k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae

g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus

s__unclassified	72368
s__unclassified	72372
s__unclassified	72375
s__unclassified	72386
s__unclassified	72392
s__unclassified	72393
s__unclassified	72404
s__unclassified	72411
s__unclassified	72419
s__unclassified	72423
s__unclassified	72425
s__unclassified	72426
s__unclassified	72432
s__unclassified	72440
s__unclassified	72446
s__unclassified	72460
s__unclassified	72463
s__unclassified	72470
s__unclassified	72472
s__unclassified	72475
s__unclassified	72480
s__unclassified	72481
s__unclassified	72483
s__unclassified	72488
s__unclassified	72489
s__unclassified	72490
s__unclassified	72492
s__unclassified	72493
s__unclassified	72501
s__unclassified	72503
s__unclassified	72504
s__unclassified	72509
s__unclassified	72515
s__unclassified	72516
s__unclassified	72517
s__unclassified	72523
s__unclassified	72532
s__unclassified	72533
s__unclassified	72535
s__unclassified	72537
s__unclassified	72539

EU457651.1 gg_id:318419 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EU454579.1 gg_id:324926 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
AY675255.1 gg_id:101305 Lactobacillus paracasei str. LPC1
EU457692.1 gg_id:336522 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU460769.1 gg_id:301721 short-beaked echidna feces clone ECH_aai37g03
AM113778.1 gg_id:140432 Lactobacillus graminis str. DSM 20719
NR_024885.1 gg_id:538781 Paralactobacillus selangorensis str. LMG 17710
GQ131183.1 gg_id:426143 Lactobacillus reuteri str. IMAU70067; HS1302
EU456756.1 gg_id:335169 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
GU125459.1 gg_id:569558 Lactobacillus alimentarius str. IMAU80037
EU452409.1 gg_id:306780 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
DQ815922.1 gg_id:168412 mouse cecum clone aab24c08
EU455875.1 gg_id:342787 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
AM905389.1 gg_id:275385 Lactobacillus cacaonum str. LMG 24285
AB257864.1 gg_id:158959 Lactobacillus camelliae MCH3-1
EU461951.1 gg_id:292302 white-faced saki feces clone Saki_aaj64c05
AY773954.1 gg_id:107854 Lactobacillus paracasei 4C
EU454930.1 gg_id:338011 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU511492.1 gg_id:273320 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak05e02
DQ103575.1 gg_id:134244 Lactobacillus casei str. AK16
EU454940.1 gg_id:340982 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EU456468.1 gg_id:322647 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
AB362730.1 gg_id:251080 Lactobacillus sakei str. NRIC 1600
L23507.1 gg_id:15143 Lactobacillus reuteri
AB362735.1 gg_id:247913 Lactobacillus pentosus str. NRIC 1732
AY690834.1 gg_id:123663 Lactobacillus nantesii str. Lp33
EU454131.1 gg_id:316490 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU456036.1 gg_id:319309 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EU456289.1 gg_id:316723 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU455211.1 gg_id:326968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
AB512775.1 gg_id:562275 Lactobacillus similis str. YIT 12117
EU456989.1 gg_id:314305 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
AF049743.1 gg_id:15206 Lactobacillus sp. str. LMG 17676
EU457691.1 gg_id:318641 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
AM905388.1 gg_id:268188 Lactobacillus fabifermentans str. LMG 24284
GQ030571.1 gg_id:428757 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw880a05c
EU508681.1 gg_id:270597 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49d02
EU509957.1 gg_id:261239 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c10
EU776728.1 gg_id:333200 Lion feces clone LI2_aae49c06
EF536364.1 gg_id:219489 Lactobacillus casei str. Zhang
EU450898.1 gg_id:344695 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N

EU457651.1	318419	1477.3	1691.9	1384.7	768.7	1396.0	1918.8
EU454579.1	324926	38.6	78.4	87.2	72.3	51.7	37.3
AY675255.1	101305	4050.6	5253.4	2810.2	1720.8	4560.9	4090.9
EU457692.1	336522	7678.4	9994.3	4593.8	2355.8	4500.7	5286.3
EU460769.1	301721	49.8	158.3	407.4	90.6	83.2	948.7
AM113778.1	140432	696.6	332.4	971.0	1324.7	726.7	736.1
NR_024885.1	538781	4417.2	4072.1	2848.1	3724.4	7708.2	5774.7
GQ131183.1	426143	1922.5	2233.7	2007.3	1348.6	2185.5	2488.7
EU456756.1	335169	2563.9	3658.4	3152.6	1589.7	5186.2	6815.6
GU125459.1	569558	4046.1	4810.7	6841.7	4832.9	3173.8	6254.9
EU452409.1	306780	61.5	141.8	539.4	100.1	133.5	108.7
DQ815922.1	168412	8249.1	8295.5	6192.6	8068.0	12007.2	11059.1
EU455875.1	342787	10671.9	12454.0	7831.8	13045.5	13625.2	12129.3
AM905389.1	275385	811.2	2054.8	2286.0	1368.9	1417.6	2678.3
AB257864.1	158959	6656.8	6027.9	5411.7	4914.5	6001.9	4791.5
EU461951.1	292302	5612.4	4891.0	4883.6	4833.1	7320.5	6588.3
AY773954.1	107854	1653.9	1898.4	2869.5	1957.7	3561.9	3489.6
EU454930.1	338011	6113.0	7116.2	2657.2	3400.4	4717.4	4040.2
EU511492.1	273320	3895.2	4979.8	5373.3	5190.9	6086.6	6873.3
DQ103575.1	134244	1728.6	2526.5	2733.8	1309.0	4252.0	3730.2
EU454940.1	340982	1822.6	2450.1	5851.0	2255.3	5698.1	6796.8
EU456468.1	322647	9403.9	11681.1	2698.6	6407.2	10995.3	9294.3
AB362730.1	251080	755.2	352.0	794.6	1244.1	723.4	842.7
L23507.1	15143	183.6	159.6	86.8	343.9	68.0	100.0
AB362735.1	247913	960.8	1047.4	1551.9	898.7	1277.2	1229.8
AY690834.1	123663	7891.3	8516.9	7056.1	5548.0	5292.5	5148.6
EU454131.1	316490	12040.2	10581.7	13649.5	10321.4	11489.7	11535.9
EU456036.1	319309	5760.0	6591.7	7851.3	5963.8	6340.5	7242.2
EU456289.1	316723	55.9	190.6	864.9	161.9	82.1	79.6
EU455211.1	326968	3384.4	4098.0	3000.0	2781.9	3325.3	4105.6
AB512775.1	562275	520.1	665.3	583.7	972.9	331.7	749.2
EU456989.1	314305	1163.1	1571.3	1816.0	1463.5	4308.3	4377.5
AF049743.1	15206	5502.4	4178.9	3047.0	2949.1	6528.6	6025.9
EU457691.1	318641	3650.9	4441.1	7136.6	4729.7	10372.5	7286.9
AM905388.1	268188	1066.7	1430.7	2329.6	2378.3	2311.5	2528.7
GQ030571.1	428757	1523.2	1148.9	2004.9	2899.8	2112.8	1311.8
EU508681.1	270597	654.9	1099.8	102.9	423.2	153.8	559.9
EU509957.1	261239	1318.9	2356.9	1194.6	880.0	1994.8	1408.0
EU776728.1	333200	1637.4	1308.5	2529.9	5508.0	1592.6	2855.6
EF536364.1	219489	2050.6	2589.2	4113.0	2359.3	1794.3	2725.6
EU450898.1	344695	961.0	1369.0	1434.0	627.4	2608.6	2138.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae

g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus

s__unclassified	72545
s__unclassified	72546
s__unclassified	72548
s__unclassified	72559
s__unclassified	72560
s__unclassified	72561
s__unclassified	72563
s__unclassified	72564
s__unclassified	72565
s__unclassified	72570
s__unclassified	72573
s__unclassified	72576
s__unclassified	72577
s__unclassified	72588
s__unclassified	72594
s__unclassified	72595
s__unclassified	72597
s__unclassified	72598
s__unclassified	72599
s__unclassified	72605
s__unclassified	72607
s__unclassified	72618
s__unclassified	72624
s__unclassified	72625
s__unclassified	72630
s__unclassified	72631
s__unclassified	72637
s__unclassified	72644
s__unclassified	72653
s__unclassified	72657
s__unclassified	72658
s__unclassified	72660
s__unclassified	72662
s__unclassified	72667
s__unclassified	72674
s__unclassified	72679
s__unclassified	72683
s__unclassified	72687
s__unclassified	72688
s__unclassified	72690
s__unclassified	72693

DQ057472.1 gg_id:134735 str. ii1366
EU511587.1 gg_id:258972 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07a10
EU451452.1 gg_id:316790 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
AY773955.1 gg_id:107855 Lactobacillus paracasei 9C
EU381123.1 gg_id:262517 Lactobacillus reuteri str. ls23
EU453529.1 gg_id:313523 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
GU458924.1 gg_id:561670 microbiota human male female forehead forearm and influence make-up skin clone
GQ421851.1 gg_id:578242 Lactobacillus buchneri str. L225
EU455189.1 gg_id:322892 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
GQ155609.1 gg_id:587513 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
X76328.1 gg_id:15144 Lactobacillus reuteri str. DSM 20016 T
AY349383.1 gg_id:92041 human oral cavity clone HT070
GU125550.1 gg_id:576646 Lactobacillus plantarum str. IMAU80128
DQ815338.1 gg_id:162668 mouse cecum clone aab46a06
EF096511.1 gg_id:180677 mouse cecum clone obob2_aaa04a10
EU456758.1 gg_id:328141 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU457050.1 gg_id:321592 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EU074832.1 gg_id:251568 Lactobacillus plantarum str. TC97
EU456918.1 gg_id:340234 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU508703.1 gg_id:259236 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49f06
AB362982.1 gg_id:247174 Lactobacillus plantarum str. LQ80
EU453721.1 gg_id:316608 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
E17066.1 gg_id:36168 Lactobacillus sp
EU474925.1 gg_id:299491 red river hog feces clone RRH_aaa04e04
FJ861112.1 gg_id:554107 Lactobacillus plantarum str. KLDS 1.0628
DQ057436.1 gg_id:133363 str. ii1204
AB290830.1 gg_id:514694 Lactobacillus equicursoris str. DI70
AB362657.1 gg_id:245705 Lactobacillus pentosus str. NRIC 0390
EU509821.1 gg_id:274002 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21f01
DQ815684.1 gg_id:169512 mouse cecum clone aab44g09
EU452068.1 gg_id:332130 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EF097607.1 gg_id:189318 mouse cecum clone SWPT20_aaa01b09
EU451715.1 gg_id:342038 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
GQ275139.1 gg_id:590798 gut symbionts are tightly linked herbivory ants extract single ant clone #163
EU507448.1 gg_id:275991 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03d04
EU456851.1 gg_id:306115 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
AM697058.1 gg_id:226751 sequencing libraries indoor dust clone BF0002B008
EU465427.1 gg_id:300717 lion feces clone LI3_aah77b08
EU451859.1 gg_id:328253 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S
EU507501.1 gg_id:259734 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b10
EU381121.1 gg_id:267051 Lactobacillus reuteri str. ls4

DQ057472.1	134735	134.8	237.0	214.3	306.5	106.1	109.3
EU511587.1	258972	6868.0	10235.9	5760.8	3900.3	4630.9	5863.0
EU451452.1	316790	1019.3	1109.0	1521.0	619.5	2605.0	2135.1
AY773955.1	107855	958.9	1017.5	1102.8	606.4	789.2	1871.8
EU381123.1	262517	1232.3	1812.1	2032.2	891.2	338.3	713.7
EU453529.1	313523	1505.7	2595.5	4467.6	1161.1	9725.3	6553.4
GU458924.1	561670	5536.5	7246.2	5219.2	5014.3	8862.7	5753.1
GQ421851.1	578242	4066.8	4596.8	2722.2	2492.0	2490.4	2397.3
EU455189.1	322892	866.3	890.3	1032.3	478.2	2579.6	1777.2
GQ155609.1	587513	179.5	479.2	890.1	264.1	147.2	382.6
X76328.1	15144	13651.8	13523.1	8983.0	9409.0	9528.6	9465.1
AY349383.1	92041	736.4	908.1	1909.2	1740.9	1152.8	1509.6
GU125550.1	576646	458.7	268.3	198.6	1362.7	306.6	345.8
DQ815338.1	162668	40.9	136.2	381.8	192.7	92.8	131.3
EF096511.1	180677	3593.3	5784.0	4838.4	3200.7	1155.0	1921.6
EU456758.1	328141	2074.6	4755.9	2268.2	2099.6	5517.5	4509.7
EU457050.1	321592	1647.4	2437.3	2382.0	1646.4	663.7	1143.5
EU074832.1	251568	1082.0	1095.1	1646.7	917.3	1445.6	1408.3
EU456918.1	340234	2526.3	2661.1	2179.4	2500.5	4293.5	4270.0
EU508703.1	259236	454.6	825.5	774.7	150.5	528.3	246.6
AB362982.1	247174	1073.0	1064.3	1653.2	1848.7	1537.1	1456.2
EU453721.1	316608	8011.9	8920.8	3208.2	6182.0	9186.2	9172.3
E17066.1	36168	6864.4	5301.1	4836.1	5735.1	6350.0	7957.3
EU474925.1	299491	2806.8	3616.7	1084.3	3147.7	5064.7	3537.5
FJ861112.1	554107	718.6	619.7	949.0	886.6	581.6	869.8
DQ057436.1	133363	6231.6	8761.8	3736.7	5959.5	5127.0	6065.6
AB290830.1	514694	1269.3	1940.0	1845.0	532.8	1435.2	899.2
AB362657.1	245705	4586.1	2821.6	2877.9	3274.0	3430.4	4546.1
EU509821.1	274002	676.6	1181.2	1749.6	868.6	1804.7	2826.4
DQ815684.1	169512	11040.1	10494.6	11903.8	12017.8	9367.1	9566.3
EU452068.1	332130	5131.8	4385.8	3701.2	4956.7	4094.5	5031.6
EF097607.1	189318	1032.7	1645.8	1593.3	967.4	1764.1	2585.2
EU451715.1	342038	998.9	1379.6	1329.8	512.6	1149.4	1337.0
GQ275139.1	590798	4858.7	4807.8	5350.6	4572.5	4424.9	6501.7
EU507448.1	275991	5211.7	4908.8	4094.2	5421.9	6681.1	5444.2
EU456851.1	306115	479.4	883.1	652.8	298.5	335.4	410.7
AM697058.1	226751	612.2	1718.0	1025.0	925.0	2419.9	2957.4
EU465427.1	300717	5787.6	8466.0	4417.2	3998.2	14346.5	7371.4
EU451859.1	328253	1867.5	2677.5	715.7	1124.8	2434.5	2246.2
EU507501.1	259734	1503.9	1283.9	3297.4	1619.2	2301.7	2937.1
EU381121.1	267051	9172.0	9474.2	6486.6	6479.5	14492.1	14033.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae

g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus

s__unclassified	72700
s__unclassified	72706
s__unclassified	72707
s__unclassified	72709
s__unclassified	72710
s__unclassified	72711
s__unclassified	72713
s__unclassified	72729
s__unclassified	72731
s__unclassified	72732
s__unclassified	72734
s__unclassified	72753
s__unclassified	72754
s__unclassified	72761
s__unclassified	72768
s__unclassified	72770
s__unclassified	72781
s__unclassified	72790
s__unclassified	72798
s__unclassified	72802
s__unclassified	72803
s__unclassified	72808
s__unclassified	72809
s__unclassified	72810
s__unclassified	72811
s__unclassified	72815
s__unclassified	72818
s__unclassified	72819
s__unclassified	72821
s__unclassified	72829
s__unclassified	72830
s__unclassified	72839
s__unclassified	72842
s__unclassified	72848
s__unclassified	72849
s__unclassified	72855
s__unclassified	72867
s__unclassified	72880
s__unclassified	72884
s__unclassified	72885
s__unclassified	72889

DQ815437.1 gg_id:171195 mouse cecum clone aab48d06
AL935261.1 gg_id:80366 Lactobacillus plantarum str. WCFS1
FM177140.1 gg_id:338585 Lactobacillus casei str. BL23
EF098024.1 gg_id:182758 mouse cecum clone SWPT12_aaa04c03
EU507563.1 gg_id:267604 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01b05
EU455156.1 gg_id:339840 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
DQ239695.1 gg_id:141655 Lactobacillus plantarum str. L2
AB470237.1 gg_id:363520 Lactobacillus sakei str. S2
EU460915.1 gg_id:296432 short-beaked echidna feces clone ECH_aai40d09
EF097172.1 gg_id:182972 mouse cecum clone SWPT18_aaa02d10
EF097176.1 gg_id:190167 mouse cecum clone SWPT18_aaa02e05
EU454503.1 gg_id:326900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU510255.1 gg_id:266771 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03f06
AY204897.1 gg_id:81036 Lactobacillus sakei str. HNSL5c
EU455625.1 gg_id:315788 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EU451160.1 gg_id:335029 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EF412985.1 gg_id:208876 Lactobacillus gallinarum str. I26
EU507280.1 gg_id:272684 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01a06
FJ405227.1 gg_id:359669 Lactobacillus casei str. ZJ3
AB368904.1 gg_id:282265 Lactobacillus plantarum str. T8-7
AF308146.1 gg_id:72717 Lactobacillus thermotolerans str. G 12
EU474952.1 gg_id:299475 red river hog feces clone RRH_aaa04g03
EU508709.1 gg_id:264123 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g05
AB362741.1 gg_id:249746 Lactobacillus pentosus str. NRIC 1753
AY735404.1 gg_id:108108 Lactobacillus plantarum str. LP1
GQ131182.1 gg_id:376168 Lactobacillus reuteri str. IMAU70066; HS1301
DQ015426.1 gg_id:130724 mouse cecum clone M3_h10
AB368903.1 gg_id:282170 Lactobacillus plantarum str. T4-5
EU074828.1 gg_id:243630 Lactobacillus plantarum str. TC41
AB162131.1 gg_id:106519 Lactobacillus nagelii str. NRIC 0559
EU457936.1 gg_id:323012 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
DQ399353.1 gg_id:154984 Lactobacillus paracasei str. SFCB2-4
EU453809.1 gg_id:318211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
GQ461596.1 gg_id:593464 Lactobacillus plantarum str. K25
EU457051.1 gg_id:317830 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU451427.1 gg_id:354114 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
GQ156407.1 gg_id:537937 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU456062.1 gg_id:308210 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
AB362731.1 gg_id:255682 Lactobacillus sakei str. NRIC 1609
GU177634.1 gg_id:578809 Lactobacillus casei str. C-1
EU474892.1 gg_id:287698 red river hog feces clone RRH_aaa04e08

DQ815437.1	171195	3681.1	4604.1	1752.3	3310.0	2736.9	3554.3
AL935261.1	80366	1134.6	1082.9	1723.9	1830.2	1512.8	1004.4
FM177140.1	338585	1848.9	2705.4	2740.1	1263.8	4252.2	3754.2
EF098024.1	182758	3599.0	6733.6	5847.6	4996.1	9677.3	7363.2
EU507563.1	267604	2093.3	2091.5	2840.5	2184.3	3046.9	3454.6
EU455156.1	339840	519.9	634.2	792.8	387.8	2543.9	1662.4
DQ239695.1	141655	811.5	1545.7	1195.2	2287.4	2233.1	2203.5
AB470237.1	363520	778.6	454.8	1095.3	1726.7	867.0	1103.1
EU460915.1	296432	87.0	137.7	325.3	172.8	153.1	485.9
EF097172.1	182972	4549.2	4942.7	4423.1	2439.2	4978.5	5373.7
EF097176.1	190167	342.7	344.8	661.2	216.5	125.9	169.2
EU454503.1	326900	356.5	605.1	710.9	213.1	1144.0	610.2
EU510255.1	266771	3570.3	6106.4	4711.5	3225.7	8481.2	9260.0
AY204897.1	81036	11861.1	14132.1	7422.5	8210.4	14658.5	10774.0
EU455625.1	315788	1202.6	2202.7	2272.7	2196.0	766.3	1463.2
EU451160.1	335029	1453.7	2382.8	3012.4	1142.9	1808.3	2121.3
EF412985.1	208876	285.5	272.3	107.1	313.7	102.9	132.9
EU507280.1	272684	1410.2	1982.7	1428.6	580.4	604.1	506.2
FJ405227.1	359669	2624.0	3489.6	2191.1	2243.9	4959.8	3616.6
AB368904.1	282265	1073.4	1046.1	1585.2	911.8	1445.8	1374.0
AF308146.1	72717	4117.8	3576.5	2290.2	2050.5	3648.2	4905.0
EU474952.1	299475	86.9	107.7	124.9	132.8	68.8	74.5
EU508709.1	264123	12207.3	16249.4	10169.2	11529.9	15426.2	13964.1
AB362741.1	249746	937.6	1186.9	1319.2	2408.6	3428.7	4894.4
AY735404.1	108108	10904.4	8727.6	7923.6	9482.7	6807.7	6125.6
GQ131182.1	376168	1768.1	5859.9	2757.1	1884.9	2299.0	3181.8
DQ015426.1	130724	28.6	1055.0	870.6	360.5	2946.5	1105.5
AB368903.1	282170	472.0	951.2	1494.9	764.5	1298.9	1339.1
EU074828.1	243630	3879.1	4054.8	4297.5	4242.0	7145.7	7953.4
AB162131.1	106519	43.7	53.1	34.7	66.1	59.1	34.0
EU457936.1	323012	2333.9	2581.3	4081.3	1052.7	8216.3	4579.0
DQ399353.1	154984	15463.0	14448.7	14756.4	12771.1	11885.6	11611.4
EU453809.1	318211	128.3	235.2	578.8	129.1	113.5	402.6
GQ461596.1	593464	793.6	1155.1	1086.5	2249.1	2262.1	1619.0
EU457051.1	317830	796.9	2058.7	1526.3	731.7	3087.0	2535.5
EU451427.1	354114	501.9	694.3	729.0	860.1	464.1	575.3
GQ156407.1	537937	5209.4	5918.7	5698.8	3268.6	3267.6	3790.0
EU456062.1	308210	580.7	1401.1	1013.3	417.4	2110.4	1900.3
AB362731.1	255682	4271.4	5221.7	4576.0	5625.1	4200.3	4001.4
GU177634.1	578809	2772.1	3074.8	2012.9	1601.1	3347.1	2648.3
EU474892.1	287698	12140.9	12282.0	5292.2	9255.5	8758.7	6347.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae

g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus

s__unclassified	72891
s__unclassified	72896
s__unclassified	72901
s__unclassified	72903
s__unclassified	72907
s__unclassified	72910
s__unclassified	72913
s__unclassified	72916
s__unclassified	72918
s__unclassified	72928
s__unclassified	72931
s__unclassified	72932
s__unclassified	72937
s__unclassified	72941
s__unclassified	72946
s__unclassified	72952
s__unclassified	72954
s__unclassified	72957
s__unclassified	72960
s__unclassified	72961
s__unclassified	72963
s__unclassified	72965
s__unclassified	72967
s__unclassified	72973
s__unclassified	72974
s__unclassified	72980
s__unclassified	72984
s__unclassified	72989
s__unclassified	72992
s__unclassified	72997
s__unclassified	72999
s__unclassified	73002
s__unclassified	73003
s__unclassified	73006
s__unclassified	73007
s__unclassified	73009
s__unclassified	73026
s__unclassified	73028
s__unclassified	73040
s__unclassified	73044
s__unclassified	73053

EU460885.1 gg_id:302664 short-beaked echidna feces clone ECH_aai39h11
EF605142.1 gg_id:229845 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU453930.1 gg_id:328325 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU453867.1 gg_id:313722 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU457601.1 gg_id:337406 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
EU455334.1 gg_id:317894 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
NR_029084.1 gg_id:576663 Lactobacillus gastricus str. Kx156A7; LMG 22113T; DSM 16045T
AB362607.1 gg_id:244469 Lactobacillus sakei str. NRIC 0126
EU510005.1 gg_id:274605 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf15e11
GU369759.1 gg_id:524305 Lactobacillus plantarum str. YM-4-5
EU452893.1 gg_id:303591 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
GQ155548.1 gg_id:512953 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AB362667.1 gg_id:258139 Lactobacillus pentosus str. NRIC 0403
GQ231436.1 gg_id:588182 Lactobacillus reuteri str. DSPV 002C
GU299083.1 gg_id:534440 Lactobacillus casei str. NQ2-2
DQ815681.1 gg_id:166336 mouse cecum clone aab44g06
AJ965487.1 gg_id:126988 Lactobacillus arizonensis str. DSM 13273
AB239468.1 gg_id:141834 Lactobacillus casei str. CP1-13
EU457018.1 gg_id:330111 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
GQ030377.1 gg_id:467257 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw877c08c
EF095994.1 gg_id:186522 mouse cecum clone lean2_aaa01f03
FJ682870.1 gg_id:530798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU454755.1 gg_id:356144 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EU460235.1 gg_id:295058 polar bear feces clone PB1_aai25b05
GQ155587.1 gg_id:513479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF096038.1 gg_id:187066 mouse cecum clone lean2_aaa02e07
AB303848.1 gg_id:257805 Monitoring Pickling Bed Fermented Rice Bran Which Dominated S-Growing Lactobac
EU439433.1 gg_id:267700 Lactobacillus plantarum str. 1L48P35
EF097557.1 gg_id:196803 mouse cecum clone SWPT19_aaa04c12
DQ815682.1 gg_id:167719 mouse cecum clone aab44g07
DQ015553.1 gg_id:135934 mouse cecum clone M3_e03_2
EU460783.1 gg_id:296454 short-beaked echidna feces clone ECH_aai37h09
EU454204.1 gg_id:347044 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
FJ678780.1 gg_id:521424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU465367.1 gg_id:302089 lion feces clone LI3_aah76b05
AB332024.2 gg_id:246232 Lactobacillus nodaensis str. IZ4B
EU526816.1 gg_id:276202 Lactobacillus plantarum str. Z6
GQ900606.1 gg_id:550314 Lactobacillus plantarum str. F34
EU505359.1 gg_id:276978 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03b09
GQ131153.1 gg_id:385174 Lactobacillus casei str. IMAU70037; BM10307
AJ242968.1 gg_id:15128 Lactobacillus gallinarum str. ATCC 33199

EU460885.1	302664	894.1	1010.8	1026.9	622.3	373.1	428.2
EF605142.1	229845	5440.9	6896.1	4445.1	6654.1	10710.5	11500.1
EU453930.1	328325	10356.0	11802.4	6074.0	7887.4	11209.5	10604.2
EU453867.1	313722	2786.4	3187.6	2470.7	2715.9	3602.3	2674.3
EU457601.1	337406	1001.0	1469.1	1667.1	730.0	293.7	502.3
EU455334.1	317894	476.9	758.9	345.4	399.5	354.1	459.6
NR_029084.1	576663	217.6	533.6	1092.1	403.8	580.5	1649.2
AB362607.1	244469	801.9	432.0	1145.7	1833.4	913.1	1105.8
EU510005.1	274605	1757.1	4409.4	2226.1	3736.5	6518.7	4680.2
GU369759.1	524305	1159.1	1048.7	1620.4	1758.7	1350.8	1272.1
EU452893.1	303591	4296.5	4614.1	4308.0	5383.8	6411.1	4682.9
GQ155548.1	512953	3593.9	4617.4	4271.0	2346.0	1889.3	3006.6
AB362667.1	258139	1048.5	888.9	1183.1	1366.1	1354.8	1186.0
GQ231436.1	588182	2066.0	2338.3	1863.6	1205.5	2220.5	2461.8
GU299083.1	534440	263.6	424.2	245.8	288.8	124.6	834.4
DQ815681.1	166336	386.8	580.7	1210.0	676.9	482.9	1551.1
AJ965487.1	126988	5763.0	5121.4	5892.3	6534.9	775.6	4576.9
AB239468.1	141834	2383.1	3147.8	2613.6	1271.6	3945.4	3288.4
EU457018.1	330111	7641.6	7848.1	3377.9	5093.1	5811.3	8383.5
GQ030377.1	467257	9591.2	8401.2	6508.2	6940.9	16739.4	12288.8
EF095994.1	186522	34.9	56.4	94.6	67.9	77.8	121.2
FJ682870.1	530798	3852.9	3833.5	2840.6	4978.4	2609.6	3525.0
EU454755.1	356144	3203.1	2665.8	2650.2	4527.7	6642.1	6023.2
EU460235.1	295058	507.9	671.0	1961.0	780.3	451.4	809.5
GQ155587.1	513479	324.1	403.0	802.2	229.1	1680.2	635.4
EF096038.1	187066	7315.8	9345.7	6936.8	6139.8	8991.9	5706.9
AB303848.1	257805	16.0	25.4	16.9	45.5	62.5	21.6
EU439433.1	267700	1027.4	1044.7	1548.1	845.3	1269.3	1303.9
EF097557.1	196803	823.9	1458.9	876.0	1460.9	871.2	784.7
DQ815682.1	167719	241.6	447.5	100.4	304.3	202.3	224.5
DQ015553.1	135934	794.4	1381.7	2822.4	1226.3	2799.8	2625.1
EU460783.1	296454	1167.4	1183.9	1263.4	1512.4	436.3	1728.4
EU454204.1	347044	1047.7	1304.2	1479.5	1296.0	868.4	1689.3
FJ678780.1	521424	8864.4	10601.1	6482.0	10120.9	9679.4	9027.6
EU465367.1	302089	7985.2	8735.1	5460.1	9317.3	8866.2	7386.9
AB332024.2	246232	580.5	755.3	3634.3	567.8	178.3	789.3
EU526816.1	276202	1265.1	1688.1	1850.4	1549.1	863.4	2907.4
GQ900606.1	550314	1067.4	1042.3	1603.4	895.1	1426.1	950.9
EU505359.1	276978	5195.8	4948.4	5897.1	5398.7	3390.0	4099.0
GQ131153.1	385174	5128.0	6440.8	3707.3	4617.2	8304.5	6747.1
AJ242968.1	15128	68.5	322.6	52.0	166.1	254.4	124.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae

g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Lactobacillus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus
g__Pediococcus

s__unclassified	73058
s__unclassified	73064
s__unclassified	73070
s__unclassified	73071
s__unclassified	73084
s__unclassified	73086
s__unclassified	73089
s__unclassified	73092
s__unclassified	73097
s__unclassified	73100
s__unclassified	73102
s__unclassified	73104
s__unclassified	73106
s__unclassified	73115
s__unclassified	73117
s__unclassified	73119
s__unclassified	73124
s__unclassified	73126
s__Pediococcus acidilactici	72099
s__Pediococcus acidilactici	72257
s__Pediococcus acidilactici	72663
s__Pediococcus acidilactici	72877
s__Pediococcus damnosus	72584
s__Pediococcus ethanolidurans	72342
s__Pediococcus ethanolidurans	72876
s__Pediococcus inopinatus	72196
s__Pediococcus parvulus	72828
s__Pediococcus parvulus	73135
s__Pediococcus pentosaceus	71886
s__Pediococcus pentosaceus	72030
s__Pediococcus pentosaceus	72211
s__Pediococcus pentosaceus	72224
s__Pediococcus pentosaceus	72297
s__Pediococcus pentosaceus	72600
s__unclassified	71827
s__unclassified	71925
s__unclassified	72176
s__unclassified	72259
s__unclassified	72274
s__unclassified	72413
s__unclassified	72555

EF536363.1 gg_id:221920 Lactobacillus plantarum str. MG3-1
AF243151.1 gg_id:22892 Lactobacillus gasseri str. KC36a
DQ815389.1 gg_id:164758 mouse cecum clone aab47d05
EU451364.1 gg_id:346613 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
GQ156345.1 gg_id:575537 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM292799.1 gg_id:187763 Lactobacillus ceti str. 142
AY253660.1 gg_id:84798 Lactobacillus ultunensis str. Kx146C1; LMG 22117T; DSM 16047T; CCUG 48460T
EU451966.1 gg_id:333408 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EU161635.1 gg_id:239571 Lactobacillus murinus str. LR
GU191837.1 gg_id:581162 Lactobacillus reuteri str. BR11
AB303841.1 gg_id:236486 Lactobacillus acetotolerans str. JCM 3825
EU511690.1 gg_id:263080 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07a08
EU504504.1 gg_id:276180 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01e09
EU547306.1 gg_id:545371 Lactobacillus delbrueckii subsp. bulgaricus str. BCS113
EU505043.1 gg_id:263220 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02a11
GQ155476.1 gg_id:593810 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM236150.1 gg_id:177499 Lactobacillus amylotrophicus str. NRRL B-4435
EU455693.1 gg_id:305429 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
AF515229.1 gg_id:56475 Pediococcus acidilactici str. RO17
AB018214.1 gg_id:15157 Pediococcus acidilactici str. LA 35
FJ915623.1 gg_id:538273 Pediococcus acidilactici str. IMAU20090; mgh10-7-2
AB018212.1 gg_id:27815 Pediococcus acidilactici str. E 7
EU331307.1 gg_id:244766 Pediococcus damnosus str. Bpe233
AB258357.1 gg_id:158048 Pediococcus siamensis MCH3-2
GU125433.1 gg_id:560139 Pediococcus ethanolidurans str. IMAU80011
AJ271383.1 gg_id:19307 Pediococcus inopinatus str. DSM 20285
EU331259.1 gg_id:239673 Pediococcus parvulus str. Bpe301
FM878597.1 gg_id:589816 Pediococcus parvulus str. LA1110
AY675245.1 gg_id:105170 Pediococcus pentosaceus str. LM2632
AB018215.1 gg_id:15152 Pediococcus pentosaceus str. LS 5
AJ305321.1 gg_id:38120 Pediococcus pentosaceus str. DSM 20336 (T)
EU080993.1 gg_id:245909 Pediococcus pentosaceus str. BMG 74
AB362987.1 gg_id:242063 Pediococcus pentosaceus str. NGRI 0305
EU483113.1 gg_id:265290 Pediococcus pentosaceus str. MY-800
EU878171.1 gg_id:328309 Pediococcus pentosaceus str. SH 740
AJ973157.1 gg_id:147407 Pediococcus stilesii str. LMG 23082 = FAIR-E
FJ378890.1 gg_id:359769 Pediococcus pentosaceus str. B-38
AJ621555.1 gg_id:113414 Pediococcus claussenii str. DSM 14800
FJ405228.1 gg_id:366574 Pediococcus claussenii str. ZJ5
AY675243.1 gg_id:104878 Pediococcus pentosaceus str. SL4
AM279764.2 gg_id:161185 Lactobacillus plantarum 7.8.2

EF536363.1	221920	1087.1	905.4	931.7	1404.6	1505.3	1260.8
AF243151.1	22892	58.5	89.5	299.7	159.7	50.7	71.7
DQ815389.1	164758	9345.7	8892.3	2767.3	8363.7	9967.1	8283.8
EU451364.1	346613	1524.2	2005.2	1368.4	1263.3	1699.3	1356.3
GQ156345.1	575537	1720.6	8325.4	3526.3	2102.8	2471.2	3299.5
AM292799.1	187763	3417.9	3827.7	2821.3	1707.2	3140.6	2776.3
AY253660.1	84798	7917.0	7740.3	8476.4	7875.0	9735.6	9519.4
EU451966.1	333408	1366.9	2887.0	1203.5	1588.9	8662.0	4197.5
EU161635.1	239571	5477.7	4554.1	6510.1	5471.6	8433.6	9505.1
GU191837.1	581162	214.6	210.8	289.6	95.6	77.4	165.5
AB303841.1	236486	677.0	859.6	2236.8	545.5	817.0	749.8
EU511690.1	263080	42.6	68.8	104.7	48.5	395.4	180.6
EU504504.1	276180	27.0	33.9	238.5	56.6	79.1	41.3
EU547306.1	545371	19.9	28.1	19.4	49.7	60.0	50.3
EU505043.1	263220	7558.7	8966.8	9760.6	3347.7	1071.7	1995.2
GQ155476.1	593810	224.3	607.5	781.0	269.6	133.4	689.7
AM236150.1	177499	13.8	27.9	17.0	40.9	41.4	12.0
EU455693.1	305429	3590.8	4000.0	3585.0	2086.7	3314.7	4796.7
AF515229.1	56475	8954.4	12012.4	4965.6	7300.3	16407.1	11721.0
AB018214.1	15157	2564.8	2713.9	4109.4	2029.0	2623.9	2845.1
FJ915623.1	538273	2396.1	2725.2	1410.1	872.7	1584.6	1084.1
AB018212.1	27815	210.7	563.4	459.4	297.4	524.8	319.6
EU331307.1	244766	4677.0	5855.2	4831.5	4324.4	4347.7	5992.4
AB258357.1	158048	2927.5	3302.1	5924.4	5266.2	4099.2	5702.9
GU125433.1	560139	2336.4	3578.6	6012.1	2198.3	3035.4	3777.0
AJ271383.1	19307	3154.8	3907.3	4923.0	4332.4	3227.8	3776.2
EU331259.1	239673	1110.9	1198.6	1164.8	372.5	1284.4	1190.7
FM878597.1	589816	1167.6	1189.6	1084.5	168.9	1043.9	800.4
AY675245.1	105170	1007.4	612.0	318.5	623.7	2503.9	1096.0
AB018215.1	15152	16496.2	16483.3	13267.8	18516.1	15141.2	16615.7
AJ305321.1	38120	830.1	616.8	974.0	786.2	2124.9	1653.3
EU080993.1	245909	798.8	582.3	1011.4	739.3	2163.8	1249.3
AB362987.1	242063	2378.5	2098.9	4447.7	3049.7	3911.7	3358.2
EU483113.1	265290	995.6	695.4	575.6	891.1	2582.2	1942.2
EU878171.1	328309	749.9	617.1	1456.0	716.7	2165.5	1141.8
AJ973157.1	147407	170.6	212.0	189.4	109.6	66.7	181.6
FJ378890.1	359769	795.0	633.0	1066.3	835.9	2173.3	1700.8
AJ621555.1	113414	4735.7	4063.4	2824.6	3808.3	5250.0	4149.5
FJ405228.1	366574	969.4	939.5	2338.6	1585.7	176.5	1066.6
AY675243.1	104878	1396.9	1081.7	1253.3	947.2	3128.4	1844.5
AM279764.2	161185	1152.0	427.4	370.9	569.8	499.7	1184.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Lactobacillaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Fructobacillus
g__Fructobacillus
g__Fructobacillus
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc

s__unclassified	71979
s__unclassified	72234
s__unclassified	72237
s__unclassified	72847
s__unclassified	73036
s__unclassified	73090
s__unclassified	72219
s__unclassified	72852
s__unclassified	72930
s__Leuconostoc citreum	71863
s__Leuconostoc citreum	71916
s__Leuconostoc citreum	72147
s__Leuconostoc citreum	72200
s__Leuconostoc citreum	72453
s__Leuconostoc citreum	72522
s__Leuconostoc citreum	72610
s__Leuconostoc fallax	72252
s__Leuconostoc mesenteroides	72140
s__Leuconostoc mesenteroides	72291
s__Leuconostoc mesenteroides	72443
s__Leuconostoc mesenteroides	72519
s__Leuconostoc mesenteroides	72757
s__Leuconostoc mesenteroides	72921
s__Leuconostoc mesenteroides	72970
s__Leuconostoc mesenteroides	73001
s__Leuconostoc mesenteroides	73037
s__Leuconostoc mesenteroides	73077
s__Leuconostoc pseudomesenteroides	71801
s__Leuconostoc pseudomesenteroides	72083
s__Leuconostoc pseudomesenteroides	72310
s__Leuconostoc pseudomesenteroides	72482
s__Leuconostoc pseudomesenteroides	72527
s__Leuconostoc pseudomesenteroides	72579
s__Leuconostoc pseudomesenteroides	72680
s__unclassified	71907
s__unclassified	72240
s__unclassified	72265
s__unclassified	72318
s__unclassified	72420
s__unclassified	72524
s__unclassified	72623

EU460868.1 gg_id:296482 short-beaked echidna feces clone ECH_aai39f03
AB240455.1 gg_id:145715 Lactobacillus halophilus str. KG34
EU460734.1 gg_id:303093 short-beaked echidna feces clone ECH_aai37b12
EU460924.1 gg_id:300991 short-beaked echidna feces clone ECH_aai40e11
EU626008.1 gg_id:277639 Lactobacillus coryniformis str. KLDS 1.0723
EU460820.1 gg_id:297646 short-beaked echidna feces clone ECH_aai38g03
AF360737.1 gg_id:67685 Leuconostoc fructosum str. DSM 20349
DQ837629.1 gg_id:163654 structures honeybee intestines and their response insecticidal proteins gut clone HB
AY169967.1 gg_id:101369 Leuconostoc pseudoficulneum str. LC51
AM157423.1 gg_id:141780 Leuconostoc citreum mother C3
AM157430.1 gg_id:143322 Leuconostoc citreum mother C4
GQ392137.1 gg_id:553432 Leuconostoc citreum str. CJGN34
FJ040200.1 gg_id:535439 Leuconostoc citreum str. C16
EU074846.1 gg_id:245787 Leuconostoc citreum str. TM319
AM157444.1 gg_id:141773 Leuconostoc citreum mother V4
AM600682.1 gg_id:226092 Leuconostoc holzapfelii str. LMG 23990 = BFE 700
AY929286.1 gg_id:113747 Leuconostoc fallax str. BFE 6749
EU074837.1 gg_id:240308 Leuconostoc mesenteroides str. CM160
GQ351321.1 gg_id:533637 Leuconostoc mesenteroides str. OR2P-2
EU074843.1 gg_id:249310 Leuconostoc mesenteroides str. AC318
FJ040199.1 gg_id:550853 Leuconostoc mesenteroides str. C12
GQ915096.1 gg_id:539665 Leuconostoc mesenteroides str. AaD8
FJ215674.1 gg_id:312330 Leuconostoc mesenteroides str. IMAU60052
EU074838.1 gg_id:238676 Leuconostoc mesenteroides str. PC216
EU074836.1 gg_id:252222 Leuconostoc mesenteroides str. CM135
EU074841.1 gg_id:247929 Leuconostoc mesenteroides str. CC317
EU177638.1 gg_id:341233 Leuconostoc mesenteroides str. ANN12
EU074839.1 gg_id:248008 Leuconostoc mesenteroides str. PM249
AF515228.1 gg_id:64385 Leuconostoc pseudomesenteroides str. RO1
EU177631.1 gg_id:337944 Leuconostoc pseudomesenteroides str. NS28
EU074840.1 gg_id:253688 Leuconostoc mesenteroides str. PM141
EU177632.1 gg_id:345546 Leuconostoc pseudomesenteroides str. NS33
FJ015056.1 gg_id:315407 Leuconostoc pseudomesenteroides str. FL6
EU337117.1 gg_id:546379 Leuconostoc pseudomesenteroides str. MC
EF121354.2 gg_id:249922 Leuconostoc citreum str. GJ7
EU574896.1 gg_id:267454 Leuconostoc mesenteroides str. NRRL B-1355
FJ749310.1 gg_id:547101 Leuconostoc lactis str. IMAU40034; QH4-6-2
FJ480207.1 gg_id:592022 Leuconostoc mesenteroides str. WCP907
AB362723.1 gg_id:238348 Leuconostoc citreum str. NRIC 1581
AB362719.1 gg_id:244448 Leuconostoc garlicum str. NRIC 1577
AB470239.1 gg_id:365285 Leuconostoc gelidum str. GD

EU460868.1	296482	1031.4	735.5	2608.5	1242.0	119.4	1094.7
AB240455.1	145715	26.7	45.1	27.5	59.7	64.1	32.7
EU460734.1	303093	3605.8	1901.9	3719.3	4146.5	1296.5	3153.9
EU460924.1	300991	4297.6	4110.9	5514.3	4364.0	4907.7	4781.1
EU626008.1	277639	132.6	211.1	339.2	89.7	80.0	208.2
EU460820.1	297646	2857.4	3787.6	5517.4	2473.3	281.1	1624.6
AF360737.1	67685	1637.9	2853.8	785.4	1398.4	2982.2	2801.3
DQ837629.1	163654	6085.1	8119.9	6341.0	3842.5	1432.5	2005.8
AY169967.1	101369	3101.2	4333.6	4273.0	1324.5	1642.3	2145.5
AM157423.1	141780	5216.6	5450.8	5089.2	3426.9	3478.8	4346.0
AM157430.1	143322	3494.9	4110.4	3609.4	2374.7	3091.0	3900.0
GQ392137.1	553432	5624.9	6043.6	5463.5	4021.5	4597.6	5478.2
FJ040200.1	535439	10282.5	9878.8	8959.5	7177.2	8569.4	7369.7
EU074846.1	245787	4996.4	5204.3	4589.1	3235.5	3432.7	4307.7
AM157444.1	141773	3663.6	3072.0	2319.3	3277.2	1939.9	3035.0
AM600682.1	226092	5203.6	5429.6	5100.4	3422.1	3466.5	4327.8
AY929286.1	113747	137.0	210.3	185.2	150.6	156.8	134.1
EU074837.1	240308	271.5	229.6	1730.7	253.7	604.3	266.5
GQ351321.1	533637	1107.7	1971.3	2454.9	962.6	2452.9	1924.5
EU074843.1	249310	2394.0	3397.8	4778.3	1886.4	2070.4	2718.4
FJ040199.1	550853	1149.3	2005.1	2587.8	967.8	2455.7	1796.8
GQ915096.1	539665	1107.3	1884.2	2472.6	789.7	2448.5	1800.6
FJ215674.1	312330	1093.6	1545.1	3688.1	1533.5	1142.7	1924.8
EU074838.1	238676	505.8	693.5	1859.0	393.2	1316.3	629.8
EU074836.1	252222	2244.0	2600.0	2349.3	3084.4	3998.8	2808.3
EU074841.1	247929	600.6	819.4	2430.4	490.6	1658.6	757.4
EU177638.1	341233	1190.5	1907.7	1478.3	889.0	2008.0	1742.6
EU074839.1	248008	319.6	261.6	2210.9	291.1	683.7	284.0
AF515228.1	64385	3101.7	4092.1	3062.0	2131.8	2113.9	3926.2
EU177631.1	337944	3359.0	4796.7	4044.7	2259.5	2430.0	3483.6
EU074840.1	253688	1808.9	1165.3	2903.1	1502.8	1427.4	1579.2
EU177632.1	345546	3182.1	4265.9	4220.2	2351.6	2743.3	3470.7
FJ015056.1	315407	1983.7	2626.6	3286.1	1363.4	1829.4	2082.2
EU337117.1	546379	1303.4	2015.6	1997.2	1104.6	921.0	1357.7
EF121354.2	249922	4962.8	5506.2	5204.7	3477.7	3720.7	4697.3
EU574896.1	267454	5362.5	4448.8	3675.2	4717.9	2706.0	4067.4
FJ749310.1	547101	5989.7	7439.7	5919.9	4109.6	3488.0	5246.9
FJ480207.1	592022	5246.9	7315.4	7434.3	5058.5	9526.6	7909.1
AB362723.1	238348	2719.6	2542.8	2092.7	3048.3	1911.9	2669.8
AB362719.1	244448	4825.4	5036.8	3068.5	4869.3	5516.6	6917.0
AB470239.1	365285	14036.1	14844.7	9993.0	8367.4	13053.8	14030.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Leuconostocaceae

g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Leuconostoc
g__Oenococcus
g__Oenococcus
g__Oenococcus
g__Oenococcus
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella
g__Weissella

s__unclassified	72629
s__unclassified	72635
s__unclassified	72646
s__unclassified	72708
s__unclassified	72807
s__unclassified	72927
s__unclassified	72987
s__unclassified	73033
s__unclassified	73096
s__Oenococcus oeni	72436
s__Oenococcus oeni	72678
s__Oenococcus oeni	72982
s__unclassified	72943
s__unclassified	71845
s__unclassified	71873
s__unclassified	72041
s__unclassified	72069
s__unclassified	72141
s__unclassified	72191
s__unclassified	72267
s__unclassified	72591
s__unclassified	72659
s__unclassified	72686
s__unclassified	72766
s__unclassified	72900
s__unclassified	72906
s__Weissella cibaria	72169
s__Weissella cibaria	72381
s__Weissella cibaria	72654
s__Weissella cibaria	72682
s__Weissella cibaria	72714
s__Weissella cibaria	73054
s__Weissella confusa	72299
s__Weissella confusa	72468
s__Weissella confusa	72993
s__Weissella confusa	73011
s__Weissella hellenica	71901
s__Weissella hellenica	72215
s__Weissella hellenica	73116
s__Weissella koreensis	72053
s__Weissella soli	72294

AM940225.1 gg_id:349734 Leuconostoc palmae str. TMW 2.694
AB362720.1 gg_id:252701 Leuconostoc garlicum str. NRIC 1578
AF111948.1 gg_id:15110 Leuconostoc citreum str. ATCC49370; KCTC3526
AB362722.1 gg_id:256844 Leuconostoc garlicum str. NRIC 1580
EU463822.1 gg_id:290159 Seba's short-tailed bat feces clone bat_aaj05d07
AY165007.4 gg_id:75964 Leuconostoc citreum str. CY2
AB022921.1 gg_id:24935 Leuconostoc gelidum str. NRIC 1778
AB362682.1 gg_id:246692 Leuconostoc mesenteroides str. NRIC 0587
AB470240.1 gg_id:363305 Leuconostoc gasicomitatum str. GC
AB054806.1 gg_id:43827 Oenococcus oeni str. 95 St.Mer-2-4
CP000411.1 gg_id:175948 Oenococcus oeni str. PSU-1
FM878590.1 gg_id:571983 Oenococcus oeni str. LA126
AB221475.1 gg_id:159865 Oenococcus kitaharae str. NRIC 0645
GU138518.1 gg_id:568005 Weissella confusa str. LSBM3-1
AB022926.1 gg_id:45087 Weissella halotolerans str. NRIC 1627
EU465515.1 gg_id:292431 lion feces clone LI3_aah78f11
AB022922.1 gg_id:43687 Weissella kandleri str. NRIC 1628
AM157446.1 gg_id:144619 Weissella confusa mother V4
EU855224.1 gg_id:352468 Weissella paramesenteroides str. CTSPL5
FJ193714.1 gg_id:346360 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi
AM157435.1 gg_id:142903 Weissella cibaria mother C4
AB015642.1 gg_id:15084 Weissella hellenica str. DS-12
EU439435.2 gg_id:560064 Weissella sp. str. 2L24P13
AM882997.1 gg_id:241383 Weissella ghanensis str. LMG 24286
EU177641.1 gg_id:320990 Weissella paramesenteroides str. NS74
EU869290.1 gg_id:331921 Weissella sp. str. JZ-1L
DQ294962.1 gg_id:143027 Weissella cibaria str. Uga57
EU074829.1 gg_id:251397 Weissella cibaria str. BC48
DQ294964.1 gg_id:142786 Weissella cibaria str. Uga69
AF477495.1 gg_id:23573 Weissella confusa str. PL9001
AF477498.1 gg_id:36439 Lactobacillus fermentum str. PL9005
AF312874.1 gg_id:22775 Weissella cibaria str. CHJ3
FJ429974.1 gg_id:565622 Weissella confusa str. C3-7
GU369772.1 gg_id:530233 Weissella confusa str. JS-7-1
FJ263453.1 gg_id:366705 Weissella confusa str. XW1
AB257595.1 gg_id:158275 Weissella salipiscis str. FS55-1
X95981.1 gg_id:15090 Weissella hellenica str. NCFB 2973
FJ654456.1 gg_id:537058 Weissella hellenica str. 138
FJ654465.1 gg_id:511014 Weissella hellenica str. 1507
DQ883229.1 gg_id:163888 Weissella koreensis str. 405
EU180607.1 gg_id:335281 Weissella soli str. NS26

AM940225.1	349734	5041.7	6243.0	5146.3	3229.3	4732.4	4901.5
AB362720.1	252701	5140.1	6712.9	6541.5	3525.4	2982.2	4023.0
AF111948.1	15110	3798.0	4223.2	3329.3	2719.7	3094.5	4431.4
AB362722.1	256844	14568.3	16865.8	8115.1	12918.5	17437.0	15638.5
EU463822.1	290159	6056.4	6514.6	6165.4	4960.1	9163.1	8055.9
AY165007.4	75964	4980.1	5450.2	6233.8	4954.4	6232.5	6035.3
AB022921.1	24935	2954.8	4501.1	4628.5	1962.8	5283.2	4088.4
AB362682.1	246692	5445.7	6139.4	7740.1	4522.6	6201.8	6333.9
AB470240.1	363305	16869.5	17983.9	12953.0	11979.8	19236.4	15278.9
AB054806.1	43827	1330.4	3229.4	2530.1	1023.8	1019.6	620.2
CP000411.1	175948	1413.8	985.7	1311.4	2066.2	478.2	774.3
FM878590.1	571983	11757.1	10618.2	7415.0	7669.8	10486.1	8715.5
AB221475.1	159865	5951.3	3993.4	5773.1	3800.0	4334.6	4198.7
GU138518.1	568005	3821.9	5780.0	3190.4	3937.4	1581.3	4796.2
AB022926.1	45087	130.4	331.6	395.8	124.8	660.2	121.6
EU465515.1	292431	6652.5	6893.6	6009.4	6362.6	6046.4	6949.6
AB022922.1	43687	86.2	201.6	288.8	132.3	95.8	370.4
AM157446.1	144619	1583.4	1784.9	2243.3	1228.5	3299.4	3119.3
EU855224.1	352468	1748.6	3694.3	3080.2	800.6	1774.4	2221.9
FJ193714.1	346360	2291.6	2119.3	816.8	4512.2	3698.5	3995.1
AM157435.1	142903	431.1	1130.1	844.9	465.5	135.0	829.4
AB015642.1	15084	2674.0	2517.0	3463.0	1878.8	3074.6	3488.8
EU439435.2	560064	405.9	1038.3	952.2	783.1	2602.2	4182.9
AM882997.1	241383	4973.5	3471.7	7613.5	5907.8	6914.4	7756.8
EU177641.1	320990	400.1	390.0	644.8	450.4	150.2	803.9
EU869290.1	331921	23.7	29.9	19.3	57.9	64.7	19.5
DQ294962.1	143027	245.0	279.2	691.1	638.1	115.7	1181.0
EU074829.1	251397	5234.0	3974.2	3581.0	5162.7	3974.6	4919.9
DQ294964.1	142786	1251.7	800.8	2845.5	1621.5	496.1	2006.8
AF477495.1	23573	4587.7	4516.9	2056.2	3162.1	601.8	968.8
AF477498.1	36439	4383.1	7074.5	3420.3	4583.0	7010.1	6399.4
AF312874.1	22775	232.8	187.5	513.7	622.1	116.0	356.2
FJ429974.1	565622	698.0	1943.9	1589.7	796.6	1337.4	2533.9
GU369772.1	530233	539.4	1172.5	1456.6	611.1	1198.2	1858.2
FJ263453.1	366705	618.5	1823.3	1457.8	680.4	1310.9	1860.8
AB257595.1	158275	3350.3	5831.4	2238.1	2075.7	2829.7	4308.9
X95981.1	15090	332.7	430.2	1004.3	262.6	626.3	652.7
FJ654456.1	537058	484.5	559.8	1203.9	343.2	610.6	1025.7
FJ654465.1	511014	484.5	562.5	1304.3	343.6	594.0	1023.3
DQ883229.1	163888	273.6	636.1	951.2	688.4	505.8	1285.6
EU180607.1	335281	2082.2	2010.7	1984.9	1239.9	1546.3	2159.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Leuconostocaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Weissella
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus
g__Lactococcus

s__Weissella viridescens	71967
s__Lactococcus garvieae	42650
s__Lactococcus garvieae	42815
s__Lactococcus garvieae	42882
s__Lactococcus garvieae	42914
s__Lactococcus garvieae	43157
s__Lactococcus garvieae	43303
s__Lactococcus garvieae	43328
s__Lactococcus garvieae	43410
s__Lactococcus garvieae	43504
s__Lactococcus garvieae	43512
s__Lactococcus garvieae	43551
s__Lactococcus garvieae	43553
s__Lactococcus garvieae	43663
s__Lactococcus garvieae	43847
s__Lactococcus garvieae	43931
s__Lactococcus garvieae	43998
s__Lactococcus lactis	42814
s__Lactococcus lactis	42908
s__Lactococcus lactis	43271
s__Lactococcus lactis	43277
s__Lactococcus lactis	43288
s__Lactococcus lactis	43335
s__Lactococcus lactis	43525
s__Lactococcus lactis	43678
s__Lactococcus lactis	43697
s__Lactococcus raffinolactis	43471
s__unclassified	42501
s__unclassified	42604
s__unclassified	42725
s__unclassified	42857
s__unclassified	42868
s__unclassified	42934
s__unclassified	42969
s__unclassified	43083
s__unclassified	43287
s__unclassified	43430
s__unclassified	43544
s__unclassified	43564
s__unclassified	43707
s__unclassified	43758

AB023236.1 gg_id:33970 Weissella viridescens str. NRIC 1536
EU775634.1 gg_id:315664 Hedgehog feces clone HH_d06
EU777721.1 gg_id:330069 Polar bear feces clone PB1_aai28f10
EU460570.1 gg_id:298506 polar bear feces clone PB2_aai22g09
EU460926.1 gg_id:299075 short-beaked echidna feces clone ECH_aai40f04
EU791208.1 gg_id:455671 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou
AB018211.1 gg_id:42931 Lactococcus garvieae str. E 1
EU460718.1 gg_id:302924 polar bear feces clone PB2_aai24h07
EU467542.1 gg_id:296207 southern three-banded armadillo feces clone arma_f03
EU775705.1 gg_id:333803 Hedgehog feces clone HH_aai36e07
EU460397.1 gg_id:302882 polar bear feces clone PB1_aai28a07
AF283499.1 gg_id:45250 Lactococcus garvieae
EU775674.1 gg_id:336969 Hedgehog feces clone HH_d10
EU460462.1 gg_id:293407 polar bear feces clone PB2_aai21b11
EU458153.1 gg_id:297489 North American black bear feces clone BB2_f02
AB244446.1 gg_id:257338 Lactococcus garvieae str. An10-2
EU460864.1 gg_id:292600 short-beaked echidna feces clone ECH_aai39e07
DQ223877.1 gg_id:173259 Lactococcus sp. str. RT5
DQ223876.1 gg_id:167936 Lactococcus lactis str. RT4
AM490366.1 gg_id:203331 Lactococcus lactis str. C22
AM157445.1 gg_id:141784 Lactococcus lactis mother V4
AJ488176.1 gg_id:66046 Lactococcus lactis str. 04
AY348313.1 gg_id:93048 Lactococcus lactis str. Akira2
AM157424.1 gg_id:141720 Lactococcus lactis mother C3
EU203156.1 gg_id:251182 Lactococcus lactis str. WH11-1
GQ337889.1 gg_id:594031 Lactococcus lactis str. KLDS4.0352
AY762104.1 gg_id:108349 Lactococcus sp. str. MKRL19
AJ133479.1 gg_id:69992 Lactococcus sp. TmLO5
EU073957.2 gg_id:240865 Lactococcus sp. Da-18
AB234513.1 gg_id:150304 termite gut homogenate clone MgMjW-44
AJ439543.2 gg_id:110020 Lactovum miscens str. anNAG3
DQ856510.1 gg_id:253776 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1N
AB089063.1 gg_id:78015 termite gut homogenate clone Rs-C68 sp.
DQ343754.1 gg_id:146404 Lactococcus piscium str. CCUG 32732
EF204369.1 gg_id:201186 Lactococcus sp. G23
EU460490.1 gg_id:294254 polar bear feces clone PB2_aai21f02
AB089061.2 gg_id:78223 termite gut homogenate clone Rs-B70
AY571411.1 gg_id:114538 termite gut clone RsaM9
EF694029.1 gg_id:256029 Lactococcus plantarum str. DSM 20686
GQ502570.1 gg_id:555286 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
AM944736.1 gg_id:270649 Enterococcus sp. str. UNK1

AB023236.1	33970	14.6	30.4	26.5	52.9	55.8	51.1
EU775634.1	315664	11869.7	10432.6	6873.1	7788.8	12263.3	10737.5
EU777721.1	330069	4945.8	4966.5	3070.9	3312.2	11300.6	6656.9
EU460570.1	298506	6432.8	5687.6	7119.2	5892.4	8365.1	6551.2
EU460926.1	299075	13945.5	10667.8	7650.9	7332.0	10973.8	9175.6
EU791208.1	455671	3323.4	3751.4	4153.7	1998.5	2531.1	3765.3
AB018211.1	42931	9256.7	7823.7	8490.9	7885.5	7858.3	5757.6
EU460718.1	302924	3198.9	2835.9	3245.5	2151.1	3476.3	2590.1
EU467542.1	296207	8429.6	7406.0	4450.5	6960.5	10836.9	8109.8
EU775705.1	333803	4489.8	2127.2	3053.3	2975.0	2846.2	3665.7
EU460397.1	302882	4104.0	3495.7	2198.5	723.8	4947.0	3876.8
AF283499.1	45250	14784.4	14162.3	10156.0	9676.1	20421.1	14048.3
EU775674.1	336969	1631.9	1636.8	2061.9	954.4	2563.8	1857.9
EU460462.1	293407	11303.1	8987.3	8089.0	8857.8	9462.9	8204.1
EU458153.1	297489	1575.8	1611.7	4855.3	1667.6	5141.1	2754.4
AB244446.1	257338	15114.2	15293.2	9784.3	13589.9	17469.5	14595.1
EU460864.1	292600	611.7	691.9	1061.9	880.1	732.4	1214.1
DQ223877.1	173259	1153.5	1455.8	2040.6	2439.9	1021.8	1232.8
DQ223876.1	167936	1286.7	3358.2	2401.5	1143.0	2855.7	2316.9
AM490366.1	203331	3457.1	4402.1	2093.1	5444.3	9472.1	8210.7
AM157445.1	141784	3884.7	5416.4	2419.1	4545.9	6867.7	5856.8
AJ488176.1	66046	2332.3	3949.5	3696.6	2518.6	4296.9	3983.7
AY348313.1	93048	76.6	215.2	310.4	104.2	96.7	116.2
AM157424.1	141720	1473.3	3117.6	3866.1	2479.0	3424.6	3536.4
EU203156.1	251182	5396.7	7439.8	5687.4	6825.0	13850.8	9726.6
GQ337889.1	594031	3024.9	4893.4	4310.4	2982.5	5113.6	4566.4
AY762104.1	108349	91.3	246.1	633.5	140.5	338.3	116.0
AJ133479.1	69992	88.2	49.8	68.2	97.4	76.9	47.3
EU073957.2	240865	3516.4	2712.7	3525.1	2715.7	2259.6	4090.4
AB234513.1	150304	1715.8	2151.7	3227.7	1212.0	1357.3	1332.8
AJ439543.2	110020	4728.6	3616.3	2353.4	9232.8	1596.3	1644.9
DQ856510.1	253776	1963.9	2563.1	3465.5	2008.0	12180.4	7262.4
AB089063.1	78015	513.3	534.9	680.2	248.6	221.6	226.4
DQ343754.1	146404	1222.4	1091.4	3768.7	616.4	1231.7	1015.9
EF204369.1	201186	1150.1	1563.8	1457.7	3528.6	1406.0	1105.5
EU460490.1	294254	5611.4	5581.6	6118.6	4619.7	3211.4	4642.2
AB089061.2	78223	1751.9	2450.3	1489.6	1765.6	2019.5	1833.3
AY571411.1	114538	407.3	1082.2	685.1	501.4	395.0	372.0
EF694029.1	256029	65.1	109.1	164.4	161.6	281.7	112.3
GQ502570.1	555286	61.2	152.4	218.3	85.7	100.3	52.2
AM944736.1	270649	12381.2	10842.1	11087.1	9531.4	8581.8	10069.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Lactococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44107
s__Streptococcus agalactiae	44807
s__Streptococcus agalactiae	45199
s__Streptococcus alactolyticus	45342
s__Streptococcus alactolyticus	45344
s__Streptococcus alactolyticus	45559
s__Streptococcus anginosus	45244
s__Streptococcus anginosus	45354
s__Streptococcus anginosus	45772
s__Streptococcus canis	45619
s__Streptococcus constellatus	45378
s__Streptococcus constellatus	45672
s__Streptococcus criceti	44621
s__Streptococcus cristatus	45375
s__Streptococcus cristatus	45762
s__Streptococcus cristatus	45888
s__Streptococcus devriesei	44889
s__Streptococcus didelphis	45798
s__Streptococcus didelphis	45850
s__Streptococcus downei	44260
s__Streptococcus downei	44342
s__Streptococcus equi	44184
s__Streptococcus equi	45528
s__Streptococcus equi	45732
s__Streptococcus ferus	45752
s__Streptococcus gordonii	44962
s__Streptococcus gordonii	45087
s__Streptococcus gordonii	45600
s__Streptococcus hyointestinalis	45078
s__Streptococcus ictaluri	45063
s__Streptococcus infantis	44154
s__Streptococcus infantis	44526
s__Streptococcus infantis	44666
s__Streptococcus infantis	44884
s__Streptococcus infantis	45658
s__Streptococcus iniae	44456
s__Streptococcus luteciae	44276
s__Streptococcus luteciae	44331
s__Streptococcus luteciae	44386
s__Streptococcus luteciae	44505
s__Streptococcus luteciae	44900

EU689104.1 gg_id:564529 Lactococcus sp. str. YM05290
NZ_AAJO01000148.1 gg_id:140424 Streptococcus agalactiae str. 18RS21
AAJO01000006.1 gg_id:139711 Streptococcus agalactiae str. 18RS21
EU473184.1 gg_id:300948 giant panda feces clone GP_1aaa04g12
AB002519.1 gg_id:15456 Streptococcus alactolyticus str. ATCC 43492
EU473340.1 gg_id:289833 giant panda feces clone GP_1aaa04h11
AB355611.1 gg_id:240886 Streptococcus anginosus str. IMU103
AY691534.1 gg_id:107288 Streptococcus anginosus str. ChDC YA1
AY986761.1 gg_id:115190 Streptococcus anginosus str. ChDC YA2
EU075058.1 gg_id:239570 Streptococcus canis str. 3-35MP
FJ557869.1 gg_id:525128 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
FJ557854.1 gg_id:527756 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
AB182324.1 gg_id:169991 Streptococcus orisuis str. NUM 1001
AJ853835.1 gg_id:108737 Streptococcus cristatus str. PD01A5
AY281090.1 gg_id:90588 Streptococcus cristatus str. ATCC 49999
AB008313.1 gg_id:15567 Streptococcus cristatus str. NCTC12479
NR_029015.1 gg_id:589575 Streptococcus devriesei str. CCUG 47156
DQ303185.1 gg_id:167230 Streptococcus didelphis str. ATCC 700828
AF176107.1 gg_id:15363 Streptococcus didelphis str. 95-3349-1
AY942561.1 gg_id:133561 Streptococcus downei str. ChDC YD1
AY942564.1 gg_id:137388 Streptococcus downei str. ChDC YD4
EF405993.1 gg_id:219796 Streptococcus subsp. equi str. Bd 5895/99
AB002516.1 gg_id:15355 Streptococcus equi subsp. zooepidemicus str. ATCC 43079
AB002515.1 gg_id:15354 Streptococcus subsp. equi str. ATCC 33398 NCTC 9682
AJ420197.1 gg_id:39498 Streptococcus ferus str. 8S1
U87827.1 gg_id:15564 aortic heart valve patient with endocarditis clone v2
AJ427479.1 gg_id:36023 Streptococcus gordonii str. DL1
AB355602.1 gg_id:243837 Streptococcus gordonii str. NUK38
AB002518.1 gg_id:15428 Streptococcus hyointestinalis str. ATCC 49169 DSM 20770
DQ462420.1 gg_id:203615 Streptococcus icataluri LS0706-05
GQ050656.1 gg_id:398932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488f1
GQ115486.1 gg_id:393307 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686c07
EU156759.1 gg_id:331335 Streptococcus infantis str. CCUG 39817
AB008315.1 gg_id:15551 Streptococcus infantis str. GTC849
GQ077246.1 gg_id:395569 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115e
EU620580.1 gg_id:279591 Streptococcus iniae str. CMS003
EU467794.1 gg_id:287876 North American black bear feces clone BB1_b04
AB002482.1 gg_id:15458 Streptococcus bovis str.ATCC 33317
AJ297214.1 gg_id:30971 Streptococcus luteciae str. NEM 760
EU461863.1 gg_id:299806 white-faced saki feces clone Saki_aaj62e05
EU467738.1 gg_id:295347 North American black bear feces clone BB1_a07

EU689104.1	564529	1690.6	2687.0	1736.0	2849.7	1051.8	1126.2
NZ_AAJO01000148.1	140424	2430.6	2943.9	3085.4	1412.8	10361.6	6950.7
AAJO01000006.1	139711	73.0	286.8	97.2	69.2	120.3	123.2
EU473184.1	300948	1779.4	1718.4	1843.8	818.9	338.7	691.9
AB002519.1	15456	2943.3	3368.8	3949.9	1939.0	2424.0	2498.8
EU473340.1	289833	3500.7	3007.5	2323.3	2589.4	3344.7	4609.6
AB355611.1	240886	106.0	1320.1	851.6	967.2	152.5	949.9
AY691534.1	107288	17562.6	17018.0	14220.3	13205.4	16365.7	16647.9
AY986761.1	115190	9963.0	10364.9	5024.2	6772.9	9820.1	11615.6
EU075058.1	239570	1011.5	1924.1	1702.2	706.3	244.9	1008.8
FJ557869.1	525128	941.1	725.7	1056.6	1093.5	1034.3	1022.2
FJ557854.1	527756	82.2	717.2	141.2	126.7	135.3	234.3
AB182324.1	169991	2981.1	2009.9	2250.1	2354.9	2446.9	2064.2
AJ853835.1	108737	25.6	212.4	34.9	45.4	59.4	19.7
AY281090.1	90588	422.8	736.2	535.6	251.0	277.8	326.9
AB008313.1	15567	65.4	674.8	218.3	89.2	128.3	74.7
NR_029015.1	589575	42.5	132.9	446.6	89.8	92.6	125.5
DQ303185.1	167230	691.0	642.3	328.6	173.0	69.0	979.8
AF176107.1	15363	3400.6	2531.5	485.4	4250.3	5592.5	6515.8
AY942561.1	133561	346.9	674.2	1670.5	483.0	1396.8	2084.6
AY942564.1	137388	1648.2	2020.3	1254.2	1414.7	3143.2	2843.4
EF405993.1	219796	1872.6	1653.5	825.2	958.4	2461.4	1573.9
AB002516.1	15355	2128.7	2687.8	1104.4	999.8	2339.6	1677.6
AB002515.1	15354	4171.3	4847.0	3271.1	3480.1	9832.3	5157.5
AJ420197.1	39498	522.8	1163.1	443.4	138.8	96.0	506.3
U87827.1	15564	793.6	920.4	142.9	634.5	896.6	727.2
AJ427479.1	36023	4256.3	4153.1	4717.7	4365.5	3974.7	4908.3
AB355602.1	243837	708.8	1545.6	1672.1	711.2	662.0	1753.7
AB002518.1	15428	1612.9	1877.4	234.7	734.2	1178.1	771.6
DQ462420.1	203615	732.4	953.1	1328.2	502.4	529.3	779.1
GQ050656.1	398932	729.8	516.9	523.1	533.0	480.1	398.7
GQ115486.1	393307	3479.9	3839.0	2948.3	3862.9	2747.9	2910.2
EU156759.1	331335	18.2	802.4	168.7	50.1	55.4	48.6
AB008315.1	15551	99.2	802.7	529.6	148.8	111.4	194.7
GQ077246.1	395569	24.1	450.3	105.3	47.1	55.0	38.0
EU620580.1	279591	130.0	793.0	625.4	161.7	184.1	127.3
EU467794.1	287876	3197.6	3610.1	4718.5	5593.5	4865.4	6586.9
AB002482.1	15458	2644.5	3433.6	2814.0	1316.0	3205.8	4323.4
AJ297214.1	30971	100.3	390.2	418.4	201.8	94.0	2460.7
EU461863.1	299806	8839.6	10386.2	9262.3	3246.3	1190.0	2477.9
EU467738.1	295347	1044.6	1082.6	2184.8	619.6	237.9	565.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus luteciae	44919
s__Streptococcus luteciae	44953
s__Streptococcus luteciae	45256
s__Streptococcus luteciae	45387
s__Streptococcus luteciae	45703
s__Streptococcus luteciae	45869
s__Streptococcus lutetiensis	45825
s__Streptococcus macedonicus	44256
s__Streptococcus minor	44366
s__Streptococcus minor	45019
s__Streptococcus minor	45538
s__Streptococcus minor	45639
s__Streptococcus mutans	44395
s__Streptococcus mutans	44413
s__Streptococcus mutans	44508
s__Streptococcus mutans	44560
s__Streptococcus mutans	44701
s__Streptococcus mutans	44779
s__Streptococcus mutans	44811
s__Streptococcus mutans	44856
s__Streptococcus mutans	44923
s__Streptococcus mutans	45014
s__Streptococcus mutans	45033
s__Streptococcus mutans	45150
s__Streptococcus mutans	45165
s__Streptococcus mutans	45168
s__Streptococcus mutans	45173
s__Streptococcus mutans	45236
s__Streptococcus mutans	45245
s__Streptococcus mutans	45265
s__Streptococcus mutans	45278
s__Streptococcus mutans	45336
s__Streptococcus mutans	45388
s__Streptococcus mutans	45415
s__Streptococcus mutans	45418
s__Streptococcus mutans	45451
s__Streptococcus mutans	45469
s__Streptococcus mutans	45554
s__Streptococcus mutans	45579
s__Streptococcus mutans	45651
s__Streptococcus mutans	45686

EU467837.1 gg_id:290948 North American black bear feces clone BB1_b03_1
EU458240.1 gg_id:295954 North American black bear feces clone BB2_e04
EU467796.1 gg_id:298722 North American black bear feces clone BB1_b07_1
EU467742.1 gg_id:291695 North American black bear feces clone BB1_b06
AJ297218.1 gg_id:21570 Streptococcus luteciae str. NEM1603
EU461969.1 gg_id:291625 white-faced saki feces clone Saki_aaj64e12
EU163444.1 gg_id:253732 Streptococcus lutetiensis str. 644
EU163501.1 gg_id:251131 Streptococcus macedonicus str. 905
EU075079.1 gg_id:246776 Streptococcus minor str. 26-59MP
AF227836.1 gg_id:70091 str. 37236
AJ409287.1 gg_id:55342 Streptococcus entericus str. CECT 5353
FJ769470.1 gg_id:545996 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana
DQ677768.1 gg_id:162458 Streptococcus mutans str. ChDC YM53; 32111
DQ677712.1 gg_id:170656 Streptococcus mutans str. ChDC YM230; PD1163-1
DQ677734.1 gg_id:173377 Streptococcus mutans str. ChDC YM204; PD32
DQ677782.1 gg_id:169174 Streptococcus mutans str. ChDC YM26; 16235
DQ677717.1 gg_id:169011 Streptococcus mutans str. ChDC YM223; PD1063
DQ677727.1 gg_id:170005 Streptococcus mutans str. ChDC YM212; PD1026
AF139600.1 gg_id:55433 Streptococcus mutans str. UA96
DQ677716.1 gg_id:164384 Streptococcus mutans str. ChDC YM225; PD1111
DQ677783.1 gg_id:170638 Streptococcus mutans str. ChDC YM29; 17135
DQ677733.1 gg_id:169266 Streptococcus mutans str. ChDC YM205; PD59
AF077835.1 gg_id:81591 Streptococcus mutans str. UA96
DQ677769.1 gg_id:171585 Streptococcus mutans str. ChDC YM51; 31125
DQ677755.1 gg_id:172601 Streptococcus mutans str. ChDC YM14; 9211
DQ677736.1 gg_id:164353 Streptococcus mutans str. ChDC YM202; PD9
DQ677787.1 gg_id:172359 Streptococcus mutans str. ChDC YM16; 9226
DQ677750.1 gg_id:166980 Streptococcus mutans str. ChDC YM79; 49215
DQ677777.1 gg_id:172519 Streptococcus mutans str. ChDC YM6; 3217
DQ677765.1 gg_id:169834 Streptococcus mutans str. ChDC YM57; 33211
DQ677737.1 gg_id:162868 Streptococcus mutans str. ChDC YM201; PD4
AY691526.1 gg_id:102599 Streptococcus mutans str. ChDC YM3
DQ677753.1 gg_id:164446 Streptococcus mutans str. ChDC YM72; 44211
DQ677786.1 gg_id:171168 Streptococcus mutans str. ChDC YM20; 10115
DQ677779.1 gg_id:167840 Streptococcus mutans str. ChDC YM34; 20235
DQ677761.1 gg_id:167048 Streptococcus mutans str. ChDC YM63; 37121
DQ677741.1 gg_id:170415 Streptococcus mutans str. ChDC YM96; 62211
DQ677758.1 gg_id:163887 Streptococcus mutans str. ChDC YM1; 1211
DQ677722.1 gg_id:171075 Streptococcus mutans str. ChDC YM217; PD1047
AF139599.1 gg_id:69287 Streptococcus mutans str. UA140
DQ677718.1 gg_id:162408 Streptococcus mutans str. ChDC YM222; PD1062

EU467837.1	290948	859.8	1312.7	2457.3	702.4	514.8	914.2
EU458240.1	295954	12625.6	11262.9	9013.6	8425.0	15275.6	15986.0
EU467796.1	298722	662.5	1352.7	2579.4	644.0	327.4	794.8
EU467742.1	291695	571.2	1194.9	2625.2	616.3	987.3	613.5
AJ297218.1	21570	93.0	419.7	723.9	212.3	106.0	2701.8
EU461969.1	291625	5103.3	4260.9	7703.0	4466.7	4151.2	6505.3
EU163444.1	253732	168.4	646.8	904.8	267.8	151.1	2582.2
EU163501.1	251131	566.6	1152.5	1515.5	469.1	894.5	2526.2
EU075079.1	246776	110.0	266.3	183.3	125.0	70.9	178.9
AF227836.1	70091	110.8	148.5	99.4	190.9	84.1	589.2
AJ409287.1	55342	77.1	65.2	162.3	89.2	116.3	201.4
FJ769470.1	545996	966.4	1399.2	1931.9	847.6	71.4	366.4
DQ677768.1	162458	3784.5	4563.5	3431.0	1430.2	1897.9	1814.7
DQ677712.1	170656	19882.5	20435.7	13794.0	15438.0	13622.5	13021.6
DQ677734.1	173377	3277.7	3596.0	4304.9	1354.3	2355.8	2417.4
DQ677782.1	169174	10262.9	8324.1	8528.6	4167.6	5713.8	4738.3
DQ677717.1	169011	3863.0	4987.9	4509.4	1688.3	3278.6	3212.0
DQ677727.1	170005	17603.6	17848.3	8861.2	13499.7	18189.6	16865.9
AF139600.1	55433	3821.6	4353.7	3605.0	1358.4	3375.1	2918.0
DQ677716.1	164384	2225.9	2723.8	2455.6	1167.0	2392.2	1950.2
DQ677783.1	170638	2903.8	4382.3	4077.5	1469.4	3448.4	3082.8
DQ677733.1	169266	8432.4	8918.2	6955.2	7989.5	13226.3	10382.1
AF077835.1	81591	6763.8	6266.1	7350.1	4721.0	5539.1	4906.8
DQ677769.1	171585	6581.8	6314.6	7749.4	2939.6	9258.8	7580.7
DQ677755.1	172601	5095.0	7882.0	5328.3	4646.9	17182.4	10160.1
DQ677736.1	164353	10780.1	12817.6	8838.2	7964.8	12454.9	10194.7
DQ677787.1	172359	1116.2	1545.4	1132.4	753.2	606.6	1042.9
DQ677750.1	166980	5465.9	5551.8	4286.0	1682.8	3679.9	3108.6
DQ677777.1	172519	3787.3	3615.3	5187.1	1727.0	4440.3	3694.6
DQ677765.1	169834	11848.1	10769.5	11422.8	9684.4	12598.6	11064.0
DQ677737.1	162868	6281.9	9227.6	5683.9	4354.9	10357.7	7157.3
AY691526.1	102599	10168.6	10945.7	7990.6	8222.5	10974.2	10107.8
DQ677753.1	164446	6893.9	7217.8	6767.9	3384.9	5875.2	4575.9
DQ677786.1	171168	4150.7	3308.1	4119.6	3187.4	3910.9	4067.7
DQ677779.1	167840	7207.3	8166.4	4751.5	3540.9	3977.7	3610.7
DQ677761.1	167048	4272.4	4654.6	4268.7	1497.9	3245.8	2955.9
DQ677741.1	170415	7620.7	8470.9	10510.5	5630.4	7253.4	6830.0
DQ677758.1	163887	4085.5	4985.9	4484.9	1619.6	3442.3	3008.8
DQ677722.1	171075	3864.1	4810.5	4577.8	1571.9	3147.3	3222.4
AF139599.1	69287	3989.3	4364.7	4019.2	1495.8	3245.6	2953.0
DQ677718.1	162408	5540.8	5652.3	6735.7	2292.1	2816.1	3849.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus mutans	45760
s__Streptococcus mutans	45862
s__Streptococcus oralis	44321
s__Streptococcus oralis	44432
s__Streptococcus oralis	44534
s__Streptococcus oralis	44562
s__Streptococcus oralis	44745
s__Streptococcus oralis	44906
s__Streptococcus oralis	45334
s__Streptococcus oralis	45425
s__Streptococcus parasanguinis	44479
s__Streptococcus parasanguinis	44874
s__Streptococcus parasanguinis	45264
s__Streptococcus parasanguinis	45778
s__Streptococcus parauberis	45793
s__Streptococcus parauberis	45794
s__Streptococcus phocae	45284
s__Streptococcus pluranimalium	45539
s__Streptococcus pneumoniae	44178
s__Streptococcus pneumoniae	44742
s__Streptococcus pneumoniae	44843
s__Streptococcus pneumoniae	44918
s__Streptococcus pneumoniae	45043
s__Streptococcus pneumoniae	45496
s__Streptococcus pneumoniae	45756
s__Streptococcus porcinus	44975
s__Streptococcus pseudopneumoniae	44153
s__Streptococcus pseudopneumoniae	44185
s__Streptococcus pseudopneumoniae	44224
s__Streptococcus pseudopneumoniae	44227
s__Streptococcus pseudopneumoniae	44243
s__Streptococcus pseudopneumoniae	44269
s__Streptococcus pseudopneumoniae	44272
s__Streptococcus pseudopneumoniae	44290
s__Streptococcus pseudopneumoniae	44318
s__Streptococcus pseudopneumoniae	44383
s__Streptococcus pseudopneumoniae	44422
s__Streptococcus pseudopneumoniae	44449
s__Streptococcus pseudopneumoniae	44482
s__Streptococcus pseudopneumoniae	44599
s__Streptococcus pseudopneumoniae	44654

AF077836.1 gg_id:82224 Streptococcus mutans str. UA140
DQ677732.1 gg_id:167860 Streptococcus mutans str. ChDC YM206; PD65
GQ112239.1 gg_id:426772 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ073529.1 gg_id:430079 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ011465.1 gg_id:498201 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792c07
FJ557749.1 gg_id:518996 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ111665.1 gg_id:428868 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY281080.1 gg_id:90116 Streptococcus oralis str. ATCC 700233
AY880050.1 gg_id:112132 Streptococcus sp. S16-08
GQ111693.1 gg_id:410090 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY281087.1 gg_id:90242 Streptococcus parasanguinis str. ATCC 15909
EU156771.1 gg_id:356452 Streptococcus parasanguinis str. ATCC 15912
AY485605.1 gg_id:102231 Streptococcus parasanguinis str. ATCC 15912
AF543299.1 gg_id:58281 Streptococcus parasanguinis str. ChDC OS49
EU081009.1 gg_id:253153 Streptococcus parauberis str. BMG 149
AY584477.1 gg_id:99803 Streptococcus parauberis str. DSM 6631
AJ621053.1 gg_id:102460 Streptococcus phocae str. CCUG 35103
EU391530.1 gg_id:534876 Streptococcus pluranimalium str. 219
NC_011072.1 gg_id:318252 Streptococcus pneumoniae str. G54
CP000920.1 gg_id:517593 Streptococcus pneumoniae str. P1031
NC_010582.1 gg_id:260561 Streptococcus pneumoniae str. CGSP14
CP000936.1 gg_id:266609 Streptococcus pneumoniae str. Hungary19A-6
NC_010582.1 gg_id:260560 Streptococcus pneumoniae str. CGSP14
CP000919.1 gg_id:530213 Streptococcus pneumoniae str. JJA
AF003930.1 gg_id:15572 Streptococcus pneumoniae str. ATCC 33400
DQ303207.1 gg_id:173018 Streptococcus pseudoporcinus str. LQ 559-98
GQ011626.1 gg_id:498040 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794d0
GQ019354.1 gg_id:490312 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189a
GQ040213.1 gg_id:458178 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw95
GQ021941.1 gg_id:487727 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ073432.1 gg_id:374596 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ000271.1 gg_id:468836 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
GQ016796.1 gg_id:492871 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825f0
GQ073552.1 gg_id:376487 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ114404.1 gg_id:374477 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
GQ007970.1 gg_id:501695 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ018379.1 gg_id:491290 Topographical and Temporal Human Skin Microbiome skin back clone nbu138d03c1
GQ111622.1 gg_id:465964 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ103077.1 gg_id:403395 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ021669.1 gg_id:487999 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ043832.1 gg_id:392907 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97

AF077836.1	82224	6726.7	6475.9	7164.4	4792.8	3514.2	3753.2
DQ677732.1	167860	5734.2	8314.4	12181.2	3510.4	12636.7	9150.4
GQ112239.1	426772	15085.4	12057.0	11887.3	8711.2	11880.4	13594.3
GQ073529.1	430079	39.5	1027.0	377.4	112.5	92.8	140.2
GQ011465.1	498201	419.0	1358.5	757.5	318.9	301.3	551.5
FJ557749.1	518996	1604.1	2014.0	1580.3	1511.7	986.7	1262.9
GQ111665.1	428868	4306.0	3562.3	4267.5	3332.1	1733.0	3024.8
AY281080.1	90116	51.4	503.1	158.7	101.8	90.0	111.4
AY880050.1	112132	2112.1	3028.0	2205.9	2910.3	677.8	1382.4
GQ111693.1	410090	422.6	683.7	631.1	281.5	256.8	379.0
AY281087.1	90242	954.5	1697.8	1218.0	543.4	670.2	680.3
EU156771.1	356452	119.1	525.4	711.1	256.5	87.7	1737.5
AY485605.1	102231	123.3	621.3	510.2	203.4	183.1	879.3
AF543299.1	58281	4061.4	4357.1	5349.6	2616.6	3237.2	4295.0
EU081009.1	253153	3629.3	3551.6	4395.6	3849.1	2098.7	2940.3
AY584477.1	99803	641.6	722.7	794.4	609.7	116.1	440.7
AJ621053.1	102460	77.3	164.0	150.7	80.7	81.5	61.7
EU391530.1	534876	67.3	181.9	101.6	146.6	64.3	565.1
NC_011072.1	318252	2105.5	3508.9	5455.0	1604.7	2858.9	5042.1
CP000920.1	517593	2246.8	3565.0	5464.7	1690.9	3045.4	5036.8
NC_010582.1	260561	1195.9	2461.0	4146.5	1180.2	2776.0	4120.3
CP000936.1	266609	1290.0	2552.4	4537.2	1225.3	2984.4	4181.4
NC_010582.1	260560	800.8	1830.0	2757.3	660.2	1036.3	2691.0
CP000919.1	530213	2267.2	3488.0	5253.1	1772.0	3186.5	4570.8
AF003930.1	15572	3172.4	4339.1	6262.6	2431.8	3262.4	5429.2
DQ303207.1	173018	791.2	1568.7	1111.0	432.0	174.0	381.9
GQ011626.1	498040	518.8	1458.1	1080.4	355.3	437.4	443.0
GQ019354.1	490312	9204.4	6372.6	6986.7	9607.2	16126.5	13112.6
GQ040213.1	458178	3040.9	3025.2	2713.3	1831.1	1726.7	1962.8
GQ021941.1	487727	6937.0	8053.6	9603.3	5353.7	8591.5	5654.2
GQ073432.1	374596	146.6	1076.0	675.0	138.1	132.5	81.2
GQ000271.1	468836	1801.5	3451.1	2847.7	1500.4	1619.9	1979.5
GQ016796.1	492871	499.9	1156.3	644.3	314.3	328.0	363.4
GQ073552.1	376487	14578.6	14480.0	7696.1	11438.5	14418.3	12807.1
GQ114404.1	374477	10068.7	10210.2	7559.8	7651.2	9123.7	8771.5
GQ007970.1	501695	36.6	628.3	67.2	62.4	74.2	43.3
GQ018379.1	491290	899.4	1681.7	922.8	223.2	271.8	341.9
GQ111622.1	465964	3455.4	2558.9	4651.6	5005.4	552.4	1130.0
GQ103077.1	403395	765.2	1026.6	327.7	101.3	97.4	102.1
GQ021669.1	487999	13578.0	14001.0	7738.5	12162.8	13679.5	13756.4
GQ043832.1	392907	2549.7	2963.3	2515.6	2055.1	1050.9	1636.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus pseudopneumoniae	44668
s__Streptococcus pseudopneumoniae	44677
s__Streptococcus pseudopneumoniae	44743
s__Streptococcus pseudopneumoniae	44781
s__Streptococcus pseudopneumoniae	44789
s__Streptococcus pseudopneumoniae	44854
s__Streptococcus pseudopneumoniae	44928
s__Streptococcus pseudopneumoniae	44997
s__Streptococcus pseudopneumoniae	45008
s__Streptococcus pseudopneumoniae	45052
s__Streptococcus pseudopneumoniae	45151
s__Streptococcus pseudopneumoniae	45254
s__Streptococcus pseudopneumoniae	45269
s__Streptococcus pseudopneumoniae	45286
s__Streptococcus pseudopneumoniae	45299
s__Streptococcus pseudopneumoniae	45304
s__Streptococcus pseudopneumoniae	45313
s__Streptococcus pseudopneumoniae	45321
s__Streptococcus pseudopneumoniae	45343
s__Streptococcus pseudopneumoniae	45356
s__Streptococcus pseudopneumoniae	45367
s__Streptococcus pseudopneumoniae	45384
s__Streptococcus pseudopneumoniae	45440
s__Streptococcus pseudopneumoniae	45467
s__Streptococcus pseudopneumoniae	45504
s__Streptococcus pseudopneumoniae	45507
s__Streptococcus pseudopneumoniae	45508
s__Streptococcus pseudopneumoniae	45525
s__Streptococcus pseudopneumoniae	45543
s__Streptococcus pseudopneumoniae	45564
s__Streptococcus pseudopneumoniae	45575
s__Streptococcus pseudopneumoniae	45582
s__Streptococcus pseudopneumoniae	45592
s__Streptococcus pseudopneumoniae	45636
s__Streptococcus pseudopneumoniae	45715
s__Streptococcus pseudopneumoniae	45786
s__Streptococcus pseudopneumoniae	45803
s__Streptococcus pseudopneumoniae	45887
s__Streptococcus pyogenes	44634
s__Streptococcus pyogenes	45224
s__Streptococcus salivarius	44274

GQ032099.1 gg_id:459269 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ116212.1 gg_id:459597 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw689c06
GQ011481.1 gg_id:498186 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792e03
GQ012738.1 gg_id:496928 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8
GQ043722.1 gg_id:454796 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97
D38483.1 gg_id:15561 Streptococcus gordonii str. NCTC7865
GQ000709.1 gg_id:469274 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ101353.1 gg_id:442140 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw494b
GQ011011.1 gg_id:498655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ114954.1 gg_id:375288 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685f02
GQ060409.1 gg_id:401159 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ037331.1 gg_id:431806 Topographical and Temporal Human Skin Microbiome skin palm clone nbu392a07c1
GQ068281.1 gg_id:440575 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148
GQ060662.1 gg_id:421166 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03h01
GQ032327.1 gg_id:433199 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu541a04
GQ095830.1 gg_id:438226 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
AY053482.1 gg_id:17851 gas hydrate clone AT425_EubB10
AY281076.1 gg_id:88205 Streptococcus mitis str. ATCC 15914
GQ073532.1 gg_id:453009 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ088993.1 gg_id:454354 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
GQ076920.1 gg_id:399933 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155
GQ026845.1 gg_id:425917 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ088086.1 gg_id:375021 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ074626.1 gg_id:444906 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164c
GQ000464.1 gg_id:469029 Topographical and Temporal Human Skin Microbiome skin palm clone nbu103h07c1
GQ032155.1 gg_id:434917 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9
GQ012673.1 gg_id:496994 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8
GQ071973.1 gg_id:386691 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190f02
GQ038042.1 gg_id:454223 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu37
GQ060519.1 gg_id:378178 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02g04
GQ043355.1 gg_id:419060 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96
GQ074070.1 gg_id:443358 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ012816.1 gg_id:496851 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8
GQ029799.1 gg_id:410188 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw927e12
GQ091881.1 gg_id:455224 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ074369.1 gg_id:392384 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162b
GQ026868.1 gg_id:426596 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ074391.1 gg_id:392084 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c
NC_011375.1 gg_id:314875 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633
CP000829.1 gg_id:319062 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633
AM157451.1 gg_id:143051 Streptococcus salivarius mother V5

GQ032099.1	459269	2138.9	1396.1	821.4	1581.5	863.8	2097.9
GQ116212.1	459597	541.6	2231.5	1753.0	529.6	643.7	909.7
GQ011481.1	498186	1745.2	1946.3	1283.4	550.3	450.7	498.4
GQ012738.1	496928	17804.3	17301.8	6700.5	14949.9	15047.1	15009.9
GQ043722.1	454796	1745.2	1978.1	1193.2	542.5	448.9	505.6
D38483.1	15561	9268.2	7728.8	6288.0	5647.4	7492.3	9635.8
GQ000709.1	469274	376.3	1002.9	547.7	262.5	293.5	387.7
GQ101353.1	442140	754.4	1019.3	299.9	86.0	98.2	109.3
GQ011011.1	498655	505.6	1225.9	989.4	613.4	347.4	436.9
GQ114954.1	375288	3485.1	2907.6	2900.4	1836.2	1752.3	1989.1
GQ060409.1	401159	4523.0	4582.6	4220.6	4223.6	4614.5	4220.5
GQ037331.1	431806	10677.0	11457.8	10471.7	11153.2	13892.3	12042.5
GQ068281.1	440575	1962.8	2566.2	2140.3	1619.8	1689.6	1825.5
GQ060662.1	421166	1624.4	1994.1	1278.0	538.7	440.7	489.8
GQ032327.1	433199	3507.2	2976.8	2913.6	1831.0	1730.3	1841.2
GQ095830.1	438226	146.6	1096.6	738.7	147.3	134.2	77.6
AY053482.1	17851	172.1	640.3	458.4	247.8	122.2	210.9
AY281076.1	88205	40.5	591.0	97.0	69.6	85.1	43.3
GQ073532.1	453009	1025.6	2019.2	1831.8	801.6	1389.0	1315.7
GQ088993.1	454354	68.4	515.0	106.9	90.5	83.4	83.9
GQ076920.1	399933	7931.1	7609.4	4269.0	5198.8	7425.3	7754.4
GQ026845.1	425917	8016.7	6700.4	4738.0	7132.1	8922.8	10374.7
GQ088086.1	375021	476.3	1427.8	762.6	325.7	404.8	389.4
GQ074626.1	444906	6709.6	7370.9	6152.3	6872.6	7408.3	7558.8
GQ000464.1	469029	336.6	1729.7	1249.6	499.9	614.5	820.7
GQ032155.1	434917	4605.3	4486.8	3918.0	3453.8	2567.6	3367.9
GQ012673.1	496994	3266.0	3049.1	2720.2	1843.8	1738.7	1842.1
GQ071973.1	386691	3245.8	4061.5	2252.3	4745.4	5344.2	4617.7
GQ038042.1	454223	30.5	942.9	28.5	51.5	65.0	22.7
GQ060519.1	378178	435.2	1172.9	510.8	275.6	289.4	333.4
GQ043355.1	419060	7937.9	8638.9	5063.5	6224.1	9544.1	8252.5
GQ074070.1	443358	3800.3	2087.0	2215.6	4502.6	2136.4	5089.4
GQ012816.1	496851	596.0	1460.5	1261.3	398.1	490.3	473.0
GQ029799.1	410188	130.3	1159.2	419.5	147.6	241.0	200.0
GQ091881.1	455224	3293.6	5624.3	1938.9	1957.0	1586.4	2245.5
GQ074369.1	392384	446.2	1417.8	1275.2	356.9	417.0	436.8
GQ026868.1	426596	40.1	734.6	116.4	72.8	73.3	67.4
GQ074391.1	392084	139.1	1010.4	469.8	254.6	178.6	139.8
NC_011375.1	314875	243.0	519.6	689.0	296.9	134.1	302.0
CP000829.1	319062	541.6	894.4	1483.0	561.0	215.0	527.5
AM157451.1	143051	283.4	821.3	775.2	469.4	110.3	3526.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus salivarius	44289
s__Streptococcus salivarius	44291
s__Streptococcus salivarius	44307
s__Streptococcus salivarius	44313
s__Streptococcus salivarius	44320
s__Streptococcus salivarius	44338
s__Streptococcus salivarius	44355
s__Streptococcus salivarius	44403
s__Streptococcus salivarius	44414
s__Streptococcus salivarius	44417
s__Streptococcus salivarius	44445
s__Streptococcus salivarius	44464
s__Streptococcus salivarius	44491
s__Streptococcus salivarius	44493
s__Streptococcus salivarius	44536
s__Streptococcus salivarius	44573
s__Streptococcus salivarius	44588
s__Streptococcus salivarius	44594
s__Streptococcus salivarius	44616
s__Streptococcus salivarius	44645
s__Streptococcus salivarius	44652
s__Streptococcus salivarius	44657
s__Streptococcus salivarius	44692
s__Streptococcus salivarius	44699
s__Streptococcus salivarius	44713
s__Streptococcus salivarius	44730
s__Streptococcus salivarius	44732
s__Streptococcus salivarius	44734
s__Streptococcus salivarius	44736
s__Streptococcus salivarius	44755
s__Streptococcus salivarius	44760
s__Streptococcus salivarius	44790
s__Streptococcus salivarius	44804
s__Streptococcus salivarius	44815
s__Streptococcus salivarius	44821
s__Streptococcus salivarius	44827
s__Streptococcus salivarius	44830
s__Streptococcus salivarius	44878
s__Streptococcus salivarius	44894
s__Streptococcus salivarius	44909
s__Streptococcus salivarius	44925

GQ067898.1 gg_id:411450 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw144a0
GQ041746.1 gg_id:399498 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932a0
GQ037788.1 gg_id:398562 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
GQ032436.1 gg_id:433098 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073305.1 gg_id:405731 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207e04c1
GQ073284.1 gg_id:395657 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c05c1
EU767000.1 gg_id:352345 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
GQ056935.1 gg_id:413299 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1038e
GQ012076.1 gg_id:497590 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw796h1
DQ327158.1 gg_id:146000 Metagenomic gut microbiome healthy human stool clone E679
GQ073122.1 gg_id:445048 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205d01c
GQ073243.1 gg_id:443817 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g05c1
GQ156099.1 gg_id:545941 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ076917.1 gg_id:450079 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155
GQ027306.1 gg_id:436913 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ016818.1 gg_id:492852 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825h0
GQ015172.1 gg_id:494494 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765c11c1
GQ073290.1 gg_id:408634 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c11c1
GQ048766.1 gg_id:405294 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5
GQ027709.1 gg_id:450712 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU766977.1 gg_id:346736 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ154798.1 gg_id:585857 Streptococcus salivarius str. CCRI 17344
GQ022123.1 gg_id:487545 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ102628.1 gg_id:413657 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ032182.1 gg_id:445687 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ032967.1 gg_id:401843 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ057589.1 gg_id:393274 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ073120.1 gg_id:419730 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c11c1
GQ009438.1 gg_id:500227 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
GQ082412.1 gg_id:402163 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11
GQ032928.1 gg_id:403958 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ076841.1 gg_id:447628 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
GQ073193.1 gg_id:465072 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206b09c
GQ027336.1 gg_id:374888 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073296.1 gg_id:401949 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207d07c
GQ076874.1 gg_id:398881 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
GQ027284.1 gg_id:415774 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073188.1 gg_id:377770 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206b04c
GQ074060.1 gg_id:438313 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
GQ032208.1 gg_id:468347 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ086295.1 gg_id:448788 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl

GQ067898.1	411450	375.1	453.8	716.5	311.8	4082.8	2135.5
GQ041746.1	399498	2260.6	1562.4	2033.0	434.2	1570.7	1823.1
GQ037788.1	398562	2269.9	2107.5	2042.4	928.0	430.7	854.6
GQ032436.1	433098	981.6	1294.2	1585.8	1319.7	2788.1	3767.2
GQ073305.1	405731	4472.9	5027.7	4517.7	3077.4	4198.4	4276.8
GQ073284.1	395657	2147.1	2151.6	2050.8	1005.6	443.3	935.6
EU767000.1	352345	1094.3	857.1	581.9	402.4	117.6	203.2
GQ056935.1	413299	2061.8	1753.9	1886.1	891.2	279.0	709.9
GQ012076.1	497590	2995.8	2803.3	2564.4	1791.0	665.2	1577.6
DQ327158.1	146000	3565.4	2212.2	1534.8	4494.1	3274.4	4105.2
GQ073122.1	445048	1611.9	2532.3	3319.6	1091.6	500.3	993.8
GQ073243.1	443817	1870.9	2444.5	2615.6	1658.0	941.6	1623.4
GQ156099.1	545941	2014.2	1965.8	2074.4	981.4	518.4	1052.3
GQ076917.1	450079	2147.0	2018.9	2051.7	1007.3	443.9	869.2
GQ027306.1	436913	2273.3	2112.4	2046.7	931.4	430.3	926.9
GQ016818.1	492852	3207.1	2728.4	2734.3	1791.4	665.5	1575.1
GQ015172.1	494494	1246.9	1070.7	1729.2	633.5	219.2	533.1
GQ073290.1	408634	2521.9	2486.9	2628.4	1859.2	635.8	1229.4
GQ048766.1	405294	1913.7	2071.5	2431.2	1572.4	623.4	1324.1
GQ027709.1	450712	15648.5	15417.5	15290.4	12299.8	12641.9	16127.7
EU766977.1	346736	7291.0	6899.9	4911.0	6255.0	1445.1	3783.4
FJ154798.1	585857	281.7	845.3	720.2	464.5	109.9	3796.3
GQ022123.1	487545	1461.7	2443.7	1085.4	1229.5	2462.3	2374.3
GQ102628.1	413657	2752.7	3747.7	2207.9	1814.2	2337.7	2300.2
GQ032182.1	445687	3216.7	2684.6	2931.5	1796.0	668.8	1472.4
GQ032967.1	401843	7198.3	5769.9	8440.1	7958.6	3308.2	4601.0
GQ057589.1	393274	2576.3	2671.1	2229.3	2287.8	2943.1	3193.9
GQ073120.1	419730	1594.6	1546.9	1754.9	882.1	244.9	558.0
GQ009438.1	500227	14522.2	13894.1	9711.6	12271.8	6488.7	8790.5
GQ082412.1	402163	3211.8	2814.4	2731.4	1788.3	667.7	1460.6
GQ032928.1	403958	3394.7	4423.7	2341.1	4757.6	575.7	1095.8
GQ076841.1	447628	3000.3	2745.7	2732.8	1794.0	666.5	1466.8
GQ073193.1	465072	9902.5	9683.8	3814.7	8071.3	5650.6	5341.1
GQ027336.1	374888	3215.2	2819.3	2735.4	1791.7	667.4	1579.5
GQ073296.1	401949	80.1	343.5	125.5	146.3	113.2	133.1
GQ076874.1	398881	1140.4	1596.8	2359.6	883.6	314.5	706.0
GQ027284.1	415774	5613.7	7699.0	1886.0	2558.7	5151.3	5092.1
GQ073188.1	377770	5942.7	5616.3	5374.0	5386.5	4125.8	4034.5
GQ074060.1	438313	3001.6	3395.2	4258.9	3481.4	4870.4	4678.8
GQ032208.1	468347	993.9	1564.4	1548.9	776.4	399.1	768.8
GQ086295.1	448788	2610.7	2661.9	3575.0	2471.8	2543.5	3086.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus salivarius	44954
s__Streptococcus salivarius	44965
s__Streptococcus salivarius	44978
s__Streptococcus salivarius	44987
s__Streptococcus salivarius	44989
s__Streptococcus salivarius	44998
s__Streptococcus salivarius	45002
s__Streptococcus salivarius	45004
s__Streptococcus salivarius	45054
s__Streptococcus salivarius	45089
s__Streptococcus salivarius	45133
s__Streptococcus salivarius	45138
s__Streptococcus salivarius	45141
s__Streptococcus salivarius	45169
s__Streptococcus salivarius	45209
s__Streptococcus salivarius	45223
s__Streptococcus salivarius	45231
s__Streptococcus salivarius	45248
s__Streptococcus salivarius	45250
s__Streptococcus salivarius	45281
s__Streptococcus salivarius	45301
s__Streptococcus salivarius	45348
s__Streptococcus salivarius	45390
s__Streptococcus salivarius	45448
s__Streptococcus salivarius	45453
s__Streptococcus salivarius	45475
s__Streptococcus salivarius	45480
s__Streptococcus salivarius	45550
s__Streptococcus salivarius	45581
s__Streptococcus salivarius	45597
s__Streptococcus salivarius	45614
s__Streptococcus salivarius	45652
s__Streptococcus salivarius	45660
s__Streptococcus salivarius	45688
s__Streptococcus salivarius	45711
s__Streptococcus salivarius	45721
s__Streptococcus salivarius	45747
s__Streptococcus salivarius	45782
s__Streptococcus salivarius	45826
s__Streptococcus salivarius	45829
s__Streptococcus salivarius	45847

GQ076786.1 gg_id:376508 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
GQ012122.1 gg_id:497544 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw797e05
FJ154797.1 gg_id:547030 Streptococcus salivarius str. ATCC 25975
GQ032902.1 gg_id:379571 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ076850.1 gg_id:445671 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
GQ043267.1 gg_id:448280 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ074824.1 gg_id:399219 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
FJ363284.1 gg_id:367277 feces adult twins and mothers; TS149 clone TS149_a01d10
GQ019319.1 gg_id:490350 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ041356.1 gg_id:452091 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
FJ154805.1 gg_id:545804 Streptococcus vestibularis str. CCRI 17387
GQ076777.1 gg_id:376055 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
GQ073340.1 gg_id:405098 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h04c1
EF463056.1 gg_id:219466 Streptococcus salivarius str. RKA2
GQ073226.1 gg_id:417324 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e07c1
GQ076892.1 gg_id:379619 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
EF463059.1 gg_id:224298 Streptococcus salivarius str. RKA5
GQ078835.1 gg_id:428382 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ073204.1 gg_id:424160 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206c08c1
GQ073389.1 gg_id:452062 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208e03c1
GQ032174.1 gg_id:418733 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073349.1 gg_id:468290 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a01c1
GQ057898.1 gg_id:393890 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ027365.1 gg_id:396642 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ007920.1 gg_id:501744 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AM157419.1 gg_id:141989 Streptococcus salivarius mother C3
GQ032472.1 gg_id:384506 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ019505.1 gg_id:490163 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190g
GQ073065.1 gg_id:378696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204f09c
GQ088234.1 gg_id:440158 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ076935.1 gg_id:386247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155
DQ801238.1 gg_id:190678 human fecal clone RL116_aaf02c02
GQ073241.1 gg_id:451593 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g03c1
GQ019428.1 gg_id:490239 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h
GQ073128.1 gg_id:374338 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205d10c1
GQ073291.1 gg_id:376264 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c12c1
GQ057595.1 gg_id:413021 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ154803.1 gg_id:549813 Streptococcus salivarius str. CCUG 7215
GQ041484.1 gg_id:426958 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
FJ363912.1 gg_id:358274 feces adult twins and mothers; TS14 clone TS14_a04g10
GQ019436.1 gg_id:490234 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190a

GQ076786.1	376508	2297.6	2083.3	2050.2	1003.0	445.1	863.0
GQ012122.1	497544	2116.7	2096.4	1910.2	930.7	428.1	925.0
FJ154797.1	547030	90.4	229.6	253.4	235.9	71.1	2727.9
GQ032902.1	379571	2219.6	2629.5	2385.7	2400.5	3252.6	3724.4
GQ076850.1	445671	1582.3	1343.7	931.5	479.6	299.6	511.4
GQ043267.1	448280	1911.3	2163.3	2268.3	1568.1	622.0	1419.3
GQ074824.1	399219	6632.4	5884.5	4668.4	5287.7	7596.1	5785.5
FJ363284.1	367277	1503.7	1003.4	1193.5	3739.4	159.0	459.0
GQ019319.1	490350	2144.0	2146.8	2046.5	1002.3	443.6	862.7
GQ041356.1	452091	1709.9	1450.6	966.0	529.6	316.6	507.0
FJ154805.1	545804	263.3	771.4	719.5	465.6	109.0	3527.7
GQ076777.1	376055	4382.3	4465.2	4408.5	2832.5	496.4	1191.0
GQ073340.1	405098	1383.9	1876.5	2165.3	1624.3	590.1	1178.3
EF463056.1	219466	213.6	689.7	673.1	282.0	91.3	2585.1
GQ073226.1	417324	6216.0	4152.7	2839.5	5566.1	2608.1	6081.1
GQ076892.1	379619	778.6	762.7	187.4	1365.5	177.3	189.0
EF463059.1	224298	256.5	768.2	766.0	394.5	95.8	3518.2
GQ078835.1	428382	4889.4	5948.5	3665.4	5843.8	7018.1	6766.2
GQ073204.1	424160	2511.5	2475.6	2599.9	1842.2	636.1	1309.9
GQ073389.1	452062	1305.3	1021.7	1388.9	3331.4	269.1	421.7
GQ032174.1	418733	2982.7	2331.6	2070.5	1167.5	2264.9	2700.9
GQ073349.1	468290	2517.7	2381.4	2476.8	1862.9	631.2	1313.5
GQ057898.1	393890	332.5	483.5	984.5	186.3	180.5	357.0
GQ027365.1	396642	7385.7	8173.0	7545.2	6025.8	8775.0	9326.2
GQ007920.1	501744	5202.3	2872.7	3278.5	5107.1	2055.3	4047.4
AM157419.1	141989	2689.5	2536.7	1748.7	3070.0	1114.9	6631.6
GQ032472.1	384506	6502.6	4938.5	851.0	4446.8	2270.7	3925.8
GQ019505.1	490163	930.2	1495.6	1550.3	782.0	397.9	775.4
GQ073065.1	378696	1570.2	1260.1	897.8	462.3	313.5	545.2
GQ088234.1	440158	2140.3	2067.2	1912.8	1001.8	466.0	927.1
GQ076935.1	386247	1606.5	1562.0	1783.1	902.3	247.0	563.4
DQ801238.1	190678	1800.5	2461.0	3272.5	1309.2	2142.2	2618.7
GQ073241.1	451593	4231.3	4127.2	1540.8	3724.3	3029.2	5029.1
GQ019428.1	490239	8351.8	6905.3	2690.5	7256.5	3288.8	6256.1
GQ073128.1	374338	4028.5	2038.8	2532.8	4075.9	2599.0	4043.5
GQ073291.1	376264	5205.0	6318.8	7807.2	5452.8	7803.8	6138.8
GQ057595.1	413021	1826.9	3261.9	2519.2	967.5	239.7	851.0
FJ154803.1	549813	238.2	657.1	711.5	393.2	96.3	3519.4
GQ041484.1	426958	591.7	1050.8	1000.0	949.1	273.0	775.7
FJ363912.1	358274	6953.8	6317.0	5330.7	9826.1	12920.2	11810.7
GQ019436.1	490234	3026.5	3827.5	4186.9	3148.8	2323.8	4671.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus salivarius	45859
s__Streptococcus salivarius	45882
s__Streptococcus salivarius	45886
s__Streptococcus sanguinis	44371
s__Streptococcus sanguinis	44451
s__Streptococcus sanguinis	45034
s__Streptococcus sanguinis	45355
s__Streptococcus sanguinis	45542
s__Streptococcus sanguinis	45595
s__Streptococcus sinensis	44665
s__Streptococcus sobrinus	44428
s__Streptococcus sobrinus	45309
s__Streptococcus sobrinus	45454
s__Streptococcus suis	44388
s__Streptococcus suis	44966
s__Streptococcus suis	45763
s__Streptococcus thermophilus	44288
s__Streptococcus thermophilus	44296
s__Streptococcus thermophilus	44330
s__Streptococcus thermophilus	44392
s__Streptococcus thermophilus	44460
s__Streptococcus thermophilus	44488
s__Streptococcus thermophilus	44502
s__Streptococcus thermophilus	44507
s__Streptococcus thermophilus	44542
s__Streptococcus thermophilus	44547
s__Streptococcus thermophilus	44583
s__Streptococcus thermophilus	44602
s__Streptococcus thermophilus	44612
s__Streptococcus thermophilus	44655
s__Streptococcus thermophilus	44764
s__Streptococcus thermophilus	44868
s__Streptococcus thermophilus	44882
s__Streptococcus thermophilus	44934
s__Streptococcus thermophilus	45070
s__Streptococcus thermophilus	45077
s__Streptococcus thermophilus	45083
s__Streptococcus thermophilus	45084
s__Streptococcus thermophilus	45086
s__Streptococcus thermophilus	45091
s__Streptococcus thermophilus	45101

GQ041461.1 gg_id:464018 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ027302.1 gg_id:380914 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ365649.1 gg_id:367692 feces adult twins and mothers; TS21 clone TS21_a01d05
GQ995676.1 gg_id:548391 Streptococcus sanguinis str. Hanzhong-A2
CP000387.1 gg_id:210400 Streptococcus sanguinis str. SK36
AB002524.1 gg_id:38234 Streptococcus sanguinis str. ATCC 10556
U87828.1 gg_id:15570 aortic heart valve patient with endocarditis clone v3
U87829.1 gg_id:15571 aortic heart valve patient with endocarditis clone v5
NC_009009.1 gg_id:205756 Streptococcus sanguinis str. SK36
NR_028833.1 gg_id:593803 Streptococcus sinensis str. HKU4; DSM 14990
AY691533.1 gg_id:107142 Streptococcus sobrinus str. ChDC YS1
DQ677799.1 gg_id:170824 Streptococcus sobrinus str. ChDC YS13; 40125
DQ677794.1 gg_id:167103 Streptococcus sobrinus str. ChDC YS206; PD1017
AJ871181.1 gg_id:110876 Streptococcus sp. 1040-02B
AF009484.1 gg_id:15515 Streptococcus suis str. 22083
DQ113766.1 gg_id:136603 dog jejunum clone J5-01
GQ101022.1 gg_id:380857 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48
GQ007632.1 gg_id:502032 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
X68418.1 gg_id:15434 Streptococcus thermophilus str. DSM 20617
GQ104143.1 gg_id:374288 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw563g1
GQ058136.1 gg_id:376543 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ155489.1 gg_id:577395 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ033163.1 gg_id:406397 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ101185.1 gg_id:408208 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
GQ031863.1 gg_id:372703 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ021918.1 gg_id:487750 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ058145.1 gg_id:416754 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ054754.1 gg_id:386599 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1100h
GQ052795.1 gg_id:404186 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ057721.1 gg_id:447223 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ031888.1 gg_id:374845 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ045675.1 gg_id:449085 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ052810.1 gg_id:451499 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ363751.1 gg_id:357648 feces adult twins and mothers; TS14 clone TS14_a02h07
DQ327131.1 gg_id:148345 Metagenomic gut microbiome healthy human stool clone E649
DQ176426.1 gg_id:139353 Streptococcus thermophilus
GU195648.1 gg_id:578630 Streptococcus thermophilus str. M4
GQ058082.1 gg_id:392901 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ069727.1 gg_id:406513 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
NC_008532.1 gg_id:197884 Streptococcus thermophilus str. LMD-9
GQ052788.1 gg_id:423913 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw

GQ041461.1	464018	17009.3	18413.7	8535.1	11561.6	15135.4	17503.8
GQ027302.1	380914	18686.3	18516.8	21395.7	14157.1	10048.8	11160.4
FJ365649.1	367692	505.1	1165.8	592.7	352.3	170.4	1098.8
GQ995676.1	548391	1731.8	2555.1	1765.7	1463.1	2437.3	5203.6
CP000387.1	210400	2608.3	4815.1	4136.4	4042.1	3941.1	5824.0
AB002524.1	38234	1390.1	1554.6	1511.7	1605.7	2049.6	2441.3
U87828.1	15570	7843.3	7157.8	4155.5	6773.5	7017.9	6070.5
U87829.1	15571	14645.2	13263.1	12275.2	10202.7	13804.0	14208.0
NC_009009.1	205756	10253.6	12056.8	6244.8	8495.1	11498.7	13652.2
NR_028833.1	593803	1050.1	1030.2	1200.8	1205.7	723.6	1727.6
AY691533.1	107142	1630.5	2283.8	2145.6	2031.3	2504.4	2903.3
DQ677799.1	170824	4471.7	5765.8	5767.3	5013.8	6327.9	5679.7
DQ677794.1	167103	12491.7	15009.3	7824.7	9090.2	13452.6	12815.8
AJ871181.1	110876	776.0	1698.0	1235.3	347.9	1359.6	846.9
AF009484.1	15515	565.5	1047.0	1536.0	672.1	206.7	470.2
DQ113766.1	136603	4358.6	4294.3	2986.1	3776.5	2576.6	4072.5
GQ101022.1	380857	819.2	1151.9	2050.6	1091.3	647.3	1345.1
GQ007632.1	502032	1528.4	1133.2	1330.9	2971.5	189.1	380.0
X68418.1	15434	8283.1	10712.6	2415.2	6127.7	6040.6	4880.5
GQ104143.1	374288	8041.8	7901.1	3824.2	5423.2	8404.4	7043.2
GQ058136.1	376543	5879.8	7770.2	4827.4	5609.5	7716.3	6910.3
GQ155489.1	577395	1906.8	1969.6	2979.9	2056.3	1457.8	3014.7
GQ033163.1	406397	12374.9	11808.6	14740.9	11932.5	14005.6	13405.5
GQ101185.1	408208	165.6	361.3	136.3	253.6	96.8	112.9
GQ031863.1	372703	89.9	293.7	109.9	212.9	120.6	90.6
GQ021918.1	487750	118.4	256.6	607.6	207.2	193.1	870.1
GQ058145.1	416754	2580.3	2744.5	1149.5	1770.8	2815.4	3022.1
GQ054754.1	386599	874.9	1110.3	2186.4	1093.6	651.9	1346.3
GQ052795.1	404186	38.5	56.2	99.0	53.7	68.1	45.5
GQ057721.1	447223	1318.3	1419.3	1792.4	1502.7	910.6	1755.0
GQ031888.1	374845	795.6	700.6	439.1	287.7	554.5	787.9
GQ045675.1	449085	13035.1	13966.5	10401.2	9661.0	9768.1	11445.1
GQ052810.1	451499	814.7	772.6	267.4	623.6	274.1	436.8
FJ363751.1	357648	4814.2	5715.8	3990.6	6277.4	11297.8	8933.3
DQ327131.1	148345	846.2	1130.5	2149.6	1001.0	638.2	1246.3
DQ176426.1	139353	5485.3	5385.0	3802.1	5460.7	4295.3	4874.9
GU195648.1	578630	74.4	286.4	148.3	101.5	84.4	2003.8
GQ058082.1	392901	875.7	1162.3	2183.4	1088.6	649.8	1251.4
GQ069727.1	406513	645.9	790.1	1980.1	1113.3	1822.7	2145.1
NC_008532.1	197884	7490.2	6330.3	7592.8	6312.0	5670.9	8225.6
GQ052788.1	423913	841.6	1061.1	2301.4	1002.8	634.2	1243.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__Streptococcus thermophilus	45125
s__Streptococcus thermophilus	45195
s__Streptococcus thermophilus	45208
s__Streptococcus thermophilus	45225
s__Streptococcus thermophilus	45282
s__Streptococcus thermophilus	45307
s__Streptococcus thermophilus	45345
s__Streptococcus thermophilus	45360
s__Streptococcus thermophilus	45382
s__Streptococcus thermophilus	45416
s__Streptococcus thermophilus	45449
s__Streptococcus thermophilus	45573
s__Streptococcus thermophilus	45574
s__Streptococcus thermophilus	45593
s__Streptococcus thermophilus	45609
s__Streptococcus thermophilus	45683
s__Streptococcus thermophilus	45690
s__Streptococcus thermophilus	45757
s__Streptococcus thermophilus	45851
s__unclassified	44157
s__unclassified	44159
s__unclassified	44160
s__unclassified	44162
s__unclassified	44164
s__unclassified	44165
s__unclassified	44167
s__unclassified	44168
s__unclassified	44173
s__unclassified	44175
s__unclassified	44176
s__unclassified	44180
s__unclassified	44181
s__unclassified	44182
s__unclassified	44183
s__unclassified	44186
s__unclassified	44189
s__unclassified	44190
s__unclassified	44191
s__unclassified	44193
s__unclassified	44197
s__unclassified	44201

GQ155655.1 gg_id:549850 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ558254.1 gg_id:517963 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
FJ749314.1 gg_id:537395 Streptococcus thermophilus str. IMAU40038; QH31-3-2
GQ031954.1 gg_id:397216 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073080.1 gg_id:443273 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204h03
DQ804818.1 gg_id:185602 human fecal clone RL385_aao81b02
DQ805013.1 gg_id:198675 human fecal clone RL385_aao84a10
GQ106050.1 gg_id:398015 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ101210.1 gg_id:411772 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
FJ364706.1 gg_id:358192 feces adult twins and mothers; TS19 clone TS19_a02a11
GQ155517.1 gg_id:557282 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ058019.1 gg_id:372435 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ048271.1 gg_id:377521 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ155829.1 gg_id:584000 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ007512.1 gg_id:502151 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ101087.1 gg_id:387080 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
GQ155483.1 gg_id:579474 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY675258.1 gg_id:101812 Streptococcus thermophilus str. ST3
DQ804809.1 gg_id:190074 human fecal clone RL385_aao81a02
AF429765.1 gg_id:71159 Streptococcus equinus str. NCDO1037T; ATCC9812
GQ074419.1 gg_id:371556 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162f
GQ032260.1 gg_id:431839 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU473988.1 gg_id:291047 giant panda feces clone GP_2aaa03g07
FJ557752.1 gg_id:519951 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ041684.1 gg_id:467380 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw931b1
GU045381.1 gg_id:587346 Streptococcus oralis str. KCOM 1408
EU458225.1 gg_id:296232 North American black bear feces clone BB2_b03_2
EU458269.1 gg_id:292189 North American black bear feces clone BB2_b03_3
FJ678567.1 gg_id:526324 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AF396922.1 gg_id:46196 Streptococcus bovis str. NCFB 2476
GQ076772.1 gg_id:459838 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
EU458273.1 gg_id:292624 North American black bear feces clone BB2_b09_2
GQ073147.1 gg_id:404881 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f05c1
EU470279.1 gg_id:294884 Grevy's zebra feces clone GZ_aaa03a08
AY858648.1 gg_id:148448 Streptococcus gallolyticus str. 329
EU460756.1 gg_id:289494 short-beaked echidna feces clone ECH_aai37e12
DQ824742.1 gg_id:187029 human fecal clone RL185_aaj72e07
AY769997.1 gg_id:113900 Streptococcus massiliensis str. 4401825
EU467782.1 gg_id:297236 North American black bear feces clone BB1_h02
EU467863.1 gg_id:289201 North American black bear feces clone BB1_g04_1
FJ684768.1 gg_id:529028 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

GQ155655.1	549850	8786.4	9532.0	6148.4	3854.8	5716.3	5850.0
FJ558254.1	517963	820.0	1315.2	1753.6	1022.8	325.6	652.7
FJ749314.1	537395	358.3	543.5	1148.3	723.5	520.8	3210.5
GQ031954.1	397216	864.6	1151.0	2155.0	1072.7	650.1	1339.2
GQ073080.1	443273	811.8	604.6	497.4	998.3	402.6	886.7
DQ804818.1	185602	860.7	1114.4	2051.2	1065.5	584.6	1158.8
DQ805013.1	198675	5272.9	5768.3	4009.1	3898.8	6881.8	5154.8
GQ106050.1	398015	6975.4	7063.9	8414.0	6475.9	6857.1	7464.2
GQ101210.1	411772	863.1	1127.9	2307.1	1076.2	651.4	1339.9
FJ364706.1	358192	1896.5	1327.9	2791.1	4525.0	1032.7	2433.2
GQ155517.1	557282	3576.8	3481.9	3770.3	3419.1	2127.3	3045.4
GQ058019.1	372435	2831.0	4033.2	3346.7	4049.8	5250.1	5926.3
GQ048271.1	377521	14433.7	13532.2	13727.5	15817.0	9018.2	9681.4
GQ155829.1	584000	2357.8	2617.1	3925.7	3785.2	2207.2	3836.3
GQ007512.1	502151	1570.5	1931.1	2045.0	3040.3	1445.2	2321.7
GQ101087.1	387080	6326.6	5140.6	2734.0	5791.7	868.9	1811.6
GQ155483.1	579474	3589.2	3282.3	3801.5	3437.8	2125.3	3051.0
AY675258.1	101812	2028.8	2807.6	1824.8	3148.7	2064.3	3885.6
DQ804809.1	190074	15731.6	12912.1	10571.9	9833.2	12308.3	11903.1
AF429765.1	71159	751.9	940.8	1493.8	359.1	120.6	3130.0
GQ074419.1	371556	3053.6	3553.8	2209.8	4244.7	1354.7	1662.4
GQ032260.1	431839	89.8	1021.3	395.8	123.1	141.8	164.6
EU473988.1	291047	1243.4	964.0	1829.2	785.5	114.9	402.1
FJ557752.1	519951	31.1	714.4	243.7	81.1	84.7	45.5
GQ041684.1	467380	1248.2	1394.5	1139.4	559.5	177.3	344.5
GU045381.1	587346	683.3	1726.7	1845.2	666.9	244.3	1203.3
EU458225.1	296232	1564.9	1884.8	2905.9	2889.0	293.4	790.6
EU458269.1	292189	4902.6	5744.2	5477.8	2518.8	1675.1	3642.8
FJ678567.1	526324	4341.3	4418.4	2748.6	4910.7	5501.7	6757.6
AF396922.1	46196	750.3	922.7	1379.7	355.7	114.6	3130.7
GQ076772.1	459838	3010.9	2360.9	529.6	1126.0	1248.8	1602.2
EU458273.1	292624	1851.7	2000.8	2609.6	788.7	441.5	936.7
GQ073147.1	404881	1814.7	1618.6	1917.4	972.3	274.4	627.2
EU470279.1	294884	7913.0	5879.6	4792.0	7610.5	9436.5	9652.2
AY858648.1	148448	124.9	354.4	790.2	151.8	208.2	206.4
EU460756.1	289494	175.8	453.8	1690.2	181.7	147.2	263.4
DQ824742.1	187029	2654.0	4034.4	876.3	1088.1	3716.5	2260.7
AY769997.1	113900	169.0	684.3	782.0	251.6	224.6	540.4
EU467782.1	297236	4935.8	4440.7	7703.1	4805.2	5771.4	6367.0
EU467863.1	289201	1252.5	1608.6	3816.6	1060.6	781.8	1088.9
FJ684768.1	529028	3566.1	4674.8	5448.0	4337.8	6727.3	6359.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44204
s__unclassified	44209
s__unclassified	44211
s__unclassified	44212
s__unclassified	44214
s__unclassified	44215
s__unclassified	44216
s__unclassified	44217
s__unclassified	44219
s__unclassified	44220
s__unclassified	44221
s__unclassified	44225
s__unclassified	44226
s__unclassified	44228
s__unclassified	44229
s__unclassified	44231
s__unclassified	44232
s__unclassified	44236
s__unclassified	44241
s__unclassified	44242
s__unclassified	44244
s__unclassified	44245
s__unclassified	44247
s__unclassified	44248
s__unclassified	44251
s__unclassified	44252
s__unclassified	44255
s__unclassified	44257
s__unclassified	44258
s__unclassified	44259
s__unclassified	44261
s__unclassified	44262
s__unclassified	44267
s__unclassified	44270
s__unclassified	44275
s__unclassified	44277
s__unclassified	44278
s__unclassified	44279
s__unclassified	44280
s__unclassified	44281
s__unclassified	44286

EU458122.1 gg_id:295579 North American black bear feces clone BB2_b03
FJ675372.1 gg_id:509952 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ156114.1 gg_id:542895 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU156788.1 gg_id:349229 Streptococcus pseudopneumoniae str. CCUG 50870
EU458191.1 gg_id:288025 North American black bear feces clone BB2_d10_1
AJ871184.1 gg_id:110043 Streptococcus sp. 1606-02B
GQ156276.1 gg_id:511755 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU458233.1 gg_id:300876 North American black bear feces clone BB2_c02_2
EU463426.1 gg_id:295495 domesticated horse feces clone horsem_aai93f11
GQ072611.1 gg_id:398533 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19
GQ069087.1 gg_id:426030 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ032546.1 gg_id:458384 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU458204.1 gg_id:291703 North American black bear feces clone BB2_f09
FJ892877.1 gg_id:574304 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
EU460889.1 gg_id:296865 short-beaked echidna feces clone ECH_aai40a06
GQ156133.1 gg_id:509836 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU475773.1 gg_id:297422 white-faced saki feces clone Saki_aaj63a10
EU461988.1 gg_id:300951 white-faced saki feces clone Saki_aaj64h04
EU474053.1 gg_id:296602 giant panda feces clone GP_2aaa02b11
EU779059.1 gg_id:316587 Prevost's squirrel feces clone SQ_aah81a03
EU471387.1 gg_id:303161 spectacled bear feces clone SB_2aaa01e06
EU772598.1 gg_id:326464 North American Black Bear feces clone BB1_c09_1
FJ679343.1 gg_id:517628 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU475742.1 gg_id:290829 white-faced saki feces clone Saki_aaj62d04
AJ305257.1 gg_id:36122 Streptococcus bovis str. NCTC11436
GQ019432.1 gg_id:490235 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h
GQ057697.1 gg_id:447655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ072785.1 gg_id:440026 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201b07
NR_029025.1 gg_id:590801 Streptococcus halichoeri str. M512/02/1; CCUG 48324
FJ558186.1 gg_id:519809 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ072303.1 gg_id:392871 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw194f05
AY525794.1 gg_id:111799 Streptococcus pneumoniae str. VN_O27
EU461851.1 gg_id:289861 white-faced saki feces clone Saki_aaj62c04
EU458245.1 gg_id:288170 North American black bear feces clone BB2_f04_2
EU467179.1 gg_id:297263 white-faced saki feces clone Saki_b01
GQ105172.1 gg_id:446697 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ110037.1 gg_id:465867 Topographical and Temporal Human Skin Microbiome skin back clone nbw658a08c1
EU458137.1 gg_id:299774 North American black bear feces clone BB2_c11
GQ032551.1 gg_id:392746 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AF124350.1 gg_id:22640 Streptococcus orisratti str. ATCC700640; A63
FJ154804.1 gg_id:561563 Streptococcus salivarius str. K12

EU458122.1	295579	708.8	1227.4	3785.3	607.2	6966.4	4619.2
FJ675372.1	509952	9914.4	9488.6	10534.4	9406.9	13150.0	12184.1
GQ156114.1	542895	1838.0	2230.6	1872.7	1714.5	1498.4	1637.0
EU156788.1	349229	437.5	1443.3	1095.1	344.7	417.2	462.9
EU458191.1	288025	1894.6	1621.1	1794.8	600.7	931.3	1482.3
AJ871184.1	110043	95.8	322.9	590.7	140.0	73.9	208.6
GQ156276.1	511755	2737.8	2160.3	3486.5	6428.1	1054.2	1269.2
EU458233.1	300876	20510.8	21043.0	17821.1	16245.3	20965.7	20681.3
EU463426.1	295495	723.2	1478.1	2904.4	694.5	366.4	880.0
GQ072611.1	398533	23.7	43.3	48.2	42.6	56.7	35.4
GQ069087.1	426030	6031.8	5708.4	4958.0	5975.0	11656.6	10852.4
GQ032546.1	458384	1176.0	1661.2	2434.9	609.9	835.8	1452.2
EU458204.1	291703	3617.0	3302.0	4610.8	2433.5	1937.2	3021.0
FJ892877.1	574304	1661.2	1158.9	1874.3	1004.3	263.8	734.9
EU460889.1	296865	352.6	788.9	2738.6	319.6	1068.4	656.8
GQ156133.1	509836	3603.2	4051.0	3838.7	4041.4	4928.3	5557.2
EU475773.1	297422	8966.8	7605.9	3514.8	8334.6	11435.7	13350.5
EU461988.1	300951	13404.7	13138.8	10144.2	10392.3	8251.1	6190.3
EU474053.1	296602	1770.9	1722.8	1846.9	810.6	333.9	682.3
EU779059.1	316587	298.7	942.7	310.7	515.9	322.1	547.2
EU471387.1	303161	2264.6	2953.2	5093.1	1876.8	4346.9	3052.1
EU772598.1	326464	3175.5	3614.6	5251.9	3601.9	7735.1	7888.5
FJ679343.1	517628	3206.0	1649.9	1307.7	2336.3	2293.1	3264.3
EU475742.1	290829	4754.5	4937.7	6565.8	4875.0	7240.5	5745.8
AJ305257.1	36122	10611.2	11011.1	7840.4	8775.2	5964.8	9634.8
GQ019432.1	490235	891.6	1607.7	1807.3	1242.7	1521.6	1335.3
GQ057697.1	447655	598.3	1012.9	774.0	615.4	196.4	265.9
GQ072785.1	440026	563.6	1421.0	710.8	329.0	294.8	444.1
NR_029025.1	590801	460.3	1054.7	1039.5	730.8	301.7	917.2
FJ558186.1	519809	10952.2	8032.6	6222.7	9842.8	8567.5	7355.7
GQ072303.1	392871	49.7	396.8	1002.4	110.0	119.0	60.8
AY525794.1	111799	1033.4	2077.9	1532.9	704.6	611.0	2250.2
EU461851.1	289861	2762.1	2927.5	3354.4	2386.0	2225.1	2687.5
EU458245.1	288170	6309.6	3117.0	1989.3	4268.1	2146.1	5733.6
EU467179.1	297263	9136.5	9485.6	7419.5	7733.1	8838.0	9995.5
GQ105172.1	446697	124.9	673.5	810.0	193.0	122.2	372.4
GQ110037.1	465867	26.3	72.5	23.0	52.1	55.4	20.9
EU458137.1	299774	14389.2	12109.6	6879.5	7256.4	13486.5	15349.6
GQ032551.1	392746	2873.3	2684.9	2601.1	1726.0	640.0	1505.9
AF124350.1	22640	7555.2	6413.1	3560.2	9310.6	10936.7	8451.3
FJ154804.1	561563	257.0	749.4	767.5	394.6	95.3	3518.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44287
s__unclassified	44292
s__unclassified	44294
s__unclassified	44299
s__unclassified	44302
s__unclassified	44305
s__unclassified	44306
s__unclassified	44308
s__unclassified	44310
s__unclassified	44314
s__unclassified	44315
s__unclassified	44316
s__unclassified	44317
s__unclassified	44323
s__unclassified	44325
s__unclassified	44327
s__unclassified	44333
s__unclassified	44335
s__unclassified	44339
s__unclassified	44341
s__unclassified	44343
s__unclassified	44344
s__unclassified	44346
s__unclassified	44353
s__unclassified	44361
s__unclassified	44363
s__unclassified	44369
s__unclassified	44370
s__unclassified	44372
s__unclassified	44373
s__unclassified	44379
s__unclassified	44380
s__unclassified	44381
s__unclassified	44384
s__unclassified	44385
s__unclassified	44387
s__unclassified	44389
s__unclassified	44391
s__unclassified	44394
s__unclassified	44396
s__unclassified	44400

GQ091903.1 gg_id:378478 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ074386.1 gg_id:465792 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c
AY134901.1 gg_id:59566 oral periodontitis clone FX003
GQ076806.1 gg_id:421906 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
EU467824.1 gg_id:302874 North American black bear feces clone BB1_g09_1
EU458201.1 gg_id:296761 North American black bear feces clone BB2_f04_1
AJ617805.1 gg_id:105608 Streptococcus mitis str. B6
GQ073665.1 gg_id:407180 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ073117.1 gg_id:372638 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c08c1
GQ091708.1 gg_id:432165 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU458275.1 gg_id:294190 North American black bear feces clone BB2_c04_2
GQ076774.1 gg_id:419654 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
EU471392.1 gg_id:294794 spectacled bear feces clone SB_2aaa03c03
EU467785.1 gg_id:297386 North American black bear feces clone BB1_h05
EU471507.1 gg_id:301767 spectacled bear feces clone SB_2aaa04f06
EU461831.1 gg_id:296458 white-faced saki feces clone Saki_aaj61g11
EU467834.1 gg_id:288953 North American black bear feces clone BB1_a10_2
EU475853.1 gg_id:295993 white-faced saki feces clone Saki_aaj62e08
GQ114957.1 gg_id:414368 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59
FJ558178.1 gg_id:528842 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
EU467902.1 gg_id:302209 North American black bear feces clone BB1_f02_2
EU461802.1 gg_id:294888 white-faced saki feces clone Saki_aaj61c11
AY281084.1 gg_id:88494 Streptococcus pneumoniae str. ATCC 6303
GQ082014.1 gg_id:413510 Topographical and Temporal Human Skin Microbiome skin back clone nbw1199a11c
FJ677072.1 gg_id:523529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU156778.1 gg_id:339761 Streptococcus pneumoniae str. CCRI-14666
EU467758.1 gg_id:291579 North American black bear feces clone BB1_d10
EU458258.1 gg_id:299395 North American black bear feces clone BB2_h04_1
GQ086143.1 gg_id:389175 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU458150.1 gg_id:289299 North American black bear feces clone BB2_e08
FJ673591.1 gg_id:518062 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
CP000262.1 gg_id:157784 Streptococcus pyogenes str. MGAS10750
EU467778.1 gg_id:294914 North American black bear feces clone BB1_g03
FJ679590.1 gg_id:525580 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU483251.1 gg_id:265868 Streptococcus sp. str. 24180-02
EU467842.1 gg_id:291050 North American black bear feces clone BB1_c02
GQ074394.1 gg_id:395063 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c
FJ558046.1 gg_id:525966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
EU470264.1 gg_id:290919 Grevy's zebra feces clone GZ_aaa01e07
GQ155707.1 gg_id:562565 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU461911.1 gg_id:303202 white-faced saki feces clone Saki_aaj63e11

GQ091903.1	378478	11869.4	10031.2	7625.8	8281.3	9417.1	10706.8
GQ074386.1	465792	1207.4	2268.5	1811.1	1530.9	640.0	1483.1
AY134901.1	59566	26.0	78.1	11.5	56.4	48.7	27.4
GQ076806.1	421906	877.9	2265.2	1888.9	725.5	511.4	1131.0
EU467824.1	302874	7159.3	6439.1	1803.2	5852.2	2850.6	5186.7
EU458201.1	296761	1128.0	2119.7	3859.6	1041.0	524.1	1185.4
AJ617805.1	105608	1342.3	2272.6	1816.5	730.5	268.7	2545.6
GQ073665.1	407180	567.3	1330.9	709.6	326.8	297.0	444.5
GQ073117.1	372638	6383.5	5480.3	2571.1	6180.1	2685.0	2767.4
GQ091708.1	432165	6802.0	6726.4	2249.9	4123.6	4755.7	5472.6
EU458275.1	294190	6864.6	5855.6	6470.7	5675.8	4301.1	5833.8
GQ076774.1	419654	1997.6	1913.1	1941.5	1013.7	425.0	810.1
EU471392.1	294794	3231.1	3304.2	6918.8	2174.9	3021.5	3085.7
EU467785.1	297386	1890.5	2666.7	4944.7	1564.2	3270.7	4878.8
EU471507.1	301767	34.7	215.9	615.8	101.0	105.3	95.9
EU461831.1	296458	7452.8	5885.7	8878.0	7123.9	7519.2	10604.3
EU467834.1	288953	8682.8	10045.7	7367.2	7823.6	8946.2	8884.9
EU475853.1	295993	708.5	1365.2	2089.1	1208.5	455.9	1222.6
GQ114957.1	414368	6677.0	6573.7	1866.2	8397.0	10888.7	10118.5
FJ558178.1	528842	751.0	1485.3	504.2	851.5	755.0	838.4
EU467902.1	302209	825.9	1300.5	2718.0	782.1	840.6	1418.6
EU461802.1	294888	1772.4	1473.9	2307.2	2846.9	187.9	544.3
AY281084.1	88494	1508.1	2732.0	8354.7	1478.0	6395.5	4551.0
GQ082014.1	413510	15364.6	14369.4	11888.2	11302.2	14410.4	14571.9
FJ677072.1	523529	5324.5	4674.5	9642.5	5834.0	2338.2	5024.8
EU156778.1	339761	1691.7	2854.3	7192.1	1563.8	4821.1	3997.9
EU467758.1	291579	7226.6	7074.3	7952.0	6131.5	6899.9	7987.4
EU458258.1	299395	63.4	412.2	101.8	94.4	82.3	267.5
GQ086143.1	389175	118.1	681.4	195.9	195.6	416.6	474.9
EU458150.1	289299	714.5	2195.7	2452.9	814.8	284.1	634.5
FJ673591.1	518062	1112.9	1364.4	1888.8	431.3	272.0	596.4
CP000262.1	157784	2326.0	3028.7	3446.2	1353.5	581.9	1212.2
EU467778.1	294914	11669.3	10290.2	10060.4	10254.9	9062.0	10010.4
FJ679590.1	525580	710.3	1649.3	2111.8	755.4	367.4	826.0
EU483251.1	265868	1386.7	1838.1	2090.0	737.0	311.2	2217.2
EU467842.1	291050	8689.7	8731.4	7370.6	7835.8	8951.4	8306.2
GQ074394.1	395063	1144.1	2293.0	1854.8	1597.5	647.4	1585.6
FJ558046.1	525966	47.2	441.8	471.9	131.2	89.8	123.2
EU470264.1	290919	4458.9	3025.1	3322.1	3773.1	1750.7	3457.1
GQ155707.1	562565	400.3	820.7	819.1	492.9	209.1	399.9
EU461911.1	303202	3720.3	4308.7	5712.1	3223.7	2252.4	3491.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44407
s__unclassified	44410
s__unclassified	44411
s__unclassified	44418
s__unclassified	44421
s__unclassified	44424
s__unclassified	44426
s__unclassified	44427
s__unclassified	44430
s__unclassified	44431
s__unclassified	44435
s__unclassified	44438
s__unclassified	44441
s__unclassified	44448
s__unclassified	44452
s__unclassified	44454
s__unclassified	44455
s__unclassified	44457
s__unclassified	44462
s__unclassified	44463
s__unclassified	44466
s__unclassified	44469
s__unclassified	44471
s__unclassified	44477
s__unclassified	44480
s__unclassified	44483
s__unclassified	44484
s__unclassified	44487
s__unclassified	44489
s__unclassified	44494
s__unclassified	44495
s__unclassified	44496
s__unclassified	44501
s__unclassified	44503
s__unclassified	44504
s__unclassified	44510
s__unclassified	44511
s__unclassified	44514
s__unclassified	44515
s__unclassified	44516
s__unclassified	44518

GQ034460.1 gg_id:455356 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
EU473383.1 gg_id:294502 giant panda feces clone GP_1aaa04f12
EU467774.1 gg_id:302237 North American black bear feces clone BB1_f09
FJ673292.1 gg_id:520118 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458129.1 gg_id:299791 North American black bear feces clone BB2_c01
EU775692.1 gg_id:343045 Hedgehog feces clone HH_d11
EU461849.1 gg_id:294466 white-faced saki feces clone Saki_aaj62b10
EU467158.1 gg_id:297683 white-faced saki feces clone Saki_c09
EU458133.1 gg_id:302604 North American black bear feces clone BB2_c05
GQ058671.1 gg_id:465504 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58
EU458141.1 gg_id:294837 North American black bear feces clone BB2_d06
EU461875.1 gg_id:291824 white-faced saki feces clone Saki_aaj62g04
EU461834.1 gg_id:301274 white-faced saki feces clone Saki_aaj61h04
FJ680001.1 gg_id:521890 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB038371.1 gg_id:42006 Streptococcus sp. str. PSH2
AY525792.1 gg_id:111812 Streptococcus pneumoniae str. SI_P7
EU458282.1 gg_id:295664 North American black bear feces clone BB2_d02_2
GQ081650.1 gg_id:437407 Topographical and Temporal Human Skin Microbiome skin back clone nbw1197g04c
EU458172.1 gg_id:289129 North American black bear feces clone BB2_h11
AJ608938.1 gg_id:107158 Streptococcus pneumoniae str. 101
FJ823146.1 gg_id:548508 Streptococcus infantis str. ToTI
EU458250.1 gg_id:288235 North American black bear feces clone BB2_g02_2
EU461821.1 gg_id:288580 white-faced saki feces clone Saki_aaj61f03
EU774846.1 gg_id:304567 Short-beaked Echidna feces clone ECH_aai39a01
GQ073297.1 gg_id:451731 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207d08c
EU467802.1 gg_id:299936 North American black bear feces clone BB1_d04_1
FJ679627.1 gg_id:522003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458256.1 gg_id:295491 North American black bear feces clone BB2_h01_1
AM774229.1 gg_id:256872 Streptococcus sp. str. 1355-03
EU461915.1 gg_id:300834 white-faced saki feces clone Saki_aaj63f06
EU461938.1 gg_id:295646 white-faced saki feces clone Saki_aaj64b02
EU458276.1 gg_id:294389 North American black bear feces clone BB2_c06_2
GQ101337.1 gg_id:461282 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493h
EU467854.1 gg_id:293702 North American black bear feces clone BB1_d12_2
EU458163.1 gg_id:288669 North American black bear feces clone BB2_g05
EU779414.1 gg_id:333660 Grevy's Zebra feces clone GZ_aaa01g10
GQ154714.1 gg_id:578309 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ675847.1 gg_id:518137 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458305.1 gg_id:290994 North American black bear feces clone BB2_g04_2
GQ057676.1 gg_id:414752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY976601.1 gg_id:124166 human cecum mucosal biopsy clone K155

GQ034460.1	455356	14175.5	14323.1	8641.7	10790.8	14795.1	14727.6
EU473383.1	294502	5908.4	7689.8	3361.6	5967.4	14195.2	8716.5
EU467774.1	302237	2422.9	2529.2	7663.2	1243.0	5392.4	5075.2
FJ673292.1	520118	1892.7	2355.4	4244.5	1813.2	922.3	1865.8
EU458129.1	299791	1466.1	1706.4	3323.3	740.1	974.9	1406.4
EU775692.1	343045	1234.9	822.5	710.1	557.1	242.6	603.1
EU461849.1	294466	523.5	1203.6	4843.8	593.6	1426.8	1872.1
EU467158.1	297683	13271.2	13011.4	10741.5	13286.3	14103.0	17153.8
EU458133.1	302604	4063.8	4103.6	3585.0	2981.3	10687.1	6955.1
GQ058671.1	465504	6984.2	5032.7	3914.6	6320.5	6711.1	5248.2
EU458141.1	294837	235.3	612.3	1381.3	310.7	144.0	290.6
EU461875.1	291824	629.1	1068.4	2354.8	626.7	517.6	862.1
EU461834.1	301274	14283.6	16035.5	7040.9	11333.8	9666.1	11505.3
FJ680001.1	521890	255.4	340.8	837.4	286.0	132.5	150.8
AB038371.1	42006	44.8	504.2	78.2	79.4	84.9	42.0
AY525792.1	111812	1222.3	1950.9	1622.2	614.5	231.5	1696.0
EU458282.1	295664	1981.3	1614.4	2706.4	847.2	342.9	688.9
GQ081650.1	437407	3782.1	3266.3	4763.2	5030.5	6425.7	6141.4
EU458172.1	289129	3128.1	3182.2	4199.7	3021.1	3758.6	4614.6
AJ608938.1	107158	419.2	1321.2	721.3	309.1	169.6	1695.5
FJ823146.1	548508	39.7	328.3	264.5	101.8	74.0	122.6
EU458250.1	288235	18178.7	15121.8	12655.3	12548.3	15927.6	19413.1
EU461821.1	288580	7924.7	7439.9	5737.3	5327.2	6363.4	6895.9
EU774846.1	304567	1774.0	2057.2	3917.0	1654.6	268.0	1592.6
GQ073297.1	451731	10698.9	10227.9	8290.7	8649.4	9976.7	9695.7
EU467802.1	299936	6386.5	9565.7	5955.8	6770.7	13761.2	10204.3
FJ679627.1	522003	5356.1	3645.2	2875.5	4393.8	6448.3	7415.1
EU458256.1	295491	370.1	534.0	1312.6	212.0	216.2	243.6
AM774229.1	256872	4733.0	4733.8	5617.9	6033.3	6576.1	7813.4
EU461915.1	300834	414.7	1055.4	1974.0	424.3	273.8	590.0
EU461938.1	295646	10708.2	9527.8	8938.7	6366.6	9365.4	9227.7
EU458276.1	294389	1287.8	2581.3	9256.5	1479.2	6406.8	5547.8
GQ101337.1	461282	764.0	1043.1	348.7	99.1	98.4	110.2
EU467854.1	293702	2219.3	2438.6	3127.7	1578.7	541.0	1828.3
EU458163.1	288669	3585.3	3726.8	3446.5	2180.9	1727.5	2166.6
EU779414.1	333660	4153.5	4532.3	5528.7	1491.8	2850.9	4738.8
GQ154714.1	578309	3155.7	2815.1	3600.2	2087.8	1040.5	1924.0
FJ675847.1	518137	3042.6	1471.0	2924.5	2929.4	1464.0	4394.9
EU458305.1	290994	12792.5	10103.3	6172.1	11125.8	14797.0	16908.0
GQ057676.1	414752	1238.5	968.2	578.5	356.5	124.4	220.4
AY976601.1	124166	17385.3	17913.0	17267.2	14694.0	14238.8	13563.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44522
s__unclassified	44525
s__unclassified	44527
s__unclassified	44529
s__unclassified	44533
s__unclassified	44535
s__unclassified	44537
s__unclassified	44539
s__unclassified	44540
s__unclassified	44541
s__unclassified	44543
s__unclassified	44549
s__unclassified	44550
s__unclassified	44551
s__unclassified	44552
s__unclassified	44553
s__unclassified	44554
s__unclassified	44557
s__unclassified	44563
s__unclassified	44564
s__unclassified	44565
s__unclassified	44566
s__unclassified	44571
s__unclassified	44572
s__unclassified	44574
s__unclassified	44575
s__unclassified	44576
s__unclassified	44577
s__unclassified	44579
s__unclassified	44580
s__unclassified	44581
s__unclassified	44584
s__unclassified	44587
s__unclassified	44589
s__unclassified	44590
s__unclassified	44592
s__unclassified	44593
s__unclassified	44598
s__unclassified	44604
s__unclassified	44605
s__unclassified	44608

EU467161.1 gg_id:288666 white-faced saki feces clone Saki_e03
EU473954.1 gg_id:301968 giant panda feces clone GP_2aaa01a05
EU458115.1 gg_id:292424 North American black bear feces clone BB2_a03
FJ675711.1 gg_id:529778 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ051339.1 gg_id:422100 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
EU467772.1 gg_id:295379 North American black bear feces clone BB1_f07
EU772573.1 gg_id:343721 North American Black Bear feces clone BB2_g11_1
GQ030437.1 gg_id:440962 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878c02c
EU461836.1 gg_id:292510 white-faced saki feces clone Saki_aaj61h07
GQ156121.1 gg_id:569797 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ043851.1 gg_id:396351 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97
EU467836.1 gg_id:299093 North American black bear feces clone BB1_b02_1
EU467810.1 gg_id:288003 North American black bear feces clone BB1_e09_1
EU467768.1 gg_id:291502 North American black bear feces clone BB1_e12
GQ016664.1 gg_id:493003 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824b0
GQ022888.1 gg_id:486781 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GU470907.1 gg_id:549026 Streptococcus mitis bv. 2 str. F0392
EU458155.1 gg_id:287652 North American black bear feces clone BB2_f04
EU458251.1 gg_id:293413 North American black bear feces clone BB2_g04_1
GU045386.1 gg_id:558644 Streptococcus oralis str. DSMZ 20395
GQ072839.1 gg_id:408605 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201g11c
FJ679770.1 gg_id:524800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458207.1 gg_id:301617 North American black bear feces clone BB2_g02_1
FJ673446.1 gg_id:527638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ112397.1 gg_id:449675 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ558181.1 gg_id:526804 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
FJ678184.1 gg_id:527125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU461987.1 gg_id:297081 white-faced saki feces clone Saki_aaj64h03
AY485604.1 gg_id:102076 Streptococcus australis str. ATCC 700641
EU458221.1 gg_id:292142 North American black bear feces clone BB2_a07_1
EU458291.1 gg_id:302636 North American black bear feces clone BB2_e02_3
EU473431.1 gg_id:301627 giant panda feces clone GP_1aaa02c05
EU467885.1 gg_id:293888 North American black bear feces clone BB1_c08_3
FJ684898.1 gg_id:518374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ558211.1 gg_id:525410 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
FJ678668.1 gg_id:523145 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ116366.1 gg_id:403611 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692b0
EU458192.1 gg_id:302661 North American black bear feces clone BB2_d12
GQ032269.1 gg_id:391176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ038600.1 gg_id:432587 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ032521.1 gg_id:396059 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw

EU467161.1	288666	5614.3	6629.1	2530.3	2599.5	5172.6	5104.4
EU473954.1	301968	1639.2	2132.3	2205.2	1487.4	699.8	1258.7
EU458115.1	292424	6483.4	9958.7	5053.2	8416.4	15983.4	11666.5
FJ675711.1	529778	431.8	277.8	979.9	405.7	155.7	235.3
GQ051339.1	422100	2285.5	1915.2	1389.2	1255.6	512.1	1084.0
EU467772.1	295379	5188.4	4500.9	4918.0	3807.0	2238.8	1801.4
EU772573.1	343721	19316.9	17275.8	12793.1	13542.2	16105.9	17997.1
GQ030437.1	440962	2664.8	3387.7	2151.4	1649.3	536.3	2053.8
EU461836.1	292510	1312.0	2552.1	2566.8	1032.5	930.4	1359.7
GQ156121.1	569797	8964.9	8434.6	8941.4	8608.2	9455.9	8459.4
GQ043851.1	396351	4962.1	3876.6	3795.7	4007.2	4236.5	4052.1
EU467836.1	299093	4026.9	2994.2	4363.3	3173.6	1998.2	3141.5
EU467810.1	288003	7430.3	7845.9	5576.0	7887.5	12171.8	11819.1
EU467768.1	291502	4485.0	5798.5	4965.7	3205.9	7760.8	7694.8
GQ016664.1	493003	2298.6	2180.7	1916.7	1002.0	443.4	1006.9
GQ022888.1	486781	83.7	476.3	93.1	123.1	67.8	59.2
GU470907.1	549026	431.1	1156.7	730.9	375.5	315.9	2363.4
EU458155.1	287652	1028.5	929.5	363.2	2260.1	3431.1	3590.7
EU458251.1	293413	1617.0	2140.8	2813.6	948.1	421.0	933.7
GU045386.1	558644	149.1	911.0	643.8	220.1	125.2	1675.4
GQ072839.1	408605	3256.5	3012.5	2672.1	1830.4	1727.2	1837.9
FJ679770.1	524800	1454.4	1493.2	2092.1	739.3	7590.2	4499.7
EU458207.1	301617	1909.2	1517.6	1512.2	611.3	934.0	1356.6
FJ673446.1	527638	294.7	838.7	1200.4	247.8	1169.2	1036.5
GQ112397.1	449675	474.0	1192.0	660.5	591.0	320.3	353.6
FJ558181.1	526804	10368.9	9634.1	7344.4	7196.0	11895.2	12004.9
FJ678184.1	527125	730.1	1269.2	2349.2	700.5	234.4	649.4
EU461987.1	297081	15444.3	13129.3	9828.8	10279.3	12743.8	14975.9
AY485604.1	102076	134.0	664.5	486.5	223.2	92.3	2399.8
EU458221.1	292142	11717.4	10816.9	6668.5	8429.1	9891.7	11769.6
EU458291.1	302636	13265.8	13389.7	9887.1	10795.3	13885.0	12080.0
EU473431.1	301627	2243.2	1951.2	1430.0	1228.6	604.4	1017.6
EU467885.1	293888	2949.2	1979.3	2672.8	3986.0	1852.7	1931.0
FJ684898.1	518374	2208.1	1833.1	3858.6	1074.2	1479.5	1954.3
FJ558211.1	525410	3209.6	2772.7	2929.6	1792.8	666.3	1581.2
FJ678668.1	523145	1724.5	2104.1	4162.8	1397.6	486.8	1503.9
GQ116366.1	403611	125.0	968.9	943.1	190.0	138.9	247.8
EU458192.1	302661	4393.1	2278.4	2120.7	5090.5	3925.5	5851.4
GQ032269.1	391176	1358.7	1509.1	1052.1	594.0	72.2	791.1
GQ038600.1	432587	120.6	382.6	297.8	177.2	105.4	304.4
GQ032521.1	396059	2288.0	1959.6	1488.5	1256.9	512.9	1090.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44609
s__unclassified	44610
s__unclassified	44615
s__unclassified	44622
s__unclassified	44623
s__unclassified	44626
s__unclassified	44629
s__unclassified	44630
s__unclassified	44632
s__unclassified	44633
s__unclassified	44635
s__unclassified	44639
s__unclassified	44641
s__unclassified	44643
s__unclassified	44644
s__unclassified	44647
s__unclassified	44648
s__unclassified	44650
s__unclassified	44651
s__unclassified	44658
s__unclassified	44659
s__unclassified	44669
s__unclassified	44673
s__unclassified	44675
s__unclassified	44676
s__unclassified	44680
s__unclassified	44681
s__unclassified	44682
s__unclassified	44684
s__unclassified	44687
s__unclassified	44688
s__unclassified	44689
s__unclassified	44698
s__unclassified	44703
s__unclassified	44705
s__unclassified	44707
s__unclassified	44708
s__unclassified	44709
s__unclassified	44711
s__unclassified	44721
s__unclassified	44722

FJ682967.1 gg_id:517809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ662826.1 gg_id:551205 Streptococcus pyogenes str. Sp4
EU460892.1 gg_id:302391 short-beaked echidna feces clone ECH_aai40b02
EU467908.1 gg_id:292450 North American black bear feces clone BB1_g03_1
GQ068224.1 gg_id:458497 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148
EU458149.1 gg_id:289551 North American black bear feces clone BB2_e07
GQ076119.1 gg_id:372054 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU458116.1 gg_id:296356 North American black bear feces clone BB2_a05
GQ013235.1 gg_id:496431 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073338.1 gg_id:418360 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h02c
GQ057439.1 gg_id:371684 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
NC_003485.1 gg_id:129068 Streptococcus pyogenes str. MGAS8232
EU535969.1 gg_id:281999 profile human microbiota antecubital fossa (inner elbow) skin clone nbt06g07
FJ676264.1 gg_id:525392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF509615.1 gg_id:225348 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
GQ101509.1 gg_id:465878 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495h
EU467763.1 gg_id:294288 North American black bear feces clone BB1_e06
EU461902.1 gg_id:295919 white-faced saki feces clone Saki_aaj63d11
EU156782.1 gg_id:350039 Streptococcus pneumoniae str. CCRI-15796
FJ678537.1 gg_id:526366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU461866.1 gg_id:298094 white-faced saki feces clone Saki_aaj62e09
EU458187.1 gg_id:302971 North American black bear feces clone BB2_c08_1
GQ074067.1 gg_id:404983 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU458210.1 gg_id:292277 North American black bear feces clone BB2_g09_1
EU458286.1 gg_id:295358 North American black bear feces clone BB2_d06_1
GQ028155.1 gg_id:406593 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ018843.1 gg_id:490825 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191d
EU458252.1 gg_id:296907 North American black bear feces clone BB2_g05_1
GQ018860.1 gg_id:490807 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f
EU458292.1 gg_id:302364 North American black bear feces clone BB2_e03_1
GQ010556.1 gg_id:499109 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ679324.1 gg_id:509856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU774903.1 gg_id:319192 Short-beaked Echidna feces clone ECH_aai38d02
GQ000869.1 gg_id:469434 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU461949.1 gg_id:297276 white-faced saki feces clone Saki_aaj64c03
EU467748.1 gg_id:289224 North American black bear feces clone BB1_c07
AM157421.1 gg_id:141768 Streptococcus parasanguinis mother C3
GQ058009.1 gg_id:449776 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU458304.1 gg_id:297241 North American black bear feces clone BB2_f10_2
FJ894952.1 gg_id:555959 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p
EU471452.1 gg_id:295151 spectacled bear feces clone SB_2aaa01f05

FJ682967.1	517809	1740.9	2498.2	4429.6	1820.2	3302.2	4380.1
FJ662826.1	551205	528.9	919.4	1371.0	545.2	203.7	508.0
EU460892.1	302391	2003.0	3016.7	2878.6	1937.3	241.6	606.2
EU467908.1	292450	500.8	1061.2	2526.1	549.6	902.3	508.8
GQ068224.1	458497	226.6	1191.4	908.2	202.6	217.4	505.9
EU458149.1	289551	4494.4	4867.6	2840.8	5081.0	6218.7	7314.7
GQ076119.1	372054	2402.7	2959.5	2475.1	2257.7	1904.0	1995.1
EU458116.1	296356	3941.2	4435.4	4016.6	4178.1	10836.4	7799.0
GQ013235.1	496431	8027.1	7291.6	3522.5	8054.0	6723.3	4018.7
GQ073338.1	418360	2010.4	1745.0	1341.7	1361.4	505.2	951.7
GQ057439.1	371684	12611.3	10030.7	9908.5	7828.9	8123.3	9722.3
NC_003485.1	129068	59.1	183.4	85.0	90.1	90.2	173.1
EU535969.1	281999	1332.1	962.0	374.7	2069.6	940.1	1729.5
FJ676264.1	525392	5689.0	5756.1	8078.4	3811.6	5180.4	6061.5
EF509615.1	225348	3979.6	4964.7	2062.5	3247.4	2695.9	4809.7
GQ101509.1	465878	1571.5	1756.4	1978.5	1558.9	1005.7	1444.8
EU467763.1	294288	2786.2	3256.2	3597.2	2894.9	1877.6	3883.1
EU461902.1	295919	13397.7	11460.4	7059.2	8828.2	11429.7	15025.3
EU156782.1	350039	510.3	1196.8	923.7	304.1	299.6	485.1
FJ678537.1	526366	8671.1	7383.9	4586.2	9325.9	11699.5	12820.8
EU461866.1	298094	1724.5	2104.1	4403.8	1397.6	486.8	1503.9
EU458187.1	302971	1597.2	2130.9	3031.8	925.9	410.5	911.5
GQ074067.1	404983	750.8	1306.2	300.8	144.9	178.4	101.5
EU458210.1	292277	1897.4	1508.0	1802.7	603.3	928.4	1337.4
EU458286.1	295358	3937.3	4635.1	5069.2	4392.4	4882.4	6085.6
GQ028155.1	406593	5165.4	5628.1	4738.7	3637.2	5132.6	4412.8
GQ018843.1	490825	62.9	759.5	642.2	136.1	95.3	153.5
EU458252.1	296907	8206.6	6890.5	5592.6	6508.0	6967.7	10584.1
GQ018860.1	490807	11984.5	11185.3	5894.0	9747.6	10253.4	8863.3
EU458292.1	302364	58.4	288.5	626.1	110.8	369.6	337.5
GQ010556.1	499109	9822.4	10059.4	5833.3	9149.6	10995.9	9769.6
FJ679324.1	509856	1552.5	1968.9	3521.7	1270.9	904.9	1543.2
EU774903.1	319192	174.4	398.5	2021.0	181.1	144.3	261.3
GQ000869.1	469434	1178.0	1326.1	1406.1	1353.2	1737.5	1731.9
EU461949.1	297276	1759.3	2627.0	4274.5	1387.7	2202.7	2560.4
EU467748.1	289224	547.4	1260.2	2839.0	591.7	979.6	643.4
AM157421.1	141768	373.7	1347.4	557.3	408.3	185.0	1470.7
GQ058009.1	449776	830.2	1087.9	1328.0	1142.1	1460.6	1685.4
EU458304.1	297241	9184.2	9797.8	5799.8	4536.3	823.9	3658.4
FJ894952.1	555959	10083.3	9182.6	5108.5	7891.9	5960.2	6726.0
EU471452.1	295151	3457.2	3528.4	4876.4	1838.1	3953.6	2862.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44723
s__unclassified	44727
s__unclassified	44728
s__unclassified	44731
s__unclassified	44735
s__unclassified	44737
s__unclassified	44747
s__unclassified	44748
s__unclassified	44750
s__unclassified	44751
s__unclassified	44753
s__unclassified	44754
s__unclassified	44757
s__unclassified	44759
s__unclassified	44763
s__unclassified	44765
s__unclassified	44767
s__unclassified	44769
s__unclassified	44770
s__unclassified	44772
s__unclassified	44774
s__unclassified	44776
s__unclassified	44778
s__unclassified	44780
s__unclassified	44783
s__unclassified	44785
s__unclassified	44786
s__unclassified	44792
s__unclassified	44793
s__unclassified	44795
s__unclassified	44806
s__unclassified	44808
s__unclassified	44813
s__unclassified	44816
s__unclassified	44817
s__unclassified	44818
s__unclassified	44820
s__unclassified	44823
s__unclassified	44825
s__unclassified	44826
s__unclassified	44829

EU458127.1 gg_id:295594 North American black bear feces clone BB2_b09
U87830.1 gg_id:15387 aortic heart valve patient with endocarditis clone v6
AB259061.1 gg_id:192739 Streptococcus dentirousetti str. NUM 1303
EU473378.1 gg_id:303070 giant panda feces clone GP_1aaa03e07
EU660341.1 gg_id:293142 Streptococcus pyogenes str. Sp30
GQ060712.1 gg_id:431280 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e07
EU467898.1 gg_id:291675 North American black bear feces clone BB1_e07_1
EU460848.1 gg_id:288152 short-beaked echidna feces clone ECH_aai39c04
AB002510.1 gg_id:15413 Streptococcus dysgalactiae V24
GU045379.1 gg_id:578793 Streptococcus oralis str. KCOM 1401
EU458169.1 gg_id:288654 North American black bear feces clone BB2_h04
EU774892.1 gg_id:353416 Short-beaked Echidna feces clone ECH_aai38e06
AF184974.1 gg_id:42170 Streptococcus australis str. AI1; ATCC 700641
GQ074435.1 gg_id:377602 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162h
EU534731.1 gg_id:286668 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18
GQ073325.1 gg_id:409438 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207g01c1
GQ032481.1 gg_id:407929 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ156288.1 gg_id:582512 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ043370.1 gg_id:446121 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96
EU467891.1 gg_id:290897 North American black bear feces clone BB1_d09_2
GQ010627.1 gg_id:499038 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU475847.1 gg_id:298266 white-faced saki feces clone Saki_g03
GQ088816.1 gg_id:422570 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU458230.1 gg_id:294980 North American black bear feces clone BB2_b08_2
GQ073229.1 gg_id:452542 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e10c1
AF335573.1 gg_id:33357 Streptococcus iniae str. Dan 1
EU461941.1 gg_id:297117 white-faced saki feces clone Saki_aaj64b06
GQ092789.1 gg_id:374841 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU461957.1 gg_id:303168 white-faced saki feces clone Saki_aaj64d06
GQ003166.1 gg_id:506496 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu19
EU470337.1 gg_id:292055 Grevy's zebra feces clone GZ_aaa03c12
DQ148957.1 gg_id:139480 Streptococcus bovis SbH8.11
GQ156147.1 gg_id:580333 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ096744.1 gg_id:446169 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU458211.1 gg_id:300882 North American black bear feces clone BB2_g10_1
EU467816.1 gg_id:298015 North American black bear feces clone BB1_f06_1
GQ069073.1 gg_id:404627 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU156767.1 gg_id:325913 Streptococcus oligofermentans str. CCUG 48365
GQ076979.1 gg_id:425421 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115
EU156773.1 gg_id:342992 Streptococcus pneumoniae str. ATCC 49619
GQ101197.1 gg_id:419981 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49

EU458127.1	295594	10667.6	13548.5	5940.8	8959.5	16353.9	14887.0
U87830.1	15387	4381.1	4412.3	4090.0	4892.8	11082.2	8127.9
AB259061.1	192739	575.3	834.6	2741.2	945.8	1631.1	2101.9
EU473378.1	303070	2833.9	2348.9	2959.5	612.4	124.0	381.4
EU660341.1	293142	7835.6	7236.6	4228.7	6513.0	6726.3	6036.4
GQ060712.1	431280	1972.9	2607.3	1123.9	697.3	617.2	760.3
EU467898.1	291675	10268.4	8418.9	7564.7	8163.2	9036.4	10815.3
EU460848.1	288152	1579.3	2178.8	3430.9	656.6	2634.5	1898.2
AB002510.1	15413	72.1	260.8	353.9	75.7	170.6	41.9
GU045379.1	578793	1522.3	1736.3	1830.0	1562.8	958.1	3364.5
EU458169.1	288654	3017.2	1702.4	3420.5	5900.2	235.7	791.7
EU774892.1	353416	174.7	414.1	1550.9	160.3	120.1	192.6
AF184974.1	42170	1138.6	1509.6	930.8	1460.8	339.1	630.5
GQ074435.1	377602	1749.8	2869.1	2066.3	1915.7	1706.1	2093.5
EU534731.1	286668	1128.9	1376.1	1324.3	1536.9	886.7	770.7
GQ073325.1	409438	2668.8	1549.8	1645.9	2852.5	1393.3	2675.0
GQ032481.1	407929	2290.1	2136.3	2283.4	1014.3	473.8	955.6
GQ156288.1	582512	42.4	158.4	76.7	72.8	65.4	94.5
GQ043370.1	446121	1836.9	1745.4	1293.1	505.8	339.6	489.9
EU467891.1	290897	6523.0	5916.4	7957.6	5114.0	5967.8	8306.0
GQ010627.1	499038	542.2	1191.5	1740.9	590.8	214.5	782.6
EU475847.1	298266	593.3	1003.3	2091.5	619.2	250.8	548.0
GQ088816.1	422570	54.2	891.1	145.0	90.7	82.7	166.3
EU458230.1	294980	17692.1	17223.3	10313.0	14348.1	17008.6	16968.5
GQ073229.1	452542	80.5	239.1	73.7	130.5	70.9	67.8
AF335573.1	33357	76.3	125.0	883.3	89.6	72.7	543.7
EU461941.1	297117	1732.2	1051.7	1463.5	3382.8	222.2	544.0
GQ092789.1	374841	4281.3	4675.8	3765.4	3014.8	3078.8	4689.8
EU461957.1	303168	293.9	586.5	1670.2	375.3	150.5	586.3
GQ003166.1	506496	8799.8	10038.2	5972.5	9448.7	11015.7	9356.3
EU470337.1	292055	1924.7	1424.8	2028.3	626.7	940.4	1244.9
DQ148957.1	139480	89.9	271.6	902.2	122.7	148.5	218.9
GQ156147.1	580333	1145.9	3272.1	3135.7	1930.6	2371.2	3134.7
GQ096744.1	446169	127.2	1156.2	566.5	161.7	236.8	209.7
EU458211.1	300882	10097.0	6991.5	6190.2	9444.6	10737.0	13719.0
EU467816.1	298015	10472.1	7657.3	6985.9	9122.0	11429.9	13525.5
GQ069073.1	404627	87.0	936.2	342.8	119.2	114.6	222.9
EU156767.1	325913	2238.1	2441.7	2352.4	999.3	1414.5	1448.5
GQ076979.1	425421	4185.5	3593.0	2267.5	4806.4	2545.1	5185.5
EU156773.1	342992	1071.1	2109.7	6251.7	1021.8	4404.1	3193.4
GQ101197.1	419981	520.1	1332.3	900.8	316.6	309.6	521.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44832
s__unclassified	44834
s__unclassified	44835
s__unclassified	44837
s__unclassified	44839
s__unclassified	44840
s__unclassified	44841
s__unclassified	44850
s__unclassified	44851
s__unclassified	44852
s__unclassified	44853
s__unclassified	44858
s__unclassified	44859
s__unclassified	44860
s__unclassified	44862
s__unclassified	44864
s__unclassified	44867
s__unclassified	44869
s__unclassified	44871
s__unclassified	44875
s__unclassified	44876
s__unclassified	44877
s__unclassified	44888
s__unclassified	44892
s__unclassified	44893
s__unclassified	44895
s__unclassified	44896
s__unclassified	44899
s__unclassified	44901
s__unclassified	44904
s__unclassified	44905
s__unclassified	44907
s__unclassified	44910
s__unclassified	44911
s__unclassified	44912
s__unclassified	44915
s__unclassified	44916
s__unclassified	44917
s__unclassified	44920
s__unclassified	44927
s__unclassified	44932

EU460730.1 gg_id:295580 short-beaked echidna feces clone ECH_aai37b08
EU458283.1 gg_id:293073 North American black bear feces clone BB2_d03_1
EU465122.1 gg_id:300671 African elephant feces clone AFYEL_aaj68d04
GQ101296.1 gg_id:419123 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493c
EU467176.1 gg_id:301477 white-faced saki feces clone Saki_a08
GQ071872.1 gg_id:459330 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw189d0
EU458234.1 gg_id:292953 North American black bear feces clone BB2_c04_1
EU458200.1 gg_id:289631 North American black bear feces clone BB2_f03_1
FJ975977.1 gg_id:571637 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
GQ077262.1 gg_id:406562 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115
EU458131.1 gg_id:298527 North American black bear feces clone BB2_c03
FJ662835.1 gg_id:565491 Streptococcus pyogenes str. Sp19
GQ072817.1 gg_id:454091 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201e08
GQ060504.1 gg_id:466552 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02e10
EU467877.1 gg_id:297939 North American black bear feces clone BB1_b06_2
EU458146.1 gg_id:300972 North American black bear feces clone BB2_e03
GQ073546.1 gg_id:459692 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo
FJ662836.1 gg_id:557233 Streptococcus pyogenes str. Sp21
EU458242.1 gg_id:298551 North American black bear feces clone BB2_f01_2
EU772612.1 gg_id:329630 North American Black Bear feces clone BB1_g02_1
EU160562.1 gg_id:332405 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc
FJ672424.1 gg_id:519177 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
CU917914.1 gg_id:568929 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU458167.1 gg_id:291884 North American black bear feces clone BB2_g11
EU467806.1 gg_id:291430 North American black bear feces clone BB1_d10_1
DQ824669.1 gg_id:193137 human fecal clone RL185_aaj71d09
GQ113281.1 gg_id:456797 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo
EU475811.1 gg_id:295833 white-faced saki feces clone Saki_a01_1
X89237.1 gg_id:135882 Streptococcus pyogenes str. serotype M49 CS101
EU467843.1 gg_id:297229 North American black bear feces clone BB1_c04_1
EU473927.1 gg_id:295065 giant panda feces clone GP_2aaa01a01
EU467830.1 gg_id:299221 North American black bear feces clone BB1_h10
DQ232533.1 gg_id:179010 Streptococcus mitis str. CIP 104996
GQ091667.1 gg_id:417572 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ057669.1 gg_id:375780 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AF003933.1 gg_id:15555 Streptococcus parasanguinis str. ATCC 15912
FJ673895.1 gg_id:518670 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY691525.1 gg_id:102441 Streptococcus mutans str. ChDC YM2
FJ558016.1 gg_id:517987 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
EU467856.1 gg_id:298009 North American black bear feces clone BB1_e05
EU458177.1 gg_id:296799 North American black bear feces clone BB2_a07

EU460730.1	295580	94.2	231.8	1295.0	121.2	116.4	143.6
EU458283.1	293073	5586.2	5973.3	4552.6	5882.4	7044.8	9017.2
EU465122.1	300671	15482.2	12622.3	14624.5	12922.4	8945.0	12835.9
GQ101296.1	419123	1752.4	1722.0	1371.6	658.2	359.1	623.5
EU467176.1	301477	13533.6	14190.7	11577.2	13496.8	15306.8	16048.5
GQ071872.1	459330	1186.0	827.1	507.7	717.3	185.9	211.5
EU458234.1	292953	1585.0	2111.5	4007.6	1187.4	485.4	1552.4
EU458200.1	289631	685.9	1473.8	2449.3	688.4	357.4	822.2
FJ975977.1	571637	87.6	308.9	150.1	112.2	65.6	47.8
GQ077262.1	406562	1705.2	1543.6	2411.7	2854.8	220.0	549.2
EU458131.1	298527	13332.3	11651.1	10100.2	11461.6	14117.1	15033.3
FJ662835.1	565491	144.9	216.3	417.6	119.8	162.7	534.3
GQ072817.1	454091	8355.0	11444.4	6664.9	8611.8	15417.2	12113.8
GQ060504.1	466552	3505.0	3022.0	2664.8	1821.4	1732.5	1969.2
EU467877.1	297939	1704.5	987.6	1769.7	3716.5	201.7	420.1
EU458146.1	300972	20153.5	19503.1	16122.0	16422.1	19493.6	21238.5
GQ073546.1	459692	2120.6	2403.3	957.4	1895.1	2306.8	2596.8
FJ662836.1	557233	4818.3	4505.8	4143.0	3585.8	4051.2	4502.5
EU458242.1	298551	2938.5	3464.9	5644.4	2718.8	2092.7	3069.4
EU772612.1	329630	976.8	2012.2	2986.9	956.5	494.2	1080.4
EU160562.1	332405	647.9	1782.0	507.5	845.0	663.0	1140.5
FJ672424.1	519177	4385.8	2763.0	3455.1	5381.1	2505.1	4943.0
CU917914.1	568929	577.7	2121.8	974.9	627.6	568.9	993.3
EU458167.1	291884	9188.5	10201.2	9879.0	11286.9	14146.6	13533.2
EU467806.1	291430	1038.1	2011.4	3186.0	972.5	508.0	1166.6
DQ824669.1	193137	14414.8	11704.9	10574.7	12424.8	17727.8	18913.8
GQ113281.1	456797	148.0	1206.2	874.6	153.2	140.5	170.9
EU475811.1	295833	9277.7	10038.6	8064.4	7818.4	8950.2	9547.5
X89237.1	135882	650.2	1369.7	1085.0	339.2	160.7	323.2
EU467843.1	297229	1350.1	2064.4	2938.8	819.8	8504.1	3781.7
EU473927.1	295065	640.7	1080.2	1415.8	597.0	288.7	566.9
EU467830.1	299221	2390.9	3158.5	1067.5	935.9	1890.6	2018.9
DQ232533.1	179010	532.7	1494.4	501.7	355.0	169.9	1057.6
GQ091667.1	417572	1470.7	1617.4	1751.0	1460.8	942.0	1335.4
GQ057669.1	375780	2665.3	2130.3	1613.0	1343.4	549.4	1210.7
AF003933.1	15555	55.1	212.7	161.5	79.6	71.5	287.5
FJ673895.1	518670	9800.0	7462.5	8553.4	6704.7	11001.5	9203.9
AY691525.1	102441	11443.2	9822.2	12566.0	8222.0	11656.1	10084.4
FJ558016.1	517987	3823.4	3913.3	1201.1	4189.7	6740.2	5029.8
EU467856.1	298009	14060.1	13049.3	15927.5	9578.7	12103.1	14128.4
EU458177.1	296799	8716.8	8151.0	8296.5	6779.7	10258.6	9075.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	44937
s__unclassified	44939
s__unclassified	44942
s__unclassified	44943
s__unclassified	44944
s__unclassified	44946
s__unclassified	44950
s__unclassified	44955
s__unclassified	44956
s__unclassified	44957
s__unclassified	44958
s__unclassified	44959
s__unclassified	44961
s__unclassified	44964
s__unclassified	44969
s__unclassified	44970
s__unclassified	44971
s__unclassified	44972
s__unclassified	44976
s__unclassified	44979
s__unclassified	44985
s__unclassified	44986
s__unclassified	44990
s__unclassified	44992
s__unclassified	44993
s__unclassified	44996
s__unclassified	44999
s__unclassified	45001
s__unclassified	45005
s__unclassified	45006
s__unclassified	45007
s__unclassified	45012
s__unclassified	45015
s__unclassified	45016
s__unclassified	45024
s__unclassified	45025
s__unclassified	45026
s__unclassified	45028
s__unclassified	45032
s__unclassified	45035
s__unclassified	45038

EU467865.1 gg_id:293109 North American black bear feces clone BB1_g07_1
EU458255.1 gg_id:292733 North American black bear feces clone BB2_g11_2
AY500370.1 gg_id:104134 Streptococcus bovis Sb5
AB264619.1 gg_id:164145 Streptococcus sp. bSSV21
EU461840.1 gg_id:294868 white-faced saki feces clone Saki_aaj62a02
AY485603.1 gg_id:101921 Streptococcus infantis str. ATCC 700779
EU461967.1 gg_id:297953 white-faced saki feces clone Saki_aaj64e08
EU467779.1 gg_id:298188 North American black bear feces clone BB1_g08
AY324611.1 gg_id:90414 Streptococcus bovis str. MPR2
GQ073778.1 gg_id:391010 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ100994.1 gg_id:451940 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48
GQ011458.1 gg_id:498208 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792b1:
AJ634751.1 gg_id:111084 Streptococcus marimammalium str. M54/01/1
EU458212.1 gg_id:291889 North American black bear feces clone BB2_h01
GQ018924.1 gg_id:490744 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d
GQ023586.1 gg_id:486084 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320c12
FJ677566.1 gg_id:530906 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AM183037.1 gg_id:253441 and its spatial composts compost clone SMB52
GQ072181.1 gg_id:391890 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193b1(
EU467826.1 gg_id:301858 North American black bear feces clone BB1_h03_1
NR_027214.1 gg_id:535803 Streptococcus pseudopneumoniae str. 108; ATCC BAA-960
EU458243.1 gg_id:296265 North American black bear feces clone BB2_f02_2
GQ155808.1 gg_id:588046 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ074087.1 gg_id:401778 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ673496.1 gg_id:527788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ155734.1 gg_id:592904 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU467871.1 gg_id:303225 North American black bear feces clone BB1_h05_2
FJ678041.1 gg_id:518979 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GU045388.1 gg_id:541157 Streptococcus mitis str. KCOM 1350
AY324610.1 gg_id:89376 Streptococcus bovis str. MPR1
EU458295.1 gg_id:295303 North American black bear feces clone BB2_e07_2
EU772625.1 gg_id:349233 North American Black Bear feces clone BB1_a08_1
GQ051010.1 gg_id:373888 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ018662.1 gg_id:491006 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu141e05
FJ673875.1 gg_id:528552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ027253.1 gg_id:388019 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU772603.1 gg_id:349682 North American Black Bear feces clone BB2_c10
EU772567.1 gg_id:350483 North American Black Bear feces clone BB2_d03
EU473235.1 gg_id:296749 giant panda feces clone GP_1aaa01e12
GQ019637.1 gg_id:490031 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu205c03
EU458213.1 gg_id:302190 North American black bear feces clone BB2_h05_1

EU467865.1	293109	661.3	1342.0	2805.9	644.6	328.8	796.0
EU458255.1	292733	4692.9	4622.6	7725.4	4091.1	3247.3	4998.2
AY500370.1	104134	6068.9	5822.5	5905.1	5770.2	4149.2	9137.5
AB264619.1	164145	8095.7	6859.3	2187.9	6662.6	3522.6	6882.9
EU461840.1	294868	2471.3	1158.8	4576.5	4580.4	194.8	717.8
AY485603.1	101921	88.1	755.9	295.1	140.3	96.2	1909.5
EU461967.1	297953	2570.4	3872.5	1635.3	1533.8	3377.3	2358.5
EU467779.1	298188	2810.6	2292.2	4359.7	3226.0	5537.0	5433.2
AY324611.1	90414	3929.5	4843.5	2361.5	3418.0	8809.6	9340.8
GQ073778.1	391010	766.7	1133.1	966.1	549.0	514.4	1303.8
GQ100994.1	451940	862.7	1067.7	460.4	117.3	127.9	150.3
GQ011458.1	498208	99.4	294.3	97.0	129.7	78.0	57.3
AJ634751.1	111084	1543.3	1250.1	1710.6	1110.0	590.5	1106.5
EU458212.1	291889	693.6	1573.9	2698.5	487.8	993.1	1308.9
GQ018924.1	490744	3228.1	2903.3	2757.3	1899.0	675.6	1582.0
GQ023586.1	486084	938.4	534.1	1015.7	1024.7	885.9	723.4
FJ677566.1	530906	1692.8	2705.7	565.5	451.2	357.7	644.5
AM183037.1	253441	134.1	205.3	275.4	229.5	145.1	105.2
GQ072181.1	391890	2668.9	3058.5	2913.7	2251.9	828.9	2151.3
EU467826.1	301858	686.4	1698.1	2449.4	685.9	356.0	822.4
NR_027214.1	535803	2419.2	3091.5	2552.9	1575.8	525.0	3375.2
EU458243.1	296265	6252.4	8620.2	6875.6	5769.1	9416.3	9269.0
GQ155808.1	588046	1754.4	2680.6	5345.3	1766.3	4208.7	3864.7
GQ074087.1	401778	5605.7	7951.1	5330.2	6249.9	8959.6	9068.1
FJ673496.1	527788	15053.1	20857.0	10005.0	13057.1	15485.3	18962.6
GQ155734.1	592904	335.7	1349.3	865.7	175.5	358.6	538.1
EU467871.1	303225	1513.2	2003.6	3470.1	1194.5	342.4	1157.4
FJ678041.1	518979	252.7	547.7	550.4	145.3	177.4	102.3
GU045388.1	541157	2408.8	3248.7	2718.2	1557.4	552.5	3290.6
AY324610.1	89376	5664.6	4997.3	5133.3	4209.3	3113.6	8806.1
EU458295.1	295303	6700.8	6289.8	3040.1	6607.6	10911.4	9223.2
EU772625.1	349233	8321.1	10600.8	5246.9	9467.5	10465.3	9332.2
GQ051010.1	373888	776.0	1559.9	1060.5	489.4	483.8	750.0
GQ018662.1	491006	860.3	1464.0	905.8	182.3	182.5	300.5
FJ673875.1	528552	276.2	545.9	1217.3	340.4	166.0	299.4
GQ027253.1	388019	4808.5	4457.3	3525.3	4301.6	7298.0	5564.6
EU772603.1	349682	1073.0	1259.7	2750.5	1371.9	285.0	672.6
EU772567.1	350483	733.7	1626.8	2911.2	699.0	347.7	826.9
EU473235.1	296749	7353.7	7444.2	5470.5	5789.3	5474.8	5830.9
GQ019637.1	490031	937.3	502.9	970.0	1019.6	886.5	733.6
EU458213.1	302190	1049.6	1360.1	1518.4	425.2	263.1	560.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45039
s__unclassified	45045
s__unclassified	45047
s__unclassified	45049
s__unclassified	45050
s__unclassified	45053
s__unclassified	45055
s__unclassified	45060
s__unclassified	45062
s__unclassified	45064
s__unclassified	45065
s__unclassified	45069
s__unclassified	45080
s__unclassified	45081
s__unclassified	45082
s__unclassified	45090
s__unclassified	45092
s__unclassified	45094
s__unclassified	45095
s__unclassified	45097
s__unclassified	45099
s__unclassified	45100
s__unclassified	45102
s__unclassified	45105
s__unclassified	45106
s__unclassified	45107
s__unclassified	45110
s__unclassified	45111
s__unclassified	45115
s__unclassified	45116
s__unclassified	45118
s__unclassified	45122
s__unclassified	45123
s__unclassified	45127
s__unclassified	45129
s__unclassified	45130
s__unclassified	45131
s__unclassified	45134
s__unclassified	45135
s__unclassified	45137
s__unclassified	45140

GQ088004.1 gg_id:430608 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GU470899.1 gg_id:558469 Streptococcus cristatus str. F0329
GQ032924.1 gg_id:416414 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU458218.1 gg_id:299212 North American black bear feces clone BB2_a03_2
GQ027310.1 gg_id:434159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ006598.1 gg_id:503066 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85d08c
GQ010315.1 gg_id:499348 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw736b1
GQ104022.1 gg_id:456295 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562a0
EU458216.1 gg_id:293266 North American black bear feces clone BB2_h10
EU458302.1 gg_id:299685 North American black bear feces clone BB2_f07_1
EU475848.1 gg_id:293772 white-faced saki feces clone Saki_aaj62b04
EU460835.1 gg_id:288716 short-beaked echidna feces clone ECH_aai39a03
DQ294302.1 gg_id:160607 Streptococcus equi Hyena M149
AF084832.1 gg_id:15483 Streptococcus sp. str. KN1
GQ091850.1 gg_id:416768 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AM157428.1 gg_id:142502 Streptococcus mitis mother C4
FJ678391.1 gg_id:513075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ155781.1 gg_id:550710 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU473460.1 gg_id:297804 Somali wild ass feces clone WA_aaa03b08
GQ030486.1 gg_id:407093 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878h11
EU473991.1 gg_id:299801 giant panda feces clone GP_2aaa04a03
GQ074320.1 gg_id:386466 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161e
FJ367135.1 gg_id:361983 feces adult twins and mothers; TS28 clone TS28_a03h09
GQ073355.1 gg_id:434919 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a09c1
EU467888.1 gg_id:294779 North American black bear feces clone BB1_c11_2
EU458114.1 gg_id:302527 North American black bear feces clone BB2_a02
FJ679191.1 gg_id:519599 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ021841.1 gg_id:487827 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB469560.1 gg_id:359502 Streptococcus sp. str. NUM 1529
EU474107.1 gg_id:290522 giant panda feces clone GP_2aaa03a05
GQ102163.1 gg_id:457320 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561g1
EU467809.1 gg_id:288523 North American black bear feces clone BB1_e06_1
EU474171.1 gg_id:289475 western lowland gorilla feces clone GORSD_2aaa04h03
EU473228.1 gg_id:294997 giant panda feces clone GP_1aaa04d08
AY442818.1 gg_id:104405 Streptococcus sp. YE54
GU045389.1 gg_id:578175 Streptococcus mitis str. KCOM 1379
GU045392.1 gg_id:512763 Streptococcus mitis str. KCOM 1286
EU458209.1 gg_id:302903 North American black bear feces clone BB2_g06_1
EU458287.1 gg_id:296176 North American black bear feces clone BB2_d09_2
FJ675732.1 gg_id:509993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ073629.1 gg_id:413473 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc

GQ088004.1	430608	9536.1	9578.4	6340.4	7281.2	8892.7	7691.9
GU470899.1	558469	40.1	413.9	92.8	60.4	73.0	152.9
GQ032924.1	416414	10486.5	10749.5	6138.4	6938.3	9359.1	11101.5
EU458218.1	299212	9181.2	10321.7	2567.6	5800.9	7179.9	7132.5
GQ027310.1	434159	2242.6	3669.8	1710.8	883.9	321.2	1277.6
GQ006598.1	503066	39.1	601.2	64.0	64.9	75.0	35.8
GQ010315.1	499348	3746.2	5113.0	4507.1	3125.7	975.1	2105.7
GQ104022.1	456295	1276.2	3262.3	2019.0	1049.6	940.4	2256.8
EU458216.1	293266	3605.8	4562.8	2297.9	2226.2	4801.3	4039.6
EU458302.1	299685	5769.6	6600.1	6849.1	4352.7	5336.5	5816.3
EU475848.1	293772	1747.2	2278.2	3757.8	1618.9	682.7	1882.3
EU460835.1	288716	9274.0	8972.1	4998.7	6344.8	8353.0	8154.9
DQ294302.1	160607	2288.2	2347.9	2125.1	1452.2	2620.2	1955.2
AF084832.1	15483	761.5	1183.5	496.1	390.3	775.5	594.3
GQ091850.1	416768	2449.3	3872.6	8243.4	2929.7	7545.3	4258.3
AM157428.1	142502	930.9	1885.2	1240.8	1379.6	1350.8	2557.9
FJ678391.1	513075	217.7	719.2	1260.1	203.7	223.6	439.7
GQ155781.1	550710	145.4	323.3	135.4	142.6	144.1	129.8
EU473460.1	297804	5752.7	3217.8	6335.1	6275.2	3532.0	4432.1
GQ030486.1	407093	1882.9	1300.5	946.7	1591.0	844.3	1516.7
EU473991.1	299801	1267.2	966.5	717.6	350.2	200.7	354.2
GQ074320.1	386466	1271.8	2197.2	2694.2	1589.6	776.1	1793.4
FJ367135.1	361983	430.5	662.4	585.9	261.4	256.6	344.9
GQ073355.1	434919	1714.3	1666.8	1782.4	851.8	251.9	603.4
EU467888.1	294779	10532.9	8769.0	9748.9	10686.7	10243.5	13490.0
EU458114.1	302527	11817.4	10879.0	7218.6	12264.7	16356.1	16138.6
FJ679191.1	519599	9313.0	8563.9	10988.5	9750.0	6882.2	7906.7
GQ021841.1	487827	452.6	1213.2	769.3	296.6	292.9	483.8
AB469560.1	359502	2066.3	1581.7	1721.1	929.1	2072.1	1932.2
EU474107.1	290522	1140.0	1270.6	1222.4	563.1	190.9	447.5
GQ102163.1	457320	1024.5	1543.4	678.7	1121.4	458.7	640.8
EU467809.1	288523	1571.0	1170.3	2989.8	3103.0	143.1	511.0
EU474171.1	289475	1748.8	2210.9	1856.4	2671.0	2221.8	2820.2
EU473228.1	294997	2381.8	1952.9	1694.6	1234.5	612.7	1074.6
AY442818.1	104405	105.8	545.1	518.3	137.9	74.1	118.5
GU045389.1	578175	466.8	1474.2	268.8	313.7	150.3	919.8
GU045392.1	512763	435.4	1318.6	698.5	308.6	365.4	388.1
EU458209.1	302903	1280.6	1912.0	2674.4	1242.5	531.8	1383.2
EU458287.1	296176	6172.7	5846.1	12150.1	4566.6	11361.1	12135.8
FJ675732.1	509993	6731.4	7541.2	7552.3	7812.0	9964.7	10421.2
GQ073629.1	413473	2665.7	1851.6	2745.0	5887.1	239.1	772.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45143
s__unclassified	45144
s__unclassified	45145
s__unclassified	45147
s__unclassified	45148
s__unclassified	45157
s__unclassified	45158
s__unclassified	45160
s__unclassified	45161
s__unclassified	45163
s__unclassified	45164
s__unclassified	45167
s__unclassified	45174
s__unclassified	45176
s__unclassified	45179
s__unclassified	45182
s__unclassified	45183
s__unclassified	45185
s__unclassified	45188
s__unclassified	45191
s__unclassified	45194
s__unclassified	45197
s__unclassified	45198
s__unclassified	45202
s__unclassified	45205
s__unclassified	45210
s__unclassified	45215
s__unclassified	45219
s__unclassified	45221
s__unclassified	45227
s__unclassified	45228
s__unclassified	45230
s__unclassified	45233
s__unclassified	45235
s__unclassified	45237
s__unclassified	45238
s__unclassified	45240
s__unclassified	45241
s__unclassified	45246
s__unclassified	45249
s__unclassified	45255

GQ111651.1 gg_id:461851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ156134.1 gg_id:581022 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU774840.1 gg_id:319809 Short-beaked Echidna feces clone ECH_aai38g08
EU772577.1 gg_id:308943 North American Black Bear feces clone BB2_g09
EU461937.1 gg_id:289435 white-faced saki feces clone Saki_aaj64a10
EU458220.1 gg_id:291672 North American black bear feces clone BB2_a06_2
EU156779.1 gg_id:334078 Streptococcus pneumoniae str. CCRI-14734
EU461935.1 gg_id:301946 white-faced saki feces clone Saki_aaj64a07
EU289129.1 gg_id:245916 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
FJ893225.1 gg_id:571456 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p
FJ676607.1 gg_id:526041 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ079517.1 gg_id:393671 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU467801.1 gg_id:297452 North American black bear feces clone BB1_d02_1
EU458173.1 gg_id:301800 North American black bear feces clone BB2_h12
AY281085.1 gg_id:90432 Streptococcus sanguinis str. ATCC 29667
EU467151.1 gg_id:298042 white-faced saki feces clone Saki_a06
EU461955.1 gg_id:301020 white-faced saki feces clone Saki_aaj64c10
FJ678419.1 gg_id:516100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ032429.1 gg_id:384627 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542h04
FJ677709.1 gg_id:519382 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ420199.1 gg_id:27408 Streptococcus macacae str. NCTC11558
EU775424.1 gg_id:336695 Western lowland gorilla feces clone GORSD_2aaa04d03
EU467754.1 gg_id:299092 North American black bear feces clone BB1_d05
GQ067186.1 gg_id:394313 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AB501126.1 gg_id:515853 Streptococcus ursoris str. NUM 1615
GQ019375.1 gg_id:490293 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189c
AY273147.1 gg_id:84371 Streptococcus pyogenes
EU467739.1 gg_id:287916 North American black bear feces clone BB1_a08
GQ023335.1 gg_id:486334 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317a09
GQ076817.1 gg_id:395887 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
GQ073289.1 gg_id:421921 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c10c1
GQ018889.1 gg_id:490779 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192a
AM420093.1 gg_id:240905 Noma subgingival plaque clone 302F04(oral)
GQ154900.1 gg_id:557859 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AY324612.1 gg_id:88822 Streptococcus bovis str. MPR4
GQ040793.1 gg_id:374127 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958g01c
DQ232536.1 gg_id:199646 Streptococcus oralis str. CIP 104985
EU461824.1 gg_id:297884 white-faced saki feces clone Saki_aaj61f09
GQ155776.1 gg_id:585008 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EF364097.1 gg_id:226980 Streptococcus henryi str. 126
FJ682683.1 gg_id:514572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

GQ111651.1	461851	460.6	643.9	225.3	167.9	506.1	210.7
GQ156134.1	581022	1494.5	2039.4	1571.6	1622.7	774.4	1474.2
EU774840.1	319809	1672.5	3305.5	4319.7	1365.3	2487.2	2374.9
EU772577.1	308943	8301.4	6573.0	5986.9	7294.7	9870.5	10882.1
EU461937.1	289435	4019.6	4843.5	4780.3	5256.7	6320.6	5465.0
EU458220.1	291672	7918.8	8822.1	6993.8	5787.5	3836.8	5567.6
EU156779.1	334078	2207.6	3418.9	9250.9	1985.7	6787.2	5293.6
EU461935.1	301946	8286.9	7850.3	5478.2	6316.4	8333.0	7042.7
EU289129.1	245916	75.8	668.5	553.1	92.2	68.6	81.3
FJ893225.1	571456	2183.7	2087.2	3581.1	2549.0	5265.9	3588.9
FJ676607.1	526041	2655.0	3618.0	5590.9	1436.2	9595.2	5224.6
GQ079517.1	393671	1494.5	1506.8	902.6	532.6	313.2	555.1
EU467801.1	297452	504.9	1087.9	2757.3	550.5	907.6	470.4
EU458173.1	301800	8310.9	8778.6	8745.4	9130.8	12652.2	11593.6
AY281085.1	90432	33.1	299.4	193.0	70.4	51.4	33.0
EU467151.1	298042	14520.3	11180.5	12674.2	11294.3	10540.4	12496.6
EU461955.1	301020	310.8	1071.9	1531.3	179.4	306.5	645.5
FJ678419.1	516100	8027.5	7784.2	7539.3	6487.2	7587.9	9634.2
GQ032429.1	384627	1638.4	3846.9	7396.8	1724.3	6685.5	5062.4
FJ677709.1	519382	13961.3	12324.4	7298.5	10915.9	10082.9	11542.6
AJ420199.1	27408	200.8	418.1	311.4	152.3	122.4	590.9
EU775424.1	336695	6299.4	5641.2	7142.7	7094.7	6666.5	6971.9
EU467754.1	299092	22.2	109.1	413.8	75.4	71.8	44.6
GQ067186.1	394313	1985.8	3639.6	1551.4	911.3	7565.9	4386.9
AB501126.1	515853	369.4	492.8	844.1	430.0	370.8	389.4
GQ019375.1	490293	57.3	829.3	593.7	136.2	105.8	164.3
AY273147.1	84371	824.8	1563.0	1489.7	869.5	238.0	781.9
EU467739.1	287916	96.8	228.2	815.6	179.4	367.0	252.7
GQ023335.1	486334	218.9	1222.8	868.3	187.0	208.7	500.8
GQ076817.1	395887	1472.0	1754.6	831.2	834.0	1718.6	1097.1
GQ073289.1	421921	2524.6	2491.6	2632.2	1862.7	635.6	1317.0
GQ018889.1	490779	56.1	845.9	631.6	133.9	106.3	177.2
AM420093.1	240905	78.3	423.7	519.7	221.1	102.0	182.1
GQ154900.1	557859	479.3	1211.6	1475.9	503.9	236.6	373.4
AY324612.1	88822	743.5	866.5	650.9	489.2	452.9	5118.5
GQ040793.1	374127	38.4	951.0	138.9	88.7	71.3	81.9
DQ232536.1	199646	51.2	229.0	142.8	115.6	81.1	1643.5
EU461824.1	297884	7968.8	8934.1	6540.8	6576.8	8463.8	8217.9
GQ155776.1	585008	2154.2	2141.7	3273.4	3209.9	2093.1	4069.1
EF364097.1	226980	451.8	2357.4	389.9	465.3	1133.8	1533.9
FJ682683.1	514572	5104.3	4242.5	6393.6	4419.7	4366.7	5517.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45257
s__unclassified	45259
s__unclassified	45266
s__unclassified	45268
s__unclassified	45273
s__unclassified	45276
s__unclassified	45290
s__unclassified	45291
s__unclassified	45293
s__unclassified	45294
s__unclassified	45295
s__unclassified	45297
s__unclassified	45298
s__unclassified	45300
s__unclassified	45306
s__unclassified	45308
s__unclassified	45311
s__unclassified	45314
s__unclassified	45320
s__unclassified	45322
s__unclassified	45323
s__unclassified	45324
s__unclassified	45325
s__unclassified	45326
s__unclassified	45327
s__unclassified	45337
s__unclassified	45340
s__unclassified	45341
s__unclassified	45349
s__unclassified	45350
s__unclassified	45351
s__unclassified	45352
s__unclassified	45357
s__unclassified	45358
s__unclassified	45362
s__unclassified	45370
s__unclassified	45372
s__unclassified	45377
s__unclassified	45385
s__unclassified	45389
s__unclassified	45391

AJ617796.1 gg_id:100642 Streptococcus pneumoniae str. HER 1055 = Hu-o8
EU471428.1 gg_id:301608 spectacled bear feces clone SB_2aaa02d04
NC_006086.1 gg_id:128611 Streptococcus pyogenes str. MGAS10394
GQ115642.1 gg_id:373633 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688h07
GQ073111.1 gg_id:429959 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c02c1
EU458224.1 gg_id:293705 North American black bear feces clone BB2_a12_1
EU467860.1 gg_id:296641 North American black bear feces clone BB1_f04_1
EU467199.1 gg_id:299664 white-faced saki feces clone Saki_g09
EU779062.1 gg_id:311993 Prevost's squirrel feces clone SQ_aah79h08
AF396920.1 gg_id:39742 Streptococcus bovis str. B315
GQ115601.1 gg_id:400616 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688b11
FJ558308.1 gg_id:516966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
EU458307.1 gg_id:289803 North American black bear feces clone BB2_h08_3
AB002522.1 gg_id:15573 Streptococcus pneumoniae str. MAFF 911410
GQ156243.1 gg_id:561883 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ076853.1 gg_id:464954 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
GQ021817.1 gg_id:487851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU467781.1 gg_id:299667 North American black bear feces clone BB1_g10
GQ023571.1 gg_id:486098 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320b09
EU458196.1 gg_id:292217 North American black bear feces clone BB2_e11
DQ318881.1 gg_id:150451 -DGGE and sequencing piglet stomachs stomach clone SY6
GQ095863.1 gg_id:435368 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
EU467163.1 gg_id:301619 white-faced saki feces clone Saki_f02
GQ102584.1 gg_id:390165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw6
EU471514.1 gg_id:294127 spectacled bear feces clone SB_2aaa01d12
EU467165.1 gg_id:300974 white-faced saki feces clone Saki_f06
EU474059.1 gg_id:302396 giant panda feces clone GP_2aaa01c07
GQ074646.1 gg_id:464930 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164f
AM157442.1 gg_id:142694 Streptococcus pneumoniae mother V4
GQ021904.1 gg_id:487765 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU458151.1 gg_id:291631 North American black bear feces clone BB2_e12
GQ032381.1 gg_id:399032 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542a07
GQ156168.1 gg_id:590723 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU460825.1 gg_id:295866 short-beaked echidna feces clone ECH_aai38g10
AJ307888.1 gg_id:63461 Streptococcus gallinaceus str. CCUG 42692
AF009507.1 gg_id:15367 Streptococcus suis str. EA1172.91
EU772622.1 gg_id:314465 North American Black Bear feces clone BB2_c10_1
EU467845.1 gg_id:287347 North American black bear feces clone BB1_c06_2
EU775569.1 gg_id:324468 Giant Panda feces clone GP_2aaa01h07
GU045397.1 gg_id:586088 Streptococcus pneumoniae str. CCARM 4033
EU473918.1 gg_id:293540 giant panda feces clone GP_2aaa04e06

AJ617796.1	100642	874.9	1791.9	1128.3	641.3	549.8	1951.0
EU471428.1	301608	5210.4	5809.7	5721.1	2823.8	4305.0	4665.8
NC_006086.1	128611	32.5	124.0	89.6	73.4	54.2	398.6
GQ115642.1	373633	80.5	256.2	217.0	120.4	117.0	276.8
GQ073111.1	429959	219.9	529.1	617.3	173.8	69.0	352.1
EU458224.1	293705	5452.9	5528.1	2256.7	6018.8	7307.9	7869.7
EU467860.1	296641	336.3	683.4	573.0	400.7	159.0	210.8
EU467199.1	299664	688.0	1433.2	2843.4	706.5	363.7	869.7
EU779062.1	311993	1864.3	3345.4	2516.3	3080.9	1608.3	3506.6
AF396920.1	39742	748.2	966.2	1016.0	338.8	92.1	3079.1
GQ115601.1	400616	4412.1	2291.1	1838.5	3542.0	1290.5	2531.4
FJ558308.1	516966	1300.1	1195.1	2254.4	1073.3	810.1	1320.7
EU458307.1	289803	4029.9	4982.1	3139.1	2386.4	1709.8	2585.6
AB002522.1	15573	1630.6	2793.3	8389.9	1565.9	6820.5	4863.6
GQ156243.1	561883	6275.5	6560.5	2483.9	5534.3	8426.7	8828.5
GQ076853.1	464954	1814.7	1616.0	2052.7	973.7	276.2	628.3
GQ021817.1	487851	62.5	542.8	263.5	108.4	87.7	73.9
EU467781.1	299667	16346.6	17347.9	9654.4	14103.5	20216.8	17526.1
GQ023571.1	486098	3048.0	3063.5	2223.1	1838.9	1642.1	2166.7
EU458196.1	292217	135.2	403.6	643.8	203.3	506.2	572.7
DQ318881.1	150451	3199.5	3206.8	3692.9	1562.6	5037.0	3664.1
GQ095863.1	435368	57.1	928.3	490.0	116.6	108.7	176.2
EU467163.1	301619	902.5	1092.4	1729.1	1206.3	1930.4	1743.4
GQ102584.1	390165	503.6	1223.5	804.0	284.1	324.7	410.6
EU471514.1	294127	1124.0	1376.3	1895.6	441.2	276.7	565.3
EU467165.1	300974	10059.9	8318.0	5939.8	9534.5	14248.2	15150.9
EU474059.1	302396	2749.7	3673.4	5384.6	3701.8	13411.7	9745.4
GQ074646.1	464930	2824.0	3014.8	2660.5	2013.1	2202.1	1962.3
AM157442.1	142694	1205.9	2401.7	1157.0	1132.3	862.0	2265.6
GQ021904.1	487765	438.5	1470.6	559.3	315.6	405.7	384.0
EU458151.1	291631	3312.0	3672.8	5193.9	2811.4	3187.5	4225.4
GQ032381.1	399032	131.3	1060.9	1032.6	122.9	83.9	125.5
GQ156168.1	590723	6629.9	6234.9	8348.2	8001.2	7616.9	8684.1
EU460825.1	295866	177.9	455.6	1690.2	179.1	148.2	265.8
AJ307888.1	63461	166.7	327.1	384.0	117.2	95.5	99.1
AF009507.1	15367	149.6	302.7	246.3	155.6	76.5	162.5
EU772622.1	314465	9347.0	7314.2	3850.4	6591.4	2573.1	3690.7
EU467845.1	287347	11522.0	10940.8	7081.7	8335.6	8935.0	9577.2
EU775569.1	324468	904.3	1475.7	1861.7	557.2	2146.5	1393.8
GU045397.1	586088	456.5	1175.3	871.7	392.0	324.5	2545.6
EU473918.1	293540	2723.2	3037.6	925.9	4063.4	3338.0	3274.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45395
s__unclassified	45396
s__unclassified	45397
s__unclassified	45398
s__unclassified	45399
s__unclassified	45402
s__unclassified	45404
s__unclassified	45405
s__unclassified	45408
s__unclassified	45412
s__unclassified	45414
s__unclassified	45422
s__unclassified	45427
s__unclassified	45428
s__unclassified	45431
s__unclassified	45434
s__unclassified	45435
s__unclassified	45437
s__unclassified	45438
s__unclassified	45439
s__unclassified	45442
s__unclassified	45444
s__unclassified	45447
s__unclassified	45455
s__unclassified	45458
s__unclassified	45468
s__unclassified	45474
s__unclassified	45476
s__unclassified	45477
s__unclassified	45478
s__unclassified	45479
s__unclassified	45481
s__unclassified	45482
s__unclassified	45483
s__unclassified	45484
s__unclassified	45485
s__unclassified	45488
s__unclassified	45489
s__unclassified	45490
s__unclassified	45491
s__unclassified	45493

EU772581.1 gg_id:354242 North American Black Bear feces clone BB2_b01
EU467869.1 gg_id:296719 North American black bear feces clone BB1_h03_2
GQ073370.1 gg_id:442986 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208c05c1
EU461864.1 gg_id:300903 white-faced saki feces clone Saki_aaj62e06
GQ040889.1 gg_id:457333 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw959g10c
AY281079.1 gg_id:89930 Streptococcus oralis str. ATCC 9811
GQ010954.1 gg_id:498711 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
DQ232534.1 gg_id:190717 Streptococcus mitis str. CIP 104997
EU475873.1 gg_id:302995 white-faced saki feces clone Saki_aaj62f09
GQ073509.1 gg_id:431778 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ113226.1 gg_id:461942 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ155674.1 gg_id:512915 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
GQ073236.1 gg_id:420071 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f09c1
EU467847.1 gg_id:288218 North American black bear feces clone BB1_c09_2
FJ677289.1 gg_id:509161 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU660342.1 gg_id:299977 Streptococcus pyogenes str. Sp32
EU461896.1 gg_id:290594 white-faced saki feces clone Saki_aaj63c10
EU458288.1 gg_id:295039 North American black bear feces clone BB2_d11
EU156784.1 gg_id:331800 Streptococcus pseudopneumoniae str. CCRI-8984
FJ679815.1 gg_id:531369 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ082003.1 gg_id:446773 Topographical and Temporal Human Skin Microbiome skin back clone nbw1198h10c
DQ016843.2 gg_id:149109 subject-specific oral microflora during initial colonization enamel human mouth; indi
DQ232537.1 gg_id:196966 Streptococcus oralis str. CIP 105158
FJ674207.1 gg_id:527106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AM941160.1 gg_id:259084 Streptococcus sp. 2923-03
GQ102114.1 gg_id:374555 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561c0
GU045383.1 gg_id:550425 Streptococcus oralis str. KCOM 1416
NR_029052.1 gg_id:538185 Streptococcus oligofermentans str. 2-4; LMG 21535
FJ674309.1 gg_id:509855 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ054576.1 gg_id:456757 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092a07c
EU458193.1 gg_id:294978 North American black bear feces clone BB2_e02_1
GQ019723.1 gg_id:489945 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu206c09
FJ672838.1 gg_id:515480 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ011178.1 gg_id:498488 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ155339.1 gg_id:546051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU458183.1 gg_id:296971 North American black bear feces clone BB2_b12_1
EU461976.1 gg_id:300448 white-faced saki feces clone Saki_aaj64f08
EU471475.1 gg_id:302979 spectacled bear feces clone SB_2aaa03d08
EU458160.1 gg_id:287785 North American black bear feces clone BB2_g02
GQ073238.1 gg_id:377455 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f11c1
AB008314.1 gg_id:15560 Streptococcus peroris str. GTC848

EU772581.1	354242	8582.9	10065.4	6685.4	7849.0	12099.5	14113.9
EU467869.1	296719	1026.3	1246.0	1648.5	397.1	239.4	533.1
GQ073370.1	442986	640.4	1371.1	1888.9	682.6	353.8	953.1
EU461864.1	300903	2095.2	2358.3	5239.5	2624.2	2138.9	2551.0
GQ040889.1	457333	1349.0	927.7	1724.4	1102.9	2097.4	1081.1
AY281079.1	89930	1240.4	873.2	1136.9	1158.0	884.9	721.7
GQ010954.1	498711	502.9	1218.3	657.4	582.4	317.9	374.2
DQ232534.1	190717	2415.2	3184.6	2539.3	1563.1	558.1	3295.4
EU475873.1	302995	12997.3	10496.1	10307.1	9397.1	9758.4	11929.9
GQ073509.1	431778	702.9	1465.8	1569.3	438.2	199.3	615.2
GQ113226.1	461942	6353.7	6146.5	6623.4	4428.7	4044.7	5236.2
GQ155674.1	512915	8483.5	6274.3	6289.5	6522.9	7806.5	4865.3
GQ073236.1	420071	2838.6	2657.9	2601.7	2001.4	667.1	1375.8
EU467847.1	288218	1164.2	1766.0	5752.6	1172.2	2531.0	2217.3
FJ677289.1	509161	16368.4	15320.2	10305.5	11565.5	15812.6	17964.2
EU660342.1	299977	340.2	429.9	331.7	1072.0	117.7	217.7
EU461896.1	290594	2359.9	1884.3	1521.9	1818.3	1750.5	2042.3
EU458288.1	295039	8235.7	7904.6	4278.3	5395.2	5632.5	5528.6
EU156784.1	331800	3260.1	3051.8	2564.6	1853.6	1856.9	1902.5
FJ679815.1	531369	809.1	1134.8	2454.5	769.1	428.4	1228.2
GQ082003.1	446773	16684.3	16925.1	10303.1	13233.0	16224.8	18302.0
DQ016843.2	149109	4061.0	3704.8	2845.4	2049.0	5723.9	2137.7
DQ232537.1	196966	970.6	1499.8	774.5	1034.2	668.4	3119.1
FJ674207.1	527106	6409.2	6310.4	6225.4	3916.7	7678.1	7391.4
AM941160.1	259084	46.3	106.6	260.5	108.4	88.4	380.9
GQ102114.1	374555	403.1	991.1	705.7	1200.4	122.6	92.9
GU045383.1	550425	3703.2	5695.7	2633.8	3048.5	8920.5	4973.9
NR_029052.1	538185	1153.5	1320.9	2371.7	991.4	996.2	1204.6
FJ674309.1	509855	258.8	591.3	1105.9	330.7	156.0	289.8
GQ054576.1	456757	50.2	110.3	55.7	52.7	69.7	47.7
EU458193.1	294978	1196.2	771.7	990.8	3108.2	214.5	401.1
GQ019723.1	489945	837.8	1632.7	1003.4	225.0	287.5	326.1
FJ672838.1	515480	2106.3	2272.8	4415.7	1648.6	486.6	1343.8
GQ011178.1	498488	434.8	1216.4	777.8	314.5	301.1	606.4
GQ155339.1	546051	5838.9	5167.8	6301.7	5580.6	4800.0	4762.7
EU458183.1	296971	4428.9	5132.0	3709.8	2672.0	10084.2	7222.1
EU461976.1	300448	591.3	945.7	1823.7	684.9	263.0	438.3
EU471475.1	302979	918.2	1536.5	1010.7	623.7	2361.5	1378.8
EU458160.1	287785	2587.3	3241.7	6478.7	1849.6	1303.4	2627.6
GQ073238.1	377455	3775.9	1926.4	2152.3	4475.5	2095.8	4378.8
AB008314.1	15560	66.5	930.9	337.6	111.3	122.7	145.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45500
s__unclassified	45502
s__unclassified	45503
s__unclassified	45505
s__unclassified	45510
s__unclassified	45512
s__unclassified	45513
s__unclassified	45514
s__unclassified	45516
s__unclassified	45517
s__unclassified	45518
s__unclassified	45519
s__unclassified	45520
s__unclassified	45522
s__unclassified	45523
s__unclassified	45524
s__unclassified	45526
s__unclassified	45529
s__unclassified	45531
s__unclassified	45536
s__unclassified	45541
s__unclassified	45544
s__unclassified	45547
s__unclassified	45549
s__unclassified	45552
s__unclassified	45555
s__unclassified	45556
s__unclassified	45558
s__unclassified	45563
s__unclassified	45568
s__unclassified	45570
s__unclassified	45572
s__unclassified	45576
s__unclassified	45577
s__unclassified	45578
s__unclassified	45585
s__unclassified	45586
s__unclassified	45587
s__unclassified	45590
s__unclassified	45596
s__unclassified	45599

GQ057678.1 gg_id:389049 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ019801.1 gg_id:489867 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu207c04
AB023576.1 gg_id:15371 Streptococcus uberis str. HN1
FJ679289.1 gg_id:526351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AF135453.1 gg_id:25587 Streptococcus bovis str. 1276
AY525790.1 gg_id:111444 Streptococcus pneumoniae str. HK_P55
FJ672957.1 gg_id:511682 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ853836.1 gg_id:108738 Streptococcus cristatus str. 0109 93830B
FJ677170.1 gg_id:525204 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458274.1 gg_id:296367 North American black bear feces clone BB2_c02_3
EU458257.1 gg_id:301824 North American black bear feces clone BB2_h02_1
EU458189.1 gg_id:303194 North American black bear feces clone BB2_d05_1
EF364098.1 gg_id:219115 Streptococcus caballi str. 151
EU467867.1 gg_id:288591 North American black bear feces clone BB1_g10_1
GQ060702.1 gg_id:420623 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d06
FJ557366.1 gg_id:524022 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
FJ679360.1 gg_id:524008 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY525791.1 gg_id:111760 Streptococcus pneumoniae str. HK_P116
FJ558253.1 gg_id:526846 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
DQ303188.1 gg_id:168087 Streptococcus mitis str. ATCC 49456
GQ111270.1 gg_id:383764 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ676643.1 gg_id:520991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458226.1 gg_id:290193 North American black bear feces clone BB2_b04_2
GQ043319.1 gg_id:439032 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU775741.1 gg_id:309550 Horse feces clone horsem_aai93e09
FJ558487.1 gg_id:530902 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
DQ303190.1 gg_id:170102 Streptococcus oralis str. CCUG 24891
GQ019394.1 gg_id:490274 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189e
GQ032401.1 gg_id:406741 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542d06
EU458208.1 gg_id:303353 North American black bear feces clone BB2_g03_1
EU774894.1 gg_id:345575 Short-beaked Echidna feces clone ECH_aai40c10
EU460725.1 gg_id:302963 short-beaked echidna feces clone ECH_aai37b01
EU475871.1 gg_id:298472 white-faced saki feces clone Saki_e02_1
EU467833.1 gg_id:301583 North American black bear feces clone BB1_a07_2
GQ086202.1 gg_id:388839 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
NC_011375.1 gg_id:314877 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633
EU467904.1 gg_id:298775 North American black bear feces clone BB1_f06_2
GQ048268.1 gg_id:451556 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
EU458272.1 gg_id:293401 North American black bear feces clone BB2_b08_3
GQ156135.1 gg_id:591692 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
Y17358.1 gg_id:26896 Streptococcus ovis str. S369-98-1

GQ057678.1	389049	2795.7	2394.5	1904.7	1447.6	582.9	1321.9
GQ019801.1	489867	2936.3	3379.4	2213.4	2251.1	3285.1	3387.8
AB023576.1	15371	3892.6	6623.1	2512.5	2444.3	4224.7	4656.5
FJ679289.1	526351	2349.5	2122.4	922.7	789.9	1172.2	1056.5
AF135453.1	25587	627.0	574.5	846.4	205.8	102.2	753.4
AY525790.1	111444	36.4	644.1	231.7	98.3	86.4	165.2
FJ672957.1	511682	13692.2	14723.5	10029.6	10249.5	12930.1	12480.8
AJ853836.1	108738	6941.9	3533.3	2944.7	3274.4	2961.4	3548.2
FJ677170.1	525204	9904.7	7709.6	5824.3	9884.4	9497.4	14965.2
EU458274.1	296367	734.2	1490.0	2911.2	704.5	371.1	827.1
EU458257.1	301824	1601.3	1593.0	1642.7	689.3	335.1	612.8
EU458189.1	303194	7763.6	6344.5	4605.2	8351.5	10793.7	13224.9
EF364098.1	219115	3124.8	2424.2	3204.2	2830.9	3977.6	2386.7
EU467867.1	288591	18967.1	16022.6	21488.5	14008.6	14973.7	19588.1
GQ060702.1	420623	4493.9	4185.9	5525.2	2866.8	3864.6	3487.8
FJ557366.1	524022	4140.2	3664.1	3230.2	3630.1	1888.4	2193.1
FJ679360.1	524008	97.4	229.3	614.3	163.3	62.9	59.0
AY525791.1	111760	969.4	2124.6	1950.8	731.2	524.6	1223.9
FJ558253.1	526846	5623.2	3465.5	2367.0	6224.2	2946.5	3458.5
DQ303188.1	168087	57.8	756.0	215.3	95.1	90.0	254.8
GQ111270.1	383764	2049.8	1475.6	2152.5	4081.6	161.7	434.0
FJ676643.1	520991	253.5	723.0	1380.5	223.3	223.2	457.8
EU458226.1	290193	56.5	150.8	451.9	94.9	324.3	418.1
GQ043319.1	439032	2351.9	2028.6	2476.8	1131.2	434.1	1128.6
EU775741.1	309550	1738.7	1722.6	3627.3	1418.6	648.8	1998.0
FJ558487.1	530902	775.3	1264.5	1271.5	485.1	481.4	640.5
DQ303190.1	170102	481.3	1081.4	887.4	415.1	325.3	2532.5
GQ019394.1	490274	2368.1	2664.5	2018.5	1908.7	931.0	1875.9
GQ032401.1	406741	109.7	1014.4	948.9	110.4	83.0	126.5
EU458208.1	303353	988.0	1711.1	3040.0	958.7	438.4	936.8
EU774894.1	345575	5515.7	6475.1	6611.7	4860.4	3125.5	4456.7
EU460725.1	302963	839.5	1247.6	2728.7	795.3	848.5	1219.6
EU475871.1	298472	9400.1	9806.7	7900.8	7978.3	9634.6	8344.0
EU467833.1	301583	5881.7	6590.9	7936.0	2943.7	1900.2	2563.1
GQ086202.1	388839	3942.6	3436.9	3859.3	4173.7	4782.2	5154.6
NC_011375.1	314877	508.5	945.6	1479.3	556.6	213.1	554.8
EU467904.1	298775	291.4	348.9	997.3	497.1	980.0	522.8
GQ048268.1	451556	3034.9	3060.3	2666.7	1818.8	1717.1	1829.3
EU458272.1	293401	11283.4	8443.8	8351.3	10074.1	7466.3	8764.7
GQ156135.1	591692	7503.5	9102.8	9533.4	5842.0	2823.1	3108.2
Y17358.1	26896	95.9	103.1	97.3	67.2	81.8	87.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45601
s__unclassified	45607
s__unclassified	45610
s__unclassified	45612
s__unclassified	45616
s__unclassified	45617
s__unclassified	45622
s__unclassified	45626
s__unclassified	45627
s__unclassified	45628
s__unclassified	45629
s__unclassified	45640
s__unclassified	45641
s__unclassified	45644
s__unclassified	45646
s__unclassified	45647
s__unclassified	45649
s__unclassified	45659
s__unclassified	45662
s__unclassified	45663
s__unclassified	45669
s__unclassified	45673
s__unclassified	45675
s__unclassified	45679
s__unclassified	45681
s__unclassified	45682
s__unclassified	45684
s__unclassified	45694
s__unclassified	45695
s__unclassified	45696
s__unclassified	45699
s__unclassified	45700
s__unclassified	45702
s__unclassified	45705
s__unclassified	45706
s__unclassified	45708
s__unclassified	45709
s__unclassified	45713
s__unclassified	45714
s__unclassified	45716
s__unclassified	45717

DQ805392.1 gg_id:184376 human fecal clone RL203_aai62a07
FJ892760.1 gg_id:550176 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p
FJ678216.1 gg_id:521294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458184.1 gg_id:296435 North American black bear feces clone BB2_c02_1
EU467771.1 gg_id:291232 North American black bear feces clone BB1_f05
EU772601.1 gg_id:322567 North American Black Bear feces clone BB2_b10
GQ078830.1 gg_id:423740 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ056825.1 gg_id:374781 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU461930.1 gg_id:299204 white-faced saki feces clone Saki_aaj63h11
GQ070655.1 gg_id:395351 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
EU460784.1 gg_id:287545 short-beaked echidna feces clone ECH_aai37h10
EU660340.1 gg_id:290080 Streptococcus pyogenes str. Sp12
GQ077236.1 gg_id:386987 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115E
EU467798.1 gg_id:294395 North American black bear feces clone BB1_c05
EU467191.1 gg_id:289185 white-faced saki feces clone Saki_e06
FJ675610.1 gg_id:518399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU473899.1 gg_id:289643 giant panda feces clone GP_2aaa02a01
EU475801.1 gg_id:287600 white-faced saki feces clone Saki_aaj64e04
EU473322.1 gg_id:295789 giant panda feces clone GP_1aaa03a08
EU458277.1 gg_id:295281 North American black bear feces clone BB2_c07_1
EU467864.1 gg_id:293154 North American black bear feces clone BB1_g05_1
FJ683535.1 gg_id:518286 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676479.1 gg_id:521992 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ072667.1 gg_id:411298 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19
EU779050.1 gg_id:333155 Prevost's squirrel feces clone SQ_aah82f11
AY525789.1 gg_id:112327 Streptococcus pneumoniae str. HK_P47
GQ076939.1 gg_id:377312 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155
AF543291.1 gg_id:58287 Streptococcus mitis str. ChDC OS41
GQ115448.1 gg_id:425877 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685g05
EU467812.1 gg_id:303216 North American black bear feces clone BB1_e11_1
GQ155692.1 gg_id:589905 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
AM396401.1 gg_id:165104 Streptococcus sp. str. DT2005WUE_IHM
EU458148.1 gg_id:298590 North American black bear feces clone BB2_e06
EU467827.1 gg_id:302755 North American black bear feces clone BB1_h05_1
EU779446.1 gg_id:309732 Grevy's Zebra feces clone GZ_aaa04g04
AF323911.1 gg_id:31706 Streptococcus gallolyticus
EU475852.1 gg_id:296662 white-faced saki feces clone Saki_e08
GQ101164.1 gg_id:430460 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49
GQ073361.1 gg_id:378214 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208b05c
DQ303194.1 gg_id:167724 Streptococcus urinalis str. CCUG 41590
EU475777.1 gg_id:292482 white-faced saki feces clone Saki_aaj61g03

DQ805392.1	184376	2673.6	2394.8	3489.7	2545.9	1354.2	2184.6
FJ892760.1	550176	1337.7	1506.7	1189.9	1526.2	363.8	586.4
FJ678216.1	521294	9295.3	9444.1	5150.9	8267.8	9593.0	8896.0
EU458184.1	296435	2200.3	2829.4	3888.8	2590.2	2472.4	3841.4
EU467771.1	291232	17026.6	17916.2	10386.2	13675.3	15521.3	16122.9
EU772601.1	322567	549.9	1045.4	2414.3	573.0	243.2	647.9
GQ078830.1	423740	1170.4	1721.5	1390.5	1083.6	393.8	626.5
GQ056825.1	374781	571.9	935.1	764.5	584.1	546.9	484.1
EU461930.1	299204	2380.2	3017.8	1924.6	810.0	1391.9	1584.1
GQ070655.1	395351	934.0	1349.4	1319.6	618.5	934.5	948.7
EU460784.1	287545	197.7	300.7	659.3	136.9	92.0	164.7
EU660340.1	290080	7279.6	7215.6	5408.0	6374.1	6824.9	6538.3
GQ077236.1	386987	368.6	615.7	295.1	1041.7	110.1	42.9
EU467798.1	294395	1362.4	2065.2	2306.3	877.8	1633.4	3161.4
EU467191.1	289185	3285.7	1712.4	5801.9	5788.0	244.7	1010.6
FJ675610.1	518399	15602.3	14814.1	14587.1	13583.3	18699.3	17193.3
EU473899.1	289643	306.2	498.2	268.7	152.8	1346.8	1191.8
EU475801.1	287600	1609.0	1943.0	2600.2	1223.2	486.8	1346.2
EU473322.1	295789	1759.1	1710.5	1837.8	799.8	329.5	675.6
EU458277.1	295281	8938.2	12500.3	4081.1	7441.6	8913.5	10687.2
EU467864.1	293154	5544.6	5012.2	5090.5	5017.1	7414.4	7781.7
FJ683535.1	518286	3635.2	4657.1	5848.8	3640.0	6099.1	6935.4
FJ676479.1	521992	5345.9	5469.8	2860.6	6350.3	7324.8	8395.8
GQ072667.1	411298	1876.0	1963.1	1279.2	546.7	425.3	531.2
EU779050.1	333155	1573.4	2003.0	1519.6	1609.1	826.0	1120.4
AY525789.1	112327	845.6	2300.5	1763.9	740.8	607.7	1146.2
GQ076939.1	377312	925.5	1319.1	541.3	133.1	291.9	543.1
AF543291.1	58287	1510.3	1325.3	2675.2	1801.8	3118.7	4046.6
GQ115448.1	425877	1869.4	1874.1	1342.7	536.3	442.4	497.5
EU467812.1	303216	8922.8	8017.1	5099.1	9960.5	13368.1	14348.3
GQ155692.1	589905	5002.5	4663.6	6030.5	5735.8	7002.1	7085.6
AM396401.1	165104	8737.1	7364.9	7321.4	4003.0	3992.4	3587.7
EU458148.1	298590	4150.1	3847.8	2998.3	2759.8	3526.5	4369.4
EU467827.1	302755	5045.6	5942.0	5934.6	6886.8	9732.5	8783.8
EU779446.1	309732	2863.8	3377.2	5304.7	2698.0	1127.2	1792.7
AF323911.1	31706	4725.0	6422.9	3871.6	3970.7	1279.6	3133.7
EU475852.1	296662	877.2	1340.8	3099.7	872.0	328.4	858.9
GQ101164.1	430460	544.7	782.7	4975.8	542.4	185.6	314.0
GQ073361.1	378214	2038.6	1419.5	2478.9	1865.4	529.8	785.8
DQ303194.1	167724	95.8	386.0	1803.9	102.1	118.9	119.1
EU475777.1	292482	2131.9	2531.1	3600.6	1316.1	773.1	1738.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus

s__unclassified	45719
s__unclassified	45720
s__unclassified	45724
s__unclassified	45725
s__unclassified	45728
s__unclassified	45729
s__unclassified	45744
s__unclassified	45746
s__unclassified	45753
s__unclassified	45754
s__unclassified	45767
s__unclassified	45771
s__unclassified	45773
s__unclassified	45785
s__unclassified	45790
s__unclassified	45792
s__unclassified	45795
s__unclassified	45796
s__unclassified	45799
s__unclassified	45804
s__unclassified	45805
s__unclassified	45806
s__unclassified	45807
s__unclassified	45808
s__unclassified	45809
s__unclassified	45814
s__unclassified	45815
s__unclassified	45817
s__unclassified	45818
s__unclassified	45822
s__unclassified	45824
s__unclassified	45827
s__unclassified	45828
s__unclassified	45832
s__unclassified	45833
s__unclassified	45835
s__unclassified	45837
s__unclassified	45841
s__unclassified	45844
s__unclassified	45845
s__unclassified	45846

AY005040.1 gg_id:28885 Streptococcus sp. oral strain str. 7A
GQ076078.1 gg_id:431953 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU341148.1 gg_id:243231 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca
AJ295853.1 gg_id:46365 Streptococcus mitis str. 209
GQ076899.1 gg_id:409566 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
EU461789.1 gg_id:298208 white-faced saki feces clone Saki_aaj61b04
GQ043419.1 gg_id:429551 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw9
EU467196.1 gg_id:299158 white-faced saki feces clone Saki_g01
EU458284.1 gg_id:297654 North American black bear feces clone BB2_d04_1
EU467823.1 gg_id:301071 North American black bear feces clone BB1_g07
FJ678805.1 gg_id:525261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ081009.1 gg_id:395948 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
EU458246.1 gg_id:299675 North American black bear feces clone BB2_f06_2
EU467808.1 gg_id:298882 North American black bear feces clone BB1_e02_1
EU458139.1 gg_id:298862 North American black bear feces clone BB2_d04
GQ155683.1 gg_id:551174 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
EU458171.1 gg_id:292100 North American black bear feces clone BB2_h08
FJ680107.1 gg_id:518559 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU660336.1 gg_id:298908 Streptococcus pyogenes str. Sp8
EU778418.1 gg_id:323518 Red Panda feces clone RP_2aaa01c07
EU458198.1 gg_id:288649 North American black bear feces clone BB2_f01_1
EU458202.1 gg_id:287473 North American black bear feces clone BB2_f06_1
EU461971.1 gg_id:299458 white-faced saki feces clone Saki_aaj64f02
Y07601.1 gg_id:15430 Streptococcus sp. str. SHV515
EU458117.1 gg_id:294121 North American black bear feces clone BB2_a06
EU772619.1 gg_id:345747 North American Black Bear feces clone BB2_c03_2
EU467750.1 gg_id:291931 North American black bear feces clone BB1_c10
AJ606047.1 gg_id:114860 Streptococcus castoreus str. M60581/03/2
FJ677268.1 gg_id:531460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ069167.1 gg_id:442582 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ673358.1 gg_id:520177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU458124.1 gg_id:302904 North American black bear feces clone BB2_b05
GQ073148.1 gg_id:406688 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f06c1
EU458223.1 gg_id:295170 North American black bear feces clone BB2_a10_1
EU467903.1 gg_id:301865 North American black bear feces clone BB1_f05_2
GQ101429.1 gg_id:407688 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495a
GQ073121.1 gg_id:397965 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c12c1
DQ798234.1 gg_id:194026 human fecal clone RL181_aah39c03
EU156776.1 gg_id:325399 Streptococcus pneumoniae str. CCRI-14589
EU467878.1 gg_id:297820 North American black bear feces clone BB1_b07_3
EU458244.1 gg_id:289054 North American black bear feces clone BB2_f03_2

AY005040.1	28885	68.7	618.4	310.9	151.2	83.9	1988.5
GQ076078.1	431953	1736.0	1939.6	1186.4	536.3	451.5	532.9
EU341148.1	243231	2519.9	2473.3	1117.9	1398.1	5507.3	4823.4
AJ295853.1	46365	2260.1	3115.6	2717.2	1558.5	544.6	3288.5
GQ076899.1	409566	768.2	850.4	1892.5	670.7	2041.5	1756.5
EU461789.1	298208	12826.6	13294.6	12363.3	10595.7	15139.3	11084.2
GQ043419.1	429551	1876.4	1955.9	1276.1	541.7	454.3	534.0
EU467196.1	299158	723.4	997.1	2111.9	646.9	249.1	648.9
EU458284.1	297654	10357.1	10187.1	4598.6	7208.1	9603.7	10997.2
EU467823.1	301071	5337.5	5092.1	4646.6	4647.2	6012.9	5517.5
FJ678805.1	525261	3510.8	3766.4	3585.8	3576.0	1945.2	3161.4
GQ081009.1	395948	9456.8	8534.7	8585.6	7454.9	7672.3	9057.0
EU458246.1	299675	2829.2	2398.1	4386.2	1197.7	3555.6	3254.6
EU467808.1	298882	976.5	1865.2	3300.5	812.5	682.7	1146.4
EU458139.1	298862	487.8	883.3	874.0	823.5	310.5	619.3
GQ155683.1	551174	10019.7	10777.7	7369.3	11648.2	12656.7	11358.7
EU458171.1	292100	4437.9	2276.2	2733.4	4081.7	1513.3	4106.4
FJ680107.1	518559	237.5	891.1	1095.1	315.2	237.2	446.4
EU660336.1	298908	745.5	854.9	1539.1	1179.1	1483.3	1451.9
EU778418.1	323518	730.9	1473.0	2665.0	705.5	372.2	894.0
EU458198.1	288649	868.1	1478.5	3118.7	1252.3	9725.5	6903.0
EU458202.1	287473	15641.0	16269.6	7783.8	11871.7	18669.9	18538.1
EU461971.1	299458	4186.2	2384.5	8664.0	3419.0	5978.7	7734.9
Y07601.1	15430	473.0	719.8	957.3	612.3	671.9	904.6
EU458117.1	294121	4249.3	5698.8	6928.8	3196.9	3951.3	4665.5
EU772619.1	345747	1441.3	1815.2	3735.7	1209.3	440.1	1230.6
EU467750.1	291931	734.2	1485.8	2466.8	702.2	371.9	895.9
AJ606047.1	114860	1474.7	4980.6	1072.7	536.8	1176.8	1162.1
FJ677268.1	531460	1280.1	2330.4	1721.0	933.2	407.7	882.2
GQ069167.1	442582	1647.8	1968.6	1906.9	1125.1	635.2	1187.9
FJ673358.1	520177	4627.3	6021.4	8625.3	7138.5	9768.7	6876.2
EU458124.1	302904	27.8	180.8	551.1	97.7	102.1	107.0
GQ073148.1	406688	2010.4	1769.9	1420.5	1361.0	507.5	951.4
EU458223.1	295170	2734.4	2647.7	1515.4	1034.7	2024.2	1163.8
EU467903.1	301865	1483.2	1693.3	3663.3	1270.3	1147.2	1436.7
GQ101429.1	407688	165.4	334.7	2068.7	308.5	119.5	103.9
GQ073121.1	397965	1906.6	2114.2	2268.8	1569.7	618.4	1416.5
DQ798234.1	194026	14195.7	14587.4	6707.2	10951.8	13870.2	13065.6
EU156776.1	325399	871.7	1958.4	5445.4	974.5	4133.2	3005.1
EU467878.1	297820	498.5	1122.6	2519.5	547.4	904.8	556.3
EU458244.1	289054	689.1	1599.6	2104.7	686.4	361.6	826.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli

o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Lactobacillales	f__Streptococcaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae

g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__Streptococcus
g__unclassified
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__Thermicanus
g__unclassified
g__unclassified

s__unclassified	45848
s__unclassified	45849
s__unclassified	45852
s__unclassified	45854
s__unclassified	45855
s__unclassified	45857
s__unclassified	45865
s__unclassified	45866
s__unclassified	45867
s__unclassified	45868
s__unclassified	45870
s__unclassified	45872
s__unclassified	45874
s__unclassified	45877
s__unclassified	45878
s__unclassified	45879
s__unclassified	45883
s__unclassified	45884
s__unclassified	45889
s__unclassified	45892
s__unclassified	45895
s__unclassified	45896
s__unclassified	44377
s__unclassified	48386
s__unclassified	48412
s__unclassified	48443
s__unclassified	48607
s__unclassified	48640
s__unclassified	48868
s__unclassified	48882
s__unclassified	48977
s__unclassified	49002
s__unclassified	49140
s__unclassified	49175
s__unclassified	49260
s__unclassified	49397
s__unclassified	49903
s__unclassified	49909
s__unclassified	49927
s__unclassified	48317
s__unclassified	48883

EU461828.1 gg_id:301841 white-faced saki feces clone Saki_aaj61g06
EU777768.1 gg_id:349666 Polar bear feces clone PB1_aai27f03
EU461813.1 gg_id:294792 white-faced saki feces clone Saki_aaj61e02
FJ678126.1 gg_id:520301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ267979.1 gg_id:563263 Surveys lactic acid yak Tibet China method fermented milk product clone IMAU 462
GQ087792.1 gg_id:375084 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU458219.1 gg_id:291040 North American black bear feces clone BB2_a04_1
AF009508.1 gg_id:15540 Streptococcus suis str. EA1832.92
AM157420.1 gg_id:142116 Streptococcus mitis mother C3
EU289036.1 gg_id:238994 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
GQ018929.1 gg_id:490737 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d
EU461983.1 gg_id:296189 white-faced saki feces clone Saki_aaj64g06
GQ030493.1 gg_id:459696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw879a10c
AM157441.1 gg_id:142633 Streptococcus parasanguinis mother V4
EF509782.1 gg_id:219258 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
EU458152.1 gg_id:292449 North American black bear feces clone BB2_f01
EU467884.1 gg_id:299150 North American black bear feces clone BB1_c06_3
GQ018857.1 gg_id:490812 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f(
EU458161.1 gg_id:293794 North American black bear feces clone BB2_g03
GQ060042.1 gg_id:441561 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
EU461878.1 gg_id:301061 white-faced saki feces clone Saki_aaj62h01
GQ074530.1 gg_id:394032 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164c
AM157443.1 gg_id:143690 Origen y potencial probiotico microbiota de la leche materna breast milk clone 5V4
EU638618.1 gg_id:337396 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638858.1 gg_id:316255 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638622.1 gg_id:319590 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638451.1 gg_id:334625 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
NR_025355.1 gg_id:534827 Thermicanus aegyptius str. ET-5b; DSM 12793
GQ079892.1 gg_id:439457 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU638737.1 gg_id:333346 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638544.1 gg_id:354384 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638577.1 gg_id:340110 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638576.1 gg_id:333359 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638435.1 gg_id:336118 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638466.1 gg_id:340259 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638734.1 gg_id:355173 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638336.1 gg_id:339047 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638556.1 gg_id:303923 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638526.1 gg_id:328129 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU638732.1 gg_id:336395 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AY518549.1 gg_id:107665 Bacillus solfatarensis str. Sol1

EU461828.1	301841	18266.9	16775.2	12978.1	14609.1	16574.1	15001.9
EU777768.1	349666	1790.4	2530.9	5019.7	1783.3	3866.2	4716.4
EU461813.1	294792	733.2	1412.0	2911.1	701.5	349.0	826.6
FJ678126.1	520301	8084.1	6691.9	3738.1	7990.2	10722.6	10494.2
GQ267979.1	563263	1854.7	1522.8	1907.0	803.1	367.8	747.2
GQ087792.1	375084	1109.3	2019.1	5289.2	1190.2	4849.1	4156.7
EU458219.1	291040	2786.9	3017.1	4286.2	1393.5	903.1	1199.5
AF009508.1	15540	1986.9	1998.7	1578.3	96.5	1837.9	1571.4
AM157420.1	142116	10441.5	14064.2	9091.4	8331.8	11676.4	12319.6
EU289036.1	238994	74.8	338.2	99.4	87.4	176.9	227.5
GQ018929.1	490737	97.6	1003.1	471.9	116.1	151.0	325.4
EU461983.1	296189	9295.6	8434.3	7174.5	6822.3	6808.4	8717.1
GQ030493.1	459696	835.7	1154.6	2204.0	847.2	278.7	915.3
AM157441.1	142633	561.2	1099.4	528.8	566.3	402.9	966.7
EF509782.1	219258	48.8	978.5	70.0	82.7	87.3	91.1
EU458152.1	292449	3508.9	5108.2	4753.1	4393.5	6241.7	4913.9
EU467884.1	299150	6564.1	6158.4	7448.4	5413.8	14204.8	14103.9
GQ018857.1	490812	689.7	1335.1	1451.2	565.2	1355.0	1420.3
EU458161.1	293794	1671.7	1344.3	660.1	1268.3	2103.2	1790.6
GQ060042.1	441561	4173.2	4361.3	4623.1	4470.8	6919.8	7022.4
EU461878.1	301061	1952.4	1904.0	3014.4	3015.0	3569.8	2244.2
GQ074530.1	394032	4088.6	4343.4	4429.3	3111.6	1429.4	2945.8
AM157443.1	143690	53.7	106.4	34.1	75.2	53.1	16.8
EU638618.1	337396	2980.3	4040.5	6268.8	3382.6	3533.9	4579.4
EU638858.1	316255	3148.1	4691.2	3883.0	2433.5	1986.7	3283.0
EU638622.1	319590	4624.7	4491.4	4886.3	7030.6	3395.8	4356.6
EU638451.1	334625	2019.5	3452.1	1574.2	1837.4	3331.0	3343.9
NR_025355.1	534827	387.8	675.9	20.6	207.9	189.4	177.8
GQ079892.1	439457	4690.3	4233.7	2847.0	4788.3	3773.9	4762.9
EU638737.1	333346	1910.6	3360.2	5272.0	2401.9	3347.9	3149.9
EU638544.1	354384	10355.0	9702.2	7596.6	10778.1	14315.8	12327.2
EU638577.1	340110	5777.1	7039.3	5608.2	4464.3	5368.4	5328.8
EU638576.1	333359	1311.9	937.2	3488.6	2837.4	180.3	804.6
EU638435.1	336118	10019.6	11166.5	3005.5	4376.2	6481.8	5391.3
EU638466.1	340259	217.0	284.7	311.2	558.2	129.3	322.4
EU638734.1	355173	11135.1	11794.4	7588.9	10716.9	6990.8	7853.4
EU638336.1	339047	1765.3	2488.3	2577.2	1664.5	500.9	1543.6
EU638556.1	303923	8224.9	11127.2	3556.8	6690.6	3027.0	3536.8
EU638526.1	328129	6650.3	7435.9	3570.6	4622.5	2860.4	3444.6
EU638732.1	336395	2295.2	2819.1	2608.5	1352.9	1206.7	1521.0
AY518549.1	107665	4474.8	4829.2	5755.4	3984.9	209.8	3752.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Thermicanales	f__Thermicanaceae
o__Thermicanales	f__Thermicanaceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__Turicibacterales	f__Turicibacteraceae
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__1B07	f__unclassified
o__1B07	f__unclassified
o__1B07	f__unclassified
o__1B07	f__unclassified
o__BSA2B-08	f__unclassified
o__BSA2B-08	f__unclassified
o__BSA2B-08	f__unclassified
o__BSA2B-08	f__unclassified
o__BSA2B-08	f__unclassified
o__Clostridiales	f__BSV43
o__Clostridiales	f__BSV43
o__Clostridiales	f__BSV43
o__Clostridiales	f__BSV43
o__Clostridiales	f__Carboxydocellaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae

g__unclassified
g__unclassified
g__Turicibacter
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfB
g__sfC
g__sfA
g__sfB
g__sfC
g__sfD
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Carboxydocella
g__unclassified
g__unclassified

s__unclassified	49303
s__unclassified	49548
s__unclassified	42642
s__unclassified	42607
s__unclassified	42751
s__unclassified	42887
s__unclassified	43040
s__unclassified	43272
s__unclassified	43283
s__unclassified	43367
s__unclassified	43393
s__unclassified	43452
s__unclassified	43467
s__unclassified	43478
s__unclassified	43526
s__unclassified	43566
s__unclassified	43712
s__unclassified	43803
s__unclassified	43864
s__unclassified	43923
s__unclassified	44049
s__unclassified	47112
s__unclassified	47903
s__unclassified	71771
s__unclassified	49470
s__unclassified	58204
s__unclassified	58463
s__unclassified	57910
s__unclassified	57868
s__unclassified	58080
s__unclassified	58255
s__unclassified	58780
s__unclassified	57828
s__unclassified	58045
s__unclassified	50442
s__unclassified	50456
s__unclassified	50473
s__unclassified	50717
s__unclassified	49104
s__unclassified	69237
s__unclassified	69244

AB042060.1 gg_id:83619 Bacillus schlegelii str. ATCC 43741T
EU638752.1 gg_id:352598 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AF349724.1 gg_id:20396 Turicibacter sanguinis
DQ015579.1 gg_id:202097 Obesity alters gut microbial ecology mouse cecum clone M3_g05_2
DQ015594.1 gg_id:202509 Obesity alters gut microbial ecology mouse cecum clone M3_h11_2
DQ015619.1 gg_id:201528 Obesity alters gut microbial ecology mouse cecum clone M3_c07_3
DQ815845.1 gg_id:171268 mouse cecum clone aab23b04
AJ400262.1 gg_id:41555 intestine clone S24-10
DQ815366.1 gg_id:171609 mouse cecum clone aab46f09
DQ015045.1 gg_id:134601 mouse cecum clone M2_d06
DQ015416.1 gg_id:201837 Obesity alters gut microbial ecology mouse cecum clone M3_g11
EU509845.1 gg_id:272578 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d03
DQ015488.1 gg_id:201366 Obesity alters gut microbial ecology mouse cecum clone M3_f09_1
FJ880353.1 gg_id:379703 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
DQ815843.1 gg_id:172983 mouse cecum clone aab23b01
DQ815565.1 gg_id:165315 mouse cecum clone aab42g09
DQ015666.1 gg_id:200054 Obesity alters gut microbial ecology mouse cecum clone M3_h01_1
DQ015508.1 gg_id:202862 Obesity alters gut microbial ecology mouse cecum clone M3_a02_2
DQ015025.1 gg_id:200030 Obesity alters gut microbial ecology mouse cecum clone M2_b01
EU509846.1 gg_id:268098 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d04
DQ015420.1 gg_id:202998 Obesity alters gut microbial ecology mouse cecum clone M3_h03
EU369151.1 gg_id:334937 libraries oyster shell clone MBHOS-02
AM500764.1 gg_id:536014 proof spatial heterogeneity hot composting clone E2
GU136560.1 gg_id:588822 Bacillus sp. str. S130(6)-2
AB308475.1 gg_id:240826 Caldaterra yamamurae str. YMO722
DQ346500.1 gg_id:153225 during composting libraries compost clone 2B16
AB233999.1 gg_id:151965 anaerobic reactor clone B-6
EU194835.1 gg_id:267680 Electricity generation thermophilic microorganisms marine Charleston harbor sedim
EF559058.1 gg_id:248820 Microbial functional groups solid waste digestor stable isotope probing thermophilic
AB175380.1 gg_id:103425 mesophilic anaerobic BSA digester clone BSA2B-08
EU358728.1 gg_id:354523 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
DQ887928.1 gg_id:167272 thermophilic anaerobic solid waste bioreactor clone GHB3F05
AM947553.1 gg_id:275685 Minor changes detected microbial structure and after three week thermophilic dige
DQ887961.1 gg_id:169373 thermophilic anaerobic solid waste bioreactor clone TIBG11
AB486136.1 gg_id:559728 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AJ229198.1 gg_id:34224 anoxic bulk soil flooded rice microcosm clone BSV43 clone
DQ129364.1 gg_id:138439 microarray level air two cities Texas urban aerosol clone AKIW782
FJ196298.1 gg_id:351034 Microbiological floras Cambrian Period Feicheng Shandong edgewise conglomerate cl
EF092457.2 gg_id:187815 Carboxydocella ferrireducens str. 019
FJ367045.1 gg_id:368252 feces adult twins and mothers; TS28 clone TS28_a02h01
DQ815751.1 gg_id:165529 mouse cecum clone aab21g12

AB042060.1	83619	2348.5	4465.8	5690.4	1917.0	3951.2	5860.9
EU638752.1	352598	3558.4	5988.1	5158.8	5154.7	5913.9	6110.6
AF349724.1	20396	136.5	246.8	718.9	120.0	197.9	765.5
DQ015579.1	202097	611.0	638.8	153.0	147.5	219.8	57.1
DQ015594.1	202509	1901.9	1698.9	1245.0	439.8	1854.9	1461.0
DQ015619.1	201528	2027.1	1641.2	2141.2	3289.0	1712.9	2691.7
DQ815845.1	171268	4607.8	3574.8	2088.2	4057.5	771.2	1262.0
AJ400262.1	41555	3130.9	1953.8	2949.9	3717.5	250.8	663.9
DQ815366.1	171609	2073.5	2726.2	3494.7	3147.8	4826.1	3994.1
DQ015045.1	134601	109.9	192.3	352.0	582.3	256.3	831.1
DQ015416.1	201837	254.2	541.8	620.4	136.4	84.8	389.0
EU509845.1	272578	2392.4	1440.9	768.4	805.5	869.9	753.0
DQ015488.1	201366	1930.9	2843.6	751.5	1249.4	3414.8	2085.0
FJ880353.1	379703	4359.9	3909.6	2735.9	1708.7	240.1	1355.1
DQ815843.1	172983	44.3	132.4	40.9	89.6	401.7	229.1
DQ815565.1	165315	4148.0	3482.2	1050.8	4757.5	1411.2	1757.7
DQ015666.1	200054	345.2	302.3	406.2	284.6	83.0	86.7
DQ015508.1	202862	8382.7	8696.2	5233.0	5877.0	7598.4	8697.2
DQ015025.1	200030	1860.6	1462.4	2199.5	1868.4	2105.5	1447.0
EU509846.1	268098	1734.6	2574.5	1692.1	1909.1	3097.9	3150.6
DQ015420.1	202998	10679.0	10666.9	5717.4	7479.2	8596.2	8153.2
EU369151.1	334937	1335.5	2135.7	2367.5	1800.4	2375.7	2414.1
AM500764.1	536014	1779.8	2681.7	2992.3	4704.9	4829.5	2934.0
GU136560.1	588822	374.9	1564.6	820.8	872.8	1270.4	1098.6
AB308475.1	240826	888.5	921.7	1490.4	208.1	579.5	861.0
DQ346500.1	153225	1461.0	1344.6	1224.5	991.0	152.2	663.5
AB233999.1	151965	7051.3	9197.6	4273.2	6011.4	6706.9	6055.7
EU194835.1	267680	230.3	444.0	1110.6	219.5	308.4	607.8
EF559058.1	248820	3612.8	5278.7	6633.6	4535.9	8539.3	6599.1
AB175380.1	103425	78.3	166.0	313.9	132.0	252.5	238.8
EU358728.1	354523	6122.6	7960.0	7495.9	9901.9	4539.3	6374.1
DQ887928.1	167272	63.2	53.1	74.8	50.7	54.3	26.6
AM947553.1	275685	8074.6	6291.3	10035.3	7049.9	6537.4	6037.9
DQ887961.1	169373	6793.1	7201.6	7690.3	6081.9	5303.6	5713.9
AB486136.1	559728	4849.8	5442.4	8658.8	5266.8	6758.9	7620.2
AJ229198.1	34224	6290.0	6867.3	3124.5	4379.3	4886.7	5909.0
DQ129364.1	138439	4575.8	6166.2	4515.3	4382.3	6992.2	4922.3
FJ196298.1	351034	3235.2	3580.2	1757.2	1309.0	2413.8	2442.8
EF092457.2	187815	45.6	81.8	120.9	83.8	84.8	63.0
FJ367045.1	368252	2143.3	1640.2	2713.6	4054.3	574.1	824.7
DQ815751.1	165529	145.6	314.6	728.6	106.0	100.2	98.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	69247
s__unclassified	69248
s__unclassified	69251
s__unclassified	69255
s__unclassified	69276
s__unclassified	69284
s__unclassified	69294
s__unclassified	69315
s__unclassified	69365
s__unclassified	69390
s__unclassified	69398
s__unclassified	69411
s__unclassified	69481
s__unclassified	69482
s__unclassified	69488
s__unclassified	69499
s__unclassified	69508
s__unclassified	69512
s__unclassified	69574
s__unclassified	69600
s__unclassified	69631
s__unclassified	69636
s__unclassified	69677
s__unclassified	69696
s__unclassified	69701
s__unclassified	69703
s__unclassified	69709
s__unclassified	69721
s__unclassified	69729
s__unclassified	69736
s__unclassified	69774
s__unclassified	69788
s__unclassified	69819
s__unclassified	69826
s__unclassified	69833
s__unclassified	69851
s__unclassified	69882
s__unclassified	69889
s__unclassified	69892
s__unclassified	69893
s__unclassified	69910

EU778320.1 gg_id:324015 feces clone RL387_aao91c02
DQ815454.1 gg_id:164595 mouse cecum clone aab48f09
GQ175436.1 gg_id:592913 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
EF445143.1 gg_id:205846 rabbit cecum clone NED2A2
AB192047.1 gg_id:142288 termite gut homogenate clone M2PT2-06
DQ015494.1 gg_id:133077 mouse cecum clone M3_g04_1
AY426451.1 gg_id:101401 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B7
AB234456.1 gg_id:146392 termite gut homogenate clone MgMjD-038
EF604609.1 gg_id:227821 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ800941.1 gg_id:197539 human fecal clone RL387_aao89f10
AB062822.1 gg_id:18245 termite gut homogenate clone BCf4-09
EU472310.1 gg_id:291318 francois langur feces clone FL_2aaa03d08
EF454103.1 gg_id:221121 termite hindgut clone 290cost002-P3L-1640
FJ881172.1 gg_id:416837 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
AB243284.1 gg_id:148219 acetone-preserved termite gut clone M2PB4a-024
AB299541.1 gg_id:237802 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G
DQ815908.1 gg_id:161771 mouse cecum clone aab24b02
DQ456434.1 gg_id:157545 pre-adolescent turkey cecum clone CFT214E5
FJ681080.1 gg_id:528434 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ815614.1 gg_id:166791 mouse cecum clone aab43f01
EF445166.1 gg_id:216356 rabbit cecum clone NED1H7
FJ881210.1 gg_id:418334 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EF604503.1 gg_id:232085 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ681260.1 gg_id:525729 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681301.1 gg_id:511624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF454637.1 gg_id:220301 termite hindgut clone 290cost002-P3L-2450
EF098915.1 gg_id:197478 mouse cecum clone SWPT1_aaa03b11
FJ367654.1 gg_id:365731 feces adult twins and mothers; TS2 clone TS2_a02a06
GQ422712.1 gg_id:552928 Human Oral Microbiome dental plaque clone CK059
AF371714.1 gg_id:69942 swine intestine clone p-4154-6Wa5
DQ456425.1 gg_id:157989 pre-adolescent turkey cecum clone CFT214F4
EU508608.1 gg_id:276402 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36b11
AB243285.1 gg_id:149668 acetone-preserved termite gut clone M2PB4a-031
DQ815372.1 gg_id:161993 mouse cecum clone aab47b03
EF604607.1 gg_id:234054 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ015370.1 gg_id:135193 mouse cecum clone M3_c05
GQ175384.1 gg_id:554511 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
GQ175467.1 gg_id:585880 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
AB009208.1 gg_id:16273 rumen clone RFN54 bacterium
EU458602.1 gg_id:299565 European rabbit feces clone RA_c03
DQ905244.1 gg_id:172163 human fecal clone 013-e8

EU778320.1	324015	2975.6	3978.1	3717.1	2302.4	4627.9	5146.6
DQ815454.1	164595	2878.9	3464.3	2071.8	4552.2	3163.1	2535.1
GQ175436.1	592913	2151.2	2236.0	2294.9	668.0	393.2	995.3
EF445143.1	205846	3456.4	3138.7	1287.7	2548.6	2757.4	3126.2
AB192047.1	142288	36.4	39.6	30.1	62.0	70.0	40.3
DQ015494.1	133077	7653.4	5770.2	4517.5	6300.0	480.0	4620.8
AY426451.1	101401	293.8	127.3	366.7	482.4	72.0	112.8
AB234456.1	146392	41.4	61.3	46.1	75.0	64.5	36.6
EF604609.1	227821	218.8	428.7	1914.2	221.2	926.7	233.3
DQ800941.1	197539	224.8	388.2	726.6	177.8	584.4	431.8
AB062822.1	18245	40.0	43.1	86.9	56.1	66.2	31.1
EU472310.1	291318	117.9	120.8	304.0	174.6	450.9	238.4
EF454103.1	221121	2796.7	3885.3	4352.0	5752.3	9049.2	13412.9
FJ881172.1	416837	6659.8	6181.6	4697.4	7432.0	6758.7	7241.2
AB243284.1	148219	3645.6	3297.4	2406.3	3035.5	3039.0	2125.2
AB299541.1	237802	1888.4	1636.0	1163.4	2253.9	865.3	1188.8
DQ815908.1	161771	1657.4	1767.8	1588.6	1921.8	3462.6	3820.1
DQ456434.1	157545	1445.9	1051.7	435.2	2114.5	260.7	195.7
FJ681080.1	528434	8451.8	9186.2	9953.8	9632.0	9776.3	6895.6
DQ815614.1	166791	2368.9	2081.1	816.4	3365.6	4008.9	3981.9
EF445166.1	216356	2016.9	2715.6	1116.5	493.1	636.1	924.2
FJ881210.1	418334	4701.9	7010.6	2674.7	6939.6	6496.3	4194.0
EF604503.1	232085	3865.9	3691.6	1962.9	5420.7	6535.7	5887.4
FJ681260.1	525729	6812.3	7079.9	3421.5	8017.8	11818.5	8825.2
FJ681301.1	511624	16859.3	14082.8	17143.7	17506.8	12963.0	11966.8
EF454637.1	220301	2365.1	2546.5	1913.9	1682.4	1898.6	2029.9
EF098915.1	197478	278.2	366.4	616.3	152.6	545.0	85.0
FJ367654.1	365731	313.2	243.3	561.3	161.1	142.2	278.4
GQ422712.1	552928	94.2	83.8	53.4	91.5	73.2	22.4
AF371714.1	69942	2111.0	2160.2	2507.9	3029.9	356.3	924.8
DQ456425.1	157989	3462.4	3445.6	1202.2	4500.6	6830.1	5467.8
EU508608.1	276402	6399.4	5989.1	4272.0	7261.3	8771.7	7104.4
AB243285.1	149668	96.8	105.2	190.1	81.8	83.3	59.5
DQ815372.1	161993	2744.0	2619.6	2369.6	4805.6	6733.9	5463.6
EF604607.1	234054	7213.1	5764.1	3621.0	4961.8	5225.9	3817.0
DQ015370.1	135193	161.4	117.7	161.5	158.0	120.6	135.1
GQ175384.1	554511	8841.0	9789.0	4504.3	6296.9	5375.0	5214.1
GQ175467.1	585880	2689.7	4557.3	6950.8	3360.7	7051.2	5922.7
AB009208.1	16273	201.4	221.4	676.3	142.2	165.0	345.6
EU458602.1	299565	3388.4	3747.2	2811.9	4547.6	5579.1	4379.1
DQ905244.1	172163	818.7	954.1	1259.7	1044.5	849.6	596.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	69934
s__unclassified	69955
s__unclassified	69968
s__unclassified	69970
s__unclassified	69986
s__unclassified	69988
s__unclassified	70017
s__unclassified	70024
s__unclassified	70027
s__unclassified	70050
s__unclassified	70052
s__unclassified	70061
s__unclassified	70080
s__unclassified	70083
s__unclassified	70107
s__unclassified	70119
s__unclassified	70121
s__unclassified	70131
s__unclassified	70132
s__unclassified	70135
s__unclassified	70138
s__unclassified	70142
s__unclassified	70157
s__unclassified	70159
s__unclassified	70175
s__unclassified	70186
s__unclassified	70189
s__unclassified	70204
s__unclassified	70207
s__unclassified	70211
s__unclassified	70220
s__unclassified	70223
s__unclassified	70237
s__unclassified	70241
s__unclassified	70242
s__unclassified	70252
s__unclassified	70254
s__unclassified	70261
s__unclassified	70266
s__unclassified	70269
s__unclassified	70279

EF602917.1 gg_id:228798 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF436324.1 gg_id:204369 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC38
GQ897552.1 gg_id:555547 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
EU845633.1 gg_id:346636 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AJ009493.1 gg_id:16086 anaerobic TCB-transforming consortium clone SJA-136
AB487703.1 gg_id:538197 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
EF436352.1 gg_id:208802 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC66
GU303307.1 gg_id:576911 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU474551.1 gg_id:288952 bighorn sheep feces clone BHSD_aaa03g05
EF063613.1 gg_id:174127 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo
AY858451.2 gg_id:110439 gastrointestinal tract zebra clone ZEBRA_12
EF603775.1 gg_id:230542 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU842417.1 gg_id:327471 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
CU925649.1 gg_id:569463 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU843209.1 gg_id:351235 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EF401880.1 gg_id:217109 human fecal clone SJTU_D_15_78
EU778048.1 gg_id:344860 Black rhinoceros feces clone RH_aaj90h01
GU302617.1 gg_id:538833 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
FJ416096.1 gg_id:359349 sediments sediment station NEC5 Northern Bering Sea clone 056M55
AB486406.1 gg_id:549867 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
CU924768.1 gg_id:550433 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AM278890.2 gg_id:231376 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
CU927708.1 gg_id:571884 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ517038.1 gg_id:513057 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
AF275916.1 gg_id:72230 anaerobic digester clone AA05
AY692049.1 gg_id:99789 UASB reactor clone M77
EU844816.1 gg_id:315276 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ800959.1 gg_id:178394 human fecal clone RL387_aao89h10
EU842554.1 gg_id:346151 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU844348.1 gg_id:330515 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB062820.1 gg_id:33347 termite gut homogenate clone BCf4-07
AY574991.1 gg_id:102360 Catabacter hongkongensis str. HKU16
EF434372.1 gg_id:215573 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont
AB486418.1 gg_id:584437 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EF688248.1 gg_id:317224 Detection microbial sludge anaerobic wastewater treatment system clone 6D9_cons
AY985462.1 gg_id:116947 human stool clone C418
CU923982.1 gg_id:551149 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU774614.1 gg_id:331966 Angola Colobus feces clone EAC_1aaa02d10
CU927863.1 gg_id:557576 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ326341.1 gg_id:145236 Metagenomic gut microbiome healthy human stool clone C332
FJ535031.1 gg_id:592702 Enhancement protein conversion volatile fatty acids accumulation during addition: ef

EF602917.1	228798	1411.7	1143.7	369.3	772.0	98.1	107.1
EF436324.1	204369	52.2	36.8	170.6	46.9	62.5	167.2
GQ897552.1	555547	497.4	325.9	1308.1	718.7	89.3	153.2
EU845633.1	346636	143.9	104.7	458.7	83.2	65.1	79.0
AJ009493.1	16086	323.6	901.2	997.0	358.6	2993.1	1297.2
AB487703.1	538197	2377.3	2175.0	5420.1	3919.5	1187.5	941.4
EF436352.1	208802	706.9	374.5	2302.0	699.0	2004.5	1197.1
GU303307.1	576911	315.7	101.3	185.7	408.1	100.2	216.2
EU474551.1	288952	320.7	284.9	1028.2	187.2	159.3	730.6
EF063613.1	174127	1492.3	2187.3	1664.4	1237.1	362.9	858.2
AY858451.2	110439	29.8	42.9	19.1	67.9	61.2	14.4
EF603775.1	230542	95.1	64.2	71.1	85.2	116.4	37.1
EU842417.1	327471	2265.8	2576.8	3890.6	2043.9	2239.8	1677.3
CU925649.1	569463	573.0	432.8	1803.3	1460.1	295.2	290.0
EU843209.1	351235	2829.9	2328.0	4452.6	2873.6	1674.1	2640.9
EF401880.1	217109	28.8	51.6	74.2	45.0	71.9	37.5
EU778048.1	344860	2347.8	1727.8	1971.3	1892.6	1012.6	980.0
GU302617.1	538833	79.2	97.1	379.4	102.0	77.3	57.3
FJ416096.1	359349	6878.8	7592.4	4489.0	5986.8	1312.7	1781.2
AB486406.1	549867	1487.6	1152.7	3487.1	472.0	160.4	920.5
CU924768.1	550433	452.7	697.0	84.5	58.1	60.0	24.3
AM278890.2	231376	743.8	994.8	1812.3	573.3	1368.8	714.4
CU927708.1	571884	2077.4	1850.5	3588.9	1680.5	1595.7	1117.8
FJ517038.1	513057	1332.6	1559.5	2699.6	1587.1	3094.9	2839.3
AF275916.1	72230	9851.7	9554.4	12683.3	8046.4	9677.2	8261.1
AY692049.1	99789	417.2	497.3	568.8	893.0	480.0	232.2
EU844816.1	315276	1391.2	2290.5	3754.8	1741.7	1726.8	1455.5
DQ800959.1	178394	191.5	260.9	231.0	112.7	121.9	89.4
EU842554.1	346151	1201.7	1087.4	3855.3	684.2	3225.6	3985.2
EU844348.1	330515	411.6	413.9	643.4	465.6	138.9	170.5
AB062820.1	33347	924.7	1038.7	1665.4	1914.9	2012.2	1816.8
AY574991.1	102360	1439.4	1171.8	2790.0	1233.5	323.6	453.4
EF434372.1	215573	38.2	44.3	98.0	47.8	71.7	23.9
AB486418.1	584437	5706.8	4537.2	5305.5	5045.7	3005.4	2742.4
EF688248.1	317224	4951.8	5570.5	3432.2	2717.3	6431.1	3171.0
AY985462.1	116947	8764.7	7642.1	7179.9	7321.6	4749.4	4512.2
CU923982.1	551149	3611.0	2285.1	2942.4	4816.7	1177.2	927.4
EU774614.1	331966	3811.3	4091.4	2550.8	3406.0	7006.1	7950.9
CU927863.1	557576	3183.0	2942.1	3119.2	4709.8	4965.1	4184.0
DQ326341.1	145236	237.8	122.3	616.1	100.1	67.2	51.4
FJ535031.1	592702	88.4	21.3	389.7	46.9	60.5	19.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Catabacteriaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Alkaliphilus
g__Alkaliphilus
g__Alkaliphilus

s__unclassified	70284
s__unclassified	70301
s__unclassified	70307
s__unclassified	70310
s__unclassified	70321
s__unclassified	70324
s__unclassified	70328
s__unclassified	70330
s__unclassified	70336
s__unclassified	70345
s__unclassified	70352
s__unclassified	70367
s__unclassified	70374
s__unclassified	70414
s__unclassified	70432
s__unclassified	70435
s__unclassified	70450
s__unclassified	70456
s__unclassified	70466
s__unclassified	70478
s__unclassified	70491
s__unclassified	70493
s__unclassified	70501
s__unclassified	70506
s__unclassified	70560
s__unclassified	70568
s__unclassified	70589
s__unclassified	70601
s__unclassified	70605
s__unclassified	70611
s__unclassified	70615
s__unclassified	70617
s__unclassified	70797
s__unclassified	70927
s__unclassified	70997
s__unclassified	71173
s__unclassified	71184
s__unclassified	71249
s__Alkaliphilus oremlandii	70216
s__Alkaliphilus transvaalensis	69959
s__Alkaliphilus transvaalensis	70477

EU843730.1 gg_id:321463 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ366077.1 gg_id:361711 feces adult twins and mothers; TS25 clone TS25_a02d10
AY854309.1 gg_id:110388 herbivore gastrointestinal tract clone Thompsons14
EU259437.1 gg_id:255950 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC61
DQ797645.1 gg_id:189301 human fecal clone RL206_aaj14b09
AJ576334.1 gg_id:105672 hindgut homogenate Pachnoda ephippiata larva clone PeH17
AF129865.1 gg_id:16131 anaerobic digestor clone HA16
EU844475.1 gg_id:338166 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AM275604.2 gg_id:231952 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
FN563365.1 gg_id:582043 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
AF129867.1 gg_id:16130 anaerobic digestor clone HB69
DQ805386.1 gg_id:177600 human fecal clone RL203_aai62a01
EU508399.1 gg_id:274619 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33a04
DQ800020.1 gg_id:188183 human fecal clone RL247_aaj23b09
AB175358.1 gg_id:107322 mesophilic anaerobic BSA digester clone BSA1B-04
AB185741.1 gg_id:107464 rumen clone U29-A02
AB486816.1 gg_id:578501 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
EU844677.1 gg_id:338831 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU771507.1 gg_id:320073 Hamadryas Baboon feces clone AFBAB_aai01h10
EU475386.1 gg_id:290991 rock hyrax feces clone RHSD_aaa02g08
AB294304.1 gg_id:205022 Microbial structure deep coal seem groundwater clone YWB35
EU844902.1 gg_id:350834 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EF434357.1 gg_id:213762 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont
U81761.2 gg_id:14133 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinBB35
DQ809166.1 gg_id:180585 human fecal clone RL308_aal82f10
EU844060.1 gg_id:339645 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU774645.1 gg_id:322962 Angola Colobus feces clone EAC_2_aaa02f05
AB486582.1 gg_id:571348 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
DQ798367.1 gg_id:177179 human fecal clone RL181_aah41f03
EU466370.1 gg_id:302115 bighorn sheep feces clone BH2_aao22f06
EU509200.1 gg_id:270441 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g05
FJ366040.1 gg_id:368527 feces adult twins and mothers; TS25 clone TS25_a02a06
AB192038.1 gg_id:142190 termite gut homogenate clone M2PB4-86
AB089007.1 gg_id:78174 termite gut homogenate clone Rs-G06
AB243282.1 gg_id:149631 acetone-preserved termite gut clone M2PB4a-013
AB192021.1 gg_id:143863 termite gut homogenate clone M2PB4-35
AB192048.1 gg_id:144142 termite gut homogenate clone M2PT2-23
AB255919.1 gg_id:169989 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr
CP000853.1 gg_id:239100 Alkaliphilus oremlandii str. OhILAs
DQ128252.1 gg_id:137817 Unique Microbial Fluids Chinese Continental Scientific Drilling drilling fluid clone CCS
EF125434.1 gg_id:176156 mangrove soil clone MSB-2D5

EU843730.1	321463	13461.5	13526.8	9228.8	10878.2	13976.3	11407.0
FJ366077.1	361711	112.0	147.0	198.8	135.9	615.5	595.6
AY854309.1	110388	954.6	901.1	289.4	273.3	886.3	362.8
EU259437.1	255950	335.0	477.0	868.8	1553.7	641.5	1211.4
DQ797645.1	189301	407.0	223.6	755.3	468.9	99.9	154.3
AJ576334.1	105672	1532.4	826.7	1197.9	379.1	620.1	336.4
AF129865.1	16131	3799.5	4748.6	3645.5	2382.7	2563.9	3191.7
EU844475.1	338166	2698.5	2567.8	4425.0	5162.6	2816.5	4319.3
AM275604.2	231952	6267.5	6472.1	8007.2	7609.9	6252.9	5346.7
FN563365.1	582043	9048.7	9647.0	8527.0	7444.4	5797.0	6074.1
AF129867.1	16130	810.9	299.0	108.4	568.2	63.2	48.9
DQ805386.1	177600	13514.2	12154.9	7819.7	10367.3	11100.2	8799.0
EU508399.1	274619	8814.4	7717.3	6750.7	5656.9	5256.2	7272.9
DQ800020.1	188183	3088.0	3264.8	1659.1	3541.9	7764.5	5601.3
AB175358.1	107322	194.8	124.0	428.8	118.4	82.4	98.0
AB185741.1	107464	967.5	1158.7	1954.5	1763.6	3900.6	4526.1
AB486816.1	578501	1615.7	1456.6	3836.7	2308.2	229.1	1140.0
EU844677.1	338831	574.5	692.0	2152.1	1834.5	1097.9	2093.7
EU771507.1	320073	1347.8	2257.2	2625.1	1788.4	964.7	817.5
EU475386.1	290991	4915.2	6311.6	1428.5	6096.8	7687.6	7214.3
AB294304.1	205022	89.2	74.9	149.4	72.7	63.6	69.2
EU844902.1	350834	2524.6	2169.9	2004.6	1531.2	1559.3	1514.6
EF434357.1	213762	42.9	46.3	71.9	73.5	53.3	61.9
U81761.2	14133	1055.1	1737.9	767.1	1237.8	477.1	481.1
DQ809166.1	180585	215.1	561.1	83.0	380.0	557.6	267.5
EU844060.1	339645	2311.6	3014.2	4146.8	1972.3	2050.5	2580.7
EU774645.1	322962	1878.7	2178.8	1931.3	1431.5	2888.6	2421.6
AB486582.1	571348	1106.7	884.3	2172.3	588.7	444.6	608.5
DQ798367.1	177179	2741.6	2427.6	1572.3	1116.9	1051.8	1407.2
EU466370.1	302115	2572.9	1290.9	3359.4	1975.8	922.2	2424.3
EU509200.1	270441	15226.9	15821.8	11510.6	14202.7	16047.9	14446.6
FJ366040.1	368527	3880.0	4141.3	1569.2	4427.9	6011.0	5215.0
AB192038.1	142190	368.4	237.8	1688.6	505.0	255.9	259.2
AB089007.1	78174	259.3	354.6	183.5	426.1	87.8	68.1
AB243282.1	149631	143.3	198.7	151.0	137.6	241.2	163.9
AB192021.1	143863	147.4	219.5	268.2	272.7	523.5	748.4
AB192048.1	144142	66.5	157.3	110.7	95.9	61.5	39.7
AB255919.1	169989	6468.5	6673.5	4194.7	2782.9	3620.5	3331.3
CP000853.1	239100	940.0	933.6	1120.3	400.9	2048.1	1701.4
DQ128252.1	137817	6241.2	4637.1	201.9	3901.7	93.9	161.2
EF125434.1	176156	5372.0	5705.0	3995.8	5189.0	1824.8	1047.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Alkaliphilus
g__Alkaliphilus
g__Alkaliphilus
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caloramator
g__Caminicella
g__Caminicella
g__Caminicella
g__Caminicella
g__Caminicella
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__Alkaliphilus transvaalensis	70581
s__unclassified	70314
s__unclassified	70514
s__unclassified	48291
s__unclassified	48294
s__unclassified	48741
s__unclassified	48893
s__unclassified	49133
s__unclassified	49718
s__unclassified	71999
s__unclassified	72109
s__unclassified	72117
s__unclassified	72130
s__unclassified	72157
s__unclassified	72162
s__unclassified	72177
s__unclassified	72228
s__unclassified	72402
s__unclassified	72736
s__unclassified	73048
s__unclassified	69953
s__unclassified	69984
s__unclassified	70037
s__unclassified	70144
s__unclassified	70451
s__Clostridium acetobutylicum	72762
s__Clostridium baratii	44362
s__Clostridium baratii	45139
s__Clostridium bifermentans	71017
s__Clostridium bifermentans	71133
s__Clostridium bowmanii	71871
s__Clostridium bowmanii	71878
s__Clostridium bowmanii	72070
s__Clostridium bowmanii	72323
s__Clostridium bowmanii	72621
s__Clostridium bowmanii	72760
s__Clostridium butyricum	44423
s__Clostridium butyricum	44938
s__Clostridium butyricum	45218
s__Clostridium butyricum	45831
s__Clostridium cellulolyticum	27653

AY569285.1 gg_id:101611 pink microbial mat clone YJQ-8
EF559033.1 gg_id:235642 Microbial functional groups solid waste digestor stable isotope probing thermophilic
AM183354.1 gg_id:169422 genetic physiological d deep-biosphere Equatorial Pacific and Peru Margin marine su
X75788.1 gg_id:16108 Caloramator indicus str. IndiB4
NR_026265.1 gg_id:564401 Caloramator proteoclasticus str. Uruguayensis; DSM 10124
AF104215.1 gg_id:16110 Caloramator coolhaasii str. Z
L09187.1 gg_id:16111 Caloramator fervidus str. RT4. B1
AF489534.1 gg_id:68459 Caloramator uzoniensis str. JW/VK-KU2
AF181848.1 gg_id:34407 Caloramator viterbiensis str. JW/MS-VS5
DQ676295.1 gg_id:220054 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
GQ906581.1 gg_id:584933 Clostridium sp. str. SW003
AB486915.1 gg_id:558768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
AB486702.1 gg_id:575035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
AB487603.1 gg_id:536237 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSRC
GQ906580.1 gg_id:558972 Clostridium sp. str. SW002
AB488197.1 gg_id:548100 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
DQ129398.1 gg_id:151986 microarray level air two cities Texas urban aerosol clone AKIW1006
AB486298.1 gg_id:554614 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
Y18179.1 gg_id:32182 Clostridium cylindrosporum str. DSM 605
DQ129395.1 gg_id:138500 microarray level air two cities Texas urban aerosol clone AKIW981
AJ431243.1 gg_id:102801 Clostridium sp. str. Dex60-61
FN356335.1 gg_id:590922 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni
AJ431244.1 gg_id:79318 Clostridium sp. str. Dex60-75
FN356332.1 gg_id:563046 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni
FN356242.1 gg_id:583876 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni
AM231183.1 gg_id:151509 Clostridium acetobutylicum str. 7 MSU
AB240207.1 gg_id:141357 Clostridium baratii str. T8
AB240209.1 gg_id:142276 Clostridium baratii str. T10
EU547723.1 gg_id:271569 Clostridium bifermentans str. SL186
EU460327.1 gg_id:299386 polar bear feces clone PB1_aai26f05
AB539899.1 gg_id:535555 Clostridium sp. str. C5S3
EF589987.2 gg_id:227564 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
AJ506120.1 gg_id:60735 Clostridium bowmanii str. DSM 14206
EF063634.1 gg_id:191245 Microbial ecology autotrophic anaerobic denitrifying UASB reactor clone R1Cb41
EF570920.1 gg_id:231269 Clostridium frigoriphilum str. 14F
AJ297443.1 gg_id:29618 Clostridium psychrophilum str. -1/C-/I
DQ831126.1 gg_id:170961 Clostridium butyricum str. W4
ABDT01000025.2 gg_id:262123 Clostridium butyricum str. 5521
AJ289705.1 gg_id:21382 Clostridium butyricum str. IBUN 125C
AM930366.1 gg_id:541328 gradual cooling stage mass and its spatial composting clone SMR62
NC_011898.1 gg_id:471235 Clostridium cellulolyticum H10 str. H10; ATCC 35319

AY569285.1	101611	1424.9	1328.5	885.0	497.5	3171.8	1914.3
EF559033.1	235642	340.7	358.6	1240.9	418.3	105.0	501.3
AM183354.1	169422	1361.7	1684.2	5226.7	1888.2	2245.1	1787.1
X75788.1	16108	3129.8	3189.3	5544.7	2420.6	1498.0	2284.7
NR_026265.1	564401	72.9	73.0	94.8	76.1	91.1	43.1
AF104215.1	16110	49.9	98.8	161.7	76.1	155.1	162.7
L09187.1	16111	80.0	102.5	136.5	129.0	112.6	153.4
AF489534.1	68459	3606.3	3137.7	907.8	746.5	4241.1	3129.1
AF181848.1	34407	39.9	79.6	45.0	49.8	45.7	22.9
DQ676295.1	220054	10006.4	10233.8	8712.4	8852.0	11024.8	9926.5
GQ906581.1	584933	12828.0	11604.8	7692.2	5683.0	5738.6	5938.7
AB486915.1	558768	7346.3	7543.7	5742.6	5323.6	3303.5	4457.7
AB486702.1	575035	252.6	107.4	587.6	113.8	127.8	104.4
AB487603.1	536237	3754.3	3387.2	4454.8	2453.3	3217.4	2870.6
GQ906580.1	558972	16047.0	16559.9	10746.5	14863.1	18225.2	15626.8
AB488197.1	548100	2155.5	968.7	2959.4	780.5	1227.6	991.5
DQ129398.1	151986	1303.1	2135.9	1501.0	1847.0	1054.2	2063.5
AB486298.1	554614	1313.2	461.1	3108.5	1034.4	1046.2	760.0
Y18179.1	32182	666.3	582.9	1214.6	118.4	140.4	527.2
DQ129395.1	138500	1430.8	741.5	1028.4	455.8	232.5	250.9
AJ431243.1	102801	22.5	32.1	23.5	43.3	63.6	26.4
FN356335.1	590922	8116.7	10302.6	7159.3	7423.1	14021.8	9331.0
AJ431244.1	79318	2551.0	2809.1	4814.5	3134.9	2308.6	1859.0
FN356332.1	563046	3042.5	2848.3	6010.7	2883.5	4742.6	5833.7
FN356242.1	583876	3861.0	3919.8	5052.3	2551.1	2228.2	2943.0
AM231183.1	151509	2787.0	2474.3	4713.5	1467.4	973.9	1455.1
AB240207.1	141357	327.3	497.5	983.1	212.9	209.4	242.4
AB240209.1	142276	1502.6	2556.2	2437.5	1127.2	1436.0	1849.3
EU547723.1	271569	87.5	171.2	138.9	76.8	45.8	68.5
EU460327.1	299386	1016.8	3143.7	1646.4	806.9	557.1	1183.7
AB539899.1	535555	1716.1	1461.5	2095.4	363.2	57.7	524.2
EF589987.2	227564	2965.9	2569.3	6036.7	1823.2	2166.7	2554.4
AJ506120.1	60735	1627.7	1383.0	4430.4	350.4	1305.5	1692.2
EF063634.1	191245	7086.2	7188.7	9329.2	6530.3	5395.1	4907.9
EF570920.1	231269	5031.8	3954.9	7631.0	2682.0	3423.4	3420.1
AJ297443.1	29618	799.6	557.0	3234.8	315.8	195.4	352.2
DQ831126.1	170961	5547.5	4993.1	2737.6	3316.3	2112.5	2149.8
ABDT01000025.2	262123	1198.8	1606.1	2843.0	801.2	463.2	848.1
AJ289705.1	21382	4883.9	5080.8	2648.8	3178.1	2430.1	2127.1
AM930366.1	541328	253.2	414.3	397.6	174.7	235.6	170.2
NC_011898.1	471235	4242.6	4129.3	4080.0	6081.8	2335.5	2961.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__Clostridium cellulovorans	72712
s__Clostridium colicanis	45774
s__Clostridium difficile	70879
s__Clostridium glycolicum	70664
s__Clostridium glycolicum	70872
s__Clostridium glycolicum	70983
s__Clostridium haemolyticum	71949
s__Clostridium haemolyticum	72168
s__Clostridium hiranonis	70638
s__Clostridium hiranonis	70642
s__Clostridium hiranonis	70696
s__Clostridium hiranonis	70703
s__Clostridium hiranonis	70704
s__Clostridium hiranonis	70726
s__Clostridium hiranonis	70732
s__Clostridium hiranonis	70738
s__Clostridium hiranonis	70741
s__Clostridium hiranonis	70809
s__Clostridium hiranonis	70813
s__Clostridium hiranonis	70833
s__Clostridium hiranonis	70836
s__Clostridium hiranonis	70869
s__Clostridium hiranonis	70881
s__Clostridium hiranonis	70885
s__Clostridium hiranonis	70901
s__Clostridium hiranonis	70912
s__Clostridium hiranonis	70929
s__Clostridium hiranonis	70944
s__Clostridium hiranonis	70947
s__Clostridium hiranonis	70981
s__Clostridium hiranonis	71006
s__Clostridium hiranonis	71014
s__Clostridium hiranonis	71039
s__Clostridium hiranonis	71082
s__Clostridium hiranonis	71085
s__Clostridium hiranonis	71100
s__Clostridium hiranonis	71111
s__Clostridium hiranonis	71161
s__Clostridium hiranonis	71172
s__Clostridium hiranonis	71176
s__Clostridium hiranonis	71179

X73438.1 gg_id:16231 Clostridium cellulovorans str. DSM 3052
FJ957870.1 gg_id:454680 Clostridium colicanis str. JPL_15
NZ_ABHE02000055.1 gg_id:559187 Clostridium difficile QCD-76w55
AY007244.1 gg_id:40074 Clostridium glycolicum str. CIN5
FJ384385.1 gg_id:359641 Clostridium glycolicum str. BG-C128
EU887819.1 gg_id:340525 Clostridium glycolicum str. SN10
L37590.1 gg_id:16126 Clostridium botulinum
AB035087.3 gg_id:22235 Clostridium novyi str. ATCC25758
EU458365.1 gg_id:288771 spotted hyena feces clone HY1_e01
FJ978743.1 gg_id:414789 feces clone CL_F_446
EU772684.1 gg_id:319770 Bush dog feces clone bdog1_aai77a07
EU776210.1 gg_id:308823 Spotted hyena feces clone HY1_d03_1
EU776124.1 gg_id:345246 Spotted hyena feces clone HY1_h10
EU772930.1 gg_id:326430 Bush dog feces clone bdog1_aai78c05
DQ800516.1 gg_id:197510 human fecal clone RL183_aah27g08
DQ800626.1 gg_id:185590 human fecal clone RL183_aao01c05
EU468360.1 gg_id:299843 lion feces clone LI2_aae48c06
EU465520.1 gg_id:287479 lion feces clone LI3_aah78g11
EU772771.1 gg_id:318578 Bush dog feces clone bdog1_d07
EU465499.1 gg_id:302610 lion feces clone LI3_aah78d08
EU772822.1 gg_id:319652 Bush dog feces clone bdog1_aai77f11
EU772713.1 gg_id:344553 Bush dog feces clone bdog1_aai80g01
EU458402.1 gg_id:290404 spotted hyena feces clone HY1_d09_2
EU776059.1 gg_id:306891 Spotted hyena feces clone HY1_f06
EU468383.1 gg_id:295187 lion feces clone LI2_aae49a09
EU467616.1 gg_id:297934 southern three-banded armadillo feces clone arma_g12_1
EU459388.1 gg_id:289373 cheetah feces clone CE3_aai06g06
EU776726.1 gg_id:305526 Lion feces clone LI1_c05_1
EU778549.1 gg_id:312781 Ring-tailed lemur feces clone RT_aai09b05
EU468210.1 gg_id:288094 lion feces clone LI1_f02_2
EU463367.1 gg_id:300475 bush dog feces clone bdog1_aai80b06
EU772883.1 gg_id:320308 Bush dog feces clone bdog1_aai79c02
EU458351.1 gg_id:301967 spotted hyena feces clone HY1_b05_1
EU773971.1 gg_id:322366 Cheetah feces clone CE3_aai06a11
EU465484.1 gg_id:293823 lion feces clone LI3_aah78b07
EU772860.1 gg_id:347235 Bush dog feces clone bdog1_aai77b09
EU772796.1 gg_id:355548 Bush dog feces clone bdog1_aai79e10
EU774859.1 gg_id:324938 Short-beaked Echidna feces clone ECH_aai37g08
EU772948.1 gg_id:310880 Bush dog feces clone bdog1_aai80a09
EU773973.1 gg_id:341829 Cheetah feces clone CE3_aai07f08
EU458412.1 gg_id:295090 spotted hyena feces clone HY1_g02_2

X73438.1	16231	169.7	297.1	375.1	207.7	709.2	199.7
FJ957870.1	454680	3728.0	3655.8	4387.5	3720.3	5449.4	4766.6
NZ_ABHE02000055.1	559187	163.0	279.4	275.2	688.9	198.4	258.1
AY007244.1	40074	896.2	1338.9	1735.8	716.8	975.9	1459.3
FJ384385.1	359641	321.4	406.0	450.1	357.3	384.3	233.3
EU887819.1	340525	2198.4	2594.5	216.5	882.3	1068.2	796.2
L37590.1	16126	9799.0	9726.5	7413.2	12308.6	11334.3	11537.2
AB035087.3	22235	1531.4	1546.9	2857.6	2335.3	1554.2	1042.9
EU458365.1	288771	8096.6	8981.9	3946.3	8596.7	11557.6	9566.5
FJ978743.1	414789	5306.2	6651.5	5228.8	4034.1	6207.9	6924.9
EU772684.1	319770	1703.3	3209.4	1853.3	2400.5	2456.6	3510.5
EU776210.1	308823	9644.5	12098.9	6060.8	9439.2	11272.1	11359.6
EU776124.1	345246	12411.7	12561.5	8487.3	10715.5	12860.9	11696.4
EU772930.1	326430	303.8	501.0	528.8	557.5	530.4	875.0
DQ800516.1	197510	64.4	282.9	143.1	58.8	62.6	24.6
DQ800626.1	185590	7930.0	7099.9	5793.2	10975.0	12773.1	9880.9
EU468360.1	299843	10531.7	12070.2	6110.1	8372.4	11277.5	9471.0
EU465520.1	287479	17560.2	16522.2	10499.7	14302.8	14977.2	13091.8
EU772771.1	318578	3420.7	5498.5	4730.1	3623.0	8332.2	7725.7
EU465499.1	302610	14735.7	14530.0	8608.9	12057.5	16201.2	12291.9
EU772822.1	319652	9595.8	11606.9	8032.7	9093.5	11037.5	10439.5
EU772713.1	344553	1598.8	1577.4	2504.3	1387.4	474.4	985.9
EU458402.1	290404	4689.8	6068.7	3463.2	3978.4	3499.8	3131.6
EU776059.1	306891	5902.2	9293.4	7175.5	7867.1	5257.0	7121.4
EU468383.1	295187	357.8	577.4	608.5	558.1	520.9	995.6
EU467616.1	297934	1506.9	1284.4	727.9	1838.6	303.1	1178.5
EU459388.1	289373	1273.8	1124.6	3106.2	1168.0	1486.2	869.7
EU776726.1	305526	445.7	961.2	758.5	259.2	180.7	157.0
EU778549.1	312781	58.0	165.0	319.8	139.0	65.1	70.4
EU468210.1	288094	10912.2	11505.8	12738.4	10676.7	7498.5	8935.9
EU463367.1	300475	4048.4	4022.2	1385.0	4604.5	3401.1	3257.8
EU772883.1	320308	987.6	700.8	1629.2	1155.6	662.2	792.3
EU458351.1	301967	7496.6	8961.0	2286.9	9530.2	12494.5	11702.4
EU773971.1	322366	3137.0	3123.4	3249.3	3663.7	3789.8	5066.5
EU465484.1	293823	3005.5	5175.0	4247.7	3894.5	1001.9	2549.6
EU772860.1	347235	585.6	566.8	751.6	1077.4	215.7	170.2
EU772796.1	355548	100.4	153.4	197.7	89.0	83.3	72.6
EU774859.1	324938	1809.0	1542.6	1610.2	3796.9	2384.2	3944.8
EU772948.1	310880	3751.9	6331.6	7062.1	5284.3	4762.5	8929.9
EU773973.1	341829	2654.8	3095.4	5350.2	4714.2	561.0	1166.5
EU458412.1	295090	601.6	1349.0	690.7	880.5	290.9	682.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__Clostridium hiranonis	71225
s__Clostridium hiranonis	71251
s__Clostridium hiranonis	71259
s__Clostridium hiranonis	71296
s__Clostridium intestinale	72438
s__Clostridium intestinale	72650
s__Clostridium irregulare	70655
s__Clostridium irregulare	71037
s__Clostridium kluyveri	72080
s__Clostridium kluyveri	72379
s__Clostridium ljungdahlii	72049
s__Clostridium metallolevans	70778
s__Clostridium metallolevans	70819
s__Clostridium metallolevans	70856
s__Clostridium metallolevans	71079
s__Clostridium metallolevans	71237
s__Clostridium neonatale	45495
s__Clostridium neonatale	45891
s__Clostridium novyi	72260
s__Clostridium paradoxum	71205
s__Clostridium paradoxum	71217
s__Clostridium paraputrificum	45270
s__Clostridium pasteurianum	71786
s__Clostridium pasteurianum	71837
s__Clostridium pasteurianum	71935
s__Clostridium perfringens	71846
s__Clostridium perfringens	72153
s__Clostridium perfringens	72179
s__Clostridium perfringens	72181
s__Clostridium perfringens	72305
s__Clostridium perfringens	72505
s__Clostridium perfringens	72587
s__Clostridium perfringens	72718
s__Clostridium perfringens	72764
s__Clostridium perfringens	72823
s__Clostridium septicum	45419
s__Clostridium sordellii	70640
s__Clostridium sordellii	70768
s__Clostridium sordellii	70802
s__Clostridium sordellii	70954
s__Clostridium sordellii	70977

EU467710.1 gg_id:290179 bush dog feces clone bdog1_g09
EU772864.1 gg_id:306149 Bush dog feces clone bdog1_aai78h05
EU773792.1 gg_id:326083 Cheetah feces clone CE3_aai06h01
EU773797.1 gg_id:339350 Cheetah feces clone CE3_aai05c02
AY781385.1 gg_id:108384 Clostridium intestinale
NR_029263.1 gg_id:578541 Clostridium intestinale str. Catt39; DSM 6191
EU887817.1 gg_id:303972 Clostridium irregulare str. SN8
X73447.1 gg_id:14214 Clostridium irregulare str. DSM 2635
CP000673.1 gg_id:254073 Clostridium kluyveri str. DSM 555
ABAJ01000001.1 gg_id:219164 Clostridium kluyveri str. DSM 555
EU828402.1 gg_id:560739 Microbial effects changeover without CO2 sparging two-stage biological and methan
EU887818.1 gg_id:342268 Clostridium metallolevans str. SN9
DQ133569.1 gg_id:138329 Clostridium metallolevans str. ASI1
EU887815.1 gg_id:324891 Clostridium metallolevans str. SN1
EU887823.1 gg_id:338957 Clostridium metallolevans str. SN16
EU887820.1 gg_id:315305 Clostridium glycolicum str. SN12
AF275949.1 gg_id:73000 Clostridium neonatale str. LCDC no.99--005
EU869244.1 gg_id:349217 Clostridium neonatale str. CM-C98
AB045606.1 gg_id:29673 Clostridium novyi str. JCM1406
Z69928.1 gg_id:14186 Clostridium paradoxum str. DSM 7308T
Z69933.1 gg_id:14196 Clostridium paradoxum str. DSM 7308T
X75907.1 gg_id:16215 Clostridium paraputrificum str. ATCC 25780
EF656616.1 gg_id:248740 Clostridium pasteurianum str. AFBR-G
EF140980.1 gg_id:175357 Clostridium pasteurianum str. CH1
AB536773.1 gg_id:572490 Clostridium pasteurianum str. JCM 1408
EU459335.1 gg_id:294957 hedgehog feces clone HH_aai36f06
AM889034.1 gg_id:237367 Clostridium perfringens JS9
FJ215327.1 gg_id:577392 Clostridium perfringens str. MOTB3
ABDU01000051.2 gg_id:270573 Clostridium perfringens C str. JGS1495
NC_003366.1 gg_id:128673 Clostridium perfringens str. 13
EU773814.1 gg_id:323142 Cheetah feces clone CE2_c01
NZ_ABOO01000021.1 gg_id:267792 Clostridium perfringens D str. JGS1721
FJ215350.1 gg_id:559845 Clostridium perfringens str. ME1
EU775668.1 gg_id:304779 Hedgehog feces clone HH_aai35d06
EU772738.1 gg_id:315982 Bush dog feces clone bdog1_aai80b01
FJ424478.1 gg_id:363985 Clostridium septicum str. SH-C24
FJ375896.1 gg_id:308996 and prevalence blaTEM genes polar bear feces clone PBF_d34
FJ375897.1 gg_id:334569 and prevalence blaTEM genes polar bear feces clone PBF_d35
FJ375892.1 gg_id:325217 and prevalence blaTEM genes polar bear feces clone PBF_d30
FJ375783.1 gg_id:354513 and prevalence blaTEM genes polar bear feces clone PBF_b12
FJ375820.1 gg_id:320883 and prevalence blaTEM genes polar bear feces clone PBF_c1

EU467710.1	290179	1888.4	2518.6	2490.1	2412.7	2124.0	2646.4
EU772864.1	306149	2295.2	4611.1	3041.5	2060.6	5044.2	6434.6
EU773792.1	326083	1908.5	1437.7	2613.1	698.9	5052.2	6280.5
EU773797.1	339350	4589.8	5204.4	4652.0	5139.5	2564.0	3808.5
AY781385.1	108384	3185.4	3198.9	3101.7	1802.4	2874.0	2374.0
NR_029263.1	578541	8478.2	9834.7	5532.9	5757.4	6191.4	5658.2
EU887817.1	303972	7965.7	7974.5	3786.0	6836.1	7593.5	6911.5
X73447.1	14214	1752.2	2192.7	2253.5	997.3	1020.7	1095.4
CP000673.1	254073	2319.8	2668.3	7647.8	1024.0	738.8	2101.7
ABAJ01000001.1	219164	1877.3	2091.5	6260.6	852.9	438.3	1103.0
EU828402.1	560739	240.4	151.1	551.8	113.6	90.7	140.6
EU887818.1	342268	2743.1	3276.2	2591.4	3508.8	2653.7	3869.0
DQ133569.1	138329	675.8	1285.8	885.1	620.4	1307.8	1303.5
EU887815.1	324891	4338.1	5813.7	3871.6	3007.5	5018.0	5277.3
EU887823.1	338957	10135.4	10939.0	5074.9	8005.1	12754.0	12965.1
EU887820.1	315305	4983.5	6203.4	3221.7	5632.4	5412.8	3880.1
AF275949.1	73000	46.6	41.3	31.1	75.5	38.2	22.4
EU869244.1	349217	473.4	731.6	3094.9	542.2	76.4	439.6
AB045606.1	29673	970.3	1447.2	1835.5	1528.0	1379.3	955.1
Z69928.1	14186	852.9	854.3	947.4	255.4	202.8	329.9
Z69933.1	14196	1755.9	1571.2	817.8	926.3	223.2	516.2
X75907.1	16215	505.8	717.4	1604.7	811.1	61.7	237.5
EF656616.1	248740	723.6	288.4	1442.1	199.8	46.0	153.4
EF140980.1	175357	9235.2	8645.1	7672.8	7619.6	6513.5	6664.8
AB536773.1	572490	1417.8	1421.8	3827.1	1025.5	250.1	525.6
EU459335.1	294957	1618.1	2079.0	2213.5	2361.5	1136.1	2167.5
AM889034.1	237367	8208.4	6481.2	6520.2	5223.6	5976.5	5580.8
FJ215327.1	577392	8189.7	7471.0	4715.1	5491.4	7272.3	7551.4
ABDU01000051.2	270573	3018.2	2996.9	3415.1	2066.9	5617.4	4955.7
NC_003366.1	128673	4958.0	4865.4	3328.4	3199.8	2823.9	2836.3
EU773814.1	323142	2163.5	1844.3	2398.2	4158.3	419.4	2423.2
NZ_ABOO01000021.1	267792	8979.9	8968.8	5569.1	8361.3	12545.5	9781.6
FJ215350.1	559845	4156.3	4268.3	4356.0	3052.1	5271.7	5536.3
EU775668.1	304779	1905.7	1306.4	1652.7	1053.4	1542.9	1830.6
EU772738.1	315982	4266.9	3746.6	5372.3	3752.9	2052.3	3828.8
FJ424478.1	363985	251.3	337.8	983.6	154.7	99.3	266.9
FJ375896.1	308996	4833.8	6123.6	5944.8	4453.2	5491.7	4975.3
FJ375897.1	334569	3883.6	4862.9	2415.1	2646.3	570.1	763.1
FJ375892.1	325217	2615.5	3109.6	1901.0	3322.5	4689.1	4100.1
FJ375783.1	354513	4593.8	6116.2	6789.1	3486.2	2102.8	3100.2
FJ375820.1	320883	398.8	779.7	389.3	158.0	98.9	224.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__Clostridium sordellii	71011
s__Clostridium sordellii	71025
s__Clostridium sordellii	71027
s__Clostridium sordellii	71077
s__Clostridium sordellii	71086
s__Clostridium sordellii	71216
s__Clostridium stercorarium	27840
s__Clostridium subterminale	72366
s__Clostridium tetani	72553
s__Clostridium thermocellum	27879
s__Clostridium thermocellum	28135
s__Clostridium thermopalmarium	72554
s__unclassified	27270
s__unclassified	27299
s__unclassified	27321
s__unclassified	27364
s__unclassified	27372
s__unclassified	27373
s__unclassified	27375
s__unclassified	27382
s__unclassified	27387
s__unclassified	27400
s__unclassified	27402
s__unclassified	27423
s__unclassified	27447
s__unclassified	27452
s__unclassified	27462
s__unclassified	27479
s__unclassified	27485
s__unclassified	27489
s__unclassified	27490
s__unclassified	27500
s__unclassified	27520
s__unclassified	27545
s__unclassified	27549
s__unclassified	27602
s__unclassified	27605
s__unclassified	27608
s__unclassified	27615
s__unclassified	27687
s__unclassified	27737

EU869242.1 gg_id:336112 Clostridium sordellii str. CM-C96
FJ375886.1 gg_id:318634 and prevalence blaTEM genes polar bear feces clone PBF_d24
FJ375781.1 gg_id:312800 and prevalence blaTEM genes polar bear feces clone PBF_b10
FJ375891.1 gg_id:304496 and prevalence blaTEM genes polar bear feces clone PBF_d29
FJ375832.1 gg_id:337750 and prevalence blaTEM genes polar bear feces clone PBF_c14
FJ375879.1 gg_id:304036 and prevalence blaTEM genes polar bear feces clone PBF_d17
AJ310082.1 gg_id:31278 Clostridium stercorarium str. DSM 8532T
EF030542.1 gg_id:190008 Clostridium botulinum str. G196
NC_004557.1 gg_id:471257 Clostridium tetani E88 str. Massachusetts
AABG04000051.1 gg_id:130271 Clostridium thermocellum str. ATCC 27405
FJ599513.1 gg_id:545541 Clostridium thermocellum str. CTL-6
NR_026112.1 gg_id:569919 Clostridium thermopalmarium str. BVP; ATCC 51427
DQ887919.1 gg_id:164481 thermophilic anaerobic solid waste bioreactor clone GHB3A06
X71856.1 gg_id:15980 Clostridium cellobioparum str. DSM 1351
AB307636.1 gg_id:271652 clay wall used Japanese traditional buildings clone B46
EF559080.1 gg_id:218474 mesophilic anaerobic digester clone B35_F_B_A02
AJ863357.1 gg_id:122896 poplar tree microcosm rhizosphere flooded clone 17RHF8
EU753611.1 gg_id:315396 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite
AY959944.2 gg_id:114917 Clostridium alkalicellum str. Z-7026
AB240379.1 gg_id:142282 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AF280831.1 gg_id:41245 bioreactor clone tbr4-15
AF482449.1 gg_id:77496 granular sludge clone R6b7
AB486179.1 gg_id:577580 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AB198481.1 gg_id:135577 termite gut wall fraction clone RsW01-052
AB294296.1 gg_id:216349 Microbial structure deep coal seem groundwater clone YWB27
AM982551.2 gg_id:278657 microbial and slurry pig straw spent bedding clone PIST-AGE08
EU703284.1 gg_id:538658 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S
AB486460.1 gg_id:574342 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
X71852.1 gg_id:15957 Clostridium papyrosolvens str. DSM 2782
AY684073.1 gg_id:130444 methanogenic enrichment 'MRE50' clone MRE50b28
CU918823.1 gg_id:556438 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB486564.1 gg_id:560650 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
FJ502269.1 gg_id:578409 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lake
EU753609.1 gg_id:353886 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite
AB374114.1 gg_id:245904 Effect temperature on microbial glucose-degrading methanogenic consortium under
GQ921436.1 gg_id:590008 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w
AF407388.1 gg_id:68943 MCB-contaminated groundwater-treating reactor clone RA9C1
AB488016.1 gg_id:579868 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
L35517.1 gg_id:15955 Bacteroides cellulosolvens
AJ229249.1 gg_id:15960 Clostridium sp. str. FCB90-1
AB240232.1 gg_id:144522 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo

EU869242.1	336112	5079.3	6219.5	5125.1	4786.4	6230.7	5919.2
FJ375886.1	318634	6857.1	8871.2	7186.5	6929.1	8694.4	7337.0
FJ375781.1	312800	4766.3	5909.2	5853.3	4119.7	5082.3	4765.5
FJ375891.1	304496	1459.3	1728.8	1778.7	1424.2	93.5	216.9
FJ375832.1	337750	3681.2	4136.3	4910.2	5642.8	7320.0	7039.5
FJ375879.1	304036	3962.7	5251.4	4449.3	3969.6	5370.9	4946.9
AJ310082.1	31278	48.1	73.6	300.2	137.9	135.1	68.7
EF030542.1	190008	779.4	666.8	2722.8	358.9	71.8	407.6
NC_004557.1	471257	159.3	139.0	126.6	89.6	63.0	42.4
AABG04000051.1	130271	1359.3	1417.1	1685.8	979.9	1138.3	1130.7
FJ599513.1	545541	1502.7	1475.5	2609.1	1914.6	2406.7	1337.4
NR_026112.1	569919	109.2	144.3	97.1	85.2	65.0	58.5
DQ887919.1	164481	149.7	154.9	930.1	144.2	93.4	110.7
X71856.1	15980	1244.8	1575.3	1475.2	1147.8	382.1	640.1
AB307636.1	271652	10197.9	10494.2	4647.3	6170.3	2765.8	3422.9
EF559080.1	218474	1810.6	1759.2	501.6	1744.8	741.2	36.8
AJ863357.1	122896	6446.7	5069.5	7433.0	2626.9	1387.4	2405.5
EU753611.1	315396	809.2	1133.1	3682.1	643.2	832.6	1479.8
AY959944.2	114917	32.8	64.0	88.8	53.9	80.2	64.2
AB240379.1	142282	2572.9	1273.9	2530.1	2742.6	1369.6	1480.0
AF280831.1	41245	3268.2	2919.3	926.9	1804.9	851.5	1812.5
AF482449.1	77496	26.4	38.3	80.7	96.0	156.9	90.6
AB486179.1	577580	373.6	436.8	2240.6	854.1	338.7	774.2
AB198481.1	135577	1123.2	3082.1	3742.4	1959.5	1833.3	2218.4
AB294296.1	216349	2897.1	3307.6	8550.4	1841.6	2835.4	3331.8
AM982551.2	278657	6792.6	7080.0	4542.5	6552.3	7891.6	6721.1
EU703284.1	538658	4081.7	6006.0	3987.2	3050.3	4047.1	4711.5
AB486460.1	574342	5493.3	5632.8	2566.3	3607.6	3919.6	5277.8
X71852.1	15957	1497.9	1313.1	4481.1	1149.5	1346.0	2110.1
AY684073.1	130444	44.4	38.6	59.7	66.9	55.9	28.0
CU918823.1	556438	8351.6	12517.2	14840.1	10226.4	9231.8	8938.7
AB486564.1	560650	8837.4	10292.5	3341.9	4802.7	7235.7	7479.8
FJ502269.1	578409	2239.8	3032.9	3843.6	1701.1	2467.4	2251.0
EU753609.1	353886	14995.7	15595.7	9250.5	11052.1	8166.7	8030.1
AB374114.1	245904	2262.2	2678.2	1609.8	1290.1	1761.8	1599.1
GQ921436.1	590008	1058.7	1390.6	1651.8	1277.6	3797.8	1620.0
AF407388.1	68943	6863.6	7217.2	3286.3	4645.3	3810.1	4384.6
AB488016.1	579868	12232.7	11584.5	7411.0	9871.5	9152.1	7758.0
L35517.1	15955	4470.2	4237.5	6489.7	7865.0	7890.8	6982.5
AJ229249.1	15960	7779.4	9230.7	5891.3	5316.5	7421.9	7056.7
AB240232.1	144522	99.8	198.1	202.5	81.7	81.0	48.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	27745
s__unclassified	27755
s__unclassified	27759
s__unclassified	27770
s__unclassified	27775
s__unclassified	27778
s__unclassified	27797
s__unclassified	27802
s__unclassified	27828
s__unclassified	27858
s__unclassified	27862
s__unclassified	27863
s__unclassified	27869
s__unclassified	27892
s__unclassified	27917
s__unclassified	27922
s__unclassified	27932
s__unclassified	27938
s__unclassified	27941
s__unclassified	27954
s__unclassified	27969
s__unclassified	27995
s__unclassified	28009
s__unclassified	28015
s__unclassified	28055
s__unclassified	28059
s__unclassified	28085
s__unclassified	28110
s__unclassified	28111
s__unclassified	28120
s__unclassified	28128
s__unclassified	28141
s__unclassified	28145
s__unclassified	28146
s__unclassified	28156
s__unclassified	28174
s__unclassified	28197
s__unclassified	44170
s__unclassified	44172
s__unclassified	44179
s__unclassified	44187

FJ825485.1 gg_id:540295 Microbial during start-up mesophilic biogas plant clone 175_BE3_2
FN436024.1 gg_id:547395 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
DQ125722.1 gg_id:136404 uranium contaminated soil clone AKAU3820
DQ125755.1 gg_id:132457 uranium contaminated soil clone AKAU3868
AB274495.1 gg_id:213313 packed-bed reactor clone CFB-6
EF586065.1 gg_id:245011 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_
DQ887967.1 gg_id:161992 thermophilic anaerobic solid waste bioreactor clone TIBE03
CR933129.1 gg_id:109994 Evry municipal wastewater treatment plant clone 013B04_B_SD_P15
DQ125655.1 gg_id:134002 uranium contaminated soil clone AKAU3717
AF050580.1 gg_id:16001 contaminated aquifer clone WCHB1-21
GQ487969.1 gg_id:550979 Microbial metal soil polluted heavy metals clone G10-80
EU250962.1 gg_id:360102 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose
AF407399.1 gg_id:48313 MCB-contaminated groundwater-treating reactor clone RA13C2
EF205577.1 gg_id:205562 among geographically regions central Tibet geothermal spring mat clone TP20
AJ318164.1 gg_id:16925 Waste-gas biofilter clone BIri47
AB011057.1 gg_id:15977 Clostridium josui str. FERM P-9684
FJ815191.2 gg_id:554015 Clostridium sp. str. A6
GU214168.1 gg_id:585365 and biota slimes Canadian paper mills slime mill taken wet section around papermal
X71854.1 gg_id:15963 Clostridium termitidis str. DSM 5396
AB487128.1 gg_id:587360 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
AJ229248.1 gg_id:15959 Clostridium sp. str. FCB45
EF559108.1 gg_id:219192 mesophilic anaerobic digester clone C35_D7_H_B_G09
AB486913.1 gg_id:572847 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0
AY330128.1 gg_id:97132 methanogenic landfill leachate bioreactor clone AC065
GQ502575.1 gg_id:564645 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
NC_011898.1 gg_id:471233 Clostridium cellulolyticum H10 str. H10; ATCC 35319
DQ069224.1 gg_id:128200 gold mine clone SRB16
AY642570.1 gg_id:153096 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali
X71847.1 gg_id:15998 Clostridium cellulolyticum str. ATCC 35319
FM994911.1 gg_id:534331 springs Velingrad region Bulgaria hot spring Mizinka clone VS-7
AB486893.1 gg_id:532875 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0
AB486146.1 gg_id:561133 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR0
AJ229216.1 gg_id:50120 anoxic bulk soil flooded rice microcosm clone BSV72 clone
AB294749.1 gg_id:211979 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobacte
GQ406191.1 gg_id:509371 Benthic submerged sinkhole ecosystems sediment clone -39-11
AB240269.1 gg_id:142277 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
EU057605.1 gg_id:252234 Clostridium sp. str. CJT-3
EU772520.1 gg_id:306873 Hamadryas Baboon feces clone BAZ_aah92f09
AY337519.1 gg_id:91168 Clostridium sp. str. L15
EU459349.1 gg_id:288632 cheetah feces clone CE3_aai05a07
FJ672914.1 gg_id:523511 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I

FJ825485.1	540295	1148.4	2582.9	3087.7	3714.1	1257.3	1549.4
FN436024.1	547395	534.8	957.6	2734.0	305.6	98.5	689.9
DQ125722.1	136404	39.3	60.5	2318.7	98.9	65.6	40.3
DQ125755.1	132457	27.2	29.9	47.7	65.3	82.7	27.5
AB274495.1	213313	39.7	78.5	136.1	90.7	371.1	114.0
EF586065.1	245011	151.7	236.6	256.7	169.2	224.7	112.2
DQ887967.1	161992	2010.5	1703.8	5118.6	1776.1	1310.7	1838.6
CR933129.1	109994	388.7	238.9	1400.7	335.7	81.7	67.2
DQ125655.1	134002	361.0	711.0	257.3	154.7	150.7	94.4
AF050580.1	16001	133.1	70.1	337.9	68.2	61.9	60.3
GQ487969.1	550979	2029.9	1869.9	2026.0	1563.0	1431.5	1414.6
EU250962.1	360102	3812.4	3537.4	2956.3	3707.4	1201.2	2057.6
AF407399.1	48313	1201.3	1661.6	1895.2	894.2	1387.9	1853.7
EF205577.1	205562	576.7	805.2	1133.1	221.9	1083.4	1179.7
AJ318164.1	16925	31.7	38.3	35.2	62.0	60.9	22.0
AB011057.1	15977	983.1	828.7	2656.8	2125.8	866.9	1348.5
FJ815191.2	554015	41.5	53.6	179.9	92.1	45.1	32.8
GU214168.1	585365	5297.3	7137.8	2042.2	1553.5	1942.2	1343.8
X71854.1	15963	2506.2	3257.1	5075.5	2309.5	2034.4	3296.5
AB487128.1	587360	2763.4	2922.9	5725.1	954.8	493.7	816.6
AJ229248.1	15959	514.5	214.1	1732.9	435.6	95.3	66.3
EF559108.1	219192	322.1	166.7	535.2	262.1	56.2	228.9
AB486913.1	572847	2389.6	3537.6	6349.6	3312.1	3583.3	2851.7
AY330128.1	97132	66.0	52.8	664.7	118.3	67.4	41.2
GQ502575.1	564645	6585.7	6678.5	6675.3	6356.9	5103.0	5959.5
NC_011898.1	471233	2606.5	2606.4	3573.1	3031.1	1787.8	2483.4
DQ069224.1	128200	157.1	155.3	2496.0	756.4	201.0	58.2
AY642570.1	153096	34.9	50.0	1455.8	107.9	47.9	14.1
X71847.1	15998	6411.3	6454.5	4711.1	7266.9	2665.4	3078.9
FM994911.1	534331	420.5	707.3	2325.6	293.7	527.6	650.6
AB486893.1	532875	1540.7	2550.0	3918.6	2026.9	2640.6	2153.8
AB486146.1	561133	569.3	358.4	2732.2	405.9	60.2	180.1
AJ229216.1	50120	1859.0	3110.6	2915.2	770.9	1631.4	1732.1
AB294749.1	211979	43.1	90.8	32.6	62.0	108.0	76.0
GQ406191.1	509371	2398.6	4441.8	5591.2	2317.6	2980.9	3201.5
AB240269.1	142277	160.7	132.6	1860.9	130.5	62.0	50.1
EU057605.1	252234	5055.3	4072.3	2501.4	3628.9	1955.3	2434.1
EU772520.1	306873	869.3	720.2	1425.4	224.8	713.1	1247.2
AY337519.1	91168	216.1	471.0	1112.4	242.7	211.9	335.3
EU459349.1	288632	2959.1	2899.8	875.3	3327.5	2382.3	4222.4
FJ672914.1	523511	727.2	556.1	1793.3	923.5	581.9	501.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	44192
s__unclassified	44194
s__unclassified	44196
s__unclassified	44200
s__unclassified	44203
s__unclassified	44208
s__unclassified	44218
s__unclassified	44222
s__unclassified	44234
s__unclassified	44235
s__unclassified	44265
s__unclassified	44282
s__unclassified	44283
s__unclassified	44295
s__unclassified	44311
s__unclassified	44319
s__unclassified	44324
s__unclassified	44328
s__unclassified	44332
s__unclassified	44347
s__unclassified	44349
s__unclassified	44358
s__unclassified	44364
s__unclassified	44368
s__unclassified	44374
s__unclassified	44382
s__unclassified	44390
s__unclassified	44397
s__unclassified	44399
s__unclassified	44406
s__unclassified	44408
s__unclassified	44420
s__unclassified	44429
s__unclassified	44444
s__unclassified	44446
s__unclassified	44447
s__unclassified	44453
s__unclassified	44497
s__unclassified	44500
s__unclassified	44506
s__unclassified	44509

FJ671575.1 gg_id:521519 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ683489.1 gg_id:519525 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473709.1 gg_id:287502 banteng feces clone BG_aaa04c08.Contig1
EU473983.1 gg_id:288648 giant panda feces clone GP_2aaa03h01
GQ458239.1 gg_id:547433 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig
EU467045.1 gg_id:291305 hedgehog feces clone HH_b05
EU459232.1 gg_id:288088 hedgehog feces clone HH_aai34e01
FJ674874.1 gg_id:531852 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AM183095.1 gg_id:241843 and its spatial composts compost clone SMC146
EU473956.1 gg_id:301835 giant panda feces clone GP_2aaa04d05
EU473643.1 gg_id:302631 banteng feces clone BG_aaa01c06.Contig1
FJ682017.1 gg_id:512879 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU459171.1 gg_id:299102 hedgehog feces clone HH_aai33b11
EU467934.1 gg_id:299336 cheetah feces clone CE2_e04
DQ196630.2 gg_id:172362 Clostridium sp. str. BL-26
FJ960229.1 gg_id:564094 bottlenose dolphin upper respiratory tract blowhole clone D9A4_121
FJ370179.1 gg_id:356848 feces adult twins and mothers; TS56 clone TS56_a01d05
EU775688.1 gg_id:315362 Hedgehog feces clone HH_aai33h06
GQ868440.1 gg_id:582630 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC518
FJ375881.1 gg_id:328969 and prevalence blaTEM genes polar bear feces clone PBF_d19
FJ683394.1 gg_id:530072 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ238608.1 gg_id:145018 Effect daidzein on piglets piglet gastrointestinal tract clone 8
EU468026.1 gg_id:294154 cheetah feces clone CE2_d12_2
EU777813.1 gg_id:322174 Polar bear feces clone PB2_aai23a05
EU474114.1 gg_id:301771 giant panda feces clone GP_2aaa02g05
EU459181.1 gg_id:291701 hedgehog feces clone HH_aai33d07
EU475570.1 gg_id:288446 babirusa feces clone BARB_aaa03g08
DQ817233.1 gg_id:172276 mouse cecum clone aaa70d07
AJ245413.1 gg_id:16236 Clostridium tertium str. ATCC 14573
EU474799.1 gg_id:292527 takin feces clone TAK_aaa01g04
DQ238613.1 gg_id:142447 Effect daidzein on piglets piglet gastrointestinal tract clone 6
FJ670668.1 gg_id:528824 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU473968.1 gg_id:295254 giant panda feces clone GP_2aaa03d03
DQ800540.1 gg_id:199214 human fecal clone RL183_aah29d02
GQ129976.1 gg_id:403839 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
FM874206.1 gg_id:356785 occupant source house mattress dust clone MC03A02
AF371844.1 gg_id:33176 swine intestine clone p-1965-s959-5
FJ679483.1 gg_id:527748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB332117.1 gg_id:247793 Continuous cultivation and structure thermophilc propionate-degrading microbial co
EU474794.1 gg_id:293733 takin feces clone TAK_aaa03c02
AB540985.1 gg_id:572196 Eubacterium moniliforme str. JCM 9990

FJ671575.1	521519	5348.5	5331.9	1769.2	5774.6	8629.7	8052.5
FJ683489.1	519525	1179.4	977.4	4014.7	665.6	1153.8	1327.3
EU473709.1	287502	6725.4	5730.9	10078.4	4188.2	1967.2	3367.8
EU473983.1	288648	5878.1	5569.8	787.1	1977.6	1287.2	1304.5
GQ458239.1	547433	2256.1	3327.2	3889.9	1470.1	7305.0	4830.4
EU467045.1	291305	431.5	248.2	883.5	179.2	78.5	224.9
EU459232.1	288088	7533.0	6621.1	5405.9	7168.5	9724.0	10752.5
FJ674874.1	531852	455.0	603.0	2921.6	318.9	152.4	364.5
AM183095.1	241843	413.8	196.2	297.8	336.6	99.7	73.5
EU473956.1	301835	7456.8	7260.3	3887.4	8928.2	11794.2	9553.9
EU473643.1	302631	778.0	761.3	1993.7	606.2	380.6	810.5
FJ682017.1	512879	1169.0	1840.2	1740.0	651.9	2840.6	1591.8
EU459171.1	299102	125.5	256.9	1422.0	222.1	89.8	135.9
EU467934.1	299336	6931.8	6884.6	6478.1	3454.3	3140.0	3358.0
DQ196630.2	172362	839.1	1060.6	3531.5	811.6	133.4	583.4
FJ960229.1	564094	1520.8	1306.3	2192.1	1557.9	2026.5	886.2
FJ370179.1	356848	5168.5	7356.8	3751.3	2725.0	10045.1	7322.4
EU775688.1	315362	5080.6	5506.1	5479.3	3653.5	4622.1	4407.2
GQ868440.1	582630	5700.5	6193.0	2689.1	6034.2	8059.4	6543.6
FJ375881.1	328969	4037.0	3780.1	3404.3	3546.2	3440.0	3301.4
FJ683394.1	530072	1423.7	2026.9	952.1	1659.8	2614.2	1734.0
DQ238608.1	145018	1106.1	2211.4	2518.6	1308.8	178.9	715.0
EU468026.1	294154	1790.5	1806.8	2263.0	2473.6	3918.1	1799.5
EU777813.1	322174	6565.0	6515.5	7504.5	4255.1	5032.0	5907.9
EU474114.1	301771	1569.3	1838.5	1077.3	2064.8	4766.0	4361.1
EU459181.1	291701	5844.0	3961.5	3663.1	5246.2	1256.6	2490.1
EU475570.1	288446	420.0	553.5	2950.6	303.1	151.6	390.2
DQ817233.1	172276	59.8	104.9	340.0	83.5	50.6	66.8
AJ245413.1	16236	1213.3	1870.9	1940.5	985.8	2068.1	1300.9
EU474799.1	292527	6335.0	5507.6	3657.9	6864.7	4267.0	5139.6
DQ238613.1	142447	7959.5	6480.2	2265.4	7232.3	12451.9	9326.3
FJ670668.1	528824	2126.9	1827.6	3122.3	1435.4	1445.3	1424.9
EU473968.1	295254	3009.1	3200.7	3347.3	1972.6	2918.9	2960.7
DQ800540.1	199214	3517.7	3563.7	2997.3	4865.5	3930.6	4475.1
GQ129976.1	403839	876.0	1318.5	1788.1	1682.7	4283.3	3962.6
FM874206.1	356785	2678.2	3748.7	7684.0	3613.7	7369.2	2934.5
AF371844.1	33176	2726.2	1849.6	5442.1	1589.9	1757.9	1615.5
FJ679483.1	527748	9965.6	7835.3	9202.2	7574.3	5380.1	5621.1
AB332117.1	247793	570.4	946.2	1742.5	304.2	114.5	643.3
EU474794.1	293733	13645.5	12631.2	5838.6	11550.1	11240.8	10623.6
AB540985.1	572196	747.2	526.3	577.3	437.4	94.3	274.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	44513
s__unclassified	44517
s__unclassified	44520
s__unclassified	44523
s__unclassified	44530
s__unclassified	44545
s__unclassified	44546
s__unclassified	44548
s__unclassified	44561
s__unclassified	44568
s__unclassified	44569
s__unclassified	44578
s__unclassified	44591
s__unclassified	44597
s__unclassified	44600
s__unclassified	44606
s__unclassified	44619
s__unclassified	44642
s__unclassified	44661
s__unclassified	44667
s__unclassified	44678
s__unclassified	44686
s__unclassified	44690
s__unclassified	44700
s__unclassified	44702
s__unclassified	44710
s__unclassified	44717
s__unclassified	44724
s__unclassified	44725
s__unclassified	44726
s__unclassified	44729
s__unclassified	44744
s__unclassified	44746
s__unclassified	44758
s__unclassified	44761
s__unclassified	44771
s__unclassified	44784
s__unclassified	44788
s__unclassified	44794
s__unclassified	44796
s__unclassified	44798

FJ375788.1 gg_id:331828 and prevalence blaTEM genes polar bear feces clone PBF_b17
X68174.1 gg_id:16213 Clostridium baratii str. ATCC27638
AM183061.1 gg_id:248563 and its spatial composts compost clone SMB82
EU464172.1 gg_id:289404 reticulated giraffe feces clone gir_aah95e03
EU473287.1 gg_id:296539 giant panda feces clone GP_1aaa04b12
EU773016.1 gg_id:333228 Banteng feces clone BG_aaa01d12.Contig1
EU473216.1 gg_id:287467 giant panda feces clone GP_1aaa01d05
AB018184.1 gg_id:40062 Eubacterium multiforme str. JCM 6484
EF559177.1 gg_id:223161 mesophilic anaerobic digester clone G35_D8_H_B_B06
EU474087.1 gg_id:295458 giant panda feces clone GP_2aaa02h06
GQ492949.1 gg_id:569263 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ881333.1 gg_id:433124 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU473365.1 gg_id:290438 giant panda feces clone GP_1aaa02b03
EU459334.1 gg_id:287565 hedgehog feces clone HH_aai36f05
DQ015563.1 gg_id:133360 mouse cecum clone M3_f01_1
EU471447.1 gg_id:291025 spectacled bear feces clone SB_2aaa03f07
EU462622.1 gg_id:302041 Sumatran orangutan feces clone orang2_aai66c04
EU472577.1 gg_id:289501 Angola colobus feces clone EAC_2_aaa03a09
EU473337.1 gg_id:292010 giant panda feces clone GP_1aaa01h01
FJ682831.1 gg_id:530824 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FM873505.1 gg_id:359728 occupant source house floor dust clone FD04G02
GQ007726.1 gg_id:501938 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ681425.1 gg_id:525936 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473883.1 gg_id:301102 giant panda feces clone GP_2aaa04c03
EU762963.1 gg_id:329216 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ793454.1 gg_id:187953 human fecal clone RL199_aaj43h11
EU460613.1 gg_id:295137 polar bear feces clone PB2_aai23d09
EU473225.1 gg_id:288164 giant panda feces clone GP_1aaa01d11
EU763600.1 gg_id:340717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ683685.1 gg_id:531765 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU474080.1 gg_id:290462 giant panda feces clone GP_2aaa03d09
DQ325781.1 gg_id:149036 Metagenomic gut microbiome healthy human stool clone B469
EU473304.1 gg_id:289102 giant panda feces clone GP_1aaa04a09
FJ684155.1 gg_id:524467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680008.1 gg_id:525078 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU459342.1 gg_id:293771 hedgehog feces clone HH_aai36g12
EU473952.1 gg_id:294441 giant panda feces clone GP_2aaa01e11
EU473891.1 gg_id:289769 giant panda feces clone GP_2aaa01h11
EU474127.1 gg_id:295740 giant panda feces clone GP_2aaa01b01
EU772351.1 gg_id:313142 Babirusa feces clone BARB_aaa01b09
GQ898543.1 gg_id:541594 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons

FJ375788.1	331828	1101.3	1633.3	2072.3	1397.5	3014.8	2040.6
X68174.1	16213	873.5	1137.4	1650.0	840.2	484.7	691.7
AM183061.1	248563	1248.8	1365.3	1021.1	378.3	322.8	559.2
EU464172.1	289404	449.1	871.7	1127.7	434.1	442.5	606.5
EU473287.1	296539	12494.0	13355.4	5577.7	9795.1	16193.3	11812.8
EU773016.1	333228	5691.2	4156.2	5830.0	5106.2	3866.3	3682.5
EU473216.1	287467	366.6	605.7	1994.7	339.7	294.6	240.5
AB018184.1	40062	4054.9	3828.5	4367.3	4599.3	4549.0	4756.2
EF559177.1	223161	20.5	32.2	32.6	34.7	50.6	14.0
EU474087.1	295458	6596.0	6764.9	4966.3	3017.4	2347.1	3546.1
GQ492949.1	569263	4807.4	5664.1	5106.6	6586.4	10665.3	9122.4
FJ881333.1	433124	513.9	1040.7	1406.2	297.2	983.9	1182.0
EU473365.1	290438	1391.1	1371.2	3432.4	767.5	1686.9	954.1
EU459334.1	287565	236.3	474.3	841.3	174.9	75.3	117.5
DQ015563.1	133360	757.5	870.2	1382.0	252.3	260.7	388.6
EU471447.1	291025	3573.5	2882.6	3513.9	1783.5	3524.6	1631.6
EU462622.1	302041	707.1	880.3	2007.2	771.2	273.5	1011.8
EU472577.1	289501	2249.1	3568.3	1231.0	3373.9	5238.2	5713.0
EU473337.1	292010	5551.3	6823.0	2833.3	4436.1	4433.3	4624.9
FJ682831.1	530824	5319.7	4821.2	2873.0	5337.8	3604.3	4634.2
FM873505.1	359728	453.2	279.5	1806.4	382.9	693.4	664.2
GQ007726.1	501938	1384.0	1355.2	3197.1	4373.7	3653.7	4871.1
FJ681425.1	525936	8598.0	8598.0	7449.0	5936.9	7890.7	7455.2
EU473883.1	301102	2417.4	2903.4	1680.7	798.1	989.9	711.5
EU762963.1	329216	2170.6	2116.5	1996.7	759.5	1519.9	1266.5
DQ793454.1	187953	2390.4	2407.6	3275.9	2496.0	7457.1	5290.3
EU460613.1	295137	2217.2	1557.3	2340.9	1445.3	1300.9	953.2
EU473225.1	288164	359.1	492.3	1356.7	234.8	221.4	394.2
EU763600.1	340717	9529.3	9700.6	9175.0	10736.9	13403.5	10716.9
FJ683685.1	531765	6467.1	4489.8	3382.3	5561.0	1652.5	2720.0
EU474080.1	290462	8325.9	7301.8	6128.3	7822.2	10756.5	9225.0
DQ325781.1	149036	7117.8	5392.9	3972.9	6173.2	7766.7	7200.3
EU473304.1	289102	244.4	304.0	1587.6	221.4	112.6	235.4
FJ684155.1	524467	2765.4	1667.0	3443.1	2182.5	2503.2	3284.2
FJ680008.1	525078	797.7	697.8	2978.0	596.1	128.5	349.0
EU459342.1	293771	1650.7	1121.8	2091.1	1203.2	1974.9	994.7
EU473952.1	294441	2543.4	3772.1	2123.2	3356.2	8061.7	9600.8
EU473891.1	289769	2685.2	2563.0	4350.2	2969.9	4570.1	3136.9
EU474127.1	295740	16620.3	15430.4	14796.3	15267.7	12804.3	11946.5
EU772351.1	313142	4029.6	4652.6	2050.5	4975.8	6158.1	7099.0
GQ898543.1	541594	7247.0	7057.7	7977.3	8865.4	10846.8	11593.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	44800
s__unclassified	44810
s__unclassified	44831
s__unclassified	44849
s__unclassified	44861
s__unclassified	44865
s__unclassified	44870
s__unclassified	44897
s__unclassified	44921
s__unclassified	44924
s__unclassified	44930
s__unclassified	44936
s__unclassified	44940
s__unclassified	44941
s__unclassified	44945
s__unclassified	44948
s__unclassified	44982
s__unclassified	45000
s__unclassified	45010
s__unclassified	45018
s__unclassified	45022
s__unclassified	45027
s__unclassified	45036
s__unclassified	45046
s__unclassified	45051
s__unclassified	45067
s__unclassified	45071
s__unclassified	45074
s__unclassified	45076
s__unclassified	45093
s__unclassified	45098
s__unclassified	45108
s__unclassified	45114
s__unclassified	45117
s__unclassified	45128
s__unclassified	45132
s__unclassified	45146
s__unclassified	45152
s__unclassified	45153
s__unclassified	45159
s__unclassified	45177

EU475622.1 gg_id:301597 babirusa feces clone BARB_aaa03f01
FJ681136.1 gg_id:512574 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801475.1 gg_id:193154 human fecal clone RL388_aao96a07
X77842.1 gg_id:16234 Clostridium sardiniense str. DSM 599
GQ458227.1 gg_id:512965 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig
DQ808504.1 gg_id:182358 human fecal clone RL239_aaj09d12
EU460604.1 gg_id:290233 polar bear feces clone PB2_aai23c07
EU774647.1 gg_id:324893 Angola Colobus feces clone EAC_1aaa02a10
FJ683095.1 gg_id:514947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ249583.1 gg_id:509782 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl
EU473255.1 gg_id:290901 giant panda feces clone GP_1aaa01f11
DQ817220.1 gg_id:169629 mouse cecum clone aaa70b08
GQ359970.1 gg_id:582866 Microbial intestinal contents and mucus yel catfish (Pelteobagrus fulvidraco) intestir
FJ682482.1 gg_id:524162 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473352.1 gg_id:287684 giant panda feces clone GP_1aaa02h03
AB018185.1 gg_id:31869 Eubacterium nitritogenes str. JCM 6485
DQ796773.1 gg_id:182452 human fecal clone RL179_aao54c09
EU772391.1 gg_id:315755 Hamadryas Baboon feces clone BAZ_e03
EU869238.1 gg_id:306622 Clostridium sp. str. CM-C81
DQ129391.1 gg_id:138056 microarray level air two cities Texas urban aerosol clone AKIW654
EU777055.1 gg_id:348224 Okapi feces clone OK2_b02_1
DQ815970.1 gg_id:164332 mouse cecum clone aaa85a09
FJ678772.1 gg_id:525918 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800727.1 gg_id:190296 human fecal clone RL183_aao02f08
EU473932.1 gg_id:301964 giant panda feces clone GP_2aaa03b11
EU459282.1 gg_id:290241 hedgehog feces clone HH_aai35e07
GU293208.1 gg_id:538968 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content
EU474817.1 gg_id:297379 takin feces clone TAK_aaa02d10
DQ815984.1 gg_id:171437 mouse cecum clone aaa85c02
EU474090.1 gg_id:295920 giant panda feces clone GP_2aaa01c04
FJ678171.1 gg_id:518018 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU761992.1 gg_id:333674 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
NR_026149.1 gg_id:534306 Clostridium quinii str. DSM 6736
GQ492067.1 gg_id:574003 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU473929.1 gg_id:288858 giant panda feces clone GP_2aaa01h06
DQ807486.1 gg_id:180069 human fecal clone RL307_aam07b11
EU777067.1 gg_id:338591 Okapi feces clone OK2_d10
FM873847.1 gg_id:359116 occupant source house mattress dust clone MB01G06
EU779088.1 gg_id:317926 Takin feces clone TAK_aaa02h01
FJ679435.1 gg_id:517527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ685390.1 gg_id:512217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

EU475622.1	301597	10203.3	10671.8	5623.8	7966.5	8247.1	7650.6
FJ681136.1	512574	2142.8	3090.1	780.1	2977.4	7044.3	4966.1
DQ801475.1	193154	3612.6	4536.6	6376.4	5098.4	6457.7	4300.9
X77842.1	16234	139.4	170.8	512.6	154.7	122.7	128.3
GQ458227.1	512965	3664.1	3904.0	4157.7	3555.7	6022.1	5529.1
DQ808504.1	182358	8917.7	8834.6	3775.5	3808.5	3329.1	3192.1
EU460604.1	290233	596.3	640.5	1233.9	386.4	1768.9	447.0
EU774647.1	324893	4803.7	5214.0	2583.0	7149.4	4450.8	5613.4
FJ683095.1	514947	5367.7	5668.8	4522.3	7619.8	5532.8	6400.9
GQ249583.1	509782	1894.3	1812.9	1641.3	1870.0	1636.8	2137.5
EU473255.1	290901	8060.7	7794.2	6512.4	5871.0	7012.6	6677.2
DQ817220.1	169629	313.9	769.9	679.7	289.0	1096.1	442.8
GQ359970.1	582866	960.8	1052.5	2775.3	855.9	381.6	802.0
FJ682482.1	524162	5157.9	4809.9	8973.4	4999.9	9338.0	5912.3
EU473352.1	287684	4610.3	4091.8	2378.0	3422.8	5681.4	3258.4
AB018185.1	31869	5789.1	6967.3	3829.0	2357.0	2958.0	2808.6
DQ796773.1	182452	3491.6	3562.8	4151.7	5132.9	4792.5	3839.1
EU772391.1	315755	3324.4	2510.2	7008.9	3495.0	3564.3	3562.8
EU869238.1	306622	272.1	601.1	679.6	230.0	334.4	367.5
DQ129391.1	138056	2060.5	1817.0	3805.6	2087.0	2109.0	3345.0
EU777055.1	348224	1208.2	1383.8	1867.3	1546.6	788.7	1013.8
DQ815970.1	164332	3314.2	3513.1	2852.4	3357.9	7845.2	6311.8
FJ678772.1	525918	1447.1	1695.2	1280.2	1110.6	639.1	844.6
DQ800727.1	190296	1202.1	1491.9	4277.9	968.2	4051.9	2439.1
EU473932.1	301964	7912.1	6931.7	5712.6	8144.3	12924.6	9962.7
EU459282.1	290241	540.4	438.0	1398.7	259.0	100.0	133.6
GU293208.1	538968	949.5	1153.6	2339.5	1361.5	412.8	845.3
EU474817.1	297379	3245.8	1991.2	4214.6	3566.9	338.8	1840.0
DQ815984.1	171437	42.3	61.8	33.9	73.7	67.1	38.6
EU474090.1	295920	8851.0	8115.4	6251.1	8256.3	7014.6	7236.0
FJ678171.1	518018	1778.2	1461.0	5885.2	1063.6	378.1	1434.4
EU761992.1	333674	444.7	1332.9	966.2	534.9	2988.1	1269.9
NR_026149.1	534306	173.9	269.0	607.6	228.1	344.4	473.5
GQ492067.1	574003	10322.8	10697.0	9885.9	9958.8	12919.4	10835.1
EU473929.1	288858	3387.3	2420.3	2074.3	1334.8	183.8	516.8
DQ807486.1	180069	2895.7	1211.9	5833.0	5386.1	350.8	507.3
EU777067.1	338591	2188.9	2550.6	2496.1	3269.2	7310.2	7658.4
FM873847.1	359116	519.0	564.9	1502.3	445.7	686.7	884.9
EU779088.1	317926	1408.5	1294.6	1653.7	219.7	162.8	424.1
FJ679435.1	517527	1360.1	1480.8	2989.8	1644.2	898.1	1848.1
FJ685390.1	512217	1426.6	1277.8	3185.7	1544.1	707.7	1710.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	45196
s__unclassified	45216
s__unclassified	45234
s__unclassified	45242
s__unclassified	45247
s__unclassified	45251
s__unclassified	45258
s__unclassified	45274
s__unclassified	45279
s__unclassified	45285
s__unclassified	45316
s__unclassified	45317
s__unclassified	45328
s__unclassified	45331
s__unclassified	45338
s__unclassified	45353
s__unclassified	45363
s__unclassified	45366
s__unclassified	45376
s__unclassified	45379
s__unclassified	45386
s__unclassified	45407
s__unclassified	45450
s__unclassified	45463
s__unclassified	45466
s__unclassified	45472
s__unclassified	45487
s__unclassified	45494
s__unclassified	45498
s__unclassified	45530
s__unclassified	45535
s__unclassified	45545
s__unclassified	45546
s__unclassified	45561
s__unclassified	45562
s__unclassified	45565
s__unclassified	45566
s__unclassified	45580
s__unclassified	45583
s__unclassified	45606
s__unclassified	45611

FJ957496.1 gg_id:426638 Microbial Anaerobes Spacecraft Clean Rooms spacecraft clean room clone JPL-S2_C1
AB020189.1 gg_id:34846 Clostridium beijerinckii str. JCM 7844
X77843.1 gg_id:16243 Clostridium caliptrosporum str. DSM 5905
NR_026013.1 gg_id:565322 Clostridium chauvoei str. 2585; ATCC 10092
EU474076.1 gg_id:287515 giant panda feces clone GP_2aaa03a12
EU777692.1 gg_id:307341 Polar bear feces clone PB2_aai22c01
DQ796807.1 gg_id:184442 human fecal clone RL179_aao54g10
FJ673626.1 gg_id:529116 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ817225.1 gg_id:168712 mouse cecum clone aaa70c01
EU474705.1 gg_id:297093 Indian rhinoceros feces clone IR_aaa03b10
EU473278.1 gg_id:289356 giant panda feces clone GP_1aaa04e09
FJ681715.1 gg_id:529490 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679026.1 gg_id:514689 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ808581.1 gg_id:195664 human fecal clone RL239_aaj10d07
EU777219.1 gg_id:319567 Okapi feces clone OK2_b04
EU473193.1 gg_id:290998 giant panda feces clone GP_1aaa01f06
EU473368.1 gg_id:287591 giant panda feces clone GP_1aaa01h05
EU777716.1 gg_id:338956 Polar bear feces clone PB1_aai28h01
AM183092.1 gg_id:252144 and its spatial composts compost clone SMC120
EU459246.1 gg_id:289622 hedgehog feces clone HH_aai34f09
AM998793.1 gg_id:283776 Clostridium saccharobutylicum str. Ox29
CP001056.1 gg_id:286203 Clostridium botulinum B str. Eklund 17B
DQ326262.1 gg_id:150131 Metagenomic gut microbiome healthy human stool clone C203
EU473286.1 gg_id:289372 giant panda feces clone GP_1aaa03c01
EU473395.1 gg_id:298080 giant panda feces clone GP_1aaa01d09
DQ810116.1 gg_id:196719 human fecal clone RL184_aao68c04
FJ678592.1 gg_id:519790 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ808820.1 gg_id:194032 human fecal clone RL243_aai85f11
FJ680093.1 gg_id:515102 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ793612.1 gg_id:197786 human fecal clone RL246_aai74d08
EU775619.1 gg_id:330962 Hedgehog feces clone HH_aai35b03
X68175.1 gg_id:16232 Clostridium baratii str. ATCC43756
X97432.1 gg_id:16227 Clostridium vincentii
FJ682951.1 gg_id:526262 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GU060306.1 gg_id:564332 Clostridium saccharobutylicum str. BS2
FJ880242.1 gg_id:429210 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ685096.1 gg_id:514508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY133085.1 gg_id:59906 TCE-contaminated site clone ccslm2120
EU473145.1 gg_id:295777 giant panda feces clone GP_1aaa01b06
DQ326540.1 gg_id:147920 Metagenomic gut microbiome healthy human stool clone C693
FJ683485.1 gg_id:522966 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

FJ957496.1	426638	5701.2	5171.0	6249.2	5369.7	5746.6	6087.6
AB020189.1	34846	5508.0	5386.1	5629.0	5001.0	3091.5	3471.0
X77843.1	16243	844.0	642.0	2895.7	613.4	1072.4	1649.6
NR_026013.1	565322	498.0	462.0	1879.3	216.4	89.3	306.9
EU474076.1	287515	216.2	267.6	943.9	156.7	90.4	178.9
EU777692.1	307341	7103.3	9022.2	5273.0	5830.9	9800.6	9001.8
DQ796807.1	184442	6917.7	8627.9	2796.0	4125.2	4158.8	3017.3
FJ673626.1	529116	3557.2	1451.2	5425.4	3624.6	2011.1	3797.0
DQ817225.1	168712	11156.6	11721.8	5340.5	7254.4	9988.3	8268.5
EU474705.1	297093	1571.5	1394.7	3524.8	649.4	715.4	901.9
EU473278.1	289356	216.6	322.3	1463.5	195.7	86.7	215.6
FJ681715.1	529490	5729.7	6499.0	4091.3	4563.9	6741.7	4531.2
FJ679026.1	514689	4103.4	2903.9	4894.0	5288.4	1715.1	3176.8
DQ808581.1	195664	629.5	630.9	1561.0	325.4	114.8	451.7
EU777219.1	319567	294.4	607.8	1825.4	257.3	98.1	209.3
EU473193.1	290998	1820.4	1987.8	2150.5	958.5	683.4	664.7
EU473368.1	287591	265.1	260.8	1093.1	188.7	57.9	153.0
EU777716.1	338956	2091.6	1773.1	1880.9	970.5	2729.9	1358.7
AM183092.1	252144	2449.5	2610.0	4346.1	2814.0	1391.3	1974.0
EU459246.1	289622	1484.5	647.0	1389.1	849.0	123.4	175.9
AM998793.1	283776	437.8	309.9	1284.0	423.7	159.6	207.6
CP001056.1	286203	1812.5	2737.4	2814.4	1063.0	1748.5	2148.8
DQ326262.1	150131	205.2	258.4	320.5	188.4	590.4	1471.7
EU473286.1	289372	4540.1	4027.3	4344.7	5763.8	9042.4	7315.6
EU473395.1	298080	4116.6	5884.7	5330.0	5027.8	7417.1	7001.1
DQ810116.1	196719	1290.0	1616.7	2724.9	952.7	3012.3	2112.1
FJ678592.1	519790	11662.6	10434.2	9127.6	9712.9	13376.2	12555.0
DQ808820.1	194032	1958.9	2232.9	1868.3	1152.0	2527.7	2230.3
FJ680093.1	515102	1748.7	1336.7	5101.7	1540.1	591.6	1754.3
DQ793612.1	197786	518.6	274.2	330.3	357.2	416.7	716.2
EU775619.1	330962	6214.5	3837.9	5531.1	3766.4	2764.2	3719.9
X68175.1	16232	8117.9	8483.8	5795.8	6404.1	10015.0	7464.1
X97432.1	16227	3660.8	5394.8	4622.1	2813.8	2859.8	3403.7
FJ682951.1	526262	7713.2	5803.3	11467.2	6686.1	3847.9	4999.1
GU060306.1	564332	675.1	425.0	2963.2	490.3	1064.9	1611.0
FJ880242.1	429210	917.1	1439.3	4309.3	1293.9	3260.1	3285.3
FJ685096.1	514508	964.2	427.7	1744.0	327.2	104.7	524.6
AY133085.1	59906	1394.4	1137.6	6343.2	865.4	111.4	896.9
EU473145.1	295777	2212.5	1987.4	1672.3	2963.5	732.4	1011.4
DQ326540.1	147920	3319.2	3156.6	4684.1	3441.2	6060.0	7876.9
FJ683485.1	522966	3835.4	3790.5	2115.2	5379.7	7246.2	5369.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	45618
s__unclassified	45621
s__unclassified	45630
s__unclassified	45642
s__unclassified	45643
s__unclassified	45648
s__unclassified	45653
s__unclassified	45654
s__unclassified	45657
s__unclassified	45691
s__unclassified	45693
s__unclassified	45712
s__unclassified	45718
s__unclassified	45722
s__unclassified	45723
s__unclassified	45726
s__unclassified	45735
s__unclassified	45750
s__unclassified	45751
s__unclassified	45761
s__unclassified	45764
s__unclassified	45765
s__unclassified	45775
s__unclassified	45779
s__unclassified	45780
s__unclassified	45800
s__unclassified	45830
s__unclassified	45838
s__unclassified	45858
s__unclassified	45861
s__unclassified	45871
s__unclassified	45885
s__unclassified	70046
s__unclassified	70651
s__unclassified	70663
s__unclassified	70665
s__unclassified	70666
s__unclassified	70679
s__unclassified	70686
s__unclassified	70690
s__unclassified	70700

AB020191.1 gg_id:49549 Clostridium beijerinckii str. JCM 7847
EU463601.1 gg_id:297513 domesticated horse feces clone horsej_aai89e09
EU775687.1 gg_id:312729 Hedgehog feces clone HH_aai33b04
DQ800651.1 gg_id:179521 human fecal clone RL183_aao01e12
FJ682021.1 gg_id:529108 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU474123.1 gg_id:295402 giant panda feces clone GP_2aaa03d05
EU474687.1 gg_id:294960 Indian rhinoceros feces clone IR_aaa04a12
FJ683569.1 gg_id:526389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ868434.1 gg_id:558476 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC512
FJ684781.1 gg_id:524895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ196631.1 gg_id:166896 Clostridium sp. str. BL-24
AJ420008.1 gg_id:76200 Clostridium colicanis str. DSM 13634
DQ808612.1 gg_id:196359 human fecal clone RL239_aaj10h09
FJ678831.1 gg_id:518772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU459179.1 gg_id:299482 hedgehog feces clone HH_aai33d05
EU463570.1 gg_id:298570 domesticated horse feces clone horsej_aai89a12
EU474011.1 gg_id:298260 giant panda feces clone GP_2aaa03f11
EU473282.1 gg_id:294306 giant panda feces clone GP_1aaa02d01
EU473204.1 gg_id:288298 giant panda feces clone GP_1aaa04a04
EU460605.1 gg_id:296166 polar bear feces clone PB2_aai23c08
AM183065.1 gg_id:237935 and its spatial composts compost clone SMB112
FJ681311.1 gg_id:530465 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473935.1 gg_id:291622 giant panda feces clone GP_2aaa04g05
FM873828.1 gg_id:361822 occupant source house mattress dust clone MB01D07
DQ800217.1 gg_id:191808 human fecal clone RL303_aal69g05
DQ800538.1 gg_id:184824 human fecal clone RL183_aah29c10
EU474813.1 gg_id:297938 takin feces clone TAK_aaa04g11
EU773874.1 gg_id:326918 Cheetah feces clone CE3_aai05f04
FJ960326.1 gg_id:571221 bottlenose dolphin upper respiratory tract blowhole clone D9A4_224
EU470820.1 gg_id:295850 red panda feces clone RP_2aaa01e02
DQ015110.1 gg_id:130878 mouse cecum clone M2_e05_1
FJ680768.1 gg_id:511288 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ810554.1 gg_id:104410 superficial sediments clone
EU475686.1 gg_id:303104 babirusa feces clone BARB_aaa03c12
EU459347.1 gg_id:296403 hedgehog feces clone HH_aai36h12
EU766580.1 gg_id:348914 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU468766.1 gg_id:298784 okapi feces clone OK3_c11_1
GQ867474.1 gg_id:582379 and prevalence blaTEM genes Arctic seals colon content clone CSG45
EU460716.1 gg_id:299954 polar bear feces clone PB2_aai24h05
AB198536.1 gg_id:135311 termite gut wall fraction clone RsW02-061
FJ375811.1 gg_id:332200 and prevalence blaTEM genes polar bear feces clone PBF_b42

AB020191.1	49549	8867.4	8322.6	6784.5	6819.9	6778.8	6286.1
EU463601.1	297513	489.4	723.7	1142.3	442.3	913.5	366.5
EU775687.1	312729	3863.5	5419.0	3751.6	1916.8	7211.3	4744.6
DQ800651.1	179521	5150.3	5122.2	4496.4	5161.9	6239.8	5694.6
FJ682021.1	529108	2082.0	2354.7	2679.8	1000.8	2183.8	1607.6
EU474123.1	295402	9500.7	9782.5	2827.8	3965.0	3675.1	5778.1
EU474687.1	294960	4651.7	3046.2	5123.4	4223.1	472.2	1772.6
FJ683569.1	526389	6388.8	7089.3	5298.1	7597.6	8872.5	8698.2
GQ868434.1	558476	4280.8	7045.6	3765.9	4598.0	5686.9	5866.8
FJ684781.1	524895	6603.8	6830.1	7092.8	6221.9	4036.1	4360.2
DQ196631.1	166896	382.5	653.7	1287.7	278.6	140.2	294.3
AJ420008.1	76200	361.1	731.3	1526.4	310.9	670.2	472.1
DQ808612.1	196359	1278.1	997.6	2456.4	1447.6	211.5	742.9
FJ678831.1	518772	3492.2	3702.8	1477.9	4259.1	6034.1	4794.9
EU459179.1	299482	2303.7	2179.1	1749.2	3579.2	4297.2	3170.5
EU463570.1	298570	886.6	1116.0	1552.5	1151.9	714.2	1080.8
EU474011.1	298260	5930.3	5631.7	2488.4	6196.7	8440.7	7596.5
EU473282.1	294306	6447.6	6449.3	3189.7	7357.1	7047.9	6313.8
EU473204.1	288298	2465.1	1958.5	3070.3	5710.9	4598.4	4412.3
EU460605.1	296166	138.5	173.1	314.0	127.8	57.7	66.6
AM183065.1	237935	407.7	271.5	821.5	340.4	124.7	423.7
FJ681311.1	530465	3655.5	2556.4	3194.3	2960.3	2111.5	2753.7
EU473935.1	291622	10286.2	10078.2	3007.3	10769.4	13659.2	10515.8
FM873828.1	361822	802.9	986.7	2642.5	814.1	1163.3	1991.2
DQ800217.1	191808	2767.4	2700.4	3426.4	2988.7	4453.1	4040.0
DQ800538.1	184824	3810.1	3381.4	2250.4	3932.1	4359.6	5028.8
EU474813.1	297938	4764.1	2149.5	4549.4	4666.8	3914.7	2635.1
EU773874.1	326918	1736.4	1074.6	1825.3	1442.2	1714.7	630.4
FJ960326.1	571221	1480.5	1285.3	2309.5	1403.0	1781.4	895.3
EU470820.1	295850	831.7	566.7	2614.3	370.9	350.6	450.9
DQ015110.1	130878	4514.5	4435.2	3968.6	4960.2	3299.4	3664.9
FJ680768.1	511288	11251.8	11147.6	6888.3	11113.2	10538.2	10605.2
AJ810554.1	104410	130.8	117.3	354.0	73.0	79.6	78.2
EU475686.1	303104	995.1	1102.5	1037.3	900.8	1015.4	757.0
EU459347.1	296403	6312.9	6915.9	1718.6	3975.3	4246.0	3818.6
EU766580.1	348914	66.2	221.4	131.4	205.3	449.0	627.9
EU468766.1	298784	3282.3	2602.5	5779.8	6902.4	982.4	1393.7
GQ867474.1	582379	3560.0	4063.3	7282.6	5172.0	6692.9	6525.6
EU460716.1	299954	684.6	784.0	1137.8	716.8	540.1	778.2
AB198536.1	135311	32.7	97.5	124.4	79.0	46.0	149.0
FJ375811.1	332200	5810.5	7411.4	5315.0	5048.7	6784.5	5206.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	70705
s__unclassified	70714
s__unclassified	70719
s__unclassified	70723
s__unclassified	70724
s__unclassified	70727
s__unclassified	70728
s__unclassified	70731
s__unclassified	70733
s__unclassified	70744
s__unclassified	70745
s__unclassified	70749
s__unclassified	70774
s__unclassified	70783
s__unclassified	70792
s__unclassified	70793
s__unclassified	70803
s__unclassified	70821
s__unclassified	70823
s__unclassified	70841
s__unclassified	70843
s__unclassified	70844
s__unclassified	70853
s__unclassified	70855
s__unclassified	70862
s__unclassified	70864
s__unclassified	70866
s__unclassified	70882
s__unclassified	70887
s__unclassified	70904
s__unclassified	70906
s__unclassified	70909
s__unclassified	70925
s__unclassified	70928
s__unclassified	70935
s__unclassified	70945
s__unclassified	70949
s__unclassified	70964
s__unclassified	70973
s__unclassified	70986
s__unclassified	70994

EU468283.1 gg_id:299186 domesticated horse feces clone horsej_f05_2
EU475598.1 gg_id:302926 babirusa feces clone BARB_aaa04d08.Contig2
EU766310.1 gg_id:344545 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU475640.1 gg_id:302964 babirusa feces clone BARB_aaa01h01
GQ491217.1 gg_id:553388 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU460543.1 gg_id:300919 polar bear feces clone PB2_aai22d08
DQ796870.1 gg_id:184692 human fecal clone RL179_aao55f12
EU472395.1 gg_id:288493 Angola colobus feces clone EAC_1aaa01b08
EU767428.1 gg_id:351406 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
FJ672948.1 gg_id:508872 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU459194.1 gg_id:295462 hedgehog feces clone HH_aai33f07
FJ681981.1 gg_id:526708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU467719.1 gg_id:303332 bush dog feces clone bdog1_d08
EU528192.1 gg_id:287156 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
FJ366771.1 gg_id:359041 feces adult twins and mothers; TS27 clone TS27_a03f08
EU460503.1 gg_id:287887 polar bear feces clone PB2_aai21g09
DQ809722.1 gg_id:176126 human fecal clone RL184_aan83c03
FJ375922.1 gg_id:309747 and prevalence blaTEM genes polar bear feces clone PBM_b9
AB075771.1 gg_id:46716 Clostridium sordellii str. ATCC 9714
DQ113681.1 gg_id:130854 dog colon clone C5-09
FJ366569.1 gg_id:368997 feces adult twins and mothers; TS27 clone TS27_a01c06
GQ458231.1 gg_id:594005 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig
FJ978707.1 gg_id:384411 feces clone CL_F_403
EU775276.1 gg_id:308502 Reticulated giraffe feces clone gir_aah94h12
FJ673530.1 gg_id:528464 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU468826.1 gg_id:291183 okapi feces clone OK3_c04_1
DQ445857.1 gg_id:156623 Clostridium sp. C01-2409
DQ810015.1 gg_id:185149 human fecal clone RL184_aao67a12
EU460560.1 gg_id:299990 polar bear feces clone PB2_aai22f08
EU775664.1 gg_id:337083 Hedgehog feces clone HH_aai35f05
FJ366714.1 gg_id:357630 feces adult twins and mothers; TS27 clone TS27_a03a04
EF682951.1 gg_id:247473 Eastern Mediterranean atmosphere clone F13_9D_FL
GQ868388.1 gg_id:541925 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC65
FJ366695.1 gg_id:369406 feces adult twins and mothers; TS27 clone TS27_a02g04
EU463306.1 gg_id:291844 bush dog feces clone bdog1_aai77e10
FJ375874.1 gg_id:316634 and prevalence blaTEM genes polar bear feces clone PBF_d11
EU459287.1 gg_id:288071 hedgehog feces clone HH_aai35f07
EU475638.1 gg_id:295162 babirusa feces clone BARB_aaa02d07
EU763479.1 gg_id:349439 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
FJ375912.1 gg_id:306812 and prevalence blaTEM genes polar bear feces clone PBM_a4
DQ798320.1 gg_id:179306 human fecal clone RL181_aah40f08

EU468283.1	299186	2084.0	1560.7	3571.0	993.9	1644.1	1755.9
EU475598.1	302926	1724.9	1737.7	2538.5	1095.6	1535.0	1890.2
EU766310.1	344545	92.7	121.5	98.1	73.3	80.9	66.0
EU475640.1	302964	4460.7	4579.4	470.3	5801.4	8179.1	5611.2
GQ491217.1	553388	1009.3	826.0	775.9	2322.7	136.1	371.7
EU460543.1	300919	134.7	300.8	435.1	67.4	107.7	65.0
DQ796870.1	184692	31.8	57.7	22.0	52.8	55.5	29.3
EU472395.1	288493	472.0	555.7	582.0	618.3	511.2	481.3
EU767428.1	351406	2860.5	3324.3	5521.3	6509.8	7521.2	8409.6
FJ672948.1	508872	10933.1	11038.0	7061.1	13065.9	15747.4	16114.1
EU459194.1	295462	3801.8	3691.7	1077.9	2708.7	2116.5	1114.7
FJ681981.1	526708	319.7	362.2	746.4	168.1	95.2	176.9
EU467719.1	303332	896.1	1188.3	1894.7	896.9	1525.8	689.3
EU528192.1	287156	1961.4	2842.1	2317.3	2164.0	2073.4	2504.4
FJ366771.1	359041	6000.2	7227.8	4823.5	7396.6	10073.6	9082.0
EU460503.1	287887	1949.4	2163.2	1489.0	4016.8	1998.3	1359.0
DQ809722.1	176126	511.3	1425.4	778.9	1124.9	408.9	1327.5
FJ375922.1	309747	4196.8	5250.3	10113.3	4390.1	5702.8	5508.6
AB075771.1	46716	552.9	1125.0	899.2	328.9	926.0	666.9
DQ113681.1	130854	507.7	763.4	167.2	170.1	333.5	182.7
FJ366569.1	368997	4304.9	6153.5	1957.8	3594.4	3969.0	5415.1
GQ458231.1	594005	1920.7	2477.4	1804.5	2553.8	3813.4	1442.5
FJ978707.1	384411	7455.0	6174.6	5057.6	5414.1	6405.1	4734.8
EU775276.1	308502	2375.0	3364.8	3849.6	4019.8	4282.1	4885.5
FJ673530.1	528464	7223.0	7461.2	3939.4	6077.6	7661.5	6305.3
EU468826.1	291183	4055.7	6002.2	2918.0	2345.4	4996.7	4624.0
DQ445857.1	156623	590.2	882.2	482.9	788.6	328.3	670.5
DQ810015.1	185149	510.2	453.6	1397.9	424.8	886.0	692.3
EU460560.1	299990	5489.6	5452.1	4835.2	4621.7	4508.3	4992.1
EU775664.1	337083	243.8	253.3	484.0	201.5	75.4	101.9
FJ366714.1	357630	2465.8	3436.2	2153.7	3983.2	2191.9	2665.7
EF682951.1	247473	3814.1	4506.1	1951.5	2201.7	3574.3	3076.8
GQ868388.1	541925	8744.7	7741.2	6956.2	7705.0	7737.4	8344.4
FJ366695.1	369406	6393.0	7114.5	2386.4	4414.6	6054.7	5392.7
EU463306.1	291844	1686.1	2468.7	1633.7	1449.1	878.6	676.3
FJ375874.1	316634	4851.8	6134.9	5947.6	4563.1	5729.2	5445.1
EU459287.1	288071	4125.7	4864.4	5135.6	4975.0	6100.1	5468.3
EU475638.1	295162	4324.3	4338.9	2877.9	5061.9	7762.2	6049.8
EU763479.1	349439	146.6	343.3	471.1	286.9	362.1	643.2
FJ375912.1	306812	562.2	1129.7	654.5	723.2	807.8	1134.6
DQ798320.1	179306	6621.2	9314.4	3923.3	6388.1	5542.4	5330.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	71008
s__unclassified	71012
s__unclassified	71016
s__unclassified	71024
s__unclassified	71030
s__unclassified	71041
s__unclassified	71049
s__unclassified	71051
s__unclassified	71052
s__unclassified	71057
s__unclassified	71062
s__unclassified	71066
s__unclassified	71070
s__unclassified	71072
s__unclassified	71074
s__unclassified	71078
s__unclassified	71090
s__unclassified	71098
s__unclassified	71099
s__unclassified	71102
s__unclassified	71103
s__unclassified	71116
s__unclassified	71120
s__unclassified	71134
s__unclassified	71148
s__unclassified	71160
s__unclassified	71162
s__unclassified	71186
s__unclassified	71187
s__unclassified	71199
s__unclassified	71201
s__unclassified	71203
s__unclassified	71204
s__unclassified	71206
s__unclassified	71214
s__unclassified	71218
s__unclassified	71223
s__unclassified	71258
s__unclassified	71260
s__unclassified	71266
s__unclassified	71271

DQ809309.1 gg_id:181731 human fecal clone RL184_aah19a09
FJ375865.1 gg_id:355523 and prevalence blaTEM genes polar bear feces clone PBF_d2
EU475172.1 gg_id:303077 visayam warty pig feces clone VWP_aaa02h09
EU773258.1 gg_id:333378 BigHorn sheep feces clone BH1_aao27f08
EU459247.1 gg_id:299625 hedgehog feces clone HH_aai34f12
DQ809435.1 gg_id:191709 human fecal clone RL184_aah20h04
EU475653.1 gg_id:297403 babirusa feces clone BARB_aaa04f06
EU488411.1 gg_id:534957 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU475631.1 gg_id:297994 babirusa feces clone BARB_aaa02f02
EU777293.1 gg_id:318173 Okapi feces clone OK3_b09_2
EU475627.1 gg_id:295791 babirusa feces clone BARB_aaa02b09
DQ113713.1 gg_id:136214 dog ileum clone I5-47
EU467066.1 gg_id:288435 hedgehog feces clone HH_b11_1
GQ867290.1 gg_id:591762 and prevalence blaTEM genes Arctic seals colon content clone WSp20
EU475100.1 gg_id:290125 visayam warty pig feces clone VWP_aaa01h04
FJ678801.1 gg_id:514611 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366693.1 gg_id:366425 feces adult twins and mothers; TS27 clone TS27_a02g02
EU475586.1 gg_id:292078 babirusa feces clone BARB_aaa03g02
EU773916.1 gg_id:332962 Cheetah feces clone CE3_aai05g07
FJ681620.1 gg_id:511228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU460520.1 gg_id:290323 polar bear feces clone PB2_aai22a08
GQ359984.1 gg_id:577153 Microbial intestinal contents and mucus yel catfish (Pelteobagrus fulvidraco) intestir
DQ799856.1 gg_id:193066 human fecal clone RL247_aaj21a04
FJ366818.1 gg_id:365641 feces adult twins and mothers; TS27 clone TS27_a04c03
EU560842.1 gg_id:534075 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir
AM697422.1 gg_id:218452 sequencing libraries indoor dust clone BF0001D037
EU468628.1 gg_id:291564 okapi feces clone OK2_f08
AM982558.1 gg_id:279235 microbial and slurry pig saw dust spent bedding clone PISD-AIH04
FJ375835.1 gg_id:348777 and prevalence blaTEM genes polar bear feces clone PBF_c17
EU465318.1 gg_id:299076 lion feces clone LI3_aah75b10
AJ810555.1 gg_id:104561 superficial sediments clone
GQ868411.1 gg_id:561998 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC812
FJ363465.1 gg_id:362524 feces adult twins and mothers; TS149 clone TS149_a03e09
DQ113746.2 gg_id:136804 dog duodenum clone D1-17
GQ492355.1 gg_id:547714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ680320.1 gg_id:526583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU475618.1 gg_id:298176 babirusa feces clone BARB_aaa01b01
EU475575.1 gg_id:293486 babirusa feces clone BARB_aaa02f04
FJ679600.1 gg_id:516687 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU462544.1 gg_id:295449 Sumatran orangutan feces clone orang1_aai56g06
FJ673752.1 gg_id:526864 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

DQ809309.1	181731	83.9	158.0	66.0	108.7	80.4	81.4
FJ375865.1	355523	6876.0	8967.2	7156.1	7018.4	7440.8	6990.4
EU475172.1	303077	4714.1	4188.9	2075.7	4952.8	9958.0	8224.5
EU773258.1	333378	2111.9	2657.9	471.3	901.1	305.0	358.2
EU459247.1	299625	7654.0	7624.2	6360.6	6956.1	13260.6	11131.5
DQ809435.1	191709	689.0	1255.1	689.3	1296.3	1255.0	835.7
EU475653.1	297403	780.4	1051.4	786.6	234.2	1575.9	1598.3
EU488411.1	534957	3740.6	3272.2	1257.5	5102.3	6083.0	5637.3
EU475631.1	297994	1673.5	2279.0	3002.4	2505.2	3395.4	2945.0
EU777293.1	318173	5467.3	5462.2	4505.0	8176.5	4993.9	3766.0
EU475627.1	295791	970.0	1487.1	1868.2	830.4	3354.6	3051.5
DQ113713.1	136214	286.9	452.3	297.1	246.1	166.6	103.1
EU467066.1	288435	13498.8	14037.7	8021.8	10654.5	14958.2	12419.2
GQ867290.1	591762	1462.9	2099.3	1561.6	1587.2	2641.9	2558.6
EU475100.1	290125	3842.4	4514.3	3749.3	2999.6	5999.5	3775.1
FJ678801.1	514611	5564.1	5397.0	3122.8	5044.0	4453.1	4979.8
FJ366693.1	366425	936.4	3722.1	1496.3	1088.9	880.6	1842.8
EU475586.1	292078	1128.7	771.4	890.4	2494.9	168.4	409.6
EU773916.1	332962	1825.2	1747.1	2136.0	1720.2	1260.2	1312.1
FJ681620.1	511228	2355.6	3383.9	2824.0	1731.9	221.9	797.9
EU460520.1	290323	5588.0	4911.4	2908.5	7254.0	7967.0	7901.7
GQ359984.1	577153	4366.5	5586.1	6785.8	3218.5	5338.6	5083.5
DQ799856.1	193066	886.2	928.2	1175.7	192.0	88.8	127.1
FJ366818.1	365641	11326.8	15576.5	6572.6	9418.6	11386.0	12195.3
EU560842.1	534075	844.9	636.0	1937.1	480.9	106.2	223.2
AM697422.1	218452	4521.9	5594.2	3033.7	6628.1	9921.8	6662.5
EU468628.1	291564	994.1	1285.4	1036.9	1577.6	2603.8	2469.4
AM982558.1	279235	94.8	407.4	542.1	212.8	559.1	789.8
FJ375835.1	348777	784.2	1130.6	1017.7	2947.7	1631.1	1875.4
EU465318.1	299076	609.7	769.3	1164.6	819.8	907.4	1158.3
AJ810555.1	104561	672.5	558.9	1197.0	305.5	1822.9	1586.3
GQ868411.1	561998	4993.5	4971.1	1836.3	5451.7	7331.9	6831.5
FJ363465.1	362524	624.3	794.7	511.7	896.0	1921.6	2488.9
DQ113746.2	136804	6247.0	6902.1	3920.0	5344.8	6057.3	6471.2
GQ492355.1	547714	1062.7	840.7	836.9	2329.8	154.9	356.6
FJ680320.1	526583	6781.2	6951.7	5575.4	7776.4	8886.1	7383.5
EU475618.1	298176	135.8	275.9	145.8	241.3	143.9	116.8
EU475575.1	293486	1712.3	1518.1	1741.6	2054.5	2176.5	2374.9
FJ679600.1	516687	1362.9	1069.8	1884.6	2433.6	134.6	360.8
EU462544.1	295449	1904.5	4613.8	2384.4	2794.2	2282.8	3493.1
FJ673752.1	526864	10705.5	9868.1	10597.1	10471.3	12963.0	11212.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	71275
s__unclassified	71276
s__unclassified	71289
s__unclassified	71776
s__unclassified	71779
s__unclassified	71781
s__unclassified	71788
s__unclassified	71796
s__unclassified	71798
s__unclassified	71800
s__unclassified	71828
s__unclassified	71831
s__unclassified	71832
s__unclassified	71849
s__unclassified	71851
s__unclassified	71858
s__unclassified	71874
s__unclassified	71884
s__unclassified	71888
s__unclassified	71891
s__unclassified	71896
s__unclassified	71914
s__unclassified	71918
s__unclassified	71937
s__unclassified	71978
s__unclassified	71995
s__unclassified	72002
s__unclassified	72005
s__unclassified	72007
s__unclassified	72011
s__unclassified	72021
s__unclassified	72024
s__unclassified	72047
s__unclassified	72054
s__unclassified	72118
s__unclassified	72163
s__unclassified	72170
s__unclassified	72199
s__unclassified	72203
s__unclassified	72245
s__unclassified	72269

AJ409003.1 gg_id:21834 human colonic clone HuCB31
FJ975999.1 gg_id:586027 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
EU475604.1 gg_id:288181 babirusa feces clone BARB_aaa02d12
EF644506.1 gg_id:255177 Structure and performance microbial involved reductive dechlorination 1122-tetrach
AB218295.1 gg_id:147444 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-7
EU828373.1 gg_id:562096 Microbial effects changeover without CO2 sparging two-stage biological and methan
EU236399.1 gg_id:295330 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92C10
DQ126679.1 gg_id:138256 Clostridium dongmakense str. HY-45-18; IMSNU 40129; KCTC 5147
L37589.1 gg_id:16150 Clostridium botulinum B str. B3
AJ810553.1 gg_id:104248 superficial sediments clone
NR_028898.1 gg_id:594284 Clostridium acidisoli str. CK74; DSM 12555
EU535463.1 gg_id:281510 profile human microbiota antecubital fossa (inner elbow) skin clone nbt25f11
NZ_ABDQ01000035.1 gg_id:263445 Clostridium botulinum C str. Eklund
EU468033.1 gg_id:291999 cheetah feces clone CE2_f03_2
GU227151.1 gg_id:574341 Clostridium tyrobutyricum str. B6-2
AB186864.1 gg_id:104466 polychlorinated dioxin dechlorinating microcosm clone TSAF01
AB486908.1 gg_id:541432 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
AB081585.1 gg_id:71518 Clostridiaceae str. A4d
NZ_ABDQ01000017.1 gg_id:264222 Clostridium botulinum C str. Eklund
AY742899.1 gg_id:106253 Clostridium crotonatovorans str. R6B
AJ229185.1 gg_id:36004 anoxic bulk soil flooded rice microcosm clone BSV20 clone
AB486626.1 gg_id:566529 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
EU474720.1 gg_id:297378 takin feces clone TAK_aaa03e09
GU476608.1 gg_id:525790 microbial biogas fermentation enrichment clone BBMC-8
AJ222546.1 gg_id:16199 Anaerobacter polyendosporus
AB486197.1 gg_id:563918 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AY395437.1 gg_id:107326 pasture soil clone EB1118
L08062.1 gg_id:16144 Clostridium tyrobutyricum str. NIZO 51
AB487095.1 gg_id:589921 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIRO
EU467918.1 gg_id:298719 cheetah feces clone CE2_a09
AB509218.1 gg_id:543607 Microbial reservior produced water oil reservoir clone HNB-13
AJ427628.1 gg_id:64232 Clostridium scatologenes str. FP
NR_029250.1 gg_id:591228 Clostridium proteolyticum str. CG; DSM 3090
AB470964.1 gg_id:535657 Clostridium sp. str. r13
AB470961.1 gg_id:571639 Clostridium sp. str. r53
EU536517.1 gg_id:279856 profile human microbiota antecubital fossa (inner elbow) skin clone nbt215c07
DQ129397.1 gg_id:137941 microarray level air two cities Texas urban aerosol clone AKIW662
EU467972.1 gg_id:297029 cheetah feces clone CE2_c12_1
EF088329.1 gg_id:177051 Clostridium hveragerdense str. AK14
AB264078.1 gg_id:190766 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-151
AY167950.1 gg_id:75821 Isolation and identification hyper-ammonia producing swine storage pits manure

AJ409003.1	21834	5475.0	6010.4	2591.4	3785.1	591.1	2930.7
FJ975999.1	586027	741.4	1213.8	1651.4	745.3	273.6	803.3
EU475604.1	288181	5051.8	4825.0	2970.5	5461.6	8241.0	6790.4
EF644506.1	255177	1377.6	551.6	4637.6	569.1	75.2	749.0
AB218295.1	147444	841.8	844.3	1227.1	316.2	1903.7	1147.6
EU828373.1	562096	963.6	1002.9	1988.4	943.6	342.8	447.2
EU236399.1	295330	1017.0	380.8	1239.4	233.2	100.3	182.7
DQ126679.1	138256	988.9	449.0	945.0	760.4	118.1	282.2
L37589.1	16150	5119.1	3938.2	3425.2	4889.4	10674.5	6467.5
AJ810553.1	104248	1334.3	849.6	2653.7	498.1	1096.8	583.7
NR_028898.1	594284	6274.4	5021.7	2971.8	5037.6	6874.8	5692.9
EU535463.1	281510	9062.3	9169.1	7526.2	9981.1	13325.7	10568.5
NZ_ABDQ01000035.1	263445	713.0	730.3	1312.7	545.9	274.7	282.5
EU468033.1	291999	8631.7	10558.6	8807.8	7165.8	11886.2	9961.9
GU227151.1	574341	8631.6	7875.5	6786.6	7626.5	6889.5	8069.8
AB186864.1	104466	374.2	134.9	270.7	426.7	70.6	47.3
AB486908.1	541432	453.7	503.1	846.7	449.2	191.7	314.6
AB081585.1	71518	3357.8	2994.6	4949.5	3160.4	1663.0	1501.6
NZ_ABDQ01000017.1	264222	1562.7	1977.2	2826.2	2171.2	921.8	828.2
AY742899.1	106253	104.5	98.7	116.8	114.4	73.2	87.3
AJ229185.1	36004	4988.8	7017.9	5019.4	6991.6	7115.0	6242.9
AB486626.1	566529	4782.4	5282.2	2756.3	4139.2	3200.5	3251.4
EU474720.1	297378	3602.8	4092.4	6398.7	3296.1	2096.0	2297.7
GU476608.1	525790	4737.5	5456.7	6250.8	6237.6	9845.3	8959.4
AJ222546.1	16199	126.3	270.6	361.6	251.9	67.1	321.5
AB486197.1	563918	155.2	186.7	273.8	167.2	125.0	219.4
AY395437.1	107326	101.7	117.3	70.3	88.8	71.5	67.9
L08062.1	16144	8762.7	8150.1	6736.3	5401.0	6414.3	7204.1
AB487095.1	589921	2165.6	1071.5	5357.5	761.0	733.4	622.9
EU467918.1	298719	11414.3	11675.7	8190.0	9699.9	11413.6	11136.8
AB509218.1	543607	8257.9	8784.8	7024.2	7590.8	4311.3	4410.5
AJ427628.1	64232	9745.5	8732.3	11149.1	6495.9	9814.0	9613.7
NR_029250.1	591228	298.2	272.0	635.7	239.4	84.3	80.5
AB470964.1	535657	4096.8	3529.0	4134.3	3670.3	1438.3	1541.2
AB470961.1	571639	5935.1	4694.4	1796.8	4483.6	2102.1	2132.4
EU536517.1	279856	14274.6	15054.7	10128.4	11420.8	17210.6	14438.6
DQ129397.1	137941	2854.2	2218.0	3409.9	4471.6	2543.6	4091.4
EU467972.1	297029	3921.4	3597.7	3196.6	4339.3	6034.0	3854.5
EF088329.1	177051	800.1	468.2	1319.7	440.8	100.1	300.8
AB264078.1	190766	5446.0	5326.4	1323.6	469.7	2692.9	3941.9
AY167950.1	75821	3600.1	3190.5	4371.6	1899.6	1693.7	1702.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	72273
s__unclassified	72278
s__unclassified	72283
s__unclassified	72314
s__unclassified	72322
s__unclassified	72330
s__unclassified	72335
s__unclassified	72343
s__unclassified	72349
s__unclassified	72358
s__unclassified	72406
s__unclassified	72409
s__unclassified	72464
s__unclassified	72478
s__unclassified	72487
s__unclassified	72520
s__unclassified	72521
s__unclassified	72542
s__unclassified	72574
s__unclassified	72590
s__unclassified	72601
s__unclassified	72609
s__unclassified	72617
s__unclassified	72651
s__unclassified	72656
s__unclassified	72691
s__unclassified	72720
s__unclassified	72723
s__unclassified	72735
s__unclassified	72740
s__unclassified	72748
s__unclassified	72758
s__unclassified	72771
s__unclassified	72776
s__unclassified	72777
s__unclassified	72780
s__unclassified	72799
s__unclassified	72812
s__unclassified	72816
s__unclassified	72827
s__unclassified	72864

AB486259.1 gg_id:582154 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EU536029.1 gg_id:287039 profile human microbiota antecubital fossa (inner elbow) skin clone nbt07c07
DQ196621.2 gg_id:167430 Clostridium sp. str. BL-28
AB470965.1 gg_id:533504 Clostridium sp. str. r22
AY858804.1 gg_id:137989 Clostridium lundensis str. DSM 17049
AY581269.1 gg_id:114950 Clostridium sp. str. HY-34-8
L37585.1 gg_id:16148 Clostridium botulinum type A
AY548785.1 gg_id:104893 Clostridium sp. str. PPf35E10
DQ680019.1 gg_id:173147 Clostridium sporogenes str. IBUN 182
DQ125892.1 gg_id:134335 uranium contaminated soil clone AKAU4146
AJ229230.1 gg_id:35306 anoxic bulk soil flooded rice microcosm clone BSV86 clone
AF407686.1 gg_id:60611 Great Artesian Basin clone R10
AB487192.1 gg_id:572576 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
AY551086.1 gg_id:102321 Clostridium sp. 17cr1
AB486869.1 gg_id:558685 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
ABDP01000045.1 gg_id:269119 Clostridium botulinum str. Bf
AB487685.1 gg_id:550171 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSRC
EU537334.1 gg_id:285059 profile human microbiota antecubital fossa (inner elbow) skin clone nbt77a02
AB218294.1 gg_id:146143 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-121
GQ503831.1 gg_id:588312 Taptapani hot water spring clone tpsrb003
EU307088.1 gg_id:257735 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AF092548.1 gg_id:16239 Clostridium gasigenes str. DSM 12272
EF197795.1 gg_id:192526 Clostridium tepidiprofundum str. SG508
AF317650.1 gg_id:31985 Clostridium thiosulfatireducens str. Lup21
NR_029246.1 gg_id:578922 Clostridium collagenovorans str. SG; DSM 3089
AB488292.1 gg_id:591402 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
FJ269106.1 gg_id:308659 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil
GQ461617.1 gg_id:581078 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial TCE Bioren
AB487999.1 gg_id:563768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
GU118536.1 gg_id:574100 Threatened Corals Provide Microbial Habitats clone Mfav_O15
AB218319.1 gg_id:148431 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-84
FJ384387.1 gg_id:368281 Clostridium sp. str. BG-C131
AB486212.1 gg_id:554530 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AB479046.1 gg_id:571847 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland ma
DQ129267.1 gg_id:137771 microarray level air two cities Texas urban aerosol clone AKIW1140
FJ167457.1 gg_id:310070 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
EU376532.1 gg_id:275993 Clostridium sp. str. SL149
AB486270.1 gg_id:586263 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EU540396.1 gg_id:280295 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114d04
EF515406.1 gg_id:224769 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a07
AB488015.1 gg_id:587690 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC

AB486259.1	582154	2775.0	2688.1	3669.5	4127.7	2733.0	2704.3
EU536029.1	287039	15158.1	16909.0	4740.9	10338.6	11403.2	9809.2
DQ196621.2	167430	228.4	346.5	526.5	137.6	52.1	105.3
AB470965.1	533504	6274.5	6561.9	2665.5	4505.9	7549.5	6305.2
AY858804.1	137989	258.0	139.8	247.1	122.5	94.2	122.1
AY581269.1	114950	738.7	370.3	2145.8	264.9	139.5	629.0
L37585.1	16148	1618.2	2018.0	1932.9	1348.9	1259.8	1237.6
AY548785.1	104893	469.7	292.2	543.6	237.4	82.1	133.0
DQ680019.1	173147	1228.8	1181.9	2450.2	827.4	830.7	812.3
DQ125892.1	134335	1017.4	1332.7	5356.2	2326.9	183.7	513.0
AJ229230.1	35306	581.7	473.9	684.0	247.8	235.6	304.8
AF407686.1	60611	5185.4	4132.8	4800.0	4680.9	2591.5	3082.9
AB487192.1	572576	4796.9	4164.3	4096.5	3422.6	4538.9	4364.8
AY551086.1	102321	1178.8	809.6	1256.0	875.9	235.8	439.1
AB486869.1	558685	2306.9	1288.8	1902.7	1461.2	311.1	301.8
ABDP01000045.1	269119	407.4	226.5	559.7	495.0	119.7	336.6
AB487685.1	550171	3417.7	3121.2	2985.4	3120.3	2130.0	1516.0
EU537334.1	285059	8175.1	8458.2	7030.7	9493.8	6744.2	7077.0
AB218294.1	146143	297.7	233.7	381.3	279.2	232.0	219.0
GQ503831.1	588312	917.5	1153.3	1644.7	676.9	440.0	891.9
EU307088.1	257735	5443.5	4749.8	10104.3	2773.1	1661.1	2881.9
AF092548.1	16239	250.3	268.7	207.2	108.5	79.8	222.7
EF197795.1	192526	597.8	562.8	216.1	109.5	120.9	114.2
AF317650.1	31985	1048.0	888.3	2427.5	505.3	247.4	842.8
NR_029246.1	578922	181.9	137.6	69.7	139.3	86.6	70.3
AB488292.1	591402	2205.0	2984.1	3260.1	3207.8	2967.6	3156.2
FJ269106.1	308659	3218.8	2301.8	5493.6	2050.8	2151.8	2383.1
GQ461617.1	581078	11052.6	10680.0	9023.3	9480.5	9903.9	13803.4
AB487999.1	563768	7991.3	7856.3	6695.2	8429.7	6450.5	6838.2
GU118536.1	574100	298.9	263.5	1539.2	136.1	51.4	181.3
AB218319.1	148431	1500.1	821.6	3071.5	496.7	280.0	571.9
FJ384387.1	368281	129.1	81.7	213.3	92.6	74.8	52.9
AB486212.1	554530	5101.5	4944.0	4835.6	4845.6	4574.8	4042.4
AB479046.1	571847	836.5	464.7	2060.7	245.1	192.7	547.1
DQ129267.1	137771	3034.7	3497.2	4742.9	3028.3	1323.9	2130.9
FJ167457.1	310070	4126.5	2589.8	6658.0	1222.1	2887.7	2986.2
EU376532.1	275993	2340.6	2550.1	1891.9	599.7	468.5	1018.5
AB486270.1	586263	4379.3	4717.9	4247.0	3925.4	3927.4	4138.9
EU540396.1	280295	5205.5	4997.3	6753.4	5569.2	6277.7	5673.3
EF515406.1	224769	7996.3	7849.7	8903.1	7764.6	7327.2	8038.2
AB488015.1	587690	3652.7	4469.0	2915.8	3509.4	5182.2	5972.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Natronincola
g__Natronincola
g__Natronincola
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina

s__unclassified	72895
s__unclassified	72902
s__unclassified	72917
s__unclassified	72926
s__unclassified	72948
s__unclassified	72955
s__unclassified	72964
s__unclassified	72991
s__unclassified	73012
s__unclassified	73019
s__unclassified	73027
s__unclassified	73029
s__unclassified	73034
s__unclassified	73035
s__unclassified	73042
s__unclassified	73067
s__unclassified	73113
s__unclassified	69945
s__unclassified	70078
s__unclassified	70507
s__unclassified	44177
s__unclassified	44322
s__unclassified	44359
s__unclassified	44360
s__unclassified	44409
s__unclassified	44442
s__unclassified	44465
s__unclassified	44519
s__unclassified	44555
s__unclassified	44559
s__unclassified	44603
s__unclassified	44625
s__unclassified	44638
s__unclassified	44649
s__unclassified	44660
s__unclassified	44740
s__unclassified	44749
s__unclassified	44802
s__unclassified	44803
s__unclassified	44812
s__unclassified	44836

AY217406.1 gg_id:81138 TCE-dechlorinating microbial community clone 7H
AB487423.1 gg_id:535222 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EU468070.1 gg_id:300313 cheetah feces clone CE2_c07_2
AB487443.1 gg_id:551963 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
AB486434.1 gg_id:587168 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EU037903.1 gg_id:240095 Clostridium mesophilum str. SW408
FJ957871.1 gg_id:417891 Clostridium sporogenes str. JPL_17
AB488261.1 gg_id:578160 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0
DQ196626.2 gg_id:167821 Clostridium sp. str. BL-22
AY667266.1 gg_id:102839 TCE-dechlorinating groundwater clone TANB101
EU073771.1 gg_id:248695 Microbial subsurface beds and methanogenic s coal enrichment clone ObedB-8G
NR_025352.1 gg_id:542995 Clostridium akagii str. CK58; DSM 12554
AB239189.1 gg_id:220242 Clone acidigenic anaerobic enriched starch thermophilic methanogenic sludge clone
AB237714.1 gg_id:139836 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW
AY548784.1 gg_id:104736 Clostridium sp. str. PPf35E8
FJ455907.1 gg_id:513952 Variations archaeal and sulfate-methane transition zone continental margin sedimen
DQ196619.1 gg_id:168422 Clostridium sp. str. BL-14
DQ675453.1 gg_id:172040 Clostridium sp. str. Z-0511
EF586022.1 gg_id:246053 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_
EU878275.1 gg_id:305185 Clostridium sp. Z-0511 str. Z-0511; DSM 18346; VKM B-2402
EU471390.1 gg_id:300773 spectacled bear feces clone SB_2aaa03a02
EU470899.1 gg_id:299498 red panda feces clone RP_2aaa01g08
EU470928.1 gg_id:295858 red panda feces clone RP_2aaa02b04
EU776817.1 gg_id:327397 Mongoose lemur feces clone ML_aaj25b03
EU778467.1 gg_id:331973 Red Panda feces clone RP_2aaa03f09
EU470764.1 gg_id:290811 red panda feces clone RP_2aaa04g03
EU777367.1 gg_id:353163 Sumatran orangutan feces clone orang1_d07_1
EU470993.1 gg_id:300606 red panda feces clone RP_2aaa01h06
EU469919.1 gg_id:289211 western lowland gorilla feces clone GOR_aag74c06
EU471360.1 gg_id:294343 spectacled bear feces clone SB_2aaa04b03
EU471368.1 gg_id:288826 spectacled bear feces clone SB_2aaa01c02
EU462444.1 gg_id:288082 Sumatran orangutan feces clone orang1_aai54g01
EU469616.1 gg_id:298985 flying fox feces clone FF_h02
EU471421.1 gg_id:303385 spectacled bear feces clone SB_2aaa03a07
EU470768.1 gg_id:298193 red panda feces clone RP_2aaa01h02
EU470933.1 gg_id:297215 red panda feces clone RP_2aaa02d08
EU462038.1 gg_id:298407 black-handed spider monkey feces clone SPIM_aaj33g03
EU470866.1 gg_id:300995 red panda feces clone RP_2aaa03g06
EU467216.1 gg_id:296163 black-handed spider monkey feces clone SPIM_c12
EU469939.1 gg_id:293118 western lowland gorilla feces clone GOR_aag74h05
EU471395.1 gg_id:295548 spectacled bear feces clone SB_2aaa01f09

AY217406.1	81138	16719.8	14531.1	10388.7	12238.6	13449.3	13929.2
AB487423.1	535222	7881.0	6486.8	7733.3	6690.2	8860.5	9941.1
EU468070.1	300313	12815.1	13656.0	3440.4	7849.8	7144.7	6496.9
AB487443.1	551963	3620.1	3409.1	5248.5	3894.6	3675.1	3929.1
AB486434.1	587168	3432.8	2767.6	4981.6	4684.6	4352.2	3885.1
EU037903.1	240095	2448.5	1724.8	3244.6	1057.2	212.4	705.2
FJ957871.1	417891	1536.1	1346.6	2294.5	921.3	979.8	1033.7
AB488261.1	578160	5145.6	5438.6	6429.3	3269.1	4046.8	5759.8
DQ196626.2	167821	6620.7	9758.8	2212.4	4540.1	4073.7	3799.0
AY667266.1	102839	2413.2	1262.9	2651.8	2585.3	470.5	1176.2
EU073771.1	248695	2226.2	2066.4	2818.2	2000.2	2377.5	2328.9
NR_025352.1	542995	975.4	871.9	854.0	211.8	117.8	240.0
AB239189.1	220242	89.6	211.2	655.6	106.0	77.7	157.2
AB237714.1	139836	1145.2	796.2	1894.6	1122.8	139.7	682.6
AY548784.1	104736	923.2	443.9	654.3	618.8	86.1	131.7
FJ455907.1	513952	3575.2	2834.6	6369.9	2447.0	3127.1	3779.8
DQ196619.1	168422	124.3	111.1	427.4	78.8	79.4	110.9
DQ675453.1	172040	1062.7	914.7	938.4	2391.9	1164.9	1218.3
EF586022.1	246053	97.9	148.1	124.5	434.4	153.8	85.9
EU878275.1	305185	7828.4	8940.6	9921.1	8840.2	7321.0	7088.0
EU471390.1	300773	944.3	1388.7	1529.7	594.0	131.1	335.5
EU470899.1	299498	2368.6	3092.5	5648.6	4170.5	4292.5	3911.4
EU470928.1	295858	8795.2	7951.7	7077.8	5131.7	549.6	4003.8
EU776817.1	327397	3866.8	1395.2	3448.1	6531.7	4980.7	3912.4
EU778467.1	331973	3265.0	3432.9	3561.0	4630.7	6323.6	6030.0
EU470764.1	290811	4883.6	4772.9	4182.5	4445.3	4151.1	4095.6
EU777367.1	353163	4264.2	4280.1	6891.5	3978.5	2440.3	3153.2
EU470993.1	300606	3405.9	3398.3	4689.7	1776.6	2806.8	2647.0
EU469919.1	289211	1371.4	1273.7	1549.8	3445.9	929.9	1755.9
EU471360.1	294343	3423.6	4971.1	2246.1	2798.4	9566.6	7401.0
EU471368.1	288826	1419.0	1347.4	3174.3	2465.0	1669.2	2362.2
EU462444.1	288082	1225.5	1229.4	3428.5	3437.4	1434.5	4602.2
EU469616.1	298985	2457.3	2407.5	3599.9	988.4	1079.1	1250.9
EU471421.1	303385	7917.7	8046.8	6652.5	6954.4	10168.9	9964.5
EU470768.1	298193	1624.0	2045.6	4196.1	966.8	1498.0	1939.2
EU470933.1	297215	7273.6	7141.9	2528.0	7657.9	5580.3	5542.8
EU462038.1	298407	4731.1	4017.7	7279.8	7280.0	5403.9	6422.5
EU470866.1	300995	352.7	683.1	926.1	615.7	87.1	107.9
EU467216.1	296163	8221.4	8441.9	3085.3	4917.1	2465.6	3230.2
EU469939.1	293118	2482.4	3299.2	3683.6	2022.0	3863.4	2705.9
EU471395.1	295548	1298.5	1906.5	1943.2	1297.1	4520.8	2573.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Sarcina
g__Tindallia
g__Tindallia
g__Tindallia

s__unclassified	44863
s__unclassified	44933
s__unclassified	44983
s__unclassified	44995
s__unclassified	45029
s__unclassified	45031
s__unclassified	45041
s__unclassified	45056
s__unclassified	45109
s__unclassified	45175
s__unclassified	45178
s__unclassified	45189
s__unclassified	45206
s__unclassified	45226
s__unclassified	45333
s__unclassified	45368
s__unclassified	45410
s__unclassified	45432
s__unclassified	45461
s__unclassified	45533
s__unclassified	45589
s__unclassified	45591
s__unclassified	45623
s__unclassified	45645
s__unclassified	45650
s__unclassified	45661
s__unclassified	45664
s__unclassified	45685
s__unclassified	45707
s__unclassified	45727
s__unclassified	45730
s__unclassified	45737
s__unclassified	45738
s__unclassified	45741
s__unclassified	45749
s__unclassified	45781
s__unclassified	45842
s__unclassified	72286
s__unclassified	70401
s__unclassified	70415
s__unclassified	70448

EU470987.1 gg_id:295473 red panda feces clone RP_2aaa03c05
EU471433.1 gg_id:288353 spectacled bear feces clone SB_2aaa04e12
EU470864.1 gg_id:289965 red panda feces clone RP_2aaa04e09
EU461261.1 gg_id:302605 hamadryas baboon feces clone BAZ_aah91f12
EU471394.1 gg_id:302208 spectacled bear feces clone SB_2aaa02c08
EU775362.1 gg_id:304758 Western lowland gorilla feces clone GOR_aag74d03
EU777443.1 gg_id:322847 Sumatran orangutan feces clone orang1_aai53a11
EU461293.1 gg_id:295126 hamadryas baboon feces clone BAZ_aah92d06
EU461294.1 gg_id:299448 hamadryas baboon feces clone BAZ_aah92d07
EU470906.1 gg_id:287378 red panda feces clone RP_2aaa01b08
EU467464.1 gg_id:293687 Sumatran orangutan feces clone orang1_h10
EU470975.1 gg_id:299372 red panda feces clone RP_2aaa03c10
EU777525.1 gg_id:341642 Sumatran orangutan feces clone orang1_aai55h09
EU470815.1 gg_id:289711 red panda feces clone RP_2aaa04b05
EU471455.1 gg_id:290626 spectacled bear feces clone SB_2aaa01c04
EU462037.1 gg_id:301778 black-handed spider monkey feces clone SPIM_aaj33g02
EU778647.1 gg_id:349573 Spectacled bear feces clone SB_2aaa03d12
EU773056.1 gg_id:336187 Banteng feces clone BG_aaa03e12.Contig1
EU470735.1 gg_id:292631 red panda feces clone RP_2aaa01a07
EU778503.1 gg_id:316285 Red Panda feces clone RP_2aaa04c01
EU462430.1 gg_id:296507 Sumatran orangutan feces clone orang1_aai54d09
EU469815.1 gg_id:298292 western lowland gorilla feces clone GOR_aag71e07
EU777615.1 gg_id:325073 Sumatran orangutan feces clone orang1_aai55g02
EU471476.1 gg_id:293333 spectacled bear feces clone SB_2aaa03c12
EU470843.1 gg_id:292525 red panda feces clone RP_2aaa02c06
EU467479.1 gg_id:289409 Sumatran orangutan feces clone orang1_f07_1
EU778399.1 gg_id:312733 Red Panda feces clone RP_2aaa02h11
EU469758.1 gg_id:293303 flying fox feces clone FF_d05
EU470773.1 gg_id:302078 red panda feces clone RP_2aaa04h10
EU467437.1 gg_id:292461 Sumatran orangutan feces clone orang1_b03
EU471327.1 gg_id:300582 spectacled bear feces clone SB_2aaa01b12
EU774131.1 gg_id:344202 Chimpanzee feces clone CHIMP12_h06
EU773439.1 gg_id:332920 Black lemur feces clone BKLE_e08_1
EU471402.1 gg_id:300228 spectacled bear feces clone SB_2aaa04h09
EU470984.1 gg_id:295643 red panda feces clone RP_2aaa01a08
EU467293.1 gg_id:288118 hamadryas baboon feces clone BAZ_f08
EU776880.1 gg_id:352379 Mongoose lemur feces clone ML_aaj26c04
EU471517.1 gg_id:290669 spectacled bear feces clone SB_2aaa01h09
AJ271455.1 gg_id:40951 Clostridium aminovorans B7FT-
AF373919.2 gg_id:28874 Tindallia californiensis str. APO
AJ271456.1 gg_id:71603 Clostridium alcaliphilum B8NS1-

EU470987.1	295473	186.6	213.4	385.8	151.1	67.9	131.8
EU471433.1	288353	8080.8	4997.8	5100.3	6684.9	8125.3	7909.2
EU470864.1	289965	1660.5	2257.5	4378.9	963.8	1467.4	1912.2
EU461261.1	302605	4205.9	3298.7	3476.2	7032.5	3666.8	4822.2
EU471394.1	302208	3903.9	3311.3	4596.8	4899.7	4053.2	3973.3
EU775362.1	304758	6157.3	6363.7	6221.1	2868.1	5780.7	5855.1
EU777443.1	322847	843.0	848.9	1205.0	521.8	1203.7	1744.4
EU461293.1	295126	2051.9	1759.3	3424.4	3819.3	2563.5	4382.9
EU461294.1	299448	7749.4	6368.3	7936.9	5170.0	2953.0	7296.3
EU470906.1	287378	2845.4	1769.0	3284.4	5566.9	1785.7	2160.4
EU467464.1	293687	2934.5	3993.3	3405.5	2697.7	7599.9	7828.4
EU470975.1	299372	1835.5	2320.4	1477.1	2315.8	518.6	1578.3
EU777525.1	341642	2894.9	3269.6	4910.0	1740.6	2448.6	2394.2
EU470815.1	289711	3025.8	3096.2	5901.2	1912.9	2321.1	2908.4
EU471455.1	290626	829.6	974.2	2077.9	440.5	496.4	868.4
EU462037.1	301778	1704.3	2278.8	3279.9	1499.4	3993.7	3168.8
EU778647.1	349573	1534.9	735.8	1657.1	322.9	535.1	359.2
EU773056.1	336187	3481.6	2986.9	6865.8	3057.7	1997.5	1259.9
EU470735.1	292631	909.6	914.4	3319.3	1056.8	169.4	1085.0
EU778503.1	316285	2155.0	1774.4	4366.5	1905.3	253.7	1648.8
EU462430.1	296507	5498.5	3950.5	5971.5	6187.7	3286.8	5174.9
EU469815.1	298292	1364.4	1720.8	2780.4	905.6	1094.7	1714.2
EU777615.1	325073	9205.7	8524.5	7489.0	9568.2	14347.6	12796.0
EU471476.1	293333	1977.1	3055.7	2176.4	1232.9	5048.1	2989.7
EU470843.1	292525	3204.2	5222.2	3575.2	1865.3	7203.8	7326.3
EU467479.1	289409	10336.9	9413.6	7611.5	10785.3	13804.6	13774.1
EU778399.1	312733	979.0	517.5	1683.0	1184.1	302.3	446.9
EU469758.1	293303	14710.6	14412.1	10490.3	11885.8	14564.6	13938.5
EU470773.1	302078	9729.3	8508.7	8313.6	7645.1	11282.5	8033.4
EU467437.1	292461	3638.4	3941.5	5656.3	2348.6	3140.9	3299.4
EU471327.1	300582	1908.4	2273.0	1996.8	1467.1	622.5	1060.7
EU774131.1	344202	2376.6	3086.2	5237.3	4344.0	4265.9	4122.8
EU773439.1	332920	7798.5	8214.7	9101.7	6944.4	9566.5	7447.3
EU471402.1	300228	341.0	223.4	411.9	213.2	231.5	244.7
EU470984.1	295643	1341.1	1251.9	3541.3	2943.7	1542.1	1760.6
EU467293.1	288118	2758.3	4001.2	2255.4	1335.6	1028.7	2382.0
EU776880.1	352379	132.1	143.2	408.4	102.6	55.7	31.6
EU471517.1	290669	784.2	1482.6	662.9	656.5	1372.5	856.1
AJ271455.1	40951	8231.9	9106.1	10921.1	11029.4	15311.9	12917.0
AF373919.2	28874	1983.4	2648.5	5518.3	3452.2	4287.6	3971.1
AJ271456.1	71603	1650.0	1954.8	5305.8	3241.6	5969.2	5138.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	44838
s__unclassified	44902
s__unclassified	45207
s__unclassified	69962
s__unclassified	69964
s__unclassified	69997
s__unclassified	70056
s__unclassified	70084
s__unclassified	70092
s__unclassified	70105
s__unclassified	70106
s__unclassified	70225
s__unclassified	70244
s__unclassified	70290
s__unclassified	70350
s__unclassified	70529
s__unclassified	70533
s__unclassified	70546
s__unclassified	71802
s__unclassified	71842
s__unclassified	71852
s__unclassified	71890
s__unclassified	71892
s__unclassified	71905
s__unclassified	71910
s__unclassified	71920
s__unclassified	71934
s__unclassified	71940
s__unclassified	71942
s__unclassified	71955
s__unclassified	71959
s__unclassified	71989
s__unclassified	71993
s__unclassified	72102
s__unclassified	72113
s__unclassified	72151
s__unclassified	72167
s__unclassified	72174
s__unclassified	72182
s__unclassified	72183
s__unclassified	72316

FJ424474.1 gg_id:364085 Clostridium sp. str. SH-C10
EU775653.1 gg_id:356516 Hedgehog feces clone HH_aai34d11
EU467043.1 gg_id:288286 hedgehog feces clone HH_a10_1
AF458779.1 gg_id:67640 Clostridium caminithermale str. DVird3
EU573106.1 gg_id:279224 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c
AB294306.1 gg_id:216573 Microbial structure deep coal seem groundwater clone YWB37
AF507894.1 gg_id:62667 Mono Lake at depth 23m station 6 July 2000 clone ML623J-36
EU443727.1 gg_id:442217 Thermotalea metallivorans str. B2-1
DQ234642.1 gg_id:141863 subsurface water clone DR546BH1103001SAD18
Y16716.1 gg_id:43181 Natronincola histidinovorans str. Z-7940T (DSM 11416)
DQ206418.1 gg_id:140290 microbial mediates arsenate reduction soda lake water clone ML-S-1
DQ643978.1 gg_id:170026 Geosporobacter subterrenus str. VNs68
DQ234901.1 gg_id:141051 Tindallia texcocoense str. IMP-300
AJ271453.1 gg_id:19154 Clostridium elmenteitii E2SE1-B
AY464940.1 gg_id:104179 Caldanaerocella colombiensis str. P4.4
GQ848202.1 gg_id:582632 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac
FM178809.1 gg_id:337073 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu
AF407695.1 gg_id:60603 Great Artesian Basin clone R82
EU458270.1 gg_id:288703 North American black bear feces clone BB2_b06_2
EU775654.1 gg_id:310410 Hedgehog feces clone HH_aai36a02
AF069742.1 gg_id:16220 Clostridium frigidicarnis str. SPL77A
EF420221.1 gg_id:208357 Mature fine processing harbour methanogenic oil sands tailings pond clone 12-10F
EU775663.1 gg_id:311928 Hedgehog feces clone HH_aai33c11
EF614838.1 gg_id:227851 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU471505.1 gg_id:300929 spectacled bear feces clone SB_2aaa01c11
DQ015091.1 gg_id:133265 mouse cecum clone M2_c01
X77676.1 gg_id:16200 Clostridium algidicarnis str. NCFB 2931
EU470498.1 gg_id:290076 red panda feces clone RP_1aaa01f09
EU775623.1 gg_id:321747 Hedgehog feces clone HH_d12
EU458271.1 gg_id:298041 North American black bear feces clone BB2_b07_3
EF687331.1 gg_id:282549 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
EU470672.1 gg_id:295461 red panda feces clone RP_1aaa04f06
EU471456.1 gg_id:288039 spectacled bear feces clone SB_2aaa01f07
AJ229222.1 gg_id:31072 anoxic bulk soil flooded rice microcosm clone BSV78 clone
EU458119.1 gg_id:296563 North American black bear feces clone BB2_a10
EU776900.1 gg_id:306522 Mongoose lemur feces clone ML_aae89h03
EU459248.1 gg_id:295190 hedgehog feces clone HH_aai34g01
FJ671124.1 gg_id:519851 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF174499.1 gg_id:180489 Clostridium sp. str. R6T
AB487300.1 gg_id:555862 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EU471302.1 gg_id:289222 red panda feces clone RP_3aaa03a04

FJ424474.1	364085	163.9	255.2	160.9	93.6	75.4	68.9
EU775653.1	356516	9916.6	9892.2	4510.4	7558.8	9454.8	7699.4
EU467043.1	288286	1666.4	1272.2	2436.9	592.1	154.0	553.0
AF458779.1	67640	1994.4	2456.8	4538.6	3160.5	489.2	774.1
EU573106.1	279224	59.5	118.4	97.5	66.9	41.7	21.5
AB294306.1	216573	1580.6	1815.7	2939.8	1068.9	713.8	1350.7
AF507894.1	62667	601.2	481.6	320.6	351.7	82.6	114.3
EU443727.1	442217	62.4	62.1	42.8	88.7	86.2	75.5
DQ234642.1	141863	39.6	54.0	54.7	74.7	89.7	35.5
Y16716.1	43181	2374.2	2058.1	4187.4	2908.0	2061.1	1860.6
DQ206418.1	140290	1264.8	1769.9	4849.9	2159.5	3297.0	2207.4
DQ643978.1	170026	1557.0	1318.6	1599.5	433.0	225.0	303.1
DQ234901.1	141051	2799.1	1814.8	4775.5	3561.9	2711.9	3506.3
AJ271453.1	19154	1003.8	813.0	874.8	1005.5	140.4	224.4
AY464940.1	104179	23.9	32.9	29.3	54.3	60.2	23.4
GQ848202.1	582632	998.2	1152.9	1592.4	236.5	154.1	281.0
FM178809.1	337073	2921.3	4369.1	1824.9	3931.6	3166.4	4992.4
AF407695.1	60603	60.3	83.4	38.3	72.4	78.4	37.6
EU458270.1	288703	2904.3	1130.6	2279.3	4636.1	2978.4	2238.5
EU775654.1	310410	1912.5	1938.5	2989.9	2188.5	12396.7	5273.7
AF069742.1	16220	80.0	178.1	941.3	136.0	92.9	91.9
EF420221.1	208357	2193.0	1691.3	579.5	1313.8	1479.8	1327.3
EU775663.1	311928	3355.1	3984.0	6345.5	2300.7	1341.0	2248.8
EF614838.1	227851	7191.6	8047.0	6951.7	6103.2	7419.2	6147.6
EU471505.1	300929	6116.6	5572.3	7129.2	5709.6	4499.8	4564.6
DQ015091.1	133265	6725.4	6331.5	2996.6	7048.8	7841.0	5890.8
X77676.1	16200	58.9	88.9	122.2	69.9	79.8	36.4
EU470498.1	290076	12777.6	12211.2	10580.8	9722.4	10078.8	9387.4
EU775623.1	321747	1343.1	2091.7	1562.1	936.4	910.1	1116.3
EU458271.1	298041	3130.8	2764.3	4639.9	2738.5	5061.8	4006.9
EF687331.1	282549	912.6	983.0	1296.5	827.8	431.6	700.5
EU470672.1	295461	4192.8	3969.2	2644.1	3765.6	4946.8	3109.7
EU471456.1	288039	9846.8	9127.4	7227.5	9869.4	9632.9	9733.2
AJ229222.1	31072	184.5	169.9	323.3	246.2	244.0	244.1
EU458119.1	296563	11108.8	10852.7	11514.9	9683.0	9831.2	8188.6
EU776900.1	306522	4478.9	5266.6	2507.8	2233.4	2174.9	3525.8
EU459248.1	295190	5233.0	4858.3	6469.5	5075.2	6149.8	5326.1
FJ671124.1	519851	4878.5	3927.3	4990.9	3786.8	4264.7	4873.5
EF174499.1	180489	158.8	134.1	141.9	111.5	70.5	60.1
AB487300.1	555862	5710.1	5170.0	6096.0	4420.0	3111.0	4041.0
EU471302.1	289222	5907.0	6441.8	7268.9	4983.7	4616.0	4768.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiaceae
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Anaerococcus

s__unclassified	72360
s__unclassified	72384
s__unclassified	72414
s__unclassified	72417
s__unclassified	72418
s__unclassified	72424
s__unclassified	72448
s__unclassified	72494
s__unclassified	72495
s__unclassified	72498
s__unclassified	72500
s__unclassified	72510
s__unclassified	72543
s__unclassified	72567
s__unclassified	72581
s__unclassified	72582
s__unclassified	72611
s__unclassified	72616
s__unclassified	72619
s__unclassified	72649
s__unclassified	72664
s__unclassified	72673
s__unclassified	72677
s__unclassified	72685
s__unclassified	72695
s__unclassified	72702
s__unclassified	72744
s__unclassified	72765
s__unclassified	72774
s__unclassified	72795
s__unclassified	72800
s__unclassified	72853
s__unclassified	72873
s__unclassified	72909
s__unclassified	72968
s__unclassified	73047
s__unclassified	73061
s__unclassified	73065
s__unclassified	73072
s__unclassified	73128
s__Anaerococcus hydrogenalis	70861

EU334518.1 gg_id:268609 Hexahydro-135-trinitro-135-triazine (RDX) mediated microbial shift under sulfate-rec
AB487835.1 gg_id:573564 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
EU459314.1 gg_id:302597 hedgehog feces clone HH_aai36b12
EU791182.1 gg_id:583383 Enteric defensins are essential regulators intestinal microbial ecology MMP7++ mou:
EU467034.1 gg_id:297538 hedgehog feces clone HH_b12
EU459211.1 gg_id:290495 hedgehog feces clone HH_aai34a09
DQ113757.1 gg_id:133349 dog duodenum clone D1-79
EU471060.1 gg_id:295623 red panda feces clone RP_3aaa03e04
GU370097.1 gg_id:530236 Clostridium sp. str. P530(2)
FJ671035.1 gg_id:530294 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AB487325.1 gg_id:570714 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EU471294.1 gg_id:298559 red panda feces clone RP_3aaa02e09
EU471296.1 gg_id:295884 red panda feces clone RP_3aaa01b07
GU370092.1 gg_id:531462 Clostridium sp. str. P410(2)
AM179918.1 gg_id:147513 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G15-
DQ378249.1 gg_id:155706 oil-polluted soil clone M29_Pitesti
AJ229181.1 gg_id:49771 unidentified eubacterium clone BSV07
EF614827.1 gg_id:228319 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
AY188850.1 gg_id:100886 Clostridium sp. str. C4/1
X80834.1 gg_id:16195 long segmented filamentous organism
EU471048.1 gg_id:298484 red panda feces clone RP_3aaa04c09
FJ672742.1 gg_id:515811 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU458241.1 gg_id:302475 North American black bear feces clone BB2_e07_1
EU470690.1 gg_id:300663 red panda feces clone RP_1aaa01a07
EU471212.1 gg_id:301163 red panda feces clone RP_3aaa03e11
DQ339713.1 gg_id:207741 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni
AB486591.1 gg_id:535624 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0
EU459196.1 gg_id:299207 hedgehog feces clone HH_aai33f09
EF512134.1 gg_id:275472 Clostridium bovipellis str. B30
AB487343.1 gg_id:586332 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
FJ675375.1 gg_id:524340 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU459197.1 gg_id:303389 hedgehog feces clone HH_aai33f10
EU471292.1 gg_id:293132 red panda feces clone RP_3aaa04d12
EU470539.1 gg_id:296716 red panda feces clone RP_1aaa02d04
AB487691.1 gg_id:541232 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
FJ670764.1 gg_id:514451 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF614891.1 gg_id:230025 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EF614886.1 gg_id:232991 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU471288.1 gg_id:288145 red panda feces clone RP_3aaa04h03
EU458168.1 gg_id:294391 North American black bear feces clone BB2_h02
GQ014753.1 gg_id:494913 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763g

EU334518.1	268609	5664.4	6136.5	4303.5	3633.8	4412.2	6617.3
AB487835.1	573564	7174.9	5997.9	8358.0	7962.0	9045.0	8104.0
EU459314.1	302597	2534.6	4224.5	4162.7	1560.9	4699.8	3322.1
EU791182.1	583383	2125.0	1378.1	2298.7	1019.9	1612.0	1115.9
EU467034.1	297538	4963.3	5707.9	3442.0	1404.7	1687.0	2851.6
EU459211.1	290495	5633.3	5317.0	6114.2	5689.1	4374.2	4261.2
DQ113757.1	133349	2376.2	1776.4	1766.2	911.0	2231.9	1021.7
EU471060.1	295623	10081.1	8377.3	6078.2	6372.4	5560.2	6384.8
GU370097.1	530236	1207.4	1439.8	3081.4	2019.5	2633.2	2923.8
FJ671035.1	530294	13718.8	13040.6	12920.5	13530.6	8692.3	10318.7
AB487325.1	570714	601.2	1018.8	247.0	222.3	146.6	275.9
EU471294.1	298559	4552.5	3842.8	6455.5	3290.7	1426.1	2603.7
EU471296.1	295884	4134.2	4110.4	4366.6	3180.1	4753.0	6438.8
GU370092.1	531462	1740.2	1468.9	3866.6	1094.9	1594.1	1348.5
AM179918.1	147513	1775.5	1499.9	2240.6	841.2	949.8	1584.5
DQ378249.1	155706	6952.0	6746.6	6634.7	3339.5	2700.1	3385.2
AJ229181.1	49771	1631.9	5045.7	2640.8	1261.9	284.5	478.1
EF614827.1	228319	2330.5	2569.7	4811.2	3486.8	1654.1	3496.6
AY188850.1	100886	2005.6	673.0	924.2	294.0	80.7	134.7
X80834.1	16195	3852.2	3515.8	4268.1	2784.0	3107.7	2967.5
EU471048.1	298484	3860.1	2895.2	4196.3	3555.7	4827.8	2818.0
FJ672742.1	515811	1225.6	1341.9	1796.8	626.5	999.0	1683.3
EU458241.1	302475	3432.8	3958.1	5394.4	2113.2	1139.0	1641.7
EU470690.1	300663	10443.0	9883.7	7990.3	10278.4	4960.4	5648.9
EU471212.1	301163	3492.8	1999.7	1722.9	4131.5	2391.4	2249.0
DQ339713.1	207741	1111.6	1186.6	4373.5	1067.3	1215.1	1276.1
AB486591.1	535624	1793.0	900.1	5149.5	1681.1	286.1	622.2
EU459196.1	299207	169.7	270.9	195.9	265.6	238.3	372.3
EF512134.1	275472	1687.7	932.0	3149.4	442.1	110.9	466.5
AB487343.1	586332	6584.5	5621.7	9963.3	6383.8	5525.3	5563.4
FJ675375.1	524340	4794.0	3635.6	957.4	2798.8	530.4	849.6
EU459197.1	303389	3752.8	3246.2	5018.1	2854.4	1482.5	2261.0
EU471292.1	293132	302.5	341.8	364.9	289.3	124.9	209.4
EU470539.1	296716	1868.8	1204.1	2417.3	2838.1	242.6	728.7
AB487691.1	541232	9068.7	6910.9	5367.0	7166.8	5760.4	6194.5
FJ670764.1	514451	1959.7	1706.8	1580.2	280.9	345.0	412.9
EF614891.1	230025	2036.8	1770.8	3251.2	5196.8	3331.7	3663.8
EF614886.1	232991	797.5	1189.6	2105.1	1510.1	780.4	992.7
EU471288.1	288145	3957.5	3873.1	2480.7	2312.0	5060.2	3668.7
EU458168.1	294391	2142.6	1917.5	2463.9	2460.4	2857.5	2850.3
GQ014753.1	494913	695.8	1559.9	646.9	1241.1	397.7	560.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus

s__Anaerococcus hydrogenalis	71089
s__Anaerococcus prevotii	70641
s__Anaerococcus prevotii	70659
s__Anaerococcus prevotii	70691
s__Anaerococcus prevotii	70818
s__Anaerococcus prevotii	70955
s__Anaerococcus prevotii	71146
s__Anaerococcus prevotii	71224
s__unclassified	70667
s__unclassified	70668
s__unclassified	70669
s__unclassified	70671
s__unclassified	70683
s__unclassified	70685
s__unclassified	70689
s__unclassified	70698
s__unclassified	70706
s__unclassified	70707
s__unclassified	70711
s__unclassified	70712
s__unclassified	70734
s__unclassified	70736
s__unclassified	70740
s__unclassified	70743
s__unclassified	70753
s__unclassified	70754
s__unclassified	70755
s__unclassified	70757
s__unclassified	70758
s__unclassified	70759
s__unclassified	70762
s__unclassified	70763
s__unclassified	70771
s__unclassified	70773
s__unclassified	70776
s__unclassified	70777
s__unclassified	70779
s__unclassified	70782
s__unclassified	70820
s__unclassified	70847
s__unclassified	70849

GQ031842.1 gg_id:452633 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ030233.1 gg_id:465730 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw875c
GQ014582.1 gg_id:495084 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw761e
GQ082223.1 gg_id:408144 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ069902.1 gg_id:436277 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw243b0
GQ001575.1 gg_id:508087 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu174f11
GQ006366.1 gg_id:503298 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu8
GQ031456.1 gg_id:414909 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw874b
GQ055843.1 gg_id:457745 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1120h
GQ016171.1 gg_id:493496 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
AF542234.1 gg_id:85988 Anaerococcus tetradius str. CCUG 46590
GQ052076.1 gg_id:384301 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu5
GQ069413.1 gg_id:387057 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ081501.1 gg_id:437020 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ047199.1 gg_id:468042 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009h
GQ029523.1 gg_id:455796 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862e08
GQ081506.1 gg_id:390253 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ081494.1 gg_id:428347 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ041827.1 gg_id:380722 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw933
GQ085212.1 gg_id:413797 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw272c
GQ094136.1 gg_id:438590 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw37C
AM183108.1 gg_id:239292 and its spatial composts compost clone SMC65
GQ016235.1 gg_id:493432 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ004504.1 gg_id:505157 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59c09c1
GQ016624.1 gg_id:493043 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ031395.1 gg_id:453253 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873b
EF419346.1 gg_id:212397 Substantial alterations cutaneous biota psoriatic lesions human skin clone 1P1-44
GQ092919.1 gg_id:400531 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ068683.1 gg_id:419268 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ094219.1 gg_id:411988 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw371
AM176528.1 gg_id:180355 Anaerococcus sp. gpac104
GQ075874.1 gg_id:427322 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ069446.1 gg_id:464288 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ091453.1 gg_id:401886 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw346c0
GQ082563.1 gg_id:390980 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ112151.1 gg_id:453052 Topographical and Temporal Human Skin Microbiome skin nare clone nbw585b08c1
GQ077289.1 gg_id:406725 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ070900.1 gg_id:452977 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ040347.1 gg_id:436008 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw953c
GQ017362.1 gg_id:492305 Topographical and Temporal Human Skin Microbiome skin nare clone nbu119h07c1
GQ075849.1 gg_id:415537 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1

GQ031842.1	452633	162.1	252.2	373.4	176.9	222.1	380.5
GQ030233.1	465730	1010.8	1480.6	1597.8	2051.9	2134.0	2597.6
GQ014582.1	495084	3923.8	3689.4	2420.7	2643.0	1946.8	2484.8
GQ082223.1	408144	3384.2	4189.9	2647.9	2825.4	3599.1	5218.4
GQ069902.1	436277	13165.9	12023.1	7359.5	7451.0	10197.1	8794.3
GQ001575.1	508087	8579.0	6938.3	3356.3	3378.5	4953.8	4111.5
GQ006366.1	503298	2974.8	3891.2	2119.5	2707.9	1725.5	1598.6
GQ031456.1	414909	8223.9	10517.6	7222.6	8769.4	11400.9	11346.7
GQ055843.1	457745	4371.2	4196.2	3765.0	6054.8	8277.2	7538.6
GQ016171.1	493496	1221.0	1675.4	4370.1	1180.6	4575.6	4552.7
AF542234.1	85988	10168.9	9351.8	7666.2	10336.4	13488.7	9832.6
GQ052076.1	384301	2753.8	4140.8	4316.7	4584.2	7873.2	6588.3
GQ069413.1	387057	13257.3	11692.5	9603.9	9141.0	9657.8	7088.3
GQ081501.1	437020	4267.5	5436.8	2267.6	4411.2	5017.4	4248.8
GQ047199.1	468042	1725.4	1525.0	978.7	476.5	239.6	422.9
GQ029523.1	455796	6315.5	4718.6	3302.6	2619.9	6587.7	4663.9
GQ081506.1	390253	10025.8	7163.2	7514.0	10244.4	5252.0	7423.2
GQ081494.1	428347	12884.6	12508.4	4733.6	9001.9	10838.5	9338.1
GQ041827.1	380722	4028.0	4960.7	1991.1	1250.6	4958.0	3694.0
GQ085212.1	413797	10355.0	8723.8	6863.5	11520.7	10672.6	9874.7
GQ094136.1	438590	12011.8	10016.8	5767.6	12811.1	8956.3	11564.7
AM183108.1	239292	2838.8	3711.3	4049.0	2065.9	6080.3	4227.4
GQ016235.1	493432	3609.2	2682.6	1538.4	3904.4	7237.6	4687.5
GQ004504.1	505157	1849.5	3062.6	2349.1	1390.8	8603.9	3847.4
GQ016624.1	493043	2773.7	1665.2	2112.4	2549.9	897.0	1062.6
GQ031395.1	453253	1703.2	2277.9	1347.3	1132.8	3568.7	2732.7
EF419346.1	212397	1407.0	1676.4	2035.3	1203.9	2335.0	1603.2
GQ092919.1	400531	4427.9	2712.7	1435.6	4068.8	2569.6	2435.4
GQ068683.1	419268	7676.9	5745.7	4629.9	9082.5	2279.8	3437.1
GQ094219.1	411988	1632.4	1256.0	1809.6	1457.1	1905.3	1800.7
AM176528.1	180355	3795.9	3816.9	1132.6	1332.1	1272.6	1087.8
GQ075874.1	427322	15752.9	15345.8	8185.9	14593.0	13426.2	10620.3
GQ069446.1	464288	3000.8	4852.8	2141.6	2566.4	11688.4	5218.9
GQ091453.1	401886	19085.9	17712.2	10396.3	12822.2	13921.9	14690.2
GQ082563.1	390980	4943.0	2990.8	3275.4	7669.2	1832.2	1922.5
GQ112151.1	453052	10692.3	9589.2	5620.1	11544.0	10670.3	9279.2
GQ077289.1	406725	5622.4	4548.8	2799.0	6996.5	4013.5	3489.5
GQ070900.1	452977	2584.9	3120.9	1276.3	1711.0	2114.7	1922.3
GQ040347.1	436008	5815.4	6793.3	4585.5	5340.5	10125.6	5040.3
GQ017362.1	492305	3834.6	4013.2	975.0	2062.5	4436.6	1637.4
GQ075849.1	415537	19848.7	19887.1	8476.2	16375.8	20438.5	16526.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus

s__unclassified	70850
s__unclassified	70852
s__unclassified	70870
s__unclassified	70876
s__unclassified	70880
s__unclassified	70883
s__unclassified	70884
s__unclassified	70888
s__unclassified	70893
s__unclassified	70905
s__unclassified	70908
s__unclassified	70913
s__unclassified	70914
s__unclassified	70926
s__unclassified	70940
s__unclassified	70959
s__unclassified	70963
s__unclassified	70966
s__unclassified	70982
s__unclassified	70992
s__unclassified	71001
s__unclassified	71003
s__unclassified	71009
s__unclassified	71010
s__unclassified	71015
s__unclassified	71020
s__unclassified	71026
s__unclassified	71045
s__unclassified	71047
s__unclassified	71067
s__unclassified	71069
s__unclassified	71071
s__unclassified	71075
s__unclassified	71081
s__unclassified	71091
s__unclassified	71096
s__unclassified	71113
s__unclassified	71118
s__unclassified	71127
s__unclassified	71132
s__unclassified	71143

GQ094304.1 gg_id:392751 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372
GQ422749.1 gg_id:574384 Anaerococcus tetradius str. F0127
GQ094326.1 gg_id:383714 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372
GQ094616.1 gg_id:415471 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372
GQ004132.1 gg_id:505530 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ016193.1 gg_id:493475 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ081492.1 gg_id:464987 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ094283.1 gg_id:392451 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372
EU931448.1 gg_id:524113 examined methods chronic venous leg ulcer clone CONR87
AM176536.1 gg_id:185333 Anaerococcus sp. gpac155
GQ040106.1 gg_id:377658 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw95
GQ071104.1 gg_id:453556 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ087168.1 gg_id:415070 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ094232.1 gg_id:394565 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw371
GQ011147.1 gg_id:498519 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ076559.1 gg_id:464143 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ070343.1 gg_id:371710 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ069466.1 gg_id:484565 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ046817.1 gg_id:395478 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ085051.1 gg_id:419213 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw270e
GQ031380.1 gg_id:451739 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873a
GQ094289.1 gg_id:424831 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372
GQ081218.1 gg_id:380367 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ004351.1 gg_id:505311 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ020017.1 gg_id:489650 Topographical and Temporal Human Skin Microbiome skin nare clone nbu202a01c1
GQ016875.1 gg_id:492792 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826e0
FM872849.1 gg_id:363159 occupant source house floor dust clone FB03F12
GQ081577.1 gg_id:384208 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ086109.1 gg_id:441795 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ044012.1 gg_id:389592 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017g(
GQ093207.1 gg_id:379387 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42
GQ070149.1 gg_id:449513 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ081583.1 gg_id:383839 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ069472.1 gg_id:463391 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ082189.1 gg_id:457901 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ080759.1 gg_id:410475 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ004581.1 gg_id:505083 Topographical and Temporal Human Skin Microbiome skin nare clone nbu60b07c1
FJ670693.1 gg_id:514078 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ089736.1 gg_id:461914 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3
GQ042145.1 gg_id:455500 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw93e
GQ081175.1 gg_id:462037 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1

GQ094304.1	392751	14535.3	13161.7	8326.4	10711.7	10202.6	10666.9
GQ422749.1	574384	3332.5	3474.0	4171.3	2965.2	3589.4	2845.5
GQ094326.1	383714	7883.0	5736.4	4091.9	8015.0	5355.1	5742.6
GQ094616.1	415471	8175.5	7126.3	4158.1	7461.9	6037.5	5626.2
GQ004132.1	505530	1285.6	1963.2	3131.7	2421.1	1828.9	3795.9
GQ016193.1	493475	3222.3	4495.5	2500.4	2652.3	4810.9	4061.3
GQ081492.1	464987	802.1	1398.0	2946.9	1287.0	4055.3	2643.7
GQ094283.1	392451	1519.2	2804.0	2409.6	2290.7	1943.2	1456.4
EU931448.1	524113	299.4	276.8	331.4	99.6	130.3	119.2
AM176536.1	185333	4132.1	3626.8	750.5	3528.8	6857.1	3742.7
GQ040106.1	377658	3217.1	3754.5	3899.0	4165.3	6269.4	6720.7
GQ071104.1	453556	3159.4	3970.6	4051.3	2155.1	6517.0	5937.8
GQ087168.1	415070	4736.9	3657.2	4229.1	4475.0	3390.9	3525.5
GQ094232.1	394565	6253.8	4020.0	5259.7	8668.4	3094.1	3351.7
GQ011147.1	498519	5996.9	6687.6	1133.7	3232.7	1927.9	1361.2
GQ076559.1	464143	9144.6	7946.8	9547.5	11270.7	11411.4	12306.9
GQ070343.1	371710	8121.4	6379.4	3478.8	7061.8	6106.0	6541.1
GQ069466.1	484565	6896.6	8535.6	3725.1	4386.5	13083.9	7850.5
GQ046817.1	395478	8908.7	7942.3	5592.3	8415.2	11064.2	7900.6
GQ085051.1	419213	5445.7	3745.6	4777.4	6699.6	7459.3	6448.1
GQ031380.1	451739	9122.4	6733.3	7475.6	7842.9	7196.2	6145.8
GQ094289.1	424831	4520.5	4169.4	836.3	2284.2	643.4	547.4
GQ081218.1	380367	7033.1	6858.3	6576.6	7349.5	9203.0	7897.5
GQ004351.1	505311	8519.6	8495.8	10958.8	7615.9	10064.5	8868.4
GQ020017.1	489650	7023.9	7840.0	8791.0	7229.2	11016.1	9024.3
GQ016875.1	492792	10073.5	11636.0	7680.5	9221.6	12586.6	11211.0
FM872849.1	363159	4880.2	5444.6	4382.6	5785.5	9706.2	6087.6
GQ081577.1	384208	9270.4	6986.2	4086.3	11576.0	9206.3	11518.8
GQ086109.1	441795	8796.3	6960.3	5244.9	5987.7	3242.9	4401.8
GQ044012.1	389592	11088.2	11208.1	8193.3	10749.9	14313.5	12100.0
GQ093207.1	379387	5145.0	3839.1	5159.5	6212.0	3814.1	3780.5
GQ070149.1	449513	8472.3	5793.1	4127.1	8110.7	5859.9	7165.1
GQ081583.1	383839	8348.7	9343.3	9435.6	9236.8	14556.4	12895.2
GQ069472.1	463391	5056.8	5134.6	1634.7	3215.1	6229.9	3516.0
GQ082189.1	457901	1795.8	3244.9	5207.9	1618.8	3029.9	4264.4
GQ080759.1	410475	2641.5	2132.5	2742.8	2242.0	2872.7	2266.8
GQ004581.1	505083	7465.2	6622.2	2193.2	7392.9	10093.0	8156.5
FJ670693.1	514078	4380.0	3103.9	3271.0	4285.0	3014.7	4709.3
GQ089736.1	461914	6732.8	7560.0	6062.3	6328.9	4918.2	7824.7
GQ042145.1	455500	7638.5	7607.6	6482.7	8396.9	9318.2	10447.9
GQ081175.1	462037	5662.4	5308.0	5381.5	6419.9	8352.2	6770.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Anaerococcus
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Finegoldia
g__Finegoldia
g__Finegoldia
g__Finegoldia
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus

s__unclassified	71153
s__unclassified	71156
s__unclassified	71163
s__unclassified	71174
s__unclassified	71183
s__unclassified	71189
s__unclassified	71191
s__unclassified	71202
s__unclassified	71213
s__unclassified	71226
s__unclassified	71228
s__unclassified	71231
s__unclassified	71233
s__unclassified	71235
s__unclassified	71236
s__unclassified	71240
s__unclassified	71241
s__unclassified	71242
s__unclassified	71247
s__unclassified	71254
s__unclassified	71281
s__unclassified	71286
s__unclassified	71290
s__Clostridium ultunense	69279
s__unclassified	69802
s__unclassified	69809
s__unclassified	69939
s__unclassified	69940
s__Finegoldia magna	70051
s__unclassified	69992
s__unclassified	70169
s__unclassified	70631
s__Helcococcus kunzii	70005
s__Helcococcus kunzii	70123
s__Helcococcus ovis	70476
s__unclassified	69963
s__unclassified	69979
s__unclassified	70040
s__unclassified	70075
s__unclassified	70128
s__unclassified	70173

GQ040514.1 gg_id:391948 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw955e
GQ060761.1 gg_id:378168 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw05b
GQ016761.1 gg_id:492904 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825c0
GQ077116.1 gg_id:375675 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1207c
FM872962.1 gg_id:367842 occupant source house floor dust clone FB02C01
GQ035694.1 gg_id:395882 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ113910.1 gg_id:375438 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ035734.1 gg_id:402899 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ085245.1 gg_id:420172 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw272h
GQ080712.1 gg_id:399798 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ081150.1 gg_id:442352 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ076712.1 gg_id:384708 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ076602.1 gg_id:392493 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ040340.1 gg_id:373833 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw953c
GQ082554.1 gg_id:465922 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
FM872684.1 gg_id:360880 occupant source house floor dust clone FA02D08
GQ052405.1 gg_id:397258 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu535f03
GQ082580.1 gg_id:443192 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ029488.1 gg_id:394661 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862b0
GQ050431.1 gg_id:437176 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu485g
GQ089886.1 gg_id:396465 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3
GQ030344.1 gg_id:408492 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw876g
GQ080678.1 gg_id:458386 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
NR_026531.1 gg_id:550421 Clostridium ultunense str. BS; DSM 10521
EF586060.1 gg_id:241189 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_
EU369163.1 gg_id:314592 libraries oyster shell clone MBFOS-04
AF550609.1 gg_id:84656 Peptostreptococcaceae bacterium 19gly3
EF586042.1 gg_id:246996 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_
AB109772.2 gg_id:87971 Finegoldia magna str. ATCC 29328
NZ_ACHM01000169.1 gg_id:470400 Finegoldia magna str. ATCC 53516
NC_010376.1 gg_id:471282 Finegoldia magna str. ATCC 29328
GQ030213.1 gg_id:446471 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw875a
NR_029237.1 gg_id:590651 Helcococcus kunzii str. 22; NCFB 2900
EU931445.1 gg_id:523124 examined methods chronic venous leg ulcer clone CONR27
AB542081.1 gg_id:541571 Helcococcus ovis str. H10-Yamagata-990517
GQ047161.1 gg_id:393130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d
FJ671232.1 gg_id:524188 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ532264.1 gg_id:162924 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
FJ959755.1 gg_id:537785 bottlenose dolphin upper respiratory tract blowhole clone D8A8_086
FJ671016.1 gg_id:512501 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ959635.1 gg_id:570400 bottlenose dolphin upper respiratory tract blowhole clone D896_235

GQ040514.1	391948	2960.8	2675.3	944.6	3675.6	4003.2	3611.4
GQ060761.1	378168	5047.1	5445.6	6001.7	6494.4	8801.1	10250.5
GQ016761.1	492904	5393.9	4696.1	3554.1	4094.9	10076.6	8711.9
GQ077116.1	375675	12170.3	11813.1	7610.6	9877.3	12683.2	10281.4
FM872962.1	367842	1779.8	3184.6	1577.0	1859.5	6299.4	2811.2
GQ035694.1	395882	3948.7	4496.0	471.2	1673.9	983.3	1043.6
GQ113910.1	375438	9978.5	8027.7	7005.1	8817.5	4725.4	5622.4
GQ035734.1	402899	4469.6	5799.3	8448.7	4436.7	3706.2	4868.6
GQ085245.1	420172	4764.4	4280.9	1922.9	1821.3	4767.2	2443.7
GQ080712.1	399798	13783.8	12243.9	9450.3	12565.2	11882.9	11311.0
GQ081150.1	442352	3447.0	4293.3	3829.6	3019.2	6278.2	5583.8
GQ076712.1	384708	11486.4	11652.0	5904.7	6691.0	10446.5	7324.3
GQ076602.1	392493	8167.6	6616.0	3816.1	9924.9	4937.6	4441.0
GQ040340.1	373833	1222.2	2128.6	1301.5	436.1	6011.4	2998.3
GQ082554.1	465922	6851.4	8739.6	6970.6	6771.7	7306.1	6920.9
FM872684.1	360880	5767.2	4032.9	1711.1	680.3	3596.0	1096.0
GQ052405.1	397258	5826.8	7729.7	4661.2	4141.1	3035.7	4222.3
GQ082580.1	443192	7348.8	8316.1	4935.3	5538.0	3639.7	5042.5
GQ029488.1	394661	8169.7	7019.4	7008.5	5344.9	7030.6	6240.1
GQ050431.1	437176	13073.3	16450.5	5824.5	8327.7	10173.8	12602.4
GQ089886.1	396465	2925.3	3324.2	2680.3	2792.6	1745.2	1764.4
GQ030344.1	408492	3121.5	3124.9	3544.6	4110.2	5158.3	6030.8
GQ080678.1	458386	13095.7	11897.4	9236.3	12674.8	12781.2	10973.1
NR_026531.1	550421	2968.1	1716.1	2609.7	2679.4	747.0	610.7
EF586060.1	241189	7558.5	6776.4	8938.4	6797.5	11786.1	8226.1
EU369163.1	314592	7643.8	5518.6	7294.6	8079.1	6581.2	7408.3
AF550609.1	84656	4607.5	3484.8	2505.6	3403.5	2265.2	1823.9
EF586042.1	246996	9547.8	7351.0	4549.8	10743.6	9470.1	8063.5
AB109772.2	87971	581.6	489.8	602.1	237.3	216.5	240.2
NZ_ACHM01000169.1	470400	2007.3	1491.3	1567.2	1133.1	824.1	999.3
NC_010376.1	471282	966.1	667.0	442.2	129.3	145.2	283.5
GQ030213.1	446471	7729.9	7651.5	9199.8	7492.6	7483.4	7219.3
NR_029237.1	590651	4875.5	4935.7	7897.1	5622.1	10444.3	8185.6
EU931445.1	523124	1910.0	3392.9	1865.6	2978.6	2903.8	2094.1
AB542081.1	541571	589.3	718.8	884.2	578.1	246.4	391.0
GQ047161.1	393130	1337.4	1399.3	2337.4	1787.2	279.9	408.8
FJ671232.1	524188	670.0	686.4	1627.7	372.9	6190.9	2911.4
DQ532264.1	162924	513.7	600.1	366.4	456.4	173.3	260.4
FJ959755.1	537785	3554.5	4329.5	1853.6	3045.8	6717.7	6248.0
FJ671016.1	512501	4603.8	4433.6	6793.8	5277.0	6869.5	5629.7
FJ959635.1	570400	1238.0	3493.1	3219.1	1753.2	1055.2	1869.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Helcococcus
g__Parvimonas
g__Parvimonas
g__Parvimonas
g__Parvimonas
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus

s__unclassified	70177
s__unclassified	70259
s__unclassified	70340
s__unclassified	70360
s__unclassified	70479
s__unclassified	70535
s__unclassified	70566
s__unclassified	70587
s__unclassified	70594
s__unclassified	70600
s__unclassified	70602
s__unclassified	70610
s__unclassified	70627
s__Parvimonas micra	69978
s__Parvimonas micra	70086
s__Parvimonas micra	70089
s__Parvimonas micra	70117
s__Peptoniphilus asaccharolyticus	69971
s__Peptoniphilus asaccharolyticus	69973
s__Peptoniphilus asaccharolyticus	69980
s__Peptoniphilus asaccharolyticus	69981
s__Peptoniphilus asaccharolyticus	69999
s__Peptoniphilus asaccharolyticus	70029
s__Peptoniphilus asaccharolyticus	70048
s__Peptoniphilus asaccharolyticus	70069
s__Peptoniphilus asaccharolyticus	70076
s__Peptoniphilus asaccharolyticus	70097
s__Peptoniphilus asaccharolyticus	70136
s__Peptoniphilus asaccharolyticus	70228
s__Peptoniphilus asaccharolyticus	70369
s__Peptoniphilus asaccharolyticus	70424
s__Peptoniphilus asaccharolyticus	70464
s__Peptoniphilus asaccharolyticus	70488
s__Peptoniphilus asaccharolyticus	70502
s__Peptoniphilus asaccharolyticus	70510
s__Peptoniphilus asaccharolyticus	70518
s__Peptoniphilus asaccharolyticus	70519
s__Peptoniphilus asaccharolyticus	70539
s__Peptoniphilus asaccharolyticus	70574
s__Peptoniphilus asaccharolyticus	70620
s__unclassified	69951

FJ671462.1 gg_id:526482 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ671406.1 gg_id:522709 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ672944.1 gg_id:527947 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ672144.1 gg_id:515690 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ959504.1 gg_id:586313 bottlenose dolphin upper respiratory tract blowhole clone D896_088
FJ670651.1 gg_id:523741 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ960157.1 gg_id:547405 bottlenose dolphin upper respiratory tract blowhole clone D9A4_043
FJ959814.1 gg_id:570444 bottlenose dolphin upper respiratory tract blowhole clone D8A8_165
FJ960159.1 gg_id:590557 bottlenose dolphin upper respiratory tract blowhole clone D9A4_045
FJ675329.1 gg_id:512373 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ674777.1 gg_id:529441 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ959441.1 gg_id:570348 bottlenose dolphin upper respiratory tract blowhole clone D896_015
FJ960145.1 gg_id:556060 bottlenose dolphin upper respiratory tract blowhole clone D9A4_031
AM176521.1 gg_id:183658 Peptostreptococcus micros gpac022
AM176532.1 gg_id:181489 Peptostreptococcus micros gpac134
AY349390.1 gg_id:92862 human oral cavity clone FJ023
AF542231.1 gg_id:83408 Peptostreptococcus micros str. ATCC 33270
GQ016336.1 gg_id:493331 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
FJ577254.2 gg_id:567933 Peptoniphilus sp. 'Oral Taxon 386' str. F0131
GQ069670.1 gg_id:437159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FJ557799.1 gg_id:524282 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ004943.1 gg_id:504719 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65a1
GQ101711.1 gg_id:392255 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw498d03
AY153431.1 gg_id:86504 Peptoniphilus indolicus str. CCUG 46591
GQ014236.1 gg_id:495429 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760e
GQ087341.1 gg_id:448805 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
AB538435.1 gg_id:583324 Peptoniphilus sp. str. JCM 8143
GQ031426.1 gg_id:387138 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873g
GQ043038.1 gg_id:405497 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012d
GQ046233.1 gg_id:430948 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ014651.1 gg_id:495015 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw762c
GQ004003.1 gg_id:505659 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67d0
GQ033299.1 gg_id:381665 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ070679.1 gg_id:456602 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ076958.1 gg_id:415523 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155
FJ557959.1 gg_id:521795 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ003957.1 gg_id:505704 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu66g0
EU526289.1 gg_id:269603 Peptoniphilus sp. str. WAL 1768N
GQ016450.1 gg_id:493216 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ031247.1 gg_id:464237 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
AF481225.1 gg_id:68341 Peptostreptococcus sp. str. E3_32

FJ671462.1	526482	2540.1	2785.8	3702.6	2825.9	8015.5	4390.8
FJ671406.1	522709	7503.3	6657.8	6811.3	4980.2	14027.7	8598.4
FJ672944.1	527947	14133.1	13526.7	11742.6	12666.5	13638.3	12332.5
FJ672144.1	515690	6249.0	7250.7	4380.3	4487.7	10607.6	7923.0
FJ959504.1	586313	5051.1	6139.1	4588.8	4909.9	4198.0	3268.8
FJ670651.1	523741	3650.3	2678.2	1574.0	3970.1	1642.2	1316.3
FJ960157.1	547405	6562.8	8044.9	6892.0	5480.8	12583.7	9136.4
FJ959814.1	570444	1966.7	2160.9	3166.1	2529.4	3237.9	2741.5
FJ960159.1	590557	4070.3	4291.3	1299.1	5493.4	4907.3	4696.7
FJ675329.1	512373	6910.8	7948.9	5245.8	7686.5	16950.7	11743.6
FJ674777.1	529441	10174.4	8884.9	2716.1	10181.4	14968.6	12960.6
FJ959441.1	570348	2337.1	3691.3	2842.9	2860.7	8777.9	6946.2
FJ960145.1	556060	3027.3	5084.8	6368.8	4013.2	9180.4	7084.1
AM176521.1	183658	3776.2	2968.5	2800.3	3496.3	3609.8	3838.7
AM176532.1	181489	4605.3	4977.7	3934.3	3447.2	5834.6	5857.6
AY349390.1	92862	2998.1	2206.0	2023.1	3200.5	3664.8	1101.9
AF542231.1	83408	4676.7	5033.2	4147.2	3748.0	6119.0	6227.8
GQ016336.1	493331	9318.9	7650.5	2506.7	6795.7	10364.3	7418.9
FJ577254.2	567933	35.2	44.0	65.1	74.3	59.6	44.7
GQ069670.1	437159	3302.2	3337.5	5922.4	3478.2	10047.8	6969.0
FJ557799.1	524282	3944.7	3761.7	2888.6	5019.6	5129.4	4304.3
GQ004943.1	504719	5671.2	6577.1	4728.6	6850.5	7638.0	5952.1
GQ101711.1	392255	1185.9	1305.7	1434.9	1533.2	1503.2	3386.5
AY153431.1	86504	206.2	301.4	735.8	249.1	503.4	746.4
GQ014236.1	495429	11760.0	12042.9	8178.6	8548.3	12112.2	8746.9
GQ087341.1	448805	1169.8	1374.7	1211.0	1802.6	1880.9	1118.6
AB538435.1	583324	247.4	249.6	106.4	899.0	84.0	68.0
GQ031426.1	387138	2833.7	2123.8	5477.7	3794.5	5015.7	1768.0
GQ043038.1	405497	2965.9	3259.9	1410.7	1432.8	700.0	1455.2
GQ046233.1	430948	996.8	1326.3	2736.3	797.6	2568.7	1876.5
GQ014651.1	495015	10528.7	8427.5	8676.3	6809.8	7100.9	6758.9
GQ004003.1	505659	5166.5	5220.0	2403.8	3543.5	8135.6	4750.8
GQ033299.1	381665	5142.8	3948.6	1665.2	5254.6	5285.2	4422.5
GQ070679.1	456602	2160.6	1578.6	4869.9	2614.1	3333.1	3373.5
GQ076958.1	415523	1316.6	1418.7	3373.0	607.1	2703.8	1754.5
FJ557959.1	521795	355.0	411.4	1371.4	449.2	146.2	292.7
GQ003957.1	505704	1472.3	1519.7	2048.2	1729.9	6122.0	5612.8
EU526289.1	269603	6387.0	5431.9	4657.6	3873.1	6100.5	4186.3
GQ016450.1	493216	4386.8	4272.0	6332.7	4248.3	9474.6	7566.7
GQ031247.1	464237	843.2	575.1	905.9	542.8	444.0	799.9
AF481225.1	68341	659.2	1225.6	3099.6	794.6	1842.1	2340.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Peptoniphilus
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Sedimentibacter
g__Soehngenia
g__Sporanaerobacter
g__Sporanaerobacter
g__Sporanaerobacter
g__Tepidimicrobium
g__Tepidimicrobium
g__Tepidimicrobium
g__Tepidimicrobium
g__Tepidimicrobium
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella

s__unclassified	70129
s__unclassified	70180
s__unclassified	70190
s__unclassified	70267
s__unclassified	70289
s__unclassified	70379
s__unclassified	69235
s__unclassified	69259
s__unclassified	69498
s__unclassified	69525
s__unclassified	69618
s__unclassified	69642
s__unclassified	69711
s__unclassified	69715
s__unclassified	69739
s__unclassified	69747
s__unclassified	69753
s__unclassified	69789
s__unclassified	69832
s__unclassified	69834
s__unclassified	69862
s__unclassified	69891
s__unclassified	69347
s__Sporanaerobacter acetigenes	69804
s__unclassified	69712
s__unclassified	69831
s__unclassified	69258
s__unclassified	69438
s__unclassified	69446
s__unclassified	69524
s__unclassified	69760
s__Tissierella praeacuta	69650
s__Tissierella praeacuta	69689
s__unclassified	69306
s__unclassified	69320
s__unclassified	69374
s__unclassified	69383
s__unclassified	69535
s__unclassified	69549
s__unclassified	69565
s__unclassified	69605

GQ082187.1 gg_id:426785 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
Y07840.1 gg_id:14275 Peptoniphilus ivorii str. DSM 10022; SBH093
EU289040.1 gg_id:249152 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
X90471.1 gg_id:14281 Peptostreptococcus sp str. 9succ1
FJ671194.1 gg_id:521628 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AY167967.1 gg_id:75475 Isolation and identification hyper-ammonia producing swine storage pits manure
FJ675039.1 gg_id:528981 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
CU919308.1 gg_id:540944 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY754832.1 gg_id:108707 Hudson river sediment clone Z35
FJ674316.1 gg_id:518267 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ825558.1 gg_id:535477 Microbial during start-up mesophilic biogas plant clone 45_BS4_8
FJ675649.1 gg_id:529080 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ168650.1 gg_id:157172 sediment-free PCB-dechlorinating enrichment culture clone JN18_A14_H
FJ671648.1 gg_id:528290 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
NR_025498.1 gg_id:569679 Sedimentibacter saalensis str. ZF2; DSM 13558
FJ674650.1 gg_id:513014 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF059533.1 gg_id:221904 Sedimentibacter sp. JN18_V27_I
CU927625.1 gg_id:567949 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ825486.1 gg_id:568699 Microbial during start-up mesophilic biogas plant clone 178_BE2_28
AF427155.1 gg_id:34493 Clostridium sp. LTR1
AY913838.1 gg_id:136382 fixed-film bioreactor clone MBR283-55
AB294744.1 gg_id:207626 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobacte
AY353956.1 gg_id:103341 Soehngenia saccharolytica str. BOR-Y
NR_025151.1 gg_id:553089 Sporanaerobacter acetigenes str. Lup33; DSM 13106
GQ461820.1 gg_id:585584 Tissierella sp. str. LBN 299
AB175360.1 gg_id:102260 mesophilic anaerobic BSA digester clone BSA1B-06
AB332034.1 gg_id:312984 Tepidimicrobium sp. str. HUT8119
AY466712.1 gg_id:101098 Clostridiales NS4-1
AB436741.1 gg_id:284303 Clostridium sp. str. AAN13
AF280824.1 gg_id:72660 bioreactor clone tbr1-9
GQ461826.1 gg_id:587283 Tepidimicrobium ferriphilum str. DSM 16624
X80833.1 gg_id:14261 Tissierella praeacuta str. ATCC 25539
GQ461802.1 gg_id:544735 Tissierella praeacuta str. AIP 224.02
FN436079.1 gg_id:567822 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
FJ675493.1 gg_id:517458 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ378266.2 gg_id:151594 oil-polluted soil clone M50_Pitesti
FJ825564.1 gg_id:561089 Microbial during start-up mesophilic biogas plant clone 62_BS5_26
AM500851.1 gg_id:560842 proof spatial heterogeneity hot composting clone F132
EU887816.1 gg_id:321681 Tissierella praeacuta str. SN5
FJ672701.1 gg_id:510178 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ461818.1 gg_id:579451 Tissierella sp. str. LBN 291

GQ082187.1	426785	1297.1	1619.4	1251.5	748.1	118.4	879.1
Y07840.1	14275	4149.6	5631.7	5249.2	5782.2	7488.9	6601.5
EU289040.1	249152	4545.5	4590.1	4152.4	4024.4	6890.9	6244.1
X90471.1	14281	360.0	511.9	194.7	2148.6	191.0	632.8
FJ671194.1	521628	2296.9	4170.4	3913.6	2664.0	2881.1	4805.4
AY167967.1	75475	34.8	37.7	29.3	44.5	75.8	35.6
FJ675039.1	528981	3725.4	3330.9	1640.8	5101.7	5577.6	5796.5
CU919308.1	540944	3035.4	4289.1	10560.8	4038.1	8103.7	6101.1
AY754832.1	108707	7974.1	7169.2	5484.7	6757.3	6855.5	6617.3
FJ674316.1	518267	2427.6	2780.2	2659.4	671.1	781.3	453.9
FJ825558.1	535477	1503.6	2818.9	1537.9	1135.5	8660.4	2568.1
FJ675649.1	529080	823.2	687.4	2828.5	586.7	1409.4	1066.7
DQ168650.1	157172	2922.1	1757.6	2731.3	1103.8	2941.3	196.4
FJ671648.1	528290	1317.2	2452.3	4529.2	1244.2	1792.8	2313.7
NR_025498.1	569679	1648.2	1920.3	574.8	1704.2	1093.9	725.6
FJ674650.1	513014	2787.5	3072.5	1434.9	1034.4	1051.1	822.2
EF059533.1	221904	3471.8	3925.2	3422.4	830.9	4140.5	765.3
CU927625.1	567949	2843.4	3493.3	4450.4	4063.0	3611.5	3803.8
FJ825486.1	568699	2467.9	1846.5	3087.1	2091.4	4493.1	3174.5
AF427155.1	34493	6148.8	6194.7	6325.7	5208.3	5046.3	5710.7
AY913838.1	136382	470.7	687.8	1480.6	801.4	140.5	485.5
AB294744.1	207626	6954.3	16284.9	2385.0	846.2	1270.6	893.0
AY353956.1	103341	522.0	710.6	624.6	382.1	295.5	714.5
NR_025151.1	553089	180.7	38.5	72.8	73.8	66.7	60.7
GQ461820.1	585584	2495.7	2412.8	4272.6	3159.3	4316.8	3451.8
AB175360.1	102260	313.5	394.5	915.4	260.3	856.7	439.5
AB332034.1	312984	106.8	335.2	80.9	57.0	82.6	80.9
AY466712.1	101098	7453.7	7139.0	3728.3	8126.0	11381.3	9980.4
AB436741.1	284303	5965.8	5196.8	9785.4	6485.1	5527.4	4226.8
AF280824.1	72660	141.3	242.5	404.9	156.4	52.0	54.4
GQ461826.1	587283	5759.2	5611.2	2359.8	2244.5	2316.0	2513.4
X80833.1	14261	1282.5	1186.8	1947.3	718.8	3256.8	2083.8
GQ461802.1	544735	1086.9	1835.8	1645.1	1255.2	5449.0	4796.4
FN436079.1	567822	5857.8	5709.8	7298.1	8128.1	10091.8	8062.4
FJ675493.1	517458	939.2	1408.4	2135.3	1349.1	870.7	1833.9
DQ378266.2	151594	6322.3	6545.2	2184.0	4753.8	7127.8	7790.7
FJ825564.1	561089	1402.6	1958.2	3038.3	2481.1	7117.1	6787.4
AM500851.1	560842	4707.2	4321.7	5036.2	4454.5	721.5	2135.3
EU887816.1	321681	5621.6	6182.9	7273.4	7119.4	7656.5	6554.4
FJ672701.1	510178	1280.8	1533.9	2102.0	760.7	192.7	1059.2
GQ461818.1	579451	178.5	237.1	1011.4	222.2	66.5	132.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis

g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__Tissierella
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	69690
s__unclassified	69722
s__unclassified	69751
s__unclassified	69821
s__unclassified	69870
s__unclassified	69236
s__unclassified	69264
s__unclassified	69275
s__unclassified	69280
s__unclassified	69286
s__unclassified	69293
s__unclassified	69316
s__unclassified	69326
s__unclassified	69332
s__unclassified	69336
s__unclassified	69386
s__unclassified	69387
s__unclassified	69396
s__unclassified	69408
s__unclassified	69409
s__unclassified	69417
s__unclassified	69430
s__unclassified	69447
s__unclassified	69458
s__unclassified	69469
s__unclassified	69471
s__unclassified	69492
s__unclassified	69500
s__unclassified	69501
s__unclassified	69506
s__unclassified	69516
s__unclassified	69527
s__unclassified	69529
s__unclassified	69540
s__unclassified	69550
s__unclassified	69553
s__unclassified	69570
s__unclassified	69572
s__unclassified	69576
s__unclassified	69596
s__unclassified	69599

FJ825528.1 gg_id:543440 Microbial during start-up mesophilic biogas plant clone 66_BS1_7
X75909.1 gg_id:14266 Clostridium sp str. BN II
AF443595.1 gg_id:88113 Clostridium sp. str. ArC6
FJ674955.1 gg_id:516090 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GU112188.1 gg_id:551545 library biogas slurry anaerobic fermentation pig manure clone 52
GU455356.1 gg_id:528917 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
GQ054096.1 gg_id:465377 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1098e
AJ002593.1 gg_id:14269 Clostridium sp.PO
GU455275.1 gg_id:530269 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
GQ028320.1 gg_id:460097 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
EF174267.1 gg_id:184280 direct activated sludge compost maturation stage clone H1-814
GQ006814.1 gg_id:502850 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88a10c
EU037326.2 gg_id:265875 structure landfill sediments receiving long-term augmentations wastes chromium co
DQ447178.1 gg_id:156727 Coexistence homoacetogens and heterotrophic sulfate-reducing synthesis gas fed la
GU455358.1 gg_id:521864 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
AB222052.1 gg_id:132531 Clostridium sp. str. EBR-02E-0599
GQ077044.1 gg_id:394722 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1206b
GQ027206.1 gg_id:434668 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EU289106.1 gg_id:242578 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
DQ887923.1 gg_id:163666 thermophilic anaerobic solid waste bioreactor clone GHB3D11
GQ461816.1 gg_id:541364 Tissierella sp. str. AIP 285.00
GU455269.1 gg_id:532271 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
DQ532342.1 gg_id:172183 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
GQ004946.1 gg_id:504716 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65b0
GQ026805.1 gg_id:447236 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ029521.1 gg_id:436394 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862e05
GU455219.1 gg_id:515391 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
DQ887969.1 gg_id:164133 thermophilic anaerobic solid waste bioreactor clone TIBG06
AY169425.1 gg_id:81585 Finegoldia magna
AM500724.1 gg_id:548585 proof spatial heterogeneity hot composting clone D18
AB294307.1 gg_id:210515 Microbial structure deep coal seem groundwater clone YWB38
EF586050.1 gg_id:240034 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_
GQ015365.1 gg_id:494301 Topographical and Temporal Human Skin Microbiome skin palm clone nbw767e08c1
GQ079937.1 gg_id:406655 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ016716.1 gg_id:492950 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824g0
EU523731.1 gg_id:261418 methanogenic microbial consortia mature oil sands tailings clone 12-2A
EU289047.1 gg_id:236547 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
FJ674639.1 gg_id:526334 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
CU919210.1 gg_id:560673 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FM873737.1 gg_id:364028 occupant source house mattress dust clone MA03H02
GQ004012.1 gg_id:505653 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67e0

FJ825528.1	543440	735.6	953.5	1570.0	806.6	276.8	604.1
X75909.1	14266	74.1	69.5	45.9	152.1	72.1	133.7
AF443595.1	88113	2104.8	568.3	7952.4	2274.4	1535.5	4113.9
FJ674955.1	516090	1327.1	1688.4	2810.4	2981.2	1154.3	1962.1
GU112188.1	551545	312.7	210.1	1238.1	287.8	60.0	136.4
GU455356.1	528917	4290.6	3270.7	1784.5	4565.4	901.4	592.0
GQ054096.1	465377	10099.4	10509.6	8159.9	6646.3	7917.1	8716.2
AJ002593.1	14269	56.6	52.3	34.6	76.3	78.1	50.2
GU455275.1	530269	12313.9	11365.2	7338.7	11811.3	7349.3	7634.8
GQ028320.1	460097	1292.6	1846.6	3734.3	1832.2	6935.3	6100.9
EF174267.1	184280	354.7	697.3	2038.0	522.8	211.2	1078.5
GQ006814.1	502850	4384.9	4395.0	5821.0	7369.2	6332.1	7234.8
EU037326.2	265875	9373.0	9660.3	3747.5	8960.4	7407.5	11476.5
DQ447178.1	156727	5566.6	4985.6	1716.2	5506.2	3808.0	6733.1
GU455358.1	521864	9520.2	13801.5	10347.4	8848.1	9418.8	9082.7
AB222052.1	132531	6480.3	5395.8	5808.9	5101.3	7326.3	5061.7
GQ077044.1	394722	350.9	256.4	683.5	188.9	349.7	923.8
GQ027206.1	434668	10999.7	9581.1	8791.4	8897.1	6594.5	5520.8
EU289106.1	242578	12644.9	12010.1	6550.3	11945.8	8574.3	7544.5
DQ887923.1	163666	898.8	1981.0	847.4	1157.8	5416.1	5467.0
GQ461816.1	541364	3484.6	4084.7	4702.6	4047.8	4071.3	4362.9
GU455269.1	532271	11325.0	11013.4	5150.0	7970.4	9965.9	8830.2
DQ532342.1	172183	9856.3	9174.6	6814.7	8441.0	12450.1	11032.4
GQ004946.1	504716	3654.7	4505.5	1381.8	5809.8	2587.3	3553.1
GQ026805.1	447236	4529.1	4065.5	4364.4	3859.3	3417.0	3368.8
GQ029521.1	436394	12371.4	10359.0	5374.7	10157.9	9908.3	9877.4
GU455219.1	515391	4595.2	5622.8	4005.2	3829.1	3195.2	3228.0
DQ887969.1	164133	36.8	39.1	53.6	55.1	67.1	40.0
AY169425.1	81585	2871.8	3193.9	1919.1	2591.7	2487.0	2345.8
AM500724.1	548585	1792.2	1992.8	1394.1	941.0	70.5	993.7
AB294307.1	210515	42.6	39.8	22.5	58.7	65.4	27.4
EF586050.1	240034	5850.6	4908.8	2929.9	4779.1	2902.0	2928.3
GQ015365.1	494301	9385.1	8320.3	3997.7	6406.4	8817.9	6830.3
GQ079937.1	406655	3088.5	3663.1	3593.8	3151.6	12548.2	8665.6
GQ016716.1	492950	9014.1	8843.5	6647.9	9094.1	8821.4	7916.3
EU523731.1	261418	1558.0	1119.4	1638.3	1389.6	345.1	1081.4
EU289047.1	236547	6888.4	6961.3	6033.8	6295.3	6730.5	6457.9
FJ674639.1	526334	3197.2	2809.3	902.7	1122.2	453.1	676.6
CU919210.1	560673	10908.0	10224.2	7886.0	10255.9	9218.5	10874.7
FM873737.1	364028	4217.6	5833.3	3383.3	6022.4	2062.9	3697.4
GQ004012.1	505653	8387.2	8041.0	7479.3	8820.9	6327.4	8375.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XI. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Acidaminobacter
g__Fusibacter
g__Fusibacter
g__Fusibacter

s__unclassified	69626
s__unclassified	69640
s__unclassified	69653
s__unclassified	69663
s__unclassified	69668
s__unclassified	69671
s__unclassified	69681
s__unclassified	69706
s__unclassified	69708
s__unclassified	69740
s__unclassified	69749
s__unclassified	69758
s__unclassified	69777
s__unclassified	69823
s__unclassified	69866
s__unclassified	69888
s__unclassified	69912
s__unclassified	69916
s__unclassified	69920
s__unclassified	69924
s__unclassified	69958
s__unclassified	69975
s__unclassified	70176
s__unclassified	70202
s__unclassified	70221
s__unclassified	70251
s__unclassified	70260
s__unclassified	70331
s__unclassified	70351
s__unclassified	70354
s__unclassified	70416
s__unclassified	70421
s__unclassified	70423
s__unclassified	70430
s__unclassified	70591
s__unclassified	70632
s__unclassified	70634
s__unclassified	70480
s__unclassified	69943
s__unclassified	70054
s__unclassified	70185

AM404396.1 gg_id:572646 Hydrocarbon-fueled sulfate reduction can sustain long-lived tubeworm aggregation
EF031088.1 gg_id:191385 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB
GQ014568.1 gg_id:495098 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw761c
AM420065.1 gg_id:253512 Noma subgingival plaque clone 301D12(oral)
GQ014275.1 gg_id:495389 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw761b
GQ087947.1 gg_id:376401 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw360g0
GQ029482.1 gg_id:374311 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862a04
EU542535.1 gg_id:276266 Effects chemical structure concentration on pathways microbial during dechlorinatio
GQ004987.1 gg_id:504675 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65f05
GQ014748.1 gg_id:494918 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763g
GQ004091.1 gg_id:505570 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu68e0
FM872671.1 gg_id:362112 occupant source house floor dust clone FA02A06
GU455253.1 gg_id:520156 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
FJ672003.1 gg_id:527552 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ032132.1 gg_id:453352 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF586044.1 gg_id:239034 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_
FM873179.1 gg_id:367696 occupant source house floor dust clone FC02H05
EF559008.1 gg_id:256589 Microbial functional groups solid waste digestor stable isotope probing thermophilic
GU455217.1 gg_id:514459 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
FJ674852.1 gg_id:522075 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU842984.1 gg_id:325610 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
GQ179692.1 gg_id:451042 Heterogeneity vaginal microbial within individuals vagina clone VE58A09
EU289054.1 gg_id:254577 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
AY207059.1 gg_id:83665 Peptostreptococcus sp. P3 str. P4P_31
GQ077578.1 gg_id:432408 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1210e(
EU289126.1 gg_id:236687 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
FJ672085.1 gg_id:524642 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GQ037136.1 gg_id:402486 Topographical and Temporal Human Skin Microbiome skin palm clone nbu389c09c1
GQ003924.1 gg_id:505737 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu66c0
GQ082499.1 gg_id:408773 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ032012.1 gg_id:379026 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ009384.1 gg_id:500281 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
EU931446.1 gg_id:523577 examined methods chronic venous leg ulcer clone CONR40
AM500842.1 gg_id:561616 proof spatial heterogeneity hot composting clone F68
GQ047234.1 gg_id:464149 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010c
GQ033406.1 gg_id:464209 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EU407217.1 gg_id:259078 household biogas digester clone GW-34
AF016691.1 gg_id:14132 Acidaminobacter hydrogenoformans str. glu 65
EU591652.1 gg_id:275236 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic
EU517558.1 gg_id:267846 methanogenic microbial consortia mature oil sands tailings clone 22-7A
AF491333.1 gg_id:85424 Fusibacter sp. str. SA1

AM404396.1	572646	616.6	613.8	669.0	805.1	687.4	969.3
EF031088.1	191385	707.9	854.4	1418.0	710.7	1852.9	1495.3
GQ014568.1	495098	2016.5	1463.5	3065.6	2140.6	524.3	565.9
AM420065.1	253512	171.5	299.8	475.2	559.9	381.6	332.3
GQ014275.1	495389	1783.8	1226.1	4037.1	1883.7	1770.9	1084.5
GQ087947.1	376401	1872.9	1735.8	2401.1	2828.2	2102.7	2306.6
GQ029482.1	374311	6044.9	4780.0	3151.3	7498.4	7409.4	6404.4
EU542535.1	276266	1596.0	1434.8	1843.9	1767.3	276.3	1132.8
GQ004987.1	504675	2663.8	2336.9	3778.5	4422.5	6600.6	6163.5
GQ014748.1	494918	3318.7	3556.4	4055.4	2611.5	3860.8	2251.7
GQ004091.1	505570	3373.7	2286.9	2481.2	4382.3	3678.1	3193.5
FM872671.1	362112	5611.7	4939.7	4791.7	5716.1	4765.7	6315.9
GU455253.1	520156	6758.5	6060.5	6495.7	6143.0	4728.9	4550.6
FJ672003.1	527552	1472.7	2090.3	1503.6	711.0	5374.2	2109.3
GQ032132.1	453352	15158.3	13272.4	12245.1	13107.0	12435.0	8077.4
EF586044.1	239034	739.7	814.9	335.7	256.7	252.6	305.0
FM873179.1	367696	10402.1	10117.2	7005.4	9798.5	12652.8	11352.7
EF559008.1	256589	1845.7	1541.8	1558.2	2196.1	529.6	1325.0
GU455217.1	514459	3722.8	3546.7	7161.9	4013.2	3445.7	4063.7
FJ674852.1	522075	9041.6	9331.3	7385.7	9474.5	14782.8	13612.4
EU842984.1	325610	9182.9	9417.3	7990.9	8554.4	11225.3	8066.8
GQ179692.1	451042	9347.7	8169.2	4481.1	8270.4	12779.3	14185.8
EU289054.1	254577	3613.9	3738.9	2592.9	6052.9	352.0	903.1
AY207059.1	83665	1246.9	705.6	1686.4	1390.1	193.1	1023.1
GQ077578.1	432408	9351.9	9492.6	12087.4	8348.8	8584.1	8783.3
EU289126.1	236687	9041.0	8860.7	6065.4	10334.3	10835.5	8271.1
FJ672085.1	524642	4036.2	4891.1	2828.8	4359.0	2090.8	2676.0
GQ037136.1	402486	3519.1	3121.5	5925.9	3552.7	2660.8	3356.7
GQ003924.1	505737	10969.0	11239.9	13994.2	9486.6	12472.0	12259.1
GQ082499.1	408773	3272.0	4132.2	5872.0	3022.6	7102.1	5352.7
GQ032012.1	379026	5044.6	5625.5	6885.4	3847.0	3619.3	3408.3
GQ009384.1	500281	889.8	1394.6	699.3	458.2	1047.3	816.6
EU931446.1	523577	326.5	158.9	1147.4	383.0	1095.4	1191.1
AM500842.1	561616	4127.1	5517.2	4005.4	6696.0	2432.6	2816.1
GQ047234.1	464149	1876.3	1716.8	2902.8	1712.9	3301.2	2656.5
GQ033406.1	464209	7508.3	7452.4	10760.0	7545.8	7814.0	7971.2
EU407217.1	259078	998.0	1688.6	2732.3	1423.2	251.3	733.3
AF016691.1	14132	364.4	618.9	794.9	451.0	1415.3	1128.8
EU591652.1	275236	146.0	116.8	423.2	136.6	127.9	307.8
EU517558.1	267846	2949.7	3053.6	5030.6	5365.5	3700.3	3926.3
AF491333.1	85424	175.3	243.0	503.2	166.4	258.6	780.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis

g__Fusibacter
g__Fusibacter
g__Fusibacter
g__Fusibacter
g__Fusibacter
g__Fusibacter
g__unclassified
g__unclassified
g__unclassified
g__Anaerovorax
g__Anaerovorax
g__Anaerovorax
g__Anaerovorax
g__Anaerovorax
g__Anaerovorax
g__Anaerovorax
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium

s__unclassified	70365
s__unclassified	70391
s__unclassified	70411
s__unclassified	70426
s__unclassified	70495
s__unclassified	70564
s__unclassified	70053
s__unclassified	70071
s__unclassified	70522
s__unclassified	70127
s__unclassified	70322
s__unclassified	70406
s__unclassified	70499
s__unclassified	70504
s__unclassified	70607
s__unclassified	70614
s__Eubacterium minutum	70520
s__unclassified	69954
s__unclassified	69972
s__unclassified	70012
s__unclassified	70066
s__unclassified	70079
s__unclassified	70082
s__unclassified	70118
s__unclassified	70126
s__unclassified	70140
s__unclassified	70178
s__unclassified	70200
s__unclassified	70229
s__unclassified	70243
s__unclassified	70273
s__unclassified	70274
s__unclassified	70292
s__unclassified	70302
s__unclassified	70465
s__unclassified	70467
s__unclassified	70471
s__unclassified	70542
s__unclassified	70545
s__unclassified	70580
s__unclassified	70586

AY570635.1 gg_id:108512 biodegraded Canadian oil reservoir clone PL-5B6
FJ167488.1 gg_id:342752 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit
GQ355042.1 gg_id:583445 structure between two geochemically distinct springs Alum Rock Park spring clone N
EU662607.1 gg_id:561558 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
AB243990.1 gg_id:245248 Methods Investigate Microbial Niigata oil well clone Niigata-22
DQ378233.1 gg_id:155716 oil-polluted soil clone M13_Pitesti
FM205000.1 gg_id:534793 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
GU208315.1 gg_id:584294 Study on Sediment Dongping Lake sediment clone Sef3-12
AF255644.1 gg_id:41951 EBPR sludge clone Ebpr14
GQ054198.1 gg_id:422335 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099g
GQ014246.1 gg_id:495420 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760f
EF562251.1 gg_id:241088 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
GQ014194.1 gg_id:495473 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760a
GQ054010.1 gg_id:426893 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1097e
EF419415.1 gg_id:213421 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6PN20
GQ009336.1 gg_id:500329 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
AJ005636.1 gg_id:14151 Eubacterium minutum str. ATCC 700079
AJ006963.1 gg_id:14160 Eubacterium sulci str. ATCC 35585
GQ502514.1 gg_id:552342 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
FJ880553.1 gg_id:426130 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EF099448.1 gg_id:178412 mouse cecum clone SWPT3_aaa03d03
DQ793597.1 gg_id:191389 human fecal clone RL246_aai74b05
EU844897.1 gg_id:344416 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
GU303039.1 gg_id:576991 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU842953.1 gg_id:332719 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ880679.1 gg_id:420891 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
FJ879943.1 gg_id:380842 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU773171.1 gg_id:324364 BigHorn sheep feces clone BH1_aao26e07
GU304138.1 gg_id:583497 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
GU304385.1 gg_id:553278 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
U13041.1 gg_id:14155 Eubacterium nodatum str. ATCC 33099
GQ458236.1 gg_id:579985 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig
EU842678.1 gg_id:340989 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
FJ687606.2 gg_id:552238 Eubacterium sp. str. WAL 14571
AF044945.1 gg_id:14152 Eubacterium sp. str. C2
EF099332.1 gg_id:181305 mouse cecum clone SWPT3_aaa01h03
EU452756.1 gg_id:318652 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83
EU469216.1 gg_id:294038 Speke's gazelle feces clone SP3_c03_2
AB034093.1 gg_id:39613 rumen clone 4C3d-12
FJ879878.1 gg_id:409369 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
GU304486.1 gg_id:592803 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium

AY570635.1	108512	4814.6	5856.5	6120.1	2541.8	3710.6	3507.8
FJ167488.1	342752	290.1	191.2	723.6	146.0	148.9	124.7
GQ355042.1	583445	6730.0	7607.3	9357.1	6348.8	5306.8	5664.8
EU662607.1	561558	1819.2	2138.8	2731.5	3154.6	2548.1	3290.1
AB243990.1	245248	325.3	251.7	2230.6	308.8	204.9	183.9
DQ378233.1	155716	128.4	144.1	503.6	119.2	219.9	439.6
FM205000.1	534793	5460.5	5244.0	8509.1	4134.4	7305.9	5918.1
GU208315.1	584294	437.3	314.0	2490.3	244.5	128.0	153.9
AF255644.1	41951	22.7	36.1	38.5	52.0	51.3	22.9
GQ054198.1	422335	716.3	1206.3	1367.3	791.7	1956.0	1763.3
GQ014246.1	495420	4671.7	4243.5	3898.9	6003.0	2981.4	2751.2
EF562251.1	241088	5040.0	6495.8	4691.7	4620.2	5010.2	4105.5
GQ014194.1	495473	2662.3	2389.3	3594.6	3214.8	1198.0	2028.2
GQ054010.1	426893	1452.9	3287.0	3466.8	1532.8	5780.6	6922.5
EF419415.1	213421	7923.9	8207.8	6734.9	7129.4	6339.3	6714.1
GQ009336.1	500329	5761.2	6008.2	5012.4	6265.5	5212.5	5271.2
AJ005636.1	14151	18.1	21.7	21.2	50.9	45.4	19.4
AJ006963.1	14160	53.9	16.9	33.0	39.6	40.6	15.2
GQ502514.1	552342	75.4	162.4	132.3	95.6	100.5	58.6
FJ880553.1	426130	7512.0	6847.7	4230.4	6972.6	5561.1	4892.2
EF099448.1	178412	7465.5	8099.8	1435.2	3150.1	3036.9	1954.1
DQ793597.1	191389	4219.6	3750.3	839.4	2928.0	4727.4	5069.8
EU844897.1	344416	7135.8	7983.7	10476.2	8374.3	13636.1	10982.7
GU303039.1	576991	6621.8	5648.5	9419.1	6996.6	6243.4	3934.7
EU842953.1	332719	2938.3	3213.4	2154.2	2024.7	808.3	2169.4
FJ880679.1	420891	800.9	632.3	611.3	1956.0	885.0	1466.6
FJ879943.1	380842	5629.1	5499.0	6390.3	3541.1	2229.7	3386.7
EU773171.1	324364	3372.3	3375.7	4870.0	3187.7	1694.4	3109.5
GU304138.1	583497	218.5	104.3	559.5	124.9	186.9	150.4
GU304385.1	553278	10158.2	10035.2	9295.6	9166.1	9708.5	8514.5
U13041.1	14155	36.5	35.6	39.4	79.8	55.6	27.5
GQ458236.1	579985	4129.2	4940.6	3469.8	3312.5	6654.5	5788.0
EU842678.1	340989	4058.3	4722.2	2272.1	3073.2	1890.5	2284.1
FJ687606.2	552238	3535.4	1808.2	4560.0	3242.0	1241.0	2568.2
AF044945.1	14152	219.2	264.0	520.6	195.8	280.9	414.8
EF099332.1	181305	254.9	145.7	832.5	151.8	105.6	64.2
EU452756.1	318652	1577.2	1471.9	304.4	2283.8	2589.4	1862.2
EU469216.1	294038	174.7	343.4	395.7	114.9	641.0	346.8
AB034093.1	39613	117.6	129.8	163.1	63.6	99.1	60.8
FJ879878.1	409369	1203.4	754.0	2218.4	1016.1	312.6	367.1
GU304486.1	592803	2263.7	2672.1	2292.0	4518.6	3995.5	2335.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis

g__Eubacterium
g__Eubacterium
g__Mogibacterium
g__Mogibacterium
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	70593
s__unclassified	70624
s__unclassified	70033
s__unclassified	70376
s__unclassified	69993
s__unclassified	70007
s__unclassified	70013
s__unclassified	70016
s__unclassified	70049
s__unclassified	70064
s__unclassified	70108
s__unclassified	70111
s__unclassified	70120
s__unclassified	70130
s__unclassified	70149
s__unclassified	70193
s__unclassified	70210
s__unclassified	70213
s__unclassified	70214
s__unclassified	70277
s__unclassified	70280
s__unclassified	70282
s__unclassified	70285
s__unclassified	70291
s__unclassified	70298
s__unclassified	70299
s__unclassified	70311
s__unclassified	70313
s__unclassified	70320
s__unclassified	70356
s__unclassified	70396
s__unclassified	70413
s__unclassified	70420
s__unclassified	70428
s__unclassified	70457
s__unclassified	70490
s__unclassified	70512
s__unclassified	70515
s__unclassified	70517
s__unclassified	70548
s__unclassified	70558

FJ983009.1 gg_id:451218 Aspects Oral Microbiome root canal clone
EU777969.1 gg_id:342539 Black rhinoceros feces clone RH_aaj90f11
Z36296.1 gg_id:14163 Mogibacterium timidum str. ATCC 33093
AB037875.1 gg_id:46159 Mogibacterium neglectum str. ATCC 700924 (=P9a-h)
AF371681.1 gg_id:36226 swine intestine clone p-3263-42A2
EU794083.1 gg_id:304402 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E28
FJ680355.1 gg_id:525024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797373.1 gg_id:189641 human fecal clone RL248_aai98e08
EU771238.1 gg_id:309179 Asiatic elephant feces clone AE1_aaa03b04
GU303467.1 gg_id:588896 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU234217.1 gg_id:239736 river and un techniques downstream Wang Yang River receiving penicillin G producti
EU457038.1 gg_id:342368 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
GU304097.1 gg_id:584897 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
GQ014713.1 gg_id:494953 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763c
FJ833233.1 gg_id:508773 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q202_47G06
GU303409.1 gg_id:583010 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU842915.1 gg_id:335229 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU470097.1 gg_id:289968 trancaspain urial feces clone TU1_aaa01h04
AY858404.3 gg_id:112328 gastrointestinal tract Grant's gazelle clone GRANT32
EU469300.1 gg_id:301283 Speke's gazelle feces clone SP3_f08_3
EU462515.1 gg_id:302242 Sumatran orangutan feces clone orang1_aai56b09
EU468647.1 gg_id:295362 okapi feces clone OK2_d11_1
DQ353910.1 gg_id:150089 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z23
GU303120.1 gg_id:580364 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
DQ325886.1 gg_id:148168 Metagenomic gut microbiome healthy human stool clone B691
GU304081.1 gg_id:577079 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU234134.1 gg_id:236437 receiving river and un techniques anaerobic process WWTP treating penicillin G prod
EU776276.1 gg_id:319547 Red Kangaroo feces clone KO1_aai42d10
DQ325813.1 gg_id:147447 Metagenomic gut microbiome healthy human stool clone B543
EU344320.1 gg_id:276794 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
GU304446.1 gg_id:586769 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
GU302749.1 gg_id:589680 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
DQ801393.1 gg_id:196828 human fecal clone RL388_aao94h07
EU463611.1 gg_id:288422 domesticated horse feces clone horsej_aai89g02
EU748523.1 gg_id:341085 neotropical folivorous flying bird adult hoatzin crop clone hoa61_11e08
EU748100.1 gg_id:307485 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42b01
DQ325766.1 gg_id:147449 Metagenomic gut microbiome healthy human stool clone B444
AF371687.1 gg_id:28381 swine intestine clone p-1032-a5
DQ394650.1 gg_id:151714 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
AY854283.1 gg_id:109624 herbivore gastrointestinal tract clone CATTLE_21
GU303390.1 gg_id:535500 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium

FJ983009.1	451218	28.7	52.1	82.8	67.4	120.5	55.3
EU777969.1	342539	8418.9	7658.4	8125.4	6424.4	6465.6	6703.9
Z36296.1	14163	685.7	698.0	708.5	929.8	426.5	601.8
AB037875.1	46159	691.1	181.3	1032.2	333.3	920.3	918.2
AF371681.1	36226	556.5	758.6	1594.1	373.7	940.5	2511.8
EU794083.1	304402	1337.4	1615.9	2523.9	1265.3	1794.3	3379.4
FJ680355.1	525024	7885.9	9879.8	5581.8	8247.4	8573.0	7435.8
DQ797373.1	189641	1776.1	2936.5	2787.0	1499.7	235.3	930.6
EU771238.1	309179	8046.5	5876.3	7784.5	7614.2	4316.3	7346.1
GU303467.1	588896	5875.9	6080.6	3911.1	3038.4	4989.1	5458.4
EU234217.1	239736	6789.6	4269.0	2790.1	6978.6	7071.0	6639.9
EU457038.1	342368	667.9	792.1	2073.7	461.7	1756.7	1990.2
GU304097.1	584897	7545.8	6433.5	6132.5	8727.8	7558.1	9398.5
GQ014713.1	494953	572.0	776.5	848.4	642.9	1228.5	587.0
FJ833233.1	508773	3293.2	2791.4	5075.9	1837.9	1062.2	1710.5
GU303409.1	583010	1711.8	2909.2	4065.3	2456.5	8012.6	5878.3
EU842915.1	335229	1975.6	2356.6	1181.1	573.0	390.2	387.6
EU470097.1	289968	5242.3	4456.0	2745.8	2351.8	4568.3	7445.4
AY858404.3	112328	45.5	22.9	41.7	48.2	57.5	40.2
EU469300.1	301283	4272.2	4011.7	4025.3	3085.8	3118.3	4385.1
EU462515.1	302242	2255.0	2432.6	3057.1	3600.9	5308.8	9697.1
EU468647.1	295362	6047.3	6295.0	5502.6	3435.5	2034.8	4081.4
DQ353910.1	150089	3547.2	3717.6	5171.6	2924.1	2808.0	2855.8
GU303120.1	580364	7474.7	11478.5	4901.4	5254.4	4669.9	6386.2
DQ325886.1	148168	474.3	670.0	721.0	440.4	483.3	1816.7
GU304081.1	577079	2797.1	2800.8	3828.9	2601.7	1459.5	2339.9
EU234134.1	236437	3405.5	3051.3	3455.1	3842.7	3542.4	3434.7
EU776276.1	319547	3382.8	3145.1	1689.5	1784.8	3147.2	2282.9
DQ325813.1	147447	133.0	177.0	799.7	143.3	48.4	87.6
EU344320.1	276794	6068.2	6463.1	9237.7	6181.5	6861.8	6077.3
GU304446.1	586769	7847.1	6613.6	2096.1	3216.3	741.7	1227.1
GU302749.1	589680	6063.5	5369.1	3763.0	3737.6	4437.3	5014.6
DQ801393.1	196828	37.2	17.5	44.3	59.0	46.7	15.0
EU463611.1	288422	1691.1	2318.9	1357.8	2140.2	1955.1	1572.0
EU748523.1	341085	2196.2	3815.4	6273.3	1630.0	6752.0	7205.3
EU748100.1	307485	10700.5	9002.9	6798.8	7106.0	8172.0	7381.1
DQ325766.1	147449	830.0	858.1	1637.8	569.3	2210.6	1549.1
AF371687.1	28381	8741.5	8347.0	6847.6	5846.1	4762.1	11616.5
DQ394650.1	151714	4991.6	7064.2	5644.4	3868.2	9793.0	7233.8
AY854283.1	109624	4908.7	6079.0	2192.0	3932.0	4487.7	3453.6
GU303390.1	535500	5553.7	4573.7	4091.8	3320.1	5252.0	2469.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__D2
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Dehalobacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Dehalobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium

s__unclassified	70583
s__unclassified	70584
s__unclassified	70616
s__unclassified	70618
s__unclassified	48224
s__unclassified	48407
s__unclassified	49070
s__unclassified	49131
s__unclassified	49363
s__unclassified	49500
s__unclassified	49545
s__unclassified	49696
s__unclassified	49823
s__unclassified	49913
s__unclassified	48236
s__unclassified	48339
s__unclassified	48392
s__unclassified	48454
s__unclassified	48469
s__unclassified	48506
s__unclassified	48510
s__unclassified	48542
s__unclassified	48572
s__unclassified	48976
s__unclassified	49003
s__unclassified	49155
s__unclassified	49210
s__unclassified	49219
s__unclassified	49228
s__unclassified	49521
s__unclassified	49556
s__unclassified	49565
s__unclassified	49575
s__unclassified	49726
s__unclassified	49747
s__Acetobacterium carbinolicum	69485
s__Acetobacterium carbinolicum	69827
s__unclassified	69324
s__unclassified	69405
s__unclassified	69427
s__unclassified	69450

GQ088939.1 gg_id:461939 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3
AB218305.1 gg_id:148228 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-3
EU775736.1 gg_id:320853 Horse feces clone horsej_aai91a05
DQ797955.1 gg_id:184240 human fecal clone RL302_aal93g12
EF586058.1 gg_id:249539 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_
EU878314.1 gg_id:510808 Investigation factors influencing production large-scale municipal biogas plant therm
EF559085.1 gg_id:223604 mesophilic anaerobic digester clone B35_F_B_E05
EU639283.1 gg_id:324728 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU591634.1 gg_id:271468 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic
AB274505.1 gg_id:203717 packed-bed reactor clone CFB-16
AY684094.1 gg_id:137161 first genome data rice I methanogens combination cultivation and techniques metha
FN563391.1 gg_id:572575 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
EU639029.1 gg_id:316446 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU358732.1 gg_id:304420 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EF603619.1 gg_id:229057 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
X86690.1 gg_id:13929 Dehalobacterium formicoaceticum str. DMC
AB486500.1 gg_id:568326 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EF603618.1 gg_id:230762 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AM943569.1 gg_id:258502 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hyper
EU259468.1 gg_id:238635 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC92
EU469050.1 gg_id:296184 Speke's gazelle feces clone SP2_e04_3
AY426448.1 gg_id:106335 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B35
EF614786.1 gg_id:229827 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EF515659.1 gg_id:227372 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
AY991064.1 gg_id:130311 mouse cecum clone C13_I13
FJ879326.1 gg_id:449353 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EF614689.1 gg_id:231836 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
GU303484.1 gg_id:575101 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU134643.1 gg_id:244028 tallgrass prarie soil clone FFCH13041
EF559162.1 gg_id:221790 mesophilic anaerobic digester clone G35_D8_L_B_E01
EU474249.1 gg_id:288109 western lowland gorilla feces clone GORSD_aaa02b06
AY990091.1 gg_id:135305 mouse cecum clone C12_E08
EF602919.1 gg_id:228772 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
CU918616.1 gg_id:545232 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ015163.1 gg_id:131268 mouse cecum clone M2_d06_2
AB546238.1 gg_id:532064 Acetobacterium carbinolicum str. Mic2c03
AB546237.1 gg_id:523930 Acetobacterium carbinolicum str. Mic2c01
AB294288.1 gg_id:213453 Microbial structure deep coal seem groundwater clone YWB19
FM178819.1 gg_id:354559 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu
X96960.1 gg_id:14231 Acetobacterium bakii str. DSM 8239
AY185326.1 gg_id:79463 Acetobacterium sp. clone AKS48

GQ088939.1	461939	59.0	34.8	40.7	155.7	59.1	34.2
AB218305.1	148228	678.8	993.2	1181.4	932.0	716.5	737.6
EU775736.1	320853	8123.7	7558.2	6813.0	3790.9	8625.3	6664.3
DQ797955.1	184240	1596.5	1624.8	4772.2	5471.7	2076.5	1122.5
EF586058.1	249539	1372.3	2409.9	1748.2	1949.7	856.2	1228.5
EU878314.1	510808	9398.7	11280.6	7676.9	3415.4	4349.0	4776.5
EF559085.1	223604	107.8	67.3	49.4	173.9	72.5	36.1
EU639283.1	324728	2115.1	2932.8	1743.3	1145.0	2758.0	3388.2
EU591634.1	271468	3457.7	5414.4	4535.7	3458.1	6847.0	5217.5
AB274505.1	203717	3606.9	5084.5	2836.2	2538.2	2852.2	3030.5
AY684094.1	137161	6387.1	6125.2	3336.4	5697.5	4287.5	3876.1
FN563391.1	572575	4078.2	5433.9	8053.3	4794.6	4770.6	4908.2
EU639029.1	316446	90.5	379.1	826.9	306.6	77.2	461.4
EU358732.1	304420	669.0	1228.0	2904.6	845.0	713.1	538.3
EF603619.1	229057	946.9	1161.1	1416.9	1467.3	4520.8	3740.3
X86690.1	13929	3911.7	1642.1	5807.1	1043.6	924.8	1158.2
AB486500.1	568326	2873.9	3004.1	5505.1	2110.6	3924.1	3652.5
EF603618.1	230762	10419.5	13067.2	7396.4	8725.9	18800.2	17834.1
AM943569.1	258502	5083.8	5387.0	6108.3	4862.9	6931.1	5504.4
EU259468.1	238635	16129.5	11526.1	15859.9	12223.4	11247.0	10308.8
EU469050.1	296184	3580.0	4675.0	4358.9	1550.3	1472.3	2474.5
AY426448.1	106335	14.2	36.2	26.2	42.3	100.2	46.3
EF614786.1	229827	8945.3	9538.2	2515.8	5791.7	5159.8	5545.8
EF515659.1	227372	35.2	70.5	70.7	66.1	68.2	35.2
AY991064.1	130311	845.7	1305.1	1912.2	1035.9	1326.3	2056.0
FJ879326.1	449353	3399.8	2825.1	5523.7	3108.2	2571.2	3719.1
EF614689.1	231836	3510.7	5007.9	2678.5	3589.0	5316.8	5737.3
GU303484.1	575101	4088.4	6176.8	5152.5	3060.8	3284.0	3450.6
EU134643.1	244028	4424.7	4371.9	3184.6	1506.0	522.2	2335.3
EF559162.1	221790	186.5	246.9	88.7	297.0	196.0	269.0
EU474249.1	288109	8867.7	9512.9	4622.1	7944.9	7816.1	10213.5
AY990091.1	135305	211.9	585.6	856.8	750.5	251.6	489.4
EF602919.1	228772	25.7	23.2	35.4	50.6	44.1	15.8
CU918616.1	545232	3210.3	3213.8	2642.6	3886.4	8238.2	6404.3
DQ015163.1	131268	223.6	336.1	483.9	880.7	236.4	601.8
AB546238.1	532064	4588.5	4591.5	6492.2	5152.1	3364.4	6002.1
AB546237.1	523930	3542.4	5217.4	6096.6	3919.1	5841.7	6328.2
AB294288.1	213453	753.9	1375.4	1791.9	481.7	2427.0	1570.2
FM178819.1	354559	9335.6	13417.6	9802.0	9365.2	9729.9	8860.1
X96960.1	14231	2220.4	2631.6	4132.5	4192.5	1283.8	1346.2
AY185326.1	79463	9188.4	9073.4	4720.0	9636.5	9129.8	8601.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Eubacteriaceae

g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Acetobacterium
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Anaerofustis
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Pseudoramibacter
g__Pseudoramibacter
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	69575
s__unclassified	69638
s__unclassified	69644
s__unclassified	69702
s__unclassified	69723
s__unclassified	69808
s__unclassified	69813
s__unclassified	69835
s__unclassified	69850
s__unclassified	69902
s__unclassified	69923
s__Anaerofustis stercorihominis	69741
s__unclassified	69243
s__unclassified	69342
s__unclassified	69371
s__unclassified	69412
s__unclassified	69443
s__unclassified	69468
s__unclassified	69669
s__unclassified	69905
s__unclassified	69913
s__Eubacterium limosum	69489
s__Eubacterium yurii	70921
s__unclassified	69354
s__unclassified	69628
s__unclassified	71061
s__unclassified	71063
s__Pseudoramibacter alactolyticus	69750
s__unclassified	69755
s__unclassified	69303
s__unclassified	69353
s__unclassified	69531
s__unclassified	69569
s__unclassified	69589
s__unclassified	69633
s__unclassified	69652
s__unclassified	69694
s__unclassified	69735
s__unclassified	69837
s__unclassified	69863
s__unclassified	69880

AY185330.1 gg_id:79459 Acetobacterium sp. clone AKS70
X96954.1 gg_id:14237 Acetobacterium woodii str. DSM 1030
AY185325.1 gg_id:79549 Acetobacterium sp. clone AKS42
AB546245.1 gg_id:522312 Acetobacterium sp. str. Mic7c05
AY185319.1 gg_id:79098 Acetobacterium sp. clone AKS04
X96958.1 gg_id:14249 Acetobacterium paludosum str. DSM 8237
DQ447180.1 gg_id:156581 Coexistence homoacetogens and heterotrophic sulfate-reducing synthesis gas fed la
AF132739.1 gg_id:14234 Acetobacterium psammolithicum str. CN-E
AY185318.1 gg_id:79515 Acetobacterium sp. clone AKS02
X96959.1 gg_id:14257 Acetobacterium fimetarium str. DSM 8238
AY185323.1 gg_id:79093 Acetobacterium sp. clone AKS29
AJ518871.2 gg_id:104008 Anaerofustis stercorihominis str. wal 14563
DQ353902.1 gg_id:148988 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z4
AB198513.1 gg_id:135410 termite gut wall fraction clone RsW01-091
EU843431.1 gg_id:319993 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ833673.1 gg_id:543902 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_77E10
DQ353937.1 gg_id:149723 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z105
EU462735.1 gg_id:291786 Sumatran orangutan feces clone orang2_aai68b12
EU844993.1 gg_id:323946 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB088988.1 gg_id:77821 termite gut homogenate clone Rs-H81 bacterium
AM691886.2 gg_id:527988 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar
AB298910.1 gg_id:275347 Eubacterium limosum str. #5
AY533381.1 gg_id:106035 Eubacterium yurii subsp. margaretiae str. ATCC 43715
EU463292.1 gg_id:294324 naked mole-rat feces clone molerat_aai72h11
AJ518868.1 gg_id:109633 Eubacterium sp. str. CS1 Van
AY533382.1 gg_id:106183 Eubacterium yurii subsp. schtitka str. ATCC 43716
AM419991.1 gg_id:247984 Noma subgingival plaque clone 102C12(oral)
AB036759.1 gg_id:46867 Pseudoramibacter alactolyticus str. 23263T
EU474929.1 gg_id:296092 red river hog feces clone RRH_aaa02e07
AF073898.1 gg_id:14253 Eubacterium aggregans str. SR12; DSM 12183
EU845579.1 gg_id:335896 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU468268.1 gg_id:302875 domesticated horse feces clone horsej_g07
DQ478748.1 gg_id:157142 UASB reactor treating brewery wastewater clone CLONG19
DQ339707.1 gg_id:214750 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni
FJ672150.1 gg_id:514900 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
GU180172.1 gg_id:554177 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
AY312403.2 gg_id:89746 Alkalibacter saccharofermentans str. Z-79820
EU843219.1 gg_id:311974 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ672463.1 gg_id:524649 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU344196.1 gg_id:274259 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ672328.1 gg_id:532190 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I

AY185330.1	79459	1218.6	1173.0	1802.5	1745.6	312.5	659.5
X96954.1	14237	444.1	1081.0	1041.4	471.7	126.1	118.3
AY185325.1	79549	2025.2	2801.3	3934.4	3171.9	3746.4	3562.8
AB546245.1	522312	1955.6	2096.9	2059.0	2831.1	3878.8	3921.7
AY185319.1	79098	3259.1	2531.9	1110.3	4605.5	5423.8	4306.7
X96958.1	14249	850.9	445.1	2750.8	422.9	419.6	841.7
DQ447180.1	156581	10716.3	13061.4	9339.6	11908.3	7766.5	7423.1
AF132739.1	14234	9258.4	9893.4	10078.2	10812.2	9637.1	10705.4
AY185318.1	79515	1643.4	2424.6	1865.1	875.8	3053.4	2785.0
X96959.1	14257	3664.3	4004.4	5252.7	7033.3	3705.7	4028.3
AY185323.1	79093	1641.7	1778.8	3044.8	1354.1	1860.4	2173.1
AJ518871.2	104008	2320.8	1293.9	1850.1	2513.0	1513.2	2192.2
DQ353902.1	148988	60.7	62.6	110.1	93.5	94.0	38.4
AB198513.1	135410	6009.3	5685.7	7437.3	7007.9	8391.9	7041.7
EU843431.1	319993	6693.9	6485.0	2741.6	4802.8	5075.0	4799.4
FJ833673.1	543902	5642.5	6162.5	6022.7	6093.9	8224.0	6408.6
DQ353937.1	149723	1915.0	1486.3	1471.5	1185.9	140.4	525.1
EU462735.1	291786	1067.3	1010.0	1020.7	4744.3	1563.0	1893.6
EU844993.1	323946	5248.9	3955.3	3816.9	6440.9	1562.0	2502.6
AB088988.1	77821	2228.6	2973.6	2739.6	1513.1	3314.6	1979.3
AM691886.2	527988	8553.8	9020.2	3553.2	9499.7	4014.0	5706.8
AB298910.1	275347	1153.1	2938.0	4636.2	770.8	2640.5	2491.8
AY533381.1	106035	3144.6	3241.5	1860.8	2295.4	4497.5	3663.8
EU463292.1	294324	1144.9	3017.3	4639.8	879.8	2656.7	1981.4
AJ518868.1	109633	136.8	402.0	298.6	86.2	77.8	36.6
AY533382.1	106183	49.8	84.2	92.4	87.1	57.7	29.1
AM419991.1	247984	1360.1	1725.0	4678.2	1423.8	3912.0	2269.2
AB036759.1	46867	32.9	42.9	48.3	79.7	70.5	35.2
EU474929.1	296092	168.3	288.7	191.0	215.1	166.3	132.3
AF073898.1	14253	51.0	43.6	60.4	71.3	70.2	50.6
EU845579.1	335896	1391.3	2396.2	2058.7	1399.2	750.3	1569.3
EU468268.1	302875	249.1	452.4	1459.3	410.6	444.2	1711.8
DQ478748.1	157142	5577.6	5003.7	6240.3	5772.7	4430.0	4573.5
DQ339707.1	214750	7356.3	6308.3	7274.2	6205.8	6422.8	6183.0
FJ672150.1	514900	6125.6	5609.9	6258.0	3970.1	3784.4	4733.1
GU180172.1	554177	4586.7	4435.4	2858.8	4545.9	3376.7	3502.6
AY312403.2	89746	344.5	397.3	360.8	340.6	156.1	214.5
EU843219.1	311974	1831.1	3310.3	6512.0	1784.4	1772.3	4053.2
FJ672463.1	524649	10955.2	9545.8	7524.2	8880.8	11471.0	9810.0
EU344196.1	274259	6118.3	4283.1	4596.9	4379.7	4111.1	5633.0
FJ672328.1	532190	4907.6	6091.1	7906.6	6400.4	9236.4	8284.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Eubacteriaceae
o__Clostridiales	f__Heliobacteriaceae
o__Clostridiales	f__Heliobacteriaceae
o__Clostridiales	f__Heliobacteriaceae
o__Clostridiales	f__Heliobacteriaceae
o__Clostridiales	f__Heliobacteriaceae
o__Clostridiales	f__Heliobacteriaceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__unclassified
g__Heliobacterium
g__Heliobacterium
g__Heliobacterium
g__Heliobacterium
g__Heliorestis
g__unclassified
g__Anaerostipes
g__Anaerostipes
g__Anaerostipes
g__Anaerostipes
g__Anaerostipes
g__Anaerostipes
g__Bacteroides
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	69900
s__Heliobacterium modesticaldum	48270
s__Heliobacterium modesticaldum	49840
s__unclassified	48267
s__unclassified	48336
s__unclassified	49391
s__unclassified	49851
s__Anaerostipes caccae	20423
s__unclassified	18502
s__unclassified	18732
s__unclassified	19222
s__unclassified	19402
s__unclassified	19423
s__Bacteroides pectinophilus	20485
s__Blautia producta	20633
s__Blautia producta	20641
s__Blautia producta	20648
s__Blautia producta	20649
s__Blautia producta	20694
s__Blautia producta	20731
s__Blautia producta	20733
s__Blautia producta	20756
s__Blautia producta	20788
s__Blautia producta	20804
s__Blautia producta	20827
s__Blautia producta	20841
s__Blautia producta	20884
s__Blautia producta	20896
s__Blautia producta	20901
s__Blautia producta	20908
s__Blautia producta	20934
s__Blautia producta	20949
s__Blautia producta	20958
s__Blautia producta	20985
s__Blautia producta	20995
s__Blautia producta	20997
s__Blautia producta	21026
s__Blautia producta	21042
s__Blautia producta	21046
s__Blautia producta	21077
s__Blautia producta	21078

AY554414.1 gg_id:103303 Alkalibacterium sp. 8B
CP000930.2 gg_id:262344 Heliobacterium modesticaldum Ice1 str. Ice1; ATCC 51547
NC_010337.1 gg_id:268302 Heliobacterium modesticaldum Ice1 str. Ice1; ATCC 51547
AB100837.1 gg_id:110646 Heliobacterium gestii str. DSM 11169
AF249678.1 gg_id:73860 Heliobacterium sulfidophilum str. BR4 (T)
NR_028721.1 gg_id:571373 Heliorestis daurensis str. BT-H1; ATCC 700798
NR_025932.1 gg_id:548015 Heliobacterium chlorum str. ATCC 35205
AF028351.1 gg_id:14069 Clostridium indolis CM971
NR_024993.1 gg_id:555445 Clostridium fimetarium str. Z-2189; DSM 9179
DQ513077.1 gg_id:161135 Microbial life fluids ridge flank crustal fluid clone FS266-27B-03
EF559143.1 gg_id:221028 mesophilic anaerobic digester clone G35_D8_L_B_A11
FJ672313.1 gg_id:524287 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AF275914.2 gg_id:72606 anaerobic digester clone AA02
ABVQ01000036.1 gg_id:561391 Bacteroides pectinophilus str. ATCC 43243
GQ493997.1 gg_id:594268 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ369932.1 gg_id:360069 feces adult twins and mothers; TS55 clone TS55_a02d10
FJ978689.1 gg_id:458990 feces clone CL_F_376
EU463007.1 gg_id:293490 southern three-banded armadillo feces clone arma_aaj56d10
FJ678747.1 gg_id:512569 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ804305.1 gg_id:195563 human fecal clone RL187_aan77g02
FJ364622.1 gg_id:368535 feces adult twins and mothers; TS19 clone TS19_a01b05
FJ978518.1 gg_id:412390 feces clone CL_F_049
DQ804223.1 gg_id:183849 human fecal clone RL187_aah70e06
EU465331.1 gg_id:290362 lion feces clone LI3_aah75d08
GQ867449.1 gg_id:578056 and prevalence blaTEM genes Arctic seals colon content clone CSG14
EU772751.1 gg_id:318444 Bush dog feces clone bdog3_aad67f09
EU468418.1 gg_id:298896 lion feces clone LI2_aae50b09
GQ491687.1 gg_id:571472 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU465525.1 gg_id:288367 lion feces clone LI3_aah78h10
AY977095.1 gg_id:119459 human cecum mucosal biopsy clone K786
FJ677562.1 gg_id:532487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY975491.1 gg_id:120281 human ascending colon mucosal biopsy clone N930
GQ491473.1 gg_id:562403 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ368564.1 gg_id:365763 feces adult twins and mothers; TS49 clone TS49_a01g11
EU462872.1 gg_id:291656 southern three-banded armadillo feces clone arma_aaj54c07
FJ364917.1 gg_id:369814 feces adult twins and mothers; TS19 clone TS19_a04g02
EU467598.1 gg_id:297131 southern three-banded armadillo feces clone arma_h05_1
FJ368665.1 gg_id:365150 feces adult twins and mothers; TS49 clone TS49_a03a07
EU465383.1 gg_id:287495 lion feces clone LI3_aah76d08
DQ803632.1 gg_id:179340 human fecal clone RL251_aaj88d11
EU458570.1 gg_id:302128 spotted hyena feces clone HY2_h05_1

AY554414.1	103303	5585.4	4822.7	3698.8	1433.0	519.5	1320.5
CP000930.2	262344	6513.4	6125.0	6817.6	4933.7	6275.2	3880.8
NC_010337.1	268302	870.4	1185.2	3707.5	917.1	3629.3	1994.1
AB100837.1	110646	653.7	875.1	986.9	340.4	204.7	504.9
AF249678.1	73860	2471.7	1870.6	1793.6	203.9	612.5	1148.8
NR_028721.1	571373	30.2	49.1	49.2	67.9	69.2	26.3
NR_025932.1	548015	66.7	137.7	451.9	82.0	440.9	551.5
AF028351.1	14069	39.8	65.6	167.6	57.9	56.1	26.2
NR_024993.1	555445	36.3	44.6	75.9	74.5	48.5	32.8
DQ513077.1	161135	266.4	324.5	108.6	278.9	63.9	69.8
EF559143.1	221028	1163.9	1767.9	2787.7	600.9	405.1	648.7
FJ672313.1	524287	405.6	837.9	2067.3	650.9	547.2	583.1
AF275914.2	72606	39.9	33.2	20.4	52.4	66.5	23.1
ABVQ01000036.1	561391	180.4	316.8	968.3	184.4	111.0	337.9
GQ493997.1	594268	699.8	677.1	359.1	755.5	411.0	762.7
FJ369932.1	360069	3660.3	1993.2	3416.9	3263.8	2071.6	3186.3
FJ978689.1	458990	4552.2	4477.1	3834.5	5359.8	3325.3	4336.2
EU463007.1	293490	1050.3	1225.5	2366.9	1560.5	651.5	1589.2
FJ678747.1	512569	177.0	625.7	225.9	274.3	95.4	45.7
DQ804305.1	195563	113.7	105.5	232.6	184.1	162.4	113.1
FJ364622.1	368535	181.1	146.4	283.0	225.4	116.4	102.2
FJ978518.1	412390	629.4	516.7	1317.4	965.0	261.2	275.2
DQ804223.1	183849	217.2	263.5	728.2	115.0	80.6	158.2
EU465331.1	290362	69.2	143.1	64.7	46.5	61.1	40.1
GQ867449.1	578056	4033.4	4606.8	5296.5	2547.8	3533.1	3405.4
EU772751.1	318444	368.5	708.8	790.8	646.2	360.0	550.7
EU468418.1	298896	1705.1	2912.9	1476.2	558.3	118.4	116.2
GQ491687.1	571472	158.5	125.5	460.5	114.6	108.8	85.5
EU465525.1	288367	1789.8	1614.5	934.4	1291.3	428.5	929.3
AY977095.1	119459	356.0	270.6	352.5	105.7	86.6	178.4
FJ677562.1	532487	8859.8	7649.3	5750.7	9499.0	11447.0	10989.3
AY975491.1	120281	3723.6	3822.4	3882.7	4995.5	5959.9	3838.7
GQ491473.1	562403	377.1	298.0	274.0	128.5	85.3	133.8
FJ368564.1	365763	154.8	270.9	113.1	108.0	250.3	238.5
EU462872.1	291656	86.1	96.7	342.0	98.5	125.5	124.1
FJ364917.1	369814	1715.2	1477.0	386.6	1207.5	307.3	233.3
EU467598.1	297131	213.2	264.9	844.4	536.9	492.3	454.0
FJ368665.1	365150	6101.2	5037.0	4579.2	6069.4	4685.4	4765.9
EU465383.1	287495	108.4	154.7	267.5	141.1	58.7	18.6
DQ803632.1	179340	2932.0	2890.4	4455.1	2828.5	4919.3	4925.4
EU458570.1	302128	914.2	510.8	484.8	435.7	784.7	1346.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__Blautia producta	21098
s__Blautia producta	21102
s__Blautia producta	21116
s__Blautia producta	21131
s__Blautia producta	21135
s__Blautia producta	21137
s__Blautia producta	21145
s__Blautia producta	21163
s__Blautia producta	21173
s__Blautia producta	21178
s__Blautia producta	21205
s__Blautia producta	21223
s__Blautia producta	21252
s__Blautia producta	21266
s__Blautia producta	21286
s__Blautia producta	21293
s__Blautia producta	21300
s__Blautia producta	21327
s__Blautia producta	21334
s__Blautia producta	21341
s__Blautia producta	21393
s__Blautia producta	21396
s__Blautia producta	21401
s__Blautia producta	21422
s__Blautia producta	21433
s__Blautia producta	21444
s__Blautia producta	21445
s__Blautia producta	21477
s__Blautia producta	21484
s__Blautia producta	21488
s__Blautia producta	21524
s__Blautia producta	21530
s__Blautia producta	21533
s__Blautia producta	21551
s__Blautia producta	21578
s__Blautia producta	21581
s__Blautia producta	21597
s__Blautia producta	21603
s__Ruminococcus obeum	20618
s__Ruminococcus obeum	20644
s__Ruminococcus obeum	20710

DQ795717.1 gg_id:191316 human fecal clone RL245_aai81b10
EU772730.1 gg_id:304309 Bush dog feces clone bdog1_aai80c10
EU463036.1 gg_id:301318 southern three-banded armadillo feces clone arma_aaj56g11
EU467565.1 gg_id:296174 southern three-banded armadillo feces clone arma_e09
DQ456327.1 gg_id:158939 pre-adolescent turkey cecum clone CFT212A8
AY980578.1 gg_id:115563 human rectum mucosal biopsy clone X564
DQ804061.1 gg_id:194041 human fecal clone RL187_aah67h08
DQ804970.1 gg_id:192897 human fecal clone RL385_aao83d06
EU465381.1 gg_id:295456 lion feces clone LI3_aah76d06
AY984413.1 gg_id:115474 human stool clone B322
FJ370721.1 gg_id:363714 feces adult twins and mothers; TS57 clone TS57_a04d11
EF403112.1 gg_id:205138 human fecal clone SJTU_B_15_05
EU462960.1 gg_id:289142 southern three-banded armadillo feces clone arma_aaj55g02
EU462816.1 gg_id:301634 southern three-banded armadillo feces clone arma_aaj53e06
GQ491355.1 gg_id:585006 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY858537.2 gg_id:109545 gastrointestinal tract eland clone ELAND_90
EU462957.1 gg_id:287601 southern three-banded armadillo feces clone arma_aaj55f09
EU771926.1 gg_id:304393 Southern three-banded armadillo feces clone arma_aaj55d07
EU465322.1 gg_id:291815 lion feces clone LI3_aah75c06
EU462823.1 gg_id:299390 southern three-banded armadillo feces clone arma_aaj53f04
EU467568.1 gg_id:292964 southern three-banded armadillo feces clone arma_f10
EU467548.1 gg_id:301090 southern three-banded armadillo feces clone arma_h01
DQ807651.1 gg_id:192025 human fecal clone RL180_aah35e03
EU467605.1 gg_id:288469 southern three-banded armadillo feces clone arma_c03_1
DQ804131.1 gg_id:181706 human fecal clone RL187_aah69a12
AM276759.2 gg_id:231704 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
GQ491435.1 gg_id:566739 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ793721.1 gg_id:194494 human fecal clone RL246_aai76b10
EU771867.1 gg_id:311777 Southern three-banded armadillo feces clone arma_h08
DQ803436.1 gg_id:176107 human fecal clone RL251_aaj85g06
AB534168.1 gg_id:537101 Blautia hansenii DSM 20583 str. JCM 14655
GQ492373.1 gg_id:564101 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU773903.1 gg_id:310173 Cheetah feces clone CE3_aai06h09
EU771961.1 gg_id:337246 Southern three-banded armadillo feces clone arma_aaj56h08
DQ804247.1 gg_id:183955 human fecal clone RL187_aah70h02
EU772709.1 gg_id:311712 Bush dog feces clone bdog1_aai79g01
EF399220.1 gg_id:211999 human fecal clone SJTU_F_13_18
FJ368791.1 gg_id:357004 feces adult twins and mothers; TS49 clone TS49_a04f03
DQ905190.1 gg_id:163706 human fecal clone 013-a11
GQ079651.1 gg_id:433152 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232g(
EF402578.1 gg_id:214316 human fecal clone SJTU_B_09_74

DQ795717.1	191316	25.9	19.0	34.9	41.1	57.3	16.8
EU772730.1	304309	38.7	139.3	100.6	92.8	59.9	125.4
EU463036.1	301318	125.3	57.6	358.1	95.2	110.0	36.3
EU467565.1	296174	7550.9	6119.5	5753.6	4950.7	5055.5	4729.0
DQ456327.1	158939	33.3	46.9	42.4	85.4	68.5	59.1
AY980578.1	115563	40.1	20.3	95.6	49.1	57.9	23.7
DQ804061.1	194041	71.8	94.9	373.8	63.9	132.2	67.9
DQ804970.1	192897	634.0	733.8	657.0	1122.1	1143.9	1437.9
EU465381.1	295456	131.3	369.7	74.9	477.8	795.6	845.7
AY984413.1	115474	798.7	587.4	2184.8	815.3	126.6	301.8
FJ370721.1	363714	209.0	409.7	401.3	130.1	107.6	61.4
EF403112.1	205138	3888.4	3994.7	2559.5	6240.5	1372.7	3365.6
EU462960.1	289142	331.6	286.4	1112.9	250.1	883.3	316.2
EU462816.1	301634	3720.0	4075.4	407.9	2307.2	1732.4	2821.4
GQ491355.1	585006	362.1	995.2	473.7	333.1	1597.6	741.4
AY858537.2	109545	12.6	29.3	23.3	54.6	60.0	21.0
EU462957.1	287601	1198.8	1594.7	2217.1	499.9	544.5	995.4
EU771926.1	304393	756.3	663.3	1065.2	416.2	810.9	340.7
EU465322.1	291815	14416.8	14725.5	10654.6	12425.4	14365.8	12672.7
EU462823.1	299390	2398.0	2261.7	2132.1	1433.6	1395.8	1902.6
EU467568.1	292964	566.9	434.4	874.8	2210.6	953.0	1578.0
EU467548.1	301090	49.6	57.0	190.2	81.3	52.6	42.0
DQ807651.1	192025	9.7	18.8	18.6	45.5	53.9	14.5
EU467605.1	288469	107.8	197.6	395.1	93.1	152.6	138.9
DQ804131.1	181706	905.2	759.9	1354.6	2882.7	573.1	2087.6
AM276759.2	231704	261.3	323.2	592.8	211.4	95.8	146.5
GQ491435.1	566739	2495.5	2235.9	3264.9	2883.9	5463.1	3260.7
DQ793721.1	194494	349.4	490.0	641.9	269.4	914.6	527.4
EU771867.1	311777	738.6	870.8	219.5	465.6	710.6	512.9
DQ803436.1	176107	410.1	468.5	555.2	2111.7	261.3	796.0
AB534168.1	537101	365.8	263.8	401.7	415.9	222.5	284.6
GQ492373.1	564101	3268.5	2932.4	712.0	1180.7	141.2	312.6
EU773903.1	310173	3438.4	5237.3	9215.6	5437.8	5923.1	7465.3
EU771961.1	337246	87.4	56.9	502.9	136.7	361.4	1573.4
DQ804247.1	183955	2469.3	1422.4	1900.9	1661.0	90.3	985.1
EU772709.1	311712	18.2	20.5	95.3	65.5	53.8	27.9
EF399220.1	211999	2649.5	3610.0	435.7	1153.3	1237.1	1276.9
FJ368791.1	357004	4261.4	2788.9	1373.5	4336.9	5674.4	6211.1
DQ905190.1	163706	4106.6	5752.1	1310.3	4314.2	2990.9	2684.7
GQ079651.1	433152	62.9	81.7	180.6	123.3	76.1	79.4
EF402578.1	214316	58.8	36.0	97.6	75.2	60.7	24.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__Ruminococcus obeum	20745
s__Ruminococcus obeum	20751
s__Ruminococcus obeum	20752
s__Ruminococcus obeum	20799
s__Ruminococcus obeum	20844
s__Ruminococcus obeum	20903
s__Ruminococcus obeum	20922
s__Ruminococcus obeum	20951
s__Ruminococcus obeum	20964
s__Ruminococcus obeum	20987
s__Ruminococcus obeum	21016
s__Ruminococcus obeum	21061
s__Ruminococcus obeum	21072
s__Ruminococcus obeum	21093
s__Ruminococcus obeum	21097
s__Ruminococcus obeum	21107
s__Ruminococcus obeum	21109
s__Ruminococcus obeum	21125
s__Ruminococcus obeum	21152
s__Ruminococcus obeum	21158
s__Ruminococcus obeum	21194
s__Ruminococcus obeum	21197
s__Ruminococcus obeum	21214
s__Ruminococcus obeum	21219
s__Ruminococcus obeum	21264
s__Ruminococcus obeum	21273
s__Ruminococcus obeum	21314
s__Ruminococcus obeum	21316
s__Ruminococcus obeum	21320
s__Ruminococcus obeum	21330
s__Ruminococcus obeum	21398
s__Ruminococcus obeum	21411
s__Ruminococcus obeum	21426
s__Ruminococcus obeum	21476
s__Ruminococcus obeum	21481
s__Ruminococcus obeum	21493
s__Ruminococcus obeum	21511
s__Ruminococcus obeum	21537
s__Ruminococcus obeum	21554
s__Ruminococcus obeum	21614
s__unclassified	17508

AY985501.1 gg_id:121327 human stool clone C466
FJ363787.1 gg_id:364910 feces adult twins and mothers; TS14 clone TS14_a03d01
EU530199.1 gg_id:268713 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1
GQ897170.1 gg_id:564568 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ367882.1 gg_id:360376 feces adult twins and mothers; TS2 clone TS2_a04f09
AY978324.1 gg_id:120310 human transverse colon mucosal biopsy clone F221
FJ366070.1 gg_id:366070 feces adult twins and mothers; TS25 clone TS25_a02d03
DQ804337.1 gg_id:176335 human fecal clone RL187_aan78c04
DQ804193.1 gg_id:180310 human fecal clone RL187_aah70b05
FJ368690.1 gg_id:360794 feces adult twins and mothers; TS49 clone TS49_a03d02
FJ367559.1 gg_id:362330 feces adult twins and mothers; TS2 clone TS2_a01a03
EU762964.1 gg_id:330799 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
FJ368669.1 gg_id:366222 feces adult twins and mothers; TS49 clone TS49_a03b03
DQ326724.1 gg_id:146107 Metagenomic gut microbiome healthy human stool clone E179
GQ077133.1 gg_id:436257 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1207e
X85101.1 gg_id:13989 Ruminococcus obeum
EF404046.1 gg_id:206980 human fecal clone SJTU_C_03_91
NZ_AAVO02000010.1 gg_id:254715 Ruminococcus obeum str. ATCC 29174
DQ804388.1 gg_id:180845 human fecal clone RL187_aan79b02
FJ371930.1 gg_id:363437 feces adult twins and mothers; TS8 clone TS8_a03h01
EF402596.1 gg_id:215785 human fecal clone SJTU_B_10_02
FJ363590.1 gg_id:361362 feces adult twins and mothers; TS14 clone TS14_a01b02
FJ363622.1 gg_id:358484 feces adult twins and mothers; TS14 clone TS14_a01d10
FJ369679.1 gg_id:362541 feces adult twins and mothers; TS51 clone TS51_a03e08
AY976610.1 gg_id:122356 human cecum mucosal biopsy clone K164
FJ368962.1 gg_id:365261 feces adult twins and mothers; TS4 clone TS4_a02f04
FJ364994.1 gg_id:366762 feces adult twins and mothers; TS1 clone TS1_a01f02
GQ897939.1 gg_id:546581 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ363819.1 gg_id:362428 feces adult twins and mothers; TS14 clone TS14_a03g02
FJ366168.1 gg_id:364536 feces adult twins and mothers; TS25 clone TS25_a03e05
AY982558.1 gg_id:118219 human descending colon mucosal biopsy clone KW23
EU728790.1 gg_id:346709 Ruminococcus sp. str. DJF_VR66
FJ363623.1 gg_id:362465 feces adult twins and mothers; TS14 clone TS14_a01d11
FJ367436.1 gg_id:368938 feces adult twins and mothers; TS29 clone TS29_a03e06
FJ366601.1 gg_id:368132 feces adult twins and mothers; TS27 clone TS27_a01f03
FJ366452.1 gg_id:366345 feces adult twins and mothers; TS26 clone TS26_a03d10
FJ368714.1 gg_id:360328 feces adult twins and mothers; TS49 clone TS49_a03f04
AY978747.1 gg_id:118593 human transverse colon mucosal biopsy clone KU92
DQ806775.1 gg_id:176537 human fecal clone RL186_aao48e10
FJ363900.1 gg_id:359930 feces adult twins and mothers; TS14 clone TS14_a04f10
DQ807635.1 gg_id:187021 human fecal clone RL180_aah35c04

AY985501.1	121327	3426.6	3585.7	561.2	1428.4	661.3	788.7
FJ363787.1	364910	929.5	749.5	290.1	245.0	100.8	86.0
EU530199.1	268713	27.9	331.5	322.6	121.1	371.8	39.6
GQ897170.1	564568	96.7	111.3	322.8	146.1	93.7	71.5
FJ367882.1	360376	42.7	98.0	239.8	92.2	66.8	42.4
AY978324.1	120310	6649.4	5713.7	2156.7	4644.5	4490.8	3832.9
FJ366070.1	366070	795.4	601.1	1238.5	1903.6	164.4	265.0
DQ804337.1	176335	360.3	156.0	537.3	920.0	54.3	87.5
DQ804193.1	180310	8853.0	9476.3	8924.9	8225.8	9478.7	10009.0
FJ368690.1	360794	3639.1	3907.0	1749.9	5012.4	6510.8	7409.1
FJ367559.1	362330	59.4	96.8	376.1	97.3	97.0	58.7
EU762964.1	330799	4310.5	5023.7	1816.5	4304.3	2344.4	3723.0
FJ368669.1	366222	7035.0	7019.1	4897.5	6786.5	10142.3	8975.1
DQ326724.1	146107	3188.5	3350.5	2520.7	1893.2	3735.0	4016.6
GQ077133.1	436257	1164.6	666.2	960.9	661.6	133.9	151.2
X85101.1	13989	67.4	71.2	438.3	102.2	65.7	42.7
EF404046.1	206980	4629.3	3874.3	1818.0	4424.8	914.0	1108.5
NZ_AAVO02000010.1	254715	56.5	118.2	323.7	107.5	71.9	53.0
DQ804388.1	180845	777.8	1170.5	495.1	293.0	1261.1	657.2
FJ371930.1	363437	2282.7	3169.1	2080.2	1236.9	3203.0	2774.4
EF402596.1	215785	37.2	55.9	107.1	96.5	44.6	19.2
FJ363590.1	361362	687.7	560.5	184.6	55.7	59.2	23.5
FJ363622.1	358484	187.6	112.7	521.5	210.6	124.5	90.6
FJ369679.1	362541	606.5	944.0	2425.8	1027.9	1386.7	1451.6
AY976610.1	122356	29.4	59.1	126.5	58.0	62.9	25.9
FJ368962.1	365261	3839.1	4192.0	4072.4	4788.7	7403.5	6293.0
FJ364994.1	366762	1178.3	1169.9	2374.3	1280.4	998.4	1064.5
GQ897939.1	546581	261.9	570.8	580.8	684.9	286.0	859.4
FJ363819.1	362428	3032.1	3558.8	2076.4	2970.5	6525.4	4354.4
FJ366168.1	364536	6935.6	8263.3	4773.9	6040.9	8065.3	8741.0
AY982558.1	118219	2415.8	3490.7	608.9	834.1	237.1	281.6
EU728790.1	346709	69.5	96.7	163.4	165.2	57.4	43.2
FJ363623.1	362465	577.1	725.4	718.1	1429.1	1932.3	1838.6
FJ367436.1	368938	49.9	106.4	343.6	96.2	78.8	48.3
FJ366601.1	368132	131.8	209.3	374.9	236.5	98.5	91.1
FJ366452.1	366345	52.7	82.1	402.0	95.6	67.2	42.3
FJ368714.1	360328	147.7	164.0	394.9	249.4	112.4	101.1
AY978747.1	118593	119.8	309.6	652.1	128.8	112.6	634.5
DQ806775.1	176537	50.4	105.1	319.9	101.1	78.6	49.9
FJ363900.1	359930	1798.4	2133.8	700.1	1506.5	2978.0	1984.5
DQ807635.1	187021	58.7	53.4	507.8	81.3	79.5	153.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	17510
s__unclassified	17595
s__unclassified	17637
s__unclassified	17646
s__unclassified	17655
s__unclassified	17684
s__unclassified	17705
s__unclassified	17834
s__unclassified	17886
s__unclassified	17914
s__unclassified	17950
s__unclassified	18096
s__unclassified	18139
s__unclassified	18150
s__unclassified	18315
s__unclassified	18399
s__unclassified	18418
s__unclassified	18563
s__unclassified	18595
s__unclassified	18670
s__unclassified	18700
s__unclassified	18920
s__unclassified	18951
s__unclassified	18955
s__unclassified	18978
s__unclassified	18991
s__unclassified	19029
s__unclassified	19097
s__unclassified	19116
s__unclassified	19136
s__unclassified	19137
s__unclassified	19250
s__unclassified	19841
s__unclassified	19877
s__unclassified	19882
s__unclassified	20617
s__unclassified	20619
s__unclassified	20620
s__unclassified	20622
s__unclassified	20623
s__unclassified	20624

DQ795429.1 gg_id:193842 human fecal clone RL178_aah54c06
DQ326454.1 gg_id:146226 Metagenomic gut microbiome healthy human stool clone C529
EU466824.1 gg_id:289535 African elephant feces clone AFEL2_aao29h11
DQ808076.1 gg_id:183267 human fecal clone RL180_aan72a03
DQ825011.1 gg_id:198532 human fecal clone RL185_aao72c02
DQ807333.1 gg_id:196082 human fecal clone RL307_aam05c04
DQ808105.1 gg_id:187385 human fecal clone RL180_aan72e11
DQ801994.1 gg_id:194896 human fecal clone RL241_aaj01e12
DQ807015.1 gg_id:185563 human fecal clone RL244_aaj45b06
DQ808195.1 gg_id:183824 human fecal clone RL180_aao73g05
DQ810151.1 gg_id:186621 human fecal clone RL184_aao68f05
DQ794894.1 gg_id:174093 human fecal clone RL310_aam37f07
EU779348.1 gg_id:303897 Somali Wild Ass feces clone WA_aaa02e07
DQ825110.1 gg_id:197657 human fecal clone RL185_aan85e05
DQ808200.1 gg_id:179609 human fecal clone RL180_aao73g10
DQ799237.1 gg_id:191132 human fecal clone RL205_aaj19e10
DQ800722.1 gg_id:178016 human fecal clone RL183_aao02f03
DQ802815.1 gg_id:184861 human fecal clone RL188_aan96h07
DQ795471.1 gg_id:197050 human fecal clone RL178_aah54g05
EU771766.1 gg_id:336948 African elephant feces clone AFEL2_aao31g05
DQ326114.1 gg_id:148619 Metagenomic gut microbiome healthy human stool clone BB74
DQ802802.1 gg_id:173917 human fecal clone RL188_aan96g04
DQ800314.1 gg_id:181003 human fecal clone RL303_aal71c11
DQ808280.1 gg_id:193210 human fecal clone RL180_aao74g04
DQ823693.1 gg_id:191950 human fecal clone RL250_aaj77g04
FJ370624.1 gg_id:359520 feces adult twins and mothers; TS57 clone TS57_a03c09
DQ803440.1 gg_id:188945 human fecal clone RL251_aaj85g11
DQ803485.1 gg_id:181226 human fecal clone RL251_aaj86d09
EU460987.1 gg_id:293389 red kangaroo feces clone KO1_aai41f04
EU771800.1 gg_id:356581 African elephant feces clone AFEL2_aao29b06
DQ057459.1 gg_id:130214 str. ic1296
DQ805983.1 gg_id:186994 human fecal clone RL186_aah59e06
DQ797262.1 gg_id:198626 human fecal clone RL248_aai97a11
DQ799354.1 gg_id:193868 human fecal clone RL305aal85c08
DQ799334.1 gg_id:176070 human fecal clone RL305aal85a09
FJ674172.1 gg_id:510818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800278.1 gg_id:179866 human fecal clone RL303_aal70g01
DQ801693.1 gg_id:183940 human fecal clone RL201_aai45e12
DQ804358.1 gg_id:189998 human fecal clone RL187_aan78e11
DQ801564.1 gg_id:198752 human fecal clone RL117_aae91d03
DQ808168.1 gg_id:187796 human fecal clone RL180_aao73d11

DQ795429.1	193842	34.8	93.1	66.8	68.0	115.5	35.1
DQ326454.1	146226	53.3	57.9	127.2	61.1	76.2	37.0
EU466824.1	289535	10.8	41.2	72.5	76.5	58.8	26.3
DQ808076.1	183267	152.5	89.8	165.6	94.4	122.3	64.4
DQ825011.1	198532	2284.3	2941.9	3225.4	2981.3	2552.7	2684.1
DQ807333.1	196082	21.9	35.8	78.5	62.5	63.2	36.6
DQ808105.1	187385	4616.3	3564.1	3674.5	2952.4	6252.3	3504.1
DQ801994.1	194896	1598.3	2287.4	650.7	1025.1	3276.8	1723.5
DQ807015.1	185563	34.0	43.4	22.3	58.1	58.2	26.1
DQ808195.1	183824	2267.7	2002.4	1919.8	1317.9	1259.5	1483.3
DQ810151.1	186621	126.3	155.4	425.1	145.3	536.6	346.3
DQ794894.1	174093	42.1	67.4	57.8	67.6	75.4	36.2
EU779348.1	303897	640.7	486.8	1582.0	1464.7	218.2	568.9
DQ825110.1	197657	21.2	38.5	139.8	59.3	181.0	93.2
DQ808200.1	179609	605.7	868.8	397.4	131.2	224.6	110.1
DQ799237.1	191132	498.9	532.8	273.4	157.5	545.3	245.2
DQ800722.1	178016	7183.3	8366.4	3408.5	5960.5	5904.9	7008.1
DQ802815.1	184861	1461.0	1776.7	398.9	163.3	625.7	334.5
DQ795471.1	197050	2266.5	2196.1	2511.5	2970.5	4370.3	3351.5
EU771766.1	336948	59.6	74.6	169.3	90.1	129.6	126.4
DQ326114.1	148619	255.2	129.7	694.4	147.7	63.3	105.6
DQ802802.1	173917	28.9	45.0	34.4	63.5	69.1	27.6
DQ800314.1	181003	3234.0	4359.4	2063.8	1904.0	1972.5	1257.9
DQ808280.1	193210	417.7	317.6	531.7	243.9	609.5	489.7
DQ823693.1	191950	3663.5	3751.6	2968.8	4305.1	4098.8	3626.5
FJ370624.1	359520	4270.6	5455.6	1416.0	3905.5	4671.9	2523.3
DQ803440.1	188945	3192.1	2944.1	1751.1	3950.4	6769.1	5750.9
DQ803485.1	181226	193.7	113.4	200.5	286.9	86.7	65.9
EU460987.1	293389	88.7	254.9	336.6	144.1	172.8	176.4
EU771800.1	356581	1141.4	1489.2	416.0	497.5	2262.6	367.3
DQ057459.1	130214	83.0	137.9	196.3	83.3	96.0	70.7
DQ805983.1	186994	2391.4	1408.9	377.3	466.0	1205.1	354.5
DQ797262.1	198626	91.3	190.9	318.1	506.5	168.7	252.0
DQ799354.1	193868	190.0	104.0	302.3	142.8	223.8	118.6
DQ799334.1	176070	652.7	562.9	947.7	388.9	247.7	554.3
FJ674172.1	510818	89.6	196.8	584.2	164.2	423.5	142.0
DQ800278.1	179866	42.5	54.5	28.8	76.8	87.3	36.3
DQ801693.1	183940	16192.2	12918.4	5468.6	10578.9	12527.3	13201.9
DQ804358.1	189998	1408.5	1593.9	1070.0	1673.8	1715.6	1350.4
DQ801564.1	198752	1230.9	1096.8	3832.8	284.7	305.9	338.1
DQ808168.1	187796	89.8	151.5	246.5	154.2	335.8	307.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20625
s__unclassified	20626
s__unclassified	20627
s__unclassified	20628
s__unclassified	20629
s__unclassified	20632
s__unclassified	20634
s__unclassified	20635
s__unclassified	20636
s__unclassified	20637
s__unclassified	20638
s__unclassified	20642
s__unclassified	20643
s__unclassified	20646
s__unclassified	20647
s__unclassified	20650
s__unclassified	20651
s__unclassified	20652
s__unclassified	20653
s__unclassified	20655
s__unclassified	20657
s__unclassified	20658
s__unclassified	20660
s__unclassified	20661
s__unclassified	20662
s__unclassified	20663
s__unclassified	20664
s__unclassified	20665
s__unclassified	20666
s__unclassified	20668
s__unclassified	20669
s__unclassified	20670
s__unclassified	20672
s__unclassified	20673
s__unclassified	20674
s__unclassified	20675
s__unclassified	20676
s__unclassified	20677
s__unclassified	20678
s__unclassified	20679
s__unclassified	20680

DQ823875.1 gg_id:188085 human fecal clone RL250_aaj80c05
EF404604.1 gg_id:208025 human fecal clone SJTU_C_13_39
FJ681567.1 gg_id:509707 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795306.1 gg_id:187002 human fecal clone RL178_aah52g06
DQ794954.1 gg_id:189588 human fecal clone RL310_aam38d06
GQ492255.1 gg_id:570706 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ800660.1 gg_id:185400 human fecal clone RL183_aao01g01
EU778183.1 gg_id:342468 feces clone RL388_aao94c02
EU766659.1 gg_id:332436 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EF403475.1 gg_id:214725 human fecal clone SJTU_A2_01_70
FJ369341.1 gg_id:359787 feces adult twins and mothers; TS50 clone TS50_a03c12
EU462921.1 gg_id:302090 southern three-banded armadillo feces clone arma_aaj55a07
GQ492965.1 gg_id:587062 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ796740.1 gg_id:177714 human fecal clone RL179_aao53h03
GQ493873.1 gg_id:571081 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ804656.1 gg_id:199135 human fecal clone RL187_aao71a01
DQ801910.1 gg_id:190027 human fecal clone RL201_aai48d05
FJ370830.1 gg_id:366957 feces adult twins and mothers; TS5 clone TS5_a01g05
FJ368442.1 gg_id:361708 feces adult twins and mothers; TS3 clone TS3_a04d06
DQ327155.1 gg_id:150223 Metagenomic gut microbiome healthy human stool clone E676
DQ808062.1 gg_id:176424 human fecal clone RL180_aan71f05
DQ808152.1 gg_id:198845 human fecal clone RL180_aao73c07
DQ808775.1 gg_id:188753 human fecal clone RL243_aai85b01
FJ365594.1 gg_id:360717 feces adult twins and mothers; TS20 clone TS20_a04g01
FJ367376.1 gg_id:359034 feces adult twins and mothers; TS29 clone TS29_a02g04
FJ673633.1 gg_id:519730 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF398335.1 gg_id:209425 human fecal clone SJTU_F_01_26
DQ824458.1 gg_id:188557 human fecal clone RL304_aal76c05
DQ795572.1 gg_id:193771 human fecal clone RL178_aan66d07
FJ365831.1 gg_id:363623 feces adult twins and mothers; TS21 clone TS21_a03e10
DQ809636.1 gg_id:179734 human fecal clone RL184_aan81h06
EU462008.1 gg_id:296699 black-handed spider monkey feces clone SPIM_aaj33c03
FJ363818.1 gg_id:362676 feces adult twins and mothers; TS14 clone TS14_a03g01
DQ804899.1 gg_id:179597 human fecal clone RL385_aao82c04
EU461755.1 gg_id:292588 mongoose lemur feces clone ML_aaj28c11
GQ046085.1 gg_id:408619 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AF371545.1 gg_id:71965 swine intestine clone p-2624-9F5
FJ368685.1 gg_id:368329 feces adult twins and mothers; TS49 clone TS49_a03c09
DQ805105.1 gg_id:188292 human fecal clone RL249_aaj81c09
DQ327067.1 gg_id:150231 Metagenomic gut microbiome healthy human stool clone E575
DQ796291.1 gg_id:185492 human fecal clone RL179_aah25c11

DQ823875.1	188085	2050.1	2412.3	1155.6	1469.5	2995.0	2348.2
EF404604.1	208025	172.9	314.3	755.5	194.5	373.2	418.5
FJ681567.1	509707	8106.0	7586.8	6279.9	7603.3	7741.0	9411.6
DQ795306.1	187002	30.7	59.8	25.8	66.6	62.1	25.5
DQ794954.1	189588	2417.6	2662.7	2693.8	2347.4	3545.1	3163.1
GQ492255.1	570706	5157.0	5143.1	5656.2	5426.9	4186.5	4290.0
DQ800660.1	185400	4090.2	3871.3	3864.6	4061.9	4282.1	3919.4
EU778183.1	342468	248.1	367.1	427.7	259.7	1649.9	919.3
EU766659.1	332436	34.4	63.2	181.4	66.9	74.3	43.2
EF403475.1	214725	28.5	25.9	53.4	62.6	62.9	30.4
FJ369341.1	359787	1998.5	1770.2	726.6	1772.1	4631.5	2723.1
EU462921.1	302090	81.9	139.6	153.6	89.5	85.4	68.0
GQ492965.1	587062	4153.3	3135.8	2969.2	5962.4	1811.5	1611.2
DQ796740.1	177714	14101.9	17542.9	5186.3	10582.2	10574.0	9216.5
GQ493873.1	571081	19.2	87.9	46.8	60.6	99.5	51.5
DQ804656.1	199135	7849.7	8010.8	9507.3	8032.8	10776.6	8541.2
DQ801910.1	190027	8957.2	10831.6	4741.0	7887.2	15884.4	13608.5
FJ370830.1	366957	13069.0	12925.3	4077.6	7970.3	6533.1	6193.7
FJ368442.1	361708	11051.0	9398.7	8050.9	5903.2	9017.9	8263.9
DQ327155.1	150223	43.8	63.6	81.5	64.8	62.8	65.0
DQ808062.1	176424	16830.2	13965.8	6686.5	10539.0	13998.7	11026.8
DQ808152.1	198845	38.1	29.2	163.2	45.3	56.4	20.7
DQ808775.1	188753	5444.5	6279.9	2025.8	3344.1	5580.7	3532.7
FJ365594.1	360717	121.3	190.6	374.6	362.5	69.1	118.4
FJ367376.1	359034	4900.9	6286.1	2491.9	3813.9	8392.7	7168.1
FJ673633.1	519730	2499.2	3092.8	1440.8	1621.9	1806.8	2138.1
EF398335.1	209425	4497.6	8687.1	2193.2	4522.5	7498.8	4910.7
DQ824458.1	188557	70.7	50.6	80.2	125.0	234.4	179.0
DQ795572.1	193771	1025.5	721.6	999.1	880.9	1270.7	1051.2
FJ365831.1	363623	514.9	481.9	821.0	741.7	811.9	385.3
DQ809636.1	179734	21.3	64.1	88.6	88.8	91.9	38.8
EU462008.1	296699	5937.5	5285.7	4445.3	7697.9	7177.8	5968.0
FJ363818.1	362676	2176.8	2638.7	1214.6	1630.8	3162.4	2686.4
DQ804899.1	179597	4740.0	6157.7	1297.2	1879.9	1725.0	1940.6
EU461755.1	292588	95.6	259.0	733.7	162.4	88.9	105.5
GQ046085.1	408619	2054.4	2060.3	3074.7	2170.6	2206.9	1449.5
AF371545.1	71965	234.6	377.7	445.7	112.9	169.5	213.1
FJ368685.1	368329	44.0	130.5	315.1	130.8	71.1	53.7
DQ805105.1	188292	154.7	297.0	222.1	115.8	100.2	86.6
DQ327067.1	150231	459.7	380.9	549.2	884.9	268.5	759.1
DQ796291.1	185492	325.8	452.4	924.6	155.0	603.6	325.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20682
s__unclassified	20683
s__unclassified	20684
s__unclassified	20685
s__unclassified	20686
s__unclassified	20687
s__unclassified	20688
s__unclassified	20689
s__unclassified	20690
s__unclassified	20691
s__unclassified	20692
s__unclassified	20693
s__unclassified	20695
s__unclassified	20696
s__unclassified	20697
s__unclassified	20700
s__unclassified	20701
s__unclassified	20703
s__unclassified	20704
s__unclassified	20705
s__unclassified	20706
s__unclassified	20708
s__unclassified	20709
s__unclassified	20711
s__unclassified	20712
s__unclassified	20713
s__unclassified	20714
s__unclassified	20715
s__unclassified	20717
s__unclassified	20720
s__unclassified	20721
s__unclassified	20722
s__unclassified	20723
s__unclassified	20725
s__unclassified	20726
s__unclassified	20727
s__unclassified	20729
s__unclassified	20730
s__unclassified	20732
s__unclassified	20734
s__unclassified	20735

DQ803581.1 gg_id:192013 human fecal clone RL251_aaj87g01
DQ802572.1 gg_id:182035 human fecal clone RL188_aan93e09
DQ803467.1 gg_id:178303 human fecal clone RL251_aaj86b08
DQ803488.1 gg_id:194155 human fecal clone RL251_aaj86e01
FJ834020.1 gg_id:540096 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q301_49A07
GQ491945.1 gg_id:560070 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ793395.1 gg_id:181678 human fecal clone RL199_aaj43b10
FJ365331.1 gg_id:358442 feces adult twins and mothers; TS20 clone TS20_a01f04
FJ367717.1 gg_id:357170 feces adult twins and mothers; TS2 clone TS2_a02g06
DQ823900.1 gg_id:178122 human fecal clone RL250_aaj80f07
DQ808806.1 gg_id:176621 human fecal clone RL243_aai85e04
DQ807520.1 gg_id:193431 human fecal clone RL307_aam07f07
FJ370181.1 gg_id:368835 feces adult twins and mothers; TS56 clone TS56_a01d07
DQ804460.1 gg_id:175586 human fecal clone RL187_aan80b09
EF398689.1 gg_id:204315 human fecal clone SJTU_F_05_07
FJ679312.1 gg_id:524376 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368258.1 gg_id:367873 feces adult twins and mothers; TS3 clone TS3_a02b04
DQ808355.1 gg_id:187289 human fecal clone RL180_aao75f07
FJ833986.1 gg_id:589328 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_82B11
DQ804066.1 gg_id:184882 human fecal clone RL187_aah68a02
GQ090418.1 gg_id:449524 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
FJ682063.1 gg_id:523934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ808292.1 gg_id:187565 human fecal clone RL180_aao74h05
FJ368724.1 gg_id:358242 feces adult twins and mothers; TS49 clone TS49_a03g02
EU779376.1 gg_id:341433 Somali Wild Ass feces clone WA_aaa01e03
DQ807930.1 gg_id:194523 human fecal clone RL180_aan69c06
DQ807157.1 gg_id:177252 human fecal clone RL244_aaj47a02
DQ803367.1 gg_id:178494 human fecal clone RL311_aam24f12
FJ369515.1 gg_id:361740 feces adult twins and mothers; TS51 clone TS51_a01e03
FJ674140.1 gg_id:532103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY960566.1 gg_id:115149 Clostridium sp. str. IE5
FJ364769.1 gg_id:364891 feces adult twins and mothers; TS19 clone TS19_a02h04
DQ804868.1 gg_id:188830 human fecal clone RL385_aao81g08
DQ804978.1 gg_id:185255 human fecal clone RL385_aao83e08
DQ797797.1 gg_id:184290 human fecal clone RL206_aaj16a02
FJ368622.1 gg_id:369716 feces adult twins and mothers; TS49 clone TS49_a02e03
DQ905909.1 gg_id:169429 human fecal clone 29c-e10
EU842917.1 gg_id:351299 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
FJ673517.1 gg_id:521392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ807843.1 gg_id:180481 human fecal clone RL180_aah37h04
FJ372363.1 gg_id:364213 feces adult twins and mothers; TS9 clone TS9_a04g03

DQ803581.1	192013	173.1	187.6	722.1	138.2	640.6	516.8
DQ802572.1	182035	112.6	103.1	88.4	138.7	153.2	199.8
DQ803467.1	178303	29.1	38.4	144.1	71.5	60.2	28.5
DQ803488.1	194155	90.6	79.8	87.8	87.7	142.0	70.6
FJ834020.1	540096	42.7	136.5	173.6	167.6	78.8	131.8
GQ491945.1	560070	1194.3	1821.8	1813.9	630.2	279.8	562.5
DQ793395.1	181678	39.4	50.5	131.7	58.8	63.0	61.0
FJ365331.1	358442	5873.4	5319.1	1322.5	6748.3	8686.8	7231.5
FJ367717.1	357170	56.8	60.1	168.2	102.8	63.6	68.8
DQ823900.1	178122	108.9	305.3	297.1	140.1	111.0	131.7
DQ808806.1	176621	51.2	42.7	100.1	64.4	56.2	34.2
DQ807520.1	193431	135.9	91.4	128.9	187.2	83.8	30.0
FJ370181.1	368835	324.6	290.8	207.1	115.4	200.4	47.2
DQ804460.1	175586	9413.4	10030.0	9161.1	8398.4	7559.6	6259.1
EF398689.1	204315	170.7	156.9	169.0	77.4	73.4	72.4
FJ679312.1	524376	95.8	69.7	453.2	98.9	103.3	61.2
FJ368258.1	367873	2681.8	3035.3	2415.1	1626.1	4615.9	4021.9
DQ808355.1	187289	5087.4	4371.9	3020.5	3589.2	3074.6	3111.0
FJ833986.1	589328	379.1	687.5	841.4	591.6	580.8	279.0
DQ804066.1	184882	22.4	28.2	48.0	40.1	76.8	24.2
GQ090418.1	449524	1730.0	2252.7	3446.4	1252.6	2446.7	1936.0
FJ682063.1	523934	2227.5	2299.0	127.7	165.6	324.4	61.1
DQ808292.1	187565	14.0	26.4	35.4	36.0	61.3	19.6
FJ368724.1	358242	5138.9	3965.4	1790.6	5746.2	6681.3	5590.7
EU779376.1	341433	2812.3	4131.4	1273.4	116.2	2062.9	2405.2
DQ807930.1	194523	170.3	123.1	147.0	385.2	73.6	44.6
DQ807157.1	177252	784.3	1068.5	1779.6	1502.9	3704.2	5147.1
DQ803367.1	178494	74.8	61.4	91.5	93.1	239.6	213.9
FJ369515.1	361740	1299.7	1334.8	122.3	76.9	92.7	55.2
FJ674140.1	532103	4198.3	4892.6	4121.0	3767.5	6482.9	6370.4
AY960566.1	115149	104.4	68.9	383.3	65.6	122.4	46.4
FJ364769.1	364891	13363.4	11873.8	14397.1	10426.5	12000.4	12081.4
DQ804868.1	188830	20.6	22.1	101.0	45.2	49.1	10.7
DQ804978.1	185255	385.8	585.5	351.2	304.3	536.9	372.7
DQ797797.1	184290	160.2	323.0	622.5	264.4	750.7	829.4
FJ368622.1	369716	21.4	31.1	21.4	55.7	61.0	18.0
DQ905909.1	169429	60.9	126.7	48.4	69.6	82.3	40.1
EU842917.1	351299	4728.4	4985.2	5696.0	3796.0	3229.4	3978.7
FJ673517.1	521392	94.9	155.7	802.2	169.1	109.0	156.6
DQ807843.1	180481	2611.7	2798.0	922.2	2027.5	1009.8	1130.7
FJ372363.1	364213	15.5	19.5	12.5	39.3	37.9	17.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20736
s__unclassified	20737
s__unclassified	20738
s__unclassified	20740
s__unclassified	20741
s__unclassified	20743
s__unclassified	20746
s__unclassified	20748
s__unclassified	20750
s__unclassified	20754
s__unclassified	20755
s__unclassified	20757
s__unclassified	20758
s__unclassified	20759
s__unclassified	20761
s__unclassified	20763
s__unclassified	20764
s__unclassified	20765
s__unclassified	20768
s__unclassified	20770
s__unclassified	20771
s__unclassified	20773
s__unclassified	20774
s__unclassified	20776
s__unclassified	20777
s__unclassified	20780
s__unclassified	20781
s__unclassified	20784
s__unclassified	20785
s__unclassified	20786
s__unclassified	20787
s__unclassified	20789
s__unclassified	20790
s__unclassified	20791
s__unclassified	20792
s__unclassified	20793
s__unclassified	20794
s__unclassified	20796
s__unclassified	20797
s__unclassified	20798
s__unclassified	20800

DQ800760.1 gg_id:184185 human fecal clone RL183_aao03b04
DQ807941.1 gg_id:197208 human fecal clone RL180_aan69e04
FJ673378.1 gg_id:515300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800119.1 gg_id:192899 human fecal clone RL247_aaj24d07
GQ493994.1 gg_id:583043 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ804040.1 gg_id:194148 human fecal clone RL187_aah67e08
FJ369151.1 gg_id:362193 feces adult twins and mothers; TS4 clone TS4_a04h05
AF371547.1 gg_id:22923 swine intestine clone p-2465-18B5
FJ680876.1 gg_id:518515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ794465.1 gg_id:175434 human fecal clone RL197_aah88c03
DQ795202.1 gg_id:179436 human fecal clone RL178_aah51e01
DQ794420.1 gg_id:181675 human fecal clone RL197_aah87e07
FJ363299.1 gg_id:358542 feces adult twins and mothers; TS149 clone TS149_a01f02
EU466833.1 gg_id:299620 African elephant feces clone AFEL2_aao30b02
EU469499.1 gg_id:288896 black lemur feces clone BKLE_a01_2
FJ680899.1 gg_id:531159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799771.1 gg_id:184890 human fecal clone RL182_aah33c01
EU462827.1 gg_id:290477 southern three-banded armadillo feces clone arma_aaj53f10
DQ799073.1 gg_id:192246 human fecal clone RL205_aaj17c03
GQ896789.1 gg_id:574406 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ804493.1 gg_id:188479 human fecal clone RL187_aan80g04
AY983069.1 gg_id:122341 human descending colon mucosal biopsy clone L312
DQ801581.1 gg_id:173802 human fecal clone RL117_aae91h12
DQ326186.1 gg_id:148423 Metagenomic gut microbiome healthy human stool clone C092
FJ677211.1 gg_id:514970 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ367463.1 gg_id:363302 feces adult twins and mothers; TS29 clone TS29_a03h04
FJ365713.1 gg_id:359758 feces adult twins and mothers; TS21 clone TS21_a02b04
FJ369196.1 gg_id:357975 feces adult twins and mothers; TS50 clone TS50_a01d06
EF398925.1 gg_id:204830 human fecal clone SJTU_F_09_12
EU462231.1 gg_id:294476 chimpanzee feces clone CHIMP1_aaj38a07
FJ367949.1 gg_id:356869 feces adult twins and mothers; TS30 clone TS30_a01f03
DQ804026.1 gg_id:186234 human fecal clone RL187_aah67c08
DQ794963.1 gg_id:178221 human fecal clone RL310_aam38e05
FJ681816.1 gg_id:516988 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682724.1 gg_id:511020 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ369965.1 gg_id:366165 feces adult twins and mothers; TS55 clone TS55_a02g10
EF398293.1 gg_id:208184 human fecal clone SJTU_F_01_72
DQ805689.1 gg_id:178495 human fecal clone RL306aal89g12
DQ804024.1 gg_id:179715 human fecal clone RL187_aah67c06
FJ879925.1 gg_id:413935 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
DQ806925.1 gg_id:195679 human fecal clone RL198_aaj75e07

DQ800760.1	184185	35.5	197.6	580.1	117.9	371.4	446.2
DQ807941.1	197208	178.5	161.9	65.6	162.3	143.0	101.7
FJ673378.1	515300	7491.6	8226.0	6807.9	6705.8	8955.9	8155.3
DQ800119.1	192899	508.6	1024.1	1549.8	1162.9	2723.3	2712.9
GQ493994.1	583043	6638.8	10210.9	3833.9	4803.4	13022.6	10284.5
DQ804040.1	194148	192.0	275.2	182.7	151.0	74.1	55.5
FJ369151.1	362193	1574.4	1448.0	793.4	488.8	1691.0	1132.3
AF371547.1	22923	14.9	18.8	13.2	32.1	55.4	20.4
FJ680876.1	518515	2594.4	2239.7	1157.9	517.1	3227.1	2110.8
DQ794465.1	175434	3517.6	4142.9	4413.2	4554.3	10303.0	7991.1
DQ795202.1	179436	35.2	54.5	80.7	61.2	58.3	31.5
DQ794420.1	181675	30.2	21.7	15.9	49.3	68.8	18.2
FJ363299.1	358542	93.4	132.2	258.1	146.3	327.3	416.0
EU466833.1	299620	91.9	71.1	136.3	93.3	92.5	49.4
EU469499.1	288896	14653.4	16053.0	10765.7	11916.8	15139.2	10872.4
FJ680899.1	531159	10003.1	8329.9	5742.4	8713.9	14903.2	12736.7
DQ799771.1	184890	45.3	67.1	94.8	101.9	85.5	38.0
EU462827.1	290477	102.8	247.2	330.0	127.2	100.0	121.9
DQ799073.1	192246	33.4	57.9	69.8	81.6	77.0	83.8
GQ896789.1	574406	3626.3	3915.5	4300.1	4517.0	6122.0	6208.7
DQ804493.1	188479	1517.2	1930.4	1644.5	1385.8	2760.0	2591.5
AY983069.1	122341	347.9	247.0	637.3	996.4	118.0	193.4
DQ801581.1	173802	2840.8	3807.0	473.8	1718.3	4481.1	2382.9
DQ326186.1	148423	76.6	168.4	420.9	176.4	346.7	40.7
FJ677211.1	514970	46.3	84.7	349.5	120.1	73.7	92.6
FJ367463.1	363302	1666.7	2323.1	2337.4	1467.3	5470.3	2534.8
FJ365713.1	359758	1726.6	1715.1	1477.4	1602.1	278.2	496.9
FJ369196.1	357975	5444.9	4355.5	5681.8	4826.4	3971.0	3971.1
EF398925.1	204830	5787.8	5778.0	3836.6	5986.9	4471.9	5269.3
EU462231.1	294476	40.7	95.2	129.3	66.3	72.1	76.9
FJ367949.1	356869	12322.1	13161.5	8375.7	9252.9	14216.8	11024.6
DQ804026.1	186234	2490.7	3197.6	497.5	2546.4	914.7	671.4
DQ794963.1	178221	53.0	44.5	66.8	77.7	58.3	37.3
FJ681816.1	516988	1602.3	1665.9	589.7	1813.3	1245.2	1264.5
FJ682724.1	511020	57.6	61.5	93.0	59.4	52.4	28.5
FJ369965.1	366165	1001.9	495.8	453.2	1060.3	3909.2	2503.0
EF398293.1	208184	1340.3	832.4	1645.6	1903.7	346.1	718.5
DQ805689.1	178495	2699.5	2958.9	2170.1	1638.9	5034.3	3476.1
DQ804024.1	179715	4899.1	5621.1	3019.1	5207.7	2065.5	3341.1
FJ879925.1	413935	59.1	84.8	229.5	63.4	49.5	45.1
DQ806925.1	195679	67.4	54.7	93.2	87.6	64.2	25.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20801
s__unclassified	20802
s__unclassified	20803
s__unclassified	20808
s__unclassified	20809
s__unclassified	20811
s__unclassified	20814
s__unclassified	20815
s__unclassified	20816
s__unclassified	20819
s__unclassified	20820
s__unclassified	20821
s__unclassified	20822
s__unclassified	20823
s__unclassified	20824
s__unclassified	20825
s__unclassified	20826
s__unclassified	20828
s__unclassified	20829
s__unclassified	20830
s__unclassified	20831
s__unclassified	20832
s__unclassified	20833
s__unclassified	20836
s__unclassified	20837
s__unclassified	20839
s__unclassified	20840
s__unclassified	20843
s__unclassified	20845
s__unclassified	20846
s__unclassified	20847
s__unclassified	20848
s__unclassified	20849
s__unclassified	20850
s__unclassified	20853
s__unclassified	20854
s__unclassified	20856
s__unclassified	20857
s__unclassified	20858
s__unclassified	20859
s__unclassified	20860

FJ676219.1 gg_id:518016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU779326.1 gg_id:342613 Visayam Warty Pig feces clone VWP_aaa04e07
EU762797.1 gg_id:305632 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
EU465456.1 gg_id:295217 lion feces clone LI3_aah77f05
DQ824386.1 gg_id:198143 human fecal clone RL304_aal75d10
FJ366844.1 gg_id:365869 feces adult twins and mothers; TS27 clone TS27_a04e06
EU472527.1 gg_id:292228 Angola colobus feces clone EAC_2_aaa01b11
DQ810056.1 gg_id:191139 human fecal clone RL184_aao67e12
FJ673488.1 gg_id:515386 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679798.1 gg_id:524019 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795686.1 gg_id:177349 human fecal clone RL178_aan68e07
EU458491.1 gg_id:299304 spotted hyena feces clone HY2_a04_1
FJ678819.1 gg_id:517547 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368482.1 gg_id:367763 feces adult twins and mothers; TS3 clone TS3_a04h07
DQ795187.1 gg_id:174286 human fecal clone RL178_aah51c05
DQ805632.1 gg_id:187239 human fecal clone RL306aal89b12
EU778834.1 gg_id:333694 Black-handed Spider Monkey feces clone SPIM_aaj35b11
FJ678972.1 gg_id:524202 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ794571.1 gg_id:192840 human fecal clone RL240_aaj29g04
FJ367473.1 gg_id:366237 feces adult twins and mothers; TS29 clone TS29_a04a02
FJ368067.1 gg_id:362389 feces adult twins and mothers; TS30 clone TS30_a03f01
DQ808129.1 gg_id:191317 human fecal clone RL180_aao73a06
DQ798248.1 gg_id:195606 human fecal clone RL181_aah39e05
DQ803705.1 gg_id:199487 human fecal clone RL200_aai57d05
FJ369569.1 gg_id:361208 feces adult twins and mothers; TS51 clone TS51_a02b04
DQ804787.1 gg_id:174796 human fecal clone RL187_aao72f12
DQ809680.1 gg_id:190956 human fecal clone RL184_aan82e07
DQ800120.1 gg_id:174967 human fecal clone RL247_aaj24d08
EU467144.1 gg_id:292859 mongoose lemur feces clone ML_aae89e06
GQ492618.1 gg_id:572387 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ799584.1 gg_id:198805 human fecal clone RL305aal88a01
EU462126.1 gg_id:300629 black-handed spider monkey feces clone SPIM_aaj35d04
EU778853.1 gg_id:343716 Black-handed Spider Monkey feces clone SPIM_aaj34h02
FJ368580.1 gg_id:364581 feces adult twins and mothers; TS49 clone TS49_a02a03
EU778515.1 gg_id:317113 Red river hog feces clone RRH_aaa03d05
DQ801893.1 gg_id:176898 human fecal clone RL201_aai48b10
GQ002337.1 gg_id:507325 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176c02
EU764414.1 gg_id:334570 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ680085.1 gg_id:516004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ824108.1 gg_id:184288 human fecal clone RL204_aaj59d11
EU776698.1 gg_id:303452 Lion feces clone LI3_aah78h03

FJ676219.1	518016	4491.3	4962.7	4215.3	5547.5	11077.5	7670.9
EU779326.1	342613	49.4	55.6	131.6	78.7	71.4	32.4
EU762797.1	305632	925.6	932.4	431.3	553.2	944.0	514.5
EU465456.1	295217	45.4	39.8	78.2	47.0	72.3	30.0
DQ824386.1	198143	199.2	371.3	233.1	364.3	204.7	474.1
FJ366844.1	365869	1845.8	2620.5	1343.9	1612.8	3279.9	2680.0
EU472527.1	292228	1634.1	1209.1	1801.1	1715.5	2836.5	1639.3
DQ810056.1	191139	937.6	189.1	2371.6	4295.3	62.5	35.8
FJ673488.1	515386	3039.3	2319.2	761.2	851.6	1354.7	478.2
FJ679798.1	524019	4425.0	3146.1	1810.0	4171.0	6275.1	7712.5
DQ795686.1	177349	375.1	477.2	993.1	165.9	1903.5	1009.6
EU458491.1	299304	33.7	75.0	211.1	99.9	40.0	35.1
FJ678819.1	517547	3738.9	3790.4	3087.5	4106.0	4508.2	4338.7
FJ368482.1	367763	27.8	52.6	74.1	70.9	47.8	20.8
DQ795187.1	174286	3511.6	3080.2	1281.2	2246.1	1804.5	1545.6
DQ805632.1	187239	7498.4	6991.7	6131.8	5975.0	841.1	5599.2
EU778834.1	333694	93.8	158.7	426.2	92.8	84.6	106.0
FJ678972.1	524202	2905.3	3006.1	2093.7	4112.7	2944.7	3928.7
DQ794571.1	192840	369.0	289.4	921.8	301.5	90.2	168.4
FJ367473.1	366237	1770.3	2453.8	4634.9	2328.1	1724.1	2246.0
FJ368067.1	362389	9922.9	12570.9	8151.0	9487.3	13306.9	12983.0
DQ808129.1	191317	2742.4	2143.3	1098.9	2090.0	3111.2	2288.4
DQ798248.1	195606	387.8	912.7	189.4	96.2	413.7	194.5
DQ803705.1	199487	8733.3	11237.7	6736.2	7560.7	11341.1	13463.9
FJ369569.1	361208	1372.5	1338.7	225.7	312.8	124.0	119.5
DQ804787.1	174796	54.7	49.6	96.5	76.9	74.5	38.4
DQ809680.1	190956	3823.2	4639.7	2817.1	4542.6	7959.5	7346.9
DQ800120.1	174967	29.6	30.0	78.3	35.1	53.2	31.5
EU467144.1	292859	1456.2	2213.5	912.4	629.9	2766.0	1510.8
GQ492618.1	572387	1838.6	4115.8	3331.1	814.4	1909.0	2666.5
DQ799584.1	198805	10092.9	9324.0	5514.9	9199.0	6261.1	7312.0
EU462126.1	300629	192.2	233.7	966.2	553.9	98.1	92.1
EU778853.1	343716	261.5	251.1	390.7	326.5	316.3	1237.1
FJ368580.1	364581	2456.9	2546.9	2826.2	4466.2	3177.1	2073.2
EU778515.1	317113	186.5	572.3	357.7	162.5	1401.6	909.2
DQ801893.1	176898	606.5	406.4	240.2	955.7	149.2	145.7
GQ002337.1	507325	378.3	583.4	623.8	401.8	1004.0	1389.6
EU764414.1	334570	26.6	64.3	131.9	67.1	63.2	40.1
FJ680085.1	516004	8671.9	8640.7	4882.0	7932.7	6984.6	7640.1
DQ824108.1	184288	813.9	1287.9	1300.6	480.0	1850.3	886.9
EU776698.1	303452	4261.7	5138.7	4194.2	4004.2	6966.0	6257.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20862
s__unclassified	20863
s__unclassified	20864
s__unclassified	20865
s__unclassified	20866
s__unclassified	20867
s__unclassified	20868
s__unclassified	20869
s__unclassified	20870
s__unclassified	20872
s__unclassified	20873
s__unclassified	20874
s__unclassified	20875
s__unclassified	20876
s__unclassified	20877
s__unclassified	20878
s__unclassified	20879
s__unclassified	20880
s__unclassified	20881
s__unclassified	20883
s__unclassified	20885
s__unclassified	20886
s__unclassified	20887
s__unclassified	20888
s__unclassified	20889
s__unclassified	20890
s__unclassified	20891
s__unclassified	20893
s__unclassified	20894
s__unclassified	20895
s__unclassified	20897
s__unclassified	20898
s__unclassified	20900
s__unclassified	20902
s__unclassified	20904
s__unclassified	20905
s__unclassified	20906
s__unclassified	20910
s__unclassified	20911
s__unclassified	20912
s__unclassified	20913

DQ799729.1 gg_id:199570 human fecal clone RL182_aah32c02
DQ809417.1 gg_id:188472 human fecal clone RL184_aah20f03
DQ805441.1 gg_id:184344 human fecal clone RL203_aai62f08
AF357567.1 gg_id:73388 mpn-isolate group 19
FJ676500.1 gg_id:510563 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AF132274.1 gg_id:72420 adult human fecal matter clone adhufec52
DQ804933.1 gg_id:196581 human fecal clone RL385_aao82g10
DQ804952.1 gg_id:187432 human fecal clone RL385_aao83b03
EU462096.1 gg_id:287668 black-handed spider monkey feces clone SPIM_aaj34h11
FJ673623.1 gg_id:509645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801879.1 gg_id:174348 human fecal clone RL201_aai48a04
AF153853.1 gg_id:13992 faecal clone adhufec35.25
DQ796760.1 gg_id:194745 human fecal clone RL179_aao54b03
FJ363676.1 gg_id:362514 feces adult twins and mothers; TS14 clone TS14_a02a05
FJ366409.1 gg_id:358537 feces adult twins and mothers; TS26 clone TS26_a02g06
DQ808220.1 gg_id:197652 human fecal clone RL180_aao74a10
FJ682086.1 gg_id:531472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ904728.1 gg_id:166362 human fecal clone 001-h6
DQ804935.1 gg_id:182308 human fecal clone RL385_aao82h01
DQ796155.1 gg_id:178646 human fecal clone RL202_aai52d05
GQ492609.1 gg_id:553609 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ326200.1 gg_id:145758 Metagenomic gut microbiome healthy human stool clone C115
DQ798716.1 gg_id:198766 human fecal clone RL181_aao00e02
FJ371877.1 gg_id:365497 feces adult twins and mothers; TS8 clone TS8_a03c04
NZ_AAVO02000004.1 gg_id:470971 Ruminococcus obeum str. ATCC 29174
EU776277.1 gg_id:340251 Red Kangaroo feces clone KO1_aai41g04
FJ364807.1 gg_id:358558 feces adult twins and mothers; TS19 clone TS19_a03d03
AY981223.1 gg_id:126425 human sigmoid colon mucosal biopsy clone G186
DQ807835.1 gg_id:198325 human fecal clone RL180_aah37g06
FJ368592.1 gg_id:368630 feces adult twins and mothers; TS49 clone TS49_a02b05
EF401712.1 gg_id:208349 human fecal clone SJTU_D_14_18
EU468139.1 gg_id:290228 lion feces clone LI1_c04
DQ807766.1 gg_id:193852 human fecal clone RL180_aah37a01
FJ366613.1 gg_id:364141 feces adult twins and mothers; TS27 clone TS27_a01g04
DQ799635.1 gg_id:192476 human fecal clone RL305aal88e08
DQ795414.1 gg_id:174625 human fecal clone RL178_aah54a12
DQ808431.1 gg_id:176519 human fecal clone RL180_aao76e04
FJ364646.1 gg_id:364097 feces adult twins and mothers; TS19 clone TS19_a01d06
DQ796801.1 gg_id:191021 human fecal clone RL179_aao54f11
FJ678562.1 gg_id:517282 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY983064.1 gg_id:125001 human descending colon mucosal biopsy clone L306

DQ799729.1	199570	134.4	238.2	353.6	124.9	1236.3	670.8
DQ809417.1	188472	2129.4	1925.7	980.6	768.3	3144.9	1503.0
DQ805441.1	184344	435.6	741.7	734.7	354.0	921.7	976.4
AF357567.1	73388	57.6	92.4	344.6	115.3	69.1	267.0
FJ676500.1	510563	2053.1	1437.2	499.2	1514.5	1205.4	482.3
AF132274.1	72420	5990.9	4303.2	3713.7	5432.7	2543.2	3572.1
DQ804933.1	196581	26.4	39.3	75.4	68.7	50.0	29.1
DQ804952.1	187432	776.5	1514.7	757.0	1494.6	1806.3	1462.1
EU462096.1	287668	972.7	987.9	901.3	988.1	1012.4	785.7
FJ673623.1	509645	4651.6	4333.3	2482.4	3696.6	4291.1	4343.4
DQ801879.1	174348	99.9	200.8	74.0	111.5	300.5	286.6
AF153853.1	13992	756.0	595.0	492.9	789.1	774.0	1923.4
DQ796760.1	194745	526.9	672.9	455.0	162.3	607.7	330.5
FJ363676.1	362514	3247.3	3585.4	5307.2	4057.4	5575.9	6072.7
FJ366409.1	358537	2640.7	2586.7	971.5	2698.9	6490.7	5301.1
DQ808220.1	197652	221.0	260.6	429.2	173.5	1399.4	1196.3
FJ682086.1	531472	3970.8	3493.2	1384.5	853.5	1204.4	494.5
DQ904728.1	166362	1004.1	1587.9	388.9	1313.0	283.2	545.6
DQ804935.1	182308	18.7	24.0	27.2	50.0	53.0	17.6
DQ796155.1	178646	44.0	120.9	206.2	74.1	81.6	28.6
GQ492609.1	553609	4489.5	6814.3	2849.9	4361.5	8124.6	8870.0
DQ326200.1	145758	1716.1	1690.6	573.0	458.1	1039.8	379.9
DQ798716.1	198766	520.9	328.4	693.3	1303.3	375.9	301.2
FJ371877.1	365497	4786.9	4133.3	3542.0	5147.1	8643.0	9250.5
NZ_AAVO02000004.1	470971	60.4	115.3	75.0	122.0	61.5	53.4
EU776277.1	340251	118.7	192.8	368.8	191.2	194.8	156.0
FJ364807.1	358558	11627.5	16036.0	4915.3	9850.3	14323.0	12494.4
AY981223.1	126425	1018.9	826.8	212.4	903.9	232.3	14.2
DQ807835.1	198325	353.9	277.7	341.1	229.5	203.5	85.6
FJ368592.1	368630	26.1	54.5	153.1	79.4	64.8	59.1
EF401712.1	208349	2511.1	2697.0	2989.4	1511.4	4987.8	3294.7
EU468139.1	290228	2552.8	3076.4	3124.8	2262.8	2772.0	2712.7
DQ807766.1	193852	4177.1	3442.8	963.6	2898.0	376.9	1234.7
FJ366613.1	364141	4877.5	5092.8	3866.3	4121.8	3555.0	3858.0
DQ799635.1	192476	1316.7	1541.3	842.5	950.3	2170.0	1121.5
DQ795414.1	174625	245.7	150.9	344.5	203.7	92.0	113.0
DQ808431.1	176519	83.2	121.5	528.3	210.4	518.6	431.9
FJ364646.1	364097	1394.7	1414.4	747.5	1069.4	1784.6	1113.3
DQ796801.1	191021	5628.8	6344.9	5056.7	5671.0	4384.5	4597.7
FJ678562.1	517282	890.3	756.1	725.4	487.1	700.7	219.6
AY983064.1	125001	612.8	1038.7	1510.6	738.4	2085.1	1276.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20914
s__unclassified	20915
s__unclassified	20916
s__unclassified	20917
s__unclassified	20919
s__unclassified	20920
s__unclassified	20921
s__unclassified	20923
s__unclassified	20924
s__unclassified	20925
s__unclassified	20926
s__unclassified	20927
s__unclassified	20929
s__unclassified	20930
s__unclassified	20931
s__unclassified	20932
s__unclassified	20935
s__unclassified	20936
s__unclassified	20941
s__unclassified	20944
s__unclassified	20946
s__unclassified	20947
s__unclassified	20948
s__unclassified	20953
s__unclassified	20954
s__unclassified	20955
s__unclassified	20956
s__unclassified	20959
s__unclassified	20960
s__unclassified	20961
s__unclassified	20963
s__unclassified	20965
s__unclassified	20966
s__unclassified	20967
s__unclassified	20968
s__unclassified	20969
s__unclassified	20971
s__unclassified	20973
s__unclassified	20974
s__unclassified	20976
s__unclassified	20979

DQ796784.1 gg_id:196862 human fecal clone RL179_aao54d10
FJ366261.1 gg_id:358843 feces adult twins and mothers; TS25 clone TS25_a04f01
FJ369162.1 gg_id:357114 feces adult twins and mothers; TS50 clone TS50_a01a06
DQ802535.1 gg_id:197244 human fecal clone RL188_aan93b03
DQ804262.1 gg_id:196986 human fecal clone RL187_aan77b05
DQ805430.1 gg_id:185521 human fecal clone RL203_aai62e04
FJ367768.1 gg_id:362466 feces adult twins and mothers; TS2 clone TS2_a03d05
FJ369199.1 gg_id:370044 feces adult twins and mothers; TS50 clone TS50_a01d09
DQ805300.1 gg_id:199508 human fecal clone RL249_aaj84g06
AJ133124.1 gg_id:22899 Ruminococcus luti str. bln9
DQ801236.1 gg_id:182962 human fecal clone RL116_aaf02b10
FJ362873.1 gg_id:368307 feces adult twins and mothers; TS13 clone TS13_a04c03
DQ825010.1 gg_id:187491 human fecal clone RL185_aao72c01
DQ806646.1 gg_id:188588 human fecal clone RL186_aao47b05
DQ905659.1 gg_id:163685 human fecal clone 014C-D5
DQ057417.1 gg_id:134268 chicken ileum/cecum clone oc44
DQ807155.1 gg_id:181330 human fecal clone RL244_aaj46h12
DQ797201.1 gg_id:187271 human fecal clone RL386_aao88c09
DQ804499.1 gg_id:185360 human fecal clone RL187_aan80h04
FJ367409.1 gg_id:361412 feces adult twins and mothers; TS29 clone TS29_a03b08
FJ363998.1 gg_id:358181 feces adult twins and mothers; TS150 clone TS150_a01g10
DQ801129.1 gg_id:183212 human fecal clone RL387_aao92f11
DQ802249.1 gg_id:189871 human fecal clone RL188_aah15a10
FJ370034.1 gg_id:368166 feces adult twins and mothers; TS55 clone TS55_a03f10
DQ805353.1 gg_id:196792 human fecal clone RL203_aai61e09
GQ493491.1 gg_id:545944 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU774067.1 gg_id:324163 Chimpanzee feces clone CHIMP1_c12
DQ798308.1 gg_id:188852 human fecal clone RL181_aah40e02
FJ363960.1 gg_id:369883 feces adult twins and mothers; TS150 clone TS150_a01d04
DQ802328.1 gg_id:182581 human fecal clone RL188_aah16b05
FJ366920.1 gg_id:360553 feces adult twins and mothers; TS28 clone TS28_a01d05
DQ803447.1 gg_id:196353 human fecal clone RL251_aaj85h09
DQ825323.1 gg_id:176089 human fecal clone RL185_aan88e07
DQ808188.1 gg_id:186103 human fecal clone RL180_aao73f09
DQ800214.1 gg_id:184636 human fecal clone RL303_aal69g02
FJ368971.1 gg_id:366601 feces adult twins and mothers; TS4 clone TS4_a02g01
EU475728.1 gg_id:300551 white-faced saki feces clone Saki_aaj63c03
FJ678854.1 gg_id:515724 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364216.1 gg_id:359342 feces adult twins and mothers; TS150 clone TS150_a04c10
DQ799793.1 gg_id:197502 human fecal clone RL182_aah33f10
FJ368939.1 gg_id:363739 feces adult twins and mothers; TS4 clone TS4_a02c12

DQ796784.1	196862	3201.8	3407.8	3072.8	3176.0	6386.6	4663.7
FJ366261.1	358843	16456.2	16295.3	11088.2	13225.0	15847.0	16458.0
FJ369162.1	357114	188.2	229.3	202.9	210.4	389.5	424.9
DQ802535.1	197244	488.1	399.7	1281.9	761.3	320.1	337.8
DQ804262.1	196986	3196.5	3650.8	991.9	3709.7	3613.7	1856.0
DQ805430.1	185521	423.4	1171.4	631.3	572.5	3908.6	1726.3
FJ367768.1	362466	4927.4	5506.6	1233.4	2171.9	1521.9	2092.4
FJ369199.1	370044	3084.8	4164.6	924.1	1805.6	1753.7	1577.3
DQ805300.1	199508	191.4	195.2	927.7	109.2	96.4	89.2
AJ133124.1	22899	380.9	382.1	455.5	215.5	203.8	241.2
DQ801236.1	182962	260.8	252.9	272.6	830.2	776.2	470.1
FJ362873.1	368307	220.5	205.9	218.3	115.9	79.8	95.2
DQ825010.1	187491	3385.2	3740.4	3285.2	3004.9	3561.2	2767.2
DQ806646.1	188588	1173.6	790.9	624.8	359.7	1130.1	366.9
DQ905659.1	163685	6386.8	6823.6	5951.7	5353.6	9333.9	8849.2
DQ057417.1	134268	3372.1	4075.7	1542.1	2346.5	3506.6	2827.9
DQ807155.1	181330	19.9	35.3	26.9	43.1	51.5	19.2
DQ797201.1	187271	128.5	46.4	168.7	72.3	62.0	54.8
DQ804499.1	185360	1492.2	1662.7	132.3	1762.7	3742.0	2345.7
FJ367409.1	361412	3631.0	3604.6	1017.4	2661.2	2869.6	2374.8
FJ363998.1	358181	1698.8	2416.4	1627.6	2755.1	4839.0	3796.6
DQ801129.1	183212	5159.9	4880.8	3898.5	4521.2	4979.9	5187.4
DQ802249.1	189871	854.9	1794.3	832.3	616.1	1071.6	583.0
FJ370034.1	368166	1881.8	2281.7	1968.6	1522.8	6001.8	3431.4
DQ805353.1	196792	1427.9	1640.0	3222.9	547.9	1555.9	1056.2
GQ493491.1	545944	1512.1	1186.3	618.1	582.1	925.9	427.7
EU774067.1	324163	29.9	81.8	290.4	73.4	74.8	118.6
DQ798308.1	188852	4420.7	3323.5	1245.4	6413.3	2922.6	2955.2
FJ363960.1	369883	71.9	153.5	134.9	96.8	353.0	142.7
DQ802328.1	182581	5586.7	5827.7	4606.3	5463.9	6646.9	5895.3
FJ366920.1	360553	1318.5	1656.3	771.9	1166.1	1599.7	1280.5
DQ803447.1	196353	1037.5	744.6	634.9	1303.7	197.8	258.4
DQ825323.1	176089	665.9	957.9	1251.1	698.5	3245.3	2940.4
DQ808188.1	186103	13.4	21.7	17.4	41.5	54.7	18.7
DQ800214.1	184636	2690.7	3980.6	1766.0	1549.5	5275.5	2830.1
FJ368971.1	366601	8283.8	7741.7	3143.9	10018.3	12580.8	10597.2
EU475728.1	300551	33.4	478.0	246.5	212.6	529.9	118.4
FJ678854.1	515724	3851.6	3858.0	1549.6	2783.5	3692.1	3189.1
FJ364216.1	359342	44.6	144.8	335.0	111.5	70.5	45.5
DQ799793.1	197502	4833.0	7125.5	3101.0	3858.9	6985.9	8585.1
FJ368939.1	363739	732.7	605.8	933.8	1435.9	1017.2	1072.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	20980
s__unclassified	20981
s__unclassified	20982
s__unclassified	20983
s__unclassified	20986
s__unclassified	20990
s__unclassified	20991
s__unclassified	20992
s__unclassified	20993
s__unclassified	20994
s__unclassified	20999
s__unclassified	21000
s__unclassified	21002
s__unclassified	21003
s__unclassified	21004
s__unclassified	21005
s__unclassified	21006
s__unclassified	21007
s__unclassified	21008
s__unclassified	21009
s__unclassified	21010
s__unclassified	21011
s__unclassified	21012
s__unclassified	21014
s__unclassified	21018
s__unclassified	21019
s__unclassified	21020
s__unclassified	21021
s__unclassified	21023
s__unclassified	21025
s__unclassified	21027
s__unclassified	21028
s__unclassified	21030
s__unclassified	21032
s__unclassified	21033
s__unclassified	21034
s__unclassified	21036
s__unclassified	21037
s__unclassified	21038
s__unclassified	21039
s__unclassified	21040

DQ800094.1 gg_id:193828 human fecal clone RL247_aaj24b02
DQ806736.1 gg_id:198868 human fecal clone RL186_aao48b04
FJ679989.1 gg_id:530488 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802544.1 gg_id:177692 human fecal clone RL188_aan93c02
DQ807801.1 gg_id:181955 human fecal clone RL180_aah37d03
EU461651.1 gg_id:294606 mongoose lemur feces clone ML_aaj26c12
FJ369921.1 gg_id:361609 feces adult twins and mothers; TS55 clone TS55_a02c11
DQ824342.1 gg_id:188584 human fecal clone RL304_aal74g05
DQ825086.1 gg_id:194112 human fecal clone RL185_aan85c02
DQ796199.1 gg_id:189049 human fecal clone RL179_aah23a09
EU774977.1 gg_id:308504 Flying Fox feces clone FF_-aag84a06
DQ798974.1 gg_id:198990 human fecal clone RL242_aaj99h04
EU466825.1 gg_id:297983 African elephant feces clone AFEL2_aao30a03
EU466972.1 gg_id:296298 African elephant feces clone AFEL2_aao32b02
FJ363105.1 gg_id:359560 feces adult twins and mothers; TS148 clone TS148_a03b04
DQ795166.1 gg_id:199748 human fecal clone RL178_aah51a02
DQ796431.1 gg_id:193150 human fecal clone RL179_aah28c03
DQ805262.1 gg_id:183936 human fecal clone RL249_aaj84a03
FJ369915.1 gg_id:367583 feces adult twins and mothers; TS55 clone TS55_a02c05
EU764574.1 gg_id:324741 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ679697.1 gg_id:516792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795521.1 gg_id:188166 human fecal clone RL178_aan65f02
FJ679919.1 gg_id:516653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU469802.1 gg_id:300479 western lowland gorilla feces clone GOR_aag71c05
AY442822.1 gg_id:99566 Ruminococcus sp. YE58
FJ370524.1 gg_id:368808 feces adult twins and mothers; TS57 clone TS57_a02a12
FJ365661.1 gg_id:365684 feces adult twins and mothers; TS21 clone TS21_a01e06
AM696975.1 gg_id:218995 sequencing libraries indoor dust clone BF0001B001
FJ363916.1 gg_id:370410 feces adult twins and mothers; TS14 clone TS14_a04h04
DQ800834.1 gg_id:188686 human fecal clone RL183_aao04a10
DQ806459.1 gg_id:174163 human fecal clone RL186_aan92h02
DQ801767.1 gg_id:189357 human fecal clone RL201_aai46e09
DQ803372.1 gg_id:191062 human fecal clone RL311_aam24g08
FJ681121.1 gg_id:519761 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU728792.1 gg_id:344947 Ruminococcus sp. str. DJF_VR70k1
FJ364765.1 gg_id:361855 feces adult twins and mothers; TS19 clone TS19_a02g10
DQ799858.1 gg_id:176933 human fecal clone RL247_aaj21a07
FJ365546.1 gg_id:369247 feces adult twins and mothers; TS20 clone TS20_a04b07
EU763193.1 gg_id:334957 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A>
FJ367161.1 gg_id:361308 feces adult twins and mothers; TS28 clone TS28_a04c03
GQ492131.1 gg_id:578713 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice

DQ800094.1	193828	1523.4	1588.1	1105.7	1011.1	2084.9	1055.0
DQ806736.1	198868	46.2	125.4	170.8	123.2	536.0	99.0
FJ679989.1	530488	67.3	49.7	342.3	97.1	81.5	63.0
DQ802544.1	177692	10275.4	9690.7	11141.3	6868.6	9506.3	8628.4
DQ807801.1	181955	27.7	59.5	353.2	66.8	71.4	199.3
EU461651.1	294606	145.7	421.1	203.3	69.1	252.5	240.9
FJ369921.1	361609	5812.4	5071.4	1701.3	1839.8	3581.8	3257.8
DQ824342.1	188584	5619.5	5240.0	2329.0	4507.8	10992.5	8341.6
DQ825086.1	194112	82.4	144.5	402.8	183.6	181.2	479.3
DQ796199.1	189049	88.6	89.9	153.2	88.0	77.9	41.4
EU774977.1	308504	6357.3	10302.8	4741.2	6239.9	11580.8	9676.6
DQ798974.1	198990	2626.2	3416.3	1140.3	2366.5	2965.3	2757.1
EU466825.1	297983	8242.2	5229.7	3235.9	5704.4	5022.8	5937.3
EU466972.1	296298	2446.9	3020.8	962.6	2586.8	2718.7	2331.0
FJ363105.1	359560	147.4	93.3	885.0	130.5	96.6	107.4
DQ795166.1	199748	47.2	51.2	92.6	79.5	71.0	46.8
DQ796431.1	193150	1015.1	695.3	465.3	406.3	596.6	204.2
DQ805262.1	183936	43.0	123.7	102.0	90.7	373.5	320.8
FJ369915.1	367583	23.8	49.0	90.0	66.3	71.2	29.9
EU764574.1	324741	118.5	95.2	535.3	99.9	66.0	37.4
FJ679697.1	516792	3252.6	4536.8	2288.4	2409.7	2982.5	3406.1
DQ795521.1	188166	140.7	109.9	150.9	179.5	95.7	112.1
FJ679919.1	516653	11872.1	13710.7	8851.2	11348.9	12378.0	9868.6
EU469802.1	300479	91.0	184.4	320.7	91.3	814.6	407.6
AY442822.1	99566	84.0	113.5	247.4	113.3	100.3	67.3
FJ370524.1	368808	235.4	227.8	431.9	112.1	155.1	184.4
FJ365661.1	365684	9385.0	8098.2	6333.4	5723.4	8933.7	7560.3
AM696975.1	218995	6386.7	6744.9	5238.0	5218.6	8114.5	7923.2
FJ363916.1	370410	151.8	139.5	282.8	170.4	193.4	137.7
DQ800834.1	188686	2974.3	2013.6	3105.6	3324.3	681.4	812.2
DQ806459.1	174163	4327.3	7263.1	3459.1	6967.5	7407.1	6075.4
DQ801767.1	189357	2400.2	1624.4	2260.9	4200.3	1768.2	949.5
DQ803372.1	191062	2566.3	2876.7	1145.5	1093.8	5340.5	3833.7
FJ681121.1	519761	446.3	409.4	76.4	120.3	185.2	103.1
EU728792.1	344947	65.9	464.7	569.5	182.6	75.4	66.0
FJ364765.1	361855	2592.2	3866.1	4150.9	4126.6	5791.8	5743.3
DQ799858.1	176933	1845.6	1475.2	1020.7	636.6	1858.3	1310.4
FJ365546.1	369247	742.5	1074.5	637.2	348.3	859.7	548.5
EU763193.1	334957	24.7	90.6	162.9	80.8	57.4	58.0
FJ367161.1	361308	3953.5	1387.1	394.0	448.3	1154.1	377.5
GQ492131.1	578713	1446.1	1906.5	823.4	1052.4	2431.7	1324.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21041
s__unclassified	21044
s__unclassified	21048
s__unclassified	21049
s__unclassified	21050
s__unclassified	21051
s__unclassified	21055
s__unclassified	21056
s__unclassified	21058
s__unclassified	21059
s__unclassified	21060
s__unclassified	21062
s__unclassified	21063
s__unclassified	21064
s__unclassified	21065
s__unclassified	21066
s__unclassified	21067
s__unclassified	21068
s__unclassified	21070
s__unclassified	21071
s__unclassified	21075
s__unclassified	21076
s__unclassified	21079
s__unclassified	21080
s__unclassified	21081
s__unclassified	21082
s__unclassified	21083
s__unclassified	21084
s__unclassified	21086
s__unclassified	21087
s__unclassified	21089
s__unclassified	21090
s__unclassified	21091
s__unclassified	21092
s__unclassified	21095
s__unclassified	21096
s__unclassified	21099
s__unclassified	21100
s__unclassified	21101
s__unclassified	21105
s__unclassified	21106

EU778140.1 gg_id:323778 feces clone RL388_aao95c12
FJ682155.1 gg_id:519441 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797815.1 gg_id:173975 human fecal clone RL206_aaj16b08
GQ492839.1 gg_id:585610 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ799779.1 gg_id:189842 human fecal clone RL182_aah33d09
DQ326493.1 gg_id:148279 Metagenomic gut microbiome healthy human stool clone C591
DQ326406.1 gg_id:149236 Metagenomic gut microbiome healthy human stool clone C448
FJ677824.1 gg_id:529004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ327590.1 gg_id:145858 Metagenomic gut microbiome healthy human stool clone EB76
GQ491902.1 gg_id:576504 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU773407.1 gg_id:311080 Black lemur feces clone BKLE_c10_3
DQ804121.1 gg_id:175988 human fecal clone RL187_aah68h08
DQ808356.1 gg_id:181831 human fecal clone RL180_aao75f08
DQ795593.1 gg_id:194234 human fecal clone RL178_aan66g03
DQ803639.1 gg_id:187496 human fecal clone RL251_aaj88e10
DQ800645.1 gg_id:180900 human fecal clone RL183_aao01e03
DQ825047.1 gg_id:191384 human fecal clone RL185_aao72f11
DQ808011.1 gg_id:174599 human fecal clone RL180_aan70f05
FJ367398.1 gg_id:368950 feces adult twins and mothers; TS29 clone TS29_a03a08
FJ370628.1 gg_id:362215 feces adult twins and mothers; TS57 clone TS57_a03d01
EU773503.1 gg_id:312986 Bonobo feces clone BNO_aaa01a01
GQ052306.1 gg_id:429460 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu534a05
DQ805014.1 gg_id:194889 human fecal clone RL385_aao84a11
DQ825038.1 gg_id:187583 human fecal clone RL185_aao72e12
EU344383.1 gg_id:258461 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EF403780.1 gg_id:204996 human fecal clone SJTU_A2_02_06
DQ808990.1 gg_id:184545 human fecal clone RL243_aai87h08
DQ807910.1 gg_id:180777 human fecal clone RL180_aah38h03
FJ363776.1 gg_id:362510 feces adult twins and mothers; TS14 clone TS14_a03c02
FJ674058.1 gg_id:531865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ806218.1 gg_id:190648 human fecal clone RL186_aah62g11
FJ683556.1 gg_id:521865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798341.1 gg_id:175589 human fecal clone RL181_aah41b11
EU467251.1 gg_id:296692 black-handed spider monkey feces clone SPIM_a03_1
DQ804949.1 gg_id:195941 human fecal clone RL385_aao83a10
FJ684827.1 gg_id:513226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370430.1 gg_id:358419 feces adult twins and mothers; TS57 clone TS57_a01a05
DQ795634.1 gg_id:199010 human fecal clone RL178_aan67d07
DQ802591.1 gg_id:195295 human fecal clone RL188_aan93g08
FJ364772.1 gg_id:357464 feces adult twins and mothers; TS19 clone TS19_a02h08
DQ804278.1 gg_id:187591 human fecal clone RL187_aan77c12

EU778140.1	323778	27.8	19.8	87.1	42.8	57.4	23.1
FJ682155.1	519441	19.9	47.9	68.6	55.5	48.3	25.6
DQ797815.1	173975	19.7	21.1	21.7	46.1	46.3	12.4
GQ492839.1	585610	3492.8	3265.0	3241.1	3661.4	6477.5	6531.3
DQ799779.1	189842	140.8	196.7	488.3	308.5	146.2	230.8
DQ326493.1	148279	56.7	80.8	256.7	103.6	92.0	63.4
DQ326406.1	149236	6938.1	6513.7	1532.7	4826.1	3091.8	4607.3
FJ677824.1	529004	188.9	184.3	207.0	92.1	80.9	31.5
DQ327590.1	145858	66.6	115.7	383.6	162.1	105.4	65.5
GQ491902.1	576504	703.2	594.9	409.8	886.6	1494.8	1014.6
EU773407.1	311080	31.4	60.2	271.2	108.1	96.0	26.7
DQ804121.1	175988	612.1	819.3	658.9	1539.5	1370.0	1271.1
DQ808356.1	181831	3362.6	3140.7	1112.3	3637.3	4248.2	5845.6
DQ795593.1	194234	336.4	535.9	1905.7	192.1	1019.4	833.5
DQ803639.1	187496	10573.4	11917.0	4460.8	5958.7	8272.7	5931.9
DQ800645.1	180900	2113.3	2014.3	1086.4	356.7	1913.8	1655.8
DQ825047.1	191384	8708.5	9366.6	3216.0	9546.5	8587.2	9798.9
DQ808011.1	174599	1840.0	2005.8	757.7	406.3	1065.9	998.5
FJ367398.1	368950	233.0	416.7	422.0	290.9	1128.2	753.4
FJ370628.1	362215	1592.2	1406.9	1184.1	1614.3	442.3	468.8
EU773503.1	312986	205.3	294.3	597.0	325.9	101.1	158.5
GQ052306.1	429460	3108.7	3244.9	135.9	1285.5	2744.3	2102.0
DQ805014.1	194889	6319.5	4547.5	3410.8	6350.8	4289.0	5847.8
DQ825038.1	187583	462.4	573.1	261.2	114.7	567.1	424.8
EU344383.1	258461	658.0	1342.5	1007.8	829.7	2649.3	2171.7
EF403780.1	204996	65.4	36.9	171.0	81.0	88.6	90.9
DQ808990.1	184545	179.3	134.9	318.0	92.0	100.1	142.8
DQ807910.1	180777	573.1	766.7	502.7	1447.4	2534.9	2302.9
FJ363776.1	362510	515.6	1039.6	1103.0	317.4	2160.7	1043.4
FJ674058.1	531865	245.1	341.8	844.3	161.2	630.4	243.9
DQ806218.1	190648	507.2	1025.7	821.1	501.1	2258.5	1171.1
FJ683556.1	521865	4088.1	3728.2	3386.1	2120.7	480.3	1496.3
DQ798341.1	175589	44.7	52.0	135.8	65.0	93.8	41.3
EU467251.1	296692	54.4	70.3	149.4	66.5	64.9	42.4
DQ804949.1	195941	26.9	27.5	58.5	48.6	58.6	18.4
FJ684827.1	513226	9626.8	9114.0	4831.0	6242.5	7296.9	6288.1
FJ370430.1	358419	7745.8	9971.5	5604.8	5817.8	7648.5	5612.0
DQ795634.1	199010	205.8	279.6	254.6	298.9	144.4	224.3
DQ802591.1	195295	199.1	120.5	143.4	474.0	273.6	288.0
FJ364772.1	357464	517.7	5955.6	4784.7	4927.9	483.2	4546.4
DQ804278.1	187591	1929.2	1344.0	1343.6	2456.8	1193.0	2266.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21108
s__unclassified	21110
s__unclassified	21111
s__unclassified	21112
s__unclassified	21113
s__unclassified	21114
s__unclassified	21115
s__unclassified	21117
s__unclassified	21119
s__unclassified	21120
s__unclassified	21122
s__unclassified	21123
s__unclassified	21124
s__unclassified	21126
s__unclassified	21127
s__unclassified	21128
s__unclassified	21129
s__unclassified	21130
s__unclassified	21132
s__unclassified	21133
s__unclassified	21134
s__unclassified	21136
s__unclassified	21138
s__unclassified	21140
s__unclassified	21141
s__unclassified	21142
s__unclassified	21143
s__unclassified	21144
s__unclassified	21146
s__unclassified	21147
s__unclassified	21149
s__unclassified	21151
s__unclassified	21154
s__unclassified	21155
s__unclassified	21157
s__unclassified	21160
s__unclassified	21161
s__unclassified	21162
s__unclassified	21164
s__unclassified	21165
s__unclassified	21166

DQ824793.1 gg_id:179080 human fecal clone RL185_aao69d02
FJ366169.1 gg_id:357289 feces adult twins and mothers; TS25 clone TS25_a03e06
FJ678441.1 gg_id:519063 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU467416.1 gg_id:296514 chimpanzee feces clone CHIMP12_c03
GQ491331.1 gg_id:575263 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ492790.1 gg_id:580891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ364998.1 gg_id:362334 feces adult twins and mothers; TS1 clone TS1_a01f06
AF349421.1 gg_id:77371 pig feces clone
FJ364211.1 gg_id:366259 feces adult twins and mothers; TS150 clone TS150_a04c05
FJ677875.1 gg_id:514708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370381.1 gg_id:360033 feces adult twins and mothers; TS56 clone TS56_a04c02
DQ798463.1 gg_id:191746 human fecal clone RL181_aan97a06
FJ678829.1 gg_id:528093 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ491285.1 gg_id:587632 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ370535.1 gg_id:365441 feces adult twins and mothers; TS57 clone TS57_a02b11
FJ367412.1 gg_id:365431 feces adult twins and mothers; TS29 clone TS29_a03c02
DQ809682.1 gg_id:195537 human fecal clone RL184_aan82e09
DQ804413.1 gg_id:173896 human fecal clone RL187_aan79e02
X95624.1 gg_id:13997 Ruminococcus hydrogenotrophicus str. S5a36
FJ366380.1 gg_id:360776 feces adult twins and mothers; TS26 clone TS26_a02c11
FJ365881.1 gg_id:364310 feces adult twins and mothers; TS21 clone TS21_a04b07
AY982924.1 gg_id:122998 human descending colon mucosal biopsy clone L118
FJ369197.1 gg_id:357853 feces adult twins and mothers; TS50 clone TS50_a01d07
AY974849.1 gg_id:118782 human ascending colon mucosal biopsy clone KG89
EU462164.1 gg_id:302830 black-handed spider monkey feces clone SPIM_aaj36c04
DQ801948.1 gg_id:193284 human fecal clone RL201_aai48h05
GQ898643.1 gg_id:569010 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ802277.1 gg_id:198083 human fecal clone RL188_aah15e06
DQ802736.1 gg_id:180297 human fecal clone RL188_aan95h08
EU462179.1 gg_id:303169 black-handed spider monkey feces clone SPIM_aaj36f06
DQ801357.1 gg_id:193389 human fecal clone RL388_aao94d11
FJ678267.1 gg_id:529473 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB218345.1 gg_id:150230 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-129
DQ799789.1 gg_id:180169 human fecal clone RL182_aah33f04
AY977739.1 gg_id:121304 human cecum mucosal biopsy clone LE08
DQ799700.1 gg_id:188200 human fecal clone RL182_aah31f10
EU768469.1 gg_id:336275 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
DQ807542.1 gg_id:197222 human fecal clone RL307_aam07h12
GQ491581.1 gg_id:567715 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ801753.1 gg_id:196693 human fecal clone RL201_aai46d04
FJ363021.1 gg_id:367919 feces adult twins and mothers; TS148 clone TS148_a02a07

DQ824793.1	179080	20.7	20.2	25.1	44.4	53.1	18.9
FJ366169.1	357289	9349.0	9119.1	6775.5	6370.8	9172.3	8342.9
FJ678441.1	519063	498.8	573.3	166.7	151.8	186.7	79.7
EU467416.1	296514	1760.4	3563.8	1314.6	923.2	6282.2	3621.7
GQ491331.1	575263	2701.6	2983.6	1943.9	3948.0	3980.3	3864.9
GQ492790.1	580891	3061.5	4037.1	1590.1	2053.4	5161.5	4952.8
FJ364998.1	362334	1402.9	1600.3	1577.7	2492.7	1365.0	1681.8
AF349421.1	77371	102.2	92.1	413.9	140.0	137.9	107.7
FJ364211.1	366259	1972.9	1436.5	1602.4	1342.9	2905.4	1775.9
FJ677875.1	514708	3567.1	4459.8	1211.5	3291.7	4943.0	4472.8
FJ370381.1	360033	2054.3	1379.4	1010.4	505.0	1182.4	365.1
DQ798463.1	191746	6724.4	6269.7	4114.7	5493.9	7327.7	7529.3
FJ678829.1	528093	2514.0	2925.8	2932.0	3549.3	5670.9	4207.1
GQ491285.1	587632	258.4	213.6	290.3	141.1	123.4	132.2
FJ370535.1	365441	3420.7	4233.1	1006.6	3435.5	1791.3	1415.3
FJ367412.1	365431	31.9	51.7	30.0	54.3	64.7	23.6
DQ809682.1	195537	46.0	39.0	91.2	72.0	52.8	24.7
DQ804413.1	173896	149.7	212.9	212.3	131.1	347.7	147.3
X95624.1	13997	1364.2	1087.2	1752.7	1796.9	196.8	215.5
FJ366380.1	360776	1887.2	2040.4	2126.8	3049.3	7084.0	8678.9
FJ365881.1	364310	1427.8	1869.3	3361.0	1240.7	1887.1	2035.6
AY982924.1	122998	169.4	135.9	1804.1	354.8	140.9	138.1
FJ369197.1	357853	120.3	195.9	236.6	121.2	104.3	188.3
AY974849.1	118782	24.7	60.7	159.9	75.3	60.8	60.3
EU462164.1	302830	130.2	227.3	703.4	162.6	153.7	178.6
DQ801948.1	193284	6910.9	5976.4	2329.6	4031.9	3460.8	3940.9
GQ898643.1	569010	1145.7	1377.5	911.3	655.5	470.9	688.4
DQ802277.1	198083	663.1	1356.3	244.0	991.1	3022.1	774.5
DQ802736.1	180297	5598.4	4429.1	2929.0	4943.3	2601.9	2591.5
EU462179.1	303169	1799.6	2092.2	775.7	1178.1	632.5	537.5
DQ801357.1	193389	41.4	74.4	127.9	69.7	74.5	71.9
FJ678267.1	529473	348.5	398.0	234.7	377.5	464.7	205.8
AB218345.1	150230	18.3	19.3	25.4	35.5	51.9	20.3
DQ799789.1	180169	8864.6	8961.5	8593.0	6997.4	9478.6	6427.5
AY977739.1	121304	23.3	34.2	17.2	47.5	49.4	13.0
DQ799700.1	188200	44.7	65.8	119.4	90.8	88.9	64.2
EU768469.1	336275	1687.7	1436.4	492.6	354.8	691.0	398.8
DQ807542.1	197222	79.7	149.0	292.2	176.8	302.4	133.5
GQ491581.1	567715	2897.4	3398.5	2114.8	2633.1	5514.9	4693.6
DQ801753.1	196693	56.2	147.8	233.8	109.8	90.0	48.2
FJ363021.1	367919	7107.8	9024.3	3755.7	5454.1	10251.9	7819.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21167
s__unclassified	21168
s__unclassified	21169
s__unclassified	21170
s__unclassified	21171
s__unclassified	21174
s__unclassified	21175
s__unclassified	21176
s__unclassified	21177
s__unclassified	21180
s__unclassified	21181
s__unclassified	21183
s__unclassified	21184
s__unclassified	21185
s__unclassified	21186
s__unclassified	21187
s__unclassified	21188
s__unclassified	21189
s__unclassified	21190
s__unclassified	21191
s__unclassified	21192
s__unclassified	21195
s__unclassified	21196
s__unclassified	21198
s__unclassified	21199
s__unclassified	21202
s__unclassified	21203
s__unclassified	21207
s__unclassified	21208
s__unclassified	21209
s__unclassified	21210
s__unclassified	21211
s__unclassified	21212
s__unclassified	21213
s__unclassified	21215
s__unclassified	21220
s__unclassified	21221
s__unclassified	21222
s__unclassified	21225
s__unclassified	21226
s__unclassified	21229

FJ369206.1 gg_id:364996 feces adult twins and mothers; TS50 clone TS50_a01e07
FJ880511.1 gg_id:384505 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ683509.1 gg_id:531675 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ803719.1 gg_id:177307 human fecal clone RL200_aai57e08
DQ809757.1 gg_id:183040 human fecal clone RL184_aan83g05
DQ796661.1 gg_id:193951 human fecal clone RL179aan76g10
DQ794215.1 gg_id:194994 human fecal clone RL176_aan59e11
EU530217.1 gg_id:262919 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1
DQ807936.1 gg_id:193031 human fecal clone RL180_aan69d10
DQ801248.1 gg_id:180078 human fecal clone RL116_aaf02h09
FJ674092.1 gg_id:517703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ079643.1 gg_id:392131 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232e(
EU772296.1 gg_id:310490 Argali sheep feces clone AS1_aao37b06.Contig1
DQ326182.1 gg_id:148131 Metagenomic gut microbiome healthy human stool clone C085
EU766231.1 gg_id:351847 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
FJ365593.1 gg_id:365207 feces adult twins and mothers; TS20 clone TS20_a04f12
DQ799673.1 gg_id:196932 human fecal clone RL305aal88h11
DQ804111.1 gg_id:174535 human fecal clone RL187_aah68f11
DQ794385.1 gg_id:184488 human fecal clone RL197_aah87a12
GQ493579.1 gg_id:580685 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ675878.1 gg_id:524722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799473.1 gg_id:194586 human fecal clone RL305aal86f12
EF399628.1 gg_id:205950 human fecal clone SJTU_E_01_40
FJ364795.1 gg_id:365988 feces adult twins and mothers; TS19 clone TS19_a03c02
EF403194.1 gg_id:215270 human fecal clone SJTU_A1_6_25
EU468183.1 gg_id:295586 lion feces clone LI1_e03_1
DQ804318.1 gg_id:183528 human fecal clone RL187_aan77h08
DQ804781.1 gg_id:189687 human fecal clone RL187_aao72f05
DQ800464.1 gg_id:183252 human fecal clone RL183_aah24h07
FJ369439.1 gg_id:359096 feces adult twins and mothers; TS50 clone TS50_a04e06
DQ801547.1 gg_id:183577 human fecal clone RL388_aao96h06
DQ804005.1 gg_id:198999 human fecal clone RL187_aah67a02
DQ057397.1 gg_id:131559 chicken ileum/cecum clone cc361
DQ803204.1 gg_id:191545 human fecal clone RL311_aam22b01
EU459628.1 gg_id:292800 ring-tailed lemur feces clone RT_aai09e08
FJ673676.1 gg_id:531582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368296.1 gg_id:359143 feces adult twins and mothers; TS3 clone TS3_a02f02
AY976522.1 gg_id:124583 human cecum mucosal biopsy clone K047
FJ368201.1 gg_id:370186 feces adult twins and mothers; TS3 clone TS3_a01d08
DQ795062.1 gg_id:194595 human fecal clone RL310_aam39g01
DQ807718.1 gg_id:175548 human fecal clone RL180_aah36d05

FJ369206.1	364996	730.3	853.0	900.2	794.1	1095.6	1300.8
FJ880511.1	384505	301.7	233.2	328.9	184.1	109.7	201.9
FJ683509.1	531675	13393.6	10858.0	6046.9	11087.6	14203.0	12169.3
DQ803719.1	177307	46.1	56.9	170.3	91.5	77.9	28.2
DQ809757.1	183040	1553.9	1674.1	410.3	1409.8	2284.6	1725.9
DQ796661.1	193951	941.9	517.0	154.3	879.9	300.1	239.5
DQ794215.1	194994	5601.7	7927.9	1846.2	3578.3	5113.1	4046.1
EU530217.1	262919	2915.7	3383.6	634.3	1717.0	1118.1	913.0
DQ807936.1	193031	7197.6	4530.7	3849.1	7593.5	3800.0	5274.8
DQ801248.1	180078	635.1	835.5	1333.2	706.3	2107.5	1553.2
FJ674092.1	517703	141.2	227.2	586.6	164.9	149.9	106.8
GQ079643.1	392131	623.1	927.6	1705.1	730.3	1476.2	1322.0
EU772296.1	310490	1713.3	1390.6	1279.8	544.6	916.1	729.3
DQ326182.1	148131	318.4	286.1	637.3	350.7	908.4	772.3
EU766231.1	351847	2552.4	2763.9	1969.2	1406.9	2871.4	3864.3
FJ365593.1	365207	3023.4	3571.8	2500.1	2427.0	2611.5	2368.1
DQ799673.1	196932	1245.0	1038.2	1658.7	1754.7	468.9	658.4
DQ804111.1	174535	596.3	783.6	582.8	1666.0	938.7	1139.7
DQ794385.1	184488	1989.8	3043.7	621.7	1041.7	1993.2	1365.4
GQ493579.1	580685	94.6	101.2	148.2	91.7	75.2	37.8
FJ675878.1	524722	7885.8	6674.4	6001.3	6238.0	4611.8	4748.1
DQ799473.1	194586	955.2	1014.9	331.1	1560.2	1790.4	1181.6
EF399628.1	205950	3553.2	3753.5	857.1	2217.4	1281.3	1420.5
FJ364795.1	365988	219.6	232.5	643.7	353.8	231.4	238.9
EF403194.1	215270	170.2	285.7	102.8	208.6	111.3	64.6
EU468183.1	295586	390.3	428.4	475.7	313.4	450.3	212.4
DQ804318.1	183528	6366.4	5508.3	4783.0	5142.2	1201.3	5683.9
DQ804781.1	189687	280.6	544.0	666.0	192.2	918.0	436.8
DQ800464.1	183252	122.0	313.5	161.3	65.7	82.5	70.9
FJ369439.1	359096	2281.0	2911.8	1985.5	1958.8	4693.6	2442.3
DQ801547.1	183577	1033.7	574.7	385.1	317.9	1091.3	1226.0
DQ804005.1	198999	93.0	123.6	221.5	169.1	154.1	226.3
DQ057397.1	131559	562.7	473.2	358.5	1987.4	113.3	507.5
DQ803204.1	191545	1864.1	2344.2	1997.3	2925.8	4521.2	4388.9
EU459628.1	292800	460.8	428.3	1638.7	1033.3	193.0	497.7
FJ673676.1	531582	6350.9	7624.8	2833.4	6589.5	12815.1	9327.5
FJ368296.1	359143	121.4	24.1	351.4	98.3	56.3	24.0
AY976522.1	124583	49.8	57.4	81.0	57.6	64.6	31.8
FJ368201.1	370186	579.8	428.3	738.6	1276.4	146.0	199.5
DQ795062.1	194595	58.9	81.6	128.3	89.6	69.4	62.3
DQ807718.1	175548	4926.1	6902.0	7616.5	5836.5	7748.1	6712.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21232
s__unclassified	21233
s__unclassified	21234
s__unclassified	21235
s__unclassified	21236
s__unclassified	21237
s__unclassified	21238
s__unclassified	21239
s__unclassified	21240
s__unclassified	21242
s__unclassified	21243
s__unclassified	21244
s__unclassified	21245
s__unclassified	21246
s__unclassified	21248
s__unclassified	21250
s__unclassified	21251
s__unclassified	21253
s__unclassified	21254
s__unclassified	21256
s__unclassified	21257
s__unclassified	21260
s__unclassified	21261
s__unclassified	21262
s__unclassified	21263
s__unclassified	21267
s__unclassified	21269
s__unclassified	21271
s__unclassified	21275
s__unclassified	21277
s__unclassified	21280
s__unclassified	21281
s__unclassified	21282
s__unclassified	21283
s__unclassified	21284
s__unclassified	21285
s__unclassified	21288
s__unclassified	21290
s__unclassified	21291
s__unclassified	21292
s__unclassified	21295

GQ175480.1 gg_id:579563 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
FJ673048.1 gg_id:522463 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ367338.1 gg_id:359066 feces adult twins and mothers; TS29 clone TS29_a02c11
DQ802497.1 gg_id:178768 human fecal clone RL188_aah18e07
EU776600.1 gg_id:331271 Lion feces clone LI2_aae50f03
EU777561.1 gg_id:337080 Sumatran orangutan feces clone orang1_aai55e12
DQ824090.1 gg_id:176724 human fecal clone RL204_aaj59b12
FJ370157.1 gg_id:367719 feces adult twins and mothers; TS56 clone TS56_a01b02
FJ364096.1 gg_id:365980 feces adult twins and mothers; TS150 clone TS150_a02h11
FJ367236.1 gg_id:360886 feces adult twins and mothers; TS29 clone TS29_a01b07
FJ674006.1 gg_id:531328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ793750.1 gg_id:181927 human fecal clone RL246_aai76f11
FJ678797.1 gg_id:529608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ175502.1 gg_id:544532 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
FJ673697.1 gg_id:518146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ807587.1 gg_id:188805 human fecal clone RL307_aam08f01
DQ804414.1 gg_id:198951 human fecal clone RL187_aan79e03
FJ879848.1 gg_id:464311 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
DQ824766.1 gg_id:176450 human fecal clone RL185_aao69a01
FJ370129.1 gg_id:365387 feces adult twins and mothers; TS55 clone TS55_a04g02
DQ824815.1 gg_id:197379 human fecal clone RL185_aao69f03
FJ679957.1 gg_id:520155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798965.1 gg_id:193337 human fecal clone RL242_aaj99g03
FJ372063.1 gg_id:361345 feces adult twins and mothers; TS9 clone TS9_a01d02
DQ806358.1 gg_id:176330 human fecal clone RL186_aan91b11
GQ896722.1 gg_id:585057 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
EF405003.1 gg_id:216807 human fecal clone SJTU_G_05_74
DQ823723.1 gg_id:177005 human fecal clone RL250_aaj78b10
DQ806093.1 gg_id:183145 human fecal clone RL186_aah61a12
GQ493166.1 gg_id:583059 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ367354.1 gg_id:363558 feces adult twins and mothers; TS29 clone TS29_a02e05
FJ680513.1 gg_id:514809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ493777.1 gg_id:587010 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ798694.1 gg_id:190120 human fecal clone RL181_aao00b12
FJ369874.1 gg_id:358576 feces adult twins and mothers; TS55 clone TS55_a01g07
DQ825195.1 gg_id:185845 human fecal clone RL185_aan86e08
EF399515.1 gg_id:204058 human fecal clone SJTU_F_11_92
GQ493460.1 gg_id:539851 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU462101.1 gg_id:288684 black-handed spider monkey feces clone SPIM_aaj35a05
EU344285.1 gg_id:264113 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU469501.1 gg_id:292310 black lemur feces clone BKLE_a03_2

GQ175480.1	579563	536.3	662.8	471.2	595.0	1493.0	1191.2
FJ673048.1	522463	2610.2	2018.7	778.5	3637.8	3741.7	3769.2
FJ367338.1	359066	1951.3	5001.9	1175.4	2305.1	1715.1	874.9
DQ802497.1	178768	796.8	1106.2	356.1	460.1	1805.0	1188.1
EU776600.1	331271	59.9	28.6	114.7	44.7	39.5	32.6
EU777561.1	337080	1807.2	1768.2	767.5	2019.7	2822.2	226.4
DQ824090.1	176724	223.4	231.7	62.6	397.8	112.1	294.6
FJ370157.1	367719	7018.6	5177.3	3502.1	5668.4	8486.4	10249.2
FJ364096.1	365980	2947.7	3488.0	719.6	1425.4	919.5	961.7
FJ367236.1	360886	8723.2	7081.9	7464.2	7690.3	7509.7	8040.2
FJ674006.1	531328	239.7	192.9	153.4	99.4	185.9	255.3
DQ793750.1	181927	299.3	417.7	99.0	229.9	66.3	51.7
FJ678797.1	529608	2597.7	306.9	1218.9	1923.1	994.0	1319.2
GQ175502.1	544532	1565.8	1057.7	875.8	1009.0	1117.8	1536.4
FJ673697.1	518146	186.3	304.0	299.7	403.6	157.4	223.4
DQ807587.1	188805	3925.0	4692.8	3752.8	2140.1	4665.0	3839.2
DQ804414.1	198951	943.1	1119.8	1542.9	1364.3	2846.9	2994.8
FJ879848.1	464311	107.3	146.2	228.6	122.7	123.6	148.3
DQ824766.1	176450	5492.1	5047.4	2278.1	1767.5	2121.7	2939.8
FJ370129.1	365387	2037.8	2078.6	2059.4	3828.2	347.5	1501.9
DQ824815.1	197379	2602.5	3499.0	688.3	2450.7	5056.7	4195.1
FJ679957.1	520155	111.6	104.5	143.4	157.0	482.8	86.9
DQ798965.1	193337	1770.7	1291.8	590.9	919.6	1046.8	492.9
FJ372063.1	361345	1003.7	1337.4	1751.1	833.9	2935.9	2464.9
DQ806358.1	176330	499.7	375.0	263.3	960.1	543.2	373.3
GQ896722.1	585057	363.5	476.2	580.2	823.7	205.2	350.4
EF405003.1	216807	939.6	566.0	763.2	1972.5	217.7	237.6
DQ823723.1	177005	21.4	44.6	66.2	64.5	56.2	36.3
DQ806093.1	183145	3654.9	3834.0	2466.2	3489.6	4850.9	4825.6
GQ493166.1	583059	423.9	525.4	338.0	250.3	930.1	1063.4
FJ367354.1	363558	404.9	695.4	1473.4	350.9	820.5	725.0
FJ680513.1	514809	1845.1	2596.2	2321.2	1323.1	3959.5	7126.2
GQ493777.1	587010	1246.3	1350.1	1347.4	520.9	518.4	728.5
DQ798694.1	190120	62.9	141.8	229.4	70.6	81.4	42.7
FJ369874.1	358576	28076.6	27436.8	16595.1	22041.1	26580.1	22866.6
DQ825195.1	185845	23.8	27.9	33.9	57.6	63.1	32.7
EF399515.1	204058	791.5	1386.0	235.4	530.4	2128.0	519.1
GQ493460.1	539851	1821.0	1474.5	1279.9	3620.6	1059.8	819.3
EU462101.1	288684	8222.8	6952.4	3250.5	7661.0	7739.5	7079.4
EU344285.1	264113	4962.5	4390.2	3602.8	2879.6	2053.0	2491.1
EU469501.1	292310	3187.5	4771.0	1802.4	5000.6	4092.3	4166.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21296
s__unclassified	21298
s__unclassified	21301
s__unclassified	21303
s__unclassified	21304
s__unclassified	21305
s__unclassified	21306
s__unclassified	21307
s__unclassified	21308
s__unclassified	21310
s__unclassified	21311
s__unclassified	21312
s__unclassified	21313
s__unclassified	21315
s__unclassified	21317
s__unclassified	21318
s__unclassified	21319
s__unclassified	21325
s__unclassified	21328
s__unclassified	21331
s__unclassified	21332
s__unclassified	21333
s__unclassified	21335
s__unclassified	21336
s__unclassified	21337
s__unclassified	21339
s__unclassified	21340
s__unclassified	21342
s__unclassified	21343
s__unclassified	21344
s__unclassified	21346
s__unclassified	21348
s__unclassified	21351
s__unclassified	21352
s__unclassified	21354
s__unclassified	21355
s__unclassified	21357
s__unclassified	21361
s__unclassified	21363
s__unclassified	21364
s__unclassified	21365

FJ678020.1 gg_id:528103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ824491.1 gg_id:178952 human fecal clone RL304_aal76f09
GQ897401.1 gg_id:562918 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
EU467434.1 gg_id:302049 chimpanzee feces clone CHIMP12_h05_2
DQ803247.1 gg_id:182728 human fecal clone RL311_aam22h02
GQ492415.1 gg_id:580087 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ325573.1 gg_id:146093 Metagenomic gut microbiome healthy human stool clone B068
FJ368900.1 gg_id:361009 feces adult twins and mothers; TS4 clone TS4_a01h05
FJ679103.1 gg_id:527140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU467241.1 gg_id:287583 black-handed spider monkey feces clone SPIM_d07
DQ326151.1 gg_id:150033 Metagenomic gut microbiome healthy human stool clone C045
DQ806462.1 gg_id:195972 human fecal clone RL186_aao45a02
DQ798304.1 gg_id:184228 human fecal clone RL181_aah40d07
GQ493558.1 gg_id:539526 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ365989.1 gg_id:361245 feces adult twins and mothers; TS25 clone TS25_a01d12
DQ793371.1 gg_id:192937 human fecal clone RL199_aaj42h06
FJ362957.1 gg_id:365345 feces adult twins and mothers; TS148 clone TS148_a01c04
FJ880700.1 gg_id:420661 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
DQ805900.1 gg_id:184238 human fecal clone RL306aal92d10
EF398596.1 gg_id:217110 human fecal clone SJTU_F_04_21
DQ805654.1 gg_id:198983 human fecal clone RL306aal89d10
FJ370553.1 gg_id:358066 feces adult twins and mothers; TS57 clone TS57_a02d09
AY977207.1 gg_id:115602 human cecum mucosal biopsy clone MT17
EF401997.1 gg_id:206178 human fecal clone SJTU_B_02_27
EU459666.1 gg_id:300510 ring-tailed lemur feces clone RT_aai10d12
FJ683591.1 gg_id:528355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802605.1 gg_id:174714 human fecal clone RL188_aan94a06
DQ793844.1 gg_id:192433 human fecal clone RL176_aah44c02
FJ362761.1 gg_id:357683 feces adult twins and mothers; TS13 clone TS13_a02g10
DQ804255.1 gg_id:186416 human fecal clone RL187_aan77a07
DQ800776.1 gg_id:193211 human fecal clone RL183_aao03c12
DQ795338.1 gg_id:182672 human fecal clone RL178_aah53b06
DQ801899.1 gg_id:185135 human fecal clone RL201_aai48c04
FJ880520.1 gg_id:436032 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
DQ809688.1 gg_id:187533 human fecal clone RL184_aan82f07
DQ810008.1 gg_id:174624 human fecal clone RL184_aao67a03
DQ804959.1 gg_id:186381 human fecal clone RL385_aao83c01
FJ363959.1 gg_id:362856 feces adult twins and mothers; TS150 clone TS150_a01d03
DQ804062.1 gg_id:177461 human fecal clone RL187_aah67h09
FJ367854.1 gg_id:369480 feces adult twins and mothers; TS2 clone TS2_a04d03
DQ905094.1 gg_id:170387 human fecal clone 2-002-h6

FJ678020.1	528103	14032.8	12218.6	4293.8	11433.3	16519.5	14338.1
DQ824491.1	178952	199.9	286.3	902.8	364.3	1167.7	1185.0
GQ897401.1	562918	56.7	68.1	178.1	72.0	55.7	52.0
EU467434.1	302049	8735.6	6994.2	5981.6	5251.9	918.7	5617.5
DQ803247.1	182728	935.0	1359.3	1602.9	1005.9	1170.3	1600.5
GQ492415.1	580087	3602.5	3679.4	3769.3	5248.0	4157.1	4989.5
DQ325573.1	146093	1304.6	939.1	1761.5	2054.3	379.4	1191.8
FJ368900.1	361009	16171.7	16848.7	5867.1	12567.6	11646.0	11139.1
FJ679103.1	527140	378.2	380.6	473.0	130.2	147.2	79.1
EU467241.1	287583	77.1	109.7	41.0	105.6	71.8	61.8
DQ326151.1	150033	268.5	247.9	691.1	286.8	240.5	156.5
DQ806462.1	195972	9140.3	9645.4	6045.4	6836.3	10638.2	9803.3
DQ798304.1	184228	3112.2	3661.8	3490.0	3627.1	7547.7	4694.0
GQ493558.1	539526	3259.5	3835.5	1544.3	2117.1	3534.5	1912.2
FJ365989.1	361245	3830.9	4257.4	2602.7	4040.5	9823.6	6574.1
DQ793371.1	192937	23.2	29.2	59.0	48.5	50.4	27.5
FJ362957.1	365345	634.9	470.5	710.5	399.3	667.1	426.5
FJ880700.1	420661	2609.8	2404.6	2339.6	2691.8	2992.2	2568.7
DQ805900.1	184238	17.5	16.7	22.2	39.3	42.6	23.8
EF398596.1	217110	706.4	1841.3	626.1	749.2	5541.3	2498.4
DQ805654.1	198983	146.7	97.4	160.2	289.6	866.2	323.6
FJ370553.1	358066	1528.3	1720.2	739.6	1810.8	2445.2	2181.5
AY977207.1	115602	27.8	34.3	117.1	47.5	68.4	20.6
EF401997.1	206178	98.6	98.9	260.6	111.0	56.1	82.4
EU459666.1	300510	4515.7	4163.5	1695.8	6727.1	9225.8	9446.2
FJ683591.1	528355	3427.3	6120.7	1911.2	3287.0	4783.0	5677.2
DQ802605.1	174714	7103.2	5845.9	4412.4	8277.0	15576.7	10228.4
DQ793844.1	192433	65.9	87.8	363.7	114.7	119.4	347.5
FJ362761.1	357683	3207.2	3098.1	2206.0	3353.8	7118.8	3687.0
DQ804255.1	186416	33.8	67.5	254.1	57.7	62.3	53.8
DQ800776.1	193211	405.3	355.7	98.9	553.5	432.7	197.0
DQ795338.1	182672	1970.5	1910.9	1217.1	2188.1	1527.8	2189.7
DQ801899.1	185135	4951.1	4374.1	3428.5	7222.3	6164.4	7849.5
FJ880520.1	436032	37.6	44.2	77.2	100.3	69.7	56.8
DQ809688.1	187533	1840.8	1983.0	800.8	1480.5	3011.7	2258.1
DQ810008.1	174624	1600.9	1656.2	2220.6	2063.8	1852.4	2057.6
DQ804959.1	186381	101.7	122.4	151.4	116.4	74.0	39.2
FJ363959.1	362856	359.9	135.8	494.9	814.2	233.4	173.1
DQ804062.1	177461	139.0	56.4	234.0	138.3	132.4	78.1
FJ367854.1	369480	30.1	98.4	87.1	91.5	71.0	81.9
DQ905094.1	170387	10320.4	10208.7	5147.1	11029.3	8300.4	9303.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21367
s__unclassified	21368
s__unclassified	21369
s__unclassified	21373
s__unclassified	21374
s__unclassified	21375
s__unclassified	21376
s__unclassified	21378
s__unclassified	21379
s__unclassified	21380
s__unclassified	21381
s__unclassified	21382
s__unclassified	21384
s__unclassified	21385
s__unclassified	21387
s__unclassified	21388
s__unclassified	21389
s__unclassified	21390
s__unclassified	21392
s__unclassified	21394
s__unclassified	21399
s__unclassified	21400
s__unclassified	21403
s__unclassified	21406
s__unclassified	21408
s__unclassified	21410
s__unclassified	21412
s__unclassified	21413
s__unclassified	21416
s__unclassified	21417
s__unclassified	21421
s__unclassified	21424
s__unclassified	21427
s__unclassified	21428
s__unclassified	21429
s__unclassified	21430
s__unclassified	21431
s__unclassified	21434
s__unclassified	21435
s__unclassified	21436
s__unclassified	21437

DQ801655.1 gg_id:179531 human fecal clone RL201_aai45a12
DQ327198.1 gg_id:149658 Metagenomic gut microbiome healthy human stool clone E729
DQ802779.1 gg_id:187866 human fecal clone RL188_aan96e01
FJ368606.1 gg_id:362131 feces adult twins and mothers; TS49 clone TS49_a02c08
DQ805395.1 gg_id:198771 human fecal clone RL203_aai62a11
DQ794663.1 gg_id:190108 human fecal clone RL240_aaj30g12
GQ492387.1 gg_id:587729 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ799186.1 gg_id:186828 human fecal clone RL205_aaj18g10
DQ805683.1 gg_id:181869 human fecal clone RL306aal89g06
DQ808174.1 gg_id:195511 human fecal clone RL180_aao73e06
FJ370752.1 gg_id:360353 feces adult twins and mothers; TS57 clone TS57_a04h02
GQ492049.1 gg_id:537067 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ833196.1 gg_id:589215 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_21E03
DQ905209.1 gg_id:166627 human fecal clone 013-b6
DQ806393.1 gg_id:185655 human fecal clone RL186_aan91f10
FJ673686.1 gg_id:526313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ805059.1 gg_id:187040 human fecal clone RL385_aao84f06
EU776195.1 gg_id:338657 Spotted hyena feces clone HY2_c05
DQ802126.1 gg_id:185798 human fecal clone RL241_aaj03d06
FJ367229.1 gg_id:367427 feces adult twins and mothers; TS29 clone TS29_a01a09
DQ824785.1 gg_id:184926 human fecal clone RL185_aao69c04
FJ684853.1 gg_id:526044 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370795.1 gg_id:359557 feces adult twins and mothers; TS5 clone TS5_a01d03
EU763793.1 gg_id:318944 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
FJ370583.1 gg_id:359794 feces adult twins and mothers; TS57 clone TS57_a02g05
EU469566.1 gg_id:289089 flying fox feces clone FF_a05
FJ370920.1 gg_id:370338 feces adult twins and mothers; TS5 clone TS5_a02g10
DQ795286.1 gg_id:199065 human fecal clone RL178_aah52e04
DQ806583.1 gg_id:194217 human fecal clone RL186_aao46d03
DQ803474.1 gg_id:176483 human fecal clone RL251_aaj86c05
DQ823702.1 gg_id:196262 human fecal clone RL250_aaj77h05
FJ363706.1 gg_id:365327 feces adult twins and mothers; TS14 clone TS14_a02c11
EU463322.1 gg_id:302321 bush dog feces clone bdog1_aai78c06
DQ804117.1 gg_id:189289 human fecal clone RL187_aah68g09
GQ491877.1 gg_id:551761 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ057452.1 gg_id:131571 str. ic1272
FJ673904.1 gg_id:516385 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ325682.1 gg_id:149909 Metagenomic gut microbiome healthy human stool clone B281
EU774663.1 gg_id:347115 Angola Colobus feces clone EAC_1aaa03b04
FJ676585.1 gg_id:525814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798720.1 gg_id:192200 human fecal clone RL181_aao00e06

DQ801655.1	179531	5547.2	6365.0	4677.2	7074.8	9038.4	9021.1
DQ327198.1	149658	50.7	36.2	107.6	50.2	85.9	39.0
DQ802779.1	187866	2793.1	2438.3	3437.2	3756.4	4492.4	4200.1
FJ368606.1	362131	11092.9	10197.6	4335.4	7533.8	11545.6	8749.8
DQ805395.1	198771	597.6	640.9	1730.4	347.2	1834.6	1878.9
DQ794663.1	190108	12191.3	12602.1	12112.9	10392.3	8172.2	7897.8
GQ492387.1	587729	3680.7	5127.3	1897.7	3030.7	10164.5	5017.7
DQ799186.1	186828	22.2	371.4	780.1	433.1	733.9	357.2
DQ805683.1	181869	2853.9	2697.9	1779.7	3803.3	6312.0	5024.3
DQ808174.1	195511	13.4	23.5	12.1	47.7	53.2	17.2
FJ370752.1	360353	635.7	1411.6	752.0	315.8	2846.8	1648.7
GQ492049.1	537067	7254.0	11147.2	3720.4	6279.5	7474.1	6856.6
FJ833196.1	589215	537.5	942.7	1044.0	358.9	341.2	740.5
DQ905209.1	166627	550.0	507.6	901.5	884.9	624.4	330.2
DQ806393.1	185655	34.4	36.0	41.6	57.5	56.4	25.7
FJ673686.1	526313	6593.9	5813.4	1875.6	2981.0	2147.7	1503.1
DQ805059.1	187040	50.2	59.3	274.8	77.0	54.6	45.6
EU776195.1	338657	55.7	122.7	158.9	158.5	150.9	169.9
DQ802126.1	185798	2342.2	2736.5	1151.0	2342.6	3011.2	3358.1
FJ367229.1	367427	392.3	427.8	908.3	556.6	310.6	142.8
DQ824785.1	184926	39.6	43.1	186.2	54.1	115.1	184.2
FJ684853.1	526044	979.1	1574.5	445.1	916.8	1794.0	1988.7
FJ370795.1	359557	1477.8	3337.0	1995.5	1372.3	1182.6	878.2
EU763793.1	318944	8218.1	9154.8	4887.2	9089.0	13486.1	12547.5
FJ370583.1	359794	7714.5	8982.5	1186.4	7409.7	6428.2	5335.3
EU469566.1	289089	4013.5	5125.2	1879.6	2903.8	6746.9	4089.0
FJ370920.1	370338	908.4	921.4	481.3	2114.2	2384.0	2070.1
DQ795286.1	199065	23.8	74.3	149.0	59.6	64.4	34.6
DQ806583.1	194217	2132.9	1318.8	632.1	638.8	1367.4	420.7
DQ803474.1	176483	25.5	62.0	89.4	76.2	59.4	39.4
DQ823702.1	196262	33.4	26.5	48.3	59.0	208.2	181.0
FJ363706.1	365327	110.1	106.1	517.7	215.6	926.6	1305.8
EU463322.1	302321	2124.7	2085.1	918.0	1443.3	977.7	653.9
DQ804117.1	189289	55.3	78.1	193.1	88.6	78.9	48.3
GQ491877.1	551761	4899.8	5454.1	2701.9	3273.8	4604.7	6802.2
DQ057452.1	131571	23.8	49.9	75.8	48.1	62.1	40.1
FJ673904.1	516385	3519.5	4637.3	1787.0	4598.8	7596.4	4842.8
DQ325682.1	149909	52.4	61.7	171.0	90.5	184.5	173.0
EU774663.1	347115	125.8	134.6	525.0	97.7	304.1	529.5
FJ676585.1	525814	8420.1	8585.6	5065.0	5332.4	9357.5	9299.2
DQ798720.1	192200	2018.4	1419.9	1121.8	2013.3	2076.6	1310.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21438
s__unclassified	21439
s__unclassified	21442
s__unclassified	21443
s__unclassified	21446
s__unclassified	21447
s__unclassified	21448
s__unclassified	21449
s__unclassified	21450
s__unclassified	21451
s__unclassified	21452
s__unclassified	21453
s__unclassified	21456
s__unclassified	21458
s__unclassified	21459
s__unclassified	21460
s__unclassified	21463
s__unclassified	21464
s__unclassified	21465
s__unclassified	21466
s__unclassified	21467
s__unclassified	21469
s__unclassified	21470
s__unclassified	21471
s__unclassified	21472
s__unclassified	21473
s__unclassified	21474
s__unclassified	21475
s__unclassified	21478
s__unclassified	21480
s__unclassified	21483
s__unclassified	21485
s__unclassified	21486
s__unclassified	21487
s__unclassified	21489
s__unclassified	21490
s__unclassified	21491
s__unclassified	21492
s__unclassified	21496
s__unclassified	21497
s__unclassified	21499

DQ804241.1 gg_id:174669 human fecal clone RL187_aah70g04
DQ805035.1 gg_id:182850 human fecal clone RL385_aao84c12
FJ370620.1 gg_id:366727 feces adult twins and mothers; TS57 clone TS57_a03c04
DQ796687.1 gg_id:197500 human fecal clone RL179_aao53b09
DQ796582.1 gg_id:197670 human fecal clone RL179aan75c08
FJ368118.1 gg_id:367639 feces adult twins and mothers; TS30 clone TS30_a04c07
DQ809130.1 gg_id:183564 human fecal clone RL308_aal82b02
GQ077072.1 gg_id:415735 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1206e
DQ799157.1 gg_id:194125 human fecal clone RL205_aaj18d04
FJ676799.1 gg_id:520380 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ804486.1 gg_id:183159 human fecal clone RL187_aan80f05
AY960563.1 gg_id:115104 Clostridium sp. str. CE6
FJ364732.1 gg_id:369530 feces adult twins and mothers; TS19 clone TS19_a02d04
DQ804248.1 gg_id:194327 human fecal clone RL187_aah70h04
DQ808467.1 gg_id:185180 human fecal clone RL180_aao76h06
DQ801496.1 gg_id:181942 human fecal clone RL388_aao96c10
FJ367468.1 gg_id:363767 feces adult twins and mothers; TS29 clone TS29_a03h09
DQ804281.1 gg_id:192533 human fecal clone RL187_aan77d07
FJ682467.1 gg_id:524374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ408999.1 gg_id:16475 human colonic clone HuCB25
AY981581.1 gg_id:126684 human sigmoid colon mucosal biopsy clone L764
EF404178.1 gg_id:207790 human fecal clone SJTU_C_05_79
EU459398.1 gg_id:294439 cheetah feces clone CE3_aai07c06
FJ369208.1 gg_id:369619 feces adult twins and mothers; TS50 clone TS50_a01e09
FJ681290.1 gg_id:528650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ806327.1 gg_id:174763 human fecal clone RL186_aan90f07
FJ833830.1 gg_id:543708 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_07G01
EU776912.1 gg_id:321453 Mongoose lemur feces clone ML_aaj28d01
GQ077026.1 gg_id:409732 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1205h
GQ491288.1 gg_id:583454 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ683504.1 gg_id:531001 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ803389.1 gg_id:186324 human fecal clone RL251_aaj85a10
FJ673117.1 gg_id:517348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673669.1 gg_id:515203 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU764302.1 gg_id:336328 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
FJ674047.1 gg_id:517387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797638.1 gg_id:181387 human fecal clone RL206_aaj14a12
DQ905829.2 gg_id:165922 human fecal clone 29E-d8
DQ805269.1 gg_id:189310 human fecal clone RL249_aaj84b03
GQ897352.1 gg_id:566202 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ824909.1 gg_id:190610 human fecal clone RL185_aao70h05

DQ804241.1	174669	110.7	396.3	352.4	145.7	568.2	113.5
DQ805035.1	182850	141.3	144.7	1057.5	198.8	248.6	411.2
FJ370620.1	366727	146.8	477.3	401.2	104.0	126.8	245.2
DQ796687.1	197500	486.5	217.0	413.5	187.5	416.5	238.3
DQ796582.1	197670	364.9	801.9	439.8	334.8	886.1	712.0
FJ368118.1	367639	10207.7	10318.4	5903.9	7224.7	10112.9	9696.5
DQ809130.1	183564	47.4	66.8	92.2	56.7	74.9	38.0
GQ077072.1	415735	1519.6	2009.0	2111.1	2973.3	4888.9	4149.8
DQ799157.1	194125	55.1	22.0	47.0	64.3	229.5	221.4
FJ676799.1	520380	1064.3	691.4	906.8	1271.2	652.8	482.0
DQ804486.1	183159	725.6	724.8	798.7	838.0	238.5	996.8
AY960563.1	115104	3737.5	2317.9	836.3	4454.0	3982.9	3159.1
FJ364732.1	369530	7758.6	8087.0	8277.8	9367.9	10811.8	11146.8
DQ804248.1	194327	7914.6	7464.8	5019.0	5224.8	7406.2	7672.1
DQ808467.1	185180	14373.2	13560.0	16380.8	11852.4	12893.8	9619.3
DQ801496.1	181942	3724.4	3717.0	3514.3	4822.6	3569.5	3938.5
FJ367468.1	363767	2520.5	2710.7	2454.3	3246.0	4852.7	3533.8
DQ804281.1	192533	12174.1	9939.9	8332.6	9998.4	14588.8	11920.6
FJ682467.1	524374	8187.6	7585.6	8570.5	7891.4	6658.7	6780.2
AJ408999.1	16475	241.8	406.8	304.9	92.9	71.0	63.8
AY981581.1	126684	66.3	75.5	358.9	104.5	89.0	75.4
EF404178.1	207790	83.7	122.3	119.0	86.7	80.0	66.7
EU459398.1	294439	183.6	293.6	607.8	144.6	288.6	212.5
FJ369208.1	369619	6737.9	6920.1	4915.7	7391.7	9009.1	7642.4
FJ681290.1	528650	12274.0	13135.7	7442.6	11779.8	13589.3	12103.8
DQ806327.1	174763	628.3	1405.3	1623.9	687.9	3670.7	1441.5
FJ833830.1	543708	86.0	293.5	247.5	95.6	179.5	114.4
EU776912.1	321453	736.3	1029.7	1218.2	985.0	2006.6	1778.7
GQ077026.1	409732	7155.8	7855.6	3942.4	4027.0	4521.4	5288.5
GQ491288.1	583454	2685.2	2855.3	3043.8	3355.8	5925.7	4507.1
FJ683504.1	531001	6163.1	6613.9	2449.3	6042.7	6743.3	7049.8
DQ803389.1	186324	217.6	377.0	374.0	282.8	1053.7	592.8
FJ673117.1	517348	163.5	382.2	436.5	241.9	108.5	78.2
FJ673669.1	515203	2423.3	2992.7	2187.8	1939.9	3480.5	2887.1
EU764302.1	336328	78.8	67.1	120.3	113.4	57.4	52.8
FJ674047.1	517387	2407.7	2265.6	1587.7	3894.1	4107.4	3712.2
DQ797638.1	181387	5573.5	4478.8	2343.8	5222.7	4030.9	1917.7
DQ905829.2	165922	11192.3	10094.3	4984.1	8802.7	7697.4	8661.2
DQ805269.1	189310	88.2	109.8	231.0	195.3	163.4	162.1
GQ897352.1	566202	449.1	1016.9	732.2	1004.0	447.8	308.6
DQ824909.1	190610	187.6	316.0	267.1	139.8	181.7	201.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21500
s__unclassified	21502
s__unclassified	21504
s__unclassified	21507
s__unclassified	21508
s__unclassified	21509
s__unclassified	21510
s__unclassified	21514
s__unclassified	21517
s__unclassified	21518
s__unclassified	21519
s__unclassified	21523
s__unclassified	21526
s__unclassified	21527
s__unclassified	21528
s__unclassified	21529
s__unclassified	21531
s__unclassified	21532
s__unclassified	21535
s__unclassified	21536
s__unclassified	21538
s__unclassified	21539
s__unclassified	21540
s__unclassified	21542
s__unclassified	21543
s__unclassified	21544
s__unclassified	21545
s__unclassified	21546
s__unclassified	21547
s__unclassified	21548
s__unclassified	21549
s__unclassified	21552
s__unclassified	21553
s__unclassified	21555
s__unclassified	21556
s__unclassified	21558
s__unclassified	21559
s__unclassified	21560
s__unclassified	21561
s__unclassified	21562
s__unclassified	21563

DQ825227.1 gg_id:194540 human fecal clone RL185_aan86h11
FM872529.1 gg_id:358675 occupant source house floor dust clone FA01F10
EU469676.1 gg_id:292633 flying fox feces clone FF_-aag84h04
FJ364608.1 gg_id:369728 feces adult twins and mothers; TS19 clone TS19_a01a03
DQ807273.1 gg_id:175296 human fecal clone RL244_aaj48d10
FJ363614.1 gg_id:365076 feces adult twins and mothers; TS14 clone TS14_a01d02
DQ824897.1 gg_id:181054 human fecal clone RL185_aao70f09
DQ806731.1 gg_id:174501 human fecal clone RL186_aao48a10
DQ905045.1 gg_id:165102 human fecal clone 2-002-d3
FJ364581.1 gg_id:366418 feces adult twins and mothers; TS15 clone TS15_a04f07
EU459631.1 gg_id:292864 ring-tailed lemur feces clone RT_aai09f02
DQ799731.1 gg_id:189522 human fecal clone RL182_aah32c08
DQ325939.1 gg_id:149178 Metagenomic gut microbiome healthy human stool clone B807
EU469413.1 gg_id:296007 black lemur feces clone BKLE_d08
FJ369499.1 gg_id:361773 feces adult twins and mothers; TS51 clone TS51_a01c10
EF401262.1 gg_id:211501 human fecal clone SJTU_D_08_02
FJ370165.1 gg_id:361226 feces adult twins and mothers; TS56 clone TS56_a01b10
GQ492725.1 gg_id:560281 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ493627.1 gg_id:569232 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ364178.1 gg_id:359500 feces adult twins and mothers; TS150 clone TS150_a03h05
DQ799855.1 gg_id:179980 human fecal clone RL247_aaj21a03
DQ802334.1 gg_id:183044 human fecal clone RL188_aah16c05
EU778311.1 gg_id:355874 feces clone RL387_aao91d11
DQ905629.1 gg_id:168527 human fecal clone 014C-A4
AB185576.1 gg_id:102704 rumen clone F24-A02
FJ680469.1 gg_id:528843 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796458.1 gg_id:177101 human fecal clone RL179_aah28f09
FJ369472.1 gg_id:365941 feces adult twins and mothers; TS50 clone TS50_a04h10
FJ370160.1 gg_id:370278 feces adult twins and mothers; TS56 clone TS56_a01b05
EU774103.1 gg_id:336133 Chimpanzee feces clone CHIMP1_f08
DQ795672.1 gg_id:174801 human fecal clone RL178_aan68b10
EU773420.1 gg_id:340910 Black lemur feces clone BKLE_f01_1
FJ975983.1 gg_id:572109 Human gut microbiome adopts alternative state bowel transplantation ileum effluent
DQ825217.1 gg_id:190683 human fecal clone RL185_aan86g10
DQ794691.1 gg_id:186166 human fecal clone RL240_aaj31b11
FJ367085.1 gg_id:356822 feces adult twins and mothers; TS28 clone TS28_a03d04
DQ805508.1 gg_id:188525 human fecal clone RL203_aai63e10
DQ806426.1 gg_id:187597 human fecal clone RL186_aan92c03
GQ491899.1 gg_id:534865 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ367501.1 gg_id:364982 feces adult twins and mothers; TS29 clone TS29_a04c08
AY169424.1 gg_id:81152 Ruminococcus obeum

DQ825227.1	194540	86.9	61.4	76.5	167.7	95.3	33.8
FM872529.1	358675	722.0	944.1	2565.6	950.2	623.5	1565.5
EU469676.1	292633	386.0	381.1	1058.7	242.2	269.2	362.0
FJ364608.1	369728	7461.3	7488.8	6585.6	7497.6	8617.1	7771.3
DQ807273.1	175296	590.1	606.9	206.9	257.2	252.1	72.7
FJ363614.1	365076	1035.3	1539.9	590.4	1362.0	784.3	1025.8
DQ824897.1	181054	126.4	215.1	497.3	116.8	102.7	96.3
DQ806731.1	174501	539.6	618.7	962.0	1001.3	824.7	1525.2
DQ905045.1	165102	7236.4	9549.3	12535.5	6488.5	12436.7	10955.9
FJ364581.1	366418	7204.3	8038.7	5785.6	5599.4	10215.9	7188.9
EU459631.1	292864	960.8	3203.8	2645.6	4621.2	2194.9	3141.2
DQ799731.1	189522	7974.3	8768.7	8734.7	6467.2	11239.2	9309.3
DQ325939.1	149178	359.5	530.4	1110.7	454.2	965.2	320.9
EU469413.1	296007	98.8	127.5	304.8	124.8	147.2	126.1
FJ369499.1	361773	1815.9	2636.5	1150.4	4398.4	5806.5	4832.3
EF401262.1	211501	43.5	123.1	104.7	59.7	133.3	118.9
FJ370165.1	361226	11108.7	11366.3	8081.5	8947.0	11690.8	9757.8
GQ492725.1	560281	3608.9	4096.8	2321.6	4172.3	7717.7	6260.6
GQ493627.1	569232	102.3	259.1	601.0	108.9	156.2	175.1
FJ364178.1	359500	16447.0	16435.8	10310.6	12912.1	19292.3	11814.5
DQ799855.1	179980	14375.1	13422.1	6728.5	10372.2	13545.0	12806.7
DQ802334.1	183044	146.2	338.5	624.6	213.4	378.6	365.3
EU778311.1	355874	1119.2	1514.2	2315.5	2127.0	4468.4	2914.8
DQ905629.1	168527	6704.1	6424.0	6980.0	6146.2	6118.1	6176.8
AB185576.1	102704	17.5	61.7	334.5	75.8	57.5	31.1
FJ680469.1	528843	4519.7	5032.0	2231.3	6881.5	4464.0	6384.9
DQ796458.1	177101	4646.8	3422.8	3614.0	2229.1	3625.7	2912.9
FJ369472.1	365941	7099.8	6180.4	2828.1	4829.0	5924.0	5202.1
FJ370160.1	370278	46.7	88.6	154.1	55.8	49.7	20.6
EU774103.1	336133	102.2	114.9	176.8	123.6	156.8	267.9
DQ795672.1	174801	704.5	468.1	1293.2	1424.5	204.7	372.7
EU773420.1	340910	250.3	509.0	372.3	221.7	418.4	439.5
FJ975983.1	572109	25.2	47.6	176.4	60.2	63.1	53.9
DQ825217.1	190683	1936.4	1737.1	476.7	590.9	1454.5	626.2
DQ794691.1	186166	11647.9	10311.2	5673.2	9703.1	15045.9	9613.5
FJ367085.1	356822	2839.4	3096.0	3457.1	3249.5	4911.2	5415.5
DQ805508.1	188525	166.6	242.8	545.9	199.0	376.0	380.4
DQ806426.1	187597	524.9	871.3	1332.5	580.1	1087.9	1527.0
GQ491899.1	534865	1538.4	2398.2	893.4	844.5	2669.4	2145.7
FJ367501.1	364982	8967.9	6828.8	5344.0	8056.3	12902.0	11307.1
AY169424.1	81152	482.0	257.1	402.6	395.1	563.0	140.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia

s__unclassified	21565
s__unclassified	21566
s__unclassified	21569
s__unclassified	21570
s__unclassified	21571
s__unclassified	21573
s__unclassified	21575
s__unclassified	21579
s__unclassified	21580
s__unclassified	21583
s__unclassified	21584
s__unclassified	21585
s__unclassified	21586
s__unclassified	21588
s__unclassified	21589
s__unclassified	21590
s__unclassified	21591
s__unclassified	21592
s__unclassified	21593
s__unclassified	21594
s__unclassified	21595
s__unclassified	21599
s__unclassified	21600
s__unclassified	21601
s__unclassified	21602
s__unclassified	21604
s__unclassified	21605
s__unclassified	21606
s__unclassified	21607
s__unclassified	21608
s__unclassified	21609
s__unclassified	21610
s__unclassified	21611
s__unclassified	21612
s__unclassified	21615
s__unclassified	21616
s__unclassified	21617
s__unclassified	21638
s__unclassified	21647
s__unclassified	21657
s__unclassified	21675

FJ364389.1 gg_id:368235 feces adult twins and mothers; TS15 clone TS15_a02d01
GQ898361.1 gg_id:581094 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ794403.1 gg_id:191306 human fecal clone RL197_aah87c10
DQ808364.1 gg_id:176416 human fecal clone RL180_aao75g04
DQ807968.1 gg_id:181844 human fecal clone RL180_aan69h11
FJ365929.1 gg_id:369888 feces adult twins and mothers; TS21 clone TS21_a04g07
DQ804897.1 gg_id:180401 human fecal clone RL385_aao82c02
EU463335.1 gg_id:289863 bush dog feces clone bdog1_aai78h02
DQ796672.1 gg_id:190370 human fecal clone RL179_aao53a06
FJ362616.1 gg_id:365574 feces adult twins and mothers; TS13 clone TS13_a01b04
DQ905859.2 gg_id:167403 human fecal clone 29E-g4
DQ803223.1 gg_id:177941 human fecal clone RL311_aam22d08
FJ879477.1 gg_id:449983 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
GQ898276.1 gg_id:549857 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ806568.1 gg_id:181584 human fecal clone RL186_aao46b10
DQ905381.1 gg_id:162651 human fecal clone 013C-A12
DQ802069.1 gg_id:175754 human fecal clone RL241_aaj02f11
EU776809.1 gg_id:354131 Mongoose lemur feces clone ML_aae88d12
EF399954.1 gg_id:211432 human fecal clone SJTU_E_06_47
FJ366059.1 gg_id:362157 feces adult twins and mothers; TS25 clone TS25_a02c02
DQ807356.1 gg_id:190415 human fecal clone RL307_aam05e05
FJ368244.1 gg_id:359889 feces adult twins and mothers; TS3 clone TS3_a01h09
FJ673226.1 gg_id:519792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673404.1 gg_id:516361 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY981104.1 gg_id:123256 human sigmoid colon mucosal biopsy clone G018
DQ809635.1 gg_id:190191 human fecal clone RL184_aan81h05
DQ804289.1 gg_id:175766 human fecal clone RL187_aan77e06
DQ805215.1 gg_id:179077 human fecal clone RL249_aaj83b11
EU728791.1 gg_id:328717 Ruminococcus sp. str. DJF_VR67
FJ679970.1 gg_id:523939 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU530242.1 gg_id:262753 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader
DQ806890.1 gg_id:185969 human fecal clone RL198_aaj74g10
FJ369700.1 gg_id:367283 feces adult twins and mothers; TS51 clone TS51_a03g05
GQ492798.1 gg_id:557714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU774068.1 gg_id:304108 Chimpanzee feces clone CHIMP1_g12
DQ806715.1 gg_id:184849 human fecal clone RL186_aao47h05
FJ364854.1 gg_id:362009 feces adult twins and mothers; TS19 clone TS19_a03h11
GQ491341.1 gg_id:563161 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ674265.1 gg_id:530490 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674119.1 gg_id:519474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673319.1 gg_id:518746 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

FJ364389.1	368235	1260.7	1762.5	554.3	1333.7	1668.7	1169.1
GQ898361.1	581094	8767.9	9653.9	5074.1	5932.7	8410.0	7764.3
DQ794403.1	191306	153.2	204.6	233.3	107.2	1196.3	1224.9
DQ808364.1	176416	214.0	152.7	413.5	194.1	152.5	118.5
DQ807968.1	181844	1513.8	2284.6	2515.1	909.6	3670.3	1954.5
FJ365929.1	369888	13207.3	13876.3	9862.2	11312.7	18892.2	14932.7
DQ804897.1	180401	2398.3	2663.7	1961.7	1482.3	2542.5	3073.3
EU463335.1	289863	3097.8	2944.5	764.1	2191.6	1145.7	738.4
DQ796672.1	190370	67.2	49.8	70.2	67.1	148.3	126.0
FJ362616.1	365574	44.6	57.6	190.4	55.6	81.6	65.3
DQ905859.2	167403	10706.1	8475.3	5682.6	7143.8	7166.9	5805.6
DQ803223.1	177941	4218.1	5610.2	1521.2	3330.9	6633.7	2684.4
FJ879477.1	449983	1438.2	1076.9	1562.4	824.2	621.0	890.5
GQ898276.1	549857	1512.7	1304.9	1189.8	2355.1	998.0	2260.1
DQ806568.1	181584	1093.8	1091.7	3068.1	256.4	287.3	328.1
DQ905381.1	162651	1940.6	2245.0	1596.4	2184.2	3723.6	4852.9
DQ802069.1	175754	471.1	680.5	996.1	396.8	425.1	547.9
EU776809.1	354131	2461.2	3834.5	2453.0	4351.5	5122.7	4739.9
EF399954.1	211432	137.3	241.7	179.5	119.0	137.2	139.6
FJ366059.1	362157	2921.0	2295.5	390.6	1810.2	2329.0	1425.4
DQ807356.1	190415	4656.8	3585.1	2626.4	3325.7	3714.5	4893.7
FJ368244.1	359889	11777.6	11268.8	9268.3	11482.7	12874.5	10374.0
FJ673226.1	519792	9074.7	9664.8	5510.7	9733.5	12097.9	9459.2
FJ673404.1	516361	99.0	96.0	445.7	108.0	75.1	75.7
AY981104.1	123256	50.5	96.3	75.0	94.5	178.0	99.1
DQ809635.1	190191	37.6	46.5	157.6	62.3	50.4	28.9
DQ804289.1	175766	73.9	94.6	232.7	132.0	98.2	70.2
DQ805215.1	179077	40.4	45.9	148.5	78.8	223.5	217.7
EU728791.1	328717	693.2	451.2	935.3	334.4	437.6	340.5
FJ679970.1	523939	5495.9	5450.3	6873.2	7858.0	9032.1	9431.5
EU530242.1	262753	9566.1	11135.7	3087.4	9192.1	7334.2	3914.7
DQ806890.1	185969	2419.6	1383.3	388.1	3160.9	2205.3	2209.5
FJ369700.1	367283	1147.5	1406.5	1314.7	1648.7	453.8	1032.2
GQ492798.1	557714	945.9	738.0	176.8	1379.0	1465.8	883.2
EU774068.1	304108	10608.6	9253.1	7237.5	8986.8	10653.0	9577.0
DQ806715.1	184849	7258.9	5608.2	2788.2	3885.9	6927.8	6561.5
FJ364854.1	362009	1153.5	1563.2	664.8	1054.0	326.6	198.7
GQ491341.1	563161	257.8	265.8	221.5	127.2	119.4	415.0
FJ674265.1	530490	5699.2	5595.6	3780.5	5082.0	721.8	482.0
FJ674119.1	519474	10420.3	9172.9	5219.6	6863.0	10013.7	8062.6
FJ673319.1	518746	2589.6	2109.9	1513.1	3042.6	5439.4	3448.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Blautia
g__Bryantella
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio

s__unclassified	21685
s__unclassified	21692
s__unclassified	21699
s__unclassified	21713
s__unclassified	21716
s__unclassified	21717
s__unclassified	21730
s__unclassified	21749
s__unclassified	21751
s__unclassified	21753
s__unclassified	21767
s__unclassified	21769
s__unclassified	21770
s__unclassified	21786
s__unclassified	21797
s__unclassified	22730
s__unclassified	22771
s__unclassified	22838
s__unclassified	22900
s__unclassified	22991
s__unclassified	23011
s__unclassified	23017
s__unclassified	23197
s__unclassified	23358
s__unclassified	23766
s__unclassified	23927
s__unclassified	27603
s__unclassified	28201
s__Bryantella formatexigens	20766
s__Butyrivibrio hungatei	23005
s__Butyrivibrio hungatei	23248
s__Butyrivibrio hungatei	23339
s__Clostridium proteoclasticum	22615
s__Clostridium proteoclasticum	22695
s__Clostridium proteoclasticum	22738
s__Clostridium proteoclasticum	22852
s__Clostridium proteoclasticum	22907
s__Clostridium proteoclasticum	23030
s__Clostridium proteoclasticum	23039
s__Clostridium proteoclasticum	23075
s__Clostridium proteoclasticum	23178

FJ680842.1 gg_id:530175 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673287.1 gg_id:511533 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674209.1 gg_id:510222 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674009.1 gg_id:522634 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680897.1 gg_id:514482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684208.1 gg_id:521014 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673372.1 gg_id:517174 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673461.1 gg_id:528243 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680913.1 gg_id:510622 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680874.1 gg_id:531676 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673170.1 gg_id:513764 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ672955.1 gg_id:515356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681846.1 gg_id:520411 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673417.1 gg_id:521442 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673550.1 gg_id:524819 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY858435.2 gg_id:111427 gastrointestinal tract Grant's gazelle clone GRANT16
EU381909.1 gg_id:267626 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
DQ673495.1 gg_id:164906 rumen fluid clone GRC30
AB270010.1 gg_id:172308 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos
EU844557.1 gg_id:310999 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU844013.1 gg_id:322677 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU468887.1 gg_id:290501 Speke's gazelle feces clone SP2_f07
DQ810011.1 gg_id:195034 human fecal clone RL184_aao67a08
DQ799482.1 gg_id:193685 human fecal clone RL305aal86g09
EU771915.1 gg_id:312589 Southern three-banded armadillo feces clone arma_g06_1
EU462163.1 gg_id:291179 black-handed spider monkey feces clone SPIM_aaj36c02
DQ804800.1 gg_id:184327 human fecal clone RL187_aao72h04
FJ369853.1 gg_id:360784 feces adult twins and mothers; TS55 clone TS55_a01e09
AJ318527.2 gg_id:94718 Bryantella formatexigens I-52
FJ794074.1 gg_id:576531 Butyrivibrio hungatei str. AR10
X89972.1 gg_id:13946 Butyrivibrio fibrisolvens str. NCDO 2398
AJ428553.1 gg_id:41384 Butyrivibrio hungatei str. JK 615
AF001772.1 gg_id:13940 rumen clone RFP4
EU844037.1 gg_id:303813 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EF436377.1 gg_id:217025 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC91
EF686628.1 gg_id:247786 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1
EU842438.1 gg_id:312418 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
GU174088.1 gg_id:569196 Microbial Bactrian camel estimated rumen clone XJC46
DQ518911.1 gg_id:227475 Butyrivibrio hungatei str. OV109
DQ392992.1 gg_id:154939 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o
AY178635.1 gg_id:98638 Butyrivibrio hungatei str. Su6

FJ680842.1	530175	1144.2	954.8	1167.7	584.3	602.4	706.5
FJ673287.1	511533	826.7	1597.4	592.3	930.4	3116.2	1637.6
FJ674209.1	510222	91.5	212.8	555.7	110.9	65.8	67.3
FJ674009.1	522634	102.5	127.7	747.0	117.7	482.5	212.0
FJ680897.1	514482	391.5	317.2	1056.3	1038.4	90.4	317.4
FJ684208.1	521014	3207.4	3338.3	1454.2	4356.9	6491.9	4643.3
FJ673372.1	517174	9027.7	7617.5	3344.4	8161.0	12527.4	10262.1
FJ673461.1	528243	1584.4	1482.1	286.3	1699.4	2063.3	1020.3
FJ680913.1	510622	4663.0	6200.3	4938.2	4968.1	8329.2	6722.2
FJ680874.1	531676	2624.8	2722.1	3247.3	1911.6	2195.0	2752.7
FJ673170.1	513764	5313.3	5100.2	4902.5	5237.9	7416.1	6353.7
FJ672955.1	515356	2443.2	2363.5	421.2	3435.3	3418.5	3900.5
FJ681846.1	520411	377.3	622.3	459.7	454.5	1646.8	1432.9
FJ673417.1	521442	5469.5	9806.5	5086.5	7182.1	5872.7	6068.5
FJ673550.1	524819	24.0	61.5	69.0	61.1	57.2	37.4
AY858435.2	111427	2697.8	4214.6	3032.4	3808.0	2873.8	3206.0
EU381909.1	267626	5420.2	5452.5	6327.6	6254.0	4549.5	4533.0
DQ673495.1	164906	15.0	34.2	33.7	53.1	52.2	30.5
AB270010.1	172308	384.3	549.6	1202.0	312.8	175.9	396.4
EU844557.1	310999	240.5	334.7	482.1	145.4	391.4	246.4
EU844013.1	322677	81.8	119.8	424.3	78.6	98.5	97.8
EU468887.1	290501	1566.3	1784.5	1762.1	1046.9	1431.5	1353.0
DQ810011.1	195034	710.5	1119.9	1258.9	977.3	3063.1	3051.7
DQ799482.1	193685	287.4	459.0	516.4	247.8	735.5	883.3
EU771915.1	312589	143.9	297.0	594.8	219.4	252.4	443.6
EU462163.1	291179	1551.8	1941.5	1519.8	1254.0	612.1	638.6
DQ804800.1	184327	17.0	33.2	85.6	46.6	72.3	38.4
FJ369853.1	360784	199.1	357.8	683.6	134.0	88.9	107.5
AJ318527.2	94718	208.9	308.5	186.3	124.6	122.9	102.5
FJ794074.1	576531	3065.6	2992.2	2343.2	2248.7	2558.3	1634.3
X89972.1	13946	23.5	28.4	59.6	37.7	57.0	41.2
AJ428553.1	41384	11856.8	9888.3	5708.6	7500.5	6443.4	7379.0
AF001772.1	13940	35.9	55.0	150.0	79.4	70.5	39.0
EU844037.1	303813	31.6	64.3	349.4	107.3	96.1	50.0
EF436377.1	217025	955.2	542.4	426.7	371.4	453.0	320.4
EF686628.1	247786	869.6	819.9	735.9	555.6	212.5	358.0
EU842438.1	312418	2191.8	2435.8	1947.7	1578.6	3028.1	3330.3
GU174088.1	569196	1741.6	687.8	561.5	1520.0	427.3	343.2
DQ518911.1	227475	9473.7	10588.1	3031.4	7978.0	10179.1	9831.7
DQ392992.1	154939	1328.1	762.2	533.0	537.1	534.8	509.8
AY178635.1	98638	1104.2	1512.2	1190.6	1737.3	2438.7	3000.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio

s__Clostridium proteoclasticum	23221
s__Clostridium proteoclasticum	23337
s__unclassified	22620
s__unclassified	22622
s__unclassified	22624
s__unclassified	22663
s__unclassified	22675
s__unclassified	22680
s__unclassified	22684
s__unclassified	22691
s__unclassified	22702
s__unclassified	22710
s__unclassified	22727
s__unclassified	22744
s__unclassified	22745
s__unclassified	22748
s__unclassified	22754
s__unclassified	22755
s__unclassified	22756
s__unclassified	22769
s__unclassified	22772
s__unclassified	22783
s__unclassified	22789
s__unclassified	22790
s__unclassified	22794
s__unclassified	22802
s__unclassified	22813
s__unclassified	22816
s__unclassified	22831
s__unclassified	22832
s__unclassified	22842
s__unclassified	22860
s__unclassified	22869
s__unclassified	22873
s__unclassified	22879
s__unclassified	22896
s__unclassified	22904
s__unclassified	22905
s__unclassified	22908
s__unclassified	22909
s__unclassified	22910

EF686558.1 gg_id:255035 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC4
FJ172816.1 gg_id:333793 Qinghai Yak Ruminal and Fungi China rumen clone RB-4H4
EU381489.1 gg_id:270511 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
FJ833606.1 gg_id:572615 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_15G02
EF686606.1 gg_id:248567 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9
EU259429.1 gg_id:244932 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC53
AB034043.1 gg_id:42145 rumen clone 5C0d-10
DQ393009.1 gg_id:154018 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
EU843345.1 gg_id:321214 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU843378.1 gg_id:313437 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU842593.1 gg_id:317110 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
AY699274.1 gg_id:105823 Butyrivibrio fibrisolvens L8
AB494757.1 gg_id:559488 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A
FJ832859.1 gg_id:576482 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_86F11
GU303840.1 gg_id:548476 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
AB270154.1 gg_id:166087 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos
FJ833278.1 gg_id:510595 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_79G10
EF445246.1 gg_id:212281 dairy cow rumen clone NED4C4
AB185815.1 gg_id:107748 rumen clone U29-H10
AB494789.1 gg_id:554405 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A
AB494805.1 gg_id:589848 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A
FJ833585.1 gg_id:560025 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_59C08
EU748391.1 gg_id:334520 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07c03
EU382023.1 gg_id:263296 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
AB494829.1 gg_id:562425 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A
AB185609.1 gg_id:100426 rumen clone F24-D09
AB034111.1 gg_id:45716 rumen clone 4C28d-22
FJ685127.1 gg_id:529667 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF686550.1 gg_id:237534 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC3
AY858397.2 gg_id:111923 gastrointestinal tract Grant's gazelle clone GRANT63
AB185548.1 gg_id:105647 rumen clone F23-E11
EU845063.1 gg_id:330080 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ832174.1 gg_id:593439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q101_33A05
DQ393006.1 gg_id:155107 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
FJ673134.1 gg_id:518548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ673488.1 gg_id:171181 rumen fluid clone GRC23
AM039826.1 gg_id:151973 Butyrivibrio hungatei str. JK684
EU998648.1 gg_id:344220 Anaerobic bio-energy process study on bioreactor fermentative hydrogen productio
AF018563.1 gg_id:13983 rumen fluid clone 12-116
EU259455.1 gg_id:250378 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC79
AF396927.1 gg_id:46567 Butyrivibrio fibrisolvens str. WV1

EF686558.1	255035	1611.1	969.7	1053.7	1633.2	606.9	615.8
FJ172816.1	333793	1707.7	1399.8	1223.0	2888.6	2838.1	2218.6
EU381489.1	270511	1629.3	2936.3	3015.2	1070.4	698.0	1582.1
FJ833606.1	572615	1334.8	2606.8	892.1	999.9	1014.6	2153.1
EF686606.1	248567	949.2	1067.2	1992.2	1288.3	2423.3	2376.5
EU259429.1	244932	1825.2	2834.6	1408.9	2432.9	3560.3	2809.8
AB034043.1	42145	393.5	375.7	436.8	1138.1	269.1	587.4
DQ393009.1	154018	39.9	87.6	545.3	91.5	60.4	31.0
EU843345.1	321214	5063.0	6639.4	4048.3	3433.2	3545.8	4019.6
EU843378.1	313437	4474.3	7249.1	2723.8	2589.2	2532.6	2554.3
EU842593.1	317110	5919.8	4671.4	3099.4	6091.7	3410.4	4093.7
AY699274.1	105823	476.7	240.4	935.2	772.1	159.7	279.4
AB494757.1	559488	3515.0	3058.1	1843.3	1608.9	1320.3	1511.5
FJ832859.1	576482	1104.3	3342.1	4095.2	3267.6	1551.2	2069.9
GU303840.1	548476	6403.1	8135.5	5352.1	5607.2	9428.7	8786.0
AB270154.1	166087	20.7	24.9	52.5	41.2	59.9	28.6
FJ833278.1	510595	502.4	447.4	1292.8	468.1	181.7	294.1
EF445246.1	212281	34.0	44.4	57.6	66.7	63.2	16.1
AB185815.1	107748	291.6	558.2	643.4	343.9	1248.7	1614.0
AB494789.1	554405	907.6	1575.2	2178.1	577.5	1787.3	1907.3
AB494805.1	589848	1085.9	1518.4	413.1	1963.9	1239.6	845.9
FJ833585.1	560025	384.2	466.3	2306.9	404.0	534.1	416.6
EU748391.1	334520	14275.0	13241.3	11985.9	12581.0	8147.5	8401.8
EU382023.1	263296	325.9	499.1	919.4	137.5	1518.2	424.4
AB494829.1	562425	1851.8	606.9	465.1	432.9	520.5	616.1
AB185609.1	100426	4717.4	5220.9	5017.2	6685.1	6745.9	6175.2
AB034111.1	45716	24.3	41.0	31.8	64.2	67.4	17.9
FJ685127.1	529667	2484.1	2296.5	906.6	3068.7	1762.1	1961.0
EF686550.1	237534	2867.7	3083.2	1422.5	4113.0	3978.1	3877.7
AY858397.2	111923	22.2	49.8	33.0	89.1	59.8	34.1
AB185548.1	105647	226.9	273.7	282.8	141.8	257.3	238.3
EU845063.1	330080	455.2	951.6	1061.4	181.7	736.0	472.6
FJ832174.1	593439	81.6	276.5	596.4	154.0	173.7	171.4
DQ393006.1	155107	170.1	268.7	100.3	1094.6	130.5	88.8
FJ673134.1	518548	53.4	220.1	334.4	140.1	608.4	188.4
DQ673488.1	171181	371.9	624.6	507.7	1174.2	842.5	1036.0
AM039826.1	151973	3862.6	2708.5	2159.5	1446.9	3545.0	2300.0
EU998648.1	344220	1211.1	571.0	2552.6	1276.3	494.5	995.3
AF018563.1	13983	5470.5	6397.5	3317.4	6442.4	7293.4	6559.4
EU259455.1	250378	4488.4	6278.6	4423.6	3086.0	3509.9	4087.1
AF396927.1	46567	6419.7	7058.0	8584.7	4809.6	8459.5	8195.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio

s__unclassified	22913
s__unclassified	22924
s__unclassified	22961
s__unclassified	22996
s__unclassified	23010
s__unclassified	23022
s__unclassified	23059
s__unclassified	23065
s__unclassified	23070
s__unclassified	23080
s__unclassified	23081
s__unclassified	23086
s__unclassified	23087
s__unclassified	23092
s__unclassified	23100
s__unclassified	23108
s__unclassified	23110
s__unclassified	23121
s__unclassified	23130
s__unclassified	23140
s__unclassified	23143
s__unclassified	23160
s__unclassified	23171
s__unclassified	23174
s__unclassified	23176
s__unclassified	23181
s__unclassified	23182
s__unclassified	23183
s__unclassified	23196
s__unclassified	23212
s__unclassified	23215
s__unclassified	23218
s__unclassified	23237
s__unclassified	23242
s__unclassified	23246
s__unclassified	23262
s__unclassified	23264
s__unclassified	23275
s__unclassified	23278
s__unclassified	23281
s__unclassified	23286

FJ172856.1 gg_id:352708 Qinghai Yak Ruminal and Fungi China rumen clone RB-3H4
EU475426.1 gg_id:292105 springbok feces clone SBSD_aaa04h10
AF001728.1 gg_id:13939 rumen clone RCP17
EU748328.1 gg_id:353814 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05b05
FJ832996.1 gg_id:571152 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q102_35C05
NR_025981.1 gg_id:554698 Butyrivibrio fibrisolvens str. ATCC 19171
GU303265.1 gg_id:544781 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU381935.1 gg_id:272045 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
EU887842.1 gg_id:313349 Butyrivibrio fibrisolvens str. H15
GU303723.1 gg_id:583937 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EU845522.1 gg_id:317020 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU259488.1 gg_id:251666 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC112
FJ832546.1 gg_id:551295 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q301_19C03
EU344292.1 gg_id:273016 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
X89973.1 gg_id:13947 Butyrivibrio fibrisolvens str. NCDO 2432
GQ402115.1 gg_id:572392 alpacas and sheep forestomach clone ALP7
FJ833317.1 gg_id:508957 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q401_47G06
EU845719.1 gg_id:329343 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EF686570.1 gg_id:257136 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC5
EU845411.1 gg_id:355326 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU468953.1 gg_id:303390 Speke's gazelle feces clone SP2_h03_1
FJ832450.1 gg_id:590844 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_35C05
GU303299.1 gg_id:562486 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU344321.1 gg_id:266983 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ172805.1 gg_id:310869 Qinghai Yak Ruminal and Fungi China rumen clone RB-2E2
AB185626.1 gg_id:101165 rumen clone F24-F04
AB034057.1 gg_id:53486 rumen clone 4C3d-2
AF084837.1 gg_id:13951 Eubacterium sp. str. TW2
EU843480.1 gg_id:333462 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ832235.1 gg_id:538459 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q102_57A08
EU469799.1 gg_id:295622 western lowland gorilla feces clone GOR_aag71b07
AY699275.1 gg_id:105974 Butyrivibrio fibrisolvens L10
DQ673500.1 gg_id:173319 rumen fluid clone GRC35
FJ684664.1 gg_id:515496 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU844205.1 gg_id:350862 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB494756.1 gg_id:550436 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A
X89976.1 gg_id:13950 Butyrivibrio fibrisolvens str. Bu 43
FJ678988.1 gg_id:511462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ832270.1 gg_id:587175 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q201_33A05
EU748148.1 gg_id:313865 neotropical folivorous flying bird adult hoatzin crop clone hoa32_08H01.F
EU844744.1 gg_id:324284 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi

FJ172856.1	352708	70.3	85.5	230.6	55.8	89.5	188.4
EU475426.1	292105	26.6	45.3	66.6	57.4	219.5	68.8
AF001728.1	13939	4689.5	5295.2	2934.2	3607.6	6856.9	5232.5
EU748328.1	353814	2840.4	4192.5	2189.1	3339.6	5252.7	5213.0
FJ832996.1	571152	8646.6	9508.1	6834.9	6821.8	9546.0	8326.8
NR_025981.1	554698	3108.4	3322.8	2706.9	2457.6	3570.3	3025.0
GU303265.1	544781	855.5	910.9	470.4	580.5	125.5	312.2
EU381935.1	272045	88.7	128.3	196.4	116.4	142.8	50.6
EU887842.1	313349	5552.4	4106.3	2763.8	5963.4	5834.9	6007.5
GU303723.1	583937	3917.5	2926.1	1632.5	4165.5	4073.2	3600.9
EU845522.1	317020	1388.0	1807.2	684.1	804.6	446.4	519.1
EU259488.1	251666	257.1	210.3	789.9	216.4	68.2	103.1
FJ832546.1	551295	394.0	460.8	942.1	212.9	245.3	1288.7
EU344292.1	273016	3204.8	3707.1	4575.7	3736.3	5395.4	4414.8
X89973.1	13947	888.6	1624.9	2178.7	906.1	5638.2	3379.7
GQ402115.1	572392	3694.8	3424.8	1275.7	4751.0	3506.9	4306.6
FJ833317.1	508957	1986.9	1280.1	1829.0	1234.0	1521.8	3829.8
EU845719.1	329343	574.8	613.5	1005.5	383.5	705.9	547.1
EF686570.1	257136	482.9	1241.7	2428.6	711.3	2761.8	2632.2
EU845411.1	355326	5666.9	7713.3	7430.1	6244.1	9312.2	9007.5
EU468953.1	303390	5957.2	7411.5	2901.5	4884.0	4089.2	3208.5
FJ832450.1	590844	130.7	160.4	462.6	87.0	89.2	62.1
GU303299.1	562486	1858.6	3208.7	830.7	612.7	513.0	243.6
EU344321.1	266983	603.9	744.9	1062.1	830.5	361.2	639.2
FJ172805.1	310869	2134.8	2320.7	1322.1	4470.6	2683.3	3072.3
AB185626.1	101165	53.3	153.2	1368.5	134.7	53.7	56.1
AB034057.1	53486	12888.5	16285.4	7314.9	9553.6	10690.1	11618.9
AF084837.1	13951	125.5	235.7	201.1	190.1	336.4	172.8
EU843480.1	333462	108.5	169.6	523.3	133.9	281.0	269.5
FJ832235.1	538459	1349.6	3077.2	2241.5	868.1	1093.9	1035.8
EU469799.1	295622	16.2	17.5	14.0	41.4	45.2	13.6
AY699275.1	105974	299.8	258.2	855.2	246.4	71.2	198.4
DQ673500.1	173319	540.9	724.1	1250.5	368.5	2070.2	1812.2
FJ684664.1	515496	10554.5	9117.8	8512.0	7342.9	9971.8	8960.6
EU844205.1	350862	2004.2	2516.8	2201.7	3003.1	864.9	1191.1
AB494756.1	550436	4941.5	4785.8	2412.3	3094.4	356.7	749.5
X89976.1	13950	1111.3	919.8	670.2	291.0	88.3	270.3
FJ678988.1	511462	7696.3	8002.3	7880.7	6269.1	6199.3	7786.9
FJ832270.1	587175	464.7	899.3	1200.4	1698.5	601.8	752.2
EU748148.1	313865	1101.8	2399.6	2190.9	1170.2	357.7	658.7
EU844744.1	324284	3945.5	4133.4	3076.5	4017.3	6173.1	6255.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Butyrivibrio
g__Catonella
g__Catonella
g__Catonella
g__Catonella
g__Catonella
g__Catonella
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	23297
s__unclassified	23300
s__unclassified	23319
s__unclassified	23333
s__unclassified	23334
s__unclassified	23354
s__unclassified	23356
s__unclassified	23365
s__unclassified	23380
s__unclassified	23385
s__unclassified	23395
s__unclassified	23399
s__unclassified	23404
s__unclassified	23412
s__unclassified	23415
s__unclassified	23419
s__unclassified	23431
s__unclassified	23548
s__unclassified	23654
s__unclassified	23657
s__unclassified	24043
s__unclassified	24139
s__unclassified	22792
s__unclassified	22796
s__unclassified	22912
s__unclassified	23044
s__unclassified	23381
s__unclassified	23384
s__Clostridium bolteae	18758
s__Clostridium bolteae	18876
s__Clostridium bolteae	18923
s__Clostridium celerecrescens	19836
s__Clostridium celerecrescens	20312
s__Clostridium hylemonae	18671
s__Clostridium piliforme	27740
s__Clostridium piliforme	27768
s__Clostridium piliforme	27902
s__Clostridium piliforme	27955
s__Clostridium piliforme	27999
s__Clostridium piliforme	28013
s__Clostridium scindens	18677

NR_029185.1 gg_id:582636 Clostridium proteoclasticum str. B316; ATCC 51982
EF436289.1 gg_id:212460 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC03
EU458792.1 gg_id:288228 Goeldi's marmoset feces clone CAL_g01_1
AJ428552.1 gg_id:29965 Clostridium proteoclasticum str. UC 142
X89975.1 gg_id:13949 Butyrivibrio fibrisolvens str. NCDO 2435
DQ256289.1 gg_id:142613 Rumen fermentation and dynamics during stepwise adaptation -concentrate diet gc
EF436453.1 gg_id:208144 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC167
EU344334.1 gg_id:260128 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
AF396926.1 gg_id:37898 Butyrivibrio fibrisolvens str. C211
EU468849.1 gg_id:287834 Speke's gazelle feces clone SP2_a02
GU302641.1 gg_id:535265 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
FJ833856.1 gg_id:578507 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_60D08
AB034049.1 gg_id:52499 rumen clone 5C0d-19
GU303019.1 gg_id:556604 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
FJ833619.1 gg_id:591679 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_08H01
GU303967.1 gg_id:544678 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
FJ834274.1 gg_id:584208 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_73A10
EU843301.1 gg_id:306119 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ278862.1 gg_id:155730 Clostridium aminophilum 152R-1b
FJ833697.1 gg_id:551575 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q101_44D06
EU998650.1 gg_id:304850 Anaerobic bio-energy process study on bioreactor fermentative hydrogen productio
GU302568.1 gg_id:557599 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
GQ115584.1 gg_id:382807 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687h1(
AM420037.1 gg_id:239814 Noma subgingival plaque clone 202A08(oral)
GU407024.1 gg_id:571776 Human Oral Microbiome oral cavity
X87151.1 gg_id:14096 Catonella morbi str. ATCC 51271
AF385556.1 gg_id:48583 crevicular epithelial cells clone BR063
NZ_ACIN02000016.1 gg_id:469479 Abiotrophia defectiva str. ATCC 49176
NZ_ABCC02000039.1 gg_id:469991 Clostridium bolteae str. ATCC BAA-613
FJ371143.1 gg_id:360723 feces adult twins and mothers; TS6 clone TS6_a01d12
AJ508452.1 gg_id:83226 Clostridium bolteae str. 16351
DQ479412.1 gg_id:157999 Clostridium sp. CYP2
FM994938.1 gg_id:537456 Clostridium celerecrescens str. HP2
AB117568.1 gg_id:111552 Clostridium hylemonae str. CT-30
D14638.1 gg_id:14113 Clostridium piliforme str. RJ
DQ352808.1 gg_id:151298 Clostridium piliforme CRL-K
DQ352807.1 gg_id:155362 Clostridium piliforme 7MTS
DQ352806.1 gg_id:153965 Clostridium piliforme
DQ352811.1 gg_id:153952 Clostridium piliforme R1
DQ352810.1 gg_id:153713 Clostridium piliforme CRL
AY244789.1 gg_id:86360 Clostridium scindens str. 2002-69680

NR_029185.1	582636	7324.7	8304.9	4410.6	5425.5	8455.8	8329.7
EF436289.1	212460	81.5	127.2	47.0	63.2	63.3	30.8
EU458792.1	288228	2499.8	4048.2	3396.2	1430.1	1053.5	3199.1
AJ428552.1	29965	15326.5	15150.8	6435.2	11495.3	12067.0	10241.6
X89975.1	13949	992.3	1107.2	1221.3	438.3	171.9	503.7
DQ256289.1	142613	503.9	225.1	43.0	118.5	176.8	59.8
EF436453.1	208144	8501.7	8354.1	5893.2	5599.1	4014.9	7359.2
EU344334.1	260128	7860.9	8252.5	8223.1	8325.7	9131.8	9179.1
AF396926.1	37898	3461.1	3508.0	6408.4	3507.9	1605.4	2530.1
EU468849.1	287834	7064.1	6018.2	7736.3	6038.9	5705.5	5405.5
GU302641.1	535265	2879.9	3225.3	1782.4	5290.2	5423.2	4957.6
FJ833856.1	578507	755.1	1360.2	2235.6	639.2	754.1	740.1
AB034049.1	52499	51.2	77.3	72.0	79.8	80.7	108.1
GU303019.1	556604	863.6	2712.8	1798.5	1146.1	756.2	1300.1
FJ833619.1	591679	1223.1	1657.5	4998.2	2559.0	811.0	2076.8
GU303967.1	544678	2387.3	3286.3	3111.6	1992.7	2660.8	3100.2
FJ834274.1	584208	689.7	1245.5	1446.4	390.0	1190.7	645.8
EU843301.1	306119	73.6	41.1	78.4	72.6	57.0	61.8
DQ278862.1	155730	18.7	343.9	24.7	45.5	700.2	460.8
FJ833697.1	551575	1880.2	3510.0	1548.6	1136.3	714.4	1484.5
EU998650.1	304850	64.1	122.1	597.4	293.3	264.0	333.3
GU302568.1	557599	10386.4	8763.0	9979.5	12551.1	9359.6	10732.6
GQ115584.1	382807	4328.2	4680.5	3617.7	3092.3	5972.3	4475.9
AM420037.1	239814	2649.0	1834.9	3695.6	3085.5	2759.5	3203.1
GU407024.1	571776	9286.1	7762.2	7432.3	5820.7	5733.1	5891.9
X87151.1	14096	97.3	163.3	592.4	148.4	174.4	90.1
AF385556.1	48583	2859.2	2381.1	3248.5	3098.7	2112.7	2794.9
NZ_ACIN02000016.1	469479	2627.5	1880.9	2636.9	1740.4	1805.0	1261.3
NZ_ABCC02000039.1	469991	58.1	41.1	264.0	68.7	53.5	35.2
FJ371143.1	360723	894.9	758.9	1356.0	1101.4	316.3	330.4
AJ508452.1	83226	45.6	65.5	252.3	73.3	109.8	37.5
DQ479412.1	157999	100.9	109.0	372.3	93.7	114.1	46.3
FM994938.1	537456	5952.7	5378.7	5345.7	5527.1	4085.1	3535.9
AB117568.1	111552	108.9	157.3	85.4	88.2	76.7	112.0
D14638.1	14113	2548.2	2830.1	3841.1	2826.8	3281.0	3849.9
DQ352808.1	151298	1935.8	1930.2	1332.7	1183.1	2701.0	2565.9
DQ352807.1	155362	2675.3	2532.8	5872.1	5357.9	2252.9	1934.8
DQ352806.1	153965	4654.8	5934.1	2501.5	3090.1	5533.4	4556.2
DQ352811.1	153952	15423.9	14884.7	7174.7	10860.5	10595.2	11737.2
DQ352810.1	153713	6726.2	8291.0	6682.2	4519.4	10217.1	7606.5
AY244789.1	86360	26.9	32.5	100.6	50.5	72.2	37.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__Clostridium scindens	19173
s__Clostridium scindens	19352
s__unclassified	17590
s__unclassified	18059
s__unclassified	18317
s__unclassified	18318
s__unclassified	18325
s__unclassified	18331
s__unclassified	18332
s__unclassified	18348
s__unclassified	18356
s__unclassified	18362
s__unclassified	18363
s__unclassified	18374
s__unclassified	18379
s__unclassified	18389
s__unclassified	18391
s__unclassified	18392
s__unclassified	18398
s__unclassified	18413
s__unclassified	18426
s__unclassified	18446
s__unclassified	18447
s__unclassified	18449
s__unclassified	18450
s__unclassified	18451
s__unclassified	18460
s__unclassified	18462
s__unclassified	18474
s__unclassified	18487
s__unclassified	18490
s__unclassified	18495
s__unclassified	18497
s__unclassified	18500
s__unclassified	18510
s__unclassified	18511
s__unclassified	18523
s__unclassified	18530
s__unclassified	18540
s__unclassified	18543
s__unclassified	18549

FJ370593.1 gg_id:368214 feces adult twins and mothers; TS57 clone TS57_a02h04
DQ799592.1 gg_id:191476 human fecal clone RL305aal88a10
DQ806965.1 gg_id:193601 human fecal clone RL198_aaj76c02
DQ801189.1 gg_id:179381 human fecal clone RL116_aaf00c04
FJ678914.1 gg_id:522609 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU451069.1 gg_id:322062 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
AY984751.1 gg_id:122545 human stool clone B711
GQ492488.1 gg_id:584140 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU462089.1 gg_id:292294 black-handed spider monkey feces clone SPIM_aaj34g08
EU504811.1 gg_id:273376 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02e11
DQ823839.1 gg_id:185281 human fecal clone RL250_aaj79g08
DQ456402.1 gg_id:157112 pre-adolescent turkey cecum clone CFT214H8
DQ801439.1 gg_id:185174 human fecal clone RL388_aao95e09
DQ799332.1 gg_id:179876 human fecal clone RL305aal85a06
EU455444.1 gg_id:342887 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU778887.1 gg_id:306692 Black-handed Spider Monkey feces clone SPIM_f10
FJ685196.1 gg_id:531394 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799688.1 gg_id:189413 human fecal clone RL182_aah31c11
FJ879747.1 gg_id:419244 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU779009.1 gg_id:341752 Prevost's squirrel feces clone SQ_aah80e08
FJ371024.1 gg_id:360061 feces adult twins and mothers; TS5 clone TS5_a04a08
GQ156416.1 gg_id:558831 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
FJ683057.1 gg_id:528893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU509444.1 gg_id:267886 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e03
DQ805861.1 gg_id:184155 human fecal clone RL306aal92a04
GQ491719.1 gg_id:560908 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ369253.1 gg_id:363341 feces adult twins and mothers; TS50 clone TS50_a02b02
EU510715.1 gg_id:269586 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39g09
DQ801354.1 gg_id:188674 human fecal clone RL388_aao94d08
DQ057375.1 gg_id:130277 chicken ileum/cecum clone cc152
DQ805819.1 gg_id:182430 human fecal clone RL306aal91e02
EU451541.1 gg_id:349757 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
EU508869.1 gg_id:270015 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37d12
EU766372.1 gg_id:328667 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
DQ825256.1 gg_id:182940 human fecal clone RL185_aan87d04
EU470204.1 gg_id:297920 trancaspain urial feces clone TU2_aaa04b02
FJ367980.1 gg_id:358986 feces adult twins and mothers; TS30 clone TS30_a02b03
FJ678396.1 gg_id:513429 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU455270.1 gg_id:340600 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S
EU763188.1 gg_id:323777 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EF399125.1 gg_id:205476 human fecal clone SJTU_F_12_07

FJ370593.1	368214	39.3	49.2	157.2	69.2	74.5	66.2
DQ799592.1	191476	28.3	54.1	53.9	66.1	83.3	21.7
DQ806965.1	193601	3352.2	2512.7	2575.0	2455.8	1435.9	1724.3
DQ801189.1	179381	28.0	45.6	245.9	42.0	75.2	57.8
FJ678914.1	522609	18.6	20.8	102.6	57.4	39.5	25.0
EU451069.1	322062	561.0	923.2	906.6	573.1	1006.1	791.3
AY984751.1	122545	2027.2	2379.3	1725.4	685.4	903.4	1151.4
GQ492488.1	584140	40.9	64.0	102.1	93.2	67.8	37.3
EU462089.1	292294	43.0	88.3	279.3	70.4	48.0	53.8
EU504811.1	273376	1340.5	1428.7	709.3	882.5	142.1	307.9
DQ823839.1	185281	55.9	180.1	328.7	91.0	66.8	85.8
DQ456402.1	157112	174.3	130.7	1272.0	260.1	267.1	265.1
DQ801439.1	185174	6709.6	7865.4	3078.2	5174.5	4923.6	4975.4
DQ799332.1	179876	36.9	57.6	137.0	48.3	60.1	35.1
EU455444.1	342887	3449.6	4489.7	3122.3	940.5	1630.7	1033.5
EU778887.1	306692	3480.4	4614.8	5119.8	3099.4	4304.2	6918.1
FJ685196.1	531394	349.8	486.9	1422.5	303.2	828.8	1113.8
DQ799688.1	189413	109.7	209.4	430.0	83.7	99.9	121.1
FJ879747.1	419244	249.7	557.7	749.2	735.0	548.6	369.3
EU779009.1	341752	3226.2	2289.7	2280.3	2370.1	2378.5	1531.4
FJ371024.1	360061	1478.9	1276.9	428.6	1604.0	2368.3	2165.7
GQ156416.1	558831	87.5	102.8	434.2	90.9	102.8	94.7
FJ683057.1	528893	3648.8	4969.0	1886.0	2207.5	3012.6	1521.8
EU509444.1	267886	530.5	892.9	1612.8	436.2	397.7	650.3
DQ805861.1	184155	33.5	33.4	90.7	54.6	62.6	22.4
GQ491719.1	560908	332.2	401.4	351.7	250.6	425.0	1249.7
FJ369253.1	363341	1128.8	1391.1	1974.6	2189.0	2471.9	3098.9
EU510715.1	269586	3089.6	3389.6	2829.4	3388.9	3155.7	3563.7
DQ801354.1	188674	285.4	456.3	419.4	103.2	268.1	150.1
DQ057375.1	130277	18.5	28.7	51.4	37.2	53.2	15.7
DQ805819.1	182430	4999.3	5743.9	3518.6	3255.5	4700.4	9120.6
EU451541.1	349757	7596.0	8084.1	3656.2	7223.8	2187.2	2159.8
EU508869.1	270015	152.6	133.0	51.5	269.9	719.2	294.8
EU766372.1	328667	33.8	35.5	57.2	67.6	52.5	29.4
DQ825256.1	182940	49.2	46.4	73.2	63.3	44.7	26.7
EU470204.1	297920	2076.0	3196.9	1593.1	1593.2	1129.4	668.2
FJ367980.1	358986	2419.5	2513.8	1695.1	3090.8	3074.6	2673.7
FJ678396.1	513429	9534.2	9287.3	3313.9	6278.7	8981.6	7151.4
EU455270.1	340600	44.8	72.6	100.8	60.2	66.1	54.4
EU763188.1	323777	8651.0	8488.6	8260.8	6475.9	8304.8	7698.8
EF399125.1	205476	87.5	59.6	119.0	68.7	71.1	46.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	18554
s__unclassified	18560
s__unclassified	18561
s__unclassified	18568
s__unclassified	18578
s__unclassified	18580
s__unclassified	18586
s__unclassified	18589
s__unclassified	18594
s__unclassified	18597
s__unclassified	18603
s__unclassified	18605
s__unclassified	18607
s__unclassified	18618
s__unclassified	18621
s__unclassified	18622
s__unclassified	18631
s__unclassified	18652
s__unclassified	18653
s__unclassified	18664
s__unclassified	18665
s__unclassified	18668
s__unclassified	18673
s__unclassified	18678
s__unclassified	18681
s__unclassified	18685
s__unclassified	18688
s__unclassified	18695
s__unclassified	18711
s__unclassified	18718
s__unclassified	18719
s__unclassified	18720
s__unclassified	18728
s__unclassified	18733
s__unclassified	18746
s__unclassified	18748
s__unclassified	18749
s__unclassified	18760
s__unclassified	18762
s__unclassified	18776
s__unclassified	18780

DQ802257.1 gg_id:183438 human fecal clone RL188_aah15b10
EU510626.1 gg_id:260811 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38d06
GQ492126.1 gg_id:573110 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ832608.1 gg_id:545139 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_31G04
DQ799840.1 gg_id:191687 human fecal clone RL182_aah34g05
DQ806982.1 gg_id:179726 human fecal clone RL198_aaj76f07
EU468527.1 gg_id:290934 okapi feces clone OK1_a07_2
EU451201.1 gg_id:329571 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
GQ491160.1 gg_id:544635 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ681675.1 gg_id:513440 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800343.1 gg_id:173900 human fecal clone RL303_aal71h03
GQ492164.1 gg_id:534016 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ326040.1 gg_id:202839 Metagenomic distal gut microbiome healthy human stool clone BA08
DQ801933.1 gg_id:190188 human fecal clone RL201_aai48f09
GQ493000.1 gg_id:537661 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ905665.1 gg_id:164419 human fecal clone 014C-D11
FJ681847.1 gg_id:523064 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368654.1 gg_id:368572 feces adult twins and mothers; TS49 clone TS49_a02h04
FJ680491.1 gg_id:519396 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366657.1 gg_id:362539 feces adult twins and mothers; TS27 clone TS27_a02c07
EU459642.1 gg_id:288103 ring-tailed lemur feces clone RT_aai09h02
EF404404.1 gg_id:209847 human fecal clone SJTU_C_09_53
FJ679391.1 gg_id:518431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU508804.1 gg_id:269313 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51c11
EU462022.1 gg_id:291771 black-handed spider monkey feces clone SPIM_aaj33d11
AB234508.1 gg_id:147442 termite gut homogenate clone MgMjW-19
EU463310.1 gg_id:291477 bush dog feces clone bdog1_aai77g06
FJ676399.1 gg_id:522177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364631.1 gg_id:366411 feces adult twins and mothers; TS19 clone TS19_a01c03
FJ677673.1 gg_id:517081 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF398872.1 gg_id:205862 human fecal clone SJTU_F_08_42
DQ905410.1 gg_id:163456 human fecal clone 013C-D7
GQ016102.1 gg_id:493565 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
DQ795830.1 gg_id:189334 human fecal clone RL245_aai83a11
EU459637.1 gg_id:298788 ring-tailed lemur feces clone RT_aai09g03
GQ493802.1 gg_id:566459 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU459728.1 gg_id:292544 ring-tailed lemur feces clone RT_aai11f10
EU462186.1 gg_id:295683 black-handed spider monkey feces clone SPIM_aaj36g03
EF398675.1 gg_id:207959 human fecal clone SJTU_F_05_23
DQ808211.1 gg_id:193699 human fecal clone RL180_aao73h09
EF401865.1 gg_id:210965 human fecal clone SJTU_D_04_32

DQ802257.1	183438	47.2	92.2	164.9	107.7	128.0	150.4
EU510626.1	260811	6785.6	5182.7	7227.6	7041.9	4255.9	5042.4
GQ492126.1	573110	194.3	97.4	176.7	410.8	64.1	35.4
FJ832608.1	545139	656.0	901.0	1031.2	528.5	1256.5	1824.5
DQ799840.1	191687	31.4	72.8	160.3	71.9	62.8	43.6
DQ806982.1	179726	730.5	1230.3	1171.5	1148.2	4848.1	3788.8
EU468527.1	290934	1171.9	1272.6	1959.9	497.3	441.0	518.6
EU451201.1	329571	3170.8	3427.0	1284.4	1822.2	3457.9	2524.8
GQ491160.1	544635	315.0	428.8	841.8	368.8	409.6	312.8
FJ681675.1	513440	771.7	1371.3	380.6	153.9	95.6	51.8
DQ800343.1	173900	37.9	61.4	216.5	68.5	152.2	57.7
GQ492164.1	534016	1695.0	1308.5	244.4	2021.0	1975.0	1591.4
DQ326040.1	202839	67.0	71.6	180.1	66.4	78.0	123.2
DQ801933.1	190188	3508.4	3917.0	5043.0	2858.1	3179.6	3274.1
GQ493000.1	537661	12117.0	10990.5	10140.1	9284.7	13317.8	12436.3
DQ905665.1	164419	152.7	261.3	613.9	153.6	106.2	121.3
FJ681847.1	523064	2753.0	2966.9	2909.4	2001.2	2460.0	3081.0
FJ368654.1	368572	3182.7	5450.5	7333.5	4008.7	5134.0	4633.5
FJ680491.1	519396	10982.5	10937.2	6924.8	7111.3	12817.8	14264.0
FJ366657.1	362539	42.0	67.0	105.1	77.6	131.7	43.0
EU459642.1	288103	363.3	291.7	425.7	455.9	423.0	366.4
EF404404.1	209847	1972.5	1579.7	487.1	1601.5	241.8	232.9
FJ679391.1	518431	2730.8	4822.3	1645.5	2255.8	4310.1	2538.8
EU508804.1	269313	5276.8	5030.5	5735.0	4841.3	9181.9	5791.6
EU462022.1	291771	265.2	785.4	684.3	174.8	201.3	192.9
AB234508.1	147442	36.5	97.6	74.7	78.6	79.7	39.5
EU463310.1	291477	103.7	185.7	259.8	103.4	107.1	86.4
FJ676399.1	522177	136.4	206.0	349.7	148.1	129.7	232.1
FJ364631.1	366411	1791.9	1162.4	2462.6	2562.1	1179.6	1969.6
FJ677673.1	517081	915.1	1206.9	2074.0	1101.5	706.5	2606.8
EF398872.1	205862	2773.7	3196.6	1942.8	1982.5	2294.6	2272.1
DQ905410.1	163456	6673.9	7185.4	3358.2	5703.8	5418.2	6053.2
GQ016102.1	493565	608.4	885.0	797.6	130.2	587.5	641.9
DQ795830.1	189334	1934.0	2535.8	2673.1	1834.0	3409.0	2086.3
EU459637.1	298788	2457.6	4444.2	4248.0	2724.0	5130.8	4992.2
GQ493802.1	566459	388.4	429.9	340.8	364.3	412.6	600.8
EU459728.1	292544	289.6	443.3	883.5	407.8	926.6	238.8
EU462186.1	295683	604.1	323.6	671.5	819.0	480.4	178.8
EF398675.1	207959	560.2	240.6	249.9	674.1	91.9	537.1
DQ808211.1	193699	762.2	381.5	795.5	718.1	124.8	251.7
EF401865.1	210965	391.1	329.9	377.3	272.1	485.8	294.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	18783
s__unclassified	18785
s__unclassified	18787
s__unclassified	18788
s__unclassified	18796
s__unclassified	18807
s__unclassified	18808
s__unclassified	18824
s__unclassified	18827
s__unclassified	18830
s__unclassified	18832
s__unclassified	18835
s__unclassified	18842
s__unclassified	18845
s__unclassified	18849
s__unclassified	18854
s__unclassified	18859
s__unclassified	18861
s__unclassified	18862
s__unclassified	18864
s__unclassified	18877
s__unclassified	18878
s__unclassified	18889
s__unclassified	18913
s__unclassified	18918
s__unclassified	18930
s__unclassified	18933
s__unclassified	18934
s__unclassified	18938
s__unclassified	18940
s__unclassified	18942
s__unclassified	18950
s__unclassified	18952
s__unclassified	18957
s__unclassified	18960
s__unclassified	18962
s__unclassified	18963
s__unclassified	18966
s__unclassified	18975
s__unclassified	18982
s__unclassified	18987

AY916317.1 gg_id:113422 human stool clone B395
EU510296.1 gg_id:259056 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04c08
FJ368701.1 gg_id:368980 feces adult twins and mothers; TS49 clone TS49_a03e03
AM405126.2 gg_id:573969 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.76
EU456172.1 gg_id:311674 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
AY984289.1 gg_id:117903 human stool clone B182
DQ808725.1 gg_id:198434 human fecal clone RL239_aaj12d08
FJ676459.1 gg_id:531723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU510783.1 gg_id:259781 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49c02
EU761737.1 gg_id:349087 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
EU009784.1 gg_id:256807 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_R38
EU463311.1 gg_id:298468 bush dog feces clone bdog1_aai77g08
EU771786.1 gg_id:313144 African elephant feces clone AFYEL_aaj65g01
EF096345.1 gg_id:185355 mouse cecum clone obob2_aaa01c07
DQ809008.1 gg_id:187682 human fecal clone RL243_aai88b05
DQ799785.1 gg_id:178610 human fecal clone RL182_aah33e05
DQ342332.1 gg_id:174153 Effect probiotics and synbiotics on gastrointestinal broilers broiler chicken intestine
GQ492903.1 gg_id:593444 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF399415.1 gg_id:207651 human fecal clone SJTU_F_15_57
DQ809996.1 gg_id:198555 human fecal clone RL184_aao66h02
FJ364704.1 gg_id:358447 feces adult twins and mothers; TS19 clone TS19_a02a09
FJ680441.1 gg_id:527271 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ362631.1 gg_id:361732 feces adult twins and mothers; TS13 clone TS13_a01c08
EU459643.1 gg_id:293128 ring-tailed lemur feces clone RT_aai09h03
FJ680851.1 gg_id:521515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU778329.1 gg_id:313557 feces clone RL116_aaf01d03
EU459610.1 gg_id:301862 ring-tailed lemur feces clone RT_aai09c01
EU009777.1 gg_id:239053 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_I27
FJ367490.1 gg_id:359444 feces adult twins and mothers; TS29 clone TS29_a04b09
NZ_AAXB02000032.1 gg_id:470236 Dorea longicatena str. DSM 13814
FJ371029.1 gg_id:356903 feces adult twins and mothers; TS5 clone TS5_a04b02
EF604799.1 gg_id:234097 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ798501.1 gg_id:181434 human fecal clone RL181_aan97e05
DQ796631.1 gg_id:199154 human fecal clone RL179aan76c06
DQ803468.1 gg_id:188970 human fecal clone RL251_aaj86b09
DQ014717.1 gg_id:130551 mouse cecum clone M1_h04_1
EU767921.1 gg_id:306209 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
DQ809818.1 gg_id:188194 human fecal clone RL184_aan84f06
EU453069.1 gg_id:355468 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
FJ680448.1 gg_id:515629 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
NZ_ACCJ01000522.1 gg_id:469972 Clostridium asparagiforme str. DSM 15981

AY916317.1	113422	40.8	89.0	146.8	84.9	176.2	41.6
EU510296.1	259056	177.7	242.8	639.5	171.2	926.2	426.3
FJ368701.1	368980	975.5	790.8	715.3	622.2	357.6	314.6
AM405126.2	573969	216.5	442.5	461.9	205.8	200.8	164.2
EU456172.1	311674	10205.1	10582.5	8534.8	10722.3	11401.2	9261.0
AY984289.1	117903	9816.7	7655.1	5339.9	8028.0	9532.0	4804.5
DQ808725.1	198434	33.4	84.2	180.9	79.1	88.8	93.6
FJ676459.1	531723	10719.4	12289.4	9098.7	7883.7	11807.6	10306.9
EU510783.1	259781	4222.0	3887.4	1886.4	1269.3	1906.0	1331.9
EU761737.1	349087	1257.6	1234.8	968.5	977.9	1761.6	1594.4
EU009784.1	256807	88.2	58.7	126.7	112.6	69.0	39.8
EU463311.1	298468	365.4	675.2	1252.1	428.5	709.2	476.4
EU771786.1	313144	3698.3	4739.5	3456.8	2144.0	2943.0	3735.6
EF096345.1	185355	1107.7	450.6	281.2	716.0	201.3	302.8
DQ809008.1	187682	4691.6	5480.6	1329.2	4798.5	5698.0	5234.7
DQ799785.1	178610	5105.2	7647.8	3107.0	6095.2	11376.6	10861.6
DQ342332.1	174153	22.4	44.6	27.7	57.1	64.7	29.7
GQ492903.1	593444	773.7	1307.2	973.0	1111.0	846.2	1088.8
EF399415.1	207651	845.0	439.7	1552.1	814.1	229.0	935.2
DQ809996.1	198555	277.7	344.0	346.8	81.6	244.8	100.0
FJ364704.1	358447	2096.2	1712.6	1002.5	998.0	411.3	205.9
FJ680441.1	527271	1025.4	950.1	227.7	966.5	248.4	75.1
FJ362631.1	361732	96.0	175.9	280.9	163.0	221.7	218.4
EU459643.1	293128	2122.2	1936.7	2995.3	1940.3	366.3	1226.2
FJ680851.1	521515	6440.8	5129.9	2986.0	4073.7	3762.5	4147.2
EU778329.1	313557	5913.1	6055.2	5635.9	4867.5	4510.2	4765.8
EU459610.1	301862	4794.3	6539.8	4682.7	4150.8	6571.0	6184.8
EU009777.1	239053	173.8	114.1	751.3	191.0	118.7	190.5
FJ367490.1	359444	1424.6	1329.7	818.7	1237.6	235.0	337.7
NZ_AAXB02000032.1	470236	1286.6	795.0	1490.2	1707.9	161.4	273.9
FJ371029.1	356903	1766.2	508.9	1617.3	546.8	71.0	245.4
EF604799.1	234097	10940.2	10511.0	8556.9	8767.4	7763.0	10295.5
DQ798501.1	181434	3973.1	5074.2	2090.7	4718.1	7128.5	6154.7
DQ796631.1	199154	1656.9	1872.3	1619.3	1879.6	5873.1	4996.9
DQ803468.1	188970	1939.0	3773.5	269.8	1384.9	1914.6	1947.1
DQ014717.1	130551	179.5	2036.4	1256.2	903.3	1709.7	1783.8
EU767921.1	306209	484.2	1136.2	644.0	747.8	3285.2	1382.9
DQ809818.1	188194	78.3	238.9	898.1	113.1	79.4	128.9
EU453069.1	355468	131.5	191.1	464.9	238.9	130.6	97.1
FJ680448.1	515629	5799.1	4436.2	3574.3	5511.3	7384.5	6904.0
NZ_ACCJ01000522.1	469972	293.5	314.5	528.3	227.9	131.4	301.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	19003
s__unclassified	19004
s__unclassified	19016
s__unclassified	19023
s__unclassified	19026
s__unclassified	19032
s__unclassified	19035
s__unclassified	19039
s__unclassified	19043
s__unclassified	19051
s__unclassified	19052
s__unclassified	19064
s__unclassified	19072
s__unclassified	19073
s__unclassified	19086
s__unclassified	19094
s__unclassified	19095
s__unclassified	19096
s__unclassified	19102
s__unclassified	19103
s__unclassified	19117
s__unclassified	19124
s__unclassified	19130
s__unclassified	19131
s__unclassified	19135
s__unclassified	19143
s__unclassified	19144
s__unclassified	19149
s__unclassified	19159
s__unclassified	19164
s__unclassified	19169
s__unclassified	19171
s__unclassified	19190
s__unclassified	19191
s__unclassified	19215
s__unclassified	19218
s__unclassified	19219
s__unclassified	19220
s__unclassified	19226
s__unclassified	19230
s__unclassified	19234

FJ365573.1 gg_id:369227 feces adult twins and mothers; TS20 clone TS20_a04e01
DQ905776.1 gg_id:167098 human fecal clone 29A-g7
DQ807951.1 gg_id:196160 human fecal clone RL180_aan69f04
FJ676983.1 gg_id:525798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681024.1 gg_id:515999 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU456668.1 gg_id:335149 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78
EU767879.1 gg_id:350481 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
FJ364032.1 gg_id:364034 feces adult twins and mothers; TS150 clone TS150_a02b10
DQ796690.1 gg_id:198124 human fecal clone RL179_aao53c04
EU509687.1 gg_id:261368 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak47b05
EU463375.1 gg_id:298858 bush dog feces clone bdog1_aai80e02
FJ367507.1 gg_id:358064 feces adult twins and mothers; TS29 clone TS29_a04d03
DQ805157.1 gg_id:193769 human fecal clone RL249_aaj82b11
FJ370811.1 gg_id:362280 feces adult twins and mothers; TS5 clone TS5_a01e09
EU510136.1 gg_id:261334 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01h03
EF098609.1 gg_id:197240 mouse cecum clone SWPT16_aaa02b03
EF098496.1 gg_id:189905 mouse cecum clone SWPT15_aaa04c05
EU461086.1 gg_id:297708 red kangaroo feces clone KO1_aai43h08
EF098635.1 gg_id:191772 mouse cecum clone SWPT16_aaa02e02
EU467257.1 gg_id:299536 black-handed spider monkey feces clone SPIM_d12_1
FJ363999.1 gg_id:370424 feces adult twins and mothers; TS150 clone TS150_a01g11
DQ799835.1 gg_id:197134 human fecal clone RL182_aah34f05
GQ492902.1 gg_id:550531 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF025255.1 gg_id:177762 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F17
DQ456162.1 gg_id:158542 pre-adolescent turkey cecum clone CFT29B5
EU767769.1 gg_id:352786 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
AF499906.1 gg_id:83271 human colonic mucosal biopsy clone ABLCf11
EU794106.1 gg_id:334661 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_U22
FJ678586.1 gg_id:522277 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ057365.1 gg_id:132892 chicken ileum/cecum clone cc112
DQ325863.1 gg_id:149131 Metagenomic gut microbiome healthy human stool clone B647
EU768387.1 gg_id:322204 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
FJ673162.1 gg_id:522205 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370677.1 gg_id:356832 feces adult twins and mothers; TS57 clone TS57_a03h07
EU459600.1 gg_id:294988 ring-tailed lemur feces clone RT_aai09a08
GQ491319.1 gg_id:542096 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU459747.1 gg_id:296770 ring-tailed lemur feces clone RT_aai12b05
EF098200.1 gg_id:183362 mouse cecum clone SWPT14_aaa02h11
FJ685226.1 gg_id:512257 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU503833.1 gg_id:269103 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01c06
DQ799122.1 gg_id:197783 human fecal clone RL205_aaj17h06

FJ365573.1	369227	1306.6	2324.1	1108.3	1876.6	4214.2	3061.5
DQ905776.1	167098	2086.7	2918.6	3005.7	1535.9	896.8	1360.8
DQ807951.1	196160	61.9	98.3	151.6	87.1	78.9	89.4
FJ676983.1	525798	1024.9	974.2	4621.6	653.7	2900.4	1511.8
FJ681024.1	515999	8930.1	9567.8	7618.6	9261.9	13211.2	11073.4
EU456668.1	335149	151.8	355.7	1033.1	272.5	280.5	244.5
EU767879.1	350481	269.2	213.0	305.3	233.3	85.8	67.6
FJ364032.1	364034	802.2	747.2	1115.4	221.1	185.3	382.2
DQ796690.1	198124	1917.2	3510.5	1639.1	1104.9	4655.7	2541.2
EU509687.1	261368	3648.6	3848.8	1363.0	1284.8	3698.8	3306.4
EU463375.1	298858	123.6	333.1	167.3	97.7	95.2	77.9
FJ367507.1	358064	9103.3	10401.7	5995.3	6698.4	12647.6	9150.9
DQ805157.1	193769	2376.0	2812.5	2397.1	2747.8	5231.7	3943.7
FJ370811.1	362280	306.8	225.5	624.0	189.7	124.3	124.0
EU510136.1	261334	142.0	166.3	615.2	124.7	295.1	244.9
EF098609.1	197240	470.7	741.1	507.1	1288.1	571.5	1359.5
EF098496.1	189905	12127.5	11021.4	9210.7	12271.8	12985.8	10678.2
EU461086.1	297708	4064.9	3382.9	2456.3	4531.4	2726.6	3855.2
EF098635.1	191772	100.5	75.6	229.0	119.8	79.7	67.2
EU467257.1	299536	266.8	199.6	377.5	131.6	122.9	119.1
FJ363999.1	370424	221.8	278.6	373.8	213.7	72.5	36.5
DQ799835.1	197134	493.5	833.7	971.4	641.6	2509.2	1750.3
GQ492902.1	550531	51.4	68.2	65.2	124.7	84.6	55.7
EF025255.1	177762	441.5	583.6	1470.8	400.1	794.2	632.6
DQ456162.1	158542	6019.2	6316.8	9809.7	6600.2	9760.7	6920.6
EU767769.1	352786	82.4	82.4	88.5	112.4	107.7	76.2
AF499906.1	83271	2125.7	1447.1	255.0	1224.7	156.4	250.1
EU794106.1	334661	2162.4	2976.6	2964.4	925.7	1127.0	1872.3
FJ678586.1	522277	4234.0	3160.4	620.8	1389.6	1082.9	892.7
DQ057365.1	132892	79.8	127.0	187.0	118.3	84.2	80.5
DQ325863.1	149131	87.3	99.3	402.0	95.0	79.7	95.7
EU768387.1	322204	2434.1	2459.7	539.9	3909.8	6449.6	4992.0
FJ673162.1	522205	8603.3	10099.4	3885.5	6657.1	8597.9	7286.8
FJ370677.1	356832	67.0	95.3	113.4	113.6	108.4	83.7
EU459600.1	294988	178.5	255.0	571.8	531.0	189.5	42.0
GQ491319.1	542096	398.8	1281.4	753.4	260.3	2690.4	1119.5
EU459747.1	296770	1023.1	1238.8	2653.2	1956.0	2948.3	2672.0
EF098200.1	183362	741.4	1800.9	1558.6	964.5	785.8	865.0
FJ685226.1	512257	3176.6	3898.5	3715.6	2386.5	643.2	1566.9
EU503833.1	269103	1039.0	792.5	1384.8	677.1	185.6	297.6
DQ799122.1	197783	25.5	32.4	53.2	63.8	57.0	31.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	19240
s__unclassified	19243
s__unclassified	19251
s__unclassified	19257
s__unclassified	19262
s__unclassified	19269
s__unclassified	19274
s__unclassified	19278
s__unclassified	19303
s__unclassified	19304
s__unclassified	19321
s__unclassified	19322
s__unclassified	19327
s__unclassified	19331
s__unclassified	19332
s__unclassified	19333
s__unclassified	19340
s__unclassified	19341
s__unclassified	19357
s__unclassified	19359
s__unclassified	19363
s__unclassified	19364
s__unclassified	19368
s__unclassified	19381
s__unclassified	19384
s__unclassified	19398
s__unclassified	19409
s__unclassified	19422
s__unclassified	19424
s__unclassified	19428
s__unclassified	19433
s__unclassified	19437
s__unclassified	19438
s__unclassified	19453
s__unclassified	19462
s__unclassified	19464
s__unclassified	19465
s__unclassified	19473
s__unclassified	19480
s__unclassified	19481
s__unclassified	19490

EF098375.1 gg_id:195470 mouse cecum clone SWPT15_aaa01h03
EU510719.1 gg_id:269618 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39h10
EU768430.1 gg_id:326928 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
FJ675705.1 gg_id:517846 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ824939.1 gg_id:180216 human fecal clone RL185_aao71c05
EU775513.1 gg_id:323595 Western lowland gorilla feces clone GORSD_aaa01c09
EU778621.1 gg_id:316740 Ring-tailed lemur feces clone RT_aai10e02
EF095977.1 gg_id:181683 mouse cecum clone lean2_aaa01c05
DQ797241.1 gg_id:184394 human fecal clone RL386_aao88g09
GQ896927.1 gg_id:554259 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
EU772874.1 gg_id:316781 Bush dog feces clone bdog1_aai79d12
AY978223.1 gg_id:117538 human transverse colon mucosal biopsy clone F032
EU451143.1 gg_id:351734 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
DQ798482.1 gg_id:180957 human fecal clone RL181_aan97c07
DQ806976.1 gg_id:197405 human fecal clone RL198_aaj76d11
EF614705.1 gg_id:231146 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU454651.1 gg_id:352861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
AY984335.1 gg_id:125016 human stool clone B234
EF098022.1 gg_id:199550 mouse cecum clone SWPT12_aaa04b11
EU454185.1 gg_id:335430 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
DQ794783.1 gg_id:187360 human fecal clone RL240_aaj32c10
DQ279737.1 gg_id:141412 Clostridium citroniae str. RMA 16102
EF098354.1 gg_id:190273 mouse cecum clone SWPT15_aaa01d07
AB234505.1 gg_id:149725 termite gut homogenate clone MgMjW-36
GQ047220.1 gg_id:424615 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010b
DQ353932.1 gg_id:146448 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z86
DQ456197.1 gg_id:157470 pre-adolescent turkey cecum clone CFT29E6
GQ867559.1 gg_id:573341 and prevalence blaTEM genes Arctic seals colon content clone CSH64
EU531926.1 gg_id:258392 Predominant role host genetics controlling gut microbiota FMF remission stool clone
EF025272.1 gg_id:175640 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N3
EU452062.1 gg_id:352160 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
DQ014807.1 gg_id:132092 mouse cecum clone M1_h08_2
AY978473.1 gg_id:119101 human transverse colon mucosal biopsy clone KP30
EF097959.1 gg_id:180717 mouse cecum clone SWPT12_aaa02h07
EF098965.1 gg_id:181568 mouse cecum clone SWPT1_aaa04a07
DQ797248.1 gg_id:198490 human fecal clone RL386_aao88h07
EF614514.1 gg_id:230096 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EF614857.1 gg_id:232638 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
DQ815496.1 gg_id:171989 mouse cecum clone aab41f05
GQ491971.1 gg_id:559976 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY975738.1 gg_id:125725 human ascending colon mucosal biopsy clone Y188

EF098375.1	195470	21.6	39.6	31.0	57.7	68.3	19.4
EU510719.1	269618	46.1	42.8	263.0	96.7	48.5	39.2
EU768430.1	326928	1240.1	1409.8	1820.1	1089.9	414.6	1072.2
FJ675705.1	517846	2051.8	906.4	760.3	647.1	1021.9	1240.1
DQ824939.1	180216	553.9	756.5	1022.9	426.8	1004.8	1520.9
EU775513.1	323595	7717.6	7647.1	6279.8	5526.4	6511.4	5852.4
EU778621.1	316740	510.9	1958.6	848.0	1396.2	119.9	998.2
EF095977.1	181683	1624.1	1925.1	2319.8	3256.6	2990.9	3867.3
DQ797241.1	184394	66.9	153.4	439.5	74.7	237.1	94.4
GQ896927.1	554259	3185.0	4024.5	3245.6	4462.1	5673.2	5925.5
EU772874.1	316781	117.6	78.7	125.0	103.2	91.6	65.2
AY978223.1	117538	113.2	126.0	1233.9	102.9	2635.3	2666.8
EU451143.1	351734	537.5	626.7	578.8	731.5	262.1	402.5
DQ798482.1	180957	33.6	40.2	49.6	51.8	55.9	30.6
DQ806976.1	197405	117.0	135.7	278.5	115.1	92.7	164.0
EF614705.1	231146	8934.0	9937.6	3883.3	7392.3	2433.9	2904.3
EU454651.1	352861	484.9	760.4	433.3	986.9	1090.7	1065.6
AY984335.1	125016	5227.9	6360.8	3308.3	1858.4	552.9	1448.7
EF098022.1	199550	14.5	10.7	17.0	41.9	43.8	20.0
EU454185.1	335430	452.1	773.4	649.7	1708.8	2993.1	2238.7
DQ794783.1	187360	38.6	25.6	230.5	53.0	46.5	23.5
DQ279737.1	141412	81.1	153.3	376.1	166.6	403.4	317.0
EF098354.1	190273	209.1	198.7	633.8	306.4	338.6	253.3
AB234505.1	149725	1473.7	633.9	1931.5	1363.1	122.5	763.2
GQ047220.1	424615	7751.6	9942.8	8008.2	7098.7	14685.9	10746.5
DQ353932.1	146448	23.8	28.3	45.2	43.8	74.0	9.3
DQ456197.1	157470	98.3	127.6	314.2	137.2	268.6	172.4
GQ867559.1	573341	9086.4	10622.2	5887.1	10949.2	14072.7	10370.6
EU531926.1	258392	2247.8	2494.8	1399.0	3274.4	1158.0	1046.2
EF025272.1	175640	2621.9	1348.2	1598.5	2933.2	2093.1	876.6
EU452062.1	352160	1590.4	2513.2	1365.8	2804.8	1450.6	2479.8
DQ014807.1	132092	18.8	28.0	67.9	73.1	40.6	15.7
AY978473.1	119101	8008.4	7082.9	3105.6	5388.0	1768.3	2463.1
EF097959.1	180717	7204.1	10059.5	4974.0	6093.2	9024.1	9957.3
EF098965.1	181568	297.3	671.7	612.2	1049.8	249.3	343.0
DQ797248.1	198490	1953.5	1654.9	559.9	1608.4	2482.4	1644.8
EF614514.1	230096	315.9	295.2	237.2	116.2	116.4	169.2
EF614857.1	232638	9170.9	9438.5	5794.9	6848.1	7782.8	7832.9
DQ815496.1	171989	2793.9	3075.9	1506.2	2743.2	6400.3	4410.0
GQ491971.1	559976	1557.0	1393.2	1690.3	1925.8	2685.4	2181.4
AY975738.1	125725	77.3	26.2	144.4	61.1	54.2	34.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	19492
s__unclassified	19495
s__unclassified	19496
s__unclassified	19504
s__unclassified	19505
s__unclassified	19507
s__unclassified	19516
s__unclassified	19531
s__unclassified	19546
s__unclassified	19550
s__unclassified	19551
s__unclassified	19554
s__unclassified	19562
s__unclassified	19566
s__unclassified	19573
s__unclassified	19574
s__unclassified	19577
s__unclassified	19591
s__unclassified	19594
s__unclassified	19599
s__unclassified	19604
s__unclassified	19611
s__unclassified	19613
s__unclassified	19619
s__unclassified	19622
s__unclassified	19627
s__unclassified	19635
s__unclassified	19637
s__unclassified	19640
s__unclassified	19643
s__unclassified	19644
s__unclassified	19645
s__unclassified	19647
s__unclassified	19648
s__unclassified	19649
s__unclassified	19650
s__unclassified	19654
s__unclassified	19659
s__unclassified	19662
s__unclassified	19664
s__unclassified	19667

FJ365651.1 gg_id:369032 feces adult twins and mothers; TS21 clone TS21_a01d07
FJ440041.1 gg_id:510813 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou
EF096677.1 gg_id:192991 mouse cecum clone SWPT11_aaa03a03
EU452637.1 gg_id:314945 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU457171.1 gg_id:311466 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU508167.1 gg_id:276240 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02c06
NR_026409.1 gg_id:559837 Desulfotomaculum guttoideum str. DSM 4024
AY977745.1 gg_id:123816 human cecum mucosal biopsy clone LE16
FJ880789.1 gg_id:458831 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU776090.1 gg_id:346658 Spotted hyena feces clone HY1_e08_2
EF614550.1 gg_id:229302 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU767569.1 gg_id:311176 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
EU510621.1 gg_id:263896 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38d01
AF092549.1 gg_id:52289 Clostridium algidixylanolyticum str. SPL73
EU457056.1 gg_id:318912 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU776542.1 gg_id:319417 Lion feces clone LI3_aah77g11
DQ798202.1 gg_id:182631 human fecal clone RL302_aal96g08
EU511054.1 gg_id:264774 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02a07
GQ493516.1 gg_id:542055 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY992804.1 gg_id:131095 mouse cecum clone C22_c07
AY991713.1 gg_id:135440 mouse cecum clone C20_a06
GQ492799.1 gg_id:583974 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF099655.1 gg_id:177473 mouse cecum clone SWPT4_aaa02e04
EF096370.1 gg_id:183391 mouse cecum clone obob2_aaa01f11
FJ680759.1 gg_id:514398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ867532.1 gg_id:587724 and prevalence blaTEM genes Arctic seals colon content clone CSH36
AY353957.1 gg_id:103489 Clostridium amygdalinum str. BR-10
EF098651.1 gg_id:197167 mouse cecum clone SWPT16_aaa02g06
EU451387.1 gg_id:351209 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EF097514.1 gg_id:189187 mouse cecum clone SWPT19_aaa03f12
EF098106.1 gg_id:174540 mouse cecum clone SWPT14_aaa01e12
EU507818.1 gg_id:272778 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01d02
EF614747.1 gg_id:233250 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
FJ365805.1 gg_id:361998 feces adult twins and mothers; TS21 clone TS21_a03c06
AY984860.1 gg_id:119032 human stool clone B831
DQ015443.1 gg_id:135545 mouse cecum clone M3_b07_1
AB234506.1 gg_id:146502 termite gut homogenate clone MgMjW-10
EU509027.1 gg_id:261702 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42c01
FJ370740.1 gg_id:357463 feces adult twins and mothers; TS57 clone TS57_a04f09
EU457966.1 gg_id:330827 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
DQ800914.1 gg_id:187219 human fecal clone RL387_aao89c01

FJ365651.1	369032	46.3	77.4	250.6	123.0	83.4	59.3
FJ440041.1	510813	385.9	377.4	2167.2	463.3	905.3	684.8
EF096677.1	192991	1857.2	1752.5	1189.0	3561.9	1282.3	1397.7
EU452637.1	314945	34.8	37.9	22.6	67.5	67.9	31.9
EU457171.1	311466	46.8	46.3	293.6	80.7	64.3	47.9
EU508167.1	276240	1432.8	1426.6	2733.7	2020.2	4783.4	3611.0
NR_026409.1	559837	1856.9	2178.0	458.5	686.0	346.4	346.0
AY977745.1	123816	668.5	675.9	894.3	453.3	2228.9	1536.6
FJ880789.1	458831	872.3	784.3	400.3	1277.3	188.1	268.8
EU776090.1	346658	2445.9	3322.8	847.7	1982.7	1901.8	2217.6
EF614550.1	229302	125.0	271.2	839.0	260.9	330.4	247.5
EU767569.1	311176	1465.4	1316.4	829.0	2034.4	244.1	443.2
EU510621.1	263896	2322.3	2100.4	526.7	1380.7	672.1	923.5
AF092549.1	52289	2110.8	1954.2	2127.6	817.2	439.0	710.6
EU457056.1	318912	16423.1	20627.2	6837.1	9712.8	12925.6	13277.1
EU776542.1	319417	10229.3	9322.0	8328.5	7914.1	5483.3	6921.8
DQ798202.1	182631	686.3	532.7	751.0	364.7	298.1	270.8
EU511054.1	264774	26.9	42.8	79.5	41.1	46.8	21.9
GQ493516.1	542055	8520.3	7081.9	7506.6	11467.8	14751.1	15205.7
AY992804.1	131095	1193.5	789.5	1318.8	2001.8	2224.9	1748.3
AY991713.1	135440	30.3	62.0	76.8	67.8	113.0	213.6
GQ492799.1	583974	8889.1	8051.6	6883.1	5774.3	6725.8	7894.1
EF099655.1	177473	42.5	54.1	153.0	73.7	78.9	45.6
EF096370.1	183391	211.5	286.7	222.9	246.4	83.5	110.4
FJ680759.1	514398	3267.5	3679.8	4663.0	3185.8	1845.0	3258.8
GQ867532.1	587724	2354.1	1580.3	2204.1	4492.4	361.7	513.3
AY353957.1	103489	1597.5	1302.7	570.8	731.4	358.9	228.3
EF098651.1	197167	5143.8	3190.7	2303.6	6451.8	3281.7	3321.1
EU451387.1	351209	1423.5	4895.2	4353.1	2887.0	6833.3	6172.8
EF097514.1	189187	8171.3	7106.7	4848.5	5889.7	7783.9	7369.4
EF098106.1	174540	1197.0	1243.6	1648.4	2561.5	1671.8	3050.8
EU507818.1	272778	12645.0	12514.1	8879.5	11261.7	9158.9	8176.3
EF614747.1	233250	2015.7	2172.8	1289.8	2825.7	1447.0	2153.3
FJ365805.1	361998	125.6	146.8	240.6	159.6	159.3	136.1
AY984860.1	119032	249.6	353.6	950.6	165.5	71.9	421.9
DQ015443.1	135545	4198.8	4791.6	515.1	3608.4	2187.2	2041.6
AB234506.1	146502	28.9	38.7	30.5	51.9	73.9	31.0
EU509027.1	261702	6111.4	6603.8	4104.6	5821.7	10190.6	7869.5
FJ370740.1	357463	1049.9	824.7	2231.8	1370.4	868.1	1901.9
EU457966.1	330827	617.7	1054.1	1218.1	1818.7	3602.6	2829.1
DQ800914.1	187219	2029.9	2815.0	3347.6	2860.0	2637.2	1777.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	19668
s__unclassified	19669
s__unclassified	19670
s__unclassified	19673
s__unclassified	19674
s__unclassified	19684
s__unclassified	19690
s__unclassified	19695
s__unclassified	19707
s__unclassified	19708
s__unclassified	19710
s__unclassified	19719
s__unclassified	19734
s__unclassified	19746
s__unclassified	19747
s__unclassified	19748
s__unclassified	19755
s__unclassified	19761
s__unclassified	19763
s__unclassified	19770
s__unclassified	19771
s__unclassified	19773
s__unclassified	19775
s__unclassified	19776
s__unclassified	19780
s__unclassified	19787
s__unclassified	19790
s__unclassified	19796
s__unclassified	19806
s__unclassified	19809
s__unclassified	19815
s__unclassified	19821
s__unclassified	19823
s__unclassified	19833
s__unclassified	19839
s__unclassified	19846
s__unclassified	19867
s__unclassified	19868
s__unclassified	19870
s__unclassified	19874
s__unclassified	19878

EF098174.1 gg_id:187843 mouse cecum clone SWPT14_aaa02f05
EU768688.1 gg_id:353667 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
GQ491558.1 gg_id:586550 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ801140.1 gg_id:195881 human fecal clone RL387_aao92h01
FJ370445.1 gg_id:365964 feces adult twins and mothers; TS57 clone TS57_a01b09
EU773398.1 gg_id:336380 Black lemur feces clone BKLE_a10_2
EU509201.1 gg_id:263138 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g06
DQ905099.1 gg_id:161968 human fecal clone 002C-a12
EU778925.1 gg_id:320055 Black-handed Spider Monkey feces clone SPIM_f09
AY993032.1 gg_id:129499 mouse cecum clone C22_p16
EU455030.1 gg_id:348772 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
DQ326829.1 gg_id:146345 Metagenomic gut microbiome healthy human stool clone E306
EU509143.1 gg_id:259818 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44g03
EF096881.1 gg_id:187921 mouse cecum clone SWPT13_aaa02b10
EU474306.1 gg_id:301475 western lowland gorilla feces clone GORSD_aaa02a05
EU457851.1 gg_id:308032 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EF096575.1 gg_id:173922 mouse cecum clone SWPT11_aaa01c11
EU508162.1 gg_id:261380 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02b10
EF096197.1 gg_id:186792 mouse cecum clone obob1_aaa02d03
EU455805.1 gg_id:346278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EU510123.1 gg_id:272390 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01f11
EU457007.1 gg_id:346275 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU459640.1 gg_id:296042 ring-tailed lemur feces clone RT_aai09g10
EF098240.1 gg_id:196497 mouse cecum clone SWPT14_aaa03e03
EU508949.1 gg_id:259909 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap40a10
GQ493246.1 gg_id:545473 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
Y18184.1 gg_id:26602 Clostridium indolis str. DSM 755
EU506499.1 gg_id:259653 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03a06
FJ369112.1 gg_id:367707 feces adult twins and mothers; TS4 clone TS4_a04d05
EF096597.1 gg_id:178199 mouse cecum clone SWPT11_aaa01f04
EU511885.1 gg_id:261220 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10e04
EU454984.1 gg_id:328536 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
FJ370230.1 gg_id:359949 feces adult twins and mothers; TS56 clone TS56_a02b02
EF098306.1 gg_id:181133 mouse cecum clone SWPT14_aaa04e07
AY993145.1 gg_id:135431 mouse cecum clone C21_g02
EU458073.1 gg_id:315358 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
GQ491281.1 gg_id:583045 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU509952.1 gg_id:269949 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c03
EU504399.1 gg_id:266896 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03f03
EU457908.1 gg_id:309360 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S
EU450910.1 gg_id:333069 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S

EF098174.1	187843	9804.1	12261.5	10662.8	8225.2	12474.7	5374.6
EU768688.1	353667	425.4	168.7	723.7	84.1	488.1	130.2
GQ491558.1	586550	9969.5	8670.6	9796.1	11436.3	10232.0	13204.5
DQ801140.1	195881	1994.1	1781.1	3334.1	1031.0	2551.9	2168.3
FJ370445.1	365964	3150.4	3121.9	2310.7	3827.7	3651.6	6013.7
EU773398.1	336380	269.9	279.5	821.7	240.4	772.1	464.1
EU509201.1	263138	1955.5	1758.4	572.5	161.8	252.5	170.8
DQ905099.1	161968	5390.2	5281.9	2329.8	3936.1	4328.4	4521.4
EU778925.1	320055	112.3	82.9	596.3	141.1	161.9	236.3
AY993032.1	129499	4682.7	7149.2	4654.7	5822.6	7918.5	8557.6
EU455030.1	348772	1903.8	1532.5	2055.7	3117.1	263.4	513.6
DQ326829.1	146345	29.0	25.3	51.2	50.1	65.3	23.7
EU509143.1	259818	4520.7	5357.5	1558.3	1384.6	1211.3	1137.7
EF096881.1	187921	27.7	66.0	148.2	65.8	245.2	141.0
EU474306.1	301475	213.2	284.2	740.1	222.8	857.2	455.9
EU457851.1	308032	5980.8	5549.7	2602.1	3914.0	3641.1	5364.6
EF096575.1	173922	324.9	724.5	2126.0	212.4	480.2	697.9
EU508162.1	261380	4959.9	3480.9	3252.2	4164.2	3502.6	2916.3
EF096197.1	186792	5672.2	5235.0	3637.2	6406.9	9594.3	8044.5
EU455805.1	346278	2546.5	3136.7	1899.9	4131.2	4525.7	5166.5
EU510123.1	272390	28.0	69.3	59.8	66.3	61.9	36.5
EU457007.1	346275	127.2	142.1	518.1	286.7	184.0	470.9
EU459640.1	296042	526.6	696.6	721.5	437.0	1312.1	962.7
EF098240.1	196497	1684.9	1642.8	1529.7	1362.1	3906.6	3164.2
EU508949.1	259909	46.9	72.4	29.9	61.9	83.4	106.4
GQ493246.1	545473	1175.9	1909.4	811.0	2859.4	4691.8	4416.4
Y18184.1	26602	137.7	121.8	385.8	107.7	93.6	65.4
EU506499.1	259653	709.3	491.5	1203.6	942.9	381.8	412.8
FJ369112.1	367707	3861.2	4071.2	4248.0	5701.6	7175.7	10808.3
EF096597.1	178199	2349.7	2369.6	1676.7	2916.7	4798.1	3867.6
EU511885.1	261220	4544.8	4427.5	1862.1	3726.9	1665.2	2471.1
EU454984.1	328536	727.8	898.5	1081.9	940.6	2261.7	2048.0
FJ370230.1	359949	4502.1	5004.8	2399.2	7000.4	6605.9	5273.7
EF098306.1	181133	400.8	852.9	34.6	421.9	336.0	466.8
AY993145.1	135431	1233.5	2318.0	1393.5	2153.9	3704.8	3398.0
EU458073.1	315358	44.4	57.8	87.5	81.4	55.4	46.4
GQ491281.1	583045	293.8	330.5	453.6	148.2	223.3	153.9
EU509952.1	269949	90.6	103.4	208.3	74.7	88.0	55.7
EU504399.1	266896	3563.6	3721.9	1734.6	1680.3	2732.4	1501.3
EU457908.1	309360	1374.7	2529.3	3334.5	1126.6	3044.2	1797.7
EU450910.1	333069	2077.5	1062.2	1107.6	1966.8	409.6	837.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	19884
s__unclassified	19886
s__unclassified	19887
s__unclassified	19888
s__unclassified	19889
s__unclassified	19890
s__unclassified	19895
s__unclassified	19898
s__unclassified	19904
s__unclassified	19906
s__unclassified	19908
s__unclassified	19910
s__unclassified	19920
s__unclassified	19929
s__unclassified	19930
s__unclassified	19934
s__unclassified	19941
s__unclassified	19942
s__unclassified	19945
s__unclassified	19954
s__unclassified	19964
s__unclassified	19967
s__unclassified	19971
s__unclassified	19975
s__unclassified	19979
s__unclassified	19982
s__unclassified	19984
s__unclassified	19990
s__unclassified	19995
s__unclassified	20008
s__unclassified	20009
s__unclassified	20010
s__unclassified	20015
s__unclassified	20018
s__unclassified	20020
s__unclassified	20021
s__unclassified	20026
s__unclassified	20037
s__unclassified	20040
s__unclassified	20041
s__unclassified	20042

EU767855.1 gg_id:332308 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
EF403444.1 gg_id:211174 human fecal clone SJTU_A2_01_30
EU508356.1 gg_id:259998 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03f08
AY992008.1 gg_id:134549 mouse cecum clone C20_p10
EF096052.1 gg_id:180458 mouse cecum clone lean2_aaa03a05
EF096277.1 gg_id:199341 mouse cecum clone obob1_aaa04a05
EU452590.1 gg_id:312205 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EF099536.1 gg_id:186085 mouse cecum clone SWPT3_aaa04f01
EF604514.1 gg_id:234516 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF614877.1 gg_id:233595 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
DQ815426.1 gg_id:166609 mouse cecum clone aab48b10
GQ492112.1 gg_id:593369 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ957873.1 gg_id:461989 Clostridium saccharolyticum str. JPL_21
EF404438.1 gg_id:209193 human fecal clone SJTU_C_10_05
FJ370463.1 gg_id:362460 feces adult twins and mothers; TS57 clone TS57_a01d06
FJ370529.1 gg_id:357221 feces adult twins and mothers; TS57 clone TS57_a02b05
FJ680978.1 gg_id:527327 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ311620.2 gg_id:90431 Clostridium hathewayi str. DSM 13479 = CCUG 43
AJ408971.1 gg_id:69958 human colonic clone HuCA19
EU463123.1 gg_id:296872 naked mole-rat feces clone molerat_aai70c02
EU509115.1 gg_id:276941 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44a08
EF099826.1 gg_id:193023 mouse cecum clone SWPT4_aaa04h05
EU510090.1 gg_id:270627 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01b12
DQ815622.1 gg_id:169045 mouse cecum clone aab43f10
DQ801685.1 gg_id:181521 human fecal clone RL201_aai45e03
FJ370676.1 gg_id:361375 feces adult twins and mothers; TS57 clone TS57_a03h06
DQ904855.1 gg_id:173777 human fecal clone 001C-c6
EU452655.1 gg_id:321921 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU511980.1 gg_id:267783 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12c04
EF406450.1 gg_id:211001 mouse colon clone control_14days-A1
EF095970.1 gg_id:178026 mouse cecum clone lean2_aaa01b07
EU450991.1 gg_id:350064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
DQ815701.1 gg_id:164638 mouse cecum clone aab21b07
EF604630.1 gg_id:231997 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU511917.1 gg_id:274132 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11c02
FJ370659.1 gg_id:367027 feces adult twins and mothers; TS57 clone TS57_a03f09
EF096886.1 gg_id:175986 mouse cecum clone SWPT13_aaa02c04
DQ015121.1 gg_id:131793 mouse cecum clone M2_f12_1
AY993011.1 gg_id:130465 mouse cecum clone C22_o10
EF098094.1 gg_id:184695 mouse cecum clone SWPT14_aaa01d09
FJ880800.1 gg_id:429698 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;

EU767855.1	332308	29.2	34.4	73.7	35.6	105.7	72.4
EF403444.1	211174	155.0	122.8	468.2	216.8	147.3	358.8
EU508356.1	259998	803.1	1280.8	810.0	464.3	1807.3	1121.8
AY992008.1	134549	777.7	518.7	1087.9	219.1	540.4	1392.8
EF096052.1	180458	1079.9	918.3	996.1	1588.4	2664.8	2329.8
EF096277.1	199341	52.1	39.0	48.9	86.7	51.9	45.1
EU452590.1	312205	5997.4	5238.9	4480.2	4115.3	4508.7	4557.6
EF099536.1	186085	9133.1	10805.1	13150.8	12140.0	13430.6	12466.8
EF604514.1	234516	74.7	171.3	603.1	87.2	84.0	146.9
EF614877.1	233595	7630.8	7313.6	6899.1	6064.0	6117.7	6150.1
DQ815426.1	166609	145.3	91.5	36.3	241.4	59.2	41.2
GQ492112.1	593369	8794.1	9839.7	7299.5	8349.2	12462.8	11026.6
FJ957873.1	461989	2468.0	3935.3	4855.5	2780.2	1660.9	2071.3
EF404438.1	209193	1515.2	698.0	631.8	1363.0	224.4	596.2
FJ370463.1	362460	9744.0	8907.4	4193.4	6349.0	9015.0	8017.3
FJ370529.1	357221	402.0	373.3	429.5	428.4	201.8	328.8
FJ680978.1	527327	560.8	518.7	424.3	754.5	130.5	490.0
AJ311620.2	90431	5967.5	7640.7	8983.8	4419.8	5090.3	5628.8
AJ408971.1	69958	4366.5	5277.0	3214.6	4358.0	9029.6	7407.2
EU463123.1	296872	48.0	84.9	149.5	108.8	80.9	213.4
EU509115.1	276941	844.4	764.6	1218.4	1162.0	1773.3	1476.7
EF099826.1	193023	3176.5	5064.3	3129.8	4072.6	1304.8	2070.7
EU510090.1	270627	927.7	802.1	1164.9	901.8	619.1	1805.9
DQ815622.1	169045	383.7	804.3	804.1	294.1	650.9	722.3
DQ801685.1	181521	2365.0	2792.7	1986.0	1674.0	1054.9	1166.4
FJ370676.1	361375	1161.5	2049.4	2536.7	807.4	4443.4	4030.4
DQ904855.1	173777	1451.7	1921.2	1951.5	1370.0	3173.9	3265.0
EU452655.1	321921	32.3	56.0	45.1	57.2	79.4	35.5
EU511980.1	267783	199.4	150.3	109.4	189.5	94.8	80.2
EF406450.1	211001	1038.8	1110.8	376.5	1130.7	1678.8	1208.7
EF095970.1	178026	215.3	256.9	360.7	213.8	620.4	411.3
EU450991.1	350064	758.2	703.0	1084.6	1090.5	969.4	1010.7
DQ815701.1	164638	2064.0	2308.0	2372.6	2688.3	4743.2	3900.0
EF604630.1	231997	600.0	736.9	835.5	232.4	158.7	268.7
EU511917.1	274132	305.9	478.8	640.2	166.2	2045.4	1317.4
FJ370659.1	367027	6271.0	7692.1	2929.6	5444.7	11116.5	9677.4
EF096886.1	175986	8000.6	10226.3	7879.9	9105.0	9994.7	8485.9
DQ015121.1	131793	1200.8	2226.0	2242.1	1779.0	4146.7	3329.4
AY993011.1	130465	32.4	51.3	156.2	83.7	98.1	77.4
EF098094.1	184695	147.4	307.1	345.2	697.2	554.4	833.3
FJ880800.1	429698	2986.6	2538.5	2061.2	4181.1	2167.1	1911.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	20044
s__unclassified	20046
s__unclassified	20055
s__unclassified	20059
s__unclassified	20068
s__unclassified	20069
s__unclassified	20070
s__unclassified	20074
s__unclassified	20098
s__unclassified	20103
s__unclassified	20108
s__unclassified	20109
s__unclassified	20112
s__unclassified	20113
s__unclassified	20114
s__unclassified	20123
s__unclassified	20125
s__unclassified	20131
s__unclassified	20135
s__unclassified	20142
s__unclassified	20145
s__unclassified	20148
s__unclassified	20150
s__unclassified	20160
s__unclassified	20171
s__unclassified	20175
s__unclassified	20185
s__unclassified	20187
s__unclassified	20188
s__unclassified	20189
s__unclassified	20191
s__unclassified	20195
s__unclassified	20199
s__unclassified	20203
s__unclassified	20210
s__unclassified	20224
s__unclassified	20225
s__unclassified	20240
s__unclassified	20242
s__unclassified	20246
s__unclassified	20248

EU507613.1 gg_id:277365 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01h09
GQ867579.1 gg_id:592345 and prevalence blaTEM genes Arctic seals colon content clone CSH88
AY978174.1 gg_id:119499 human cecum mucosal biopsy clone LJ63
DQ507245.1 gg_id:159259 Clostridium sp. str. AIP 321.05
EU454693.1 gg_id:329126 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EU511227.1 gg_id:273077 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04f11
EU510407.1 gg_id:270065 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b01
DQ803584.1 gg_id:179758 human fecal clone RL251_aaj87g05
DQ800728.1 gg_id:183498 human fecal clone RL183_aao02f09
FJ370516.1 gg_id:368577 feces adult twins and mothers; TS57 clone TS57_a02a04
EF098834.1 gg_id:181808 mouse cecum clone SWPT1_aaa01f07
FJ363546.1 gg_id:358915 feces adult twins and mothers; TS149 clone TS149_a04e06
EF097971.1 gg_id:176671 mouse cecum clone SWPT12_aaa03b07
EU507789.1 gg_id:264568 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04h05
EF402492.1 gg_id:213448 human fecal clone SJTU_B_08_62
GQ492185.1 gg_id:584906 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF099713.1 gg_id:196088 mouse cecum clone SWPT4_aaa03c11
GQ493377.1 gg_id:590324 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU762698.1 gg_id:307338 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EU504212.1 gg_id:275307 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04c04
EU509514.1 gg_id:273179 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59g12
EU509781.1 gg_id:276663 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48h05
EU508759.1 gg_id:271646 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50e12
EU504370.1 gg_id:260529 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03b11
EU776687.1 gg_id:331571 Lion feces clone LI3_aah76a12
EF098153.1 gg_id:181711 mouse cecum clone SWPT14_aaa02c08
EU451008.1 gg_id:345101 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU776759.1 gg_id:310803 Mongoose lemur feces clone ML_aaj25c02
FJ364698.1 gg_id:362665 feces adult twins and mothers; TS19 clone TS19_a02a02
EU778969.1 gg_id:331575 Prevost's squirrel feces clone SQ_aah82g09
EU452394.1 gg_id:352370 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU767660.1 gg_id:304352 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
DQ815778.1 gg_id:167848 mouse cecum clone aab22b11
EU862317.1 gg_id:344422 Clostridium sp. str. C9
EU451858.1 gg_id:326644 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79
EF614479.1 gg_id:234428 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
DQ815462.1 gg_id:162517 mouse cecum clone aab41a11
EU939444.1 gg_id:342085 Fecal wild pygmy loris feces clone WF16S_304
EU454659.1 gg_id:313237 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EF099107.1 gg_id:196760 mouse cecum clone SWPT2_aaa02d03
EU456764.1 gg_id:311165 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N

EU507613.1	277365	143.4	172.0	858.5	159.3	357.1	1087.3
GQ867579.1	592345	406.2	187.4	435.6	112.5	84.0	79.9
AY978174.1	119499	2076.8	1722.7	1488.3	471.1	438.5	662.3
DQ507245.1	159259	4939.6	9298.0	3175.9	6147.1	5835.7	5026.1
EU454693.1	329126	2966.9	2701.3	3610.7	3943.0	2226.5	1941.0
EU511227.1	273077	39.1	47.7	37.6	63.1	86.4	31.8
EU510407.1	270065	2145.2	2481.7	2155.8	2544.8	3205.2	1755.4
DQ803584.1	179758	4593.1	3625.7	4052.9	5729.9	4500.5	4828.1
DQ800728.1	183498	891.5	48.2	1376.5	741.0	657.7	481.9
FJ370516.1	368577	14383.7	11177.9	10928.9	8586.9	10245.3	12920.9
EF098834.1	181808	714.9	1272.6	1327.8	2097.2	2707.6	2557.0
FJ363546.1	358915	26.1	35.3	63.9	71.4	72.0	38.7
EF097971.1	176671	4754.2	6241.0	3643.3	5059.0	4740.3	5595.9
EU507789.1	264568	16.0	17.6	52.6	62.1	66.7	22.1
EF402492.1	213448	21.7	31.6	69.6	59.1	49.8	38.2
GQ492185.1	584906	2657.4	587.2	2851.2	5536.8	3255.9	4535.9
EF099713.1	196088	1833.4	2120.7	3014.4	2035.3	4560.8	4024.9
GQ493377.1	590324	447.0	349.6	743.8	500.7	412.6	1662.8
EU762698.1	307338	255.2	223.8	2927.4	4093.9	397.8	823.9
EU504212.1	275307	3518.8	5819.5	2545.6	3338.5	5332.5	4437.8
EU509514.1	273179	3385.6	2342.9	400.1	1613.4	2731.2	2114.8
EU509781.1	276663	5728.1	5480.4	5323.0	4297.3	6732.5	6981.2
EU508759.1	271646	7793.4	7113.0	2821.4	8915.8	11439.0	10366.8
EU504370.1	260529	3728.9	3618.2	1979.8	2132.2	1682.4	1279.6
EU776687.1	331571	4629.2	4652.1	5707.9	4868.0	6181.7	8417.4
EF098153.1	181711	680.4	1250.8	1666.9	454.9	5504.9	3775.0
EU451008.1	345101	7115.5	8315.6	5391.4	6972.5	10191.7	11395.4
EU776759.1	310803	51.4	76.5	242.2	83.0	457.5	632.3
FJ364698.1	362665	132.9	126.2	532.5	404.9	140.2	268.4
EU778969.1	331575	536.6	616.7	977.6	558.0	965.4	924.1
EU452394.1	352370	194.7	267.9	525.6	345.0	478.3	1060.0
EU767660.1	304352	88.7	77.1	173.4	125.4	79.7	27.6
DQ815778.1	167848	122.8	124.1	65.1	136.1	109.0	160.8
EU862317.1	344422	2039.2	1603.7	809.2	704.1	2621.8	2257.8
EU451858.1	326644	30.7	91.4	563.9	70.3	113.4	133.9
EF614479.1	234428	404.9	364.5	742.4	734.7	152.5	162.8
DQ815462.1	162517	4069.1	3812.5	2606.6	3801.3	3665.4	2700.3
EU939444.1	342085	2316.7	2793.8	4295.2	1303.8	4618.9	3887.9
EU454659.1	313237	1120.7	1677.0	2036.0	411.1	468.5	810.0
EF099107.1	196760	22.9	31.5	51.0	47.9	122.6	98.5
EU456764.1	311165	5360.0	3814.5	3501.9	5788.9	6279.8	6328.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	20250
s__unclassified	20251
s__unclassified	20264
s__unclassified	20265
s__unclassified	20266
s__unclassified	20271
s__unclassified	20274
s__unclassified	20275
s__unclassified	20279
s__unclassified	20281
s__unclassified	20283
s__unclassified	20285
s__unclassified	20298
s__unclassified	20300
s__unclassified	20306
s__unclassified	20311
s__unclassified	20321
s__unclassified	20323
s__unclassified	20327
s__unclassified	20332
s__unclassified	20336
s__unclassified	20337
s__unclassified	20347
s__unclassified	20361
s__unclassified	20366
s__unclassified	20370
s__unclassified	20372
s__unclassified	20379
s__unclassified	20383
s__unclassified	20387
s__unclassified	20390
s__unclassified	20392
s__unclassified	20394
s__unclassified	20395
s__unclassified	20397
s__unclassified	20399
s__unclassified	20405
s__unclassified	20412
s__unclassified	20422
s__unclassified	20425
s__unclassified	20429

GQ492511.1 gg_id:540206 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EF098230.1 gg_id:193707 mouse cecum clone SWPT14_aaa03d02
EU503837.1 gg_id:258710 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01d01
AY991756.1 gg_id:134785 mouse cecum clone C20_c17
EF098778.1 gg_id:191205 mouse cecum clone SWPT16_aaa04g08
EU510985.1 gg_id:267672 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52h01
DQ801002.1 gg_id:184794 human fecal clone RL387_aao90g03
AY982046.1 gg_id:123136 human sigmoid colon mucosal biopsy clone P435
AF371598.1 gg_id:27071 swine intestine clone p-3568-9F3
DQ015626.1 gg_id:133410 mouse cecum clone M3_d03_3
EU456432.1 gg_id:337754 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EU509482.1 gg_id:260401 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59a12
EU451347.1 gg_id:328290 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EU506494.1 gg_id:267348 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa02h07
AY991972.1 gg_id:133932 mouse cecum clone C20_n14
EF098724.1 gg_id:188587 mouse cecum clone SWPT16_aaa04a03
GQ867464.1 gg_id:594104 and prevalence blaTEM genes Arctic seals colon content clone CSG33
EF098257.1 gg_id:184092 mouse cecum clone SWPT14_aaa03g02
EU451916.1 gg_id:351322 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
GQ867496.1 gg_id:589252 and prevalence blaTEM genes Arctic seals colon content clone CSG68
AY976468.1 gg_id:121417 human ascending colon mucosal biopsy clone LZ74
EU451067.1 gg_id:333330 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EU766772.1 gg_id:332005 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EF096317.1 gg_id:177372 mouse cecum clone obob1_aaa04g09
AM932636.1 gg_id:566204 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications
AB075772.1 gg_id:70424 Clostridium sphenoides str. ATCC 19403
AM183091.1 gg_id:253465 and its spatial composts compost clone SMC62
AY305309.1 gg_id:99786 butyrate-producing M62/1
DQ905158.1 gg_id:165137 human fecal clone 002C-f12
EF096776.1 gg_id:195356 mouse cecum clone SWPT11_aaa04e04
EU764399.1 gg_id:321397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
EF096298.1 gg_id:176380 mouse cecum clone obob1_aaa04d03
FJ364572.1 gg_id:362759 feces adult twins and mothers; TS15 clone TS15_a04e07
EF099498.1 gg_id:191020 mouse cecum clone SWPT3_aaa04a04
AF357570.1 gg_id:71692 mpn-isolate group 22
EU504147.1 gg_id:263865 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02c04
GQ492220.1 gg_id:592784 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU506722.1 gg_id:265652 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55b07
EU452778.1 gg_id:312718 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
FJ370778.1 gg_id:370100 feces adult twins and mothers; TS5 clone TS5_a01b08
EU504001.1 gg_id:268581 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03h01

GQ492511.1	540206	16741.9	10476.7	5604.3	7631.1	10551.6	9226.9
EF098230.1	193707	1679.9	1666.2	1916.2	3801.7	1845.3	2628.2
EU503837.1	258710	49.5	130.2	303.5	92.9	119.6	36.6
AY991756.1	134785	4715.2	8072.2	3484.2	5410.8	6435.4	6714.5
EF098778.1	191205	1154.1	1213.4	1956.5	2301.3	476.1	845.9
EU510985.1	267672	395.7	521.2	711.2	530.5	1075.6	1270.8
DQ801002.1	184794	821.0	1045.2	790.1	236.0	178.8	272.4
AY982046.1	123136	1655.1	1615.6	251.9	321.5	618.3	264.5
AF371598.1	27071	99.5	66.4	251.8	70.4	73.3	101.2
DQ015626.1	133410	32.3	32.2	37.6	71.5	87.3	44.4
EU456432.1	337754	14.7	33.6	13.8	41.6	50.9	22.3
EU509482.1	260401	1452.2	2573.8	695.0	194.0	1274.2	491.9
EU451347.1	328290	6582.6	6152.1	4870.0	4855.7	9003.1	6339.7
EU506494.1	267348	3052.7	3179.0	1745.0	4309.2	3656.9	3151.9
AY991972.1	133932	23.2	40.3	54.7	56.3	73.4	50.1
EF098724.1	188587	410.7	392.5	1399.8	1223.5	1452.9	1073.9
GQ867464.1	594104	771.3	688.5	1164.4	914.7	156.3	221.0
EF098257.1	184092	147.4	283.2	1023.2	120.3	149.7	244.0
EU451916.1	351322	104.4	190.5	355.4	177.4	75.1	125.2
GQ867496.1	589252	2394.4	1337.9	1018.1	2126.1	499.2	1189.5
AY976468.1	121417	7390.4	5278.9	2919.7	3494.2	7138.7	5634.2
EU451067.1	333330	18.9	29.1	55.0	40.6	59.1	15.8
EU766772.1	332005	1427.0	2027.2	1082.9	1546.9	1501.4	1689.0
EF096317.1	177372	1010.0	766.8	121.3	782.6	220.6	533.6
AM932636.1	566204	757.2	692.0	1325.1	1426.6	804.3	289.1
AB075772.1	70424	5677.3	7254.6	4090.7	5501.7	7585.9	6935.3
AM183091.1	253465	35.9	35.9	180.7	69.6	67.6	36.4
AY305309.1	99786	21.8	26.7	24.1	27.0	53.2	39.5
DQ905158.1	165137	5840.1	5138.2	3047.7	6460.1	582.3	1721.1
EF096776.1	195356	4181.2	6160.6	3861.1	3764.7	9984.8	6775.5
EU764399.1	321397	2641.8	2481.9	595.7	1514.5	2708.6	1234.1
EF096298.1	176380	5069.1	5891.4	4011.8	9843.5	8837.3	9170.7
FJ364572.1	362759	862.1	1177.6	4886.9	1411.0	1149.1	1973.4
EF099498.1	191020	4130.4	4101.8	1690.0	2269.2	1679.2	1146.9
AF357570.1	71692	3687.3	4003.4	940.9	3514.2	3315.0	3503.2
EU504147.1	263865	2761.9	1832.0	2692.8	673.8	1048.3	1206.1
GQ492220.1	592784	1023.5	2749.0	2215.7	535.3	792.3	1282.8
EU506722.1	265652	1867.1	4128.0	1373.6	1642.5	7803.5	6296.4
EU452778.1	312718	348.9	396.9	188.4	218.8	61.6	66.6
FJ370778.1	370100	376.3	263.8	513.6	393.5	72.4	37.5
EU504001.1	268581	691.7	1181.3	241.0	133.0	83.5	117.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	20432
s__unclassified	20435
s__unclassified	20450
s__unclassified	20452
s__unclassified	20453
s__unclassified	20454
s__unclassified	20460
s__unclassified	20462
s__unclassified	20472
s__unclassified	20475
s__unclassified	20481
s__unclassified	20493
s__unclassified	20496
s__unclassified	20497
s__unclassified	20502
s__unclassified	20506
s__unclassified	20511
s__unclassified	20512
s__unclassified	20513
s__unclassified	20517
s__unclassified	20521
s__unclassified	20524
s__unclassified	20531
s__unclassified	20534
s__unclassified	20549
s__unclassified	20556
s__unclassified	20557
s__unclassified	20560
s__unclassified	20565
s__unclassified	20568
s__unclassified	20569
s__unclassified	20573
s__unclassified	20580
s__unclassified	20586
s__unclassified	20590
s__unclassified	20591
s__unclassified	20593
s__unclassified	20598
s__unclassified	20600
s__unclassified	20603
s__unclassified	20610

EU503912.1 gg_id:267090 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02e02
EF098723.1 gg_id:199322 mouse cecum clone SWPT16_aaa04a02
FJ371935.1 gg_id:358495 feces adult twins and mothers; TS8 clone TS8_a03h06
DQ808448.1 gg_id:180386 human fecal clone RL180_aao76f10
EU503586.1 gg_id:266131 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01f02
FM204998.1 gg_id:564961 Prokaryote shifts and reductive dehalogenase redundancy response electron donor
EU451441.1 gg_id:355374 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EU510210.1 gg_id:258218 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h12
EU508100.1 gg_id:276628 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa04a04
DQ807984.1 gg_id:177535 human fecal clone RL180_aan70b12
EF097084.1 gg_id:175044 mouse cecum clone SWPT18_aaa01b09
EU453023.1 gg_id:331317 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EF099459.1 gg_id:188117 mouse cecum clone SWPT3_aaa03e02
EU474426.1 gg_id:292669 western lowland gorilla feces clone GORSD_aaa01a07
EF096430.1 gg_id:182604 mouse cecum clone obob2_aaa02f12
EF398816.1 gg_id:213808 human fecal clone SJTU_F_07_51
DQ795209.1 gg_id:182723 human fecal clone RL178_aah51e09
EU511939.1 gg_id:263503 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11e10
EF025256.1 gg_id:185151 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F18
EF098495.1 gg_id:181368 mouse cecum clone SWPT15_aaa04c02
EU506432.1 gg_id:270960 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01f09
EU511857.1 gg_id:260996 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10a07
EU773389.1 gg_id:332584 BigHorn sheep feces clone BH1_aao26e10
EU456147.1 gg_id:316007 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU508222.1 gg_id:275907 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03f09
GQ897835.1 gg_id:557850 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AB114225.1 gg_id:97871 Clostridium sp. str. B556-1
X71855.1 gg_id:13973 Clostridium xylanolyticum str. ATCC 4963
EF604530.1 gg_id:233313 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ014635.1 gg_id:134263 mouse cecum clone M1_h08
DQ799555.1 gg_id:184320 human fecal clone RL305aal87f04
EF099548.1 gg_id:185301 mouse cecum clone SWPT3_aaa04g06
EU506240.1 gg_id:261109 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c06
FJ880755.1 gg_id:416185 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU455733.1 gg_id:321446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU508176.1 gg_id:272386 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02e07
EF098641.1 gg_id:183428 mouse cecum clone SWPT16_aaa02e12
EU504073.1 gg_id:272742 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04h05
DQ798869.1 gg_id:177286 human fecal clone RL242_aaj98d09
EF096053.1 gg_id:177043 mouse cecum clone lean2_aaa03a06
EU456428.1 gg_id:347190 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N

EU503912.1	267090	348.8	1751.4	1959.6	2027.9	191.1	1170.0
EF098723.1	199322	497.3	968.2	2042.1	249.5	289.5	423.1
FJ371935.1	358495	952.2	1852.8	734.0	540.9	2802.4	2970.5
DQ808448.1	180386	1084.0	1078.1	163.6	183.5	97.3	303.1
EU503586.1	266131	4575.0	4547.6	3234.1	3502.0	5015.0	3480.5
FM204998.1	564961	164.5	57.3	375.3	131.1	95.2	44.8
EU451441.1	355374	3939.8	5936.1	2924.2	2471.7	5545.3	5279.6
EU510210.1	258218	1239.1	1737.8	978.0	1234.9	1624.3	754.9
EU508100.1	276628	4383.8	3538.3	1649.7	4830.4	4063.0	5352.7
DQ807984.1	177535	53.5	64.8	339.9	83.3	70.7	62.1
EF097084.1	175044	1696.0	1090.0	1185.0	4064.3	1069.9	2543.7
EU453023.1	331317	5245.3	2772.8	2132.4	4444.3	8841.4	5094.4
EF099459.1	188117	7052.0	6090.3	2624.1	7106.3	5586.6	4489.7
EU474426.1	292669	81.3	287.8	77.5	128.5	136.0	91.7
EF096430.1	182604	6523.8	7927.7	6404.0	5619.2	9141.7	8796.8
EF398816.1	213808	2459.7	2787.8	521.0	1501.7	2682.7	2359.2
DQ795209.1	182723	80.5	92.9	404.0	84.3	65.4	62.6
EU511939.1	263503	8099.5	8676.3	7372.2	6567.7	5390.9	5628.0
EF025256.1	185151	6258.9	5876.2	7046.4	5878.3	5613.8	7338.6
EF098495.1	181368	94.9	330.9	527.4	1366.6	298.3	934.7
EU506432.1	270960	6844.9	5916.7	3075.1	5689.3	11467.4	6121.1
EU511857.1	260996	32.8	28.9	125.7	58.9	51.0	40.3
EU773389.1	332584	558.2	932.2	1687.9	268.4	347.8	336.6
EU456147.1	316007	3678.1	4388.3	5220.6	2499.6	3523.1	2773.0
EU508222.1	275907	942.2	913.3	1219.7	1791.4	734.4	1151.1
GQ897835.1	557850	1050.8	817.7	741.5	1060.1	89.6	135.6
AB114225.1	97871	8387.6	4262.5	8607.0	6475.2	5230.9	6253.3
X71855.1	13973	95.9	175.3	368.0	515.9	134.1	147.5
EF604530.1	233313	6077.1	5975.1	6382.5	5890.7	5243.2	5835.8
DQ014635.1	134263	545.5	523.3	477.0	626.5	1780.3	1235.6
DQ799555.1	184320	537.2	915.9	221.8	354.4	123.1	504.0
EF099548.1	185301	110.1	339.5	503.5	165.5	1036.8	805.5
EU506240.1	261109	8464.0	7735.4	3766.5	7916.4	8721.1	9097.9
FJ880755.1	416185	4917.0	7243.9	5961.1	6771.9	11264.5	7836.8
EU455733.1	321446	118.8	274.6	140.9	100.9	246.5	146.9
EU508176.1	272386	7902.1	10484.5	1647.4	1954.9	3801.9	1572.4
EF098641.1	183428	37.6	141.6	148.5	447.2	87.7	45.3
EU504073.1	272742	1658.2	1324.3	1704.6	3361.4	2672.2	3648.8
DQ798869.1	177286	649.4	616.2	1283.9	970.7	969.5	690.7
EF096053.1	177043	7654.4	8900.4	1415.3	7894.2	6024.3	4192.1
EU456428.1	347190	23.1	32.4	78.2	61.2	235.0	32.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	20611
s__unclassified	20612
s__unclassified	20615
s__unclassified	20616
s__unclassified	20631
s__unclassified	20778
s__unclassified	20813
s__unclassified	20818
s__unclassified	20933
s__unclassified	20950
s__unclassified	21121
s__unclassified	21156
s__unclassified	21249
s__unclassified	21265
s__unclassified	21297
s__unclassified	21360
s__unclassified	21650
s__unclassified	21702
s__unclassified	21742
s__unclassified	21758
s__unclassified	21780
s__unclassified	22641
s__unclassified	22649
s__unclassified	22652
s__unclassified	22655
s__unclassified	22656
s__unclassified	22681
s__unclassified	22682
s__unclassified	22683
s__unclassified	22688
s__unclassified	22689
s__unclassified	22692
s__unclassified	22697
s__unclassified	22701
s__unclassified	22703
s__unclassified	22724
s__unclassified	22734
s__unclassified	22760
s__unclassified	22762
s__unclassified	22785
s__unclassified	22787

AB114231.1 gg_id:95658 Clostridium sp. str. Kas401-4
EF098553.1 gg_id:185587 mouse cecum clone SWPT16_aaa01c07
EU506380.1 gg_id:275913 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64e10
EF096792.1 gg_id:173865 mouse cecum clone SWPT11_aaa04g04
DQ015610.1 gg_id:129538 mouse cecum clone M3_b09_3
DQ798924.1 gg_id:176924 human fecal clone RL242_aaj99b07
EF098774.1 gg_id:188527 mouse cecum clone SWPT16_aaa04g01
EU511784.1 gg_id:275362 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09b12.Contig2
EU777890.1 gg_id:333030 European rabbit feces clone RA_c12
EU777843.1 gg_id:317693 European rabbit feces clone RA_d04
EU771662.1 gg_id:324837 African elephant feces clone AFYEL_aaj67h11
EU450997.1 gg_id:351184 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EF097574.1 gg_id:193509 mouse cecum clone SWPT19_aaa04f03
EU777852.1 gg_id:353339 European rabbit feces clone RA_c07
EU458606.1 gg_id:302763 European rabbit feces clone RA_c11
EU453414.1 gg_id:304920 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EF099092.1 gg_id:189272 mouse cecum clone SWPT2_aaa02b04
EU454774.1 gg_id:314424 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU506185.1 gg_id:274509 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02f05
EF097951.1 gg_id:188402 mouse cecum clone SWPT12_aaa02g05
EU506150.1 gg_id:276190 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa01a10
EU530312.1 gg_id:259761 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
DQ807567.1 gg_id:196575 human fecal clone RL307_aam08d02
DQ904659.1 gg_id:163667 human fecal clone 001-b9
DQ815335.1 gg_id:165437 mouse cecum clone aab45g07
EU511089.1 gg_id:274060 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02e08
EF098104.1 gg_id:186332 mouse cecum clone SWPT14_aaa01e09
FJ364077.1 gg_id:367361 feces adult twins and mothers; TS150 clone TS150_a02g01
AY984246.1 gg_id:125031 human stool clone B137
DQ802434.1 gg_id:196091 human fecal clone RL188_aah17f09
DQ014768.1 gg_id:131073 mouse cecum clone M1_e02_2
EU453995.1 gg_id:338442 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
FJ367695.1 gg_id:367805 feces adult twins and mothers; TS2 clone TS2_a02e03
DQ825146.1 gg_id:185864 human fecal clone RL185_aan85h06
FJ371087.1 gg_id:369473 feces adult twins and mothers; TS5 clone TS5_a04g05
AY977088.1 gg_id:118015 human cecum mucosal biopsy clone K778
DQ808251.1 gg_id:198086 human fecal clone RL180_aao74d08
FJ369137.1 gg_id:361894 feces adult twins and mothers; TS4 clone TS4_a04f10
FJ369095.1 gg_id:357512 feces adult twins and mothers; TS4 clone TS4_a04b08
FJ368954.1 gg_id:359028 feces adult twins and mothers; TS4 clone TS4_a02e06
DQ807363.1 gg_id:187991 human fecal clone RL307_aam05f02

AB114231.1	95658	430.6	697.9	506.9	1379.8	1493.5	3617.6
EF098553.1	185587	52.4	68.1	142.9	78.1	61.4	70.1
EU506380.1	275913	1021.4	1217.6	1067.9	597.6	908.1	1391.4
EF096792.1	173865	3790.9	3829.6	307.3	4413.1	3635.6	4718.1
DQ015610.1	129538	21.3	38.8	81.5	64.9	84.0	54.9
DQ798924.1	176924	2148.6	1958.8	1060.4	789.6	3607.3	1730.4
EF098774.1	188527	3060.8	3542.2	1073.3	2358.7	3392.9	1302.7
EU511784.1	275362	19.0	31.2	19.7	50.2	51.1	18.3
EU777890.1	333030	1589.0	1930.3	2653.2	1796.8	2158.5	1525.8
EU777843.1	317693	1328.1	1526.3	1841.6	1118.5	2543.9	3071.7
EU771662.1	324837	3814.6	4045.3	1080.2	6855.9	5172.0	5881.4
EU450997.1	351184	7381.1	7368.2	7928.2	6467.9	5999.8	6749.6
EF097574.1	193509	39.2	35.6	77.2	64.0	79.1	78.3
EU777852.1	353339	3990.2	5166.5	2357.6	3000.9	8126.4	8338.2
EU458606.1	302763	141.3	147.6	291.0	127.8	139.0	139.3
EU453414.1	304920	99.8	42.4	219.8	55.5	104.8	114.3
EF099092.1	189272	51.1	95.8	78.3	90.6	71.5	62.6
EU454774.1	314424	6026.2	7593.2	7490.4	7764.5	7762.1	9667.4
EU506185.1	274509	319.3	278.1	699.3	477.6	707.6	516.8
EF097951.1	188402	850.3	1061.3	1298.2	631.2	1491.2	1151.5
EU506150.1	276190	2424.2	3002.6	1923.4	1904.5	3631.5	3371.8
EU530312.1	259761	7927.3	7066.6	7255.2	5418.5	4962.6	6485.1
DQ807567.1	196575	1223.5	2264.5	1244.1	790.7	4167.6	2549.3
DQ904659.1	163667	269.8	383.2	1084.2	568.1	397.8	769.7
DQ815335.1	165437	48.8	58.9	104.9	54.9	133.8	27.2
EU511089.1	274060	441.6	457.5	1311.5	746.2	404.0	492.1
EF098104.1	186332	683.8	975.9	1005.5	983.8	705.1	895.4
FJ364077.1	367361	202.3	165.4	140.9	93.0	60.4	66.3
AY984246.1	125031	126.7	181.2	341.9	318.4	281.7	1390.4
DQ802434.1	196091	476.1	308.7	235.6	166.3	2721.3	1135.0
DQ014768.1	131073	2350.2	2170.0	910.8	1144.5	1616.2	1167.8
EU453995.1	338442	5734.9	5121.8	1722.3	3518.2	4324.6	3275.2
FJ367695.1	367805	6701.4	6693.5	7400.4	5172.2	9180.9	9977.3
DQ825146.1	185864	693.4	869.3	454.3	302.8	347.6	303.9
FJ371087.1	369473	317.4	320.8	397.7	2443.1	519.2	474.5
AY977088.1	118015	276.3	499.8	588.2	135.7	1879.6	805.3
DQ808251.1	198086	37.5	83.9	121.4	67.3	64.0	37.9
FJ369137.1	361894	595.5	814.2	471.8	1899.6	101.7	165.2
FJ369095.1	357512	1871.2	2071.0	2307.2	2609.4	3659.2	4465.5
FJ368954.1	359028	8684.8	8966.3	4828.6	9714.2	13897.1	15986.1
DQ807363.1	187991	125.0	208.1	624.4	260.6	496.9	798.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	22808
s__unclassified	22811
s__unclassified	22814
s__unclassified	22826
s__unclassified	22829
s__unclassified	22835
s__unclassified	22847
s__unclassified	22855
s__unclassified	22864
s__unclassified	22868
s__unclassified	22892
s__unclassified	22933
s__unclassified	22936
s__unclassified	22940
s__unclassified	22951
s__unclassified	22954
s__unclassified	23003
s__unclassified	23013
s__unclassified	23018
s__unclassified	23025
s__unclassified	23062
s__unclassified	23076
s__unclassified	23077
s__unclassified	23102
s__unclassified	23105
s__unclassified	23136
s__unclassified	23165
s__unclassified	23167
s__unclassified	23173
s__unclassified	23180
s__unclassified	23194
s__unclassified	23211
s__unclassified	23222
s__unclassified	23229
s__unclassified	23243
s__unclassified	23263
s__unclassified	23272
s__unclassified	23280
s__unclassified	23288
s__unclassified	23317
s__unclassified	23320

FJ369046.1 gg_id:361922 feces adult twins and mothers; TS4 clone TS4_a03f03
DQ015254.1 gg_id:132281 mouse cecum clone M2_1b08
FJ371331.1 gg_id:370049 feces adult twins and mothers; TS6 clone TS6_a03f11
AY994021.1 gg_id:136633 Abundant and fungal microbiota murine intestine clone 41-1
DQ799304.1 gg_id:181834 human fecal clone RL205_aaj20e03
FJ369123.1 gg_id:365644 feces adult twins and mothers; TS4 clone TS4_a04e06
AY981455.1 gg_id:122012 human sigmoid colon mucosal biopsy clone L545
EU766751.1 gg_id:329944 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
AY984564.1 gg_id:123233 human stool clone B503
EF098881.1 gg_id:187852 mouse cecum clone SWPT1_aaa02e12
FJ367781.1 gg_id:357957 feces adult twins and mothers; TS2 clone TS2_a03e07
DQ904722.1 gg_id:171410 human fecal clone 001-h12
AY984690.1 gg_id:121570 human stool clone B642
EF099816.1 gg_id:192408 mouse cecum clone SWPT4_aaa04g01
FJ369040.1 gg_id:365086 feces adult twins and mothers; TS4 clone TS4_a03e09
DQ823933.1 gg_id:196107 human fecal clone RL204_aaj57b03
FJ368977.1 gg_id:358255 feces adult twins and mothers; TS4 clone TS4_a02g07
EU504262.1 gg_id:275676 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01c09
DQ905526.1 gg_id:162294 human fecal clone 014-g1
EU508369.1 gg_id:258165 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04a08
FJ371424.1 gg_id:359347 feces adult twins and mothers; TS6 clone TS6_a04g10
FJ370956.1 gg_id:363515 feces adult twins and mothers; TS5 clone TS5_a03c03
EF404993.1 gg_id:216746 human fecal clone SJTU_G_05_59
FJ369087.1 gg_id:357218 feces adult twins and mothers; TS4 clone TS4_a04a12
DQ904930.1 gg_id:171783 human fecal clone 002-b1
AY978695.1 gg_id:119824 human transverse colon mucosal biopsy clone KT72
EU453964.1 gg_id:318008 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EF403201.1 gg_id:210539 human fecal clone SJTU_A1_6_40
AY984776.1 gg_id:116238 human stool clone B738
AY975938.1 gg_id:120535 human ascending colon mucosal biopsy clone LS45
AY982876.1 gg_id:120781 human descending colon mucosal biopsy clone L046
AY983028.1 gg_id:123310 human descending colon mucosal biopsy clone L258
AY980512.1 gg_id:127137 human rectum mucosal biopsy clone X243
FJ368858.1 gg_id:364039 feces adult twins and mothers; TS4 clone TS4_a01d09
AY982766.1 gg_id:126286 human descending colon mucosal biopsy clone KZ01
EU508235.1 gg_id:275799 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04a07
FJ368923.1 gg_id:366377 feces adult twins and mothers; TS4 clone TS4_a02b08
DQ802136.1 gg_id:176587 human fecal clone RL241_aaj03e08
FJ371276.1 gg_id:357312 feces adult twins and mothers; TS6 clone TS6_a03a10
EF400450.1 gg_id:212481 human fecal clone SJTU_E_13_50
EF401232.1 gg_id:206701 human fecal clone SJTU_D_07_54

FJ369046.1	361922	2587.4	3126.4	1256.7	2979.8	517.2	824.6
DQ015254.1	132281	228.6	1003.6	391.8	1073.4	1843.8	4544.5
FJ371331.1	370049	366.5	594.2	592.8	530.5	204.0	1164.7
AY994021.1	136633	4397.6	6802.8	5326.4	4765.9	5670.8	5018.6
DQ799304.1	181834	319.4	106.1	66.2	435.7	87.2	51.3
FJ369123.1	365644	158.5	45.5	394.7	98.9	306.4	308.1
AY981455.1	122012	4260.0	3374.0	1185.2	4389.8	5275.2	5120.4
EU766751.1	329944	1761.1	2337.7	2648.1	2337.7	2902.6	4766.6
AY984564.1	123233	2130.2	172.5	1201.8	3582.9	2613.8	3655.0
EF098881.1	187852	597.0	581.3	197.9	742.9	95.1	135.9
FJ367781.1	357957	119.0	163.9	609.0	144.3	130.5	503.8
DQ904722.1	171410	85.0	99.1	161.6	103.4	66.9	53.4
AY984690.1	121570	1790.5	459.1	1225.1	2836.5	3450.1	2980.2
EF099816.1	192408	136.3	271.8	312.2	112.1	99.4	253.3
FJ369040.1	365086	1058.4	1543.2	797.3	1934.2	1775.7	1102.3
DQ823933.1	196107	2476.9	2796.8	5278.1	3412.4	5506.5	4593.0
FJ368977.1	358255	3568.6	4409.5	2921.7	4200.6	4834.9	5868.2
EU504262.1	275676	58.0	83.7	94.7	65.6	60.8	38.2
DQ905526.1	162294	538.1	472.8	147.5	187.5	403.7	242.4
EU508369.1	258165	352.0	290.8	280.7	333.4	2250.3	991.4
FJ371424.1	359347	49.8	38.1	85.4	79.7	66.0	47.0
FJ370956.1	363515	96.0	85.4	59.2	212.4	62.9	30.6
EF404993.1	216746	214.6	185.1	486.9	324.2	139.7	165.5
FJ369087.1	357218	112.1	228.0	688.3	145.7	179.8	343.2
DQ904930.1	171783	1965.4	1499.0	350.5	466.3	87.0	126.3
AY978695.1	119824	2483.5	2220.3	491.5	866.2	758.5	667.8
EU453964.1	318008	1230.2	1168.2	759.7	611.1	959.2	803.5
EF403201.1	210539	302.5	596.6	980.5	237.2	530.6	502.6
AY984776.1	116238	84.9	242.0	144.4	95.7	101.4	73.5
AY975938.1	120535	2879.3	3522.8	5726.9	1783.9	2783.6	1748.4
AY982876.1	120781	3664.2	4624.0	477.6	2597.8	1686.4	1844.3
AY983028.1	123310	38.2	53.7	82.7	167.1	49.8	82.6
AY980512.1	127137	57.1	81.4	295.6	73.6	66.7	40.9
FJ368858.1	364039	5540.9	6798.3	5241.1	4302.3	4872.7	4162.9
AY982766.1	126286	88.4	60.6	457.4	199.1	353.3	380.5
EU508235.1	275799	3984.9	3780.2	2443.8	2947.3	2461.2	2255.7
FJ368923.1	366377	231.5	199.7	2308.4	639.2	2953.3	466.7
DQ802136.1	176587	39.8	45.5	165.8	110.3	64.5	51.4
FJ371276.1	357312	21.5	26.5	39.4	44.9	38.1	16.6
EF400450.1	212481	195.4	232.5	548.1	146.7	132.6	195.1
EF401232.1	206701	944.0	1177.0	976.4	1650.0	1248.7	3115.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	23324
s__unclassified	23342
s__unclassified	23359
s__unclassified	23369
s__unclassified	23376
s__unclassified	23382
s__unclassified	23386
s__unclassified	23402
s__unclassified	23423
s__unclassified	23434
s__unclassified	23464
s__unclassified	23471
s__unclassified	23484
s__unclassified	23489
s__unclassified	23503
s__unclassified	23520
s__unclassified	23522
s__unclassified	23543
s__unclassified	23544
s__unclassified	23567
s__unclassified	23568
s__unclassified	23579
s__unclassified	23581
s__unclassified	23589
s__unclassified	23591
s__unclassified	23595
s__unclassified	23597
s__unclassified	23599
s__unclassified	23618
s__unclassified	23667
s__unclassified	23677
s__unclassified	23695
s__unclassified	23701
s__unclassified	23706
s__unclassified	23726
s__unclassified	23731
s__unclassified	23733
s__unclassified	23739
s__unclassified	23740
s__unclassified	23767
s__unclassified	23774

DQ823905.1 gg_id:197197 human fecal clone RL250_aaj80g04
AY916166.1 gg_id:114387 human transverse colon biopsy clone M629
EU776782.1 gg_id:321095 Mongoose lemur feces clone ML_aaj28f07
FJ369014.1 gg_id:370235 feces adult twins and mothers; TS4 clone TS4_a03c07
FJ369150.1 gg_id:367923 feces adult twins and mothers; TS4 clone TS4_a04h04
AY985171.1 gg_id:116565 human stool clone BB95
DQ801872.1 gg_id:183711 human fecal clone RL201_aai47h08
AY982502.1 gg_id:123023 human sigmoid colon mucosal biopsy clone MN06
EF604966.1 gg_id:235081 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604534.1 gg_id:234956 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF097988.1 gg_id:181415 mouse cecum clone SWPT12_aaa03f06
EU511999.1 gg_id:271804 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12e04
EF099490.1 gg_id:174338 mouse cecum clone SWPT3_aaa03g12
EF602819.1 gg_id:228836 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU457160.1 gg_id:352799 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EU451365.1 gg_id:327720 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU452796.1 gg_id:315001 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU776507.1 gg_id:325848 Lion feces clone LI3_aah76a09
EF098165.1 gg_id:197600 mouse cecum clone SWPT14_aaa02e04
EU454540.1 gg_id:305112 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU453875.1 gg_id:307093 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EF098455.1 gg_id:197759 mouse cecum clone SWPT15_aaa03e04
EU509194.1 gg_id:272159 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f11
EU504518.1 gg_id:267353 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g04
EU454074.1 gg_id:353177 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EF605183.1 gg_id:228046 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU509790.1 gg_id:275349 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b01
AY992530.1 gg_id:132673 mouse cecum clone C23_h21
EU506415.1 gg_id:259154 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01d10
EU455283.1 gg_id:345503 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EF098479.1 gg_id:190699 mouse cecum clone SWPT15_aaa03h11
EF097776.1 gg_id:192131 mouse cecum clone SWPT20_aaa03f01
EF097342.1 gg_id:176950 mouse cecum clone SWPT19_aaa01c11
AY991902.1 gg_id:135378 mouse cecum clone C20_k03
EU504157.1 gg_id:266061 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02e02
EU510843.1 gg_id:277200 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak50b04
EU474262.1 gg_id:296041 western lowland gorilla feces clone GORSD_aaa01e03
EU453646.1 gg_id:315974 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EF602818.1 gg_id:228511 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF604535.1 gg_id:235067 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ881305.1 gg_id:428954 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;

DQ823905.1	197197	3695.2	2679.1	5903.1	6177.3	1032.8	1574.5
AY916166.1	114387	39.4	49.8	165.3	58.2	42.9	36.8
EU776782.1	321095	104.2	64.1	195.8	101.4	90.5	45.2
FJ369014.1	370235	63.7	138.2	166.9	89.4	70.6	56.2
FJ369150.1	367923	2832.5	3231.4	3208.2	4096.9	7489.6	5978.9
AY985171.1	116565	585.7	359.5	638.4	2382.7	939.2	602.4
DQ801872.1	183711	3854.3	3351.7	2032.6	3316.5	3616.0	2466.7
AY982502.1	123023	53.2	38.7	70.7	52.8	73.9	41.1
EF604966.1	235081	3696.9	3722.4	3146.4	3800.0	4618.7	3368.5
EF604534.1	234956	10694.1	12242.7	10187.2	10010.4	14394.7	11015.0
EF097988.1	181415	716.5	1025.4	3340.2	1134.6	3588.5	4275.6
EU511999.1	271804	26.0	37.3	41.2	56.7	47.4	18.1
EF099490.1	174338	532.3	644.6	91.7	433.9	135.3	115.2
EF602819.1	228836	1148.0	1397.7	1194.0	1245.2	2528.1	1417.1
EU457160.1	352799	37.5	80.5	47.3	81.7	45.4	44.2
EU451365.1	327720	71.1	124.8	291.5	108.1	216.0	216.4
EU452796.1	315001	76.7	74.7	520.0	92.2	60.8	89.6
EU776507.1	325848	417.3	911.8	591.0	327.2	2360.8	1158.3
EF098165.1	197600	278.9	258.9	410.3	594.5	75.1	116.1
EU454540.1	305112	10070.6	11940.5	12517.9	8715.5	14837.3	10500.3
EU453875.1	307093	3211.8	3180.1	4886.8	2472.5	4067.6	3340.5
EF098455.1	197759	31.0	37.8	87.6	55.7	63.1	28.7
EU509194.1	272159	6809.2	6922.2	1199.7	5413.6	3154.5	2816.2
EU504518.1	267353	250.6	243.3	741.6	284.0	480.7	442.9
EU454074.1	353177	486.6	290.7	677.4	512.7	359.8	280.3
EF605183.1	228046	2770.1	2551.0	866.0	2268.3	2843.8	2114.5
EU509790.1	275349	104.7	130.6	299.5	113.5	93.2	88.0
AY992530.1	132673	15.4	28.7	50.7	56.5	70.0	25.2
EU506415.1	259154	2150.2	2397.3	2368.8	2331.4	4354.8	2886.5
EU455283.1	345503	4487.0	2860.3	3545.8	5733.7	4599.0	3588.1
EF098479.1	190699	109.7	218.1	349.8	165.8	297.5	182.9
EF097776.1	192131	1376.6	696.5	1036.9	2099.3	1528.6	825.3
EF097342.1	176950	2736.2	3878.2	2756.5	3905.6	4418.6	6133.4
AY991902.1	135378	1307.3	165.4	2964.9	2510.1	82.7	72.4
EU504157.1	266061	157.4	164.7	605.9	245.0	138.2	277.8
EU510843.1	277200	193.9	135.1	1347.6	179.0	290.4	207.9
EU474262.1	296041	171.7	223.6	626.4	155.2	123.6	190.5
EU453646.1	315974	271.1	311.6	419.9	100.8	117.1	192.3
EF602818.1	228511	2097.8	1900.8	718.1	3269.7	3701.7	2867.9
EF604535.1	235067	11894.3	12142.8	12476.1	9913.8	12380.0	11564.5
FJ881305.1	428954	172.8	118.4	276.9	118.3	330.2	133.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	23786
s__unclassified	23787
s__unclassified	23796
s__unclassified	23830
s__unclassified	23847
s__unclassified	23853
s__unclassified	23854
s__unclassified	23862
s__unclassified	23867
s__unclassified	23871
s__unclassified	23891
s__unclassified	23904
s__unclassified	23905
s__unclassified	23907
s__unclassified	23922
s__unclassified	23932
s__unclassified	23935
s__unclassified	23951
s__unclassified	23963
s__unclassified	23972
s__unclassified	23981
s__unclassified	23999
s__unclassified	24004
s__unclassified	24006
s__unclassified	24008
s__unclassified	24011
s__unclassified	24018
s__unclassified	24021
s__unclassified	24034
s__unclassified	24044
s__unclassified	24046
s__unclassified	24051
s__unclassified	24059
s__unclassified	24060
s__unclassified	24087
s__unclassified	24099
s__unclassified	24101
s__unclassified	24103
s__unclassified	24107
s__unclassified	24113
s__unclassified	24121

EF098318.1 gg_id:182632 mouse cecum clone SWPT14_aaa04f12
EU452296.1 gg_id:326031 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
AY991846.1 gg_id:135402 mouse cecum clone C20_h05
EU455602.1 gg_id:330278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EF096300.1 gg_id:198463 mouse cecum clone obob1_aaa04d10
EF098746.1 gg_id:199211 mouse cecum clone SWPT16_aaa04c10
EF096344.1 gg_id:180694 mouse cecum clone obob2_aaa01c06
EU510446.1 gg_id:274237 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38g05
EU453143.1 gg_id:352769 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU454296.1 gg_id:304917 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EF098140.1 gg_id:174184 mouse cecum clone SWPT14_aaa02b01
EU451037.1 gg_id:352146 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EF604634.1 gg_id:232681 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AY991811.1 gg_id:132756 mouse cecum clone C20_f17
EU451512.1 gg_id:341100 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU503823.1 gg_id:264544 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01b06
EU510959.1 gg_id:258626 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52d07
EF098083.1 gg_id:194848 mouse cecum clone SWPT14_aaa01c05
EU506320.1 gg_id:273558 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63b10
AY992877.1 gg_id:130280 mouse cecum clone C22_g16
AM932538.1 gg_id:567954 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications
DQ015189.1 gg_id:132741 mouse cecum clone M2_g02_2
EF095964.1 gg_id:187871 mouse cecum clone lean2_aaa01a05
EU457571.1 gg_id:349645 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S
EU474428.1 gg_id:287507 western lowland gorilla feces clone GORSD_aaa01a10
EF096058.1 gg_id:190496 mouse cecum clone lean2_aaa03b08
AY991913.1 gg_id:129978 mouse cecum clone C20_k14
AM932611.1 gg_id:537301 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications
FJ879176.1 gg_id:403497 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU504967.1 gg_id:273683 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h09
EF098676.1 gg_id:180508 mouse cecum clone SWPT16_aaa03c07
DQ014804.1 gg_id:131642 mouse cecum clone M1_h04_2
DQ815639.1 gg_id:163445 mouse cecum clone aab44b08
DQ014926.1 gg_id:133348 mouse cecum clone M1_1e10
EU454486.1 gg_id:311129 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S
EF099794.1 gg_id:197183 mouse cecum clone SWPT4_aaa04d06
EU511991.1 gg_id:262335 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12d06
EU006205.1 gg_id:240405 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
EF098596.1 gg_id:174631 mouse cecum clone SWPT16_aaa01h10
EU454164.1 gg_id:321642 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU504734.1 gg_id:260278 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01c09

EF098318.1	182632	10056.1	10129.2	2520.7	4504.2	5240.4	5981.7
EU452296.1	326031	777.6	997.5	923.8	622.6	2493.4	2749.3
AY991846.1	135402	9214.8	9419.5	8876.3	8795.4	12127.5	11915.3
EU455602.1	330278	6687.4	7196.0	2062.9	5193.8	6664.7	5221.3
EF096300.1	198463	7085.7	6851.9	5127.8	5363.3	5240.4	4583.4
EF098746.1	199211	31.9	57.7	49.4	50.3	66.9	28.5
EF096344.1	180694	3479.4	2354.7	1831.6	3129.2	2297.9	3556.3
EU510446.1	274237	600.1	554.1	712.6	836.6	138.3	240.3
EU453143.1	352769	1376.6	1771.6	854.1	844.4	2241.9	1175.0
EU454296.1	304917	8750.5	7949.7	4679.3	6269.2	7471.9	6905.9
EF098140.1	174184	1484.4	1113.4	1716.1	1804.2	2029.9	1178.9
EU451037.1	352146	1084.3	1207.5	745.5	967.4	1679.3	1374.0
EF604634.1	232681	5932.0	5013.1	2687.8	4617.1	3202.5	3486.0
AY991811.1	132756	178.5	176.5	561.4	253.3	170.7	109.0
EU451512.1	341100	30.5	48.6	82.4	59.5	94.4	25.1
EU503823.1	264544	36.3	46.9	71.1	54.6	53.6	35.7
EU510959.1	258626	13.1	46.5	50.0	48.8	47.6	21.8
EF098083.1	194848	889.0	1526.3	937.3	882.5	2575.4	1862.9
EU506320.1	273558	5298.6	4538.6	753.6	3044.6	521.1	990.2
AY992877.1	130280	189.1	186.4	389.0	106.2	184.5	264.8
AM932538.1	567954	6064.4	5181.6	2843.1	4139.0	7011.3	4936.5
DQ015189.1	132741	125.4	227.0	159.2	199.0	205.0	277.6
EF095964.1	187871	42.7	37.5	53.1	46.3	46.9	26.6
EU457571.1	349645	255.4	346.4	393.3	137.8	192.2	302.5
EU474428.1	287507	279.1	662.1	1365.4	460.4	1025.6	1781.6
EF096058.1	190496	56.3	63.0	253.0	95.4	53.0	39.1
AY991913.1	129978	62.0	79.6	62.9	89.2	94.0	49.9
AM932611.1	537301	120.6	169.0	102.8	116.9	65.3	65.1
FJ879176.1	403497	9319.2	10043.7	3484.2	5328.3	5359.6	4901.4
EU504967.1	273683	1340.4	1548.3	1665.7	847.0	2072.2	2161.0
EF098676.1	180508	1991.2	1930.5	1713.3	2459.0	2577.2	2744.1
DQ014804.1	131642	1148.0	1717.7	495.3	1974.0	546.8	624.7
DQ815639.1	163445	179.5	134.2	227.3	61.0	75.8	130.6
DQ014926.1	133348	1706.6	1424.3	3171.4	3077.9	2330.2	2409.9
EU454486.1	311129	85.6	187.4	314.6	131.5	333.6	295.3
EF099794.1	197183	10233.5	8715.4	8618.4	10039.7	11044.0	14109.9
EU511991.1	262335	2363.7	2874.5	4821.0	2087.5	3047.4	3209.5
EU006205.1	240405	5295.3	4361.0	775.2	3123.2	644.1	897.5
EF098596.1	174631	2663.1	2339.2	2115.2	2768.2	1216.9	2336.8
EU454164.1	321642	21.8	37.0	55.6	50.3	42.5	26.8
EU504734.1	260278	56.5	64.5	41.7	78.6	75.1	67.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	24134
s__unclassified	24149
s__unclassified	24150
s__unclassified	24156
s__unclassified	24159
s__unclassified	24361
s__unclassified	27273
s__unclassified	27275
s__unclassified	27281
s__unclassified	27285
s__unclassified	27292
s__unclassified	27298
s__unclassified	27300
s__unclassified	27306
s__unclassified	27307
s__unclassified	27315
s__unclassified	27326
s__unclassified	27331
s__unclassified	27333
s__unclassified	27334
s__unclassified	27338
s__unclassified	27341
s__unclassified	27342
s__unclassified	27343
s__unclassified	27344
s__unclassified	27348
s__unclassified	27354
s__unclassified	27356
s__unclassified	27369
s__unclassified	27378
s__unclassified	27385
s__unclassified	27386
s__unclassified	27388
s__unclassified	27398
s__unclassified	27403
s__unclassified	27405
s__unclassified	27410
s__unclassified	27412
s__unclassified	27414
s__unclassified	27417
s__unclassified	27419

DQ014621.1 gg_id:133579 mouse cecum clone M1_g03
EF098295.1 gg_id:187235 mouse cecum clone SWPT14_aaa04c12
EU454820.1 gg_id:316984 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU506201.1 gg_id:264427 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03e06
EU451646.1 gg_id:343917 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EU776893.1 gg_id:350052 Mongoose lemur feces clone ML_aae87d11
EU766933.1 gg_id:352649 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ824440.1 gg_id:197356 human fecal clone RL304_aal76a10
GQ503859.1 gg_id:564639 Captain bheri clone Ecwsrb022
AB234493.1 gg_id:146488 termite gut homogenate clone MgMjR-083
EU768108.1 gg_id:329703 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
AB234484.1 gg_id:147741 termite gut homogenate clone MgMjR-030
EU504190.1 gg_id:258283 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03g02
DQ798696.1 gg_id:198678 human fecal clone RL181_aao00c02
AY349389.1 gg_id:92430 human oral cavity clone JM048
FJ978593.1 gg_id:384675 feces clone CL_F_197
FJ676837.1 gg_id:525104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802531.1 gg_id:187163 human fecal clone RL188_aan93a09
DQ905267.1 gg_id:171220 human fecal clone 013-g8
AB088949.1 gg_id:77909 termite gut homogenate clone Rs-D68 bacterium
AY974898.1 gg_id:116267 human ascending colon mucosal biopsy clone KH90
DQ802285.1 gg_id:181634 human fecal clone RL188_aah15f04
AY975299.1 gg_id:124921 human ascending colon mucosal biopsy clone N540
DQ803552.1 gg_id:199212 human fecal clone RL251_aaj87d02
NR_029269.1 gg_id:584986 Clostridium propionicum str. X2; DSM 1682
GQ448418.1 gg_id:557186 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g
FJ362869.1 gg_id:363216 feces adult twins and mothers; TS13 clone TS13_a04b10
EU748174.1 gg_id:321561 neotropical folivorous flying bird adult hoatzin crop clone hoa31_73A10.F
EF399587.1 gg_id:205933 human fecal clone SJTU_F_06_63
AY992923.1 gg_id:130491 mouse cecum clone C22_i22
GU304319.1 gg_id:563613 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
DQ799077.1 gg_id:180319 human fecal clone RL205_aaj17c08
DQ327495.1 gg_id:150500 Metagenomic gut microbiome healthy human stool clone EA67
EF402203.1 gg_id:204121 human fecal clone SJTU_B_04_90
DQ804300.1 gg_id:197231 human fecal clone RL187_aan77f07
EU763532.1 gg_id:327125 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
EU472163.1 gg_id:295754 francois langur feces clone FL_2aaa03h11
EF434346.1 gg_id:210179 human infant gastrointestinal tract microbiota stool baby 3 12 weeks old clone 1099
DQ799640.1 gg_id:175400 human fecal clone RL305aal88f01
EU761814.1 gg_id:347117 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
EU250957.1 gg_id:370405 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose

DQ014621.1	133579	5558.0	6818.2	3748.5	4117.9	9974.8	6399.5
EF098295.1	187235	26.2	28.7	28.5	48.3	55.7	26.0
EU454820.1	316984	2219.0	1923.5	2730.1	1577.4	693.4	1120.7
EU506201.1	264427	1282.8	1147.5	967.6	4248.6	2292.1	2194.1
EU451646.1	343917	987.7	1619.1	2363.4	1163.0	1035.0	1690.0
EU776893.1	350052	1769.7	2419.5	1379.0	1437.7	2691.4	2391.0
EU766933.1	352649	88.3	100.3	204.2	98.2	169.4	150.7
DQ824440.1	197356	2600.3	3860.4	2505.7	2075.5	2097.6	2174.7
GQ503859.1	564639	6612.3	10049.7	5636.3	5836.6	14936.4	11891.7
AB234493.1	146488	347.2	204.5	1080.7	433.9	75.7	153.2
EU768108.1	329703	3749.7	4755.6	2620.3	2268.2	5121.2	5143.7
AB234484.1	147741	221.2	308.9	144.0	106.7	292.7	157.3
EU504190.1	258283	1280.3	1863.0	2400.5	2052.2	1696.4	1320.4
DQ798696.1	198678	2979.1	1540.9	576.6	2853.7	1167.6	1443.5
AY349389.1	92430	1684.5	851.0	146.4	1695.7	304.7	379.8
FJ978593.1	384675	61.0	47.1	167.0	104.5	58.4	41.1
FJ676837.1	525104	469.3	427.5	1774.0	1070.3	420.6	667.6
DQ802531.1	187163	3586.6	5313.5	5684.7	5150.7	4720.2	6983.7
DQ905267.1	171220	1719.9	2247.3	841.6	820.2	399.6	562.3
AB088949.1	77909	3014.7	4236.8	1913.5	2256.1	3977.8	3567.4
AY974898.1	116267	3234.1	2891.8	1471.3	6671.5	2054.4	2610.6
DQ802285.1	181634	689.1	729.6	1480.3	593.8	919.9	884.5
AY975299.1	124921	2648.7	1562.1	1844.4	4312.9	1057.4	2771.4
DQ803552.1	199212	86.0	152.6	241.1	173.6	572.6	224.3
NR_029269.1	584986	5117.2	5999.0	2998.8	4865.8	8230.1	9969.2
GQ448418.1	557186	6242.5	7082.0	4794.8	6105.3	9451.7	8097.4
FJ362869.1	363216	10797.3	9545.8	10799.0	15314.0	5240.8	8851.0
EU748174.1	321561	7377.7	7806.4	8859.7	7099.4	7057.4	8635.4
EF399587.1	205933	65.0	86.1	109.2	70.4	90.2	94.7
AY992923.1	130491	2269.2	1974.1	1068.7	578.5	213.7	310.8
GU304319.1	563613	4635.7	5742.1	5526.7	5356.1	7293.3	6382.4
DQ799077.1	180319	52.0	69.2	177.8	63.4	223.7	152.1
DQ327495.1	150500	1749.2	1734.6	1676.1	952.7	1694.1	1397.9
EF402203.1	204121	149.5	170.2	541.2	171.9	276.8	223.4
DQ804300.1	197231	41.9	57.2	448.2	163.5	864.1	629.3
EU763532.1	327125	274.9	709.2	390.0	99.9	294.5	512.5
EU472163.1	295754	2262.5	3312.0	4356.2	2393.0	4205.6	4127.8
EF434346.1	210179	1890.6	1327.4	1113.9	1144.7	258.8	222.8
DQ799640.1	175400	3880.5	4158.0	1219.9	5431.5	6147.8	7155.9
EU761814.1	347117	323.6	447.7	490.2	112.2	263.1	199.1
EU250957.1	370405	76.5	127.3	201.8	97.5	184.7	53.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	27420
s__unclassified	27424
s__unclassified	27426
s__unclassified	27443
s__unclassified	27446
s__unclassified	27449
s__unclassified	27468
s__unclassified	27473
s__unclassified	27474
s__unclassified	27491
s__unclassified	27497
s__unclassified	27499
s__unclassified	27509
s__unclassified	27510
s__unclassified	27532
s__unclassified	27537
s__unclassified	27538
s__unclassified	27539
s__unclassified	27554
s__unclassified	27570
s__unclassified	27574
s__unclassified	27577
s__unclassified	27579
s__unclassified	27587
s__unclassified	27590
s__unclassified	27593
s__unclassified	27599
s__unclassified	27619
s__unclassified	27622
s__unclassified	27624
s__unclassified	27636
s__unclassified	27637
s__unclassified	27664
s__unclassified	27671
s__unclassified	27673
s__unclassified	27680
s__unclassified	27696
s__unclassified	27698
s__unclassified	27703
s__unclassified	27707
s__unclassified	27708

EU850610.1 gg_id:335773 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF446
AB185777.1 gg_id:105659 rumen clone U29-D06
FJ368953.1 gg_id:358649 feces adult twins and mothers; TS4 clone TS4_a02e05
FJ364499.1 gg_id:365900 feces adult twins and mothers; TS15 clone TS15_a03f08
AB288892.1 gg_id:201079 termite gut homogenate clone BOf2-23
DQ799135.1 gg_id:185370 human fecal clone RL205_aaj18a11
EU763056.1 gg_id:313769 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ803148.1 gg_id:182190 human fecal clone RL311_aam21b06
AM275397.2 gg_id:231161 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
AF371679.1 gg_id:32467 swine intestine clone p-4247-4Wa3
AB234448.1 gg_id:148473 termite gut homogenate clone MgMjR-070
AB192216.1 gg_id:143980 termite gut homogenate clone RsTu1-66
GQ449057.1 gg_id:547906 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g
EF603661.1 gg_id:229062 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ502561.1 gg_id:563998 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
EU763577.1 gg_id:308853 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EF097077.1 gg_id:175307 mouse cecum clone SWPT18_aaa01a12
AM420271.1 gg_id:251150 Noma subgingival plaque clone 702B06(oral)
AY986119.1 gg_id:118835 human stool clone D461
EU510399.1 gg_id:268620 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37h12
AB198664.1 gg_id:135632 termite gut fluid and protists fraction clone RsC01-098
EU472066.1 gg_id:289449 francois langur feces clone FL_1aaa03g05
AY684405.2 gg_id:110059 mucosal biopsies human intestine clone HuDI72
DQ807168.1 gg_id:176088 human fecal clone RL244_aaj47b01
AY916283.1 gg_id:113415 human sigmoid colon biopsy clone G075
AY984500.1 gg_id:121072 human stool clone B424
DQ797242.1 gg_id:174520 human fecal clone RL386_aao88g10
FJ366310.1 gg_id:361864 feces adult twins and mothers; TS26 clone TS26_a01b09
DQ825193.1 gg_id:188567 human fecal clone RL185_aan86e06
GQ175485.1 gg_id:591118 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
NR_026151.1 gg_id:539658 Clostridium colinum str. DSM 6011
EU850560.1 gg_id:347796 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF369
EU768799.1 gg_id:318400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
EU283547.1 gg_id:277790 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A889
EU842731.1 gg_id:318679 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EF603946.1 gg_id:233761 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AB192057.1 gg_id:142092 termite gut homogenate clone M1NP2-32
AJ811979.1 gg_id:196159 human biopsies Human ulcerative colitis biopsy clone UC9-31
DQ647100.1 gg_id:256583 Microbial structure -temperature oil-field produced water Troll formations North Se
EU764416.1 gg_id:329193 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
DQ456412.1 gg_id:157611 pre-adolescent turkey cecum clone CFT214G6

EU850610.1	335773	8136.0	7014.8	868.0	3404.4	4247.5	4557.2
AB185777.1	105659	241.6	102.4	299.1	118.9	93.5	244.9
FJ368953.1	358649	6520.0	5942.4	2590.3	8237.9	3709.4	5808.7
FJ364499.1	365900	2754.0	2781.8	639.9	449.0	3512.8	2602.5
AB288892.1	201079	69.2	78.9	134.2	61.6	53.0	23.5
DQ799135.1	185370	7940.4	8776.5	8168.0	8439.3	8320.9	9432.4
EU763056.1	313769	92.9	302.1	722.3	138.8	716.3	1131.3
DQ803148.1	182190	784.7	343.1	754.5	405.5	1604.6	488.8
AM275397.2	231161	146.7	154.3	156.7	163.4	408.4	227.3
AF371679.1	32467	47.8	81.8	69.3	88.7	45.3	25.5
AB234448.1	148473	528.8	529.6	2343.0	1238.6	3830.5	5345.5
AB192216.1	143980	36.9	59.2	90.2	69.5	88.6	44.7
GQ449057.1	547906	1555.6	2081.7	3486.6	2710.9	1693.5	3225.6
EF603661.1	229062	11327.1	10525.1	6012.5	6180.2	6335.4	6131.4
GQ502561.1	563998	126.0	235.0	663.5	120.3	827.6	422.9
EU763577.1	308853	16.5	25.1	35.0	27.6	54.3	34.9
EF097077.1	175307	3360.5	3990.5	2091.4	4167.6	2777.7	1766.1
AM420271.1	251150	1276.0	1503.5	1136.3	2864.8	827.5	670.0
AY986119.1	118835	1944.6	1778.1	1239.2	3312.4	256.3	539.3
EU510399.1	268620	281.3	261.9	725.5	295.4	125.1	170.2
AB198664.1	135632	33.2	96.4	199.0	77.9	79.1	39.1
EU472066.1	289449	2965.1	4315.3	6245.0	3082.0	8824.7	5896.8
AY684405.2	110059	936.9	1113.4	787.5	392.3	258.3	753.7
DQ807168.1	176088	5439.1	5170.8	1987.3	12134.6	5821.7	5757.3
AY916283.1	113415	66.2	98.3	152.3	86.8	58.4	20.0
AY984500.1	121072	6934.5	6815.1	1476.6	6717.2	688.5	1098.1
DQ797242.1	174520	932.8	483.3	790.9	917.4	403.1	1223.8
FJ366310.1	361864	6846.7	6335.8	5130.3	5735.0	7680.1	8220.4
DQ825193.1	188567	4301.3	5993.4	2597.3	4452.0	8900.3	7550.3
GQ175485.1	591118	1813.0	1732.4	3501.9	1369.9	2188.3	2882.2
NR_026151.1	539658	234.9	212.5	1347.1	203.0	496.6	395.5
EU850560.1	347796	1871.3	2853.9	2549.4	1172.8	2542.0	2277.4
EU768799.1	318400	182.4	299.5	821.1	815.6	1495.5	880.0
EU283547.1	277790	1396.5	1767.6	2263.8	1010.3	1722.1	1822.9
EU842731.1	318679	76.6	100.2	58.9	66.3	102.0	71.3
EF603946.1	233761	2069.5	2482.1	554.1	1128.6	1713.8	1160.9
AB192057.1	142092	5697.9	9787.3	6245.4	7180.4	12531.7	9176.8
AJ811979.1	196159	227.6	485.0	926.7	339.4	974.9	566.4
DQ647100.1	256583	680.9	257.8	392.7	509.1	209.7	28.6
EU764416.1	329193	87.7	123.6	193.2	145.3	619.8	266.6
DQ456412.1	157611	38.6	66.4	58.7	63.5	77.0	41.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	27721
s__unclassified	27725
s__unclassified	27733
s__unclassified	27734
s__unclassified	27735
s__unclassified	27738
s__unclassified	27747
s__unclassified	27748
s__unclassified	27751
s__unclassified	27754
s__unclassified	27762
s__unclassified	27767
s__unclassified	27779
s__unclassified	27782
s__unclassified	27787
s__unclassified	27788
s__unclassified	27790
s__unclassified	27800
s__unclassified	27812
s__unclassified	27818
s__unclassified	27819
s__unclassified	27821
s__unclassified	27826
s__unclassified	27833
s__unclassified	27842
s__unclassified	27843
s__unclassified	27847
s__unclassified	27854
s__unclassified	27859
s__unclassified	27861
s__unclassified	27864
s__unclassified	27885
s__unclassified	27886
s__unclassified	27899
s__unclassified	27900
s__unclassified	27903
s__unclassified	27906
s__unclassified	27918
s__unclassified	27920
s__unclassified	27923
s__unclassified	27925

AY160776.1 gg_id:95195 termite intestinal tract clone COB P4-9
AB062841.1 gg_id:26279 termite gut homogenate clone BCf8-25
AY985062.1 gg_id:126206 human stool clone BA71
DQ802414.1 gg_id:180986 human fecal clone RL188_aah17d07
DQ799668.1 gg_id:190728 human fecal clone RL305aal88h06
FJ676210.1 gg_id:518083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF603789.1 gg_id:232266 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
AY979358.1 gg_id:127662 human transverse colon mucosal biopsy clone Z695
AM943572.1 gg_id:264963 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype
AB192012.1 gg_id:143098 termite gut homogenate clone M2PB4-40
FJ684344.1 gg_id:520882 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ879150.1 gg_id:430468 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EF403013.1 gg_id:217103 human fecal clone SJTU_B_15_58
AB192210.1 gg_id:141614 termite gut homogenate clone RsTu1-57
DQ797516.1 gg_id:176077 human fecal clone RL248_aaj00d07
FJ678223.1 gg_id:520821 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766302.1 gg_id:310536 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B
AY571391.1 gg_id:114703 termite gut clone RsaHw471
EU511960.1 gg_id:262308 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12a02
EU505619.1 gg_id:262012 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa03e07
DQ905770.2 gg_id:164968 Effect bowel preparation and colonoscopy on post-procedure intestinal microbiota
EU344188.1 gg_id:275416 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
AB062772.1 gg_id:37128 termite gut homogenate clone BCf1-11
AB234445.1 gg_id:145498 termite gut homogenate clone MgMjD-060
DQ802465.1 gg_id:178262 human fecal clone RL188_aah18b04
AY981965.1 gg_id:127759 human sigmoid colon mucosal biopsy clone P096
FJ365463.1 gg_id:362977 feces adult twins and mothers; TS20 clone TS20_a03b11
EU765802.1 gg_id:317793 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B
EU475248.1 gg_id:298150 bonobo feces clone BNO_aaa03f12
FJ366941.1 gg_id:360303 feces adult twins and mothers; TS28 clone TS28_a01f02
EU488294.1 gg_id:540852 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
DQ206415.1 gg_id:140502 microbial mediates arsenate reduction soda lake water clone ML-AsS-9
EF096990.1 gg_id:187515 mouse cecum clone SWPT13_aaa03g10
EU768713.1 gg_id:339985 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
EU344547.1 gg_id:263432 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
DQ904757.1 gg_id:162278 human fecal clone 001B-c11
GQ493719.1 gg_id:578445 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AJ576348.1 gg_id:102471 hindgut homogenate Pachnoda ephippiata larva clone PeH31
EU775142.1 gg_id:348992 Francois Langur feces clone FL_1aaa04a08
AB192223.1 gg_id:142182 termite gut homogenate clone RsTu1-83
FJ679144.1 gg_id:524841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

AY160776.1	95195	6863.3	9008.0	8024.0	6960.2	12316.8	9567.2
AB062841.1	26279	69.6	105.0	142.0	55.6	101.5	48.3
AY985062.1	126206	264.6	531.1	483.7	395.7	366.0	624.2
DQ802414.1	180986	6574.1	6486.2	6811.3	6956.1	5169.2	6316.0
DQ799668.1	190728	93.2	230.5	406.2	133.9	367.0	477.1
FJ676210.1	518083	390.2	613.7	1964.5	390.7	1604.2	1063.9
EF603789.1	232266	6016.2	5166.1	1233.2	4533.4	3118.4	4425.4
AY979358.1	127662	2178.5	1850.5	2279.3	4408.7	2140.7	3683.5
AM943572.1	264963	5255.1	6920.3	2884.5	4436.2	7434.7	5675.9
AB192012.1	143098	48.7	62.8	164.9	62.9	77.3	43.6
FJ684344.1	520882	577.9	504.0	784.7	599.2	245.6	292.1
FJ879150.1	430468	311.7	825.0	760.4	147.6	344.4	55.7
EF403013.1	217103	2659.2	4785.9	2411.9	774.7	6339.5	2756.8
AB192210.1	141614	2022.9	2215.8	1957.3	1717.5	1256.7	962.8
DQ797516.1	176077	29.6	32.3	36.0	48.8	45.8	17.1
FJ678223.1	520821	98.2	150.2	342.5	170.4	254.5	332.7
EU766302.1	310536	5239.3	5401.5	1556.9	3863.8	3912.6	5485.7
AY571391.1	114703	83.1	66.1	59.8	99.0	140.0	259.3
EU511960.1	262308	81.0	149.3	315.6	247.4	132.6	167.7
EU505619.1	262012	894.1	1001.4	645.7	384.4	608.5	509.2
DQ905770.2	164968	1869.1	1994.4	4664.0	3326.6	3132.7	3635.6
EU344188.1	275416	9628.6	9614.0	9202.9	8047.1	8324.3	8147.4
AB062772.1	37128	7003.6	10757.0	5315.0	5596.8	6136.2	4810.1
AB234445.1	145498	31.0	41.7	27.8	53.5	55.3	24.7
DQ802465.1	178262	165.0	381.8	176.5	220.2	1909.1	627.0
AY981965.1	127759	6022.8	8067.5	4154.2	4729.4	14031.0	9272.4
FJ365463.1	362977	903.1	630.5	1154.0	1828.3	355.4	349.1
EU765802.1	317793	1846.5	1741.2	3137.1	5644.0	1880.8	2836.8
EU475248.1	298150	210.5	276.1	901.7	165.4	284.1	252.9
FJ366941.1	360303	47.4	50.1	46.5	46.1	81.8	57.2
EU488294.1	540852	1891.0	1460.0	850.3	1514.6	1106.5	934.5
DQ206415.1	140502	329.2	282.4	608.8	838.6	148.1	138.3
EF096990.1	187515	7491.1	8964.5	4721.8	7206.4	4258.9	4191.5
EU768713.1	339985	289.1	501.2	1524.7	249.5	1034.3	567.2
EU344547.1	263432	3296.9	3122.4	4016.0	6159.4	8779.2	7847.4
DQ904757.1	162278	96.6	117.6	196.0	375.9	74.9	100.0
GQ493719.1	578445	58.0	154.4	787.3	176.9	66.4	29.4
AJ576348.1	102471	87.5	146.4	384.3	182.2	184.7	80.3
EU775142.1	348992	893.1	1150.7	3111.4	876.9	1664.8	1937.1
AB192223.1	142182	2553.7	2994.5	2899.8	2913.4	6801.0	4540.2
FJ679144.1	524841	5566.8	5096.0	4187.2	3475.4	6838.9	6184.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium

s__unclassified	27929
s__unclassified	27943
s__unclassified	27949
s__unclassified	27962
s__unclassified	27963
s__unclassified	27964
s__unclassified	27965
s__unclassified	27967
s__unclassified	27970
s__unclassified	27972
s__unclassified	27973
s__unclassified	27976
s__unclassified	27984
s__unclassified	27987
s__unclassified	27991
s__unclassified	27994
s__unclassified	28004
s__unclassified	28007
s__unclassified	28011
s__unclassified	28025
s__unclassified	28032
s__unclassified	28036
s__unclassified	28038
s__unclassified	28042
s__unclassified	28048
s__unclassified	28052
s__unclassified	28061
s__unclassified	28063
s__unclassified	28067
s__unclassified	28071
s__unclassified	28075
s__unclassified	28092
s__unclassified	28095
s__unclassified	28099
s__unclassified	28102
s__unclassified	28136
s__unclassified	28137
s__unclassified	28138
s__unclassified	28142
s__unclassified	28143
s__unclassified	28162

AY985458.1 gg_id:125070 human stool clone C413
GQ502538.1 gg_id:552353 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
GQ249495.1 gg_id:587669 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor
DQ905185.1 gg_id:168289 human fecal clone 002C-h6
FJ681873.1 gg_id:509718 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802242.1 gg_id:184702 human fecal clone RL188_aah15a02
DQ804469.1 gg_id:195799 human fecal clone RL187_aan80d02
AB198449.1 gg_id:135337 termite gut wall fraction clone RsW01-009
EU843061.1 gg_id:345031 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ802280.1 gg_id:195605 human fecal clone RL188_aah15e10
EU508139.1 gg_id:269912 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01c09
EF402988.1 gg_id:206523 human fecal clone SJTU_B_15_24
DQ824134.1 gg_id:177731 human fecal clone RL204_aaj59g08
AY984216.1 gg_id:119151 human stool clone B105
AY974917.1 gg_id:121020 human ascending colon mucosal biopsy clone KI37
EU765496.1 gg_id:354397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
AY571393.1 gg_id:114620 termite gut clone RsaHf312
EU777270.1 gg_id:351986 Okapi feces clone OK3_b06_1
EU762778.1 gg_id:320202 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
DQ327161.1 gg_id:148112 Metagenomic gut microbiome healthy human stool clone E682
DQ804246.1 gg_id:181537 human fecal clone RL187_aah70g10
AY667250.1 gg_id:105725 TCE-dechlorinating groundwater clone TANB5
EU344412.1 gg_id:275216 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
DQ799449.1 gg_id:192133 human fecal clone RL305aal86d08
FJ833638.1 gg_id:549831 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_36D05
EF123527.1 gg_id:242805 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
AY985856.1 gg_id:126931 human stool clone D130
EF559166.1 gg_id:218171 mesophilic anaerobic digester clone G35_D8_H_B_B09
AB198443.1 gg_id:135362 termite gut wall fraction clone RsW01-001
EU765511.1 gg_id:304969 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
FJ372276.1 gg_id:366470 feces adult twins and mothers; TS9 clone TS9_a03g02
DQ905850.2 gg_id:168659 human fecal clone 29E-f6
EF400772.1 gg_id:213176 human fecal clone SJTU_D_01_33
EF097198.1 gg_id:177969 mouse cecum clone SWPT18_aaa02h12
EU850609.1 gg_id:324705 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF444
EU765712.1 gg_id:354597 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
FJ365526.1 gg_id:358859 feces adult twins and mothers; TS20 clone TS20_a03h07
EU762397.1 gg_id:345086 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
DQ904836.1 gg_id:167327 human fecal clone 001C-b10
DQ815362.1 gg_id:171881 mouse cecum clone aab46f02
EU762524.1 gg_id:344336 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›

AY985458.1	125070	372.9	631.0	1018.8	214.8	4848.9	2526.1
GQ502538.1	552353	2912.2	3789.5	2980.0	3646.2	1427.7	1080.0
GQ249495.1	587669	3854.9	4449.8	4674.3	3726.3	4647.9	3633.3
DQ905185.1	168289	5828.6	5047.2	4582.1	9654.8	6754.4	5025.3
FJ681873.1	509718	4072.0	5438.1	6792.6	4040.0	12416.2	9973.2
DQ802242.1	184702	2516.3	1004.3	2177.9	3749.5	4266.6	2948.5
DQ804469.1	195799	126.7	140.5	103.1	304.7	78.4	73.2
AB198449.1	135337	73.8	145.3	137.9	85.9	568.2	338.8
EU843061.1	345031	1577.4	2076.8	3249.5	1592.2	1796.6	2291.0
DQ802280.1	195605	623.2	4142.1	1486.3	2424.6	2879.9	4607.1
EU508139.1	269912	2166.1	2677.9	3290.4	2338.1	2148.8	1864.7
EF402988.1	206523	33.1	37.8	132.7	42.4	55.4	31.6
DQ824134.1	177731	33.9	65.2	39.8	53.2	87.1	41.6
AY984216.1	119151	5060.9	4652.9	2735.4	7717.7	1035.1	1396.2
AY974917.1	121020	5245.6	4733.0	2188.1	7988.6	1763.8	2877.7
EU765496.1	354397	1011.7	1191.7	756.5	1745.0	3098.5	1456.6
AY571393.1	114620	300.8	788.3	588.5	292.4	498.8	847.2
EU777270.1	351986	463.0	483.9	1311.2	380.1	617.3	804.1
EU762778.1	320202	32.5	59.4	236.0	66.0	320.9	203.6
DQ327161.1	148112	424.8	590.8	1331.7	93.8	1736.2	1428.3
DQ804246.1	181537	1533.2	2075.4	1294.0	1732.0	2728.2	2205.1
AY667250.1	105725	2952.6	3010.7	3105.4	947.8	483.1	1140.4
EU344412.1	275216	3415.3	4369.3	4821.3	2322.7	3387.8	3489.5
DQ799449.1	192133	41.6	29.5	125.5	48.5	62.7	35.0
FJ833638.1	549831	1723.2	3481.1	4908.9	2005.9	4966.6	3465.2
EF123527.1	242805	3091.1	4210.6	3935.3	3936.3	4005.1	5384.1
AY985856.1	126931	2328.3	4423.8	3007.3	1894.5	614.3	1142.7
EF559166.1	218171	748.6	438.7	1954.4	642.6	890.9	459.0
AB198443.1	135362	8047.1	11742.2	7999.6	7326.7	14285.2	9505.4
EU765511.1	304969	839.3	739.8	1068.1	596.2	674.6	1347.0
FJ372276.1	366470	3413.8	4026.6	2253.6	5341.0	9753.0	8696.9
DQ905850.2	168659	5252.7	6417.7	6156.3	6033.1	7636.0	5673.5
EF400772.1	213176	26.1	122.1	105.0	56.5	78.8	22.2
EF097198.1	177969	6413.1	5261.1	1284.2	9100.6	4316.3	5161.7
EU850609.1	324705	1481.2	2539.2	1882.5	455.2	724.9	1205.0
EU765712.1	354597	1296.9	825.3	1240.1	2347.9	129.4	740.2
FJ365526.1	358859	1067.5	1016.6	163.4	1069.3	1544.1	1411.3
EU762397.1	345086	7982.6	9130.5	5247.9	6536.0	9034.3	8264.6
DQ904836.1	167327	3451.8	3132.5	1482.0	4445.4	5668.0	5362.7
DQ815362.1	171881	16.3	13.6	63.9	49.1	66.5	14.6
EU762524.1	344336	42.5	64.9	167.3	131.5	45.7	167.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Clostridium
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	28165
s__unclassified	28169
s__unclassified	28170
s__unclassified	28177
s__unclassified	28187
s__unclassified	28190
s__unclassified	72104
s__unclassified	72122
s__unclassified	72351
s__unclassified	72427
s__unclassified	72833
s__unclassified	72958
s__Clostridium phytofermentans	21775
s__Clostridium sp. SS2/1	19426
s__Clostridium sp. SS2/1	19435
s__Clostridium sp. SS2/1	19448
s__Clostridium sp. SS2/1	19450
s__Clostridium sp. SS2/1	19460
s__Clostridium sp. SS2/1	19463
s__Clostridium sp. SS2/1	19469
s__Clostridium sp. SS2/1	19479
s__Clostridium sp. SS2/1	19488
s__Clostridium sp. SS2/1	19526
s__Clostridium sp. SS2/1	19553
s__Clostridium sp. SS2/1	19557
s__Clostridium sp. SS2/1	19595
s__Clostridium sp. SS2/1	19612
s__Clostridium sp. SS2/1	19615
s__Clostridium sp. SS2/1	19625
s__Clostridium sp. SS2/1	19646
s__Clostridium sp. SS2/1	19698
s__Clostridium sp. SS2/1	19699
s__Clostridium sp. SS2/1	19730
s__Clostridium sp. SS2/1	19732
s__Clostridium sp. SS2/1	19756
s__Clostridium sp. SS2/1	19801
s__Clostridium sp. SS2/1	19838
s__Clostridium sp. SS2/1	19900
s__Clostridium sp. SS2/1	19936
s__Clostridium sp. SS2/1	19951
s__Clostridium sp. SS2/1	19965

EU766596.1 gg_id:308206 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
AY984211.1 gg_id:124785 human stool clone B096
GQ503877.1 gg_id:587633 Captain bheri clone Ecwsrb040
EU772692.1 gg_id:303460 Bush dog feces clone bdog1_g03_1
GQ896694.1 gg_id:572516 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s
FJ363376.1 gg_id:367825 feces adult twins and mothers; TS149 clone TS149_a02e04
AB192032.1 gg_id:141363 termite gut homogenate clone M2PB4-29
AB031328.1 gg_id:51807 Clostridium sp. str. NT-2
AB031327.1 gg_id:42607 Clostridium sp. str. NT-1
AB192044.1 gg_id:142702 termite gut homogenate clone M2PT2-80
AB192040.1 gg_id:144949 termite gut homogenate clone M1NP1-74
AB192050.1 gg_id:141770 termite gut homogenate clone M1PT4-74
NC_010001.1 gg_id:235413 Clostridium phytofermentans str. ISDg
AY984142.1 gg_id:117209 human stool clone B024
DQ799529.1 gg_id:197814 human fecal clone RL305aal87d02
AY974814.1 gg_id:115535 human ascending colon mucosal biopsy clone KG10
EU767854.1 gg_id:355893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
DQ801417.1 gg_id:180622 human fecal clone RL388_aao95c05
DQ325736.1 gg_id:149889 Metagenomic gut microbiome healthy human stool clone B384
DQ799434.1 gg_id:198495 human fecal clone RL305aal86c03
AY982887.1 gg_id:123174 human descending colon mucosal biopsy clone L059
DQ802029.1 gg_id:187229 human fecal clone RL241_aaj02a12
EU767909.1 gg_id:332048 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
GQ897100.1 gg_id:576132 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AY974968.1 gg_id:116469 human ascending colon mucosal biopsy clone KJ23
AY979886.1 gg_id:118682 human rectum mucosal biopsy clone E169
EU466940.1 gg_id:302490 African elephant feces clone AFEL2_aao31f06
GQ896926.1 gg_id:544108 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s
FJ365323.1 gg_id:369831 feces adult twins and mothers; TS20 clone TS20_a01e07
DQ799405.1 gg_id:194052 human fecal clone RL305aal85h02
FJ367911.1 gg_id:362741 feces adult twins and mothers; TS30 clone TS30_a01a05
EU766707.1 gg_id:342338 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
AY985965.1 gg_id:126527 human stool clone D264
FJ366554.1 gg_id:357369 feces adult twins and mothers; TS27 clone TS27_a01b03
FJ371073.1 gg_id:368129 feces adult twins and mothers; TS5 clone TS5_a04f02
DQ801052.1 gg_id:183701 human fecal clone RL387_aao91d12
FJ369451.1 gg_id:363138 feces adult twins and mothers; TS50 clone TS50_a04f10
AY981557.1 gg_id:116122 human sigmoid colon mucosal biopsy clone L712
EU764116.1 gg_id:346508 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
FJ364563.1 gg_id:357007 feces adult twins and mothers; TS15 clone TS15_a04d09
EU768317.1 gg_id:323354 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5

EU766596.1	308206	1582.8	1270.8	760.6	1180.6	1138.2	442.7
AY984211.1	124785	7045.2	5623.3	3895.9	4477.1	3986.4	4236.7
GQ503877.1	587633	6458.4	7527.1	6006.0	7835.3	9421.7	7303.2
EU772692.1	303460	249.0	221.1	521.7	401.6	129.6	98.2
GQ896694.1	572516	691.5	1661.7	961.9	631.7	2074.1	1069.4
FJ363376.1	367825	163.7	456.3	177.7	114.0	108.3	298.5
AB192032.1	141363	36.5	75.0	38.1	44.8	93.6	36.5
AB031328.1	51807	23.3	31.6	34.1	63.2	50.2	13.8
AB031327.1	42607	37.6	155.9	120.5	77.1	118.2	90.6
AB192044.1	142702	5504.3	6964.6	7550.0	6421.3	10059.8	7523.3
AB192040.1	144949	187.5	225.5	476.7	139.4	207.4	222.1
AB192050.1	141770	46.0	107.2	404.4	81.7	71.8	79.6
NC_010001.1	235413	243.3	201.4	403.2	318.3	139.6	138.3
AY984142.1	117209	2254.3	1866.4	2683.7	487.8	3354.4	3219.8
DQ799529.1	197814	436.4	407.8	619.0	365.2	162.3	272.0
AY974814.1	115535	4667.7	3809.5	5046.5	4228.1	3870.0	4234.2
EU767854.1	355893	150.4	154.7	330.8	68.0	86.0	89.9
DQ801417.1	180622	545.9	582.4	380.2	315.5	467.2	386.0
DQ325736.1	149889	111.7	39.9	46.6	79.4	83.6	29.5
DQ799434.1	198495	601.6	1215.9	1459.6	1722.8	1363.1	678.6
AY982887.1	123174	1098.2	723.4	1424.9	1781.9	1010.7	1052.0
DQ802029.1	187229	2315.9	1770.2	1373.8	3013.2	1768.2	1582.1
EU767909.1	332048	92.1	201.5	108.6	70.8	137.6	43.9
GQ897100.1	576132	7210.2	10470.0	6110.9	6839.0	11966.9	8353.6
AY974968.1	116469	1288.4	713.7	1119.8	364.4	794.5	326.8
AY979886.1	118682	17071.9	16565.1	13906.4	13964.8	13145.8	13899.2
EU466940.1	302490	511.9	630.0	1180.7	200.9	662.7	752.6
GQ896926.1	544108	1793.5	2797.5	2714.1	2369.1	2425.8	2944.5
FJ365323.1	369831	185.2	159.8	45.5	72.9	106.5	29.9
DQ799405.1	194052	1098.9	474.2	508.6	206.2	458.4	192.2
FJ367911.1	362741	13604.7	14189.0	8214.0	9801.0	10255.0	11151.5
EU766707.1	342338	2239.6	2085.6	2511.1	839.8	2414.3	1699.4
AY985965.1	126527	598.9	750.2	1473.4	418.8	1011.0	927.8
FJ366554.1	357369	811.3	505.9	1128.3	319.2	872.8	684.0
FJ371073.1	368129	3414.8	3859.0	4231.6	3987.2	3773.7	4766.1
DQ801052.1	183701	271.5	275.6	242.6	114.7	132.5	58.2
FJ369451.1	363138	271.6	389.4	985.1	154.2	108.7	252.6
AY981557.1	116122	2237.8	1705.4	1456.9	1611.2	1808.3	2264.0
EU764116.1	346508	1265.1	1123.1	1728.1	300.5	1792.1	1339.4
FJ364563.1	357007	1405.5	2418.9	1633.5	2134.4	3619.6	2871.9
EU768317.1	323354	5849.9	7915.4	4993.8	5269.6	11679.5	9347.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__Clostridium sp. SS2/1	20003
s__Clostridium sp. SS2/1	20011
s__Clostridium sp. SS2/1	20022
s__Clostridium sp. SS2/1	20080
s__Clostridium sp. SS2/1	20085
s__Clostridium sp. SS2/1	20086
s__Clostridium sp. SS2/1	20089
s__Clostridium sp. SS2/1	20172
s__Clostridium sp. SS2/1	20201
s__Clostridium sp. SS2/1	20245
s__Clostridium sp. SS2/1	20254
s__Clostridium sp. SS2/1	20324
s__Clostridium sp. SS2/1	20358
s__Clostridium sp. SS2/1	20388
s__Clostridium sp. SS2/1	20406
s__Clostridium sp. SS2/1	20407
s__Clostridium sp. SS2/1	20410
s__Clostridium sp. SS2/1	20430
s__Clostridium sp. SS2/1	20461
s__Clostridium sp. SS2/1	20486
s__Clostridium sp. SS2/1	20515
s__Clostridium sp. SS2/1	20540
s__Clostridium sp. SS2/1	20578
s__Clostridium sp. SS2/1	20599
s__Clostridium sp. SS2/1	20602
s__Clostridium sp. SS2/1	20604
s__Coprococcus catus	23582
s__Coprococcus catus	23948
s__Coprococcus catus	24036
s__Coprococcus catus	24158
s__Coprococcus catus	24169
s__Coprococcus eutactus	24232
s__unclassified	17492
s__unclassified	18257
s__unclassified	18271
s__unclassified	18322
s__unclassified	18324
s__unclassified	18335
s__unclassified	18337
s__unclassified	18345
s__unclassified	18360

AY981319.1 gg_id:116252 human sigmoid colon mucosal biopsy clone G335
EU764418.1 gg_id:343960 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
DQ802338.1 gg_id:187157 human fecal clone RL188_aah16d02
DQ326159.1 gg_id:149198 Metagenomic gut microbiome healthy human stool clone C054
GQ896992.1 gg_id:583202 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ365267.1 gg_id:362811 feces adult twins and mothers; TS1 clone TS1_a04h01
GQ077508.1 gg_id:412854 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1209f0
AY978337.1 gg_id:121737 human transverse colon mucosal biopsy clone F244
EU763747.1 gg_id:341629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
GQ079269.1 gg_id:437713 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230f0
ABGC03000035.1 gg_id:268313 Clostridium sp. str. SS2/1
AY982970.1 gg_id:122388 human descending colon mucosal biopsy clone L179
FJ367689.1 gg_id:358527 feces adult twins and mothers; TS2 clone TS2_a02d07
DQ797631.1 gg_id:183214 human fecal clone RL206_aaj13h11
AY981134.1 gg_id:122205 human sigmoid colon mucosal biopsy clone G056
GQ896955.1 gg_id:573003 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AY979901.1 gg_id:119323 human rectum mucosal biopsy clone E209
GQ897021.1 gg_id:538339 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AY977059.1 gg_id:124905 human cecum mucosal biopsy clone K747
FJ365360.1 gg_id:367646 feces adult twins and mothers; TS20 clone TS20_a02a03
AY981748.1 gg_id:124788 human sigmoid colon mucosal biopsy clone LB84
FJ370820.1 gg_id:368282 feces adult twins and mothers; TS5 clone TS5_a01f06
DQ326449.1 gg_id:148389 Metagenomic gut microbiome healthy human stool clone C521
FJ366327.1 gg_id:367179 feces adult twins and mothers; TS26 clone TS26_a01d10
DQ798712.1 gg_id:176221 human fecal clone RL181_aao00d10
FJ368314.1 gg_id:356764 feces adult twins and mothers; TS3 clone TS3_a02g10
DQ905606.1 gg_id:166598 human fecal clone 014B-G2
DQ803327.1 gg_id:187518 human fecal clone RL311_aam24a11
DQ795759.1 gg_id:179147 human fecal clone RL245_aai81h08
AY983324.1 gg_id:125323 human descending colon mucosal biopsy clone A386
AY977551.1 gg_id:121101 human cecum mucosal biopsy clone W357
EU768039.1 gg_id:331250 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
DQ807186.1 gg_id:188131 human fecal clone RL244_aaj47c10
DQ823980.1 gg_id:181649 human fecal clone RL204_aaj57g01
DQ799470.1 gg_id:198583 human fecal clone RL305aal86f09
AB494744.1 gg_id:589475 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A
DQ796782.1 gg_id:185703 human fecal clone RL179_aao54d08
FJ879449.1 gg_id:382721 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
AY975195.1 gg_id:121393 human ascending colon mucosal biopsy clone KN24
FJ364970.1 gg_id:365093 feces adult twins and mothers; TS1 clone TS1_a01d01
FJ024722.1 gg_id:330731 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp

AY981319.1	116252	7697.6	7278.9	4818.8	5661.9	3978.8	4753.4
EU764418.1	343960	1349.4	1468.8	1953.2	807.5	1777.4	1530.6
DQ802338.1	187157	669.4	449.1	1405.2	364.9	1404.1	892.6
DQ326159.1	149198	158.7	344.0	137.4	91.6	163.2	108.3
GQ896992.1	583202	1863.8	1161.0	1474.7	1954.2	159.9	345.8
FJ365267.1	362811	1935.0	1987.1	2220.0	803.5	2259.1	2091.3
GQ077508.1	412854	5175.4	6613.4	4360.1	1938.7	4766.1	4559.5
AY978337.1	121737	1415.3	1428.7	1180.9	720.5	1325.0	1382.6
EU763747.1	341629	719.7	676.6	1615.8	301.1	906.8	1151.1
GQ079269.1	437713	807.7	428.0	449.6	186.3	448.7	178.1
ABGC03000035.1	268313	2592.8	1629.1	3677.3	2600.0	628.7	830.0
AY982970.1	122388	2600.6	1671.9	2424.1	5544.1	2468.3	3593.4
FJ367689.1	358527	768.1	592.3	1478.2	366.6	1311.4	831.3
DQ797631.1	183214	2925.1	3205.4	6968.9	1467.8	4532.4	4813.3
AY981134.1	122205	14901.8	12870.9	16034.8	12780.2	10268.8	10373.4
GQ896955.1	573003	1888.7	1146.2	1012.3	1896.7	113.7	268.1
AY979901.1	119323	1798.3	1987.6	2223.5	806.4	2265.7	1942.8
GQ897021.1	538339	3558.3	3278.7	936.1	3969.7	5273.4	4583.3
AY977059.1	124905	4056.7	4703.2	6276.7	3193.9	4306.0	4575.7
FJ365360.1	367646	8543.2	10490.8	8006.8	8227.0	13656.4	14961.1
AY981748.1	124788	1328.8	1109.6	2060.8	422.6	1808.0	1378.2
FJ370820.1	368282	1241.5	953.6	505.0	2074.4	101.0	198.4
DQ326449.1	148389	287.8	249.5	565.0	114.3	109.3	103.8
FJ366327.1	367179	578.5	367.8	403.5	517.1	76.4	60.8
DQ798712.1	176221	7805.0	7284.7	5605.0	5419.2	4829.1	5538.0
FJ368314.1	356764	5849.5	5584.8	2197.0	8133.2	8700.6	8288.8
DQ905606.1	166598	3813.0	3802.3	2464.3	2579.9	1794.0	1921.6
DQ803327.1	187518	635.1	1246.4	1543.6	371.5	617.8	2329.8
DQ795759.1	179147	10015.8	9773.2	5286.0	7778.1	10274.3	9217.6
AY983324.1	125323	6730.9	7857.9	3746.0	5967.7	7108.9	4564.2
AY977551.1	121101	234.0	302.4	1317.3	352.6	1035.0	899.3
EU768039.1	331250	64.5	66.6	80.9	93.8	67.5	42.3
DQ807186.1	188131	92.6	171.5	536.9	206.6	473.5	398.6
DQ823980.1	181649	21.1	31.9	22.9	40.5	72.6	17.2
DQ799470.1	198583	183.9	273.2	212.2	181.8	1314.5	1119.8
AB494744.1	589475	496.0	152.9	720.4	121.9	81.7	67.9
DQ796782.1	185703	724.2	1016.9	855.3	1293.5	2409.6	1753.3
FJ879449.1	382721	83.2	168.6	432.3	129.6	378.2	143.4
AY975195.1	121393	901.9	634.6	2153.7	993.7	233.5	414.6
FJ364970.1	365093	5648.4	4651.6	3806.5	4260.4	9012.7	6616.5
FJ024722.1	330731	240.9	450.6	608.6	705.4	536.8	1109.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	18373
s__unclassified	18376
s__unclassified	18381
s__unclassified	18383
s__unclassified	18397
s__unclassified	18409
s__unclassified	18424
s__unclassified	18452
s__unclassified	18467
s__unclassified	18478
s__unclassified	18480
s__unclassified	18491
s__unclassified	18493
s__unclassified	18503
s__unclassified	18545
s__unclassified	18573
s__unclassified	18577
s__unclassified	18633
s__unclassified	18635
s__unclassified	18654
s__unclassified	18656
s__unclassified	18672
s__unclassified	18674
s__unclassified	18683
s__unclassified	18724
s__unclassified	18734
s__unclassified	18741
s__unclassified	18767
s__unclassified	18774
s__unclassified	18797
s__unclassified	18802
s__unclassified	18826
s__unclassified	18848
s__unclassified	18855
s__unclassified	18867
s__unclassified	18885
s__unclassified	18895
s__unclassified	18909
s__unclassified	18916
s__unclassified	19009
s__unclassified	19012

EF098253.1 gg_id:188643 mouse cecum clone SWPT14_aaa03f07
EU504306.1 gg_id:259989 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02b02
EU473641.1 gg_id:299118 banteng feces clone BG_aaa04d05.Contig1
AY756592.1 gg_id:108706 Siwhaho sediment clone LJ3
FJ880192.1 gg_id:434572 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ880748.1 gg_id:378068 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU778880.1 gg_id:353577 Black-handed Spider Monkey feces clone SPIM_aaj36b05
EU507949.1 gg_id:265576 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa04b05
EU507971.1 gg_id:277133 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01a03
EU771949.1 gg_id:319153 Southern three-banded armadillo feces clone arma_aaj53g07
EU508268.1 gg_id:266726 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04h08
DQ105656.1 gg_id:137353 pig feces clone DGGE band K2
FJ879330.1 gg_id:441799 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EF655642.1 gg_id:245596 dye containing wastewater treatment biofilm reactor clone B29
EU508881.1 gg_id:263014 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37f10
DQ815812.1 gg_id:172622 mouse cecum clone aab22f06
EU794200.1 gg_id:355318 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K22
EU456821.1 gg_id:312892 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU504348.1 gg_id:262939 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02g11
EU452929.1 gg_id:309206 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EF632747.1 gg_id:237273 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
GQ493671.1 gg_id:574714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AF349416.1 gg_id:77449 pig feces clone
EU773327.1 gg_id:322137 BigHorn sheep feces clone BH1_aao26e11
FJ679990.1 gg_id:531052 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ793657.1 gg_id:178682 human fecal clone RL246_aai75b10
FJ879661.1 gg_id:418999 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
AB486484.1 gg_id:561193 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EU850551.1 gg_id:326833 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF351
GQ491405.1 gg_id:583711 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
X71853.1 gg_id:14099 Clostridium populeti str. ATCC 35295
AY212660.1 gg_id:99173 water 20 m downstream manure clone 213ds20
EU466237.1 gg_id:291890 bighorn sheep feces clone BH1_aao28e12
EU506241.1 gg_id:272369 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c07
EF602871.1 gg_id:232283 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AY977415.1 gg_id:122556 human cecum mucosal biopsy clone W090
FJ879205.1 gg_id:423041 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU470217.1 gg_id:302864 trancaspain urial feces clone TU2_aaa03h09
DQ071475.1 gg_id:231128 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc10
EU794284.1 gg_id:322231 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_N36
DQ803800.1 gg_id:177788 human fecal clone RL200_aai58e10

EF098253.1	188643	39.4	68.2	57.7	72.1	59.0	24.7
EU504306.1	259989	26.6	43.6	254.1	57.7	82.4	135.8
EU473641.1	299118	1727.2	1806.9	2396.0	1620.8	4122.3	2993.7
AY756592.1	108706	291.7	199.2	763.6	1091.9	102.7	170.3
FJ880192.1	434572	317.1	332.0	836.4	1217.1	971.1	934.2
FJ880748.1	378068	9808.8	9437.1	11268.7	7143.4	9307.8	7832.1
EU778880.1	353577	569.0	710.3	3000.9	337.8	2087.0	1420.5
EU507949.1	265576	93.7	130.4	420.1	255.2	479.4	117.0
EU507971.1	277133	1535.4	3013.4	4174.9	2320.1	6827.4	5019.9
EU771949.1	319153	241.4	301.5	1206.9	366.8	1063.5	913.4
EU508268.1	266726	4104.6	3734.7	5006.6	4957.9	4216.1	5416.1
DQ105656.1	137353	180.3	181.5	66.9	201.8	155.5	284.1
FJ879330.1	441799	225.6	204.8	515.3	139.1	207.1	299.2
EF655642.1	245596	686.0	608.9	1555.7	324.1	98.1	318.2
EU508881.1	263014	10460.2	9680.5	8585.5	10555.0	9833.7	10141.1
DQ815812.1	172622	615.9	518.7	591.8	270.5	412.0	254.6
EU794200.1	355318	975.0	1083.2	4681.1	1532.4	2109.0	1578.0
EU456821.1	312892	531.6	492.8	410.4	955.9	576.2	915.1
EU504348.1	262939	140.2	179.8	1009.8	157.1	310.7	192.5
EU452929.1	309206	5132.4	5403.2	3536.8	5121.3	4766.6	5575.1
EF632747.1	237273	6985.5	6939.8	7488.4	8553.4	7558.3	6100.7
GQ493671.1	574714	370.8	366.4	413.0	273.2	628.6	374.5
AF349416.1	77449	327.8	449.1	361.3	494.5	153.3	268.7
EU773327.1	322137	180.2	123.5	249.2	148.2	193.9	113.3
FJ679990.1	531052	29.9	42.2	83.8	79.0	115.8	116.8
DQ793657.1	178682	2101.2	2586.3	2157.7	2035.3	3122.8	1841.7
FJ879661.1	418999	844.0	577.4	933.5	1341.7	179.8	154.8
AB486484.1	561193	610.6	571.4	2322.9	403.5	169.5	448.7
EU850551.1	326833	188.1	262.4	839.0	146.8	1441.6	1422.5
GQ491405.1	583711	1947.3	1913.4	1191.5	2667.8	2520.0	2433.3
X71853.1	14099	226.2	493.1	1335.4	177.6	61.4	178.4
AY212660.1	99173	34.4	37.8	35.0	60.3	77.7	35.1
EU466237.1	291890	808.9	813.0	2105.6	1222.9	1802.3	1225.7
EU506241.1	272369	1940.4	1297.2	2157.3	3437.2	567.4	1001.0
EF602871.1	232283	2817.4	3741.2	3721.3	4680.9	7352.1	4366.8
AY977415.1	122556	39.3	59.8	127.0	59.0	53.4	34.9
FJ879205.1	423041	6755.2	6182.3	8332.0	6855.7	7432.7	6980.7
EU470217.1	302864	893.3	650.8	249.1	198.1	299.7	286.2
DQ071475.1	231128	70.9	136.0	53.6	103.6	65.4	53.7
EU794284.1	322231	242.9	320.2	1412.5	301.8	1090.9	425.3
DQ803800.1	177788	497.5	393.7	675.6	1008.8	1869.6	945.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19018
s__unclassified	19045
s__unclassified	19046
s__unclassified	19059
s__unclassified	19062
s__unclassified	19082
s__unclassified	19092
s__unclassified	19098
s__unclassified	19133
s__unclassified	19162
s__unclassified	19166
s__unclassified	19170
s__unclassified	19182
s__unclassified	19211
s__unclassified	19227
s__unclassified	19242
s__unclassified	19264
s__unclassified	19287
s__unclassified	19292
s__unclassified	19298
s__unclassified	19302
s__unclassified	19308
s__unclassified	19316
s__unclassified	19349
s__unclassified	19350
s__unclassified	19351
s__unclassified	19375
s__unclassified	19382
s__unclassified	19386
s__unclassified	19387
s__unclassified	19391
s__unclassified	19403
s__unclassified	19407
s__unclassified	19413
s__unclassified	19416
s__unclassified	19419
s__unclassified	19420
s__unclassified	19421
s__unclassified	19429
s__unclassified	19430
s__unclassified	19431

EU504286.1 gg_id:259281 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01g05
EF095995.1 gg_id:182621 mouse cecum clone lean2_aaa01f04
EU779113.1 gg_id:308857 Takin feces clone TAK_aaa03e11
FJ366481.1 gg_id:358834 feces adult twins and mothers; TS26 clone TS26_a03h07
DQ815966.1 gg_id:169701 mouse cecum clone aab24h11
FJ365126.1 gg_id:370305 feces adult twins and mothers; TS1 clone TS1_a03b10
EU508740.1 gg_id:267400 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50c10
FJ679327.1 gg_id:515632 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU452548.1 gg_id:315309 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU509492.1 gg_id:273301 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59c09
EU456838.1 gg_id:324615 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
GQ491245.1 gg_id:538885 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU774776.1 gg_id:311610 Angola Colobus feces clone EAC_1aaa01e03
FJ672488.1 gg_id:531825 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU460964.1 gg_id:301879 red kangaroo feces clone KO1_aai41b07
DQ808993.1 gg_id:175596 human fecal clone RL243_aai87h11
AY534872.1 gg_id:102328 Clostridium sp. str. IMSNU 40011
EU508308.1 gg_id:274455 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02d01
EU461740.1 gg_id:294791 mongoose lemur feces clone ML_aaj28b01
DQ793567.1 gg_id:184905 human fecal clone RL246_aai73f04
FJ678549.1 gg_id:519866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ868402.1 gg_id:580793 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC81
DQ800844.1 gg_id:178970 human fecal clone RL183_aao04c02
FJ542922.1 gg_id:520231 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EF515538.1 gg_id:225599 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
EU509215.1 gg_id:268028 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46a03
EU773313.1 gg_id:323365 BigHorn sheep feces clone BH1_aao25a09
EU466172.1 gg_id:291475 bighorn sheep feces clone BH1_aao27d08
EU453188.1 gg_id:328453 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU473636.1 gg_id:300295 banteng feces clone BG_aaa02h01.Contig1
FJ672606.1 gg_id:527413 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
NR_025796.1 gg_id:552538 Clostridium jejuense str. HY-35-12; IMSNU 40003
GQ493826.1 gg_id:572045 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU509517.1 gg_id:274400 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59h07
FJ371671.1 gg_id:369597 feces adult twins and mothers; TS7 clone TS7_a04h09
FJ362613.1 gg_id:364756 feces adult twins and mothers; TS13 clone TS13_a01b01
EF071231.1 gg_id:195514 library survey and quantitative measurement major mucosa- IBD human colonic muc
EU462354.1 gg_id:288857 chimpanzee feces clone CHIMP1_aaj40g10
FJ363762.1 gg_id:365692 feces adult twins and mothers; TS14 clone TS14_a03a10
DQ327549.1 gg_id:145426 Metagenomic gut microbiome healthy human stool clone EB31
DQ798564.1 gg_id:179518 human fecal clone RL181_aan98d01

EU504286.1	259281	1898.7	1099.4	1981.0	1352.2	1397.7	1099.8
EF095995.1	182621	232.9	275.0	706.2	266.7	658.8	340.1
EU779113.1	308857	123.8	108.1	460.9	117.1	171.5	455.3
FJ366481.1	358834	802.8	1408.3	1185.2	733.1	5066.4	1872.3
DQ815966.1	169701	2022.7	1131.4	737.3	812.2	630.7	946.0
FJ365126.1	370305	388.4	324.0	450.9	449.3	86.6	49.9
EU508740.1	267400	30.8	43.0	92.6	63.6	58.6	187.8
FJ679327.1	515632	7243.0	7552.2	3760.5	6033.2	11585.4	10246.9
EU452548.1	315309	3664.9	4714.2	1405.9	2156.9	3745.0	1671.8
EU509492.1	273301	300.2	550.7	740.4	257.8	430.1	508.3
EU456838.1	324615	1439.9	1658.8	1446.3	943.4	2067.2	996.0
GQ491245.1	538885	86.5	106.0	270.5	117.5	165.2	116.0
EU774776.1	311610	489.9	47.1	449.2	496.3	384.4	715.0
FJ672488.1	531825	1444.2	2267.2	1657.6	1063.7	841.6	940.8
EU460964.1	301879	246.6	334.8	557.3	272.5	152.1	267.8
DQ808993.1	175596	89.5	128.2	855.1	159.1	168.7	154.7
AY534872.1	102328	37.9	35.9	469.6	100.8	59.1	37.8
EU508308.1	274455	9144.5	9304.9	5151.4	8764.4	12350.5	11045.3
EU461740.1	294791	69.3	100.6	409.9	121.3	87.2	138.1
DQ793567.1	184905	1187.6	1403.6	217.6	208.9	103.3	29.1
FJ678549.1	519866	25.1	22.7	46.1	43.6	175.1	62.7
GQ868402.1	580793	2635.5	2139.8	2047.5	4232.5	1144.5	1466.9
DQ800844.1	178970	99.9	110.6	289.6	99.4	110.3	102.3
FJ542922.1	520231	2582.5	1786.1	3857.1	2831.7	3055.5	2088.9
EF515538.1	225599	6615.5	5910.3	5904.6	5964.3	6172.2	6283.0
EU509215.1	268028	3478.4	3580.3	1364.1	5493.3	5136.1	4741.1
EU773313.1	323365	248.6	309.6	2006.5	430.2	812.2	595.7
EU466172.1	291475	2222.9	2185.8	2089.5	1120.4	2271.8	1975.3
EU453188.1	328453	291.3	375.1	358.7	506.5	230.8	303.4
EU473636.1	300295	733.2	677.0	411.4	1393.9	248.6	406.2
FJ672606.1	527413	1332.1	2325.5	754.5	362.9	530.8	399.8
NR_025796.1	552538	153.1	207.5	336.3	175.4	97.6	192.2
GQ493826.1	572045	2923.8	4288.5	1201.3	2624.3	2808.3	3288.5
EU509517.1	274400	7021.2	4630.8	3611.8	5822.3	8576.8	7526.2
FJ371671.1	369597	36.3	33.6	45.2	68.2	78.6	32.1
FJ362613.1	364756	664.2	602.2	910.7	365.3	1146.2	1278.5
EF071231.1	195514	1770.0	1970.5	982.7	1098.8	837.8	646.4
EU462354.1	288857	7090.3	4821.1	6216.6	4714.3	7048.4	5083.4
FJ363762.1	365692	79.4	367.2	150.6	102.7	146.9	126.9
DQ327549.1	145426	31.0	57.0	324.0	74.3	61.0	25.2
DQ798564.1	179518	1012.7	2559.1	135.4	86.7	86.3	156.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19439
s__unclassified	19440
s__unclassified	19442
s__unclassified	19444
s__unclassified	19446
s__unclassified	19447
s__unclassified	19451
s__unclassified	19458
s__unclassified	19459
s__unclassified	19467
s__unclassified	19468
s__unclassified	19471
s__unclassified	19472
s__unclassified	19474
s__unclassified	19476
s__unclassified	19483
s__unclassified	19489
s__unclassified	19491
s__unclassified	19493
s__unclassified	19494
s__unclassified	19497
s__unclassified	19499
s__unclassified	19502
s__unclassified	19503
s__unclassified	19506
s__unclassified	19510
s__unclassified	19511
s__unclassified	19512
s__unclassified	19513
s__unclassified	19520
s__unclassified	19521
s__unclassified	19522
s__unclassified	19523
s__unclassified	19525
s__unclassified	19530
s__unclassified	19535
s__unclassified	19537
s__unclassified	19538
s__unclassified	19543
s__unclassified	19545
s__unclassified	19547

DQ327529.1 gg_id:147480 Metagenomic gut microbiome healthy human stool clone EB11
AM277382.2 gg_id:229853 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
DQ802766.1 gg_id:183853 human fecal clone RL188_aan96c08
FJ367837.1 gg_id:358360 feces adult twins and mothers; TS2 clone TS2_a04b07
DQ325827.1 gg_id:145051 Metagenomic gut microbiome healthy human stool clone B566
FJ679258.1 gg_id:524214 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY976512.1 gg_id:119285 human cecum mucosal biopsy clone K034
GQ896896.1 gg_id:580242 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ801081.1 gg_id:177184 human fecal clone RL387_aao91h04
DQ796707.1 gg_id:183325 human fecal clone RL179_aao53d11
EU762664.1 gg_id:318085 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ801445.1 gg_id:175981 human fecal clone RL388_aao95f05
DQ801596.1 gg_id:193594 human fecal clone RL117_aae92c08
FJ367849.1 gg_id:370336 feces adult twins and mothers; TS2 clone TS2_a04c09
GQ897203.1 gg_id:545113 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AF371638.1 gg_id:29079 swine intestine clone p-1894-s962-3
DQ801802.1 gg_id:189572 human fecal clone RL201_aai47a04
EU762248.1 gg_id:346684 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EF399973.1 gg_id:213155 human fecal clone SJTU_E_07_14
FJ367910.1 gg_id:365889 feces adult twins and mothers; TS30 clone TS30_a01a04
AY976640.1 gg_id:116094 human cecum mucosal biopsy clone K204
DQ327315.1 gg_id:147899 Metagenomic gut microbiome healthy human stool clone E863
AM697161.1 gg_id:227258 sequencing libraries indoor dust clone BF0001C002
AY981729.1 gg_id:120484 human sigmoid colon mucosal biopsy clone LB21
EU467096.1 gg_id:300902 mongoose lemur feces clone ML_aae88b05
DQ807097.1 gg_id:192077 human fecal clone RL244_aaj46b10
FJ370064.1 gg_id:370074 feces adult twins and mothers; TS55 clone TS55_a04a07
FJ368444.1 gg_id:357429 feces adult twins and mothers; TS3 clone TS3_a04d09
DQ325631.1 gg_id:146452 Metagenomic gut microbiome healthy human stool clone B171
DQ796741.1 gg_id:192388 human fecal clone RL179_aao53h04
FJ371070.1 gg_id:364813 feces adult twins and mothers; TS5 clone TS5_a04e11
FJ682996.1 gg_id:519242 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678681.1 gg_id:528608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ806889.1 gg_id:190886 human fecal clone RL198_aaj74g09
DQ798252.1 gg_id:176633 human fecal clone RL181_aah39e11
GQ001531.1 gg_id:508130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu174b1
FJ363666.1 gg_id:357596 feces adult twins and mothers; TS14 clone TS14_a01h07
FJ367676.1 gg_id:368233 feces adult twins and mothers; TS2 clone TS2_a02c06
DQ799669.1 gg_id:197638 human fecal clone RL305aal88h07
AY981488.1 gg_id:127177 human sigmoid colon mucosal biopsy clone L591
FJ368089.1 gg_id:356961 feces adult twins and mothers; TS30 clone TS30_a03h04

DQ327529.1	147480	233.6	345.0	606.5	82.8	437.8	453.3
AM277382.2	229853	301.1	435.5	447.1	238.9	92.7	129.0
DQ802766.1	183853	68.3	52.0	351.7	72.6	86.4	44.3
FJ367837.1	358360	17345.3	15709.7	16909.3	15614.5	13527.5	14762.4
DQ325827.1	145051	3166.2	4626.4	3233.4	2643.0	5428.7	4721.1
FJ679258.1	524214	54.8	157.9	259.7	114.8	550.1	168.5
AY976512.1	119285	762.6	2350.6	821.9	329.3	398.3	1215.7
GQ896896.1	580242	1684.3	1228.1	960.2	1922.8	118.3	249.5
DQ801081.1	177184	491.0	536.3	1678.3	1063.5	1849.1	2377.0
DQ796707.1	183325	121.8	116.1	636.1	108.8	227.4	111.2
EU762664.1	318085	338.9	127.1	638.3	87.1	60.0	38.5
DQ801445.1	175981	10.8	16.0	56.8	45.8	48.7	17.3
DQ801596.1	193594	144.1	1429.4	324.6	2568.4	611.6	578.3
FJ367849.1	370336	1036.9	1087.5	2783.6	526.0	2094.1	3067.6
GQ897203.1	545113	2487.6	1971.7	3848.7	3621.2	4053.1	4028.1
AF371638.1	29079	85.5	53.5	154.0	67.8	61.1	33.3
DQ801802.1	189572	307.8	575.9	906.0	148.5	687.3	630.0
EU762248.1	346684	104.1	280.0	138.1	98.5	207.6	85.1
EF399973.1	213155	3573.1	3338.5	1303.2	2034.5	83.7	377.9
FJ367910.1	365889	4097.9	4927.4	4727.8	4746.2	8389.5	6247.3
AY976640.1	116094	965.4	1290.3	1895.2	1822.8	1292.4	1259.9
DQ327315.1	147899	6566.1	5190.2	3221.4	4812.8	2651.1	5313.5
AM697161.1	227258	6556.4	6024.3	3038.9	6216.5	3936.1	3799.9
AY981729.1	120484	325.3	562.0	1099.7	210.0	754.0	759.2
EU467096.1	300902	326.2	518.5	1038.9	194.7	697.0	662.4
DQ807097.1	192077	10780.9	10632.4	8649.9	9653.8	5924.5	3455.8
FJ370064.1	370074	311.6	334.1	214.5	1373.1	584.3	447.8
FJ368444.1	357429	28.7	50.0	61.6	67.8	84.6	22.7
DQ325631.1	146452	3429.9	4417.0	3625.3	4094.1	5477.7	5601.5
DQ796741.1	192388	487.2	298.1	436.7	195.5	145.8	220.7
FJ371070.1	364813	1590.3	1493.8	330.2	2432.8	943.5	1105.6
FJ682996.1	519242	38.5	30.3	104.5	51.8	53.2	27.4
FJ678681.1	528608	2175.0	3521.6	1519.0	2960.3	4129.2	6705.6
DQ806889.1	190886	4064.9	4959.9	2773.0	4074.9	6007.2	7389.8
DQ798252.1	176633	3717.6	3137.4	2425.9	3303.0	6761.4	4475.3
GQ001531.1	508130	55.0	140.8	111.3	72.2	78.1	39.2
FJ363666.1	357596	138.3	338.7	250.7	109.4	142.5	286.0
FJ367676.1	368233	2748.2	2888.9	4108.2	1648.1	1191.9	2439.1
DQ799669.1	197638	1368.8	1461.5	473.4	1121.7	1919.9	1548.5
AY981488.1	127177	228.1	285.8	331.4	92.1	75.9	65.1
FJ368089.1	356961	4758.5	3825.6	714.7	6178.8	7178.5	6337.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19552
s__unclassified	19555
s__unclassified	19556
s__unclassified	19558
s__unclassified	19560
s__unclassified	19564
s__unclassified	19567
s__unclassified	19568
s__unclassified	19571
s__unclassified	19572
s__unclassified	19575
s__unclassified	19578
s__unclassified	19583
s__unclassified	19587
s__unclassified	19588
s__unclassified	19589
s__unclassified	19590
s__unclassified	19596
s__unclassified	19597
s__unclassified	19598
s__unclassified	19600
s__unclassified	19601
s__unclassified	19602
s__unclassified	19605
s__unclassified	19606
s__unclassified	19608
s__unclassified	19610
s__unclassified	19616
s__unclassified	19621
s__unclassified	19624
s__unclassified	19628
s__unclassified	19630
s__unclassified	19634
s__unclassified	19639
s__unclassified	19641
s__unclassified	19651
s__unclassified	19652
s__unclassified	19653
s__unclassified	19655
s__unclassified	19657
s__unclassified	19672

DQ801897.1 gg_id:189731 human fecal clone RL201_aai48c02
FJ362791.1 gg_id:366121 feces adult twins and mothers; TS13 clone TS13_a03c03
FJ370352.1 gg_id:360418 feces adult twins and mothers; TS56 clone TS56_a03h01
FJ365716.1 gg_id:357752 feces adult twins and mothers; TS21 clone TS21_a02b07
FJ366917.1 gg_id:368931 feces adult twins and mothers; TS28 clone TS28_a01d02
AM275455.2 gg_id:234340 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
DQ798714.1 gg_id:193231 human fecal clone RL181_aao00d12
EU466792.1 gg_id:303125 African elephant feces clone AFEL2_aao29e11
FJ363689.1 gg_id:357535 feces adult twins and mothers; TS14 clone TS14_a02b06
DQ807937.1 gg_id:195481 human fecal clone RL180_aan69d11
DQ326713.1 gg_id:148649 Metagenomic gut microbiome healthy human stool clone E168
DQ797422.1 gg_id:190985 human fecal clone RL248_aai99b08
EU763441.1 gg_id:330946 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
AY979955.1 gg_id:119081 human rectum mucosal biopsy clone K838
AY981292.1 gg_id:120019 human sigmoid colon mucosal biopsy clone G288
EU466835.1 gg_id:303384 African elephant feces clone AFEL2_aao30b04
FJ368522.1 gg_id:368771 feces adult twins and mothers; TS49 clone TS49_a01d01
FJ368896.1 gg_id:358153 feces adult twins and mothers; TS4 clone TS4_a01h01
DQ327483.1 gg_id:146465 Metagenomic gut microbiome healthy human stool clone EA53
AY977072.1 gg_id:123375 human cecum mucosal biopsy clone K760
FJ676090.1 gg_id:521570 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ367114.1 gg_id:360063 feces adult twins and mothers; TS28 clone TS28_a03f09
FJ679823.1 gg_id:516527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ369460.1 gg_id:358560 feces adult twins and mothers; TS50 clone TS50_a04g09
DQ801252.1 gg_id:189002 human fecal clone RL388_aao93a04
FJ369397.1 gg_id:368336 feces adult twins and mothers; TS50 clone TS50_a04a04
DQ071523.1 gg_id:230528 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc31
AY981621.1 gg_id:122358 human sigmoid colon mucosal biopsy clone L858
DQ795404.1 gg_id:198270 human fecal clone RL178_aah53h12
AY981324.1 gg_id:120304 human sigmoid colon mucosal biopsy clone G341
AY976872.1 gg_id:120572 human cecum mucosal biopsy clone K513
FJ370090.1 gg_id:363987 feces adult twins and mothers; TS55 clone TS55_a04c10
DQ795084.1 gg_id:174110 human fecal clone RL310_aam40a06
FJ676204.1 gg_id:527356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679996.1 gg_id:521075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ807278.1 gg_id:177041 human fecal clone RL244_aaj48e06
EU761890.1 gg_id:341191 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
EU762096.1 gg_id:356215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ368085.1 gg_id:363354 feces adult twins and mothers; TS30 clone TS30_a03g10
DQ796540.1 gg_id:189217 human fecal clone RL179aan74d05
FJ370864.1 gg_id:358427 feces adult twins and mothers; TS5 clone TS5_a02b07

DQ801897.1	189731	2883.0	3475.6	772.0	2011.8	2780.2	3523.4
FJ362791.1	366121	1312.7	1287.4	519.4	3238.3	926.2	1391.4
FJ370352.1	360418	1841.2	906.8	1395.3	2568.2	818.5	559.2
FJ365716.1	357752	3677.3	2611.1	5202.0	4565.2	4583.1	5008.6
FJ366917.1	368931	6680.7	6119.8	2891.2	8340.3	4712.4	6312.9
AM275455.2	234340	2302.8	1417.2	1442.8	2139.4	892.0	424.5
DQ798714.1	193231	1259.0	194.3	1404.4	1453.9	55.3	113.4
EU466792.1	303125	580.8	365.4	820.6	268.2	815.5	661.4
FJ363689.1	357535	4451.8	4107.4	6884.5	6480.0	5494.8	5799.9
DQ807937.1	195481	55.7	84.2	57.3	54.3	119.9	44.5
DQ326713.1	148649	579.2	358.9	836.8	283.4	867.4	644.8
DQ797422.1	190985	1295.2	3138.3	663.2	596.5	3224.3	2273.2
EU763441.1	330946	122.3	214.1	141.8	73.5	95.1	70.0
AY979955.1	119081	163.9	274.0	252.5	79.3	84.3	93.2
AY981292.1	120019	5350.5	4002.4	11351.9	7273.3	4444.4	7797.7
EU466835.1	303384	1030.2	1026.9	1677.8	2891.9	901.9	1726.1
FJ368522.1	368771	8564.0	8813.6	10753.5	8411.2	6632.4	6940.7
FJ368896.1	358153	5184.2	5517.7	4079.1	6827.7	9597.7	9774.9
DQ327483.1	146465	674.4	358.8	966.8	321.6	1051.1	817.2
AY977072.1	123375	531.6	356.0	477.6	232.9	490.6	235.6
FJ676090.1	521570	304.7	495.1	922.5	134.0	776.9	642.4
FJ367114.1	360063	9843.2	7956.3	1924.1	10395.1	12060.4	13586.1
FJ679823.1	516527	7563.5	7284.1	3139.6	8523.9	11785.9	9209.2
FJ369460.1	358560	1210.7	867.2	1250.9	351.5	1546.8	1016.6
DQ801252.1	189002	7530.2	6638.0	2609.5	8352.0	8172.9	7445.6
FJ369397.1	368336	1101.5	1384.8	1236.1	1287.9	2342.8	2881.7
DQ071523.1	230528	17.0	30.3	18.9	54.5	56.6	13.6
AY981621.1	122358	4968.6	4452.5	3877.6	11409.0	3906.0	8197.3
DQ795404.1	198270	86.5	117.9	1054.2	154.4	560.7	344.3
AY981324.1	120304	130.0	243.7	673.5	146.5	305.1	549.3
AY976872.1	120572	234.6	349.1	690.7	141.7	109.4	203.7
FJ370090.1	363987	599.2	654.5	856.5	1184.9	208.3	275.4
DQ795084.1	174110	268.0	304.1	316.8	174.1	160.1	172.5
FJ676204.1	527356	208.1	174.0	223.6	226.2	224.9	129.3
FJ679996.1	521075	305.6	458.6	930.3	138.2	769.4	642.5
DQ807278.1	177041	228.5	305.4	654.6	92.7	403.2	505.3
EU761890.1	341191	2939.2	2552.4	2359.0	3686.2	818.5	1078.3
EU762096.1	356215	685.1	508.6	576.0	191.5	584.6	640.0
FJ368085.1	363354	50.3	162.6	92.0	80.9	86.0	52.7
DQ796540.1	189217	1837.2	2085.6	367.4	2001.2	2842.6	2063.8
FJ370864.1	358427	940.7	754.6	500.4	2078.1	109.7	191.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19675
s__unclassified	19676
s__unclassified	19678
s__unclassified	19681
s__unclassified	19682
s__unclassified	19686
s__unclassified	19691
s__unclassified	19694
s__unclassified	19697
s__unclassified	19700
s__unclassified	19701
s__unclassified	19702
s__unclassified	19704
s__unclassified	19706
s__unclassified	19711
s__unclassified	19712
s__unclassified	19713
s__unclassified	19714
s__unclassified	19715
s__unclassified	19717
s__unclassified	19726
s__unclassified	19729
s__unclassified	19733
s__unclassified	19736
s__unclassified	19740
s__unclassified	19741
s__unclassified	19742
s__unclassified	19743
s__unclassified	19744
s__unclassified	19745
s__unclassified	19750
s__unclassified	19751
s__unclassified	19753
s__unclassified	19754
s__unclassified	19759
s__unclassified	19762
s__unclassified	19764
s__unclassified	19765
s__unclassified	19766
s__unclassified	19772
s__unclassified	19774

AY984430.1 gg_id:125789 human stool clone B340
EU778575.1 gg_id:343934 Ring-tailed lemur feces clone RT_aai09h05
AY981483.1 gg_id:118911 human sigmoid colon mucosal biopsy clone L585
FJ370346.1 gg_id:361594 feces adult twins and mothers; TS56 clone TS56_a03g04
AY974859.1 gg_id:118535 human ascending colon mucosal biopsy clone KH11
AY983020.1 gg_id:125747 human descending colon mucosal biopsy clone L248
FJ370319.1 gg_id:363682 feces adult twins and mothers; TS56 clone TS56_a03d07
FJ370085.1 gg_id:369111 feces adult twins and mothers; TS55 clone TS55_a04c05
EU763087.1 gg_id:323066 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
DQ327031.1 gg_id:148868 Metagenomic gut microbiome healthy human stool clone E536
AY974985.1 gg_id:124294 human ascending colon mucosal biopsy clone KJ58
FJ364648.1 gg_id:369711 feces adult twins and mothers; TS19 clone TS19_a01d08
AY960568.1 gg_id:114994 Anaerostipes sp. str. IE4
GQ002290.1 gg_id:507372 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu175f09
DQ326965.1 gg_id:146256 Metagenomic gut microbiome healthy human stool clone E458
DQ805381.1 gg_id:197515 human fecal clone RL203_aai61h08
EU762235.1 gg_id:349852 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
FJ679950.1 gg_id:513542 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678623.1 gg_id:513783 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ326798.1 gg_id:145333 Metagenomic gut microbiome healthy human stool clone E267
FJ369427.1 gg_id:368844 feces adult twins and mothers; TS50 clone TS50_a04d03
EU762763.1 gg_id:344399 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
EU767808.1 gg_id:356162 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
DQ796479.1 gg_id:192913 human fecal clone RL179_aah28h11
AY984899.1 gg_id:122801 human stool clone B880
DQ795217.1 gg_id:178717 human fecal clone RL178_aah51f05
DQ327118.1 gg_id:145284 Metagenomic gut microbiome healthy human stool clone E636
FJ368110.1 gg_id:360474 feces adult twins and mothers; TS30 clone TS30_a04b09
DQ807820.1 gg_id:184457 human fecal clone RL180_aah37f02
FJ362753.1 gg_id:363486 feces adult twins and mothers; TS13 clone TS13_a02g02
DQ326681.1 gg_id:147258 Metagenomic gut microbiome healthy human stool clone E128
DQ807882.1 gg_id:182054 human fecal clone RL180_aah38d06
DQ326470.1 gg_id:147326 Metagenomic gut microbiome healthy human stool clone C559
GQ047165.1 gg_id:402005 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d
GQ047276.1 gg_id:402052 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010g
DQ801729.1 gg_id:184590 human fecal clone RL201_aai46b03
DQ804603.1 gg_id:193691 human fecal clone RL187_aao70c01
DQ327576.1 gg_id:150150 Metagenomic gut microbiome healthy human stool clone EB60
AY983034.1 gg_id:127613 human descending colon mucosal biopsy clone L265
FJ367163.1 gg_id:359737 feces adult twins and mothers; TS28 clone TS28_a04c05
DQ798590.1 gg_id:195395 human fecal clone RL181_aan98f09

AY984430.1	125789	85.6	228.4	306.9	89.9	156.1	332.9
EU778575.1	343934	1630.1	1429.1	2358.4	2779.8	3325.8	2915.4
AY981483.1	118911	2484.4	3746.1	319.5	1152.5	1230.8	1626.7
FJ370346.1	361594	7864.6	10502.3	8188.2	7875.3	19777.3	14385.7
AY974859.1	118535	9066.1	8861.3	3452.8	4880.8	2763.2	3279.6
AY983020.1	125747	553.4	862.0	553.8	2013.8	225.7	767.4
FJ370319.1	363682	52.3	34.3	78.7	54.6	89.0	140.2
FJ370085.1	369111	28.4	20.8	32.9	50.3	56.5	16.8
EU763087.1	323066	12361.9	8141.2	1684.4	6131.9	6430.8	7421.7
DQ327031.1	148868	499.8	758.6	1354.5	808.3	462.1	630.5
AY974985.1	124294	11262.7	14742.9	8591.7	8282.7	15531.0	12378.4
FJ364648.1	369711	1587.7	1872.8	2435.3	1497.9	3704.7	4280.2
AY960568.1	114994	80.4	134.0	62.3	509.2	55.5	22.5
GQ002290.1	507372	642.5	542.5	1269.4	1084.7	365.0	1165.4
DQ326965.1	146256	581.4	338.5	816.9	268.2	860.9	715.3
DQ805381.1	197515	1978.7	2002.5	1367.3	1383.4	2922.2	95.7
EU762235.1	349852	708.2	585.4	1061.3	248.5	980.2	802.2
FJ679950.1	513542	1666.0	1923.9	5211.9	2225.8	3558.0	2728.6
FJ678623.1	513783	384.6	546.0	179.0	93.8	89.8	50.1
DQ326798.1	145333	527.9	582.0	344.5	481.4	1504.1	1036.6
FJ369427.1	368844	135.4	183.5	244.5	124.5	297.6	177.9
EU762763.1	344399	313.2	622.3	637.5	154.8	319.7	279.3
EU767808.1	356162	10381.5	10023.2	8748.0	8264.5	10744.6	10696.7
DQ796479.1	192913	1229.1	1054.9	1617.9	1912.4	1625.4	1366.9
AY984899.1	122801	139.2	198.2	104.2	81.7	68.9	29.0
DQ795217.1	178717	3236.0	2360.2	915.8	1032.3	5207.0	2678.4
DQ327118.1	145284	8679.4	7918.7	6319.3	8913.6	7616.8	8017.7
FJ368110.1	360474	325.9	454.5	772.4	232.6	360.2	420.3
DQ807820.1	184457	682.8	569.4	565.4	249.8	259.8	472.8
FJ362753.1	363486	3907.7	3826.0	2713.0	3804.1	6043.3	4364.0
DQ326681.1	147258	19965.3	14788.6	18711.7	14503.3	12316.2	13353.3
DQ807882.1	182054	527.5	730.7	1011.7	264.6	1654.9	1248.8
DQ326470.1	147326	6809.9	5710.8	4815.4	7095.0	5201.3	6615.5
GQ047165.1	402005	613.0	466.2	1056.6	245.0	984.4	803.4
GQ047276.1	402052	517.1	689.8	902.3	1179.5	472.8	660.5
DQ801729.1	184590	59.0	71.3	207.0	72.1	87.4	38.0
DQ804603.1	193691	54.3	145.5	161.4	70.5	70.5	58.8
DQ327576.1	150150	20.2	23.7	31.4	50.0	64.7	15.7
AY983034.1	127613	1375.5	1073.7	1112.6	1749.7	1522.6	1470.7
FJ367163.1	359737	3806.7	4919.1	570.7	3439.4	2435.2	2572.8
DQ798590.1	195395	1022.9	2465.7	410.1	122.2	106.7	267.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19778
s__unclassified	19779
s__unclassified	19781
s__unclassified	19784
s__unclassified	19785
s__unclassified	19786
s__unclassified	19791
s__unclassified	19792
s__unclassified	19793
s__unclassified	19798
s__unclassified	19800
s__unclassified	19803
s__unclassified	19810
s__unclassified	19811
s__unclassified	19813
s__unclassified	19820
s__unclassified	19826
s__unclassified	19829
s__unclassified	19830
s__unclassified	19831
s__unclassified	19835
s__unclassified	19840
s__unclassified	19842
s__unclassified	19843
s__unclassified	19844
s__unclassified	19845
s__unclassified	19847
s__unclassified	19850
s__unclassified	19853
s__unclassified	19858
s__unclassified	19859
s__unclassified	19860
s__unclassified	19863
s__unclassified	19864
s__unclassified	19865
s__unclassified	19866
s__unclassified	19871
s__unclassified	19872
s__unclassified	19875
s__unclassified	19879
s__unclassified	19881

DQ326017.1 gg_id:145413 Metagenomic gut microbiome healthy human stool clone B955
DQ905930.1 gg_id:173503 human fecal clone 29c-h8
FJ683219.1 gg_id:515754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795343.1 gg_id:182566 human fecal clone RL178_aah53b12
FJ363496.1 gg_id:366870 feces adult twins and mothers; TS149 clone TS149_a03h09
FJ365779.1 gg_id:362106 feces adult twins and mothers; TS21 clone TS21_a02h08
FJ369957.1 gg_id:361190 feces adult twins and mothers; TS55 clone TS55_a02g02
EU766947.1 gg_id:348387 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ364681.1 gg_id:357195 feces adult twins and mothers; TS19 clone TS19_a01g07
DQ796685.1 gg_id:194298 human fecal clone RL179_aao53b07
FJ364929.1 gg_id:361669 feces adult twins and mothers; TS19 clone TS19_a04h04
AY978349.1 gg_id:119014 human transverse colon mucosal biopsy clone F280
FJ679203.1 gg_id:512803 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ365787.1 gg_id:364446 feces adult twins and mothers; TS21 clone TS21_a03a06
DQ806364.1 gg_id:175387 human fecal clone RL186_aan91c08
DQ798516.1 gg_id:194999 human fecal clone RL181_aan97f11
FJ371032.1 gg_id:366081 feces adult twins and mothers; TS5 clone TS5_a04b06
FJ367605.1 gg_id:368886 feces adult twins and mothers; TS2 clone TS2_a01e01
EF400396.1 gg_id:214689 human fecal clone SJTU_E_12_81
FJ367811.1 gg_id:359780 feces adult twins and mothers; TS2 clone TS2_a03h03
AY983090.1 gg_id:117012 human descending colon mucosal biopsy clone L337
AY976510.1 gg_id:122853 human cecum mucosal biopsy clone K032
FJ365724.1 gg_id:365011 feces adult twins and mothers; TS21 clone TS21_a02c05
FJ363664.1 gg_id:357558 feces adult twins and mothers; TS14 clone TS14_a01h05
DQ326796.1 gg_id:146454 Metagenomic gut microbiome healthy human stool clone E265
FJ368651.1 gg_id:359189 feces adult twins and mothers; TS49 clone TS49_a02g11
FJ679210.1 gg_id:516896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796804.1 gg_id:176547 human fecal clone RL179_aao54g05
FJ363631.1 gg_id:360786 feces adult twins and mothers; TS14 clone TS14_a01e08
FJ679121.1 gg_id:531815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370243.1 gg_id:364800 feces adult twins and mothers; TS56 clone TS56_a02c06
DQ326407.1 gg_id:146736 Metagenomic gut microbiome healthy human stool clone C450
FJ369995.1 gg_id:367250 feces adult twins and mothers; TS55 clone TS55_a03c04
EU466813.1 gg_id:295177 African elephant feces clone AFEL2_aao29g10
AY984705.1 gg_id:126730 human stool clone B658
DQ326469.1 gg_id:147499 Metagenomic gut microbiome healthy human stool clone C556
DQ803244.1 gg_id:174137 human fecal clone RL311_aam22g08
DQ795368.1 gg_id:192243 human fecal clone RL178_aah53e04
FJ369837.1 gg_id:359199 feces adult twins and mothers; TS55 clone TS55_a01d04
DQ801534.1 gg_id:174920 human fecal clone RL388_aao96g04
DQ807884.1 gg_id:192300 human fecal clone RL180_aah38d09

DQ326017.1	145413	1159.0	1706.8	553.5	2037.7	3501.0	3150.6
DQ905930.1	173503	586.8	707.6	1058.8	2241.0	1514.3	1109.6
FJ683219.1	515754	642.4	958.2	708.6	1954.4	314.0	540.9
DQ795343.1	182566	2594.5	3333.7	1880.7	1559.9	3875.5	2045.3
FJ363496.1	366870	8672.7	7040.0	3878.0	7871.7	5078.0	5158.1
FJ365779.1	362106	10800.9	12810.5	8703.0	8613.9	7159.9	6033.1
FJ369957.1	361190	5469.0	5731.8	3350.2	2631.2	2891.4	4693.3
EU766947.1	348387	1192.7	645.9	520.1	290.4	790.3	289.1
FJ364681.1	357195	1651.0	1880.3	1695.3	4522.7	1742.7	1811.6
DQ796685.1	194298	2933.2	3353.0	3005.6	2334.7	4759.5	3708.6
FJ364929.1	361669	879.7	637.9	972.8	1232.6	115.8	148.7
AY978349.1	119014	5628.2	5764.4	2629.3	5564.7	6997.0	6097.3
FJ679203.1	512803	224.4	391.8	538.4	93.6	354.8	213.5
FJ365787.1	364446	719.5	1325.6	779.2	522.3	3803.3	4086.0
DQ806364.1	175387	2684.9	3439.6	1377.8	2719.5	5006.8	4551.5
DQ798516.1	194999	103.6	210.6	420.1	103.8	161.0	286.6
FJ371032.1	366081	8633.9	9119.1	5821.6	7717.6	4476.4	8601.5
FJ367605.1	368886	992.6	1088.6	2303.2	1154.9	3539.8	2849.3
EF400396.1	214689	3568.1	3095.4	660.4	1107.9	2587.3	3236.6
FJ367811.1	359780	544.0	339.1	820.2	270.9	866.8	661.3
AY983090.1	117012	270.7	354.3	959.0	144.8	155.0	169.6
AY976510.1	122853	1394.8	945.6	334.8	301.2	717.1	258.1
FJ365724.1	365011	2358.1	4017.6	1079.6	1500.8	2833.6	3073.6
FJ363664.1	357558	2904.5	3081.0	3884.7	2016.0	5669.7	4117.8
DQ326796.1	146454	52.4	142.7	95.0	74.4	70.6	44.8
FJ368651.1	359189	518.7	228.7	264.7	154.8	442.0	402.8
FJ679210.1	516896	2619.0	2322.9	2701.6	4230.0	3505.6	3316.4
DQ796804.1	176547	555.5	1128.1	1037.9	1500.5	1970.9	2918.3
FJ363631.1	360786	7701.6	5795.8	4131.6	6600.3	3649.6	4586.4
FJ679121.1	531815	774.1	706.7	240.7	307.8	329.8	191.4
FJ370243.1	364800	6201.2	6194.7	8243.9	5654.3	7922.8	6969.8
DQ326407.1	146736	308.4	529.3	902.6	148.4	726.8	677.3
FJ369995.1	367250	360.0	598.4	1069.3	163.7	848.6	757.9
EU466813.1	295177	1389.6	493.1	899.2	327.8	785.9	391.4
AY984705.1	126730	1818.8	1801.4	1780.6	595.7	910.7	1198.8
DQ326469.1	147499	208.4	132.7	156.8	116.5	123.9	184.3
DQ803244.1	174137	757.7	1389.4	888.0	226.0	351.0	419.1
DQ795368.1	192243	159.7	334.0	569.0	142.9	163.8	441.3
FJ369837.1	359199	783.0	304.4	418.6	239.8	888.8	268.9
DQ801534.1	174920	48.5	50.4	33.8	47.4	65.6	39.4
DQ807884.1	192300	159.6	641.5	158.3	144.0	1589.8	986.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19883
s__unclassified	19885
s__unclassified	19905
s__unclassified	19909
s__unclassified	19911
s__unclassified	19912
s__unclassified	19913
s__unclassified	19917
s__unclassified	19918
s__unclassified	19919
s__unclassified	19923
s__unclassified	19925
s__unclassified	19927
s__unclassified	19928
s__unclassified	19931
s__unclassified	19932
s__unclassified	19938
s__unclassified	19940
s__unclassified	19943
s__unclassified	19944
s__unclassified	19946
s__unclassified	19947
s__unclassified	19949
s__unclassified	19952
s__unclassified	19953
s__unclassified	19957
s__unclassified	19958
s__unclassified	19959
s__unclassified	19961
s__unclassified	19962
s__unclassified	19969
s__unclassified	19972
s__unclassified	19974
s__unclassified	19976
s__unclassified	19978
s__unclassified	19980
s__unclassified	19983
s__unclassified	19989
s__unclassified	19991
s__unclassified	19993
s__unclassified	19994

AY981322.1 gg_id:118449 human sigmoid colon mucosal biopsy clone G338
DQ798578.1 gg_id:181113 human fecal clone RL181_aan98e05
GQ898585.1 gg_id:553014 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AY981405.1 gg_id:126052 human sigmoid colon mucosal biopsy clone L458
FJ367771.1 gg_id:363066 feces adult twins and mothers; TS2 clone TS2_a03d08
FJ370019.1 gg_id:357288 feces adult twins and mothers; TS55 clone TS55_a03e05
FJ364702.1 gg_id:360169 feces adult twins and mothers; TS19 clone TS19_a02a07
FJ370368.1 gg_id:363012 feces adult twins and mothers; TS56 clone TS56_a04a07
DQ795587.1 gg_id:185404 human fecal clone RL178_aan66f07
DQ795615.1 gg_id:176336 human fecal clone RL178_aan67a11
DQ795236.1 gg_id:179617 human fecal clone RL178_aah51h01
DQ806129.1 gg_id:198401 human fecal clone RL186_aah61f03
AY977058.1 gg_id:121722 human cecum mucosal biopsy clone K746
DQ795245.1 gg_id:189081 human fecal clone RL178_aah51h10
FJ370088.1 gg_id:368843 feces adult twins and mothers; TS55 clone TS55_a04c08
FJ678759.1 gg_id:527751 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ794536.1 gg_id:194931 human fecal clone RL240_aaj29c07
DQ327360.1 gg_id:146102 Metagenomic gut microbiome healthy human stool clone E916
FJ365088.1 gg_id:356729 feces adult twins and mothers; TS1 clone TS1_a02f10
FJ369862.1 gg_id:363055 feces adult twins and mothers; TS55 clone TS55_a01f07
FJ372207.1 gg_id:360381 feces adult twins and mothers; TS9 clone TS9_a03a02
GQ090517.1 gg_id:401779 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
DQ801721.1 gg_id:199183 human fecal clone RL201_aai46a06
FJ369989.1 gg_id:363307 feces adult twins and mothers; TS55 clone TS55_a03b09
FJ366965.1 gg_id:367240 feces adult twins and mothers; TS28 clone TS28_a01h03
FJ363816.1 gg_id:370034 feces adult twins and mothers; TS14 clone TS14_a03f11
DQ796388.1 gg_id:185876 human fecal clone RL179_aah26e12
FJ370071.1 gg_id:361092 feces adult twins and mothers; TS55 clone TS55_a04b03
AY979995.1 gg_id:118321 human rectum mucosal biopsy clone K936
DQ799666.1 gg_id:199237 human fecal clone RL305aal88h04
DQ325976.1 gg_id:147194 Metagenomic gut microbiome healthy human stool clone B875
AY981491.1 gg_id:126530 human sigmoid colon mucosal biopsy clone L595
DQ795475.1 gg_id:180860 human fecal clone RL178_aah54g11
FJ365982.1 gg_id:364181 feces adult twins and mothers; TS25 clone TS25_a01d05
DQ327604.1 gg_id:148762 Metagenomic gut microbiome healthy human stool clone EB94
AY981519.1 gg_id:115463 human sigmoid colon mucosal biopsy clone L646
FJ367595.1 gg_id:365617 feces adult twins and mothers; TS2 clone TS2_a01d03
DQ327512.1 gg_id:147432 Metagenomic gut microbiome healthy human stool clone EA87
AY980228.1 gg_id:119170 human rectum mucosal biopsy clone KF73
EU530468.1 gg_id:269215 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M7
DQ795430.1 gg_id:187643 human fecal clone RL178_aah54c07

AY981322.1	118449	656.4	1164.8	1277.9	734.7	883.6	1778.9
DQ798578.1	181113	59.5	143.5	140.9	75.4	80.6	100.8
GQ898585.1	553014	189.2	107.2	60.2	160.8	73.6	42.0
AY981405.1	126052	4035.0	6271.5	4020.7	3218.7	10444.4	5703.2
FJ367771.1	363066	1493.3	1662.7	4050.7	839.7	1942.6	2773.2
FJ370019.1	357288	894.0	1377.8	999.4	1207.8	3386.0	3281.9
FJ364702.1	360169	803.3	606.7	815.2	1108.1	679.7	950.5
FJ370368.1	363012	2847.7	2100.0	1916.0	4023.1	2397.1	3493.1
DQ795587.1	185404	1495.5	1740.1	1507.8	842.1	898.9	1205.6
DQ795615.1	176336	825.9	826.1	912.5	320.6	178.9	411.5
DQ795236.1	179617	1989.5	2151.7	3194.1	2537.8	1700.2	2284.9
DQ806129.1	198401	217.5	298.5	662.4	134.7	340.6	457.2
AY977058.1	121722	251.2	308.5	685.3	130.5	148.0	144.8
DQ795245.1	189081	7920.0	7136.5	6489.9	8766.1	6946.5	7101.8
FJ370088.1	368843	939.6	1160.6	1548.0	298.3	1861.8	1208.8
FJ678759.1	527751	11239.7	8556.3	5152.7	12213.9	11722.5	9921.2
DQ794536.1	194931	8918.5	5980.4	2479.9	6737.1	8047.7	10292.3
DQ327360.1	146102	4459.0	4860.3	5431.1	2779.8	4976.7	5081.0
FJ365088.1	356729	965.0	1500.9	1096.6	759.5	211.0	411.9
FJ369862.1	363055	503.9	475.5	469.6	1026.4	101.4	182.0
FJ372207.1	360381	204.1	389.9	172.1	106.3	166.7	275.9
GQ090517.1	401779	330.4	473.0	749.3	1874.5	407.6	1973.5
DQ801721.1	199183	682.6	552.3	1054.8	240.3	978.1	793.3
FJ369989.1	363307	747.2	917.2	905.4	1219.6	285.0	499.7
FJ366965.1	367240	5083.7	3886.5	6429.3	6137.6	6386.1	6694.3
FJ363816.1	370034	9979.0	10697.6	10543.8	7694.2	16574.2	14021.3
DQ796388.1	185876	38.1	47.9	77.3	69.9	145.5	75.6
FJ370071.1	361092	1493.4	2236.8	3109.0	577.9	2329.6	1915.1
AY979995.1	118321	221.9	303.2	594.8	88.8	380.2	509.1
DQ799666.1	199237	8198.5	8848.2	3101.0	6693.6	7085.6	7039.4
DQ325976.1	147194	1312.1	1129.5	161.7	1213.1	291.7	512.5
AY981491.1	126530	344.2	518.8	257.4	83.2	59.5	74.6
DQ795475.1	180860	31.0	127.7	266.4	63.5	75.5	51.4
FJ365982.1	364181	1038.6	1698.0	767.3	1222.8	2965.1	3287.6
DQ327604.1	148762	248.5	298.8	1227.1	193.8	924.6	1238.8
AY981519.1	115463	88.3	163.2	256.6	87.5	95.0	80.8
FJ367595.1	365617	6335.5	7257.7	7405.2	5948.5	9317.5	7773.1
DQ327512.1	147432	113.8	249.0	904.5	192.1	173.4	370.7
AY980228.1	119170	917.2	1398.5	1619.3	845.2	3269.3	2071.9
EU530468.1	269215	407.5	338.7	186.1	192.8	78.2	137.8
DQ795430.1	187643	480.8	881.5	1432.6	325.0	1472.0	1785.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	19996
s__unclassified	19998
s__unclassified	20001
s__unclassified	20004
s__unclassified	20012
s__unclassified	20013
s__unclassified	20014
s__unclassified	20016
s__unclassified	20024
s__unclassified	20027
s__unclassified	20028
s__unclassified	20029
s__unclassified	20030
s__unclassified	20031
s__unclassified	20032
s__unclassified	20033
s__unclassified	20035
s__unclassified	20038
s__unclassified	20039
s__unclassified	20043
s__unclassified	20045
s__unclassified	20048
s__unclassified	20050
s__unclassified	20051
s__unclassified	20052
s__unclassified	20054
s__unclassified	20056
s__unclassified	20060
s__unclassified	20063
s__unclassified	20064
s__unclassified	20065
s__unclassified	20066
s__unclassified	20067
s__unclassified	20072
s__unclassified	20073
s__unclassified	20075
s__unclassified	20078
s__unclassified	20079
s__unclassified	20082
s__unclassified	20088
s__unclassified	20091

AY981657.1 gg_id:121345 human sigmoid colon mucosal biopsy clone L934
DQ327565.1 gg_id:149526 Metagenomic gut microbiome healthy human stool clone EB49
DQ795890.1 gg_id:188526 human fecal clone RL245_aai84a10
EU763685.1 gg_id:304317 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
GQ897929.1 gg_id:586117 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ803171.1 gg_id:185017 human fecal clone RL311_aam21e05
AY983132.1 gg_id:115404 human descending colon mucosal biopsy clone L392
FJ365852.1 gg_id:366076 feces adult twins and mothers; TS21 clone TS21_a03g11
FJ368044.1 gg_id:369944 feces adult twins and mothers; TS30 clone TS30_a03c03
DQ824042.1 gg_id:182512 human fecal clone RL204_aaj58e09
FJ368850.1 gg_id:358018 feces adult twins and mothers; TS4 clone TS4_a01d01
DQ799778.1 gg_id:184382 human fecal clone RL182_aah33d02
AY982803.1 gg_id:118990 human descending colon mucosal biopsy clone KZ48
AY982947.1 gg_id:120341 human descending colon mucosal biopsy clone L150
FJ367115.1 gg_id:361458 feces adult twins and mothers; TS28 clone TS28_a03f10
FJ369352.1 gg_id:363050 feces adult twins and mothers; TS50 clone TS50_a03d11
DQ326570.1 gg_id:150134 Metagenomic gut microbiome healthy human stool clone E003
FJ365681.1 gg_id:361061 feces adult twins and mothers; TS21 clone TS21_a01g05
FJ370380.1 gg_id:366297 feces adult twins and mothers; TS56 clone TS56_a04c01
GQ047248.1 gg_id:373386 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010e
AY981351.1 gg_id:118041 human sigmoid colon mucosal biopsy clone G370
FJ672871.1 gg_id:518121 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ365880.1 gg_id:369955 feces adult twins and mothers; TS21 clone TS21_a04b06
FJ368830.1 gg_id:367061 feces adult twins and mothers; TS4 clone TS4_a01b03
AY984592.1 gg_id:127691 human stool clone B532
DQ807010.1 gg_id:199158 human fecal clone RL244_aaj45b01
DQ803217.1 gg_id:190799 human fecal clone RL311_aam22c07
FJ370984.1 gg_id:368313 feces adult twins and mothers; TS5 clone TS5_a03e10
DQ327407.1 gg_id:146980 Metagenomic gut microbiome healthy human stool clone E966
AY982992.1 gg_id:122440 human descending colon mucosal biopsy clone L213
DQ806816.1 gg_id:199262 human fecal clone RL198_aaj73b09
FJ370062.1 gg_id:363104 feces adult twins and mothers; TS55 clone TS55_a04a05
FJ679229.1 gg_id:528140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY981289.1 gg_id:119080 human sigmoid colon mucosal biopsy clone G285
FJ367926.1 gg_id:357891 feces adult twins and mothers; TS30 clone TS30_a01c04
DQ802357.1 gg_id:178821 human fecal clone RL188_aah16f01
FJ369824.1 gg_id:363186 feces adult twins and mothers; TS55 clone TS55_a01c03
FJ365682.1 gg_id:362783 feces adult twins and mothers; TS21 clone TS21_a01g06
DQ807636.1 gg_id:185429 human fecal clone RL180_aah35c05
FJ365938.1 gg_id:367945 feces adult twins and mothers; TS21 clone TS21_a04h06
DQ798388.1 gg_id:183609 human fecal clone RL181_aah41h06

AY981657.1	121345	12064.6	11847.1	1445.8	5837.0	3759.0	3662.9
DQ327565.1	149526	401.4	443.7	1055.7	327.4	366.8	502.4
DQ795890.1	188526	80.7	134.0	245.2	90.8	76.4	147.7
EU763685.1	304317	120.8	252.2	645.7	117.0	171.0	298.6
GQ897929.1	586117	1662.6	979.9	923.5	1902.2	109.4	225.5
DQ803171.1	185017	3059.6	6101.5	6109.3	2846.3	12384.2	9629.0
AY983132.1	115404	2249.7	1802.5	4279.6	1539.0	509.8	938.0
FJ365852.1	366076	7506.4	6364.7	5674.1	9066.7	9140.4	9833.7
FJ368044.1	369944	1109.1	1529.4	4034.4	1683.8	1078.9	1683.6
DQ824042.1	182512	3306.4	3614.0	3497.6	2236.1	3732.6	2960.2
FJ368850.1	358018	4854.2	7031.5	3986.3	4190.6	12225.6	6782.6
DQ799778.1	184382	1505.0	1529.9	3679.2	713.6	3780.8	3883.1
AY982803.1	118990	89.2	214.2	420.6	129.3	153.4	471.0
AY982947.1	120341	5510.2	5177.3	3771.5	6260.9	7161.5	7472.0
FJ367115.1	361458	830.4	675.6	761.1	1876.3	122.5	226.2
FJ369352.1	363050	1204.5	1124.2	327.1	3229.5	932.2	1944.9
DQ326570.1	150134	600.1	415.8	868.3	281.2	872.0	695.7
FJ365681.1	361061	10285.6	9101.5	13369.7	9796.0	6746.9	9372.0
FJ370380.1	366297	2475.9	2173.2	2152.4	3811.5	2858.1	1962.3
GQ047248.1	373386	460.8	936.3	645.9	195.3	435.5	497.8
AY981351.1	118041	1189.7	867.0	820.7	2814.6	1657.2	2399.7
FJ672871.1	518121	94.5	132.8	281.4	81.3	152.3	103.8
FJ365880.1	369955	993.3	2712.4	173.7	101.2	180.8	153.9
FJ368830.1	367061	593.6	622.8	821.8	1125.6	163.4	274.0
AY984592.1	127691	193.1	288.5	204.6	100.0	77.5	62.1
DQ807010.1	199158	2201.2	3202.1	904.7	2694.2	2889.7	75.5
DQ803217.1	190799	577.8	412.2	1010.0	238.6	1046.9	851.7
FJ370984.1	368313	5471.3	6974.8	3697.1	3330.6	4078.5	3954.9
DQ327407.1	146980	579.8	334.4	833.1	283.3	916.3	693.3
AY982992.1	122440	1200.4	1847.7	721.0	2074.8	2673.6	3808.1
DQ806816.1	199262	5766.0	6298.0	7089.4	5663.8	8630.4	7245.1
FJ370062.1	363104	971.1	1867.8	815.8	516.4	2472.9	1870.3
FJ679229.1	528140	2376.8	5625.2	1575.3	834.3	2077.8	2351.0
AY981289.1	119080	75.1	175.9	233.9	85.1	155.9	262.5
FJ367926.1	357891	2893.4	2670.3	885.1	3714.7	4988.3	6932.4
DQ802357.1	178821	545.7	381.8	1020.5	2211.7	909.1	1580.0
FJ369824.1	363186	307.7	480.4	1038.5	197.4	740.4	662.2
FJ365682.1	362783	140.1	215.9	762.6	171.8	220.1	735.6
DQ807636.1	185429	2519.3	2156.6	2491.3	2859.6	2872.4	2661.3
FJ365938.1	367945	481.8	500.8	223.7	96.2	74.6	58.3
DQ798388.1	183609	2191.6	4057.3	1800.5	2439.8	8337.3	4747.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	20092
s__unclassified	20094
s__unclassified	20097
s__unclassified	20099
s__unclassified	20105
s__unclassified	20110
s__unclassified	20116
s__unclassified	20122
s__unclassified	20126
s__unclassified	20129
s__unclassified	20130
s__unclassified	20132
s__unclassified	20137
s__unclassified	20140
s__unclassified	20143
s__unclassified	20144
s__unclassified	20151
s__unclassified	20158
s__unclassified	20159
s__unclassified	20161
s__unclassified	20163
s__unclassified	20166
s__unclassified	20167
s__unclassified	20168
s__unclassified	20169
s__unclassified	20170
s__unclassified	20174
s__unclassified	20176
s__unclassified	20180
s__unclassified	20183
s__unclassified	20190
s__unclassified	20192
s__unclassified	20194
s__unclassified	20197
s__unclassified	20198
s__unclassified	20202
s__unclassified	20207
s__unclassified	20208
s__unclassified	20209
s__unclassified	20211
s__unclassified	20212

FJ364479.1 gg_id:367115 feces adult twins and mothers; TS15 clone TS15_a03d11
FJ678170.1 gg_id:520887 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY985660.1 gg_id:116406 human stool clone C666
FJ363359.1 gg_id:367937 feces adult twins and mothers; TS149 clone TS149_a02c11
AY975186.1 gg_id:126668 human ascending colon mucosal biopsy clone KN08
DQ808141.1 gg_id:179395 human fecal clone RL180_aao73b07
FJ370188.1 gg_id:361470 feces adult twins and mothers; TS56 clone TS56_a01e05
GQ898491.1 gg_id:565351 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ365837.1 gg_id:363010 feces adult twins and mothers; TS21 clone TS21_a03f06
FJ370337.1 gg_id:356973 feces adult twins and mothers; TS56 clone TS56_a03f06
DQ794645.1 gg_id:198329 human fecal clone RL240_aaj30f03
DQ325767.1 gg_id:148012 Metagenomic gut microbiome healthy human stool clone B445
FJ363137.1 gg_id:366756 feces adult twins and mothers; TS148 clone TS148_a03e08
FJ370944.1 gg_id:361071 feces adult twins and mothers; TS5 clone TS5_a03b02
EU466973.1 gg_id:290543 African elephant feces clone AFEL2_aao32b04
EU767156.1 gg_id:335982 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ799484.1 gg_id:184523 human fecal clone RL305aal86h01
AY978359.1 gg_id:121691 human transverse colon mucosal biopsy clone F306
DQ325826.1 gg_id:147221 Metagenomic gut microbiome healthy human stool clone B565
DQ823952.1 gg_id:188128 human fecal clone RL204_aaj57d04
FJ371333.1 gg_id:367760 feces adult twins and mothers; TS6 clone TS6_a03g01
EU764364.1 gg_id:303428 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
DQ325851.1 gg_id:147212 Metagenomic gut microbiome healthy human stool clone B626
GQ897976.1 gg_id:579613 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
EU762013.1 gg_id:350368 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ369357.1 gg_id:367975 feces adult twins and mothers; TS50 clone TS50_a03e06
DQ802600.1 gg_id:188331 human fecal clone RL188_aan93h09
FJ369422.1 gg_id:360753 feces adult twins and mothers; TS50 clone TS50_a04c09
FJ370009.1 gg_id:363126 feces adult twins and mothers; TS55 clone TS55_a03d06
FJ369117.1 gg_id:366010 feces adult twins and mothers; TS4 clone TS4_a04d10
FJ372009.1 gg_id:358234 feces adult twins and mothers; TS8 clone TS8_a04g02
AM275420.2 gg_id:232700 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
AY979987.1 gg_id:116730 human rectum mucosal biopsy clone K910
FJ365630.1 gg_id:365873 feces adult twins and mothers; TS21 clone TS21_a01b08
FJ683843.1 gg_id:529625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678187.1 gg_id:519886 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ016070.1 gg_id:493598 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
EU466989.1 gg_id:291504 African elephant feces clone AFEL2_aao32d03
FJ368053.1 gg_id:364459 feces adult twins and mothers; TS30 clone TS30_a03d06
FJ367714.1 gg_id:361615 feces adult twins and mothers; TS2 clone TS2_a02g03
DQ798732.1 gg_id:186891 human fecal clone RL181_aao00f09

FJ364479.1	367115	6088.1	6460.4	3094.8	4830.9	3279.7	3205.5
FJ678170.1	520887	2286.0	2842.1	1303.7	2406.7	3947.0	2752.0
AY985660.1	116406	1297.4	2111.7	1786.3	542.7	866.1	2036.1
FJ363359.1	367937	267.6	427.1	715.1	129.9	336.9	244.8
AY975186.1	126668	1580.4	1367.1	2049.1	4853.1	1585.3	3016.3
DQ808141.1	179395	555.3	500.2	615.5	581.9	556.2	1003.4
FJ370188.1	361470	312.1	278.2	562.5	105.5	87.9	95.0
GQ898491.1	565351	1722.7	1099.3	1468.9	2192.3	159.3	112.2
FJ365837.1	363010	913.4	1355.9	274.2	3254.9	1173.8	1202.0
FJ370337.1	356973	302.7	166.1	515.1	149.3	200.6	153.9
DQ794645.1	198329	4179.9	5343.2	6596.2	3466.2	2582.5	2958.9
DQ325767.1	148012	1344.0	1321.8	3618.2	755.0	3310.0	4155.1
FJ363137.1	366756	1922.5	1945.2	2484.1	897.6	2909.3	2684.4
FJ370944.1	361071	590.4	325.8	698.7	213.6	894.4	717.4
EU466973.1	290543	600.8	355.0	695.7	222.3	908.1	792.6
EU767156.1	335982	314.0	545.5	930.9	146.4	740.7	651.4
DQ799484.1	184523	4385.2	5397.2	2314.6	4084.0	3474.3	3272.4
AY978359.1	121691	96.2	234.1	312.2	103.2	162.3	367.0
DQ325826.1	147221	9502.6	7700.6	4252.9	7798.6	5536.3	6178.3
DQ823952.1	188128	905.8	1244.7	465.4	398.3	961.9	2221.4
FJ371333.1	367760	30.6	70.2	64.4	50.3	61.6	49.4
EU764364.1	303428	801.6	793.1	1749.8	295.4	1455.3	1744.8
DQ325851.1	147212	134.8	156.1	315.0	74.7	290.0	193.0
GQ897976.1	579613	2214.9	2661.0	2623.3	2287.4	3395.1	3259.6
EU762013.1	350368	670.7	661.2	937.7	506.6	132.2	286.2
FJ369357.1	367975	1337.7	1395.0	3606.6	747.1	3527.1	4154.9
DQ802600.1	188331	4356.7	4155.9	2653.9	4464.2	2613.0	2220.6
FJ369422.1	360753	273.0	434.4	932.2	144.6	780.6	642.3
FJ370009.1	363126	958.2	1498.6	3313.3	1125.7	2323.0	1747.1
FJ369117.1	366010	4967.0	5395.1	3982.7	4800.0	6593.7	4486.7
FJ372009.1	358234	2313.1	2711.7	1195.8	1449.9	3399.9	3098.0
AM275420.2	232700	4374.5	3954.9	3320.9	4222.5	7020.0	4284.4
AY979987.1	116730	191.9	240.2	365.6	83.8	78.4	70.5
FJ365630.1	365873	120.5	205.9	127.8	73.3	88.9	59.7
FJ683843.1	529625	1002.1	732.3	2924.1	310.5	581.3	1564.6
FJ678187.1	519886	1014.2	1319.8	212.1	1670.5	1749.9	1247.9
GQ016070.1	493598	7857.9	9022.8	4003.6	6515.1	8895.6	6669.0
EU466989.1	291504	635.6	725.8	1385.2	532.7	594.7	710.6
FJ368053.1	364459	2635.9	2809.6	1640.4	3555.3	6067.9	4897.3
FJ367714.1	361615	8713.8	7431.2	6613.9	6535.1	5749.3	7532.8
DQ798732.1	186891	2041.2	3281.6	1703.5	634.9	589.4	670.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	20215
s__unclassified	20216
s__unclassified	20217
s__unclassified	20219
s__unclassified	20220
s__unclassified	20222
s__unclassified	20223
s__unclassified	20227
s__unclassified	20229
s__unclassified	20236
s__unclassified	20237
s__unclassified	20239
s__unclassified	20244
s__unclassified	20247
s__unclassified	20253
s__unclassified	20255
s__unclassified	20257
s__unclassified	20261
s__unclassified	20263
s__unclassified	20267
s__unclassified	20268
s__unclassified	20273
s__unclassified	20278
s__unclassified	20282
s__unclassified	20288
s__unclassified	20292
s__unclassified	20295
s__unclassified	20299
s__unclassified	20307
s__unclassified	20309
s__unclassified	20314
s__unclassified	20315
s__unclassified	20316
s__unclassified	20325
s__unclassified	20329
s__unclassified	20333
s__unclassified	20335
s__unclassified	20338
s__unclassified	20342
s__unclassified	20343
s__unclassified	20345

GQ898623.1 gg_id:579103 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ327601.1 gg_id:145551 Metagenomic gut microbiome healthy human stool clone EB91
EU466881.1 gg_id:299300 African elephant feces clone AFEL2_aao30g08
DQ793763.1 gg_id:194417 human fecal clone RL246_aai76h08
DQ327598.1 gg_id:147399 Metagenomic gut microbiome healthy human stool clone EB86
EU766663.1 gg_id:353149 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ368064.1 gg_id:358567 feces adult twins and mothers; TS30 clone TS30_a03e08
AY981109.1 gg_id:123392 human sigmoid colon mucosal biopsy clone G023
AY976729.1 gg_id:118744 human cecum mucosal biopsy clone K322
FJ362679.1 gg_id:361660 feces adult twins and mothers; TS13 clone TS13_a01h01
DQ797842.1 gg_id:198743 human fecal clone RL206_aaj16e03
FJ363626.1 gg_id:358857 feces adult twins and mothers; TS14 clone TS14_a01e02
DQ807991.1 gg_id:195146 human fecal clone RL180_aan70c08
FJ370084.1 gg_id:367682 feces adult twins and mothers; TS55 clone TS55_a04c04
DQ807187.1 gg_id:178805 human fecal clone RL244_aaj47c11
FJ365909.1 gg_id:365938 feces adult twins and mothers; TS21 clone TS21_a04e01
FJ369328.1 gg_id:359727 feces adult twins and mothers; TS50 clone TS50_a03b08
FJ363648.1 gg_id:362322 feces adult twins and mothers; TS14 clone TS14_a01g01
DQ798687.1 gg_id:181548 human fecal clone RL181_aao00b04
DQ799737.1 gg_id:189763 human fecal clone RL182_aah32d07
FJ371007.1 gg_id:363139 feces adult twins and mothers; TS5 clone TS5_a03h03
FJ676935.1 gg_id:527583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ408972.1 gg_id:72481 human colonic clone HuCA20
AY977012.1 gg_id:115635 human cecum mucosal biopsy clone K686
FJ368155.1 gg_id:363118 feces adult twins and mothers; TS30 clone TS30_a04h05
EU768210.1 gg_id:310205 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
AY978510.1 gg_id:120323 human transverse colon mucosal biopsy clone KQ08
FJ366548.1 gg_id:365979 feces adult twins and mothers; TS27 clone TS27_a01a09
DQ796764.1 gg_id:195420 human fecal clone RL179_aao54b08
GQ898666.1 gg_id:573178 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ368131.1 gg_id:367336 feces adult twins and mothers; TS30 clone TS30_a04e04
AY981390.1 gg_id:123610 human sigmoid colon mucosal biopsy clone L434
EU767800.1 gg_id:335052 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
GQ898549.1 gg_id:538276 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ795463.1 gg_id:195174 human fecal clone RL178_aah54f07
FJ371311.1 gg_id:366504 feces adult twins and mothers; TS6 clone TS6_a03e02
GQ079184.1 gg_id:468250 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229e(
AY975126.1 gg_id:118960 human ascending colon mucosal biopsy clone KM16
FJ368054.1 gg_id:360490 feces adult twins and mothers; TS30 clone TS30_a03d07
FJ682827.1 gg_id:514693 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682413.1 gg_id:524658 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

GQ898623.1	579103	3814.1	2766.3	2739.6	3177.1	1550.8	1091.5
DQ327601.1	145551	209.0	318.4	595.8	86.2	366.4	260.1
EU466881.1	299300	6650.6	6225.3	3439.2	8393.9	10245.5	10600.9
DQ793763.1	194417	19.0	22.5	18.8	42.2	64.8	20.8
DQ327598.1	147399	907.3	1394.8	1474.8	966.2	487.6	2172.0
EU766663.1	353149	830.2	1325.5	3114.6	596.0	740.3	1145.5
FJ368064.1	358567	11042.1	11101.2	9083.7	7900.3	6295.8	8794.5
AY981109.1	123392	30.7	32.7	46.3	61.2	55.0	29.0
AY976729.1	118744	2023.7	3489.5	2725.8	2664.2	4958.8	4325.0
FJ362679.1	361660	562.3	385.6	879.1	288.2	870.9	646.9
DQ797842.1	198743	78.6	182.7	167.7	88.3	59.1	47.4
FJ363626.1	358857	6684.7	6466.8	5329.4	6282.9	3713.1	4465.7
DQ807991.1	195146	1584.2	1105.8	2038.6	932.1	1186.2	1777.0
FJ370084.1	367682	6062.9	6842.1	6789.2	6029.4	5186.7	4759.5
DQ807187.1	178805	2074.0	2498.9	1388.5	1473.4	3573.6	2898.0
FJ365909.1	365938	4891.6	6433.1	1784.7	3237.5	3273.6	5438.6
FJ369328.1	359727	1373.1	973.0	522.1	2962.9	1626.4	1274.5
FJ363648.1	362322	534.7	323.2	676.8	237.0	518.1	648.0
DQ798687.1	181548	995.9	2536.5	150.6	107.7	188.6	145.2
DQ799737.1	189763	651.1	905.9	2186.2	461.6	2436.6	3565.6
FJ371007.1	363139	951.1	1084.8	1440.5	295.0	1395.5	1261.0
FJ676935.1	527583	44.9	32.0	68.9	54.9	63.9	36.3
AJ408972.1	72481	7613.5	5442.9	6489.4	6604.8	7026.8	9762.6
AY977012.1	115635	87.7	218.1	243.3	91.3	90.3	106.1
FJ368155.1	363118	5698.0	6286.9	4208.3	7440.4	9615.8	9106.8
EU768210.1	310205	518.0	305.7	448.3	221.7	490.8	224.3
AY978510.1	120323	4516.9	4595.5	2845.1	6714.5	2862.4	5256.6
FJ366548.1	365979	334.0	595.9	903.6	177.1	762.1	706.1
DQ796764.1	195420	3363.1	5267.3	4027.9	3537.0	8898.7	5226.8
GQ898666.1	573178	3490.6	2267.6	1782.4	3122.4	558.6	486.3
FJ368131.1	367336	3039.6	3197.6	3235.2	3019.7	2302.3	1509.0
AY981390.1	123610	745.6	849.1	2886.8	773.2	2261.5	1288.3
EU767800.1	335052	93.2	253.1	123.0	68.2	125.8	42.7
GQ898549.1	538276	5942.4	4417.9	5228.1	6427.2	5822.9	4818.4
DQ795463.1	195174	1774.0	1578.4	1756.5	395.1	218.7	642.0
FJ371311.1	366504	8903.1	8883.5	4583.3	7409.4	7779.7	8835.5
GQ079184.1	468250	330.6	205.6	392.5	99.8	57.8	37.6
AY975126.1	118960	286.2	410.8	565.4	334.9	120.7	187.0
FJ368054.1	360490	548.4	373.5	736.2	269.5	870.4	645.1
FJ682827.1	514693	2313.7	4279.7	333.9	1048.1	1574.1	1113.6
FJ682413.1	524658	5613.0	3808.9	2568.9	4724.1	6497.0	6578.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	20350
s__unclassified	20351
s__unclassified	20354
s__unclassified	20355
s__unclassified	20359
s__unclassified	20360
s__unclassified	20365
s__unclassified	20368
s__unclassified	20371
s__unclassified	20373
s__unclassified	20375
s__unclassified	20376
s__unclassified	20377
s__unclassified	20378
s__unclassified	20380
s__unclassified	20381
s__unclassified	20382
s__unclassified	20384
s__unclassified	20385
s__unclassified	20386
s__unclassified	20389
s__unclassified	20393
s__unclassified	20398
s__unclassified	20400
s__unclassified	20401
s__unclassified	20403
s__unclassified	20404
s__unclassified	20413
s__unclassified	20415
s__unclassified	20416
s__unclassified	20417
s__unclassified	20420
s__unclassified	20426
s__unclassified	20427
s__unclassified	20428
s__unclassified	20434
s__unclassified	20436
s__unclassified	20437
s__unclassified	20440
s__unclassified	20441
s__unclassified	20442

DQ803317.1 gg_id:181169 human fecal clone RL311_aam23h09
DQ794798.1 gg_id:178201 human fecal clone RL240_aaj32e03
FJ370014.1 gg_id:363968 feces adult twins and mothers; TS55 clone TS55_a03d11
AY981272.1 gg_id:121932 human sigmoid colon mucosal biopsy clone G264
EF399741.1 gg_id:214326 human fecal clone SJTU_E_02_80
EU467094.1 gg_id:302260 mongoose lemur feces clone ML_aae88b02
FJ365465.1 gg_id:359239 feces adult twins and mothers; TS20 clone TS20_a03c02
DQ808298.1 gg_id:197637 human fecal clone RL180_aao75a02
AY976950.1 gg_id:121006 human cecum mucosal biopsy clone K611
EU767253.1 gg_id:347629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
DQ327506.1 gg_id:145154 Metagenomic gut microbiome healthy human stool clone EA80
FJ370957.1 gg_id:369037 feces adult twins and mothers; TS5 clone TS5_a03c04
FJ370095.1 gg_id:357176 feces adult twins and mothers; TS55 clone TS55_a04d03
DQ795794.1 gg_id:198960 human fecal clone RL245_aai82e05
DQ799849.1 gg_id:178896 human fecal clone RL182_aah34h07
AY979988.1 gg_id:115875 human rectum mucosal biopsy clone K917
FJ367600.1 gg_id:362701 feces adult twins and mothers; TS2 clone TS2_a01d08
EU466760.1 gg_id:289045 African elephant feces clone AFEL2_aao29b01
EF399837.1 gg_id:215378 human fecal clone SJTU_E_03_90
DQ905506.1 gg_id:173012 human fecal clone 014-d9
DQ806249.1 gg_id:190058 human fecal clone RL186_aan89c09
EU767773.1 gg_id:318758 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3
DQ327206.1 gg_id:147131 Metagenomic gut microbiome healthy human stool clone E737
EU451337.1 gg_id:330473 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
EU763884.1 gg_id:346114 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
AY975189.1 gg_id:121776 human ascending colon mucosal biopsy clone KN15
DQ795244.1 gg_id:195491 human fecal clone RL178_aah51h09
DQ799441.1 gg_id:196073 human fecal clone RL305aal86c10
EU762316.1 gg_id:328305 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A>
DQ326456.1 gg_id:146072 Metagenomic gut microbiome healthy human stool clone C531
FJ370419.1 gg_id:357103 feces adult twins and mothers; TS56 clone TS56_a04h04
AY978700.1 gg_id:126318 human transverse colon mucosal biopsy clone KT78
GQ897549.1 gg_id:592235 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ799818.1 gg_id:195604 human fecal clone RL182_aah34c02
GQ001498.1 gg_id:508164 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173g01
GQ897613.1 gg_id:535749 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ796531.1 gg_id:197819 human fecal clone RL179aan74c03
FJ364639.1 gg_id:358860 feces adult twins and mothers; TS19 clone TS19_a01c11
EU762312.1 gg_id:317534 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A>
FJ367738.1 gg_id:361646 feces adult twins and mothers; TS2 clone TS2_a03a07
DQ327267.1 gg_id:145585 Metagenomic gut microbiome healthy human stool clone E811

DQ803317.1	181169	1940.7	1809.8	2746.9	2073.7	2739.5	2467.6
DQ794798.1	178201	579.7	687.6	1058.3	274.5	496.9	461.6
FJ370014.1	363968	202.3	423.4	182.3	115.3	152.6	178.8
AY981272.1	121932	1377.7	1006.7	1872.7	2950.0	117.4	242.6
EF399741.1	214326	4467.5	4198.1	5321.4	5082.7	5604.2	5919.7
EU467094.1	302260	3717.9	4433.6	1556.4	3856.3	4941.9	4399.4
FJ365465.1	359239	309.1	294.2	305.5	53.1	610.7	362.3
DQ808298.1	197637	124.0	59.4	93.0	78.5	56.5	28.1
AY976950.1	121006	10435.1	9420.8	9824.5	10506.5	8328.5	10569.0
EU767253.1	347629	12105.7	13497.0	11582.6	9850.9	11393.8	11542.9
DQ327506.1	145154	22.4	60.5	42.9	49.9	114.5	25.7
FJ370957.1	369037	1184.6	1035.3	464.0	3233.4	910.6	1617.5
FJ370095.1	357176	985.6	801.2	2916.6	1327.3	242.4	441.1
DQ795794.1	198960	1041.5	1158.2	1659.4	1870.1	4771.6	6170.8
DQ799849.1	178896	653.0	906.8	2356.4	462.3	2439.4	3295.1
AY979988.1	115875	5064.0	4813.1	4454.2	4707.4	4781.9	4833.1
FJ367600.1	362701	218.8	273.7	467.6	129.1	699.3	370.8
EU466760.1	289045	6040.2	6919.5	9162.9	4702.7	7686.5	6342.0
EF399837.1	215378	507.2	559.5	159.7	177.8	78.4	55.7
DQ905506.1	173012	1733.2	1022.0	922.3	1888.9	113.0	248.2
DQ806249.1	190058	387.4	39.3	88.2	270.8	84.9	68.9
EU767773.1	318758	185.4	251.7	176.6	92.7	69.0	27.9
DQ327206.1	147131	34.5	25.4	107.3	60.9	53.5	22.8
EU451337.1	330473	716.2	1049.2	1218.5	409.3	1324.5	1007.1
EU763884.1	346114	15107.6	15246.8	9867.0	12289.2	13871.6	13753.3
AY975189.1	121776	1025.2	1011.8	1807.7	533.6	584.0	720.8
DQ795244.1	195491	1025.6	1271.9	2622.2	764.4	1552.1	1868.7
DQ799441.1	196073	2418.1	2151.8	3137.0	5197.7	858.0	2425.3
EU762316.1	328305	147.1	211.9	702.7	138.8	577.7	295.6
DQ326456.1	146072	1432.0	1394.7	3616.1	748.7	3303.2	4155.1
FJ370419.1	357103	5113.9	5211.3	4035.0	4552.6	6236.4	6458.0
AY978700.1	126318	7791.5	7395.9	3450.6	5934.6	4453.0	4438.7
GQ897549.1	592235	981.1	900.3	776.2	1423.6	175.8	137.3
DQ799818.1	195604	1035.1	889.9	2030.0	1805.2	1622.4	1500.5
GQ001498.1	508164	498.5	227.5	287.7	164.6	475.3	414.4
GQ897613.1	535749	1747.7	1292.3	989.5	1953.9	145.4	307.4
DQ796531.1	197819	51.8	121.1	132.3	61.3	71.8	62.2
FJ364639.1	358860	398.5	541.4	1050.7	128.3	583.7	333.9
EU762312.1	317534	190.0	270.5	637.8	125.8	339.3	446.4
FJ367738.1	361646	504.9	398.6	210.7	105.8	54.0	30.8
DQ327267.1	145585	232.4	320.8	649.4	79.6	433.9	493.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	20443
s__unclassified	20445
s__unclassified	20446
s__unclassified	20455
s__unclassified	20457
s__unclassified	20458
s__unclassified	20459
s__unclassified	20463
s__unclassified	20466
s__unclassified	20468
s__unclassified	20470
s__unclassified	20473
s__unclassified	20476
s__unclassified	20478
s__unclassified	20483
s__unclassified	20484
s__unclassified	20488
s__unclassified	20491
s__unclassified	20492
s__unclassified	20494
s__unclassified	20498
s__unclassified	20499
s__unclassified	20503
s__unclassified	20504
s__unclassified	20507
s__unclassified	20510
s__unclassified	20514
s__unclassified	20516
s__unclassified	20522
s__unclassified	20525
s__unclassified	20535
s__unclassified	20537
s__unclassified	20538
s__unclassified	20541
s__unclassified	20543
s__unclassified	20544
s__unclassified	20545
s__unclassified	20548
s__unclassified	20551
s__unclassified	20553
s__unclassified	20554

DQ809721.1 gg_id:189440 human fecal clone RL184_aan83c02
DQ071480.1 gg_id:233648 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc17
DQ799325.1 gg_id:189701 human fecal clone RL205_aaj20h09
DQ326644.1 gg_id:147888 Metagenomic gut microbiome healthy human stool clone E081
AY978654.1 gg_id:117354 human transverse colon mucosal biopsy clone KS83
AY980149.1 gg_id:121657 human rectum mucosal biopsy clone KD47
DQ794967.1 gg_id:181815 human fecal clone RL310_aam38e09
DQ808460.1 gg_id:184002 human fecal clone RL180_aao76g10
DQ807035.1 gg_id:197041 human fecal clone RL244_aaj45d05
DQ801333.1 gg_id:181853 human fecal clone RL388_aao94b05
DQ809690.1 gg_id:174111 human fecal clone RL184_aan82f09
DQ795390.1 gg_id:174199 human fecal clone RL178_aah53g06
FJ369506.1 gg_id:368371 feces adult twins and mothers; TS51 clone TS51_a01d05
AY981426.1 gg_id:117920 human sigmoid colon mucosal biopsy clone L493
FJ370030.1 gg_id:364149 feces adult twins and mothers; TS55 clone TS55_a03f06
EU762347.1 gg_id:310421 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
DQ796749.1 gg_id:190462 human fecal clone RL179_aao53h12
DQ807697.1 gg_id:174347 human fecal clone RL180_aah36b03
AY977087.1 gg_id:119004 human cecum mucosal biopsy clone K777
DQ327521.1 gg_id:148085 Metagenomic gut microbiome healthy human stool clone EB01
DQ798618.1 gg_id:193664 human fecal clone RL181_aan99b01
DQ796586.1 gg_id:190899 human fecal clone RL179aan75d03
FJ370968.1 gg_id:365622 feces adult twins and mothers; TS5 clone TS5_a03d05
DQ796228.1 gg_id:191484 human fecal clone RL179_aah23d06
EF400068.1 gg_id:214474 human fecal clone SJTU_E_08_47
DQ800930.1 gg_id:180095 human fecal clone RL387_aao89e01
DQ809583.1 gg_id:182505 human fecal clone RL184_aan81b10
EU762022.1 gg_id:306696 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
AY982998.1 gg_id:121493 human descending colon mucosal biopsy clone L222
AY981259.1 gg_id:122690 human sigmoid colon mucosal biopsy clone G246
DQ327481.1 gg_id:148410 Metagenomic gut microbiome healthy human stool clone EA51
DQ801679.1 gg_id:183837 human fecal clone RL201_aai45d03
DQ327280.1 gg_id:145739 Metagenomic gut microbiome healthy human stool clone E824
DQ798547.1 gg_id:188522 human fecal clone RL181_aan98b01
DQ807958.1 gg_id:178681 human fecal clone RL180_aan69g07
DQ807688.1 gg_id:178919 human fecal clone RL180_aah35h11
EU774084.1 gg_id:355900 Chimpanzee feces clone CHIMP1_aaj39e07
AY981171.1 gg_id:122120 human sigmoid colon mucosal biopsy clone G118
AY978339.1 gg_id:121348 human transverse colon mucosal biopsy clone F251
DQ796894.1 gg_id:185065 human fecal clone RL179_aao56a11
FJ364707.1 gg_id:360128 feces adult twins and mothers; TS19 clone TS19_a02a12

DQ809721.1	189440	87.2	215.0	98.8	142.3	127.3	202.0
DQ071480.1	233648	53.9	92.4	149.7	80.6	52.7	49.3
DQ799325.1	189701	1353.4	1302.6	1521.5	3233.4	1597.4	1812.8
DQ326644.1	147888	3269.9	3546.4	3019.0	2443.0	7175.9	5687.1
AY978654.1	117354	7935.5	8146.7	9815.4	6864.1	6948.7	6152.8
AY980149.1	121657	9856.6	10613.2	3113.4	6532.8	9967.6	9386.3
DQ794967.1	181815	10435.5	10402.3	4314.7	7820.5	14137.2	9097.7
DQ808460.1	184002	298.5	506.7	932.7	149.7	744.7	613.7
DQ807035.1	197041	31.6	41.0	160.7	79.7	59.8	29.5
DQ801333.1	181853	1099.4	1257.0	2047.2	841.0	2048.5	1317.2
DQ809690.1	174111	299.1	170.7	231.0	162.7	75.8	112.7
DQ795390.1	174199	111.9	236.5	426.8	113.7	113.0	271.8
FJ369506.1	368371	1255.6	1183.5	2139.3	414.8	1814.8	1481.3
AY981426.1	117920	125.9	230.6	637.6	131.1	348.0	475.9
FJ370030.1	364149	2603.9	4025.8	5977.0	2610.6	8569.7	4160.5
EU762347.1	310421	12561.3	11062.5	6881.0	9213.9	9660.6	10005.4
DQ796749.1	190462	10289.8	10217.5	13288.2	8695.9	7835.3	8443.3
DQ807697.1	174347	293.2	386.2	979.7	149.5	807.4	899.9
AY977087.1	119004	265.4	358.1	974.9	182.6	509.6	348.3
DQ327521.1	148085	49.2	40.0	244.5	76.5	78.1	70.4
DQ798618.1	193664	67.1	72.0	156.7	108.7	252.2	195.4
DQ796586.1	190899	46.6	46.6	148.9	62.1	95.7	62.9
FJ370968.1	365622	302.9	262.7	521.6	362.7	90.9	52.7
DQ796228.1	191484	2512.8	4350.5	1628.8	2205.3	1573.7	1289.5
EF400068.1	214474	3940.4	2882.7	2824.1	3199.6	1464.4	1069.1
DQ800930.1	180095	129.6	163.8	666.2	132.7	551.3	284.1
DQ809583.1	182505	272.8	160.9	96.5	83.0	56.5	37.2
EU762022.1	306696	92.2	97.0	431.0	119.1	89.8	86.8
AY982998.1	121493	113.6	238.4	587.2	96.0	139.0	134.6
AY981259.1	122690	123.4	300.2	594.5	107.2	82.2	117.1
DQ327481.1	148410	11195.3	9310.4	5693.5	3852.2	1496.8	3075.5
DQ801679.1	183837	51.3	76.6	108.8	70.6	76.7	40.9
DQ327280.1	145739	1336.3	1586.5	2168.8	1236.9	2827.0	4084.9
DQ798547.1	188522	1842.5	3287.5	1287.3	2003.1	1293.4	1540.0
DQ807958.1	178681	1006.5	1503.2	1296.4	1402.6	2013.7	1343.3
DQ807688.1	178919	295.7	490.1	875.2	138.7	727.1	666.1
EU774084.1	355900	5474.6	6136.8	2277.8	3624.7	4090.5	2860.7
AY981171.1	122120	866.6	797.3	776.7	2374.3	1172.5	1999.3
AY978339.1	121348	216.3	367.7	1007.2	261.6	273.5	1144.4
DQ796894.1	185065	1715.5	1253.5	1425.4	3344.7	1695.5	2529.3
FJ364707.1	360128	4400.0	8017.3	2561.9	3209.6	12318.3	8323.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	20563
s__unclassified	20566
s__unclassified	20567
s__unclassified	20570
s__unclassified	20572
s__unclassified	20574
s__unclassified	20575
s__unclassified	20576
s__unclassified	20577
s__unclassified	20579
s__unclassified	20582
s__unclassified	20583
s__unclassified	20584
s__unclassified	20587
s__unclassified	20594
s__unclassified	20595
s__unclassified	20601
s__unclassified	20606
s__unclassified	20608
s__unclassified	20609
s__unclassified	21626
s__unclassified	21637
s__unclassified	21643
s__unclassified	21648
s__unclassified	21649
s__unclassified	21656
s__unclassified	21659
s__unclassified	21667
s__unclassified	21671
s__unclassified	21673
s__unclassified	21677
s__unclassified	21678
s__unclassified	21681
s__unclassified	21686
s__unclassified	21689
s__unclassified	21690
s__unclassified	21700
s__unclassified	21708
s__unclassified	21711
s__unclassified	21712
s__unclassified	21721

EU764211.1 gg_id:327552 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
DQ326455.1 gg_id:150341 Metagenomic gut microbiome healthy human stool clone C530
FJ679429.1 gg_id:521644 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ807570.1 gg_id:179871 human fecal clone RL307_aam08d05
EU762986.1 gg_id:326433 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
AY982774.1 gg_id:124418 human descending colon mucosal biopsy clone KZ12
DQ808101.1 gg_id:175303 human fecal clone RL180_aan72e04
FJ367908.1 gg_id:367092 feces adult twins and mothers; TS30 clone TS30_a01a02
AM697416.1 gg_id:222230 sequencing libraries indoor dust clone BF0001D031
EU766710.1 gg_id:307860 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
AY983055.1 gg_id:119891 human descending colon mucosal biopsy clone L291
GQ897330.1 gg_id:547913 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
GQ088675.1 gg_id:404865 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
AY978399.1 gg_id:121158 human transverse colon mucosal biopsy clone F383
FJ682604.1 gg_id:528062 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
NZ_ABGC03000041.1 gg_id:469957 Clostridium sp. str. SS2/1
EU762728.1 gg_id:329976 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ807693.1 gg_id:184566 human fecal clone RL180_aah36a07
FJ678363.1 gg_id:532186 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795253.1 gg_id:192263 human fecal clone RL178_aah52b02
AB486353.1 gg_id:579188 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EF602816.1 gg_id:233515 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
AY330126.1 gg_id:95597 methanogenic landfill leachate bioreactor clone AC036
AF371667.1 gg_id:32727 swine intestine clone p-1612-c5
AJ229203.1 gg_id:38211 anoxic bulk soil flooded rice microcosm clone BSV51
EF602953.1 gg_id:231295 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
EF602951.1 gg_id:232130 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
EU779322.1 gg_id:336501 Visayam Warty Pig feces clone VWP_aaa04d03
AM932651.1 gg_id:560203 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications
DQ815773.1 gg_id:172705 mouse cecum clone aab22b06
FJ365173.1 gg_id:364390 feces adult twins and mothers; TS1 clone TS1_a03g03
X77839.1 gg_id:14090 Clostridium polysaccharolyticum str. DSM 1801
AF371666.1 gg_id:25842 swine intestine clone p-204-o5
EU504957.1 gg_id:259762 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g09
AB488370.1 gg_id:532832 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
AB264067.1 gg_id:196195 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-50
EU656014.1 gg_id:283710 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone
EU503974.1 gg_id:277385 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03e03
AB264071.1 gg_id:177681 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-96
EF559115.1 gg_id:222851 mesophilic anaerobic digester clone C35_D7_H_B_B05
EU598268.1 gg_id:270815 Production purification and alkaliphilic xylanase microbial EMSD5 compost clone OTU

EU764211.1	327552	88.3	326.3	219.0	115.9	239.3	389.8
DQ326455.1	150341	89.6	206.2	348.1	46.6	57.5	69.6
FJ679429.1	521644	57.9	109.6	256.9	57.8	41.1	33.5
DQ807570.1	179871	2350.6	2560.7	2186.3	2539.7	3381.8	4085.1
EU762986.1	326433	3983.1	4679.6	2928.4	5576.8	1649.3	4318.5
AY982774.1	124418	11229.3	10514.7	9148.3	10325.7	3180.8	5786.5
DQ808101.1	175303	4784.0	5620.5	2029.6	4388.0	6497.0	8217.2
FJ367908.1	367092	10711.5	12904.3	13382.6	9532.2	14165.6	14309.4
AM697416.1	222230	454.9	563.4	775.3	124.3	307.0	236.2
EU766710.1	307860	758.8	860.0	1351.0	719.4	710.7	1193.1
AY983055.1	119891	5468.3	6989.0	819.8	3043.2	1035.8	1051.6
GQ897330.1	547913	142.7	154.0	745.3	175.8	153.7	232.5
GQ088675.1	404865	59.7	41.6	141.6	80.3	99.8	130.2
AY978399.1	121158	229.3	284.2	625.0	123.4	94.8	107.7
FJ682604.1	528062	296.5	501.9	941.0	153.0	739.6	608.8
NZ_ABGC03000041.1	469957	2530.0	1675.4	2347.3	2118.9	371.0	503.2
EU762728.1	329976	4664.9	7134.4	6458.4	3934.6	5682.6	5049.2
DQ807693.1	184566	565.0	530.3	496.8	251.3	131.0	432.0
FJ678363.1	532186	3793.9	4451.7	1477.4	2295.7	2427.7	1835.3
DQ795253.1	192263	31.5	86.8	62.7	100.3	190.1	94.3
AB486353.1	579188	69.4	189.0	855.1	157.1	64.3	75.6
EF602816.1	233515	2676.7	2964.7	2197.9	2545.0	6117.6	4992.2
AY330126.1	95597	345.6	603.5	1414.3	329.4	306.2	194.2
AF371667.1	32727	68.0	111.6	88.3	85.7	69.0	53.4
AJ229203.1	38211	696.9	599.0	1483.5	303.6	265.5	1297.2
EF602953.1	231295	1616.8	1261.1	3808.5	1725.0	8579.9	6275.4
EF602951.1	232130	2501.2	3988.8	4085.3	2896.6	3289.5	3291.0
EU779322.1	336501	1041.9	541.0	1884.5	331.2	479.5	506.0
AM932651.1	560203	1781.1	2141.3	2141.7	1032.9	2682.3	2977.9
DQ815773.1	172705	133.6	83.9	144.5	97.0	204.8	65.3
FJ365173.1	364390	20.2	46.1	138.0	54.9	64.8	24.3
X77839.1	14090	24.7	35.5	26.1	58.4	59.4	21.1
AF371666.1	25842	20.3	31.9	22.9	53.5	48.4	16.8
EU504957.1	259762	1788.6	2926.6	688.5	783.7	2483.8	2321.4
AB488370.1	532832	155.3	361.6	1034.3	460.7	138.0	175.5
AB264067.1	196195	1950.3	1554.4	3533.0	1868.5	599.0	1591.9
EU656014.1	283710	2229.2	3685.5	2528.7	1995.8	4440.7	5894.5
EU503974.1	277385	1875.7	2036.3	2491.2	1155.9	4399.4	3950.7
AB264071.1	177681	7414.4	6833.7	8005.6	6100.7	5529.0	6730.7
EF559115.1	222851	2769.9	1752.9	1136.2	3075.3	3686.6	3370.8
EU598268.1	270815	4672.7	3362.2	2809.4	2865.7	1437.3	1632.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	21725
s__unclassified	21727
s__unclassified	21728
s__unclassified	21739
s__unclassified	21745
s__unclassified	21747
s__unclassified	21754
s__unclassified	21789
s__unclassified	21795
s__unclassified	21806
s__unclassified	21810
s__unclassified	21811
s__unclassified	21814
s__unclassified	21823
s__unclassified	21826
s__unclassified	21827
s__unclassified	22618
s__unclassified	22621
s__unclassified	22623
s__unclassified	22627
s__unclassified	22628
s__unclassified	22629
s__unclassified	22633
s__unclassified	22653
s__unclassified	22654
s__unclassified	22657
s__unclassified	22660
s__unclassified	22662
s__unclassified	22665
s__unclassified	22666
s__unclassified	22694
s__unclassified	22705
s__unclassified	22711
s__unclassified	22713
s__unclassified	22714
s__unclassified	22716
s__unclassified	22718
s__unclassified	22723
s__unclassified	22729
s__unclassified	22732
s__unclassified	22739

EF097888.1 gg_id:180065 mouse cecum clone SWPT12_aaa01d03
EU474886.1 gg_id:302836 red river hog feces clone RRH_aaa02c04
EF559119.1 gg_id:220781 mesophilic anaerobic digester clone C35_D7_H_B_H01
AJ229234.1 gg_id:14101 Clostridium sp. str. XB90
EU655971.1 gg_id:286598 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone
X71858.1 gg_id:14089 Clostridium polysaccharolyticum str. DSM 1801
AM982562.1 gg_id:278018 microbial and slurry pig saw dust spent bedding clone PISD-AIH08
AB487614.1 gg_id:541647 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
EF603083.1 gg_id:233089 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
AB486227.1 gg_id:575834 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AJ229214.1 gg_id:23653 anoxic bulk soil flooded rice microcosm clone BSV70 clone
EU358714.1 gg_id:308774 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EF603181.1 gg_id:229938 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
AB487451.1 gg_id:540943 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
EF445208.1 gg_id:205597 rabbit cecum clone NED2H8
AM500788.1 gg_id:540532 proof spatial heterogeneity hot composting clone E72
FJ365944.1 gg_id:367453 feces adult twins and mothers; TS25 clone TS25_a01a03
DQ795967.1 gg_id:189870 human fecal clone RL202_aai49e10
DQ798524.1 gg_id:182948 human fecal clone RL181_aan97g08
AF371659.1 gg_id:25904 swine intestine clone p-197-o5
DQ326932.1 gg_id:145977 Metagenomic gut microbiome healthy human stool clone E423
DQ798374.1 gg_id:196045 human fecal clone RL181_aah41g01
AY212770.1 gg_id:101237 equine manure clone wet68
AB218343.1 gg_id:145097 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-172
DQ795043.1 gg_id:175342 human fecal clone RL310_aam39e04
GQ040652.1 gg_id:446057 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957b10
EU777587.1 gg_id:312054 Sumatran orangutan feces clone orang1_aai56c10
FJ370200.1 gg_id:361563 feces adult twins and mothers; TS56 clone TS56_a01f10
GQ040758.1 gg_id:439855 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958d01
FJ364231.1 gg_id:362190 feces adult twins and mothers; TS150 clone TS150_a04e04
FN563398.1 gg_id:594380 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
AB185572.1 gg_id:102090 rumen clone F23-H10
FJ368245.1 gg_id:365926 feces adult twins and mothers; TS3 clone TS3_a02a01
EU748480.1 gg_id:327697 neotropical folivorous flying bird adult hoatzin crop clone hoa61_09e11
EU009810.1 gg_id:246937 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_E48
DQ806056.1 gg_id:177612 human fecal clone RL186_aah60e10
AF001738.1 gg_id:14079 rumen clone RF5
DQ905358.1 gg_id:169063 human fecal clone 013B-G11
DQ803139.1 gg_id:177960 human fecal clone RL311_aam21a01
DQ325775.1 gg_id:148628 Metagenomic gut microbiome healthy human stool clone B461
EU775348.1 gg_id:335703 Western lowland gorilla feces clone GOR_aag73h05

EF097888.1	180065	29.6	60.3	69.6	79.2	103.7	43.1
EU474886.1	302836	306.1	373.5	802.9	827.1	736.0	1369.3
EF559119.1	220781	3228.7	3710.4	4636.0	2581.4	2827.6	3716.4
AJ229234.1	14101	4793.1	7023.1	4774.7	3967.8	5068.5	5430.9
EU655971.1	286598	3422.7	3340.7	5785.8	5169.2	8232.3	7774.3
X71858.1	14089	5292.9	3915.4	2934.1	5420.7	5428.4	4867.9
AM982562.1	278018	2746.2	2642.0	2622.7	2825.7	4301.7	4313.8
AB487614.1	541647	599.8	841.1	1004.8	368.4	213.7	250.1
EF603083.1	233089	1827.2	2029.8	1791.8	722.8	2555.9	2448.5
AB486227.1	575834	1752.8	2005.9	6450.0	1708.8	2006.1	2242.6
AJ229214.1	23653	20.9	38.4	51.9	71.5	70.2	48.0
EU358714.1	308774	1258.2	1061.8	3121.5	412.3	483.1	401.6
EF603181.1	229938	7856.7	10158.2	7306.7	7952.2	8809.2	11643.0
AB487451.1	540943	626.3	740.3	1462.8	370.0	234.2	349.3
EF445208.1	205597	3435.6	3252.9	2772.2	3061.0	3191.9	2263.6
AM500788.1	540532	2351.8	2217.1	2102.9	1117.4	1471.1	1120.7
FJ365944.1	367453	1328.3	1083.8	146.5	1898.2	1563.7	1680.4
DQ795967.1	189870	28.3	44.4	75.6	59.2	70.0	25.2
DQ798524.1	182948	285.5	235.2	1075.6	244.6	143.5	142.3
AF371659.1	25904	114.6	145.1	470.4	224.3	130.5	208.8
DQ326932.1	145977	7956.3	6920.2	10111.9	6368.3	6940.3	6486.4
DQ798374.1	196045	307.7	247.5	649.1	179.9	267.7	181.3
AY212770.1	101237	20.2	42.5	168.1	97.2	54.5	22.2
AB218343.1	145097	22.9	32.1	25.4	57.8	63.2	29.5
DQ795043.1	175342	48.9	53.0	51.3	80.0	80.4	40.0
GQ040652.1	446057	8720.7	8998.3	3119.6	6386.6	7619.0	6951.0
EU777587.1	312054	7181.4	6275.0	6239.9	7001.5	6618.1	7377.3
FJ370200.1	361563	1606.2	1875.1	925.6	3398.0	2833.2	4167.3
GQ040758.1	439855	20.9	65.5	334.1	58.4	64.3	25.8
FJ364231.1	362190	1108.6	800.5	1089.5	554.8	2111.3	1357.3
FN563398.1	594380	692.7	1304.3	1047.9	556.1	2285.6	2957.3
AB185572.1	102090	3851.1	2599.0	3163.0	3851.3	1910.7	2468.9
FJ368245.1	365926	1068.4	834.1	1105.0	1278.5	2663.4	2469.9
EU748480.1	327697	3019.0	3832.6	3024.9	1721.3	4777.0	6400.2
EU009810.1	246937	4234.4	4358.3	1741.4	6127.0	6910.2	8376.5
DQ806056.1	177612	6248.7	6411.3	4467.3	6191.7	7345.2	7315.9
AF001738.1	14079	20.9	26.7	51.6	45.8	38.0	22.3
DQ905358.1	169063	4388.9	4483.9	5170.4	2944.3	4547.2	5410.8
DQ803139.1	177960	262.3	150.4	259.0	568.2	67.4	72.5
DQ325775.1	148628	93.3	333.2	285.9	79.6	65.4	50.7
EU775348.1	335703	45.8	91.8	112.8	275.2	71.6	111.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	22741
s__unclassified	22743
s__unclassified	22746
s__unclassified	22752
s__unclassified	22761
s__unclassified	22766
s__unclassified	22767
s__unclassified	22774
s__unclassified	22780
s__unclassified	22784
s__unclassified	22791
s__unclassified	22793
s__unclassified	22797
s__unclassified	22799
s__unclassified	22801
s__unclassified	22804
s__unclassified	22807
s__unclassified	22810
s__unclassified	22817
s__unclassified	22820
s__unclassified	22827
s__unclassified	22828
s__unclassified	22834
s__unclassified	22839
s__unclassified	22843
s__unclassified	22850
s__unclassified	22854
s__unclassified	22857
s__unclassified	22859
s__unclassified	22876
s__unclassified	22878
s__unclassified	22880
s__unclassified	22881
s__unclassified	22887
s__unclassified	22891
s__unclassified	22902
s__unclassified	22915
s__unclassified	22918
s__unclassified	22920
s__unclassified	22926
s__unclassified	22927

DQ802401.1 gg_id:177232 human fecal clone RL188_aah17c04
FJ363598.1 gg_id:363673 feces adult twins and mothers; TS14 clone TS14_a01b10
EU471606.1 gg_id:297180 Asiatic elephant feces clone AE1_aaa03b08
FJ369768.1 gg_id:368229 feces adult twins and mothers; TS51 clone TS51_a04e12
DQ797873.1 gg_id:174394 human fecal clone RL206_aaj16h04
FJ369407.1 gg_id:368023 feces adult twins and mothers; TS50 clone TS50_a04b05
DQ797064.1 gg_id:198736 human fecal clone RL386_aao86e03
DQ797794.1 gg_id:176294 human fecal clone RL206_aaj15h11
DQ804235.1 gg_id:180498 human fecal clone RL187_aah70f08
FM873638.1 gg_id:367860 occupant source house mattress dust clone MA01H09
AB218300.1 gg_id:148304 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-73
DQ824467.1 gg_id:189373 human fecal clone RL304_aal76d03
GQ897362.1 gg_id:566033 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ369269.1 gg_id:364786 feces adult twins and mothers; TS50 clone TS50_a02c08
DQ325553.1 gg_id:146945 Metagenomic gut microbiome healthy human stool clone B015
DQ803271.1 gg_id:187948 human fecal clone RL311_aam23c01
FJ362754.1 gg_id:363879 feces adult twins and mothers; TS13 clone TS13_a02g03
EU778160.1 gg_id:316598 feces clone RL388_aao96f07
DQ795004.1 gg_id:178146 human fecal clone RL310_aam39a05
FJ369227.1 gg_id:367762 feces adult twins and mothers; TS50 clone TS50_a01g07
FJ832200.1 gg_id:560995 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q101_82B11
FJ371026.1 gg_id:368983 feces adult twins and mothers; TS5 clone TS5_a04a11
DQ807249.1 gg_id:191769 human fecal clone RL244_aaj48b05
DQ327417.1 gg_id:148635 Metagenomic gut microbiome healthy human stool clone E976
DQ806335.1 gg_id:184069 human fecal clone RL186_aan90g07
DQ116006.1 gg_id:130051 bovine teat canal clone D-51
FJ673323.1 gg_id:515572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ326427.1 gg_id:147279 Metagenomic gut microbiome healthy human stool clone C482
EU844987.1 gg_id:343667 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB218299.1 gg_id:145431 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-71
DQ795466.1 gg_id:182270 human fecal clone RL178_aah54f12
DQ804374.1 gg_id:174474 human fecal clone RL187_aan78h05
FJ363791.1 gg_id:364298 feces adult twins and mothers; TS14 clone TS14_a03d05
EF436361.1 gg_id:205445 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC75
DQ794583.1 gg_id:192428 human fecal clone RL240_aaj29h05
DQ798651.1 gg_id:189815 human fecal clone RL181_aan99e10
DQ800500.1 gg_id:179320 human fecal clone RL183_aah27e04
DQ802270.1 gg_id:188481 human fecal clone RL188_aah15d08
DQ803722.1 gg_id:181406 human fecal clone RL200_aai57e11
FJ364143.1 gg_id:369413 feces adult twins and mothers; TS150 clone TS150_a03e05
DQ798129.1 gg_id:184829 human fecal clone RL302_aal95h02

DQ802401.1	177232	2150.1	3356.9	965.7	3689.3	1084.8	2294.7
FJ363598.1	363673	4233.0	3256.8	1914.4	5274.5	4080.4	4594.7
EU471606.1	297180	1172.6	1172.1	1823.5	2356.8	715.2	1709.9
FJ369768.1	368229	9405.4	7693.7	8391.4	4393.8	6195.8	5103.9
DQ797873.1	174394	264.9	283.2	492.5	558.7	1565.0	681.8
FJ369407.1	368023	10341.4	12149.0	6996.5	10169.7	9545.3	9295.0
DQ797064.1	198736	45.4	60.9	47.0	89.1	102.8	63.7
DQ797794.1	176294	1659.3	1526.0	1609.0	2881.6	180.1	541.5
DQ804235.1	180498	203.2	181.0	350.4	174.7	143.1	90.1
FM873638.1	367860	9077.3	9568.0	2944.4	2879.2	3947.7	4275.5
AB218300.1	148304	5390.7	4377.9	1198.2	4998.6	6879.1	6960.7
DQ824467.1	189373	169.3	160.8	345.6	637.7	148.8	235.1
GQ897362.1	566033	911.6	797.3	876.7	595.6	248.4	745.8
FJ369269.1	364786	603.1	624.4	773.9	918.9	335.7	242.9
DQ325553.1	146945	40.8	63.4	464.7	94.7	119.4	85.4
DQ803271.1	187948	9644.8	9905.6	8207.9	7883.1	10356.3	9297.3
FJ362754.1	363879	3683.6	4288.2	3315.2	5337.5	7121.2	5313.8
EU778160.1	316598	63.3	52.6	140.8	83.7	54.5	72.5
DQ795004.1	178146	58.2	44.3	169.0	104.9	58.0	51.0
FJ369227.1	367762	54.7	33.9	52.2	47.9	41.4	25.2
FJ832200.1	560995	3796.8	3695.5	1717.9	331.0	1825.5	2596.2
FJ371026.1	368983	9858.3	12804.2	7473.4	11123.2	13398.9	11308.0
DQ807249.1	191769	24.7	47.8	89.2	52.0	75.1	27.2
DQ327417.1	148635	237.6	390.3	199.7	128.8	208.6	257.9
DQ806335.1	184069	4946.3	4858.9	3325.4	3302.4	2813.3	2652.1
DQ116006.1	130051	3336.5	4347.2	5252.6	2496.0	4843.0	4985.8
FJ673323.1	515572	1602.3	1523.1	2257.0	781.4	6327.7	3442.8
DQ326427.1	147279	52.7	89.6	78.4	85.6	89.9	57.5
EU844987.1	343667	3030.8	3392.4	3502.4	4800.5	3311.6	3804.8
AB218299.1	145431	159.1	134.8	542.5	137.0	362.4	337.5
DQ795466.1	182270	960.7	1413.4	2359.1	1724.4	1940.2	1348.0
DQ804374.1	174474	451.0	499.5	866.5	160.6	123.0	343.3
FJ363791.1	364298	2864.2	3137.1	2046.4	2128.2	2521.6	2310.8
EF436361.1	205445	2481.9	2967.4	2725.1	1285.9	2006.3	3950.0
DQ794583.1	192428	4227.7	5352.9	3791.4	2648.9	4051.1	4067.1
DQ798651.1	189815	8792.1	8461.6	9370.6	9772.8	10616.8	9848.9
DQ800500.1	179320	1418.8	1556.3	2242.1	2817.1	2994.0	2811.0
DQ802270.1	188481	12128.2	12048.1	4851.6	9188.9	10406.7	10732.4
DQ803722.1	181406	6244.0	4665.1	3773.2	2970.5	282.2	3392.6
FJ364143.1	369413	919.3	970.2	501.9	1516.0	2287.1	1213.8
DQ798129.1	184829	493.8	516.5	1788.1	317.5	2062.7	1139.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	22934
s__unclassified	22937
s__unclassified	22945
s__unclassified	22950
s__unclassified	22957
s__unclassified	22959
s__unclassified	22963
s__unclassified	22966
s__unclassified	22969
s__unclassified	22970
s__unclassified	22971
s__unclassified	22982
s__unclassified	22990
s__unclassified	22993
s__unclassified	22995
s__unclassified	23008
s__unclassified	23012
s__unclassified	23035
s__unclassified	23037
s__unclassified	23038
s__unclassified	23057
s__unclassified	23060
s__unclassified	23061
s__unclassified	23063
s__unclassified	23068
s__unclassified	23072
s__unclassified	23073
s__unclassified	23084
s__unclassified	23085
s__unclassified	23090
s__unclassified	23113
s__unclassified	23119
s__unclassified	23120
s__unclassified	23122
s__unclassified	23126
s__unclassified	23131
s__unclassified	23139
s__unclassified	23144
s__unclassified	23146
s__unclassified	23152
s__unclassified	23158

FJ366225.1 gg_id:361112 feces adult twins and mothers; TS25 clone TS25_a04b10
DQ795259.1 gg_id:176125 human fecal clone RL178_aah52b08
FJ370766.1 gg_id:359863 feces adult twins and mothers; TS5 clone TS5_a01a06
EU771423.1 gg_id:320284 Asiatic elephant feces clone AE2_aaa04e11
EU776147.1 gg_id:308045 Spotted hyena feces clone HY2_g06
DQ794005.1 gg_id:196443 human fecal clone RL176_aah46e07
DQ796513.1 gg_id:194330 human fecal clone RL179aan73f11
FJ369329.1 gg_id:368073 feces adult twins and mothers; TS50 clone TS50_a03b09
FJ363846.1 gg_id:358422 feces adult twins and mothers; TS14 clone TS14_a04a09
DQ794651.1 gg_id:185791 human fecal clone RL240_aaj30f09
AF001702.1 gg_id:14091 rumen clone RC10
DQ806145.1 gg_id:197745 human fecal clone RL186_aah61g10
DQ325786.1 gg_id:148837 Metagenomic gut microbiome healthy human stool clone B477
GQ448774.1 gg_id:540224 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g
EU778980.1 gg_id:313823 Prevost's squirrel feces clone SQ_aah81a06
FJ371206.1 gg_id:363385 feces adult twins and mothers; TS6 clone TS6_a02b07
FJ364508.1 gg_id:361833 feces adult twins and mothers; TS15 clone TS15_a03g07
DQ803194.1 gg_id:183984 human fecal clone RL311_aam21h10
AY960565.1 gg_id:114912 Clostridium sp. str. ID11
DQ796396.1 gg_id:190307 human fecal clone RL179_aah26f11
FJ368662.1 gg_id:360088 feces adult twins and mothers; TS49 clone TS49_a03a04
DQ793914.1 gg_id:189485 human fecal clone RL176_aah45c03
DQ795696.1 gg_id:191766 human fecal clone RL178_aan68g08
GQ897258.1 gg_id:568646 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
EU344679.1 gg_id:275370 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
AF371665.1 gg_id:71089 swine intestine clone p-30-a5
EF445260.1 gg_id:211734 dairy cow rumen clone NED4D11
EU622674.1 gg_id:279487 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
FJ363493.1 gg_id:362863 feces adult twins and mothers; TS149 clone TS149_a03h05
FJ368627.1 gg_id:367884 feces adult twins and mothers; TS49 clone TS49_a02e08
DQ809618.1 gg_id:197865 human fecal clone RL184_aan81f05
DQ795109.1 gg_id:176491 human fecal clone RL310_aam40d01
DQ327256.1 gg_id:149461 Metagenomic gut microbiome healthy human stool clone E795
DQ803199.1 gg_id:188592 human fecal clone RL311_aam22a05
EU381987.1 gg_id:271750 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
DQ805127.1 gg_id:192315 human fecal clone RL249_aaj81f03
EU762969.1 gg_id:315028 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
DQ796218.1 gg_id:174256 human fecal clone RL179_aah23c07
EU473489.1 gg_id:296607 Somali wild ass feces clone WA_aaa01b03
DQ796700.1 gg_id:181100 human fecal clone RL179_aao53d03
FJ368814.1 gg_id:366752 feces adult twins and mothers; TS49 clone TS49_a04h10

FJ366225.1	361112	1123.6	1040.4	1470.9	1790.1	1270.8	1460.6
DQ795259.1	176125	12.3	14.0	15.3	35.6	45.4	18.2
FJ370766.1	359863	11224.7	11181.7	5870.5	9701.7	10877.0	11404.3
EU771423.1	320284	1523.0	2186.9	4883.4	2659.3	4311.5	4103.0
EU776147.1	308045	183.2	212.6	96.0	172.7	267.8	187.4
DQ794005.1	196443	17.2	24.4	20.6	40.7	61.4	18.8
DQ796513.1	194330	537.3	623.7	746.6	1200.2	1639.9	986.6
FJ369329.1	368073	1618.4	2996.5	621.9	4138.1	4613.3	3472.1
FJ363846.1	358422	74.0	191.3	137.7	180.8	175.6	119.7
DQ794651.1	185791	368.4	567.5	1814.1	358.6	1759.4	1108.7
AF001702.1	14091	50.2	68.2	83.7	57.9	86.4	43.6
DQ806145.1	197745	34.8	44.7	73.8	75.0	54.2	63.7
DQ325786.1	148837	8676.8	8177.5	4991.0	4743.9	9321.0	7569.0
GQ448774.1	540224	5422.3	6559.3	5670.8	5034.2	6590.0	4610.4
EU778980.1	313823	981.0	607.4	1778.3	1644.4	312.6	320.5
FJ371206.1	363385	8077.9	9796.5	5834.0	7046.7	6267.0	6647.3
FJ364508.1	361833	7544.1	10185.5	4642.8	5177.2	6458.3	5738.5
DQ803194.1	183984	4490.3	5619.8	3041.4	4046.8	5864.7	3817.2
AY960565.1	114912	1386.2	916.7	155.8	152.2	139.8	97.3
DQ796396.1	190307	969.5	2433.8	2645.2	852.8	4594.9	3518.1
FJ368662.1	360088	910.9	969.1	833.8	1345.3	1176.7	1338.6
DQ793914.1	189485	2106.7	1791.5	2085.3	1432.3	3615.5	3683.8
DQ795696.1	191766	4819.2	3247.9	2612.1	5754.9	1265.8	1124.6
GQ897258.1	568646	5829.9	5471.4	4800.7	3658.3	3863.2	3717.3
EU344679.1	275370	1604.6	2855.3	4170.0	1698.5	429.5	1372.9
AF371665.1	71089	63.3	68.6	90.5	93.9	56.4	55.1
EF445260.1	211734	169.1	135.3	235.7	148.0	73.7	69.6
EU622674.1	279487	46.2	38.1	259.2	86.3	60.6	40.7
FJ363493.1	362863	2718.7	3780.9	2572.7	1123.1	902.2	1366.3
FJ368627.1	367884	4147.1	4203.6	6302.0	3700.8	3291.3	3460.2
DQ809618.1	197865	259.4	119.5	591.8	111.1	67.7	55.4
DQ795109.1	176491	1717.7	1547.1	627.1	295.6	1003.8	729.7
DQ327256.1	149461	1896.7	1748.0	1785.2	1397.9	2465.9	1678.4
DQ803199.1	188592	3531.6	3620.2	1849.2	3555.3	4531.2	3832.8
EU381987.1	271750	593.3	928.3	1251.7	692.6	2684.5	1915.0
DQ805127.1	192315	4026.9	3290.9	736.0	3587.3	2825.2	2842.7
EU762969.1	315028	4124.8	6224.2	1402.5	4608.1	3971.9	3981.2
DQ796218.1	174256	4721.0	3460.3	2228.5	5669.4	1428.2	2997.2
EU473489.1	296607	2191.8	3516.1	2442.6	1793.4	8036.8	4451.3
DQ796700.1	181100	1381.4	1285.7	1002.5	1483.2	355.7	324.2
FJ368814.1	366752	91.4	226.2	246.9	78.4	83.8	45.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	23159
s__unclassified	23161
s__unclassified	23166
s__unclassified	23168
s__unclassified	23169
s__unclassified	23187
s__unclassified	23192
s__unclassified	23201
s__unclassified	23202
s__unclassified	23204
s__unclassified	23205
s__unclassified	23209
s__unclassified	23213
s__unclassified	23216
s__unclassified	23224
s__unclassified	23226
s__unclassified	23227
s__unclassified	23228
s__unclassified	23236
s__unclassified	23239
s__unclassified	23245
s__unclassified	23254
s__unclassified	23256
s__unclassified	23269
s__unclassified	23274
s__unclassified	23277
s__unclassified	23284
s__unclassified	23289
s__unclassified	23291
s__unclassified	23310
s__unclassified	23327
s__unclassified	23329
s__unclassified	23332
s__unclassified	23346
s__unclassified	23364
s__unclassified	23377
s__unclassified	23389
s__unclassified	23397
s__unclassified	23408
s__unclassified	23417
s__unclassified	23424

FJ363809.1 gg_id:363624 feces adult twins and mothers; TS14 clone TS14_a03f01
DQ797571.1 gg_id:199052 human fecal clone RL206_aaj13b10
DQ795156.1 gg_id:186048 human fecal clone RL310_aam40h03
DQ824600.1 gg_id:185299 human fecal clone RL185_aaj70c05
DQ803202.1 gg_id:189745 human fecal clone RL311_aam22a09
GU303697.1 gg_id:570450 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
FJ362975.1 gg_id:362583 feces adult twins and mothers; TS148 clone TS148_a01d10
FJ364128.1 gg_id:362262 feces adult twins and mothers; TS150 clone TS150_a03c12
EU467012.1 gg_id:291448 African elephant feces clone AFEL2_aao32f10
FJ368288.1 gg_id:369224 feces adult twins and mothers; TS3 clone TS3_a02e04
EU774091.1 gg_id:315176 Chimpanzee feces clone CHIMP12_e08_1
FJ364204.1 gg_id:369896 feces adult twins and mothers; TS150 clone TS150_a04b09
DQ799390.1 gg_id:189715 human fecal clone RL305aal85f10
EU775922.1 gg_id:331309 Horse feces clone horsej_aai90c10
DQ327173.1 gg_id:148579 Metagenomic gut microbiome healthy human stool clone E701
GQ090630.1 gg_id:381579 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
DQ802518.1 gg_id:190122 human fecal clone RL188_aah18h02
FJ366839.1 gg_id:362391 feces adult twins and mothers; TS27 clone TS27_a04e01
EU845683.1 gg_id:311395 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ809784.1 gg_id:190984 human fecal clone RL184_aan84b08
FJ368263.1 gg_id:364272 feces adult twins and mothers; TS3 clone TS3_a02b09
DQ904646.1 gg_id:170104 human fecal clone 001-a7
DQ327003.1 gg_id:147218 Metagenomic gut microbiome healthy human stool clone E504
EU772020.1 gg_id:324961 Argali sheep feces clone AS1_aao38e09.Contig1
DQ805673.1 gg_id:183956 human fecal clone RL306aal89f08
FJ363898.1 gg_id:363738 feces adult twins and mothers; TS14 clone TS14_a04f08
DQ798645.1 gg_id:198540 human fecal clone RL181_aan99e03
FJ833076.1 gg_id:510859 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_82B11
DQ794056.1 gg_id:177942 human fecal clone RL176_aan57d05
DQ805407.1 gg_id:194366 human fecal clone RL203_aai62b11
EU843494.1 gg_id:314618 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ363471.1 gg_id:357829 feces adult twins and mothers; TS149 clone TS149_a03f03
EF404127.1 gg_id:215034 human fecal clone SJTU_C_05_14
FJ368805.1 gg_id:361224 feces adult twins and mothers; TS49 clone TS49_a04g08
DQ326977.1 gg_id:149713 Metagenomic gut microbiome healthy human stool clone E472
EU775401.1 gg_id:335601 Western lowland gorilla feces clone GOR_aag74d01
EU843844.1 gg_id:308974 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ810039.1 gg_id:192338 human fecal clone RL184_aao67d03
AF001756.1 gg_id:14080 rumen clone RF24
EU451291.1 gg_id:326416 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EU456777.1 gg_id:351561 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N

FJ363809.1	363624	216.8	422.2	181.2	1198.7	391.2	290.5
DQ797571.1	199052	1514.0	1641.9	426.2	2261.2	2167.0	889.7
DQ795156.1	186048	17.6	24.3	18.5	46.5	56.8	23.1
DQ824600.1	185299	62.0	164.0	250.1	131.9	527.2	151.0
DQ803202.1	189745	4053.8	2303.5	1283.6	1740.5	2422.2	2425.9
GU303697.1	570450	537.8	707.6	537.0	901.0	528.4	348.6
FJ362975.1	362583	167.3	162.8	206.0	297.8	303.2	278.4
FJ364128.1	362262	583.7	1204.7	181.0	1846.7	1712.6	1630.4
EU467012.1	291448	39.5	48.7	91.0	98.9	64.8	48.1
FJ368288.1	369224	33.0	45.4	37.1	69.5	74.4	33.0
EU774091.1	315176	734.3	582.9	1509.4	3544.0	907.9	1603.5
FJ364204.1	369896	1058.0	2202.4	737.0	665.7	3802.3	2933.3
DQ799390.1	189715	5331.7	3627.3	1828.4	3204.6	1874.7	2929.5
EU775922.1	331309	571.8	718.8	903.1	272.4	401.7	655.3
DQ327173.1	148579	2128.8	2929.5	2455.0	3594.5	5336.4	3909.9
GQ090630.1	381579	13471.5	14895.8	10616.3	9201.8	15969.7	19593.7
DQ802518.1	190122	8437.3	9746.3	3819.5	4478.5	5584.9	7311.7
FJ366839.1	362391	5843.9	6205.1	3443.5	7665.8	9818.9	9540.4
EU845683.1	311395	4214.8	4032.8	3215.1	808.1	3743.5	3083.1
DQ809784.1	190984	160.4	264.3	488.3	137.8	108.1	180.0
FJ368263.1	364272	472.4	521.6	147.5	148.7	89.9	129.8
DQ904646.1	170104	22.6	25.0	13.7	37.9	52.7	15.4
DQ327003.1	147218	10155.3	9270.3	2740.9	8503.1	7024.2	4938.6
EU772020.1	324961	4460.2	4760.9	3316.0	3744.9	5328.9	6044.6
DQ805673.1	183956	28.9	21.8	24.6	53.9	61.9	13.1
FJ363898.1	363738	89.0	89.3	202.5	83.3	76.3	54.1
DQ798645.1	198540	5829.0	5955.9	3463.6	7633.4	4981.2	5194.1
FJ833076.1	510859	871.7	1298.6	1070.6	1321.7	1071.2	1323.1
DQ794056.1	177942	41.6	44.1	25.8	65.0	99.6	36.8
DQ805407.1	194366	1027.6	1439.3	1229.7	2244.4	4625.5	5663.3
EU843494.1	314618	7397.5	7065.2	5870.6	4230.8	10014.8	9474.3
FJ363471.1	357829	70.9	140.8	64.1	107.7	378.4	446.6
EF404127.1	215034	77.0	119.4	595.1	112.2	105.4	97.1
FJ368805.1	361224	40.4	93.9	129.2	82.6	110.1	41.1
DQ326977.1	149713	6575.4	6815.8	3945.7	4933.6	5263.2	4538.7
EU775401.1	335601	405.9	410.5	773.1	488.4	523.5	478.2
EU843844.1	308974	1374.0	2233.4	1668.1	1236.9	10549.2	3948.3
DQ810039.1	192338	23.5	51.6	28.1	37.8	54.9	22.3
AF001756.1	14080	288.3	287.7	475.4	196.1	282.8	753.6
EU451291.1	326416	189.1	316.3	169.0	115.9	237.7	167.6
EU456777.1	351561	8435.3	9503.1	6997.4	10090.1	10750.2	8371.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	23448
s__unclassified	23449
s__unclassified	23452
s__unclassified	23453
s__unclassified	23469
s__unclassified	23478
s__unclassified	23481
s__unclassified	23493
s__unclassified	23498
s__unclassified	23527
s__unclassified	23531
s__unclassified	23534
s__unclassified	23545
s__unclassified	23552
s__unclassified	23561
s__unclassified	23569
s__unclassified	23571
s__unclassified	23628
s__unclassified	23649
s__unclassified	23655
s__unclassified	23659
s__unclassified	23669
s__unclassified	23674
s__unclassified	23683
s__unclassified	23694
s__unclassified	23720
s__unclassified	23730
s__unclassified	23749
s__unclassified	23750
s__unclassified	23772
s__unclassified	23779
s__unclassified	23780
s__unclassified	23803
s__unclassified	23805
s__unclassified	23813
s__unclassified	23818
s__unclassified	23836
s__unclassified	23848
s__unclassified	23855
s__unclassified	23858
s__unclassified	23861

AY975445.1 gg_id:124342 human ascending colon mucosal biopsy clone N835
EU748175.1 gg_id:334172 neotropical folivorous flying bird adult hoatzin crop clone hoa31_49A07.F
FJ364202.1 gg_id:368228 feces adult twins and mothers; TS150 clone TS150_a04b07
GQ896848.1 gg_id:586637 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ777934.1 gg_id:167252 rat feces clone R-1199(2)
EU453406.1 gg_id:354240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
AF371676.1 gg_id:21698 swine intestine clone p-273-o5
EU765884.1 gg_id:343785 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
GU302756.1 gg_id:557137 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
AY976184.1 gg_id:127439 human ascending colon mucosal biopsy clone LV91
EU452252.1 gg_id:319038 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
FJ679395.1 gg_id:522077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU453604.1 gg_id:353050 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU778332.1 gg_id:321304 feces clone RL388_aao93h04
EU456462.1 gg_id:313333 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S
AF001721.1 gg_id:14020 rumen clone RC35
DQ808884.1 gg_id:176257 human fecal clone RL243_aai86e11
FJ881245.1 gg_id:430739 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
DQ797115.1 gg_id:199013 human fecal clone RL386_aao87b10
EF098232.1 gg_id:184535 mouse cecum clone SWPT14_aaa03d04
FJ679670.1 gg_id:524122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681388.1 gg_id:515129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ825335.1 gg_id:178362 human fecal clone RL185_aan88g03
EU452326.1 gg_id:333914 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
FJ879304.1 gg_id:411214 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
AF371677.1 gg_id:36892 swine intestine clone p-2409-55G5
EU344224.1 gg_id:260496 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU455186.1 gg_id:333786 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
FJ834237.1 gg_id:567961 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q301_78F10
FJ367885.1 gg_id:359911 feces adult twins and mothers; TS2 clone TS2_a04g01
FJ680195.1 gg_id:530278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU452990.1 gg_id:332816 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU462618.1 gg_id:295074 Sumatran orangutan feces clone orang2_aai66b12
EU456680.1 gg_id:318224 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
EF098586.1 gg_id:188120 mouse cecum clone SWPT16_aaa01g06
FJ678722.1 gg_id:525789 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ815697.1 gg_id:163142 mouse cecum clone aab21b02
EU509978.1 gg_id:268910 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24h05
EU530167.1 gg_id:258321 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1
EU748382.1 gg_id:323463 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07h08
EU450938.1 gg_id:306993 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S

AY975445.1	124342	2096.6	1521.2	1027.9	1352.2	3172.6	72.3
EU748175.1	334172	1094.3	2284.6	2563.0	1183.0	2458.6	2174.7
FJ364202.1	368228	7460.7	6769.0	6236.9	6783.3	11976.1	10070.5
GQ896848.1	586637	31.0	35.1	30.5	57.7	57.5	30.8
DQ777934.1	167252	3921.0	5784.9	2550.3	4291.1	3269.2	3317.7
EU453406.1	354240	1788.0	2461.1	1534.5	2741.5	2369.9	3436.7
AF371676.1	21698	260.7	466.1	597.4	951.3	404.0	967.4
EU765884.1	343785	1468.0	994.7	1674.2	882.5	1064.6	867.7
GU302756.1	557137	7335.3	8416.6	7525.4	6078.2	9577.6	8017.5
AY976184.1	127439	314.8	197.4	1027.7	330.7	111.3	229.2
EU452252.1	319038	2721.5	2063.0	2810.2	3001.6	954.7	2046.3
FJ679395.1	522077	4772.2	5306.3	597.7	4472.1	6629.0	6969.5
EU453604.1	353050	374.1	709.5	1697.4	934.9	1824.0	1411.2
EU778332.1	321304	56.7	162.0	76.3	154.7	287.1	148.2
EU456462.1	313333	4110.2	4157.6	5213.6	3419.5	3177.1	2869.7
AF001721.1	14020	68.9	111.0	131.5	113.5	80.5	49.4
DQ808884.1	176257	3901.6	6411.9	3880.1	7893.4	4597.0	5998.4
FJ881245.1	430739	2775.0	2235.4	3628.2	3123.6	2483.3	1571.5
DQ797115.1	199013	577.6	777.3	2059.4	541.6	1716.2	923.7
EF098232.1	184535	2768.0	3363.0	684.2	3731.0	3143.2	2746.0
FJ679670.1	524122	4365.5	2445.4	2710.6	4800.0	992.7	934.2
FJ681388.1	515129	2239.8	2003.5	1933.0	688.9	873.9	781.3
DQ825335.1	178362	31.8	37.2	55.9	50.1	131.8	42.9
EU452326.1	333914	2043.1	2413.6	2151.1	3950.1	3047.5	3998.3
FJ879304.1	411214	372.9	218.4	721.2	1211.9	91.8	72.4
AF371677.1	36892	49.3	54.4	124.0	80.5	73.8	51.8
EU344224.1	260496	258.8	596.1	3862.1	565.4	370.8	813.0
EU455186.1	333786	66.1	102.4	188.6	106.2	138.5	96.6
FJ834237.1	567961	394.4	501.2	611.6	246.0	1672.7	668.8
FJ367885.1	359911	67.3	120.0	228.8	94.6	62.4	83.7
FJ680195.1	530278	48.2	122.4	283.9	82.7	142.9	371.1
EU452990.1	332816	962.4	1259.1	731.4	285.8	573.3	510.9
EU462618.1	295074	1382.9	1396.3	582.9	2293.8	144.6	738.2
EU456680.1	318224	1852.1	1849.0	1769.4	3824.3	1322.1	3523.7
EF098586.1	188120	5992.9	5774.9	4240.3	6278.2	6171.2	6727.8
FJ678722.1	525789	2630.2	3110.3	1925.1	3321.7	5727.1	5870.0
DQ815697.1	163142	273.3	121.2	153.4	490.2	82.9	206.1
EU509978.1	268910	3127.0	2750.6	3029.4	3236.0	1938.5	1473.4
EU530167.1	258321	217.1	159.9	802.0	204.7	78.5	175.3
EU748382.1	323463	35.5	90.6	239.9	77.5	90.5	73.0
EU450938.1	306993	699.3	631.7	987.4	815.9	691.3	1019.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	23878
s__unclassified	23881
s__unclassified	23888
s__unclassified	23906
s__unclassified	23908
s__unclassified	23909
s__unclassified	23911
s__unclassified	23923
s__unclassified	23928
s__unclassified	23945
s__unclassified	23949
s__unclassified	23952
s__unclassified	23955
s__unclassified	23959
s__unclassified	23962
s__unclassified	23964
s__unclassified	23977
s__unclassified	23991
s__unclassified	24019
s__unclassified	24025
s__unclassified	24027
s__unclassified	24037
s__unclassified	24049
s__unclassified	24052
s__unclassified	24072
s__unclassified	24092
s__unclassified	24093
s__unclassified	24094
s__unclassified	24100
s__unclassified	24118
s__unclassified	24123
s__unclassified	24127
s__unclassified	24133
s__unclassified	24140
s__unclassified	24141
s__unclassified	24145
s__unclassified	24148
s__unclassified	24152
s__unclassified	24164
s__unclassified	24165
s__unclassified	24166

FJ370152.1 gg_id:362250 feces adult twins and mothers; TS56 clone TS56_a01a07
EU455391.1 gg_id:329314 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
AF371675.1 gg_id:106258 swine intestine clone p-653-a5
DQ799657.1 gg_id:173934 human fecal clone RL305aal88g06
EU503857.1 gg_id:275869 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01f04
EU344496.1 gg_id:261381 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU450979.1 gg_id:356010 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
FJ685073.1 gg_id:517182 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU453671.1 gg_id:314503 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S
FJ368515.1 gg_id:358624 feces adult twins and mothers; TS49 clone TS49_a01c05
EU456865.1 gg_id:337710 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EF614592.1 gg_id:234914 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU456162.1 gg_id:320303 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N
FJ680692.1 gg_id:523749 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680968.1 gg_id:521604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU457567.1 gg_id:336011 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
EU454285.1 gg_id:331683 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
FJ684591.1 gg_id:520237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ832915.1 gg_id:565563 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_13E02
FJ368425.1 gg_id:370307 feces adult twins and mothers; TS3 clone TS3_a04b11
EU457237.1 gg_id:339073 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
FJ678929.1 gg_id:519545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801232.1 gg_id:192443 human fecal clone RL116_aaf02b01
FJ681054.1 gg_id:521401 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FM874014.1 gg_id:369502 occupant source house mattress dust clone MB05B06
FJ679944.1 gg_id:520788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU467116.1 gg_id:297642 mongoose lemur feces clone ML_aae88f01
EU842491.1 gg_id:347828 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU006303.1 gg_id:257049 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
FJ364129.1 gg_id:366721 feces adult twins and mothers; TS150 clone TS150_a03d02
FJ880839.1 gg_id:435285 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU455671.1 gg_id:353454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EF098785.1 gg_id:182446 mouse cecum clone SWPT16_aaa04h06
EU344398.1 gg_id:261634 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ681916.1 gg_id:523731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU457797.1 gg_id:319812 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
DQ809672.1 gg_id:189574 human fecal clone RL184_aan82d09
EU461523.1 gg_id:299398 black rhinoceros feces clone RH_aaj91f01
EU763756.1 gg_id:324502 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
FJ372350.1 gg_id:360928 feces adult twins and mothers; TS9 clone TS9_a04e12
EU505012.1 gg_id:272499 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f02

FJ370152.1	362250	2420.7	3262.3	2853.8	2392.5	5042.3	3646.2
EU455391.1	329314	243.7	252.0	171.9	89.4	131.0	87.4
AF371675.1	106258	2128.3	2844.6	3931.1	1673.3	4436.3	4079.9
DQ799657.1	173934	113.8	84.5	165.2	87.8	76.4	49.7
EU503857.1	275869	1115.2	1102.4	1767.4	1030.5	723.1	829.9
EU344496.1	261381	936.9	1191.8	1180.7	989.6	2317.3	2668.8
EU450979.1	356010	659.9	659.7	298.2	94.7	93.8	88.4
FJ685073.1	517182	12606.4	12449.1	4908.5	10449.2	13139.5	14574.9
EU453671.1	314503	97.0	177.0	248.8	191.3	706.6	539.4
FJ368515.1	358624	4020.7	3795.0	3471.1	4128.9	5705.3	6430.4
EU456865.1	337710	10019.2	12199.3	7665.3	10125.8	17582.9	12795.4
EF614592.1	234914	6881.8	7370.6	6661.5	5259.8	7916.4	6126.3
EU456162.1	320303	2452.6	2534.0	1531.9	4069.7	3015.5	3851.2
FJ680692.1	523749	2437.9	2015.0	1864.5	1295.6	594.0	563.3
FJ680968.1	521604	3587.4	4197.5	6135.7	3360.7	4536.3	4988.0
EU457567.1	336011	1061.3	1662.3	1532.7	2695.9	3105.4	4700.0
EU454285.1	331683	6920.6	8793.2	2065.3	6957.1	5393.4	4289.8
FJ684591.1	520237	1082.9	447.9	738.9	283.3	197.0	184.3
FJ832915.1	565563	148.2	140.0	1443.5	117.8	164.2	234.8
FJ368425.1	370307	473.4	426.8	484.6	291.5	1467.4	1137.8
EU457237.1	339073	5065.6	3965.5	2549.5	6983.1	5488.6	7338.8
FJ678929.1	519545	7201.5	5842.4	5963.7	4735.3	5857.1	5224.0
DQ801232.1	192443	1109.0	979.6	645.3	623.0	1301.6	1111.6
FJ681054.1	521401	1598.3	1177.1	733.4	1498.1	2975.0	2794.2
FM874014.1	369502	1820.6	3633.4	557.7	272.1	706.7	677.7
FJ679944.1	520788	307.1	474.8	480.5	193.4	398.7	367.8
EU467116.1	297642	158.4	212.7	1029.7	165.5	92.4	267.0
EU842491.1	347828	1412.8	1841.8	2086.9	533.4	2719.7	2526.0
EU006303.1	257049	37.3	57.0	32.0	55.9	54.4	113.7
FJ364129.1	366721	6841.2	8927.4	6452.7	6497.7	8029.0	9843.2
FJ880839.1	435285	1633.4	2039.7	3000.5	1204.9	2300.2	1909.9
EU455671.1	353454	577.5	469.7	1855.1	332.4	317.4	381.9
EF098785.1	182446	10652.2	9474.4	4335.8	13410.9	10810.0	11181.4
EU344398.1	261634	1262.8	596.4	2265.1	1554.3	61.5	287.3
FJ681916.1	523731	1732.8	2131.9	1526.1	1032.6	2963.5	1753.3
EU457797.1	319812	6325.9	6700.2	5044.5	6883.4	7471.4	5906.5
DQ809672.1	189574	2106.3	2699.1	1019.2	3629.6	1438.3	600.6
EU461523.1	299398	4026.4	3570.7	2451.4	5752.0	1913.9	2534.2
EU763756.1	324502	16.7	29.7	23.2	47.9	58.1	21.1
FJ372350.1	360928	447.4	360.0	289.7	241.5	1380.5	1080.8
EU505012.1	272499	1230.5	816.0	752.7	3324.8	318.8	335.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus

s__unclassified	24176
s__unclassified	24177
s__unclassified	24185
s__unclassified	24186
s__unclassified	24190
s__unclassified	24193
s__unclassified	24195
s__unclassified	24199
s__unclassified	24200
s__unclassified	24205
s__unclassified	24207
s__unclassified	24209
s__unclassified	24211
s__unclassified	24212
s__unclassified	24213
s__unclassified	24221
s__unclassified	24223
s__unclassified	24228
s__unclassified	24229
s__unclassified	24230
s__unclassified	24233
s__unclassified	24235
s__unclassified	24236
s__unclassified	24238
s__unclassified	24242
s__unclassified	24243
s__unclassified	24245
s__unclassified	24248
s__unclassified	24252
s__unclassified	24255
s__unclassified	24257
s__unclassified	24258
s__unclassified	24261
s__unclassified	24266
s__unclassified	24268
s__unclassified	24269
s__unclassified	24270
s__unclassified	24272
s__unclassified	24276
s__unclassified	24281
s__unclassified	24286

EU766491.1 gg_id:331255 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
FJ880110.1 gg_id:452592 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU766273.1 gg_id:306643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU764369.1 gg_id:306379 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
EU381441.1 gg_id:266392 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
DQ794425.1 gg_id:181500 human fecal clone RL197_aah87e12
FJ833469.1 gg_id:584481 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_61E08
DQ797246.1 gg_id:177482 human fecal clone RL386_aao88h04
DQ794364.1 gg_id:188621 human fecal clone RL197_aah86e07
EU844552.1 gg_id:319145 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU381898.1 gg_id:261290 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
FJ363635.1 gg_id:366757 feces adult twins and mothers; TS14 clone TS14_a01e12
EU469257.1 gg_id:302339 Speke's gazelle feces clone SP3_h08_1
DQ797019.1 gg_id:199305 human fecal clone RL386_aao85h05
EU778230.1 gg_id:339621 feces clone RL388_aao94f07
DQ794527.1 gg_id:186724 human fecal clone RL240_aaj29b08
AB185762.1 gg_id:99824 rumen clone U29-C01
DQ794949.1 gg_id:180449 human fecal clone RL310_aam38c12
AF371657.1 gg_id:20421 swine intestine clone p-444-o3
DQ824117.1 gg_id:192060 human fecal clone RL204_aaj59e08
FJ366191.1 gg_id:358337 feces adult twins and mothers; TS25 clone TS25_a03g05
EF686576.1 gg_id:253222 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6
EU381470.1 gg_id:263808 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU766374.1 gg_id:325264 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
DQ794376.1 gg_id:183192 human fecal clone RL197_aah86g11
EU842292.1 gg_id:331206 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
AF371650.1 gg_id:34731 swine intestine clone p-1895-s962-3
EU766433.1 gg_id:350577 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU777196.1 gg_id:340572 Okapi feces clone OK1_g03_1
EU766213.1 gg_id:354961 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU381880.1 gg_id:260787 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
NR_024661.1 gg_id:573803 Eubacterium ruminantium str. GA195; ATCC 17233
FJ833266.1 gg_id:538611 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_49A07
EU843008.1 gg_id:343422 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU778151.1 gg_id:343981 feces clone RL388_aao96e11
DQ824189.1 gg_id:194572 human fecal clone RL204_aaj60f02
AY854269.2 gg_id:109798 herbivore gastrointestinal tract clone CATTLE_7
NZ_AAYW02000018.1 gg_id:469946 Clostridium sp. str. L2-50
EU344603.1 gg_id:268215 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
DQ824605.1 gg_id:177984 human fecal clone RL185_aaj70c10
EU844383.1 gg_id:322159 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi

EU766491.1	331255	123.5	134.7	228.7	175.7	78.0	97.3
FJ880110.1	452592	5287.9	6579.4	4116.0	3614.5	6704.4	6350.8
EU766273.1	306643	3063.1	1854.3	694.2	445.6	219.8	119.8
EU764369.1	306379	27.5	43.4	53.1	57.1	50.1	25.3
EU381441.1	266392	258.8	573.7	1184.6	321.4	2054.5	1476.2
DQ794425.1	181500	11832.9	12120.7	6407.5	9131.7	12930.4	12351.2
FJ833469.1	584481	1124.5	1698.0	896.9	758.3	490.1	485.1
DQ797246.1	177482	3232.2	3472.3	2686.4	4270.8	5352.3	4389.2
DQ794364.1	188621	152.8	208.7	230.0	95.0	527.4	222.5
EU844552.1	319145	2030.3	1084.8	2479.6	1026.4	124.3	434.1
EU381898.1	261290	502.4	326.9	945.8	275.4	156.1	547.9
FJ363635.1	366757	2292.8	2526.4	2218.2	2065.0	3998.6	3898.6
EU469257.1	302339	172.8	320.6	706.5	173.1	688.1	804.4
DQ797019.1	199305	71.4	44.1	233.9	87.9	57.1	43.8
EU778230.1	339621	2111.3	2847.8	698.5	1296.5	57.9	1371.0
DQ794527.1	186724	9549.6	8072.5	7176.8	6603.5	8889.3	7310.6
AB185762.1	99824	2890.0	3416.9	2557.7	3470.8	4978.8	4041.2
DQ794949.1	180449	4661.7	5462.3	341.8	4836.3	1691.0	1464.2
AF371657.1	20421	2273.2	1381.8	1840.4	2026.9	1055.4	1280.7
DQ824117.1	192060	818.3	1066.9	350.5	447.5	152.7	601.3
FJ366191.1	358337	8796.5	10253.4	3269.9	6060.9	5194.9	5765.5
EF686576.1	253222	1987.4	2088.5	4625.0	1098.2	523.4	1374.3
EU381470.1	263808	3216.0	1619.5	4233.5	3458.5	1095.2	2204.0
EU766374.1	325264	6957.6	5327.0	5728.0	8327.8	4391.2	5439.7
DQ794376.1	183192	695.1	819.9	291.2	3742.8	990.5	1075.2
EU842292.1	331206	1431.3	1304.5	1560.3	580.1	173.6	188.1
AF371650.1	34731	1276.4	1784.4	4869.6	1873.1	1548.1	2013.3
EU766433.1	350577	958.5	950.0	980.1	1327.8	1809.8	2423.7
EU777196.1	340572	4073.6	4682.7	1285.7	3651.9	1802.6	2456.2
EU766213.1	354961	6086.0	4880.3	6473.2	4596.0	5871.5	5850.4
EU381880.1	260787	468.9	631.2	685.9	467.7	637.7	698.4
NR_024661.1	573803	689.8	1198.5	1771.9	563.2	1719.2	1741.2
FJ833266.1	538611	1694.6	2740.1	1424.0	1276.4	1190.7	1871.5
EU843008.1	343422	1463.8	1397.5	778.0	1202.6	181.5	463.4
EU778151.1	343981	1750.8	1377.0	2868.6	5170.9	2140.4	3621.1
DQ824189.1	194572	128.7	201.8	107.2	153.8	67.5	96.2
AY854269.2	109798	3047.0	3030.6	3222.2	643.1	7031.1	5873.2
NZ_AAYW02000018.1	469946	758.7	903.8	1838.2	468.8	397.1	651.7
EU344603.1	268215	1589.5	1874.4	3004.7	1638.6	3485.0	3664.4
DQ824605.1	177984	2147.4	2508.5	3088.4	5125.0	3656.5	4157.9
EU844383.1	322159	5602.4	3828.8	5096.0	5954.4	2687.6	3020.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Coprococcus
g__Dorea
g__Dorea

s__unclassified	24288
s__unclassified	24293
s__unclassified	24300
s__unclassified	24308
s__unclassified	24313
s__unclassified	24314
s__unclassified	24318
s__unclassified	24319
s__unclassified	24321
s__unclassified	24323
s__unclassified	24326
s__unclassified	24327
s__unclassified	24328
s__unclassified	24330
s__unclassified	24331
s__unclassified	24334
s__unclassified	24337
s__unclassified	24343
s__unclassified	24345
s__unclassified	24348
s__unclassified	24349
s__unclassified	24351
s__unclassified	24352
s__unclassified	24354
s__unclassified	24355
s__unclassified	24359
s__unclassified	24363
s__unclassified	24366
s__unclassified	24367
s__unclassified	24368
s__unclassified	24370
s__unclassified	24372
s__unclassified	24374
s__unclassified	24377
s__unclassified	24380
s__unclassified	24381
s__unclassified	24383
s__unclassified	24385
s__unclassified	27620
s__Dorea formicigenerans	18387
s__Dorea formicigenerans	18552

FJ881307.1 gg_id:430497 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU764626.1 gg_id:353279 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ680393.1 gg_id:514136 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU764391.1 gg_id:340570 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
EU381742.1 gg_id:274577 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
AB034069.1 gg_id:23219 rumen clone 5C3d-11
DQ794599.1 gg_id:198802 human fecal clone RL240_aaj30b01
EU748298.1 gg_id:327252 neotropical folivorous flying bird adult hoatzin crop clone hoa46_69E09
EU771329.1 gg_id:346606 Asiatic elephant feces clone AE2_aaa04a09
EU766512.1 gg_id:322878 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU842325.1 gg_id:341204 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU471590.1 gg_id:300123 Asiatic elephant feces clone AE1_aaa03b02
EF445162.1 gg_id:209524 rabbit cecum clone NED3B2
EU766402.1 gg_id:326396 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU748309.1 gg_id:322189 neotropical folivorous flying bird adult hoatzin crop clone hoa46_33A05
AY442828.1 gg_id:100506 culturable kangaroo Macropus giganteus Eastern grey Kangaroo forestomach conter
AY985384.1 gg_id:124285 human stool clone C321
AB034025.1 gg_id:25995 rumen clone 4C0d-12
EU778254.1 gg_id:354254 feces clone RL387_aao89b04
DQ799915.1 gg_id:195196 human fecal clone RL247_aaj21g12
EU766173.1 gg_id:324453 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
DQ801370.1 gg_id:182943 human fecal clone RL388_aao94f01
DQ801418.1 gg_id:196850 human fecal clone RL388_aao95c06
EU764601.1 gg_id:346821 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
EU381551.1 gg_id:274876 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU842621.1 gg_id:342811 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU381639.1 gg_id:266062 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU766527.1 gg_id:345136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU622773.1 gg_id:278439 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
DQ794497.1 gg_id:174019 human fecal clone RL197_aah88f11
FJ681890.1 gg_id:524260 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795023.1 gg_id:182681 human fecal clone RL310_aam39c06
AY985444.1 gg_id:127752 human stool clone C391
AB185807.1 gg_id:103066 rumen clone U29-G09
EF436389.1 gg_id:209741 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC103
EU843953.1 gg_id:324835 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU764717.1 gg_id:356540 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ833666.1 gg_id:571186 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_91C12
EU774771.1 gg_id:345211 Angola Colobus feces clone EAC_1aaa01e02
NZ_AAXA02000006.1 gg_id:270584 Dorea formicigenerans str. ATCC 27755
NZ_AAXA02000015.1 gg_id:470237 Dorea formicigenerans str. ATCC 27755

FJ881307.1	430497	256.9	623.0	294.2	369.1	1642.6	1538.9
EU764626.1	353279	3286.1	1011.0	1422.1	3715.3	2994.8	2639.2
FJ680393.1	514136	10115.1	10018.8	4821.6	10166.4	7538.8	7917.8
EU764391.1	340570	4527.9	4923.8	8849.5	7748.7	4053.5	5352.2
EU381742.1	274577	197.6	135.6	697.9	163.7	162.8	777.7
AB034069.1	23219	39.4	55.6	59.6	69.4	67.8	27.9
DQ794599.1	198802	3299.5	2786.5	1454.1	2558.9	6743.8	4643.5
EU748298.1	327252	675.4	1267.3	1046.7	1987.4	391.5	797.9
EU771329.1	346606	511.5	659.6	2884.0	415.3	1152.2	1060.1
EU766512.1	322878	1917.9	3962.5	2321.7	1888.7	5463.3	3742.4
EU842325.1	341204	713.6	468.6	1665.6	347.8	425.2	912.4
EU471590.1	300123	2365.5	3414.7	2032.5	2140.8	4949.6	4382.4
EF445162.1	209524	48.6	64.8	69.0	60.8	70.2	31.7
EU766402.1	326396	2015.6	3771.4	2402.4	2914.1	5011.8	4829.9
EU748309.1	322189	9741.4	9509.5	6229.4	8803.3	9353.2	14477.9
AY442828.1	100506	29.1	35.7	35.8	69.5	207.5	47.8
AY985384.1	124285	5509.7	4817.4	3758.6	4434.9	8573.3	6594.5
AB034025.1	25995	3254.7	2393.2	2072.1	1493.0	2581.2	2280.7
EU778254.1	354254	567.3	443.2	1003.7	965.3	812.4	1284.6
DQ799915.1	195196	1132.0	275.5	1524.8	576.5	2463.2	1594.5
EU766173.1	324453	31.6	47.2	51.4	60.4	58.2	31.3
DQ801370.1	182943	9439.9	10400.6	3916.1	7876.2	10579.1	7557.6
DQ801418.1	196850	49.9	116.0	68.7	55.4	87.1	44.3
EU764601.1	346821	404.2	283.4	413.6	740.2	95.5	143.6
EU381551.1	274876	2565.4	2535.2	3129.3	3336.6	2697.3	4102.3
EU842621.1	342811	965.0	803.3	3189.8	639.3	244.1	819.2
EU381639.1	266062	4951.7	6528.0	8544.0	6475.6	3898.2	4744.8
EU766527.1	345136	1833.0	2291.3	1599.9	747.1	3433.4	3263.8
EU622773.1	278439	1301.2	1821.9	2330.7	1549.9	2865.6	3038.2
DQ794497.1	174019	237.0	404.5	290.2	392.7	1230.3	350.3
FJ681890.1	524260	3893.7	4298.2	3265.7	4407.1	4998.6	5350.9
DQ795023.1	182681	35.9	25.0	35.8	67.1	345.1	75.3
AY985444.1	127752	497.0	496.9	1734.3	335.8	150.4	296.6
AB185807.1	103066	30.9	47.9	62.2	73.9	70.1	24.5
EF436389.1	209741	914.1	1281.0	1266.7	471.6	1081.6	1076.8
EU843953.1	324835	413.8	468.3	299.6	282.6	310.3	205.5
EU764717.1	356540	560.7	402.1	1665.2	780.4	381.5	556.4
FJ833666.1	571186	2052.0	1769.4	2024.2	908.0	1830.5	1202.5
EU774771.1	345211	53.2	69.8	121.9	111.0	71.0	27.7
NZ_AAXA02000006.1	270584	206.5	209.4	274.2	277.8	184.0	164.9
NZ_AAXA02000015.1	470237	1701.6	1277.8	2243.5	1333.6	258.2	373.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea

s__Dorea formicigenerans	18587
s__Dorea formicigenerans	18646
s__Dorea formicigenerans	18727
s__Dorea formicigenerans	18935
s__Dorea formicigenerans	19005
s__Dorea formicigenerans	19022
s__Dorea formicigenerans	19057
s__Dorea formicigenerans	19113
s__Dorea formicigenerans	19276
s__unclassified	18378
s__unclassified	18410
s__unclassified	18414
s__unclassified	18429
s__unclassified	18430
s__unclassified	18434
s__unclassified	18461
s__unclassified	18492
s__unclassified	18499
s__unclassified	18526
s__unclassified	18531
s__unclassified	18535
s__unclassified	18551
s__unclassified	18642
s__unclassified	18666
s__unclassified	18687
s__unclassified	18712
s__unclassified	18722
s__unclassified	18725
s__unclassified	18740
s__unclassified	18744
s__unclassified	18747
s__unclassified	18763
s__unclassified	18800
s__unclassified	18847
s__unclassified	18850
s__unclassified	18866
s__unclassified	18869
s__unclassified	18886
s__unclassified	18888
s__unclassified	18899
s__unclassified	18917

AY982268.1 gg_id:122518 human sigmoid colon mucosal biopsy clone MI08
AY976232.1 gg_id:127502 human ascending colon mucosal biopsy clone LW62
FJ364307.1 gg_id:357959 feces adult twins and mothers; TS15 clone TS15_a01d08
AY984686.1 gg_id:124107 human stool clone B638
NZ_AAXA02000014.1 gg_id:261912 Dorea formicigenerans str. ATCC 27755
NZ_AAXA02000007.1 gg_id:470229 Dorea formicigenerans str. ATCC 27755
AY976895.1 gg_id:127343 human cecum mucosal biopsy clone K540
NZ_AAXA02000015.1 gg_id:470238 Dorea formicigenerans str. ATCC 27755
NZ_AAXA02000016.1 gg_id:470230 Dorea formicigenerans str. ATCC 27755
GQ491673.1 gg_id:592412 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY979418.1 gg_id:118945 human transverse colon mucosal biopsy clone M021
EF399958.1 gg_id:215996 human fecal clone SJTU_E_06_56
AY979373.1 gg_id:117508 human transverse colon mucosal biopsy clone Z722
AY981371.1 gg_id:119304 human sigmoid colon mucosal biopsy clone G395
FJ370209.1 gg_id:366476 feces adult twins and mothers; TS56 clone TS56_a01g09
AY983402.1 gg_id:116631 human descending colon mucosal biopsy clone A582
AY983685.1 gg_id:118813 human descending colon mucosal biopsy clone NP92
AY978285.1 gg_id:127553 human transverse colon mucosal biopsy clone F145
FJ362919.1 gg_id:364583 feces adult twins and mothers; TS13 clone TS13_a04g06
AY979732.1 gg_id:118674 human transverse colon mucosal biopsy clone M475
AY975739.1 gg_id:115877 human ascending colon mucosal biopsy clone Y189
EU530238.1 gg_id:275687 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader
DQ327389.1 gg_id:145925 Metagenomic gut microbiome healthy human stool clone E947
AY979917.1 gg_id:123588 human rectum mucosal biopsy clone E239
AY983171.1 gg_id:123677 human descending colon mucosal biopsy clone A067
AF357564.1 gg_id:70405 mpn-isolate group 16
FJ365595.1 gg_id:359355 feces adult twins and mothers; TS20 clone TS20_a04g02
FJ371402.1 gg_id:367855 feces adult twins and mothers; TS6 clone TS6_a04e07
FJ368583.1 gg_id:369057 feces adult twins and mothers; TS49 clone TS49_a02a06
AY981801.1 gg_id:127835 human sigmoid colon mucosal biopsy clone NU02
FJ369873.1 gg_id:358282 feces adult twins and mothers; TS55 clone TS55_a01g06
AY977989.1 gg_id:115924 human cecum mucosal biopsy clone LH22
AY983625.1 gg_id:116382 human descending colon mucosal biopsy clone NO65
FJ371197.1 gg_id:359382 feces adult twins and mothers; TS6 clone TS6_a02a10
AY981721.1 gg_id:120659 human sigmoid colon mucosal biopsy clone LB02
AY978748.1 gg_id:123331 human transverse colon mucosal biopsy clone KU94
FJ368698.1 gg_id:363888 feces adult twins and mothers; TS49 clone TS49_a03d10
AY975351.1 gg_id:116850 human ascending colon mucosal biopsy clone N632
FJ365936.1 gg_id:365459 feces adult twins and mothers; TS21 clone TS21_a04h04
AY982434.1 gg_id:117037 human sigmoid colon mucosal biopsy clone ML48
FJ365581.1 gg_id:359797 feces adult twins and mothers; TS20 clone TS20_a04e09

AY982268.1	122518	3836.4	6054.2	642.4	2317.0	1027.5	1657.3
AY976232.1	127502	147.8	66.2	342.7	104.1	115.6	109.6
FJ364307.1	357959	312.1	154.1	336.2	142.0	199.3	137.3
AY984686.1	124107	7083.4	8026.9	5543.7	7976.1	11573.2	12410.7
NZ_AAXA02000014.1	261912	1264.5	712.6	1522.3	1244.0	157.5	180.3
NZ_AAXA02000007.1	470229	1376.3	937.5	2125.5	1301.7	259.2	303.8
AY976895.1	127343	593.7	1155.5	471.3	71.7	74.2	108.6
NZ_AAXA02000015.1	470238	1495.0	1254.7	1679.6	1405.9	159.7	165.3
NZ_AAXA02000016.1	470230	1546.4	1346.1	1764.7	1577.5	239.8	288.9
GQ491673.1	592412	337.2	363.6	490.2	396.8	81.0	36.3
AY979418.1	118945	1039.5	2108.3	650.9	665.5	1657.7	1641.1
EF399958.1	215996	1090.0	478.8	1058.6	1150.0	182.7	147.7
AY979373.1	117508	479.9	689.3	711.7	195.6	890.0	816.9
AY981371.1	119304	21.6	31.7	59.0	51.0	73.5	35.1
FJ370209.1	366476	448.9	370.6	381.4	249.8	85.7	97.4
AY983402.1	116631	141.2	78.6	295.0	105.5	57.8	90.9
AY983685.1	118813	363.0	501.7	438.2	137.8	121.4	156.3
AY978285.1	127553	271.2	365.8	669.2	184.1	775.8	773.9
FJ362919.1	364583	6311.3	5838.1	3801.6	5591.2	8676.7	8869.8
AY979732.1	118674	251.5	307.4	636.5	151.3	139.1	213.5
AY975739.1	115877	273.6	309.5	634.8	150.5	139.1	212.3
EU530238.1	275687	3239.8	4589.2	2572.3	2458.1	2570.9	3790.2
DQ327389.1	145925	4372.8	6992.2	3299.7	4588.5	4665.6	4011.2
AY979917.1	123588	28.3	49.3	152.9	68.1	96.0	75.2
AY983171.1	123677	228.3	336.6	188.0	79.5	136.5	97.2
AF357564.1	70405	1043.8	1110.9	1837.2	1978.5	441.2	721.3
FJ365595.1	359355	241.0	595.6	138.6	114.7	256.9	221.9
FJ371402.1	367855	821.6	1648.3	1237.5	1107.0	2642.2	2715.2
FJ368583.1	369057	158.0	256.1	338.3	107.1	135.6	166.4
AY981801.1	127835	14200.1	8938.5	10604.3	8888.0	10577.6	11353.1
FJ369873.1	358282	271.7	311.6	622.2	151.8	136.8	207.5
AY977989.1	115924	173.6	158.6	441.6	109.3	162.5	120.3
AY983625.1	116382	1215.7	1921.8	884.3	316.6	256.3	399.5
FJ371197.1	359382	554.9	662.7	351.5	407.1	76.2	41.3
AY981721.1	120659	141.1	275.0	172.0	72.3	113.7	109.3
AY978748.1	123331	32.7	48.1	153.1	64.8	97.4	74.6
FJ368698.1	363888	157.6	253.5	83.5	135.9	167.7	1037.9
AY975351.1	116850	62.6	29.1	155.0	67.3	47.1	32.8
FJ365936.1	365459	5697.8	5834.7	4777.0	4654.9	7451.3	6155.8
AY982434.1	117037	641.8	1450.5	1180.5	752.8	2462.6	2841.2
FJ365581.1	359797	6217.7	9403.7	3755.1	4369.2	6469.2	9831.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Dorea
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Epulopiscium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium

s__unclassified	18922
s__unclassified	18924
s__unclassified	18986
s__unclassified	19002
s__unclassified	19078
s__unclassified	19087
s__unclassified	19089
s__unclassified	19150
s__unclassified	19172
s__unclassified	19179
s__unclassified	19185
s__unclassified	19192
s__unclassified	19232
s__unclassified	19241
s__unclassified	19267
s__unclassified	19307
s__unclassified	19312
s__unclassified	19325
s__unclassified	19367
s__unclassified	19376
s__unclassified	19389
s__unclassified	19394
s__Epulopiscium sp.	27320
s__Epulopiscium sp.	27519
s__Epulopiscium sp.	27598
s__Epulopiscium sp.	27805
s__unclassified	27441
s__unclassified	27582
s__unclassified	27678
s__unclassified	27763
s__unclassified	27910
s__unclassified	27934
s__unclassified	27961
s__unclassified	28149
s__Eubacterium cellulosolvens	23792
s__Eubacterium cellulosolvens	23899
s__unclassified	17862
s__unclassified	18015
s__unclassified	18504
s__unclassified	19049
s__unclassified	19390

FJ367363.1 gg_id:362982 feces adult twins and mothers; TS29 clone TS29_a02f03
FJ365317.1 gg_id:366565 feces adult twins and mothers; TS20 clone TS20_a01d12
AY979478.1 gg_id:119402 human transverse colon mucosal biopsy clone M104
DQ326308.1 gg_id:145731 Metagenomic gut microbiome healthy human stool clone C279
FJ367538.1 gg_id:363533 feces adult twins and mothers; TS29 clone TS29_a04g03
AY976662.1 gg_id:119238 human cecum mucosal biopsy clone K229
FJ369025.1 gg_id:360317 feces adult twins and mothers; TS4 clone TS4_a03d06
EU762250.1 gg_id:309236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A›
FJ370139.1 gg_id:359846 feces adult twins and mothers; TS55 clone TS55_a04h02
AY982186.1 gg_id:119083 human sigmoid colon mucosal biopsy clone MG65
AY979159.1 gg_id:119223 human transverse colon mucosal biopsy clone Z211
DQ796594.1 gg_id:184918 human fecal clone RL179aan75e08
DQ327584.1 gg_id:150493 Metagenomic gut microbiome healthy human stool clone EB69
GQ491661.1 gg_id:558736 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ368807.1 gg_id:365239 feces adult twins and mothers; TS49 clone TS49_a04g10
FJ365443.1 gg_id:360796 feces adult twins and mothers; TS20 clone TS20_a02h09
FJ365464.1 gg_id:367576 feces adult twins and mothers; TS20 clone TS20_a03c01
EF401324.1 gg_id:204922 human fecal clone SJTU_D_08_81
AY977329.1 gg_id:119218 human cecum mucosal biopsy clone MV44
FJ367466.1 gg_id:365137 feces adult twins and mothers; TS29 clone TS29_a03h07
AY981492.1 gg_id:119712 human sigmoid colon mucosal biopsy clone L596
AY977315.1 gg_id:116123 human cecum mucosal biopsy clone MV19
M99573.1 gg_id:14129 Epulopiscium sp str. morphotype A2
AF067413.1 gg_id:14121 Epulopiscium fishelsoni str. Red Sea A1
AF067414.1 gg_id:14130 Epulopiscium fishelsoni str. Red Sea A2
M99574.1 gg_id:14128 Epulopiscium sp str. morphotype B
GQ340245.1 gg_id:580674 Prokaryotic Marathonas Reservoir Greece water column clone VE07-92-BAC
AM500767.1 gg_id:558007 proof spatial heterogeneity hot composting clone E6
EU468764.1 gg_id:294143 okapi feces clone OK3_c09_1
DQ113748.1 gg_id:136518 dog duodenum clone D1-26
U22331.1 gg_id:14126 "Metabacterium polyspora"
EU475028.1 gg_id:291710 red river hog feces clone RRH_aaa02f06
EU470379.1 gg_id:299376 Grevy's zebra feces clone GZ_aaa01c09
U22332.1 gg_id:14127 "Metabacterium polyspora"
X71860.1 gg_id:13988 Eubacterium cellulosolvens 6 str. ATCC 43171
AB372004.1 gg_id:312201 Eubacterium cellulosolvens str. NE13
DQ824305.1 gg_id:192536 human fecal clone RL304_aal74c01
EU778103.1 gg_id:332313 feces clone RL387_aao89a11.Contig2
DQ795815.1 gg_id:196272 human fecal clone RL245_aai82g10
DQ801788.1 gg_id:197940 human fecal clone RL201_aai46g10
DQ805487.1 gg_id:189396 human fecal clone RL203_aai63c09

FJ367363.1	362982	1155.5	1258.4	1201.9	1940.7	687.1	1840.4
FJ365317.1	366565	1409.1	1063.8	1174.8	2736.8	529.8	1290.4
AY979478.1	119402	21.4	67.7	261.0	74.4	158.2	115.9
DQ326308.1	145731	5604.8	5532.4	3288.6	4606.6	4096.8	4589.5
FJ367538.1	363533	3953.8	3577.7	1407.7	4429.3	6471.7	4693.9
AY976662.1	119238	48.6	77.0	34.1	52.9	49.1	27.7
FJ369025.1	360317	1047.9	1397.9	1263.6	106.4	263.7	429.9
EU762250.1	309236	3448.8	4540.6	2259.3	2160.7	4494.7	4065.8
FJ370139.1	359846	290.6	352.2	318.4	353.4	75.2	17.7
AY982186.1	119083	473.4	896.0	1603.5	678.4	1990.3	1525.2
AY979159.1	119223	36.7	50.4	160.7	70.0	99.9	79.1
DQ796594.1	184918	7433.2	7010.5	2915.6	5901.1	4447.6	4413.1
DQ327584.1	150493	994.3	926.3	835.1	340.0	288.1	250.4
GQ491661.1	558736	3790.3	3923.2	4554.9	5552.0	8755.4	9856.8
FJ368807.1	365239	914.9	926.5	980.8	482.6	200.2	323.7
FJ365443.1	360796	138.9	180.1	203.3	121.0	379.4	361.0
FJ365464.1	367576	24.7	29.1	114.6	65.5	56.3	51.4
EF401324.1	204922	1474.7	1259.7	2103.8	1383.8	247.6	356.0
AY977329.1	119218	956.5	1656.7	1557.0	780.5	2589.7	2650.9
FJ367466.1	365137	952.4	463.0	1275.0	1818.0	293.8	269.9
AY981492.1	119712	499.7	1002.3	1163.5	215.6	1214.4	1477.1
AY977315.1	116123	2201.2	2506.9	1409.6	3059.7	6953.0	5071.3
M99573.1	14129	2824.2	2833.6	2639.6	2134.2	1172.6	2398.6
AF067413.1	14121	31.6	53.9	63.5	43.0	66.4	281.7
AF067414.1	14130	3024.9	3525.2	2470.2	2993.9	5778.6	7046.8
M99574.1	14128	1187.4	752.6	882.6	1091.7	623.1	1014.5
GQ340245.1	580674	4785.4	3937.8	6905.4	3193.4	4443.3	5569.8
AM500767.1	558007	22.7	72.9	164.0	94.6	59.0	77.2
EU468764.1	294143	2899.2	4429.4	5087.2	5103.2	6944.6	5333.8
DQ113748.1	136518	57.8	70.5	56.9	76.2	148.6	39.8
U22331.1	14126	638.6	1625.2	1148.3	1045.3	192.8	406.0
EU475028.1	291710	2491.1	2085.3	3589.8	4422.1	2425.4	3355.4
EU470379.1	299376	46.4	80.8	206.6	94.8	66.5	239.1
U22332.1	14127	2976.0	3688.3	1302.3	2304.6	3946.6	3070.7
X71860.1	13988	35.5	49.5	79.8	71.3	72.2	36.7
AB372004.1	312201	256.5	143.5	293.6	382.8	137.2	375.8
DQ824305.1	192536	22.1	32.8	28.3	57.6	62.0	26.9
EU778103.1	332313	66.0	92.4	428.3	99.8	145.9	108.2
DQ795815.1	196272	59.7	90.1	85.0	89.6	75.0	53.6
DQ801788.1	197940	4310.5	4182.7	7566.4	4055.0	6708.6	4604.2
DQ805487.1	189396	397.7	335.7	839.7	174.5	276.0	174.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium

s__unclassified	19401
s__unclassified	19727
s__unclassified	19799
s__unclassified	19916
s__unclassified	20107
s__unclassified	20286
s__unclassified	20747
s__unclassified	20852
s__unclassified	20937
s__unclassified	20938
s__unclassified	21053
s__unclassified	21347
s__unclassified	21534
s__unclassified	21557
s__unclassified	22616
s__unclassified	22632
s__unclassified	22638
s__unclassified	22639
s__unclassified	22643
s__unclassified	22644
s__unclassified	22647
s__unclassified	22650
s__unclassified	22671
s__unclassified	22674
s__unclassified	22678
s__unclassified	22679
s__unclassified	22687
s__unclassified	22696
s__unclassified	22698
s__unclassified	22699
s__unclassified	22700
s__unclassified	22704
s__unclassified	22708
s__unclassified	22715
s__unclassified	22717
s__unclassified	22720
s__unclassified	22721
s__unclassified	22725
s__unclassified	22726
s__unclassified	22731
s__unclassified	22733

DQ798666.1 gg_id:181876 human fecal clone RL181_aan99g07
EU464403.1 gg_id:290405 hamadryas baboon feces clone AFBAB_aai04d09
EU464298.1 gg_id:292341 hamadryas baboon feces clone AFBAB_aai02b02
AY960569.1 gg_id:114929 Ruminococcus sp. str. ID1
EU464283.1 gg_id:299741 hamadryas baboon feces clone AFBAB_aai01f10
EU464338.1 gg_id:295189 hamadryas baboon feces clone AFBAB_aai03a06
DQ804789.1 gg_id:182724 human fecal clone RL187_aao72g02
FJ676752.1 gg_id:522551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU381497.1 gg_id:275224 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU773576.1 gg_id:312780 Goeldi's Marmoset feces clone CAL_g05
DQ085084.1 gg_id:137650 goat rumen clone A10
EU530321.1 gg_id:273681 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
DQ071485.1 gg_id:233103 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc8
DQ797410.1 gg_id:195175 human fecal clone RL248_aai99a05
EU466910.1 gg_id:288208 African elephant feces clone AFEL2_aao31c03
FJ364061.1 gg_id:366656 feces adult twins and mothers; TS150 clone TS150_a02e06
FJ363785.1 gg_id:363228 feces adult twins and mothers; TS14 clone TS14_a03c11
FJ677666.1 gg_id:527303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798613.1 gg_id:198740 human fecal clone RL181_aan99a06
AJ408978.1 gg_id:111446 human colonic clone HuCA27
FJ362772.1 gg_id:357827 feces adult twins and mothers; TS13 clone TS13_a03a04
DQ824940.1 gg_id:181111 human fecal clone RL185_aao71c06
GQ493324.1 gg_id:580898 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AY977502.1 gg_id:127727 human cecum mucosal biopsy clone W257
DQ796051.1 gg_id:177746 human fecal clone RL202_aai50g07
DQ795677.1 gg_id:180329 human fecal clone RL178_aan68d01
DQ823941.1 gg_id:174799 human fecal clone RL204_aaj57c01
FJ372061.1 gg_id:366033 feces adult twins and mothers; TS9 clone TS9_a01c12
DQ797635.1 gg_id:180628 human fecal clone RL206_aaj14a05
DQ795675.1 gg_id:190177 human fecal clone RL178_aan68c05
DQ798351.1 gg_id:189315 human fecal clone RL181_aah41d03
DQ795022.1 gg_id:176238 human fecal clone RL310_aam39c05
GQ897243.1 gg_id:539595 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ674180.1 gg_id:518553 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795460.1 gg_id:175261 human fecal clone RL178_aah54f04
FJ683955.1 gg_id:529512 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679615.1 gg_id:512352 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ685186.1 gg_id:516143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ794499.1 gg_id:184670 human fecal clone RL197_aah88g03
DQ801131.1 gg_id:189661 human fecal clone RL387_aao92g01
DQ796378.1 gg_id:196021 human fecal clone RL179_aah26e02

DQ798666.1	181876	1920.5	2403.1	3690.7	2397.4	2512.1	3653.6
EU464403.1	290405	1377.0	1303.9	749.1	184.8	375.9	947.3
EU464298.1	292341	172.7	363.0	927.4	258.1	861.3	984.0
AY960569.1	114929	483.7	484.7	620.5	355.1	163.1	1262.3
EU464283.1	299741	72.3	73.8	221.1	82.7	75.8	99.1
EU464338.1	295189	1326.6	991.1	1384.5	2884.8	234.4	363.2
DQ804789.1	182724	24.7	33.0	50.9	63.8	68.0	19.6
FJ676752.1	522551	4193.7	4101.7	2107.1	2507.7	3209.2	3475.9
EU381497.1	275224	270.8	533.4	716.4	335.6	325.8	486.0
EU773576.1	312780	2219.3	1726.4	779.2	2225.5	207.3	534.3
DQ085084.1	137650	4912.2	4710.3	4490.6	5656.8	4647.2	5131.0
EU530321.1	273681	60.5	92.8	337.2	73.8	99.6	57.9
DQ071485.1	233103	18.0	34.1	41.9	52.6	55.9	23.6
DQ797410.1	195175	4215.9	4444.6	3235.0	2551.9	4241.2	4171.4
EU466910.1	288208	1565.3	1693.6	2604.1	3445.2	1435.6	2733.8
FJ364061.1	366656	949.5	1435.9	2526.5	989.9	1104.0	2013.2
FJ363785.1	363228	41.9	83.6	181.8	84.7	138.7	101.7
FJ677666.1	527303	3529.0	4519.4	2839.4	4194.8	7004.7	5168.0
DQ798613.1	198740	2266.1	1655.7	2594.9	1530.6	1591.9	1528.2
AJ408978.1	111446	463.1	514.5	916.1	842.4	847.1	1157.0
FJ362772.1	357827	395.9	326.5	673.7	686.9	173.1	215.7
DQ824940.1	181111	33.3	34.5	143.1	67.6	262.8	151.7
GQ493324.1	580898	2778.7	3215.3	1607.5	2081.2	2841.7	2714.8
AY977502.1	127727	5591.3	6030.5	4711.6	4779.9	6440.6	4865.5
DQ796051.1	177746	10034.2	11881.6	7457.6	6432.7	11057.6	8777.2
DQ795677.1	180329	239.6	582.0	1296.7	155.1	511.7	448.6
DQ823941.1	174799	4620.1	6572.2	4077.0	2531.5	9142.9	6857.2
FJ372061.1	366033	971.9	1423.5	1505.3	1222.4	1876.5	1469.9
DQ797635.1	180628	8131.7	4233.5	6475.0	7234.4	8185.3	7049.9
DQ795675.1	190177	14376.6	17831.7	10657.4	11807.9	18193.6	14688.4
DQ798351.1	189315	10983.6	11872.6	6527.1	8638.3	9291.8	9361.6
DQ795022.1	176238	224.9	249.1	189.3	94.2	89.4	56.1
GQ897243.1	539595	7053.4	4713.5	1849.3	5766.4	7908.4	8027.9
FJ674180.1	518553	3298.0	910.4	1586.1	3744.4	3008.6	2263.7
DQ795460.1	175261	35.9	39.9	61.4	60.0	54.7	50.6
FJ683955.1	529512	4831.9	5247.1	3859.0	4709.8	9572.4	6765.1
FJ679615.1	512352	248.6	158.8	146.6	1739.4	140.5	152.8
FJ685186.1	516143	1852.8	2449.2	3525.4	1763.6	3544.3	3212.4
DQ794499.1	184670	14.4	101.5	236.7	95.0	53.4	20.9
DQ801131.1	189661	628.7	1219.5	2036.7	402.4	896.3	1124.4
DQ796378.1	196021	39.9	49.8	62.1	81.2	53.6	36.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium

s__unclassified	22735
s__unclassified	22737
s__unclassified	22750
s__unclassified	22751
s__unclassified	22758
s__unclassified	22759
s__unclassified	22764
s__unclassified	22777
s__unclassified	22778
s__unclassified	22782
s__unclassified	22788
s__unclassified	22803
s__unclassified	22805
s__unclassified	22806
s__unclassified	22812
s__unclassified	22821
s__unclassified	22823
s__unclassified	22830
s__unclassified	22836
s__unclassified	22840
s__unclassified	22849
s__unclassified	22856
s__unclassified	22858
s__unclassified	22861
s__unclassified	22862
s__unclassified	22863
s__unclassified	22870
s__unclassified	22871
s__unclassified	22872
s__unclassified	22874
s__unclassified	22875
s__unclassified	22884
s__unclassified	22885
s__unclassified	22886
s__unclassified	22889
s__unclassified	22890
s__unclassified	22899
s__unclassified	22901
s__unclassified	22903
s__unclassified	22906
s__unclassified	22914

DQ806062.1 gg_id:190798 human fecal clone RL186_aah60f10
AY982478.1 gg_id:116264 human sigmoid colon mucosal biopsy clone MM39
FJ682393.1 gg_id:528101 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799588.1 gg_id:196948 human fecal clone RL305aal88a06
DQ795610.1 gg_id:175007 human fecal clone RL178_aan67a03
DQ796306.1 gg_id:183552 human fecal clone RL179_aah25e07
AY980794.1 gg_id:126997 human rectum mucosal biopsy clone LO11
FJ369908.1 gg_id:364287 feces adult twins and mothers; TS55 clone TS55_a02b08
FJ366270.1 gg_id:370023 feces adult twins and mothers; TS25 clone TS25_a04f10
FJ370213.1 gg_id:368038 feces adult twins and mothers; TS56 clone TS56_a01h01
FJ368827.1 gg_id:365391 feces adult twins and mothers; TS4 clone TS4_a01a12
FJ685443.1 gg_id:529808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ369265.1 gg_id:363127 feces adult twins and mothers; TS50 clone TS50_a02c04
FJ684743.1 gg_id:519921 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796869.1 gg_id:196394 human fecal clone RL179_aao55f11
FJ678359.1 gg_id:514400 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370858.1 gg_id:365636 feces adult twins and mothers; TS5 clone TS5_a02a12
FJ365451.1 gg_id:362642 feces adult twins and mothers; TS20 clone TS20_a03a09
DQ800958.1 gg_id:199174 human fecal clone RL387_aao89h08
DQ807460.1 gg_id:186561 human fecal clone RL307_aam06h03
DQ825285.1 gg_id:174225 human fecal clone RL185_aan87g06
DQ809837.1 gg_id:182381 human fecal clone RL184_aao65a01
FJ369804.1 gg_id:360862 feces adult twins and mothers; TS55 clone TS55_a01a07
EF402093.1 gg_id:206645 human fecal clone SJTU_B_03_57
DQ805865.1 gg_id:198078 human fecal clone RL306aal92a08
DQ797393.1 gg_id:195255 human fecal clone RL248_aai98g07
DQ326329.1 gg_id:145360 Metagenomic gut microbiome healthy human stool clone C318
FJ679248.1 gg_id:528560 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ369063.1 gg_id:366153 feces adult twins and mothers; TS4 clone TS4_a03g10
DQ802012.1 gg_id:198227 human fecal clone RL241_aaj01g11
FJ369432.1 gg_id:366979 feces adult twins and mothers; TS50 clone TS50_a04d08
DQ798560.1 gg_id:196287 human fecal clone RL181_aan98c07
DQ807627.1 gg_id:182679 human fecal clone RL180_aah35b04
DQ802564.1 gg_id:179762 human fecal clone RL188_aan93e01
DQ802492.1 gg_id:178191 human fecal clone RL188_aah18d11
DQ795623.1 gg_id:193991 human fecal clone RL178_aan67c02
DQ807694.1 gg_id:195485 human fecal clone RL180_aah36a08
AY979910.1 gg_id:127325 human rectum mucosal biopsy clone E224
DQ802322.1 gg_id:195976 human fecal clone RL188_aah16a08
FJ372011.1 gg_id:367354 feces adult twins and mothers; TS8 clone TS8_a04g04
DQ795329.1 gg_id:192403 human fecal clone RL178_aah53a07

DQ806062.1	190798	34.8	40.5	60.2	75.3	67.9	37.6
AY982478.1	116264	6387.3	6493.0	3040.2	8373.8	6170.7	6300.9
FJ682393.1	528101	3111.5	2882.3	4326.4	1672.8	2206.4	2163.4
DQ799588.1	196948	979.6	837.9	1764.2	714.7	1441.5	1139.9
DQ795610.1	175007	4714.2	4755.5	4721.9	4420.6	9260.8	7307.0
DQ796306.1	183552	27.8	30.5	76.9	71.6	57.1	35.1
AY980794.1	126997	7011.4	5819.0	6701.2	6534.1	2806.5	5941.1
FJ369908.1	364287	3365.5	6420.3	2521.7	2794.7	9579.1	5513.4
FJ366270.1	370023	1806.6	2147.8	2122.7	1565.8	5485.1	5283.0
FJ370213.1	368038	27.9	44.8	62.8	38.5	181.8	183.2
FJ368827.1	365391	6430.9	7724.0	7090.6	6855.1	13636.6	14115.4
FJ685443.1	529808	4736.1	5052.1	873.1	2983.9	2256.8	2172.9
FJ369265.1	363127	2473.2	3734.4	286.1	1161.2	1364.7	1215.8
FJ684743.1	519921	50.3	59.6	63.7	104.6	77.7	46.7
DQ796869.1	196394	68.8	118.7	678.7	119.7	274.1	511.4
FJ678359.1	514400	3980.8	4256.5	3382.1	4141.3	6445.1	4725.3
FJ370858.1	365636	165.8	378.2	130.4	112.9	95.4	54.6
FJ365451.1	362642	7770.6	13094.7	4523.3	7711.3	9518.5	8706.6
DQ800958.1	199174	86.5	95.1	120.9	54.7	130.4	78.3
DQ807460.1	186561	25.3	49.6	30.5	64.5	71.0	22.1
DQ825285.1	174225	2862.5	2621.4	1329.4	3867.1	5421.2	4173.5
DQ809837.1	182381	7006.1	8119.6	3130.5	5409.5	2404.5	2871.0
FJ369804.1	360862	3567.6	3520.2	1351.4	980.4	1996.6	2439.3
EF402093.1	206645	2959.4	4488.5	1233.3	1529.0	5520.6	3606.6
DQ805865.1	198078	245.8	397.4	485.3	219.3	253.2	680.4
DQ797393.1	195255	3829.0	5146.0	5873.5	3643.3	2452.5	3259.2
DQ326329.1	145360	20.1	16.2	70.3	56.3	207.9	137.5
FJ679248.1	528560	1307.6	1448.0	898.0	1031.9	612.9	696.4
FJ369063.1	366153	3513.4	3830.8	1657.0	2418.0	6671.4	4376.7
DQ802012.1	198227	5340.0	5752.8	3597.8	4138.1	5433.1	4816.9
FJ369432.1	366979	563.2	1171.3	678.6	335.8	213.6	887.0
DQ798560.1	196287	135.4	181.2	1104.5	130.8	70.2	80.4
DQ807627.1	182679	6629.5	10553.1	3377.4	5689.3	9549.7	7216.1
DQ802564.1	179762	3895.7	2603.8	949.1	4073.6	5479.5	4571.7
DQ802492.1	178191	12735.3	12561.1	13491.0	11316.1	13479.2	13569.7
DQ795623.1	193991	2315.0	2761.0	2980.2	2082.9	6592.9	4607.1
DQ807694.1	195485	156.0	182.4	509.2	147.8	168.1	95.4
AY979910.1	127325	794.1	1585.3	3077.0	378.8	2268.0	1525.2
DQ802322.1	195976	282.4	523.2	850.6	504.3	671.6	576.1
FJ372011.1	367354	12719.5	13604.9	4812.7	9685.8	10242.7	9113.4
DQ795329.1	192403	2885.9	5322.8	4000.1	2852.2	7097.4	4735.1

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium
g__Eubacterium

s__unclassified	22916
s__unclassified	22917
s__unclassified	22919
s__unclassified	22923
s__unclassified	22928
s__unclassified	22929
s__unclassified	22930
s__unclassified	22931
s__unclassified	22938
s__unclassified	22941
s__unclassified	22942
s__unclassified	22944
s__unclassified	22948
s__unclassified	22953
s__unclassified	22955
s__unclassified	22958
s__unclassified	22960
s__unclassified	22967
s__unclassified	22968
s__unclassified	22977
s__unclassified	22981
s__unclassified	22983
s__unclassified	22997
s__unclassified	22998
s__unclassified	23002
s__unclassified	23004
s__unclassified	23006
s__unclassified	23014
s__unclassified	23024
s__unclassified	23029
s__unclassified	23032
s__unclassified	23033
s__unclassified	23036
s__unclassified	23040
s__unclassified	23042
s__unclassified	23045
s__unclassified	23046
s__unclassified	23049
s__unclassified	23054
s__unclassified	23055
s__unclassified	23056

DQ799427.1 gg_id:189378 human fecal clone RL305aal86b05
FJ362651.1 gg_id:360092 feces adult twins and mothers; TS13 clone TS13_a01e06
DQ905789.2 gg_id:167882 human fecal clone 29E-a1
DQ804596.1 gg_id:176409 human fecal clone RL187_aao70b06
DQ795087.1 gg_id:183505 human fecal clone RL310_aam40a09
DQ325743.1 gg_id:149614 Metagenomic gut microbiome healthy human stool clone B394
FJ370065.1 gg_id:369212 feces adult twins and mothers; TS55 clone TS55_a04a08
FJ369870.1 gg_id:365861 feces adult twins and mothers; TS55 clone TS55_a01g03
AY986125.1 gg_id:121971 human stool clone D468
DQ801863.1 gg_id:178337 human fecal clone RL201_aai47g09
DQ807737.1 gg_id:203199 human fecal clone RL180_aah36f02
DQ801836.1 gg_id:190239 human fecal clone RL201_aai47e02
DQ800317.1 gg_id:192672 human fecal clone RL303_aal71d06
FJ364400.1 gg_id:361003 feces adult twins and mothers; TS15 clone TS15_a02e02
DQ325916.1 gg_id:145806 Metagenomic gut microbiome healthy human stool clone B756
DQ806845.1 gg_id:183809 human fecal clone RL198_aaj73g08
DQ809522.1 gg_id:177501 human fecal clone RL184_aah22c02
FJ679540.1 gg_id:519626 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY983629.1 gg_id:121240 human descending colon mucosal biopsy clone NO71
DQ801904.1 gg_id:195152 human fecal clone RL201_aai48c10
FJ369919.1 gg_id:357017 feces adult twins and mothers; TS55 clone TS55_a02c09
EU771665.1 gg_id:304410 African elephant feces clone AFEL2_aao31f04
GQ492513.1 gg_id:576103 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ370081.1 gg_id:361880 feces adult twins and mothers; TS55 clone TS55_a04c01
DQ794770.1 gg_id:180070 human fecal clone RL240_aaj32b06
DQ806610.1 gg_id:182539 human fecal clone RL186_aao46f10
FJ365518.1 gg_id:362419 feces adult twins and mothers; TS20 clone TS20_a03g09
FJ678279.1 gg_id:532113 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802730.1 gg_id:186283 human fecal clone RL188_aan95g12
DQ798222.1 gg_id:173959 human fecal clone RL181_aah39a11
EU469505.1 gg_id:290281 black lemur feces clone BKLE_a12_3
EU771816.1 gg_id:310632 African elephant feces clone AFEL2_aao32a11
DQ807876.1 gg_id:179509 human fecal clone RL180_aah38c10
EU761798.1 gg_id:347926 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
DQ799845.1 gg_id:195911 human fecal clone RL182_aah34h02
DQ809883.1 gg_id:198942 human fecal clone RL184_aao65e03
FJ363951.1 gg_id:360540 feces adult twins and mothers; TS150 clone TS150_a01c07
DQ802103.1 gg_id:186515 human fecal clone RL241_aaj03b04
GQ897156.1 gg_id:578032 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ369904.1 gg_id:362722 feces adult twins and mothers; TS55 clone TS55_a02b04
FJ365750.1 gg_id:368316 feces adult twins and mothers; TS21 clone TS21_a02e10

DQ799427.1	189378	7433.7	5346.2	4816.2	5338.4	6882.1	9270.1
FJ362651.1	360092	668.3	899.2	1258.5	482.9	3835.6	4124.2
DQ905789.2	167882	118.8	286.6	104.9	96.2	286.1	437.5
DQ804596.1	176409	708.9	1138.1	698.1	180.7	338.0	415.7
DQ795087.1	183505	72.2	133.0	670.1	135.2	302.6	181.6
DQ325743.1	149614	138.9	199.2	1067.9	172.7	161.7	419.5
FJ370065.1	369212	88.3	107.7	254.0	129.9	122.6	120.9
FJ369870.1	365861	115.3	161.1	306.7	320.0	855.5	988.4
AY986125.1	121971	265.1	502.0	894.3	259.2	385.0	385.9
DQ801863.1	178337	6624.6	9301.6	6250.0	7960.3	12335.6	10164.3
DQ807737.1	203199	170.9	189.3	521.9	210.7	511.7	630.1
DQ801836.1	190239	1819.7	951.9	1702.7	755.5	1176.7	1368.3
DQ800317.1	192672	1582.0	1438.8	209.2	393.2	344.1	301.8
FJ364400.1	361003	5412.5	6311.4	6461.1	5717.8	9742.9	5858.6
DQ325916.1	145806	7668.5	10606.7	5968.9	6307.8	7635.5	8011.3
DQ806845.1	183809	26.6	15.8	63.4	78.5	70.4	26.8
DQ809522.1	177501	5660.9	6566.0	7338.8	5942.1	5109.7	5136.7
FJ679540.1	519626	280.5	739.3	1574.1	481.7	1104.1	1233.4
AY983629.1	121240	4467.7	4641.4	4862.1	6265.5	3701.0	3848.2
DQ801904.1	195152	2475.6	3185.7	1465.7	3262.4	3152.1	3362.8
FJ369919.1	357017	3490.2	4871.8	1894.1	3769.2	10678.2	6102.4
EU771665.1	304410	20.7	36.6	43.1	58.8	79.4	29.7
GQ492513.1	576103	6523.9	8249.6	7527.9	5569.6	12761.0	9484.4
FJ370081.1	361880	337.0	261.4	420.8	418.4	232.0	195.3
DQ794770.1	180070	1246.9	1006.3	1388.6	2349.5	1784.3	1371.0
DQ806610.1	182539	2701.8	3551.7	1985.4	2819.5	6210.9	4140.3
FJ365518.1	362419	1990.0	2152.6	1881.8	2274.5	1519.3	1729.8
FJ678279.1	532113	2965.5	3140.6	195.3	3353.2	3566.5	3497.6
DQ802730.1	186283	13.6	47.9	212.3	85.2	59.5	24.1
DQ798222.1	173959	5616.3	8542.5	4618.0	4627.5	9489.2	7127.5
EU469505.1	290281	26.3	41.5	49.3	87.7	59.9	24.6
EU771816.1	310632	4650.0	3079.8	376.9	2351.1	3601.7	3049.2
DQ807876.1	179509	73.0	96.8	168.3	69.7	149.0	99.0
EU761798.1	347926	2271.8	1767.1	3364.6	1520.2	1632.1	1330.5
DQ799845.1	195911	29.0	37.2	41.5	61.5	77.6	62.3
DQ809883.1	198942	73.9	96.7	191.0	107.4	246.0	96.6
FJ363951.1	360540	2405.9	2559.7	2126.2	2470.0	2297.5	2406.3
DQ802103.1	186515	97.8	100.1	319.0	100.4	83.1	80.8
GQ897156.1	578032	108.5	294.6	801.3	207.3	465.9	363.3
FJ369904.1	362722	797.3	1211.5	457.2	1585.5	3579.6	3201.4
FJ365750.1	368316	12022.5	11383.7	8086.8	10049.7	11959.5	11722.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia