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GQ867579.1 gg_id:592345 and prevalence blaTEM genes Arctic seals colon content clone CSH88 GQ867
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DQ507245.1 gg_id:159259 Clostridium sp. str. AIP 321.05 DQ507
EU454693.1 gg_id:329126 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU454
EU511227.1 gg_id:273077 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04f11 EU511
EU510407.1 gg_id:270065 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b01 EU510
DQ803584.1 gg_id:179758 human fecal clone RL251_aaj87g05 DQ803
DQ800728.1 gg_id:183498 human fecal clone RL183_aao02f09 DQ800
FJ370516.1 gg_id:368577 feces adult twins and mothers; TS57 clone TS57_a02a04 FJ3705
EF098834.1 gg_id:181808 mouse cecum clone SWPT1_aaa01f07 EF0988
FJ363546.1 gg_id:358915 feces adult twins and mothers; TS149 clone TS149_a04e06 FJ3635
EF097971.1 gg_id:176671 mouse cecum clone SWPT12_aaa03b07 EF0979
EU507789.1 gg_id:264568 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04h05 EU507
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EU509781.1 gg_id:276663 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48h05 EU509
EU508759.1 gg_id:271646 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50e12 EU508
EU504370.1 gg_id:260529 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03b11 EU504
EU776687.1 gg_id:331571 Lion feces clone LI3_aah76a12 EU776
EF098153.1 gg_id:181711 mouse cecum clone SWPT14_aaa02c08 EF0981
EU451008.1 gg_id:345101 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
EU776759.1 gg_id:310803 Mongoose lemur feces clone ML_aaj25c02 EU776
FJ364698.1 gg_id:362665 feces adult twins and mothers; TS19 clone TS19_a02a02 FJ3646
EU778969.1 gg_id:331575 Prevost's squirrel feces clone SQ_aah82g09 EU778
EU452394.1 gg_id:352370 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
EU767660.1 gg_id:304352 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
DQ815778.1 gg_id:167848 mouse cecum clone aab22b11 DQ815
EU862317.1 gg_id:344422 Clostridium sp. str. C9 EU862
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EF614479.1 gg_id:234428 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6144
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EU766772.1 gg_id:332005 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
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AM932636.1 gg_id:566204 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
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AM183091.1 gg_id:253465 and its spatial composts compost clone SMC62 AM183
AY305309.1 gg_id:99786 butyrate-producing M62/1 AY3053
DQ905158.1 gg_id:165137 human fecal clone 002C-f12 DQ905
EF096776.1 gg_id:195356 mouse cecum clone SWPT11_aaa04e04 EF0967
EU764399.1 gg_id:321397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
EF096298.1 gg_id:176380 mouse cecum clone obob1_aaa04d03 EF0962
FJ364572.1 gg_id:362759 feces adult twins and mothers; TS15 clone TS15_a04e07 FJ3645
EF099498.1 gg_id:191020 mouse cecum clone SWPT3_aaa04a04 EF0994
AF357570.1 gg_id:71692 mpn-isolate group 22 AF3575
EU504147.1 gg_id:263865 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02c04 EU5041
GQ492220.1 gg_id:592784 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU506722.1 gg_id:265652 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55b07 EU5067
EU452778.1 gg_id:312718 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4527
FJ370778.1 gg_id:370100 feces adult twins and mothers; TS5 clone TS5_a01b08 FJ3707
EU504001.1 gg_id:268581 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03h01 EU5040

22037.2	4838.2	5017.2	6344.2	3937.4	3361.3	6245.4	4320.4	6721.8	5687.8	7042.9
547.5	2733.2	2794.4	3135.1	3569.6	2926.9	2763.6	4088.5	1863.4	1182.3	2972.5
62.0	309.5	510.5	526.6	202.4	417.1	232.9	590.1	90.9	111.2	161.9
3595.2	3733.5	3775.9	4018.6	4240.0	3623.7	4610.4	3467.3	4069.6	4093.9	3325.2
342.8	2779.8	3010.0	3266.2	3795.3	2773.6	3546.3	3511.6	2395.1	564.7	2875.7
1029.1	1127.7	1665.1	1394.9	1038.6	1197.5	1191.9	1328.8	791.5	704.1	850.8
46.1	1168.4	1308.2	1352.6	1041.4	833.5	1338.1	408.4	1356.7	443.3	666.9
386.2	540.8	502.7	581.2	480.8	939.2	547.0	652.4	449.2	1482.6	389.9
55.1	504.6	959.4	738.5	195.4	779.4	385.4	952.8	268.3	143.8	624.7
47.8	51.0	34.6	69.9	56.8	53.3	50.5	72.6	25.4	25.3	41.3
37.3	23.1	31.2	31.1	16.0	34.4	19.3	19.4	24.2	24.3	20.6
269.9	1225.2	1517.5	1708.8	928.3	924.7	1320.3	1310.2	511.1	382.4	488.6
11750.8	4251.5	5422.7	5307.6	3826.7	4859.0	4503.9	4908.6	4513.5	3560.3	5263.7
3416.1	2767.3	3387.7	2155.8	1868.5	2118.9	1685.8	2212.2	2401.9	2502.0	2497.1
33.7	46.1	83.8	49.3	38.9	58.6	43.2	31.5	44.5	26.3	48.4
347.6	1591.9	1798.6	1994.5	1510.8	2344.4	1732.4	2440.4	1116.3	893.8	1467.8
32.5	1906.7	1728.4	1346.6	979.8	985.8	1773.9	1422.2	1411.2	1536.5	1263.9
145.1	820.5	1160.1	1116.7	1286.4	974.6	1250.2	1023.7	425.9	222.6	792.0
60.6	1004.1	1492.1	1728.2	299.4	920.9	620.2	1470.0	223.1	115.2	757.1
142.1	1721.2	1928.1	1698.3	1410.2	1353.4	2009.4	1972.5	1906.4	1488.8	1281.2
18048.9	2562.7	2103.7	2488.5	2560.7	2292.7	2698.0	2692.0	2359.0	2624.6	3017.5
34.7	48.1	68.4	79.0	25.3	34.4	30.4	13.3	18.4	19.4	24.9
183.7	1394.9	1967.3	2062.9	1277.8	1572.2	1870.5	1214.9	2204.4	686.0	1333.8
218.2	278.8	220.5	537.1	227.5	239.6	274.3	315.4	198.4	162.7	217.3
151.7	883.5	1198.0	1621.3	1176.6	1174.0	1280.6	1400.2	934.1	470.7	633.6
8322.8	3717.9	5119.3	4289.3	3389.7	4463.6	4400.2	4566.6	4919.6	4342.6	6475.0
37.9	325.8	765.0	689.8	157.8	321.4	275.6	380.7	89.1	30.0	225.8
26.0	31.2	41.6	58.9	31.8	57.9	45.8	186.7	29.3	50.1	28.5
606.4	4944.1	5843.8	6302.5	2728.2	5097.3	3468.9	5103.7	4539.1	4410.9	5679.8
8262.4	3889.2	4179.9	3258.2	3787.1	3601.9	3493.5	3318.7	3953.4	5110.6	3306.1
2977.8	1033.7	1197.2	1283.3	1003.8	963.6	807.1	1441.7	677.1	693.0	368.9
7602.5	3946.2	4252.0	4003.0	3770.4	3819.3	4340.1	3600.2	3582.6	5522.3	3960.0
1061.6	3904.5	4637.8	3795.6	5287.0	4011.6	4429.5	3893.8	2732.3	1657.6	3045.5
163.0	2445.1	2238.1	2464.2	2300.8	2713.0	2839.9	2610.2	2159.0	1397.6	1720.1
5596.3	3425.0	4385.0	4055.7	2959.7	3334.6	3794.9	3703.7	3623.5	2626.1	4083.7
588.1	1737.4	2033.8	2767.5	1754.8	2188.9	2946.3	2106.7	4806.9	2103.6	5118.6
1056.8	2694.6	3225.9	4186.0	3013.6	3015.1	2734.4	3322.0	2119.5	681.4	2057.6
5461.5	2498.2	2941.8	1906.8	2248.3	2597.9	2098.7	3359.4	2005.5	2801.2	1917.5
41.3	332.8	377.5	358.6	156.2	345.0	176.0	498.7	165.0	89.2	221.3
63.7	699.7	735.4	556.2	358.3	601.6	346.9	671.2	604.0	819.8	399.7
42.4	418.6	694.3	760.2	641.2	350.4	716.4	488.9	92.2	130.8	212.3

5102.0	5274.2	4600.0
1723.0	2801.1	2964.7
589.5	394.6	485.8
3647.7	4951.2	4397.1
1273.3	3875.1	2651.1
1496.8	1587.6	1986.7
1049.5	1187.0	1336.4
544.3	1293.3	340.9
1230.3	624.9	749.2
75.4	35.1	64.9
16.9	34.2	21.3
2056.9	1253.8	3745.1
4386.6	6419.9	6024.6
1811.8	3459.0	1848.7
44.7	72.5	38.1
1905.0	2185.2	2454.0
1009.0	994.9	1413.1
991.4	1075.3	1287.8
2012.0	1305.3	1464.5
2081.4	1511.9	2157.7
2700.8	3050.9	2780.9
39.8	52.4	82.9
1908.7	2346.5	1827.2
350.6	192.0	309.7
1493.1	1577.5	1329.0
5231.2	4457.5	4346.6
377.8	320.8	627.7
323.8	76.3	106.8
5976.2	4842.8	6349.0
3522.9	4809.8	4294.4
1874.5	2121.3	1462.0
3211.9	5502.3	3270.6
4208.7	3233.9	4597.7
2643.7	2779.4	3748.0
3199.7	3342.8	3759.8
1737.3	2140.9	2337.2
3033.1	3912.5	3776.4
2855.2	3099.0	3435.5
625.8	372.0	604.5
932.1	618.5	1404.0
425.6	560.2	600.2

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
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
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EU503912.1 gg_id:267090 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02e02 EU503
EF098723.1 gg_id:199322 mouse cecum clone SWPT16_aaa04a02 EF0987
FJ371935.1 gg_id:358495 feces adult twins and mothers; TS8 clone TS8_a03h06 FJ3719
DQ808448.1 gg_id:180386 human fecal clone RL180_aao76f10 DQ808
EU503586.1 gg_id:266131 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01f02 EU503
FM204998.1 gg_id:564961 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM204
EU451441.1 gg_id:355374 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU451
EU510210.1 gg_id:258218 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h12 EU510
EU508100.1 gg_id:276628 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa04a04 EU508
DQ807984.1 gg_id:177535 human fecal clone RL180_aan70b12 DQ807
EF097084.1 gg_id:175044 mouse cecum clone SWPT18_aaa01b09 EF097
EU453023.1 gg_id:331317 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EF099459.1 gg_id:188117 mouse cecum clone SWPT3_aaa03e02 EF0994
EU474426.1 gg_id:292669 western lowland gorilla feces clone GORSD_aaa01a07 EU474
EF096430.1 gg_id:182604 mouse cecum clone obob2_aaa02f12 EF0964
EF398816.1 gg_id:213808 human fecal clone SJTU_F_07_51 EF3988
DQ795209.1 gg_id:182723 human fecal clone RL178_aah51e09 DQ795
EU511939.1 gg_id:263503 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11e10 EU511
EF025256.1 gg_id:185151 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F18 EF0252
EF098495.1 gg_id:181368 mouse cecum clone SWPT15_aaa04c02 EF0984
EU506432.1 gg_id:270960 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01f09 EU506
EU511857.1 gg_id:260996 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10a07 EU511
EU773389.1 gg_id:332584 BigHorn sheep feces clone BH1_aao26e10 EU773
EU456147.1 gg_id:316007 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU456
EU508222.1 gg_id:275907 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03f09 EU508
GQ897835.1 gg_id:557850 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AB114225.1 gg_id:97871 Clostridium sp. str. B556-1 AB114
X71855.1 gg_id:13973 Clostridium xylanolyticum str. ATCC 4963 X71855
EF604530.1 gg_id:233313 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
DQ014635.1 gg_id:134263 mouse cecum clone M1_h08 DQ014
DQ799555.1 gg_id:184320 human fecal clone RL305aal87f04 DQ799
EF099548.1 gg_id:185301 mouse cecum clone SWPT3_aaa04g06 EF0995
EU506240.1 gg_id:261109 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c06 EU506
FJ880755.1 gg_id:416185 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU455733.1 gg_id:321446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU508176.1 gg_id:272386 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02e07 EU508
EF098641.1 gg_id:183428 mouse cecum clone SWPT16_aaa02e12 EF0986
EU504073.1 gg_id:272742 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04h05 EU504
DQ798869.1 gg_id:177286 human fecal clone RL242_aaj98d09 DQ798
EF096053.1 gg_id:177043 mouse cecum clone lean2_aaa03a06 EF0960
EU456428.1 gg_id:347190 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456

246.3	1809.9	2432.1	2744.6	712.0	1675.7	1144.0	1564.6	1683.1	2362.7	1746.3
79.9	1817.2	1971.1	2179.8	2992.8	1980.8	2882.6	1882.4	1270.8	1386.8	1433.2
4637.9	1228.8	1458.2	1698.9	895.7	1342.4	1065.0	2430.2	494.0	1327.3	711.6
46.8	782.1	1954.5	366.2	527.7	549.0	327.1	561.2	308.1	351.9	296.3
4689.9	3969.5	3613.0	4533.9	4562.3	3964.1	4423.7	4901.4	4213.9	3871.7	3900.0
42.6	736.6	1095.2	1328.4	115.3	902.3	507.6	2662.7	175.6	273.5	667.7
6726.7	2079.2	2418.2	2370.5	2061.6	2288.3	2670.7	2210.3	1822.2	1640.3	2512.5
635.6	2020.9	2207.2	1823.1	1890.2	2017.2	1466.6	2093.6	2318.5	2345.4	1538.0
1728.1	2644.9	2765.5	2958.4	2810.1	2772.1	2901.5	2920.9	3037.4	2196.2	2999.1
36.8	416.2	309.6	527.3	138.1	244.6	156.2	323.5	88.0	57.0	99.6
302.6	1385.3	1684.6	999.2	709.1	1085.4	966.0	1181.8	1299.7	2228.1	682.6
5224.3	2228.3	2193.6	2452.7	1919.8	2372.4	2197.9	2500.6	3205.1	3161.6	2622.7
5527.9	3257.6	3496.7	3816.1	2860.9	3040.9	3224.0	3098.2	2625.6	2080.3	4461.1
57.8	123.2	246.3	316.6	130.6	107.3	91.9	218.3	82.2	56.0	133.9
12383.7	4589.0	6147.1	5198.7	4551.0	4525.3	5079.4	4349.0	9862.4	7193.2	5792.7
584.8	915.4	1456.4	1719.5	607.8	905.7	935.7	1348.6	482.8	458.1	1216.3
48.0	652.5	1081.3	1356.7	272.9	552.0	416.9	1535.5	451.3	96.9	249.5
10063.1	6791.5	7532.0	7110.3	7777.9	6724.9	10136.0	7520.5	8923.8	5244.3	7936.1
8664.9	4688.7	4488.9	5066.3	4335.6	4330.1	4741.7	4042.9	7023.8	5128.8	6176.5
109.9	795.2	1187.4	1245.2	551.5	810.5	525.1	805.7	493.2	447.5	656.9
13560.3	3808.5	3344.3	3501.8	3520.1	3822.7	3702.8	3520.2	5180.8	5364.4	2116.4
26.9	347.0	518.5	953.5	22.0	110.6	60.1	223.9	43.6	15.7	220.3
240.5	1681.9	2259.2	2806.3	1645.9	2027.1	2240.4	2371.0	1063.2	695.5	1521.1
7654.8	3174.8	2716.0	3255.8	3500.6	3166.0	3041.0	3158.7	4275.2	3127.6	3984.6
167.2	1644.0	2191.6	1654.4	1143.3	1940.3	1527.7	1941.3	929.7	1147.3	1740.8
78.7	978.0	1427.1	1290.9	454.8	1076.9	1483.9	1240.8	506.4	196.3	864.2
13095.4	6893.9	6691.6	7439.4	5098.8	6252.6	5994.9	7979.7	6585.7	4675.2	6865.2
597.0	809.3	1256.4	1346.0	729.1	1438.7	594.0	3192.8	431.2	888.4	1090.0
11254.0	4455.9	3995.5	4569.6	4885.0	5131.0	4533.4	4194.3	5985.6	5323.1	6494.3
274.4	717.8	1216.8	870.3	771.2	763.6	678.1	1019.6	712.9	627.1	957.2
91.5	451.6	661.0	661.2	287.3	394.6	356.2	662.8	192.6	616.6	292.5
296.9	633.7	929.4	1132.2	1035.3	1082.2	962.3	1134.8	423.7	510.6	522.4
12180.8	5320.3	6225.5	6926.6	4947.5	5640.2	5301.8	4511.3	6131.5	4938.2	6789.1
11705.0	5043.2	5491.5	5735.8	5891.2	5579.9	5809.5	5469.7	4674.0	3682.9	5465.5
68.1	161.0	416.0	491.0	210.1	199.6	226.4	269.2	121.0	61.3	135.7
461.2	1749.6	2159.2	2107.9	1671.9	1676.0	2073.5	2427.0	2008.3	1246.5	1848.5
40.4	165.7	175.1	167.7	105.0	147.1	152.7	276.0	525.7	477.0	203.2
284.2	1896.7	1776.6	1335.4	951.6	1376.6	1115.0	1121.9	2330.2	2546.3	2374.7
136.9	2031.1	2454.7	3191.3	1871.9	2247.3	2982.3	2988.1	897.5	986.0	2050.0
2273.8	3041.4	3188.5	2706.7	2727.0	2734.4	2424.1	2690.8	3512.7	2905.3	2602.0
65.3	108.4	165.0	165.8	89.4	105.1	89.3	102.1	42.2	31.5	56.6

2030.1	2385.1	2384.6
1888.7	1848.9	3392.9
3233.0	1468.5	2075.1
423.8	635.0	305.3
3912.4	4549.5	4677.0
4399.3	790.7	1603.2
2531.6	3121.0	2630.4
2318.0	2112.8	2556.3
2554.3	3395.6	2719.3
347.4	330.0	449.3
1161.6	1524.1	1439.9
2154.7	3765.3	2258.6
2778.3	3941.7	3003.7
275.9	193.3	134.4
4551.0	5789.8	4727.9
1472.6	1187.2	1623.6
2003.4	757.1	1479.5
6289.0	7662.6	7942.1
3940.2	5676.6	4367.6
849.1	1051.1	942.9
3429.0	5705.6	3607.8
460.8	176.6	186.8
2406.2	2206.9	1877.5
804.1	2733.6	2926.3
1833.0	1868.4	1548.2
839.8	832.3	1088.5
10073.3	4977.4	6590.3
3548.8	1217.7	1872.0
4008.2	5554.0	4880.2
510.0	1441.6	1046.0
524.2	923.6	1219.0
984.9	1554.7	1180.3
4143.8	5742.1	5510.8
5702.3	6540.4	6490.2
323.5	359.8	331.2
1648.7	1990.7	1863.9
191.7	401.8	207.4
1350.6	1505.4	1000.4
3470.9	2554.7	3705.2
2637.0	3957.4	3738.1
241.1	187.8	148.6

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AB114231.1 gg_id:95658 Clostridium sp. str. Kas401-4	AB114
EF098553.1 gg_id:185587 mouse cecum clone SWPT16_aaa01c07	EF0985
EU506380.1 gg_id:275913 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64e10	EU5063
EF096792.1 gg_id:173865 mouse cecum clone SWPT11_aaa04g04	EF0967
DQ015610.1 gg_id:129538 mouse cecum clone M3_b09_3	DQ015
DQ798924.1 gg_id:176924 human fecal clone RL242_aaj99b07	DQ798
EF098774.1 gg_id:188527 mouse cecum clone SWPT16_aaa04g01	EF0987
EU511784.1 gg_id:275362 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09b12.Contig2	EU5117
EU777890.1 gg_id:333030 European rabbit feces clone RA_c12	EU7778
EU777843.1 gg_id:317693 European rabbit feces clone RA_d04	EU7778
EU771662.1 gg_id:324837 African elephant feces clone AFYEL_aaj67h11	EU7716
EU450997.1 gg_id:351184 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S	EU4509
EF097574.1 gg_id:193509 mouse cecum clone SWPT19_aaa04f03	EF0975
EU777852.1 gg_id:353339 European rabbit feces clone RA_c07	EU7778
EU458606.1 gg_id:302763 European rabbit feces clone RA_c11	EU4586
EU453414.1 gg_id:304920 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N	EU4534
EF099092.1 gg_id:189272 mouse cecum clone SWPT2_aaa02b04	EF0990
EU454774.1 gg_id:314424 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S	EU4547
EU506185.1 gg_id:274509 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02f05	EU5061
EF097951.1 gg_id:188402 mouse cecum clone SWPT12_aaa02g05	EF0979
EU506150.1 gg_id:276190 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa01a10	EU5061
EU530312.1 gg_id:259761 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4	EU5303
DQ807567.1 gg_id:196575 human fecal clone RL307_aam08d02	DQ807
DQ904659.1 gg_id:163667 human fecal clone 001-b9	DQ904
DQ815335.1 gg_id:165437 mouse cecum clone aab45g07	DQ815
EU511089.1 gg_id:274060 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02e08	EU5110
EF098104.1 gg_id:186332 mouse cecum clone SWPT14_aaa01e09	EF0981
FJ364077.1 gg_id:367361 feces adult twins and mothers; TS150 clone TS150_a02g01	FJ3640
AY984246.1 gg_id:125031 human stool clone B137	AY9842
DQ802434.1 gg_id:196091 human fecal clone RL188_aah17f09	DQ802
DQ014768.1 gg_id:131073 mouse cecum clone M1_e02_2	DQ014
EU453995.1 gg_id:338442 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S	EU4539
FJ367695.1 gg_id:367805 feces adult twins and mothers; TS2 clone TS2_a02e03	FJ3676
DQ825146.1 gg_id:185864 human fecal clone RL185_aan85h06	DQ825
FJ371087.1 gg_id:369473 feces adult twins and mothers; TS5 clone TS5_a04g05	FJ3710
AY977088.1 gg_id:118015 human cecum mucosal biopsy clone K778	AY9770
DQ808251.1 gg_id:198086 human fecal clone RL180_aao74d08	DQ808
FJ369137.1 gg_id:361894 feces adult twins and mothers; TS4 clone TS4_a04f10	FJ3691
FJ369095.1 gg_id:357512 feces adult twins and mothers; TS4 clone TS4_a04b08	FJ3690
FJ368954.1 gg_id:359028 feces adult twins and mothers; TS4 clone TS4_a02e06	FJ3689
DQ807363.1 gg_id:187991 human fecal clone RL307_aam05f02	DQ807

145.3	1569.2	1691.3	1515.2	952.9	1288.1	900.6	2792.8	680.0	714.7	702.2
90.9	234.6	344.3	264.3	128.3	181.5	181.6	129.8	83.1	272.2	120.4
1740.3	1615.5	1532.4	1332.4	1282.2	1311.7	920.7	1451.4	1283.8	1154.3	1331.6
1314.0	1953.1	2424.2	2020.0	2797.6	1931.1	3701.0	2133.1	1394.0	1970.5	2011.9
59.3	107.8	140.2	117.9	165.3	53.7	131.3	130.4	50.1	45.9	52.1
870.6	1875.0	1526.4	2089.5	2307.7	1745.3	1894.4	3672.9	1560.2	1491.5	1526.5
1305.2	830.6	1127.1	1139.4	997.8	1207.2	1215.0	980.4	742.8	1478.4	657.2
31.0	31.3	71.4	69.1	46.8	82.7	53.8	57.2	24.4	27.1	34.9
3367.7	2526.2	3332.3	2860.4	2181.4	2736.7	2718.9	2787.0	1512.0	828.4	2800.4
867.5	2566.1	3416.1	3602.8	3148.7	2401.8	2947.0	2632.7	1403.7	1255.9	1691.0
3803.2	1945.9	2321.9	2268.1	1757.8	1894.4	1944.1	1877.9	1797.2	1810.2	1351.5
10426.6	5368.7	4654.4	5370.2	3905.7	4843.7	5830.7	4725.1	6039.1	5304.2	9435.0
38.3	302.5	246.9	247.1	118.6	115.2	91.5	156.1	34.2	24.2	58.1
11348.8	2846.2	2846.4	3148.3	2872.9	2684.8	2731.6	2943.1	2637.9	1727.9	2705.2
89.9	460.8	740.4	925.0	295.9	377.2	271.5	637.4	188.0	94.7	418.9
50.2	401.4	550.3	807.3	323.0	203.4	398.9	383.3	88.3	47.3	162.6
48.0	79.7	110.3	38.1	28.9	84.9	67.8	36.1	36.8	79.9	82.7
10127.7	6105.5	5744.6	5702.4	5851.1	5392.0	6464.0	5561.9	7929.5	5663.6	8462.1
759.7	1229.0	1382.7	1470.4	1452.2	1291.9	1483.8	1110.1	696.0	697.3	733.9
122.6	1391.3	1725.2	1633.3	1248.1	1360.9	1794.9	1876.9	871.2	586.7	1200.4
1236.5	2210.1	2966.9	3129.6	2790.7	2084.4	2820.7	2110.3	1905.7	1356.4	2606.4
5840.0	4591.9	5596.8	4735.8	4186.9	5327.0	4143.0	5307.1	5573.4	4346.2	5356.2
6657.2	2340.2	3127.6	2693.3	2604.6	2626.2	2177.2	2481.2	2960.6	2793.4	2215.0
508.2	1242.8	1917.2	1644.0	1892.9	1971.0	1628.1	1698.3	1197.9	391.7	2817.6
57.4	237.5	463.3	764.2	54.5	105.6	121.8	293.2	51.0	24.2	126.1
418.8	3131.2	1910.2	1709.4	1679.9	1992.0	1204.5	1600.1	2560.4	1489.5	1430.8
78.5	1083.2	1782.7	1853.8	1843.2	1175.1	1772.5	1602.8	985.7	927.3	1353.2
38.0	575.2	821.3	674.9	163.3	357.4	248.6	748.3	113.7	72.0	355.8
325.0	532.1	696.8	800.5	742.8	593.9	465.1	1184.4	441.0	234.0	329.8
6122.0	466.8	579.0	800.4	657.9	883.5	415.2	891.4	256.0	144.7	211.6
368.7	1780.5	1933.9	1873.3	950.0	1093.3	1070.1	1314.1	1034.1	1117.5	903.0
1543.6	2599.6	2969.9	2884.1	2268.9	1974.3	2333.5	2201.0	2207.7	3041.3	2258.2
10534.8	5436.3	5799.1	4823.2	6881.1	5441.2	6057.6	5134.2	9216.1	7498.7	7285.0
279.3	1103.4	1421.8	1390.1	733.2	667.6	685.2	1123.0	288.4	291.2	628.2
83.6	1138.2	1580.6	1308.6	869.3	1640.0	1193.4	1347.9	1468.0	636.4	773.5
1503.7	1031.4	1370.7	1795.8	831.0	891.1	714.3	1643.0	428.9	356.0	562.9
41.1	279.3	347.8	444.9	126.4	202.9	144.4	319.3	32.1	29.7	168.5
85.8	1023.1	1083.6	920.8	254.2	469.8	289.0	518.4	481.7	1134.0	324.8
1821.1	1934.7	1778.6	1999.6	2447.0	1775.7	1895.8	2109.5	2169.3	2012.2	2360.1
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64.9	579.3	1028.8	1114.1	438.3	577.0	571.7	1047.4	193.1	109.9	402.9

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178.1	377.3	136.9
1520.4	1956.5	1389.9
2282.0	2323.2	2174.1
103.9	117.7	103.6
2851.0	2677.2	1227.0
688.6	1832.1	989.8
58.8	155.2	62.0
2419.7	3142.3	3608.7
3386.9	3177.0	3146.5
1855.4	2857.9	1994.8
4316.7	5371.5	5133.8
199.4	186.2	156.2
3322.3	4137.7	3799.2
720.3	746.8	883.4
452.6	466.0	628.4
594.9	35.3	115.3
4888.0	5749.4	5273.5
1001.3	1423.9	1172.6
1876.3	1855.2	3759.2
2072.5	2794.0	3015.5
5434.2	6071.4	4655.6
4038.2	2743.0	3011.7
1933.8	1749.4	1765.7
252.6	348.2	129.8
1826.1	1189.0	1109.1
1228.3	1898.5	1849.4
751.4	728.1	688.2
1629.1	951.5	1025.3
1186.9	1825.0	799.3
1504.4	1417.9	1699.8
2333.2	2511.8	3408.3
4586.0	5686.5	5087.9
1222.9	1179.8	2481.0
1523.2	1237.6	1494.4
1946.4	1581.0	1468.5
397.0	253.2	288.1
763.1	728.9	839.8
2196.5	2775.1	2241.2
3837.9	6238.1	4447.3
1113.1	874.3	952.0

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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DQ015254.1 gg_id:132281 mouse cecum clone M2_1b08 DQ015
FJ371331.1 gg_id:370049 feces adult twins and mothers; TS6 clone TS6_a03f11 FJ3713
AY994021.1 gg_id:136633 Abundant and fungal microbiota murine intestine clone 41-1 AY994
DQ799304.1 gg_id:181834 human fecal clone RL205_aaj20e03 DQ799
FJ369123.1 gg_id:365644 feces adult twins and mothers; TS4 clone TS4_a04e06 FJ3691
AY981455.1 gg_id:122012 human sigmoid colon mucosal biopsy clone L545 AY981
EU766751.1 gg_id:329944 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
AY984564.1 gg_id:123233 human stool clone B503 AY984
EF098881.1 gg_id:187852 mouse cecum clone SWPT1_aaa02e12 EF0988
FJ367781.1 gg_id:357957 feces adult twins and mothers; TS2 clone TS2_a03e07 FJ3677
DQ904722.1 gg_id:171410 human fecal clone 001-h12 DQ904
AY984690.1 gg_id:121570 human stool clone B642 AY984
EF099816.1 gg_id:192408 mouse cecum clone SWPT4_aaa04g01 EF0998
FJ369040.1 gg_id:365086 feces adult twins and mothers; TS4 clone TS4_a03e09 FJ3690
DQ823933.1 gg_id:196107 human fecal clone RL204_aaj57b03 DQ823
FJ368977.1 gg_id:358255 feces adult twins and mothers; TS4 clone TS4_a02g07 FJ3689
EU504262.1 gg_id:275676 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01c09 EU504
DQ905526.1 gg_id:162294 human fecal clone 014-g1 DQ905
EU508369.1 gg_id:258165 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04a08 EU508
FJ371424.1 gg_id:359347 feces adult twins and mothers; TS6 clone TS6_a04g10 FJ3714
FJ370956.1 gg_id:363515 feces adult twins and mothers; TS5 clone TS5_a03c03 FJ3709
EF404993.1 gg_id:216746 human fecal clone SJTU_G_05_59 EF4049
FJ369087.1 gg_id:357218 feces adult twins and mothers; TS4 clone TS4_a04a12 FJ3690
DQ904930.1 gg_id:171783 human fecal clone 002-b1 DQ904
AY978695.1 gg_id:119824 human transverse colon mucosal biopsy clone KT72 AY978
EU453964.1 gg_id:318008 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EF403201.1 gg_id:210539 human fecal clone SJTU_A1_6_40 EF4032
AY984776.1 gg_id:116238 human stool clone B738 AY984
AY975938.1 gg_id:120535 human ascending colon mucosal biopsy clone LS45 AY975
AY982876.1 gg_id:120781 human descending colon mucosal biopsy clone L046 AY982
AY983028.1 gg_id:123310 human descending colon mucosal biopsy clone L258 AY983
AY980512.1 gg_id:127137 human rectum mucosal biopsy clone X243 AY980
FJ368858.1 gg_id:364039 feces adult twins and mothers; TS4 clone TS4_a01d09 FJ3688
AY982766.1 gg_id:126286 human descending colon mucosal biopsy clone KZ01 AY982
EU508235.1 gg_id:275799 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04a07 EU508
FJ368923.1 gg_id:366377 feces adult twins and mothers; TS4 clone TS4_a02b08 FJ3689
DQ802136.1 gg_id:176587 human fecal clone RL241_aaj03e08 DQ802
FJ371276.1 gg_id:357312 feces adult twins and mothers; TS6 clone TS6_a03a10 FJ3712
EF400450.1 gg_id:212481 human fecal clone SJTU_E_13_50 EF4004
EF401232.1 gg_id:206701 human fecal clone SJTU_D_07_54 EF4012

131.2	1930.2	2016.3	1968.7	1592.6	1740.3	1919.4	1833.7	1945.3	3742.9	1486.1
601.5	393.2	529.9	555.8	572.9	453.6	559.0	402.1	287.5	179.6	254.9
51.1	1192.2	1410.8	1051.2	330.2	579.1	378.1	748.1	532.4	1276.2	363.7
3973.1	4076.1	5503.7	4325.5	3728.9	3557.6	4683.9	4040.3	4292.2	5084.6	4575.6
87.9	100.6	75.9	125.7	103.1	97.2	128.8	78.7	147.8	56.4	167.7
74.3	785.6	1142.7	1140.9	570.9	921.2	1029.0	1319.7	141.7	116.9	665.4
2947.7	1761.8	1667.0	1400.1	1620.2	1479.1	1729.5	1370.0	2014.7	1652.3	2168.8
1095.9	2975.9	3008.1	3598.4	2850.6	2575.5	2642.3	3926.1	1835.4	3185.4	2868.6
397.5	2756.1	2076.5	2058.5	1321.3	2745.2	2015.1	2286.5	1448.0	3046.5	1519.5
64.9	801.7	565.1	391.2	422.5	590.5	385.2	499.0	1180.9	575.0	374.6
41.2	943.1	1464.3	1481.1	287.7	675.3	462.1	1310.4	278.5	137.8	556.1
58.8	337.4	525.0	529.6	190.7	781.5	248.0	619.5	139.3	96.0	288.6
693.9	1366.7	1689.4	1813.8	1560.4	1746.1	1139.1	2072.1	966.8	1638.9	961.0
96.6	306.2	361.7	423.1	335.7	199.6	413.4	305.6	134.3	109.1	166.3
583.9	1993.0	1814.9	1614.5	1340.8	1829.1	1297.4	1675.0	2471.9	1701.9	1254.7
681.1	3205.6	3886.2	3560.7	4338.2	3432.9	4480.3	3772.1	3302.4	2174.7	4711.1
6164.0	3982.9	4533.5	4330.8	3507.8	3580.1	3146.6	3290.3	3578.6	3441.5	3418.2
35.3	84.0	126.7	240.1	232.0	192.0	73.8	75.9	47.7	23.2	42.3
64.2	135.5	211.1	158.7	169.6	123.1	229.1	50.2	92.3	89.7	146.7
240.3	435.9	493.9	643.8	513.8	410.1	368.7	457.4	400.7	338.8	257.6
42.6	271.3	447.0	498.7	97.1	296.9	193.8	604.8	87.7	75.1	196.4
43.1	130.7	172.9	177.8	81.3	143.6	64.8	247.4	243.0	248.3	154.4
57.2	657.2	1123.8	1080.6	252.0	570.0	530.8	966.7	458.9	157.6	466.0
55.7	1063.1	1487.4	2154.4	258.6	549.8	310.9	829.6	143.0	111.3	337.1
57.3	690.4	1169.7	1106.1	240.9	863.6	610.3	1289.2	276.7	131.7	675.5
75.9	742.4	1378.5	1056.0	829.1	847.6	899.1	979.3	313.5	501.9	545.8
263.2	1092.5	1209.8	1200.5	711.4	760.5	750.6	902.7	595.7	489.3	600.3
439.5	1648.7	2363.2	2730.3	975.1	1270.0	1012.7	2374.1	1033.9	368.9	1927.7
42.4	255.5	504.9	662.8	66.3	129.4	128.6	462.5	69.4	78.2	185.1
926.3	4966.9	5754.6	5677.3	4180.0	4467.8	4925.3	4984.7	3178.1	2221.2	4783.1
706.8	763.6	1249.4	1161.8	699.3	922.3	853.1	1186.5	416.5	421.1	959.4
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64.5	628.1	1035.7	1212.3	64.1	456.3	132.0	1413.5	97.9	134.0	115.2
3895.0	3978.3	5767.4	4711.5	3783.3	4751.3	4787.6	4900.9	3490.5	3447.0	4606.4
360.1	520.6	511.4	728.5	479.0	552.1	434.9	908.6	221.5	279.5	259.4
5453.8	3066.2	2979.2	3438.0	3195.6	2889.6	3095.6	4028.9	5003.7	3138.1	1319.0
2077.5	1510.5	2395.1	1739.7	1977.1	1493.0	1599.6	4348.4	562.9	738.9	2530.7
44.4	608.5	872.4	1141.6	115.5	730.7	233.5	1024.1	124.2	58.0	293.0
51.2	86.4	179.2	136.3	13.7	53.2	26.5	110.7	27.4	14.9	44.5
55.9	700.1	1082.7	1398.9	501.4	867.0	410.9	845.2	275.8	232.4	449.2
129.6	1399.6	1569.4	1244.2	823.1	1263.0	927.8	2211.3	757.3	547.1	841.9

1901.7	2135.2	2261.1
523.9	866.9	1043.2
1271.5	872.2	1004.2
4053.7	4570.6	5266.2
71.1	166.4	71.8
1509.7	647.1	971.9
1195.5	2146.4	1801.9
3750.4	3459.2	4354.4
2756.3	2454.9	2840.1
938.9	487.2	724.4
1664.2	1261.0	1315.6
652.6	761.8	265.1
2497.9	2648.8	2131.9
186.0	513.9	657.8
1807.2	1594.2	2655.8
2977.7	4598.6	4687.7
3597.3	4954.1	3224.6
90.0	132.4	102.1
117.0	236.1	186.3
575.3	771.2	557.7
741.1	501.2	619.3
193.4	244.1	170.4
1202.0	791.5	826.2
1029.7	1183.0	623.4
1570.8	1140.8	1590.5
1047.6	1173.8	1567.5
1090.8	1006.8	1390.8
2459.5	2164.7	2190.4
696.9	323.1	312.4
3998.7	4794.2	5841.4
910.3	1464.6	810.6
222.4	179.0	131.8
1885.0	562.9	1041.5
5103.1	5587.4	5974.8
975.7	1076.8	1233.4
3940.7	1908.4	3186.6
4012.9	1915.6	3242.0
1190.8	939.1	347.6
105.8	124.6	60.6
865.2	572.4	758.9
3033.1	1248.2	1571.0

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DQ823905.1 gg_id:197197 human fecal clone RL250_aaj80g04 DQ823
AY916166.1 gg_id:114387 human transverse colon biopsy clone M629 AY916
EU776782.1 gg_id:321095 Mongoose lemur feces clone ML_aaj28f07 EU776
FJ369014.1 gg_id:370235 feces adult twins and mothers; TS4 clone TS4_a03c07 FJ3690
FJ369150.1 gg_id:367923 feces adult twins and mothers; TS4 clone TS4_a04h04 FJ3691
AY985171.1 gg_id:116565 human stool clone BB95 AY985
DQ801872.1 gg_id:183711 human fecal clone RL201_aai47h08 DQ801
AY982502.1 gg_id:123023 human sigmoid colon mucosal biopsy clone MN06 AY982
EF604966.1 gg_id:235081 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF604
EF604534.1 gg_id:234956 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
EF097988.1 gg_id:181415 mouse cecum clone SWPT12_aaa03f06 EF0979
EU511999.1 gg_id:271804 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12e04 EU511
EF099490.1 gg_id:174338 mouse cecum clone SWPT3_aaa03g12 EF0994
EF602819.1 gg_id:228836 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EU457160.1 gg_id:352799 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU457
EU451365.1 gg_id:327720 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU451
EU452796.1 gg_id:315001 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
EU776507.1 gg_id:325848 Lion feces clone LI3_aah76a09 EU776
EF098165.1 gg_id:197600 mouse cecum clone SWPT14_aaa02e04 EF0981
EU454540.1 gg_id:305112 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU454
EU453875.1 gg_id:307093 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EF098455.1 gg_id:197759 mouse cecum clone SWPT15_aaa03e04 EF0984
EU509194.1 gg_id:272159 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f11 EU509
EU504518.1 gg_id:267353 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g04 EU504
EU454074.1 gg_id:353177 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU454
EF605183.1 gg_id:228046 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EU509790.1 gg_id:275349 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b01 EU509
AY992530.1 gg_id:132673 mouse cecum clone C23_h21 AY992
EU506415.1 gg_id:259154 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01d10 EU506
EU455283.1 gg_id:345503 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EF098479.1 gg_id:190699 mouse cecum clone SWPT15_aaa03h11 EF0984
EF097776.1 gg_id:192131 mouse cecum clone SWPT20_aaa03f01 EF0977
EF097342.1 gg_id:176950 mouse cecum clone SWPT19_aaa01c11 EF0973
AY991902.1 gg_id:135378 mouse cecum clone C20_k03 AY991
EU504157.1 gg_id:266061 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02e02 EU504
EU510843.1 gg_id:277200 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak50b04 EU510
EU474262.1 gg_id:296041 western lowland gorilla feces clone GORSD_aaa01e03 EU474
EU453646.1 gg_id:315974 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EF602818.1 gg_id:228511 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EF604535.1 gg_id:235067 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
FJ881305.1 gg_id:428954 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813

499.2	7676.4	6266.6	5924.4	4216.3	5723.6	5103.9	4739.5	7779.4	3621.6	5869.1
41.2	388.5	828.2	1171.7	110.8	731.4	186.0	1017.1	157.4	79.6	202.7
52.2	337.2	646.8	648.9	251.6	808.4	324.6	518.0	110.7	72.4	220.9
48.8	296.4	478.2	461.3	59.8	141.9	87.9	243.1	53.6	26.0	55.9
4461.5	4339.4	4545.0	4276.3	3137.4	3966.6	3210.7	3610.3	3809.8	4894.2	3066.5
67.1	1780.5	1088.0	860.3	778.3	1074.9	775.1	656.3	1966.0	1497.1	753.5
4900.9	2805.3	2459.2	2754.0	2983.8	2086.0	3184.5	2389.7	2310.3	2323.2	2421.3
50.2	237.4	396.0	522.1	47.4	138.9	61.9	141.1	46.6	24.6	129.9
1366.5	1891.7	2674.9	2235.4	1821.0	2090.6	2152.6	2456.9	2025.6	2830.4	1704.1
20094.5	8465.7	8599.6	9464.7	8682.9	7961.1	9854.7	8057.9	9697.1	9877.3	10966.9
1699.1	2538.1	3262.2	2820.6	2378.4	3023.3	2583.5	3249.3	2121.7	1204.0	2657.4
39.0	156.0	388.9	403.7	43.2	114.0	77.4	382.2	52.5	25.6	187.9
79.0	313.3	305.9	241.4	174.5	171.7	161.6	217.8	167.7	124.2	94.5
818.5	1073.6	1466.5	1669.8	1473.4	1181.1	1337.1	1795.4	796.2	552.6	1233.4
33.1	125.3	125.7	186.0	47.7	51.3	38.3	101.2	27.5	23.1	33.7
32.1	472.5	636.3	745.8	802.9	496.3	590.9	585.4	128.2	61.5	248.0
42.2	891.5	905.0	1695.8	274.8	397.6	195.9	682.7	154.4	80.2	109.8
1113.2	970.7	1257.9	1357.9	343.7	962.5	571.6	1436.7	508.9	474.7	898.7
61.1	579.5	679.1	783.4	350.6	589.2	523.8	1391.9	832.5	244.8	408.7
10154.6	7226.0	6742.4	7207.2	6880.1	6396.4	8025.0	6607.4	9187.0	7955.7	7362.0
726.3	3266.9	3528.8	3781.8	3080.7	3133.2	4169.0	3657.5	2262.5	2027.3	3121.4
28.5	169.1	241.4	352.3	61.6	92.0	76.6	131.9	33.9	22.8	89.1
694.8	2932.3	1874.3	1659.5	1338.5	1819.2	1541.2	2301.8	3024.4	2093.9	1660.9
146.7	907.6	1169.4	1853.9	706.9	880.7	879.5	1580.7	366.2	211.7	541.4
74.0	866.4	1260.9	1151.1	680.8	817.2	752.4	616.3	416.3	745.0	728.8
1583.0	1242.0	1464.5	1848.7	1446.5	1178.2	1148.1	1905.4	662.1	413.1	1023.7
38.1	638.7	1039.9	1192.6	347.7	563.0	459.9	1007.7	296.8	133.9	504.0
36.4	97.2	128.9	113.9	33.7	34.8	44.3	51.0	20.5	22.2	28.0
661.9	2591.5	3296.1	4384.0	2869.9	2734.6	2572.5	3531.1	2439.6	2844.1	2034.2
5230.4	3562.2	2884.4	2440.0	2592.8	2872.9	2788.2	2836.5	4059.6	3777.7	2675.6
199.6	401.3	725.4	691.1	429.4	487.3	466.2	666.8	190.6	161.2	289.4
2385.9	401.4	403.1	380.6	432.0	499.7	341.8	498.9	204.9	257.2	337.1
2022.1	3281.7	3451.5	3440.1	3056.7	3013.3	2795.4	3542.2	2978.9	2601.0	1770.1
101.1	3577.5	4720.9	3595.7	1633.2	3352.0	3373.9	3299.5	2950.2	1624.3	3475.2
117.9	1026.7	1468.7	2036.0	414.0	736.3	577.8	1213.6	258.3	123.3	458.0
213.0	1067.3	1452.8	1379.6	1562.7	1277.4	1648.1	1549.2	313.4	188.8	627.0
54.0	615.3	917.4	1068.2	708.8	702.1	726.7	1340.4	351.4	165.6	817.4
60.3	579.7	1108.0	1166.5	367.0	685.4	372.1	1160.2	270.9	90.3	452.6
1678.5	1074.0	1112.0	937.3	762.7	768.7	787.7	908.7	882.0	1010.0	1068.1
25024.5	8106.4	8072.6	8717.4	8945.6	7716.4	10145.4	7489.4	12151.6	12534.0	11394.0
93.6	481.5	695.0	649.5	366.7	451.5	452.9	701.3	218.9	110.3	314.8

4722.8	4197.7	4899.2
1175.0	959.7	717.8
924.4	601.6	702.1
312.5	239.7	322.0
4154.9	3864.5	4446.3
581.8	721.1	808.6
2309.0	2728.6	2575.4
151.3	294.3	313.1
2366.5	3177.1	3337.5
9298.9	8173.6	8434.1
3645.1	3570.3	5162.2
354.7	190.2	335.4
272.4	339.1	243.8
2046.3	2286.5	1815.3
126.2	132.3	128.3
671.6	772.3	887.7
1472.9	585.4	1844.5
1391.1	1282.7	1318.2
1216.7	811.6	513.6
6134.7	7834.8	7104.5
3690.6	3643.9	4137.9
216.8	240.2	207.4
1684.2	2451.1	2091.7
2007.5	1318.5	2574.9
1013.9	1256.4	1254.3
2168.0	2037.3	2308.7
1367.9	817.3	708.8
77.2	69.4	44.4
4791.2	3608.4	4201.6
2589.7	3001.9	3078.4
655.5	692.0	987.2
415.1	891.5	448.7
3947.9	4665.8	3743.3
2268.4	2965.3	2857.3
1912.1	1272.4	1176.0
1942.9	921.7	3199.1
1123.3	813.9	1276.2
1074.6	880.7	975.6
907.5	1550.2	762.5
7638.0	8322.5	7708.7
982.7	882.4	1178.8

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Clostridium
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EF098318.1 gg_id:182632 mouse cecum clone SWPT14_aaa04f12 EF0983
EU452296.1 gg_id:326031 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
AY991846.1 gg_id:135402 mouse cecum clone C20_h05 AY9918
EU455602.1 gg_id:330278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
EF096300.1 gg_id:198463 mouse cecum clone obob1_aaa04d10 EF0963
EF098746.1 gg_id:199211 mouse cecum clone SWPT16_aaa04c10 EF0987
EF096344.1 gg_id:180694 mouse cecum clone obob2_aaa01c06 EF0963
EU510446.1 gg_id:274237 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38g05 EU510
EU453143.1 gg_id:352769 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
EU454296.1 gg_id:304917 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454
EF098140.1 gg_id:174184 mouse cecum clone SWPT14_aaa02b01 EF0981
EU451037.1 gg_id:352146 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EF604634.1 gg_id:232681 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
AY991811.1 gg_id:132756 mouse cecum clone C20_f17 AY9918
EU451512.1 gg_id:341100 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EU503823.1 gg_id:264544 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01b06 EU503
EU510959.1 gg_id:258626 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52d07 EU510
EF098083.1 gg_id:194848 mouse cecum clone SWPT14_aaa01c05 EF0980
EU506320.1 gg_id:273558 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63b10 EU506
AY992877.1 gg_id:130280 mouse cecum clone C22_g16 AY9928
AM932538.1 gg_id:567954 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ015189.1 gg_id:132741 mouse cecum clone M2_g02_2 DQ015
EF095964.1 gg_id:187871 mouse cecum clone lean2_aaa01a05 EF0959
EU457571.1 gg_id:349645 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU457
EU474428.1 gg_id:287507 western lowland gorilla feces clone GORSD_aaa01a10 EU4744
EF096058.1 gg_id:190496 mouse cecum clone lean2_aaa03b08 EF0960
AY991913.1 gg_id:129978 mouse cecum clone C20_k14 AY9919
AM932611.1 gg_id:537301 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
FJ879176.1 gg_id:403497 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EU504967.1 gg_id:273683 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h09 EU5049
EF098676.1 gg_id:180508 mouse cecum clone SWPT16_aaa03c07 EF0986
DQ014804.1 gg_id:131642 mouse cecum clone M1_h04_2 DQ014
DQ815639.1 gg_id:163445 mouse cecum clone aab44b08 DQ815
DQ014926.1 gg_id:133348 mouse cecum clone M1_1e10 DQ014
EU454486.1 gg_id:311129 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4544
EF099794.1 gg_id:197183 mouse cecum clone SWPT4_aaa04d06 EF0997
EU511991.1 gg_id:262335 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12d06 EU5119
EU006205.1 gg_id:240405 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0062
EF098596.1 gg_id:174631 mouse cecum clone SWPT16_aaa01h10 EF0985
EU454164.1 gg_id:321642 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4541
EU504734.1 gg_id:260278 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01c09 EU5047

1433.7	2477.6	3122.7	3783.3	2434.8	2750.6	2888.3	3705.1	3715.2	3809.5	3621.4
4088.1	1715.4	2010.0	1777.5	1306.5	1608.6	1645.1	1489.0	1904.7	1431.1	2201.3
15337.6	6412.2	5617.4	7035.1	5258.3	4878.7	6321.0	6640.7	8234.0	6992.6	7925.0
2897.0	4049.4	3555.7	2970.6	3467.0	3507.8	3020.7	3415.1	3579.4	3461.2	3187.7
7285.5	3890.7	4175.5	4585.4	4355.1	4160.6	4406.4	4213.0	4926.8	5067.1	4507.1
45.3	68.5	43.9	102.1	36.7	106.9	82.8	397.1	33.6	70.3	60.4
1318.1	2063.3	2218.9	2403.8	2461.9	2122.2	2616.1	2359.1	1183.0	1056.0	1356.4
54.2	1168.7	1936.6	2338.5	667.7	1378.6	1183.5	1887.3	315.0	189.1	1051.5
1598.9	644.4	782.2	607.1	841.1	687.3	855.7	1173.3	463.8	864.8	458.4
16663.3	4087.4	3670.5	4815.7	3756.6	3917.5	4171.0	3762.6	5944.7	4893.7	5603.1
2980.3	2372.4	2316.8	2325.9	2226.4	2120.0	2660.1	2014.5	2052.4	1057.0	2502.5
187.8	612.4	936.2	1114.4	766.0	802.8	1245.8	967.6	649.7	2163.0	478.9
943.5	3280.2	4154.2	3487.3	2673.1	3243.0	3074.5	3181.1	4073.2	2450.8	3904.5
98.3	792.3	948.5	932.6	713.0	871.3	929.4	1246.0	714.9	653.6	355.5
45.6	109.6	217.3	221.8	97.7	82.0	109.5	122.3	42.1	37.9	65.5
55.1	286.5	318.2	362.0	50.3	446.0	358.4	1233.4	47.6	144.8	139.3
32.4	45.1	59.9	98.4	79.2	69.1	58.9	79.2	25.6	43.0	32.4
789.9	1287.8	1735.5	1629.5	1258.4	1008.7	1395.6	1363.4	682.8	1113.6	1217.1
189.9	2102.1	1810.0	1622.1	1326.8	1712.1	1269.2	1623.5	2232.4	2261.9	1308.7
110.3	419.1	781.8	966.0	353.8	670.9	359.5	1164.0	185.7	112.6	362.8
7528.8	3952.2	3931.5	4559.5	4228.1	3749.7	5783.8	4498.3	3859.2	3755.4	3789.7
111.2	204.2	275.6	381.5	208.2	237.4	273.3	309.2	207.2	128.4	198.4
38.7	112.1	135.3	147.8	55.1	73.0	50.9	112.2	54.1	75.8	40.4
123.0	1078.7	1524.7	1796.4	352.3	729.4	496.7	1304.5	419.8	668.0	671.9
108.6	2286.9	2364.8	2199.1	1633.6	1768.4	1598.5	1956.4	958.7	344.9	1425.2
45.5	256.8	254.3	502.2	238.6	522.7	221.8	1075.6	88.1	207.0	162.9
56.5	89.4	174.0	311.3	59.2	72.7	69.3	100.8	48.9	34.5	122.1
40.1	238.4	313.9	363.0	94.4	317.8	206.8	644.2	54.8	153.7	146.0
2889.2	4663.7	5171.7	4746.9	2696.1	3821.5	2989.0	4169.4	2496.5	1800.4	4193.9
2525.9	1298.9	1903.8	1878.6	1955.1	1282.5	1718.2	1729.3	996.5	505.5	1146.3
905.3	1778.3	2125.1	1994.8	989.5	1639.9	1323.8	2030.7	1515.5	1357.1	1652.4
94.2	1165.4	1265.8	1116.6	1230.2	861.1	967.4	816.8	562.6	413.8	835.4
35.1	455.4	794.9	954.6	94.5	186.7	127.3	480.1	66.8	40.1	181.4
1646.9	3922.9	3046.5	3130.9	3492.3	3814.1	3334.7	3553.5	3896.2	6616.1	2731.7
174.5	309.5	441.3	482.4	244.4	306.4	341.1	318.6	205.1	165.4	276.4
17234.0	7798.1	7822.2	8164.5	7595.2	7512.9	8104.3	6882.2	8569.3	7217.2	9962.4
978.2	3378.5	4847.0	4720.9	4274.4	3982.6	3301.3	4340.1	2781.3	1698.0	3485.0
150.9	1148.9	1102.5	1058.3	796.8	870.9	818.2	915.5	1179.8	852.2	849.8
318.6	2228.9	2712.4	2613.2	3820.8	2570.9	3411.7	1769.0	1548.8	706.3	2215.9
37.1	276.5	381.4	480.9	67.7	81.0	77.9	245.3	25.7	36.6	63.1
52.5	33.2	40.3	59.6	39.8	38.2	38.4	37.0	42.3	27.2	39.8

2992.7	4106.0	4972.1
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720.5	156.8	220.2
1715.6	2836.7	2765.1
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1236.2	873.8	1175.5
3354.9	5179.2	3688.0
3420.9	2299.9	2094.1
876.5	1112.2	885.0
2683.3	2985.8	3096.8
1777.3	649.9	1505.1
145.7	118.8	89.6
2329.4	259.2	1500.7
95.7	216.7	150.8
1428.3	1482.5	1607.1
1697.7	1702.6	2007.2
1415.0	629.1	1432.3
4688.9	6032.2	5105.4
241.7	260.8	354.0
171.6	186.7	318.4
1695.4	1185.4	3023.2
1955.9	1892.3	2688.1
1691.6	486.2	1173.8
115.7	89.7	75.5
1210.2	332.3	1276.3
4264.3	4166.1	4578.2
1928.2	1850.8	2417.7
1544.5	2696.3	3295.3
849.1	1609.1	977.3
441.0	528.6	205.3
2855.5	2745.3	2965.9
308.4	497.2	575.0
6710.9	9010.8	7012.4
3268.0	4138.0	6201.5
1079.1	1171.5	1159.2
2210.6	3169.3	3815.0
365.2	262.0	101.6
44.8	44.7	41.5

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o__Clostridiales	f__Lachnospiraceae

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DQ014621.1 gg_id:133579 mouse cecum clone M1_g03 DQ014
EF098295.1 gg_id:187235 mouse cecum clone SWPT14_aaa04c12 EF0982
EU454820.1 gg_id:316984 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4548
EU506201.1 gg_id:264427 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03e06 EU5062
EU451646.1 gg_id:343917 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4516
EU776893.1 gg_id:350052 Mongoose lemur feces clone ML_aae87d11 EU7768
EU766933.1 gg_id:352649 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7669
DQ824440.1 gg_id:197356 human fecal clone RL304_aal76a10 DQ824
GQ503859.1 gg_id:564639 Captain bheri clone Ecwsrb022 GQ503
AB234493.1 gg_id:146488 termite gut homogenate clone MgMjR-083 AB2344
EU768108.1 gg_id:329703 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7681
AB234484.1 gg_id:147741 termite gut homogenate clone MgMjR-030 AB2344
EU504190.1 gg_id:258283 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03g02 EU5041
DQ798696.1 gg_id:198678 human fecal clone RL181_aao00c02 DQ798
AY349389.1 gg_id:92430 human oral cavity clone JM048 AY3493
FJ978593.1 gg_id:384675 feces clone CL_F_197 FJ9785
FJ676837.1 gg_id:525104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
DQ802531.1 gg_id:187163 human fecal clone RL188_aan93a09 DQ802
DQ905267.1 gg_id:171220 human fecal clone 013-g8 DQ905
AB088949.1 gg_id:77909 termite gut homogenate clone Rs-D68 bacterium AB0889
AY974898.1 gg_id:116267 human ascending colon mucosal biopsy clone KH90 AY9748
DQ802285.1 gg_id:181634 human fecal clone RL188_aah15f04 DQ802
AY975299.1 gg_id:124921 human ascending colon mucosal biopsy clone N540 AY9752
DQ803552.1 gg_id:199212 human fecal clone RL251_aaj87d02 DQ803
NR_029269.1 gg_id:584986 Clostridium propionicum str. X2; DSM 1682 NR_029
GQ448418.1 gg_id:557186 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ362869.1 gg_id:363216 feces adult twins and mothers; TS13 clone TS13_a04b10 FJ3628
EU748174.1 gg_id:321561 neotropical folivorous flying bird adult hoatzin crop clone hoa31_73A10.F EU7481
EF399587.1 gg_id:205933 human fecal clone SJTU_F_06_63 EF3995
AY992923.1 gg_id:130491 mouse cecum clone C22_i22 AY9929
GU304319.1 gg_id:563613 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
DQ799077.1 gg_id:180319 human fecal clone RL205_aaj17c08 DQ799
DQ327495.1 gg_id:150500 Metagenomic gut microbiome healthy human stool clone EA67 DQ327
EF402203.1 gg_id:204121 human fecal clone SJTU_B_04_90 EF4022
DQ804300.1 gg_id:197231 human fecal clone RL187_aan77f07 DQ804
EU763532.1 gg_id:327125 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7635
EU472163.1 gg_id:295754 francois langur feces clone FL_2aaa03h11 EU4721
EF434346.1 gg_id:210179 human infant gastrointestinal tract microbiota stool baby 3 12 weeks old clone 10999 EF4343
DQ799640.1 gg_id:175400 human fecal clone RL305aal88f01 DQ799
EU761814.1 gg_id:347117 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
EU250957.1 gg_id:370405 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU2509

10664.8	4065.8	4047.3	4767.1	4158.8	3977.6	4490.9	4028.7	4757.8	5089.1	5049.5
29.8	26.9	38.9	42.5	25.1	20.5	30.1	35.6	26.3	20.7	24.3
264.8	3673.3	5867.8	5057.7	3324.8	4142.3	3156.8	3925.8	2425.3	3477.8	3665.7
123.3	1109.9	950.8	868.8	596.4	773.0	598.8	855.6	485.9	435.7	521.5
1363.2	2012.3	2422.8	2644.6	2981.2	2813.8	3070.5	4199.6	1311.8	4364.1	1839.0
1559.4	1364.8	1272.7	1222.1	1179.4	1323.2	1283.2	1145.3	1805.6	1475.0	867.6
41.9	269.5	361.6	441.7	130.7	275.2	220.2	417.3	213.1	73.0	372.1
280.2	2437.5	4524.1	3763.3	2179.2	3460.9	2827.6	3565.1	2151.6	1680.6	2774.8
8180.7	4839.1	5248.3	4613.7	5299.4	4964.2	6044.8	4999.5	6132.8	4146.6	5668.3
47.6	1809.1	1349.2	1363.1	523.6	1416.3	552.9	2213.9	668.1	276.8	2581.6
2479.9	3444.6	4111.1	4076.5	4222.4	3279.6	4782.3	3553.9	3627.8	1108.2	3977.7
52.9	163.2	248.3	275.3	181.5	144.6	179.0	162.3	90.6	24.4	119.6
236.2	2653.4	3468.1	3851.2	3115.5	2370.3	3358.3	3178.8	1318.4	1139.7	2158.9
1631.3	610.4	578.4	618.9	598.7	643.9	448.0	570.6	443.4	322.7	657.5
502.8	543.8	398.6	480.3	413.8	294.4	555.9	471.7	643.9	164.3	363.0
24.3	368.1	790.4	1035.2	137.2	592.0	441.0	1066.7	196.3	73.6	710.9
682.8	3611.1	3715.0	4214.1	2003.1	2859.8	2057.8	3096.9	2403.5	1598.8	2122.6
3884.7	4533.6	5137.0	5899.5	5883.9	5526.6	5584.4	4904.2	3079.7	6097.6	4970.2
75.4	1658.9	2946.0	1864.5	1068.8	2187.7	1204.0	2928.2	933.2	281.7	1569.8
2067.9	2296.9	2786.1	3113.0	2064.4	2182.9	3912.4	2193.2	2204.8	1514.6	2330.4
943.7	2813.5	2851.9	2064.3	1982.6	2503.2	2086.4	2456.5	2795.3	1906.6	1841.8
287.1	2623.7	2671.8	3323.3	1546.8	2237.8	2098.7	2226.6	1632.7	1107.3	1643.4
1161.7	1731.1	2483.7	2523.5	2896.4	2371.2	3100.1	2335.7	1545.8	4281.8	1749.7
136.7	424.9	654.5	992.8	529.2	638.1	399.7	924.4	622.2	486.9	400.3
10447.5	3110.5	3899.2	3609.5	2956.3	3241.5	3201.0	3252.7	5210.4	7445.6	3911.8
9948.2	5568.0	5934.3	5790.9	6295.0	5560.2	5803.5	6111.9	5702.0	6228.0	6247.1
21598.4	9723.8	8005.3	6448.7	6666.5	9077.7	6588.1	7580.4	10856.1	6439.0	8022.4
3118.8	7612.4	9026.7	9263.4	7141.9	7921.5	9109.5	8495.9	8197.2	8467.5	8814.8
67.0	277.5	356.7	398.9	198.4	411.7	161.7	476.8	250.2	1014.0	220.9
91.2	883.1	1448.7	905.3	614.9	1125.7	664.9	1394.5	386.4	259.5	933.6
4862.7	3703.7	4931.7	5118.9	5126.6	4802.5	5014.5	4958.7	4014.8	3004.3	4453.3
62.4	208.7	321.2	486.8	275.0	225.0	384.8	472.5	71.4	96.5	296.6
140.8	1739.7	2416.7	2191.9	1414.7	1680.5	1591.9	2185.6	2338.5	1406.9	1704.8
36.4	721.0	1138.4	1335.8	385.7	772.5	637.5	1411.2	374.7	161.4	926.8
211.4	528.2	989.2	1200.4	220.3	722.4	600.6	942.2	295.9	85.8	1326.3
86.9	812.8	1524.1	1530.3	447.7	845.6	594.5	1694.0	745.7	336.1	685.0
2849.6	4130.1	4734.4	4842.6	5794.8	4649.1	5136.1	6990.5	4169.9	2536.6	4936.7
139.5	1669.3	1508.9	1400.4	1069.5	1228.1	479.2	1485.8	1580.0	383.8	782.8
2882.6	2176.7	3162.6	2537.6	2295.2	2119.5	3217.1	2326.7	2115.1	1554.9	2734.5
74.8	666.9	1283.2	1022.2	1021.7	813.1	1118.3	966.8	252.5	202.5	586.2
42.7	377.8	496.0	513.0	292.6	398.8	215.9	726.4	239.9	215.6	286.0

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24.5	44.2	34.1
3030.7	3807.3	3794.5
852.8	1308.8	713.5
4392.8	2867.9	4727.4
1500.2	1962.4	1326.6
583.0	330.9	829.5
2949.3	3985.7	4704.7
4833.7	5571.1	4961.2
1603.3	1065.4	1336.2
3499.9	3915.4	4510.7
155.4	197.2	181.6
3460.2	3041.4	4044.5
456.1	1001.5	513.0
269.9	604.3	447.2
1356.6	453.4	1219.7
4652.2	2096.3	2025.7
5365.2	6858.8	5472.4
3101.4	2788.2	4551.0
2614.1	2880.1	3082.6
2243.2	2096.7	2385.9
2432.9	2374.1	3363.0
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353.2	826.9	432.9
701.5	1179.2	1545.1
4787.1	5420.1	5866.4
195.3	326.8	432.5
2093.7	2855.0	3127.8
1605.6	1053.5	1703.2
673.8	385.6	609.5
1627.9	1545.0	1546.4
4561.7	4801.1	4313.2
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746.8	1397.8	2390.8
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o__Clostridiales	f__Lachnospiraceae

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AB185777.1 gg_id:105659 rumen clone U29-D06 AB185
FJ368953.1 gg_id:358649 feces adult twins and mothers; TS4 clone TS4_a02e05 FJ3689
FJ364499.1 gg_id:365900 feces adult twins and mothers; TS15 clone TS15_a03f08 FJ3644
AB288892.1 gg_id:201079 termite gut homogenate clone BOf2-23 AB288
DQ799135.1 gg_id:185370 human fecal clone RL205_aaj18a11 DQ799
EU763056.1 gg_id:313769 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
DQ803148.1 gg_id:182190 human fecal clone RL311_aam21b06 DQ803
AM275397.2 gg_id:231161 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
AF371679.1 gg_id:32467 swine intestine clone p-4247-4Wa3 AF371
AB234448.1 gg_id:148473 termite gut homogenate clone MgMjR-070 AB234
AB192216.1 gg_id:143980 termite gut homogenate clone RsTu1-66 AB192
GQ449057.1 gg_id:547906 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ449
EF603661.1 gg_id:229062 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
GQ502561.1 gg_id:563998 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU763577.1 gg_id:308853 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EF097077.1 gg_id:175307 mouse cecum clone SWPT18_aaa01a12 EF097
AM420271.1 gg_id:251150 Noma subgingival plaque clone 702B06(oral) AM420
AY986119.1 gg_id:118835 human stool clone D461 AY986
EU510399.1 gg_id:268620 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37h12 EU510
AB198664.1 gg_id:135632 termite gut fluid and protists fraction clone RsC01-098 AB198
EU472066.1 gg_id:289449 francois langur feces clone FL_1aaa03g05 EU472
AY684405.2 gg_id:110059 mucosal biopsies human intestine clone HuDI72 AY684
DQ807168.1 gg_id:176088 human fecal clone RL244_aaj47b01 DQ807
AY916283.1 gg_id:113415 human sigmoid colon biopsy clone G075 AY916
AY984500.1 gg_id:121072 human stool clone B424 AY984
DQ797242.1 gg_id:174520 human fecal clone RL386_aao88g10 DQ797
FJ366310.1 gg_id:361864 feces adult twins and mothers; TS26 clone TS26_a01b09 FJ3663
DQ825193.1 gg_id:188567 human fecal clone RL185_aan86e06 DQ825
GQ175485.1 gg_id:591118 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
NR_026151.1 gg_id:539658 Clostridium colinum str. DSM 6011 NR_02
EU850560.1 gg_id:347796 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF369 EU850
EU768799.1 gg_id:318400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
EU283547.1 gg_id:277790 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A889 EU283
EU842731.1 gg_id:318679 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF603946.1 gg_id:233761 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6039
AB192057.1 gg_id:142092 termite gut homogenate clone M1NP2-32 AB192
AJ811979.1 gg_id:196159 human biopsies Human ulcerative colitis biopsy clone UC9-31 AJ8119
DQ647100.1 gg_id:256583 Microbial structure -temperature oil-field produced water Troll formations North Se DQ647
EU764416.1 gg_id:329193 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU764
DQ456412.1 gg_id:157611 pre-adolescent turkey cecum clone CFT214G6 DQ456

762.3	1525.3	1943.7	1745.3	2107.0	1710.4	2040.7	1993.6	1468.1	1615.5	1513.2
91.3	302.1	457.1	541.9	365.1	466.6	337.3	469.2	109.6	68.6	246.1
4701.8	1671.5	1846.6	2034.5	1232.6	1784.1	1344.4	1452.7	1916.1	2330.4	1745.3
845.8	2087.2	2225.7	2137.4	2023.9	1725.5	1006.5	1437.0	1275.8	512.5	905.7
46.0	37.6	45.6	52.5	53.8	38.6	37.6	38.2	47.5	18.1	55.3
10537.1	5780.7	5940.9	5340.4	5777.9	6777.9	6892.2	6411.9	4711.8	3594.3	6889.7
233.5	1007.8	1910.4	1508.8	1119.3	1585.7	1210.5	2497.0	463.2	720.7	1295.4
2520.9	1525.6	2070.8	1665.6	1924.1	1782.3	1944.5	1906.4	2016.7	553.8	2341.8
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197.6	468.9	844.5	608.8	892.2	570.9	813.6	801.8	441.6	292.6	537.1
35.8	89.7	132.2	113.3	31.7	35.8	26.3	77.8	23.5	31.7	18.3
646.5	3240.5	2986.9	2498.3	2098.3	2872.9	2647.2	2043.2	3894.2	2985.2	2901.7
562.3	2619.2	2068.1	2603.2	1854.3	1495.1	1578.2	1820.4	4190.7	1295.6	1505.2
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83.2	1254.4	2011.9	2522.3	591.9	1330.9	986.5	1580.4	563.0	206.9	1163.4
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3351.4	2129.4	2263.1	2031.6	1728.9	2339.7	1970.2	2168.6	2338.0	1508.1	2616.5
33.6	213.3	333.1	251.5	161.5	235.4	301.1	385.5	184.6	27.2	130.3
250.4	3193.7	2653.8	1612.9	1891.9	2447.1	1809.7	2699.5	2847.9	2400.9	1919.2
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2861.5	2458.7	3102.6	3157.4	3389.8	2309.1	3281.9	2902.1	2027.5	1055.2	1699.0
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1694.6	2787.4	3139.0	3708.6	3292.6	3028.8	3142.1	3629.5	2100.8	1108.8	2319.6
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152.2	902.7	1611.4	1122.3	949.2	1003.7	1012.2	1322.9	1001.1	951.2	769.3
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1533.0	2015.6	2155.2
274.9	703.3	2563.2
304.6	121.2	130.2
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56.0	61.3	45.5
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4796.5	4814.3	4889.6
498.6	813.6	930.0
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1905.9	1981.7	2176.2
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836.6	969.9	1472.7
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1608.8	1463.8	1494.1
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92.0	311.2	110.4
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AB062841.1 gg_id:26279 termite gut homogenate clone BCf8-25 AB0628
AY985062.1 gg_id:126206 human stool clone BA71 AY9850
DQ802414.1 gg_id:180986 human fecal clone RL188_aah17d07 DQ802
DQ799668.1 gg_id:190728 human fecal clone RL305aal88h06 DQ799
FJ676210.1 gg_id:518083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
EF603789.1 gg_id:232266 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6037
AY979358.1 gg_id:127662 human transverse colon mucosal biopsy clone Z695 AY9793
AM943572.1 gg_id:264963 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype AM943
AB192012.1 gg_id:143098 termite gut homogenate clone M2PB4-40 AB1920
FJ684344.1 gg_id:520882 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ879150.1 gg_id:430468 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EF403013.1 gg_id:217103 human fecal clone SJTU_B_15_58 EF4030
AB192210.1 gg_id:141614 termite gut homogenate clone RsTu1-57 AB1922
DQ797516.1 gg_id:176077 human fecal clone RL248_aaj00d07 DQ797
FJ678223.1 gg_id:520821 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU766302.1 gg_id:310536 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
AY571391.1 gg_id:114703 termite gut clone RsaHw471 AY5713
EU511960.1 gg_id:262308 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12a02 EU5119
EU505619.1 gg_id:262012 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa03e07 EU5056
DQ905770.2 gg_id:164968 Effect bowel preparation and colonoscopy on post-procedure intestinal microbiota DQ905
EU344188.1 gg_id:275416 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3441
AB062772.1 gg_id:37128 termite gut homogenate clone BCf1-11 AB0627
AB234445.1 gg_id:145498 termite gut homogenate clone MgMjD-060 AB2344
DQ802465.1 gg_id:178262 human fecal clone RL188_aah18b04 DQ802
AY981965.1 gg_id:127759 human sigmoid colon mucosal biopsy clone P096 AY9819
FJ365463.1 gg_id:362977 feces adult twins and mothers; TS20 clone TS20_a03b11 FJ3654
EU765802.1 gg_id:317793 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
EU475248.1 gg_id:298150 bonobo feces clone BNO_aaa03f12 EU4752
FJ366941.1 gg_id:360303 feces adult twins and mothers; TS28 clone TS28_a01f02 FJ3669
EU488294.1 gg_id:540852 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4882
DQ206415.1 gg_id:140502 microbial mediates arsenate reduction soda lake water clone ML-AsS-9 DQ206
EF096990.1 gg_id:187515 mouse cecum clone SWPT13_aaa03g10 EF0969
EU768713.1 gg_id:339985 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7687
EU344547.1 gg_id:263432 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3445
DQ904757.1 gg_id:162278 human fecal clone 001B-c11 DQ904
GQ493719.1 gg_id:578445 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AJ576348.1 gg_id:102471 hindgut homogenate Pachnoda ephippiata larva clone PeH31 AJ5763
EU775142.1 gg_id:348992 Francois Langur feces clone FL_1aaa04a08 EU7751
AB192223.1 gg_id:142182 termite gut homogenate clone RsTu1-83 AB1922
FJ679144.1 gg_id:524841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791

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44.4	228.2	622.7	431.9	242.9	210.2	372.0	362.8	162.7	50.1	269.7
126.5	443.4	944.7	720.2	276.1	457.1	435.6	800.6	347.1	355.1	837.8
9767.8	4063.8	3328.4	3605.4	3393.4	3791.1	3633.9	3539.1	5177.0	5102.3	5163.8
64.3	636.0	1341.8	948.4	587.3	564.8	765.6	975.3	322.5	213.9	577.3
436.3	2753.0	3391.1	3575.3	2665.7	3030.2	3972.2	3940.5	1099.6	692.3	2164.3
2539.5	1918.2	1965.5	1499.1	1921.7	1764.2	1820.3	2285.5	2125.1	868.5	2774.1
2407.2	3176.9	2898.9	2489.8	2134.4	2707.8	2319.1	2570.7	3374.0	3823.1	2129.2
4448.6	4070.9	4564.3	4693.3	3824.8	3559.0	4333.4	5578.8	4314.9	3984.1	5012.4
53.7	357.7	578.1	305.4	276.7	377.6	207.8	300.3	227.5	45.6	262.0
70.9	974.6	1208.6	1504.2	520.0	885.1	620.6	1163.3	413.4	1327.4	657.4
93.5	608.5	964.9	1223.5	568.8	693.1	560.7	831.7	1380.2	316.0	377.6
4330.0	3118.4	4205.8	3945.5	3123.0	3141.0	2848.5	4321.0	2805.6	2908.0	3042.3
439.2	1835.1	2929.7	3282.3	2484.8	1938.4	2466.8	2657.3	2143.8	372.3	2266.1
43.8	126.6	138.8	139.0	68.9	189.1	63.7	90.6	41.8	38.8	74.3
102.0	494.1	736.6	916.2	425.5	439.8	632.1	784.4	287.3	151.0	435.9
3174.0	1898.3	1817.0	2286.0	1708.2	2478.6	1982.0	1640.6	2556.8	1725.8	3398.5
92.5	101.8	169.1	133.4	112.8	109.3	195.4	186.6	78.6	31.8	84.4
57.3	405.3	569.7	1018.1	531.8	380.6	464.0	579.7	179.5	173.8	287.9
827.4	868.9	1375.7	1761.8	571.2	1146.2	758.9	2031.9	365.7	167.4	384.2
913.9	4196.4	4831.4	3708.4	4893.5	5091.1	4569.0	4647.0	2933.2	2794.3	3787.2
14560.4	6969.4	8027.2	8793.5	7743.8	7494.7	8414.1	8512.2	7650.0	9420.0	9005.2
6525.0	5163.5	5153.7	5595.7	5329.6	5510.9	5167.5	5058.5	5318.9	3624.3	5719.8
43.7	41.3	85.8	43.0	45.7	54.5	53.8	59.4	24.8	21.8	37.1
128.4	392.0	454.0	488.1	151.5	169.8	112.7	255.3	257.9	127.8	100.9
9666.2	5509.7	5650.4	5846.1	5510.0	5486.6	6036.2	5566.4	5803.3	6987.6	5883.4
834.1	2320.2	2411.9	1785.4	1903.8	2505.7	1890.7	2632.0	3995.5	2179.6	2035.8
558.7	4203.1	3845.5	5527.1	3890.0	4267.9	2873.6	4671.0	3793.7	5228.1	2613.4
231.2	1247.8	1818.3	1841.8	673.5	900.1	1269.4	1139.1	223.0	105.0	988.8
62.8	117.7	123.6	121.2	54.9	55.3	47.7	60.4	47.3	32.1	80.8
2516.2	1686.3	2122.9	2535.3	1005.2	1861.1	1342.6	2605.6	837.3	755.5	1595.3
46.8	596.7	927.9	852.1	560.3	595.5	442.8	951.8	373.6	294.1	646.3
789.5	5457.3	5246.3	4450.6	4981.6	4415.2	4367.6	4110.9	5188.1	5604.9	3950.8
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1963.3	4257.7	5331.3	3961.0	3232.6	4559.0	3806.2	3948.0	5359.1	6727.3	4900.4
41.3	224.8	643.9	730.6	166.8	192.4	231.8	315.3	89.5	56.0	159.8
80.5	289.5	208.3	226.5	99.6	251.8	118.4	465.9	495.3	125.0	109.5
77.8	443.1	854.4	545.7	387.4	500.4	351.1	901.4	350.5	96.7	676.3
435.7	3076.5	3975.5	3477.5	2425.7	2884.8	3503.9	3565.6	1846.8	964.7	2209.2
3210.3	2219.7	2942.4	3247.5	3284.2	3249.3	3347.0	3262.5	1658.0	2129.0	2032.4
6996.3	3401.3	4475.5	4227.4	3587.7	3710.2	4159.5	3879.2	3710.5	3547.1	4839.6

4977.6	7255.2	6942.8
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532.5	758.7	2101.0
3215.1	4197.1	3706.3
571.6	1215.3	2261.5
3127.7	4126.6	4629.6
1314.2	2161.4	1767.4
2244.1	2762.4	2924.0
4187.3	4193.8	5174.9
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761.0	1369.4	1292.7
1784.0	897.6	762.6
5231.4	3353.3	6138.9
1933.5	2500.6	1924.8
56.6	83.4	370.6
464.9	742.5	631.9
1496.7	2370.2	1791.6
208.9	236.7	169.5
692.7	824.2	1610.1
2454.4	1189.0	1876.0
3935.4	3927.8	6042.9
8354.3	8430.4	9838.7
4355.4	6676.3	5314.5
87.7	57.9	60.4
465.7	519.6	546.1
5546.2	6371.5	7105.0
1561.3	3689.4	2440.0
4071.4	3717.6	4635.7
782.2	1233.3	1735.5
78.6	117.4	69.2
2214.0	1843.2	2607.5
677.1	742.7	613.7
3907.7	5118.8	6295.9
2924.9	2571.8	2656.8
4140.5	4682.7	4988.8
243.8	417.5	218.9
463.2	557.9	170.6
554.7	567.7	964.0
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2931.4	5342.2	4725.2
3681.2	4791.9	5362.0

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o__Clostridiales	f__Lachnospiraceae

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AY985458.1 gg_id:125070 human stool clone C413 AY9854
GQ502538.1 gg_id:552353 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
GQ249495.1 gg_id:587669 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor GQ249
DQ905185.1 gg_id:168289 human fecal clone 002C-h6 DQ905
FJ681873.1 gg_id:509718 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
DQ802242.1 gg_id:184702 human fecal clone RL188_aah15a02 DQ802
DQ804469.1 gg_id:195799 human fecal clone RL187_aan80d02 DQ804
AB198449.1 gg_id:135337 termite gut wall fraction clone RsW01-009 AB1984
EU843061.1 gg_id:345031 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ802280.1 gg_id:195605 human fecal clone RL188_aah15e10 DQ802
EU508139.1 gg_id:269912 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01c09 EU508
EF402988.1 gg_id:206523 human fecal clone SJTU_B_15_24 EF4029
DQ824134.1 gg_id:177731 human fecal clone RL204_aaj59g08 DQ824
AY984216.1 gg_id:119151 human stool clone B105 AY9842
AY974917.1 gg_id:121020 human ascending colon mucosal biopsy clone KI37 AY9749
EU765496.1 gg_id:354397 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU7654
AY571393.1 gg_id:114620 termite gut clone RsaHf312 AY5713
EU777270.1 gg_id:351986 Okapi feces clone OK3_b06_1 EU777
EU762778.1 gg_id:320202 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ327161.1 gg_id:148112 Metagenomic gut microbiome healthy human stool clone E682 DQ327
DQ804246.1 gg_id:181537 human fecal clone RL187_aah70g10 DQ804
AY667250.1 gg_id:105725 TCE-dechlorinating groundwater clone TANB5 AY667
EU344412.1 gg_id:275216 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ799449.1 gg_id:192133 human fecal clone RL305aal86d08 DQ799
FJ833638.1 gg_id:549831 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_36D05 FJ8336
EF123527.1 gg_id:242805 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbe EF1235
AY985856.1 gg_id:126931 human stool clone D130 AY9858
EF559166.1 gg_id:218171 mesophilic anaerobic digester clone G35_D8_H_B_B09 EF5591
AB198443.1 gg_id:135362 termite gut wall fraction clone RsW01-001 AB1984
EU765511.1 gg_id:304969 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
FJ372276.1 gg_id:366470 feces adult twins and mothers; TS9 clone TS9_a03g02 FJ3722
DQ905850.2 gg_id:168659 human fecal clone 29E-f6 DQ905
EF400772.1 gg_id:213176 human fecal clone SJTU_D_01_33 EF4007
EF097198.1 gg_id:177969 mouse cecum clone SWPT18_aaa02h12 EF0971
EU850609.1 gg_id:324705 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF444 EU850
EU765712.1 gg_id:354597 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
FJ365526.1 gg_id:358859 feces adult twins and mothers; TS20 clone TS20_a03h07 FJ3655
EU762397.1 gg_id:345086 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ904836.1 gg_id:167327 human fecal clone 001C-b10 DQ904
DQ815362.1 gg_id:171881 mouse cecum clone aab46f02 DQ815
EU762524.1 gg_id:344336 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762

8693.7	1430.8	2154.2	2176.3	2466.3	2354.1	2460.5	3000.7	613.9	815.4	1591.0
2005.5	3158.7	3747.3	2978.8	2303.6	3032.8	2475.4	2909.3	3673.7	1463.0	2055.5
2228.1	5574.0	5386.8	6651.0	6633.9	7029.7	6886.9	5854.2	4356.7	4788.8	4543.0
10260.3	3778.1	4219.6	3899.1	2895.3	3374.1	3329.6	3974.2	3635.2	4505.6	3562.9
8144.3	6123.2	6096.1	6644.5	8236.3	5856.5	8100.3	6814.5	5581.6	6423.1	5262.2
312.1	2949.6	5223.5	3292.7	5131.8	4604.6	3302.9	4958.4	2479.8	2619.8	3360.6
62.0	160.4	179.5	126.5	144.3	106.3	155.2	164.7	239.3	234.3	117.8
322.1	249.6	396.9	285.4	433.5	251.0	462.7	311.2	205.7	253.7	209.6
177.2	2669.8	3386.5	2527.1	2429.3	2637.8	3227.2	2805.9	1948.8	1512.3	2117.8
3900.8	1845.9	2387.1	1888.5	1419.9	1853.6	1648.3	2557.3	2194.4	3216.6	2449.9
950.7	3153.9	4540.9	4757.3	3485.1	3394.2	3819.2	3677.2	2972.6	1312.9	2993.1
47.5	124.6	146.8	129.4	45.8	124.7	60.0	356.1	19.7	24.9	101.1
37.2	34.1	31.5	49.1	28.1	35.8	32.9	43.6	27.6	21.1	27.4
209.2	3677.1	3651.4	2870.3	2429.2	3407.8	2190.7	3410.8	2762.1	2682.5	3058.6
699.4	2501.4	2662.6	1913.2	1729.4	2543.7	1945.1	2261.6	2370.1	1572.5	2638.9
3129.1	956.8	1148.5	979.8	699.7	1114.2	972.8	1107.5	896.4	718.0	818.2
65.3	593.0	920.7	973.0	1188.2	885.1	1243.2	1043.1	268.6	255.7	401.7
137.9	1295.6	2261.1	2025.9	1059.2	1185.7	2041.3	1738.1	861.3	326.8	902.8
48.8	249.3	653.6	748.6	430.1	258.7	463.3	722.4	122.0	159.4	411.5
140.0	1199.6	1842.6	1619.6	1286.7	1520.0	1592.0	1888.7	761.5	1003.6	1078.2
1292.3	1799.7	2012.3	1322.1	1416.1	2378.5	1612.4	1946.1	2368.4	2957.8	1293.2
62.8	2378.4	3838.5	3281.6	2102.8	3037.2	2282.5	4254.2	1782.9	766.2	3729.4
5852.7	4534.7	5559.0	5969.7	5110.0	5115.9	4820.1	5784.8	4661.4	3979.9	4768.8
35.6	276.7	668.7	359.1	254.0	316.4	354.1	542.3	99.2	117.4	269.0
2564.2	4698.5	5136.1	5478.1	5325.0	5039.8	6331.2	5623.4	3554.3	2907.4	3956.9
8083.4	4930.3	4764.4	4539.9	4714.2	4556.2	4527.1	5840.2	5155.5	4668.7	4643.8
760.0	3537.8	3986.5	3757.2	3930.2	3922.8	5057.3	3403.1	3806.0	2176.9	3472.6
1074.3	2279.5	2277.3	2329.9	2350.8	2200.3	2044.4	3029.9	1530.7	1134.7	1889.3
8819.6	7821.8	7849.2	8339.3	8734.5	7558.3	9039.3	7747.8	8157.7	6280.0	9541.6
520.7	1702.7	2703.1	2094.6	2050.9	1765.6	2499.0	2506.4	1007.8	748.9	1227.9
6345.4	3302.2	4320.5	3469.5	3657.8	3400.5	4451.3	3470.5	2900.6	2216.7	3078.1
2854.5	5240.4	5172.1	5078.7	4520.9	4693.7	4349.9	4767.6	6788.1	4139.9	5679.5
44.1	369.7	328.1	198.5	508.3	358.9	147.2	231.0	84.2	79.8	203.6
1804.7	3078.0	2940.1	2458.8	2874.0	2294.1	2477.4	2372.0	4183.0	3996.3	3102.2
147.5	2585.7	3144.2	2782.9	2597.2	2588.5	2858.1	3318.2	1356.1	506.4	2267.8
144.0	2253.0	2737.6	2077.2	1701.1	2653.4	2947.7	2494.4	3301.0	2374.7	1642.3
797.3	346.8	839.5	775.8	428.0	287.9	332.7	430.5	272.9	139.0	230.1
7266.7	5521.7	5629.1	4669.3	4995.4	5958.8	5846.7	5222.7	6542.6	4454.4	6597.6
4239.8	1995.3	2474.5	2577.9	1606.3	1636.5	1800.8	2107.4	2175.7	2445.7	2628.3
40.5	40.4	46.3	59.5	26.9	15.8	15.8	39.2	16.1	16.9	16.3
38.3	586.2	1134.1	1130.0	189.9	1041.5	200.2	1316.5	559.6	985.4	433.6

1951.8	4007.7	3636.9
2251.8	2845.2	3166.7
6299.4	7410.1	7763.2
3826.2	4420.5	4869.3
6347.3	7134.2	6529.0
3355.0	4859.8	4471.6
69.6	305.9	128.6
292.9	512.0	555.3
2294.2	3461.0	4279.2
2105.1	2990.5	3202.8
4230.9	3929.9	5059.0
130.8	114.3	85.5
39.5	36.3	73.8
2780.1	3077.4	5201.4
1597.6	1790.9	2016.8
1589.2	2474.2	1812.0
969.1	1062.3	1584.8
2399.6	1683.6	2476.2
253.3	574.0	531.4
1598.6	2103.7	2971.6
1649.3	2022.4	2527.1
2694.8	2903.2	3748.4
5210.5	5931.9	5904.3
745.7	530.1	806.0
5040.2	5253.6	7047.4
4696.4	5178.8	5327.1
2984.6	4394.6	5527.3
2992.4	2168.1	2701.3
8220.1	8451.6	7716.7
1537.8	2297.3	2412.7
3323.3	4872.3	4252.9
3850.4	4854.9	4474.6
209.9	310.8	718.4
2286.1	2919.6	2707.7
2732.9	2549.2	4581.5
1660.5	2932.3	2094.2
334.8	950.7	483.9
3679.3	8563.1	6993.5
1784.3	2298.9	1768.1
12.2	15.1	20.2
1267.1	1843.0	631.3

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s__Clostridium phytofermentans	21775
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EU766596.1 gg_id:308206 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
AY984211.1 gg_id:124785 human stool clone B096 AY9842
GQ503877.1 gg_id:587633 Captain bheri clone Ecwsrb040 GQ503
EU772692.1 gg_id:303460 Bush dog feces clone bdog1_g03_1 EU7726
GQ896694.1 gg_id:572516 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ363376.1 gg_id:367825 feces adult twins and mothers; TS149 clone TS149_a02e04 FJ3633
AB192032.1 gg_id:141363 termite gut homogenate clone M2PB4-29 AB1920
AB031328.1 gg_id:51807 Clostridium sp. str. NT-2 AB0313
AB031327.1 gg_id:42607 Clostridium sp. str. NT-1 AB0313
AB192044.1 gg_id:142702 termite gut homogenate clone M2PT2-80 AB1920
AB192040.1 gg_id:144949 termite gut homogenate clone M1NP1-74 AB1920
AB192050.1 gg_id:141770 termite gut homogenate clone M1PT4-74 AB1920
NC_010001.1 gg_id:235413 Clostridium phytofermentans str. ISDg NC_010
AY984142.1 gg_id:117209 human stool clone B024 AY9841
DQ799529.1 gg_id:197814 human fecal clone RL305aal87d02 DQ799
AY974814.1 gg_id:115535 human ascending colon mucosal biopsy clone KG10 AY9748
EU767854.1 gg_id:355893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7678
DQ801417.1 gg_id:180622 human fecal clone RL388_aao95c05 DQ801
DQ325736.1 gg_id:149889 Metagenomic gut microbiome healthy human stool clone B384 DQ325
DQ799434.1 gg_id:198495 human fecal clone RL305aal86c03 DQ799
AY982887.1 gg_id:123174 human descending colon mucosal biopsy clone L059 AY9828
DQ802029.1 gg_id:187229 human fecal clone RL241_aaj02a12 DQ802
EU767909.1 gg_id:332048 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7679
GQ897100.1 gg_id:576132 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AY974968.1 gg_id:116469 human ascending colon mucosal biopsy clone KJ23 AY9749
AY979886.1 gg_id:118682 human rectum mucosal biopsy clone E169 AY9798
EU466940.1 gg_id:302490 African elephant feces clone AFEL2_aao31f06 EU4669
GQ896926.1 gg_id:544108 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ365323.1 gg_id:369831 feces adult twins and mothers; TS20 clone TS20_a01e07 FJ3653
DQ799405.1 gg_id:194052 human fecal clone RL305aal85h02 DQ799
FJ367911.1 gg_id:362741 feces adult twins and mothers; TS30 clone TS30_a01a05 FJ3679
EU766707.1 gg_id:342338 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
AY985965.1 gg_id:126527 human stool clone D264 AY9859
FJ366554.1 gg_id:357369 feces adult twins and mothers; TS27 clone TS27_a01b03 FJ3665
FJ371073.1 gg_id:368129 feces adult twins and mothers; TS5 clone TS5_a04f02 FJ3710
DQ801052.1 gg_id:183701 human fecal clone RL387_aao91d12 DQ801
FJ369451.1 gg_id:363138 feces adult twins and mothers; TS50 clone TS50_a04f10 FJ3694
AY981557.1 gg_id:116122 human sigmoid colon mucosal biopsy clone L712 AY9815
EU764116.1 gg_id:346508 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7641
FJ364563.1 gg_id:357007 feces adult twins and mothers; TS15 clone TS15_a04d09 FJ3645
EU768317.1 gg_id:323354 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7683

385.6	1245.1	1834.7	2120.0	899.2	1146.3	976.4	1666.9	507.4	305.1	928.4
1497.3	2785.7	3489.2	4194.0	2722.1	2749.6	3269.9	2891.9	2381.7	87.6	3904.2
3948.2	5101.5	4654.0	4450.9	4830.1	4465.8	5333.3	5172.6	5337.2	6264.7	4431.7
41.3	927.9	1390.2	1691.1	438.4	894.8	425.9	1423.0	938.2	251.1	538.1
696.3	1285.0	1649.6	1597.9	1632.1	1210.3	1576.6	1570.8	668.5	629.5	1089.9
65.6	424.5	635.9	642.9	263.9	411.4	271.7	611.0	740.2	284.2	356.9
41.0	101.9	127.9	104.9	115.1	115.8	42.3	127.6	34.3	51.0	76.6
34.7	20.0	24.6	48.3	25.7	24.1	23.6	22.3	11.2	22.3	28.7
109.5	77.5	108.7	119.6	164.0	144.1	133.2	360.3	131.0	43.5	120.5
13488.0	5745.0	6301.3	6335.7	5431.2	6142.6	5995.5	6325.1	6737.1	9546.0	7091.5
141.6	537.2	750.4	784.1	460.2	652.6	1058.8	1057.8	253.8	153.0	796.8
35.7	523.6	663.5	545.7	492.0	786.7	330.3	1072.6	310.8	654.8	375.6
48.0	540.9	1723.2	1006.7	430.6	1133.8	960.5	1317.9	635.5	166.1	1363.8
2358.7	2732.0	3174.0	3727.9	2706.7	2337.8	2237.8	2711.5	1532.6	768.5	2847.7
36.5	837.8	1460.9	1281.0	794.9	845.3	946.7	898.5	507.5	225.0	512.8
5339.5	3764.2	3700.8	3874.6	2990.7	3375.8	3435.5	3286.1	4088.2	3211.7	4626.8
42.7	860.4	1478.5	1454.1	506.8	799.6	503.1	2107.1	338.0	936.3	1107.3
337.8	1581.8	1433.3	1043.8	777.8	1239.3	928.1	1151.1	1068.1	587.0	1118.8
42.0	369.5	435.7	447.3	87.4	274.0	115.0	293.6	217.3	43.2	268.3
89.2	1327.3	1525.7	1529.5	723.6	1012.8	1077.3	1085.2	864.8	444.4	990.3
188.4	1827.5	1743.5	1646.0	1193.8	1927.0	1309.9	2309.9	4845.5	2983.9	2201.3
654.4	2812.1	2879.7	2828.8	1495.5	2327.1	1725.0	2691.8	1739.0	961.5	2508.3
105.1	434.5	518.9	455.2	210.4	349.2	184.0	346.5	204.8	144.8	273.2
12689.3	5311.2	5252.0	5209.6	5145.9	5157.8	5442.5	4999.4	5282.9	5827.7	6701.4
1905.6	2415.9	3084.8	3653.0	1089.0	2005.4	1539.8	2626.9	1166.1	745.1	3292.6
9175.0	8139.0	7717.2	6908.1	5672.2	7355.2	6496.7	5858.1	12149.2	12152.8	10268.2
157.7	1331.1	1903.1	1932.8	997.7	1295.4	1148.4	1832.9	670.9	336.9	1580.5
245.0	2476.6	3085.2	2827.7	2425.6	2432.7	3184.4	2638.1	1512.4	3862.5	2377.6
50.2	216.4	254.6	202.0	92.2	146.7	114.9	140.3	130.2	47.2	108.3
1115.7	1128.3	1830.0	1355.4	1019.1	1047.9	713.6	946.8	663.4	509.9	984.8
7565.4	6692.5	6175.9	6425.4	5593.3	5784.6	6482.6	5933.3	8326.3	5270.3	9982.9
2576.4	2411.3	2772.3	3191.0	2080.5	2019.2	1886.3	2083.6	1444.3	1648.2	1794.6
307.5	1525.6	2258.4	2479.6	1061.1	1539.1	1308.2	2259.2	747.2	331.8	1848.8
1410.9	1391.5	1740.4	2019.5	1021.8	1369.5	1120.5	1532.2	900.9	426.9	1415.9
1168.9	4332.4	5255.2	5879.7	2923.1	3807.5	3432.8	4385.5	4849.9	4222.5	6679.8
62.5	809.8	1415.5	1067.3	356.5	796.3	551.3	1417.5	518.1	125.1	703.7
156.5	1313.9	1830.0	1802.4	1058.8	1175.6	1020.5	2017.4	580.7	375.2	1098.6
1966.5	1519.8	1604.2	1963.9	1161.9	1259.6	1231.9	917.8	1074.3	716.7	1137.1
1218.2	1703.6	2135.6	2187.2	1501.1	1515.4	1289.9	1580.4	1162.4	670.5	1572.3
928.8	1696.3	2488.3	2540.8	1639.8	2219.2	1427.3	2797.3	1273.6	1859.4	1780.5
12973.2	4656.7	5148.1	5174.6	4432.1	5381.3	4582.3	5494.4	6419.2	4693.1	6265.2

1841.9	1688.0	1868.4
2333.8	3052.9	3253.5
5269.6	6395.3	6104.3
2213.3	1135.3	1512.2
1516.8	1661.9	1593.5
441.0	715.5	608.5
139.3	138.1	469.7
16.5	30.9	19.7
140.1	186.3	68.5
5916.8	7165.7	6576.1
590.0	561.1	840.1
960.4	1196.1	1155.7
1467.6	756.5	1227.4
2993.2	3482.0	3096.1
809.1	960.6	1514.5
3527.5	4168.9	3501.2
1554.1	1019.5	915.3
1313.2	1361.2	750.2
243.7	280.2	104.0
1082.8	1354.8	1041.1
1714.6	2542.7	1668.9
2342.1	3210.2	1983.2
363.1	495.4	260.5
5132.6	6016.6	5309.5
3061.3	2545.2	1778.6
6287.9	9158.1	6787.3
1994.4	1413.8	1929.7
2487.4	3879.5	2838.9
178.1	196.1	71.8
1205.5	1672.9	1171.4
5355.2	5638.4	6599.4
2709.8	3109.1	2845.7
2771.8	1711.2	2796.7
2239.1	1749.8	1984.4
4186.8	4405.4	4106.6
1182.7	1457.8	849.7
2175.8	1493.7	2143.8
1557.7	2459.9	3059.0
1908.0	2026.3	1949.3
3278.7	2895.0	2757.6
5012.0	6393.3	5253.3

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o__Clostridiales	f__Lachnospiraceae

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AY981319.1 gg_id:116252 human sigmoid colon mucosal biopsy clone G335 AY9813
EU764418.1 gg_id:343960 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7644
DQ802338.1 gg_id:187157 human fecal clone RL188_aah16d02 DQ802
DQ326159.1 gg_id:149198 Metagenomic gut microbiome healthy human stool clone C054 DQ326
GQ896992.1 gg_id:583202 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ896
FJ365267.1 gg_id:362811 feces adult twins and mothers; TS1 clone TS1_a04h01 FJ3652
GQ077508.1 gg_id:412854 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1209f0 GQ077
AY978337.1 gg_id:121737 human transverse colon mucosal biopsy clone F244 AY9783
EU763747.1 gg_id:341629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7637
GQ079269.1 gg_id:437713 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230f0 GQ079
ABGC03000035.1 gg_id:268313 Clostridium sp. str. SS2/1 ABGC0
AY982970.1 gg_id:122388 human descending colon mucosal biopsy clone L179 AY9829
FJ367689.1 gg_id:358527 feces adult twins and mothers; TS2 clone TS2_a02d07 FJ3676
DQ797631.1 gg_id:183214 human fecal clone RL206_aaj13h11 DQ797
AY981134.1 gg_id:122205 human sigmoid colon mucosal biopsy clone G056 AY9811
GQ896955.1 gg_id:573003 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ896
AY979901.1 gg_id:119323 human rectum mucosal biopsy clone E209 AY9799
GQ897021.1 gg_id:538339 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AY977059.1 gg_id:124905 human cecum mucosal biopsy clone K747 AY9770
FJ365360.1 gg_id:367646 feces adult twins and mothers; TS20 clone TS20_a02a03 FJ3653
AY981748.1 gg_id:124788 human sigmoid colon mucosal biopsy clone LB84 AY9817
FJ370820.1 gg_id:368282 feces adult twins and mothers; TS5 clone TS5_a01f06 FJ3708
DQ326449.1 gg_id:148389 Metagenomic gut microbiome healthy human stool clone C521 DQ326
FJ366327.1 gg_id:367179 feces adult twins and mothers; TS26 clone TS26_a01d10 FJ3663
DQ798712.1 gg_id:176221 human fecal clone RL181_aao00d10 DQ798
FJ368314.1 gg_id:356764 feces adult twins and mothers; TS3 clone TS3_a02g10 FJ3683
DQ905606.1 gg_id:166598 human fecal clone 014B-G2 DQ905
DQ803327.1 gg_id:187518 human fecal clone RL311_aam24a11 DQ803
DQ795759.1 gg_id:179147 human fecal clone RL245_aai81h08 DQ795
AY983324.1 gg_id:125323 human descending colon mucosal biopsy clone A386 AY9833
AY977551.1 gg_id:121101 human cecum mucosal biopsy clone W357 AY9775
EU768039.1 gg_id:331250 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7680
DQ807186.1 gg_id:188131 human fecal clone RL244_aaj47c10 DQ807
DQ823980.1 gg_id:181649 human fecal clone RL204_aaj57g01 DQ823
DQ799470.1 gg_id:198583 human fecal clone RL305aal86f09 DQ799
AB494744.1 gg_id:589475 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
DQ796782.1 gg_id:185703 human fecal clone RL179_aao54d08 DQ796
FJ879449.1 gg_id:382721 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
AY975195.1 gg_id:121393 human ascending colon mucosal biopsy clone KN24 AY9751
FJ364970.1 gg_id:365093 feces adult twins and mothers; TS1 clone TS1_a01d01 FJ3649
FJ024722.1 gg_id:330731 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp FJ0247

845.6	3916.8	4608.8	4046.3	4073.8	3418.2	3882.1	4462.5	4787.5	2901.7	5476.2
2103.9	2126.3	2920.4	3256.3	1807.9	2067.9	1895.3	2802.2	1105.3	574.9	2368.7
1520.6	1725.2	2520.8	2586.2	1476.8	1696.6	1403.4	2404.7	908.1	457.7	2033.9
100.5	418.8	543.1	456.3	254.0	404.0	263.5	419.7	200.8	225.1	254.9
145.7	2124.1	3038.1	3196.8	909.0	2103.4	1462.9	3315.2	876.2	493.8	2406.3
1502.1	2059.8	2774.4	2854.0	2034.8	1863.3	1828.1	2198.5	1333.6	781.3	1955.1
1863.7	3308.9	4317.4	3967.3	3527.0	3587.2	3573.3	3880.9	3504.3	4301.3	3507.7
1476.9	1460.7	1931.3	2108.9	1515.7	1368.9	1377.5	1458.2	875.1	437.7	1268.5
463.6	2176.5	2967.1	2799.3	1866.2	1696.6	1343.5	2691.1	1119.2	517.5	1252.5
1113.2	1121.4	1575.3	1241.3	1021.4	1057.9	720.1	1069.1	651.5	560.3	1011.3
412.7	2235.2	2926.9	3159.9	1268.1	2486.7	1899.0	3379.3	1112.8	827.6	2763.9
1305.3	2817.6	3403.2	2672.0	2948.7	3195.9	2260.1	3275.6	1916.9	2830.9	2623.7
1524.9	1761.4	2457.4	2575.3	1404.1	1714.6	1369.8	2358.9	936.5	467.2	2011.0
841.4	3677.7	3885.3	4919.7	3852.5	4043.4	639.6	3695.5	3430.1	3470.8	4487.5
9074.2	8805.4	8230.9	8601.7	6969.8	7994.5	8163.3	7633.5	13300.9	11796.7	12151.5
48.0	1606.0	2499.5	2409.2	610.3	1938.2	1129.2	2896.5	780.4	419.1	2454.8
1506.3	2082.2	2638.2	2872.2	1905.7	1999.3	1836.8	2082.7	1435.9	786.3	2104.3
2544.3	1561.3	2070.5	1938.0	1254.6	1621.2	1462.0	1704.1	1511.2	1566.2	2405.0
3491.7	4147.3	4329.1	4991.2	4714.6	3840.7	4433.6	3704.4	3071.4	3817.6	3648.3
13647.3	6002.2	6425.8	6333.1	6209.4	5838.4	6374.2	5632.4	9228.9	8859.9	9315.9
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57.6	724.6	752.4	901.4	333.9	561.5	394.6	744.5	1304.2	1050.7	498.2
3901.5	3692.3	3506.2	3676.7	4004.4	3195.7	5072.8	4051.7	4218.5	5342.4	5238.6
5060.2	2135.1	2759.5	2966.0	2443.5	2072.4	2411.4	2079.3	2950.8	3389.0	3990.6
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366.7	1513.6	1938.0	2385.4	1356.7	1902.0	1624.4	1904.7	769.2	840.1	1195.1
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1230.7	821.3	929.7	856.4	806.9	593.6	547.3	654.2	348.8	276.5	341.0
47.3	946.1	1944.9	2058.9	471.4	1175.2	1065.3	1997.5	542.2	172.7	1773.3
369.2	964.7	992.3	1441.8	464.2	621.4	460.9	847.5	371.4	277.0	628.4
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77.2	2384.3	2018.2	1630.8	1482.3	1607.3	1373.1	1616.1	3391.0	1024.2	1291.4
9120.2	3446.0	3543.9	3013.8	2941.4	3066.5	2877.9	2860.9	3519.8	3354.5	2825.6
309.0	1167.6	1575.9	1187.1	659.7	1220.4	1120.3	1397.8	539.0	310.7	1054.8

2298.5	3932.1	4318.6
3664.0	2671.1	3839.2
2866.3	2149.4	2960.8
428.4	638.3	381.5
3906.9	1832.2	2783.6
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3614.7	3961.5	5002.1
1932.2	1795.7	1964.5
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1422.4	1793.2	1305.8
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o__Clostridiales	f__Lachnospiraceae
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o__Clostridiales	f__Lachnospiraceae

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EF098253.1 gg_id:188643 mouse cecum clone SWPT14_aaa03f07 EF0982
EU504306.1 gg_id:259989 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02b02 EU5043
EU473641.1 gg_id:299118 banteng feces clone BG_aaa04d05.Contig1 EU4736
AY756592.1 gg_id:108706 Siwhaho sediment clone LJ3 AY7565
FJ880192.1 gg_id:434572 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
FJ880748.1 gg_id:378068 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU778880.1 gg_id:353577 Black-handed Spider Monkey feces clone SPIM_aaj36b05 EU7788
EU507949.1 gg_id:265576 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa04b05 EU5079
EU507971.1 gg_id:277133 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01a03 EU5079
EU771949.1 gg_id:319153 Southern three-banded armadillo feces clone arma_aaj53g07 EU7719
EU508268.1 gg_id:266726 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04h08 EU5082
DQ105656.1 gg_id:137353 pig feces clone DGGE band K2 DQ105
FJ879330.1 gg_id:441799 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EF655642.1 gg_id:245596 dye containing wastewater treatment biofilm reactor clone B29 EF6556
EU508881.1 gg_id:263014 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37f10 EU5088
DQ815812.1 gg_id:172622 mouse cecum clone aab22f06 DQ815
EU794200.1 gg_id:355318 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K22 EU7942
EU456821.1 gg_id:312892 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4568
EU504348.1 gg_id:262939 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02g11 EU5043
EU452929.1 gg_id:309206 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4529
EF632747.1 gg_id:237273 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
GQ493671.1 gg_id:574714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AF349416.1 gg_id:77449 pig feces clone AF3494
EU773327.1 gg_id:322137 BigHorn sheep feces clone BH1_aao26e11 EU7733
FJ679990.1 gg_id:531052 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ793657.1 gg_id:178682 human fecal clone RL246_aai75b10 DQ793
FJ879661.1 gg_id:418999 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
AB486484.1 gg_id:561193 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
EU850551.1 gg_id:326833 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF351 EU8505
GQ491405.1 gg_id:583711 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
X71853.1 gg_id:14099 Clostridium populeti str. ATCC 35295 X71853
AY212660.1 gg_id:99173 water 20 m downstream manure clone 213ds20 AY2126
EU466237.1 gg_id:291890 bighorn sheep feces clone BH1_aao28e12 EU4662
EU506241.1 gg_id:272369 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c07 EU5062
EF602871.1 gg_id:232283 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
AY977415.1 gg_id:122556 human cecum mucosal biopsy clone W090 AY9774
FJ879205.1 gg_id:423041 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU470217.1 gg_id:302864 trancaspain urial feces clone TU2_aaa03h09 EU4702
DQ071475.1 gg_id:231128 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc10 DQ071
EU794284.1 gg_id:322231 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_N36 EU7942
DQ803800.1 gg_id:177788 human fecal clone RL200_aai58e10 DQ803

35.1	117.2	194.5	152.2	267.6	89.9	216.2	144.4	33.2	32.7	40.4
36.3	295.4	397.9	563.1	267.3	197.1	167.3	489.5	92.0	91.0	137.2
1434.3	3886.7	4949.5	4923.0	3299.6	5030.9	3143.8	5070.4	3644.2	3404.5	3568.6
36.8	686.1	710.6	1004.1	187.2	984.8	338.4	1101.2	264.0	170.0	788.5
296.0	905.8	1510.2	1681.3	1109.4	993.1	1132.0	1084.9	398.1	250.4	772.2
5519.6	6716.4	8085.2	6258.9	5318.9	7680.4	6775.1	6899.2	7997.5	8580.0	7621.3
96.3	2593.7	4021.2	4193.9	1533.1	2579.8	2049.1	3882.2	1303.1	510.5	2959.0
58.9	412.9	544.6	841.4	224.8	239.5	183.3	291.2	126.5	68.6	136.0
3209.8	3512.7	3355.0	4280.8	4627.5	2171.1	5313.4	3190.5	2097.0	2418.4	2692.2
2075.2	1757.7	1905.9	2251.9	901.7	1111.6	1207.9	1603.1	723.7	292.7	1548.2
7704.2	6015.2	6180.4	5372.7	4777.6	5454.4	5561.4	4840.1	7386.5	3812.3	5089.5
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41.5	863.1	1244.2	1352.3	386.9	943.5	702.2	1673.8	292.6	127.0	856.0
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13335.5	6805.3	6306.8	8095.8	6029.3	6203.2	6693.3	5592.6	7462.7	7884.5	9631.5
556.8	1377.3	1416.5	1583.8	1097.4	1177.5	901.5	2086.8	919.6	276.5	1123.6
147.8	3178.9	4156.3	3717.4	3732.8	3480.6	4014.2	4078.2	1829.7	1423.0	3087.5
99.3	1068.0	2890.0	1960.0	935.9	1128.3	965.3	1395.0	863.0	1967.3	1190.5
87.1	727.6	1301.3	1821.9	1085.9	775.5	951.7	1020.0	315.4	201.1	640.3
2856.8	3319.4	3038.1	3164.0	2596.5	2514.1	3027.6	2966.9	4047.4	2892.8	3755.6
2863.7	5825.1	6907.6	6240.7	5110.1	5542.9	6174.2	5613.8	5548.8	4316.5	7056.7
94.8	773.3	807.2	895.8	459.2	505.4	508.0	880.9	679.5	139.3	430.3
57.3	936.1	1429.1	1559.9	680.8	1085.4	863.6	1880.3	385.0	193.6	1137.9
374.4	760.3	900.3	1342.3	284.0	306.4	223.4	637.6	150.2	42.1	339.2
54.2	137.1	467.2	212.7	75.0	120.4	134.7	248.8	94.0	33.9	96.7
451.3	1585.0	2630.8	2146.3	2130.5	1900.3	2446.6	1977.8	1320.3	1674.3	1194.1
34.2	1075.4	1877.3	2337.9	544.4	1233.0	863.1	1627.0	430.9	251.9	1375.4
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38.7	92.5	178.7	137.1	71.5	171.1	125.5	217.6	42.5	46.9	105.1
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40.3	72.9	123.5	83.5	51.6	66.4	43.2	107.9	63.0	47.8	55.6
62.3	2124.9	3254.8	3277.6	1659.4	2473.7	2146.1	3495.0	1121.2	515.9	2600.6
1910.4	866.1	1791.9	1163.5	761.4	1116.1	999.6	1457.4	524.6	318.2	699.6

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769.6	818.3	1490.4
1682.0	1601.9	1404.3
6641.5	7511.1	7193.9
4309.5	3162.7	5668.2
501.3	571.7	1745.9
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989.4	1649.2	1749.9
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3952.4	1554.3	2593.7
5893.9	7425.4	5978.3
1923.4	1934.7	2213.4
3242.9	3633.9	5175.0
1342.8	1917.8	2245.1
492.6	1095.7	1502.0
2356.7	2617.4	3014.7
4913.1	6099.5	6633.4
744.7	631.4	637.8
1898.0	1137.9	2037.7
1048.7	764.0	400.9
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5819.4	3342.2	6285.8
1287.6	1396.7	1785.9
1641.4	1286.8	1967.6
4999.1	1642.2	2799.5
68.3	60.4	90.9
1724.8	1642.9	1391.4
2529.5	3406.5	3331.9
3331.1	3878.8	4446.6
196.4	179.0	212.1
4630.1	4913.1	4183.9
867.0	862.7	976.5
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1586.7	1634.6	1099.9

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
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EU504286.1 gg_id:259281 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01g05 EU504
EF095995.1 gg_id:182621 mouse cecum clone lean2_aaa01f04 EF0959
EU779113.1 gg_id:308857 Takin feces clone TAK_aaa03e11 EU779
FJ366481.1 gg_id:358834 feces adult twins and mothers; TS26 clone TS26_a03h07 FJ3664
DQ815966.1 gg_id:169701 mouse cecum clone aab24h11 DQ815
FJ365126.1 gg_id:370305 feces adult twins and mothers; TS1 clone TS1_a03b10 FJ3651
EU508740.1 gg_id:267400 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50c10 EU508
FJ679327.1 gg_id:515632 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU452548.1 gg_id:315309 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4525
EU509492.1 gg_id:273301 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59c09 EU509
EU456838.1 gg_id:324615 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4568
GQ491245.1 gg_id:538885 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU774776.1 gg_id:311610 Angola Colobus feces clone EAC_1aaa01e03 EU774
FJ672488.1 gg_id:531825 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU460964.1 gg_id:301879 red kangaroo feces clone KO1_aai41b07 EU460
DQ808993.1 gg_id:175596 human fecal clone RL243_aai87h11 DQ808
AY534872.1 gg_id:102328 Clostridium sp. str. IMSNU 40011 AY5348
EU508308.1 gg_id:274455 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02d01 EU5083
EU461740.1 gg_id:294791 mongoose lemur feces clone ML_aaj28b01 EU461
DQ793567.1 gg_id:184905 human fecal clone RL246_aai73f04 DQ793
FJ678549.1 gg_id:519866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GQ868402.1 gg_id:580793 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC81 GQ868
DQ800844.1 gg_id:178970 human fecal clone RL183_aao04c02 DQ800
FJ542922.1 gg_id:520231 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EF515538.1 gg_id:225599 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EU509215.1 gg_id:268028 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46a03 EU509
EU773313.1 gg_id:323365 BigHorn sheep feces clone BH1_aao25a09 EU7733
EU466172.1 gg_id:291475 bighorn sheep feces clone BH1_aao27d08 EU4661
EU453188.1 gg_id:328453 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4531
EU473636.1 gg_id:300295 banteng feces clone BG_aaa02h01.Contig1 EU4736
FJ672606.1 gg_id:527413 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6726
NR_025796.1 gg_id:552538 Clostridium jejuense str. HY-35-12; IMSNU 40003 NR_02
GQ493826.1 gg_id:572045 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509517.1 gg_id:274400 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59h07 EU5095
FJ371671.1 gg_id:369597 feces adult twins and mothers; TS7 clone TS7_a04h09 FJ3716
FJ362613.1 gg_id:364756 feces adult twins and mothers; TS13 clone TS13_a01b01 FJ3626
EF071231.1 gg_id:195514 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0712
EU462354.1 gg_id:288857 chimpanzee feces clone CHIMP1_aaj40g10 EU4623
FJ363762.1 gg_id:365692 feces adult twins and mothers; TS14 clone TS14_a03a10 FJ3637
DQ327549.1 gg_id:145426 Metagenomic gut microbiome healthy human stool clone EB31 DQ327
DQ798564.1 gg_id:179518 human fecal clone RL181_aan98d01 DQ798

1582.9	2406.1	2059.8	2070.2	2164.9	2110.8	1880.8	2825.3	2993.6	752.2	2932.3
153.0	1175.7	977.2	580.1	751.5	1020.5	806.8	1092.7	685.5	175.1	876.4
57.3	597.0	1018.2	1066.2	576.4	899.9	705.3	936.9	180.2	171.8	513.6
454.2	1350.3	1809.9	1908.9	955.7	1153.4	1290.7	1932.9	1177.8	805.1	1114.4
145.8	1694.4	2333.3	2393.9	984.1	1897.2	1412.1	4153.7	669.3	369.1	1701.4
48.4	782.8	807.3	652.1	277.0	480.3	343.4	362.4	551.2	933.2	374.5
52.7	92.9	123.3	123.5	73.4	104.6	79.3	2622.1	97.1	122.1	1640.7
8995.2	3113.1	4226.9	3459.3	3649.4	2995.6	4657.5	3701.4	5182.8	2667.1	3877.0
1942.0	1515.8	1639.1	1723.1	1253.8	1622.0	1676.3	2038.5	1631.5	1385.6	1819.7
126.9	1327.1	2655.4	1691.6	1236.8	1244.6	1036.9	1824.2	671.6	1046.8	1686.5
747.1	583.6	2563.6	2749.3	2774.5	1984.8	4049.6	2472.7	1753.8	1136.9	2886.7
52.6	404.6	453.0	507.3	223.1	348.7	221.5	594.3	334.5	104.8	251.3
246.5	1251.4	1481.2	1328.6	1288.3	1078.3	1395.8	1505.4	927.5	729.8	843.4
166.6	1529.2	2067.9	1672.6	1290.4	1397.6	1539.7	1647.4	1087.8	581.9	1516.9
64.2	803.1	1009.8	940.9	817.1	785.0	1039.1	911.1	242.9	97.5	396.2
74.9	519.4	766.1	725.7	526.4	549.8	355.8	573.5	310.3	257.0	351.7
45.6	189.8	231.3	245.4	137.7	286.5	329.8	600.6	56.5	31.5	247.7
13369.6	4730.2	4574.7	5008.3	5476.7	4736.4	4851.2	4452.5	6360.6	6841.5	5647.7
34.2	807.6	1275.8	1476.4	424.6	906.1	847.1	1350.1	425.8	36.6	1084.6
79.2	379.3	702.8	525.1	255.8	357.3	268.5	640.6	282.1	126.4	125.3
39.1	56.6	92.8	80.0	46.5	57.7	59.6	58.8	21.1	25.7	31.9
111.2	1818.9	2352.5	2137.4	1230.8	1621.3	2107.5	2324.1	962.1	777.4	1283.3
72.6	335.8	594.0	451.6	222.2	652.2	309.2	1070.6	178.1	124.9	378.4
209.6	3901.0	5110.2	5445.0	3551.9	3891.6	4254.3	4385.9	3175.4	1393.2	4213.2
10443.0	4098.7	3881.6	4867.0	3673.0	3714.5	4082.3	3795.5	5152.2	3962.6	4980.4
5749.8	2200.8	2014.9	2189.0	2570.1	2001.6	2448.5	2232.0	2532.4	1883.2	2490.4
97.4	2880.5	3318.4	4004.8	2381.7	2008.7	2066.9	3003.3	934.9	908.1	1984.5
1178.7	2178.3	3135.5	2284.9	2301.7	2330.1	2364.2	2549.5	1938.4	1507.0	2213.9
39.8	341.5	575.2	626.3	234.9	395.0	409.5	484.0	268.6	220.1	477.9
83.8	281.3	485.1	451.6	416.3	281.2	439.7	411.4	273.4	217.6	562.4
208.5	1542.4	2444.5	2716.4	1794.2	2284.4	2307.9	2660.6	993.6	1918.0	1926.1
86.1	958.3	1753.0	931.6	386.2	1150.6	477.1	2170.4	287.6	572.5	1394.4
2242.6	1326.6	1654.2	1372.6	1273.9	1000.7	1440.2	1186.5	1470.9	854.9	1171.0
6512.5	2609.7	2687.3	2887.4	2827.3	2425.3	3012.7	2718.5	3288.4	3615.4	4608.5
33.0	159.2	197.9	210.6	29.3	95.3	53.4	81.2	73.7	25.8	126.1
118.8	887.2	1203.0	1245.5	1191.0	1157.7	919.6	1367.3	600.4	714.9	885.6
745.4	1787.5	2259.1	2626.0	1266.3	1954.8	1473.5	2494.9	831.3	387.1	1776.4
15290.4	5080.4	5713.3	6949.2	5273.7	4887.0	6644.4	5090.6	5689.6	3715.5	4842.2
97.9	344.6	388.3	376.7	374.0	313.4	381.3	516.3	153.1	159.4	190.0
42.5	495.2	1074.7	1539.3	188.6	561.0	212.3	1175.5	152.0	83.9	469.2
68.0	248.0	363.6	440.0	200.7	195.7	238.3	385.3	84.5	300.9	169.0

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2290.9	2233.7	1965.1
4432.9	2069.7	3468.7
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1686.4	2349.9	1946.3
1436.7	1721.1	2136.0
2302.3	2284.5	2136.1
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2006.6	2384.3	2218.9
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1792.7	2347.9	3697.7
416.8	481.5	786.2
386.7	512.7	313.1
2729.8	2249.4	2584.2
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1968.1	734.0	774.6
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o__Clostridiales	f__Lachnospiraceae

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AM277382.2 gg_id:229853 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
DQ802766.1 gg_id:183853 human fecal clone RL188_aan96c08 DQ802
FJ367837.1 gg_id:358360 feces adult twins and mothers; TS2 clone TS2_a04b07 FJ3678
DQ325827.1 gg_id:145051 Metagenomic gut microbiome healthy human stool clone B566 DQ325
FJ679258.1 gg_id:524214 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
AY976512.1 gg_id:119285 human cecum mucosal biopsy clone K034 AY9765
GQ896896.1 gg_id:580242 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ801081.1 gg_id:177184 human fecal clone RL387_aao91h04 DQ801
DQ796707.1 gg_id:183325 human fecal clone RL179_aao53d11 DQ796
EU762664.1 gg_id:318085 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ801445.1 gg_id:175981 human fecal clone RL388_aao95f05 DQ801
DQ801596.1 gg_id:193594 human fecal clone RL117_aae92c08 DQ801
FJ367849.1 gg_id:370336 feces adult twins and mothers; TS2 clone TS2_a04c09 FJ3678
GQ897203.1 gg_id:545113 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AF371638.1 gg_id:29079 swine intestine clone p-1894-s962-3 AF371
DQ801802.1 gg_id:189572 human fecal clone RL201_aai47a04 DQ801
EU762248.1 gg_id:346684 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EF399973.1 gg_id:213155 human fecal clone SJTU_E_07_14 EF3999
FJ367910.1 gg_id:365889 feces adult twins and mothers; TS30 clone TS30_a01a04 FJ3679
AY976640.1 gg_id:116094 human cecum mucosal biopsy clone K204 AY9766
DQ327315.1 gg_id:147899 Metagenomic gut microbiome healthy human stool clone E863 DQ327
AM697161.1 gg_id:227258 sequencing libraries indoor dust clone BF0001C002 AM697
AY981729.1 gg_id:120484 human sigmoid colon mucosal biopsy clone LB21 AY9817
EU467096.1 gg_id:300902 mongoose lemur feces clone ML_aae88b05 EU467
DQ807097.1 gg_id:192077 human fecal clone RL244_aaj46b10 DQ807
FJ370064.1 gg_id:370074 feces adult twins and mothers; TS55 clone TS55_a04a07 FJ3700
FJ368444.1 gg_id:357429 feces adult twins and mothers; TS3 clone TS3_a04d09 FJ3684
DQ325631.1 gg_id:146452 Metagenomic gut microbiome healthy human stool clone B171 DQ325
DQ796741.1 gg_id:192388 human fecal clone RL179_aao53h04 DQ796
FJ371070.1 gg_id:364813 feces adult twins and mothers; TS5 clone TS5_a04e11 FJ3710
FJ682996.1 gg_id:519242 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ678681.1 gg_id:528608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ806889.1 gg_id:190886 human fecal clone RL198_aaj74g09 DQ806
DQ798252.1 gg_id:176633 human fecal clone RL181_aah39e11 DQ798
GQ001531.1 gg_id:508130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu174b11 GQ001
FJ363666.1 gg_id:357596 feces adult twins and mothers; TS14 clone TS14_a01h07 FJ3636
FJ367676.1 gg_id:368233 feces adult twins and mothers; TS2 clone TS2_a02c06 FJ3676
DQ799669.1 gg_id:197638 human fecal clone RL305aal88h07 DQ799
AY981488.1 gg_id:127177 human sigmoid colon mucosal biopsy clone L591 AY9814
FJ368089.1 gg_id:356961 feces adult twins and mothers; TS30 clone TS30_a03h04 FJ3680

73.3	498.2	669.9	631.4	361.7	505.6	425.7	599.5	337.1	154.6	428.3
36.7	1115.7	1249.3	1394.0	820.3	1029.9	726.6	1830.1	499.9	217.3	859.7
72.2	1092.8	1987.7	1400.3	138.5	1109.5	452.5	778.0	753.7	44.3	1016.3
20601.0	8474.1	7744.1	9557.0	7875.4	8387.0	8583.1	7470.2	15439.4	10735.4	12851.2
2163.1	3012.4	3721.9	3910.9	3419.0	2716.4	3562.0	2767.5	3690.4	3793.5	3338.4
225.9	438.0	522.4	713.5	107.2	237.7	302.1	316.0	148.6	57.5	245.7
480.1	1475.3	1850.9	1982.3	1687.7	1503.0	1947.9	1688.9	961.7	3146.4	1026.7
45.8	1731.0	2356.5	2643.9	859.6	1986.3	1272.8	2955.2	924.1	422.7	2306.4
1244.6	3163.3	2559.8	2089.2	2179.4	2783.4	1620.1	2118.9	2884.1	1580.1	2106.8
266.2	546.0	640.7	866.1	83.6	326.7	296.6	486.9	125.1	56.8	335.3
38.8	755.9	1175.3	889.0	350.5	906.7	483.7	1239.4	591.4	245.8	630.8
38.3	50.8	108.2	121.1	73.5	87.0	86.8	204.3	36.5	17.1	62.8
107.2	704.6	1178.6	798.9	364.6	433.1	545.9	779.7	581.8	202.0	589.0
318.0	2432.6	2974.2	2917.3	3370.2	2355.9	2853.3	2686.0	1418.6	832.1	2442.8
446.6	2687.3	2939.4	2447.8	1284.1	1902.7	1643.2	1910.2	2896.5	3481.9	3098.4
59.1	301.7	638.1	583.0	69.9	350.8	284.7	413.0	83.2	40.3	315.0
146.7	1043.4	1276.2	1499.7	761.5	766.6	677.1	1158.6	465.0	182.6	797.2
94.3	566.3	635.0	572.0	367.0	471.6	351.2	649.8	250.7	179.6	255.5
224.9	1809.9	2752.6	2720.9	889.9	1871.3	1232.4	2899.6	980.1	491.0	1883.7
4997.3	2885.6	2820.0	4042.0	2444.1	2622.8	2684.1	2507.5	4476.4	4500.1	5184.4
219.8	2722.0	2142.0	1889.3	1974.3	1344.7	2278.0	1315.6	2570.1	3088.8	1857.5
739.2	2687.3	2050.2	2056.7	2677.6	1932.8	2197.5	2162.9	3345.5	1521.7	2310.3
2143.6	3477.5	4515.4	4211.4	2423.1	3587.1	3169.1	4631.0	3903.4	1518.6	4275.5
174.0	1324.2	1714.8	2046.0	978.8	1151.9	983.2	1688.5	706.6	365.0	1306.0
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2147.5	4804.9	6143.7	6054.3	5880.1	5435.2	6061.6	5481.8	7475.4	5727.9	8997.0
123.2	355.6	374.2	260.6	206.6	236.7	341.7	208.0	358.1	139.1	400.7
32.1	183.9	233.5	144.3	91.4	105.2	102.4	161.6	52.1	42.3	114.4
5369.3	2565.2	3158.4	3096.4	2633.7	2552.6	2678.3	2599.0	6229.3	3731.7	2971.3
39.8	833.2	1399.4	1446.2	266.6	906.1	662.4	1313.1	317.4	103.5	889.8
171.0	301.0	349.1	326.8	219.6	230.4	223.5	295.8	235.8	214.8	381.4
24.3	154.1	328.8	311.1	65.3	79.6	94.2	189.6	30.1	34.5	134.4
4788.8	1624.5	2049.3	1891.9	2207.6	1680.4	1956.2	1787.5	1294.5	2831.5	1447.4
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86.7	562.8	621.5	717.9	559.8	443.9	560.2	799.0	166.6	182.3	381.7
590.6	1829.4	2381.4	2099.5	1168.4	1776.8	1519.5	2041.9	2279.7	2516.7	2077.1
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39.7	620.3	698.1	673.3	433.2	531.0	407.6	992.4	304.2	136.2	258.1
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1824.1	1039.5	2347.7
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483.9	381.2	359.1
1823.3	2247.4	2069.1
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2256.7	1910.9	1645.7
600.7	421.0	510.3
1493.4	964.2	986.9
115.6	384.8	72.6
653.1	873.0	699.8
2447.1	2616.7	3548.2
2193.7	1864.2	3119.8
436.1	368.5	114.9
1145.6	1014.3	1424.7
556.4	742.3	622.5
2757.3	1665.1	2221.9
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1771.9	2242.9	2307.6
1650.0	2110.8	1690.7
5285.7	3882.1	4626.5
1943.7	1371.9	1834.0
1759.1	1164.6	1712.3
5119.7	5526.1	4937.3
218.4	499.6	148.9
185.9	185.4	267.1
2694.6	3521.0	2790.2
1678.1	685.3	1171.3
188.8	373.7	140.5
216.1	366.0	692.0
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4812.7	5332.8	3957.7
2682.4	3404.5	2810.1
186.6	312.5	421.8
542.7	715.0	1301.6
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o__Clostridiales	f__Lachnospiraceae

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FJ362791.1 gg_id:366121 feces adult twins and mothers; TS13 clone TS13_a03c03 FJ3627
FJ370352.1 gg_id:360418 feces adult twins and mothers; TS56 clone TS56_a03h01 FJ3703
FJ365716.1 gg_id:357752 feces adult twins and mothers; TS21 clone TS21_a02b07 FJ3657
FJ366917.1 gg_id:368931 feces adult twins and mothers; TS28 clone TS28_a01d02 FJ3669
AM275455.2 gg_id:234340 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
DQ798714.1 gg_id:193231 human fecal clone RL181_aao00d12 DQ798
EU466792.1 gg_id:303125 African elephant feces clone AFEL2_aao29e11 EU466
FJ363689.1 gg_id:357535 feces adult twins and mothers; TS14 clone TS14_a02b06 FJ3636
DQ807937.1 gg_id:195481 human fecal clone RL180_aan69d11 DQ807
DQ326713.1 gg_id:148649 Metagenomic gut microbiome healthy human stool clone E168 DQ326
DQ797422.1 gg_id:190985 human fecal clone RL248_aai99b08 DQ797
EU763441.1 gg_id:330946 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7634
AY979955.1 gg_id:119081 human rectum mucosal biopsy clone K838 AY9799
AY981292.1 gg_id:120019 human sigmoid colon mucosal biopsy clone G288 AY9812
EU466835.1 gg_id:303384 African elephant feces clone AFEL2_aao30b04 EU4668
FJ368522.1 gg_id:368771 feces adult twins and mothers; TS49 clone TS49_a01d01 FJ3685
FJ368896.1 gg_id:358153 feces adult twins and mothers; TS4 clone TS4_a01h01 FJ3688
DQ327483.1 gg_id:146465 Metagenomic gut microbiome healthy human stool clone EA53 DQ327
AY977072.1 gg_id:123375 human cecum mucosal biopsy clone K760 AY9770
FJ676090.1 gg_id:521570 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
FJ367114.1 gg_id:360063 feces adult twins and mothers; TS28 clone TS28_a03f09 FJ3671
FJ679823.1 gg_id:516527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ369460.1 gg_id:358560 feces adult twins and mothers; TS50 clone TS50_a04g09 FJ3694
DQ801252.1 gg_id:189002 human fecal clone RL388_aao93a04 DQ801
FJ369397.1 gg_id:368336 feces adult twins and mothers; TS50 clone TS50_a04a04 FJ3693
DQ071523.1 gg_id:230528 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc31 DQ071
AY981621.1 gg_id:122358 human sigmoid colon mucosal biopsy clone L858 AY9816
DQ795404.1 gg_id:198270 human fecal clone RL178_aah53h12 DQ795
AY981324.1 gg_id:120304 human sigmoid colon mucosal biopsy clone G341 AY9813
AY976872.1 gg_id:120572 human cecum mucosal biopsy clone K513 AY9768
FJ370090.1 gg_id:363987 feces adult twins and mothers; TS55 clone TS55_a04c10 FJ3700
DQ795084.1 gg_id:174110 human fecal clone RL310_aam40a06 DQ795
FJ676204.1 gg_id:527356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
FJ679996.1 gg_id:521075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ807278.1 gg_id:177041 human fecal clone RL244_aaj48e06 DQ807
EU761890.1 gg_id:341191 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
EU762096.1 gg_id:356215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7620
FJ368085.1 gg_id:363354 feces adult twins and mothers; TS30 clone TS30_a03g10 FJ3680
DQ796540.1 gg_id:189217 human fecal clone RL179aan74d05 DQ796
FJ370864.1 gg_id:358427 feces adult twins and mothers; TS5 clone TS5_a02b07 FJ3708

1979.5	1669.9	1868.7	1733.2	648.9	1294.1	973.1	1378.2	1579.2	752.9	1435.8
90.7	1309.1	1098.1	1126.4	722.1	795.8	545.7	1076.5	710.6	367.1	652.0
1918.4	2903.5	2704.6	2547.9	1744.7	2347.0	1621.9	1383.7	2863.7	2323.8	1867.3
2402.0	3935.9	4296.5	4215.1	2947.8	3307.3	2566.1	3152.9	3926.6	3313.7	4747.8
1734.9	4619.8	4235.6	3396.2	3608.2	3473.1	2701.0	3572.6	4547.2	2605.7	3653.0
2208.1	1989.4	2796.3	2843.2	1552.5	2544.0	1791.6	2828.4	1331.4	660.7	2579.8
37.5	2094.4	1990.5	2157.1	1190.3	1874.0	2239.3	2475.3	3886.0	2331.8	2048.3
1290.6	1228.8	1587.5	1821.7	1014.8	1078.7	840.3	1263.1	712.7	307.2	1189.6
4858.4	4339.1	4453.2	5026.5	4063.9	4098.9	4376.2	3680.5	5776.3	4541.9	6748.2
97.6	222.0	350.6	298.8	99.6	192.1	154.5	259.0	64.5	47.3	206.4
1283.0	1246.8	1642.3	1931.2	981.3	1124.5	926.2	1414.1	721.4	308.4	1176.3
817.6	973.3	1414.5	2073.2	1010.3	1070.7	983.1	1499.2	622.1	963.6	812.2
62.4	446.3	702.9	903.9	191.1	329.8	231.0	928.2	136.1	389.1	588.8
72.8	656.9	891.8	862.7	517.2	611.6	498.8	1065.2	312.3	243.9	531.3
16160.6	8579.2	6490.3	5142.9	5449.7	6832.5	5038.8	5840.1	13059.5	7670.4	6960.0
692.9	2673.8	2844.4	2485.6	3037.3	2185.6	1900.3	2913.4	1807.7	1019.3	1811.3
3323.5	8102.2	8227.9	8068.0	7095.2	6957.5	7467.4	7688.0	7568.8	5719.6	8591.9
5369.7	3351.2	3551.0	4305.8	3268.4	3033.5	3395.6	3176.8	5368.3	4477.8	5774.1
1622.0	1368.7	1777.2	1991.7	1117.7	1194.9	1037.9	1591.6	776.0	383.6	1239.2
1121.3	872.3	1154.9	1154.4	834.3	829.3	616.6	1000.6	654.8	296.8	967.8
150.4	917.4	1217.8	1417.9	629.3	718.0	658.7	1013.7	448.3	177.8	715.6
9906.2	3086.5	3369.9	3066.5	3075.0	2564.4	2802.8	2607.4	4390.7	4102.8	4687.9
8843.0	3788.4	3604.5	4152.8	3022.8	3338.0	3496.2	3176.8	5378.4	3820.6	4540.8
2219.7	2090.6	2278.0	2774.3	1694.0	1815.3	1406.1	1527.5	1090.3	748.8	1632.9
8686.1	3774.7	3646.1	3669.2	3531.5	3009.8	3651.4	3366.2	5071.6	4417.3	4600.0
1954.3	1373.0	1536.6	1399.6	1329.2	1231.7	1272.2	1701.0	1802.6	1485.2	1109.2
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3423.1	6443.3	7396.3	4904.8	4529.6	5031.3	4144.3	4378.9	5058.1	3961.6	5908.5
53.8	1130.4	1512.6	1911.7	1097.0	1056.9	1077.1	1813.0	395.5	214.9	910.4
122.5	897.5	1248.3	1379.5	819.8	591.0	648.3	1001.0	328.4	173.5	589.1
153.8	993.4	1396.9	1368.0	684.1	903.9	818.3	1498.5	446.1	291.1	769.4
148.5	1529.8	1551.0	1564.9	846.4	1071.7	939.7	1115.5	1017.4	1021.1	850.3
47.1	855.1	1369.5	1627.1	258.4	537.9	548.4	1103.8	352.8	733.5	1181.8
536.8	1082.0	1077.5	924.9	637.1	799.7	908.9	1239.1	895.6	520.0	792.6
170.1	940.1	1284.4	1457.8	619.6	699.8	678.9	1005.8	443.5	176.9	693.4
68.4	536.5	660.6	758.5	346.7	450.8	400.3	576.2	381.8	167.8	492.3
38.9	2092.5	2017.6	1718.9	1512.5	1701.5	1745.0	1973.4	4024.8	2510.1	2167.6
1263.3	1222.9	1543.8	1536.2	1185.4	973.6	741.9	945.6	602.8	360.3	887.0
35.3	332.4	292.4	340.1	249.7	208.1	228.6	360.6	126.4	92.4	237.0
3626.4	743.3	846.3	893.3	1087.7	764.9	934.5	750.2	711.7	500.6	826.3
66.2	1015.7	977.9	761.6	560.5	630.3	499.7	782.7	725.7	900.2	520.2

1037.7	1560.9	1194.8
838.9	1181.0	862.7
2325.0	2554.1	2791.1
3785.8	4186.7	3212.0
2833.5	3978.4	2670.7
4671.5	2604.1	3250.4
1817.9	1805.5	1695.6
1829.2	1390.8	1573.7
3917.9	4158.0	4283.6
494.3	245.3	230.1
1936.4	1490.1	1641.3
1693.5	1811.3	1053.7
744.2	350.9	327.0
1023.4	833.1	1045.1
5984.1	5409.4	4816.1
2889.5	2480.5	3301.5
6652.3	6633.9	7066.2
3201.3	3604.7	2910.4
2120.8	1640.1	1814.5
1443.6	1161.8	1325.8
1100.9	938.9	1157.5
2450.9	4183.0	2580.9
3060.6	4759.6	3103.8
2276.3	2933.1	2133.4
3786.4	4483.4	3849.4
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4802.8	5796.8	4286.0
2544.7	1203.7	2338.4
1056.2	922.4	1681.0
1542.1	1141.8	1598.2
1287.4	1262.0	1704.4
693.3	1143.0	428.3
877.6	673.2	780.5
1103.9	946.8	1230.5
603.6	539.6	596.2
1789.9	2194.0	1539.8
1231.7	1544.4	1548.1
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655.0	1194.0	1146.1
778.4	907.9	1335.5

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AY984430.1 gg_id:125789 human stool clone B340 AY9844
EU778575.1 gg_id:343934 Ring-tailed lemur feces clone RT_aai09h05 EU7785
AY981483.1 gg_id:118911 human sigmoid colon mucosal biopsy clone L585 AY9814
FJ370346.1 gg_id:361594 feces adult twins and mothers; TS56 clone TS56_a03g04 FJ3703
AY974859.1 gg_id:118535 human ascending colon mucosal biopsy clone KH11 AY9748
AY983020.1 gg_id:125747 human descending colon mucosal biopsy clone L248 AY9830
FJ370319.1 gg_id:363682 feces adult twins and mothers; TS56 clone TS56_a03d07 FJ3703
FJ370085.1 gg_id:369111 feces adult twins and mothers; TS55 clone TS55_a04c05 FJ3700
EU763087.1 gg_id:323066 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7630
DQ327031.1 gg_id:148868 Metagenomic gut microbiome healthy human stool clone E536 DQ327
AY974985.1 gg_id:124294 human ascending colon mucosal biopsy clone KJ58 AY9749
FJ364648.1 gg_id:369711 feces adult twins and mothers; TS19 clone TS19_a01d08 FJ3646
AY960568.1 gg_id:114994 Anaerostipes sp. str. IE4 AY9605
GQ002290.1 gg_id:507372 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu175f09 GQ002
DQ326965.1 gg_id:146256 Metagenomic gut microbiome healthy human stool clone E458 DQ326
DQ805381.1 gg_id:197515 human fecal clone RL203_aai61h08 DQ805
EU762235.1 gg_id:349852 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7622
FJ679950.1 gg_id:513542 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ678623.1 gg_id:513783 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ326798.1 gg_id:145333 Metagenomic gut microbiome healthy human stool clone E267 DQ326
FJ369427.1 gg_id:368844 feces adult twins and mothers; TS50 clone TS50_a04d03 FJ3694
EU762763.1 gg_id:344399 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7627
EU767808.1 gg_id:356162 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7678
DQ796479.1 gg_id:192913 human fecal clone RL179_aah28h11 DQ796
AY984899.1 gg_id:122801 human stool clone B880 AY9848
DQ795217.1 gg_id:178717 human fecal clone RL178_aah51f05 DQ795
DQ327118.1 gg_id:145284 Metagenomic gut microbiome healthy human stool clone E636 DQ327
FJ368110.1 gg_id:360474 feces adult twins and mothers; TS30 clone TS30_a04b09 FJ3681
DQ807820.1 gg_id:184457 human fecal clone RL180_aah37f02 DQ807
FJ362753.1 gg_id:363486 feces adult twins and mothers; TS13 clone TS13_a02g02 FJ3627
DQ326681.1 gg_id:147258 Metagenomic gut microbiome healthy human stool clone E128 DQ326
DQ807882.1 gg_id:182054 human fecal clone RL180_aah38d06 DQ807
DQ326470.1 gg_id:147326 Metagenomic gut microbiome healthy human stool clone C559 DQ326
GQ047165.1 gg_id:402005 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d GQ047
GQ047276.1 gg_id:402052 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010g GQ047
DQ801729.1 gg_id:184590 human fecal clone RL201_aai46b03 DQ801
DQ804603.1 gg_id:193691 human fecal clone RL187_aao70c01 DQ804
DQ327576.1 gg_id:150150 Metagenomic gut microbiome healthy human stool clone EB60 DQ327
AY983034.1 gg_id:127613 human descending colon mucosal biopsy clone L265 AY9830
FJ367163.1 gg_id:359737 feces adult twins and mothers; TS28 clone TS28_a04c05 FJ3671
DQ798590.1 gg_id:195395 human fecal clone RL181_aan98f09 DQ798

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38.4	367.5	613.5	682.1	376.5	537.6	340.9	593.5	284.7	282.7	557.3
18865.3	8077.8	7569.4	7948.9	8325.9	7830.7	8511.6	7363.6	10250.3	11694.0	8306.9
206.4	2078.9	3004.2	2983.1	1901.7	2073.8	2251.1	2904.8	4523.8	2031.3	2786.7
196.4	900.0	2310.0	1280.4	637.5	613.5	627.2	932.6	1517.3	184.0	1372.0
23.7	229.4	315.5	375.5	209.2	172.0	276.4	260.0	69.4	34.1	235.6
23.8	134.9	263.7	288.2	40.4	89.9	89.1	160.1	32.3	23.4	215.0
5267.8	1991.0	1709.8	1870.0	1786.2	1648.2	2363.3	1814.8	3037.9	2826.8	2883.4
487.6	3159.5	2309.1	2344.3	2015.4	2290.3	1473.7	2075.7	3136.5	1480.0	1669.5
11140.9	7125.8	6670.9	7611.0	7746.8	7819.8	8565.8	7154.0	14680.9	10317.7	9283.5
2387.9	2278.1	2787.4	2866.6	2299.9	1792.9	1960.2	2474.3	2061.9	1884.2	1734.6
25.6	127.8	218.0	226.4	68.7	69.3	117.3	109.9	51.3	22.3	66.6
205.0	1222.0	1828.0	1349.1	676.5	1046.7	1341.3	1549.5	694.0	319.6	1068.3
1384.0	1217.1	1555.8	1807.0	998.1	1009.5	832.7	1238.9	711.6	326.3	1115.4
6779.6	1355.2	1650.3	636.2	1555.6	1272.5	1551.5	1760.9	1339.8	1066.4	1404.1
1360.2	1448.3	1879.0	2021.9	1282.1	1124.3	958.0	1511.3	685.8	384.0	1179.5
271.2	3094.8	4510.2	4047.5	3505.3	3016.2	2878.4	3799.9	2257.2	1263.1	3829.3
59.0	430.1	1125.3	969.7	199.0	419.5	313.6	480.0	63.6	33.2	454.8
213.1	717.4	899.5	793.5	519.6	673.6	598.3	1053.0	470.9	266.5	654.8
154.3	899.7	782.5	674.6	579.6	534.9	376.4	637.8	419.6	141.8	339.5
54.2	724.9	880.2	858.0	700.0	695.1	614.0	1116.3	400.5	297.0	724.2
15861.1	5956.2	5290.8	7857.2	5488.9	5388.6	5904.4	5071.6	13509.1	8564.9	9025.8
1375.8	1903.4	1601.9	1609.9	1422.9	1612.9	1923.9	1717.7	1348.2	531.3	1726.0
31.3	436.5	492.8	433.7	340.8	320.9	238.9	683.5	188.6	91.8	137.3
12780.2	1040.7	1243.1	1244.0	1743.1	2292.0	1158.5	1461.5	1080.0	663.8	977.1
2144.9	3273.5	2832.4	2636.7	1782.9	3113.7	2853.1	2945.5	3477.5	2253.9	2928.1
175.7	999.2	1415.8	1841.6	495.5	723.5	826.9	1037.4	513.2	167.8	728.2
100.3	1018.0	1499.2	1764.0	917.4	1087.7	1301.8	1463.9	635.4	299.6	1088.3
4487.1	1641.9	1998.3	1944.6	1656.9	1532.6	2349.7	2132.0	2370.3	2912.4	2213.5
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5612.2	4003.9	4264.7	4013.8	3414.1	3711.3	3942.6	3728.6	3291.7	3657.8	4248.6
1483.3	1423.2	1956.7	1954.5	1462.0	1218.6	997.2	1518.3	714.6	333.6	1284.5
157.7	1319.9	2128.6	1316.8	1090.5	1135.8	1013.3	1713.6	982.5	479.1	1549.0
47.9	365.5	824.3	696.0	206.1	528.5	315.3	1046.5	174.0	100.2	432.8
37.5	452.3	437.8	472.9	432.5	399.1	187.0	1220.7	158.3	102.9	587.9
23.2	72.1	178.6	93.2	34.3	57.4	38.8	93.2	24.0	22.0	102.9
143.6	2219.8	2280.0	2276.6	1336.5	1867.6	1475.2	2718.7	3869.8	2495.2	2450.6
661.2	781.3	918.0	861.3	732.0	701.3	521.4	948.4	1567.1	759.5	1158.8
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573.5	644.7	988.2
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7717.9	8674.0	8974.1
2424.5	2734.4	3516.5
779.2	1254.5	755.6
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187.7	209.9	128.0
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2393.3	1780.0	1861.2
7884.0	7613.2	8369.5
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1348.0	1492.7	1237.9
1846.6	1397.7	1534.7
1657.9	1878.7	1369.0
1895.9	1853.2	2245.9
2875.5	3228.4	4170.9
800.3	390.6	414.6
722.1	932.4	1356.9
611.8	671.6	378.0
772.4	957.3	1823.1
5679.5	6398.2	5832.9
1295.4	2041.4	2246.5
371.9	549.5	541.1
1666.9	2172.0	1486.6
2008.2	3716.0	2831.8
1421.7	932.9	1232.1
2194.1	1211.2	1508.0
2324.8	2551.6	2637.7
8163.3	9737.8	9753.1
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1429.4	1803.6	2259.3
1241.0	795.8	1024.9
870.6	491.2	1034.8
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584.2	1055.4	745.9
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o__Clostridiales	f__Lachnospiraceae

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DQ905930.1 gg_id:173503 human fecal clone 29c-h8 DQ905
FJ683219.1 gg_id:515754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
DQ795343.1 gg_id:182566 human fecal clone RL178_aah53b12 DQ795
FJ363496.1 gg_id:366870 feces adult twins and mothers; TS149 clone TS149_a03h09 FJ3634
FJ365779.1 gg_id:362106 feces adult twins and mothers; TS21 clone TS21_a02h08 FJ3657
FJ369957.1 gg_id:361190 feces adult twins and mothers; TS55 clone TS55_a02g02 FJ3699
EU766947.1 gg_id:348387 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ364681.1 gg_id:357195 feces adult twins and mothers; TS19 clone TS19_a01g07 FJ3646
DQ796685.1 gg_id:194298 human fecal clone RL179_aao53b07 DQ796
FJ364929.1 gg_id:361669 feces adult twins and mothers; TS19 clone TS19_a04h04 FJ3649
AY978349.1 gg_id:119014 human transverse colon mucosal biopsy clone F280 AY978
FJ679203.1 gg_id:512803 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ365787.1 gg_id:364446 feces adult twins and mothers; TS21 clone TS21_a03a06 FJ3657
DQ806364.1 gg_id:175387 human fecal clone RL186_aan91c08 DQ806
DQ798516.1 gg_id:194999 human fecal clone RL181_aan97f11 DQ798
FJ371032.1 gg_id:366081 feces adult twins and mothers; TS5 clone TS5_a04b06 FJ3710
FJ367605.1 gg_id:368886 feces adult twins and mothers; TS2 clone TS2_a01e01 FJ3676
EF400396.1 gg_id:214689 human fecal clone SJTU_E_12_81 EF4003
FJ367811.1 gg_id:359780 feces adult twins and mothers; TS2 clone TS2_a03h03 FJ3678
AY983090.1 gg_id:117012 human descending colon mucosal biopsy clone L337 AY983
AY976510.1 gg_id:122853 human cecum mucosal biopsy clone K032 AY976
FJ365724.1 gg_id:365011 feces adult twins and mothers; TS21 clone TS21_a02c05 FJ3657
FJ363664.1 gg_id:357558 feces adult twins and mothers; TS14 clone TS14_a01h05 FJ3636
DQ326796.1 gg_id:146454 Metagenomic gut microbiome healthy human stool clone E265 DQ326
FJ368651.1 gg_id:359189 feces adult twins and mothers; TS49 clone TS49_a02g11 FJ3686
FJ679210.1 gg_id:516896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
DQ796804.1 gg_id:176547 human fecal clone RL179_aao54g05 DQ796
FJ363631.1 gg_id:360786 feces adult twins and mothers; TS14 clone TS14_a01e08 FJ3636
FJ679121.1 gg_id:531815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
FJ370243.1 gg_id:364800 feces adult twins and mothers; TS56 clone TS56_a02c06 FJ3702
DQ326407.1 gg_id:146736 Metagenomic gut microbiome healthy human stool clone C450 DQ326
FJ369995.1 gg_id:367250 feces adult twins and mothers; TS55 clone TS55_a03c04 FJ3699
EU466813.1 gg_id:295177 African elephant feces clone AFEL2_aao29g10 EU466
AY984705.1 gg_id:126730 human stool clone B658 AY984
DQ326469.1 gg_id:147499 Metagenomic gut microbiome healthy human stool clone C556 DQ326
DQ803244.1 gg_id:174137 human fecal clone RL311_aam22g08 DQ803
DQ795368.1 gg_id:192243 human fecal clone RL178_aah53e04 DQ795
FJ369837.1 gg_id:359199 feces adult twins and mothers; TS55 clone TS55_a01d04 FJ3698
DQ801534.1 gg_id:174920 human fecal clone RL388_aao96g04 DQ801
DQ807884.1 gg_id:192300 human fecal clone RL180_aah38d09 DQ807

1357.2	695.5	882.0	1061.2	657.6	704.4	559.2	896.9	423.9	1307.9	602.4
1004.3	1756.2	2831.6	1870.4	1700.7	1667.7	1724.7	2005.2	1327.1	714.8	1533.0
188.2	1535.0	2210.9	1446.2	1045.5	1066.7	1051.1	1343.4	1344.3	615.0	1354.3
1223.1	1769.2	2494.8	2151.9	1933.5	1976.6	1995.9	2428.9	1521.7	3531.1	1884.4
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3666.7	7870.9	7930.4	7512.3	6214.4	7003.9	6460.7	7461.4	7873.9	5579.7	10206.7
4988.6	3392.1	3116.8	3756.0	4252.0	3615.4	4634.9	2465.9	2993.2	7458.3	2718.5
2171.6	1089.3	1236.9	1241.1	974.6	1111.9	707.2	560.5	873.9	363.2	978.2
787.2	2924.4	2721.3	2442.8	2245.6	2653.4	2364.3	2336.6	2248.0	2224.1	1960.0
11361.1	3665.0	3430.7	3248.9	2989.6	2864.9	3035.8	3040.5	4289.1	2530.4	5149.8
66.2	1803.6	2341.3	1620.3	1104.4	1639.3	1131.8	1979.9	1283.3	1545.0	1655.4
6241.7	2458.2	2663.9	2787.8	2415.6	2100.4	2579.1	2334.1	3625.8	3257.8	3766.7
73.3	551.1	765.2	724.2	360.0	473.5	359.0	550.7	367.1	144.7	590.0
1344.9	1595.4	1679.2	1885.4	1024.5	989.1	1139.7	1612.5	867.9	391.7	968.0
4733.4	1711.7	2202.8	2367.7	1982.9	1753.1	1737.9	2412.1	1588.6	1115.7	1652.5
96.7	666.5	1010.1	1049.6	532.8	468.8	432.7	831.6	250.6	92.4	431.8
1331.6	6521.3	6337.1	5801.5	7114.6	5454.4	5860.9	5848.0	7173.4	5630.4	5227.3
2127.0	1827.3	2729.5	3153.8	1455.0	2199.0	1915.1	2850.9	1558.8	776.0	2140.4
917.9	1194.8	1520.0	1702.1	755.5	887.3	1241.0	1490.5	507.1	272.2	782.8
1388.6	1239.4	1495.8	1826.4	943.1	1088.5	841.4	1187.0	770.6	331.0	1198.6
142.7	1169.3	1684.1	1650.5	899.5	1077.2	900.9	1821.1	587.2	282.3	983.2
280.1	1014.5	1135.8	1045.7	621.7	561.3	539.4	1186.2	618.3	424.5	550.5
633.3	1846.1	2400.3	3395.2	1771.1	1597.7	1749.2	2246.6	1977.9	942.5	2016.9
553.7	2643.3	2889.5	2923.6	3054.3	2825.8	2636.3	2944.7	3696.5	2758.2	2709.3
49.6	379.1	458.1	441.0	294.1	297.3	224.6	447.8	175.0	58.2	266.9
1280.1	704.1	886.3	863.6	528.5	611.5	500.7	514.0	401.7	222.8	572.3
784.4	3141.2	2424.6	2507.2	1698.8	2438.2	2274.1	2176.2	3065.0	1839.2	3299.4
200.7	1129.6	1528.1	1187.4	1189.7	1047.7	1179.7	1647.6	816.5	1432.3	789.1
666.1	6358.7	5243.5	6183.2	4643.0	4928.3	4751.0	5633.0	11076.0	4907.2	6186.1
256.0	1249.4	1267.6	1707.4	782.6	1030.2	743.9	2129.4	663.3	220.9	853.7
7290.3	5149.4	4674.2	5442.6	4418.0	4954.9	4683.9	4306.7	7792.0	5852.9	5806.2
152.2	1031.6	1244.5	1485.0	744.8	716.9	670.0	1136.0	464.0	192.2	747.5
176.0	1070.4	1386.4	1524.5	792.7	836.2	743.9	1148.7	491.6	207.3	882.2
2169.3	1699.2	2165.8	1755.6	1353.6	1822.8	1185.8	1626.0	1260.4	538.5	4518.6
439.0	1041.4	1162.6	1525.1	973.4	1093.0	1512.0	930.0	1527.1	1189.0	1677.2
40.6	224.5	282.4	296.3	270.1	167.2	400.0	210.7	126.5	55.6	156.5
79.7	799.3	1201.2	1181.9	618.5	1072.7	940.8	1100.6	479.0	708.4	803.1
169.1	1546.3	2069.2	1774.8	1046.5	1088.9	950.6	1530.8	635.1	123.2	733.4
2525.9	804.8	831.2	872.8	901.3	815.9	598.2	122.4	703.1	297.1	829.0
60.5	77.4	107.9	148.4	39.6	68.4	91.5	168.4	60.4	28.8	90.6
385.9	394.5	469.3	468.0	328.8	332.0	300.9	374.0	327.1	470.4	233.7

920.2	1346.9	341.2
2019.7	1339.4	1783.9
1172.1	1715.4	1744.1
2099.7	2272.3	3269.3
2714.2	4058.7	3876.3
6322.4	8407.2	6746.7
3576.7	4832.2	3717.8
1342.2	1623.8	1246.4
2205.0	2145.5	3408.7
2816.8	2984.8	3175.7
2121.4	1879.9	2254.3
2440.1	3202.1	2846.3
592.1	535.0	700.6
1498.0	1821.9	2133.3
2181.7	2519.3	2978.7
942.3	698.0	1188.2
4955.6	6406.2	6552.3
2526.8	3019.6	3558.8
1342.5	1848.4	1852.8
1860.8	1405.4	1578.1
2019.5	1331.7	1954.2
947.3	1564.6	1301.6
1967.7	2698.4	2280.6
2964.3	3095.3	3734.1
293.3	308.6	651.3
1579.2	1019.2	692.4
1925.9	2498.7	1318.5
2046.3	1487.7	1270.3
5060.1	5323.6	4519.6
1504.0	1593.8	1070.8
4105.1	5547.2	4924.4
1164.1	1021.2	1385.7
1115.7	992.5	1312.1
2576.4	2347.7	2076.9
981.4	1098.1	1166.4
205.6	220.3	100.2
1225.0	1250.7	1192.7
1309.9	1090.1	2536.2
853.7	1276.3	752.5
157.3	100.8	82.3
515.5	634.2	410.0

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AY981322.1 gg_id:118449 human sigmoid colon mucosal biopsy clone G338 AY9813
DQ798578.1 gg_id:181113 human fecal clone RL181_aan98e05 DQ798
GQ898585.1 gg_id:553014 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
AY981405.1 gg_id:126052 human sigmoid colon mucosal biopsy clone L458 AY9814
FJ367771.1 gg_id:363066 feces adult twins and mothers; TS2 clone TS2_a03d08 FJ3677
FJ370019.1 gg_id:357288 feces adult twins and mothers; TS55 clone TS55_a03e05 FJ3700
FJ364702.1 gg_id:360169 feces adult twins and mothers; TS19 clone TS19_a02a07 FJ3647
FJ370368.1 gg_id:363012 feces adult twins and mothers; TS56 clone TS56_a04a07 FJ3703
DQ795587.1 gg_id:185404 human fecal clone RL178_aan66f07 DQ795
DQ795615.1 gg_id:176336 human fecal clone RL178_aan67a11 DQ795
DQ795236.1 gg_id:179617 human fecal clone RL178_aah51h01 DQ795
DQ806129.1 gg_id:198401 human fecal clone RL186_aah61f03 DQ806
AY977058.1 gg_id:121722 human cecum mucosal biopsy clone K746 AY977(
DQ795245.1 gg_id:189081 human fecal clone RL178_aah51h10 DQ795
FJ370088.1 gg_id:368843 feces adult twins and mothers; TS55 clone TS55_a04c08 FJ3700
FJ678759.1 gg_id:527751 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ794536.1 gg_id:194931 human fecal clone RL240_aaj29c07 DQ794
DQ327360.1 gg_id:146102 Metagenomic gut microbiome healthy human stool clone E916 DQ327
FJ365088.1 gg_id:356729 feces adult twins and mothers; TS1 clone TS1_a02f10 FJ3650
FJ369862.1 gg_id:363055 feces adult twins and mothers; TS55 clone TS55_a01f07 FJ3698
FJ372207.1 gg_id:360381 feces adult twins and mothers; TS9 clone TS9_a03a02 FJ3722
GQ090517.1 gg_id:401779 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
DQ801721.1 gg_id:199183 human fecal clone RL201_aai46a06 DQ801
FJ369989.1 gg_id:363307 feces adult twins and mothers; TS55 clone TS55_a03b09 FJ3699
FJ366965.1 gg_id:367240 feces adult twins and mothers; TS28 clone TS28_a01h03 FJ3669
FJ363816.1 gg_id:370034 feces adult twins and mothers; TS14 clone TS14_a03f11 FJ3638
DQ796388.1 gg_id:185876 human fecal clone RL179_aah26e12 DQ796
FJ370071.1 gg_id:361092 feces adult twins and mothers; TS55 clone TS55_a04b03 FJ3700
AY979995.1 gg_id:118321 human rectum mucosal biopsy clone K936 AY9799
DQ799666.1 gg_id:199237 human fecal clone RL305aal88h04 DQ799
DQ325976.1 gg_id:147194 Metagenomic gut microbiome healthy human stool clone B875 DQ325
AY981491.1 gg_id:126530 human sigmoid colon mucosal biopsy clone L595 AY9814
DQ795475.1 gg_id:180860 human fecal clone RL178_aah54g11 DQ795
FJ365982.1 gg_id:364181 feces adult twins and mothers; TS25 clone TS25_a01d05 FJ3659
DQ327604.1 gg_id:148762 Metagenomic gut microbiome healthy human stool clone EB94 DQ327
AY981519.1 gg_id:115463 human sigmoid colon mucosal biopsy clone L646 AY9815
FJ367595.1 gg_id:365617 feces adult twins and mothers; TS2 clone TS2_a01d03 FJ3675
DQ327512.1 gg_id:147432 Metagenomic gut microbiome healthy human stool clone EA87 DQ327
AY980228.1 gg_id:119170 human rectum mucosal biopsy clone KF73 AY9802
EU530468.1 gg_id:269215 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M7 EU5304
DQ795430.1 gg_id:187643 human fecal clone RL178_aah54c07 DQ795

1389.7	1080.4	1373.9	2058.2	1541.5	1016.9	1943.5	1120.1	738.6	1883.7	822.7
66.8	427.2	521.9	697.3	298.5	275.2	345.5	485.5	148.2	136.6	270.2
40.5	487.9	810.8	792.1	202.4	541.6	296.7	953.3	193.1	79.9	619.5
4032.8	3842.5	4218.7	3591.4	4332.4	3915.6	4303.3	4025.4	4588.2	5089.0	2519.2
296.9	3128.4	2993.9	2828.3	2927.4	2319.2	2701.5	2876.9	2318.3	1306.9	2868.1
2784.3	1105.5	1070.7	1458.0	1196.5	1008.3	1550.2	1138.9	1663.7	1971.2	1583.1
160.6	1012.5	1510.7	1611.5	712.0	1315.0	1070.2	1925.2	753.6	503.6	1404.3
1314.8	2476.0	2287.0	3223.9	1840.8	2054.5	2208.7	2181.8	2701.1	903.3	3730.3
540.3	1701.9	2274.1	2356.2	1095.4	1801.7	1504.8	2312.7	1477.5	746.8	1649.1
56.9	996.2	1230.7	1370.7	1163.5	1121.3	1235.1	1131.2	396.4	175.3	711.3
894.3	2293.9	2786.8	3449.3	1942.8	1694.1	2273.7	2152.7	1115.1	893.4	2477.7
100.6	1029.3	1358.2	1456.6	738.5	742.2	602.8	1126.7	375.6	262.4	727.9
146.4	849.0	1247.0	1228.2	530.7	764.7	720.7	1310.1	410.8	209.5	615.8
6634.9	3064.1	3224.1	2890.1	2966.7	3025.7	3111.1	2971.2	3965.6	4374.1	3918.5
1323.3	1667.0	1980.7	2314.5	1376.2	1444.6	1176.3	1389.7	1116.1	546.3	1589.1
10421.4	5083.8	4304.1	4482.6	3429.0	3670.8	4199.3	4084.8	5428.7	4488.4	6349.8
10904.9	2387.1	2611.9	2457.1	2593.2	1983.4	2432.3	2143.2	3479.4	3199.7	3224.3
384.5	3354.6	3964.5	4790.0	3641.1	2842.7	3054.7	3308.7	5516.6	3139.2	3956.0
152.2	1437.7	1562.4	1599.5	932.1	1368.8	1280.9	1248.1	1674.8	2388.1	1130.0
55.7	1134.9	1142.7	824.5	639.4	824.9	599.4	788.2	957.2	1033.8	595.3
43.1	389.1	667.8	608.9	243.4	389.9	517.2	509.4	176.6	404.5	371.6
199.0	1069.1	1513.3	1335.4	893.2	1098.4	1048.0	1072.1	613.3	595.7	1020.0
1361.9	1442.3	1892.0	2015.6	1276.4	1187.3	950.7	1504.7	730.6	357.1	1231.7
164.2	1889.0	1828.7	1684.9	1116.0	1337.3	1200.8	1335.2	1066.4	1541.7	1018.7
2136.1	5853.0	4799.6	5223.2	4292.9	4524.8	4345.7	4441.4	5013.8	3549.8	4831.3
29204.5	5812.0	5721.8	7556.0	6346.7	5354.1	6701.3	5963.1	8866.7	7371.0	7060.9
37.8	227.0	316.6	427.4	78.9	120.5	167.7	239.8	83.3	25.6	128.5
209.7	2584.5	3651.5	3383.9	2520.3	2428.0	2189.6	3112.3	2292.2	869.4	2888.9
72.0	505.4	611.6	689.6	301.0	434.7	355.4	533.4	336.9	142.6	460.2
3089.2	3923.0	3684.1	3198.0	2796.5	2758.1	3092.7	3447.9	6229.3	4144.7	4136.5
35.3	551.2	705.3	735.1	572.4	480.0	612.1	611.7	399.9	248.4	440.4
37.8	783.3	643.6	575.4	704.1	609.8	473.2	1110.2	406.1	246.3	298.4
21.4	492.7	946.3	1125.8	1482.3	390.6	1776.8	982.1	138.4	120.7	307.6
2377.3	1194.2	1380.5	1400.9	1437.6	1025.5	1242.0	1191.3	1948.9	1646.7	1210.3
213.5	1178.9	1606.1	1975.2	914.0	685.0	827.7	1226.4	416.3	129.0	554.7
125.0	510.2	596.3	690.5	225.7	300.0	258.6	528.7	153.4	68.9	335.0
12049.2	6262.3	6858.6	6719.0	6659.3	6168.4	6874.9	6176.4	10113.4	6897.7	6350.0
43.2	474.5	1022.4	1327.2	229.8	354.0	322.2	566.3	157.5	61.3	190.6
4006.7	1318.6	2147.6	2087.2	998.9	1758.5	1420.9	1833.5	1098.8	656.8	1486.9
37.1	729.6	1146.2	1406.4	180.0	704.2	403.7	1378.4	269.4	91.9	791.4
254.3	1791.2	1653.5	2219.7	2677.3	1563.5	2118.2	2279.8	1262.3	460.4	1530.9

994.9	1628.5	910.3
494.8	478.1	435.4
1064.3	369.9	759.2
4460.2	5015.8	4761.0
2638.8	2524.3	3232.3
1106.4	1075.6	998.6
1960.2	1568.6	2020.7
1628.8	2722.2	2005.1
1974.9	2312.9	2160.6
1010.0	1210.8	2422.0
2771.3	2225.9	2439.8
1195.3	1156.5	1798.2
1416.3	1010.9	1476.9
2764.3	2948.0	3281.6
1828.3	1919.7	1939.9
3684.1	5651.9	3683.1
2028.5	3241.5	2282.0
3391.3	3374.0	3477.8
1262.8	1570.3	2980.5
864.5	879.0	1168.4
578.1	650.6	632.3
1520.3	1333.2	1001.9
1890.4	1833.7	2257.7
1459.3	1619.5	2144.1
4130.1	5638.4	4226.5
7127.8	7461.4	7680.3
414.8	318.0	195.9
2873.9	2824.2	3281.0
582.0	499.1	580.9
2638.7	4877.2	5379.3
562.0	721.5	736.2
802.6	835.4	1254.8
741.9	353.9	196.8
1198.6	1219.0	1067.0
1446.8	1120.1	596.5
497.0	428.8	641.8
6588.5	7231.2	8006.7
614.0	708.1	608.2
1875.9	2623.6	2578.7
1637.3	571.4	802.5
2014.0	1713.1	3859.1

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AY981657.1 gg_id:121345 human sigmoid colon mucosal biopsy clone L934 AY9816
DQ327565.1 gg_id:149526 Metagenomic gut microbiome healthy human stool clone EB49 DQ327
DQ795890.1 gg_id:188526 human fecal clone RL245_aai84a10 DQ795
EU763685.1 gg_id:304317 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
GQ897929.1 gg_id:586117 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ803171.1 gg_id:185017 human fecal clone RL311_aam21e05 DQ803
AY983132.1 gg_id:115404 human descending colon mucosal biopsy clone L392 AY9831
FJ365852.1 gg_id:366076 feces adult twins and mothers; TS21 clone TS21_a03g11 FJ3658
FJ368044.1 gg_id:369944 feces adult twins and mothers; TS30 clone TS30_a03c03 FJ3680
DQ824042.1 gg_id:182512 human fecal clone RL204_aaj58e09 DQ824
FJ368850.1 gg_id:358018 feces adult twins and mothers; TS4 clone TS4_a01d01 FJ3688
DQ799778.1 gg_id:184382 human fecal clone RL182_aah33d02 DQ799
AY982803.1 gg_id:118990 human descending colon mucosal biopsy clone KZ48 AY9828
AY982947.1 gg_id:120341 human descending colon mucosal biopsy clone L150 AY9829
FJ367115.1 gg_id:361458 feces adult twins and mothers; TS28 clone TS28_a03f10 FJ3671
FJ369352.1 gg_id:363050 feces adult twins and mothers; TS50 clone TS50_a03d11 FJ3693
DQ326570.1 gg_id:150134 Metagenomic gut microbiome healthy human stool clone E003 DQ326
FJ365681.1 gg_id:361061 feces adult twins and mothers; TS21 clone TS21_a01g05 FJ3656
FJ370380.1 gg_id:366297 feces adult twins and mothers; TS56 clone TS56_a04c01 FJ3703
GQ047248.1 gg_id:373386 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010e GQ047
AY981351.1 gg_id:118041 human sigmoid colon mucosal biopsy clone G370 AY9813
FJ672871.1 gg_id:518121 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ365880.1 gg_id:369955 feces adult twins and mothers; TS21 clone TS21_a04b06 FJ3658
FJ368830.1 gg_id:367061 feces adult twins and mothers; TS4 clone TS4_a01b03 FJ3688
AY984592.1 gg_id:127691 human stool clone B532 AY9845
DQ807010.1 gg_id:199158 human fecal clone RL244_aaj45b01 DQ807
DQ803217.1 gg_id:190799 human fecal clone RL311_aam22c07 DQ803
FJ370984.1 gg_id:368313 feces adult twins and mothers; TS5 clone TS5_a03e10 FJ3709
DQ327407.1 gg_id:146980 Metagenomic gut microbiome healthy human stool clone E966 DQ327
AY982992.1 gg_id:122440 human descending colon mucosal biopsy clone L213 AY9829
DQ806816.1 gg_id:199262 human fecal clone RL198_aaj73b09 DQ806
FJ370062.1 gg_id:363104 feces adult twins and mothers; TS55 clone TS55_a04a05 FJ3700
FJ679229.1 gg_id:528140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
AY981289.1 gg_id:119080 human sigmoid colon mucosal biopsy clone G285 AY9812
FJ367926.1 gg_id:357891 feces adult twins and mothers; TS30 clone TS30_a01c04 FJ3679
DQ802357.1 gg_id:178821 human fecal clone RL188_aah16f01 DQ802
FJ369824.1 gg_id:363186 feces adult twins and mothers; TS55 clone TS55_a01c03 FJ3698
FJ365682.1 gg_id:362783 feces adult twins and mothers; TS21 clone TS21_a01g06 FJ3656
DQ807636.1 gg_id:185429 human fecal clone RL180_aah35c05 DQ807
FJ365938.1 gg_id:367945 feces adult twins and mothers; TS21 clone TS21_a04h06 FJ3659
DQ798388.1 gg_id:183609 human fecal clone RL181_aah41h06 DQ798

411.4	1696.2	2883.6	2508.8	1444.5	1824.5	1773.4	2277.5	1970.7	1950.1	2526.3
166.3	1892.0	1975.4	1904.4	1116.7	1452.7	1257.8	1604.2	1129.3	424.1	1987.0
23.9	299.1	392.7	541.4	174.0	206.2	174.2	364.4	60.4	45.5	235.7
106.4	892.4	1267.2	1485.0	745.7	687.5	591.6	1156.5	398.5	177.1	704.0
44.2	1573.9	2197.4	2356.6	695.3	1879.5	1163.8	2708.8	812.6	392.7	2098.5
2982.4	4159.5	4888.7	5480.4	5249.2	3925.5	5352.9	6319.2	3089.6	2519.5	5713.9
107.2	3171.0	2832.6	4622.9	4007.1	3055.0	3683.5	3651.5	3327.6	910.6	3752.8
5131.0	4070.6	3885.2	3257.7	3357.5	3372.3	3093.7	3234.5	5035.7	3842.3	4626.9
519.1	3944.8	4236.3	5451.4	4998.5	3575.4	5050.4	4563.2	4238.8	2202.9	3563.7
11337.9	1503.6	1781.7	1710.1	1375.2	1431.7	1685.7	1625.9	2239.1	2611.6	2164.6
7262.1	3809.7	3755.1	4433.9	3927.5	3588.3	4383.7	3655.6	4763.6	4011.5	3469.7
1675.4	3080.3	3490.5	3835.9	4267.8	3236.8	3739.9	3210.6	2082.4	919.4	3481.5
104.8	669.4	867.9	1115.3	596.0	460.9	439.2	852.6	257.3	78.1	339.2
10253.6	3248.3	3126.6	3670.4	2709.0	2749.0	3021.8	3022.5	5998.3	4126.1	3790.3
40.2	1879.9	1785.1	1309.4	823.3	1360.2	798.4	1236.5	1979.3	1843.3	959.8
110.7	1174.7	1148.1	598.8	481.3	717.1	393.0	874.0	429.6	293.3	747.7
1141.5	1221.2	1566.7	1838.6	1086.3	1084.0	879.1	1296.4	757.2	324.5	1193.0
15217.9	8206.0	6865.1	6796.5	6295.3	6859.8	6394.3	6399.1	10809.7	8604.8	9444.5
947.2	4079.4	3420.4	2857.6	2074.7	2141.5	2224.5	2851.0	4161.3	4181.1	2835.0
60.1	826.3	1098.0	897.1	653.2	799.9	749.1	1021.5	427.9	691.5	733.1
159.7	1200.0	1774.8	1689.5	1419.2	1861.4	1094.7	2645.6	690.0	1055.9	1613.5
132.8	440.7	592.1	671.3	143.4	265.4	250.4	389.5	145.6	66.6	322.2
53.6	310.6	488.2	776.9	231.0	276.0	483.5	767.7	139.4	170.0	413.7
161.2	1546.5	1511.9	1490.7	896.1	1051.5	882.1	1082.2	972.3	1076.4	881.0
49.0	489.9	525.5	527.5	347.8	442.1	341.3	726.4	235.1	120.1	202.9
4286.9	1374.3	1573.8	572.6	1253.9	1357.2	1342.0	1538.5	2143.1	1369.9	1496.4
1358.0	1406.1	1915.0	1989.1	1344.0	1169.3	956.4	1484.8	700.1	354.9	1254.7
1789.8	3243.5	4982.5	4164.8	3398.8	3438.0	3444.9	3891.3	1622.6	3870.8	3580.8
1375.8	1235.0	1610.6	1916.6	965.8	1052.4	918.6	1389.9	720.4	327.6	1102.9
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1531.3	1105.9	1433.4	1179.8	1128.6	1004.2	1341.5	1430.7	609.7	1376.4	1073.3
1400.5	3216.6	3078.2	4105.6	3122.8	2580.8	2884.3	3871.1	1850.4	768.4	2532.2
92.4	481.4	660.0	675.7	395.1	300.2	316.5	455.4	186.3	64.7	262.5
2605.6	1267.3	1874.3	1648.9	1550.2	1291.1	1269.0	1213.4	2377.5	1569.2	2107.6
228.6	1946.2	694.8	2360.6	1738.8	2203.1	1196.9	1742.7	1304.0	1330.1	1576.6
170.9	1196.3	1606.6	1877.1	764.5	1048.3	824.8	1487.7	679.5	261.5	1202.6
159.9	694.8	1051.1	1231.5	181.4	365.7	485.0	750.6	291.9	57.9	369.7
1226.2	2855.9	2294.5	2482.0	1986.8	2250.3	2144.0	2422.0	2713.0	1563.5	2503.6
58.2	1036.7	1260.2	880.8	510.6	878.7	493.5	1372.0	417.0	407.4	714.7
4811.7	3140.5	3173.2	2955.4	3481.7	2767.8	2810.3	3334.6	2634.7	3347.5	2695.1

2046.6	3228.4	2878.9
1486.6	1466.0	1320.8
305.5	508.5	1065.8
1488.8	915.4	1602.8
3568.0	1411.1	2666.9
5058.4	6265.3	5514.2
3434.0	2491.7	5559.7
2864.1	4045.4	2587.8
4594.5	4126.2	5056.7
1278.4	2030.4	1362.5
3791.4	3818.8	4537.1
3133.2	3416.6	4483.2
806.3	858.0	1603.1
3118.1	3932.6	3328.5
1354.3	1296.7	2141.3
1107.7	575.2	516.6
1846.4	1434.1	1514.9
6927.7	6227.7	7078.7
2886.3	3337.0	3223.6
859.7	1129.9	1460.5
2817.2	1590.9	2552.3
466.3	344.8	379.9
444.6	354.1	409.1
1246.3	1203.7	1665.7
486.2	651.0	715.4
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1840.9	1807.5	2423.9
2810.4	4053.3	3444.3
1953.8	1497.0	1602.3
1044.9	1612.8	1033.0
4591.0	5716.8	4788.0
1301.5	1304.8	1794.6
3213.3	2877.5	3955.5
396.2	453.8	762.5
1142.0	1537.8	1418.3
1984.8	1196.5	1901.5
1789.8	1176.8	1715.1
851.6	746.3	779.3
2254.1	2717.3	2627.8
2516.4	1056.8	1352.0
2985.6	3526.1	3960.6

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
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FJ364479.1 gg_id:367115 feces adult twins and mothers; TS15 clone TS15_a03d11 FJ3644
FJ678170.1 gg_id:520887 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
AY985660.1 gg_id:116406 human stool clone C666 AY9856
FJ363359.1 gg_id:367937 feces adult twins and mothers; TS149 clone TS149_a02c11 FJ3633
AY975186.1 gg_id:126668 human ascending colon mucosal biopsy clone KN08 AY9751
DQ808141.1 gg_id:179395 human fecal clone RL180_aao73b07 DQ808
FJ370188.1 gg_id:361470 feces adult twins and mothers; TS56 clone TS56_a01e05 FJ3701
GQ898491.1 gg_id:565351 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ365837.1 gg_id:363010 feces adult twins and mothers; TS21 clone TS21_a03f06 FJ3658
FJ370337.1 gg_id:356973 feces adult twins and mothers; TS56 clone TS56_a03f06 FJ3703
DQ794645.1 gg_id:198329 human fecal clone RL240_aaj30f03 DQ794
DQ325767.1 gg_id:148012 Metagenomic gut microbiome healthy human stool clone B445 DQ325
FJ363137.1 gg_id:366756 feces adult twins and mothers; TS148 clone TS148_a03e08 FJ3631
FJ370944.1 gg_id:361071 feces adult twins and mothers; TS5 clone TS5_a03b02 FJ3709
EU466973.1 gg_id:290543 African elephant feces clone AFEL2_aao32b04 EU466
EU767156.1 gg_id:335982 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ799484.1 gg_id:184523 human fecal clone RL305aal86h01 DQ799
AY978359.1 gg_id:121691 human transverse colon mucosal biopsy clone F306 AY9783
DQ325826.1 gg_id:147221 Metagenomic gut microbiome healthy human stool clone B565 DQ325
DQ823952.1 gg_id:188128 human fecal clone RL204_aaj57d04 DQ823
FJ371333.1 gg_id:367760 feces adult twins and mothers; TS6 clone TS6_a03g01 FJ3713
EU764364.1 gg_id:303428 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
DQ325851.1 gg_id:147212 Metagenomic gut microbiome healthy human stool clone B626 DQ325
GQ897976.1 gg_id:579613 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU762013.1 gg_id:350368 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
FJ369357.1 gg_id:367975 feces adult twins and mothers; TS50 clone TS50_a03e06 FJ3693
DQ802600.1 gg_id:188331 human fecal clone RL188_aan93h09 DQ802
FJ369422.1 gg_id:360753 feces adult twins and mothers; TS50 clone TS50_a04c09 FJ3694
FJ370009.1 gg_id:363126 feces adult twins and mothers; TS55 clone TS55_a03d06 FJ3700
FJ369117.1 gg_id:366010 feces adult twins and mothers; TS4 clone TS4_a04d10 FJ3691
FJ372009.1 gg_id:358234 feces adult twins and mothers; TS8 clone TS8_a04g02 FJ3720
AM275420.2 gg_id:232700 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
AY979987.1 gg_id:116730 human rectum mucosal biopsy clone K910 AY9799
FJ365630.1 gg_id:365873 feces adult twins and mothers; TS21 clone TS21_a01b08 FJ3656
FJ683843.1 gg_id:529625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
FJ678187.1 gg_id:519886 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ016070.1 gg_id:493598 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
EU466989.1 gg_id:291504 African elephant feces clone AFEL2_aao32d03 EU466
FJ368053.1 gg_id:364459 feces adult twins and mothers; TS30 clone TS30_a03d06 FJ3680
FJ367714.1 gg_id:361615 feces adult twins and mothers; TS2 clone TS2_a02g03 FJ3677
DQ798732.1 gg_id:186891 human fecal clone RL181_aao00f09 DQ798

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1238.2	2111.4	2548.0	2189.9	1317.5	1597.4	1537.4	1843.3	2052.6	1174.4	2073.2
589.3	1885.3	2341.8	3166.4	2295.4	1515.0	1701.7	1876.9	1460.8	473.2	1481.7
71.7	688.2	1092.6	1050.5	521.0	733.1	463.2	1160.9	459.4	213.4	979.9
372.4	2953.9	3019.0	2587.8	3267.7	3395.2	2301.2	3611.8	2047.6	2315.8	2228.6
428.4	1326.7	1426.5	1624.7	795.1	1277.4	732.7	710.9	1384.1	269.4	848.1
252.1	869.0	1271.2	1285.5	247.2	599.8	464.4	1008.6	315.8	153.5	481.5
109.7	1285.4	1870.8	2238.6	592.4	1679.1	1104.7	2272.0	1137.5	403.9	2200.9
829.7	938.8	914.0	918.9	825.4	649.8	528.4	1258.4	501.5	169.5	485.0
768.7	1753.6	1781.6	2385.3	978.5	1439.0	769.2	1661.9	1101.3	339.5	1488.2
2010.9	4950.7	4845.3	5570.6	4232.6	4779.7	5436.1	5056.3	3185.3	2366.9	4866.4
1670.4	2827.4	3024.6	3648.1	4079.1	2797.5	3472.4	2689.5	2103.7	833.0	2715.3
7701.0	2418.6	2460.2	3704.1	2345.4	1940.3	879.1	2509.3	2088.7	974.6	1924.7
1488.5	993.5	1215.3	1444.8	854.5	758.9	759.6	651.4	588.7	248.9	649.9
1290.7	1015.6	1171.1	1452.9	915.4	743.4	742.5	641.9	603.1	267.4	692.0
153.9	974.0	1271.9	1480.5	679.1	732.0	668.8	1019.5	457.8	180.5	784.4
525.1	2359.7	2535.5	1987.3	2072.8	2265.3	2240.5	2376.5	2953.0	1370.0	3419.4
114.1	632.1	842.0	884.5	599.7	379.5	466.3	594.4	222.7	110.3	332.7
3421.1	4373.4	4047.5	4864.1	4131.4	4166.4	3918.8	4251.3	5750.1	3005.7	5627.7
212.4	1695.5	1828.0	1762.1	1320.9	1347.8	1282.1	1481.4	414.0	329.3	1494.7
54.6	156.8	215.4	335.6	65.5	71.9	90.1	106.8	32.9	38.9	68.8
235.6	1994.5	2068.3	2211.7	2193.9	1793.4	1931.5	2367.4	1105.8	587.7	1946.6
74.0	703.9	1138.1	1245.2	362.0	676.1	569.4	1215.0	248.9	567.0	853.7
3419.2	2831.3	3179.8	3350.3	3004.3	2880.0	3540.9	2667.7	2032.1	3307.8	2456.3
53.1	1373.6	1354.3	1169.7	835.8	1138.3	834.3	1343.6	1337.3	1482.7	754.8
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653.6	3108.3	3714.5	3528.6	1948.1	2653.5	2250.6	2666.9	3330.0	1867.4	3756.4
188.8	1001.4	1272.9	1517.5	616.1	757.9	682.8	948.4	522.0	180.1	784.9
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46.7	403.8	693.5	750.2	181.7	315.1	212.9	964.2	127.0	383.4	580.4
45.8	1998.7	3503.1	2543.0	2060.1	2028.2	2284.1	3188.8	1517.5	493.6	1844.7
3081.6	626.5	728.9	1067.7	293.2	533.1	623.8	880.8	552.1	260.4	728.8
9556.8	4447.9	3621.4	3675.7	3228.8	3789.5	3618.2	3603.7	6347.3	4666.1	4287.5
142.5	1464.8	1827.5	1717.2	1527.1	1436.7	1343.9	1333.0	1555.7	457.2	1500.9
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170.8	923.4	1187.6	1512.1	1340.0	1088.1	1691.5	1351.5	479.4	1197.3	779.2

3869.8	4176.4	4406.2
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2017.3	1920.1	2963.2
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3854.7	2409.2	4422.6
1111.0	1185.6	1210.0
966.6	849.2	694.7
2603.8	1175.6	2015.2
892.4	1198.1	1230.7
1347.9	1160.0	1345.7
4136.2	4972.5	6966.5
2897.4	3238.3	4043.1
2837.2	2888.9	3263.0
1149.7	1223.0	1195.7
1137.5	1213.3	1081.9
1074.3	930.3	1162.8
1781.5	2230.1	2804.2
563.6	643.0	954.4
3686.9	4423.6	5021.7
1508.4	1702.4	1191.9
267.4	211.5	89.8
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3374.8	4246.3	3602.5
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2914.9	3033.2	3957.8
2289.5	2290.5	2183.4
1102.9	930.8	1250.7
2235.9	2646.8	3434.6
4009.7	4416.8	4944.3
1193.0	1567.6	1138.5
5498.7	4170.7	4568.0
749.5	806.6	935.7
701.4	304.8	300.7
2670.3	2661.7	4128.8
863.4	1043.0	569.7
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1643.1	1404.0	1573.2
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
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GQ898623.1 gg_id:579103 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ327601.1 gg_id:145551 Metagenomic gut microbiome healthy human stool clone EB91 DQ327
EU466881.1 gg_id:299300 African elephant feces clone AFEL2_aao30g08 EU466
DQ793763.1 gg_id:194417 human fecal clone RL246_aai76h08 DQ793
DQ327598.1 gg_id:147399 Metagenomic gut microbiome healthy human stool clone EB86 DQ327
EU766663.1 gg_id:353149 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ368064.1 gg_id:358567 feces adult twins and mothers; TS30 clone TS30_a03e08 FJ3680
AY981109.1 gg_id:123392 human sigmoid colon mucosal biopsy clone G023 AY981
AY976729.1 gg_id:118744 human cecum mucosal biopsy clone K322 AY976
FJ362679.1 gg_id:361660 feces adult twins and mothers; TS13 clone TS13_a01h01 FJ3626
DQ797842.1 gg_id:198743 human fecal clone RL206_aaj16e03 DQ797
FJ363626.1 gg_id:358857 feces adult twins and mothers; TS14 clone TS14_a01e02 FJ3636
DQ807991.1 gg_id:195146 human fecal clone RL180_aan70c08 DQ807
FJ370084.1 gg_id:367682 feces adult twins and mothers; TS55 clone TS55_a04c04 FJ3700
DQ807187.1 gg_id:178805 human fecal clone RL244_aaj47c11 DQ807
FJ365909.1 gg_id:365938 feces adult twins and mothers; TS21 clone TS21_a04e01 FJ3659
FJ369328.1 gg_id:359727 feces adult twins and mothers; TS50 clone TS50_a03b08 FJ3693
FJ363648.1 gg_id:362322 feces adult twins and mothers; TS14 clone TS14_a01g01 FJ3636
DQ798687.1 gg_id:181548 human fecal clone RL181_aao00b04 DQ798
DQ799737.1 gg_id:189763 human fecal clone RL182_aah32d07 DQ799
FJ371007.1 gg_id:363139 feces adult twins and mothers; TS5 clone TS5_a03h03 FJ3710
FJ676935.1 gg_id:527583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
AJ408972.1 gg_id:72481 human colonic clone HuCA20 AJ4089
AY977012.1 gg_id:115635 human cecum mucosal biopsy clone K686 AY977
FJ368155.1 gg_id:363118 feces adult twins and mothers; TS30 clone TS30_a04h05 FJ3681
EU768210.1 gg_id:310205 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AY978510.1 gg_id:120323 human transverse colon mucosal biopsy clone KQ08 AY978
FJ366548.1 gg_id:365979 feces adult twins and mothers; TS27 clone TS27_a01a09 FJ3665
DQ796764.1 gg_id:195420 human fecal clone RL179_aao54b08 DQ796
GQ898666.1 gg_id:573178 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ368131.1 gg_id:367336 feces adult twins and mothers; TS30 clone TS30_a04e04 FJ3681
AY981390.1 gg_id:123610 human sigmoid colon mucosal biopsy clone L434 AY981
EU767800.1 gg_id:335052 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
GQ898549.1 gg_id:538276 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ795463.1 gg_id:195174 human fecal clone RL178_aah54f07 DQ795
FJ371311.1 gg_id:366504 feces adult twins and mothers; TS6 clone TS6_a03e02 FJ3713
GQ079184.1 gg_id:468250 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229e GQ079
AY975126.1 gg_id:118960 human ascending colon mucosal biopsy clone KM16 AY975
FJ368054.1 gg_id:360490 feces adult twins and mothers; TS30 clone TS30_a03d07 FJ3680
FJ682827.1 gg_id:514693 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ682413.1 gg_id:524658 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824

1071.5	2808.1	3774.6	4187.6	1485.9	3059.1	2133.7	4072.1	1948.4	972.5	3640.3
62.2	477.8	596.7	680.6	322.4	383.4	325.5	435.8	397.1	149.5	472.5
7061.3	2779.3	2952.5	3659.8	2320.3	2468.7	2771.2	2128.8	4426.1	3882.7	4328.3
40.3	18.8	21.9	22.4	17.2	12.6	14.0	13.1	15.7	14.4	21.1
908.7	878.8	1271.1	1410.5	1344.9	803.3	1672.2	986.5	434.9	1837.0	693.4
87.1	3697.0	4654.8	3294.3	3054.7	3449.6	2685.4	3102.8	2612.5	1063.4	2768.8
10577.4	4882.8	4283.8	5352.2	3946.9	4365.6	4313.5	4074.4	7873.4	5460.7	6282.6
30.1	119.8	220.4	122.7	56.7	112.0	77.0	80.7	100.1	29.5	109.2
1449.2	2493.0	2869.8	2719.0	2391.4	2240.8	2463.5	2448.4	1433.8	2996.0	1863.2
1302.1	1265.4	1568.5	1897.9	1014.6	1124.3	909.0	1232.7	788.0	327.8	1225.9
41.8	795.4	704.1	752.8	515.3	622.3	395.2	1256.2	353.5	140.8	552.0
4161.0	4139.3	4679.6	5024.7	3605.4	4035.9	4115.7	4112.5	5970.2	4186.8	5270.9
2146.7	2088.7	2607.3	2752.1	2208.9	2831.3	2000.3	2552.6	1553.5	2150.9	2303.2
8148.2	4029.0	3516.2	3728.7	3350.2	3689.2	3466.4	3810.6	4596.7	3820.4	5414.1
3079.3	1470.5	1755.8	1707.4	1384.7	1370.3	1557.9	1677.2	2546.8	1633.5	1419.9
8140.8	2028.0	2445.7	2506.0	2247.0	2153.3	2447.3	2322.8	2696.4	3118.2	1938.1
2550.3	1149.1	1125.9	1209.2	1428.8	1016.0	1211.5	437.6	798.1	389.7	1055.9
1261.9	1069.6	1474.3	1628.1	973.4	941.3	707.4	1007.6	624.9	274.2	1048.1
50.9	267.6	392.6	405.7	210.7	232.8	258.3	432.4	107.5	249.5	209.9
317.8	1924.5	1912.2	2482.9	3024.3	2040.3	2717.0	1843.3	1274.4	506.9	1805.7
1289.2	1685.8	2355.4	2441.9	1469.1	1569.7	1164.8	1778.9	1098.6	535.4	1826.0
28.0	224.2	470.5	468.8	69.9	160.1	125.2	319.0	89.2	35.9	316.3
7024.7	5447.6	5729.7	5964.0	5360.7	5058.1	5840.2	5117.9	5439.7	5327.8	6647.2
64.9	554.5	780.0	742.7	469.1	443.7	372.3	846.0	245.2	180.5	473.1
5396.9	4444.1	4520.1	5186.7	3807.9	3838.1	3888.5	3850.6	6297.0	4848.4	6367.2
1120.5	787.8	1104.8	1078.5	701.1	816.2	547.5	826.8	629.6	278.3	992.1
870.0	2535.2	2213.6	2241.8	2707.1	2299.2	2391.1	2860.5	3358.5	2863.1	2121.9
170.8	1041.4	1322.1	1552.1	674.4	812.3	751.7	993.8	561.7	262.5	803.1
3045.2	4200.5	4141.9	4190.3	3657.9	3784.7	4040.5	3847.5	4956.9	3361.5	4547.5
1050.2	2309.0	3142.3	3599.8	1062.6	2601.7	1754.7	3520.4	1407.0	684.5	3001.7
3468.3	1748.1	2775.8	3642.8	1481.2	2021.8	2665.2	3265.6	2737.6	1665.6	2467.7
771.2	2236.2	2846.3	3774.5	1464.8	2189.4	2082.9	2664.7	1658.4	494.3	1959.1
91.1	474.8	520.8	454.1	329.1	398.1	252.8	495.1	214.3	162.1	199.9
10800.8	3588.5	3809.7	4057.0	2517.6	3520.9	3449.7	4135.6	4335.1	3711.6	4640.7
62.4	1384.4	1657.9	1931.7	1033.5	1188.1	1483.8	1450.2	818.6	248.9	918.0
7170.8	4278.7	3540.6	4076.4	2965.8	3605.5	3524.1	3207.8	7372.0	5376.7	4130.0
31.7	806.5	1270.6	1149.4	376.7	741.8	435.3	1184.4	410.3	340.0	504.3
38.5	1058.0	1279.5	1866.1	522.1	1005.6	901.5	1684.1	464.7	282.4	848.1
1284.3	1260.8	1671.0	1964.0	994.6	1135.7	954.8	1430.4	677.4	309.6	1185.9
753.0	672.2	946.8	1043.9	469.8	583.3	773.1	949.9	366.5	252.4	534.0
6964.3	4200.1	3641.3	3644.6	3025.0	3196.2	3139.4	3251.6	4234.8	2625.4	7540.6

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532.5	479.2	513.1
2455.9	3579.2	2360.8
25.2	29.3	18.0
955.0	1205.8	661.9
3211.5	2904.6	3039.8
3944.9	5111.0	3579.4
70.3	198.5	365.1
2744.4	3862.7	2861.3
1863.7	1449.7	1631.4
680.7	521.4	1569.8
3743.0	4616.7	4086.8
3612.8	3087.2	3982.1
3697.6	4374.7	3601.2
1607.4	2064.0	2098.1
2164.0	2743.8	2423.7
1100.2	1613.9	1327.4
1642.0	1272.0	1499.2
400.7	374.1	428.5
1827.6	1738.2	2921.8
2350.3	1978.7	2358.6
463.4	236.8	227.4
4624.6	6269.9	5954.4
759.2	595.0	954.7
3944.5	4007.8	3918.6
1333.6	1026.6	1049.7
2694.3	3419.7	3018.5
1158.8	1069.4	1361.4
3629.1	4613.0	3778.8
4785.0	2242.7	3151.0
2392.7	2518.3	2556.6
3108.9	3203.6	3712.7
436.5	636.5	535.2
4652.5	3744.5	4953.8
1262.1	1728.9	1803.6
3032.4	5257.3	3958.1
1182.2	1205.0	1188.4
1714.2	1224.2	2356.1
1946.6	1598.6	1652.0
777.2	1070.1	1542.6
3854.5	4345.8	3251.7

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DQ794798.1 gg_id:178201 human fecal clone RL240_aaj32e03 DQ794
FJ370014.1 gg_id:363968 feces adult twins and mothers; TS55 clone TS55_a03d11 FJ3700
AY981272.1 gg_id:121932 human sigmoid colon mucosal biopsy clone G264 AY9812
EF399741.1 gg_id:214326 human fecal clone SJTU_E_02_80 EF3997
EU467094.1 gg_id:302260 mongoose lemur feces clone ML_aae88b02 EU467
FJ365465.1 gg_id:359239 feces adult twins and mothers; TS20 clone TS20_a03c02 FJ3654
DQ808298.1 gg_id:197637 human fecal clone RL180_aao75a02 DQ808
AY976950.1 gg_id:121006 human cecum mucosal biopsy clone K611 AY976
EU767253.1 gg_id:347629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ327506.1 gg_id:145154 Metagenomic gut microbiome healthy human stool clone EA80 DQ327
FJ370957.1 gg_id:369037 feces adult twins and mothers; TS5 clone TS5_a03c04 FJ3709
FJ370095.1 gg_id:357176 feces adult twins and mothers; TS55 clone TS55_a04d03 FJ3700
DQ795794.1 gg_id:198960 human fecal clone RL245_aai82e05 DQ795
DQ799849.1 gg_id:178896 human fecal clone RL182_aah34h07 DQ799
AY979988.1 gg_id:115875 human rectum mucosal biopsy clone K917 AY979
FJ367600.1 gg_id:362701 feces adult twins and mothers; TS2 clone TS2_a01d08 FJ3676
EU466760.1 gg_id:289045 African elephant feces clone AFEL2_aao29b01 EU466
EF399837.1 gg_id:215378 human fecal clone SJTU_E_03_90 EF3998
DQ905506.1 gg_id:173012 human fecal clone 014-d9 DQ905
DQ806249.1 gg_id:190058 human fecal clone RL186_aan89c09 DQ806
EU767773.1 gg_id:318758 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
DQ327206.1 gg_id:147131 Metagenomic gut microbiome healthy human stool clone E737 DQ327
EU451337.1 gg_id:330473 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU763884.1 gg_id:346114 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
AY975189.1 gg_id:121776 human ascending colon mucosal biopsy clone KN15 AY975
DQ795244.1 gg_id:195491 human fecal clone RL178_aah51h09 DQ795
DQ799441.1 gg_id:196073 human fecal clone RL305aal86c10 DQ799
EU762316.1 gg_id:328305 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU762
DQ326456.1 gg_id:146072 Metagenomic gut microbiome healthy human stool clone C531 DQ326
FJ370419.1 gg_id:357103 feces adult twins and mothers; TS56 clone TS56_a04h04 FJ3704
AY978700.1 gg_id:126318 human transverse colon mucosal biopsy clone KT78 AY978
GQ897549.1 gg_id:592235 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ799818.1 gg_id:195604 human fecal clone RL182_aah34c02 DQ799
GQ001498.1 gg_id:508164 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173g01 GQ001
GQ897613.1 gg_id:535749 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ796531.1 gg_id:197819 human fecal clone RL179aan74c03 DQ796
FJ364639.1 gg_id:358860 feces adult twins and mothers; TS19 clone TS19_a01c11 FJ3646
EU762312.1 gg_id:317534 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU762
FJ367738.1 gg_id:361646 feces adult twins and mothers; TS2 clone TS2_a03a07 FJ3677
DQ327267.1 gg_id:145585 Metagenomic gut microbiome healthy human stool clone E811 DQ327

6209.5	2416.4	2594.4	2624.6	2387.4	2161.8	2487.6	2353.6	2699.1	2151.9	2777.3
187.0	1558.1	2255.4	2089.9	682.9	1368.2	1022.1	1942.2	697.6	288.0	1118.6
48.1	594.1	726.8	586.9	414.4	540.7	466.2	583.1	276.0	418.3	395.3
43.4	2664.9	2510.3	2491.9	1712.7	1986.2	1755.6	2062.4	3186.1	2439.9	1596.3
3513.4	4320.3	4067.3	3908.3	3357.2	3608.5	3859.6	3999.8	4896.9	2762.2	4898.3
2705.2	2596.7	2598.7	3717.6	2833.8	2129.0	2235.4	2421.4	1472.9	975.5	2192.8
104.9	743.4	1133.8	415.6	306.1	646.4	502.5	895.6	436.8	212.2	855.0
45.7	298.2	328.9	367.0	93.8	219.3	93.0	268.8	127.4	52.2	65.7
10073.8	6413.9	5057.6	5488.8	4658.4	5533.9	5805.4	5449.7	7831.7	5578.3	6251.7
15345.3	7049.0	7042.1	9030.1	4997.2	6254.1	6916.4	6498.1	10807.4	8598.5	12759.4
85.9	122.7	196.9	176.6	71.3	63.7	107.0	99.2	56.8	28.2	67.3
100.4	1266.7	1199.8	918.3	523.5	959.5	544.4	1000.3	483.3	351.4	771.8
86.1	2299.7	2664.5	3051.6	2417.9	2339.6	2402.4	2173.5	1490.9	869.7	1648.8
4262.4	1482.1	2075.5	1704.9	1271.6	1399.8	1490.1	1726.5	2196.5	1191.3	1441.2
339.8	1926.5	1936.4	2514.0	3029.1	2051.9	2723.6	1871.9	1179.4	475.9	1840.5
1470.2	5038.4	4481.0	4962.7	3916.6	4268.9	3695.1	4247.4	5800.8	2980.1	4685.4
91.7	810.2	1231.5	1094.6	753.0	854.0	1205.1	1144.9	593.7	172.1	1023.9
9047.2	4840.3	5127.8	4981.3	4607.1	4452.5	4865.4	4006.6	4918.6	5185.7	4962.8
56.7	1242.6	1621.6	1306.2	579.4	1299.5	671.2	1887.0	535.3	345.7	1261.8
42.1	1464.1	2299.8	2399.9	541.2	1788.1	1070.2	2701.2	794.7	361.2	2085.7
66.5	169.1	199.6	47.3	114.0	143.8	130.2	104.3	216.8	167.4	139.0
44.9	504.2	567.4	565.8	352.1	435.1	354.9	760.0	220.5	130.7	246.0
30.6	235.2	445.1	391.4	50.9	225.8	97.0	272.7	93.5	27.1	194.6
279.0	1510.0	2024.3	2042.6	1288.8	1700.9	2092.4	2760.0	835.4	1434.5	1457.4
17436.2	5566.2	5357.8	6309.3	4898.5	5021.9	5596.4	5064.0	11306.6	6878.3	7846.7
147.2	1858.6	2049.4	1908.2	1734.6	1680.7	1626.7	2068.2	1747.0	679.0	1750.3
256.7	2596.3	3115.2	3644.8	2742.1	2847.3	2885.6	3870.9	1559.3	702.3	3002.7
676.5	2575.5	3093.1	2696.3	2941.3	2176.6	3061.6	2602.9	3946.2	1293.9	2429.2
138.1	795.1	1145.9	1343.9	399.2	602.4	525.7	947.2	328.8	135.3	688.5
1667.5	2809.0	3195.8	3614.9	4337.0	2785.0	3444.1	2863.4	2094.2	777.0	2704.4
5299.5	2972.3	3175.5	3276.5	2864.0	3451.6	2905.7	2514.2	4511.5	3061.1	4213.3
2127.4	4318.2	3757.2	3547.1	2843.8	3497.2	3051.3	3582.8	5560.7	4456.6	3937.5
48.4	1374.0	1737.6	2006.3	766.7	1244.1	1061.4	2019.6	816.3	405.6	1360.2
253.9	2843.2	1908.6	2694.2	2273.2	1206.5	2598.8	1398.4	2967.1	2713.0	2204.2
1397.5	609.8	702.4	902.8	510.7	490.0	473.7	288.3	381.7	182.0	424.9
49.8	1761.1	2400.2	2689.7	901.1	1921.4	1340.4	3006.0	893.5	500.5	2205.7
66.7	355.6	456.0	604.2	281.7	207.7	264.6	350.6	97.1	126.0	209.0
96.1	925.8	1352.2	1392.1	544.7	939.3	736.1	1583.1	615.9	224.9	1030.3
95.7	1013.6	1447.6	1434.8	777.0	760.7	572.7	1175.3	392.7	231.4	744.6
32.1	899.8	1274.8	1084.3	473.0	695.4	483.6	1309.9	381.5	518.1	591.7
71.0	473.7	633.5	699.1	347.1	458.0	416.6	570.9	335.7	151.6	418.6

2211.1	2399.2	2428.5
1681.3	1406.9	1488.3
580.3	803.0	802.4
2124.8	2419.3	3451.5
4873.9	3765.7	4023.6
3143.4	3196.8	2921.8
1367.1	637.3	555.9
339.8	296.0	110.3
5031.0	5625.3	4555.8
4896.8	7146.8	6203.6
153.0	153.9	89.5
1623.8	851.3	701.8
2162.0	2185.3	3507.9
1614.3	1808.6	1748.2
1810.4	1733.9	2921.9
4562.5	4601.1	7515.2
1065.3	964.5	1432.5
4321.3	5175.5	4251.6
3131.1	1177.9	1790.1
3338.3	1237.0	2167.3
150.7	278.7	144.9
484.6	658.0	706.0
452.8	361.0	460.0
2441.2	2000.1	2746.5
4289.2	7251.8	4597.6
2004.8	2091.3	2735.4
4262.6	2374.3	4911.0
2248.8	3535.5	3737.8
1048.7	780.9	1208.9
2886.3	3026.6	4030.9
2826.8	3924.3	3003.5
3590.6	4841.9	5348.7
2191.8	1304.4	2058.4
1859.6	2278.5	2152.3
882.5	999.1	554.6
3760.9	1669.5	3072.1
464.7	423.8	379.8
1073.4	1161.0	1383.0
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611.3	552.0	632.1

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DQ071480.1 gg_id:233648 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc17 DQ071
DQ799325.1 gg_id:189701 human fecal clone RL205_aaj20h09 DQ799
DQ326644.1 gg_id:147888 Metagenomic gut microbiome healthy human stool clone E081 DQ326
AY978654.1 gg_id:117354 human transverse colon mucosal biopsy clone KS83 AY978
AY980149.1 gg_id:121657 human rectum mucosal biopsy clone KD47 AY980
DQ794967.1 gg_id:181815 human fecal clone RL310_aam38e09 DQ794
DQ808460.1 gg_id:184002 human fecal clone RL180_aao76g10 DQ808
DQ807035.1 gg_id:197041 human fecal clone RL244_aaj45d05 DQ807
DQ801333.1 gg_id:181853 human fecal clone RL388_aao94b05 DQ801
DQ809690.1 gg_id:174111 human fecal clone RL184_aan82f09 DQ809
DQ795390.1 gg_id:174199 human fecal clone RL178_aah53g06 DQ795
FJ369506.1 gg_id:368371 feces adult twins and mothers; TS51 clone TS51_a01d05 FJ3695
AY981426.1 gg_id:117920 human sigmoid colon mucosal biopsy clone L493 AY981
FJ370030.1 gg_id:364149 feces adult twins and mothers; TS55 clone TS55_a03f06 FJ3700
EU762347.1 gg_id:310421 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ796749.1 gg_id:190462 human fecal clone RL179_aao53h12 DQ796
DQ807697.1 gg_id:174347 human fecal clone RL180_aah36b03 DQ807
AY977087.1 gg_id:119004 human cecum mucosal biopsy clone K777 AY977
DQ327521.1 gg_id:148085 Metagenomic gut microbiome healthy human stool clone EB01 DQ327
DQ798618.1 gg_id:193664 human fecal clone RL181_aan99b01 DQ798
DQ796586.1 gg_id:190899 human fecal clone RL179aan75d03 DQ796
FJ370968.1 gg_id:365622 feces adult twins and mothers; TS5 clone TS5_a03d05 FJ3709
DQ796228.1 gg_id:191484 human fecal clone RL179_aah23d06 DQ796
EF400068.1 gg_id:214474 human fecal clone SJTU_E_08_47 EF4000
DQ800930.1 gg_id:180095 human fecal clone RL387_aao89e01 DQ800
DQ809583.1 gg_id:182505 human fecal clone RL184_aan81b10 DQ809
EU762022.1 gg_id:306696 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
AY982998.1 gg_id:121493 human descending colon mucosal biopsy clone L222 AY982
AY981259.1 gg_id:122690 human sigmoid colon mucosal biopsy clone G246 AY981
DQ327481.1 gg_id:148410 Metagenomic gut microbiome healthy human stool clone EA51 DQ327
DQ801679.1 gg_id:183837 human fecal clone RL201_aai45d03 DQ801
DQ327280.1 gg_id:145739 Metagenomic gut microbiome healthy human stool clone E824 DQ327
DQ798547.1 gg_id:188522 human fecal clone RL181_aan98b01 DQ798
DQ807958.1 gg_id:178681 human fecal clone RL180_aan69g07 DQ807
DQ807688.1 gg_id:178919 human fecal clone RL180_aah35h11 DQ807
EU774084.1 gg_id:355900 Chimpanzee feces clone CHIMP1_aaj39e07 EU774
AY981171.1 gg_id:122120 human sigmoid colon mucosal biopsy clone G118 AY981
AY978339.1 gg_id:121348 human transverse colon mucosal biopsy clone F251 AY978
DQ796894.1 gg_id:185065 human fecal clone RL179_aao56a11 DQ796
FJ364707.1 gg_id:360128 feces adult twins and mothers; TS19 clone TS19_a02a12 FJ3647

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28.2	407.1	613.7	610.1	182.6	379.6	189.2	553.3	77.1	33.3	335.5
500.1	2111.9	3316.3	3053.5	1403.9	1795.9	2133.1	2643.8	1004.2	346.1	2459.3
6668.1	2282.9	2469.6	3546.5	2363.3	1953.2	2231.9	2428.7	2076.1	1778.3	1855.7
11164.4	6332.4	6186.7	6670.2	6354.1	6106.0	6991.3	5670.7	7204.5	6797.6	9366.4
18798.5	5910.3	5417.2	6911.7	5635.9	5320.4	6351.1	5374.4	11312.1	5825.5	8159.4
19469.6	4721.9	5263.3	5397.7	4800.4	4504.8	5000.7	5649.3	5809.9	5106.1	5331.4
161.0	974.9	1195.2	1481.8	632.3	734.6	670.1	957.5	460.2	182.1	785.9
29.8	369.5	740.1	1605.0	68.5	289.5	210.9	769.4	119.0	52.1	424.1
1429.3	21.1	1386.8	879.9	825.1	1162.9	1599.0	1245.1	2258.9	893.6	2147.1
61.7	759.2	923.2	1197.0	178.7	669.9	368.5	999.8	219.2	81.8	602.0
91.4	787.6	1069.5	1138.8	698.9	544.0	495.8	1052.4	319.2	116.5	464.9
1344.2	2104.8	2832.1	2809.5	1764.0	1963.5	1677.5	2578.9	1338.7	837.1	2210.8
99.0	774.9	1130.4	1285.6	617.2	498.3	536.7	820.1	314.7	114.3	505.8
3306.8	3595.6	4433.7	4178.5	3973.4	3636.7	4893.0	3655.3	3669.0	3057.5	2743.7
12823.0	5955.2	6212.8	5697.7	3963.3	5070.4	5908.9	5545.4	8516.2	6162.6	7904.8
10820.3	7233.0	6554.3	8451.8	7193.8	6745.1	7709.7	6839.7	14943.8	8966.5	9814.9
186.6	1022.6	1281.0	1696.9	624.5	746.3	739.4	1027.7	537.3	215.6	755.5
146.7	1242.9	1839.4	1853.1	756.4	1133.7	927.4	1958.3	566.1	250.1	1292.3
143.4	424.0	534.2	706.0	36.0	228.3	206.5	275.2	155.2	43.1	273.5
55.3	441.8	561.6	761.8	194.6	252.1	317.5	488.1	177.4	56.9	286.0
42.4	316.1	526.7	548.6	156.3	295.4	191.8	512.7	112.1	42.9	319.1
56.6	708.9	1360.2	420.2	211.6	473.2	258.3	403.5	540.3	1078.8	449.5
1026.4	1793.7	1589.5	1767.4	1398.6	1545.9	1927.0	1826.5	1174.6	548.7	1914.4
1010.8	2919.0	3962.4	4409.3	1497.3	3183.5	2184.1	4234.1	1826.7	917.6	3724.6
146.4	781.8	1024.2	1293.8	309.2	588.0	484.8	867.3	317.8	139.5	665.4
60.8	708.8	973.9	800.0	268.8	563.6	289.5	600.0	347.9	294.4	440.8
128.4	620.2	943.9	988.3	210.9	528.8	310.2	862.1	302.0	93.0	534.7
129.4	808.4	975.1	1142.8	659.8	495.6	493.6	839.9	303.9	131.5	433.8
126.6	937.6	1038.8	1238.3	853.6	575.8	556.7	1076.5	373.8	157.4	469.5
697.9	3654.6	3960.9	4021.9	4661.4	3507.2	5210.7	4616.9	2155.6	2479.9	4260.0
35.9	270.6	383.7	454.3	92.8	137.2	187.8	279.6	80.2	39.4	175.0
3012.4	2573.2	2575.6	3808.2	2463.8	1994.0	1771.0	2638.2	1576.6	515.3	1507.6
238.3	1514.6	1952.4	1933.4	1597.4	1806.6	1548.7	1839.3	1148.1	1953.5	1297.2
1791.7	1902.7	1947.7	2012.8	1263.4	1629.9	1524.7	1911.8	3241.8	1707.7	1851.1
151.4	947.1	1194.4	1409.1	601.4	696.3	605.2	973.8	440.8	172.3	757.1
735.5	2817.1	3710.8	4421.6	3131.4	2933.1	3603.8	3555.3	4296.8	5413.1	2574.2
100.9	1121.4	1403.7	1373.0	1621.8	1459.5	1029.4	1849.2	694.9	1134.9	871.7
321.3	1561.6	1730.4	2574.7	1330.1	986.2	1012.9	1295.0	574.5	258.3	640.1
1988.0	2479.1	2390.0	2018.2	2069.8	1925.9	1755.1	2036.5	1981.2	1646.3	2183.5
8271.0	3775.3	4181.6	2940.9	4009.6	3506.1	3215.2	4393.4	2795.1	4999.0	3144.0

429.8	428.1	508.5
606.8	470.1	775.7
2176.2	2062.4	2906.5
3103.1	3304.4	3213.7
6553.5	6845.6	5823.2
6028.1	6364.2	6952.3
4410.2	6577.7	5225.4
1076.4	933.0	1163.6
954.8	551.7	599.9
794.9	1143.3	1009.9
1361.7	531.7	771.1
1043.1	796.4	1626.1
3028.6	2583.1	2876.6
923.4	776.1	1491.6
3302.2	4574.3	4497.2
4290.6	5845.3	6874.2
7687.6	7469.7	7684.1
1147.5	975.8	1290.3
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419.3	268.6	369.8
599.6	480.5	387.4
781.0	375.3	493.9
358.5	450.1	559.6
1199.0	1852.6	1308.6
5462.7	2935.7	4006.8
1077.9	762.9	1239.2
581.8	476.6	344.9
1048.0	521.0	872.5
853.0	763.2	1141.7
961.0	868.1	1642.1
3581.2	4489.6	4528.8
397.4	312.8	190.8
2919.2	2953.4	2834.2
1998.6	1962.7	2682.8
1538.8	2439.7	1444.5
1071.5	886.0	1109.6
3447.1	4014.9	4549.3
1746.7	1341.1	2129.7
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1507.6	2426.0	2075.2
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU764211.1 gg_id:327552 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
DQ326455.1 gg_id:150341 Metagenomic gut microbiome healthy human stool clone C530 DQ326
FJ679429.1 gg_id:521644 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ807570.1 gg_id:179871 human fecal clone RL307_aam08d05 DQ807
EU762986.1 gg_id:326433 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
AY982774.1 gg_id:124418 human descending colon mucosal biopsy clone KZ12 AY9827
DQ808101.1 gg_id:175303 human fecal clone RL180_aan72e04 DQ808
FJ367908.1 gg_id:367092 feces adult twins and mothers; TS30 clone TS30_a01a02 FJ3679
AM697416.1 gg_id:222230 sequencing libraries indoor dust clone BF0001D031 AM697
EU766710.1 gg_id:307860 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
AY983055.1 gg_id:119891 human descending colon mucosal biopsy clone L291 AY983
GQ897330.1 gg_id:547913 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ088675.1 gg_id:404865 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ088
AY978399.1 gg_id:121158 human transverse colon mucosal biopsy clone F383 AY9783
FJ682604.1 gg_id:528062 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
NZ_ABGC03000041.1 gg_id:469957 Clostridium sp. str. SS2/1 NZ_AB
EU762728.1 gg_id:329976 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ807693.1 gg_id:184566 human fecal clone RL180_aah36a07 DQ807
FJ678363.1 gg_id:532186 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
DQ795253.1 gg_id:192263 human fecal clone RL178_aah52b02 DQ795
AB486353.1 gg_id:579188 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EF602816.1 gg_id:233515 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
AY330126.1 gg_id:95597 methanogenic landfill leachate bioreactor clone AC036 AY3301
AF371667.1 gg_id:32727 swine intestine clone p-1612-c5 AF3716
AJ229203.1 gg_id:38211 anoxic bulk soil flooded rice microcosm clone BSV51 AJ2292
EF602953.1 gg_id:231295 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6029
EF602951.1 gg_id:232130 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6029
EU779322.1 gg_id:336501 Visayam Warty Pig feces clone VWP_aaa04d03 EU7793
AM932651.1 gg_id:560203 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ815773.1 gg_id:172705 mouse cecum clone aab22b06 DQ815
FJ365173.1 gg_id:364390 feces adult twins and mothers; TS1 clone TS1_a03g03 FJ3651
X77839.1 gg_id:14090 Clostridium polysaccharolyticum str. DSM 1801 X77839
AF371666.1 gg_id:25842 swine intestine clone p-204-o5 AF3716
EU504957.1 gg_id:259762 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g09 EU5049
AB488370.1 gg_id:532832 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4883
AB264067.1 gg_id:196195 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-50 AB2640
EU656014.1 gg_id:283710 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6560
EU503974.1 gg_id:277385 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03e03 EU5039
AB264071.1 gg_id:177681 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-96 AB2640
EF559115.1 gg_id:222851 mesophilic anaerobic digester clone C35_D7_H_B_B05 EF5591
EU598268.1 gg_id:270815 Production purification and alkaliphilic xylanase microbial EMSD5 compost clone OTU EU5982

193.0	428.8	506.6	613.4	406.4	335.8	445.5	491.8	142.6	126.6	216.3
35.9	933.9	1391.4	1964.4	403.3	596.4	483.9	1452.7	295.1	895.0	1093.4
37.7	372.4	660.8	501.2	172.4	356.7	333.4	413.7	136.1	58.2	272.9
3463.3	2561.7	3708.0	3499.7	2569.3	2401.5	3436.8	3603.0	1391.5	1309.9	4489.3
1037.7	3772.2	3480.8	3290.5	2865.6	2942.4	2866.2	3256.8	4745.5	4069.0	3154.5
1156.7	6625.9	7155.4	5747.9	4742.5	5510.2	5492.0	5933.9	7539.8	6092.6	8290.3
4614.5	3229.0	3577.0	4697.6	2993.0	3290.5	3377.6	3385.6	3667.2	2640.2	4599.3
21050.8	8257.7	7814.5	7771.1	7432.1	7411.6	8404.2	8366.6	11681.3	10720.1	12027.3
61.4	881.6	1512.5	1405.5	859.6	919.4	768.5	1111.6	484.7	144.8	844.1
639.8	2078.6	1554.3	2331.3	1609.2	1530.7	1620.3	1515.1	1235.7	1221.4	1129.0
163.1	1091.4	1671.4	1612.7	1002.7	1122.1	972.0	1734.0	1196.0	596.8	1020.0
44.0	948.0	1564.1	1205.7	457.7	1230.9	849.8	1206.8	469.5	173.4	733.2
31.8	409.0	665.3	737.8	160.0	344.1	371.2	666.2	180.3	50.5	276.1
137.8	833.9	1201.1	1175.0	474.0	781.9	664.2	1287.0	393.4	192.0	630.4
176.5	1015.2	1286.7	1535.4	635.5	771.2	695.4	975.4	487.4	183.8	814.4
68.9	2459.6	3619.4	3594.2	1090.2	2627.3	1717.9	3790.6	1289.6	764.6	3229.3
3287.1	5734.4	5351.0	7252.5	7291.2	5453.4	6759.6	5526.6	7069.1	4943.2	6431.9
82.2	1395.0	1533.5	1897.4	1099.1	1143.9	1357.4	1399.0	644.3	426.7	833.6
802.8	1736.9	2248.4	2540.3	1281.6	1397.9	1460.1	1723.0	1058.8	638.8	1413.2
43.0	273.6	368.0	419.4	115.0	184.3	185.5	340.7	117.6	25.7	178.6
36.0	1072.9	2684.8	1491.2	738.1	1718.0	833.6	2129.8	538.1	142.6	1794.5
7222.4	2009.7	2144.8	2144.6	1666.4	1941.6	2122.5	2315.4	1590.4	1689.7	2127.2
71.5	1735.3	3233.4	3060.8	1689.6	2706.2	1991.0	2839.8	911.9	787.0	2633.4
27.0	101.4	253.3	219.6	132.0	107.8	119.7	146.5	67.0	86.3	89.2
148.1	1745.4	3234.1	2992.1	1437.3	2302.1	2037.4	2731.4	714.1	366.6	2087.8
10527.6	2881.8	2887.0	3387.7	3032.3	2595.6	3839.1	3289.1	2577.8	1112.0	2754.1
354.3	3730.5	4559.5	4057.4	4159.4	3487.2	5938.3	3279.0	2308.5	2843.5	4433.4
393.8	2365.3	2941.1	2274.7	1499.7	2318.1	1813.0	3010.3	1877.2	2541.5	1917.6
836.9	1720.0	2116.9	2203.7	2076.1	1804.5	2724.2	2060.0	2831.5	1271.2	1852.9
59.6	127.8	212.1	344.6	41.3	120.0	100.4	201.3	60.7	40.2	96.2
36.0	97.7	100.2	148.8	69.7	94.2	69.9	110.2	37.0	26.9	51.5
46.3	27.7	29.8	32.9	26.3	23.8	26.3	22.5	19.6	18.0	26.4
38.9	20.3	17.0	26.9	21.8	15.1	19.0	17.2	11.6	13.4	15.4
6737.3	1228.1	1368.6	1228.0	1398.6	1619.8	1183.8	1577.1	988.9	868.3	1585.3
41.5	1414.9	2650.4	2182.4	1312.3	1864.5	1619.0	2558.3	665.6	455.2	1669.3
111.7	4337.2	4945.5	4714.2	2553.2	4204.1	3302.2	5447.2	3167.5	1541.1	3788.3
1238.9	2739.5	2871.3	2948.6	2873.5	2664.2	3580.0	3354.1	4322.2	2507.7	3086.5
3536.8	2527.2	2948.0	3981.5	3296.4	2959.9	3206.3	3014.5	2066.9	1102.0	2455.6
12495.2	5220.5	4412.8	5538.2	4451.0	7683.9	4738.1	4372.3	8956.7	5639.4	9178.9
2123.3	1087.2	1274.0	1392.3	1224.8	1008.9	1346.5	1040.0	1097.8	962.1	1233.8
122.8	3623.6	3971.7	3729.3	2852.1	3408.5	3995.1	4110.2	3018.4	2058.8	2955.0

428.6	608.8	783.9
1614.0	708.4	527.3
678.5	407.5	768.9
2772.2	3792.1	5166.1
3624.9	3689.3	3579.8
5195.0	5243.6	5126.9
2573.2	3825.9	2886.9
7256.3	8796.2	7874.8
1233.2	999.9	1006.8
1329.2	1658.4	1988.9
1416.3	1945.6	2203.6
1014.4	721.0	1203.6
736.3	619.0	667.2
1394.7	959.8	1461.7
1090.6	943.5	1277.8
4440.3	2335.7	3479.9
6005.3	5384.2	8205.4
1931.3	1707.2	1918.5
1872.2	1784.4	2355.6
433.2	414.2	203.5
2895.1	1339.5	3377.1
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4089.0	2342.1	2747.3
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3129.8	2160.4	3197.2
3873.1	4667.8	3365.2
3399.1	4819.2	5698.8
3130.5	2182.6	3913.4
2654.5	2143.8	3128.8
123.1	119.1	167.6
133.1	72.6	36.7
32.3	40.1	26.2
16.5	20.5	14.3
1612.3	2296.7	1593.4
2648.7	1756.9	3337.1
6049.1	3720.8	5641.5
3382.7	3289.0	4234.0
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4203.9	5437.0	4703.9
446.5	1865.7	817.3
3552.4	3112.6	4844.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
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EF097888.1 gg_id:180065 mouse cecum clone SWPT12_aaa01d03 EF0978
EU474886.1 gg_id:302836 red river hog feces clone RRH_aaa02c04 EU4748
EF559119.1 gg_id:220781 mesophilic anaerobic digester clone C35_D7_H_B_H01 EF5591
AJ229234.1 gg_id:14101 Clostridium sp. str. XB90 AJ2292
EU655971.1 gg_id:286598 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6559
X71858.1 gg_id:14089 Clostridium polysaccharolyticum str. DSM 1801 X71858
AM982562.1 gg_id:278018 microbial and slurry pig saw dust spent bedding clone PISD-AIH08 AM982
AB487614.1 gg_id:541647 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4876
EF603083.1 gg_id:233089 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
AB486227.1 gg_id:575834 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR0 AB4862
AJ229214.1 gg_id:23653 anoxic bulk soil flooded rice microcosm clone BSV70 clone AJ2292
EU358714.1 gg_id:308774 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EF603181.1 gg_id:229938 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
AB487451.1 gg_id:540943 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4874
EF445208.1 gg_id:205597 rabbit cecum clone NED2H8 EF4452
AM500788.1 gg_id:540532 proof spatial heterogeneity hot composting clone E72 AM500
FJ365944.1 gg_id:367453 feces adult twins and mothers; TS25 clone TS25_a01a03 FJ3659
DQ795967.1 gg_id:189870 human fecal clone RL202_aai49e10 DQ795
DQ798524.1 gg_id:182948 human fecal clone RL181_aan97g08 DQ798
AF371659.1 gg_id:25904 swine intestine clone p-197-o5 AF3716
DQ326932.1 gg_id:145977 Metagenomic gut microbiome healthy human stool clone E423 DQ326
DQ798374.1 gg_id:196045 human fecal clone RL181_aah41g01 DQ798
AY212770.1 gg_id:101237 equine manure clone wet68 AY2127
AB218343.1 gg_id:145097 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-172 AB2183
DQ795043.1 gg_id:175342 human fecal clone RL310_aam39e04 DQ795
GQ040652.1 gg_id:446057 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957b10 GQ040
EU777587.1 gg_id:312054 Sumatran orangutan feces clone orang1_aai56c10 EU7775
FJ370200.1 gg_id:361563 feces adult twins and mothers; TS56 clone TS56_a01f10 FJ3702
GQ040758.1 gg_id:439855 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958d01 GQ040
FJ364231.1 gg_id:362190 feces adult twins and mothers; TS150 clone TS150_a04e04 FJ3642
FN563398.1 gg_id:594380 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
AB185572.1 gg_id:102090 rumen clone F23-H10 AB1855
FJ368245.1 gg_id:365926 feces adult twins and mothers; TS3 clone TS3_a02a01 FJ3682
EU748480.1 gg_id:327697 neotropical folivorous flying bird adult hoatzin crop clone hoa61_09e11 EU7484
EU009810.1 gg_id:246937 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_E48 EU0098
DQ806056.1 gg_id:177612 human fecal clone RL186_aah60e10 DQ806
AF001738.1 gg_id:14079 rumen clone RF5 AF0017
DQ905358.1 gg_id:169063 human fecal clone 013B-G11 DQ905
DQ803139.1 gg_id:177960 human fecal clone RL311_aam21a01 DQ803
DQ325775.1 gg_id:148628 Metagenomic gut microbiome healthy human stool clone B461 DQ325
EU775348.1 gg_id:335703 Western lowland gorilla feces clone GOR_aag73h05 EU7753

59.8	278.3	536.9	808.3	159.7	100.7	106.8	413.9	51.5	25.1	96.5
160.5	1163.6	1366.5	1385.6	1004.0	1024.9	930.1	1668.7	644.8	390.6	824.2
4799.4	4121.2	5078.2	4555.4	3494.7	4795.7	2435.3	5168.3	3443.7	4153.1	4340.5
4453.1	3548.5	5532.9	4637.8	5014.0	3624.3	4943.3	4802.9	6028.8	3373.0	4059.8
4993.6	5084.3	5508.7	5551.8	6031.0	5391.8	5328.9	5975.8	4944.5	4051.6	4688.0
3886.9	2656.1	3291.2	2215.6	1762.7	3251.1	1850.3	2818.2	3145.9	3100.0	4117.9
605.2	2521.6	3496.0	2523.1	3926.1	3378.3	2221.5	3318.3	3057.4	2800.7	2301.4
102.9	1589.5	2992.4	3290.1	1247.7	2602.7	1460.3	3058.9	944.1	989.2	2308.7
1017.8	2196.8	2279.3	2343.9	1583.9	2143.9	2454.7	2205.8	2252.6	1297.4	2602.8
276.8	4559.1	5668.8	6103.0	5421.5	5123.7	4584.3	5809.1	3437.9	3003.0	4175.8
43.9	156.5	528.7	344.4	131.5	519.2	191.6	566.4	309.0	33.0	517.2
291.2	2387.6	3499.3	3600.9	1840.1	3104.8	2161.9	3613.7	1186.6	1221.8	2190.5
2573.4	7109.7	6264.3	7001.1	6877.4	6330.7	8316.1	6530.6	10099.7	6995.4	7517.6
46.5	2153.9	3588.4	3377.2	2097.1	2868.9	2584.6	4199.1	1100.4	362.8	2774.1
751.5	2455.0	2721.8	3000.7	2199.3	2365.7	2224.7	2681.0	1935.1	1921.0	2709.8
298.7	1669.8	3038.3	2534.5	1670.9	2182.1	2107.1	3536.7	1734.9	720.5	2720.2
974.3	786.8	1759.1	740.4	644.7	714.0	509.0	930.6	779.3	229.4	729.4
47.9	141.9	235.4	233.6	79.3	121.5	154.3	170.9	53.2	66.3	91.3
43.5	1279.2	2245.6	2494.3	721.5	1617.8	1158.8	1933.0	358.7	170.0	1603.2
50.8	573.1	686.0	804.7	400.5	577.0	665.9	617.7	158.0	103.4	276.1
4895.2	5068.4	5619.1	5079.9	3468.5	5801.3	4731.1	5099.4	6852.7	5537.5	7819.6
163.7	908.6	1489.9	1058.7	652.2	1150.0	845.7	1512.9	443.1	224.2	765.2
43.9	272.8	433.0	496.5	209.3	259.1	666.4	458.1	36.4	56.8	148.0
42.1	22.5	21.8	28.8	22.2	20.9	22.6	17.9	19.5	17.8	21.7
32.4	43.0	54.6	83.3	46.5	52.3	61.4	42.8	46.9	33.8	35.3
4677.5	3566.1	2905.3	2988.5	2529.2	2845.5	2764.5	2954.8	4840.4	4973.3	3595.8
4999.1	3501.5	3922.9	3791.5	3965.5	3504.5	3467.4	3245.3	4751.7	3938.2	5308.1
333.5	1580.9	1555.5	1603.9	1118.8	1282.2	1337.8	2088.0	2652.2	2544.6	2181.1
37.0	149.0	93.1	270.1	34.9	114.8	149.9	69.2	36.4	17.5	60.5
440.3	1157.9	1122.7	937.8	674.3	954.2	1007.2	818.2	1412.0	584.1	2387.9
436.1	1764.1	2298.6	2501.3	1716.2	1982.8	2288.7	2456.7	949.0	413.8	1230.7
1517.9	2824.6	3208.2	3181.9	3117.3	2863.7	3250.4	3157.7	3668.1	2089.1	3775.0
3120.1	1244.2	1071.1	1394.7	956.1	1030.0	1614.0	1090.7	1343.8	1313.2	916.0
5533.4	2984.0	3456.4	3781.4	3533.9	2740.0	3483.2	2221.8	3991.2	1733.4	2928.2
3561.7	2592.1	2414.5	2498.9	2192.8	2332.8	2077.0	2879.4	2043.2	1514.1	2410.0
7885.7	3931.2	4345.1	3967.5	2875.5	4152.3	3418.0	4495.2	5399.9	4366.1	6193.7
46.4	35.8	50.9	52.7	36.8	66.2	30.1	58.1	11.8	21.8	40.3
5549.3	3418.3	4093.5	4046.9	3208.8	3413.7	3502.4	3553.1	4796.9	4247.8	4135.4
61.7	652.6	725.4	626.6	403.3	758.1	453.0	631.5	924.9	1091.0	450.1
369.8	245.5	544.4	449.0	142.2	293.3	216.9	348.8	51.7	28.8	150.3
90.5	157.1	233.3	364.7	84.3	98.5	132.9	106.1	73.9	37.7	73.1

398.1	447.2	361.7
1177.6	1064.8	1165.5
5812.3	4427.4	6930.5
3895.4	4530.3	4636.5
6476.5	4904.7	6241.6
2786.1	3477.8	2396.1
3480.0	2953.2	3508.6
3896.7	1934.5	3003.8
2713.3	2307.5	2803.4
7156.5	5486.3	9745.3
364.3	77.9	186.3
4171.0	3677.7	5164.2
6377.8	8515.6	7187.7
4747.4	1935.0	4084.0
2735.8	2975.8	3757.5
4106.9	2443.5	2600.9
601.2	1336.2	647.3
201.5	162.3	284.3
1931.7	2012.0	3754.2
696.5	741.0	662.5
4942.1	6291.1	5763.8
1572.7	1348.9	1733.1
552.8	345.4	214.8
35.1	30.0	21.4
54.4	86.2	72.6
2515.8	3977.7	3828.2
2904.1	4480.4	2944.4
1346.0	2351.5	1192.7
107.5	108.9	242.8
567.6	1532.4	636.3
2965.2	2331.8	2148.0
3167.1	2872.5	2796.0
1285.3	1235.0	1430.1
3261.0	4055.3	3224.2
2592.1	3245.1	2030.9
4179.1	5393.6	4662.5
42.6	74.6	96.2
2945.2	4065.9	3704.8
469.2	767.0	496.2
202.9	528.2	382.9
168.4	216.7	167.0

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
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
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DQ802401.1 gg_id:177232 human fecal clone RL188_aah17c04 DQ802
FJ363598.1 gg_id:363673 feces adult twins and mothers; TS14 clone TS14_a01b10 FJ3635
EU471606.1 gg_id:297180 Asiatic elephant feces clone AE1_aaa03b08 EU471
FJ369768.1 gg_id:368229 feces adult twins and mothers; TS51 clone TS51_a04e12 FJ3697
DQ797873.1 gg_id:174394 human fecal clone RL206_aaj16h04 DQ797
FJ369407.1 gg_id:368023 feces adult twins and mothers; TS50 clone TS50_a04b05 FJ3694
DQ797064.1 gg_id:198736 human fecal clone RL386_aao86e03 DQ797
DQ797794.1 gg_id:176294 human fecal clone RL206_aaj15h11 DQ797
DQ804235.1 gg_id:180498 human fecal clone RL187_aah70f08 DQ804
FM873638.1 gg_id:367860 occupant source house mattress dust clone MA01H09 FM873
AB218300.1 gg_id:148304 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-73 AB218
DQ824467.1 gg_id:189373 human fecal clone RL304_aal76d03 DQ824
GQ897362.1 gg_id:566033 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
FJ369269.1 gg_id:364786 feces adult twins and mothers; TS50 clone TS50_a02c08 FJ3692
DQ325553.1 gg_id:146945 Metagenomic gut microbiome healthy human stool clone B015 DQ325
DQ803271.1 gg_id:187948 human fecal clone RL311_aam23c01 DQ803
FJ362754.1 gg_id:363879 feces adult twins and mothers; TS13 clone TS13_a02g03 FJ3627
EU778160.1 gg_id:316598 feces clone RL388_aao96f07 EU778
DQ795004.1 gg_id:178146 human fecal clone RL310_aam39a05 DQ795
FJ369227.1 gg_id:367762 feces adult twins and mothers; TS50 clone TS50_a01g07 FJ3692
FJ832200.1 gg_id:560995 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q101_82B11 FJ8322
FJ371026.1 gg_id:368983 feces adult twins and mothers; TS5 clone TS5_a04a11 FJ3710
DQ807249.1 gg_id:191769 human fecal clone RL244_aaj48b05 DQ807
DQ327417.1 gg_id:148635 Metagenomic gut microbiome healthy human stool clone E976 DQ327
DQ806335.1 gg_id:184069 human fecal clone RL186_aan90g07 DQ806
DQ116006.1 gg_id:130051 bovine teat canal clone D-51 DQ116
FJ673323.1 gg_id:515572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ326427.1 gg_id:147279 Metagenomic gut microbiome healthy human stool clone C482 DQ326
EU844987.1 gg_id:343667 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB218299.1 gg_id:145431 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-71 AB218
DQ795466.1 gg_id:182270 human fecal clone RL178_aah54f12 DQ795
DQ804374.1 gg_id:174474 human fecal clone RL187_aan78h05 DQ804
FJ363791.1 gg_id:364298 feces adult twins and mothers; TS14 clone TS14_a03d05 FJ3637
EF436361.1 gg_id:205445 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC75 EF4363
DQ794583.1 gg_id:192428 human fecal clone RL240_aaj29h05 DQ794
DQ798651.1 gg_id:189815 human fecal clone RL181_aan99e10 DQ798
DQ800500.1 gg_id:179320 human fecal clone RL183_aah27e04 DQ800
DQ802270.1 gg_id:188481 human fecal clone RL188_aah15d08 DQ802
DQ803722.1 gg_id:181406 human fecal clone RL200_aai57e11 DQ803
FJ364143.1 gg_id:369413 feces adult twins and mothers; TS150 clone TS150_a03e05 FJ3641
DQ798129.1 gg_id:184829 human fecal clone RL302_aal95h02 DQ798

897.4	1944.9	1692.9	1405.5	1578.7	2008.7	1436.0	1489.8	2444.2	1257.1	1053.7
1524.7	3181.5	2637.0	2752.8	2590.8	2756.4	2657.6	2690.8	3022.7	2204.2	2081.0
332.6	2279.2	2317.7	2035.2	2048.3	2153.8	2768.8	1703.0	857.8	1005.3	1163.6
5552.6	4953.0	4498.5	6807.3	5281.7	4744.8	5831.2	4675.8	7192.7	3272.5	5505.9
130.8	539.4	838.8	779.0	462.0	548.6	589.8	744.4	407.5	162.2	630.8
12978.5	6069.9	5026.9	5466.0	4991.0	5875.2	5587.6	5344.8	8376.4	7426.7	9570.9
92.4	53.2	83.1	239.3	52.2	42.8	49.5	51.2	49.6	44.2	45.3
201.3	2451.9	2527.9	2079.6	1506.5	2028.9	1752.6	1974.5	2713.6	2037.7	1631.2
61.7	446.2	1626.7	506.9	239.4	613.1	298.6	620.7	261.6	81.8	451.1
1891.2	2394.7	2657.9	2582.2	2323.4	2521.8	2950.2	2131.9	2280.7	1426.0	3108.1
5338.9	2178.4	2125.2	2140.3	1123.3	1586.0	1868.3	1822.4	2204.5	2212.3	2815.1
71.0	661.8	1155.5	1377.9	570.8	621.1	565.9	525.0	340.5	204.9	416.4
310.2	1270.0	1407.7	1189.4	1337.3	1112.9	1495.0	1384.2	1020.0	724.7	1030.0
147.9	834.4	1409.0	1770.9	526.1	1333.5	776.4	1426.4	1032.8	635.4	915.8
31.6	474.3	567.5	722.1	277.5	509.3	225.4	632.1	117.2	34.2	267.3
22919.9	6505.9	6579.6	7218.4	6220.2	6015.1	7121.0	6240.3	10343.1	6758.0	10273.2
1592.8	3550.0	4275.3	4687.6	3326.6	3705.2	4175.2	3745.5	3714.4	4840.6	4123.7
52.8	232.7	429.4	552.2	82.2	158.5	122.8	245.6	109.5	30.2	177.0
44.2	336.9	603.9	582.1	150.4	493.5	229.1	736.3	120.4	47.6	224.8
47.0	99.4	171.1	133.7	86.2	100.7	65.6	161.2	51.3	27.2	83.3
637.4	982.8	2396.8	2893.7	2169.9	1798.9	2169.2	1943.7	304.4	182.3	1862.2
13769.7	5387.7	5780.0	5044.9	5485.3	5303.4	5051.6	5131.0	8726.8	7234.7	8215.2
66.7	120.2	162.5	137.3	125.7	105.7	108.7	301.2	49.4	23.5	100.3
129.4	381.7	619.2	499.7	436.4	473.3	459.1	622.5	390.8	644.4	431.0
2233.4	2810.1	4034.3	2664.5	2404.6	4014.1	2739.6	3261.1	2537.0	4499.3	3677.2
2963.5	4097.6	5113.8	5113.3	5341.0	4226.6	5475.1	4238.5	3067.0	2332.4	3833.2
2917.0	2992.5	3054.7	3346.0	2793.1	3236.5	2937.5	3856.9	2919.1	1391.9	3058.6
44.7	129.5	148.5	219.5	125.7	85.6	100.2	79.2	43.3	42.5	44.8
2250.5	2798.8	3123.7	3165.3	3415.4	3014.7	3677.4	3209.2	3758.7	1984.0	2839.5
76.9	803.8	1243.1	1237.5	600.7	828.7	602.1	1392.3	352.0	155.1	769.6
821.6	2220.0	2208.3	2225.2	3381.2	2216.9	3519.0	2015.5	909.4	1001.8	994.8
93.6	908.8	1494.2	1334.7	812.3	596.6	896.2	1084.1	722.4	106.2	474.2
2271.1	1106.4	1341.5	915.5	828.0	1185.9	941.4	1108.6	1799.2	1660.7	1104.1
1285.0	2179.4	2626.2	2959.5	2921.3	2840.3	2856.5	3160.2	1380.3	750.4	2282.9
13648.1	2878.4	2424.4	2822.2	3215.6	2480.6	2943.1	2379.6	4417.7	2883.9	4115.3
13799.8	8243.2	6442.0	6981.6	6588.4	6501.0	8018.6	6353.5	7438.4	5676.4	8742.2
1108.5	2599.4	3552.6	3468.8	2152.9	2724.8	2134.2	3391.2	1746.9	1291.1	2629.0
20162.7	3872.4	4688.1	5520.9	3472.6	4190.6	4234.0	3586.7	6102.3	5085.8	6362.2
1293.4	2862.1	2822.7	3547.0	2885.1	2996.7	3515.9	2546.2	1451.0	954.8	3239.7
704.2	1018.1	1252.4	1049.0	819.9	974.4	1006.2	1270.6	1941.9	1140.6	1419.4
3535.6	1950.2	2533.7	3003.0	1997.4	2205.6	2157.0	2293.7	1489.7	1403.3	2196.5

1335.8	2293.5	1454.0
2614.6	3013.9	3280.5
1745.8	2177.2	2965.7
4008.8	5142.2	5162.7
1060.2	752.9	782.9
4689.7	5798.8	5451.5
60.5	80.5	47.1
2398.5	1860.2	2933.7
455.3	689.1	703.2
1911.2	3007.7	3064.4
1508.4	2585.0	2184.0
576.4	783.3	721.1
1200.9	1261.3	1850.1
1507.0	1278.2	1724.0
466.9	627.6	1147.3
6389.6	7919.1	8613.0
3486.0	5596.4	4601.2
243.3	412.5	518.3
946.3	592.6	868.9
117.7	158.3	71.1
2496.6	2579.9	2073.2
4796.9	6314.8	5258.1
186.1	185.7	154.3
615.0	520.4	783.7
2323.4	3755.5	4118.2
3938.8	4947.0	4991.5
3815.3	4067.1	4307.6
201.9	70.2	1123.5
3401.3	3207.4	3396.7
1347.7	1116.9	1543.2
2115.4	2541.2	2816.5
1061.9	1340.6	1760.8
925.1	1486.4	791.2
3723.1	2403.8	3328.4
2447.9	2855.6	2567.3
5770.7	6519.3	5851.5
3195.3	3400.1	3680.2
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2172.1	2761.6	3684.3
1031.0	1725.9	898.1
2651.3	2023.6	2923.5

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
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FJ366225.1 gg_id:361112 feces adult twins and mothers; TS25 clone TS25_a04b10 FJ3662
DQ795259.1 gg_id:176125 human fecal clone RL178_aah52b08 DQ795
FJ370766.1 gg_id:359863 feces adult twins and mothers; TS5 clone TS5_a01a06 FJ3707
EU771423.1 gg_id:320284 Asiatic elephant feces clone AE2_aaa04e11 EU771
EU776147.1 gg_id:308045 Spotted hyena feces clone HY2_g06 EU776
DQ794005.1 gg_id:196443 human fecal clone RL176_aah46e07 DQ794
DQ796513.1 gg_id:194330 human fecal clone RL179aan73f11 DQ796
FJ369329.1 gg_id:368073 feces adult twins and mothers; TS50 clone TS50_a03b09 FJ3693
FJ363846.1 gg_id:358422 feces adult twins and mothers; TS14 clone TS14_a04a09 FJ3638
DQ794651.1 gg_id:185791 human fecal clone RL240_aaj30f09 DQ794
AF001702.1 gg_id:14091 rumen clone RC10 AF001
DQ806145.1 gg_id:197745 human fecal clone RL186_aah61g10 DQ806
DQ325786.1 gg_id:148837 Metagenomic gut microbiome healthy human stool clone B477 DQ325
GQ448774.1 gg_id:540224 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU778980.1 gg_id:313823 Prevost's squirrel feces clone SQ_aah81a06 EU778
FJ371206.1 gg_id:363385 feces adult twins and mothers; TS6 clone TS6_a02b07 FJ3712
FJ364508.1 gg_id:361833 feces adult twins and mothers; TS15 clone TS15_a03g07 FJ3645
DQ803194.1 gg_id:183984 human fecal clone RL311_aam21h10 DQ803
AY960565.1 gg_id:114912 Clostridium sp. str. ID11 AY960
DQ796396.1 gg_id:190307 human fecal clone RL179_aah26f11 DQ796
FJ368662.1 gg_id:360088 feces adult twins and mothers; TS49 clone TS49_a03a04 FJ3686
DQ793914.1 gg_id:189485 human fecal clone RL176_aah45c03 DQ793
DQ795696.1 gg_id:191766 human fecal clone RL178_aan68g08 DQ795
GQ897258.1 gg_id:568646 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU344679.1 gg_id:275370 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
AF371665.1 gg_id:71089 swine intestine clone p-30-a5 AF371
EF445260.1 gg_id:211734 dairy cow rumen clone NED4D11 EF4452
EU622674.1 gg_id:279487 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
FJ363493.1 gg_id:362863 feces adult twins and mothers; TS149 clone TS149_a03h05 FJ3634
FJ368627.1 gg_id:367884 feces adult twins and mothers; TS49 clone TS49_a02e08 FJ3686
DQ809618.1 gg_id:197865 human fecal clone RL184_aan81f05 DQ809
DQ795109.1 gg_id:176491 human fecal clone RL310_aam40d01 DQ795
DQ327256.1 gg_id:149461 Metagenomic gut microbiome healthy human stool clone E795 DQ327
DQ803199.1 gg_id:188592 human fecal clone RL311_aam22a05 DQ803
EU381987.1 gg_id:271750 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ805127.1 gg_id:192315 human fecal clone RL249_aaj81f03 DQ805
EU762969.1 gg_id:315028 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ796218.1 gg_id:174256 human fecal clone RL179_aah23c07 DQ796
EU473489.1 gg_id:296607 Somali wild ass feces clone WA_aaa01b03 EU473
DQ796700.1 gg_id:181100 human fecal clone RL179_aao53d03 DQ796
FJ368814.1 gg_id:366752 feces adult twins and mothers; TS49 clone TS49_a04h10 FJ3688

229.6	2655.7	1781.6	2124.0	2015.9	1267.1	2359.3	1323.3	3631.8	3601.4	1756.0
40.7	13.2	11.0	14.0	17.1	12.2	11.6	12.5	15.5	17.2	16.4
12264.2	6250.8	5932.6	6547.1	4377.8	6273.4	5290.3	5245.7	11478.4	8283.6	8548.0
5043.0	4550.3	4298.2	4875.8	5077.3	4906.6	4588.3	4070.6	3140.5	3322.5	3364.0
339.8	329.3	387.2	452.0	504.9	246.1	207.7	344.5	255.3	60.0	275.1
47.1	27.7	33.8	37.1	26.4	32.0	25.1	31.2	28.6	42.5	26.3
966.8	1191.8	1578.0	1723.8	766.7	1104.3	1106.2	1591.8	673.2	403.0	914.5
794.9	1067.1	1134.1	1266.6	637.5	947.1	1233.9	827.9	1020.2	729.9	861.0
633.5	406.3	492.8	616.5	189.9	201.1	257.3	395.8	320.6	271.7	508.2
4217.3	1092.8	1242.2	1718.7	1455.4	1107.3	2081.8	1724.4	1488.0	579.9	1183.4
31.4	90.2	271.6	259.4	178.4	172.1	228.3	257.5	67.8	50.4	124.4
37.5	226.1	303.5	394.4	105.9	141.5	133.4	269.5	70.0	67.9	155.3
8537.2	4847.5	5488.4	4988.1	5040.4	5541.6	4344.5	5000.2	5728.2	5554.6	5081.9
898.8	7080.9	7810.0	7289.2	6749.9	6381.8	7404.3	6901.4	6633.1	4587.1	6080.0
1539.8	1250.5	1189.2	1097.4	785.9	1090.7	842.2	1015.7	568.0	793.4	1184.7
4863.8	6449.8	5966.9	5543.8	4234.4	5670.0	5024.3	5517.3	9278.0	7613.4	8439.3
2514.1	3623.7	4300.5	4736.1	4217.3	3945.7	4332.5	4445.5	3828.4	3186.0	4191.6
8321.7	4238.1	3447.8	3747.2	1943.2	3660.4	2897.3	3614.5	2878.4	2490.8	3894.6
64.8	286.6	369.5	330.1	339.4	311.9	349.2	402.8	233.2	71.2	467.3
164.2	2486.0	2760.3	2840.7	2703.4	3014.0	2603.3	3252.4	2514.1	3235.5	2905.8
890.7	1757.9	2335.8	1664.1	971.0	1524.7	1171.8	2230.3	766.5	343.4	1692.9
4874.4	2259.8	3168.0	3221.7	2229.6	1942.1	2394.4	2704.0	1126.4	511.9	1483.6
539.9	3559.8	4028.5	3333.3	3064.7	4023.2	3818.8	3335.4	3905.0	2903.8	3538.9
2709.7	3859.5	3094.5	4199.3	3928.7	3689.0	4520.2	3230.8	2389.9	2485.6	4125.5
130.8	3593.9	4147.8	4217.1	4633.2	3811.1	5351.2	3331.3	2185.1	3277.6	3264.6
45.3	170.8	234.6	269.5	96.6	162.4	191.7	179.8	52.1	39.0	181.7
25.0	391.4	800.0	690.1	207.7	505.9	325.7	641.3	110.2	171.8	409.4
37.4	418.5	488.8	540.3	191.9	517.7	397.5	541.7	124.1	125.4	242.5
108.5	1551.1	2246.0	1992.5	1202.9	2511.9	2574.0	2521.1	1341.6	1373.0	1447.7
4102.7	4472.1	4991.2	5152.8	4394.0	5576.0	4706.7	4138.7	4077.9	3306.8	5845.5
51.1	795.5	558.9	1245.3	152.9	314.8	182.6	561.9	105.5	63.4	129.3
354.6	895.7	1186.2	1464.6	542.2	887.0	589.6	1213.5	485.4	386.0	672.7
1804.6	1996.2	2216.1	2595.0	1532.3	2749.6	2020.6	2261.2	2396.8	829.4	2342.0
5746.0	2335.6	2844.7	2804.9	1667.1	2506.5	2275.9	2685.2	2883.2	2853.2	2401.6
1859.5	1502.2	1796.0	2391.1	1455.4	1497.2	1836.5	1666.4	974.1	817.9	1051.7
3318.4	744.3	895.9	687.0	782.0	1035.1	803.0	882.9	626.1	654.4	706.5
4003.4	1450.3	1719.0	1770.6	1253.6	1633.6	1488.2	1460.1	2077.5	1538.1	2350.0
370.2	2910.0	3374.2	2923.3	1945.1	2356.9	2339.3	1251.2	2633.0	2220.5	3072.6
4489.5	3928.4	3094.8	3416.2	3352.8	3510.3	3615.3	3675.4	3299.3	1363.9	2792.0
92.4	1264.3	1557.7	1837.7	1055.5	1135.4	1508.7	1518.6	740.4	490.1	1102.4
66.5	433.1	601.6	693.3	433.4	355.1	468.7	542.1	99.5	93.1	195.5

1803.5	2170.2	2025.8
14.8	20.9	11.9
4734.8	6584.9	5183.9
4649.2	5269.6	4077.4
491.3	655.4	352.2
29.3	51.5	64.4
1956.0	1975.3	2169.2
1132.3	1362.3	1366.2
321.7	249.7	396.9
1434.6	1654.0	1485.0
197.1	170.3	282.3
332.8	334.8	495.8
5294.1	6567.2	6399.8
7455.2	7427.4	10152.1
1047.5	1221.2	766.3
5405.7	6246.4	6656.4
3828.0	4701.5	5404.2
4068.4	3468.4	4215.0
327.3	427.3	235.4
3632.0	2985.6	2780.3
2090.3	1823.3	1535.5
2612.2	2908.9	3186.7
3544.7	3317.9	3081.0
3125.5	3571.0	4670.8
3821.1	3938.3	6174.9
177.6	254.6	259.2
699.7	707.4	846.9
795.7	441.0	564.0
1530.1	2197.0	2989.4
4009.2	4429.9	5466.0
723.7	658.9	655.7
1363.6	1054.1	1906.2
2487.3	2711.8	2230.3
2463.1	3046.8	3486.7
1865.8	2520.4	2845.4
559.1	1961.1	735.2
1639.8	1632.5	1579.9
2401.4	3367.9	2757.3
3885.8	3807.7	3060.5
1450.4	1356.4	3144.4
791.4	519.4	600.2

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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

g__Coprococcus
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FJ363809.1 gg_id:363624 feces adult twins and mothers; TS14 clone TS14_a03f01 FJ3638
DQ797571.1 gg_id:199052 human fecal clone RL206_aaj13b10 DQ797
DQ795156.1 gg_id:186048 human fecal clone RL310_aam40h03 DQ795
DQ824600.1 gg_id:185299 human fecal clone RL185_aaj70c05 DQ824
DQ803202.1 gg_id:189745 human fecal clone RL311_aam22a09 DQ803
GU303697.1 gg_id:570450 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ362975.1 gg_id:362583 feces adult twins and mothers; TS148 clone TS148_a01d10 FJ3629
FJ364128.1 gg_id:362262 feces adult twins and mothers; TS150 clone TS150_a03c12 FJ3641
EU467012.1 gg_id:291448 African elephant feces clone AFEL2_aao32f10 EU467
FJ368288.1 gg_id:369224 feces adult twins and mothers; TS3 clone TS3_a02e04 FJ3682
EU774091.1 gg_id:315176 Chimpanzee feces clone CHIMP12_e08_1 EU774
FJ364204.1 gg_id:369896 feces adult twins and mothers; TS150 clone TS150_a04b09 FJ3642
DQ799390.1 gg_id:189715 human fecal clone RL305aal85f10 DQ799
EU775922.1 gg_id:331309 Horse feces clone horsej_aai90c10 EU775
DQ327173.1 gg_id:148579 Metagenomic gut microbiome healthy human stool clone E701 DQ327
GQ090630.1 gg_id:381579 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
DQ802518.1 gg_id:190122 human fecal clone RL188_aah18h02 DQ802
FJ366839.1 gg_id:362391 feces adult twins and mothers; TS27 clone TS27_a04e01 FJ3668
EU845683.1 gg_id:311395 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
DQ809784.1 gg_id:190984 human fecal clone RL184_aan84b08 DQ809
FJ368263.1 gg_id:364272 feces adult twins and mothers; TS3 clone TS3_a02b09 FJ3682
DQ904646.1 gg_id:170104 human fecal clone 001-a7 DQ904
DQ327003.1 gg_id:147218 Metagenomic gut microbiome healthy human stool clone E504 DQ327
EU772020.1 gg_id:324961 Argali sheep feces clone AS1_aao38e09.Contig1 EU772
DQ805673.1 gg_id:183956 human fecal clone RL306aal89f08 DQ805
FJ363898.1 gg_id:363738 feces adult twins and mothers; TS14 clone TS14_a04f08 FJ3638
DQ798645.1 gg_id:198540 human fecal clone RL181_aan99e03 DQ798
FJ833076.1 gg_id:510859 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_82B11 FJ8330
DQ794056.1 gg_id:177942 human fecal clone RL176_aan57d05 DQ794
DQ805407.1 gg_id:194366 human fecal clone RL203_aai62b11 DQ805
EU843494.1 gg_id:314618 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ363471.1 gg_id:357829 feces adult twins and mothers; TS149 clone TS149_a03f03 FJ3634
EF404127.1 gg_id:215034 human fecal clone SJTU_C_05_14 EF4041
FJ368805.1 gg_id:361224 feces adult twins and mothers; TS49 clone TS49_a04g08 FJ3688
DQ326977.1 gg_id:149713 Metagenomic gut microbiome healthy human stool clone E472 DQ326
EU775401.1 gg_id:335601 Western lowland gorilla feces clone GOR_aag74d01 EU775
EU843844.1 gg_id:308974 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ810039.1 gg_id:192338 human fecal clone RL184_aao67d03 DQ810
AF001756.1 gg_id:14080 rumen clone RF24 AF001
EU451291.1 gg_id:326416 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU451
EU456777.1 gg_id:351561 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU456

107.4	284.7	411.3	442.8	298.9	281.7	291.4	222.7	153.1	141.6	174.6
1224.4	826.2	899.7	960.4	1207.7	882.8	743.9	919.0	766.8	778.9	729.2
48.3	24.5	23.4	21.1	19.6	17.0	18.6	17.4	20.9	13.4	17.8
70.6	595.7	554.7	437.7	866.7	439.1	793.2	523.0	247.6	231.3	216.1
6798.6	2415.0	1421.8	2275.8	2202.8	2764.8	1850.0	1749.5	1685.7	1009.7	3250.3
104.5	452.8	1139.4	768.7	555.5	560.2	878.7	659.1	298.2	174.4	367.0
269.7	1553.4	1092.3	60.9	1071.2	1339.0	657.5	816.3	905.2	536.4	401.1
514.3	533.3	310.3	468.8	399.0	389.1	609.1	431.3	446.5	359.2	471.9
54.9	216.3	366.8	175.2	241.6	365.8	162.7	424.0	98.4	131.8	89.3
56.5	32.6	64.3	90.2	38.7	50.2	50.0	61.1	36.4	21.9	48.3
218.0	2058.6	503.3	1658.3	2097.8	2153.2	1216.8	1965.4	1387.6	1350.1	1303.0
1151.7	1037.3	1227.9	1074.4	1235.5	1094.7	1458.0	1318.3	1009.3	2123.1	1037.2
1670.7	2099.3	2404.6	2542.3	1933.0	2080.8	2056.9	2149.0	1812.0	1336.6	2493.2
91.5	927.9	1545.1	1217.0	809.1	1431.8	1093.8	2741.5	661.6	355.8	935.0
2177.0	2770.2	3590.2	2963.4	2850.2	3548.1	2571.7	3155.0	2930.7	2883.1	3650.8
31532.6	8211.9	8453.6	8184.7	6370.2	8000.1	8569.3	7853.2	11189.3	9825.6	15903.7
4416.2	3110.1	3043.5	1833.3	3997.7	3111.2	4106.4	3119.2	3625.4	3520.2	4835.1
8684.3	2963.8	3203.8	3383.3	2804.6	2977.0	2988.8	2819.3	4139.8	3874.3	4883.7
999.4	3014.6	3454.6	3094.9	3378.6	2890.3	4485.1	3480.4	2582.2	1726.5	2697.9
60.3	781.9	1082.6	893.2	774.1	1107.5	774.3	1206.4	583.4	453.7	693.3
62.6	189.5	270.3	222.0	262.7	232.5	204.9	261.9	652.1	72.0	125.9
46.7	26.0	37.7	39.8	14.9	11.7	12.2	18.0	24.4	15.5	16.2
2316.9	3464.6	3325.8	3665.1	2214.3	3534.9	2949.2	2782.9	4355.4	5805.6	3646.7
3611.6	3746.7	3553.7	3732.4	3676.8	3242.3	4402.1	3659.2	3257.2	1636.3	3473.2
38.5	110.2	115.4	158.9	43.5	51.4	73.5	49.8	20.1	25.4	42.6
38.4	209.6	254.2	217.4	241.7	223.1	217.5	203.7	47.0	36.9	82.0
3771.8	4075.5	4342.5	3940.0	3555.4	4741.2	5335.5	5430.4	6704.0	4104.0	5537.1
508.5	1519.1	1803.2	2440.0	1600.9	1407.8	1515.8	1420.2	731.4	747.7	636.2
83.8	33.1	32.1	46.0	51.0	23.1	36.0	30.1	36.0	23.7	32.3
3432.7	1447.4	1700.1	1758.4	2214.5	2517.4	1609.1	1954.9	1776.1	1603.1	1369.7
9915.7	5747.9	6362.7	6035.8	6937.7	5539.2	6557.4	6401.2	4348.2	4457.3	5003.4
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87.2	248.8	336.6	471.7	173.9	218.5	201.8	464.4	120.5	83.4	229.9
4984.7	4026.2	4900.8	4884.6	4105.9	4068.1	4491.9	4667.0	3462.4	2526.0	5081.8
86.4	809.0	1175.1	1064.9	514.2	774.7	893.4	855.4	483.5	532.2	944.4
4393.3	3408.5	3053.0	3170.6	2690.5	3523.4	2863.8	3344.5	2969.6	2405.1	2504.9
42.4	21.9	54.8	38.6	38.3	26.3	29.9	19.0	29.6	16.9	27.6
59.0	713.5	1061.1	774.9	775.1	783.8	736.3	719.0	296.4	242.5	433.7
56.0	461.8	662.3	673.3	395.9	411.1	482.7	533.8	227.9	136.0	433.9
19516.4	4763.3	4849.4	4603.4	4221.3	4117.6	4448.8	3839.1	7514.8	5358.5	6128.4

228.0	408.5	415.2
998.8	1593.7	1486.6
21.4	22.2	18.1
510.7	903.9	788.0
1850.7	2948.9	1682.1
692.3	1098.4	985.0
809.4	895.9	735.9
355.5	911.5	296.3
320.5	368.2	452.1
77.2	126.7	67.6
2124.4	1351.0	1904.7
1142.1	1610.0	1776.8
2008.7	2814.9	2270.2
2977.6	1377.3	3302.9
3229.7	2928.9	3063.1
7649.7	9302.7	8923.5
2968.7	3617.5	3337.1
3043.3	4113.8	3305.2
3129.8	3514.5	4392.1
1320.6	995.0	1256.7
208.6	397.7	228.9
23.0	31.9	56.0
2529.3	5120.2	4109.8
3562.0	3475.1	3272.1
89.6	97.2	62.2
132.8	204.9	176.7
3844.6	4687.3	4955.0
2280.2	2263.8	1474.5
30.1	34.4	32.9
1750.1	2693.9	2469.1
5882.9	6883.6	7268.8
187.5	272.6	272.5
394.4	592.3	1017.6
784.0	256.4	497.7
4992.9	5400.1	4629.6
942.4	1157.5	1517.6
3758.2	4693.5	3154.7
33.5	42.4	32.0
669.5	1060.1	1794.0
643.2	456.9	532.3
3670.3	5905.6	3762.6

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

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Coprococcus
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AY975445.1 gg_id:124342 human ascending colon mucosal biopsy clone N835 AY975
EU748175.1 gg_id:334172 neotropical folivorous flying bird adult hoatzin crop clone hoa31_49A07.F EU748
FJ364202.1 gg_id:368228 feces adult twins and mothers; TS150 clone TS150_a04b07 FJ3642
GQ896848.1 gg_id:586637 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ777934.1 gg_id:167252 rat feces clone R-1199(2) DQ777
EU453406.1 gg_id:354240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
AF371676.1 gg_id:21698 swine intestine clone p-273-o5 AF371
EU765884.1 gg_id:343785 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
GU302756.1 gg_id:557137 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
AY976184.1 gg_id:127439 human ascending colon mucosal biopsy clone LV91 AY976
EU452252.1 gg_id:319038 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU452
FJ679395.1 gg_id:522077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU453604.1 gg_id:353050 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU453
EU778332.1 gg_id:321304 feces clone RL388_aao93h04 EU778
EU456462.1 gg_id:313333 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79 EU456
AF001721.1 gg_id:14020 rumen clone RC35 AF001
DQ808884.1 gg_id:176257 human fecal clone RL243_aai86e11 DQ808
FJ881245.1 gg_id:430739 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
DQ797115.1 gg_id:199013 human fecal clone RL386_aao87b10 DQ797
EF098232.1 gg_id:184535 mouse cecum clone SWPT14_aaa03d04 EF0982
FJ679670.1 gg_id:524122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
FJ681388.1 gg_id:515129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ825335.1 gg_id:178362 human fecal clone RL185_aan88g03 DQ825
EU452326.1 gg_id:333914 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU452
FJ879304.1 gg_id:411214 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
AF371677.1 gg_id:36892 swine intestine clone p-2409-55G5 AF371
EU344224.1 gg_id:260496 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU455186.1 gg_id:333786 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU455
FJ834237.1 gg_id:567961 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q301_78F10 FJ8342
FJ367885.1 gg_id:359911 feces adult twins and mothers; TS2 clone TS2_a04g01 FJ3678
FJ680195.1 gg_id:530278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU452990.1 gg_id:332816 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
EU462618.1 gg_id:295074 Sumatran orangutan feces clone orang2_aai66b12 EU462
EU456680.1 gg_id:318224 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU456
EF098586.1 gg_id:188120 mouse cecum clone SWPT16_aaa01g06 EF0985
FJ678722.1 gg_id:525789 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ815697.1 gg_id:163142 mouse cecum clone aab21b02 DQ815
EU509978.1 gg_id:268910 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24h05 EU509
EU530167.1 gg_id:258321 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
EU748382.1 gg_id:323463 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07h08 EU748
EU450938.1 gg_id:306993 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU450

4850.4	1333.1	1811.6	937.9	1143.8	1747.0	1268.6	2272.0	1476.7	974.5	1710.3
238.6	2104.7	3038.6	2758.6	2700.3	2755.7	3417.3	2403.2	1892.6	1282.4	2269.0
7788.1	5885.2	6231.5	5926.1	6202.8	5695.1	6068.6	6708.1	6989.5	5073.0	7508.6
32.1	52.9	67.3	52.0	56.7	56.9	56.3	45.9	22.3	21.7	22.6
1510.4	3546.3	4391.5	4492.3	2396.0	2864.0	3158.3	4877.1	4911.3	1009.8	3779.1
425.6	3395.0	2794.9	2635.7	2439.6	2519.3	2286.7	2625.1	2677.5	3724.3	1688.7
138.2	1240.0	1663.5	1645.5	908.7	1087.3	1240.3	1534.0	597.2	943.0	971.1
47.6	1627.7	1707.5	1968.1	2390.4	2156.1	2265.6	2112.3	1427.5	1135.2	1480.9
10378.1	6193.9	6103.5	7031.8	7901.0	7249.4	6878.2	6934.3	8113.9	4684.3	7559.5
51.1	1420.6	2508.8	2625.6	931.2	1253.9	1835.0	2306.9	414.1	198.1	1579.3
1046.0	2525.0	3396.2	3144.0	1898.7	2692.6	2343.1	3626.0	1768.1	1741.0	2716.1
2322.3	1633.1	1497.1	1691.5	962.5	1265.4	1464.0	1366.3	2087.5	1826.0	2354.5
152.2	1143.0	2030.4	1758.0	1422.5	1162.6	1495.2	1497.5	732.9	1586.4	1029.0
89.6	87.1	206.2	196.6	142.2	199.2	180.9	285.8	85.4	73.3	159.1
2257.3	3751.7	5141.8	4365.5	2928.1	3969.2	3784.1	4536.6	2894.9	3385.1	4318.7
43.7	178.2	186.6	324.9	112.7	89.2	115.6	181.5	70.9	44.6	77.8
1955.6	5498.9	4882.7	4337.9	4736.9	4762.0	4035.4	4859.1	4551.8	5770.6	4162.9
8674.6	4474.3	4217.4	4349.3	2622.6	3938.8	1997.5	4180.7	3574.8	3251.0	3367.8
830.8	748.7	2275.9	2079.3	1876.5	1875.6	2386.4	1722.8	1400.8	472.6	2431.3
2011.6	703.4	1077.5	843.6	694.6	945.9	607.1	998.6	1112.3	745.2	827.9
3129.2	3861.6	4229.3	2781.6	3043.4	3408.8	2451.8	3589.5	4033.4	6910.2	2697.8
64.5	2252.2	3375.7	3626.8	3041.6	2763.2	4190.6	3481.6	1040.1	944.2	2354.4
33.2	60.4	199.0	86.1	78.4	101.1	71.5	326.2	62.8	33.4	48.8
690.0	5247.5	4004.0	3209.2	3737.2	3334.9	3079.1	2683.6	3468.1	1978.8	2527.7
46.8	880.6	1478.6	1446.4	374.9	1071.3	1058.1	1458.1	539.3	379.2	871.2
54.0	344.5	1121.1	576.1	108.3	632.1	363.1	552.4	186.3	48.9	701.4
161.9	2585.8	2823.3	3749.8	2821.2	2695.2	2965.1	2940.9	840.6	642.2	1716.6
57.2	250.6	476.4	440.7	247.7	326.0	239.1	372.5	204.0	48.0	234.8
463.0	780.4	1198.2	1490.8	612.5	790.3	551.8	995.8	367.3	507.9	504.7
34.5	254.2	572.4	374.7	253.9	284.2	241.0	391.4	102.8	31.0	195.3
40.8	521.3	1041.6	578.6	816.9	552.7	697.0	807.3	157.2	443.7	487.0
105.5	884.5	1575.6	1284.2	732.0	1126.6	852.2	1172.4	510.7	742.6	886.5
406.9	2214.0	1685.1	1459.5	1255.4	1706.5	1091.9	1449.5	1835.8	958.0	1023.6
1516.5	2716.9	2431.3	2205.5	1630.0	2058.0	1669.5	1685.9	2499.9	2169.2	1911.3
7292.9	4949.5	4333.9	4140.0	3812.3	4031.1	4383.4	4445.1	4678.2	4328.1	4425.0
4524.2	2686.5	2816.1	2619.1	1897.5	2149.8	1974.6	2332.5	2364.7	1109.1	2472.6
45.3	713.5	916.8	787.0	227.0	830.9	652.0	1057.2	421.7	83.8	725.3
96.5	3273.1	4726.6	4794.9	3728.6	3906.5	4483.2	4299.5	2648.6	1031.2	3863.5
34.2	1187.9	1567.2	1707.7	857.2	968.4	1478.7	1512.2	318.0	192.5	1025.1
55.0	329.5	581.0	514.8	255.4	284.5	375.1	398.8	127.5	47.6	157.6
188.6	1158.0	2121.3	1733.2	1564.2	1622.7	2044.0	1718.7	925.5	295.7	1216.2

2021.9	2101.9	1866.0
2295.9	2438.6	3287.2
5378.0	6463.5	6822.0
37.8	56.7	52.1
4406.5	3599.5	3782.5
2416.2	2471.5	3123.7
1620.5	1660.4	1520.1
1818.5	1528.2	2312.5
8259.7	7418.2	7593.9
2636.7	1407.7	2765.3
3302.0	3484.2	3251.9
1198.4	2029.9	1468.6
1502.6	2584.5	3177.7
456.5	178.3	160.9
4408.9	5244.1	4483.7
156.1	169.8	244.6
4493.1	5190.4	6725.5
3920.3	4918.9	4859.5
1648.9	1989.5	2057.0
828.4	2552.5	906.6
3004.7	3201.3	3735.3
3064.6	2583.2	4606.0
251.4	168.4	155.1
3299.5	2358.0	3080.2
885.3	1005.5	1729.1
371.8	382.3	668.5
2623.9	2247.1	3066.6
505.1	833.4	477.4
1268.3	1229.9	1224.0
299.3	475.3	474.4
817.1	653.3	1337.5
1214.9	1619.5	1080.0
1428.9	1657.2	1606.9
1843.1	2306.9	1745.1
3496.0	5089.5	5561.5
2430.9	3043.5	2619.5
1516.3	809.1	1068.3
4296.0	3408.5	6258.5
1720.1	1147.4	1999.8
580.6	586.7	799.5
1823.5	3732.3	2149.1

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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FJ370152.1 gg_id:362250 feces adult twins and mothers; TS56 clone TS56_a01a07 FJ3701
EU455391.1 gg_id:329314 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
AF371675.1 gg_id:106258 swine intestine clone p-653-a5 AF3716
DQ799657.1 gg_id:173934 human fecal clone RL305aal88g06 DQ799
EU503857.1 gg_id:275869 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01f04 EU5038
EU344496.1 gg_id:261381 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
EU450979.1 gg_id:356010 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU450
FJ685073.1 gg_id:517182 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
EU453671.1 gg_id:314503 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4536
FJ368515.1 gg_id:358624 feces adult twins and mothers; TS49 clone TS49_a01c05 FJ3685
EU456865.1 gg_id:337710 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4568
EF614592.1 gg_id:234914 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU456162.1 gg_id:320303 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4561
FJ680692.1 gg_id:523749 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ680968.1 gg_id:521604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU457567.1 gg_id:336011 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4575
EU454285.1 gg_id:331683 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4542
FJ684591.1 gg_id:520237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ832915.1 gg_id:565563 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_13E02 FJ8329
FJ368425.1 gg_id:370307 feces adult twins and mothers; TS3 clone TS3_a04b11 FJ3684
EU457237.1 gg_id:339073 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4572
FJ678929.1 gg_id:519545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ801232.1 gg_id:192443 human fecal clone RL116_aaf02b01 DQ801
FJ681054.1 gg_id:521401 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FM874014.1 gg_id:369502 occupant source house mattress dust clone MB05B06 FM874
FJ679944.1 gg_id:520788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU467116.1 gg_id:297642 mongoose lemur feces clone ML_aae88f01 EU4671
EU842491.1 gg_id:347828 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
EU006303.1 gg_id:257049 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0063
FJ364129.1 gg_id:366721 feces adult twins and mothers; TS150 clone TS150_a03d02 FJ3641
FJ880839.1 gg_id:435285 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU455671.1 gg_id:353454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4556
EF098785.1 gg_id:182446 mouse cecum clone SWPT16_aaa04h06 EF0987
EU344398.1 gg_id:261634 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
FJ681916.1 gg_id:523731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU457797.1 gg_id:319812 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4577
DQ809672.1 gg_id:189574 human fecal clone RL184_aan82d09 DQ809
EU461523.1 gg_id:299398 black rhinoceros feces clone RH_aaj91f01 EU4615
EU763756.1 gg_id:324502 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7637
FJ372350.1 gg_id:360928 feces adult twins and mothers; TS9 clone TS9_a04e12 FJ3723
EU505012.1 gg_id:272499 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f02 EU5050

3926.8	2553.0	2887.4	2732.0	2888.4	3263.9	3034.1	2647.7	3260.2	2751.3	2933.9
52.9	210.9	431.3	476.5	239.7	261.6	281.6	356.5	142.5	61.7	231.4
5196.2	4515.5	4504.8	4817.7	4036.5	4507.2	5855.2	5276.1	2925.3	2638.7	3557.2
35.3	305.6	548.2	498.0	223.0	394.9	293.7	533.9	149.0	131.5	315.1
123.0	1566.1	2106.5	1882.1	1366.5	1503.6	1426.2	1699.3	873.2	1196.2	1374.1
596.4	1894.0	2307.0	2743.0	1477.2	1411.9	1741.9	1999.3	1695.9	972.0	1739.6
40.2	269.9	448.3	559.0	247.0	373.2	388.2	463.8	117.9	59.2	254.0
20478.5	5038.6	5135.0	5153.4	3990.4	5547.1	4673.8	5449.1	5315.5	5475.1	7541.3
1030.8	489.5	474.1	542.9	564.1	410.3	516.1	500.8	229.5	106.4	263.2
5191.9	2633.1	3129.6	2868.2	2392.8	2817.6	2491.6	2970.5	3523.3	5434.3	3535.3
21681.3	6874.5	7114.3	7226.2	6611.5	6711.0	7571.0	6528.8	11259.9	8688.0	9928.7
14062.2	5334.3	5211.0	6059.6	4892.6	5391.5	5899.3	5919.7	5201.8	4502.0	7403.2
2221.5	2034.4	1732.8	1593.9	1625.3	1616.5	1457.1	1471.9	1847.0	1179.3	1315.2
143.5	2195.5	3404.7	3211.5	2015.2	2139.1	2505.8	3013.4	1663.8	717.0	2840.8
5302.0	5873.5	5353.6	6700.8	5637.2	5568.8	5926.5	6160.1	5086.7	3602.2	5938.7
721.7	1792.4	1617.0	1939.8	1718.6	1325.8	1120.1	1445.2	1092.7	1132.5	1445.3
683.9	1814.4	3991.5	3909.1	3458.9	3687.7	1763.3	4055.2	1236.4	1724.2	1485.8
353.2	1488.0	2100.6	2308.4	787.8	1487.2	895.8	3065.2	666.5	284.4	1406.3
103.3	1292.2	1613.9	2968.3	508.5	1274.4	818.4	1638.1	315.1	148.6	684.0
1089.9	1115.1	1352.0	1471.4	1376.0	1036.9	1187.8	1182.0	561.3	262.4	833.0
2460.7	2914.0	2879.6	3131.9	2783.0	2634.3	2802.9	2839.8	2386.3	2046.0	3089.6
9814.3	4826.5	4891.3	4749.6	4083.1	4481.9	4244.2	5140.0	5823.2	3544.5	6487.0
989.5	1161.9	1268.6	1506.5	2410.6	1549.5	1496.2	1346.1	898.5	324.0	1017.9
234.1	826.2	1532.9	1408.7	1157.7	1130.8	1150.3	1311.7	1028.3	1019.8	798.5
88.2	408.0	789.9	685.5	645.9	465.9	629.2	935.9	250.6	112.7	321.9
48.2	709.8	1116.8	1028.7	510.7	1036.4	652.0	1415.8	473.0	175.3	712.2
50.8	1655.7	2370.5	1884.7	1211.0	1471.2	1817.8	1887.5	693.7	194.8	841.9
1596.7	2322.8	2823.9	3121.2	2780.6	2397.1	3790.5	3462.2	2294.8	1433.7	2855.9
47.7	74.4	106.7	91.1	72.2	76.0	66.7	114.9	42.5	85.7	62.2
2857.9	6193.2	5805.9	6024.9	4386.1	5254.2	5835.9	5537.0	7034.9	3471.5	6639.8
714.9	2731.3	3762.9	3769.1	1733.9	2444.1	2666.2	4004.6	1609.7	895.8	3034.5
113.8	1585.9	2319.6	1936.3	1503.5	1679.2	1492.4	2105.7	1041.6	771.4	1524.9
14660.6	5024.4	4911.8	5557.4	4654.5	4511.6	4985.3	4457.5	6057.5	3764.7	6875.6
53.1	1580.3	1698.0	1986.5	792.6	1308.7	1044.5	1691.2	2153.0	1887.9	1072.6
1613.4	2094.2	2992.8	3144.7	2314.0	2116.8	3161.2	3008.4	2114.3	740.2	2448.2
10752.3	3984.8	3585.0	3633.9	3998.3	3881.0	3499.7	3626.9	4673.1	3709.8	5284.8
778.3	2324.4	1834.6	1503.7	1345.3	1998.2	1400.5	1627.2	1958.7	2221.3	1383.4
847.6	4524.3	4891.1	4216.4	3771.2	3925.4	4110.7	4447.7	6151.1	5682.4	3854.4
40.1	20.2	34.9	36.0	15.7	14.3	24.3	32.6	23.1	13.6	33.5
1496.7	666.5	865.9	757.8	1141.4	732.1	643.7	731.4	373.5	146.9	380.4
131.8	2058.1	1657.9	1258.2	1128.9	1447.4	1203.0	1436.5	2224.5	1731.3	1212.1

2625.8	3769.1	3599.1
454.0	568.9	685.2
6269.1	4545.3	5557.9
426.7	616.1	566.8
1872.0	1871.9	1683.9
1799.7	1614.9	1691.8
490.1	533.3	576.5
5768.7	5782.5	5182.9
671.0	876.6	673.5
3577.2	3239.1	3353.5
6345.9	9442.9	6829.9
6159.0	7327.8	5881.3
1540.9	2219.5	1668.5
2612.2	3154.5	3037.5
5862.0	6572.1	7140.5
1914.0	1653.3	1592.4
2983.4	4639.2	2907.5
2870.5	1810.1	1788.6
1979.0	1499.0	1525.8
1175.3	1573.3	1648.7
2733.3	4141.8	2443.2
4052.9	5175.1	4127.2
1290.1	1930.2	2039.4
1995.0	1377.5	1131.1
538.7	973.1	2163.8
1733.5	1102.7	1546.3
1902.8	1305.9	3398.4
3596.9	2483.2	4304.3
97.0	98.1	43.8
4872.8	5344.4	5670.7
3132.2	3521.3	2689.6
2103.0	2225.4	2440.0
4228.8	5411.2	4696.9
1342.9	1639.2	1467.5
2597.6	2375.7	3475.2
3536.8	4463.9	3727.8
1736.7	1888.5	1895.9
3801.2	4674.4	4624.2
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820.1	1439.7	1008.4
1367.2	1626.6	1619.3

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU766491.1 gg_id:331255 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ880110.1 gg_id:452592 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU766273.1 gg_id:306643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU764369.1 gg_id:306379 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU381441.1 gg_id:266392 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3814
DQ794425.1 gg_id:181500 human fecal clone RL197_aah87e12 DQ794
FJ833469.1 gg_id:584481 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_61E08 FJ8334
DQ797246.1 gg_id:177482 human fecal clone RL386_aao88h04 DQ797
DQ794364.1 gg_id:188621 human fecal clone RL197_aah86e07 DQ794
EU844552.1 gg_id:319145 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8445
EU381898.1 gg_id:261290 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
FJ363635.1 gg_id:366757 feces adult twins and mothers; TS14 clone TS14_a01e12 FJ3636
EU469257.1 gg_id:302339 Speke's gazelle feces clone SP3_h08_1 EU469
DQ797019.1 gg_id:199305 human fecal clone RL386_aao85h05 DQ797
EU778230.1 gg_id:339621 feces clone RL388_aao94f07 EU778
DQ794527.1 gg_id:186724 human fecal clone RL240_aaj29b08 DQ794
AB185762.1 gg_id:99824 rumen clone U29-C01 AB185
DQ794949.1 gg_id:180449 human fecal clone RL310_aam38c12 DQ794
AF371657.1 gg_id:20421 swine intestine clone p-444-o3 AF3716
DQ824117.1 gg_id:192060 human fecal clone RL204_aaj59e08 DQ824
FJ366191.1 gg_id:358337 feces adult twins and mothers; TS25 clone TS25_a03g05 FJ3661
EF686576.1 gg_id:253222 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6! EF6865
EU381470.1 gg_id:263808 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3814
EU766374.1 gg_id:325264 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
DQ794376.1 gg_id:183192 human fecal clone RL197_aah86g11 DQ794
EU842292.1 gg_id:331206 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
AF371650.1 gg_id:34731 swine intestine clone p-1895-s962-3 AF3716
EU766433.1 gg_id:350577 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU777196.1 gg_id:340572 Okapi feces clone OK1_g03_1 EU7771
EU766213.1 gg_id:354961 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7662
EU381880.1 gg_id:260787 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
NR_024661.1 gg_id:573803 Eubacterium ruminantium str. GA195; ATCC 17233 NR_024
FJ833266.1 gg_id:538611 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_49A07 FJ8332
EU843008.1 gg_id:343422 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8430
EU778151.1 gg_id:343981 feces clone RL388_aao96e11 EU7781
DQ824189.1 gg_id:194572 human fecal clone RL204_aaj60f02 DQ824
AY854269.2 gg_id:109798 herbivore gastrointestinal tract clone CATTLE_7 AY8542
NZ_AAYW02000018.1 gg_id:469946 Clostridium sp. str. L2-50 NZ_AA
EU344603.1 gg_id:268215 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
DQ824605.1 gg_id:177984 human fecal clone RL185_aaj70c10 DQ824
EU844383.1 gg_id:322159 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443

59.3	424.7	651.6	573.6	426.1	418.8	443.5	547.6	200.6	118.0	306.9
7461.5	3241.4	4512.8	5513.2	2323.9	3229.9	4872.9	5045.4	4364.9	2485.8	6397.6
107.7	992.8	918.7	843.8	238.1	858.2	304.9	1031.4	309.5	898.5	159.8
40.5	123.6	304.6	226.7	99.9	157.3	148.2	142.1	74.0	24.5	137.9
116.7	1206.3	1582.0	1717.9	1185.8	1416.9	982.6	1605.6	635.0	632.1	961.0
20756.1	4769.3	4784.4	4906.5	4256.1	4374.2	4819.3	4108.2	7595.1	6730.4	8383.5
153.7	1746.5	2473.1	2793.1	1402.9	1972.8	1512.7	3469.5	1216.4	2650.9	1414.3
3879.6	3080.2	3005.7	3289.2	2944.4	2927.5	3742.2	3242.2	2684.1	2434.0	3240.3
104.2	349.6	624.2	258.1	190.9	291.7	475.2	288.6	342.6	88.0	522.3
339.1	2531.9	3267.8	3778.9	1518.3	2809.3	2196.0	3460.7	1732.7	738.1	3508.1
48.1	1106.4	1886.1	2000.5	855.6	1050.9	1434.0	1652.4	793.0	387.1	1064.4
1559.7	2249.5	2270.1	2203.0	2003.8	2096.2	2067.5	2565.5	2656.6	3425.4	2593.8
217.1	1463.7	2160.3	1649.0	950.7	1626.1	1266.1	2090.7	864.5	2002.9	1516.1
38.4	479.3	784.0	793.3	111.4	314.2	186.8	445.2	119.2	57.0	352.9
41.0	727.3	1047.4	1056.5	1065.4	899.1	1238.8	1255.7	1171.6	1322.0	950.2
19223.2	4964.3	4769.3	5424.4	5576.6	5397.6	3242.3	4793.0	7109.3	5243.9	8047.3
2567.8	2524.6	3586.6	2635.8	2673.3	3049.5	2348.6	2597.5	2647.9	2782.9	3183.3
65.7	493.0	885.6	502.3	410.1	371.3	329.6	389.0	337.2	271.5	640.6
873.8	2428.2	3434.2	2946.3	2022.1	2911.7	2435.7	3653.8	2492.2	3279.2	2440.1
110.8	1149.6	1094.2	739.8	562.7	757.3	557.6	860.9	532.6	615.8	609.0
6829.1	3124.4	3511.4	2994.2	2635.1	2796.6	2776.7	3157.6	2939.4	3339.5	3713.0
1255.7	3909.0	5107.0	5359.8	4722.2	4906.0	5811.7	5792.7	4093.0	2476.7	5044.5
2095.1	3401.7	3840.0	3898.9	3875.0	3558.7	3311.5	3904.1	2965.5	1554.1	4185.1
2276.2	4621.8	5172.1	3837.2	3648.6	4504.6	3494.5	4127.3	5455.4	5417.3	3926.0
84.0	579.1	543.1	562.3	517.2	467.0	530.7	585.2	402.7	264.6	578.7
79.9	1908.4	2853.4	3081.4	774.4	1837.2	1493.3	2708.0	984.3	438.1	1719.1
1460.9	3637.7	4707.8	5455.3	4083.7	3627.4	4471.2	4418.8	2096.0	1846.4	4103.7
2252.0	1598.8	1727.3	1679.3	1096.5	1145.8	1047.2	1854.4	845.5	420.7	1476.2
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5538.5	3653.1	5020.9	4270.3	3050.8	3638.5	3549.1	3975.4	4642.9	3895.7	4947.9
220.2	1654.7	2214.7	2204.3	1202.9	1458.8	1246.3	2412.6	858.5	1445.1	1591.4
358.7	1171.3	1245.3	1424.7	1893.3	1111.8	2049.5	1305.0	870.5	578.0	1311.9
500.2	1281.0	2190.8	2404.8	1772.3	2086.6	2267.6	2316.0	712.3	1281.6	1513.8
174.2	1550.2	1674.8	2007.4	1043.2	1062.1	1094.3	1776.6	1435.4	348.5	1333.8
400.7	3828.3	3784.2	2979.8	3658.5	3969.1	2663.7	3615.7	2880.6	1811.9	2480.9
39.0	267.6	466.6	303.8	95.3	200.7	192.3	225.8	115.6	98.6	238.2
8486.2	2828.9	3960.3	3899.2	3099.8	3017.9	3663.5	3679.9	2736.3	2338.0	2948.5
1855.5	1717.3	1682.5	2033.9	2104.0	1730.8	2115.8	1813.7	1345.3	1064.1	1766.9
2019.3	3500.4	4359.0	4402.2	4749.6	4951.7	5030.2	5049.5	3385.8	5611.0	3366.0
2033.4	2890.4	3451.6	3730.1	4208.3	3405.0	3927.5	4039.1	2713.1	2406.2	2715.5
1873.0	5509.4	5485.9	6280.7	5879.1	4323.6	4465.3	4734.5	5499.4	3521.1	5270.2

653.3	752.1	729.6
4073.3	3517.6	4501.1
920.2	903.5	502.9
252.9	360.6	309.2
1854.3	2223.8	2189.7
3779.3	5740.7	4254.7
2793.5	2503.9	3512.5
3179.4	3405.9	3290.2
979.4	891.8	244.2
3623.0	2781.5	3181.3
1986.0	1552.6	2363.7
2470.3	2472.2	2460.3
2663.9	2182.3	2603.1
595.2	670.6	626.6
994.9	1243.9	1290.3
4484.4	5584.4	5052.6
2919.2	4584.5	3208.8
321.0	698.2	464.9
4206.1	3397.8	4381.0
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2416.3	3677.1	3038.5
6068.6	4249.4	6686.8
3820.5	3803.7	4796.3
3918.3	4452.4	3004.2
486.3	841.1	554.0
2957.6	2046.6	2886.0
4801.1	4194.3	5561.9
1714.0	1434.1	1914.7
1817.7	2299.7	2100.4
3278.3	4699.2	3882.4
2435.3	2344.0	2915.8
1514.2	1196.2	1980.7
1973.2	2120.4	2939.6
2067.1	1515.0	2018.1
4133.0	3065.5	3397.6
433.8	431.6	508.0
4301.3	4566.7	5894.9
2312.6	1729.0	2691.0
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3817.0	4577.8	3931.6
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g__Coprococcus
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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; FJ8813
EU764626.1 gg_id:353279 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
FJ680393.1 gg_id:514136 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU764391.1 gg_id:340570 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
EU381742.1 gg_id:274577 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3817
AB034069.1 gg_id:23219 rumen clone 5C3d-11 AB0340
DQ794599.1 gg_id:198802 human fecal clone RL240_aaj30b01 DQ794
EU748298.1 gg_id:327252 neotropical folivorous flying bird adult hoatzin crop clone hoa46_69E09 EU7482
EU771329.1 gg_id:346606 Asiatic elephant feces clone AE2_aaa04a09 EU7713
EU766512.1 gg_id:322878 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU842325.1 gg_id:341204 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
EU471590.1 gg_id:300123 Asiatic elephant feces clone AE1_aaa03b02 EU4715
EF445162.1 gg_id:209524 rabbit cecum clone NED3B2 EF4451
EU766402.1 gg_id:326396 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU748309.1 gg_id:322189 neotropical folivorous flying bird adult hoatzin crop clone hoa46_33A05 EU7483
AY442828.1 gg_id:100506 culturable kangaroo Macropus giganteus Eastern grey Kangaroo forestomach conter AY4428
AY985384.1 gg_id:124285 human stool clone C321 AY9853
AB034025.1 gg_id:25995 rumen clone 4C0d-12 AB0340
EU778254.1 gg_id:354254 feces clone RL387_aao89b04 EU7782
DQ799915.1 gg_id:195196 human fecal clone RL247_aaj21g12 DQ799
EU766173.1 gg_id:324453 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7661
DQ801370.1 gg_id:182943 human fecal clone RL388_aao94f01 DQ801
DQ801418.1 gg_id:196850 human fecal clone RL388_aao95c06 DQ801
EU764601.1 gg_id:346821 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
EU381551.1 gg_id:274876 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3815
EU842621.1 gg_id:342811 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
EU381639.1 gg_id:266062 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3816
EU766527.1 gg_id:345136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU622773.1 gg_id:278439 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
DQ794497.1 gg_id:174019 human fecal clone RL197_aah88f11 DQ794
FJ681890.1 gg_id:524260 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
DQ795023.1 gg_id:182681 human fecal clone RL310_aam39c06 DQ795
AY985444.1 gg_id:127752 human stool clone C391 AY9854
AB185807.1 gg_id:103066 rumen clone U29-G09 AB1858
EF436389.1 gg_id:209741 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC103 EF4363
EU843953.1 gg_id:324835 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8439
EU764717.1 gg_id:356540 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7647
FJ833666.1 gg_id:571186 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_91C12 FJ8336
EU774771.1 gg_id:345211 Angola Colobus feces clone EAC_1aaa01e02 EU7747
NZ_AAXA02000006.1 gg_id:270584 Dorea formicigenerans str. ATCC 27755 NZ_AA
NZ_AAXA02000015.1 gg_id:470237 Dorea formicigenerans str. ATCC 27755 NZ_AA

595.9	400.6	654.0	695.4	445.5	456.7	705.8	595.7	316.6	94.6	249.8
236.2	2066.9	3028.3	2234.4	2431.0	2675.3	1710.6	3428.8	1680.7	1923.6	2172.4
3197.7	5956.7	6507.0	6632.1	6582.6	6085.6	6114.7	5435.9	5869.0	6981.7	6012.2
2874.9	7873.4	8041.7	7521.0	5949.4	6553.9	6490.2	6350.7	5537.6	4337.7	6025.0
87.8	745.7	1039.4	1212.3	635.5	613.8	820.2	973.5	448.7	153.3	567.4
33.1	70.1	153.0	125.2	150.1	107.4	79.6	200.4	28.3	31.2	48.8
9323.7	1296.4	1503.9	1496.7	1376.6	1329.1	1280.8	1821.5	1073.7	1444.5	1504.4
174.3	1987.9	3174.2	2374.7	1608.0	2278.4	1823.3	2776.6	1658.5	2283.5	2123.5
1077.8	2899.5	3392.7	3558.3	2495.9	3178.3	2832.5	3174.7	1192.9	1730.6	1765.3
2253.8	3011.3	2836.3	2852.7	2229.0	1997.3	1886.0	2394.8	3244.7	799.5	2251.5
75.0	1717.1	2087.2	2176.3	1906.7	1780.0	2672.0	2097.7	587.0	431.6	1494.8
2564.3	2987.5	2930.7	3280.9	3589.8	2570.7	3871.1	2911.0	1359.2	2610.4	2062.0
48.4	164.3	213.9	167.2	67.0	99.0	89.4	150.2	62.9	32.8	76.9
2835.0	3250.3	3063.6	2942.7	2759.0	2395.4	2514.9	3231.6	3418.9	980.6	2150.8
9186.3	6488.7	6268.5	7678.0	6983.6	6229.0	6728.8	7089.8	6868.3	7120.4	7418.0
41.3	41.9	59.8	53.3	43.7	34.8	32.5	43.1	28.5	20.8	32.2
16287.7	3141.7	3528.5	2355.5	3085.7	3238.7	3208.0	3263.7	4186.0	3654.5	3107.2
3151.0	1392.1	1314.8	1040.2	899.4	1391.0	1063.1	1133.7	2598.3	9.6	1639.5
128.8	1388.6	1924.1	2279.9	1343.8	1306.5	1147.6	2078.6	563.8	297.7	891.0
9764.2	1569.5	1939.2	2367.5	2029.8	1565.5	1677.5	2365.3	1532.0	725.3	1542.3
29.8	176.7	313.4	192.1	73.2	190.4	155.3	157.8	60.8	35.5	141.5
7132.4	5057.5	5470.3	4884.5	4382.6	4552.5	4954.6	4705.6	7325.9	5639.3	6250.9
31.4	197.6	248.3	226.4	207.7	136.5	181.4	139.7	39.3	86.3	121.1
75.6	607.5	1031.8	701.4	308.2	582.9	390.0	659.2	537.0	380.7	551.6
887.0	2815.3	4448.9	4093.1	3340.2	3059.1	3524.4	3878.7	2659.9	740.1	3239.3
76.0	2565.5	3671.9	3977.9	3669.9	2597.5	3660.2	3328.8	1566.8	628.3	1993.2
945.4	6746.4	7235.8	7200.7	7602.6	6625.2	7418.7	6965.5	7585.6	5528.0	6741.7
2111.2	1967.3	2226.3	1982.8	1754.0	1696.7	1659.7	2168.8	1468.0	826.2	1642.4
4282.5	2525.5	3614.2	4224.9	2581.9	2342.9	2476.0	3668.9	1411.2	894.2	1906.0
696.4	323.7	384.2	271.9	330.1	292.4	222.3	437.4	203.0	358.0	214.9
2196.9	3433.8	4223.7	3596.0	3728.5	3792.3	3918.4	3604.1	3127.9	3276.0	3449.1
552.9	251.8	351.7	111.7	193.3	243.3	208.5	271.1	79.5	39.4	51.8
29.0	2418.8	3911.7	4043.2	1839.1	2971.6	2730.6	3904.5	979.9	437.8	2652.9
49.7	45.6	58.1	44.6	47.1	32.1	64.5	41.9	36.2	28.8	40.3
144.7	1648.9	2357.0	2301.3	1652.7	1549.5	1793.5	2576.7	1395.8	739.6	1655.5
103.5	637.5	912.5	1152.8	278.2	462.0	426.4	905.4	316.9	249.2	551.9
553.6	2813.3	2285.7	1925.6	1895.9	2062.2	1214.2	1571.8	2574.6	1314.3	1691.8
986.3	2314.1	3899.4	3635.9	2394.3	3339.6	2991.2	4080.2	1921.9	3506.4	2492.3
34.4	241.5	377.4	428.0	170.1	304.3	236.2	383.8	140.0	84.9	165.7
63.1	568.5	656.6	831.9	380.4	564.7	304.7	996.7	107.9	238.8	523.1
76.8	1769.9	3374.7	3189.1	1135.5	2412.2	2344.4	2909.2	634.9	586.5	2189.4

517.3	898.1	1011.2
2862.4	2429.7	2417.1
6142.5	7700.7	6986.1
7504.6	6938.7	6442.0
1108.4	669.5	318.4
165.1	298.9	167.4
1863.9	2311.3	2220.0
1912.0	2534.3	2476.7
3903.4	3436.0	4633.8
2666.1	2522.2	3061.5
1640.5	2483.8	2575.4
3393.6	3143.7	4339.2
110.1	155.1	79.6
3339.9	2554.1	3166.6
6185.8	7486.5	6718.4
40.8	57.8	55.5
3386.4	4544.5	3410.1
950.6	2260.4	1526.3
2344.9	1813.9	2769.2
2120.1	2464.5	2762.2
383.9	333.9	333.8
3985.8	5196.4	4693.5
182.2	271.1	377.8
641.2	1219.1	945.7
3688.2	4092.3	4527.1
3620.7	3071.9	4842.6
7176.7	6511.8	10603.8
2400.1	2169.0	1719.6
3906.5	3084.4	4698.2
278.5	446.5	394.3
3821.0	5528.2	4619.5
602.5	460.8	265.5
5217.3	2838.6	4598.8
54.8	36.7	39.3
2084.1	2556.9	3080.3
1049.0	792.2	641.6
2012.5	1360.7	1329.2
3806.4	3688.9	4900.1
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1175.0	662.0	825.1
2482.9	1692.8	2637.3

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o__Clostridiales	f__Lachnospiraceae
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o__Clostridiales	f__Lachnospiraceae

g__Dorea
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AY982268.1 gg_id:122518 human sigmoid colon mucosal biopsy clone MI08 AY9822
AY976232.1 gg_id:127502 human ascending colon mucosal biopsy clone LW62 AY9762
FJ364307.1 gg_id:357959 feces adult twins and mothers; TS15 clone TS15_a01d08 FJ3643
AY984686.1 gg_id:124107 human stool clone B638 AY9846
NZ_AAXA02000014.1 gg_id:261912 Dorea formicigenerans str. ATCC 27755 NZ_AA
NZ_AAXA02000007.1 gg_id:470229 Dorea formicigenerans str. ATCC 27755 NZ_AA
AY976895.1 gg_id:127343 human cecum mucosal biopsy clone K540 AY9768
NZ_AAXA02000015.1 gg_id:470238 Dorea formicigenerans str. ATCC 27755 NZ_AA
NZ_AAXA02000016.1 gg_id:470230 Dorea formicigenerans str. ATCC 27755 NZ_AA
GQ491673.1 gg_id:592412 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY979418.1 gg_id:118945 human transverse colon mucosal biopsy clone M021 AY9794
EF399958.1 gg_id:215996 human fecal clone SJTU_E_06_56 EF3999
AY979373.1 gg_id:117508 human transverse colon mucosal biopsy clone Z722 AY9793
AY981371.1 gg_id:119304 human sigmoid colon mucosal biopsy clone G395 AY9813
FJ370209.1 gg_id:366476 feces adult twins and mothers; TS56 clone TS56_a01g09 FJ3702
AY983402.1 gg_id:116631 human descending colon mucosal biopsy clone A582 AY9834
AY983685.1 gg_id:118813 human descending colon mucosal biopsy clone NP92 AY9836
AY978285.1 gg_id:127553 human transverse colon mucosal biopsy clone F145 AY9782
FJ362919.1 gg_id:364583 feces adult twins and mothers; TS13 clone TS13_a04g06 FJ3629
AY979732.1 gg_id:118674 human transverse colon mucosal biopsy clone M475 AY9797
AY975739.1 gg_id:115877 human ascending colon mucosal biopsy clone Y189 AY9757
EU530238.1 gg_id:275687 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU5302
DQ327389.1 gg_id:145925 Metagenomic gut microbiome healthy human stool clone E947 DQ327
AY979917.1 gg_id:123588 human rectum mucosal biopsy clone E239 AY9799
AY983171.1 gg_id:123677 human descending colon mucosal biopsy clone A067 AY9831
AF357564.1 gg_id:70405 mpn-isolate group 16 AF3575
FJ365595.1 gg_id:359355 feces adult twins and mothers; TS20 clone TS20_a04g02 FJ3655
FJ371402.1 gg_id:367855 feces adult twins and mothers; TS6 clone TS6_a04e07 FJ3714
FJ368583.1 gg_id:369057 feces adult twins and mothers; TS49 clone TS49_a02a06 FJ3685
AY981801.1 gg_id:127835 human sigmoid colon mucosal biopsy clone NU02 AY9818
FJ369873.1 gg_id:358282 feces adult twins and mothers; TS55 clone TS55_a01g06 FJ3698
AY977989.1 gg_id:115924 human cecum mucosal biopsy clone LH22 AY9779
AY983625.1 gg_id:116382 human descending colon mucosal biopsy clone NO65 AY9836
FJ371197.1 gg_id:359382 feces adult twins and mothers; TS6 clone TS6_a02a10 FJ3711
AY981721.1 gg_id:120659 human sigmoid colon mucosal biopsy clone LB02 AY9817
AY978748.1 gg_id:123331 human transverse colon mucosal biopsy clone KU94 AY9787
FJ368698.1 gg_id:363888 feces adult twins and mothers; TS49 clone TS49_a03d10 FJ3686
AY975351.1 gg_id:116850 human ascending colon mucosal biopsy clone N632 AY9753
FJ365936.1 gg_id:365459 feces adult twins and mothers; TS21 clone TS21_a04h04 FJ3659
AY982434.1 gg_id:117037 human sigmoid colon mucosal biopsy clone ML48 AY9824
FJ365581.1 gg_id:359797 feces adult twins and mothers; TS20 clone TS20_a04e09 FJ3655

307.1	705.1	1182.7	1024.1	724.7	803.1	733.8	1206.1	598.8	530.2	904.6
100.1	710.9	932.2	984.9	454.2	743.1	494.1	1159.6	341.9	198.3	687.2
870.2	1386.5	1273.7	1405.0	1058.1	1012.6	658.6	1583.4	704.0	303.2	1017.7
13788.0	4176.5	4697.1	4901.3	4059.3	4019.9	4146.6	4400.5	5278.7	4155.8	7398.1
59.6	1405.4	2204.9	2370.5	566.1	1570.9	1401.5	1626.7	363.8	130.6	1463.0
74.0	1675.2	2810.7	2876.2	935.6	2171.4	2160.8	2370.1	543.4	244.8	1808.7
28.3	1065.5	1188.8	1270.5	1010.5	773.5	787.3	1246.4	317.6	277.2	691.3
59.4	1364.3	2256.2	2391.8	674.5	1668.1	1383.9	1622.4	281.0	126.7	1667.4
102.4	1166.8	2143.8	2605.6	764.4	1810.8	1559.7	1994.3	383.6	307.5	1487.9
50.6	844.1	1119.7	629.9	289.2	477.9	329.7	403.1	503.8	951.8	311.8
1495.1	1065.4	1199.0	1168.0	1360.1	1048.5	1099.1	1215.7	935.2	956.2	990.8
36.6	1660.7	1620.2	1722.1	593.3	1300.5	486.7	2152.5	235.4	256.8	1193.4
155.5	1252.4	1621.4	1548.1	1148.7	1348.5	1110.2	1960.7	603.0	792.6	1263.6
40.9	100.0	153.0	130.9	87.2	94.8	67.2	217.2	46.8	42.4	128.8
54.6	711.8	1001.4	689.0	360.0	622.3	319.7	951.3	447.3	983.6	736.9
43.0	646.9	927.8	828.2	412.0	749.2	379.3	1115.4	304.8	377.5	727.5
94.3	853.1	1107.5	1084.4	583.1	909.2	586.8	1420.6	409.3	639.2	851.2
119.1	772.1	1234.5	1130.7	1035.1	968.7	955.0	1641.9	474.4	551.3	956.2
13803.8	3793.3	3916.5	4169.3	3817.5	3675.9	4167.7	4031.8	4266.3	4426.9	4461.8
50.2	961.0	1669.2	1215.8	751.8	1268.8	811.8	1853.2	536.3	518.4	1238.4
49.8	947.3	1613.4	1204.2	748.5	1340.8	812.5	1944.4	515.2	521.0	1181.5
850.0	3296.0	3150.0	3061.1	3620.7	2928.8	3567.3	3717.7	1919.3	3520.1	3045.4
1643.9	4167.0	3611.3	3976.3	4549.0	3349.6	4440.0	3789.8	3473.8	3604.1	5057.2
44.3	178.3	233.2	319.7	269.3	220.0	291.1	290.1	75.6	37.3	177.4
49.3	200.1	334.6	342.2	279.5	227.6	335.2	390.8	90.9	99.5	224.4
161.8	1767.5	1974.5	1813.4	1323.0	1796.7	1712.6	1879.2	1300.4	1042.1	2066.9
57.6	262.6	382.5	361.3	281.2	320.2	334.7	491.9	167.0	414.3	186.5
1758.4	1499.6	1954.7	1706.2	1464.8	1467.6	1415.4	1731.3	1287.5	1512.8	1688.5
48.2	463.8	790.4	662.6	487.9	573.0	461.5	979.6	230.9	417.9	570.0
14035.2	7663.1	7039.1	7876.7	7911.3	7768.7	9525.7	6550.5	11441.3	8604.0	10551.7
36.6	910.5	1409.3	1180.4	687.6	1311.1	818.1	1743.1	464.7	549.2	959.9
69.4	1073.2	1284.1	973.4	622.7	1270.5	743.9	1570.6	468.7	223.2	781.6
116.8	1139.6	1596.2	1841.3	1680.5	1381.3	1368.9	2075.9	460.6	491.2	1234.4
57.0	592.5	577.9	364.7	234.0	395.5	236.7	271.0	449.5	819.9	288.9
60.4	262.9	453.1	472.2	399.9	311.8	365.5	531.5	136.6	50.1	390.3
41.4	162.8	196.4	236.0	249.5	213.2	271.5	269.0	75.2	40.8	153.4
29.7	177.5	201.8	256.4	83.1	128.7	115.4	212.6	83.4	107.1	86.5
47.1	363.4	622.4	472.3	186.2	490.8	222.1	775.6	217.2	71.7	517.1
7508.3	3857.8	4205.0	4136.9	3681.9	3765.6	4080.9	4249.2	4932.2	3100.5	7946.3
1986.6	1193.5	1630.8	1458.4	1644.3	1384.2	1409.7	1653.6	1121.1	1016.4	1362.5
19914.6	5956.8	5284.9	5234.7	5569.6	4831.8	5241.4	5235.4	4152.6	4178.6	7486.0

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1177.4	885.4	1125.0
998.7	1322.0	965.3
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1263.9	875.9	1477.1
2003.1	1317.4	2223.4
1457.5	1298.3	1326.7
1459.8	979.5	1425.3
1816.7	1212.1	1577.1
578.9	707.7	807.3
1247.4	1355.5	1240.4
3061.3	1255.2	2110.6
2126.1	1589.1	2202.6
152.9	116.5	123.1
884.9	705.6	838.0
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1975.6	1268.6	1808.5
1961.0	1255.4	1805.1
3212.5	3621.6	4615.1
2468.9	3892.6	5139.8
277.9	167.7	233.5
379.1	249.7	308.6
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586.3	326.5	666.8
2288.9	2057.1	1792.8
943.2	615.4	794.8
7474.9	8374.1	7181.6
2016.2	1237.4	1694.6
1917.6	1079.3	1470.5
2351.6	1523.2	2184.4
431.3	424.5	517.8
348.3	304.3	327.4
266.6	151.5	229.2
482.2	217.5	148.1
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1669.1	1617.2	1774.9
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FJ367363.1 gg_id:362982 feces adult twins and mothers; TS29 clone TS29_a02f03	FJ3673
FJ365317.1 gg_id:366565 feces adult twins and mothers; TS20 clone TS20_a01d12	FJ3653
AY979478.1 gg_id:119402 human transverse colon mucosal biopsy clone M104	AY9794
DQ326308.1 gg_id:145731 Metagenomic gut microbiome healthy human stool clone C279	DQ326
FJ367538.1 gg_id:363533 feces adult twins and mothers; TS29 clone TS29_a04g03	FJ3675
AY976662.1 gg_id:119238 human cecum mucosal biopsy clone K229	AY9766
FJ369025.1 gg_id:360317 feces adult twins and mothers; TS4 clone TS4_a03d06	FJ3690
EU762250.1 gg_id:309236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A>	EU762
FJ370139.1 gg_id:359846 feces adult twins and mothers; TS55 clone TS55_a04h02	FJ3701
AY982186.1 gg_id:119083 human sigmoid colon mucosal biopsy clone MG65	AY9821
AY979159.1 gg_id:119223 human transverse colon mucosal biopsy clone Z211	AY9791
DQ796594.1 gg_id:184918 human fecal clone RL179aan75e08	DQ796
DQ327584.1 gg_id:150493 Metagenomic gut microbiome healthy human stool clone EB69	DQ327
GQ491661.1 gg_id:558736 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ491
FJ368807.1 gg_id:365239 feces adult twins and mothers; TS49 clone TS49_a04g10	FJ3688
FJ365443.1 gg_id:360796 feces adult twins and mothers; TS20 clone TS20_a02h09	FJ3654
FJ365464.1 gg_id:367576 feces adult twins and mothers; TS20 clone TS20_a03c01	FJ3654
EF401324.1 gg_id:204922 human fecal clone SJTU_D_08_81	EF4013
AY977329.1 gg_id:119218 human cecum mucosal biopsy clone MV44	AY9773
FJ367466.1 gg_id:365137 feces adult twins and mothers; TS29 clone TS29_a03h07	FJ3674
AY981492.1 gg_id:119712 human sigmoid colon mucosal biopsy clone L596	AY9814
AY977315.1 gg_id:116123 human cecum mucosal biopsy clone MV19	AY9773
M99573.1 gg_id:14129 Epulopiscium sp str. morphotype A2	M9957
AF067413.1 gg_id:14121 Epulopiscium fishelsoni str. Red Sea A1	AF0674
AF067414.1 gg_id:14130 Epulopiscium fishelsoni str. Red Sea A2	AF0674
M99574.1 gg_id:14128 Epulopiscium sp str. morphotype B	M9957
GQ340245.1 gg_id:580674 Prokaryotic Marathonas Reservoir Greece water column clone VE07-92-BAC	GQ340
AM500767.1 gg_id:558007 proof spatial heterogeneity hot composting clone E6	AM500
EU468764.1 gg_id:294143 okapi feces clone OK3_c09_1	EU4687
DQ113748.1 gg_id:136518 dog duodenum clone D1-26	DQ113
U22331.1 gg_id:14126 "Metabacterium polyspora"	U22331
EU475028.1 gg_id:291710 red river hog feces clone RRH_aaa02f06	EU4750
EU470379.1 gg_id:299376 Grevy's zebra feces clone GZ_aaa01c09	EU4703
U22332.1 gg_id:14127 "Metabacterium polyspora"	U22332
X71860.1 gg_id:13988 Eubacterium cellulosolvens 6 str. ATCC 43171	X71860
AB372004.1 gg_id:312201 Eubacterium cellulosolvens str. NE13	AB3720
DQ824305.1 gg_id:192536 human fecal clone RL304_aal74c01	DQ824
EU778103.1 gg_id:332313 feces clone RL387_aao89a11.Contig2	EU7781
DQ795815.1 gg_id:196272 human fecal clone RL245_aai82g10	DQ795
DQ801788.1 gg_id:197940 human fecal clone RL201_aai46g10	DQ801
DQ805487.1 gg_id:189396 human fecal clone RL203_aai63c09	DQ805

130.8	2178.0	1796.6	1624.7	1702.4	1679.1	1630.5	1749.5	1109.7	1144.6	1322.7
437.9	3049.0	2607.2	2459.4	1323.4	2129.7	1241.0	1182.0	1986.3	1681.5	1379.5
29.4	278.1	363.3	369.7	422.8	431.5	450.0	603.3	143.4	50.5	272.4
1919.3	4191.6	3665.3	4063.8	5238.0	3409.8	3954.6	3831.6	3474.9	4126.5	4353.4
4218.0	2151.6	1880.8	2148.8	1591.1	1773.5	1771.0	1943.6	2169.9	2156.8	2579.3
43.6	57.8	64.1	128.3	45.2	75.9	82.5	71.5	28.5	46.3	44.8
49.6	1617.9	1905.0	2071.7	1737.0	1651.8	1784.3	2575.9	938.2	338.7	1458.1
10877.2	2623.2	2369.2	2148.8	1961.0	2074.9	2274.7	2103.3	3144.7	2033.3	4158.2
38.2	566.8	519.8	288.1	218.1	376.4	257.2	239.5	436.2	800.0	350.7
183.0	1819.6	2286.6	2239.5	1925.3	2155.8	2238.0	2427.0	1448.1	735.9	1354.6
48.7	204.7	294.0	276.8	274.8	243.6	270.4	351.0	123.6	46.0	292.5
2458.5	3731.9	3541.5	2950.9	2451.8	3501.8	2755.7	3210.8	5320.5	3734.5	4320.4
393.1	1706.7	1511.7	1921.2	1518.0	1400.4	1209.4	1739.4	1681.0	693.3	1551.9
3640.9	4820.4	4949.6	4641.3	4502.0	4743.8	4416.2	4998.5	7004.0	6409.7	5518.0
65.5	1594.4	1596.6	1722.9	1365.6	1461.6	1429.2	1563.5	1141.8	1132.6	1205.8
114.2	653.1	461.9	504.6	456.4	359.8	466.8	587.3	246.6	213.4	280.2
44.4	232.3	360.4	338.8	138.3	234.9	143.3	453.6	114.3	236.0	360.2
75.9	1519.7	2921.0	2836.4	887.6	2133.0	2185.7	2424.4	488.4	242.9	1801.0
1649.0	1896.9	2461.3	2233.3	1874.2	2391.4	1859.3	2761.8	1411.7	1513.9	1907.4
86.5	2453.7	2197.2	2598.8	1830.7	2103.3	2314.9	2229.1	3700.0	3365.9	2093.9
180.7	1282.4	1676.1	1647.2	2207.0	1663.2	1936.1	2161.9	711.3	435.6	1136.8
1933.8	1735.9	1763.6	1951.8	1791.1	1615.7	1934.3	1626.0	1273.4	1060.7	1867.4
1760.7	2896.4	3321.1	4141.3	3699.0	3331.4	2311.4	5239.5	3663.1	3056.1	3854.7
29.8	182.2	172.4	219.8	210.6	239.2	186.1	705.4	71.9	22.3	175.2
7669.7	3682.4	3425.0	4462.4	5008.6	3804.0	3770.5	4856.9	3111.4	2011.5	3701.5
96.8	1721.0	1649.2	1661.4	968.0	1125.9	1392.7	1868.5	2100.0	525.7	1477.5
2678.1	7410.9	9013.2	7204.4	5081.5	7342.1	5399.1	8643.2	4677.1	3599.8	10245.0
43.6	180.9	537.3	447.3	195.9	268.1	111.9	876.7	54.1	126.6	300.0
2827.2	5205.5	5557.9	5311.9	5521.9	4969.4	5380.5	5625.0	4473.9	3796.3	4342.2
41.5	66.7	61.3	68.8	64.6	55.2	77.8	71.8	38.2	32.6	90.4
144.3	1695.6	2671.2	2272.1	1773.0	2050.8	1936.2	3087.0	915.7	1218.5	1596.5
745.7	3573.9	4826.6	4404.5	4332.9	3860.9	4175.1	4231.1	2997.2	1559.7	4252.5
40.1	374.0	366.3	332.0	228.9	365.7	298.8	475.2	183.8	511.0	154.5
4985.0	2334.8	2839.2	2766.4	2408.6	2424.6	2566.3	2992.1	2911.8	1492.2	2914.4
53.7	81.6	199.2	284.2	49.1	89.9	55.2	163.8	29.8	37.0	56.5
43.7	404.7	668.7	814.8	222.4	437.9	285.1	898.8	445.8	101.9	250.3
35.1	60.8	51.1	41.9	32.5	41.6	42.1	40.5	28.9	18.5	28.9
49.1	750.9	1134.2	1298.4	817.7	756.6	638.1	1089.0	138.1	88.0	446.5
50.2	179.9	300.3	254.6	161.4	200.5	123.6	367.6	74.8	56.0	144.6
1397.7	3076.6	4655.4	5028.0	3862.2	4094.2	5480.5	4588.4	2730.0	1805.6	4609.4
744.1	1654.7	1499.8	1814.4	1778.6	1397.8	1256.2	2145.3	799.7	377.5	1492.2

1842.6	1598.9	2207.0
1981.6	2158.8	2093.2
451.5	250.0	390.5
2481.4	3985.8	5146.1
1938.7	2118.7	1743.1
59.4	122.9	113.0
2697.3	2040.8	3076.1
1886.9	2375.5	72.0
324.2	411.7	472.9
2511.7	2927.1	2711.9
311.1	173.7	252.6
2671.7	4655.2	3880.8
68.0	1999.3	2050.4
4955.8	5963.8	4761.9
1847.7	1510.6	1830.8
490.5	451.9	447.8
305.7	247.1	233.2
1967.4	1321.2	2064.4
3183.6	2456.5	2808.5
2269.8	2648.5	1957.3
1834.0	1560.6	1866.6
1675.2	2012.4	1591.5
3870.2	3007.4	3714.9
258.8	235.6	101.0
4715.4	4516.4	5435.5
1720.5	1147.4	1039.7
7379.8	7079.4	6766.1
241.5	166.7	334.5
5381.9	5522.3	5827.0
102.6	69.4	90.7
2805.7	3143.1	4224.6
3819.3	4280.3	5121.7
434.9	785.1	2260.8
2840.8	3790.3	4137.6
258.7	162.8	123.2
1801.3	630.0	702.6
51.1	35.6	70.3
1369.4	810.7	1970.1
301.7	351.6	382.5
4127.6	4438.7	4104.2
1589.4	1515.1	1583.7

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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DQ798666.1 gg_id:181876 human fecal clone RL181_aan99g07 DQ798
EU464403.1 gg_id:290405 hamadryas baboon feces clone AFBAB_aai04d09 EU4644
EU464298.1 gg_id:292341 hamadryas baboon feces clone AFBAB_aai02b02 EU4642
AY960569.1 gg_id:114929 Ruminococcus sp. str. ID1 AY9605
EU464283.1 gg_id:299741 hamadryas baboon feces clone AFBAB_aai01f10 EU4642
EU464338.1 gg_id:295189 hamadryas baboon feces clone AFBAB_aai03a06 EU4643
DQ804789.1 gg_id:182724 human fecal clone RL187_aao72g02 DQ804
FJ676752.1 gg_id:522551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
EU381497.1 gg_id:275224 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3814
EU773576.1 gg_id:312780 Goeldi's Marmoset feces clone CAL_g05 EU7735
DQ085084.1 gg_id:137650 goat rumen clone A10 DQ085
EU530321.1 gg_id:273681 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
DQ071485.1 gg_id:233103 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc8 DQ071
DQ797410.1 gg_id:195175 human fecal clone RL248_aai99a05 DQ797
EU466910.1 gg_id:288208 African elephant feces clone AFEL2_aao31c03 EU4669
FJ364061.1 gg_id:366656 feces adult twins and mothers; TS150 clone TS150_a02e06 FJ3640
FJ363785.1 gg_id:363228 feces adult twins and mothers; TS14 clone TS14_a03c11 FJ3637
FJ677666.1 gg_id:527303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
DQ798613.1 gg_id:198740 human fecal clone RL181_aan99a06 DQ798
AJ408978.1 gg_id:111446 human colonic clone HuCA27 AJ4089
FJ362772.1 gg_id:357827 feces adult twins and mothers; TS13 clone TS13_a03a04 FJ3627
DQ824940.1 gg_id:181111 human fecal clone RL185_aao71c06 DQ824
GQ493324.1 gg_id:580898 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY977502.1 gg_id:127727 human cecum mucosal biopsy clone W257 AY9775
DQ796051.1 gg_id:177746 human fecal clone RL202_aai50g07 DQ796
DQ795677.1 gg_id:180329 human fecal clone RL178_aan68d01 DQ795
DQ823941.1 gg_id:174799 human fecal clone RL204_aaj57c01 DQ823
FJ372061.1 gg_id:366033 feces adult twins and mothers; TS9 clone TS9_a01c12 FJ3720
DQ797635.1 gg_id:180628 human fecal clone RL206_aaj14a05 DQ797
DQ795675.1 gg_id:190177 human fecal clone RL178_aan68c05 DQ795
DQ798351.1 gg_id:189315 human fecal clone RL181_aah41d03 DQ798
DQ795022.1 gg_id:176238 human fecal clone RL310_aam39c05 DQ795
GQ897243.1 gg_id:539595 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ674180.1 gg_id:518553 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ795460.1 gg_id:175261 human fecal clone RL178_aah54f04 DQ795
FJ683955.1 gg_id:529512 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FJ679615.1 gg_id:512352 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
FJ685186.1 gg_id:516143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
DQ794499.1 gg_id:184670 human fecal clone RL197_aah88g03 DQ794
DQ801131.1 gg_id:189661 human fecal clone RL387_aao92g01 DQ801
DQ796378.1 gg_id:196021 human fecal clone RL179_aah26e02 DQ796

3903.8	1963.3	2237.1	2278.6	2968.7	2235.9	2856.9	2767.5	2425.6	1525.1	2004.2
91.0	601.0	1214.8	1144.3	436.5	868.2	725.9	901.5	382.8	1462.8	628.0
245.1	1250.4	1550.9	1993.0	1535.9	1202.7	1524.0	2007.7	585.9	272.4	543.2
113.2	1438.3	1377.3	1330.0	651.2	803.0	685.6	1080.6	460.7	1282.0	693.4
42.5	447.9	709.9	744.5	60.4	272.6	223.4	631.8	127.6	24.8	321.0
152.4	3313.2	2458.7	2031.6	1508.5	2308.4	1795.1	2089.0	3529.7	3048.1	1894.2
47.1	106.7	200.9	116.8	53.4	81.1	60.9	78.7	24.7	19.8	64.9
4260.3	1889.6	2304.4	2364.5	1117.5	1789.8	1847.6	2174.9	2478.3	2505.1	2599.4
45.5	1507.1	2036.8	2244.1	804.6	1457.2	1142.6	2423.4	823.4	1153.3	1385.8
152.3	1470.6	1603.6	1293.0	980.8	1045.3	926.0	982.3	1215.5	960.8	458.0
6783.7	3520.6	3661.5	3466.7	3576.9	3969.3	3634.0	3475.8	3897.0	4126.2	4853.4
49.5	637.2	943.0	998.6	107.5	376.9	193.0	576.4	107.3	69.5	217.2
41.2	61.5	84.1	81.9	46.5	44.2	242.4	26.6	49.7	18.7	80.6
11368.2	3689.6	3816.7	4871.3	3748.1	4203.3	4584.3	4201.9	4512.8	2624.4	4695.1
361.8	3107.0	3613.3	2947.9	3324.1	3337.5	2827.0	3603.9	1764.8	1890.6	2133.6
287.1	2366.8	2670.5	3354.0	2482.5	2148.3	2616.2	2484.4	828.5	1029.1	1438.9
53.8	234.4	458.2	462.1	358.7	170.1	214.3	285.3	49.7	42.8	188.8
3181.5	3234.1	3778.2	3624.7	3575.7	2762.0	3601.3	2674.5	2572.9	1941.1	3431.6
2890.4	2059.5	2136.7	2807.3	866.2	2244.9	2355.6	2361.8	2237.7	1375.2	2075.3
301.2	1596.7	1841.9	2183.1	1588.1	1587.1	1375.9	1961.8	1132.8	592.3	1042.3
66.2	1316.1	1283.6	1058.3	1550.8	1085.2	1221.2	1020.1	587.3	1175.7	815.6
38.1	226.2	438.4	417.7	569.9	91.2	482.1	250.1	40.7	30.8	130.4
5818.4	1726.2	1706.5	1357.1	1214.3	1617.5	1547.9	1397.0	2358.1	1509.0	2375.1
3901.3	3983.4	3878.4	3600.8	3943.9	3033.8	3717.7	3415.0	3554.2	3064.1	6358.9
4743.2	8175.5	8456.2	7721.3	8163.4	7454.0	7470.5	7909.2	8912.7	6530.1	6760.9
223.2	1154.5	1998.2	1549.7	1486.5	1098.5	1712.2	1136.4	585.4	326.7	736.5
3352.8	3422.1	3327.9	3264.1	4719.0	3687.0	4045.8	3611.2	3151.6	2591.5	3771.1
736.0	1305.6	1668.5	1370.2	1258.1	1352.1	1404.1	1888.2	890.8	1206.5	1183.9
8551.1	5878.9	6271.6	5823.3	4842.7	5164.4	5822.4	4903.4	7466.7	7128.4	9559.1
30840.1	9233.4	8643.8	8730.0	7560.6	7496.8	8903.7	6346.8	12626.4	9762.8	18880.7
10390.3	6734.9	6748.0	6226.1	6217.6	5381.7	6141.7	5084.0	8306.2	5598.3	9131.8
43.7	338.2	792.5	545.3	241.2	252.4	233.6	443.6	105.4	58.4	368.4
7569.3	2410.6	1702.1	2611.8	2762.7	1531.8	2426.6	1976.6	2814.3	2309.2	4184.5
210.5	2502.5	2718.5	2469.4	3593.8	3078.3	2024.3	3087.6	1665.7	1911.1	2125.3
34.0	233.7	238.8	180.1	71.8	133.7	90.0	157.8	34.9	55.2	60.9
12259.2	3998.3	3342.6	2704.4	3277.4	3594.3	3413.1	3819.3	4462.9	5502.4	3255.6
34.7	480.9	364.2	369.9	343.5	244.8	212.4	364.0	379.6	128.2	131.6
878.3	2819.2	2625.1	2542.7	2021.1	2056.2	2230.8	2403.9	2735.6	2180.9	3546.8
31.0	324.0	538.9	409.5	639.2	196.5	536.1	346.6	94.6	43.8	206.8
675.6	2365.1	2480.4	2598.7	2428.6	2303.7	2459.0	2033.1	1779.9	760.4	1838.9
36.4	340.9	424.3	499.8	102.8	126.3	157.6	143.2	29.0	23.2	52.5

2481.8	2120.0	3031.1
788.6	1142.7	898.0
1706.6	1708.5	2071.9
1637.3	1504.8	2497.0
689.5	622.1	944.2
1842.1	2680.5	2926.5
170.6	118.4	124.0
2289.5	2232.2	1851.4
2209.7	2077.2	2477.7
1288.8	934.7	892.5
3416.4	3627.9	3284.5
835.0	798.2	742.0
48.0	50.2	79.4
3475.5	5341.4	4403.4
3620.6	2642.0	3838.0
2583.8	2812.4	2889.2
275.6	339.1	466.0
2599.5	3955.2	3711.5
3136.0	2286.0	2839.7
2160.3	1911.8	1956.1
899.9	1116.7	1333.4
260.0	274.7	379.1
1740.2	1879.6	1608.3
3733.1	3315.7	4663.2
6859.0	8825.4	7411.8
1130.5	1615.6	2860.2
3311.8	4429.4	3818.1
1487.2	1788.9	2002.7
4889.3	5998.5	5530.6
8207.8	9161.4	7625.3
5885.5	6340.7	5907.0
438.7	638.0	1177.6
1828.1	3457.9	2209.5
3092.7	2379.5	2454.9
158.9	204.8	238.5
4151.1	5669.6	3679.6
332.2	356.7	967.8
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Eubacterium
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AY982478.1 gg_id:116264 human sigmoid colon mucosal biopsy clone MM39 AY9824
FJ682393.1 gg_id:528101 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
DQ799588.1 gg_id:196948 human fecal clone RL305aal88a06 DQ799
DQ795610.1 gg_id:175007 human fecal clone RL178_aan67a03 DQ795
DQ796306.1 gg_id:183552 human fecal clone RL179_aah25e07 DQ796
AY980794.1 gg_id:126997 human rectum mucosal biopsy clone LO11 AY9807
FJ369908.1 gg_id:364287 feces adult twins and mothers; TS55 clone TS55_a02b08 FJ3699
FJ366270.1 gg_id:370023 feces adult twins and mothers; TS25 clone TS25_a04f10 FJ3662
FJ370213.1 gg_id:368038 feces adult twins and mothers; TS56 clone TS56_a01h01 FJ3702
FJ368827.1 gg_id:365391 feces adult twins and mothers; TS4 clone TS4_a01a12 FJ3688
FJ685443.1 gg_id:529808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ369265.1 gg_id:363127 feces adult twins and mothers; TS50 clone TS50_a02c04 FJ3692
FJ684743.1 gg_id:519921 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ796869.1 gg_id:196394 human fecal clone RL179_aao55f11 DQ796
FJ678359.1 gg_id:514400 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
FJ370858.1 gg_id:365636 feces adult twins and mothers; TS5 clone TS5_a02a12 FJ3708
FJ365451.1 gg_id:362642 feces adult twins and mothers; TS20 clone TS20_a03a09 FJ3654
DQ800958.1 gg_id:199174 human fecal clone RL387_aao89h08 DQ800
DQ807460.1 gg_id:186561 human fecal clone RL307_aam06h03 DQ807
DQ825285.1 gg_id:174225 human fecal clone RL185_aan87g06 DQ825
DQ809837.1 gg_id:182381 human fecal clone RL184_aao65a01 DQ809
FJ369804.1 gg_id:360862 feces adult twins and mothers; TS55 clone TS55_a01a07 FJ3698
EF402093.1 gg_id:206645 human fecal clone SJTU_B_03_57 EF4020
DQ805865.1 gg_id:198078 human fecal clone RL306aal92a08 DQ805
DQ797393.1 gg_id:195255 human fecal clone RL248_aai98g07 DQ797
DQ326329.1 gg_id:145360 Metagenomic gut microbiome healthy human stool clone C318 DQ326
FJ679248.1 gg_id:528560 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ369063.1 gg_id:366153 feces adult twins and mothers; TS4 clone TS4_a03g10 FJ3690
DQ802012.1 gg_id:198227 human fecal clone RL241_aaj01g11 DQ802
FJ369432.1 gg_id:366979 feces adult twins and mothers; TS50 clone TS50_a04d08 FJ3694
DQ798560.1 gg_id:196287 human fecal clone RL181_aan98c07 DQ798
DQ807627.1 gg_id:182679 human fecal clone RL180_aah35b04 DQ807
DQ802564.1 gg_id:179762 human fecal clone RL188_aan93e01 DQ802
DQ802492.1 gg_id:178191 human fecal clone RL188_aah18d11 DQ802
DQ795623.1 gg_id:193991 human fecal clone RL178_aan67c02 DQ795
DQ807694.1 gg_id:195485 human fecal clone RL180_aah36a08 DQ807
AY979910.1 gg_id:127325 human rectum mucosal biopsy clone E224 AY9799
DQ802322.1 gg_id:195976 human fecal clone RL188_aah16a08 DQ802
FJ372011.1 gg_id:367354 feces adult twins and mothers; TS8 clone TS8_a04g04 FJ3720
DQ795329.1 gg_id:192403 human fecal clone RL178_aah53a07 DQ795

32.4	160.0	275.3	319.5	32.0	93.9	83.8	223.5	58.0	28.5	121.6
2511.1	2945.3	2786.4	2596.2	2736.6	2848.4	3193.7	3450.9	4725.5	2152.8	3477.3
2063.9	5248.4	5588.3	3851.7	4037.7	4756.4	3477.6	4952.8	5769.7	5952.7	4463.7
291.5	818.1	1169.7	1315.4	2155.2	1380.4	1693.0	1366.4	388.7	163.7	1019.3
7742.0	4984.1	5109.8	5587.6	5551.0	4916.5	6823.4	5647.3	7784.2	4969.9	5674.7
27.8	114.4	165.7	190.3	52.7	89.7	51.7	209.2	32.3	29.8	133.2
10427.1	4672.6	5001.1	5427.0	4004.9	4543.3	4555.8	4227.1	5634.1	6347.6	6079.7
5473.8	3793.7	3364.6	3008.2	2640.6	2870.2	2974.7	3269.8	2783.5	3639.6	3140.0
2810.2	2417.3	2666.1	2850.6	4297.5	2636.4	3585.9	3386.8	1914.3	964.4	2208.8
56.5	125.6	182.4	189.8	84.9	170.9	103.0	202.0	46.2	95.3	112.3
13216.2	6290.4	6180.9	6555.4	6395.9	6308.2	7191.9	5601.9	8445.7	7398.5	6968.7
1396.8	996.3	1458.4	923.8	1438.8	1073.7	976.1	1583.7	1465.9	350.4	1316.3
49.8	482.0	670.2	792.1	343.5	366.9	315.8	468.6	227.8	304.6	636.8
48.4	251.2	256.2	328.4	55.5	125.6	61.9	171.0	48.5	37.0	143.9
102.6	866.2	1130.3	1356.9	1108.8	853.7	1224.0	1221.3	183.3	119.8	553.3
4575.8	2416.4	2765.0	2771.9	2493.7	2239.5	2138.3	2371.4	2817.7	4712.9	3769.2
52.9	320.2	582.6	598.0	67.9	209.2	153.2	475.9	87.8	36.4	303.2
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36.4	44.9	85.7	106.5	21.0	26.6	39.4	84.7	31.4	24.4	87.0
3435.6	1763.6	2024.3	1401.3	1252.2	1266.3	1282.6	1483.3	1830.0	1819.8	2519.8
1318.0	4445.1	3750.4	3168.5	2589.5	3672.7	2420.4	3162.3	4903.5	4250.8	4489.5
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249.2	242.5	299.8	236.2	202.0	236.4	232.4	492.7	169.3	213.4	283.3
4319.0	6732.8	5695.9	5743.7	4514.6	5411.9	5757.0	5421.4	6694.7	5186.9	6111.0
39.8	159.7	229.4	212.1	21.4	87.2	66.8	106.6	20.2	15.2	55.3
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3810.7	2121.6	2073.4	2022.4	2292.5	2308.7	2173.1	2739.2	1862.9	2477.9	1989.8
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7432.5	4463.6	4186.3	3703.8	3586.2	3382.9	3793.5	3369.3	4903.7	4340.6	5083.2
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25110.6	8055.8	7018.0	7778.8	7235.4	7598.2	7898.3	6952.9	9658.6	8402.8	14421.8
8319.0	2750.8	3707.5	4369.1	2451.8	2899.3	2597.6	4027.5	2028.9	2401.4	2869.4
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2728.6	1031.2	2550.6	2830.7	3523.1	1638.5	4019.4	3153.4	999.9	1019.8	2393.2
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286.7	229.0	266.2
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4893.9	2867.8	3043.2
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2940.4	2979.3	2868.8
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FJ362651.1 gg_id:360092 feces adult twins and mothers; TS13 clone TS13_a01e06 FJ3626
DQ905789.2 gg_id:167882 human fecal clone 29E-a1 DQ905
DQ804596.1 gg_id:176409 human fecal clone RL187_aao70b06 DQ804
DQ795087.1 gg_id:183505 human fecal clone RL310_aam40a09 DQ795
DQ325743.1 gg_id:149614 Metagenomic gut microbiome healthy human stool clone B394 DQ325
FJ370065.1 gg_id:369212 feces adult twins and mothers; TS55 clone TS55_a04a08 FJ3700
FJ369870.1 gg_id:365861 feces adult twins and mothers; TS55 clone TS55_a01g03 FJ3698
AY986125.1 gg_id:121971 human stool clone D468 AY986
DQ801863.1 gg_id:178337 human fecal clone RL201_aai47g09 DQ801
DQ807737.1 gg_id:203199 human fecal clone RL180_aah36f02 DQ807
DQ801836.1 gg_id:190239 human fecal clone RL201_aai47e02 DQ801
DQ800317.1 gg_id:192672 human fecal clone RL303_aal71d06 DQ800
FJ364400.1 gg_id:361003 feces adult twins and mothers; TS15 clone TS15_a02e02 FJ3644
DQ325916.1 gg_id:145806 Metagenomic gut microbiome healthy human stool clone B756 DQ325
DQ806845.1 gg_id:183809 human fecal clone RL198_aaj73g08 DQ806
DQ809522.1 gg_id:177501 human fecal clone RL184_aah22c02 DQ809
FJ679540.1 gg_id:519626 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
AY983629.1 gg_id:121240 human descending colon mucosal biopsy clone NO71 AY983
DQ801904.1 gg_id:195152 human fecal clone RL201_aai48c10 DQ801
FJ369919.1 gg_id:357017 feces adult twins and mothers; TS55 clone TS55_a02c09 FJ3699
EU771665.1 gg_id:304410 African elephant feces clone AFEL2_aao31f04 EU771
GQ492513.1 gg_id:576103 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ370081.1 gg_id:361880 feces adult twins and mothers; TS55 clone TS55_a04c01 FJ3700
DQ794770.1 gg_id:180070 human fecal clone RL240_aaj32b06 DQ794
DQ806610.1 gg_id:182539 human fecal clone RL186_aao46f10 DQ806
FJ365518.1 gg_id:362419 feces adult twins and mothers; TS20 clone TS20_a03g09 FJ3655
FJ678279.1 gg_id:532113 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
DQ802730.1 gg_id:186283 human fecal clone RL188_aan95g12 DQ802
DQ798222.1 gg_id:173959 human fecal clone RL181_aah39a11 DQ798
EU469505.1 gg_id:290281 black lemur feces clone BKLE_a12_3 EU469
EU771816.1 gg_id:310632 African elephant feces clone AFEL2_aao32a11 EU771
DQ807876.1 gg_id:179509 human fecal clone RL180_aah38c10 DQ807
EU761798.1 gg_id:347926 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
DQ799845.1 gg_id:195911 human fecal clone RL182_aah34h02 DQ799
DQ809883.1 gg_id:198942 human fecal clone RL184_aao65e03 DQ809
FJ363951.1 gg_id:360540 feces adult twins and mothers; TS150 clone TS150_a01c07 FJ3639
DQ802103.1 gg_id:186515 human fecal clone RL241_aaj03b04 DQ802
GQ897156.1 gg_id:578032 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ369904.1 gg_id:362722 feces adult twins and mothers; TS55 clone TS55_a02b04 FJ3699
FJ365750.1 gg_id:368316 feces adult twins and mothers; TS21 clone TS21_a02e10 FJ3657

13109.9	4638.0	4173.1	4738.6	4699.2	4778.3	4710.1	3803.4	4421.0	3922.0	5885.4
2430.4	1166.2	1410.3	1720.8	1887.5	1213.3	1557.7	1300.3	541.2	290.9	870.3
416.1	466.0	667.6	718.7	396.8	432.0	187.1	602.3	262.0	101.0	308.6
45.8	714.2	1293.0	1067.0	398.2	785.0	604.1	948.7	282.8	672.7	1009.0
90.0	894.9	940.9	1140.2	1868.5	1296.9	1530.0	1464.0	304.5	233.4	297.5
50.8	1512.8	2221.2	2050.0	860.1	1676.2	1385.6	1839.0	450.0	1235.9	1075.1
90.2	404.3	503.4	567.0	177.5	454.4	296.4	1117.6	137.3	146.8	209.1
2192.9	561.2	944.8	1052.6	412.6	549.3	405.1	895.3	291.3	142.4	635.1
124.2	1112.3	1913.0	1430.1	1302.8	1116.7	1350.3	858.9	408.1	414.6	693.8
9337.5	6073.3	6247.7	6376.0	5750.0	5522.9	8704.6	6045.9	7727.1	5159.6	7933.6
248.5	876.3	1005.3	1173.9	1017.7	720.7	738.7	1055.8	310.2	200.9	568.6
394.9	1746.8	2288.4	3018.5	1397.1	2019.9	1100.9	2620.8	1655.0	597.3	2469.2
76.8	349.3	597.3	441.4	312.8	463.6	296.9	638.5	215.4	123.9	550.3
7357.1	6258.1	4746.4	5534.3	4966.6	4989.0	5102.8	4902.6	4907.1	4266.9	9909.4
23332.8	4733.1	4959.8	5026.4	5176.2	4724.8	5569.7	4828.7	7015.7	5073.0	6848.6
40.5	155.0	255.8	333.2	30.6	101.3	75.2	235.8	33.2	26.4	126.5
8961.1	4859.0	5541.9	5468.2	4506.7	5241.8	5651.0	4371.3	4704.6	3151.5	6666.1
115.0	1455.6	1824.3	2043.3	1240.4	1233.5	1309.7	1679.7	624.1	281.7	817.5
7849.7	4624.5	5692.6	4892.2	4073.0	5253.0	4639.9	4335.1	6342.6	4546.2	4665.6
395.1	1648.9	2023.5	1884.5	1888.3	2152.6	1734.2	2521.4	1546.8	2575.1	2096.2
7936.1	2936.5	2760.6	2507.2	3217.9	2898.7	2969.5	3020.2	2309.3	3348.0	2405.2
38.9	86.2	77.4	83.3	29.1	45.7	54.3	46.8	29.9	26.7	31.8
13793.4	7117.6	6871.7	7320.6	8284.9	7012.7	8370.0	6284.7	6084.2	6483.7	7717.5
46.0	753.6	790.8	683.9	367.8	550.8	313.1	577.7	478.1	815.0	542.4
1847.9	2131.9	1981.7	1937.1	1678.4	1941.9	1600.8	1888.6	1684.0	2061.1	1822.4
7737.5	1790.7	1913.3	2191.8	1889.9	1700.1	1796.7	1979.2	1884.1	1974.9	2174.3
2436.2	1474.2	1387.4	1119.2	1266.0	1121.6	1215.2	1404.6	1112.4	907.8	1259.5
1184.7	1351.9	1831.4	1765.2	1449.2	1136.0	1366.5	1757.7	1105.3	1725.7	1481.4
46.7	288.1	395.6	512.8	486.2	273.2	398.3	280.8	49.9	44.7	76.0
11148.9	5106.8	4877.2	5489.1	4414.5	4176.0	5407.7	3883.7	6229.8	3157.3	6154.1
81.5	151.9	211.9	240.1	87.9	93.7	66.1	171.1	44.6	29.4	101.4
6490.1	2840.6	3108.4	3094.7	2568.7	2597.1	2443.5	2675.1	3607.3	3238.0	3181.5
104.5	458.5	422.1	502.3	617.1	356.6	698.3	450.4	137.6	50.0	367.2
732.9	3183.9	3742.3	3909.0	2460.4	3005.4	3259.5	4264.5	2326.1	4212.3	4129.5
46.5	132.0	140.1	81.5	64.1	92.3	67.4	164.4	35.4	118.0	133.2
704.4	456.5	592.8	762.2	440.4	444.2	168.7	588.9	94.9	68.8	335.3
2837.8	2454.2	2700.0	2559.2	2374.7	2080.4	2318.8	2670.2	2458.5	2462.4	2487.4
50.8	533.7	933.8	899.7	151.1	351.6	368.5	645.1	169.1	63.1	554.5
47.0	952.9	1272.3	1109.4	898.9	1005.7	1410.5	1091.6	229.0	1055.9	540.4
974.9	776.1	1107.4	1325.3	1379.2	915.4	780.2	1127.9	429.0	1222.9	610.4
27073.8	6229.8	6741.4	7164.8	5793.0	5534.9	4460.8	5652.8	8872.6	6885.7	9342.7

4100.5	4936.2	4165.9
1757.5	1774.6	1874.5
685.0	711.3	835.6
923.3	1096.5	1180.4
1178.5	1175.4	1386.5
2083.0	1461.3	2269.5
1706.9	490.4	967.1
622.4	759.9	868.9
1275.6	1349.3	1898.0
6236.2	6528.8	6109.7
1347.8	819.8	1042.5
2245.9	2391.3	2326.6
343.8	381.6	836.4
5805.7	5423.2	5575.2
4664.7	6633.9	5462.2
83.4	166.5	110.9
3717.6	4826.5	5143.5
1647.8	1867.6	1889.6
4347.1	4608.4	5689.6
2314.0	2191.6	3044.0
3072.5	3263.5	3930.5
87.5	70.3	88.5
6306.6	7082.2	7806.1
792.7	550.4	1048.2
2399.2	2881.2	2649.3
2267.5	3381.0	2734.6
2519.7	1522.9	1075.1
1626.2	1770.6	2080.3
612.8	396.5	482.2
4774.8	4768.3	4247.0
177.9	129.5	151.5
2666.3	2784.3	2670.6
676.4	316.7	1388.7
4131.5	3892.5	4046.0
138.3	187.7	160.4
619.4	871.7	1952.9
2430.6	2491.8	3079.0
407.6	471.6	1063.3
1288.9	1077.5	1013.2
1340.2	1962.6	1162.4
5209.2	6498.0	5437.8

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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FJ685262.1 gg_id:528647 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
DQ802645.1 gg_id:175705 human fecal clone RL188_aan94f06 DQ802
FJ673255.1 gg_id:514971 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
DQ802337.1 gg_id:185372 human fecal clone RL188_aah16c11 DQ802
DQ795045.1 gg_id:193452 human fecal clone RL310_aam39e06 DQ795
DQ800815.1 gg_id:180261 human fecal clone RL183_aao03g10 DQ800
EU765102.1 gg_id:329212 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ672991.1 gg_id:517310 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
AJ811983.1 gg_id:187930 human biopsies Human ulcerative colitis biopsy clone UC9-54 AJ8119
EU767603.1 gg_id:307060 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
FJ369453.1 gg_id:365272 feces adult twins and mothers; TS50 clone TS50_a04g01 FJ3694
DQ796031.1 gg_id:185031 human fecal clone RL202_aai50e03 DQ796
EU767247.1 gg_id:339714 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ678499.1 gg_id:511955 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
DQ807440.1 gg_id:176585 human fecal clone RL307_aam06f06 DQ807
GQ896598.1 gg_id:584945 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ365768.1 gg_id:367260 feces adult twins and mothers; TS21 clone TS21_a02g06 FJ3657
EU776829.1 gg_id:329520 Mongoose lemur feces clone ML_aaj27g06 EU776
DQ800034.1 gg_id:188008 human fecal clone RL247_aaj23d01 DQ800
FJ369901.1 gg_id:366175 feces adult twins and mothers; TS55 clone TS55_a02b01 FJ3699
DQ810109.1 gg_id:186519 human fecal clone RL184_aao68b09 DQ810
FJ369742.1 gg_id:362935 feces adult twins and mothers; TS51 clone TS51_a04c08 FJ3697
DQ794487.1 gg_id:188965 human fecal clone RL197_aah88e08 DQ794
FJ683151.1 gg_id:520674 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU763969.1 gg_id:315472 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
DQ807650.1 gg_id:176734 human fecal clone RL180_aah35e01 DQ807
GQ491970.1 gg_id:547083 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ796953.1 gg_id:194935 human fecal clone RL179_aao56h07 DQ796
DQ805288.1 gg_id:188213 human fecal clone RL249_aaj84e10 DQ805
FJ371018.1 gg_id:360947 feces adult twins and mothers; TS5 clone TS5_a04a02 FJ3710
FJ363766.1 gg_id:367562 feces adult twins and mothers; TS14 clone TS14_a03b03 FJ3637
DQ807846.1 gg_id:181642 human fecal clone RL180_aah37h08 DQ807
FJ372359.1 gg_id:367858 feces adult twins and mothers; TS9 clone TS9_a04f09 FJ3723
DQ825288.1 gg_id:188792 human fecal clone RL185_aan87h02 DQ825
FJ365134.1 gg_id:363400 feces adult twins and mothers; TS1 clone TS1_a03c08 FJ3651
EU466767.1 gg_id:287951 African elephant feces clone AFEL2_aao29c01 EU466
FJ684613.1 gg_id:514920 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
GQ897903.1 gg_id:547836 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ796868.1 gg_id:184057 human fecal clone RL179_aao55f10 DQ796
AY979303.1 gg_id:115974 human transverse colon mucosal biopsy clone Z551 AY9793

44.4	255.4	402.0	288.8	240.9	249.1	270.3	336.6	94.8	115.6	154.4
44.9	531.4	682.9	733.3	52.5	233.8	225.9	618.9	79.6	49.3	286.4
590.6	1777.9	2318.4	2465.6	2434.6	2135.7	2767.2	2014.4	1200.5	2046.3	1414.6
2492.1	1781.3	1612.6	1642.0	1746.0	1362.2	1665.9	1454.6	1258.6	1183.6	2004.9
25234.9	5642.1	5608.4	5788.6	6108.7	5866.0	6764.0	4327.5	8429.5	7315.1	8541.8
46.8	466.3	465.1	370.5	367.2	325.9	287.0	739.8	326.7	134.8	265.1
509.6	2333.4	2794.5	3322.9	2950.1	3047.1	3813.6	2263.7	1401.2	1288.9	3671.1
1005.9	6975.9	6504.6	5806.6	6057.6	6776.2	5184.2	5546.8	5358.1	4601.2	4601.4
8209.3	3232.6	3619.7	3168.3	3574.0	3101.1	3242.8	2972.8	1586.5	3405.5	3420.5
933.5	1899.1	2773.3	2192.8	2030.2	1845.6	2060.8	2024.2	1183.9	767.3	2056.9
98.8	804.2	1447.1	1688.7	651.6	673.5	744.3	1260.9	217.0	186.4	772.2
2749.0	2555.7	2198.8	2409.1	2829.0	2078.1	2719.7	2218.1	2059.5	1999.7	3447.8
112.8	803.4	257.3	1019.3	176.1	750.0	1283.7	834.6	284.9	239.1	502.8
5546.4	4715.0	5490.2	5643.8	4649.1	4737.0	5047.7	5018.0	4934.9	4790.7	6624.4
140.7	627.5	846.4	721.1	734.3	484.3	655.7	684.2	417.8	248.7	463.3
258.6	2092.8	2071.3	2368.2	2075.5	1734.4	2201.7	2053.2	998.8	993.5	1705.4
133.6	1286.5	1923.6	1269.8	802.8	1505.9	744.4	1740.3	518.1	721.4	1106.1
5354.6	1868.6	2210.0	2449.6	1679.3	1672.9	1820.0	1881.4	1870.7	1143.1	1965.8
4221.9	1295.7	1704.4	1735.5	1832.2	2092.6	2272.9	1652.9	685.9	245.1	879.4
36.6	148.3	172.7	229.4	570.5	171.6	223.3	93.7	18.9	27.7	34.2
61.0	212.0	253.3	319.7	74.8	90.9	57.8	147.9	43.5	54.4	152.9
39.7	512.1	649.4	633.0	660.3	484.7	487.5	864.4	276.3	412.9	444.8
5462.0	4169.7	3976.8	4375.0	3865.6	3803.0	3978.0	3698.2	4547.5	3124.3	7102.9
666.8	1381.5	1353.0	1092.4	1557.1	1180.8	1191.7	1381.3	1655.9	820.2	900.8
797.3	754.8	922.8	721.4	722.1	757.8	745.9	1268.3	616.0	849.4	565.6
7860.2	2423.0	2798.1	3575.1	3281.4	2549.3	2862.1	2848.0	3173.4	2498.4	3871.7
49.7	625.4	854.6	1085.7	1103.0	499.1	681.4	963.4	143.9	101.6	465.0
70.1	1005.2	941.6	706.7	2031.1	878.5	566.0	498.3	877.7	1597.5	519.9
2951.1	2222.4	3197.7	3099.1	1953.4	2574.1	2471.3	2746.9	1591.9	1867.1	2202.9
1372.1	2078.5	2051.4	2112.3	2666.6	2150.7	2567.2	1730.4	2494.1	1844.9	1723.5
1162.6	3461.7	3049.9	2043.1	2301.0	2470.4	1957.0	2271.9	1888.3	1489.5	3976.9
161.6	739.9	1172.4	909.4	1202.4	791.2	1120.7	678.9	327.4	218.3	510.3
560.4	1958.3	2536.2	2464.8	2850.7	1934.7	2886.8	2588.2	1168.6	1129.2	1592.5
18358.2	5677.2	6480.8	7540.1	6301.7	6295.4	6446.0	5663.2	9433.0	5119.5	11332.1
244.9	1623.9	1617.1	1713.8	2387.6	1723.0	2242.1	1968.3	490.9	349.4	911.6
37.7	83.1	114.0	99.0	50.6	59.7	53.3	74.1	20.2	22.5	49.7
3059.7	2658.5	3061.2	2515.2	2087.8	2393.9	2456.7	2884.8	2227.4	1981.8	3015.5
3170.3	3408.0	2669.4	1718.6	1783.8	2292.2	1523.5	1962.1	3162.4	2227.7	3346.5
15920.0	4660.3	4231.9	4535.1	3766.3	3929.7	4623.6	3866.9	4935.1	3839.6	6509.9
125.2	445.1	840.7	629.6	640.7	586.6	573.7	977.9	235.8	165.7	559.4
46.9	857.4	1378.5	1413.4	787.6	879.0	903.2	1573.2	287.8	205.4	692.5

661.9	399.3	949.1
534.3	321.0	296.2
1995.8	2784.9	2349.4
1373.7	2038.3	1414.8
4895.9	5718.3	5425.6
776.5	539.4	796.5
1850.7	1578.0	2884.7
5829.3	4708.2	5813.1
4204.1	3730.8	4086.0
1920.1	3191.9	2569.8
1210.7	718.2	1170.3
2115.1	2536.3	2292.0
1033.6	849.8	1418.0
4567.8	5863.3	6497.5
713.3	726.0	910.3
1921.6	1860.8	2294.9
1764.6	1198.5	1544.7
1788.0	2047.9	2289.3
1653.0	2198.7	3144.9
136.9	180.9	207.4
160.3	158.0	130.5
682.8	1030.6	1532.9
3404.9	4437.0	4439.3
950.3	1601.8	1983.8
2110.6	1098.6	1258.3
2797.0	4012.5	3292.0
833.3	605.9	1078.1
591.4	1069.9	1400.6
2763.8	3045.0	2429.9
1935.5	2121.7	2551.0
2517.7	2638.1	2010.3
744.8	788.0	1262.7
2234.3	2277.9	2957.7
6186.6	5484.9	6826.1
1536.4	1422.1	1969.6
176.8	80.7	255.7
2996.1	3092.4	3317.2
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4276.7	5382.0	3718.6
909.8	780.5	1120.5
1743.9	1418.5	1584.0

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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DQ798838.1 gg_id:188018 human fecal clone RL242_aaj98a07 DQ798
EU761735.1 gg_id:321203 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ366263.1 gg_id:366003 feces adult twins and mothers; TS25 clone TS25_a04f03 FJ3662
EU461775.1 gg_id:301025 mongoose lemur feces clone ML_aaj28g03 EU461
FJ366421.1 gg_id:364710 feces adult twins and mothers; TS26 clone TS26_a03a02 FJ3664
EU763962.1 gg_id:305501 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
GQ006869.1 gg_id:502796 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g06c GQ006
FJ365392.1 gg_id:362829 feces adult twins and mothers; TS20 clone TS20_a02d02 FJ3653
AY978332.1 gg_id:119050 human transverse colon mucosal biopsy clone F237 AY9783
GQ090639.1 gg_id:389523 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
DQ904902.1 gg_id:173658 human fecal clone 001C-g7 DQ904
FJ369949.1 gg_id:367658 feces adult twins and mothers; TS55 clone TS55_a02f06 FJ3699
FJ370113.1 gg_id:364878 feces adult twins and mothers; TS55 clone TS55_a04e09 FJ3701
FJ673736.1 gg_id:528127 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
DQ802688.1 gg_id:193128 human fecal clone RL188_aan95c02 DQ802
DQ803382.1 gg_id:191172 human fecal clone RL311_aam24h11 DQ803
AY980926.1 gg_id:123426 human rectum mucosal biopsy clone LR38 AY9809
DQ795760.1 gg_id:176845 human fecal clone RL245_aai81h09 DQ795
DQ806962.1 gg_id:194870 human fecal clone RL198_aaj76b10 DQ806
DQ808330.1 gg_id:196701 human fecal clone RL180_aao75d03 DQ808
DQ798132.1 gg_id:180983 human fecal clone RL302_aal95h06 DQ798
FJ369204.1 gg_id:362227 feces adult twins and mothers; TS50 clone TS50_a01e04 FJ3692
FJ365694.1 gg_id:369815 feces adult twins and mothers; TS21 clone TS21_a01h07 FJ3656
DQ807877.1 gg_id:188165 human fecal clone RL180_aah38c11 DQ807
FJ365904.1 gg_id:358905 feces adult twins and mothers; TS21 clone TS21_a04d08 FJ3659
FJ365475.1 gg_id:358481 feces adult twins and mothers; TS20 clone TS20_a03c12 FJ3654
DQ805397.1 gg_id:188087 human fecal clone RL203_aai62b01 DQ805
FJ364848.1 gg_id:357191 feces adult twins and mothers; TS19 clone TS19_a03h05 FJ3648
DQ804124.1 gg_id:179837 human fecal clone RL187_aah68h11 DQ804
DQ799398.1 gg_id:181828 human fecal clone RL305aal85g07 DQ799
EU842279.1 gg_id:313296 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU843831.1 gg_id:354158 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8438
EU474950.1 gg_id:292979 red river hog feces clone RRH_aaa03d10 EU4749
AM277070.2 gg_id:232273 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
AB034054.1 gg_id:44311 rumen clone 3C3d-15 AB0340
DQ673542.1 gg_id:163539 rumen fluid clone GRC77 DQ673
EU842352.1 gg_id:308021 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
AB494806.1 gg_id:565292 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
AY854287.2 gg_id:110748 herbivore gastrointestinal tract clone CATTLE_25 AY8542
AF202264.1 gg_id:41867 Syntrophococcus sucromutans str. S195 AF2022
EU458753.1 gg_id:288604 Goeldi's marmoset feces clone CAL_d12_2 EU4587

38.8	91.1	132.3	111.7	45.2	82.8	79.3	100.3	98.9	68.4	50.5
7753.0	4117.5	4459.3	4299.7	2103.7	3464.1	4064.7	3800.3	4391.0	3505.0	4806.2
931.1	1056.1	1157.0	1325.6	1322.7	1131.0	1115.7	1672.6	605.5	338.5	921.4
1633.4	4239.5	3727.0	3159.8	2789.1	3444.8	3083.1	3569.9	4390.7	4720.1	3666.6
2753.6	5125.0	5775.3	6687.8	5918.6	4911.5	5275.4	5357.7	5785.8	4403.1	5256.3
1701.9	311.1	427.9	374.4	226.0	327.6	221.4	323.5	266.5	243.0	324.7
455.4	1476.3	2176.6	1685.7	1091.1	1365.0	1028.7	1486.6	985.6	1475.2	1074.0
2167.2	474.7	526.1	403.3	946.0	401.9	355.3	766.0	328.7	201.1	357.3
185.5	767.8	834.9	916.6	1092.8	810.6	848.6	963.4	394.3	244.2	501.9
9408.5	3831.4	2358.6	3493.0	3644.8	3618.8	4900.7	3170.0	5179.2	3865.4	5071.0
69.3	513.6	711.4	758.6	413.1	424.6	505.2	626.4	229.1	58.5	421.8
34.9	753.1	1180.4	1415.7	465.7	805.4	700.9	1154.5	158.3	292.2	734.0
264.3	2280.5	1943.7	1134.7	822.0	1551.0	844.0	1138.9	1702.6	897.6	1383.5
35.4	491.1	648.5	801.1	123.2	226.4	245.7	541.8	69.4	45.1	242.6
57.1	96.9	98.8	95.3	44.9	70.7	31.8	88.4	61.6	54.4	74.9
4895.3	2943.8	3031.2	3042.8	3954.5	2896.1	3550.2	3391.1	2463.6	3934.4	2355.6
40.9	768.9	816.7	919.1	420.0	656.0	348.9	935.2	82.9	70.7	360.4
35.3	209.7	259.8	435.9	60.7	63.8	63.9	126.5	24.4	31.9	48.6
48.3	304.7	385.2	396.7	104.9	200.3	283.8	271.2	60.8	33.4	121.2
1068.8	5768.4	6092.6	6441.4	5076.6	5395.1	4860.5	5520.7	5361.7	3676.2	5936.3
246.4	2274.4	2456.9	3087.8	1375.6	2318.7	2269.0	2908.8	737.7	588.5	1390.5
233.5	1121.3	1668.5	2187.9	356.3	731.6	491.6	1672.2	455.4	326.9	765.0
3358.4	3050.4	3546.5	3359.3	3148.8	2759.5	3160.8	2723.7	3376.2	3504.1	3598.8
1342.4	1069.0	1170.5	1207.9	1462.8	1245.5	1217.6	990.4	1092.0	828.9	1134.5
112.6	1392.6	1365.0	1181.4	1151.6	1356.9	999.3	1394.0	976.8	1825.6	933.7
156.6	1797.8	2523.1	2190.7	1568.1	1841.3	1612.8	2207.2	1916.2	1576.4	1650.4
11908.7	4992.8	4322.2	5448.0	6186.4	4852.3	4726.6	4327.2	6617.1	5098.7	9553.0
54.3	918.4	955.5	980.5	1047.1	824.4	779.2	967.3	369.7	606.1	521.8
56.4	246.3	482.7	478.3	225.4	389.6	298.5	343.6	67.5	79.3	246.9
78.2	555.3	694.5	666.9	1126.6	420.6	596.1	400.8	450.7	397.3	362.3
50.5	897.1	1327.2	1117.1	390.6	472.3	405.4	1310.9	313.5	640.2	612.8
2729.9	1502.5	2585.0	1770.1	1163.3	1601.8	1203.3	2576.6	1063.2	2680.7	1561.6
10592.1	5514.0	5017.1	6169.1	4082.6	5059.3	6060.2	4722.9	5732.7	5082.7	5636.6
35.1	180.6	372.5	629.6	61.8	264.8	190.1	774.7	69.9	113.5	181.4
73.7	983.7	1236.3	1588.1	1136.9	935.5	1072.0	1072.4	150.1	311.0	477.4
57.9	268.6	299.4	308.6	239.1	328.7	174.5	358.9	380.8	44.5	202.6
71.3	497.3	915.0	1144.4	253.4	299.1	143.9	463.4	161.4	592.8	212.1
6081.8	4040.9	4647.8	5462.0	4877.1	3802.2	5971.4	4349.8	4559.1	3985.3	4813.9
38.9	1421.9	1933.1	1332.1	775.9	1037.3	658.6	1290.9	326.7	275.4	817.1
141.8	1043.8	1305.4	989.5	1037.8	1218.9	1023.3	1701.6	813.3	1699.8	676.4
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109.8	127.0	90.4
2369.8	3938.7	5246.0
2577.9	1752.4	1519.7
4292.2	4421.9	4958.5
5017.8	6080.8	5536.6
368.3	867.0	437.2
1736.8	2228.2	1758.2
733.7	740.0	1021.3
905.4	1346.1	1361.7
3227.4	4901.6	3212.8
657.5	606.8	1033.4
966.3	812.0	1502.8
980.2	1389.7	1073.5
510.4	394.8	311.1
79.9	85.4	131.3
3019.0	4110.0	4045.3
449.9	516.5	1267.5
181.3	299.4	129.0
521.7	529.2	194.9
4564.7	4878.0	4994.9
2823.1	2507.3	3841.9
2394.5	1201.8	1483.4
2768.9	4381.8	3362.3
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1491.5	1035.2	1733.3
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1199.4	735.1	1517.9
764.2	371.2	259.1
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1062.5	921.4	751.8
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5544.6	6095.0	5429.0
929.7	238.5	524.9
1300.1	1191.6	2414.3
231.4	262.4	249.6
581.9	720.0	743.3
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Eubacterium
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g__Johnsonella
g__Johnsonella
g__Lachnobacterium
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s__unclassified	23759
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s__unclassified	23874
s__unclassified	23925
s__unclassified	23937
s__unclassified	23973
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s__unclassified	24102
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s__Lachnobacterium bovis	18075
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s__unclassified	17870

AB034113.1 gg_id:29937 rumen clone 4C28d-24 AB034
DQ326866.1 gg_id:149699 Metagenomic gut microbiome healthy human stool clone E348 DQ326
FJ367602.1 gg_id:358858 feces adult twins and mothers; TS2 clone TS2_a01d10 FJ3676
GU304530.1 gg_id:572313 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU458712.1 gg_id:297942 Goeldi's marmoset feces clone CAL_a12_1 EU458
FJ673087.1 gg_id:525259 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
EU844621.1 gg_id:349401 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ804183.1 gg_id:195096 human fecal clone RL187_aah69h07 DQ804
GU304233.1 gg_id:594513 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU302772.1 gg_id:533877 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU842324.1 gg_id:356261 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ394607.1 gg_id:151675 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
Y18191.1 gg_id:25317 Syntrophococcus sucromutans str. DSM 3224 Y18191
DQ057372.1 gg_id:136044 chicken ileum/cecum clone cc142 DQ057
AM420242.1 gg_id:235970 Noma subgingival plaque clone 201G01(oral) AM420
FJ976324.1 gg_id:591273 Interindividual healthy human oral microbiota mouth clone 10B859 FJ9763
AF298662.1 gg_id:35683 Lachnobacterium bovis str. LRC 5357 AF298
DQ809911.1 gg_id:182324 human fecal clone RL184_aao65g12 DQ809
EU454692.1 gg_id:313804 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU454
DQ797186.1 gg_id:186096 human fecal clone RL386_aao88b04 DQ797
EF095986.1 gg_id:174276 mouse cecum clone lean2_aaa01d08 EF0959
AF396923.1 gg_id:24050 Eubacterium sp. str. C12b AF3969
DQ810111.1 gg_id:187960 human fecal clone RL184_aao68b11 DQ810
EF404492.1 gg_id:209085 human fecal clone SJTU_C_10_90 EF4044
EU779311.1 gg_id:306866 Visayam Warty Pig feces clone VWP_aaa02f12 EU7793
EU777208.1 gg_id:325580 Okapi feces clone OK1_f05 EU777
FJ365281.1 gg_id:359139 feces adult twins and mothers; TS20 clone TS20_a01a08 FJ3652
EU747905.1 gg_id:328207 neotropical folivorous flying bird adult hoatzin crop clone hoa11_54F07 EU747
DQ015039.1 gg_id:133516 mouse cecum clone M2_c11 DQ015
FJ679958.1 gg_id:521213 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
AF202259.1 gg_id:16477 Eubacterium oxidoreducens str. G2-2 AF2022
EF097686.1 gg_id:196519 mouse cecum clone SWPT20_aaa02c09 EF0976
FJ671752.1 gg_id:532247 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6717
EU450958.1 gg_id:310414 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU450
FJ672619.1 gg_id:515002 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6726
DQ326964.1 gg_id:147198 Metagenomic gut microbiome healthy human stool clone E457 DQ326
FJ671540.1 gg_id:528645 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6715
AF202258.1 gg_id:38558 Eubacterium oxidoreducens str. DAS110 AF2022
FJ684882.1 gg_id:526046 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU504541.1 gg_id:266664 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa02b09 EU5045
DQ810115.1 gg_id:180450 human fecal clone RL184_aao68c03 DQ810

58.5	755.8	1424.1	1307.4	306.5	660.8	416.3	817.5	212.6	151.3	775.2
76.9	870.0	1334.2	1531.2	565.4	748.6	967.4	1340.7	349.2	392.1	662.9
57.9	567.6	760.9	1070.5	326.8	486.2	355.5	1375.0	257.5	358.2	368.6
645.7	2186.7	3202.2	3209.1	1837.2	2244.2	2347.0	2753.1	703.1	705.1	1819.0
210.7	1737.7	2611.0	2286.4	1484.4	1563.6	1733.1	2234.0	2125.8	1300.5	1617.0
196.0	1406.5	2829.1	1460.0	835.8	1159.6	1049.1	1286.4	713.3	522.5	1473.7
30.8	429.6	645.0	777.1	88.6	252.7	169.2	482.9	55.3	72.7	279.2
29.9	40.8	95.1	146.3	11.3	30.2	13.1	131.3	11.6	21.0	57.3
1737.6	2177.5	2263.6	2286.5	2136.5	2078.6	2298.2	2212.5	909.4	1422.5	1068.6
971.8	1008.1	1534.9	1736.8	990.4	1135.5	987.2	1583.9	804.6	487.8	864.4
57.5	275.0	175.2	189.9	125.3	248.0	183.6	206.4	77.2	135.4	87.8
132.2	1672.5	2088.9	2297.8	982.6	1370.9	1398.1	2478.6	660.5	350.2	991.3
740.6	2118.8	3024.7	3420.5	1738.8	1724.6	1697.0	2406.6	691.0	1037.4	1810.1
42.3	391.4	558.0	737.0	360.4	407.7	571.1	511.8	161.4	504.8	441.9
166.0	1940.7	2470.7	2349.2	1236.9	1344.6	1341.2	1775.3	2635.9	357.0	1232.8
693.0	2991.8	3213.1	3398.4	2480.7	2797.3	2800.7	3093.1	2896.1	2128.4	2258.4
53.8	333.5	471.5	571.1	128.1	245.6	160.7	460.6	102.2	89.2	188.6
111.0	652.8	1329.6	1497.1	149.1	270.1	166.2	386.3	138.3	131.4	392.9
693.8	2148.8	2493.3	2904.1	1899.8	2108.3	2002.9	2786.6	1169.0	1408.6	1928.6
63.0	105.5	179.0	95.0	75.8	159.6	133.2	46.6	44.6	68.9	59.7
41.5	208.5	468.9	254.1	90.4	169.1	184.4	166.0	53.5	24.7	186.0
108.2	840.4	1327.0	1301.9	814.3	994.4	926.0	1777.2	347.8	609.2	733.4
82.9	906.1	1180.0	1303.6	551.6	1318.9	697.1	1360.5	525.4	999.4	897.8
145.4	448.1	893.9	875.5	501.3	589.0	632.3	663.1	549.6	217.0	758.5
97.1	599.2	999.5	1177.3	652.8	724.0	931.4	1181.6	413.8	98.0	601.4
60.4	819.1	1333.5	1463.4	625.4	725.2	755.7	948.3	229.7	61.3	478.5
4466.8	2133.8	2945.4	2957.2	1660.2	1661.3	1789.5	2042.1	1803.0	1692.8	2317.4
65.2	929.1	1257.4	1534.6	455.3	879.3	677.6	1305.4	332.1	142.3	725.9
47.4	91.2	214.1	136.7	79.1	91.8	72.2	178.1	32.7	14.5	66.1
404.9	1730.0	1696.3	1622.2	1677.7	1657.6	1552.9	1907.6	1807.2	1470.6	1293.8
88.9	455.4	693.8	831.2	294.5	508.2	379.6	1069.2	133.4	57.7	220.6
403.7	505.5	517.0	594.4	664.4	394.8	517.0	456.9	391.1	222.9	370.3
104.8	777.4	1287.6	1528.4	1109.8	968.4	1255.9	1061.3	285.5	175.0	530.8
15005.9	6922.6	5362.9	7690.9	7498.6	6477.7	7641.0	6873.9	7191.5	5605.5	7009.9
30.5	731.4	1270.4	1211.7	508.7	924.7	660.1	1040.8	255.1	165.3	472.4
15183.8	4463.8	4039.6	4567.8	3711.2	3997.9	4413.8	4309.9	6435.2	4517.0	7078.3
6283.7	2382.9	2289.4	2505.8	1451.7	1955.4	2130.5	2312.3	2221.3	1990.1	3500.3
154.3	825.6	1564.9	1671.1	705.3	1034.8	653.0	1648.0	366.4	416.5	764.5
51.1	2264.4	2346.8	2282.7	2352.8	2736.4	2098.6	2602.8	1189.7	314.5	1163.4
4391.4	5179.7	4949.9	5623.1	4742.6	4515.3	4266.8	5326.8	4880.0	2638.9	5539.0
981.3	1826.9	3435.4	2935.4	1784.5	1657.5	2793.0	2629.8	822.2	273.5	1195.7

674.3	775.4	931.4
1676.2	1533.2	1877.0
1429.3	892.3	971.9
3695.2	2569.5	3110.6
2262.8	2071.5	1838.2
1361.3	1370.5	1113.7
400.6	376.5	634.3
75.2	88.9	34.4
2219.7	2292.4	3656.8
1933.4	1633.6	1546.8
211.6	293.9	860.0
2459.3	1600.1	2198.7
2898.1	2925.7	3385.0
602.4	631.3	699.9
1536.2	1963.7	3001.9
2930.3	2984.4	4098.1
638.2	507.7	315.9
856.2	743.9	798.1
3013.8	2405.3	3322.8
182.9	113.0	153.0
83.1	211.3	107.7
2252.8	1412.4	1510.0
1918.7	1219.0	1074.1
806.7	1002.5	1842.7
1047.1	1016.3	1174.2
1180.4	1006.3	1758.6
2439.6	3038.3	3493.4
1596.2	1007.7	1431.7
92.8	174.3	225.0
2031.0	1646.7	1909.4
1319.0	493.8	577.5
513.5	653.9	593.9
1380.3	1011.0	1294.0
6534.8	7623.6	8074.3
1332.6	1184.5	1312.2
4948.4	5142.3	4195.5
2320.2	2962.9	1869.4
1904.9	1152.1	1215.6
2996.4	2752.0	5756.8
5050.9	5534.6	4696.3
2795.1	2346.4	3383.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Lachnobacterium
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s__unclassified	19484
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s__unclassified	19723
s__unclassified	19752
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s__unclassified	19782

EU124830.1 gg_id:242741 Eubacterium rangiferina R3_91_1 EU1248
FJ363613.1 gg_id:370350 feces adult twins and mothers; TS14 clone TS14_a01d01 FJ3636
DQ815815.1 gg_id:172307 mouse cecum clone aab22f10 DQ815
DQ825322.1 gg_id:182980 human fecal clone RL185_aan88e06 DQ825
EF603794.1 gg_id:234887 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
AF371614.1 gg_id:48120 swine intestine clone p-2184-s959-3 AF3716
EU771470.1 gg_id:320066 Hamadryas Baboon feces clone AFBAB_aai02b09 EU7714
AY992989.1 gg_id:132525 mouse cecum clone C22_n03 AY9929
EU452953.1 gg_id:319558 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4529
DQ800573.1 gg_id:189216 human fecal clone RL183_aah30b02 DQ800
FJ880786.1 gg_id:421538 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU503863.1 gg_id:264345 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01g01 EU5038
EU455016.1 gg_id:341227 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4550
EU451134.1 gg_id:351978 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4511
AF396924.1 gg_id:23277 Eubacterium sp. str. C124b AF3969
AB009213.1 gg_id:14027 rumen clone RFN66 bacterium AB0092
EU774428.1 gg_id:343474 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1(EU7744
CR933122.1 gg_id:110000 Evry municipal wastewater treatment plant clone 013F01_B_SD_P15 CR9331
EU775845.1 gg_id:347744 Horse feces clone horsem_aai95b05 EU7758
AY699277.1 gg_id:106290 Lachnospira pectinoschiza M81 AY6992
EU764725.1 gg_id:331441 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7647
EU762854.1 gg_id:322408 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7628
FJ372106.1 gg_id:366903 feces adult twins and mothers; TS9 clone TS9_a01g11 FJ3721
EU774171.1 gg_id:356644 Chimpanzee feces clone CHIMP1_e07 EU7741
FJ368392.1 gg_id:369652 feces adult twins and mothers; TS3 clone TS3_a03h01 FJ3683
DQ797586.1 gg_id:197341 human fecal clone RL206_aaj13d03 DQ797
DQ823650.1 gg_id:178001 human fecal clone RL250_aaj77b04 DQ823
EU765893.1 gg_id:329161 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
EU774962.1 gg_id:318124 Flying Fox feces clone FF_a06_2 EU7749
FJ369956.1 gg_id:366229 feces adult twins and mothers; TS55 clone TS55_a02g01 FJ3699
DQ806710.1 gg_id:199421 human fecal clone RL186_aao47g12 DQ806
EU762889.1 gg_id:326533 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7628
EU762896.1 gg_id:346419 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7628
DQ796214.1 gg_id:181427 human fecal clone RL179_aah23c03 DQ796
EU768290.1 gg_id:308000 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7682
EU766675.1 gg_id:324045 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7666
DQ777931.1 gg_id:164628 rat feces clone R-1330 DQ777
EU768588.1 gg_id:314431 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7685
GQ896729.1 gg_id:555632 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do : GQ896
EU767220.1 gg_id:338700 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7672
EU764213.1 gg_id:313911 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7642

72.7	1259.7	1648.7	1667.5	843.5	908.5	1039.2	1962.7	748.0	160.7	914.5
154.3	429.1	664.1	593.2	335.0	426.2	325.8	558.1	209.4	125.2	393.4
76.3	366.6	213.4	141.4	156.7	309.1	109.0	125.9	368.0	40.7	119.8
40.2	112.2	161.9	189.3	83.3	118.6	98.9	124.4	43.5	26.9	99.2
564.8	1746.7	2323.5	2433.5	1939.3	1546.3	2309.8	1748.8	935.3	1188.7	1646.5
52.6	39.1	42.2	31.6	20.5	26.0	18.0	23.1	24.7	24.5	27.9
217.4	586.4	1008.8	1271.3	277.0	794.0	591.4	1264.4	199.6	158.6	591.7
79.7	1009.4	1420.9	1703.0	841.7	848.5	1143.4	1443.9	337.5	222.4	685.6
301.0	1818.9	2143.5	2175.6	1401.8	1492.1	1649.0	1882.8	1099.8	934.0	1551.3
13228.2	4248.4	3701.8	3637.3	3844.5	3719.6	3523.9	3753.0	4275.1	4450.8	4310.3
318.3	2310.6	3000.4	3797.4	1906.5	1625.7	1902.1	2120.5	1015.8	1067.0	1563.8
3151.9	2096.3	2607.7	3587.8	2042.5	1677.8	1889.5	2042.6	1969.1	1362.3	1600.3
380.4	2114.3	2089.6	2208.9	2123.0	2144.8	2049.1	2353.5	1375.1	1397.8	1551.5
11975.0	4707.3	4375.4	4584.6	4075.9	4149.2	4557.5	4231.0	5247.6	3408.2	5010.6
1327.8	831.5	1089.1	902.0	734.4	755.0	865.9	1230.3	923.8	1093.4	910.2
47.5	95.1	97.3	114.8	102.9	84.0	125.9	162.5	45.1	34.9	56.1
46.4	1548.9	1840.5	2003.5	1083.0	1409.2	845.3	1791.6	814.1	553.8	1139.7
2849.9	923.5	1022.2	1077.2	565.4	743.8	630.0	1231.1	457.0	280.2	1296.7
374.2	5476.8	5645.1	5355.6	2411.7	4715.8	4599.5	5044.6	6209.2	4394.6	5975.8
94.8	44.2	508.7	476.0	792.1	518.0	720.0	575.3	290.7	279.0	230.4
6839.6	5435.9	5424.7	5571.0	5529.5	6327.2	6354.9	5266.2	7024.5	5492.8	7272.3
83.9	318.9	709.9	613.8	288.5	403.1	312.3	884.5	223.9	327.3	325.7
54.6	1841.2	1776.6	1734.3	1807.6	2044.8	1819.0	2124.8	3114.3	2315.4	1320.0
7654.2	4566.1	4522.4	4705.0	4392.6	4711.9	4538.6	4494.2	8556.0	5542.8	5935.1
6605.1	1417.5	1485.6	1942.5	1480.6	1820.4	1581.8	1558.2	1998.4	1814.2	2241.8
245.0	794.6	1026.3	985.0	744.0	804.0	1497.6	1304.8	454.7	598.6	621.4
324.9	979.8	1720.3	1755.2	618.4	1405.2	1407.4	2148.5	489.0	381.5	2076.8
3369.4	1658.6	1691.8	1633.4	1283.7	1407.4	1811.5	1507.8	2068.3	1691.4	1722.1
8003.9	4543.6	4900.3	4393.1	3769.5	3962.4	1774.1	3921.2	5095.2	3728.3	5401.7
6045.2	4119.4	3697.7	3828.8	3627.6	3596.9	3751.0	3316.2	5697.8	3959.6	4078.0
447.7	1405.9	2467.1	1996.6	2278.3	1996.3	227.4	2001.2	1582.1	1115.7	1290.6
6595.8	2869.3	2582.0	2652.4	2647.3	2726.8	3274.5	3308.8	2884.6	3653.4	2456.0
1079.7	3470.5	3336.6	3152.3	3846.8	3018.4	3634.1	2862.4	4836.1	3390.7	2416.1
48.7	25.7	22.2	25.1	22.0	25.7	21.8	23.1	27.4	23.6	20.2
1234.9	4840.2	5248.1	4457.0	4004.7	4597.7	4606.6	5269.8	5379.8	3267.3	5344.3
442.1	1445.0	1900.3	2177.1	1198.6	1510.6	1237.5	2562.9	960.8	1232.7	1151.9
111.1	2056.7	3048.9	3170.7	1604.5	2213.9	2105.8	2680.8	1221.7	1116.3	1871.9
2180.5	1868.1	2889.5	2814.3	1494.6	1937.2	1936.7	2817.4	2039.6	1240.9	2566.1
14660.0	4299.2	3873.9	4485.3	5004.5	4468.5	5201.5	6004.3	4932.7	5070.9	6626.3
526.8	59.2	185.1	172.8	91.9	95.5	100.7	244.5	60.9	39.3	107.0
196.3	860.0	1033.9	1135.7	460.4	721.2	626.0	1340.1	276.6	178.3	637.6

1773.1	1553.7	2443.6
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71.7	126.6	70.1
140.4	199.3	148.5
1953.1	2466.7	2847.0
26.4	39.2	48.8
1573.6	872.6	1176.6
1430.0	1204.0	3001.5
2155.1	1729.5	2856.7
5664.5	5479.5	3956.3
2948.4	2836.8	3899.3
2127.4	2006.0	2714.1
2402.1	2333.7	3769.1
4514.8	4522.8	5866.6
1341.4	1344.3	815.7
100.9	112.8	121.6
1710.1	1948.4	1751.8
916.4	1091.0	787.6
4805.5	2913.9	2638.0
594.7	699.5	629.4
4405.9	8222.4	5595.1
630.0	821.0	575.7
1403.6	1737.0	1537.5
4404.4	5966.6	5201.6
1193.1	2444.0	1379.7
797.7	1437.8	1409.6
1968.2	1121.1	1606.5
1337.8	2366.8	2142.0
3903.0	4327.4	4280.5
3352.4	4986.6	4103.3
1816.1	1984.6	1923.3
2953.0	2972.8	3412.7
2742.4	4128.0	3043.6
26.7	35.6	25.0
3786.3	4323.9	3569.0
3009.2	2248.4	2080.9
3180.3	2541.2	2683.6
2797.9	2698.7	2634.1
4063.3	5674.3	5135.7
393.5	162.5	107.7
1286.4	1038.9	1392.1

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Lachnospira
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DQ905269.1 gg_id:173712 human fecal clone 013-h10 DQ905
AY984236.1 gg_id:115781 human stool clone B127 AY9842
DQ809979.1 gg_id:191888 human fecal clone RL184_aao66f05 DQ809
AY985110.1 gg_id:117562 human stool clone BB29 AY9851
AY984128.1 gg_id:127670 human stool clone B006 AY9841
EU764940.1 gg_id:345064 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7649
FJ364464.1 gg_id:364002 feces adult twins and mothers; TS15 clone TS15_a03c07 FJ3644
EU764204.1 gg_id:306597 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7642
EF401947.1 gg_id:210023 human fecal clone SJTU_B_01_68 EF4019
AY985042.1 gg_id:117998 human stool clone BA47 AY9850
EU764772.1 gg_id:313876 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
EU762935.1 gg_id:308990 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU7629
FJ368313.1 gg_id:368585 feces adult twins and mothers; TS3 clone TS3_a02g09 FJ3683
AY978042.1 gg_id:115457 human cecum mucosal biopsy clone LH86 AY9780
AY985080.1 gg_id:119690 human stool clone BA91 AY9850
DQ809187.1 gg_id:180837 human fecal clone RL308_aal83a10 DQ809
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FJ368843.1 gg_id:367761 feces adult twins and mothers; TS4 clone TS4_a01c05 FJ3688
EF403111.1 gg_id:210835 human fecal clone SJTU_B_09_55 EF4031
FJ372341.1 gg_id:358191 feces adult twins and mothers; TS9 clone TS9_a04e02 FJ3723
DQ794864.1 gg_id:198909 human fecal clone RL310_aam37c06 DQ794
AY977819.1 gg_id:116949 human cecum mucosal biopsy clone LF12 AY9778
EU764742.1 gg_id:317221 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
GU269544.1 gg_id:580185 Lactobacillus rogosae str. ATCC 27753 GU269
FJ364997.1 gg_id:361723 feces adult twins and mothers; TS1 clone TS1_a01f05 FJ3649
AF371643.1 gg_id:46667 swine intestine clone p-268-o5 AF3716
AF371645.1 gg_id:33320 swine intestine clone p-1692-b3 AF3716
EU763400.1 gg_id:306126 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7634
GQ079268.1 gg_id:403144 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230e1 GQ079
EU775973.1 gg_id:350865 Spotted hyena feces clone HY2_d06_1 EU7759
EU763204.1 gg_id:316227 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU7632
AY984967.1 gg_id:122272 human stool clone B958 AY9849
AY981468.1 gg_id:118941 human sigmoid colon mucosal biopsy clone L567 AY9814
EU763791.1 gg_id:337443 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7637
EU763637.1 gg_id:336435 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
DQ797159.1 gg_id:181148 human fecal clone RL386_aao87f12 DQ797
EF405098.1 gg_id:213526 human fecal clone SJTU_G_07_89 EF4050
EU776399.1 gg_id:323020 Red Kangaroo feces clone KO2_aai17c03 EU7763
AY984574.1 gg_id:122511 human stool clone B514 AY9845
EU764099.1 gg_id:320038 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7640

195.7	1643.0	1846.8	1789.1	1922.5	1585.9	2948.1	2011.2	952.3	1432.6	1226.6
79.6	2787.1	2476.8	2162.3	1410.6	2178.2	2086.0	2583.2	2544.3	1355.7	2080.0
41.1	511.9	821.0	991.9	167.8	402.4	281.7	993.0	207.5	445.5	286.6
13084.5	4525.2	4735.6	3017.0	5177.0	5194.3	4992.6	5252.7	6841.0	5452.5	6344.0
58.4	685.9	914.8	1093.5	929.5	642.9	1346.4	797.1	510.1	550.4	950.8
10689.6	5849.2	5005.6	5022.7	4724.9	5145.4	4416.5	5426.6	5474.2	6291.7	3625.9
1851.9	2988.0	4509.4	4226.4	3875.8	4300.0	3765.7	4760.2	3406.9	4326.6	2997.3
717.0	2387.9	2462.6	2309.1	1911.6	1990.3	2306.3	2580.7	4105.6	2650.7	2931.0
39.8	34.9	95.9	74.5	22.6	152.9	30.6	83.0	22.1	13.6	56.1
24.9	401.0	744.1	533.6	159.4	389.7	273.4	1279.2	167.0	150.1	327.3
8380.1	7457.9	7411.7	7596.1	6706.8	6628.9	7750.9	7396.7	8174.4	4601.0	7672.5
6976.6	3984.6	3883.8	3494.5	3319.5	3490.6	3773.7	3459.8	5195.1	6258.8	3456.6
216.3	547.6	614.7	744.5	390.0	479.3	306.1	618.8	283.2	97.0	310.4
54.4	383.3	602.9	484.6	262.7	430.8	268.3	483.2	208.2	284.4	281.4
48.8	1406.2	991.6	1074.9	111.9	1054.8	649.3	995.1	859.8	1270.9	501.8
1742.1	3339.4	4144.7	3965.6	2559.8	3204.1	3026.4	3972.4	2064.1	830.2	3637.4
56.0	154.6	203.0	221.4	66.5	155.9	72.4	320.5	46.2	43.9	90.6
8867.7	2657.0	2767.2	3538.2	2303.4	2897.7	2700.1	2666.7	3943.7	5564.7	3889.4
169.8	1893.7	2822.0	1678.5	1152.4	1688.6	1369.7	2147.2	1795.3	1640.8	2284.5
39.3	221.9	422.8	548.8	138.9	188.4	286.1	394.6	301.7	212.1	114.8
223.2	2574.5	1736.5	2356.6	1841.0	2692.5	2068.7	2562.7	1764.4	1966.4	1692.6
36.2	212.2	308.8	434.6	277.1	378.9	166.2	432.4	78.1	86.4	121.1
29.4	136.4	263.5	211.6	85.1	181.7	85.5	401.0	56.9	37.3	117.0
63.4	2538.3	3344.3	2826.2	2757.7	2256.6	2347.2	3637.9	1269.3	2078.9	1632.8
2920.5	4184.2	4510.9	4790.3	2315.9	3338.2	2969.5	4794.3	4058.5	1014.8	3318.4
498.4	356.2	503.7	527.1	140.2	304.5	337.0	358.8	387.5	355.3	487.6
15582.5	5653.5	5992.1	6477.1	5207.6	4966.6	6061.0	5422.7	7815.5	6810.0	6823.9
172.4	341.4	451.1	503.0	180.7	233.6	182.2	367.4	121.2	56.1	259.4
112.4	318.6	418.1	506.9	193.2	413.5	289.5	993.6	139.8	137.4	265.6
37.4	1422.9	1803.5	2105.9	756.2	1325.6	1085.0	1954.0	403.5	291.7	1532.8
395.5	880.1	1422.6	1456.8	864.1	1074.4	831.1	1505.9	502.0	604.5	802.8
34.4	694.3	1056.7	1610.2	353.9	850.1	502.0	1647.5	454.0	216.6	503.3
1094.9	1416.8	1429.7	1875.9	1379.5	1513.2	1894.7	1644.3	1064.1	603.7	965.5
1655.0	3276.9	3972.9	4123.1	4916.1	4376.8	4064.7	4760.1	4221.0	3586.8	3155.8
4179.5	1216.7	1477.0	1666.6	1155.7	1584.7	1233.2	1619.8	1389.5	478.9	1524.9
7330.5	3163.4	3318.9	4864.0	479.5	3135.0	3179.0	4003.5	3794.6	2657.0	3681.7
2208.4	1240.8	1410.9	1290.7	1310.8	1402.2	1227.6	1378.8	991.4	1954.6	973.8
37.0	418.0	427.6	530.3	198.3	260.8	306.2	669.4	199.6	109.4	275.9
583.0	1449.2	2054.3	1753.1	1142.7	1452.1	1303.5	1639.4	793.8	329.5	1452.0
3639.5	1066.2	1043.4	1120.3	679.3	573.8	1204.5	2090.8	1197.5	1137.6	848.8
45.0	482.3	818.6	848.9	257.3	825.0	421.6	1315.6	203.5	240.9	685.8

1451.3	2278.1	3316.2
1863.2	2168.5	3194.8
980.2	738.5	602.8
4134.5	5466.0	4530.3
605.2	144.8	1331.0
6136.5	5898.0	4551.1
3501.3	4550.2	4832.1
2069.2	2725.4	2343.6
99.1	88.2	64.0
1931.8	524.3	851.6
7056.8	8025.9	7811.0
3594.7	5018.2	3725.8
367.2	576.0	359.7
459.0	565.9	594.5
1242.7	716.6	1058.1
4154.8	3397.2	5088.7
282.2	335.8	284.5
2773.2	3997.7	2525.4
1107.4	2722.9	2046.9
344.8	530.1	140.5
2350.6	2083.5	2642.6
569.0	449.3	440.3
441.8	172.4	247.8
4411.7	3266.4	3049.7
5453.7	3423.9	4028.3
352.1	585.8	333.7
5953.2	5672.1	7276.2
439.2	538.2	214.8
1028.8	631.9	889.6
1754.7	1769.8	3632.1
1479.0	1802.8	1849.8
1681.9	1134.2	1737.1
1358.7	1772.1	1463.6
4314.3	5154.0	4688.7
1767.1	1702.3	1731.6
4507.0	4061.4	3816.3
1512.4	2257.9	2011.1
496.9	401.0	502.8
1561.2	2400.7	2046.5
1944.9	1863.3	1303.7
1305.2	442.5	632.2

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU768746.1 gg_id:310660 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU764783.1 gg_id:348687 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EF403988.1 gg_id:216944 human fecal clone SJTU_C_03_25 EF4039
EF098210.1 gg_id:188538 mouse cecum clone SWPT14_aaa03b02 EF0982
EU457079.1 gg_id:315578 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EU006207.1 gg_id:235351 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF099065.1 gg_id:197605 mouse cecum clone SWPT2_aaa01g04 EF0990
EU503939.1 gg_id:261265 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03a04 EU5039
EF604796.1 gg_id:229388 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
GQ079602.1 gg_id:411792 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231g GQ079
FJ983011.1 gg_id:411796 Aspects Oral Microbiome root canal clone FJ9830
AY278618.1 gg_id:86715 Lachnospiraceae genomosp. C1 AY278
GU304388.1 gg_id:541114 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU304566.1 gg_id:538862 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU381462.1 gg_id:262031 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
GQ026254.1 gg_id:378008 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
GU303144.1 gg_id:560505 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
GU302622.1 gg_id:533634 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU843160.1 gg_id:313325 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ000726.1 gg_id:469291 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ000
FJ557577.1 gg_id:526062 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5575
NR_029097.1 gg_id:546988 Oribacterium sinus str. AIP 354.02; CIP 107991 NR_02
FJ577249.2 gg_id:571357 Oribacterium sp. oral taxon 078 str. F0262 FJ5772
FJ557800.1 gg_id:524676 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
AF481222.1 gg_id:55615 oral endodontic infection clone MCE10_236 AF4812
EU557017.1 gg_id:343309 Detection microorganisms involved infectious endocarditis cultivation techniques inf EU557
AM697318.1 gg_id:225814 sequencing libraries indoor dust clone BF0002C015 AM697
FJ577261.2 gg_id:566635 Oribacterium sinus str. F0268 FJ5772
FJ557719.1 gg_id:528375 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
X95893.1 gg_id:14046 Pseudobutyrivibrio ruminis str. DSM 9787 X95893
AJ428549.1 gg_id:18666 Pseudobutyrivibrio ruminis str. JK 626 AJ4285
U77337.1 gg_id:14054 Butyrivibrio fibrisolvens str. AR27 U7733
AY347530.1 gg_id:92464 Butyrivibrio fibrisolvens str. 0/10 AY3475
AB004910.1 gg_id:14048 Butyrivibrio fibrisolvens str. T63 Bovine rumen AB0049
AF202262.1 gg_id:26725 Pseudobutyrivibrio ruminis str. pC-XS7 AF2022
EU259460.1 gg_id:252825 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC84 EU2594
AB009190.1 gg_id:14062 rumen clone RFN34 bacterium AB0091
EU850527.1 gg_id:314838 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF314 EU8505
AF202260.1 gg_id:19835 Pseudobutyrivibrio ruminis str. pC-XS2 AF2022
AB494819.1 gg_id:532771 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
EU381773.1 gg_id:261201 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381

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48.8	518.0	865.6	1143.4	207.4	497.4	267.5	827.4	248.3	129.2	356.5
38.6	185.1	296.0	417.7	104.7	152.2	161.3	240.6	61.6	37.4	90.8
87.6	3324.9	5397.8	3773.1	2830.8	4042.0	2438.9	6262.7	2898.9	6081.8	3216.8
3433.2	4736.0	6277.5	5776.6	3901.6	4248.7	4494.5	4384.6	4792.5	906.3	6123.4
5728.5	3432.9	5005.8	4528.3	3104.0	4128.7	2465.0	4343.8	5746.3	5648.7	3635.0
943.9	1404.5	1591.6	1445.3	1266.9	1139.1	1603.6	1388.2	1291.9	887.5	1961.1
54.6	965.7	1689.6	1452.5	596.4	1040.3	971.5	1497.0	421.3	166.0	763.5
7697.3	5227.2	6091.9	6088.7	5406.3	5779.2	5871.2	5692.9	6313.3	4332.6	6720.5
71.4	484.5	1259.0	1075.7	1015.2	588.8	943.3	750.1	382.9	113.4	581.5
1748.1	1483.0	1963.7	2016.7	995.3	1710.1	1732.1	2144.0	1221.6	748.5	1488.3
11117.0	5923.0	6135.9	6260.0	5639.7	5563.7	6878.0	5752.0	6316.0	6228.3	6637.9
111.3	2535.5	3619.5	2107.6	1508.1	1898.7	2099.2	2614.7	1391.5	826.3	1779.9
5678.4	2855.5	4068.5	3033.5	2973.7	3012.9	3571.9	3744.8	2187.3	1162.2	2588.1
76.1	594.2	1759.5	978.1	426.7	1002.0	704.8	1209.5	250.8	486.2	766.7
36.3	266.2	472.7	485.4	65.3	178.1	177.0	300.8	64.8	43.8	131.5
374.3	939.3	2177.2	1517.7	503.8	1001.8	846.4	1450.8	312.2	267.7	675.0
36.4	233.3	478.5	540.3	134.0	96.4	114.9	218.5	70.4	31.1	97.7
1244.9	2056.6	2808.6	2249.9	1882.4	2309.9	1919.6	2013.6	1263.3	1053.8	3015.9
251.4	2647.7	3239.5	3399.5	2841.9	2997.0	4040.9	3500.4	1576.1	864.1	2904.1
565.9	543.3	934.3	799.2	411.5	723.2	511.5	1362.0	287.4	222.9	363.4
64.7	876.5	1318.4	1544.6	1175.3	969.1	1265.2	1488.7	458.9	278.1	660.6
76.0	1317.1	1955.3	2508.9	668.8	1146.3	1107.0	2411.8	612.5	156.4	1691.6
1514.3	2515.9	2604.5	3209.6	2928.0	2705.7	3763.1	3399.2	2960.7	259.1	3418.2
5213.3	2695.6	3297.8	4173.7	4101.1	3146.5	3340.5	4713.4	1512.1	652.8	2870.0
1699.4	3422.0	3106.2	3465.1	3100.4	2888.4	4201.9	3221.1	2383.0	1973.8	2739.0
4186.6	1292.1	1608.1	1951.4	1356.0	1441.9	1151.5	2078.4	783.5	286.2	1349.0
75.1	932.6	1366.2	1779.5	1222.3	1009.4	1327.5	1642.2	436.7	277.8	881.5
505.1	2632.3	3476.0	3563.4	2092.8	2748.5	2311.3	3634.5	1484.2	938.0	1842.0
333.5	1551.8	1898.7	1948.7	1240.1	1211.5	1047.4	1603.9	740.7	182.9	2026.2
3232.8	1885.2	1955.5	2153.2	1490.5	1565.7	1441.1	1842.5	2038.5	1270.7	1927.4
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19238.8	4117.0	4328.1	5198.1	4707.0	4394.7	5382.9	4604.6	5343.9	6453.7	6256.0
44.8	825.7	1273.2	1184.2	472.7	781.2	706.8	1090.4	262.0	255.9	834.1
41.5	1856.8	2265.0	2048.9	802.2	1849.3	1160.5	2258.7	806.8	270.1	1392.9
53.0	493.7	769.0	877.5	210.4	569.4	515.1	950.9	160.9	95.1	394.5
35.3	1634.2	2362.3	2690.7	304.3	730.5	488.4	1296.1	166.6	158.9	985.0
34.5	891.8	1250.9	1059.9	520.3	965.9	732.9	1110.4	383.2	453.8	731.8
41.7	512.6	724.9	834.4	127.7	291.5	182.5	802.1	117.8	154.0	513.3
137.3	1721.3	2464.7	2588.8	1065.8	1632.7	1362.5	2672.1	741.9	482.9	1788.5

466.4	672.9	844.8
859.9	729.9	392.3
251.6	288.3	265.8
4310.3	3954.4	5954.3
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3932.8	4297.8	4784.2
1384.6	1369.7	1640.2
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1948.2	2427.6	1887.2
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1986.9	1912.1	3789.8
4460.7	2781.3	5663.8
1328.7	1031.6	2606.0
345.3	458.9	336.8
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2629.6	2714.5	2873.1
3437.2	4366.8	5517.0
1570.1	1293.8	1684.2
1850.8	1296.1	1513.6
2242.2	1644.9	2050.0
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3039.0	3537.3	3361.0
2755.4	1953.3	1685.7
2312.7	1250.3	1679.0
4400.1	2785.2	3668.7
2352.9	1267.6	2449.0
1959.8	3218.8	1628.0
583.4	598.0	666.3
5035.2	3580.4	5179.2
5499.3	6183.6	6214.3
1162.9	699.2	959.0
1949.3	1702.6	2478.3
1252.5	396.9	535.1
1582.4	1069.8	1408.2
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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s__Eubacterium rectale	17444

AJ518873.1 gg_id:110723 Lachnobacterium sp. str. wal 14165 AJ5188
FJ189565.1 gg_id:324159 digester anaerobic sludge clone EUB_44 FJ1895
AB494897.1 gg_id:548133 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB4948
EU714407.1 gg_id:558581 Butyrivibrio sp EU7144
EF436347.1 gg_id:214287 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC61 EF4363
U41167.1 gg_id:14040 Butyrivibrio fibrisolvens str. 49 U4116
U77339.1 gg_id:14045 Butyrivibrio fibrisolvens str. H10b U7733
EU850519.1 gg_id:352051 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF296 EU850
X89979.1 gg_id:14063 Butyrivibrio fibrisolvens str. NCDO 2397 X89979
DQ326446.1 gg_id:147832 Metagenomic gut microbiome healthy human stool clone C516 DQ326
EU850564.1 gg_id:316947 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF374 EU850
AJ250365.2 gg_id:45953 Butyrivibrio fibrisolvens str. 16.4 human feaces AJ2503
U41169.1 gg_id:14058 Butyrivibrio fibrisolvens str. OB189 U4116
FJ189567.1 gg_id:333967 digester anaerobic sludge clone EUB_46 FJ1895
AF105403.1 gg_id:14049 Butyrivibrio fibrisolvens str. LP1265 AF1054
DQ673524.1 gg_id:164682 rumen fluid clone GRC59 DQ673
AF264034.1 gg_id:36852 Butyrivibrio cf. fibrisolvens EAT6 AF2640
EF400193.1 gg_id:206647 human fecal clone SJTU_E_10_11 EF4001
EU381442.1 gg_id:266929 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3814
AF202261.1 gg_id:74850 Pseudobutyrivibrio ruminis str. pC-XS6 AF2022
AY699284.1 gg_id:102017 Pseudobutyrivibrio ruminis M80 AY6992
AJ428550.1 gg_id:21769 Pseudobutyrivibrio xylanivorans str. JK 23/2 AJ4285
AY699285.1 gg_id:102170 Pseudobutyrivibrio ruminis L4 AY6992
EU381523.1 gg_id:263930 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3815
AY981718.1 gg_id:122818 human sigmoid colon mucosal biopsy clone LA93 AY9817
GQ079203.1 gg_id:440226 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229g GQ079
EU466812.1 gg_id:301799 African elephant feces clone AFEL2_aao29g08 EU4668
DQ808014.1 gg_id:191640 human fecal clone RL180_aan70f09 DQ808
FJ363716.1 gg_id:366125 feces adult twins and mothers; TS14 clone TS14_a02d10 FJ3637
FJ364199.1 gg_id:364692 feces adult twins and mothers; TS150 clone TS150_a04b04 FJ3641
FJ364099.1 gg_id:364744 feces adult twins and mothers; TS150 clone TS150_a03a03 FJ3640
AY978397.1 gg_id:122629 human transverse colon mucosal biopsy clone F381 AY9783
FJ368518.1 gg_id:361275 feces adult twins and mothers; TS49 clone TS49_a01c08 FJ3685
DQ801440.1 gg_id:187047 human fecal clone RL388_aao95e10 DQ801
DQ795403.1 gg_id:175682 human fecal clone RL178_aah53h10 DQ795
FJ370978.1 gg_id:358935 feces adult twins and mothers; TS5 clone TS5_a03e04 FJ3709
FJ364642.1 gg_id:364428 feces adult twins and mothers; TS19 clone TS19_a01d02 FJ3646
DQ794462.1 gg_id:198095 human fecal clone RL197_aah88b11 DQ794
FJ684267.1 gg_id:524363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ363938.1 gg_id:365290 feces adult twins and mothers; TS150 clone TS150_a01b05 FJ3639
DQ795520.1 gg_id:180861 human fecal clone RL178_aan65f01 DQ795

48.2	256.8	215.7	206.9	59.5	136.8	79.1	134.1	222.6	22.0	100.5
39.5	908.2	1586.4	1352.5	434.6	854.2	608.0	1244.4	338.6	190.2	838.3
233.0	2202.4	3274.5	3041.1	2407.9	2334.1	1953.9	2796.2	1095.9	1014.6	925.8
126.5	636.2	988.4	1046.6	362.8	680.8	570.3	950.7	229.3	132.8	538.3
42.1	144.5	246.1	289.7	146.9	208.6	230.8	167.6	81.4	27.9	130.3
43.0	561.3	1203.6	1314.8	433.4	840.2	517.0	882.6	161.9	151.6	405.6
34.6	936.5	1464.9	1460.7	394.0	959.3	632.3	1271.7	334.6	127.5	796.8
61.4	918.9	1463.2	1881.7	698.1	1045.0	681.2	1432.6	527.9	143.2	889.3
47.7	996.9	1526.4	1532.9	458.0	1039.1	922.8	1357.9	389.4	159.1	907.3
145.2	481.7	653.6	852.4	744.0	585.4	648.4	804.2	471.0	103.8	376.7
50.5	905.4	1451.2	1465.0	535.2	823.9	759.2	1357.1	257.6	231.4	880.9
24.8	274.7	569.5	682.9	161.5	360.2	252.8	462.1	114.7	36.3	477.7
31.9	333.4	405.1	497.4	286.2	383.8	475.2	694.6	144.9	720.0	410.4
143.4	1260.3	2054.4	1620.7	746.0	1112.1	928.0	1745.2	590.0	1173.0	1456.3
67.9	1394.2	1612.1	1793.3	614.9	1616.2	1140.8	1913.7	781.0	176.8	1206.3
112.5	763.9	1165.0	1170.2	626.8	762.8	765.6	1051.3	280.8	137.3	660.8
12354.0	3237.7	3265.1	3648.9	2159.3	3130.4	3038.3	3934.8	3056.9	2589.7	3841.1
187.1	770.1	793.4	869.0	510.5	514.8	623.8	897.4	514.5	316.7	459.1
44.6	448.3	680.9	553.7	307.1	408.0	461.3	734.6	244.8	129.0	471.8
26.8	292.2	626.3	604.7	302.0	378.5	381.8	660.6	343.7	78.4	265.5
183.9	2316.9	3161.7	3213.2	1669.9	2286.1	2248.4	2526.9	906.2	993.8	2099.0
3231.5	1516.3	1437.6	1538.9	1433.6	1221.2	1541.8	1418.9	2017.2	1667.8	1836.5
41.8	37.5	29.6	24.0	28.3	45.9	17.9	31.0	26.3	19.3	22.0
68.1	2275.0	3392.8	3360.3	1081.4	2054.1	1440.9	3404.8	1118.4	933.5	2951.3
6671.7	3322.5	3293.8	3462.9	2747.6	3429.0	3895.4	3288.8	4128.0	3239.4	4239.1
4628.6	6061.5	5983.2	5996.4	4687.6	5966.4	6135.4	5902.4	7374.1	7489.4	6494.2
20297.6	8688.2	8076.9	7786.1	7074.4	7926.4	8801.2	8280.8	9997.4	7789.8	10013.4
1021.7	899.7	1306.4	1513.3	875.4	747.0	967.4	1498.7	688.1	274.2	664.3
37.2	316.4	600.3	589.7	188.9	579.9	220.2	414.9	88.4	1251.1	213.1
49.5	122.2	237.5	274.8	103.0	203.3	147.9	250.1	28.8	294.5	100.0
2182.9	2757.4	3150.9	2836.9	2259.3	3047.2	2493.8	2452.0	3633.3	4161.7	3505.7
38.6	175.1	289.2	254.6	368.0	190.2	300.9	237.3	74.0	53.0	109.9
93.7	1021.1	1401.3	1657.9	1331.9	1299.0	1839.7	1614.6	492.7	946.7	750.1
35.4	112.3	111.4	93.4	81.7	65.9	156.7	74.6	58.2	29.7	43.1
1326.1	2598.3	1863.6	2333.0	1090.5	1229.9	1132.7	1918.3	892.7	638.7	1613.1
40.1	98.2	252.6	493.4	55.4	83.2	73.3	229.2	26.9	24.2	43.2
19111.4	6004.9	5692.5	5826.1	6015.3	5473.1	5943.0	5377.1	7731.9	7879.0	8104.3
52.4	1408.0	1375.5	1559.7	1236.9	1405.8	2049.9	1763.8	1099.4	1448.9	564.6
41.1	202.6	480.2	426.1	112.1	293.3	164.1	352.7	61.6	132.8	123.5
54.3	1009.3	1411.9	1290.3	752.5	1495.3	800.4	1077.0	592.3	2112.4	673.5
850.7	1515.1	2117.8	2125.0	1957.4	1407.5	1907.0	2231.6	1261.2	1101.8	1855.9

228.0	82.8	68.8
1306.0	1151.6	1131.4
2625.7	2431.1	5504.2
1158.5	788.5	843.3
167.8	347.2	705.8
773.6	878.2	1360.7
1182.4	845.2	1289.0
1732.7	1076.0	1359.3
2090.6	752.4	1159.0
893.2	816.1	837.3
1593.9	821.5	1010.5
225.4	234.7	378.4
629.4	400.1	516.8
1496.6	1496.7	1530.4
2384.7	1162.3	1668.6
1235.8	1048.4	1164.5
4261.4	3850.3	4196.1
861.4	1079.4	705.7
615.2	502.1	508.9
864.8	477.1	813.1
3119.7	2588.1	3524.6
1079.1	2716.0	1276.1
49.0	39.7	52.1
3678.0	2208.0	2877.2
3193.0	3398.7	3589.8
5791.6	6240.1	6017.0
7663.7	9495.8	7872.6
1153.2	2797.4	1084.4
792.8	448.5	459.2
497.9	166.6	237.6
2712.5	2783.6	2175.4
226.7	306.6	310.2
2022.6	1086.1	1666.5
61.6	134.9	380.5
1848.8	2276.3	2189.2
456.0	283.9	162.0
5375.5	6529.4	5529.5
1609.8	1448.5	1624.1
919.6	271.8	325.5
1453.1	1314.6	1177.0
2168.5	2644.6	1882.9

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

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Roseburia
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s__Eubacterium rectale	17446
s__Eubacterium rectale	17447
s__Eubacterium rectale	17448
s__Eubacterium rectale	17452
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s__Eubacterium rectale	17521
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s__Eubacterium rectale	17534

FJ364556.1 gg_id:367193 feces adult twins and mothers; TS15 clone TS15_a04d02 FJ3645
FJ679964.1 gg_id:529974 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
AY976130.1 gg_id:117542 human ascending colon mucosal biopsy clone LV14 AY976
FJ371875.1 gg_id:357002 feces adult twins and mothers; TS8 clone TS8_a03c02 FJ3718
DQ808157.1 gg_id:187482 human fecal clone RL180_aao73c12 DQ808
AY979857.1 gg_id:122721 human rectum mucosal biopsy clone E057 AY979
DQ794838.1 gg_id:177582 human fecal clone RL310_aam37a02 DQ794
DQ800915.1 gg_id:194884 human fecal clone RL387_aao89c04 DQ800
FJ364158.1 gg_id:362914 feces adult twins and mothers; TS150 clone TS150_a03f08 FJ3641
EU764351.1 gg_id:334650 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
DQ805790.1 gg_id:198020 human fecal clone RL306aal91b02 DQ805
FJ371251.1 gg_id:363990 feces adult twins and mothers; TS6 clone TS6_a02g04 FJ3712
FJ369440.1 gg_id:360757 feces adult twins and mothers; TS50 clone TS50_a04e07 FJ3694
FJ371774.1 gg_id:367085 feces adult twins and mothers; TS8 clone TS8_a02a10 FJ3717
FJ364188.1 gg_id:370117 feces adult twins and mothers; TS150 clone TS150_a04a04 FJ3641
EU767090.1 gg_id:327648 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
EU767068.1 gg_id:349303 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ801829.1 gg_id:190224 human fecal clone RL201_aai47d05 DQ801
DQ798542.1 gg_id:192358 human fecal clone RL181_aan98a06 DQ798
FJ684023.1 gg_id:530357 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
DQ802220.1 gg_id:185239 human fecal clone RL241_aaj04f07 DQ802
FJ684345.1 gg_id:522356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
EU764528.1 gg_id:318888 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU466840.1 gg_id:291245 African elephant feces clone AFEL2_aao30b12 EU466
DQ794811.1 gg_id:181538 human fecal clone RL240_aaj32f08 DQ794
EU763453.1 gg_id:306351 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ365494.1 gg_id:360494 feces adult twins and mothers; TS20 clone TS20_a03e08 FJ3654
EU766711.1 gg_id:322225 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ327015.1 gg_id:146118 Metagenomic gut microbiome healthy human stool clone E516 DQ327
DQ802105.1 gg_id:195859 human fecal clone RL241_aaj03b06 DQ802
DQ795257.1 gg_id:196798 human fecal clone RL178_aah52b06 DQ795
DQ824892.1 gg_id:198763 human fecal clone RL185_aao70f03 DQ824
FJ367156.1 gg_id:367005 feces adult twins and mothers; TS28 clone TS28_a04b08 FJ3671
DQ809314.1 gg_id:192285 human fecal clone RL184_aah19b02 DQ809
EU771586.1 gg_id:304401 African elephant feces clone AFEL2_aao31f01 EU771
FJ366967.1 gg_id:368053 feces adult twins and mothers; TS28 clone TS28_a01h06 FJ3669
DQ795483.1 gg_id:193808 human fecal clone RL178_aah54h08 DQ795
EU768273.1 gg_id:328685 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
GQ038693.1 gg_id:399803 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu521f01 GQ038
EU762799.1 gg_id:303965 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU762
EU767159.1 gg_id:352608 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767

6539.0	3215.3	3691.7	3876.5	3682.7	3685.0	3190.2	3708.1	2518.8	3416.6	2972.8
40.4	182.1	370.2	426.6	110.8	266.8	236.8	416.1	37.9	32.3	137.8
11101.0	3876.8	4135.6	4495.7	3562.1	3785.3	4507.9	4130.7	4484.6	4620.1	4147.6
1286.3	3392.4	4016.8	4015.4	2608.2	3452.8	3366.0	3506.7	3068.7	2536.7	3209.2
45.4	704.9	1325.5	1299.3	263.1	927.6	444.7	2005.8	332.8	211.7	692.6
106.7	717.3	182.1	630.1	597.6	679.4	692.3	791.9	1243.1	807.1	896.8
75.5	416.1	756.0	600.8	214.9	435.0	172.4	643.6	92.0	175.3	255.9
12396.3	4742.5	4842.2	4976.7	4824.1	4570.0	5174.4	4368.0	8299.1	6334.1	7051.9
411.6	5355.3	4007.8	2881.5	2376.3	3567.9	2763.5	3098.6	5272.1	6635.9	3499.8
68.3	643.9	954.6	965.0	156.2	593.1	279.2	1133.2	317.3	201.9	583.5
17508.0	8797.9	7740.9	8545.6	7290.1	7244.8	8194.7	7259.6	9261.5	7179.4	12768.3
41.4	382.2	600.6	534.2	448.4	458.1	496.2	720.5	127.2	210.3	229.5
76.9	1661.4	1582.9	1738.1	669.2	1304.7	1050.9	1231.7	1065.3	1065.5	808.9
100.0	1256.7	1533.2	1822.8	1262.9	1517.3	1450.5	1588.4	750.3	410.9	1062.7
6600.0	2817.4	2737.3	2884.4	2272.6	2328.3	2553.0	2333.4	3645.1	3082.0	4534.7
39.3	133.7	319.4	241.6	98.6	227.3	156.8	280.2	42.3	139.0	88.6
63.8	429.3	943.7	837.3	255.6	459.8	373.3	701.1	121.6	55.6	276.3
44.5	367.3	589.8	594.7	216.0	406.5	328.5	514.2	271.2	63.8	309.8
72.7	359.9	581.3	444.7	236.4	462.0	314.1	586.4	78.3	89.6	287.7
52.5	30.1	31.5	35.7	31.2	16.1	21.9	25.1	24.2	24.8	23.3
49.4	657.4	1104.8	1022.9	397.0	832.8	668.1	772.7	265.0	648.6	524.2
4793.5	3117.5	3231.1	3774.9	3261.1	3257.4	3982.9	4265.8	2457.3	3961.0	3364.4
63.8	1263.6	1488.6	1539.9	1030.5	1317.3	1076.4	1840.5	648.6	1204.3	1169.1
77.6	431.0	595.4	603.2	582.4	443.5	497.6	529.1	170.4	206.2	268.7
4925.1	3796.9	3739.0	4165.3	4708.5	4491.4	4040.3	5092.5	4316.5	5620.4	4016.8
69.0	1810.3	2224.8	2152.2	1212.5	1394.9	1965.0	1910.5	572.2	323.5	1541.1
105.1	1224.3	1569.4	1713.1	1613.6	1435.4	1072.3	1249.4	1415.3	370.7	770.0
10038.8	3427.3	3669.5	4124.8	2891.0	3172.5	3179.6	3013.4	4197.6	3134.4	4886.4
66.4	785.0	1157.9	1385.0	1490.2	1140.2	1501.5	1573.0	378.1	89.7	826.3
190.7	1862.4	2773.9	2067.2	1332.6	1760.4	1139.1	2611.8	1290.8	396.6	4038.7
106.0	486.1	651.3	604.1	628.1	519.3	510.4	686.9	290.3	711.3	378.0
3339.6	2322.3	2122.5	2340.5	1952.4	1508.3	2116.4	2182.2	1801.2	1736.2	4415.3
90.2	2264.5	3088.9	2703.6	2050.9	2272.2	2456.0	2363.8	1425.9	674.9	1874.0
1260.6	8311.2	5427.6	4722.7	3843.6	5059.5	4771.1	4997.1	10160.4	8699.1	5707.6
62.2	1908.5	1443.0	2295.8	2093.8	1798.7	2115.3	2535.6	816.4	550.8	1507.9
63.5	1205.9	1933.5	1652.8	882.8	1600.0	1060.0	1901.8	821.2	1366.3	1534.4
39.2	402.5	422.8	782.8	170.9	264.6	206.2	390.9	88.2	44.1	103.8
254.2	2397.0	2530.4	2459.8	1147.0	2281.8	1365.7	2761.5	2159.8	4032.7	2808.0
421.5	1457.7	2057.0	2370.7	1313.6	1512.8	1455.9	2207.5	994.4	526.5	1465.0
196.5	1734.4	1801.1	1688.8	1627.0	1677.6	2218.5	1756.8	1001.7	1727.2	1238.8
216.8	839.3	1277.6	1051.1	569.8	913.9	503.6	1195.0	394.3	1047.7	559.4

3458.8	4647.1	4447.3
879.0	221.6	386.7
4066.2	5069.7	4551.3
3967.8	4223.8	4145.0
1832.2	1147.8	1275.0
727.2	827.5	782.2
1141.7	728.4	700.4
4394.2	5556.6	4379.6
3157.0	3899.2	2801.1
1338.3	836.2	1027.7
7407.4	8334.1	7554.9
1224.8	484.1	727.7
1792.8	1482.7	1673.6
2706.0	1318.4	2500.9
2389.8	3077.4	2470.2
660.8	201.3	222.5
1350.1	844.5	1140.0
641.2	975.4	3866.3
591.1	480.8	725.3
25.8	37.6	22.1
939.7	1082.4	788.8
4455.8	3581.6	3498.0
1875.3	1757.8	1647.3
729.6	649.4	844.8
4301.3	5567.8	5251.0
2037.3	1905.5	2184.9
1508.5	1472.7	1249.3
3484.7	3426.1	3010.0
1874.5	1013.8	1991.6
2491.0	2156.2	2209.1
606.6	839.9	636.8
1893.8	2638.8	2112.9
2629.4	3772.1	4169.1
4416.0	7844.9	6703.4
2921.1	1916.8	3507.4
2159.3	1959.8	1667.6
663.9	385.8	526.7
2359.3	2305.6	1832.5
2276.0	2236.3	3847.8
2049.5	2097.9	2517.9
1577.8	1069.4	1442.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Roseburia
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s__Eubacterium rectale	17535
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s__Eubacterium rectale	17539
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s__Eubacterium rectale	17621

FM873062.1 gg_id:369242 occupant source house floor dust clone FC01F07 FM873
FJ685466.1 gg_id:514531 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ367319.1 gg_id:366355 feces adult twins and mothers; TS29 clone TS29_a02b03 FJ3673
EU530216.1 gg_id:260086 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
EU531915.1 gg_id:266916 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU762836.1 gg_id:325955 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7628
EU767257.1 gg_id:322662 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU768525.1 gg_id:312541 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU7685
AF371600.1 gg_id:73370 swine intestine clone p-1701-b3 AF3716
GQ129843.1 gg_id:462891 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
DQ801833.1 gg_id:175994 human fecal clone RL201_aai47d10 DQ801
FJ370262.1 gg_id:363790 feces adult twins and mothers; TS56 clone TS56_a02e10 FJ3702
DQ806829.1 gg_id:189007 human fecal clone RL198_aaj73e06 DQ806
EU466963.1 gg_id:294109 African elephant feces clone AFEL2_aao31h07 EU466
FJ678204.1 gg_id:522117 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ365454.1 gg_id:365282 feces adult twins and mothers; TS20 clone TS20_a03b01 FJ3654
FJ371131.1 gg_id:360819 feces adult twins and mothers; TS6 clone TS6_a01c10 FJ3711
FJ363291.1 gg_id:360701 feces adult twins and mothers; TS149 clone TS149_a01e06 FJ3632
DQ825097.1 gg_id:193400 human fecal clone RL185_aan85d02 DQ825
DQ795533.1 gg_id:187545 human fecal clone RL178_aan65g10 DQ795
DQ802108.1 gg_id:182412 human fecal clone RL241_aaj03b10 DQ802
FJ370203.1 gg_id:365078 feces adult twins and mothers; TS56 clone TS56_a01g02 FJ3702
DQ807826.1 gg_id:183743 human fecal clone RL180_aah37f09 DQ807
AY980662.1 gg_id:126910 human rectum mucosal biopsy clone LL61 AY980
DQ326747.1 gg_id:145280 Metagenomic gut microbiome healthy human stool clone E207 DQ326
FJ364366.1 gg_id:362761 feces adult twins and mothers; TS15 clone TS15_a02b01 FJ3643
DQ808385.1 gg_id:182934 human fecal clone RL180_aao76a03 DQ808
FJ366984.1 gg_id:369024 feces adult twins and mothers; TS28 clone TS28_a02b03 FJ3669
DQ326692.1 gg_id:148261 Metagenomic gut microbiome healthy human stool clone E143 DQ326
DQ905879.1 gg_id:170118 human fecal clone 29c-a2 DQ905
FJ678682.1 gg_id:527684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
DQ795650.1 gg_id:191147 human fecal clone RL178_aan67g05 DQ795
FJ684683.1 gg_id:520217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
DQ805854.1 gg_id:176658 human fecal clone RL306aal91h07 DQ805
FJ369457.1 gg_id:365386 feces adult twins and mothers; TS50 clone TS50_a04g06 FJ3694
EU768472.1 gg_id:309993 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ825093.1 gg_id:181338 human fecal clone RL185_aan85c09 DQ825
DQ808391.1 gg_id:192447 human fecal clone RL180_aao76a09 DQ808
FJ679037.1 gg_id:516514 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ800966.1 gg_id:194840 human fecal clone RL387_aao90a06 DQ800
DQ905661.1 gg_id:168592 human fecal clone 014C-D7 DQ905

1946.4	5987.9	4476.8	3685.0	2502.1	4297.1	3387.5	3924.8	5348.4	6893.5	5183.9
57.7	606.1	1204.9	910.6	311.3	661.8	521.5	818.8	203.2	118.2	383.7
212.7	1081.2	1090.7	1229.9	880.4	1099.1	1055.1	1764.6	834.1	832.1	989.6
46.5	137.9	177.2	237.8	129.2	118.3	92.4	135.4	35.5	42.9	51.6
8694.3	4305.0	4083.9	3913.7	5225.8	4165.8	5045.9	4466.6	3480.0	3994.1	3769.2
56.7	318.0	574.9	521.5	205.8	391.9	257.8	458.1	167.7	89.8	399.6
21284.3	5508.9	5624.9	4865.0	5132.6	4920.7	5398.1	5081.7	8295.3	7522.7	4756.3
4568.2	4408.4	5323.3	5000.1	4029.6	4983.1	4737.6	6137.1	4889.6	3871.6	9019.2
244.3	1528.3	2217.9	2383.8	642.3	1178.5	942.0	1587.6	581.4	812.1	1240.0
818.1	2348.2	3122.8	2482.5	1208.9	2099.2	1499.9	2514.4	1654.4	1551.7	1931.7
186.7	663.7	1016.4	1213.4	417.8	653.7	792.4	791.8	349.7	124.7	373.5
1309.2	1362.6	1764.3	1551.4	1444.2	1491.6	1484.6	1426.5	2206.9	1644.1	1532.9
144.4	604.0	835.8	1009.9	356.4	563.3	431.8	602.6	655.6	236.0	574.4
10532.0	4691.9	4324.1	4244.6	3931.4	4726.9	4162.7	4504.6	7417.4	5059.8	6677.0
554.2	4632.3	4933.3	4766.4	4826.4	3818.8	6752.9	4625.1	3299.3	4304.3	4103.5
11768.1	1887.2	1896.3	2441.4	2323.3	1848.1	2066.4	2379.1	1362.3	1787.0	1459.8
501.7	3069.3	2837.4	2540.1	1964.9	2835.8	2097.4	2507.9	2493.1	3575.3	1920.3
4777.0	4915.8	4749.0	5379.3	4013.4	5097.1	4228.1	4604.0	5009.8	3982.0	7500.4
62.3	541.8	841.7	1045.5	1068.4	817.2	1089.0	1088.9	285.4	312.0	464.2
63.6	161.0	410.1	307.1	72.5	150.0	108.3	250.7	27.6	47.3	96.9
74.4	200.3	292.1	242.4	160.9	263.0	246.1	382.8	590.9	490.4	287.6
331.4	1920.9	1960.0	1863.8	991.9	1726.1	1105.3	1884.5	1353.3	1153.4	1129.5
6015.2	5257.5	4618.6	4805.4	3929.8	4269.1	4455.1	5454.4	5011.0	3799.8	11924.3
10072.5	3122.6	3298.0	3866.1	3593.4	3236.0	3741.4	3714.3	4335.9	3891.1	3340.7
82.7	3632.7	3086.8	2926.2	1942.5	3063.7	3868.7	3886.1	5677.7	4395.9	2770.1
13006.0	6065.3	5296.7	5695.8	6464.4	5477.0	5881.3	5925.5	6368.0	4862.3	6054.7
1399.6	2428.8	2832.9	2615.7	2476.9	2456.8	2794.2	2662.2	3207.7	2250.0	2442.8
260.6	1669.1	1760.4	1867.8	1049.2	1587.5	1470.2	1794.6	2777.2	2327.6	1994.1
44.5	284.9	626.9	496.9	59.1	305.3	181.9	266.5	166.6	40.5	294.3
4607.7	1990.2	1891.1	2376.5	2040.2	1844.0	1983.1	1878.2	3003.0	1289.0	2608.7
90.1	1277.5	2108.7	1961.0	1726.7	2059.3	2218.5	2150.8	797.0	2002.4	1066.5
62.6	451.9	860.3	946.7	950.1	717.2	989.8	960.9	239.9	262.2	399.2
7158.7	3886.1	4960.1	4255.7	3648.5	4238.0	4332.2	4919.3	4720.8	6946.5	4329.9
2928.5	3853.4	2915.4	3006.9	2503.8	2904.0	2673.3	2746.6	4475.4	3592.4	2596.5
2568.1	538.5	913.9	963.6	610.2	578.0	509.6	818.5	432.3	169.7	323.1
134.1	1501.0	1520.8	1560.5	879.1	1374.3	1065.9	1890.2	2294.4	1861.4	1274.4
256.4	873.1	922.8	1066.2	1015.7	975.8	873.7	1438.3	779.8	247.3	1262.5
56.5	200.5	162.2	195.5	28.3	65.0	39.2	94.8	40.1	43.5	32.8
12652.2	3660.4	3851.1	3770.5	3411.8	3582.1	3839.1	3549.4	5392.8	4142.5	4706.3
322.3	503.3	676.4	752.4	615.1	581.6	351.4	604.2	201.5	128.4	260.7
115.3	2030.6	2494.6	1684.8	607.5	1267.5	939.0	1053.9	1935.3	1115.1	1617.1

3691.9	4433.8	3013.7
914.3	762.8	1354.2
1389.1	1025.1	1239.9
219.5	217.9	102.7
4430.8	4609.1	6638.8
709.6	390.7	550.0
5002.7	6299.9	6026.7
4947.9	7233.5	5538.2
1786.7	1880.0	1550.6
2608.7	2753.6	2788.5
1345.7	783.3	859.9
1501.8	1783.9	1855.2
1133.7	681.3	511.9
3769.0	5053.7	4251.9
4021.5	7680.2	7098.4
3092.2	3032.4	3323.8
2837.8	2612.3	3062.0
4349.3	4881.6	5240.6
1184.6	800.3	1251.2
696.9	182.2	171.6
370.7	442.9	317.9
2387.4	2006.3	2321.5
2372.1	4860.7	5122.6
4286.5	4164.9	5211.2
3252.3	3750.2	3057.6
6053.5	5830.8	7058.0
2684.7	2870.1	3478.8
1920.1	2095.8	1766.1
302.8	224.0	570.5
2340.3	2672.7	1985.9
2623.6	1541.0	2186.7
1133.7	660.7	964.4
4025.6	5117.0	4411.2
2510.1	3990.7	2757.5
1276.8	1246.1	506.6
2145.8	2013.3	1470.8
1153.3	1417.2	1029.6
90.7	129.0	70.1
4274.4	3966.3	3635.1
1359.4	617.8	744.9
997.8	1429.4	761.6

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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FJ365503.1 gg_id:368774 feces adult twins and mothers; TS20 clone TS20_a03f05 FJ3655
FJ682618.1 gg_id:527893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
FJ685051.1 gg_id:524554 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
FJ364930.1 gg_id:361763 feces adult twins and mothers; TS19 clone TS19_a04h06 FJ3649
FJ365815.1 gg_id:368017 feces adult twins and mothers; TS21 clone TS21_a03d05 FJ3658
FJ364034.1 gg_id:358949 feces adult twins and mothers; TS150 clone TS150_a02b12 FJ3640
FJ365849.1 gg_id:363597 feces adult twins and mothers; TS21 clone TS21_a03g07 FJ3658
DQ801961.1 gg_id:194918 human fecal clone RL241_aaj01a10 DQ801
FJ369277.1 gg_id:360219 feces adult twins and mothers; TS50 clone TS50_a02d06 FJ3692
FJ371240.1 gg_id:367197 feces adult twins and mothers; TS6 clone TS6_a02f02 FJ3712
DQ795543.1 gg_id:197014 human fecal clone RL178_aan65h12 DQ795
FJ369288.1 gg_id:358809 feces adult twins and mothers; TS50 clone TS50_a02e09 FJ3692
FJ678398.1 gg_id:514172 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
DQ795387.1 gg_id:196516 human fecal clone RL178_aah53g02 DQ795
FJ679566.1 gg_id:518807 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU778355.1 gg_id:352864 feces clone RL388_aao93b11 EU778
DQ807445.1 gg_id:189908 human fecal clone RL307_aam06f11 DQ807
DQ795642.1 gg_id:185901 human fecal clone RL178_aan67f02 DQ795
FJ369224.1 gg_id:366354 feces adult twins and mothers; TS50 clone TS50_a01g03 FJ3692
FJ369777.1 gg_id:358289 feces adult twins and mothers; TS51 clone TS51_a04f10 FJ3697
DQ327557.1 gg_id:146527 Metagenomic gut microbiome healthy human stool clone EB40 DQ327
FJ367937.1 gg_id:359488 feces adult twins and mothers; TS30 clone TS30_a01d07 FJ3679
DQ905520.1 gg_id:173210 human fecal clone 014-f31 DQ905
DQ806541.1 gg_id:179229 human fecal clone RL186_aao45h03 DQ806
FJ369536.1 gg_id:361729 feces adult twins and mothers; TS51 clone TS51_a01g02 FJ3695
DQ802070.1 gg_id:175760 human fecal clone RL241_aaj02f12 DQ802
FJ367978.1 gg_id:359012 feces adult twins and mothers; TS30 clone TS30_a02b01 FJ3679
FJ364903.1 gg_id:364092 feces adult twins and mothers; TS19 clone TS19_a04e11 FJ3649
DQ905882.1 gg_id:168946 human fecal clone 29c-b1 DQ905
FJ368551.1 gg_id:368217 feces adult twins and mothers; TS49 clone TS49_a01f10 FJ3685
EU466961.1 gg_id:296786 African elephant feces clone AFEL2_aao31h05 EU466
AY981367.1 gg_id:119815 human sigmoid colon mucosal biopsy clone G390 AY9813
DQ794832.1 gg_id:177312 human fecal clone RL240_aaj32h08 DQ794
DQ795401.1 gg_id:179074 human fecal clone RL178_aah53h06 DQ795
DQ807853.1 gg_id:198176 human fecal clone RL180_aah38a07 DQ807
EU768747.1 gg_id:352627 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ685239.1 gg_id:517956 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
FJ679585.1 gg_id:523170 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
DQ326759.1 gg_id:150073 Metagenomic gut microbiome healthy human stool clone E221 DQ326
EU767099.1 gg_id:323352 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
DQ905498.1 gg_id:164993 human fecal clone 014-d10 DQ905

200.2	508.3	571.6	605.0	403.1	511.3	371.3	672.0	252.1	154.7	323.6
50.1	366.7	673.5	761.6	266.1	418.8	366.2	540.2	102.4	94.5	292.5
3544.6	1309.6	1029.5	1083.3	1098.8	986.9	1033.4	1044.6	1515.1	1894.8	1051.4
90.8	1409.9	1868.7	1530.6	1455.9	1242.0	1274.1	2351.7	1097.5	812.1	985.7
58.3	1278.2	1635.4	1521.8	1414.1	1661.8	1664.3	1701.3	702.1	897.2	955.4
75.7	560.1	545.3	674.7	290.6	371.6	431.2	545.1	742.3	682.9	311.3
3374.1	2342.5	2340.6	2172.0	1880.6	2164.1	1902.1	2563.4	2610.2	1319.8	2532.1
8185.1	2363.4	2536.9	2394.1	2012.0	2138.4	2373.4	2050.0	3600.8	2050.1	3590.1
1412.0	258.0	409.4	556.3	365.5	463.1	322.1	562.2	215.2	106.2	280.1
63.9	631.9	1086.1	1328.2	617.3	741.1	748.1	1092.6	326.9	79.8	588.6
2833.2	2769.3	2775.8	3399.2	2740.8	2828.0	3001.5	3250.8	2486.9	3854.3	3154.1
126.2	2005.5	2200.1	2588.6	1882.4	2289.0	1479.8	3242.8	977.0	517.9	1594.9
328.3	1181.5	1296.0	1165.2	455.6	757.3	732.5	1594.9	696.8	712.3	725.4
352.5	2374.7	2675.9	2427.1	2523.6	2278.1	2277.4	2406.4	2692.1	2589.3	3052.5
39499.2	11444.8	7478.3	8193.1	7703.1	7284.7	10052.7	8580.5	13018.6	9372.8	12030.4
40.8	657.5	890.1	891.5	393.0	618.8	377.8	397.1	319.1	116.5	483.4
102.2	656.3	1231.5	1169.0	955.7	814.5	900.4	1009.1	528.7	421.1	600.8
600.5	2724.1	3033.0	3554.0	3202.6	3181.5	3402.5	4935.4	1736.9	2639.7	2773.0
1128.0	2166.6	2867.1	2094.6	1328.8	1976.9	1485.7	2241.0	1804.5	1410.2	2719.0
2542.4	1796.0	1966.1	1756.8	2052.5	2131.3	2320.6	2170.1	1528.9	2320.8	1762.6
47.6	222.1	376.8	469.5	248.8	300.2	231.2	372.7	64.9	80.0	110.9
15955.0	7541.1	6770.0	7923.6	8156.2	7845.6	8131.3	7131.0	9485.6	7186.8	9268.0
118.5	1061.7	1365.7	1638.7	342.8	766.6	571.5	1072.9	226.3	165.9	871.5
55.3	548.4	976.6	986.7	393.3	761.3	552.7	969.1	184.3	363.0	411.5
75.4	1182.9	1842.2	1815.5	1176.8	1676.8	1615.3	2000.5	583.0	872.4	981.2
2667.7	1444.7	2447.7	2165.4	1399.7	1962.6	1720.7	1857.0	1158.9	1803.1	1302.6
6118.1	3766.5	3431.6	3696.5	3198.6	3907.8	3388.5	3448.8	4444.8	4580.9	5283.0
2078.2	1624.8	1864.6	1855.0	1567.6	1421.0	1469.9	1421.5	2352.9	917.4	2078.0
49.4	190.7	377.4	428.5	96.6	212.2	169.6	263.3	36.4	34.6	109.5
3734.6	4939.0	5148.7	4862.1	4723.8	4681.2	5292.1	4599.1	5433.0	3874.8	6309.0
465.3	1362.2	1564.8	1536.9	1190.2	1269.4	1123.5	1428.5	993.8	1152.5	1051.1
79.1	1172.9	1319.0	1464.0	1210.7	1200.8	1671.7	1664.0	504.6	564.4	588.1
70.4	241.3	507.0	493.2	137.6	243.4	201.9	327.2	75.3	76.7	166.9
11332.1	4701.1	4396.0	4258.5	4538.2	2694.7	4238.2	3548.6	6963.6	4307.6	6164.9
2036.3	3173.8	1638.7	3068.1	3029.4	2905.0	3419.4	2544.7	2131.0	1396.9	2495.3
44.2	40.5	54.2	43.6	52.0	30.5	47.6	48.6	17.5	22.2	27.3
15511.0	4715.0	5338.5	4251.3	4787.4	4651.5	5535.5	4536.5	6166.8	5403.5	2719.1
352.0	1343.6	2187.6	2142.9	945.2	1210.0	1199.2	1552.6	959.7	668.6	1150.1
48.3	213.8	247.2	384.9	96.4	261.4	99.0	270.5	71.3	49.2	103.1
17383.2	8272.9	6417.2	7017.3	5912.4	6339.6	7226.3	6868.6	7505.7	6598.4	9664.3
115.7	852.0	1179.2	1363.8	264.2	604.8	415.4	893.8	188.2	143.4	585.7

948.8	601.1	712.1
1328.0	463.8	608.4
1206.1	1609.9	1169.4
2402.4	2280.8	1556.1
1972.5	1338.5	2286.7
464.6	696.0	372.9
2909.5	2318.5	2607.1
2301.4	2526.2	177.2
850.7	811.5	687.7
1276.8	812.1	1121.0
2937.5	2977.6	2862.1
4387.7	2020.8	4001.7
1727.1	2186.2	1090.0
2641.4	2130.3	2467.1
7293.9	14758.1	8505.0
864.4	689.4	741.3
1440.6	1045.3	1449.9
4081.0	2977.3	3817.7
2083.3	2234.4	1728.8
2198.2	2301.4	2901.9
1054.2	314.5	389.0
7669.8	8408.1	8164.0
920.5	1468.6	921.8
1292.0	908.7	1279.9
2073.1	1511.8	2097.9
2430.6	2614.4	2139.8
3593.9	4180.7	3056.9
1565.1	1720.0	1764.4
767.9	195.1	286.3
4048.7	4674.9	4581.1
1522.6	2157.0	2012.5
1571.4	1549.4	1610.9
712.4	269.5	307.5
3311.6	4890.5	4284.0
2501.6	2993.7	3386.0
37.0	37.2	42.2
4991.2	4900.6	4943.2
1832.5	1749.5	2304.9
689.2	235.6	301.1
6410.6	6681.0	6424.9
926.2	1144.7	631.9

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o__Clostridiales	f__Lachnospiraceae
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s__Eubacterium rectale	17818

DQ905630.1 gg_id:162644 human fecal clone 014C-A5 DQ905
FJ685450.1 gg_id:521707 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
DQ808230.1 gg_id:186955 human fecal clone RL180_aao74b09 DQ808
DQ798354.1 gg_id:194115 human fecal clone RL181_aah41d07 DQ798
FJ364703.1 gg_id:360709 feces adult twins and mothers; TS19 clone TS19_a02a08 FJ3647
DQ825327.1 gg_id:180271 human fecal clone RL185_aan88f05 DQ825
EU762972.1 gg_id:329548 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ364641.1 gg_id:367198 feces adult twins and mothers; TS19 clone TS19_a01d01 FJ3646
FJ369275.1 gg_id:369410 feces adult twins and mothers; TS50 clone TS50_a02d04 FJ3692
DQ806442.1 gg_id:175827 human fecal clone RL186_aan92e03 DQ806
FJ372329.1 gg_id:362286 feces adult twins and mothers; TS9 clone TS9_a04d01 FJ3723
FJ673905.1 gg_id:520426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY983645.1 gg_id:124589 human descending colon mucosal biopsy clone NP02 AY983
DQ802190.1 gg_id:186848 human fecal clone RL241_aaj04c05 DQ802
DQ794617.1 gg_id:181590 human fecal clone RL240_aaj30c10 DQ794
EU768411.1 gg_id:316275 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ802179.1 gg_id:177125 human fecal clone RL241_aaj04b03 DQ802
FJ363350.1 gg_id:365129 feces adult twins and mothers; TS149 clone TS149_a02c01 FJ3633
FJ364057.1 gg_id:367480 feces adult twins and mothers; TS150 clone TS150_a02e02 FJ3640
DQ824774.1 gg_id:180624 human fecal clone RL185_aao69b01 DQ824
FJ678132.1 gg_id:509736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ079253.1 gg_id:400680 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d GQ079
DQ795352.1 gg_id:186105 human fecal clone RL178_aah53c10 DQ795
AY985878.1 gg_id:116625 human stool clone D156 AY985
DQ805494.1 gg_id:178281 human fecal clone RL203_aai63d06 DQ805
AY976767.1 gg_id:124156 human cecum mucosal biopsy clone K370 AY976
DQ806036.1 gg_id:175467 human fecal clone RL186_aah60c05 DQ806
DQ795457.1 gg_id:180457 human fecal clone RL178_aah54f01 DQ795
DQ801712.1 gg_id:193745 human fecal clone RL201_aai45h04 DQ801
EU762504.1 gg_id:317649 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ326990.1 gg_id:146423 Metagenomic gut microbiome healthy human stool clone E487 DQ326
DQ798642.1 gg_id:198695 human fecal clone RL181_aan99d10 DQ798
DQ905512.1 gg_id:170573 human fecal clone 014-e5 DQ905
AY980949.1 gg_id:117339 human rectum mucosal biopsy clone V010 AY980
DQ802310.1 gg_id:189471 human fecal clone RL188_aah15h07 DQ802
DQ795477.1 gg_id:194671 human fecal clone RL178_aah54h01 DQ795
FJ684922.1 gg_id:511827 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
DQ800950.1 gg_id:197252 human fecal clone RL387_aao89g11 DQ800
DQ327093.1 gg_id:145310 Metagenomic gut microbiome healthy human stool clone E608 DQ327
FJ368960.1 gg_id:365060 feces adult twins and mothers; TS4 clone TS4_a02f01 FJ3689
DQ905122.1 gg_id:165496 human fecal clone 002C-c11 DQ905

520.3	1588.7	2181.7	1627.4	1222.5	1498.2	1333.0	1603.7	1650.0	2247.8	1359.8
330.5	2680.4	2965.9	2666.0	1451.2	2548.6	2421.3	3295.3	1819.3	1666.5	1864.0
55.2	489.9	733.2	932.3	269.7	608.8	323.6	624.0	211.5	311.2	200.2
363.1	2687.5	2216.6	2128.1	1554.3	2003.8	1758.1	2296.6	2619.6	1991.3	2418.4
11009.5	5202.1	4790.1	5177.1	5750.1	4542.7	5274.9	4108.8	6834.1	6703.7	7273.6
49.1	44.6	201.7	98.4	17.8	30.1	27.9	44.8	27.7	22.6	25.7
895.6	4967.8	3515.3	3579.0	2531.0	3511.9	3881.5	4189.0	4511.4	2839.4	5335.8
11053.5	4675.3	4143.5	5072.3	5050.5	4192.2	4536.0	4284.1	5582.5	4988.5	5624.8
1063.3	1271.9	2133.1	2277.1	1335.7	1725.2	1164.6	2086.4	915.9	1385.9	920.9
1143.2	1206.1	1935.6	1870.4	923.9	1363.3	1105.9	1610.4	952.5	1433.8	1215.7
81.7	866.3	1277.0	1466.8	621.8	906.0	739.5	1432.8	390.4	269.7	945.1
3759.4	2145.4	2075.1	1873.6	1304.9	1815.7	1605.6	1024.9	2727.6	2217.4	1803.2
412.6	1469.6	2685.3	2438.5	1355.5	1691.1	1692.7	2063.4	1803.6	1621.1	2474.5
996.1	2219.3	3028.1	2042.7	1627.4	2097.0	1741.9	1950.3	4911.3	2850.4	2839.1
3679.7	4588.5	3810.4	5314.7	4619.0	4065.3	5042.5	4598.6	4960.2	3382.1	7922.9
1360.5	512.7	774.9	743.0	423.2	609.9	499.5	654.4	576.0	439.2	632.9
49.8	276.0	406.8	420.9	281.7	249.0	221.1	269.6	83.4	124.3	137.4
1798.9	6349.8	6805.6	6052.8	4648.9	5701.6	5768.0	5811.6	7698.9	7784.5	7834.8
49.4	445.0	795.0	681.6	263.3	590.3	361.3	546.0	247.9	624.0	304.9
8389.5	3844.5	3532.9	4040.5	4026.2	3203.2	4844.0	5886.0	3643.6	2989.4	4255.3
139.8	1223.5	1636.1	1750.2	1034.0	1266.3	1016.0	1665.3	1783.1	1117.8	1417.1
6637.4	2749.9	2887.5	2861.7	2221.3	2494.1	2371.0	2352.7	3034.4	2592.2	3465.4
294.1	581.6	411.8	398.4	464.6	495.8	531.1	475.0	383.2	430.7	274.2
186.4	1550.3	3041.8	2959.3	554.5	1701.1	678.4	3362.1	570.8	351.7	1428.4
39.8	103.5	236.4	146.6	94.4	79.8	68.5	99.7	43.4	27.8	57.6
45.4	752.8	756.0	744.2	344.9	608.9	461.0	1131.9	771.0	374.5	309.5
31.0	216.4	109.9	90.0	67.7	60.8	48.8	21.3	20.6	39.5	86.6
121.5	414.9	838.1	877.0	266.8	584.4	314.5	883.1	311.8	93.0	320.7
59.5	730.8	1075.4	1043.8	68.0	796.1	315.1	1870.1	267.3	268.9	694.3
5992.5	4781.4	5331.4	4075.4	3532.2	3992.3	3658.4	3749.8	7125.4	5588.4	5148.7
53.4	386.9	833.6	597.0	203.9	569.6	341.6	508.1	252.4	175.2	504.7
5807.9	3099.3	3002.2	2783.6	3230.1	3302.3	2161.1	3137.2	2209.8	3049.4	1853.8
16292.5	4676.2	4117.6	3075.7	4171.8	3956.5	3702.4	4137.7	5881.0	6096.4	3786.9
106.7	1523.6	1545.2	1893.0	1797.2	1529.1	2631.4	2220.4	688.4	1296.7	823.4
116.3	600.1	1602.4	1273.4	788.7	744.2	577.3	1377.4	667.8	620.0	638.3
1357.9	1115.3	1502.8	1158.7	1057.9	1155.9	1144.4	1656.4	902.7	1538.4	979.8
49.7	566.6	1000.2	901.2	598.8	838.4	652.9	1013.5	212.1	424.6	402.7
71.2	685.1	1245.7	1463.4	605.6	1206.0	470.3	1644.3	334.0	1173.0	701.3
945.8	6177.0	4387.5	3148.9	3147.6	4951.7	2108.1	3599.4	5304.7	3556.2	2619.3
367.5	1130.0	1543.2	1480.6	1050.6	1107.5	1054.6	1378.5	634.1	475.3	871.9
60.0	205.5	197.4	293.1	75.8	158.8	115.2	150.4	115.7	62.6	113.8

1383.1	1828.0	1753.0
2965.6	4891.0	3375.6
1210.9	490.3	491.5
2489.5	2164.0	3096.4
4589.5	5249.6	4701.8
41.6	38.8	53.8
2706.5	3964.7	3287.6
4293.6	5025.1	4388.1
2632.7	2429.1	2523.2
2168.7	1547.0	1624.2
1890.3	1142.7	970.1
2058.2	2539.4	1855.5
2300.6	2873.1	2509.3
1851.3	2333.2	1870.8
3943.5	6392.8	4562.1
532.3	1350.3	532.0
310.7	400.6	468.3
4782.4	5423.4	5694.8
710.9	704.2	798.9
4370.2	3988.6	4325.3
1942.3	1782.3	1323.7
2744.1	3539.0	2192.2
404.6	637.7	543.9
1392.9	1278.8	1855.0
117.0	136.9	110.7
1147.9	957.2	1636.7
56.5	194.0	164.8
1301.6	917.3	869.5
3538.3	695.5	1512.8
4400.9	4616.8	4727.2
1022.7	647.9	908.2
3544.0	2446.1	2573.1
3743.5	5176.8	3743.5
1991.3	2270.7	2476.0
1737.8	1426.0	922.1
1244.0	1439.2	1596.7
2022.8	814.1	952.4
2301.7	1549.2	2097.0
4201.2	3640.4	2336.3
1205.5	2053.5	1087.9
187.2	256.4	127.4

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
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Roseburia
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s__Eubacterium rectale	17819
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FJ679854.1 gg_id:519508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ684593.1 gg_id:510279 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU466766.1 gg_id:290571 African elephant feces clone AFEL2_aao29b12 EU466
DQ801365.1 gg_id:189974 human fecal clone RL388_aao94e07 DQ801
DQ798551.1 gg_id:187599 human fecal clone RL181_aan98b07 DQ798
FJ367608.1 gg_id:362114 feces adult twins and mothers; TS2 clone TS2_a01e04 FJ3676
FJ365782.1 gg_id:369492 feces adult twins and mothers; TS21 clone TS21_a03a01 FJ3657
FJ680167.1 gg_id:524523 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU763571.1 gg_id:339729 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
DQ805954.1 gg_id:198934 human fecal clone RL186_aah59b07 DQ805
FJ370172.1 gg_id:357262 feces adult twins and mothers; TS56 clone TS56_a01c07 FJ3701
EU530175.1 gg_id:259373 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
FJ684449.1 gg_id:525584 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
DQ802659.1 gg_id:184827 human fecal clone RL188_aan94g11 DQ802
EU466978.1 gg_id:302677 African elephant feces clone AFEL2_aao32c01 EU466
EU778085.1 gg_id:341146 feces clone RL388_aao93c02 EU778
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DQ798526.1 gg_id:192445 human fecal clone RL181_aan97g10 DQ798
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FJ369582.1 gg_id:359744 feces adult twins and mothers; TS51 clone TS51_a02c06 FJ3695
DQ806738.1 gg_id:197999 human fecal clone RL186_aao48b06 DQ806
FJ364203.1 gg_id:362529 feces adult twins and mothers; TS150 clone TS150_a04b08 FJ3642
FJ676724.1 gg_id:518187 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
DQ801645.1 gg_id:195963 human fecal clone RL201_aai45a02 DQ801
DQ807759.1 gg_id:184100 human fecal clone RL180_aah36h04 DQ807
DQ802206.1 gg_id:177793 human fecal clone RL241_aaj04d12 DQ802
FJ370216.1 gg_id:358910 feces adult twins and mothers; TS56 clone TS56_a01h05 FJ3702
GQ042977.1 gg_id:416953 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011f GQ042
FJ368587.1 gg_id:358837 feces adult twins and mothers; TS49 clone TS49_a02a10 FJ3685
DQ793232.1 gg_id:179396 human fecal clone RL199_aaj41b02 DQ793
DQ802375.1 gg_id:190144 human fecal clone RL188_aah16h03 DQ802
FJ682654.1 gg_id:517334 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
DQ801699.1 gg_id:179678 human fecal clone RL201_aai45f09 DQ801
DQ801830.1 gg_id:197323 human fecal clone RL201_aai47d07 DQ801
DQ806212.1 gg_id:199111 human fecal clone RL186_aah62g01 DQ806
DQ806685.1 gg_id:184421 human fecal clone RL186_aao47e09 DQ806
FJ370817.1 gg_id:362130 feces adult twins and mothers; TS5 clone TS5_a01f03 FJ3708
DQ809761.1 gg_id:190930 human fecal clone RL184_aan83g09 DQ809
EU466896.1 gg_id:300009 African elephant feces clone AFEL2_aao31a06 EU466
DQ804763.1 gg_id:187743 human fecal clone RL187_aao72d07 DQ804
FJ365693.1 gg_id:367779 feces adult twins and mothers; TS21 clone TS21_a01h06 FJ3656

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2722.2	1443.0	2500.2	1763.0	1217.0	1683.0	1691.3	1469.4	1170.3	2198.6	1548.3
249.1	922.7	1057.0	1389.8	454.7	671.5	513.0	1158.6	930.8	117.1	853.6
4330.3	4699.7	5021.6	3673.9	3038.4	3533.9	3221.6	4045.1	5177.0	7651.3	4243.6
1911.2	2478.7	2579.9	3264.0	2840.6	3004.6	3127.5	3904.6	1798.8	3294.8	2506.8
63.6	816.9	1368.0	1459.5	533.2	894.2	699.0	1181.0	402.0	367.1	619.1
11829.4	3139.3	3663.6	3717.2	3255.1	3186.6	3567.8	3522.9	3974.8	3972.9	4646.0
62.3	137.8	319.9	325.9	88.2	222.0	199.6	250.3	34.2	116.6	122.5
2706.4	6660.9	5996.5	6147.7	5980.7	6110.6	6648.7	8794.8	6106.5	5659.0	6408.8
38.8	251.0	588.9	579.5	92.9	250.1	210.9	538.8	83.5	61.6	256.7
6681.0	4239.4	4188.3	4044.8	4308.4	5657.4	4886.6	4484.2	6363.9	6808.0	3855.0
156.9	1334.6	2038.2	2256.6	1686.5	1929.8	1270.8	2651.6	1045.1	971.5	1371.0
5616.9	1449.2	1635.0	1486.8	1498.1	1588.7	1426.0	1630.3	1286.7	1787.8	1109.7
24251.4	8134.3	8445.8	7506.5	7674.0	7523.8	8314.4	6745.0	13713.9	10997.3	11188.7
3686.9	1311.6	1505.5	1480.0	883.7	1047.6	1459.1	1748.9	1119.4	747.9	1486.2
64.9	163.6	167.9	311.9	67.6	72.8	77.9	202.2	83.0	34.3	55.8
117.2	1017.6	1436.4	1703.7	334.3	792.2	582.1	1135.2	235.0	164.8	818.0
316.6	1239.4	980.6	1428.4	1044.7	1300.2	1218.5	2910.2	726.8	1189.8	1234.4
51.3	86.6	157.1	176.6	77.8	95.3	76.3	118.7	31.7	41.3	59.3
130.6	827.1	857.1	837.1	543.3	716.1	1443.6	1115.4	198.2	762.5	292.3
25617.4	6260.2	6233.1	7118.3	6766.2	6555.5	6969.0	6272.4	8779.7	6524.1	10028.8
1790.7	3495.4	2934.5	4988.7	3683.5	3253.1	3432.9	4304.8	2977.3	1307.4	4685.9
48.6	576.7	959.6	926.8	607.1	813.1	662.3	1030.8	229.0	427.6	414.4
50.5	26.1	21.3	17.6	17.6	18.6	22.1	15.2	20.0	27.9	17.3
2429.5	1222.8	2050.2	2358.3	2533.3	1933.2	2188.0	2403.0	1440.0	1021.5	1833.4
51.0	625.1	636.6	825.7	430.1	757.3	365.9	773.3	119.7	59.2	252.1
40.3	284.5	497.0	627.4	69.9	232.3	93.2	593.4	95.3	79.4	237.4
61.2	360.7	742.1	867.5	54.2	228.0	111.5	435.7	72.4	27.5	202.5
58.7	92.1	138.8	151.1	47.3	67.7	39.2	68.4	34.9	27.9	54.3
484.3	535.4	630.4	557.9	167.2	303.1	296.5	511.9	131.1	163.5	317.8
54.9	188.5	293.8	322.0	276.2	206.4	314.1	411.6	71.8	50.4	126.5
5840.5	1558.2	1620.6	1790.1	1635.0	1569.3	1692.9	1862.6	1258.4	1488.5	954.2
3561.6	2484.5	1532.2	2911.1	2613.4	2317.9	2768.9	2651.0	2445.0	1344.1	3317.3
3413.7	1045.3	2028.4	2279.2	2847.8	1857.8	2352.6	2030.8	1687.9	1549.5	2290.7
33.6	341.2	699.2	550.4	201.9	720.9	275.1	591.4	92.6	1446.3	180.5
5374.2	3613.6	4715.0	6540.8	4726.8	4359.9	5144.6	4490.7	2974.3	3583.3	4732.1
966.3	2587.7	2247.0	1335.4	1700.6	2480.3	1744.9	1339.1	1692.0	1294.7	811.5
2424.0	2316.6	2115.0	2516.6	1439.7	1952.3	2528.4	1995.3	2414.0	1455.7	2055.8
7829.6	4958.1	3850.0	4600.2	4201.8	4433.5	3062.4	4657.0	4482.8	3252.2	5835.3
45.6	294.2	465.3	522.1	341.4	290.6	351.0	422.2	200.0	64.7	252.6
7423.8	3503.0	3217.4	3518.3	2880.7	2884.5	3510.3	3192.4	3761.8	3634.3	4577.3

2443.1	2162.7	2188.8
1772.8	2775.3	2371.7
836.8	1191.3	993.4
3734.1	5577.3	5815.6
3855.7	3119.2	3101.5
1541.0	1278.8	1297.3
3869.4	4755.7	4082.2
390.3	244.5	166.6
7173.9	7787.8	8283.2
374.6	271.4	415.9
5182.6	7576.0	4942.6
2575.1	2038.4	1721.6
2716.1	1738.1	1594.5
7087.3	7638.6	8604.0
1402.6	2136.4	1896.3
224.5	221.9	163.7
1097.3	1431.8	959.3
1798.9	1392.0	1422.2
147.8	174.5	126.2
1254.9	717.4	933.2
7006.3	8091.1	7404.1
3647.1	3980.4	3974.4
1911.6	844.1	1005.9
19.9	16.3	14.0
2885.7	2677.3	3513.0
695.7	763.5	1179.4
630.3	506.5	97.3
558.0	456.3	310.5
102.5	179.6	57.1
402.7	843.1	333.2
447.9	311.1	436.1
2815.8	2573.7	2420.3
2689.4	3592.3	3721.5
2465.6	2752.8	2573.2
1264.3	469.2	449.9
3885.7	3854.8	4945.4
1574.5	1614.2	2165.9
2130.0	2491.1	2212.9
4650.6	5063.5	5451.2
577.1	352.8	650.3
3477.0	4536.2	3304.7

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
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Roseburia
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s__Eubacterium rectale	17908
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s__Eubacterium rectale	17910
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s__Eubacterium rectale	17987

FJ368001.1 gg_id:361921 feces adult twins and mothers; TS30 clone TS30_a02e05 FJ3680
DQ794968.1 gg_id:185516 human fecal clone RL310_aam38e10 DQ794
FJ363257.1 gg_id:358710 feces adult twins and mothers; TS149 clone TS149_a01b06 FJ3632
FJ685440.1 gg_id:512889 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
DQ904907.1 gg_id:167248 human fecal clone 001C-h12 DQ904
FJ678707.1 gg_id:512903 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ680145.1 gg_id:523776 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
DQ807568.1 gg_id:181379 human fecal clone RL307_aam08d03 DQ807
FJ676360.1 gg_id:517278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
DQ802464.1 gg_id:188240 human fecal clone RL188_aah18b03 DQ802
DQ806524.1 gg_id:183247 human fecal clone RL186_aao45f09 DQ806
FJ365687.1 gg_id:358679 feces adult twins and mothers; TS21 clone TS21_a01g11 FJ3656
AM697090.1 gg_id:227371 sequencing libraries indoor dust clone BF0002B040 AM697
FJ368351.1 gg_id:357963 feces adult twins and mothers; TS3 clone TS3_a03d01 FJ3683
DQ794647.1 gg_id:186583 human fecal clone RL240_aaj30f05 DQ794
FJ364097.1 gg_id:363592 feces adult twins and mothers; TS150 clone TS150_a03a01 FJ3640
DQ798013.1 gg_id:197372 human fecal clone RL302_aal94e08 DQ798
AY978123.1 gg_id:124624 human cecum mucosal biopsy clone LI93 AY978
DQ808367.1 gg_id:190580 human fecal clone RL180_aao75g07 DQ808
FJ368631.1 gg_id:360078 feces adult twins and mothers; TS49 clone TS49_a02f01 FJ3686
FJ368860.1 gg_id:369361 feces adult twins and mothers; TS4 clone TS4_a01d11 FJ3688
EU466855.1 gg_id:297190 African elephant feces clone AFEL2_aao30d07 EU466
DQ801237.1 gg_id:198348 human fecal clone RL116_aaf02b11 DQ801
FJ363362.1 gg_id:369270 feces adult twins and mothers; TS149 clone TS149_a02d02 FJ3633
DQ810154.1 gg_id:190787 human fecal clone RL184_aao68f08 DQ810
EU762167.1 gg_id:324760 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ366995.1 gg_id:363238 feces adult twins and mothers; TS28 clone TS28_a02c02 FJ3669
FJ684040.1 gg_id:512570 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
FJ364786.1 gg_id:367532 feces adult twins and mothers; TS19 clone TS19_a03b03 FJ3647
DQ326959.1 gg_id:145511 Metagenomic gut microbiome healthy human stool clone E452 DQ326
DQ804771.1 gg_id:176789 human fecal clone RL187_aao72e04 DQ804
FJ682239.1 gg_id:517986 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
DQ794822.1 gg_id:196420 human fecal clone RL240_aaj32g10 DQ794
DQ806119.1 gg_id:198071 human fecal clone RL186_aah61d09 DQ806
FJ367199.1 gg_id:357309 feces adult twins and mothers; TS28 clone TS28_a04f10 FJ3671
GQ079144.1 gg_id:414860 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229a GQ079
DQ802617.1 gg_id:192223 human fecal clone RL188_aan94b08 DQ802
DQ824777.1 gg_id:197066 human fecal clone RL185_aao69b04 DQ824
DQ801920.1 gg_id:191525 human fecal clone RL201_aai48e03 DQ801
FJ365286.1 gg_id:360736 feces adult twins and mothers; TS20 clone TS20_a01b03 FJ3652
AY977654.1 gg_id:124009 human cecum mucosal biopsy clone LD06 AY977

5120.8	3439.4	3481.6	3619.8	3008.9	3594.6	3384.0	3606.7	3612.7	3231.5	4493.5
10234.0	7255.3	6465.0	6888.8	7987.5	6024.1	7557.6	6679.9	8340.2	6052.0	8272.4
53.8	277.8	378.8	412.5	135.8	239.3	137.5	396.3	53.7	64.5	102.9
30.6	846.2	1556.1	1533.5	1827.3	1445.6	1741.7	2060.9	607.9	832.2	1237.3
48.3	416.7	541.1	704.3	137.5	241.4	199.2	327.9	54.3	36.7	144.5
3836.3	552.3	857.3	818.5	396.6	494.5	448.9	616.4	615.1	458.0	547.2
65.9	1188.0	2065.5	1737.6	1236.2	1325.0	1829.6	1748.8	878.4	346.2	1210.4
51.1	318.1	488.7	623.4	189.2	353.4	244.4	308.9	80.3	62.7	178.4
47.5	1441.3	2221.5	1736.7	1994.4	2160.2	1878.5	2339.8	1198.3	1758.0	1319.6
1220.8	3786.5	4264.8	3772.3	3054.5	3496.0	2073.5	4017.1	7788.2	5062.8	5022.0
32.5	116.1	309.2	262.6	78.3	223.4	71.3	228.1	47.6	103.9	75.0
50.8	1869.7	1928.8	2001.4	1150.7	1732.0	1525.1	1819.3	945.1	1346.2	1256.0
5886.6	4927.6	4743.4	5456.9	6382.1	5952.3	6034.4	5191.9	4656.9	7262.2	5521.8
478.2	3635.4	3442.6	4007.0	4248.4	3600.1	4042.8	4251.5	2935.0	3295.8	2962.6
1575.9	1999.1	1640.8	2061.2	2439.9	1684.4	2513.6	1950.8	1124.3	1803.1	1740.7
3537.5	2199.6	2418.7	2479.3	2197.1	2371.0	2410.5	2508.4	1971.1	3019.6	2391.8
3573.8	2807.5	3254.4	2818.7	2409.5	2382.6	2527.1	1930.8	2535.9	1566.8	3958.2
43.2	212.4	361.5	326.0	158.2	266.5	142.8	311.1	46.5	55.2	134.9
50.1	314.0	479.3	569.1	205.1	332.4	243.0	724.3	157.8	163.1	254.5
46.1	219.0	369.0	447.4	133.0	238.6	214.4	382.2	65.6	66.8	133.9
5827.4	3376.4	2818.3	3598.9	3346.5	3422.6	3105.2	3744.3	4004.3	4019.6	4924.4
72.5	1519.3	2222.5	2820.9	687.2	1167.4	1061.5	1990.5	329.5	216.6	834.2
546.8	1742.4	2249.0	2243.4	2208.6	1973.2	2591.2	2805.2	1151.0	2193.3	1498.3
4985.7	6203.2	5125.3	4911.2	4647.9	4742.9	4847.0	5073.1	7915.5	6055.7	7170.7
58.1	463.2	617.2	638.3	371.3	423.8	415.9	747.6	324.2	397.1	266.0
2184.1	3734.4	4008.8	4813.0	4855.9	4105.4	3882.4	5529.5	4425.8	6693.6	3609.2
33.9	202.2	236.8	443.8	67.6	82.6	91.4	134.3	44.2	28.5	51.5
50.4	253.4	505.6	685.1	83.0	277.8	180.7	377.5	47.3	35.7	152.9
12314.7	6561.8	5940.3	5363.8	5326.2	5679.9	5684.9	5294.8	7620.9	6598.0	7058.9
60.0	581.8	741.4	678.7	254.4	513.3	343.4	741.7	805.3	605.8	351.7
49.3	369.0	371.3	430.3	73.3	67.5	88.8	224.6	99.9	35.8	50.3
15270.5	7098.9	6357.8	6377.9	5211.9	5645.5	7630.1	6712.1	8032.0	4813.5	10858.3
461.5	8452.7	9155.1	6828.3	6541.4	7620.7	7614.5	6294.7	6710.4	7890.2	6980.8
41.8	96.2	185.1	129.7	139.4	71.6	130.9	118.6	150.7	100.3	87.7
781.0	1916.1	2915.6	2820.0	2264.1	1961.1	2408.5	2124.5	1803.6	637.7	2393.5
40.2	31.0	36.8	41.1	45.2	37.8	51.4	41.1	24.1	25.3	26.6
457.6	1717.2	1959.9	2648.0	1560.7	1584.0	2132.2	1054.2	1147.5	975.7	1717.4
2762.4	1941.2	1984.3	2163.4	2201.6	1794.7	2610.5	2666.7	1793.2	1360.5	1398.0
41.7	69.4	149.0	223.4	60.0	96.4	69.3	157.8	48.9	21.5	64.5
674.8	1951.9	2823.4	2337.0	2145.0	2239.7	1709.5	1808.5	1490.2	1167.6	1545.8
102.7	538.5	910.9	1114.4	855.6	467.0	562.2	790.6	304.9	131.5	388.2

3082.4	4703.0	3274.6
5892.5	8613.4	6936.5
537.8	464.9	474.4
1889.9	1503.7	2081.2
542.7	507.3	224.9
428.2	1287.6	513.1
1724.0	1689.5	2860.9
416.5	334.3	864.1
2173.5	1776.8	2865.4
4169.6	3827.1	3541.2
375.3	279.9	229.9
1803.0	2230.9	3041.0
5341.0	9135.7	5757.3
3507.0	2899.1	3939.7
2452.7	1871.7	2195.2
2851.4	2974.8	3145.5
3387.2	2331.1	2766.7
1245.9	204.1	560.3
597.1	571.0	370.4
981.2	268.3	524.6
3384.5	3164.5	2777.5
3214.7	1664.8	1366.4
2456.2	2402.6	3246.0
4511.0	6507.8	4467.8
883.4	636.2	809.7
5825.7	4639.3	4091.0
216.1	220.6	125.1
793.0	396.1	329.2
5114.0	5960.0	6123.3
1201.1	851.9	604.6
404.2	371.4	559.6
5594.0	8454.7	6711.6
6194.5	7342.4	7800.9
105.3	219.9	87.4
2094.4	2832.1	3188.6
41.1	56.0	40.3
1726.0	1665.5	1622.7
2449.0	2117.8	2981.3
175.2	106.8	96.9
2699.0	1904.4	2269.4
1083.6	2194.9	2715.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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g__Roseburia
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s__Eubacterium rectale	17988
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s__Eubacterium rectale	18009
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s__Eubacterium rectale	18092

FJ370282.1 gg_id:367961 feces adult twins and mothers; TS56 clone TS56_a02g11 FJ3702
FJ367008.1 gg_id:369749 feces adult twins and mothers; TS28 clone TS28_a02d05 FJ3670
FJ363179.1 gg_id:359795 feces adult twins and mothers; TS148 clone TS148_a04b01 FJ3631
FJ677840.1 gg_id:526445 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ676810.1 gg_id:521922 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
DQ798572.1 gg_id:199615 human fecal clone RL181_aan98d10 DQ798
GQ009488.1 gg_id:500178 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU466856.1 gg_id:302746 African elephant feces clone AFEL2_aao30d08 EU466
DQ809092.1 gg_id:178997 human fecal clone RL308_aal81d01 DQ809
EU466947.1 gg_id:294228 African elephant feces clone AFEL2_aao31g01 EU466
FJ371069.1 gg_id:358681 feces adult twins and mothers; TS5 clone TS5_a04e10 FJ3710
FJ369242.1 gg_id:367699 feces adult twins and mothers; TS50 clone TS50_a02a01 FJ3692
FJ370882.1 gg_id:359543 feces adult twins and mothers; TS5 clone TS5_a02d02 FJ3708
DQ806134.1 gg_id:175208 human fecal clone RL186_aah61f08 DQ806
DQ795621.1 gg_id:182233 human fecal clone RL178_aan67b09 DQ795
FJ363075.1 gg_id:358806 feces adult twins and mothers; TS148 clone TS148_a02f09 FJ3630
FJ366916.1 gg_id:365844 feces adult twins and mothers; TS28 clone TS28_a01d01 FJ3669
AY982934.1 gg_id:120934 human descending colon mucosal biopsy clone L134 AY982
DQ805972.1 gg_id:196955 human fecal clone RL186_aah59d07 DQ805
DQ795652.1 gg_id:190044 human fecal clone RL178_aan67g08 DQ795
FJ370353.1 gg_id:368817 feces adult twins and mothers; TS56 clone TS56_a03h02 FJ3703
FJ366299.1 gg_id:365573 feces adult twins and mothers; TS26 clone TS26_a01a07 FJ3662
DQ797907.1 gg_id:194546 human fecal clone RL302_aal93c07 DQ797
FJ370891.1 gg_id:368548 feces adult twins and mothers; TS5 clone TS5_a02d11 FJ3708
DQ804730.1 gg_id:185930 human fecal clone RL187_aao72a03 DQ804
EU762626.1 gg_id:331056 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
GQ079168.1 gg_id:409786 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229d GQ079
DQ806222.1 gg_id:191921 human fecal clone RL186_aah62h03 DQ806
FJ371061.1 gg_id:363317 feces adult twins and mothers; TS5 clone TS5_a04e02 FJ3710
EU467000.1 gg_id:289357 African elephant feces clone AFEL2_aao32e07 EU467
DQ905858.2 gg_id:164028 human fecal clone 29E-g3 DQ905
FJ684372.1 gg_id:522736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ366338.1 gg_id:363459 feces adult twins and mothers; TS26 clone TS26_a01e11 FJ3663
DQ801160.1 gg_id:186450 human fecal clone RL116_aae99d03 DQ801
DQ801269.1 gg_id:184910 human fecal clone RL388_aao93c04 DQ801
DQ798514.1 gg_id:187339 human fecal clone RL181_aan97f09 DQ798
FJ364191.1 gg_id:362123 feces adult twins and mothers; TS150 clone TS150_a04a07 FJ3641
EU763418.1 gg_id:312883 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ685507.1 gg_id:515275 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6855
DQ807832.1 gg_id:186292 human fecal clone RL180_aah37g03 DQ807
DQ797700.1 gg_id:198093 human fecal clone RL206_aaj14g09 DQ797

817.2	1066.9	1226.0	1047.6	574.7	422.6	643.0	929.0	793.0	639.4	673.0
6068.3	2070.0	2310.7	2000.6	1754.1	1890.3	2044.3	1988.0	3433.2	2742.5	2217.8
52.2	347.8	694.4	916.0	108.6	349.4	176.5	428.8	61.8	46.1	175.3
3189.7	4271.8	5306.1	5958.1	4941.8	4525.0	6271.5	5215.6	5439.0	3949.1	6391.3
8659.2	3981.0	3788.0	4323.5	4040.8	3522.6	4379.3	4756.3	4392.1	2907.8	4081.2
2535.5	4525.5	4299.9	4285.1	3461.1	3963.6	3305.3	5365.5	5570.7	5119.4	5349.5
67.6	2094.6	1410.3	875.0	929.1	1803.4	1282.4	922.0	2116.5	1352.7	933.6
55.7	314.7	895.1	906.6	155.4	299.2	212.2	362.7	65.1	178.6	165.5
58.6	501.2	671.5	664.0	901.0	629.3	755.7	575.3	212.7	132.0	335.1
39.7	435.6	737.8	826.6	425.0	551.7	366.7	833.4	517.1	257.0	838.2
79.0	708.2	846.9	1055.8	531.0	702.1	689.5	675.9	542.3	201.8	480.6
96.2	470.3	988.5	883.1	359.9	507.5	450.1	518.9	257.9	67.8	277.6
15733.9	6642.0	6484.8	5957.4	5714.1	5361.4	6977.0	6421.2	7629.8	7773.0	6011.4
1494.0	1886.3	1599.2	2202.6	1862.1	1373.6	1833.3	1449.8	1343.0	896.4	1292.4
1977.2	2852.0	2638.2	1419.5	2649.1	2216.1	2984.1	3092.2	2662.2	1848.7	3597.9
38.6	54.4	71.6	96.0	51.6	62.2	65.0	71.4	26.2	32.0	35.9
49.1	322.0	713.2	684.5	257.7	526.3	386.0	584.7	176.8	469.8	309.5
668.8	2083.1	2814.9	2566.8	1665.8	2090.4	2601.6	2605.4	1336.2	1712.4	2043.8
1262.5	2056.4	2512.4	2451.1	1730.8	2049.4	3012.1	2091.2	2374.8	1509.0	2836.2
15372.6	4467.2	4402.7	5350.1	4179.2	4298.3	4166.9	5242.7	5540.4	7977.7	5356.0
108.4	1632.0	1753.2	1577.2	855.6	1581.6	1369.3	1783.7	948.2	1692.7	1082.1
53.3	587.7	633.8	827.1	296.1	813.0	265.3	744.5	105.5	362.8	238.7
51.9	1619.0	1869.2	2243.3	2036.3	1814.2	3394.9	2099.9	856.4	806.4	1649.2
3037.8	5434.9	3610.3	2447.6	1947.6	3528.5	2812.0	2747.3	4607.5	3388.1	2466.9
36.9	469.1	1271.5	1283.8	186.5	513.6	349.0	963.7	118.7	68.1	748.1
60.1	505.0	833.1	1035.7	389.3	630.0	637.7	926.7	248.1	521.2	329.7
493.8	2002.7	2915.6	1578.0	1336.0	1866.3	1179.7	1658.2	2826.0	3500.5	3854.2
340.1	985.1	1564.2	1576.2	844.4	1073.5	1006.5	1387.5	614.9	514.6	902.4
246.7	627.6	780.1	725.5	396.8	533.0	522.2	740.2	442.6	316.7	498.0
2925.6	2112.5	2094.1	2631.5	2401.2	1859.6	2204.8	2002.8	1879.8	1589.2	3267.1
5136.6	1939.2	2052.1	2442.6	1811.7	1954.0	1957.8	2283.2	2396.4	2437.7	2334.9
8590.4	2466.1	1752.3	2125.8	1794.3	1769.5	296.4	2393.2	1946.3	936.5	1875.1
659.7	510.6	757.1	726.7	450.9	854.6	401.1	768.6	317.7	1252.3	366.4
110.9	866.1	1190.9	1268.6	1165.9	974.2	1096.4	1498.0	890.1	1035.8	593.6
47.7	522.0	959.6	273.6	470.7	1488.7	321.5	1039.5	530.5	3756.6	622.2
1708.3	3100.0	2212.6	2548.2	2008.8	2460.3	2052.2	2930.2	2801.0	2303.8	1696.7
3642.8	2746.5	2925.7	2658.8	2160.4	2509.9	2079.9	2356.0	3004.9	1608.1	3874.7
7850.1	3290.0	3454.7	3142.1	1374.2	2820.2	3324.6	3452.0	4617.6	3738.6	4318.3
4637.0	5793.8	6553.7	5260.5	5066.3	5364.8	7656.6	5003.6	7404.8	5739.5	7200.9
35.3	66.2	68.5	103.3	24.7	27.3	25.3	30.8	35.2	28.0	38.9
1045.5	1716.9	1666.1	1770.5	1532.7	1584.3	1545.3	1664.8	1419.4	1001.6	1947.1

1417.2	1307.7	1205.8
2142.8	3041.5	1920.9
1125.7	447.2	374.8
5264.0	5537.6	4987.7
5247.1	5052.0	4524.5
4398.7	4472.5	3939.3
1498.6	913.2	2261.2
766.4	541.0	421.2
539.8	710.1	1056.6
761.8	775.9	770.8
1089.1	857.7	932.4
933.1	714.4	715.7
5185.9	7778.7	6873.8
1990.7	2284.3	1820.5
2617.7	3572.6	3158.2
122.2	103.0	61.4
810.3	740.2	501.8
2436.3	2848.2	2671.5
2074.2	2947.1	3294.3
5239.5	5997.4	4312.6
1469.2	1996.8	2008.9
806.0	700.0	1086.0
2076.1	1091.5	2952.9
2827.0	3385.0	3501.5
1607.2	650.9	823.5
1170.9	1046.3	656.2
1854.5	1765.6	1375.0
1501.2	1376.4	1977.1
854.0	814.2	506.3
2808.2	2918.4	2114.4
1998.0	2005.4	1804.2
2241.0	4011.3	2682.0
770.9	1116.8	961.5
1358.8	1768.3	1073.3
1664.0	1170.1	1054.4
2461.7	2807.4	2244.3
2900.0	2588.2	2814.1
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4403.3	4968.7	4266.6
63.6	67.0	28.7
1591.7	2424.2	1302.7

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g__Roseburia
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s__Eubacterium rectale	18093
s__Eubacterium rectale	18095
s__Eubacterium rectale	18099
s__Eubacterium rectale	18101
s__Eubacterium rectale	18110
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s__Eubacterium rectale	18177
s__Eubacterium rectale	18180

DQ795667.1 gg_id:198090 human fecal clone RL178_aan68a12 DQ795
FJ684405.1 gg_id:528385 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
DQ798746.1 gg_id:182742 human fecal clone RL181_aao00g12 DQ798
FJ371157.1 gg_id:366810 feces adult twins and mothers; TS6 clone TS6_a01f02 FJ3711
FJ365684.1 gg_id:362085 feces adult twins and mothers; TS21 clone TS21_a01g08 FJ3656
DQ806452.1 gg_id:176365 human fecal clone RL186_aan92f10 DQ806
GQ079595.1 gg_id:442940 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231f0 GQ079
EU768219.1 gg_id:306963 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
DQ327352.1 gg_id:148544 Metagenomic gut microbiome healthy human stool clone E907 DQ327
FJ364209.1 gg_id:369549 feces adult twins and mothers; TS150 clone TS150_a04c03 FJ3642
EU763899.1 gg_id:335439 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7638
FJ364351.1 gg_id:358621 feces adult twins and mothers; TS15 clone TS15_a01h08 FJ3643
EU762879.1 gg_id:334484 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7628
FJ369459.1 gg_id:370323 feces adult twins and mothers; TS50 clone TS50_a04g08 FJ3694
EU776763.1 gg_id:311423 Mongoose lemur feces clone ML_aaj27a09 EU7767
EU762980.1 gg_id:340350 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7629
FJ369896.1 gg_id:360143 feces adult twins and mothers; TS55 clone TS55_a02a07 FJ3698
EU765367.1 gg_id:308641 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU7653
EU763604.1 gg_id:315672 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
DQ807644.1 gg_id:182440 human fecal clone RL180_aah35d06 DQ807
FJ369013.1 gg_id:362038 feces adult twins and mothers; TS4 clone TS4_a03c06 FJ3690
FJ364207.1 gg_id:365481 feces adult twins and mothers; TS150 clone TS150_a04c01 FJ3642
FJ368975.1 gg_id:361772 feces adult twins and mothers; TS4 clone TS4_a02g05 FJ3689
FJ371059.1 gg_id:367050 feces adult twins and mothers; TS5 clone TS5_a04d11 FJ3710
DQ808283.1 gg_id:186962 human fecal clone RL180_aao74g07 DQ808
FJ363277.1 gg_id:364103 feces adult twins and mothers; TS149 clone TS149_a01d02 FJ3632
DQ808131.1 gg_id:182892 human fecal clone RL180_aao73a08 DQ808
DQ806615.1 gg_id:197527 human fecal clone RL186_aao46g04 DQ806
DQ325783.1 gg_id:148413 Metagenomic gut microbiome healthy human stool clone B473 DQ325
DQ327426.1 gg_id:148870 Metagenomic gut microbiome healthy human stool clone E985 DQ327
DQ802630.1 gg_id:195582 human fecal clone RL188_aan94c12 DQ802
FJ364463.1 gg_id:368556 feces adult twins and mothers; TS15 clone TS15_a03c06 FJ3644
FJ371335.1 gg_id:364555 feces adult twins and mothers; TS6 clone TS6_a03g03 FJ3713
FJ368262.1 gg_id:364326 feces adult twins and mothers; TS3 clone TS3_a02b08 FJ3682
DQ905146.1 gg_id:161984 human fecal clone 002C-e11 DQ905
DQ806197.1 gg_id:190602 human fecal clone RL186_aah62e05 DQ806
FJ362862.1 gg_id:362903 feces adult twins and mothers; TS13 clone TS13_a04b03 FJ3628
FJ362755.1 gg_id:362203 feces adult twins and mothers; TS13 clone TS13_a02g04 FJ3627
FJ370350.1 gg_id:368308 feces adult twins and mothers; TS56 clone TS56_a03g09 FJ3703
EU763912.1 gg_id:346172 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7639
EU766779.1 gg_id:306617 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667

126.5	2020.7	1870.2	1995.6	1878.0	1889.7	1610.4	2605.3	1731.9	2649.1	2466.2
2009.9	2720.0	3463.1	2936.9	3001.4	2677.5	3182.5	3239.5	2952.5	2452.6	3064.0
1213.4	2068.8	1953.2	2133.6	1929.8	1854.9	1849.7	1969.5	2302.3	2878.1	1422.9
8451.2	3897.9	3529.7	3919.9	4359.0	3171.6	3748.0	3683.6	3917.2	5212.7	4110.9
61.1	1494.6	1601.2	1353.1	1513.2	1169.0	2084.8	1286.7	1121.7	759.4	1314.0
19854.7	6858.4	5500.9	6833.7	5815.9	6224.7	6051.1	6868.6	6781.4	5094.5	8972.9
47.1	152.6	290.7	389.5	89.5	152.0	84.8	286.6	47.2	47.4	66.0
78.5	1136.7	1532.0	1879.9	753.8	1346.1	1286.3	1770.8	786.4	536.9	961.0
49.3	198.6	303.0	414.9	126.2	214.9	416.0	318.6	201.0	79.9	98.0
52.0	1413.8	1464.5	1867.8	307.8	887.0	325.0	529.0	427.4	401.0	255.9
195.3	1234.8	1564.3	1837.7	1835.4	1419.2	1699.4	1958.4	628.6	303.9	1242.3
1213.2	5752.7	5467.4	5293.6	5594.1	4801.0	6107.9	5958.8	4056.3	5735.2	4238.0
13690.9	4233.8	4842.7	4796.8	4754.4	4423.4	4775.6	4725.5	6071.8	6352.0	4679.9
266.4	340.1	319.2	483.1	415.3	466.1	333.2	376.7	232.8	71.6	256.0
4409.4	2779.2	3257.5	4002.1	2730.2	2859.8	3524.8	3688.5	1943.9	1674.0	3201.1
1079.1	1669.7	1643.1	1474.2	1382.2	1733.7	1109.1	2610.9	1604.2	2455.3	2049.8
236.5	2341.9	2864.0	2715.0	2596.7	2530.4	2535.3	2753.4	1585.6	1028.2	1432.1
30076.7	8470.1	8097.3	8790.7	7789.5	7417.9	8617.7	7613.3	10197.9	10676.2	11398.8
71.4	118.1	197.8	129.9	78.4	85.4	94.9	177.6	46.3	25.5	67.5
80.6	381.7	633.9	794.3	562.1	416.3	591.6	811.6	381.6	103.7	234.2
96.1	412.0	921.4	872.1	467.0	565.6	603.3	689.7	156.7	144.5	328.5
13375.7	5050.8	4872.5	6447.0	4939.7	4965.5	5374.3	5472.1	6546.3	5466.7	5726.4
43.8	315.2	480.8	499.3	194.7	535.1	170.9	491.9	148.6	593.2	188.9
450.9	7369.3	5791.0	5244.7	3995.0	6591.3	5633.8	6402.9	5070.3	3675.1	6647.2
594.3	484.4	706.1	643.6	472.7	793.8	462.1	770.5	349.6	401.6	614.4
40.4	393.3	335.2	659.7	131.2	195.9	145.0	299.8	56.1	59.6	66.9
86.5	4097.4	4406.6	5026.5	4873.9	4119.8	4703.6	3785.7	2127.8	2669.8	3691.0
50.2	119.4	180.6	135.4	75.2	78.6	112.1	102.0	34.3	38.7	50.7
2283.5	3011.5	2475.4	2476.0	1981.7	2347.3	2192.1	2553.3	2240.7	1615.4	1696.5
148.0	843.9	1147.1	1081.2	824.4	887.2	1270.7	1309.7	583.7	316.9	565.5
71.2	2325.6	3135.4	3177.7	2689.5	2479.9	3379.8	3290.3	2023.8	1013.9	2497.8
884.5	1401.7	1451.7	1639.7	985.0	1209.5	710.8	1663.9	785.7	429.3	1089.5
58.8	172.3	309.5	291.0	129.0	183.4	147.4	204.5	121.4	336.7	106.8
8855.5	2580.5	2375.1	2320.6	1680.9	2138.7	1845.9	2464.5	2886.4	2601.6	2158.5
195.5	1490.6	1558.7	479.1	263.8	791.6	288.2	749.3	1639.7	1258.3	1191.5
43.5	619.9	1022.4	1003.8	531.0	757.6	406.6	1030.5	396.8	492.3	669.4
542.7	269.0	497.9	362.3	385.9	270.7	411.4	400.7	387.1	170.8	226.6
58.5	473.4	422.4	300.1	366.2	290.0	405.9	732.3	213.0	479.2	265.1
2699.9	2786.3	2713.9	2884.3	2609.9	2630.3	2952.6	2916.3	1972.0	2202.8	2290.4
44.9	575.6	679.9	638.2	417.5	656.4	362.8	743.2	127.6	108.9	254.4
214.8	3657.7	3079.3	2481.8	1698.7	2739.0	1722.0	2379.2	3624.4	3018.3	2553.6

2329.4	1970.9	2515.1
3470.9	2873.1	3469.7
2326.4	2747.3	1407.7
2842.3	3661.6	4324.8
1061.2	1650.1	1751.7
6036.0	7099.8	5577.4
368.5	366.0	222.2
2074.6	1822.8	2354.4
920.4	238.5	364.4
1214.4	1185.7	2402.9
1841.2	1604.8	1794.3
4235.2	5859.3	6543.6
5201.2	6256.1	4985.9
408.3	511.5	410.6
3595.1	2877.1	4523.5
2001.5	1632.5	1662.5
2191.0	3093.9	3773.6
7630.5	8745.1	8500.6
164.8	160.6	156.3
839.3	1400.7	571.8
866.2	1106.8	638.0
5132.5	5265.3	5606.9
1051.2	678.4	325.5
5265.0	6235.2	5643.3
913.7	794.5	976.9
548.1	296.6	345.3
3810.1	3548.8	3896.2
160.8	128.3	106.4
2444.5	3093.0	2972.2
1259.8	1462.9	1680.0
3827.7	3174.1	4221.2
1880.7	1328.7	1226.1
340.8	318.9	182.3
2637.1	2658.5	2645.4
444.2	615.5	325.7
1413.4	1088.7	829.1
464.3	828.1	413.2
268.1	616.5	996.4
2976.8	2875.3	2995.5
1348.9	483.2	751.7
2376.9	2482.9	3891.2

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
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Roseburia
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s__Eubacterium rectale	18181
s__Eubacterium rectale	18182
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DQ807815.1 gg_id:182994 human fecal clone RL180_aah37e09 DQ807
FJ679947.1 gg_id:531715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
FJ363921.1 gg_id:369590 feces adult twins and mothers; TS14 clone TS14_a04h11 FJ3639
FJ370315.1 gg_id:364928 feces adult twins and mothers; TS56 clone TS56_a03d02 FJ3703
DQ795566.1 gg_id:193977 human fecal clone RL178_aan66d01 DQ795
DQ808026.1 gg_id:193343 human fecal clone RL180_aan70h08 DQ808
FJ684744.1 gg_id:524474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ806741.1 gg_id:192923 human fecal clone RL186_aao48b09 DQ806
FJ684927.1 gg_id:517856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
DQ904800.1 gg_id:162220 human fecal clone 001B-f7 DQ904
FJ684978.1 gg_id:529927 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ369414.1 gg_id:368691 feces adult twins and mothers; TS50 clone TS50_a04b12 FJ3694
DQ798553.1 gg_id:198159 human fecal clone RL181_aan98b09 DQ798
DQ795385.1 gg_id:187809 human fecal clone RL178_aah53f11 DQ795
FJ363967.1 gg_id:357135 feces adult twins and mothers; TS150 clone TS150_a01d12 FJ3639
DQ803172.1 gg_id:178123 human fecal clone RL311_aam21e06 DQ803
DQ824944.1 gg_id:176391 human fecal clone RL185_aao71c12 DQ824
EU762004.1 gg_id:324073 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
EU466805.1 gg_id:301604 African elephant feces clone AFEL2_aao29g01 EU466
FJ370280.1 gg_id:368376 feces adult twins and mothers; TS56 clone TS56_a02g08 FJ3702
FJ371042.1 gg_id:367397 feces adult twins and mothers; TS5 clone TS5_a04c04 FJ3710
FJ371163.1 gg_id:368473 feces adult twins and mothers; TS6 clone TS6_a01f09 FJ3711
DQ802612.1 gg_id:180645 human fecal clone RL188_aan94b02 DQ802
FJ363008.1 gg_id:365189 feces adult twins and mothers; TS148 clone TS148_a01h01 FJ3630
DQ808019.1 gg_id:190672 human fecal clone RL180_aan70g06 DQ808
DQ809580.1 gg_id:183969 human fecal clone RL184_aan81b05 DQ809
FJ369996.1 gg_id:358126 feces adult twins and mothers; TS55 clone TS55_a03c05 FJ3699
AY976660.1 gg_id:126762 human cecum mucosal biopsy clone K226 AY976
FJ677317.1 gg_id:519781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ370363.1 gg_id:360803 feces adult twins and mothers; TS56 clone TS56_a03h12 FJ3703
EU466891.1 gg_id:294818 African elephant feces clone AFEL2_aao30h08 EU466
FJ369156.1 gg_id:363988 feces adult twins and mothers; TS4 clone TS4_a04h11 FJ3691
FJ673219.1 gg_id:529666 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ678155.1 gg_id:528673 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
DQ809907.1 gg_id:187555 human fecal clone RL184_aao65g08 DQ809
FJ684461.1 gg_id:515520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
DQ905807.2 gg_id:164453 human fecal clone 29E-b8 DQ905
DQ804644.1 gg_id:183733 human fecal clone RL187_aao70g09 DQ804
DQ810076.1 gg_id:190298 human fecal clone RL184_aao67g11 DQ810
FJ362918.1 gg_id:358696 feces adult twins and mothers; TS13 clone TS13_a04g05 FJ3629
DQ798438.1 gg_id:193735 human fecal clone RL181_aah42f06 DQ798

73.0	674.4	847.4	854.5	742.3	576.0	846.2	744.6	388.6	195.9	590.8
173.3	583.6	833.2	760.7	608.0	697.7	504.6	926.0	224.9	153.2	304.2
1425.3	1107.5	1254.0	1268.5	936.8	954.7	996.0	1194.7	1001.8	884.6	956.3
1581.6	2772.8	2801.4	2574.3	2214.9	2796.4	2281.1	2291.9	2408.0	1931.5	2121.4
18281.7	7424.8	6548.8	6904.6	6864.1	6124.1	6852.1	5885.3	9377.1	6525.4	9933.8
1348.3	4223.8	4217.8	4227.8	3049.5	3567.9	4234.9	4121.7	7362.3	5198.5	4753.2
4825.3	5192.1	4178.8	4364.0	3802.9	4451.6	4186.8	4374.4	4478.8	3598.5	4410.1
46.4	229.6	445.7	479.2	141.3	280.3	245.3	370.9	77.5	136.2	146.0
52.7	240.6	492.7	513.8	169.8	243.5	313.5	233.1	81.3	51.5	148.0
1306.9	1740.8	1402.2	1837.5	1986.3	1740.0	1181.1	1426.7	926.5	739.3	1073.9
5441.8	3615.2	3065.3	3585.7	3061.1	2947.0	3053.2	3837.7	3824.5	4465.8	4327.2
53.5	544.1	805.3	904.1	149.6	507.0	265.4	441.4	148.0	337.2	277.6
111.7	3772.9	3030.6	1544.3	1244.8	2669.1	1298.1	2095.4	2341.4	3081.3	1574.4
435.4	3509.4	3967.1	3872.5	2742.4	3612.8	3704.4	4553.3	2441.8	5889.0	3342.1
4095.9	2981.8	3217.4	3554.3	3177.6	2962.6	2664.6	3345.4	2367.4	1878.9	2924.7
19397.0	6440.4	6541.6	6414.5	6420.5	5490.9	7783.5	6841.9	6388.6	6388.6	6542.0
69.8	1246.1	1926.5	1813.9	1110.2	1632.6	897.6	1914.6	783.4	2430.5	1421.3
617.7	826.6	1134.9	1254.4	458.6	831.4	712.1	1454.3	466.8	994.6	728.2
74.0	922.2	841.9	801.4	304.0	650.4	405.0	814.5	621.1	421.2	387.6
51.4	106.3	148.9	148.6	71.3	123.1	75.6	158.3	46.5	121.8	92.0
7579.0	2890.5	2290.3	2633.2	1738.6	2176.8	2704.7	2987.2	3862.1	2641.2	2101.1
50.0	515.7	880.4	915.1	597.7	758.0	612.6	945.9	196.3	385.8	374.1
12743.5	4508.4	4448.7	4568.2	4086.1	4436.0	4174.7	4573.8	4248.5	5452.1	5141.2
415.6	1538.0	2310.2	2135.1	1914.2	2307.4	2003.6	2316.3	1466.2	4198.7	2167.8
68.4	258.6	307.9	351.9	113.7	97.2	135.2	196.1	64.2	68.5	113.4
567.8	721.7	958.5	949.3	598.8	613.4	583.3	755.5	672.9	604.9	522.6
79.2	854.2	1107.8	1010.2	710.9	1164.1	812.8	934.6	514.1	1385.7	487.1
249.2	1420.3	1741.9	1962.9	990.4	1477.2	1124.8	1625.5	1191.2	573.6	1195.2
71.5	649.6	1203.6	1250.5	210.0	650.8	302.4	990.7	64.3	54.4	312.0
7770.0	6373.1	5760.5	6405.0	5247.9	5446.7	5950.1	5688.7	5280.4	5510.2	6803.0
112.2	1522.8	2580.0	2130.6	1100.7	2165.5	1608.1	1919.7	1105.7	1739.6	1390.7
611.6	917.8	802.1	951.6	483.7	795.2	614.0	662.8	580.7	300.1	433.2
79.7	1177.0	1600.2	1901.8	838.1	1489.7	1345.2	1937.4	789.5	538.3	969.2
5777.5	2606.6	2173.0	2319.3	1824.5	1930.2	2265.8	1960.9	2681.9	2454.7	3013.3
39.4	775.6	1315.3	1339.3	639.9	867.1	891.2	1094.8	491.7	272.2	727.6
585.3	2057.9	2990.4	2630.2	1944.2	2123.2	2612.1	1887.2	1194.6	1499.0	2115.4
125.7	3110.6	2996.2	2600.6	1773.1	2279.7	2423.1	2409.2	2983.8	2329.0	2717.7
75.1	570.3	804.0	1160.3	108.9	353.1	621.5	731.3	303.6	70.4	267.9
36.0	337.6	287.6	279.8	130.2	121.3	124.3	216.3	38.6	61.6	107.4
2491.2	6049.4	5534.0	5863.5	5220.0	5358.1	5706.5	5580.0	10417.2	6263.3	6388.4
4519.4	3622.1	3728.2	4023.7	3017.5	3596.5	3549.9	3209.8	4617.4	2594.6	6373.0

1038.5	1034.0	880.6
1885.3	643.6	772.7
1530.0	1623.4	1601.9
2691.3	2748.9	2399.6
5727.8	9172.5	6360.4
3834.5	4606.5	3736.4
4040.4	4705.5	5003.8
826.4	298.1	323.7
203.3	363.8	292.1
1469.9	1879.0	1520.9
2904.4	4469.2	3233.3
1063.7	588.1	529.2
2087.1	2210.5	4283.7
3604.8	5375.3	4273.4
3721.7	2975.2	3402.8
5881.0	7364.1	7597.5
2551.0	1891.4	1888.4
1431.1	1586.6	998.8
1647.0	821.6	762.7
160.4	171.4	167.6
2482.7	3760.6	2587.2
1732.1	846.8	846.0
5056.5	5322.1	4570.4
2464.3	2667.0	2984.1
260.1	306.6	311.9
975.4	1073.8	809.2
1050.4	1199.3	930.8
1187.5	1382.6	1395.5
1748.3	646.1	768.6
5819.6	5940.0	6238.4
2673.6	2866.1	1990.2
861.3	731.6	762.9
2275.3	1933.4	2740.6
2441.7	3283.3	1911.5
1970.8	883.9	1700.0
2358.7	2807.1	3132.6
2460.1	1673.0	1844.1
822.1	669.9	677.8
169.6	414.0	437.8
5623.4	5780.3	5291.2
3608.9	3530.4	2626.8

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
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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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

g__Roseburia
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s__Eubacterium rectale	18286
s__Eubacterium rectale	18288
s__Eubacterium rectale	18293
s__Eubacterium rectale	18294
s__Eubacterium rectale	18296
s__Eubacterium rectale	18298
s__Eubacterium rectale	18302
s__Eubacterium rectale	18305
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s__Eubacterium rectale	18311
s__Eubacterium rectale	18606
s__Eubacterium rectale	18782
s__Eubacterium rectale	19146
s__Eubacterium rectale	19324
s__Eubacterium rectale	21302
s__Eubacterium rectale	21512
s__Roseburia faecis	17708
s__Roseburia faecis	17733
s__Roseburia faecis	17762
s__Roseburia faecis	17782
s__Roseburia faecis	17785
s__Roseburia faecis	17801
s__Roseburia faecis	17871
s__Roseburia faecis	17925
s__Roseburia faecis	18007
s__Roseburia faecis	18051
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s__Roseburia faecis	18105
s__Roseburia faecis	18122
s__Roseburia faecis	18136
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s__Roseburia faecis	18280
s__Roseburia faecis	18295
s__unclassified	17449
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s__unclassified	17453

DQ798007.1 gg_id:187875 human fecal clone RL302_aal94d11 DQ798
EU768041.1 gg_id:350250 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
DQ794795.1 gg_id:193556 human fecal clone RL240_aaj32d10 DQ794
EU768316.1 gg_id:330961 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ806617.1 gg_id:197873 human fecal clone RL186_aao46g07 DQ806
FJ368207.1 gg_id:368611 feces adult twins and mothers; TS3 clone TS3_a01e03 FJ3682
DQ798454.1 gg_id:189241 human fecal clone RL181_aah42h03 DQ798
DQ798242.1 gg_id:179996 human fecal clone RL181_aah39d05 DQ798
DQ798182.1 gg_id:175518 human fecal clone RL302_aal96e08 DQ798
FJ363366.1 gg_id:360526 feces adult twins and mothers; TS149 clone TS149_a02d06 FJ3633
DQ807352.1 gg_id:178011 human fecal clone RL307_aam05d12 DQ807
DQ805671.1 gg_id:175635 human fecal clone RL306aal89f06 DQ805
DQ801962.1 gg_id:186097 human fecal clone RL241_aaj01a11 DQ801
DQ794835.1 gg_id:176340 human fecal clone RL240_aaj32h11 DQ794
DQ801420.1 gg_id:198605 human fecal clone RL388_aao95c08 DQ801
DQ824792.1 gg_id:197864 human fecal clone RL185_aao69d01 DQ824
DQ825066.1 gg_id:195105 human fecal clone RL185_aao72h10 DQ825
FJ363558.1 gg_id:359682 feces adult twins and mothers; TS149 clone TS149_a04f06 FJ3635
EU728794.1 gg_id:314893 Roseburia sp. str. DJF_VR77 EU728
FJ685213.1 gg_id:516832 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
EU531971.1 gg_id:260732 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
DQ905089.1 gg_id:166670 human fecal clone 2-002-h1 DQ905
FJ672970.1 gg_id:517938 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ797487.1 gg_id:186077 human fecal clone RL248_aaj00a02 DQ797
DQ325547.1 gg_id:145765 Metagenomic gut microbiome healthy human stool clone B003 DQ325
FJ681797.1 gg_id:520892 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
DQ825293.1 gg_id:181390 human fecal clone RL185_aan87h10 DQ825
FJ362949.1 gg_id:363026 feces adult twins and mothers; TS148 clone TS148_a01b06 FJ3629
FJ367069.1 gg_id:358597 feces adult twins and mothers; TS28 clone TS28_a03b08 FJ3670
EU768128.1 gg_id:317350 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU508660.1 gg_id:261837 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36h11 EU508
FJ685484.1 gg_id:514579 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
DQ808419.1 gg_id:179885 human fecal clone RL180_aao76d03 DQ808
DQ807601.1 gg_id:177520 human fecal clone RL307_aam08g07 DQ807
FJ685032.1 gg_id:509017 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
AF371608.1 gg_id:107098 swine intestine clone p-5-a5 AF371
DQ825299.1 gg_id:177772 human fecal clone RL185_aan88a07 DQ825
AF371610.1 gg_id:26201 swine intestine clone p-969-s962-5 AF371
FJ680909.1 gg_id:514384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ824430.1 gg_id:176014 human fecal clone RL304_aal75h09 DQ824
FJ682651.1 gg_id:512204 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826

7316.8	5471.3	4673.0	4992.2	5137.8	4727.4	4996.3	4872.8	4359.5	3781.8	5603.4
85.0	342.0	531.5	610.1	245.7	314.2	344.8	783.5	206.4	37.1	246.8
163.3	1740.6	2011.6	2173.4	1679.6	1907.0	1915.3	2462.6	2188.0	1956.8	1557.2
102.7	966.1	1157.1	1043.1	856.7	799.9	1057.4	874.7	926.0	525.2	436.1
7913.0	3946.4	3737.5	4937.9	3569.5	3776.5	3739.0	3429.3	4420.7	3308.8	4895.8
6188.3	3658.5	3048.0	3466.5	3358.6	3421.6	3853.5	4554.5	2792.5	3528.3	2703.2
1375.8	1427.3	1387.4	1676.1	1157.2	1696.0	1120.0	2074.4	1086.8	2212.9	1845.4
2701.2	1691.8	1695.6	1973.3	1756.5	1542.2	1522.6	1658.9	1389.2	1099.5	1697.3
5706.2	3349.1	4321.3	3740.5	3356.0	3512.2	3403.5	2974.7	3894.9	2876.0	4413.4
47.7	273.5	476.2	608.1	69.3	186.0	134.9	312.3	95.7	193.6	162.4
4986.7	983.5	965.3	970.6	1441.1	938.0	1194.3	1068.3	726.6	397.3	769.6
3730.2	1602.1	1597.2	1704.7	1672.0	443.4	1094.7	1582.1	1175.9	1157.9	1696.7
1446.8	5271.1	4994.2	4942.9	5164.9	4662.1	5154.2	4212.1	4892.1	1458.5	4205.0
89.4	536.6	1153.6	866.3	449.8	635.0	530.1	988.0	244.6	451.3	554.9
1007.5	3085.3	3073.2	3048.6	2551.1	3243.5	2970.2	4463.2	1909.4	2307.2	2639.6
188.3	2032.6	1237.8	708.1	831.5	1443.6	463.0	828.6	1679.4	491.3	639.4
3019.1	1635.4	1246.2	1590.8	1269.3	1221.6	1324.8	1576.3	1278.7	971.9	1758.3
2101.1	3166.9	1702.3	3006.0	2701.3	2874.0	2424.2	2826.7	4818.6	3670.6	3771.8
275.6	2368.7	3488.3	3135.8	1587.8	2843.4	2322.9	3175.9	1020.5	1115.0	2641.2
55.7	300.4	378.5	509.0	158.5	226.9	270.7	490.9	312.6	197.1	208.0
895.1	3010.9	3494.5	3600.2	1834.8	2597.9	2173.5	4165.8	1340.3	2921.0	2516.3
41.3	1348.5	2063.6	1929.7	1662.4	1633.4	1716.3	2261.2	950.5	533.8	1024.3
1277.6	1091.4	1382.8	2189.4	1049.5	999.1	1290.9	985.1	789.3	760.5	1054.9
1575.7	1761.7	2434.7	1607.2	1588.1	1881.6	1568.6	1406.0	2705.6	1760.3	1251.9
38.3	694.3	1410.5	904.1	399.2	1110.1	569.9	1195.5	697.7	154.5	961.2
44.8	299.9	591.4	608.0	132.0	312.7	294.1	633.3	145.7	105.7	209.3
35.4	1743.5	2104.8	2394.6	1062.5	1056.7	2548.1	2803.8	1303.7	157.7	1207.5
97.3	620.7	1169.6	872.6	230.6	458.6	314.1	488.2	290.2	224.1	442.8
42.0	381.4	613.0	590.3	154.0	377.3	343.1	408.3	115.2	50.6	179.2
1716.8	2373.8	2719.7	2765.3	1250.3	2100.3	1841.7	1893.9	2366.4	2546.0	2060.0
240.7	1379.8	1705.8	1846.9	1807.1	1564.4	2064.4	1695.3	758.2	400.4	939.1
558.2	2644.5	2762.1	2466.1	1275.5	2091.8	2189.8	3005.4	2022.3	2196.0	1948.6
467.0	1743.0	849.1	1700.6	2512.6	1662.8	1744.9	1858.3	2140.6	1214.3	1660.7
133.6	333.8	481.6	420.0	368.6	359.6	400.9	474.4	368.7	404.8	345.7
6251.2	2349.9	1918.1	2153.5	1749.6	2379.4	1675.0	2068.4	1805.7	1408.2	2423.0
196.9	1339.2	1776.0	2083.3	1339.5	1256.7	1526.6	1960.6	640.5	244.5	1399.5
2178.9	886.6	991.3	1195.4	965.0	972.3	857.2	312.9	676.6	364.1	811.6
52.7	544.9	697.4	857.3	749.2	651.2	953.7	847.7	260.3	256.7	735.8
10914.6	5094.4	5150.1	5519.0	4586.0	4420.0	4819.4	4628.5	5409.1	5166.6	6865.6
42.3	373.5	282.5	160.4	168.0	207.4	293.0	333.0	439.7	322.4	196.1
189.4	3796.2	3773.1	4308.5	2864.9	2865.1	2916.5	3497.4	3023.1	2714.7	4149.5

4518.8	5751.2	5334.0
445.7	656.4	2147.6
2569.2	2147.9	2230.7
1022.5	770.8	822.6
3575.8	4809.6	3492.7
3660.8	3909.0	3977.4
1731.0	1206.7	1315.8
1875.7	2057.2	1689.4
3381.8	3759.4	3158.8
377.0	352.1	243.2
1206.2	1316.5	1952.5
1236.6	2546.3	1562.7
4328.3	4792.9	6088.5
777.0	1098.0	1412.8
4087.8	4513.6	5906.6
878.1	688.1	633.2
1545.5	1846.7	1125.2
2557.2	2794.7	2248.6
3809.6	3106.9	2730.6
451.8	478.8	335.0
4147.5	2787.5	3809.9
1916.1	1633.1	1939.9
1473.6	1403.3	1546.8
1392.4	3008.2	2035.8
895.5	805.5	922.7
387.2	469.4	795.0
3102.2	1608.9	2833.0
825.7	782.4	1002.1
518.5	456.7	419.9
2530.8	2675.6	1987.4
1733.3	1752.5	3428.3
3015.4	2715.8	3054.8
1841.9	3228.2	1698.5
407.4	324.1	591.1
1844.1	1918.6	1712.1
2049.3	1677.3	2858.1
1350.5	1737.1	979.1
814.6	561.3	633.3
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385.9	404.9	252.3
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DQ807054.1 gg_id:183928 human fecal clone RL244_aaj45f04 DQ807
EU461258.1 gg_id:300235 hamadryas baboon feces clone BAZ_aah91f09 EU461
DQ809931.1 gg_id:182676 human fecal clone RL184_aao66a09 DQ809
FJ679610.1 gg_id:530857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU765539.1 gg_id:351850 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ684629.1 gg_id:525474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ679897.1 gg_id:510518 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
DQ805120.1 gg_id:193105 human fecal clone RL249_aaj81e02 DQ805
AF371602.1 gg_id:45296 swine intestine clone p-61-a5 AF3716
AY916373.1 gg_id:113909 human stool clone D522 AY9163
EU775400.1 gg_id:313850 Western lowland gorilla feces clone GORSD_2aaa01a04 EU7754
FJ363002.1 gg_id:358798 feces adult twins and mothers; TS148 clone TS148_a01g06 FJ3630
DQ804753.1 gg_id:198208 human fecal clone RL187_aao72c05 DQ804
DQ807158.1 gg_id:196312 human fecal clone RL244_aaj47a03 DQ807
EU762661.1 gg_id:323781 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU7626
DQ794669.1 gg_id:187633 human fecal clone RL240_aaj30h06 DQ794
DQ532269.1 gg_id:162623 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
DQ801408.1 gg_id:197953 human fecal clone RL388_aao95b07 DQ801
DQ808024.1 gg_id:192415 human fecal clone RL180_aan70h06 DQ808
FJ684308.1 gg_id:519190 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
FJ681565.1 gg_id:518940 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
AM500721.1 gg_id:562038 proof spatial heterogeneity hot composting clone D14 AM500
DQ808441.1 gg_id:195207 human fecal clone RL180_aao76f02 DQ808
GQ448613.1 gg_id:560963 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU778522.1 gg_id:311704 Red river hog feces clone RRH_aaa04f09 EU7785
FJ371198.1 gg_id:358875 feces adult twins and mothers; TS6 clone TS6_a02a11 FJ3711
EU794281.1 gg_id:316489 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K16 EU7942
DQ800180.1 gg_id:185651 human fecal clone RL303_aal69c07 DQ800
FJ679371.1 gg_id:526154 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ678578.1 gg_id:532316 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ803526.1 gg_id:181189 human fecal clone RL251_aaj87a02 DQ803
EU779266.1 gg_id:326170 Trancaspian Urial feces clone TU2_aaa03c05 EU7792
DQ823907.1 gg_id:194053 human fecal clone RL250_aaj80g06 DQ823
FJ685118.1 gg_id:512836 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
DQ794531.1 gg_id:195493 human fecal clone RL240_aaj29b12 DQ794
DQ803843.1 gg_id:199643 human fecal clone RL200_aai59a09 DQ803
FJ680496.1 gg_id:522134 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
DQ824821.1 gg_id:198616 human fecal clone RL185_aao69f09 DQ824
EU771355.1 gg_id:333279 Asiatic elephant feces clone AE2_aaa01f10 EU7713
GQ448639.1 gg_id:537357 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448

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59.3	299.5	530.0	555.3	517.4	305.0	453.7	492.9	220.2	128.7	175.7
49.2	479.6	628.1	793.0	66.5	295.4	220.7	797.7	74.0	99.9	172.0
13058.6	5214.4	5016.4	5967.0	4861.4	5162.7	5208.8	5286.2	5980.2	6370.0	5719.7
42.6	372.3	581.6	682.2	150.8	304.0	298.6	474.6	116.2	40.7	518.6
208.2	1435.2	2376.7	1965.5	421.4	1294.0	744.2	2295.9	514.7	283.5	2090.7
45.4	593.2	876.7	1066.5	424.3	788.1	431.0	1170.5	176.2	95.6	586.1
44.0	430.8	844.0	608.7	222.9	667.3	147.9	1281.8	262.3	130.4	465.2
61.1	105.7	139.3	158.3	153.3	147.9	144.0	180.1	75.5	67.0	162.9
1410.7	1793.7	1953.4	1941.1	1334.1	1553.9	1446.8	1460.4	1452.9	474.8	1065.5
291.7	1068.8	1519.2	1150.4	822.3	1036.6	1319.4	903.5	1014.7	1746.3	1440.1
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72.6	318.4	450.5	594.1	122.8	156.5	212.6	183.8	45.8	40.6	116.3
352.4	2435.6	2713.1	2285.8	1853.2	1791.4	1881.7	1980.0	2640.1	1739.0	1500.5
86.7	923.1	1523.0	1485.4	738.1	1100.0	883.2	1426.0	483.2	236.5	917.0
85.7	1390.1	1706.4	1397.1	921.7	1304.1	952.4	1289.6	2002.5	627.6	806.7
181.9	1198.5	2367.3	1904.5	730.5	1100.9	613.7	1878.2	433.2	499.5	1178.6
30.5	65.0	183.8	293.5	21.9	68.5	38.5	127.2	22.1	18.9	60.0
68.6	651.1	759.9	1234.1	265.9	514.2	336.0	956.4	170.5	107.8	367.6
41.3	843.5	1187.2	1467.9	528.3	704.5	822.4	1313.9	177.0	88.1	406.3
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136.9	417.8	589.0	599.0	265.9	482.8	282.5	563.6	858.5	516.0	509.2
41.9	980.4	1267.4	1303.6	797.1	872.3	1151.4	1122.0	340.4	251.3	536.9
29.9	108.4	272.0	417.0	24.1	146.2	177.0	256.1	56.9	29.9	277.5
156.7	1421.8	2232.8	2368.3	983.7	1629.7	1286.7	2087.8	873.3	520.7	1600.6
36.8	575.9	552.4	653.7	330.3	372.7	318.4	477.1	78.2	86.1	187.5
16159.2	8225.0	6193.8	4846.7	5133.3	6635.8	4913.4	5317.1	9728.1	5674.3	6950.8
217.7	789.9	1196.7	1371.4	1439.6	1077.2	1272.2	1565.2	742.6	641.9	1368.8
45.8	141.4	328.7	365.8	103.9	202.8	72.4	230.0	111.2	77.6	127.8
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105.6	420.5	348.6	372.5	610.3	422.1	317.6	482.1	205.1	118.2	214.1
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1425.9	751.5	2156.2
148.3	291.1	342.1
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804.1	1099.3	1236.9
3112.7	2121.9	3715.6
314.6	322.5	278.4
2115.5	1740.7	2853.7
1525.7	1101.1	1920.7
1127.0	1113.3	1370.4
1652.5	1696.2	1674.1
94.5	80.4	63.6
1158.5	842.6	820.9
1542.3	942.8	1177.4
3454.9	2123.4	3633.8
5445.8	4754.1	6985.2
1087.5	702.0	786.0
601.8	776.1	537.4
1293.9	1409.3	1662.5
97.1	158.5	182.9
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724.6	484.4	510.8
5087.1	4820.4	4345.2
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4096.7	4724.7	4369.6
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EU475449.1 gg_id:300222 springbok feces clone SBSD_aaa03e11 EU475
DQ825116.1 gg_id:188518 human fecal clone RL185_aan85e11 DQ825
DQ794708.1 gg_id:194924 human fecal clone RL240_aaj31d09 DQ794
FJ685347.1 gg_id:517683 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
FJ679922.1 gg_id:519541 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU771887.1 gg_id:353124 Southern three-banded armadillo feces clone arma_h05 EU7718
AY804148.1 gg_id:109014 Roseburia hominis str. A2-181 AY8041
EU761654.1 gg_id:342151 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7616
DQ806172.1 gg_id:187102 human fecal clone RL186_aah62b08 DQ806
EU470290.1 gg_id:290396 Grevy's zebra feces clone GZ_aaa03d08 EU470
FJ683400.1 gg_id:515910 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU766898.1 gg_id:303749 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7668
FJ365665.1 gg_id:368905 feces adult twins and mothers; TS21 clone TS21_a01e10 FJ3656
EU469042.1 gg_id:302163 Speke's gazelle feces clone SP2_d07_2 EU469
DQ823842.1 gg_id:192656 human fecal clone RL250_aaj79g11 DQ823
DQ824936.1 gg_id:191922 human fecal clone RL185_aao71c02 DQ824
EU776480.1 gg_id:355196 Red Kangaroo feces clone KO1_aai42d01 EU776
FJ679487.1 gg_id:511003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ807467.1 gg_id:190076 human fecal clone RL307_aam06h11 DQ807
EU467554.1 gg_id:303176 southern three-banded armadillo feces clone arma_b02 EU467
FJ683023.1 gg_id:516480 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ363524.1 gg_id:369164 feces adult twins and mothers; TS149 clone TS149_a04c03 FJ3635
AF371613.1 gg_id:102506 swine intestine clone p-1590-c5 AF371
FJ678227.1 gg_id:528045 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ685493.1 gg_id:524968 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
EU475261.1 gg_id:288961 bonobo feces clone BNO_aaa04h02 EU475
DQ810132.1 gg_id:178071 human fecal clone RL184_aao68d09 DQ810
FJ674108.1 gg_id:518613 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ676788.1 gg_id:525401 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
AF371605.1 gg_id:41673 swine intestine clone p-2176-s959-3 AF371
DQ795660.1 gg_id:198494 human fecal clone RL178_aan67h09 DQ795
FJ684548.1 gg_id:510026 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU468940.1 gg_id:295804 Speke's gazelle feces clone SP2_f02_1 EU468
FJ369883.1 gg_id:362595 feces adult twins and mothers; TS55 clone TS55_a01h04 FJ3698
DQ904912.1 gg_id:169255 human fecal clone 001C-h7 DQ904
FJ370075.1 gg_id:359007 feces adult twins and mothers; TS55 clone TS55_a04b07 FJ3700
FJ677285.1 gg_id:521162 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
AF371616.1 gg_id:50105 swine intestine clone p-2195-s959-3 AF371
FJ684730.1 gg_id:525544 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ797220.1 gg_id:185851 human fecal clone RL386_aao88e09 DQ797
FJ371315.1 gg_id:356867 feces adult twins and mothers; TS6 clone TS6_a03e06 FJ3713

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628.0	483.4	769.9	893.6	345.4	400.6	273.6	739.6	207.9	1244.7	304.2
50.2	168.9	353.9	461.6	54.8	70.2	67.9	206.2	62.4	31.6	95.3
11678.3	3048.2	3624.4	3551.9	2676.6	2583.6	3099.9	2875.6	3564.7	3316.8	4201.5
7334.4	1921.6	1820.7	2028.4	1692.2	1575.5	1702.9	1677.0	296.0	1931.5	1996.5
199.4	1610.7	2550.7	2276.6	1356.8	1916.1	1409.8	2732.7	1242.8	772.9	1483.2
451.4	2650.9	3292.7	3767.7	2421.3	2844.6	2863.3	3795.9	1383.3	624.4	2908.5
10012.9	6419.7	5908.8	5908.3	5286.0	5741.1	5498.0	5155.1	7886.4	8893.9	7448.3
52.8	1683.6	1683.5	1936.7	1020.3	1512.5	1931.2	1977.1	2850.6	2686.1	1596.3
107.2	2534.0	3138.6	3171.1	2382.3	2582.1	2585.7	3165.1	1255.0	775.2	2070.9
6774.7	3986.7	4170.6	4342.2	3722.5	4161.1	4402.0	3831.9	3964.9	4494.8	4506.6
331.3	1351.2	1225.7	1456.9	1024.3	936.2	1010.6	1168.2	1701.7	674.7	888.3
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75.4	1040.9	1546.9	1356.3	1489.5	1201.7	1227.8	1550.7	675.1	743.1	1006.6
72.5	86.8	161.2	100.2	96.2	117.0	84.8	87.6	44.4	22.2	55.1
611.3	1759.4	2266.0	2814.4	1653.8	1496.4	1893.0	1340.5	759.7	442.4	1085.1
34.1	874.5	1092.8	1476.4	290.7	771.1	618.5	1588.1	177.6	259.1	355.7
106.6	1361.9	1918.3	1923.1	1165.7	1446.2	1680.3	1986.9	850.9	463.4	1302.9
2566.4	2851.9	3896.0	3750.7	3252.6	2907.2	4081.7	3963.9	2760.7	1848.9	2172.2
54.3	1274.6	1713.9	2057.5	935.4	1170.9	1101.1	1402.6	443.4	237.2	864.6
1621.1	1583.2	1824.5	2726.9	1313.6	1347.1	1322.2	1547.9	1190.1	1430.3	1902.8
687.0	1050.5	1349.2	1344.5	850.8	1370.2	843.4	1314.1	799.5	1964.3	1515.7
70.0	685.2	1064.1	1363.8	682.3	794.3	668.4	1035.1	185.3	138.2	587.2
1469.0	497.0	512.9	433.5	485.8	593.6	549.5	669.1	265.9	713.2	314.1
189.9	2252.9	3663.5	4172.7	1822.2	2853.8	1061.3	3475.4	1568.0	920.8	2933.9
30.7	293.7	325.7	373.2	128.6	341.9	279.3	848.6	110.0	103.0	185.5
54.3	161.7	195.5	246.8	55.7	62.4	78.9	99.8	29.3	31.4	40.8
7896.4	5492.6	5772.9	6122.3	4852.0	5645.9	5571.7	6349.7	5796.2	6068.0	6753.0
176.3	1264.6	1473.2	1144.8	1502.9	1307.2	1303.2	2631.7	926.9	2534.2	793.9
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42.2	156.1	261.8	381.8	63.5	120.7	79.0	243.3	27.2	32.6	79.0
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425.5	1149.0	1341.9	1642.9	1336.5	869.5	1136.0	991.6	439.6	631.4	689.7
217.8	1396.2	1707.5	1490.2	1257.8	1219.3	1291.8	1550.2	2057.7	1345.0	1071.1
48.8	1498.1	1335.8	1376.4	746.3	985.3	726.6	1044.2	793.8	588.9	680.1
35.6	967.3	1328.7	1411.4	521.9	1077.2	864.1	1540.2	392.4	172.6	1106.0
1496.0	3876.7	3423.5	3607.8	3415.9	3218.1	3507.9	3767.8	2540.0	4484.8	4335.0
278.2	960.9	1600.4	1975.7	634.9	1079.5	711.4	1439.3	465.4	181.6	1219.1
728.3	4296.3	3165.5	2030.9	2684.1	3085.1	2461.2	3186.5	5378.1	3206.2	2862.8

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936.4	1149.2	575.5
228.6	178.0	156.8
3347.4	3452.5	3059.8
1900.7	2216.2	1863.3
3038.4	2303.5	2934.4
4368.9	2744.1	4147.3
5781.6	6995.1	5422.9
1684.4	1856.9	1580.1
2501.6	2405.8	2964.6
4291.3	5490.9	4990.3
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3387.2	3323.1	3669.0
2008.7	979.1	1170.0
266.2	141.8	275.6
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2042.7	1900.4	2954.3
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892.8	408.0	684.0
208.5	205.1	410.8
6705.3	6369.1	5983.2
3215.4	1922.2	1684.8
4787.2	3326.6	3716.0
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1349.9	1419.1	1774.0
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FJ678723.1 gg_id:517172 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
EF031002.1 gg_id:182065 Effect mannan-oligosaccharides on piglets weaning piglet colon digesta clone A135 EF0310
EU767317.1 gg_id:306890 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7673
FJ679664.1 gg_id:529516 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU465773.1 gg_id:292249 argali sheep feces clone AS2_aao35b12 EU4657
AF371612.1 gg_id:34520 swine intestine clone p-2743-24E5 AF3716
EU764833.1 gg_id:329313 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
FJ678286.1 gg_id:509840 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AM055815.1 gg_id:149843 Roseburia intestinalis str. XB6B4 AM055
FJ684488.1 gg_id:525426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
AF371611.1 gg_id:28914 swine intestine clone p-2418-55G5 AF3716
EU843513.1 gg_id:315537 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8435
AB264068.1 gg_id:187447 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-52 AB2640
DQ808335.1 gg_id:184864 human fecal clone RL180_aao75d09 DQ808
EF640148.1 gg_id:254376 pig feces clone lcy29 EF6401
EU775805.1 gg_id:308426 Horse feces clone horsem_aai95b06 EU7758
EU468534.1 gg_id:300517 okapi feces clone OK1_c01_1 EU4685
FJ675990.1 gg_id:521896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU465689.1 gg_id:292399 argali sheep feces clone AS2_aao33e11 EU4656
FJ679322.1 gg_id:524772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
DQ809444.1 gg_id:175532 human fecal clone RL184_aah21a08 DQ809
FJ370372.1 gg_id:359147 feces adult twins and mothers; TS56 clone TS56_a04b02 FJ3703
DQ810104.1 gg_id:194650 human fecal clone RL184_aao68b03 DQ810
FJ365821.1 gg_id:367958 feces adult twins and mothers; TS21 clone TS21_a03d11 FJ3658
EU470174.1 gg_id:293104 trancaspain urial feces clone TU2_aaa01c05 EU4701
DQ807462.1 gg_id:180878 human fecal clone RL307_aam06h05 DQ807
DQ823759.1 gg_id:179472 human fecal clone RL250_aaj78f11 DQ823
DQ800407.1 gg_id:178751 human fecal clone RL303_aal72g10 DQ800
FJ679215.1 gg_id:509388 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
GU303692.1 gg_id:541602 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ681210.1 gg_id:511432 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
EU763109.1 gg_id:311820 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU7631
DQ801750.1 gg_id:190597 human fecal clone RL201_aai46c12 DQ801
EU776429.1 gg_id:347998 Red Kangaroo feces clone KO1_aai41d11 EU7764
FJ364889.1 gg_id:358847 feces adult twins and mothers; TS19 clone TS19_a04d04 FJ3648
FJ679311.1 gg_id:520754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ678871.1 gg_id:513703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EU765254.1 gg_id:313766 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU7652
EU469078.1 gg_id:299126 Speke's gazelle feces clone SP3_b01 EU4690
FJ364609.1 gg_id:365492 feces adult twins and mothers; TS19 clone TS19_a01a04 FJ3646

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911.9	4240.8	3252.9	3072.4	3059.7	3618.0	3761.3	3410.1	4135.8	1992.2	3369.4
29.4	159.0	272.5	287.4	57.1	259.7	104.0	638.7	59.1	56.7	99.8
43.9	470.3	610.4	703.7	305.6	254.9	328.2	479.5	119.1	162.4	209.4
50.2	246.3	409.3	607.0	106.5	219.0	178.7	193.2	59.3	83.7	194.3
32.1	92.6	159.1	262.7	52.8	58.0	63.6	96.9	30.6	21.7	73.7
4320.9	4592.4	4296.8	5810.4	2913.7	3021.3	3206.0	3643.7	3869.8	2527.8	3350.1
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70.8	84.7	190.1	275.5	48.2	114.0	153.8	143.3	38.4	25.1	93.7
93.6	967.7	1208.8	1549.1	679.2	1107.3	649.4	1650.0	598.9	141.5	1026.5
122.0	46.6	62.3	237.8	22.4	19.3	20.1	158.4	36.7	10.3	92.7
413.2	320.1	447.5	407.9	411.2	402.3	347.8	390.6	258.4	566.0	328.9
45.5	128.6	148.5	253.6	82.6	87.8	84.6	198.5	47.0	32.0	100.0
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1328.2	1902.3	2589.3	2778.5	1594.7	1840.4	2065.5	2467.8	2602.2	1563.9	1988.6
1265.5	3284.1	3025.9	3083.1	1080.2	2817.4	2254.9	3292.5	3459.1	2985.7	2489.5
48.4	411.8	649.4	745.1	229.4	489.3	296.6	782.2	146.0	311.3	399.9
10386.6	2869.0	2773.7	3509.8	3929.2	2689.7	1426.5	3116.4	2331.0	2000.4	2856.9
35.7	1634.6	2115.1	2208.1	296.8	1139.3	723.5	1895.7	351.0	205.1	1043.2
3830.0	2411.4	2541.8	2447.8	2293.1	2925.0	2673.6	2782.6	2878.0	1487.1	2249.9
46.5	108.2	168.5	265.0	36.7	118.7	182.3	166.5	51.9	45.8	55.7
1876.1	2754.3	2861.2	2563.3	1745.7	3048.3	1838.0	2735.1	2246.6	4490.0	1976.4
46.9	874.3	1491.6	1707.7	463.4	907.0	672.5	1648.6	495.4	134.3	912.0
1890.3	3620.6	2446.8	2555.9	2149.2	2214.6	3225.7	2856.1	5279.2	1102.8	1986.6
91.6	387.1	632.8	785.0	149.5	210.8	214.4	458.9	112.9	109.4	190.6
87.0	109.9	148.7	107.0	183.2	110.8	127.2	111.7	86.5	92.1	110.6
280.5	1746.6	1594.2	2467.5	1482.6	2649.5	1326.3	2554.3	653.8	3674.1	1339.9
282.9	1219.3	1618.0	2340.0	982.4	1569.3	1075.3	1736.7	1387.5	1141.3	1474.7
18326.0	4290.9	4442.7	4563.7	4268.5	4001.6	4528.2	4250.3	1439.3	4960.9	4249.5
1258.2	996.6	1507.5	1132.8	785.5	1131.1	780.9	1200.4	695.9	1010.1	988.7
35.3	607.4	1001.4	1012.3	498.2	473.7	1364.6	905.6	142.7	102.1	596.0
32.8	1243.9	1737.7	2448.1	664.9	1114.4	1073.8	2398.9	296.2	290.9	1213.8
781.5	1783.1	1677.0	2746.5	1676.3	2329.9	1394.7	2518.8	1049.8	4026.4	1133.1
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1736.7	1639.4	1531.2	1896.6	1064.0	1077.9	1071.4	1478.2	974.3	304.7	1097.6
6129.7	322.5	385.1	493.4	615.6	386.4	443.8	688.4	236.6	150.4	180.0
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1213.8	2273.1	2569.6	2938.8	1230.7	1566.6	1311.6	2021.9	1575.8	1226.8	1295.2

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600.4	522.8	1187.8
437.5	404.7	355.3
166.8	124.8	123.5
3787.8	4118.1	3905.2
1978.8	1463.1	2430.1
1309.0	481.0	720.6
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1800.9	1148.9	981.4
281.1	60.5	195.8
446.4	817.4	555.3
190.0	157.8	162.2
2837.7	3528.0	2490.6
3137.3	2303.5	2820.7
3480.7	3697.0	2490.0
1067.4	410.1	634.2
3214.2	3979.1	3634.2
2656.0	1334.0	1617.2
2369.4	2552.5	2789.2
411.2	173.5	278.3
2473.2	3350.7	2927.9
1199.2	982.1	839.7
1991.5	2600.9	1949.1
845.3	454.6	410.4
104.0	387.4	135.6
2169.6	3633.5	2133.6
1466.0	1894.5	1394.0
4611.6	4725.1	4811.6
1261.1	1919.8	1156.6
935.7	630.0	411.5
2438.3	1469.1	1861.7
1982.8	3258.2	2094.7
1940.9	1409.7	2175.5
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1426.9	1863.4	2487.0
2341.6	2829.3	2748.7

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Roseburia
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FJ678840.1 gg_id:518748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
DQ794800.1 gg_id:189208 human fecal clone RL240_aaj32e06 DQ794
DQ808114.1 gg_id:197930 human fecal clone RL180_aan72g05 DQ808
DQ808312.1 gg_id:176297 human fecal clone RL180_aao75b06 DQ808
DQ806958.1 gg_id:188023 human fecal clone RL198_aaj76b05 DQ806
DQ804676.1 gg_id:191824 human fecal clone RL187_aao71c03 DQ804
DQ804890.1 gg_id:183646 human fecal clone RL385_aao82b06 DQ804
DQ805075.1 gg_id:182506 human fecal clone RL385_aao84h05 DQ805
DQ804129.1 gg_id:184729 human fecal clone RL187_aah69a08 DQ804
DQ804292.1 gg_id:193702 human fecal clone RL187_aan77e09 DQ804
DQ802458.1 gg_id:178851 human fecal clone RL188_aah18a04 DQ802
DQ799741.1 gg_id:188039 human fecal clone RL182_aah32e04 DQ799
FJ367517.1 gg_id:357232 feces adult twins and mothers; TS29 clone TS29_a04e03 FJ3675
DQ905906.1 gg_id:165146 human fecal clone 29c-e3 DQ905
DQ804408.1 gg_id:190890 human fecal clone RL187_aan79d06 DQ804
EU139255.1 gg_id:245108 Ruminococcus gnavus str. A2 EU139
DQ326730.1 gg_id:146113 Metagenomic gut microbiome healthy human stool clone E185 DQ326
AY976547.1 gg_id:125145 human cecum mucosal biopsy clone K079 AY976
FJ371092.1 gg_id:370360 feces adult twins and mothers; TS5 clone TS5_a04h01 FJ3710
DQ803534.1 gg_id:178103 human fecal clone RL251_aaj87b02 DQ803
FJ370684.1 gg_id:363436 feces adult twins and mothers; TS57 clone TS57_a04a04 FJ3706
FJ978683.1 gg_id:381895 feces clone CL_F_368 FJ9786
FJ370711.1 gg_id:357618 feces adult twins and mothers; TS57 clone TS57_a04c10 FJ3707
FJ371142.1 gg_id:359605 feces adult twins and mothers; TS6 clone TS6_a01d11 FJ3711
GQ001490.1 gg_id:508171 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173f05 GQ001
GQ492701.1 gg_id:560581 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492877.1 gg_id:583406 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU530390.1 gg_id:264290 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
EU776668.1 gg_id:342397 Lion feces clone LI3_aah76c02 EU776
FJ364832.1 gg_id:358009 feces adult twins and mothers; TS19 clone TS19_a03f10 FJ3648
DQ803563.1 gg_id:198251 human fecal clone RL251_aaj87e03 DQ803
GQ493596.1 gg_id:570712 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368938.1 gg_id:369562 feces adult twins and mothers; TS4 clone TS4_a02c11 FJ3689
NZ_AAVP02000025.1 gg_id:470974 Ruminococcus torques str. ATCC 27756 NZ_AA
NZ_AAVP02000040.1 gg_id:470983 Ruminococcus torques str. ATCC 27756 NZ_AA
DQ808089.1 gg_id:180432 human fecal clone RL180_aan72c10 DQ808
FJ370299.1 gg_id:363908 feces adult twins and mothers; TS56 clone TS56_a03b03 FJ3702
FJ367673.1 gg_id:358748 feces adult twins and mothers; TS2 clone TS2_a02c03 FJ3676
GQ175509.1 gg_id:592688 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ327420.1 gg_id:145342 Metagenomic gut microbiome healthy human stool clone E979 DQ327

72.8	829.1	1275.8	1316.6	544.3	945.8	723.2	1311.9	341.1	592.9	813.5
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42.6	57.1	57.4	88.0	35.1	41.8	54.3	49.1	34.7	29.4	31.2
124.3	1569.4	1266.9	1759.4	1583.3	1596.7	1900.7	1423.1	916.8	554.8	1956.9
36.9	142.8	316.7	139.8	167.3	171.4	113.9	301.9	72.7	134.4	96.7
59.5	1053.7	1580.0	1306.1	202.0	1051.7	611.4	2618.5	2288.6	1321.9	722.1
1610.0	1060.6	1670.2	1996.9	512.3	939.1	1009.0	1498.4	1794.6	1575.9	1436.8
41.4	390.0	1052.7	878.7	359.5	440.1	515.2	668.9	190.6	187.8	318.7
117.0	4524.5	4631.3	4653.4	2107.4	3210.4	2767.6	3274.2	3790.3	3890.5	3656.6
52.0	647.4	1119.0	1328.7	258.9	408.6	396.6	629.3	389.9	598.1	301.2
724.2	60.1	568.6	287.7	358.3	390.5	457.4	408.1	624.5	696.2	374.7
1581.6	1959.3	3145.5	2499.9	1266.6	1813.4	1526.5	3175.7	1279.2	2306.2	2251.9
97.9	926.5	1444.3	1145.8	743.2	973.3	1046.2	1777.1	2265.7	1301.7	1172.9
596.8	4476.5	4652.8	4676.0	4129.2	4384.0	4543.6	4182.7	5540.7	5254.6	4788.3
49.0	385.6	551.2	552.3	233.3	272.9	447.4	423.1	87.6	62.7	199.9
50.4	342.6	488.9	572.2	147.0	275.7	254.2	639.0	116.7	77.8	255.4
112.4	1500.0	2158.8	2200.1	1091.6	1237.5	1529.7	1824.4	1379.9	704.9	1070.7
2589.7	822.2	821.1	462.2	569.5	770.5	554.3	641.8	778.6	548.0	613.4
5863.2	3199.5	3341.1	3320.5	2846.8	3055.1	3583.7	3109.5	4207.9	2960.6	3760.7
118.7	2874.3	3138.6	2626.1	1479.4	1463.1	1536.7	2287.7	2800.2	1657.5	1512.2
5675.1	2400.4	2315.0	2384.3	1623.0	1946.7	2166.6	2588.6	3331.1	2597.8	2103.8
74.8	1954.5	2335.6	2295.5	1044.5	1389.7	1407.7	2356.7	1055.0	1266.8	1590.2
10132.4	2105.2	2117.7	2559.6	1845.7	1078.9	2370.6	1877.4	3101.2	2760.5	3584.6
7403.9	6346.1	6105.3	7512.2	5812.7	5907.7	6069.4	5642.4	5484.0	5037.5	7253.3
40.0	630.9	1038.0	1213.5	180.1	464.1	353.0	664.5	471.5	332.6	514.0
46.1	1836.3	3234.8	3604.8	697.4	2060.4	2078.2	2712.8	1076.4	817.4	2109.5
123.3	2050.0	2478.3	3023.6	1604.0	1419.9	1724.5	2284.0	1091.7	514.8	1340.7
564.8	1395.0	1208.8	1174.2	931.5	1068.0	1329.8	1383.7	1676.0	859.8	1052.0
40.9	189.1	391.8	344.5	60.1	214.0	173.5	196.7	75.8	23.5	125.8
57.9	975.5	881.1	883.2	634.2	930.1	662.2	636.0	1326.8	797.6	587.1
426.0	2287.7	1833.3	1938.5	1868.7	829.5	2054.7	1120.3	2634.6	1931.7	2272.5
80.0	1965.9	2916.8	3200.1	946.0	2168.0	1709.8	3411.6	979.5	536.2	2850.8
1877.6	1811.3	2172.4	3043.0	1637.4	2218.9	1825.6	3103.4	1115.0	512.8	3160.7
31.6	235.3	537.8	281.1	88.4	334.5	144.9	201.2	147.5	689.1	238.8
742.5	1933.8	2445.1	2222.2	1130.5	1551.4	1551.7	2377.4	1041.3	589.8	1693.7
52.3	1076.2	1480.0	1516.2	416.9	1018.5	739.0	1587.9	486.5	255.7	919.3
311.1	4209.2	3232.8	2851.0	2219.8	2447.9	2579.5	3917.5	3544.6	2693.9	2405.9
59.5	519.3	728.9	795.1	226.0	443.1	311.9	738.0	235.2	200.5	525.8

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1490.6	1172.9	697.8
2474.3	3202.9	2462.7
47.4	88.9	58.2
1154.3	1448.1	158.8
476.8	367.2	555.7
2706.9	1288.6	1415.3
1175.9	1211.9	1491.7
657.8	510.6	892.6
3020.7	3595.9	4173.4
594.9	505.6	679.6
533.7	1113.6	383.2
2369.4	2253.9	2392.4
1310.9	1445.7	1025.3
5108.9	4699.0	5312.9
501.7	370.0	396.9
589.6	381.2	262.9
1804.6	1327.8	2853.0
488.7	1474.2	238.8
2940.9	3923.3	3395.5
3900.5	1842.6	2769.2
2437.1	2856.9	1773.2
2263.7	1829.6	2096.6
1810.7	3778.1	1972.1
5626.7	9222.8	6203.0
736.9	953.1	719.1
2493.0	1667.9	2430.8
2873.7	1699.6	2682.7
1091.2	1780.2	1671.3
329.5	201.9	208.3
1475.1	841.2	796.8
1695.1	2329.2	1496.9
4497.9	1786.0	2918.6
3568.0	2090.1	2975.8
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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DQ808229.1 gg_id:193028 human fecal clone RL180_aao74b08 DQ808
AY169415.1 gg_id:81063 Clostridium nexile AY1694
DQ057458.1 gg_id:129692 str. ic1294 DQ057
DQ798745.1 gg_id:175808 human fecal clone RL181_aao00g11 DQ798
FJ685386.1 gg_id:522632 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
AF357572.1 gg_id:71434 mpn-isolate group 24 AF3575
DQ327599.1 gg_id:148987 Metagenomic gut microbiome healthy human stool clone EB87 DQ327
FJ364788.1 gg_id:363667 feces adult twins and mothers; TS19 clone TS19_a03b05 FJ3647
DQ777926.1 gg_id:167187 rat feces clone R-1314 DQ777
DQ802435.1 gg_id:175850 human fecal clone RL188_aah17f12 DQ802
DQ795961.1 gg_id:186203 human fecal clone RL202_aai49e01 DQ795
FJ673341.1 gg_id:527086 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ372163.1 gg_id:358901 feces adult twins and mothers; TS9 clone TS9_a02d11 FJ3721
AY980571.1 gg_id:116438 human rectum mucosal biopsy clone X534 AY9805
EU469092.1 gg_id:302395 Speke's gazelle feces clone SP3_d02 EU469
FJ679086.1 gg_id:517721 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
EU771983.1 gg_id:332500 Southern three-banded armadillo feces clone arma_aaj55h03 EU7719
GQ493206.1 gg_id:554500 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ366545.1 gg_id:363122 feces adult twins and mothers; TS27 clone TS27_a01a06 FJ3665
FJ367647.1 gg_id:369694 feces adult twins and mothers; TS2 clone TS2_a01h09 FJ3676
DQ803493.1 gg_id:180842 human fecal clone RL251_aaj86e06 DQ803
FJ678322.1 gg_id:517797 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
DQ798635.1 gg_id:178087 human fecal clone RL181_aan99c09 DQ798
FJ369755.1 gg_id:369217 feces adult twins and mothers; TS51 clone TS51_a04d10 FJ3697
GQ024140.1 gg_id:485529 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ024
FJ366542.1 gg_id:358321 feces adult twins and mothers; TS27 clone TS27_a01a03 FJ3665
FJ366284.1 gg_id:366435 feces adult twins and mothers; TS25 clone TS25_a04h02 FJ3662
DQ798232.1 gg_id:190939 human fecal clone RL181_aah39b11 DQ798
DQ800457.1 gg_id:174053 human fecal clone RL183_aah24g09 DQ800
FJ365747.1 gg_id:370361 feces adult twins and mothers; TS21 clone TS21_a02e07 FJ3657
GQ492527.1 gg_id:588966 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU462778.1 gg_id:296010 southern three-banded armadillo feces clone arma_aaj53a03 EU462
DQ803522.1 gg_id:195999 human fecal clone RL251_aaj86h08 DQ803
GQ493221.1 gg_id:547807 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ057412.1 gg_id:136507 chicken ileum/cecum clone oc10 DQ057
FJ364768.1 gg_id:362436 feces adult twins and mothers; TS19 clone TS19_a02h03 FJ3647
AY985538.1 gg_id:123198 human stool clone C514 AY9855
FJ682931.1 gg_id:513285 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GQ491685.1 gg_id:547567 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY985811.1 gg_id:120639 human stool clone D066 AY9858

223.5	770.9	1225.4	1194.6	821.4	894.2	855.0	1122.1	1166.8	546.5	865.6
230.1	184.2	242.0	239.2	233.7	167.2	130.3	155.1	143.2	32.4	173.3
152.3	1723.8	2309.6	2498.1	1174.8	1785.4	1727.9	3325.0	809.0	425.1	1915.3
100.7	559.6	900.9	1077.0	559.0	542.8	562.4	1021.7	852.5	142.6	394.5
4211.7	1966.6	1853.3	1006.0	2460.0	2281.8	2125.8	2155.0	1723.0	1977.8	1868.7
232.7	1038.1	1503.4	1496.0	875.4	1133.1	1043.2	1586.1	606.5	969.6	954.9
53.5	71.4	134.7	130.6	53.2	61.3	43.7	125.8	35.7	38.5	66.0
119.5	219.4	468.1	328.0	122.2	146.1	210.1	264.7	106.3	31.5	130.1
434.4	815.4	1187.2	1068.0	836.6	780.9	1048.4	929.9	860.9	829.5	806.5
334.4	3170.1	3921.5	4415.6	1976.4	3943.8	2319.1	4244.5	2276.9	835.0	2872.1
12825.9	7806.4	7370.6	6885.4	6054.2	6766.6	6879.8	6302.6	9292.2	7439.5	10061.0
2978.6	2744.9	3273.1	3026.1	2518.0	2567.4	3447.6	2637.2	3426.1	3102.0	3982.8
9182.0	6668.3	6699.0	8302.1	7465.0	7296.8	8172.6	6288.9	8760.2	6121.8	8916.4
38.8	455.6	610.2	734.5	183.1	169.7	202.3	485.6	86.6	70.2	169.2
1007.0	1650.8	2274.4	2312.3	1310.3	2271.7	1332.9	2628.6	836.6	402.5	1585.9
41.3	324.0	516.2	533.8	150.5	512.7	327.1	986.7	152.4	94.8	240.7
5582.4	1944.0	2362.7	2542.5	2483.9	1890.8	2571.9	2581.4	1596.2	2349.9	1622.1
10614.3	4416.6	4420.0	4175.9	2534.0	4010.0	4458.0	4675.2	6074.1	3378.7	4980.6
30.9	92.5	143.9	119.0	127.0	109.9	77.9	136.9	30.5	63.2	52.0
387.4	1505.7	2264.5	2118.9	924.9	1585.8	1394.3	2014.4	1022.5	779.0	1728.3
33.8	69.5	82.0	93.8	92.4	76.6	91.9	91.7	38.8	36.4	50.8
175.9	322.0	371.4	365.4	365.1	287.8	354.1	329.0	208.0	285.4	187.8
9582.7	3478.1	3641.1	3013.4	3222.1	3169.2	3174.4	3738.3	4076.6	5366.0	2855.7
3571.7	3987.8	4144.4	3833.4	3703.6	3859.5	3678.4	3218.3	5205.5	2973.8	2909.8
412.5	1515.4	2427.6	2065.0	1170.1	1933.3	1663.2	2266.0	1371.8	915.1	1979.4
5810.3	2813.5	3050.8	2868.1	2605.5	2434.0	3907.1	2627.3	3614.8	3289.6	2803.3
38.9	2900.8	2150.7	2056.1	2128.2	1482.4	3032.4	1914.7	3451.5	3243.1	2129.2
386.5	1442.1	2011.4	2091.7	1031.7	1221.7	1333.9	1656.5	796.5	1051.1	1624.6
41.8	125.6	156.4	192.0	90.0	122.3	184.3	223.8	45.8	31.6	70.8
4848.6	2963.9	3592.7	3132.1	2621.6	1407.3	3489.5	2675.7	4009.1	3055.4	3084.9
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731.7	3346.4	4180.4	3326.0	2564.7	3283.7	2589.3	3200.4	3647.2	4329.2	3992.3
34.6	186.4	105.6	356.4	53.6	182.2	90.6	533.4	38.8	68.8	73.7
359.4	2773.8	3254.1	2998.2	1843.3	3170.3	3149.1	3097.3	2925.9	4068.8	3377.0
43.1	715.8	1007.8	900.8	365.8	696.0	553.3	889.9	441.7	284.8	771.6
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72.4	1305.3	2188.5	2050.2	1102.7	1994.8	1511.2	2137.4	829.9	247.2	1362.5
48.1	361.8	513.4	497.0	471.5	547.6	447.4	454.8	152.0	227.0	209.8
175.8	1903.0	2197.6	1877.1	1120.6	1612.2	1369.4	1727.6	1214.1	391.0	2006.9
659.2	2081.0	2436.3	2756.8	1405.2	1807.3	1962.8	2243.8	1759.9	1992.0	2200.3

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148.8	333.9	174.6
4043.0	2034.5	3097.6
936.7	882.8	1754.6
2443.9	3860.2	2244.0
2141.7	1578.4	1861.2
128.6	91.9	148.6
172.5	205.3	329.0
856.6	1134.9	1574.6
5353.5	3144.2	4462.6
5781.8	7331.1	6469.7
2251.9	3519.1	3108.5
6305.9	8131.7	6194.6
550.8	771.7	927.2
3205.7	2285.9	2948.3
1519.8	685.2	1066.7
2922.8	2983.6	3157.8
2910.4	4411.2	3797.0
380.9	126.1	286.2
2625.1	1751.4	2201.6
78.5	172.9	186.4
301.2	543.4	301.2
3695.3	4589.9	3409.7
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2504.7	3627.3	3427.1
1888.5	2484.2	2007.9
1981.3	1679.3	1982.8
259.1	186.7	477.7
2535.0	3854.9	2997.0
1300.4	1105.6	2336.2
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2988.2	2914.1	4354.8
655.9	194.5	396.1
3224.5	2681.3	2764.1
899.9	667.3	960.4
980.9	1331.0	1665.5
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o__Clostridiales	f__Lachnospiraceae
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AY960570.1 gg_id:114982 Clostridium sp. str. ID3 AY9605
FJ679547.1 gg_id:526660 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU530323.1 gg_id:277190 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
FJ366445.1 gg_id:362418 feces adult twins and mothers; TS26 clone TS26_a03d03 FJ3664
EF403738.1 gg_id:216096 human fecal clone SJTU_A2_06_28 EF4037
FJ676553.1 gg_id:519968 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
DQ801898.1 gg_id:178400 human fecal clone RL201_aai48c03 DQ801
FJ368926.1 gg_id:369231 feces adult twins and mothers; TS4 clone TS4_a02b11 FJ3689
EU766717.1 gg_id:329034 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7667
FJ365955.1 gg_id:365845 feces adult twins and mothers; TS25 clone TS25_a01b02 FJ3659
DQ796049.1 gg_id:182889 human fecal clone RL202_aai50g04 DQ796
AY980909.1 gg_id:115735 human rectum mucosal biopsy clone LQ93 AY9809
GQ021410.1 gg_id:488258 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
X73443.1 gg_id:14036 Clostridium nexile str. DSM 1787 X73443
DQ327213.1 gg_id:149534 Metagenomic gut microbiome healthy human stool clone E745 DQ327
GQ493793.1 gg_id:551202 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368206.1 gg_id:369005 feces adult twins and mothers; TS3 clone TS3_a01e02 FJ3682
EU776331.1 gg_id:327642 Red Kangaroo feces clone KO2_aai19a05 EU7763
FJ368881.1 gg_id:358849 feces adult twins and mothers; TS4 clone TS4_a01f08 FJ3688
EU773269.1 gg_id:349002 BigHorn sheep feces clone BH1_aao26g08 EU7732
AY985663.1 gg_id:118706 human stool clone C669 AY9856
DQ798375.1 gg_id:176842 human fecal clone RL181_aah41g02 DQ798
GQ493167.1 gg_id:562750 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF398618.1 gg_id:216342 human fecal clone SJTU_F_05_92 EF3986
DQ327425.1 gg_id:145721 Metagenomic gut microbiome healthy human stool clone E984 DQ327
DQ796068.1 gg_id:189296 human fecal clone RL202_aai51a09 DQ796
GQ493326.1 gg_id:542986 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU779209.1 gg_id:344114 Trancaspian Urial feces clone TU2_aaa02g10 EU7792
EU467575.1 gg_id:293464 southern three-banded armadillo feces clone arma_a12_1 EU4675
GQ491592.1 gg_id:574834 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ364682.1 gg_id:362668 feces adult twins and mothers; TS19 clone TS19_a01g08 FJ3646
DQ326912.1 gg_id:148744 Metagenomic gut microbiome healthy human stool clone E403 DQ326
EU775324.1 gg_id:310303 Reticulated giraffe feces clone gir_aah93e01 EU7753
GQ493654.1 gg_id:564762 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ808801.1 gg_id:179408 human fecal clone RL243_aai85d10 DQ808
EF025296.1 gg_id:181332 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N28 EF0252
DQ905636.1 gg_id:162162 human fecal clone 014C-B1 DQ905
DQ905098.1 gg_id:168567 human fecal clone 002C-a10 DQ905
DQ798406.1 gg_id:180049 human fecal clone RL181_aah42b04 DQ798
FJ367447.1 gg_id:365554 feces adult twins and mothers; TS29 clone TS29_a03f09 FJ3674
FJ685477.1 gg_id:527884 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854

40.9	387.2	769.9	713.1	377.5	608.5	633.3	1036.0	220.1	59.3	460.5
1194.4	648.6	753.1	739.5	471.3	566.3	842.2	741.4	738.5	367.4	485.6
4108.2	3178.0	3156.9	3584.0	2981.9	3025.8	3412.3	3337.0	2884.5	3401.1	3814.0
1626.8	360.8	486.6	629.4	167.6	437.5	268.7	1164.6	274.7	200.0	282.3
58.3	907.8	1621.5	1811.1	540.8	1141.1	844.9	1402.5	376.3	676.2	879.5
518.6	2471.9	3197.4	2427.2	2998.6	2485.9	2934.3	2401.0	2279.2	1160.8	1516.5
801.6	2245.1	2576.9	2574.4	1982.1	2212.6	1784.5	2835.8	2426.9	822.8	2881.6
2954.6	4197.0	2922.0	3410.4	3374.3	2962.1	3279.4	2519.9	4186.6	2919.8	3955.6
412.9	1161.9	1201.6	1593.2	630.7	986.0	998.1	1550.9	426.8	103.0	817.9
373.4	1082.1	1543.3	1520.6	773.0	896.4	989.1	1285.3	492.5	883.8	1135.4
1438.6	1757.2	1901.5	1898.5	2068.3	1963.8	1994.4	2639.1	844.3	1353.5	966.4
386.0	1159.4	1568.1	1630.5	716.4	948.4	1079.6	1192.2	718.5	663.1	1184.2
3729.0	5522.5	6570.5	5560.4	4879.4	4891.9	6027.9	5386.3	7694.1	5510.5	7601.6
17739.8	7074.6	7633.7	7521.0	7029.1	6974.0	7450.1	6836.0	10684.6	10607.0	9503.3
326.1	2001.1	2766.2	2776.8	2173.1	1973.3	3062.6	2228.6	2074.6	2020.3	2285.5
1445.8	2420.6	2820.9	2810.5	1561.3	2769.6	1737.4	2531.2	1576.9	1574.8	1576.2
67.7	905.5	1541.7	1540.3	596.7	795.1	571.9	1274.3	361.7	155.7	708.5
5554.2	3849.1	4124.2	4817.3	3765.8	3709.7	3962.4	4063.8	4045.8	4303.1	4778.3
728.1	2210.9	3178.6	3050.2	2239.9	3253.0	2852.6	3676.9	1678.8	1189.8	2829.4
394.0	411.4	491.9	789.6	484.4	587.7	440.1	626.6	172.5	42.3	291.4
5924.0	5489.6	4692.9	4673.2	3830.8	4558.7	4437.8	4727.5	6169.8	5247.3	7431.2
250.2	1584.3	2419.4	1841.9	832.3	1385.2	970.7	2398.0	587.3	376.4	1517.6
2867.7	8139.5	6795.3	6577.9	6123.2	6615.4	6120.3	6322.1	9221.7	5207.3	8488.5
39.0	966.5	1493.7	1611.4	598.1	1290.5	1632.6	1910.8	323.6	213.0	887.5
432.1	702.3	1023.3	893.8	722.3	646.9	958.6	743.6	749.4	783.6	682.3
371.6	2087.2	2680.0	2601.2	1401.4	2353.7	2482.3	3337.3	1865.7	2100.8	2338.6
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15111.4	3962.7	3426.7	3550.8	3803.9	3778.6	4074.6	3561.0	6300.8	6016.2	5100.6
35.3	229.4	381.6	410.7	189.2	306.0	495.5	438.7	59.4	66.8	158.6
14312.3	4831.6	5661.7	5524.0	5387.2	4537.6	5729.3	5747.0	7113.2	4729.7	5433.0
78.2	1302.1	2024.9	1721.1	741.5	1427.1	994.1	1894.1	810.6	391.9	1371.8
54.6	640.7	997.3	970.8	257.2	624.5	258.0	1050.8	583.7	198.0	759.3
991.6	1629.8	1866.8	1939.8	825.3	1097.8	1076.3	1696.2	826.8	792.9	1804.1
63.4	220.5	357.0	326.3	153.9	175.8	138.0	267.1	122.7	90.4	102.3
47.3	402.4	570.0	492.5	219.2	375.9	413.3	490.0	193.7	50.5	217.2
3545.7	2012.8	2376.0	2282.2	2322.9	2301.1	2166.9	2307.7	2251.0	3851.2	1835.7
36.0	18.1	16.1	21.7	20.3	13.2	13.1	11.2	12.7	10.5	20.6
109.6	360.4	765.4	547.0	233.0	521.1	475.6	808.9	242.6	115.1	435.4
158.2	1892.8	2342.7	2218.8	1347.4	1319.0	1533.3	1727.3	853.2	632.3	1337.1
35.9	530.6	928.0	1158.7	65.6	462.7	243.0	796.3	125.9	83.5	359.4
83.6	441.3	819.9	788.1	305.3	522.7	281.1	910.0	232.3	116.3	434.8

767.9	468.1	742.9
676.9	1268.4	1123.1
3820.4	4481.9	4187.1
1615.2	804.6	870.0
1464.3	1330.2	1285.3
2805.2	2735.6	4342.0
2500.1	2269.8	2673.3
2396.0	3398.7	2811.8
1603.8	1665.1	1588.4
1609.4	1230.0	1647.2
2900.4	2225.5	2733.9
1538.4	1185.2	1438.9
4834.3	5280.3	4811.7
7302.3	8183.6	8246.6
2060.3	2985.6	3287.7
3437.1	2497.2	2939.6
1423.7	989.2	2212.5
3743.6	6216.3	4113.4
4652.3	2895.7	4181.1
437.4	986.9	724.0
4254.8	4774.0	3776.6
2569.8	2225.9	2353.2
6490.0	6741.9	5416.1
3093.3	1052.7	2024.6
686.6	981.2	1395.6
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1870.4	2312.8	2057.0
3298.7	5235.7	3655.3
866.9	229.5	708.6
4880.1	5951.7	5433.4
2054.4	1453.0	2009.3
1290.2	1218.9	1184.5
1831.7	1696.6	1151.6
357.4	362.3	345.5
479.5	457.7	670.1
2790.0	3106.4	2905.4
15.2	17.6	16.6
801.5	594.0	532.0
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1423.1	694.5	510.9
985.8	782.3	1034.7

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GQ491386.1 gg_id:550514 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ491753.1 gg_id:582093 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ367105.1 gg_id:363445 feces adult twins and mothers; TS28 clone TS28_a03e12 FJ3671
EF025288.1 gg_id:186138 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N19 EF0252
AY977361.1 gg_id:122326 human cecum mucosal biopsy clone MV96 AY9773
AY975495.1 gg_id:123346 human ascending colon mucosal biopsy clone N940 AY9754
EU462858.1 gg_id:294353 southern three-banded armadillo feces clone arma_aaj54b02 EU4628
FJ371270.1 gg_id:363882 feces adult twins and mothers; TS6 clone TS6_a03a04 FJ3712
EU460121.1 gg_id:294538 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU4601
DQ905700.1 gg_id:165183 human fecal clone 014C-H7 DQ905
DQ327461.1 gg_id:147500 Metagenomic gut microbiome healthy human stool clone EA26 DQ327
FJ366644.1 gg_id:367111 feces adult twins and mothers; TS27 clone TS27_a02b04 FJ3666
AY985305.1 gg_id:121455 human stool clone C209 AY9853
DQ327008.1 gg_id:145570 Metagenomic gut microbiome healthy human stool clone E509 DQ327
AY979201.1 gg_id:115705 human transverse colon mucosal biopsy clone Z319 AY9792
DQ071521.1 gg_id:234309 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc28 DQ071
DQ326193.1 gg_id:145742 Metagenomic gut microbiome healthy human stool clone C107 DQ326
DQ809019.1 gg_id:198527 human fecal clone RL243_aai88c09 DQ809
DQ905039.1 gg_id:171469 human fecal clone 2-002-c9 DQ905
FJ366564.1 gg_id:362281 feces adult twins and mothers; TS27 clone TS27_a01c01 FJ3665
FJ371136.1 gg_id:364899 feces adult twins and mothers; TS6 clone TS6_a01d04 FJ3711
DQ801852.1 gg_id:174404 human fecal clone RL201_aai47f07 DQ801
AY982542.1 gg_id:123324 human descending colon mucosal biopsy clone KW06 AY9825
FJ679307.1 gg_id:514046 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
DQ905574.1 gg_id:162631 human fecal clone 014B-D5 DQ905
FJ678369.1 gg_id:514646 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
DQ802167.1 gg_id:197674 human fecal clone RL241_aaj03h10 DQ802
EU461359.1 gg_id:301990 red kangaroo feces clone KO2_aai18f06 EU4613
DQ793683.1 gg_id:199555 human fecal clone RL246_aai75e10 DQ793
EF025237.1 gg_id:197579 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_B29 EF0252
GQ493983.1 gg_id:536295 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ802748.1 gg_id:180617 human fecal clone RL188_aan96b01 DQ802
FJ368586.1 gg_id:356788 feces adult twins and mothers; TS49 clone TS49_a02a09 FJ3685
L76604.1 gg_id:14012 Ruminococcus torques str. ATCC 27756 L76604
DQ800430.1 gg_id:175474 human fecal clone RL183_aah24c02 DQ800
EU461414.1 gg_id:298557 red kangaroo feces clone KO2_aai20f10 EU4614
AY979054.1 gg_id:120691 human transverse colon mucosal biopsy clone NJ62 AY9790
DQ793576.1 gg_id:182245 human fecal clone RL246_aai73g11 DQ793
DQ327087.1 gg_id:147259 Metagenomic gut microbiome healthy human stool clone E601 DQ327
FJ367828.1 gg_id:369417 feces adult twins and mothers; TS2 clone TS2_a04a09 FJ3678

340.2	1395.8	1751.5	1780.2	1126.1	1297.9	1397.5	1670.7	860.9	816.5	1520.2
117.4	1795.3	2108.4	1831.9	1331.5	1849.1	1694.6	2012.8	1124.9	995.5	1714.4
50.2	1031.3	1450.2	1569.5	1030.0	1435.2	1340.0	2195.0	593.8	416.5	1006.4
7987.0	2988.8	2727.2	3137.5	2440.1	2480.6	2730.5	2295.2	4301.7	3108.8	5089.4
5182.1	1370.4	1933.4	1935.0	1542.0	1354.2	2013.6	1780.0	1314.1	483.0	1368.2
134.5	2495.5	3924.6	3659.1	3560.0	2938.3	3743.3	3583.4	2219.9	2118.5	2805.6
155.6	744.4	1129.9	1303.2	534.6	619.8	979.3	1011.3	691.9	441.0	464.1
228.4	1370.8	1377.9	1496.4	1807.5	1267.3	2282.6	1453.6	535.5	284.6	720.6
36.2	854.2	1002.5	930.8	666.3	819.3	478.9	1256.9	419.3	95.1	411.9
47.3	662.9	1009.5	1031.8	138.2	427.1	323.8	533.8	53.7	28.6	275.2
116.2	1619.9	1872.3	2151.4	1310.9	1501.3	1463.4	1952.2	3085.1	1585.5	1740.8
1252.1	4739.9	4383.5	3809.1	3012.9	5105.9	3387.0	4478.7	4268.8	2238.8	4869.7
61.7	1837.7	2577.6	2329.6	735.9	1781.2	1074.1	2401.7	1100.7	1009.9	1744.3
723.4	2206.2	2782.8	2856.5	1304.0	2120.4	1928.5	2700.0	1871.1	2020.2	2262.0
37.0	807.9	1329.6	1181.9	440.5	759.7	490.4	1188.8	296.7	245.3	752.3
805.7	1570.3	1918.0	2125.7	1251.6	1399.3	1890.9	1655.1	1959.0	1950.0	1414.4
474.9	683.9	1086.3	1147.0	599.8	786.1	644.7	1077.3	365.4	550.6	647.4
276.7	1023.8	1294.9	1298.8	709.9	880.5	472.9	1658.8	468.1	997.3	675.6
54.9	306.2	847.9	607.6	409.4	443.4	456.0	736.0	335.0	247.6	615.1
4616.2	2573.8	2675.6	2666.8	2165.4	2525.1	3066.1	2464.3	2636.9	1512.2	3092.9
808.4	2374.2	3153.3	3204.2	1498.3	2414.8	2215.6	2997.9	2188.1	2168.8	2432.1
4246.7	3744.1	4215.4	4079.1	4209.5	4276.9	4416.6	4278.9	4524.0	3229.8	3167.9
49.5	152.1	406.9	331.9	207.3	120.7	270.7	214.7	110.9	50.4	125.3
3956.3	9465.6	7529.4	7481.3	6584.6	6493.5	6703.5	6384.6	10524.0	6414.1	8751.6
176.3	1540.1	1843.1	1236.1	1399.7	1520.7	1745.7	1621.0	926.9	553.2	1203.2
145.5	1622.5	1893.4	2148.4	1492.3	1547.6	2033.0	1721.1	1464.8	388.7	1152.2
2643.5	1180.2	1378.2	1851.4	1510.2	1349.3	2442.7	1477.2	855.4	1604.3	816.0
1522.4	4973.4	5089.7	5017.8	5748.8	4572.4	5230.1	4656.5	6217.2	3160.8	5891.1
6457.4	1856.9	2224.6	2394.7	1982.5	1810.6	458.2	2297.0	1406.5	845.7	1702.4
184.4	1744.8	1377.5	1100.1	864.9	1441.4	1396.1	1164.5	632.7	1449.9	792.1
809.5	1106.2	1337.6	1036.3	1173.3	1069.4	1020.1	1216.1	957.6	1594.5	924.8
422.0	2697.1	3634.3	3879.6	2072.5	3012.6	3474.1	4730.7	1342.9	1232.7	3622.6
5072.6	4892.3	4558.3	5253.0	5213.7	4648.5	5777.5	4860.4	8033.8	6432.8	6265.3
4331.8	3257.5	3839.8	4384.6	3930.0	3553.1	4791.8	3407.6	3022.8	2481.1	3221.8
3734.2	1400.8	1630.6	1611.2	1006.5	1508.6	1176.0	1390.4	1795.3	1537.8	1900.4
119.2	723.4	1011.4	870.0	761.6	775.3	839.8	998.5	447.4	471.1	587.1
47.3	246.1	290.9	361.9	167.8	55.3	144.2	237.0	106.7	70.3	107.8
112.8	1066.6	1373.6	1636.2	620.0	838.5	837.5	1770.4	684.7	131.8	699.5
46.2	173.8	426.5	477.7	406.5	476.0	340.4	356.2	95.7	57.5	136.9
750.3	1807.3	2187.5	2421.0	1435.8	1592.7	2152.5	1884.7	2107.4	2087.0	1641.9
23964.0	8361.1	5940.2	9071.5	6900.8	7531.7	8119.6	7260.7	11001.2	8037.6	11695.8

1966.5	1726.9	2057.6
2431.8	1684.2	2060.7
2419.5	1311.6	2121.6
2547.4	3210.1	2498.4
1856.4	1857.0	1531.2
2749.0	2850.3	6153.6
992.7	1270.5	1054.8
1375.2	1494.0	2294.0
775.5	1205.1	1658.3
1147.2	557.4	1269.9
1963.8	2333.9	1655.4
4644.8	4431.9	4212.0
3331.0	1769.4	2490.7
3457.8	2482.1	2898.8
1630.5	797.0	1530.2
1766.8	1970.4	2077.8
1250.9	1277.3	1398.9
1674.9	1419.7	1995.8
438.7	608.1	424.1
2487.1	2639.5	2544.6
3732.7	2805.7	3135.3
4242.8	5018.5	4260.5
171.2	248.2	588.3
6862.4	6726.7	7086.3
1170.8	2383.0	2251.3
1474.1	2018.2	3173.8
1566.9	1848.7	1595.5
4657.5	5346.7	5095.5
2810.0	2510.4	2512.7
1476.9	1290.0	1554.9
1426.2	1145.5	1576.7
4429.1	2925.3	4102.8
5206.2	5438.5	4389.2
3519.0	4581.1	4631.5
1415.5	2217.5	1385.0
1061.4	1134.9	1384.7
353.7	300.7	359.8
1836.8	1292.9	1965.3
528.2	331.0	528.4
2007.3	2246.2	2262.0
6989.8	8002.1	6858.1

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

g__Ruminococcus
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EU771714.1 gg_id:350396 African elephant feces clone AFEL2_aao31e06 EU771
DQ794277.1 gg_id:194984 human fecal clone RL176_aan60e06 DQ794
EU462421.1 gg_id:294022 Sumatran orangutan feces clone orang1_aai54c04 EU462
FJ372057.1 gg_id:359245 feces adult twins and mothers; TS9 clone TS9_a01c08 FJ3720
DQ802397.1 gg_id:194364 human fecal clone RL188_aah17b10 DQ802
DQ326751.1 gg_id:145473 Metagenomic gut microbiome healthy human stool clone E211 DQ326
EU776162.1 gg_id:350594 Spotted hyena feces clone HY2_c04 EU776
FJ368890.1 gg_id:366086 feces adult twins and mothers; TS4 clone TS4_a01g06 FJ3688
AY978933.1 gg_id:121792 human transverse colon mucosal biopsy clone NG68 AY9789
EU776398.1 gg_id:352712 Red Kangaroo feces clone KO2_aai17b07 EU776
FJ678828.1 gg_id:525532 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
DQ905491.1 gg_id:171386 human fecal clone 014-c3 DQ905
AY684374.2 gg_id:110259 mucosal biopsies human intestine clone HuRC33 AY6843
AY981433.1 gg_id:125763 human sigmoid colon mucosal biopsy clone L513 AY9814
GQ492339.1 gg_id:558380 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU772087.1 gg_id:345846 Argali sheep feces clone AS1_aao37b09.Contig1 EU772
FJ677219.1 gg_id:519710 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
EU462886.1 gg_id:299608 southern three-banded armadillo feces clone arma_aaj54e02 EU4628
DQ801672.1 gg_id:183663 human fecal clone RL201_aai45c08 DQ801
FJ684877.1 gg_id:523542 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
DQ326812.1 gg_id:150070 Metagenomic gut microbiome healthy human stool clone E282 DQ326
AY978964.1 gg_id:124012 human transverse colon mucosal biopsy clone NH49 AY9789
GQ492583.1 gg_id:552770 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ326786.1 gg_id:147939 Metagenomic gut microbiome healthy human stool clone E253 DQ326
DQ798077.1 gg_id:189787 human fecal clone RL302_aal95c05 DQ798
DQ326720.1 gg_id:149825 Metagenomic gut microbiome healthy human stool clone E175 DQ326
AY978934.1 gg_id:123993 human transverse colon mucosal biopsy clone NG70 AY9789
AY985948.1 gg_id:121913 human stool clone D246 AY9859
FJ364610.1 gg_id:369632 feces adult twins and mothers; TS19 clone TS19_a01a05 FJ3646
DQ327441.1 gg_id:146930 Metagenomic gut microbiome healthy human stool clone EA04 DQ327
FJ366624.1 gg_id:363033 feces adult twins and mothers; TS27 clone TS27_a01h05 FJ3666
FJ366100.1 gg_id:360703 feces adult twins and mothers; TS25 clone TS25_a02f11 FJ3661
EU774442.1 gg_id:325255 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1! EU774
DQ905638.1 gg_id:167163 human fecal clone 014C-B3 DQ905
DQ802606.1 gg_id:179151 human fecal clone RL188_aan94a08 DQ802
FJ680721.1 gg_id:527909 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU773805.1 gg_id:314832 Cheetah feces clone CE3_aai07d08 EU7738
EU459677.1 gg_id:287645 ring-tailed lemur feces clone RT_aai10g01 EU4596
DQ805533.1 gg_id:184597 human fecal clone RL203_aai63h01 DQ805
EU776169.1 gg_id:333386 Spotted hyena feces clone HY1_f11 EU776

9688.0	5303.6	4902.7	4912.8	5807.5	5458.2	5682.9	4802.2	5828.7	5370.8	4732.4
202.7	2237.7	3520.2	2337.1	2345.9	2086.3	2946.6	2296.7	1079.8	1816.5	2463.9
918.6	2005.6	1969.1	1727.7	1189.3	1385.9	1862.1	2354.4	994.4	1515.4	1401.2
222.3	1241.4	1421.2	1584.4	1242.6	1491.5	1560.5	1303.8	987.2	770.8	980.8
98.9	1845.1	2094.0	1768.5	1281.4	1599.5	1112.1	1925.2	1284.9	1438.6	1572.2
73.7	1307.3	1665.4	944.9	552.3	1069.4	746.7	952.6	1135.5	527.9	863.5
340.2	1275.7	1894.0	1771.1	730.6	1291.4	1107.2	1716.4	705.5	630.4	1485.5
43.7	898.0	1090.3	1090.6	527.2	835.9	521.9	929.1	207.5	279.4	575.8
204.0	629.0	1208.9	1098.4	498.8	578.0	546.3	510.4	317.8	347.2	509.6
890.4	2533.7	3103.2	3070.0	1800.1	2573.4	2472.9	3080.7	2208.5	2423.1	2780.2
344.1	2800.8	3059.2	4243.7	3042.8	3531.3	2506.0	3446.9	2418.2	3079.5	2786.6
720.0	1480.8	2122.5	2324.9	2101.7	1554.1	1954.8	1646.3	1548.3	1251.5	2223.7
1835.5	3327.7	4375.6	4087.8	1915.8	3424.1	4057.0	3806.8	4392.8	4325.5	3188.1
4182.4	4177.9	3933.6	4242.9	4199.9	3609.1	3764.7	4281.6	3437.2	2567.3	5421.3
800.2	1811.6	2316.7	2832.7	2308.8	2022.4	3098.3	2080.6	1143.1	2024.8	1307.6
1025.6	1812.0	2116.6	2217.9	2126.1	1634.4	1956.0	1733.9	2164.2	554.1	2110.2
217.5	2026.4	2609.2	2396.5	2771.3	2621.1	2180.4	3062.2	1887.8	2175.0	2124.6
834.9	843.2	1120.1	837.0	863.8	993.3	877.1	1131.8	914.8	1465.4	744.8
74.3	659.4	905.0	970.5	379.2	507.3	768.3	627.7	155.6	68.2	511.7
55.0	1743.8	2495.7	2096.9	948.5	1810.2	1278.2	2575.9	946.7	363.2	1809.9
15101.0	6878.7	6198.5	6721.3	5778.6	6385.0	6515.1	5925.7	9278.4	7011.8	8607.6
406.6	790.6	1182.8	1056.6	748.9	802.4	879.1	941.9	829.0	771.3	834.1
8097.0	3886.3	3660.9	3796.0	3368.0	3489.3	4001.2	3519.4	4334.2	3723.2	4303.2
22160.0	5402.0	5082.9	5242.2	6023.0	5025.2	5441.2	5216.3	7772.4	7156.7	5812.1
234.1	1866.5	2389.0	1554.9	1114.0	1813.4	1324.5	1923.8	1117.7	763.9	2333.7
2752.3	3003.7	2759.2	2808.5	2542.1	2559.3	2904.8	2751.2	2464.2	1536.4	3399.4
86.6	1241.3	1788.2	2100.1	650.1	1208.1	672.2	1527.2	1094.7	426.3	914.9
21942.2	6549.0	5569.6	6292.6	5521.6	6043.5	6348.7	5161.1	9691.0	5828.5	10763.3
897.9	1690.7	1666.3	1875.7	2045.5	1443.1	2255.8	1637.0	1738.8	1581.2	1151.0
781.0	1971.7	2280.2	2621.0	1868.9	1819.8	2319.5	2107.1	2252.6	2360.8	1865.2
377.5	1878.6	2855.4	1384.9	1173.6	1604.4	1152.7	1690.6	1336.6	902.7	1770.2
757.5	1993.8	2544.0	2824.5	1313.6	1963.3	1974.5	2305.0	1787.2	1982.2	2099.1
28.6	254.5	537.8	405.7	156.5	254.9	90.2	267.7	53.5	78.1	161.8
1773.1	2648.7	3155.8	2861.7	2021.3	2327.6	2424.0	2444.6	1779.1	1750.5	3953.9
485.5	1294.6	2161.7	2293.2	935.8	1574.7	2311.4	1624.9	820.5	582.1	1440.6
123.2	495.6	634.6	927.2	370.9	542.9	435.3	838.4	151.9	41.6	329.4
88.9	584.4	906.9	729.4	876.0	640.6	942.5	949.5	402.4	186.9	373.2
545.4	1344.3	1584.7	1528.0	1111.3	1511.2	1216.4	1844.9	767.9	295.7	1147.1
914.7	3675.6	2629.6	2413.4	2535.7	2888.3	1736.7	2523.5	2440.9	1492.6	2655.6
36.9	229.8	394.0	561.0	87.2	226.9	135.6	547.6	58.5	75.8	139.8
45.6	180.2	269.5	181.3	88.8	195.1	78.7	162.3	55.8	101.4	114.9

5998.1	5540.9	6281.2
2109.0	2275.7	2100.7
2587.6	1653.2	2140.7
1307.6	882.0	2914.7
1999.0	1651.7	2234.4
844.4	1004.6	854.1
2350.2	1427.8	1902.8
1160.1	1262.2	1043.9
747.1	806.5	1035.8
3574.4	3148.6	3669.5
2761.4	3911.3	3963.7
1732.8	2075.7	1772.4
3554.2	3495.0	3341.7
4762.5	4169.2	3785.7
2100.2	2300.4	2382.8
2230.0	2028.0	2188.9
2735.0	2278.5	2651.2
1162.3	1280.7	1302.4
551.4	696.1	1807.6
2773.6	2153.6	3214.1
5572.4	6167.9	5659.3
875.3	1081.5	1576.7
3243.1	5063.1	4404.8
5404.5	6805.9	5549.9
2040.4	1937.9	1572.0
2135.1	3566.8	2216.3
2001.0	1531.4	1484.9
5378.3	6210.4	5943.9
2090.6	1723.1	1847.1
2224.9	2500.1	2458.4
1838.9	2735.1	1627.5
2764.7	2386.2	2376.2
320.1	472.5	441.9
2431.6	2989.1	2024.5
1218.0	1452.1	1618.7
832.1	1242.1	1059.9
1661.3	548.0	1078.5
2070.4	1240.9	1989.0
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1135.7	320.9	369.9
281.3	130.6	239.4

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o__Clostridiales	f__Lachnospiraceae

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GQ175422.1 gg_id:514030 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
EU461126.1 gg_id:295914 red kangaroo feces clone KO1_aai44g04 EU461
DQ802367.1 gg_id:190902 human fecal clone RL188_aah16g02 DQ802
EU009853.1 gg_id:249142 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_V48 EU009
AY985749.1 gg_id:124089 human stool clone C781 AY985
DQ808135.1 gg_id:173994 human fecal clone RL180_aao73a12 DQ808
EU773162.1 gg_id:339111 BigHorn sheep feces clone BH2_aao24f09 EU773
GQ493675.1 gg_id:550701 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ491641.1 gg_id:592348 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ802682.1 gg_id:189136 human fecal clone RL188_aan95b04 DQ802
EF025300.1 gg_id:185972 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N32 EF0253
DQ802106.1 gg_id:188521 human fecal clone RL241_aaj03b07 DQ802
DQ905513.1 gg_id:167330 human fecal clone 014-e6 DQ905
DQ327068.1 gg_id:145530 Metagenomic gut microbiome healthy human stool clone E576 DQ327
DQ797240.1 gg_id:198105 human fecal clone RL386_aao88g07 DQ797
FJ371212.1 gg_id:360981 feces adult twins and mothers; TS6 clone TS6_a02c03 FJ3712
EU469310.1 gg_id:291426 Speke's gazelle feces clone SP3_g10_2 EU469
FJ370786.1 gg_id:359968 feces adult twins and mothers; TS5 clone TS5_a01c06 FJ3707
EU773988.1 gg_id:333309 Cheetah feces clone CE3_aai06g03 EU773
FJ368092.1 gg_id:370388 feces adult twins and mothers; TS30 clone TS30_a03h07 FJ3680
FJ369085.1 gg_id:359707 feces adult twins and mothers; TS4 clone TS4_a04a09 FJ3690
DQ800102.1 gg_id:185775 human fecal clone RL247_aaj24b10 DQ800
DQ327379.1 gg_id:146834 Metagenomic gut microbiome healthy human stool clone E936 DQ327
DQ071519.1 gg_id:234113 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc26 DQ071
DQ905559.1 gg_id:170503 human fecal clone 014B-C2 DQ905
AY977233.1 gg_id:122429 human cecum mucosal biopsy clone MT69 AY977
DQ805113.1 gg_id:184911 human fecal clone RL249_aaj81d05 DQ805
EU462882.1 gg_id:293600 southern three-banded armadillo feces clone arma_aaj54d09 EU462
FJ364879.1 gg_id:360138 feces adult twins and mothers; TS19 clone TS19_a04c04 FJ3648
FJ366558.1 gg_id:359733 feces adult twins and mothers; TS27 clone TS27_a01b07 FJ3665
DQ794475.1 gg_id:193297 human fecal clone RL197_aah88d03 DQ794
FJ678742.1 gg_id:523496 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ366836.1 gg_id:366783 feces adult twins and mothers; TS27 clone TS27_a04d10 FJ3668
FJ368994.1 gg_id:367327 feces adult twins and mothers; TS4 clone TS4_a03a06 FJ3689
FJ371218.1 gg_id:362500 feces adult twins and mothers; TS6 clone TS6_a02c09 FJ3712
FJ369934.1 gg_id:359266 feces adult twins and mothers; TS55 clone TS55_a02e01 FJ3699
FJ371690.1 gg_id:359323 feces adult twins and mothers; TS8 clone TS8_a01b07 FJ3716
DQ326814.1 gg_id:146704 Metagenomic gut microbiome healthy human stool clone E285 DQ326
FJ368753.1 gg_id:365790 feces adult twins and mothers; TS49 clone TS49_a04b03 FJ3687
FJ362751.1 gg_id:368009 feces adult twins and mothers; TS13 clone TS13_a02f11 FJ3627

2664.0	4652.5	4424.3	3683.4	3406.8	3792.3	3866.6	3881.7	7067.0	4331.9	4285.1
6136.4	4725.7	4489.7	4609.4	5005.1	4556.3	5239.3	4822.9	5985.6	7204.9	3929.6
59.1	334.9	483.6	512.6	321.4	299.1	316.5	362.2	105.8	58.6	127.4
65.6	171.2	345.1	311.5	253.6	227.9	327.4	362.6	84.9	224.1	139.9
74.7	510.8	840.8	938.6	469.2	566.7	656.7	791.1	243.1	122.6	300.8
191.0	2352.1	4167.3	2360.0	1381.4	2465.4	1519.3	2991.4	2018.0	1013.1	3650.1
42.2	88.4	155.1	151.6	97.2	144.1	103.9	228.5	55.0	39.6	106.3
28.4	2139.9	2252.3	1186.3	1766.0	2160.0	1773.1	1176.9	4450.4	4730.9	626.1
58.0	394.9	367.1	281.1	194.1	313.0	153.8	207.2	290.7	460.2	271.0
80.6	1090.6	1629.3	1583.4	626.1	1178.0	788.7	1496.7	677.2	214.2	1427.1
602.9	2559.6	3691.5	4166.2	1594.2	2908.2	3385.3	3288.5	2040.5	2032.5	2796.6
48.5	95.4	118.8	105.9	50.0	112.8	61.9	182.8	54.5	45.3	80.2
815.8	2161.2	2558.4	2274.9	1704.3	1955.4	2417.0	2103.6	2458.2	1517.7	2703.0
188.4	1099.7	2257.6	2135.4	745.7	1649.1	1509.6	1618.2	613.2	226.8	1074.5
936.6	1668.4	2045.0	2213.2	1641.3	1801.2	1939.0	1874.4	2248.9	2168.5	1644.2
124.2	2094.6	1679.3	1763.5	1967.3	1663.0	2005.2	1810.6	2012.0	1793.0	1187.9
35.6	181.7	362.7	368.7	247.1	201.9	243.0	1023.3	55.4	29.6	199.1
79.3	2970.6	4871.9	4743.9	1356.6	3862.4	3235.5	4894.3	1564.3	710.6	3763.3
864.9	2379.9	2048.4	1723.3	1522.4	1852.3	1312.3	1672.2	1567.9	1253.5	1212.1
953.6	1989.7	2607.6	2846.8	1341.4	2133.9	2010.7	3090.9	1172.2	534.7	2113.3
447.3	1090.4	1588.8	1471.1	947.6	1019.1	1191.0	1104.2	769.7	1004.2	1272.9
6457.1	2113.8	2532.9	1945.2	1748.6	2267.1	2602.7	1891.0	1291.1	2165.2	3264.3
58.7	507.3	1156.7	1094.5	403.2	807.5	741.2	769.5	533.0	470.9	1075.2
40.0	91.5	98.3	109.6	45.6	51.2	34.5	73.2	49.4	31.3	62.6
210.6	724.1	805.4	834.5	748.2	697.4	869.5	796.4	446.2	206.8	623.3
33.9	524.1	749.0	841.6	144.7	470.9	286.0	886.7	229.1	79.5	607.6
755.6	2197.7	2767.0	2711.3	1450.6	2253.7	2126.7	2607.7	2012.5	2058.8	2683.6
6913.8	4012.2	3527.2	4875.8	4587.5	3571.9	4722.8	3505.7	4576.3	4363.8	6107.8
4662.5	5129.1	5818.4	4860.8	4522.7	4989.5	4806.3	6711.3	6126.0	3398.4	5228.8
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808.0	1950.5	2440.9	2709.2	1282.4	1775.8	1897.7	2171.5	1881.9	2044.4	1981.0
1710.4	1126.9	1168.5	1222.1	994.5	1203.3	1419.3	1495.3	1068.5	818.4	1181.5
55.6	266.0	433.0	567.1	103.0	226.1	220.7	346.5	76.7	61.7	211.1
6444.3	2010.0	2376.4	2450.8	2018.3	2167.8	2078.8	2824.7	1929.6	2267.3	2271.7
15057.1	8942.2	8211.3	8394.2	10151.9	7135.0	9342.5	7755.0	11888.8	9073.4	11218.3
100.2	2550.4	2107.2	1535.4	1113.8	1868.2	1122.2	1388.6	2070.6	2214.1	1453.1
80.0	1004.5	1467.9	1694.7	579.0	1097.2	612.9	1848.1	481.2	572.9	778.8
404.9	2250.5	3428.5	2671.4	1484.4	2150.7	2019.5	2951.5	1498.8	1326.1	2612.4
396.1	847.5	1255.3	1123.6	840.0	848.9	1064.3	987.8	813.0	781.6	853.5
822.3	2053.4	2751.5	2707.8	1447.7	2252.7	2125.3	2606.5	2154.5	2188.0	2463.2
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5010.7	5520.0	5593.4
577.8	374.7	538.7
519.7	262.8	347.2
847.1	731.5	885.4
3565.4	2949.9	2935.5
313.2	221.1	222.5
1347.8	983.2	1357.3
496.0	233.5	387.5
1758.2	1263.3	1773.0
3227.9	2578.7	3017.1
181.3	149.4	176.2
1499.5	1695.1	1560.0
1322.1	1396.3	1716.3
1945.7	2200.1	2337.4
1845.6	1669.8	2144.1
514.6	257.6	315.2
5478.4	2904.0	4757.0
1592.0	2641.6	1566.9
3659.5	1952.9	2985.9
1166.3	1420.0	1785.1
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865.4	1023.0	1364.4
108.0	100.9	93.9
715.2	786.2	1041.4
1104.2	493.3	709.2
3086.3	2701.4	3056.2
3776.5	4314.1	3415.7
5940.6	5424.7	5851.4
2956.5	4546.7	4134.8
2629.6	2226.3	2280.0
1125.4	2026.2	1038.8
377.3	430.7	344.9
3526.9	3486.2	3254.8
7280.2	8208.6	6852.6
1589.6	1566.6	2486.3
1942.2	1272.8	1494.8
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o__Clostridiales	f__Lachnospiraceae

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DQ905618.1 gg_id:172273 human fecal clone 014B-H3 DQ905
FJ366699.1 gg_id:358617 feces adult twins and mothers; TS27 clone TS27_a02g08 FJ3666
DQ804059.1 gg_id:196967 human fecal clone RL187_aah67h03 DQ804
DQ456170.1 gg_id:157302 pre-adolescent turkey cecum clone CFT29C1 DQ456
DQ805425.1 gg_id:174604 human fecal clone RL203_aai62d11 DQ805
AY980918.1 gg_id:116825 human rectum mucosal biopsy clone LR25 AY9809
DQ905539.1 gg_id:165398 human fecal clone 014B-A6 DQ905
GQ493410.1 gg_id:585983 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ797428.1 gg_id:175273 human fecal clone RL248_aai99c03 DQ797
FJ678344.1 gg_id:515194 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
FJ368787.1 gg_id:363239 feces adult twins and mothers; TS49 clone TS49_a04e09 FJ3687
GQ493082.1 gg_id:583836 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF025247.1 gg_id:176435 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F9 EF0252
DQ795782.1 gg_id:192966 human fecal clone RL245_aai82c11 DQ795
DQ326809.1 gg_id:150159 Metagenomic gut microbiome healthy human stool clone E279 DQ326
FJ673649.1 gg_id:517277 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ802042.1 gg_id:190560 human fecal clone RL241_aaj02c09 DQ802
EF399287.1 gg_id:212960 human fecal clone SJTU_F_14_03 EF3992
EU773335.1 gg_id:310492 BigHorn sheep feces clone BH1_aao25f07 EU7733
FJ682187.1 gg_id:522697 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
DQ799008.1 gg_id:183370 human fecal clone RL242_aak00c11 DQ799
FJ363264.1 gg_id:362565 feces adult twins and mothers; TS149 clone TS149_a01c01 FJ3632
FJ673945.1 gg_id:512723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
GQ491988.1 gg_id:581922 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ364762.1 gg_id:362461 feces adult twins and mothers; TS19 clone TS19_a02g07 FJ3647
GQ493078.1 gg_id:536373 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ326651.1 gg_id:147001 Metagenomic gut microbiome healthy human stool clone E090 DQ326
DQ801918.1 gg_id:192071 human fecal clone RL201_aai48e01 DQ801
EU460132.1 gg_id:292073 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU460
DQ823822.1 gg_id:191551 human fecal clone RL250_aaj79e10 DQ823
EU776463.1 gg_id:349343 Red Kangaroo feces clone KO1_aai44e01 EU7764
GQ021445.1 gg_id:488223 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
EU458416.1 gg_id:300405 spotted hyena feces clone HY1_g09_2 EU4584
GQ493968.1 gg_id:537542 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY978915.1 gg_id:122685 human transverse colon mucosal biopsy clone NG29 AY9789
AY592220.1 gg_id:101163 marine ANAMMOX sediment clone AY592220 AY5922
FJ366840.1 gg_id:358475 feces adult twins and mothers; TS27 clone TS27_a04e02 FJ3668
FJ678821.1 gg_id:525885 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ675824.1 gg_id:513990 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
EF403531.1 gg_id:211175 human fecal clone SJTU_A2_03_09 EF4035

73.5	470.0	687.0	969.3	707.7	684.2	1116.2	735.2	339.0	96.0	410.9
4051.3	2718.1	3574.9	3734.4	2120.7	3320.5	2936.9	3538.0	2432.5	2114.9	4112.9
2912.3	5650.0	4086.5	4151.3	3319.0	4070.4	3807.1	3732.5	5556.2	2963.7	5882.0
57.9	43.2	54.4	46.8	33.2	42.8	34.2	70.6	31.8	36.1	30.4
92.0	551.1	910.5	957.1	351.0	567.5	489.9	728.9	145.0	79.2	306.1
95.5	1670.0	2454.9	1595.1	504.2	1283.5	1469.9	1417.1	1758.8	1181.7	1798.3
52.3	292.9	271.9	387.2	150.0	212.5	261.2	511.4	55.4	66.1	148.0
528.2	1659.7	2361.3	2851.9	1216.8	1982.4	2033.2	2582.9	1252.5	1130.8	1813.5
155.5	1762.5	1819.3	1862.4	2342.0	1859.5	2606.8	2015.9	1452.0	1874.7	1311.9
7985.9	3241.3	3039.9	3061.8	3260.3	3198.6	3122.6	3475.4	3642.5	3196.6	3112.3
3355.2	2408.0	2824.2	3523.1	2757.4	3215.4	3224.5	3839.7	2682.3	1181.8	2465.1
181.0	3020.3	3817.6	2854.7	1795.5	2063.4	1905.5	2110.4	3022.9	1793.9	3074.9
1380.8	5797.5	4417.9	3226.4	3218.0	3878.4	2742.5	3477.0	4558.8	3065.6	4509.5
129.7	1158.1	1228.6	1492.6	1222.9	1190.6	1238.3	1391.8	949.5	1065.4	1106.7
4111.3	2177.0	2572.3	2870.7	2442.0	2687.7	3260.4	2649.3	3749.9	4706.7	3751.1
71.4	1279.3	2004.7	2136.4	735.0	1480.2	849.0	1822.7	1062.2	415.8	972.7
24139.1	8513.5	8032.3	8551.9	8144.7	7860.3	8826.2	7535.1	8299.3	10670.0	9614.4
88.3	204.8	307.8	341.7	320.2	84.6	413.4	251.5	138.7	134.6	155.0
492.1	2160.8	3437.4	3103.4	1793.5	2484.5	2809.9	2565.9	1398.8	1923.1	2283.2
922.7	1595.8	1612.6	1806.3	1986.8	1382.4	2506.6	1382.3	450.0	665.9	944.1
34.4	198.1	327.8	478.1	105.4	297.6	169.3	397.4	93.4	92.9	99.6
98.8	362.1	643.9	652.5	265.7	274.5	564.3	363.2	248.4	110.2	233.8
65.3	976.3	1014.0	1432.8	1053.4	1088.5	2122.1	1246.8	1084.8	1698.4	629.4
376.6	581.5	943.8	1000.5	505.0	539.1	1083.4	930.3	441.7	135.8	640.9
216.5	2317.4	2493.1	2371.2	2312.6	2415.1	2521.5	2225.3	1636.5	1462.2	2509.1
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141.0	1329.7	1236.9	738.8	1142.7	959.8	548.7	751.4	1012.9	471.6	771.2
34.9	460.3	665.5	585.9	123.2	521.3	101.4	729.8	245.9	259.4	560.2
5074.2	1940.2	2366.5	1984.2	1524.2	1847.2	1820.7	1814.2	2475.0	2072.0	2345.0
70.8	895.8	1366.7	1695.0	299.4	868.3	470.8	1542.8	363.3	504.7	832.2
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107.9	2499.3	2464.6	2374.4	2401.7	2733.4	2456.7	3695.1	2083.6	584.4	1353.0
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3731.6	4000.8	3437.3	3346.6	2656.1	3384.3	3018.3	3223.8	6364.7	5222.7	3902.2
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7812.6	2402.8	2446.1	2903.0	2320.9	2393.2	2411.3	2620.7	2923.6	2688.8	3653.3
598.8	2594.6	3676.1	4141.9	3430.0	2907.1	4086.5	2849.1	2710.6	4169.4	3342.1
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4155.9	3487.6	3851.3
3400.3	4267.1	3397.2
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787.2	544.7	848.8
1305.6	2009.7	1133.3
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2649.5	2182.5	2834.9
2243.0	2316.3	2356.7
2727.8	2988.8	5105.2
4122.1	3458.0	2879.9
2425.5	2429.1	2466.9
3687.0	4123.4	3259.9
1184.2	1701.3	1127.1
2198.3	3564.5	2919.1
2429.4	1609.1	1669.4
7564.6	9852.1	8530.0
263.4	381.6	308.2
2432.7	2133.1	3285.6
1418.6	1666.8	2839.1
755.5	372.8	321.1
350.6	431.7	603.5
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972.2	704.4	606.0
2508.4	2376.2	2728.3
2559.0	2798.4	2709.4
921.8	1099.7	506.5
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2765.8	1355.0	1661.8
3547.4	2953.0	3441.6
5937.9	6921.7	5949.3
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3107.6	4733.1	4277.2
599.3	587.9	1280.4
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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DQ905580.1 gg_id:167959 human fecal clone 014B-D11 DQ905
DQ800037.1 gg_id:196179 human fecal clone RL247_aaj23d05 DQ800
GQ088713.1 gg_id:433719 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ088
AJ315979.1 gg_id:100067 Ruminococcus sp. str. 14531 AJ3159
DQ808256.1 gg_id:190340 human fecal clone RL180_aao74e01 DQ808
AY981922.1 gg_id:122665 human sigmoid colon mucosal biopsy clone NZ40 AY9819
FJ683488.1 gg_id:516265 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
DQ805608.1 gg_id:196505 human fecal clone RL203_aai64h05 DQ805
GQ491205.1 gg_id:578251 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ456364.1 gg_id:157516 pre-adolescent turkey cecum clone CFT212E4 DQ456
EU772704.1 gg_id:341622 Bush dog feces clone bdog1_aai80e08 EU772
DQ071536.1 gg_id:234421 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc23 DQ071
EF399161.1 gg_id:216134 human fecal clone SJTU_F_12_47 EF3991
GQ493957.1 gg_id:582233 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ369466.1 gg_id:367857 feces adult twins and mothers; TS50 clone TS50_a04h04 FJ3694
DQ800183.1 gg_id:195002 human fecal clone RL303_aal69d01 DQ800
DQ796321.1 gg_id:199585 human fecal clone RL179_aah25g04 DQ796
FJ367966.1 gg_id:369900 feces adult twins and mothers; TS30 clone TS30_a01h04 FJ3679
EU530425.1 gg_id:271120 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M6 EU5304
GQ175466.1 gg_id:593066 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ905611.1 gg_id:169787 human fecal clone 014B-G8 DQ905
EU475485.1 gg_id:290548 springbok feces clone SBSD_aaa02c06 EU4754
FJ365141.1 gg_id:367587 feces adult twins and mothers; TS1 clone TS1_a03d04 FJ3651
FJ369760.1 gg_id:358260 feces adult twins and mothers; TS51 clone TS51_a04e04 FJ3697
EF403443.1 gg_id:204152 human fecal clone SJTU_A2_01_29 EF4034
DQ796893.1 gg_id:185834 human fecal clone RL179_aao56a10 DQ796
GQ493314.1 gg_id:583398 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ806984.1 gg_id:192413 human fecal clone RL198_aaj76f09 DQ806
EU466859.1 gg_id:291755 African elephant feces clone AFEL2_aao30d11 EU4668
FJ366049.1 gg_id:365527 feces adult twins and mothers; TS25 clone TS25_a02b03 FJ3660
DQ807268.1 gg_id:195172 human fecal clone RL244_aaj48d02 DQ807
AY978903.1 gg_id:118349 human transverse colon mucosal biopsy clone NF82 AY9789
FJ369930.1 gg_id:359000 feces adult twins and mothers; TS55 clone TS55_a02d08 FJ3699
FJ369122.1 gg_id:364608 feces adult twins and mothers; TS4 clone TS4_a04e05 FJ3691
FJ370133.1 gg_id:366858 feces adult twins and mothers; TS55 clone TS55_a04g06 FJ3701
FJ366834.1 gg_id:368301 feces adult twins and mothers; TS27 clone TS27_a04d08 FJ3668
AY981879.1 gg_id:127442 human sigmoid colon mucosal biopsy clone NX61 AY9818
EU530240.1 gg_id:261540 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-aden EU5302
FJ364056.1 gg_id:357671 feces adult twins and mothers; TS150 clone TS150_a02d11 FJ3640
EU530356.1 gg_id:274877 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303

63.9	621.7	948.9	914.6	325.6	689.0	473.9	990.2	563.8	337.1	620.9
7656.1	6123.7	7339.0	7104.8	5301.1	6499.6	6562.1	7250.9	7924.4	6234.7	8518.0
42.6	969.2	1684.6	1467.4	821.6	1463.3	1037.5	1711.9	766.2	421.0	1508.4
53.0	405.1	521.0	723.9	301.3	435.0	536.8	537.0	230.1	477.2	271.1
1585.6	2930.1	2838.2	2688.2	2237.5	3521.2	2072.6	3426.4	3130.0	861.8	3035.6
79.6	425.0	641.7	746.1	143.2	526.9	322.9	1517.4	187.9	217.3	392.8
875.6	1881.6	2253.8	2481.2	1619.5	1718.4	2235.5	2125.1	2023.8	2192.2	1683.3
2238.4	1443.0	1153.8	1471.1	2368.2	1129.8	2499.3	1216.4	400.8	317.1	517.9
40.2	25.6	40.9	24.3	25.1	21.2	19.3	20.5	20.3	36.6	16.5
16686.6	6250.6	5329.0	4768.8	4696.5	5763.5	4515.7	4506.7	8216.8	5683.9	6027.0
819.2	2461.4	2962.5	3265.6	3865.2	2756.2	2753.1	2548.6	2130.7	1611.3	6483.9
908.8	1512.2	2215.9	2363.8	1387.4	1856.4	1896.2	2711.0	1546.4	1186.2	1758.6
1662.2	831.1	1402.4	1217.0	1090.8	1014.7	1209.4	1281.3	656.6	337.8	1238.8
15243.9	4407.2	5033.5	5220.4	5552.5	4157.2	5168.5	4841.2	6420.3	3466.6	4362.8
1056.8	2922.4	3050.4	2679.9	2251.9	2536.7	2507.5	2787.8	2934.3	1067.0	2686.4
123.1	1018.4	1692.6	1517.2	1829.5	1634.3	2225.5	1810.8	896.6	360.2	1024.0
984.8	192.5	383.8	400.4	479.8	225.6	283.3	420.6	284.8	246.6	214.6
1672.6	2428.1	1988.3	1498.4	1818.1	1739.8	1879.3	1557.3	1869.9	1448.2	1135.4
3585.5	3935.6	3489.7	4156.1	2838.5	3375.1	2412.5	2797.8	2423.3	1156.6	2378.7
489.5	3135.3	4158.7	3211.8	2599.0	2949.2	2144.9	3222.1	2263.5	1608.2	2614.0
67.4	1053.2	1464.7	1534.5	1329.4	982.0	1182.8	1453.6	1268.6	246.5	810.0
11616.6	5359.5	5327.6	6309.9	5719.3	5734.2	5933.0	5282.4	6031.6	6345.8	7729.3
158.0	1088.0	1473.7	1585.6	830.3	1295.7	995.9	2395.6	426.1	197.4	1011.7
413.7	1476.3	2142.9	1856.2	1000.8	1623.6	1487.8	1854.8	1065.2	861.9	1991.9
3178.2	1966.7	2026.4	1882.9	1577.3	1667.1	2006.3	1767.3	3792.5	1717.5	3006.6
165.4	1020.8	1538.7	1637.6	1074.4	965.5	1621.9	1544.8	835.4	350.5	1053.0
287.3	870.6	1453.4	1271.8	518.3	886.6	873.0	1062.3	727.8	852.7	544.4
783.6	717.8	935.5	843.9	595.1	707.0	680.3	715.4	981.0	446.0	709.5
698.2	821.4	1083.3	997.3	690.9	718.4	698.9	833.7	1265.2	986.0	1018.4
789.6	3392.0	3577.4	3146.7	1866.4	2909.6	2491.5	3090.1	4233.6	4216.8	4394.7
343.5	1483.3	2058.4	2127.3	1121.4	1239.1	1363.9	1669.8	751.3	1060.8	1461.6
3724.1	1910.6	2425.2	1978.2	2136.0	2132.2	2030.4	1660.3	2985.0	1730.3	2890.0
7947.7	1748.6	1980.1	2110.9	1548.3	1662.3	1565.8	1762.2	2340.3	1303.4	2130.6
34.3	304.9	1126.3	1328.2	296.7	475.7	416.1	937.4	758.8	98.1	600.2
3249.0	3458.3	3103.1	3529.5	2051.1	3138.4	2900.1	3118.9	3031.8	2254.7	3629.0
247.8	574.2	680.7	719.5	565.8	493.3	644.1	792.2	239.3	103.5	340.8
54.1	818.9	1561.1	1345.8	506.4	1246.7	639.7	1406.5	416.3	206.3	794.4
7343.5	4016.0	4595.2	4388.5	3844.6	3307.0	4338.4	4218.8	4037.0	2296.2	5579.3
44.0	763.3	1151.1	1227.3	505.4	784.9	916.9	891.3	190.0	64.7	487.8
3749.9	2427.4	2566.1	2890.1	3098.2	2473.7	2673.6	2562.4	3287.6	3598.0	2620.7
783.2	1995.2	3609.1	3080.1	1561.2	2415.8	2999.8	2644.7	1499.9	2255.7	2258.2

1258.1	894.9	956.1
6922.7	6785.6	7300.7
1848.6	1470.6	1741.6
606.2	469.4	767.1
2992.0	2830.2	3235.4
1457.6	556.1	965.1
2249.1	2414.4	2689.8
2017.4	1461.3	1899.9
19.9	21.1	31.9
4829.6	5452.4	4563.1
2891.8	3284.5	2408.8
2843.9	2276.6	3032.7
905.3	1220.1	1197.4
5050.3	4989.5	4980.9
2344.4	2741.9	2889.6
1815.5	1567.2	2047.9
339.0	1665.2	371.6
1390.9	2041.1	1353.3
3459.5	3879.0	3705.6
3319.1	3116.2	4044.2
1529.6	1765.4	3198.9
5671.8	7085.4	5533.4
2559.0	1175.0	1932.6
2259.6	1880.4	2244.6
1603.1	2212.8	1761.8
1563.1	1312.6	2287.4
919.6	1285.7	1605.3
743.6	1112.3	924.2
941.9	1548.6	649.4
3277.7	3302.4	3396.0
1987.7	1709.6	2032.3
1521.7	2023.6	2532.6
1477.0	2802.3	2362.4
847.3	566.0	628.9
3269.5	3416.7	3485.6
576.1	1073.4	965.9
1963.7	1220.4	1569.4
3850.3	5496.5	5004.2
679.6	946.7	1780.4
2750.1	3335.8	2977.2
2140.2	2115.5	2664.1

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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EU469335.1 gg_id:294672 springbok feces clone SBK_f10 EU469
FJ370238.1 gg_id:357633 feces adult twins and mothers; TS56 clone TS56_a02c01 FJ3702
DQ800341.1 gg_id:193624 human fecal clone RL303_aal71g11 DQ800
GQ493418.1 gg_id:583336 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ370128.1 gg_id:364901 feces adult twins and mothers; TS55 clone TS55_a04g01 FJ3701
DQ808113.1 gg_id:184492 human fecal clone RL180_aan72g04 DQ808
AY982654.1 gg_id:124568 human descending colon mucosal biopsy clone KX45 AY9826
FJ367173.1 gg_id:359446 feces adult twins and mothers; TS28 clone TS28_a04d05 FJ3671
FJ369758.1 gg_id:361222 feces adult twins and mothers; TS51 clone TS51_a04e02 FJ3697
DQ905477.1 gg_id:164148 human fecal clone 014-b1 DQ905
FJ370411.1 gg_id:368396 feces adult twins and mothers; TS56 clone TS56_a04g05 FJ3704
FJ365992.1 gg_id:360267 feces adult twins and mothers; TS25 clone TS25_a01e03 FJ3659
FJ683878.1 gg_id:525278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
AY980425.1 gg_id:126180 human rectum mucosal biopsy clone N328 AY9804
EU771578.1 gg_id:321693 African elephant feces clone AFEL2_aao32d12 EU7715
FJ371364.1 gg_id:367266 feces adult twins and mothers; TS6 clone TS6_a04b01 FJ3713
FJ680888.1 gg_id:521005 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EU460182.1 gg_id:297182 mammals their gut microbes eastern black and white colobus feces clone COL_aai16 EU4601
DQ798904.1 gg_id:177911 human fecal clone RL242_aaj98h05 DQ798
EU462919.1 gg_id:297641 southern three-banded armadillo feces clone arma_aaj55a04 EU4629
EU776069.1 gg_id:342110 Spotted hyena feces clone HY2_d06 EU7760
AF399956.1 gg_id:44493 Shuttleworthia satelles str. VPI D143K-13 AF3999
AF371623.1 gg_id:39567 swine intestine clone p-986-s962-5 AF3716
AB034118.1 gg_id:34221 rumen clone 2C28d-12 AB0341
EU842536.1 gg_id:348474 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
AB034061.1 gg_id:23832 rumen clone 5C3d-20 AB0340
GQ040708.1 gg_id:384462 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957g08c GQ040
GQ038576.1 gg_id:467322 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ044889.1 gg_id:442935 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ044
AY958930.1 gg_id:137153 Microbes on human vaginal epithelium clone rRNA157 AY9589
GQ040803.1 gg_id:464655 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958g12c GQ040
GQ037634.1 gg_id:392847 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
GQ036308.1 gg_id:414882 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362f04c1 GQ036
GQ037663.1 gg_id:455181 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
GQ038522.1 gg_id:455063 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ040952.1 gg_id:468028 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw960e04c GQ040
AY959202.1 gg_id:134747 Microbes on human vaginal epithelium clone rRNA429 AY9592
GQ042994.1 gg_id:399643 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011h GQ042
GQ043923.1 gg_id:396628 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
CR933136.1 gg_id:111355 Evry municipal wastewater treatment plant clone 012F03_B_SD_P15 CR9331
AF001901.2 gg_id:245935 Selenomonas lipolytica str. CF1B AF0019

6382.0	3682.7	3429.8	3813.0	2929.0	2911.5	3319.2	3117.9	3741.0	3769.1	4620.3
56.7	334.6	579.3	635.8	257.0	396.8	279.6	503.1	189.3	164.4	345.0
1570.7	1028.4	1213.0	1143.7	1188.6	1118.0	1447.4	1055.6	1065.9	1600.1	1250.4
24705.9	5824.1	4887.6	5426.6	4857.0	5354.4	5497.4	5257.9	9134.7	6306.3	7628.8
469.7	2651.8	2066.7	1799.4	2605.0	2310.2	2335.7	2091.6	1479.9	1989.0	1006.4
63.6	93.0	148.3	178.6	95.1	113.9	176.0	146.7	86.0	50.3	91.5
6685.8	3514.9	3600.9	4043.5	3305.7	3627.0	4507.9	3940.4	4406.7	4527.2	3373.5
27638.5	5649.3	4988.6	5639.5	5847.5	4836.1	5374.8	4968.2	10252.0	7318.8	8620.4
673.7	2791.5	3305.5	3148.7	2156.3	3669.2	2827.5	3152.3	2214.0	2482.5	2940.2
160.5	2137.4	2962.5	3545.6	1768.9	2296.8	3153.2	2222.7	1389.5	1273.3	2338.2
1763.6	937.7	1399.6	1333.5	726.2	900.0	754.4	1146.3	732.0	889.1	1112.6
39.7	45.2	280.8	334.6	119.4	110.4	175.6	134.9	34.5	40.0	29.2
6388.4	1995.5	2178.4	2428.5	1938.3	1989.9	3024.2	2040.7	2144.2	2975.4	2273.3
860.9	5444.0	5056.2	5417.7	3297.1	4857.5	4821.4	4253.9	6304.3	6439.1	5122.7
38.4	393.1	729.4	711.7	279.3	453.4	371.3	659.8	119.3	32.1	178.4
702.8	2128.9	2438.1	2789.7	1836.0	2004.8	1984.7	2361.0	2014.0	2298.6	2287.0
5290.3	4693.1	5096.4	4879.3	4977.9	4845.9	5614.6	4193.1	3324.8	3173.9	4739.3
24.1	304.8	477.3	583.0	111.5	277.2	210.2	363.9	41.2	16.0	249.1
69.6	166.4	321.3	217.4	215.5	149.5	298.2	96.9	123.4	39.5	69.5
10390.9	4764.7	5468.3	5548.1	5752.2	5306.5	6084.0	5088.5	7476.3	6088.3	6410.5
1972.5	3012.3	3736.7	3767.5	2452.2	2943.9	2677.0	3202.2	1616.2	2475.5	2202.8
68.9	184.1	404.1	432.3	72.8	240.8	67.0	363.8	151.6	195.7	279.7
233.4	2850.8	2529.6	1900.1	1800.1	2514.2	1942.0	2369.2	1940.8	981.9	1310.2
48.8	166.5	190.0	247.6	188.9	202.5	220.1	289.6	78.1	47.9	91.3
383.6	967.8	1358.7	1571.2	638.9	801.8	820.5	1215.8	474.8	161.2	690.5
43.5	123.4	163.9	269.6	135.5	112.3	224.6	167.8	43.7	40.6	175.1
201.2	2628.8	2420.2	3400.8	2587.8	2568.7	2826.3	4003.2	1570.3	578.7	2856.8
1206.7	2211.3	2232.4	2480.1	1692.7	1663.4	1687.4	1925.6	1700.9	1017.0	1252.4
926.4	3658.5	4216.3	4246.3	2548.3	2955.6	3486.8	3554.8	3285.8	2569.0	4141.4
1606.7	4818.6	4978.2	5171.4	4589.4	4804.3	4705.9	5385.2	4946.9	3528.7	7043.0
4535.1	6246.6	6570.8	6872.6	5691.5	5827.6	5974.4	6934.0	6501.1	4198.6	5951.0
1973.8	3031.5	3045.8	3373.5	2340.9	2588.0	2597.3	2918.9	2690.5	1754.2	2615.1
1469.3	5432.5	4732.7	5510.0	4699.4	4642.7	4932.4	5534.9	5050.2	3256.1	4375.6
8578.9	6692.8	6694.7	6443.1	5571.6	5996.9	5968.0	5947.2	8633.8	6991.9	6368.8
1766.8	5252.8	5006.6	6544.3	4774.6	4928.1	4682.0	6364.1	2774.1	1304.8	4434.5
3376.2	2092.6	2291.5	2468.8	1941.4	1939.6	1899.8	2358.4	1725.2	962.0	1500.4
3900.1	2474.3	2764.4	2138.7	1578.8	2194.4	1949.5	2538.1	2480.8	2510.2	2596.6
523.0	1921.2	1989.1	1007.2	971.3	1215.1	1210.8	1044.3	1307.9	1441.3	1318.8
505.1	3812.6	3280.1	5323.3	3423.1	3198.1	3284.6	4821.0	2195.0	769.0	2642.7
54.8	211.3	182.0	220.8	150.9	134.9	167.6	43.0	76.8	53.7	132.5
24413.8	6232.4	5971.8	6542.5	6887.9	5641.2	7384.8	6399.5	9406.4	7927.0	9681.6

3424.8	3293.4	3494.7
441.8	588.0	495.7
1193.1	1377.5	1238.5
4866.0	5558.8	4816.2
2240.8	1956.4	1875.8
217.9	147.9	144.4
4142.4	4658.4	5478.3
4585.9	5389.5	4663.7
3436.0	3043.8	3624.3
1775.2	1918.7	2103.7
1015.6	1359.7	892.6
201.3	184.6	347.5
1920.6	2518.4	2597.9
4925.5	4858.1	5909.3
941.7	533.6	866.7
2859.4	2462.5	2341.0
3946.3	4660.7	5972.7
486.3	315.0	625.4
540.0	204.0	357.6
4944.7	7086.1	6176.2
3499.5	4061.3	3281.0
344.1	397.0	537.2
2116.1	1623.4	2277.3
199.6	183.5	245.0
1709.1	1282.8	2008.6
390.1	173.1	428.9
2768.0	3477.3	2603.7
2311.5	2653.5	2408.5
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5728.2	6591.9	5774.4
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193.8	140.7	390.4
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o__Clostridiales	f__Lachnospiraceae

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DQ824919.1 gg_id:198557 human fecal clone RL185_aao71a03 DQ824
EU764646.1 gg_id:356232 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU474631.1 gg_id:290036 Indian rhinoceros feces clone IR_aaa03f07 EU474
FJ676414.1 gg_id:517632 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU843986.1 gg_id:320857 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ823660.1 gg_id:196625 human fecal clone RL250_aaj77c04 DQ823
EU842482.1 gg_id:355827 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU508972.1 gg_id:264231 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41a03 EU508
EU764906.1 gg_id:330442 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
AF001754.1 gg_id:14043 rumen clone RF22 AF001
DQ807023.1 gg_id:187981 human fecal clone RL244_aaj45c03 DQ807
EU506378.1 gg_id:259787 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64e07 EU506
EU767793.1 gg_id:305459 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
AB185510.1 gg_id:107149 rumen clone F23-A07 AB185
EU778970.1 gg_id:306939 Prevost's squirrel feces clone SQ_aah82b05 EU778
EU381472.1 gg_id:259924 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU381
AB494831.1 gg_id:588390 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EF099443.1 gg_id:182320 mouse cecum clone SWPT3_aaa03c09 EF0994
FJ365654.1 gg_id:358016 feces adult twins and mothers; TS21 clone TS21_a01d11 FJ3656
AJ408980.1 gg_id:36059 human colonic clone HuCA29 AJ4089
FJ370965.1 gg_id:366716 feces adult twins and mothers; TS5 clone TS5_a03d02 FJ3709
EU475072.1 gg_id:297562 visayam warty pig feces clone VWP_aaa03a02 EU475
FJ371068.1 gg_id:364246 feces adult twins and mothers; TS5 clone TS5_a04e09 FJ3710
FJ372184.1 gg_id:357652 feces adult twins and mothers; TS9 clone TS9_a02f11 FJ3721
EU843157.1 gg_id:336336 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ675901.1 gg_id:520529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU764581.1 gg_id:328417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
DQ801965.1 gg_id:198450 human fecal clone RL241_aaj01b03 DQ801
EU748359.1 gg_id:344470 neotropical folivorous flying bird adult hoatzin crop clone hoa5_08e06 EU748
EU842506.1 gg_id:327661 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU381804.1 gg_id:272076 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU845648.1 gg_id:322259 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AB494940.1 gg_id:563363 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
EU764734.1 gg_id:318895 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
FJ881160.1 gg_id:454363 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
DQ824783.1 gg_id:176334 human fecal clone RL185_aao69c02 DQ824
EU843223.1 gg_id:324536 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF436448.1 gg_id:211900 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC162 EF4364
DQ085080.1 gg_id:129331 goat rumen clone A5 DQ085
EU452145.1 gg_id:343630 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
FJ364058.1 gg_id:363352 feces adult twins and mothers; TS150 clone TS150_a02e03 FJ3640

53.7	101.0	157.6	183.2	60.3	84.1	64.9	123.9	32.0	27.9	56.9
2893.7	685.0	897.6	1220.9	276.6	566.5	481.2	614.1	360.5	265.0	498.6
6478.3	3821.6	3609.5	4025.1	3478.4	3462.9	2770.3	3896.6	4296.0	2771.9	4386.3
486.1	2648.1	3569.9	3416.7	2666.0	3182.5	2840.9	3786.2	2382.8	2118.5	3100.5
41.5	221.2	270.4	284.4	301.5	174.0	201.6	351.2	96.6	56.7	157.9
125.7	547.5	598.9	488.9	399.7	478.6	517.0	585.7	912.5	619.3	376.5
146.4	2193.3	2665.9	2844.8	2911.6	2361.8	3670.1	2477.0	2060.1	746.7	2023.7
1123.1	2476.1	2245.4	2981.4	2015.7	1726.0	1906.8	1842.0	2455.7	2828.6	2442.8
78.8	865.6	1391.5	1361.7	390.0	710.6	736.3	1024.3	456.1	330.2	476.9
32.8	395.5	664.5	618.2	188.8	430.0	383.9	683.2	197.3	127.3	619.8
49.5	985.4	1395.9	1245.5	621.2	1192.7	820.3	1336.5	510.5	1139.9	918.0
1533.1	3861.9	3712.9	4781.2	3850.1	3379.8	2704.4	3861.0	3318.3	3174.1	3423.2
16788.9	4379.0	4614.0	4977.8	3964.3	4182.5	5331.0	3984.2	6608.9	5357.1	6117.2
5178.3	3289.1	3534.9	3663.5	2991.9	3482.2	3018.9	3796.7	3860.0	2965.4	3832.4
32.5	12.3	14.7	17.9	8.7	12.2	14.8	13.2	11.6	14.0	13.6
62.7	939.3	1620.2	1386.6	1067.3	968.3	1123.2	1435.6	458.2	544.9	822.2
646.0	2039.0	1878.6	1755.4	2131.3	1643.9	1959.0	1864.5	2013.9	1100.0	1149.9
3840.6	2038.1	2892.9	3047.3	2847.3	2340.1	3202.4	2630.0	2455.6	1158.8	2054.7
7139.2	3463.3	3424.3	3663.9	3069.2	3315.2	3436.9	3357.4	3858.2	3499.8	3463.6
307.5	6175.8	5375.5	4620.7	3719.5	4765.2	3719.2	5025.3	6001.2	3642.4	3845.7
84.1	435.2	650.2	646.3	381.0	495.5	602.3	609.9	219.0	404.5	352.7
270.9	1254.3	2113.4	2140.9	1277.2	1325.5	1417.0	1546.2	747.1	405.4	1300.0
1283.0	2983.8	3278.9	3600.0	2745.3	3022.8	2956.4	2875.9	2802.2	3330.2	3071.3
53.2	981.4	1271.6	1731.2	633.1	669.2	497.9	1097.5	188.7	398.0	615.1
11339.2	5484.9	5678.4	5905.7	4719.1	5669.7	5973.7	4730.9	5561.3	5095.8	5791.9
9139.5	7634.6	6860.7	6499.5	5587.1	7617.0	6264.7	6462.5	9603.6	9142.5	7774.0
4691.6	1942.0	2106.5	2535.0	1441.2	1751.9	1983.5	1512.7	2366.9	1659.0	1892.7
35.0	146.5	123.1	117.4	140.2	139.8	71.9	333.5	86.9	38.9	70.7
487.6	3473.9	4194.0	3889.3	3436.9	3595.5	4156.6	4130.2	5915.9	2608.3	3954.3
1578.9	3124.0	3698.6	4195.1	2710.1	2702.3	2974.1	2519.6	2581.6	906.1	2738.4
116.6	1144.7	1393.0	1372.8	868.7	891.5	708.8	1248.3	482.2	112.6	757.7
153.2	2090.4	3508.8	2172.7	1237.3	1615.1	1426.1	2031.9	834.5	507.5	2385.2
54.2	1142.8	1565.1	2216.5	826.5	781.4	625.7	1365.1	283.5	155.1	611.9
42.2	333.6	511.0	567.6	93.3	263.4	269.8	411.7	91.5	59.5	185.7
47.4	1538.2	2030.2	2632.0	1384.6	1565.2	1038.8	1890.6	885.1	909.0	1020.3
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51.0	964.5	1447.1	1461.8	624.4	997.3	703.3	1077.4	278.4	211.1	630.4
390.9	1241.3	1983.3	2074.9	881.0	1108.2	856.3	1758.6	1272.4	609.6	1039.8
55.0	42.3	105.8	74.6	34.7	70.1	67.0	121.9	56.7	18.9	37.5
403.6	1276.0	2038.6	2101.2	1830.3	1924.4	2064.9	1882.7	1080.4	652.3	1215.9

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898.6	1238.8	936.4
3069.9	4452.2	4096.5
4389.9	2623.2	5095.7
287.2	369.4	253.3
501.9	919.9	417.5
2555.1	2742.8	3189.6
1995.1	2458.4	2081.7
1583.9	1458.5	907.9
684.1	327.0	839.5
1482.7	1461.5	1274.2
3423.7	4183.0	4411.3
3907.8	5279.9	3966.7
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1250.7	1536.4	1968.5
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3257.3	4062.2	4392.7
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608.3	743.9	758.4
2192.9	1984.2	3136.0
3007.1	3152.6	3622.3
1196.5	1300.8	1551.8
4548.6	5937.3	5197.2
6737.2	7771.8	9175.1
1702.5	2855.1	2937.4
201.1	139.5	128.7
3745.6	4107.1	4886.8
2869.8	4346.0	3316.4
1255.3	1154.8	906.2
2228.7	2106.9	1951.6
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546.4	476.5	756.7
2241.5	2429.0	2985.8
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EU473665.1 gg_id:295809 banteng feces clone BG_aaa03g03.Contig1 EU473
CU924276.1 gg_id:533480 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EU474684.1 gg_id:288613 Indian rhinoceros feces clone IR_aaa03c10 EU474
AY212759.1 gg_id:101469 equine manure clone wet56 AY212
EU475048.1 gg_id:300451 visayam warty pig feces clone VWP_aaa03b10 EU475
EU504049.1 gg_id:274744 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04e09 EU504
EF099366.1 gg_id:196089 mouse cecum clone SWPT3_aaa02c11 EF0993
EU462315.1 gg_id:292740 chimpanzee feces clone CHIMP1_aaj39h09 EU462
EU511654.1 gg_id:261627 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08d01 EU511
EF402928.1 gg_id:215475 human fecal clone SJTU_B_14_32 EF402
EU843891.1 gg_id:355825 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
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EU764777.1 gg_id:317602 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU775529.1 gg_id:327067 Western lowland gorilla feces clone GORSD_aaa01c02 EU775
DQ806726.1 gg_id:195865 human fecal clone RL186_aao48a05 DQ806
AY984619.1 gg_id:119853 human stool clone B560 AY984
EF436303.1 gg_id:207063 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC17 EF4363
DQ815835.1 gg_id:171399 mouse cecum clone aab22h11 DQ815
AY976863.1 gg_id:116931 human cecum mucosal biopsy clone K494 AY976
EU765422.1 gg_id:329718 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EF405506.1 gg_id:211212 human fecal clone SJTU_G_03_14 EF4055
AB269957.1 gg_id:165372 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
EU778577.1 gg_id:319197 Ring-tailed lemur feces clone RT_aai10h06 EU778
EU844338.1 gg_id:354628 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ364291.1 gg_id:363811 feces adult twins and mothers; TS15 clone TS15_a01c01 FJ3642
DQ797879.1 gg_id:180291 human fecal clone RL206_aaj16h11 DQ797
EU767612.1 gg_id:337628 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
EU509375.1 gg_id:266331 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48h01 EU509
EF098843.1 gg_id:195655 mouse cecum clone SWPT1_aaa01h07 EF0988
EU843456.1 gg_id:313821 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
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DQ904692.1 gg_id:163013 human fecal clone 001-e6 DQ904
GQ897562.1 gg_id:579146 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU842762.1 gg_id:324723 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ807051.1 gg_id:198426 human fecal clone RL244_aaj45e12 DQ807
EU508907.1 gg_id:274688 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap38c12 EU508
DQ794511.1 gg_id:181258 human fecal clone RL240_aaj29a02 DQ794
EF099418.1 gg_id:180743 mouse cecum clone SWPT3_aaa02h11 EF0994
EU474961.1 gg_id:288246 red river hog feces clone RRH_aaa03c08 EU474

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3063.6	2896.0	2895.9	3614.3	2359.9	2888.9	3198.0	2800.5	3706.0	3115.0	4211.7
53.6	194.3	310.8	206.9	248.3	135.3	270.3	431.0	293.7	210.3	126.8
5889.3	5539.2	5502.4	6306.4	4903.9	4462.6	5610.1	6369.8	5548.3	6023.5	5524.7
421.0	2497.7	3050.8	2964.3	2965.6	3059.6	2023.3	4288.5	1847.1	2332.9	2450.1
5049.7	4324.9	4455.3	5399.9	5940.2	4291.2	4527.8	5055.7	2554.4	1416.8	3720.4
46.8	673.1	1246.9	1535.0	184.5	838.8	569.7	1384.2	421.7	111.5	874.7
1733.0	3753.8	3838.7	3547.8	3013.0	3218.8	4009.4	3739.3	4851.0	2307.7	3627.2
1398.7	776.7	1358.4	1507.2	388.7	687.9	584.7	1182.4	449.5	253.7	629.4
5602.9	6352.9	7143.2	6378.5	4800.2	5305.4	5051.1	5839.6	6006.9	3684.5	7422.2
232.3	1726.4	2645.2	2451.7	1139.5	1300.2	999.3	1897.5	388.9	688.7	1187.1
14546.0	5151.3	5807.6	5648.8	4178.8	4976.0	4501.4	4010.1	7803.8	5169.4	5650.1
64.5	409.9	812.7	811.6	481.5	447.2	284.1	744.6	252.3	114.4	262.4
38.0	328.9	520.8	668.5	301.8	211.2	436.2	370.8	76.2	67.6	171.4
9108.7	3698.4	4029.1	3305.2	2874.9	3564.2	2616.1	3610.0	2799.3	2017.9	3732.0
57.3	860.4	1369.4	1068.4	613.8	966.2	735.3	1135.9	521.8	584.2	804.5
34.7	437.3	768.7	1034.0	87.6	343.0	373.2	491.8	80.1	31.2	336.5
358.2	2268.0	2161.4	1851.9	2092.9	2340.8	1714.7	1832.8	2337.0	2021.8	1527.9
34.6	74.7	115.0	132.4	45.7	48.2	52.4	65.8	35.5	35.8	44.2
41.6	305.6	486.8	549.2	298.4	141.7	467.6	292.2	61.6	68.5	226.9
31.4	383.2	569.4	748.4	130.4	461.9	222.9	613.3	103.5	92.5	261.5
153.4	997.1	1655.2	1631.8	1591.3	1421.3	1226.9	1633.8	539.1	632.2	1057.6
48.2	194.2	452.3	714.8	34.9	164.2	87.6	271.0	54.0	29.3	137.7
41.6	1208.0	1848.6	2237.4	635.9	1179.2	980.7	2109.7	450.6	326.8	1368.9
3099.1	4420.3	4701.7	4672.3	3486.0	3471.0	4737.2	3445.7	4153.0	2367.1	4410.0
37.8	400.1	576.2	801.6	49.1	211.0	127.5	455.0	51.3	20.4	243.2
447.9	1820.1	2419.9	2938.5	1676.8	1722.2	1609.9	2218.1	1124.4	950.7	1048.8
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84.6	781.9	995.9	1153.4	490.4	812.9	596.3	1121.6	275.8	140.2	696.5
2535.9	2401.6	2780.2	3005.2	2041.7	2141.3	2328.4	2505.8	2192.5	1992.6	3387.8
1444.6	891.4	947.6	1438.2	995.3	707.1	770.9	1182.6	515.2	556.9	752.9
963.4	1540.4	2197.7	2137.3	1243.4	1106.4	1433.1	1344.7	851.6	840.3	1234.1
165.8	296.9	423.3	396.9	302.3	284.2	276.4	376.7	87.9	152.3	134.0
457.5	2972.6	2877.6	2679.4	1927.9	2629.8	2466.0	2395.5	3804.5	3624.2	3178.6
35.4	497.6	818.4	931.7	309.6	447.6	314.7	834.4	238.8	169.1	666.9

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3086.3	5040.1	2666.8
266.2	195.2	239.4
5541.6	5327.2	5505.3
3363.9	3387.5	3673.4
4495.4	4717.5	5937.3
1341.5	935.2	1898.7
3011.2	3515.3	3703.0
1398.1	1211.7	1096.0
4689.5	6199.8	5047.8
1756.1	1666.5	1989.4
4449.7	5310.8	5405.0
1024.8	621.9	325.5
575.0	391.7	298.8
3535.1	4170.6	4561.5
1235.4	1289.0	1142.2
660.9	485.8	672.6
2825.8	1851.4	2489.2
38.2	104.7	51.9
450.1	425.3	286.3
829.0	513.2	498.5
1650.8	1266.1	1657.0
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3842.0	5533.1	4185.9
597.0	360.4	497.4
2580.1	2055.9	2753.8
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DQ796024.1 gg_id:187005 human fecal clone RL202_aai50d07 DQ796
EF614671.1 gg_id:227590 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
DQ801769.1 gg_id:177873 human fecal clone RL201_aai46e11 DQ801
FJ362608.1 gg_id:362404 feces adult twins and mothers; TS13 clone TS13_a01a08 FJ3626
DQ673466.1 gg_id:164693 rumen fluid clone GRC01 DQ673
EU474604.1 gg_id:292247 Indian rhinoceros feces clone IR_aaa02b09 EU474
EU462046.1 gg_id:292941 black-handed spider monkey feces clone SPIM_aaj33h05 EU462
DQ796017.1 gg_id:194230 human fecal clone RL202_aai50c10 DQ796
EU506317.1 gg_id:270744 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63b07 EU5063
EU778340.1 gg_id:322310 feces clone RL117_aae92f02 EU7783
FJ678071.1 gg_id:521048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
EU779298.1 gg_id:355697 Visayam Warty Pig feces clone VWP_aaa02f06 EU779
DQ796249.1 gg_id:181622 human fecal clone RL179_aah23f09 DQ796
EU844216.1 gg_id:304808 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU844334.1 gg_id:303851 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
DQ808327.1 gg_id:198696 human fecal clone RL180_aao75c11 DQ808
EU844587.1 gg_id:306615 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8445
EU475295.1 gg_id:299401 rock hyrax feces clone RHSD_aaa03c06 EU475
FJ679775.1 gg_id:511342 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
EU777936.1 gg_id:334954 Black rhinoceros feces clone RH_aaj91f07 EU777
EU844336.1 gg_id:343465 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
EU504063.1 gg_id:268933 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04g04 EU5040
EU774295.1 gg_id:322505 Chimpanzee feces clone CHIMP1_aaj37d11 EU774
EU771121.1 gg_id:326860 Asiatic elephant feces clone AE3_aaa02g04 EU771
EU452297.1 gg_id:315880 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU452
EU506324.1 gg_id:269957 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63c10 EU5063
EU842673.1 gg_id:338660 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU843208.1 gg_id:327837 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF614701.1 gg_id:230367 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EU843030.1 gg_id:337355 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU765561.1 gg_id:332840 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
EU509086.1 gg_id:271643 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43c12 EU5090
DQ801403.1 gg_id:195792 human fecal clone RL388_aao95a11 DQ801
EF100070.1 gg_id:179793 mouse cecum clone SWPT5_aaa04c05 EF1000
AM932637.1 gg_id:574327 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
EU468273.1 gg_id:299484 domesticated horse feces clone horsej_a03_1 EU468
GU303565.1 gg_id:578995 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AY452000.1 gg_id:104971 human intestine clone Muc3-3 AY4520
EU471818.1 gg_id:295444 Asiatic elephant feces clone AE2_aaa02h11 EU4718
FJ678005.1 gg_id:516960 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780

361.9	1694.7	1877.0	2398.8	1096.6	1561.5	1525.9	2053.9	716.4	433.8	1145.8
2550.8	1601.1	1686.4	2356.9	1774.4	1564.9	1286.7	1838.7	887.1	304.9	1057.2
259.9	2822.2	3438.4	3277.3	2250.1	3014.2	3075.3	3547.2	2705.4	2114.3	2057.1
55.0	1102.6	1100.5	1034.5	683.9	1516.0	528.7	2711.8	716.8	2050.0	703.8
29.6	49.1	65.0	88.8	28.3	62.7	26.6	64.2	30.6	16.9	53.0
655.2	1520.3	1772.4	2075.0	1770.1	1389.5	1456.5	1459.2	816.4	379.2	975.1
606.7	1336.5	1844.3	2255.0	1123.9	1212.4	1711.1	1930.3	702.3	386.5	1103.2
274.2	1644.2	2198.0	2711.2	871.5	1198.5	1179.0	1942.3	401.2	166.9	847.4
654.5	719.1	626.3	594.7	662.0	735.9	746.5	869.4	254.9	423.4	590.2
2226.6	4202.3	3968.0	4482.8	4438.0	3727.9	3941.7	4408.5	3534.4	2379.1	3256.2
1224.6	1375.7	1561.1	1090.7	2452.6	1574.3	1936.9	1751.5	1114.1	406.1	1012.1
5993.3	2332.2	2705.3	3247.1	2840.4	2689.3	2428.2	2296.5	1695.7	2984.0	1576.5
48.5	1038.5	1740.3	968.4	582.0	1191.0	528.9	1345.2	758.3	150.8	1258.8
83.2	326.0	525.3	662.6	159.7	217.5	241.3	446.0	65.8	50.6	186.3
3124.4	4491.2	4726.1	5718.3	4912.7	4519.0	5238.8	4640.2	4813.5	3387.9	5712.4
3483.6	2392.6	3019.1	2781.9	1741.4	2901.4	2256.6	3951.0	2295.7	3671.1	3629.7
90.1	338.6	719.6	680.7	295.9	376.6	350.1	439.8	246.4	254.7	261.0
4481.7	5330.3	4689.5	4587.3	3866.4	4284.6	4528.5	4490.2	6025.2	3953.8	4839.5
61.4	949.7	1552.7	1768.2	541.9	1262.3	957.1	1851.4	647.9	253.4	858.1
6339.8	2155.4	2988.3	2236.6	1943.3	2356.4	2172.6	2417.4	2723.4	2407.1	2759.7
472.9	707.7	941.4	1128.0	648.4	950.9	499.3	1069.8	430.3	1132.4	479.4
5652.3	5263.8	4623.6	5086.9	3532.1	4332.6	4642.6	4390.5	5306.0	3040.9	4756.5
952.3	442.6	550.0	497.7	465.5	482.1	434.7	500.6	210.3	318.7	266.7
32.1	672.3	947.9	921.7	539.2	477.3	760.3	961.9	263.9	204.1	434.7
2646.9	5330.1	4442.5	4998.2	4369.7	4185.1	4054.4	4275.9	4238.7	3026.9	3060.6
1025.8	1286.1	1608.1	2179.6	1522.4	1217.5	1657.6	1885.4	525.7	582.3	1162.5
41.1	916.5	1350.0	1697.9	998.5	989.4	1008.9	988.7	374.1	354.1	553.0
390.5	2326.8	3413.8	2651.9	1763.8	2675.5	1982.4	3781.8	1772.6	1568.9	2748.1
19098.3	5190.0	4874.8	5681.9	4485.0	5070.4	5546.6	4748.2	7830.8	5644.4	9157.7
642.4	2588.4	3118.5	3161.7	2581.2	3083.9	3448.6	3340.8	2075.8	2151.3	2505.0
1540.4	2480.8	3243.6	3687.7	2160.3	2033.5	2320.4	3058.3	1067.1	371.4	1858.0
747.7	211.9	276.2	270.9	192.2	317.6	256.9	256.4	180.7	71.0	179.7
12073.6	4880.6	4654.5	5782.0	5213.7	5220.2	4808.5	5373.7	5493.6	4061.7	4910.0
42.3	731.8	1045.9	1354.3	547.9	606.5	501.8	878.4	256.7	165.8	354.3
138.9	360.5	380.5	488.6	294.8	204.2	274.7	375.0	182.2	54.2	203.7
49.8	338.4	696.5	735.4	30.4	330.7	270.2	626.4	149.9	22.4	338.0
370.8	1632.2	2554.0	1953.8	1739.4	1853.6	2264.7	2473.4	811.2	602.4	1269.4
37.3	519.7	884.5	614.5	255.2	461.9	419.5	683.3	185.4	171.9	319.5
59.1	639.6	1062.7	1375.3	469.1	499.8	454.1	697.6	229.7	129.2	403.9
273.8	791.3	930.0	888.1	606.3	814.3	837.8	1177.0	719.9	734.0	845.0
57.8	1030.6	1549.5	1664.8	853.9	1036.7	1064.4	1243.0	342.4	441.6	776.3

2263.2	1804.3	1921.1
1965.2	1904.8	1704.2
3078.0	3215.1	4676.5
2900.6	1388.2	1654.7
52.7	81.6	64.0
1966.8	2200.7	1864.1
1623.6	1799.7	1398.0
2185.2	1871.6	2906.8
495.8	735.1	601.0
4389.5	4796.4	4536.6
1870.6	1860.4	1959.4
2879.8	4162.7	2901.7
1605.3	877.7	1473.9
425.2	629.0	286.6
4426.0	5490.4	5466.7
3928.4	2643.3	3398.1
895.3	356.4	1084.7
4820.3	4476.1	4666.0
1594.1	1331.8	2419.2
2894.1	2662.8	3023.2
1104.5	1645.4	631.0
4060.1	3864.8	5360.2
478.3	670.7	745.1
1047.6	731.0	706.0
3730.3	4035.7	4219.0
1916.3	1665.9	1956.6
1186.9	1010.7	2591.0
4249.3	2948.2	3156.1
4592.8	7040.2	5009.9
2985.5	2569.3	5037.1
3141.7	2927.1	3936.8
214.2	667.8	217.7
4856.8	5755.1	6674.5
1116.9	1139.5	1538.3
528.7	420.9	957.9
545.8	495.3	621.0
2490.1	2801.2	2309.0
548.3	770.2	1179.5
879.3	843.6	1057.7
773.0	1179.0	797.5
1531.1	1434.5	1611.3

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EU506389.1 gg_id:268192 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64g08 EU506
DQ795469.1 gg_id:193259 human fecal clone RL178_aah54g03 DQ795
AF371587.1 gg_id:68843 swine intestine clone p-393-o3 AF371
FJ363009.1 gg_id:358695 feces adult twins and mothers; TS148 clone TS148_a01h02 FJ3630
EU844524.1 gg_id:335411 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ370373.1 gg_id:367241 feces adult twins and mothers; TS56 clone TS56_a04b03 FJ3703
EU844158.1 gg_id:339661 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU764930.1 gg_id:315002 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU452492.1 gg_id:343968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU452
EU850566.1 gg_id:328186 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF376 EU850
DQ807313.1 gg_id:190874 human fecal clone RL307_aam05a04 DQ807
EU457580.1 gg_id:312869 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
DQ801250.1 gg_id:198511 human fecal clone RL388_aao93a02 DQ801
AF371629.1 gg_id:49854 swine intestine clone p-3848-23G3 AF371
FJ881223.1 gg_id:466102 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
AM932616.1 gg_id:564042 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ800420.1 gg_id:192952 human fecal clone RL183_aah24a07 DQ800
EU508979.1 gg_id:268027 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41b12 EU508
AY858542.2 gg_id:109966 gastrointestinal tract eland clone ELAND_95 AY858
DQ810002.1 gg_id:177830 human fecal clone RL184_aao66h08 DQ810
DQ799884.1 gg_id:194960 human fecal clone RL247_aaj21d02 DQ799
EU471607.1 gg_id:296697 Asiatic elephant feces clone AE1_aaa03d11 EU471
EU457025.1 gg_id:306833 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EU456417.1 gg_id:348748 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
DQ807358.1 gg_id:192404 human fecal clone RL307_aam05e07 DQ807
EU842275.1 gg_id:353780 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ809266.1 gg_id:197951 human fecal clone RL308_aal84d06 DQ809
EF614892.1 gg_id:233371 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU509053.1 gg_id:267522 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42f10 EU509
EU452320.1 gg_id:307380 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU452
DQ801873.1 gg_id:196540 human fecal clone RL201_aai47h09 DQ801
EU843271.1 gg_id:334890 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU842906.1 gg_id:307550 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU462328.1 gg_id:296165 chimpanzee feces clone CHIMP1_aaj40c03 EU462
DQ808320.1 gg_id:190565 human fecal clone RL180_aao75c03 DQ808
EU776757.1 gg_id:312291 Mongoose lemur feces clone ML_aae89c03 EU776
EU506267.1 gg_id:267393 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61h02 EU506
EU843291.1 gg_id:316384 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU844631.1 gg_id:341544 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU842443.1 gg_id:303440 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU504118.1 gg_id:262724 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01f05 EU504

6080.1	5118.9	5415.2	5868.7	5777.8	5119.0	4734.7	5018.2	5830.2	5136.0	5023.7
41.6	352.6	660.8	559.2	239.6	407.0	404.2	632.8	137.1	50.7	315.8
42.3	28.2	26.9	38.7	24.0	27.8	19.8	30.0	15.7	17.7	19.3
566.0	2431.8	2253.7	1852.6	1816.1	2053.0	1646.0	2277.9	2819.7	2434.0	1850.2
73.5	1050.3	1426.9	1551.7	315.5	700.2	407.6	1467.3	372.3	185.0	714.0
58.8	1836.1	2179.8	2635.8	651.6	1692.7	1033.0	2770.3	1177.3	333.3	1593.8
40.6	391.0	634.7	608.5	329.6	393.1	366.6	460.5	259.7	146.9	340.3
68.5	656.9	960.7	1333.2	322.2	576.1	562.0	1002.2	734.5	504.6	526.2
4860.8	5376.2	5737.7	5913.3	4753.6	5911.2	5666.2	5718.0	6699.0	4538.7	5222.1
2370.5	2693.2	3091.3	3175.9	2226.3	2618.8	1722.6	3415.5	1985.2	1472.0	3087.4
99.8	740.2	1319.7	1309.4	817.3	1468.0	1077.4	877.7	364.5	167.0	497.3
1377.4	2225.1	1917.7	1569.4	1293.7	1859.8	1292.0	1853.2	1951.4	1484.1	1361.4
1685.0	2987.4	3394.1	3483.2	1734.3	3444.4	3214.6	3602.5	2322.8	3170.2	4091.6
61.0	39.5	35.5	41.0	51.4	37.1	54.9	34.5	28.9	23.2	26.6
8565.5	6542.0	5706.9	6186.7	6619.8	5420.6	6172.9	5225.1	7427.4	4355.1	5008.1
57.4	452.2	829.5	995.4	150.0	359.0	382.9	490.5	63.0	28.7	170.3
32.4	835.7	1123.6	1424.1	48.0	272.2	180.3	518.0	56.0	26.1	361.4
28843.3	8791.6	7002.3	8544.2	10131.7	7775.5	8075.8	7628.8	7097.6	6033.5	6394.2
43.2	62.9	103.9	75.9	41.8	48.3	59.7	91.8	37.4	26.1	56.6
47.5	561.3	1151.8	719.1	584.8	780.8	735.7	1489.0	421.7	442.9	780.6
10032.2	3533.8	3905.7	3692.3	3095.9	3229.6	2728.3	1653.5	5840.2	3352.0	4784.5
110.1	794.7	1114.1	997.1	454.1	748.6	1017.7	1065.5	448.8	179.0	984.5
624.7	2559.3	3061.0	3734.4	2374.0	2986.4	3079.6	3842.5	2395.0	1373.7	2222.5
15961.5	5022.6	5735.5	6022.8	4855.6	5142.3	7215.4	5826.9	9169.8	5759.9	6894.0
470.1	993.9	1519.1	1461.1	1291.5	1088.3	1409.8	1305.5	949.5	296.8	1244.0
478.0	1489.6	2259.1	2726.6	679.2	1496.7	1090.9	1800.9	640.3	319.9	1225.5
118.6	378.4	732.7	844.6	329.2	304.6	257.1	400.5	93.2	50.9	108.9
157.2	1726.1	2086.7	2661.6	1724.7	1857.0	2008.6	1754.3	1493.4	1285.8	1354.1
21246.7	6298.6	5528.8	6754.9	6148.9	6534.1	6287.3	5699.8	9122.7	8803.5	6429.0
51.9	964.8	1613.2	1668.8	791.1	1076.6	1683.4	2072.4	495.3	1326.9	1133.3
106.1	1052.4	1149.8	1312.0	853.1	1036.5	1273.8	1966.3	269.8	259.5	580.0
592.9	2134.1	2779.2	2865.6	1862.4	2066.2	2172.4	2704.5	1330.5	907.6	2008.1
225.5	1289.2	1703.2	1963.5	1724.1	1252.1	2065.1	1596.9	668.5	410.8	1000.5
188.3	1237.2	1673.1	1900.5	1780.7	1321.4	1868.5	1955.0	1111.0	471.4	981.3
2801.1	2325.2	2706.8	3266.0	2460.8	2096.5	2404.5	2726.0	1615.3	1594.3	1697.7
239.7	1478.2	1774.9	2042.2	1769.3	1879.5	1692.7	2244.3	1194.0	695.5	1285.9
3984.6	4340.7	4425.0	4702.3	4663.0	3835.4	4463.4	4999.6	5739.4	2606.0	4012.5
12249.6	3961.1	3834.0	4048.1	3368.8	3609.4	4341.6	4479.4	6756.2	4446.3	7869.7
484.3	1172.6	1421.2	1603.6	1692.4	1260.3	2273.6	1402.6	864.9	468.3	693.1
71.9	940.9	1808.9	1428.8	973.3	1239.1	1185.7	1764.2	563.6	1843.1	1004.2
809.6	1490.4	2588.0	2762.7	2054.5	1921.0	2531.6	2200.9	664.0	308.2	1608.5

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2247.2	2558.9	2362.0
1726.1	1407.2	1362.0
2470.1	1369.9	2022.1
488.0	485.4	539.7
905.1	1071.0	967.3
4768.5	4537.3	8313.1
3428.9	3947.5	3905.8
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1345.1	2396.1	1562.8
2498.8	4261.0	4135.3
31.2	40.6	46.7
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678.6	513.6	617.3
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7681.1	8362.4	8637.3
75.3	116.4	259.7
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2886.9	4608.9	3069.2
776.3	861.8	879.2
3946.0	3290.8	6930.9
4224.3	5581.5	6453.6
1114.4	1454.4	3073.9
2351.2	1937.7	3304.4
401.3	734.4	728.5
1786.8	1960.7	3377.1
5597.0	7521.3	7330.1
1490.0	942.6	2038.0
2614.5	925.5	1314.1
3624.7	2751.4	3672.3
1402.2	1125.3	1707.7
1499.1	2239.8	2302.9
3890.2	3428.5	1858.7
2014.5	1888.7	1587.7
3666.7	4593.8	4513.1
3701.1	5685.3	4151.4
1535.3	2461.0	1948.6
1751.5	1342.9	1844.7
2737.2	2414.3	2740.5

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DQ805761.1 gg_id:198536 human fecal clone RL306aal90g01 DQ805
EU775906.1 gg_id:346045 Horse feces clone horsej_aai92b04 EU775
AB494776.1 gg_id:533469 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EU779476.1 gg_id:332126 Grevy's Zebra feces clone GZ_aaa03b02 EU779
EU765017.1 gg_id:330857 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
FJ370855.1 gg_id:358762 feces adult twins and mothers; TS5 clone TS5_a02a09 FJ3708
EF436398.1 gg_id:203828 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC112 EF4363
DQ905416.1 gg_id:171279 human fecal clone 013C-E1 DQ905
DQ327057.1 gg_id:149210 Metagenomic gut microbiome healthy human stool clone E565 DQ327
DQ796618.1 gg_id:176808 human fecal clone RL179aan75h10 DQ796
FJ440065.1 gg_id:543500 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
EU764750.1 gg_id:345111 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
FJ677970.1 gg_id:518355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
DQ807812.1 gg_id:178809 human fecal clone RL180_aah37e05 DQ807
EU457826.1 gg_id:334406 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU844166.1 gg_id:313671 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ797348.1 gg_id:188157 human fecal clone RL248_aai98c03 DQ797
EU764962.1 gg_id:346771 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU765688.1 gg_id:303913 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ394610.1 gg_id:155943 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU767891.1 gg_id:305959 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
DQ796417.1 gg_id:173948 human fecal clone RL179_aah28a05 DQ796
EF100022.1 gg_id:195008 mouse cecum clone SWPT5_aaa03f04 EF1000
EF614690.1 gg_id:229185 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
DQ796693.1 gg_id:184508 human fecal clone RL179_aao53c08 DQ796
EU765426.1 gg_id:353963 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ795094.1 gg_id:189624 human fecal clone RL310_aam40b07 DQ795
EU455844.1 gg_id:331471 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU455
EU771831.1 gg_id:336761 African elephant feces clone AFEL2_aao29a04 EU771
EF399751.1 gg_id:207688 human fecal clone SJTU_E_02_95 EF3997
EF099347.1 gg_id:192378 mouse cecum clone SWPT3_aaa02a09 EF0993
DQ795921.1 gg_id:174251 human fecal clone RL202_aai49a01 DQ795
DQ905702.1 gg_id:173453 human fecal clone 014C-H11 DQ905
DQ799891.1 gg_id:177055 human fecal clone RL247_aaj21d09 DQ799
DQ809456.1 gg_id:196167 human fecal clone RL184_aah21c01 DQ809
EF436294.1 gg_id:217080 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC08 EF4362
GU174105.1 gg_id:582627 Microbial Bactrian camel estimated rumen clone XJC73 GU174
EU465612.1 gg_id:289452 argali sheep feces clone AS1_aao39f12.Contig1 EU465
DQ799897.1 gg_id:197545 human fecal clone RL247_aaj21e05 DQ799
EU766081.1 gg_id:352304 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
AY992999.1 gg_id:131132 mouse cecum clone C22_n20 AY992

37.9	406.8	738.2	872.2	405.9	485.0	526.2	775.1	88.3	86.4	423.8
89.3	467.8	668.6	753.4	705.5	471.5	796.3	413.7	267.2	91.3	302.1
37.6	367.6	636.8	575.6	243.9	333.0	247.4	311.5	127.9	125.7	182.0
506.6	2711.8	2748.8	3127.1	2387.8	3024.1	2801.0	3083.8	4031.5	3349.4	2350.3
278.6	2424.7	3279.1	1440.6	753.3	1112.7	695.0	1793.0	607.6	886.3	890.2
14788.3	4722.7	3514.1	3814.6	3964.4	4547.5	4468.6	3832.5	6291.6	6771.7	5910.8
1509.8	2067.3	2496.6	2047.8	1941.9	1613.3	1580.2	2722.7	1192.3	950.2	1525.8
308.7	2614.5	3215.3	2840.2	2614.9	3093.3	2002.8	3241.8	1483.1	2312.5	1882.9
63.5	1634.3	1892.1	2260.8	1952.2	1494.2	1811.4	1997.7	401.8	189.4	634.0
520.1	2882.1	3695.9	3328.7	2704.2	2976.8	3221.2	3695.4	3947.1	2521.3	3416.8
56.8	420.3	678.0	763.5	568.3	504.6	437.6	817.1	433.0	256.1	400.8
1212.5	942.5	1317.8	1470.5	1114.1	1070.1	986.2	1391.6	715.5	1558.2	861.5
918.3	1196.4	1387.6	1347.1	1148.9	1179.1	1110.3	1281.2	1086.3	817.0	1279.4
78.0	2949.8	2323.8	2063.9	1257.1	2383.1	1700.0	1963.4	1922.3	1289.6	1913.5
210.9	2197.4	3739.6	4741.9	1421.8	2171.8	1981.3	2889.2	1039.6	576.9	2340.0
4430.1	3570.6	3875.1	4638.1	3742.9	2908.6	3221.6	3947.6	3667.4	237.7	3594.2
102.1	596.3	743.1	878.2	478.0	558.4	577.7	711.5	251.9	124.6	408.5
3278.6	2785.2	3417.1	1977.0	1042.5	1705.6	1174.7	2150.7	1005.1	2848.7	1712.0
15712.0	3570.3	3589.0	4471.4	2895.2	3154.9	3718.8	3722.3	5625.7	4407.4	4712.9
27260.6	5056.6	4169.7	4576.5	4173.1	4069.5	5213.6	4270.8	6194.1	5561.9	2430.9
4204.5	2170.3	2618.9	3003.2	1962.7	2368.5	2233.1	3213.2	1677.1	1885.4	1645.0
49.9	312.3	562.8	752.4	157.3	376.5	404.5	681.5	128.3	100.7	365.2
231.8	2258.6	3266.8	3286.1	2837.7	3313.7	2307.6	3869.8	2749.8	3720.7	2131.5
5893.5	3827.7	4673.9	4280.1	4116.7	4499.9	3166.9	4600.2	6036.5	6219.7	4660.5
179.8	628.7	1035.7	1305.8	902.8	512.5	838.6	823.8	233.1	115.4	364.2
11140.6	2888.1	3565.9	3751.0	3139.6	3036.9	4081.5	3716.8	3507.9	2815.8	3500.0
257.0	1422.6	1996.6	3038.8	929.2	1011.3	1488.1	1649.7	589.2	445.4	929.4
17727.2	10786.4	11745.7	12629.3	11703.0	11341.9	12623.4	11205.2	17320.2	10978.1	13569.4
64.4	428.2	719.2	672.7	576.1	402.3	473.9	650.1	470.6	615.4	519.1
146.8	2155.3	3165.1	4476.5	2236.1	1840.6	2291.6	2536.5	902.6	809.2	1852.6
899.1	7257.1	8298.4	7395.5	5390.4	6941.5	7673.3	7942.7	5805.9	5921.0	8117.2
3103.4	2703.8	3483.8	2276.2	2428.1	2663.3	2182.7	2721.1	3595.5	4076.7	2774.1
3211.3	2916.9	3800.2	4214.9	2984.2	2782.7	3325.8	3266.0	2173.3	1912.9	2496.2
3650.4	3605.1	4029.3	3330.7	3345.4	3202.1	4398.2	3677.1	3348.4	2395.6	3948.2
493.1	1260.9	1397.3	1596.2	1474.0	1182.4	1761.3	1674.6	726.4	352.7	869.9
1002.8	2882.3	2961.1	3059.4	2552.0	3428.6	3213.1	3345.1	2339.8	1388.1	2796.6
39.8	522.9	1105.5	1355.8	105.6	472.0	234.8	985.0	105.2	71.7	288.7
285.7	714.9	1306.2	1205.9	384.7	856.3	739.5	1195.8	478.3	198.9	848.8
4926.0	2403.4	2840.0	2480.5	2316.9	2448.9	2255.4	2828.7	2253.6	1655.8	2536.5
965.3	1260.6	1797.5	2003.8	1663.0	1354.3	1271.5	1799.7	650.9	615.8	1212.1
824.6	2701.1	4197.9	4412.7	2716.1	2705.1	2843.0	3890.6	1508.0	966.0	2212.4

1185.4	520.3	728.9
728.5	731.6	2366.1
381.0	449.4	411.6
3247.9	3212.3	3009.0
1778.9	1405.6	1052.7
3610.3	5175.7	3954.5
2305.7	3093.9	2729.6
3404.3	2772.9	3339.8
2531.2	1875.4	3210.5
3770.7	3374.5	3865.0
776.6	766.2	541.0
1451.1	1857.1	1617.5
1412.1	1763.6	1493.8
1858.9	1986.3	2152.5
3185.5	3129.9	4007.0
4485.3	3185.4	4209.0
768.7	637.5	469.1
2073.4	2321.5	2192.6
3355.9	5213.6	3419.9
4560.9	5666.2	5281.9
3177.1	3425.8	3158.1
633.2	441.8	538.5
3142.2	3137.6	4372.6
4354.3	5367.5	5554.0
847.3	776.6	1116.0
3819.8	4705.7	3786.7
2248.4	1961.9	2826.9
9686.0	9035.9	15008.7
608.4	626.7	362.0
3339.6	2142.9	3786.1
6361.7	7005.5	8190.0
2729.5	2512.0	2663.4
3134.6	3564.3	3411.0
2514.9	4276.3	4094.9
1803.7	1536.6	1422.0
4043.9	3689.1	3429.4
935.9	554.4	577.0
869.3	961.8	1280.4
3025.8	4124.0	3831.2
1663.6	1459.4	2095.2
3347.4	3099.8	6565.5

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EU510165.1 gg_id:274045 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02c10 EU510
DQ808203.1 gg_id:191208 human fecal clone RL180_aao73h01 DQ808
DQ806608.1 gg_id:190932 human fecal clone RL186_aao46f08 DQ806
AF001718.1 gg_id:13999 rumen clone RC34 AF001
DQ797022.1 gg_id:178882 human fecal clone RL386_aao85h08 DQ797
DQ796022.1 gg_id:175721 human fecal clone RL202_aai50d05 DQ796
DQ794548.1 gg_id:182451 human fecal clone RL240_aaj29d11 DQ794
EU842898.1 gg_id:328139 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ365859.1 gg_id:365314 feces adult twins and mothers; TS21 clone TS21_a03h06 FJ3658
EU765797.1 gg_id:336866 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU506386.1 gg_id:259190 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64f09 EU506
EU510847.1 gg_id:276067 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak50c02 EU510
FJ370807.1 gg_id:370047 feces adult twins and mothers; TS5 clone TS5_a01e05 FJ3708
DQ801853.1 gg_id:195173 human fecal clone RL201_aai47f08 DQ801
EU844476.1 gg_id:306013 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ365832.1 gg_id:363955 feces adult twins and mothers; TS21 clone TS21_a03e11 FJ3658
EU474876.1 gg_id:288437 red river hog feces clone RRH_aaa03c12 EU474
DQ796317.1 gg_id:200365 human fecal clone RL179_aah25f10 DQ796
EU768242.1 gg_id:331476 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU474916.1 gg_id:289660 red river hog feces clone RRH_aaa01f06 EU474
EU844386.1 gg_id:334091 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU843064.1 gg_id:324476 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU778117.1 gg_id:319097 feces clone RL388_aao94b02 EU778
FJ363402.1 gg_id:368090 feces adult twins and mothers; TS149 clone TS149_a02g09 FJ3634
EU778852.1 gg_id:325329 Black-handed Spider Monkey feces clone SPIM_aaj34g06 EU778
EU474666.1 gg_id:296902 Indian rhinoceros feces clone IR_aaa01c12 EU474
EU845645.1 gg_id:338052 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU765583.1 gg_id:315521 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ823853.1 gg_id:195918 human fecal clone RL250_aaj80a02 DQ823
EU844596.1 gg_id:354870 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB185654.1 gg_id:107082 rumen clone F24-H10 AB185
DQ805090.1 gg_id:182927 human fecal clone RL249_aaj81b03 DQ805
DQ798299.1 gg_id:183039 human fecal clone RL181_aah40d02 DQ798
EU344217.1 gg_id:271477 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
GU302535.1 gg_id:560114 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EF614553.1 gg_id:233021 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU842162.1 gg_id:327127 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
AY854275.2 gg_id:110361 herbivore gastrointestinal tract clone CATTLE_13 AY854
DQ794823.1 gg_id:180003 human fecal clone RL240_aaj32g11 DQ794
DQ815758.1 gg_id:171564 mouse cecum clone aab21h09 DQ815

80.8	705.7	857.2	1211.1	811.7	595.2	890.6	790.8	240.5	92.8	361.4
4475.4	2739.9	2753.3	3027.6	2516.9	2689.6	2301.5	2648.2	3577.2	3588.0	2302.0
55.2	162.7	269.4	241.5	176.4	139.2	145.1	212.6	63.1	69.5	89.7
454.7	1835.1	2167.3	2519.2	2682.4	1873.1	2687.9	2901.2	1694.2	1570.1	1471.4
50.3	85.0	110.7	95.1	112.6	94.4	104.7	82.9	44.2	43.8	84.3
47.9	248.6	395.1	356.1	69.9	197.7	110.2	410.4	88.0	25.1	182.8
28167.2	6963.1	8098.1	7608.8	6830.6	6555.2	7524.5	6411.7	13242.5	8682.8	10125.2
4527.5	1575.7	1549.4	1574.4	2147.0	1842.4	1503.3	1843.5	972.5	2854.5	1070.5
4978.4	6228.4	6587.5	7227.5	5907.6	6920.5	6458.8	7894.9	5223.8	6656.0	7636.2
4335.5	2032.5	2270.5	2285.4	1599.4	1816.8	1546.9	2157.5	2620.5	1846.5	1977.4
6091.8	3966.3	3786.5	4000.2	3652.9	3551.2	4220.8	3782.6	5794.0	3682.4	4568.7
1992.6	5638.0	5898.9	6280.4	6115.2	5659.0	6011.7	6160.0	5722.5	4131.5	5776.8
2095.4	4293.1	4517.6	4267.2	3425.3	4096.2	4429.5	4330.0	5409.6	2648.2	3816.6
102.9	584.2	752.5	624.4	780.3	605.0	798.5	802.2	267.2	194.3	384.5
41.2	288.7	313.0	273.3	264.4	305.4	194.7	653.1	73.4	82.3	134.8
72.6	604.5	623.9	704.8	549.1	586.4	733.4	651.9	301.5	311.8	337.8
897.6	2289.4	2677.8	2902.9	2873.3	2164.9	3401.4	3157.0	3637.7	2505.8	2744.6
217.7	1143.9	1648.4	2172.5	646.3	852.1	712.1	1613.4	340.8	342.9	1030.7
378.5	247.9	380.6	365.5	476.4	440.8	551.3	487.3	230.5	201.1	249.4
34.7	145.5	273.8	437.4	28.2	152.3	78.3	333.3	41.7	34.9	58.8
2823.1	3688.4	3395.9	3230.0	2251.7	2906.1	2749.8	3446.8	3188.9	1657.4	3716.9
57.7	432.5	753.4	836.7	295.0	431.4	440.7	544.5	496.3	110.1	371.9
121.6	652.4	1101.8	1201.7	313.6	473.3	303.6	1175.7	304.6	243.0	496.7
1272.8	1076.3	1244.0	2274.1	1144.5	1164.7	888.0	1594.6	272.8	187.2	763.3
26.1	298.0	511.3	636.2	124.1	259.6	190.3	458.4	80.6	31.5	178.5
67.8	304.6	669.8	883.7	159.7	214.9	179.9	660.9	335.8	57.7	274.0
1783.9	2846.1	3285.0	3149.3	2772.3	2550.3	4192.9	2815.6	2590.2	1213.6	3150.0
2725.1	3560.8	3865.2	4833.1	4934.5	3371.0	4852.6	3700.6	3587.0	1219.8	5064.0
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212.4	2520.5	4183.4	2324.1	1057.2	1498.9	1451.0	2006.7	661.6	238.7	2607.4
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2915.3	5338.5	7143.0	7210.4	7054.7	6094.8	7071.6	5135.9	4573.1	3141.6	5363.6
1830.4	2091.7	1943.3	2138.9	1729.2	1825.8	2357.2	1814.7	2299.8	1948.3	2413.7
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1919.1	6005.7	5834.9	5957.6	4887.4	5401.3	4979.8	6257.9	4948.0	3505.3	6230.3
40.8	27.7	33.0	50.1	25.3	29.9	26.4	25.1	19.0	19.8	30.7
40.8	367.3	410.4	263.1	252.0	509.0	277.0	1051.8	129.7	73.6	230.5
33.7	197.6	349.6	345.0	66.1	235.3	52.8	509.5	39.6	56.9	92.0

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177.0	242.6	298.1
3363.3	3592.3	2172.5
78.4	103.4	87.4
435.3	237.3	344.0
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2015.7	2294.4	1829.7
7582.7	7023.5	7966.2
1840.3	2806.0	1957.8
3354.3	4534.9	3777.0
5985.2	5829.0	7774.8
3612.9	4232.0	5325.2
1062.7	594.5	775.5
660.2	354.9	328.0
677.1	1159.1	974.9
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1773.1	1294.8	899.1
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EU506524.1 gg_id:267714 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03d11 EU506
GU304168.1 gg_id:537874 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU773362.1 gg_id:325181 BigHorn sheep feces clone BH1_aao27c08 EU773
EU456200.1 gg_id:330064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
FJ363698.1 gg_id:364134 feces adult twins and mothers; TS14 clone TS14_a02c03 FJ3636
DQ795198.1 gg_id:179497 human fecal clone RL178_aah51d08 DQ795
EF098102.1 gg_id:191098 mouse cecum clone SWPT14_aaa01e07 EF0981
EU511649.1 gg_id:264993 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08c04 EU511
FJ825526.1 gg_id:570049 Microbial during start-up mesophilic biogas plant clone 68_BS1_3 FJ8255
FJ369018.1 gg_id:369718 feces adult twins and mothers; TS4 clone TS4_a03c11 FJ3690
DQ798894.1 gg_id:189679 human fecal clone RL242_aaj98g06 DQ798
FJ367760.1 gg_id:364753 feces adult twins and mothers; TS2 clone TS2_a03c08 FJ3677
DQ795223.1 gg_id:186212 human fecal clone RL178_aah51f11 DQ795
EU748192.1 gg_id:323465 neotropical folivorous flying bird adult hoatzin crop clone hoa31_70F09.F EU748
EU344216.1 gg_id:270176 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU467112.1 gg_id:289734 mongoose lemur feces clone ML_aae88e06 EU467
EU456937.1 gg_id:344726 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
AY980044.1 gg_id:119655 human rectum mucosal biopsy clone KA62 AY980
AJ576367.1 gg_id:103464 hindgut homogenate Pachnoda ephippiata larva clone PeH54 AJ5763
EU462885.1 gg_id:293078 southern three-banded armadillo feces clone arma_aaj54e01 EU462
EU468602.1 gg_id:299571 okapi feces clone OK1_g12_2 EU468
DQ804842.1 gg_id:180577 human fecal clone RL385_aao81d10 DQ804
FJ880208.1 gg_id:410895 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EF099088.1 gg_id:192491 mouse cecum clone SWPT2_aaa02a12 EF0990
DQ795319.1 gg_id:186286 human fecal clone RL178_aah52h07 DQ795
EF071156.1 gg_id:177665 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU503880.1 gg_id:264974 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02a03 EU5038
GQ448783.1 gg_id:561027 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU762314.1 gg_id:305841 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ015573.1 gg_id:132165 mouse cecum clone M3_f11_2 DQ015
EU465560.1 gg_id:296474 argali sheep feces clone AS1_aao37f12.Contig1 EU465
EU772019.1 gg_id:347774 Argali sheep feces clone AS1_aao40a02.Contig1 EU772
EU474450.1 gg_id:297770 bighorn sheep feces clone BHSD_aaa04a10 EU474
EU474651.1 gg_id:288023 Indian rhinoceros feces clone IR_aaa02d10 EU474
EU771577.1 gg_id:323075 African elephant feces clone AFYEL_aaj65b12 EU771
EU452317.1 gg_id:354783 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
GQ448122.1 gg_id:593548 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
DQ800565.1 gg_id:191804 human fecal clone RL183_aah29g10 DQ800
EU842210.1 gg_id:332157 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU462132.1 gg_id:293232 black-handed spider monkey feces clone SPIM_aaj35e04 EU462
EU470436.1 gg_id:287580 Grevy's zebra feces clone GZ_aaa03a04 EU470

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1415.5	1894.3	2519.9	2753.1	2323.7	1955.9	2454.7	2612.8	627.1	751.3	1770.0
275.3	1198.6	1469.7	1267.3	1623.2	1481.6	1585.0	1269.5	1178.5	824.1	795.1
3071.1	1872.2	1623.3	1927.0	1612.6	1423.9	1765.3	1650.7	2183.6	1933.1	2633.3
52.5	169.8	92.1	144.4	37.6	41.3	37.3	65.0	37.8	37.9	33.8
35.6	387.2	507.5	443.0	270.9	243.8	409.3	281.9	60.6	32.8	133.1
241.7	2173.3	3067.6	3400.9	971.3	1966.5	1612.4	2978.5	1502.5	943.8	1795.9
142.1	2590.2	3104.0	3673.9	2520.0	2253.1	3016.2	2958.6	1336.5	2095.9	1899.3
32.3	54.1	59.5	52.1	49.5	37.3	170.7	47.4	13.6	15.8	27.8
123.3	1216.9	1441.1	1523.6	647.2	880.9	837.2	1425.1	951.3	165.9	1093.3
49.6	1315.7	1572.6	2094.9	1411.6	1469.6	1570.6	1705.2	720.1	271.7	1083.2
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157.4	474.7	590.0	666.5	289.7	396.7	467.2	372.9	139.5	78.0	154.6
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25639.1	8562.9	7416.9	8063.7	6771.1	7857.7	8279.2	7012.5	10400.3	8434.0	12204.4
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123.8	1538.2	2232.7	2996.0	545.1	1181.3	784.3	2152.6	719.1	229.1	1197.0
63.4	204.4	331.8	346.5	245.6	247.1	224.8	289.6	67.9	66.5	137.4
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34.0	1260.8	2540.6	2173.3	835.5	1077.7	1692.9	1985.6	616.6	232.8	1008.3
34.0	679.9	1201.4	1234.6	440.3	581.2	562.8	640.8	219.7	155.7	409.2
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2696.6	2841.8	2443.0
1475.2	1675.2	2166.2
1496.8	2600.8	1370.1
94.5	73.9	72.1
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3736.8	2615.4	2940.6
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GQ448680.1 gg_id:508842 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU470127.1 gg_id:294901 trancaspain urial feces clone TU2_aaa02c06 EU470
EU762903.1 gg_id:348227 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU462107.1 gg_id:301234 black-handed spider monkey feces clone SPIM_aaj35b02 EU462
NR_025206.1 gg_id:538986 Hespellia porcina str. PC80; NRRL B-23458 NR_02
EU774075.1 gg_id:314104 Chimpanzee feces clone CHIMP12_f09_1 EU774
EU885021.1 gg_id:326380 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone AG6 EU885
EU773057.1 gg_id:352263 Banteng feces clone BG_aaa03g10.Contig1 EU773
FJ364927.1 gg_id:367389 feces adult twins and mothers; TS19 clone TS19_a04h02 FJ3649
EU504389.1 gg_id:268835 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03e02.Cont EU504
FJ681188.1 gg_id:528390 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ879956.1 gg_id:434509 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
EF099809.1 gg_id:189189 mouse cecum clone SWPT4_aaa04f05 EF0998
EU766137.1 gg_id:332258 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
FJ673344.1 gg_id:513208 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU455182.1 gg_id:305212 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU455
AB189705.1 gg_id:112766 alkaline-enriched termite gut homogenate clone Pl-10e-26 AB189
DQ115999.1 gg_id:130419 bovine teat canal clone D-11 DQ115
AB234461.1 gg_id:150502 termite gut homogenate clone MgMjD-052 AB234
FJ371271.1 gg_id:365753 feces adult twins and mothers; TS6 clone TS6_a03a05 FJ3712
FJ881315.1 gg_id:409738 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
GQ491814.1 gg_id:581719 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ815380.1 gg_id:172243 mouse cecum clone aab47c06 DQ815
EU775175.1 gg_id:335003 Francois Langur feces clone FL_1aaa04b03 EU775
DQ014763.1 gg_id:135537 mouse cecum clone M1_d07_2 DQ014
EU506281.1 gg_id:273602 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap62b09 EU506
EF096045.1 gg_id:182619 mouse cecum clone lean2_aaa02g06 EF096
EU843876.1 gg_id:312849 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU772090.1 gg_id:326539 Argali sheep feces clone AS1_aao37e01.Contig1 EU772
AY858464.2 gg_id:110874 gastrointestinal tract zebra clone ZEBRA_25 AY858
EU505206.1 gg_id:270480 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04e02 EU505
AY983846.1 gg_id:124428 human descending colon mucosal biopsy clone M954 AY983
AF371576.1 gg_id:36647 swine intestine clone p-247-o5 AF371
FJ681025.1 gg_id:515460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EF100059.1 gg_id:199250 mouse cecum clone SWPT5_aaa04b04 EF100
EU462951.1 gg_id:289874 southern three-banded armadillo feces clone arma_aaj55e12 EU462
FJ535038.1 gg_id:509070 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350
EF099457.1 gg_id:194292 mouse cecum clone SWPT3_aaa03d12 EF0994
AF371584.1 gg_id:68844 swine intestine clone p-2876-6C5 AF371
EU472103.1 gg_id:292909 francois langur feces clone FL_1aaa02b04 EU472

7896.5	2493.8	2699.9	2912.1	2214.4	2257.4	2648.7	2658.2	2310.1	1265.3	2936.1
242.4	2570.1	2472.9	2301.2	2430.5	2265.2	2204.3	2913.0	2401.3	1502.3	2003.2
55.5	598.5	768.8	983.1	524.3	619.5	571.4	1032.5	335.6	94.7	443.1
67.8	110.3	216.8	130.8	91.5	155.9	97.4	263.1	86.2	34.4	151.4
130.2	2913.1	3747.0	3919.7	1663.5	2898.7	2249.1	4013.3	1920.7	949.6	3169.4
61.3	92.8	185.3	141.4	55.7	145.4	127.3	145.5	48.7	18.2	117.0
248.3	436.6	526.2	591.7	576.9	394.8	591.7	495.0	186.0	241.3	339.1
169.1	1822.3	2640.2	2736.9	1524.1	2046.5	2119.2	2949.2	906.0	1466.5	1810.8
5726.9	3637.6	3480.1	3778.6	3756.1	3825.8	4317.4	3444.9	3053.4	2553.5	3204.9
38.4	231.0	457.3	304.5	56.7	44.6	41.8	68.0	82.4	49.8	44.4
402.4	4357.7	3584.3	2797.3	3216.9	3660.7	2862.6	2979.3	3833.9	3652.4	2780.2
2273.2	3375.8	4448.2	4632.5	3925.5	3447.5	4913.9	4356.0	5058.5	4749.3	5615.4
2247.6	4505.9	3910.6	3096.0	2360.1	3582.5	2215.3	3419.4	4396.3	4699.9	2911.7
8366.0	2557.4	2960.3	2759.3	2959.6	2561.7	2754.1	2693.0	636.4	1959.9	3287.6
298.5	2567.0	2641.4	1962.6	2077.9	1678.4	2421.5	2333.2	2858.4	2894.7	2459.2
57.1	708.7	1215.9	1102.9	619.3	645.7	1064.4	821.4	249.4	223.5	728.9
5723.8	3212.6	2700.8	2716.3	2691.1	2984.7	2966.3	3109.8	5340.2	4244.1	2655.2
118.5	768.3	975.6	957.0	689.3	788.1	945.0	924.4	360.1	274.9	961.1
37.8	1055.3	1523.7	1550.2	204.5	999.6	438.3	1667.4	324.5	298.1	1028.3
74.3	542.8	1077.4	627.4	447.7	600.8	635.5	811.6	234.2	99.4	382.2
158.1	2142.9	3180.3	2778.3	2222.3	2960.6	2893.4	2900.2	1175.5	700.6	1811.4
166.5	1176.9	2134.5	2214.6	721.9	1045.1	896.7	1369.5	404.1	171.7	998.4
672.1	1967.4	1210.1	1499.9	1235.4	1360.9	1599.9	1252.5	2330.6	1119.6	988.8
16233.2	6158.6	5577.8	6540.3	6805.6	4785.9	5965.2	5161.2	7519.6	7434.4	6576.3
10521.2	4958.3	5642.0	5782.4	4681.6	4838.9	5505.4	5250.6	2843.7	2127.1	5631.9
6245.0	3103.4	3509.2	2855.0	2814.3	3281.5	3799.6	2634.3	5479.7	3716.2	3951.4
3160.5	3270.0	3221.9	2448.1	1981.4	3335.0	2264.5	3176.4	2672.5	1418.2	3452.5
925.9	2084.9	2400.4	2430.2	1754.8	1762.9	1722.4	2460.8	1957.5	1348.6	2341.3
208.7	1824.0	2245.6	2848.1	2384.8	1943.5	2683.0	2805.2	944.1	167.9	1245.4
186.7	1310.8	1524.4	1282.3	925.0	1104.2	1358.0	1141.2	896.9	661.1	900.9
44.6	1305.2	2419.9	2340.9	803.9	1417.6	1444.4	1748.6	656.4	116.6	1800.7
544.7	3145.7	3335.6	3106.7	2577.2	2554.6	2949.3	2720.0	1815.2	740.3	2684.4
46.4	505.0	401.5	585.7	368.7	410.0	468.0	620.3	246.9	30.6	280.7
54.1	265.4	492.2	601.4	148.9	255.0	139.5	699.9	87.4	88.0	167.5
20295.3	6564.5	6964.9	7821.6	6225.4	6018.7	7582.2	7144.7	8769.1	6830.4	10052.2
28.0	78.1	111.2	107.6	71.4	71.8	78.4	113.3	48.3	52.9	62.8
8396.8	5710.4	6135.2	6684.5	4784.6	5709.1	5284.3	5923.2	7389.0	5669.0	7123.0
58.4	973.7	1810.2	1641.3	843.1	1137.9	942.9	1537.5	340.5	163.1	1227.6
134.4	361.7	816.8	516.2	189.9	366.9	263.1	460.9	192.1	183.9	288.1
47.9	632.3	521.0	782.0	608.7	336.1	1711.8	814.7	120.6	166.4	224.2
46.6	716.4	1078.8	1377.0	164.3	925.9	504.2	1984.1	298.9	220.7	689.3

2527.6	2296.5	2892.0
2160.3	2004.1	2798.8
952.8	716.6	1185.1
196.8	122.4	141.4
4580.4	2588.8	4156.1
60.2	111.5	126.9
516.6	569.1	826.5
3277.8	2223.1	2239.5
4211.6	3788.0	4160.6
246.3	241.7	238.2
3008.1	3367.5	4543.8
4127.8	5005.9	3569.3
3686.4	3536.9	5394.7
2480.3	3260.1	5552.1
2321.4	2638.1	3330.4
1080.1	941.4	893.4
2580.1	4541.1	2909.6
1076.0	1223.2	1314.4
1186.8	731.7	830.6
567.2	713.5	890.9
2865.4	3316.3	4862.2
1686.1	1963.3	2638.4
1342.0	1554.1	1238.3
5037.2	6265.3	5557.8
5764.0	5199.0	5658.5
2541.4	3797.0	2651.8
3197.5	3451.6	4520.2
1971.9	2344.7	2003.5
2328.5	2320.4	3147.0
1186.6	803.6	2371.8
2046.1	1529.7	3192.7
2179.8	2667.9	2523.4
660.6	777.2	739.2
1009.9	684.9	409.3
5776.7	7150.2	5948.0
112.9	141.4	124.5
6262.5	6679.6	7782.2
1392.4	1575.1	1791.6
293.7	608.4	229.0
772.6	602.6	651.7
2465.7	869.6	1472.4

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EF097936.1 gg_id:198808 mouse cecum clone SWPT12_aaa02d08 EF0979
EU776142.1 gg_id:352869 Spotted hyena feces clone HY2_g07_1 EU776
DQ392993.1 gg_id:154021 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ392
GQ896946.1 gg_id:583958 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ896
GU304201.1 gg_id:557646 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
AB192028.1 gg_id:142325 termite gut homogenate clone M1PT4-46 AB192
EU474658.1 gg_id:296471 Indian rhinoceros feces clone IR_aaa04b03 EU474
GQ448094.1 gg_id:547287 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
FJ681179.1 gg_id:510481 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
FJ681895.1 gg_id:527278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
EU844275.1 gg_id:356280 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ809132.1 gg_id:187268 human fecal clone RL308_aal82b08 DQ809
EF099847.1 gg_id:190768 mouse cecum clone SWPT5_aaa01c03 EF0998
DQ807837.1 gg_id:197400 human fecal clone RL180_aah37g08 DQ807
EU467569.1 gg_id:290468 southern three-banded armadillo feces clone arma_f11 EU467
AY983157.1 gg_id:121649 human descending colon mucosal biopsy clone A042 AY983
EU505009.1 gg_id:276548 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01e10 EU505
FJ681350.1 gg_id:519742 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ804908.1 gg_id:197002 human fecal clone RL385_aao82d06 DQ804
EF097641.1 gg_id:189739 mouse cecum clone SWPT20_aaa01f09 EF0976
EU451955.1 gg_id:320373 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU451
EU472379.1 gg_id:294869 Angola colobus feces clone EAC_1aaa02a01 EU472
FJ880090.1 gg_id:454763 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU772719.1 gg_id:318651 Bush dog feces clone bdog1_b10_1 EU772
EU466173.1 gg_id:300529 bighorn sheep feces clone BH1_aao27d09 EU466
EU776207.1 gg_id:307217 Spotted hyena feces clone HY2_d02_3 EU776
DQ805004.1 gg_id:192396 human fecal clone RL385_aao83h11 DQ805
EF404593.1 gg_id:209736 human fecal clone SJTU_C_13_24 EF4045
GQ493107.1 gg_id:564188 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ815637.1 gg_id:167512 mouse cecum clone aab44b06 DQ815
AY975277.1 gg_id:118129 human ascending colon mucosal biopsy clone N504 AY975
EU468743.1 gg_id:289743 okapi feces clone OK3_e07 EU468
EU505213.1 gg_id:268085 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04e11 EU505
EU458328.1 gg_id:302494 spotted hyena feces clone HY1_e08 EU458
EU980608.1 gg_id:349074 Eubacterium contortum str. Ala-1 EU980
EU748182.1 gg_id:347442 neotropical folivorous flying bird adult hoatzin crop clone hoa31_71G09.F EU748
EF398528.1 gg_id:217083 human fecal clone SJTU_F_03_04 EF3985
EU775008.1 gg_id:306413 Francois Langur feces clone FL_1aaa01g04 EU775
DQ800395.1 gg_id:181233 human fecal clone RL303_aal72f05 DQ800
GQ897421.1 gg_id:585480 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU778351.1 gg_id:304327 feces clone RL117_aae92d06 EU778

328.3	617.0	987.6	1042.9	570.2	686.0	944.4	964.9	387.3	122.6	846.4
727.5	783.6	955.0	764.5	803.1	612.7	626.2	889.6	291.8	223.6	626.4
29.1	388.8	472.0	479.7	122.1	352.1	345.8	597.7	119.9	79.3	238.5
3640.4	2002.2	2284.9	2772.2	1415.9	2245.9	1788.9	1692.3	1896.4	527.8	2495.6
3095.6	4291.0	4746.6	4073.6	4273.4	5111.2	3981.8	4439.1	4964.1	4141.0	4073.8
59.0	203.2	333.4	574.8	238.4	305.0	228.0	443.6	121.6	62.0	206.8
9040.1	9224.4	7977.6	7159.0	6883.7	7250.4	6708.8	6644.4	10637.3	7464.7	11063.1
525.9	2044.9	3176.9	2953.2	1937.5	2189.5	2834.7	2592.9	2632.2	1012.5	1971.8
58.0	2100.1	2988.8	3435.0	495.6	1683.0	1348.4	2730.0	621.6	286.8	1664.3
260.8	2009.0	3234.0	3270.3	1749.7	2306.4	2272.6	2674.9	915.0	2388.8	1860.2
76.5	1532.8	1705.0	1930.3	1242.1	1511.5	1772.2	2320.6	826.5	199.2	1010.8
45.1	401.5	465.1	456.9	250.3	329.7	448.3	688.1	385.0	178.2	326.1
517.8	1673.8	2835.7	2911.0	2320.4	1803.1	2344.7	2199.6	1674.4	1185.6	1705.7
121.5	551.0	1028.3	825.3	771.0	1056.6	453.5	1022.1	363.6	603.7	591.8
83.2	936.5	964.7	1076.4	740.1	801.7	801.2	1195.2	517.7	132.4	577.7
97.1	2700.6	2228.6	1549.3	1165.8	2099.0	1301.7	1817.6	2603.6	3546.7	1530.1
1212.0	3633.1	4202.7	4155.7	3551.3	4245.8	3121.1	4181.6	5456.4	3860.4	4229.2
85.7	1473.0	1439.2	1771.4	765.7	1093.5	818.5	1400.9	1615.2	751.6	1055.6
38.8	368.3	429.0	777.5	400.5	189.2	323.1	336.0	39.1	38.7	83.3
3036.2	4757.7	5861.9	4955.9	4799.8	4482.6	4349.5	4738.8	8090.5	5823.5	5333.7
1569.8	4432.7	5254.7	4729.9	4364.6	4199.0	5606.0	4247.5	5576.1	4307.7	4374.0
1109.8	2212.0	2820.6	2603.1	2021.0	2195.0	2024.5	2854.2	1495.2	1635.7	4114.2
1554.1	3306.6	3203.9	3042.3	1681.5	2577.6	1776.8	2947.5	2389.9	2127.2	1956.8
79.1	724.4	815.3	888.3	1028.3	697.4	890.2	839.1	422.4	883.6	324.6
1661.3	2783.7	2767.3	2589.4	2093.9	2544.3	2424.7	3048.8	2376.3	1519.4	2580.9
3196.6	1954.4	2407.9	2543.8	2080.5	1941.2	2027.1	2521.9	1997.9	1504.9	2323.9
422.7	1535.3	2268.8	2016.4	1446.8	1619.6	2067.8	1457.7	2600.0	733.6	1600.1
3549.2	4049.6	3032.9	2998.7	3014.9	2994.8	3054.1	3108.4	4354.4	2389.0	2727.1
90.9	842.4	1242.8	865.0	785.9	777.7	752.0	849.5	479.0	146.8	589.4
303.7	752.5	1288.4	1377.0	668.2	1083.5	928.4	1469.1	606.4	209.2	821.7
34.4	130.0	286.5	252.6	234.0	144.9	203.4	237.3	56.7	47.8	165.9
504.7	1157.6	1277.3	985.0	887.2	924.7	1081.9	985.5	1120.9	695.8	1393.3
3154.4	2361.9	2696.5	2705.8	2484.5	2510.2	2771.9	2541.4	2906.9	2405.0	3202.4
30.6	113.9	167.5	184.9	77.6	153.8	164.7	159.4	68.3	39.4	84.7
295.4	3275.8	3911.2	4234.6	4416.1	3971.1	2747.2	5566.4	2486.3	2805.5	3180.0
47.5	195.0	381.8	434.4	92.9	281.7	175.1	286.4	89.4	54.1	132.9
375.7	4305.9	5137.3	4547.0	3134.4	4955.5	3065.4	4478.7	3795.7	2602.2	3698.9
28.3	42.5	90.0	97.8	57.0	55.3	33.8	100.7	34.0	102.8	33.5
41.0	35.8	93.4	102.9	30.8	43.7	35.3	78.0	34.7	27.9	43.0
36.0	1177.8	2918.4	2708.9	986.7	1967.6	1435.8	2258.2	865.5	181.8	2136.5
438.4	1363.8	1506.5	1599.8	1483.6	1274.7	1943.5	1863.1	1305.9	875.3	1656.9

857.9	943.1	738.0
910.4	980.2	874.9
503.2	405.6	351.5
3456.5	2444.5	2085.6
3554.0	5078.9	4583.1
563.7	487.8	469.3
6618.7	9750.8	6726.0
3126.3	2380.7	3852.3
3307.4	1578.3	2302.7
2886.1	2669.5	4367.1
3125.2	1588.0	2796.9
433.8	410.7	498.5
2526.5	2162.8	3656.0
891.4	700.8	851.1
1700.9	1153.2	1687.9
1872.4	1907.2	2529.6
3627.6	4260.3	3526.7
1492.0	1383.1	943.8
421.1	377.4	373.3
4893.4	5929.2	5033.6
3984.9	5721.9	5308.1
2777.5	3240.5	2902.2
3122.7	2315.1	4190.9
1171.0	1035.3	1215.6
3524.2	3077.7	3487.1
2814.7	2942.9	3601.5
2070.5	1735.7	3631.3
3996.2	3681.5	3477.0
1398.1	738.1	1370.6
1645.3	1261.9	2049.9
152.7	224.3	163.8
671.9	916.0	755.4
2382.1	3047.4	2580.9
220.1	155.2	211.9
5004.1	3268.3	5006.1
295.0	277.3	339.7
5056.8	2908.3	4723.8
130.3	118.0	64.7
100.7	97.3	59.5
2875.6	1382.8	3432.8
2145.3	1505.8	2057.9

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EU508425.1 gg_id:260553 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33d02 EU508
FJ673298.1 gg_id:525987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ172888.1 gg_id:335488 Qinghai Yak Ruminal and Fungi China rumen clone RB-12 FJ1728
EU474433.1 gg_id:301633 bighorn sheep feces clone BHSD_aaa04d09 EU474
AJ576351.1 gg_id:106393 hindgut homogenate Pachnoda ephippiata larva clone PeH35 AJ5763
EF100006.1 gg_id:195934 mouse cecum clone SWPT5_aaa03d11 EF1000
EU777278.1 gg_id:331240 Okapi feces clone OK1_f11_3 EU777
EU845293.1 gg_id:335032 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU768480.1 gg_id:349094 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ815643.1 gg_id:165434 mouse cecum clone aab44c02 DQ815
EF400639.1 gg_id:210200 human fecal clone SJTU_E_16_22 EF4006
EU774752.1 gg_id:309534 Angola Colobus feces clone EAC_2_aaa02h06 EU774
EU466324.1 gg_id:297982 bighorn sheep feces clone BH2_aao21h07 EU466
DQ805037.1 gg_id:190503 human fecal clone RL385_aao84d04 DQ805
DQ793840.1 gg_id:177359 human fecal clone RL176_aah44b09 DQ793
AY685919.1 gg_id:105684 feces clone 2C12 AY685
FJ880101.1 gg_id:467666 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
DQ800557.1 gg_id:190849 human fecal clone RL183_aah29f10 DQ800
DQ394642.1 gg_id:151401 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
AY854368.1 gg_id:110858 herbivore gastrointestinal tract clone Thompsons96 AY854
EF605060.1 gg_id:232620 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6050
EU510082.1 gg_id:273594 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01a12 EU510
EF100115.1 gg_id:181063 mouse cecum clone SWPT5_aaa04h06 EF1001
EU466107.1 gg_id:302407 bighorn sheep feces clone BH1_aao26a05 EU466
EF402474.1 gg_id:208509 human fecal clone SJTU_B_08_38 EF4024
FJ677261.1 gg_id:530104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
EU775776.1 gg_id:336149 Horse feces clone horsem_aai93d05 EU775
FJ374228.1 gg_id:365377 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg FJ3742
EF099407.1 gg_id:175432 mouse cecum clone SWPT3_aaa02g12 EF0994
EU454544.1 gg_id:303841 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
GQ448134.1 gg_id:508984 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
EF603792.1 gg_id:230215 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6037
AY991938.1 gg_id:134424 mouse cecum clone C20_m01 AY991
EU454263.1 gg_id:329122 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU454
AB189708.1 gg_id:113610 alkaline-enriched termite gut homogenate clone Pl-9.2e-11 AB189
EU776029.1 gg_id:327493 Spotted hyena feces clone HY1_a10 EU776
EU462996.1 gg_id:289304 southern three-banded armadillo feces clone arma_aaj56c08 EU462
FJ364165.1 gg_id:358603 feces adult twins and mothers; TS150 clone TS150_a03g03 FJ3641
EU475432.1 gg_id:299124 springbok feces clone SBSD_aaa03b12 EU475
GQ451207.1 gg_id:553492 Fecal Yunnan snub-nosed monkey feces clone J60 GQ451
EU462878.1 gg_id:296516 southern three-banded armadillo feces clone arma_aaj54d04 EU462

15332.1	4494.1	5003.0	5247.4	4975.9	4263.1	4704.9	5186.3	5849.4	5514.6	5262.1
19114.1	9458.6	8398.0	8797.6	7595.8	8389.0	8354.9	7309.7	11568.4	10167.0	12507.2
42.4	886.2	946.6	904.5	534.0	859.1	354.4	1605.4	1316.7	498.0	729.4
70.1	530.3	678.9	960.2	248.0	314.5	346.3	496.2	122.2	105.6	295.1
2693.3	3160.5	4406.9	4209.0	3646.9	3464.9	4533.6	3690.6	3373.7	2252.9	3230.9
197.5	1410.7	1653.7	1588.2	1504.9	1567.3	1602.8	1390.7	1205.0	379.7	1368.8
2635.7	1688.7	2197.6	2569.5	1148.1	1603.0	1457.6	2318.7	984.8	384.4	2137.6
849.6	7195.9	8365.4	5606.4	4583.4	5420.4	4564.4	5672.4	4377.9	7840.6	4979.7
46.1	931.8	1542.9	1423.6	382.9	851.8	1336.6	1043.4	335.1	78.9	1076.6
8317.9	3090.8	3448.7	3668.5	3200.8	2739.1	3374.0	2857.2	4126.9	4132.3	5688.4
13761.0	4155.4	3972.2	4222.0	4259.5	3910.9	4563.9	4072.0	5717.1	4030.5	5812.6
798.7	2790.4	2720.2	3056.8	2684.0	2934.3	3729.1	3425.5	3238.6	3386.7	3623.5
175.4	1642.8	2544.9	2750.0	813.7	1265.4	969.8	1810.5	437.0	241.9	1205.4
878.5	1698.4	1878.9	1907.6	834.2	1397.9	1170.5	1734.1	1804.7	2104.1	1848.3
40.9	67.4	135.8	171.5	117.2	67.9	144.3	255.4	51.4	24.6	68.1
65.3	46.0	78.8	57.8	39.2	50.7	41.9	68.3	37.7	38.2	47.1
8784.9	2870.6	2682.6	2885.1	2505.3	2672.6	3181.0	3039.4	2846.2	4850.4	2678.5
31.7	477.3	711.3	862.4	310.0	292.9	348.6	504.4	80.5	56.8	215.2
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37.1	46.4	96.8	83.1	74.2	54.6	90.1	95.1	37.6	19.6	48.3
543.3	2163.7	3103.5	4030.9	3122.4	3066.1	3079.8	2655.9	1218.8	565.3	1967.5
57.2	1544.0	2968.2	3649.4	728.2	1288.4	994.0	1866.6	391.0	184.2	1366.5
550.4	2820.8	3637.3	3643.7	2620.5	2524.5	3068.8	4506.2	2498.9	1342.2	2817.1
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4839.7	3938.7	5005.8	4255.8	5238.6	3829.2	6342.1	4207.9	3380.9	1671.2	3605.0
265.8	1454.9	1963.0	1858.7	2527.6	1967.9	2366.7	1261.0	936.4	405.7	1175.7
571.2	4041.3	3484.3	3080.1	3116.8	3140.9	3944.8	3763.3	3925.6	3512.6	3144.7
12132.3	4398.9	4749.5	4952.7	4947.1	4626.3	5244.9	5428.1	4092.2	3056.2	4834.8
924.6	2423.9	3110.0	3604.9	1908.6	2449.2	2216.0	3126.4	1177.8	2214.6	1870.2
3070.8	1896.0	2584.5	2551.2	1991.1	1808.6	3332.5	2123.2	2096.2	1263.6	2531.1
9380.9	5068.9	4079.4	4259.5	2771.2	4075.4	3177.6	4072.7	2776.0	3209.9	3447.4
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49.6	1186.9	1477.3	1336.7	932.9	939.7	875.5	1150.8	513.8	378.1	638.7
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301.5	2288.1	2059.1	2912.5	2170.8	3016.4	1913.7	3297.1	1056.2	3766.9	1415.8
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1416.9	1571.9	1913.0
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5105.2	6154.8	6684.6
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615.9	720.6	772.0
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1464.2	1725.8	1949.0
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EU381863.1 gg_id:275824 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EF099982.1 gg_id:192504 mouse cecum clone SWPT5_aaa03b04 EF0999
AF371572.1 gg_id:30587 swine intestine clone p-1028-a5 AF3715
DQ801366.1 gg_id:192603 human fecal clone RL388_aao94e08 DQ801
GQ448108.1 gg_id:511234 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
EU779178.1 gg_id:322604 Trancaspian Urial feces clone TU2_aaa01g09 EU779
EU466206.1 gg_id:296103 bighorn sheep feces clone BH1_aao28a06 EU466
EU844598.1 gg_id:339911 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ824503.1 gg_id:188818 human fecal clone RL304_aal76g12 DQ824
EU457086.1 gg_id:335869 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
DQ014911.1 gg_id:131235 mouse cecum clone M1_1d02 DQ014
EU456638.1 gg_id:325690 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
EF096497.1 gg_id:193742 mouse cecum clone obob2_aaa03g10 EF0964
AY854316.1 gg_id:110434 herbivore gastrointestinal tract clone Thompsons28a AY8543
FJ681090.1 gg_id:527934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EU467418.1 gg_id:298916 chimpanzee feces clone CHIMP12_c08_2 EU467
FJ681436.1 gg_id:530379 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
EU344395.1 gg_id:276882 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU455309.1 gg_id:336015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
FJ684450.1 gg_id:529810 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
EU764744.1 gg_id:340178 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU504860.1 gg_id:266418 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03d07 EU5048
FJ676498.1 gg_id:515269 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU842591.1 gg_id:310078 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ834059.1 gg_id:569871 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q401_57A08 FJ8340
FJ880210.1 gg_id:375678 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU470158.1 gg_id:294440 trancaspain urial feces clone TU2_aaa02e06 EU470
DQ806761.1 gg_id:178295 human fecal clone RL186_aao48d06 DQ806
EF097997.1 gg_id:183706 mouse cecum clone SWPT12_aaa03g07 EF0979
EU456570.1 gg_id:344418 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU456
GQ448746.1 gg_id:569582 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
DQ015243.1 gg_id:135600 mouse cecum clone M2_g05_1 DQ015
EF099755.1 gg_id:194822 mouse cecum clone SWPT4_aaa03h03 EF0997
AY984693.1 gg_id:123923 human stool clone B646 AY984
GU304124.1 gg_id:568828 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
DQ327400.1 gg_id:146248 Metagenomic gut microbiome healthy human stool clone E958 DQ327
EU459778.1 gg_id:301110 ring-tailed lemur feces clone RT_aai12f06 EU459
EU344291.1 gg_id:263629 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU765488.1 gg_id:306345 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ879182.1 gg_id:461837 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
FJ372006.1 gg_id:360555 feces adult twins and mothers; TS8 clone TS8_a04f09 FJ3720

76.8	2095.7	2870.0	3390.3	882.6	2040.9	1562.7	3439.1	985.0	484.5	1911.4
889.9	522.1	748.2	881.6	638.1	562.7	609.6	767.9	462.3	136.4	546.2
38.6	21.8	29.3	34.3	27.2	24.4	30.7	27.8	32.1	36.6	37.6
237.7	2692.6	3776.5	4883.1	1965.8	1961.6	1954.6	2734.4	1245.5	966.1	2523.1
448.7	872.8	1411.6	1171.9	1108.2	948.2	1055.6	780.6	592.7	723.4	959.8
115.7	2129.2	2265.2	1892.7	1635.2	1945.7	1490.2	1715.3	2612.9	2086.4	1828.4
585.8	1077.6	1379.7	737.3	642.7	681.5	832.2	833.9	2439.5	887.6	1096.7
4156.1	3725.3	3323.0	3743.5	3010.8	2901.5	3123.3	3558.4	2369.9	1109.3	3454.5
33.9	91.8	180.8	143.9	45.5	86.9	45.1	170.5	63.2	27.1	141.4
25878.5	6069.4	5235.9	5595.7	5076.2	5056.6	5718.6	5022.3	7753.6	5598.5	10437.3
3947.5	5627.0	5690.5	6270.3	6814.9	6524.2	7311.9	6505.9	9626.9	8943.5	7165.1
184.7	256.0	489.5	326.0	221.2	269.2	257.3	689.2	212.6	366.1	382.6
135.8	675.4	1094.5	1459.3	690.6	519.2	866.9	761.6	279.1	216.6	265.6
145.5	699.9	844.5	824.0	512.9	726.7	774.7	1339.6	622.4	115.1	400.8
111.1	1409.7	1422.1	1477.3	1443.0	1272.2	1425.5	1558.5	1114.7	230.7	914.0
83.9	617.9	1077.9	1091.9	312.6	783.5	799.4	560.1	278.9	91.9	705.0
52.0	753.9	934.2	899.1	259.8	769.2	482.0	1071.9	345.3	146.5	648.9
108.3	3178.7	3186.9	2926.2	2424.2	2844.3	2675.9	2337.3	1459.1	1442.0	1669.8
889.2	1388.5	1814.8	1932.2	1367.5	1576.7	1656.2	1943.9	1296.5	911.4	1276.9
3699.2	1534.7	2262.5	2253.3	1894.1	1515.9	2561.5	2463.9	698.4	280.5	3191.8
67.5	390.5	465.7	734.7	427.5	447.5	673.1	485.3	149.7	41.5	308.1
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40.2	219.3	419.2	532.1	65.6	329.5	77.4	274.2	58.3	23.0	95.8
7630.2	4875.3	5592.0	5721.8	5761.4	5078.4	5986.8	5374.5	6088.5	4819.9	5288.5
133.2	2168.6	2886.3	3168.7	2388.9	2596.4	2857.9	2897.6	1176.2	1549.8	2154.3
233.0	739.9	1401.7	1382.1	367.8	544.0	449.3	1381.2	395.5	124.6	757.9
938.7	2674.5	2880.0	3300.5	1835.8	2318.8	2133.9	2806.8	1103.7	491.7	1642.4
183.8	407.3	401.9	635.7	709.4	395.9	874.3	434.8	222.4	117.7	250.4
544.3	2631.4	2448.1	2008.6	1668.0	2500.0	1436.4	2382.3	2271.6	1881.3	1901.3
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69.1	1975.2	2354.4	2093.3	1858.8	1792.8	1531.3	3101.1	1243.1	744.5	1627.1
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180.9	1134.5	1934.4	2269.0	318.4	708.8	559.8	1082.3	271.9	125.0	802.0
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10627.2	5694.5	4723.7	4807.5	4132.0	4834.4	4438.8	4630.5	5859.7	4913.2	5769.4
618.3	1059.3	1124.8	851.5	656.2	1012.1	786.4	999.9	890.1	441.0	704.2
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98.9	2231.5	2627.0	1860.7	1422.4	1693.9	1950.4	2391.3	2024.8	1302.1	2040.5
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27.4	33.3	28.4
3277.3	3466.0	3201.9
1050.9	1808.6	1823.8
1806.8	1890.5	1857.5
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3664.1	4463.8	4284.2
112.6	97.8	25.0
4666.7	5416.4	4964.6
5511.9	8377.1	6760.4
424.8	578.1	1037.8
929.5	694.2	563.7
1605.4	871.0	1330.8
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2986.9	3122.2	5392.8
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1941.1	2180.0	3016.9
517.7	584.2	793.7
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3617.0	2107.8	3175.3
605.3	814.2	519.0
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2591.3	1864.7	3017.3
3732.6	5176.6	3879.2
1516.4	1125.5	1052.0
631.2	368.2	495.5
4599.6	5237.4	5418.3
747.0	727.5	780.5
924.8	686.9	767.9
9347.0	8873.4	12700.3
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905.6	889.9	765.8
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EU843346.1 gg_id:320160 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
FJ880002.1 gg_id:422064 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
DQ799732.1 gg_id:186277 human fecal clone RL182_aah32c09 DQ799
FJ684162.1 gg_id:521496 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
AY979259.1 gg_id:121548 human transverse colon mucosal biopsy clone Z451 AY9792
FJ364252.1 gg_id:357134 feces adult twins and mothers; TS150 clone TS150_a04g06 FJ3642
FJ368503.1 gg_id:369439 feces adult twins and mothers; TS49 clone TS49_a01b05 FJ3685
EU504933.1 gg_id:261354 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04d10 EU5049
FJ372249.1 gg_id:361166 feces adult twins and mothers; TS9 clone TS9_a03d09 FJ3722
AB189707.1 gg_id:114381 alkaline-enriched termite gut homogenate clone Pl-9.2e-7 AB1897
EU505482.1 gg_id:276364 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa01c12 EU5054
DQ799097.1 gg_id:184518 human fecal clone RL205_aaj17e10 DQ799
DQ803685.1 gg_id:176975 human fecal clone RL200_aai57b07 DQ803
FJ684251.1 gg_id:524289 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
AY981916.1 gg_id:120368 human sigmoid colon mucosal biopsy clone NZ24 AY9819
AY858432.2 gg_id:111982 gastrointestinal tract Grant's gazelle clone GRANT13 AY8584
EU776923.1 gg_id:304639 Mongoose lemur feces clone ML_aaj25d09 EU7769
DQ815938.1 gg_id:172389 mouse cecum clone aab24e09 DQ815
EU508357.1 gg_id:262020 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03f09 EU5083
EU452436.1 gg_id:324146 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4524
EF098632.1 gg_id:191109 mouse cecum clone SWPT16_aaa02d10 EF0986
FJ370616.1 gg_id:364175 feces adult twins and mothers; TS57 clone TS57_a03b11 FJ3706
EU344425.1 gg_id:277063 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
DQ794421.1 gg_id:196508 human fecal clone RL197_aah87e08 DQ794
EU452744.1 gg_id:314970 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4527
EU845471.1 gg_id:311964 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8454
EU768086.1 gg_id:317898 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7680
AJ576422.1 gg_id:106224 midgut homogenate Pachnoda ephippiata larva clone PeM68 AJ5764
EU466243.1 gg_id:299008 bighorn sheep feces clone BH1_aao28f11 EU4662
DQ805323.1 gg_id:188989 human fecal clone RL203_aai61b09 DQ805
EU469747.1 gg_id:291950 flying fox feces clone FF_b07_2 EU4697
EF099777.1 gg_id:185770 mouse cecum clone SWPT4_aaa04b10 EF0997
EU776775.1 gg_id:331886 Mongoose lemur feces clone ML_aae87b05 EU7767
EU463079.1 gg_id:299910 naked mole-rat feces clone molerat_aai69f02 EU4630
AF371599.1 gg_id:43159 swine intestine clone p-1512-b5 AF3715
EU530171.1 gg_id:272886 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU5301
AY980257.1 gg_id:126883 human rectum mucosal biopsy clone MW68 AY9802
EU470201.1 gg_id:288049 trancaspain urial feces clone TU2_aaa02a05 EU4702
EU503967.1 gg_id:275366 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d06 EU5039
EU778572.1 gg_id:313741 Ring-tailed lemur feces clone RT_aai09b11 EU7785

33.6	374.9	530.1	606.0	296.1	339.0	280.3	324.6	168.7	90.0	130.9
182.8	1896.3	2034.6	2229.9	1567.2	1732.8	1974.8	2035.4	646.6	534.9	1749.0
2765.9	2937.3	3177.3	3912.8	3045.4	3156.4	3379.6	3470.2	2866.5	1752.6	3529.3
32.1	1146.1	1332.1	1485.6	2635.5	1190.8	1284.2	1696.4	277.7	184.4	523.9
112.6	778.9	1212.0	1173.4	1160.9	881.5	959.9	1476.9	379.9	502.1	895.7
46.4	321.2	558.6	564.3	137.5	341.8	195.4	432.5	130.2	76.9	456.2
5498.8	2907.4	2900.1	2991.2	3207.8	3174.0	2854.0	2634.7	4362.2	2951.9	4500.9
45.8	22.5	37.2	37.7	35.3	24.5	36.6	24.3	21.6	16.4	16.5
4843.4	8335.3	7717.4	8348.3	7997.4	6909.4	9220.5	6380.0	6683.7	4726.8	6856.0
431.2	939.5	681.9	839.0	784.9	651.7	449.1	1021.5	432.3	167.2	570.1
32.0	275.4	804.5	756.9	525.1	744.0	563.3	655.9	230.8	94.4	420.7
49.9	24.9	26.6	28.8	19.2	15.3	22.6	27.1	33.3	29.8	23.5
70.8	449.5	620.3	607.2	1326.5	488.4	785.6	472.1	160.0	417.8	290.7
72.8	176.1	186.1	204.7	139.6	128.1	124.0	349.2	90.9	85.4	127.5
42.9	668.2	804.0	1014.4	139.2	503.1	326.8	799.9	122.3	79.4	496.9
42.2	2686.5	2723.4	2594.6	2198.1	2298.2	3138.0	2381.0	5238.0	3041.2	4102.0
70.5	446.4	781.2	968.3	568.0	541.8	648.3	848.1	215.6	72.7	433.2
46.5	679.7	1206.8	1255.1	502.8	647.0	762.9	1212.5	211.9	149.1	603.4
4666.9	2622.5	3084.3	2979.2	2345.8	2815.1	2920.9	2816.9	3289.0	3013.3	3812.2
47.1	978.3	1536.9	2165.1	358.0	740.0	624.8	1107.7	264.6	239.6	465.6
7638.0	3908.1	4286.5	3873.1	3587.6	3515.5	3799.6	3734.5	5663.3	4580.1	6789.3
1039.9	139.3	165.0	192.7	135.0	129.1	123.1	141.7	207.3	108.4	157.5
4564.5	3431.1	3807.6	2932.8	2262.9	3406.0	3005.5	2564.6	4577.6	2940.0	4675.2
1052.1	2854.9	3189.8	3535.3	3159.2	2743.5	3328.8	3072.2	1586.6	2863.8	2621.5
78.9	674.1	2068.3	196.9	251.8	311.2	139.4	281.8	161.5	171.1	154.0
959.7	2030.8	2322.0	2215.0	2427.6	2410.9	2452.3	1942.2	2364.0	934.0	2125.6
2821.9	2927.9	2866.5	3473.7	3779.8	2264.8	2447.3	2646.0	4990.7	1116.5	2715.8
25.8	13.8	13.6	14.8	13.2	10.3	16.7	9.9	13.1	13.9	17.6
121.7	1566.9	2151.4	2252.4	1122.2	1663.5	2073.7	1522.0	848.7	179.1	1212.1
13853.3	6164.4	5463.0	4928.4	4846.0	5125.0	6040.3	5351.1	6139.0	4383.6	4634.6
467.0	2645.3	1945.5	3209.7	4610.5	3145.2	3772.7	3210.3	2084.3	1209.2	2110.2
24.3	1230.9	1866.9	2167.6	288.5	665.8	431.7	1342.6	455.2	82.3	560.1
57.3	1031.0	1694.5	2240.0	902.0	1091.5	1165.9	2274.1	473.6	330.3	913.9
90.3	2215.5	2406.9	2406.8	2536.1	2205.4	2241.5	2773.9	644.4	387.2	1118.8
656.0	3486.9	4863.4	5075.0	4384.6	4200.0	4849.4	4948.4	2120.9	1611.6	3574.5
33.6	66.6	91.2	93.2	53.0	63.2	57.9	51.7	32.3	27.8	45.6
67.8	787.4	960.7	1025.3	232.9	559.6	312.9	1060.3	262.0	93.8	897.4
314.0	778.6	889.5	1002.5	906.7	725.6	722.0	1244.1	347.4	878.9	668.7
249.3	1353.3	1966.3	1963.7	668.7	1348.7	1311.4	2321.3	716.5	595.0	1372.1
40.3	189.1	436.9	707.5	69.4	162.6	186.8	217.8	62.0	30.6	115.5
779.8	539.5	1051.6	771.8	405.8	496.6	425.4	794.4	581.4	706.5	438.1

666.6	476.1	497.4
2162.3	1867.1	2346.5
3479.1	4121.7	4857.1
1664.1	1094.0	1677.0
1285.2	1416.8	1281.6
562.6	340.5	517.3
2930.0	3686.6	3318.1
25.8	35.5	38.9
6772.9	7620.6	8395.6
887.0	921.7	620.6
786.6	432.4	1169.6
17.6	29.9	21.4
475.1	559.4	674.3
241.2	173.9	369.1
744.5	624.0	709.5
2193.4	3258.3	2315.6
927.3	580.6	906.6
1197.6	563.5	962.6
2227.6	3977.7	2524.6
1358.1	1429.3	1082.1
3532.4	5203.4	3853.4
118.0	596.0	143.0
2529.3	4083.5	3323.4
2954.3	3031.7	3503.4
249.7	345.2	391.6
2037.2	2073.3	2898.5
3080.1	2552.5	3610.9
9.2	21.1	15.7
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4575.2	5220.6	5649.7
3457.5	3272.6	3071.6
2177.1	1123.7	1326.7
2521.8	1221.1	2406.2
2767.1	1725.8	2266.3
4817.5	3565.2	4586.9
52.5	90.8	60.2
1519.2	637.9	1095.4
1233.7	1180.8	1297.2
2940.5	1267.1	1772.4
256.6	274.9	153.1
674.3	972.1	470.6

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o__Clostridiales	f__Lachnospiraceae

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DQ815312.1 gg_id:171565 mouse cecum clone aab45c08 DQ815
EU470427.1 gg_id:289929 Grevy's zebra feces clone GZ_aaa01a02 EU470
EF097990.1 gg_id:178106 mouse cecum clone SWPT12_aaa03f08 EF0979
EF099192.1 gg_id:173850 mouse cecum clone SWPT2_aaa03f07 EF0991
FJ364892.1 gg_id:360165 feces adult twins and mothers; TS19 clone TS19_a04d08 FJ3648
EU509896.1 gg_id:261764 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak23d01 EU5098
GQ402116.1 gg_id:580171 alpacas and sheep forestomach clone ALP4 GQ402
GQ448593.1 gg_id:541415 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU844125.1 gg_id:354188 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
GQ448779.1 gg_id:586290 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
DQ803682.1 gg_id:192159 human fecal clone RL200_aai57b04 DQ803
EU451081.1 gg_id:305919 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU451
DQ815320.1 gg_id:171333 mouse cecum clone aab45d09 DQ815
FJ366764.1 gg_id:362448 feces adult twins and mothers; TS27 clone TS27_a03f01 FJ3667
EU844936.1 gg_id:350330 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
EU456846.1 gg_id:329416 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU4568
AF371640.1 gg_id:31249 swine intestine clone p-1051-a5 AF3716
EU456659.1 gg_id:334243 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU4566
EF099478.1 gg_id:178814 mouse cecum clone SWPT3_aaa03f10 EF0994
DQ801377.1 gg_id:181823 human fecal clone RL388_aao94f11 DQ801
EU456554.1 gg_id:323101 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU4565
DQ815728.1 gg_id:162201 mouse cecum clone aab21e06 DQ815
FJ365251.1 gg_id:363014 feces adult twins and mothers; TS1 clone TS1_a04f04 FJ3652
FJ879589.1 gg_id:393167 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
FJ369960.1 gg_id:359128 feces adult twins and mothers; TS55 clone TS55_a02g05 FJ3699
DQ800978.1 gg_id:181028 human fecal clone RL387_aao90c04 DQ800
AM237879.1 gg_id:213401 Selective colonization insoluble human faecal faeces clone D1B-6.5-48h-6 AM237
EU468116.1 gg_id:287540 bush dog feces clone bdog3_aad68c08 EU468
EU455153.1 gg_id:334568 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU455
EU469112.1 gg_id:295574 Speke's gazelle feces clone SP3_f08 EU469
EU381677.1 gg_id:259223 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU472185.1 gg_id:291887 francois langur feces clone FL_2aaa03b06 EU472
EU776095.1 gg_id:345340 Spotted hyena feces clone HY1_f07_3 EU776
FJ367192.1 gg_id:363919 feces adult twins and mothers; TS28 clone TS28_a04f02 FJ3671
FJ680926.1 gg_id:519613 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ794797.1 gg_id:177828 human fecal clone RL240_aaj32d12 DQ794
FJ879226.1 gg_id:453454 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
AY978280.1 gg_id:115403 human transverse colon mucosal biopsy clone F136 AY9782
EU454694.1 gg_id:343321 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU4546
EU764912.1 gg_id:329115 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7649
EU451699.1 gg_id:352956 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU4516

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437.4	1589.3	1703.9	2417.5	1342.6	1644.5	1306.3	2157.2	499.8	1989.3	1290.7
46.2	879.2	795.4	1122.2	693.1	741.2	765.8	610.3	333.0	282.9	263.9
1976.2	3579.1	4406.8	4442.9	4558.6	3857.9	5112.8	3879.9	3800.0	5330.1	3731.4
7280.0	3723.6	3864.1	4512.7	3875.8	3829.4	3500.5	4555.1	4985.8	2673.2	5865.8
127.6	2246.9	2565.8	2295.8	2790.4	2090.5	2342.4	1502.6	2284.7	805.0	1409.0
3739.1	2658.9	3405.7	3049.7	4002.4	2632.6	3259.8	3040.8	3662.5	2223.4	3356.2
46.8	593.2	801.2	976.6	498.7	769.0	591.5	1489.0	157.8	110.9	428.5
379.2	1435.1	1907.6	1968.5	1111.3	1230.4	1319.7	1985.4	952.0	381.8	1170.0
158.4	3081.3	3719.3	3466.9	2760.0	2841.9	2386.8	3529.5	1373.0	1443.2	2712.7
2757.7	1266.1	1447.1	1773.6	1216.0	1601.6	1689.3	1423.0	1267.5	1700.6	863.0
991.7	3570.0	3704.9	3205.8	1324.0	3008.5	3086.9	3828.5	2641.1	3106.5	3043.2
450.7	1700.3	2383.6	2955.4	3252.4	2321.1	3731.4	2595.4	2268.4	2367.3	2378.8
5884.9	2520.7	2523.1	2457.5	2196.4	1979.4	2149.5	2423.1	2288.6	2204.7	3271.2
4237.0	4336.7	4673.7	5341.1	5579.1	4606.0	5246.7	4754.2	3795.6	4942.5	7049.1
578.8	1591.7	2509.3	1704.0	1884.7	2187.2	1766.0	2278.6	1213.7	1613.1	2330.3
31.5	18.5	21.9	22.6	19.6	14.7	14.2	16.0	17.6	18.7	19.7
4318.0	6340.2	6310.7	5450.4	4612.4	6029.1	5349.5	5884.4	9786.9	8778.2	7452.7
5567.7	3601.3	4278.4	3721.0	3731.3	3595.7	4370.4	3762.5	4197.9	4244.5	4197.5
2723.4	2202.0	3315.7	2665.5	3072.2	3354.7	2531.1	2884.9	2593.1	3111.0	2689.2
16268.8	5283.0	4835.5	4357.5	4019.4	4498.2	4595.4	3886.5	6595.9	3405.7	6267.9
5955.0	4352.5	5722.9	6271.0	4799.0	4830.9	4904.1	4894.1	5908.2	4935.7	5295.7
6940.6	2065.6	1934.8	1786.5	1717.8	1900.6	1988.9	1903.1	3013.9	2784.3	2224.2
299.5	1840.7	2594.7	1617.8	1413.2	1709.3	1523.7	1760.4	1470.3	897.0	2489.2
72.7	744.4	1254.5	1494.8	221.6	970.3	816.4	1292.0	190.5	62.2	768.0
39.6	466.6	740.9	592.2	343.3	368.4	503.9	539.6	59.0	65.3	296.4
53.2	1536.9	2506.4	3464.1	1189.9	1082.6	1608.0	1802.9	475.6	138.1	754.4
123.9	501.9	641.8	396.6	407.2	435.1	528.6	550.0	265.7	118.1	581.7
120.1	1520.3	3275.6	1677.7	1119.5	1285.4	1168.1	1644.0	1066.2	581.1	1778.5
699.0	3645.1	3738.4	3493.9	3005.4	3667.2	3012.7	3756.0	2756.4	3802.4	2508.5
122.2	2258.9	2479.5	3005.9	3328.2	2041.7	3262.0	2870.8	987.1	1175.1	1595.2
52.6	1353.0	1946.7	2008.9	681.5	1291.4	1717.0	1790.0	515.8	424.4	1361.3
8893.9	3745.2	3377.8	4225.8	3511.9	3514.9	3576.9	3653.7	3581.9	2263.2	4449.1
40.3	1359.0	1333.4	1365.2	664.1	1024.1	828.9	1091.7	352.0	199.1	762.6
987.6	588.9	1042.2	1018.7	454.2	645.3	615.2	1119.9	484.7	262.8	785.6
1883.6	969.5	916.3	1799.0	1458.2	1218.2	879.7	1260.2	458.4	233.2	775.1
20138.7	5353.6	6836.4	5983.7	4669.7	5050.6	5739.2	5154.5	8127.4	8144.9	8581.3
44.6	1727.6	2855.9	2558.1	926.7	2275.5	2241.2	2610.7	680.8	193.6	1735.1
3153.5	4783.2	4889.9	5282.3	5152.5	4234.0	4914.3	4862.2	4509.1	4500.2	4031.7
30.7	686.3	887.6	865.2	419.4	724.6	386.1	2054.3	271.8	86.9	492.0
45.1	1783.5	2463.1	2678.1	881.8	1898.1	1099.5	3286.5	856.5	595.1	1549.4

4371.0	3958.0	4051.5
1586.8	2209.2	1530.2
607.8	754.3	1435.1
3639.8	5673.2	6219.2
3265.7	4682.3	4653.8
1270.7	1913.3	3871.7
2536.6	2718.1	3041.5
2008.8	717.1	1844.1
1811.4	1817.2	1738.8
3270.5	3605.7	3454.4
1695.4	2045.8	2268.1
3919.6	3599.8	6614.1
1709.5	3405.7	4033.3
2631.0	2634.4	2525.8
4881.8	5524.0	4622.8
2270.9	2277.1	2709.3
22.6	24.0	22.2
5763.1	6341.2	8903.8
3273.0	4387.6	3908.2
3149.1	4080.2	2618.1
4073.9	4399.2	3555.5
5553.0	5452.7	5516.3
1958.8	2945.5	2175.7
1803.7	2194.1	2554.7
1072.6	579.1	1005.6
373.7	573.8	926.6
2183.9	1794.8	2667.4
497.7	708.8	607.2
1425.8	2282.3	2112.1
4116.9	2880.8	4163.7
3016.4	2208.1	2721.5
2055.8	1099.9	1959.6
3443.2	4072.4	3440.1
1280.4	843.3	1385.3
1003.3	1320.5	665.9
1006.1	1707.3	1824.3
6006.2	6815.5	5836.5
2430.6	1275.4	2092.8
4321.3	5867.4	6201.6
1787.3	900.6	1041.6
3320.0	2113.0	2286.6

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AB494826.1 gg_id:541394 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
DQ804535.1 gg_id:185497 human fecal clone RL187_aao69d05 DQ804
EU773555.1 gg_id:331026 Goeldi's Marmoset feces clone CAL_b10 EU7735
FJ372060.1 gg_id:359030 feces adult twins and mothers; TS9 clone TS9_a01c11 FJ3720
FJ685170.1 gg_id:514222 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EU468709.1 gg_id:301510 okapi feces clone OK2_b10_1 EU4687
EU504227.1 gg_id:270304 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04f02 EU5042
EU455142.1 gg_id:329968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4551
EU776077.1 gg_id:324236 Spotted hyena feces clone HY2_e05_2 EU7760
FJ366998.1 gg_id:360962 feces adult twins and mothers; TS28 clone TS28_a02c05 FJ3669
EF402522.1 gg_id:212503 human fecal clone SJTU_B_09_07 EF4025
DQ809709.1 gg_id:179228 human fecal clone RL184_aan83a07 DQ809
EU842695.1 gg_id:327336 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
EF098880.1 gg_id:180762 mouse cecum clone SWPT1_aaa02e11 EF0988
AY916257.1 gg_id:112783 human rectum biopsy clone E024 AY9162
AY982764.1 gg_id:117348 human descending colon mucosal biopsy clone KY95 AY9827
FJ879404.1 gg_id:393396 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
FJ880637.1 gg_id:430724 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EU457036.1 gg_id:347908 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4570
EF099497.1 gg_id:187234 mouse cecum clone SWPT3_aaa04a03 EF0994
EU474350.1 gg_id:298395 western lowland gorilla feces clone GORSD_aaa03f05 EU4743
EF099720.1 gg_id:178173 mouse cecum clone SWPT4_aaa03d09 EF0997
DQ823850.1 gg_id:182653 human fecal clone RL250_aaj79h07 DQ823
EU462890.1 gg_id:290502 southern three-banded armadillo feces clone arma_aaj54e11 EU4628
FJ879324.1 gg_id:420244 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
DQ795542.1 gg_id:197996 human fecal clone RL178_aan65h09 DQ795
FJ681380.1 gg_id:532377 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ534957.1 gg_id:578649 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5349
EU454243.1 gg_id:325636 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4542
GQ451310.1 gg_id:584137 Fecal Yunnan snub-nosed monkey feces clone J328 GQ451
EU344239.1 gg_id:271586 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
EU766938.1 gg_id:345367 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7669
EU503840.1 gg_id:261277 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01d04 EU5038
AY985158.1 gg_id:123338 human stool clone BB82 AY9851
NZ_AAVL02000015.1 gg_id:470392 Eubacterium ventriosum str. ATCC 27560 NZ_AA
AY977923.1 gg_id:126385 human cecum mucosal biopsy clone LG38 AY9779
EU504089.1 gg_id:268080 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01b01 EU5040
DQ802226.1 gg_id:184577 human fecal clone RL241_aaj04g04 DQ802
FJ364071.1 gg_id:360291 feces adult twins and mothers; TS150 clone TS150_a02f06 FJ3640
EU467357.1 gg_id:294041 chimpanzee feces clone CHIMP12_c10 EU4673
FJ679672.1 gg_id:530383 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796

826.7	5153.2	6613.3	5782.0	4602.7	4557.2	5213.6	5271.3	4897.4	4182.7	4294.6
538.4	2177.0	2265.6	1699.5	2237.9	2011.5	2680.4	1943.9	2458.0	1242.1	1854.4
125.1	449.5	903.3	520.9	900.8	589.7	1094.5	665.5	234.7	144.7	295.6
7940.3	3732.7	4140.2	4160.4	3700.2	3739.5	3737.6	4650.1	6840.6	5011.5	4993.4
2536.7	3369.1	2907.7	2456.6	2411.8	2494.5	3109.7	2457.8	2373.1	3730.5	2144.8
9322.5	3809.2	3638.6	3516.3	3172.8	3958.9	4172.4	3554.0	5226.4	4498.5	3571.1
36.8	628.0	706.5	803.7	608.7	459.6	529.0	549.3	391.8	180.5	505.1
740.2	1969.8	2489.7	1803.8	1068.4	1961.6	1116.7	2585.7	637.7	2468.3	1830.9
1012.1	2741.2	3277.9	3358.9	2415.0	2856.3	3543.5	3348.0	2623.1	1161.1	2671.7
1292.3	733.4	769.5	1026.6	1120.3	932.6	775.2	842.6	581.9	594.3	640.8
1564.0	2677.2	3747.1	4564.5	3073.4	2968.9	2492.8	3080.1	2248.9	2109.9	2488.5
4668.3	1120.2	1454.3	1502.1	1456.0	1766.0	1953.2	2338.2	1356.4	814.4	1014.0
4599.0	5228.0	5803.5	5504.1	6164.3	6285.1	5105.1	6777.8	7110.5	6551.3	6605.9
59.0	579.9	1094.2	1390.0	324.1	599.3	428.7	1077.1	245.8	110.2	683.6
8802.6	3408.0	3117.2	3569.3	3725.7	3462.8	3132.4	4324.2	4390.7	3440.8	6495.5
2370.1	740.6	1070.1	824.4	808.2	817.7	691.0	965.0	843.7	751.7	939.1
52.3	450.1	971.4	1115.2	132.4	386.1	242.7	696.5	106.1	103.7	288.4
11963.3	4867.4	4737.5	4526.8	3689.4	3966.7	4182.4	4293.3	4676.9	4649.1	4363.1
85.8	850.0	1528.8	1332.6	656.7	1069.8	819.9	1571.6	809.9	530.4	780.7
30422.7	10552.6	10011.4	11346.4	11165.1	9228.4	12456.0	10118.9	13938.9	11095.9	14783.7
58.8	48.1	56.5	71.6	57.3	35.9	148.8	44.4	29.6	18.6	30.0
26.7	667.6	1470.3	1307.2	410.6	677.8	858.6	1159.2	288.0	69.8	553.8
44.7	262.9	354.6	382.7	153.7	167.6	184.3	231.4	115.8	76.8	180.5
30.7	617.8	1137.6	1264.5	329.9	823.3	493.6	1321.6	207.6	122.3	492.7
935.0	3696.7	3657.4	4098.7	3520.2	3909.6	3250.7	3350.9	4584.2	4467.4	4544.4
5774.2	2164.8	2299.8	1979.7	1099.5	2305.4	2160.2	2149.8	3408.5	3013.6	3029.4
2654.7	2741.9	3503.4	3529.1	3700.8	2551.1	4120.3	3729.9	4483.0	1618.9	2848.6
77.9	1411.5	2190.2	2418.8	867.0	1377.0	1689.6	1921.2	553.9	295.6	1187.2
247.8	2181.3	3732.6	2788.8	2344.4	2265.0	2463.5	2717.2	2859.6	1724.2	2379.8
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61.4	1432.2	2307.3	2685.2	814.1	1564.7	1317.9	2555.9	488.9	312.2	1699.1
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69.5	1248.0	1632.9	1888.4	1377.6	978.0	1325.2	1382.9	820.8	356.0	701.3
3113.1	3721.3	3746.9	3839.1	3061.4	3233.0	3414.4	3634.3	3569.6	2916.6	3445.6
54.9	79.8	115.3	105.7	195.5	70.0	217.8	85.1	25.5	28.2	39.6
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6491.4	3660.5	4559.5	4610.5	4552.5	3820.6	4037.2	4340.4	3255.7	3749.8	3949.7
47.7	575.2	764.7	871.3	1258.6	614.4	886.2	616.7	107.5	80.8	197.8
73.2	802.1	1372.6	578.7	283.6	730.4	357.5	804.1	548.9	861.8	574.4
169.9	1270.6	116.9	1520.1	1445.7	1575.4	784.5	1246.8	1210.1	742.8	833.2
2135.2	2639.1	2480.2	3030.8	2089.2	2253.6	2211.8	2316.5	3301.4	2077.1	2346.1

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2025.0	1820.9	2310.7
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3898.7	5241.7	4441.7
2288.8	3260.8	4359.5
3650.3	4767.8	4337.0
431.2	987.2	501.4
2554.8	2823.4	3547.1
3181.6	3146.5	5000.2
881.7	1174.4	852.5
3428.5	3708.7	2556.1
3186.3	2016.8	3379.5
5610.9	6071.8	5989.2
1273.5	687.9	1754.7
3573.8	3970.3	3939.6
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856.7	644.2	441.9
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1581.1	1811.0	1972.7
10567.8	10534.4	11364.0
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1028.9	791.8	953.0
2956.0	3427.4	4936.7
1581.5	2967.9	1600.0
4073.6	3286.4	5235.0
1808.1	1855.1	2376.9
3174.3	2943.9	5265.2
4475.6	3316.1	4672.4
3126.7	1719.7	2694.8
2361.6	2481.7	3146.4
1398.2	2149.2	2313.4
3405.7	3693.0	3420.3
56.6	90.2	63.6
123.9	190.1	122.6
4734.4	6044.9	4913.4
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GU269550.1 gg_id:554176 Eubacterium uniforme str. X3C39 GU269
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AM697093.1 gg_id:222849 sequencing libraries indoor dust clone BF0002B043 AM697
EU462978.1 gg_id:298904 southern three-banded armadillo feces clone arma_aaj56a06 EU462
EU842359.1 gg_id:327905 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ015646.1 gg_id:130175 mouse cecum clone M3_f03_2 DQ015
EU509051.1 gg_id:268982 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42f08 EU509
DQ795297.1 gg_id:179333 human fecal clone RL178_aah52f06 DQ795
EU778846.1 gg_id:307536 Black-handed Spider Monkey feces clone SPIM_aaj35e06 EU778
DQ815716.1 gg_id:163512 mouse cecum clone aab21d04 DQ815
EU471878.1 gg_id:300250 Asiatic elephant feces clone AE3_aaa04c05 EU471
AB189704.1 gg_id:113709 alkaline-enriched termite gut homogenate clone Pl-10e-23 AB189
DQ808148.1 gg_id:190954 human fecal clone RL180_aao73c03 DQ808
DQ795170.1 gg_id:177111 human fecal clone RL178_aah51a09 DQ795
FJ879504.1 gg_id:384843 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU454004.1 gg_id:319241 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU454
DQ796523.1 gg_id:175978 human fecal clone RL179aan74a10 DQ796
EU104043.1 gg_id:330750 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ680896.1 gg_id:519636 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
GQ458226.1 gg_id:570367 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
EU461336.1 gg_id:292387 red kangaroo feces clone KO2_aai17g02 EU461
AF371590.1 gg_id:42492 swine intestine clone p-228-o5 AF371
EU468485.1 gg_id:301058 okapi feces clone OK1_g03 EU468
GQ449180.1 gg_id:584396 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ449
FJ369574.1 gg_id:360851 feces adult twins and mothers; TS51 clone TS51_a02b09 FJ3695
AY978112.1 gg_id:122693 human cecum mucosal biopsy clone LI81 AY978
AY854367.1 gg_id:110168 herbivore gastrointestinal tract clone Thompsons93 AY854
AF371577.1 gg_id:69988 swine intestine clone p-386-o3 AF371
EU475501.1 gg_id:301156 springbok feces clone SBSD_aaa01f12 EU475
DQ824228.1 gg_id:181843 human fecal clone RL304_aal73b10 DQ824
EU764199.1 gg_id:314290 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
EF405404.1 gg_id:213236 human fecal clone SJTU_G_01_39 EF4054
DQ673494.1 gg_id:169584 rumen fluid clone GRC29 DQ673
AY978565.1 gg_id:116993 human transverse colon mucosal biopsy clone KR31 AY978
EF403815.1 gg_id:215738 human fecal clone SJTU_A2_03_12 EF4038
FJ879683.1 gg_id:397857 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
ABOU02000049.1 gg_id:329241 Ruminococcus lactaris str. ATCC 29176 ABOU0
EF614791.1 gg_id:232247 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
AY977164.1 gg_id:125656 human cecum mucosal biopsy clone MS39 AY977
DQ796824.1 gg_id:184472 human fecal clone RL179_aao55a08 DQ796
FJ879430.1 gg_id:387084 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794

227.7	636.6	1267.5	904.5	413.1	740.7	622.3	1378.8	317.0	201.4	498.6
60.3	613.2	1034.3	1145.9	153.3	315.7	411.6	754.7	61.1	58.5	260.5
51.5	1204.9	2030.3	1907.8	548.1	1440.4	597.4	2183.4	338.0	542.3	1676.1
475.6	770.9	1474.2	1804.7	1175.3	939.1	1450.3	1188.2	397.8	178.1	935.7
54.0	287.2	528.4	710.3	229.5	338.3	316.4	514.3	166.2	82.8	340.4
2340.6	3419.8	2614.7	3298.3	2246.1	2526.8	2837.7	2802.0	3041.8	3417.6	3091.6
59.3	923.4	1485.6	1926.4	780.3	900.5	906.8	1574.6	297.5	173.7	824.8
1622.0	1699.7	1545.9	534.4	1119.8	1378.4	1429.1	1677.4	2068.7	1770.3	1461.8
49.9	268.2	521.0	706.9	633.1	195.0	324.0	259.8	68.0	71.8	107.2
3310.1	1944.7	2161.5	2209.2	1404.3	1693.5	1628.8	1862.8	1410.1	1510.2	1263.9
183.0	1372.4	1896.0	2110.0	768.8	1163.0	1576.0	1891.9	666.5	310.1	1180.5
49.6	1089.1	2136.2	1921.2	970.0	1346.1	934.1	1595.4	525.4	145.2	1044.7
38.7	56.5	121.1	103.0	82.7	56.3	111.3	103.1	25.1	23.1	67.3
89.5	1286.2	1465.0	2104.8	1965.3	1585.5	2015.1	2064.0	633.7	601.0	845.6
52.7	423.2	874.0	940.3	177.9	483.7	296.5	795.3	182.4	65.9	365.2
169.7	1805.9	2032.0	1674.7	1081.0	1350.3	1212.8	1859.2	1676.0	1320.4	1542.3
40.5	1151.8	1370.7	1400.4	1384.0	1306.4	1550.7	1329.5	712.0	326.5	1185.2
244.5	4829.0	5676.5	6168.8	4283.3	5190.8	4746.7	6350.3	3401.2	1863.2	6223.3
9637.7	6178.8	7015.3	7249.9	6015.0	6229.4	7177.9	6335.3	7303.0	6491.9	9580.9
34.4	824.5	1050.1	1365.1	121.7	585.4	371.7	1164.9	181.5	132.8	691.2
56.1	1491.3	1694.7	1782.7	1785.7	1364.7	2059.1	2293.4	639.1	556.9	719.6
47.2	41.9	76.5	66.3	80.3	54.2	71.9	45.8	26.8	16.9	39.8
908.8	2742.4	3226.2	3567.0	2743.6	2805.2	2857.0	3109.1	2308.9	3545.4	3107.1
158.2	1204.1	1622.7	1551.4	1139.9	1434.2	1619.7	2549.0	596.2	292.6	808.8
12673.5	9476.4	7407.7	9755.7	9439.2	8957.2	10231.2	7860.6	12468.9	10592.0	13021.5
51.3	968.1	1729.2	1135.6	453.7	1094.8	604.0	2022.8	545.1	181.3	1132.9
5259.6	2983.1	3420.8	1987.1	2446.2	2620.5	2389.9	3252.4	3259.7	2936.2	2723.8
1122.8	1040.8	1069.0	1284.0	1153.9	1155.1	1067.0	1224.9	595.8	729.4	702.4
42.1	687.3	864.5	1355.4	182.2	821.4	354.7	1248.8	163.2	168.0	322.3
676.2	4206.7	5297.2	5284.8	4101.1	4527.0	7678.9	4723.3	4817.9	3799.8	5536.1
44.8	458.7	696.2	685.5	383.5	644.0	546.3	1294.7	149.1	257.8	364.7
95.1	1159.2	2242.6	2003.9	1100.5	1523.3	2107.0	1674.6	608.7	217.5	1641.7
112.2	387.7	732.9	824.4	275.5	423.6	350.2	671.6	625.3	107.7	421.2
544.7	3031.2	3585.1	2996.3	2582.2	2679.9	3067.9	3142.9	4191.5	2891.8	4600.0
160.7	593.6	633.9	695.9	513.9	608.9	697.7	828.1	284.7	276.6	397.8
55.2	549.8	1053.9	1099.6	291.1	383.8	354.6	696.4	117.3	193.1	238.1
46.6	393.5	736.2	686.9	145.6	464.0	659.5	463.6	149.5	31.8	322.8
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14929.6	5586.7	4852.4	5321.3	4012.2	4520.9	4599.2	4214.2	5917.8	5487.3	4905.1
32.6	328.6	714.4	778.8	80.9	139.9	150.4	277.4	27.0	15.3	73.2
4712.8	2740.5	3326.7	3061.3	2358.0	2453.3	2808.9	2889.2	2966.0	2349.9	2360.8

1653.8	830.1	1731.2
899.6	595.3	640.3
2747.9	1271.8	1940.4
1124.9	1453.9	1972.5
647.5	420.7	527.2
2481.4	3291.3	3122.4
2533.1	1022.5	1575.3
1665.3	1928.2	1400.0
569.5	378.6	785.3
2150.1	2441.7	1815.4
1823.4	1664.5	2652.2
1638.6	1473.6	1577.9
45.0	110.4	140.5
2476.2	1555.6	2814.4
800.3	730.4	839.2
1655.9	1990.6	2205.7
1631.7	1271.7	1687.4
6572.8	5198.9	6198.4
6633.0	6894.2	5914.1
1073.4	754.4	570.0
3255.2	1355.8	4750.5
43.9	103.3	72.0
3230.3	3358.5	3967.7
2472.7	939.6	2124.0
9038.5	9726.1	8414.5
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2572.4	3150.4	3376.2
1128.3	1399.9	1230.4
1551.0	811.1	1071.7
4783.4	5017.4	6095.6
1813.1	826.4	1308.9
1114.7	1313.7	1939.8
437.9	755.7	720.5
2855.7	3499.7	2588.4
703.8	1069.2	881.9
1042.8	982.4	487.1
289.7	193.4	361.2
2393.7	4195.5	4343.5
4528.3	3972.4	4055.1
564.8	510.0	595.7
3049.2	3438.4	3047.3

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DQ795275.1 gg_id:179563 human fecal clone RL178_aah52d04 DQ795
DQ794948.1 gg_id:193833 human fecal clone RL310_aam38c09 DQ794
EU457579.1 gg_id:329555 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
EU456496.1 gg_id:304607 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU456
FJ880297.1 gg_id:409686 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU474332.1 gg_id:292386 western lowland gorilla feces clone GORSD_aaa03c11 EU474
GQ493316.1 gg_id:545025 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ492842.1 gg_id:568186 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ364456.1 gg_id:364861 feces adult twins and mothers; TS15 clone TS15_a03b09 FJ3644
DQ796395.1 gg_id:189819 human fecal clone RL179_aah26f09 DQ796
GQ493872.1 gg_id:547852 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU460145.1 gg_id:294491 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU460
EU775154.1 gg_id:303502 Francois Langur feces clone FL_1aaa03a07 EU775
EU845368.1 gg_id:304394 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EF096845.1 gg_id:197765 mouse cecum clone SWPT13_aaa01f02 EF0968
AY985707.1 gg_id:126405 human stool clone C728 AY985
EF402585.1 gg_id:208154 human fecal clone SJTU_B_09_84 EF4025
GQ897228.1 gg_id:563056 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ492934.1 gg_id:535640 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ801473.1 gg_id:175987 human fecal clone RL388_aao96a03 DQ801
GU174117.1 gg_id:567011 Microbial Bactrian camel estimated rumen clone XJC97 GU174
EU764770.1 gg_id:340567 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU763008.1 gg_id:303930 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ372260.1 gg_id:360965 feces adult twins and mothers; TS9 clone TS9_a03e09 FJ3722
EF640147.1 gg_id:248923 pig feces clone lcy22 EF6401
DQ794444.1 gg_id:192127 human fecal clone RL197_aah87g12 DQ794
NZ_ABWN01000012.1 gg_id:469890 Butyrivibrio crossotus str. DSM 2876 NZ_AB
DQ794722.1 gg_id:181041 human fecal clone RL240_aaj31e11 DQ794
DQ238618.1 gg_id:144395 Effect daidzein on piglets piglet gastrointestinal tract clone 1 DQ238
AB270022.1 gg_id:162110 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
GQ492433.1 gg_id:571748 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU468256.1 gg_id:293542 domesticated horse feces clone horsej_c12_1 EU468
DQ793269.1 gg_id:195777 human fecal clone RL199_aaj41e08 DQ793
EU763093.1 gg_id:343283 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
DQ805756.1 gg_id:179905 human fecal clone RL306aal90f08 DQ805
AM696759.1 gg_id:223303 sequencing libraries indoor dust clone BF0001A046 AM696
EU765093.1 gg_id:353263 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU844548.1 gg_id:340280 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ371396.1 gg_id:359178 feces adult twins and mothers; TS6 clone TS6_a04d11 FJ3713
EF404326.1 gg_id:211540 human fecal clone SJTU_C_08_40 EF4043
DQ794863.1 gg_id:189600 human fecal clone RL310_aam37c05 DQ794

48.6	23.9	20.2	28.0	27.7	22.4	21.9	24.2	22.0	23.0	22.7
1350.1	954.7	1245.3	1272.7	950.8	1353.9	1088.7	1549.8	1272.8	278.8	876.2
416.9	1250.6	1323.3	1464.9	852.9	1023.2	1118.9	1250.8	874.7	813.7	747.4
201.8	945.8	1506.4	1705.2	846.2	537.3	1024.5	1533.8	1318.0	212.1	1164.7
439.4	978.6	1476.3	1812.5	1469.6	1004.5	1294.2	1394.5	588.8	959.8	1118.3
76.5	548.7	667.7	898.0	400.1	424.1	557.3	535.4	197.6	83.6	364.7
178.2	673.1	1509.0	1127.6	1159.0	1070.6	1087.7	1251.2	672.3	1419.2	836.0
252.3	2047.3	2581.0	2228.3	1696.0	2243.4	1936.4	2664.5	2424.2	1534.2	1892.2
27435.1	9253.2	8685.5	10895.9	9310.1	7944.8	12113.6	7673.5	13595.5	12975.4	13151.3
3773.1	2906.9	2993.8	1688.4	3454.1	3004.1	3590.5	3155.0	3588.8	3015.0	4777.9
546.6	2253.8	3101.2	3364.7	2589.0	1865.9	2518.2	2630.7	1039.9	1328.8	1843.8
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769.9	2060.9	2957.8	2975.3	1385.2	1915.4	1965.9	2279.6	890.2	694.7	1318.3
37.9	800.2	1048.1	1190.6	218.4	449.5	176.7	2200.6	108.8	174.9	615.3
1113.2	439.1	548.7	528.4	527.1	436.1	465.3	502.9	304.3	287.8	379.0
14297.4	7891.8	7534.3	9684.9	8042.4	7028.1	9877.3	6827.7	11025.9	9802.3	7824.3
147.8	722.1	986.2	1080.3	1152.9	583.4	1677.7	844.6	357.9	200.1	399.3
3306.6	2992.0	3384.3	4738.3	4086.3	3911.2	4242.6	3287.7	2588.0	5746.8	2823.8
6601.6	6907.6	6793.8	7031.7	7282.0	6447.7	6258.9	6620.6	7928.0	8661.3	7411.3
958.9	1848.4	2991.2	2360.2	2145.0	2053.4	2943.4	2603.9	2586.8	2790.3	2796.4
64.7	743.4	802.6	1003.8	669.9	630.5	1174.4	1192.2	489.7	269.8	513.8
1938.6	1444.8	1813.3	1857.8	1341.8	1461.9	1332.3	2384.9	1066.3	468.2	1421.6
1377.7	1614.8	1452.0	1592.5	1257.1	1249.5	1249.1	1992.8	929.9	847.2	839.5
64.1	549.2	1275.0	978.3	301.0	603.7	461.1	941.3	308.1	132.2	666.7
233.3	2314.9	2347.7	2842.1	3447.9	2681.7	3611.4	2861.9	1396.9	832.8	1794.1
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40.4	28.3	62.3	45.5	40.3	30.0	34.6	38.0	26.8	26.6	36.2
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41.7	61.6	89.2	117.6	34.3	62.4	21.8	195.1	26.2	18.6	31.6
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735.7	3387.6	3586.1	3425.3	2789.7	3500.8	3494.1	4425.8	3580.1	3343.5	3579.9
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30.9	118.2	247.7	288.6	182.5	120.7	351.1	201.3	32.9	35.5	71.6
105.0	1437.7	1868.6	1891.7	1589.2	1231.1	1060.1	2303.9	1359.2	279.6	1125.7
45.3	80.4	207.0	177.8	43.1	94.9	66.6	172.4	40.3	38.1	55.3
220.8	849.1	1294.2	1062.7	1301.5	976.9	1489.3	1237.4	661.7	1030.9	880.7
28.6	994.2	1768.2	2244.3	252.0	627.7	379.3	1329.3	269.9	107.0	771.5
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7745.8	4165.8	3540.7	4475.5	3355.5	3778.7	4244.3	3623.9	5088.0	6116.7	6575.2
16170.4	6364.4	6899.5	8075.3	6811.0	6000.6	7339.8	6939.1	6455.3	5163.3	8318.7
10435.3	5178.3	4772.9	5107.1	3702.7	3744.0	3970.3	3259.2	3994.1	4358.5	4592.5

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1225.6	1286.6	1582.0
1681.0	1959.3	1783.2
1501.0	1476.4	1350.6
758.6	584.2	802.8
1163.3	1236.3	1954.5
3181.2	3085.9	2893.8
7694.4	9622.9	8500.7
2950.1	3525.8	3257.0
3045.6	2808.0	4122.1
2063.0	1597.4	2254.5
2678.1	2416.4	3802.1
1435.3	723.1	581.0
418.6	958.0	466.0
6864.9	7463.1	7717.8
553.6	806.8	1369.1
5380.1	4493.3	3935.0
6166.5	7615.1	7612.2
2312.4	3369.4	2534.5
866.7	996.3	1226.2
1883.6	2029.2	1965.2
2976.6	1712.9	1646.2
842.6	1111.0	900.0
2586.2	2420.6	3820.8
908.6	1077.9	840.5
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105.7	96.3	51.4
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2221.9	1999.6	2049.5
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2130.2	2112.9	3028.7
295.3	106.1	73.3
1004.7	1011.6	1800.6
1381.9	1079.4	1099.7
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o__Clostridiales	f__Lachnospiraceae
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EU463610.1 gg_id:301233 domesticated horse feces clone horsej_aai89g01 EU463
DQ804158.1 gg_id:191714 human fecal clone RL187_aah69d12 DQ804
DQ795164.1 gg_id:187782 human fecal clone RL310_aam40h12 DQ795
EU762952.1 gg_id:348169 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU471977.1 gg_id:301388 francois langur feces clone FL_1aaa04a10 EU471
FJ679710.1 gg_id:526071 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
AJ409005.1 gg_id:24781 human colonic clone HuCB40 AJ409
EU764765.1 gg_id:327131 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU764
DQ806689.1 gg_id:195805 human fecal clone RL186_aao47f01 DQ806
EU504017.1 gg_id:261336 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04b01 EU504
DQ801110.1 gg_id:193230 human fecal clone RL387_aao92d01 DQ801
EU456575.1 gg_id:332340 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
FJ367597.1 gg_id:361213 feces adult twins and mothers; TS2 clone TS2_a01d05 FJ3675
EU530233.1 gg_id:262722 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ade EU530
DQ800976.1 gg_id:188512 human fecal clone RL387_aao90c01 DQ800
EU765965.1 gg_id:311303 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
EU462891.1 gg_id:294487 southern three-banded armadillo feces clone arma_aaj54e12 EU462
DQ798871.1 gg_id:190477 human fecal clone RL242_aaj98d11 DQ798
DQ799606.1 gg_id:192915 human fecal clone RL305aal88b12 DQ799
AY985782.1 gg_id:116743 human stool clone D026 AY985
DQ806051.1 gg_id:193217 human fecal clone RL186_aah60e03 DQ806
GQ493445.1 gg_id:546052 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AB494755.1 gg_id:547665 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
AB494779.1 gg_id:579311 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EF404061.1 gg_id:213816 human fecal clone SJTU_C_04_19 EF404
FJ368330.1 gg_id:361635 feces adult twins and mothers; TS3 clone TS3_a03a08 FJ3683
FJ372168.1 gg_id:367125 feces adult twins and mothers; TS9 clone TS9_a02e06 FJ3721
FJ833467.1 gg_id:510062 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_55G07 FJ8334
EU766528.1 gg_id:316083 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
EF403438.1 gg_id:211181 human fecal clone SJTU_A2_01_21 EF4034
EF402531.1 gg_id:215047 human fecal clone SJTU_B_09_16 EF4025
EU381610.1 gg_id:264313 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU458460.1 gg_id:291414 spotted hyena feces clone HY2_a01 EU458
EU344729.1 gg_id:261203 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU776091.1 gg_id:305313 Spotted hyena feces clone HY1_g06_1 EU776
DQ801360.1 gg_id:199664 human fecal clone RL388_aao94e02 DQ801
EF403976.1 gg_id:204178 human fecal clone SJTU_C_03_11 EF4039
EU772690.1 gg_id:321253 Bush dog feces clone bdog1_aai79a04 EU772
EU463034.1 gg_id:294961 southern three-banded armadillo feces clone arma_aaj56g08 EU463
FJ672959.1 gg_id:515271 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ372102.1 gg_id:366666 feces adult twins and mothers; TS9 clone TS9_a01g07 FJ3721

186.8	1714.7	2039.5	2369.3	815.8	1455.2	1685.2	2652.9	593.8	322.8	1866.1
40.1	310.2	555.9	627.9	253.0	268.7	221.2	408.4	111.5	49.3	114.7
41.9	70.1	65.6	63.4	69.8	65.6	47.9	68.0	41.4	45.7	38.3
2109.3	5508.8	5293.0	4873.5	3958.2	4204.4	4421.8	5323.5	5477.0	3529.0	5575.7
900.2	2989.0	3841.0	3860.0	2331.6	2862.8	2695.8	3203.8	1245.3	1965.3	2048.8
409.3	482.1	628.5	724.3	862.1	465.6	293.3	681.6	89.7	94.3	202.7
95.7	701.9	947.4	1289.5	700.5	706.6	597.7	903.2	472.3	150.0	672.3
13129.5	5506.3	5294.4	5398.7	5338.7	5184.0	6652.8	5027.6	6319.2	7227.2	6349.8
38.7	27.5	52.8	65.4	21.6	13.3	21.8	24.8	17.1	12.9	23.0
55.7	428.1	626.3	714.9	257.0	386.4	357.0	580.3	107.8	90.1	218.4
44.8	129.7	497.1	159.1	85.6	274.6	68.1	601.9	251.5	36.2	247.4
80.4	1303.1	1793.0	1843.6	1722.6	1351.0	1535.8	1783.6	681.5	347.9	919.8
7488.5	1737.6	1458.8	2110.9	2532.3	1676.5	1937.7	1712.0	2572.4	1789.0	2535.5
2283.8	2117.6	3328.5	3016.1	1100.0	1969.9	1949.4	2831.0	1477.4	1036.7	2221.6
417.9	2335.6	2735.1	2822.7	1021.4	1538.4	1459.9	1772.1	2305.0	3174.4	2710.0
5391.1	5866.0	6300.6	6201.3	5211.5	4976.5	6777.8	5168.3	5353.1	4033.9	6812.3
3355.3	1209.0	1399.4	1530.2	880.5	1365.4	1263.0	1451.2	1497.3	2149.1	1179.0
31.6	230.8	316.9	271.7	112.0	152.9	191.7	297.7	84.1	25.5	95.9
9625.1	1472.3	1737.2	1964.9	1959.1	1577.8	1920.0	1882.7	1763.4	1416.9	1870.0
25.2	1520.1	2138.8	2276.9	517.5	1274.0	997.3	2332.2	555.4	287.6	1247.0
5083.4	6512.6	5691.8	5363.2	5547.0	5588.0	4920.8	5239.8	9064.2	9332.3	7019.8
3334.9	5592.4	5308.5	4958.6	4551.6	5221.1	5078.3	4543.1	6132.7	5466.6	6121.8
10610.5	6807.4	8010.3	7860.7	5854.1	6778.1	8175.9	7802.4	8707.8	5657.5	9074.8
871.8	2448.8	3556.7	4449.9	1529.0	2066.8	2240.7	3395.7	1584.3	1315.6	2704.5
1443.5	1771.0	2203.9	3198.0	2533.0	1971.7	2887.9	1922.2	1157.7	796.2	1996.4
260.7	992.8	1425.9	1499.2	969.0	939.5	798.8	1242.4	701.3	534.3	853.0
14687.9	5187.8	3138.3	4767.9	5646.4	4564.8	5284.7	4441.9	8365.7	7532.6	5619.0
5942.5	3946.9	5163.7	6089.1	4488.5	4541.7	5238.8	5005.3	3745.5	2234.5	5140.8
490.1	2160.4	2178.1	2207.1	2111.6	2415.8	2235.7	2863.8	2097.1	2974.9	2025.1
176.1	1064.1	1765.5	2248.6	1039.5	805.1	1075.9	1038.8	407.8	253.9	1077.5
1791.0	2835.9	2633.0	2950.2	3714.0	2964.8	4379.6	3306.1	2914.0	2883.1	2737.5
2995.7	1588.9	2912.1	2292.8	1967.6	2053.6	1691.4	2432.2	1172.5	1983.9	1423.8
82.9	1245.6	1779.7	1908.7	638.7	1308.1	1224.8	1747.6	466.1	163.4	944.3
269.9	1513.2	2224.7	2479.4	953.8	1574.8	1555.6	2458.4	592.1	387.6	1228.1
66.7	355.0	403.2	347.4	584.0	333.3	407.6	339.7	171.8	88.0	243.8
1244.1	3043.4	3783.1	3996.7	3874.1	3135.2	4644.7	3061.6	1989.9	2335.5	2797.6
906.0	1292.6	1352.5	2075.1	1275.1	903.4	1533.7	1772.0	689.3	313.0	971.8
48.5	405.1	749.5	571.5	346.5	485.1	489.0	539.0	123.5	127.6	311.5
46.1	65.4	124.1	113.3	82.5	129.6	134.6	143.6	26.2	14.0	49.5
10791.9	3921.7	4885.9	4666.6	4159.9	3766.1	3857.0	4032.2	4948.8	2556.5	5968.2
1250.1	932.3	1698.5	1610.6	1199.1	1101.2	1004.2	1402.6	750.7	1614.2	833.7

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5572.7	4192.5	4603.4
3643.5	3425.6	4175.3
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780.0	836.2	992.3
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665.0	392.9	692.6
264.3	563.3	132.7
2235.3	1473.3	2047.9
1817.8	2086.1	1947.6
3309.1	3006.0	4196.8
1880.9	1881.5	2021.7
5658.4	5521.6	5285.2
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2105.1	2681.9	2371.4
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4831.6	7371.8	6840.9
4605.6	5446.9	5728.8
6739.0	7933.9	7525.6
3571.8	3043.4	3398.7
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1531.8	1394.8	1680.2
4535.0	6132.2	4613.9
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2000.9	3457.5	3173.3
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1233.4	928.2	1175.0
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EU764169.1 gg_id:313307 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
DQ805640.1 gg_id:187186 human fecal clone RL306aal89c08 DQ805
EU764896.1 gg_id:326551 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
DQ800186.1 gg_id:179739 human fecal clone RL303_aal69d04 DQ800
DQ807113.1 gg_id:193448 human fecal clone RL244_aaj46d10 DQ807
DQ800347.1 gg_id:194544 human fecal clone RL303_aal71h08 DQ800
FJ369646.1 gg_id:357203 feces adult twins and mothers; TS51 clone TS51_a03b06 FJ3696
EF686632.1 gg_id:236124 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
FJ676668.1 gg_id:517208 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
DQ798631.1 gg_id:187263 human fecal clone RL181_aan99c05 DQ798
FJ367334.1 gg_id:365800 feces adult twins and mothers; TS29 clone TS29_a02c07 FJ3673
EU465588.1 gg_id:294898 argali sheep feces clone AS1_aao38g05.Contig1 EU465
EU530260.1 gg_id:269131 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
EU464132.1 gg_id:301675 reticulated giraffe feces clone gir_aah94e03 EU464
EU766619.1 gg_id:312462 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU771550.1 gg_id:338071 Hamadryas Baboon feces clone AFBAB_aai03e10 EU771
DQ342330.1 gg_id:183867 Effect probiotics and synbiotics on gastrointestinal broilers broiler chicken intestine DQ342
EU762071.1 gg_id:308387 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
EU381927.1 gg_id:263820 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ793293.1 gg_id:178534 human fecal clone RL199_aaj41h03 DQ793
DQ809972.1 gg_id:182879 human fecal clone RL184_aao66e09 DQ809
AF371558.1 gg_id:36611 swine intestine clone p-3022-SwA5 AF371
DQ793638.1 gg_id:180227 human fecal clone RL246_aai74h02 DQ793
GQ502571.1 gg_id:590175 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU381592.1 gg_id:275820 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ676977.1 gg_id:531283 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
DQ797151.1 gg_id:196381 human fecal clone RL386_aao87f02 DQ797
FJ368198.1 gg_id:368834 feces adult twins and mothers; TS3 clone TS3_a01d05 FJ3681
EU471825.1 gg_id:290640 Asiatic elephant feces clone AE2_aaa01g09 EU471
EU462992.1 gg_id:294733 southern three-banded armadillo feces clone arma_aaj56c04 EU462
DQ801551.1 gg_id:188196 human fecal clone RL388_aao96h11 DQ801
AF371593.1 gg_id:68842 swine intestine clone p-4575-4Wb3 AF371
DQ326817.1 gg_id:150407 Metagenomic gut microbiome healthy human stool clone E290 DQ326
EU465902.1 gg_id:302429 African elephant feces clone AFEL3_aao13g05 EU465
FJ368441.1 gg_id:364589 feces adult twins and mothers; TS3 clone TS3_a04d05 FJ3684
GQ898745.1 gg_id:565505 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
DQ057383.1 gg_id:130103 chicken ileum/cecum clone cc186 DQ057
EU771866.1 gg_id:333067 Southern three-banded armadillo feces clone arma_aaj56e09 EU771
EU381536.1 gg_id:260158 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
DQ805270.1 gg_id:192488 human fecal clone RL249_aaj84b05 DQ805
EF402051.1 gg_id:203933 human fecal clone SJTU_B_02_93 EF402

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165.9	519.9	649.2	840.9	637.6	544.8	526.1	757.2	301.3	729.5	466.9
52.8	435.8	732.4	803.2	501.3	428.7	537.4	632.3	201.1	113.5	409.6
1152.8	1221.7	1794.9	1849.0	1316.3	1326.7	1518.8	1741.7	904.6	1543.3	1168.2
29.8	4.7	6.8	10.9	6.4	7.4	7.0	5.8	8.2	6.6	7.5
156.0	2421.1	3071.3	3020.8	2441.1	2621.3	3078.8	3222.7	2223.7	1212.1	3261.0
65.7	536.0	626.3	650.1	293.0	568.6	467.7	508.8	75.7	64.5	279.0
75.3	1691.5	2720.2	3641.2	1284.3	1298.1	1701.2	1624.2	915.5	334.5	938.2
273.7	527.8	950.6	1059.0	537.4	435.8	669.2	1152.3	394.3	33.9	746.0
129.0	664.0	806.9	1231.1	207.9	314.6	143.9	526.8	214.6	72.1	308.6
4899.5	1742.8	2070.9	2002.4	1823.3	1690.5	1215.7	1779.6	1639.9	1554.5	2307.2
1340.9	946.6	1174.1	1241.8	916.7	882.9	1109.5	1276.6	671.9	1193.8	744.8
27.3	2846.1	3751.1	2657.8	1423.6	2365.9	2253.2	3110.7	2335.5	1182.5	2657.8
1949.1	4425.6	5305.9	6022.2	3545.8	4438.6	4247.1	4266.7	2707.0	1813.8	4457.2
759.1	1155.3	1936.4	2054.8	1190.6	1237.5	2062.6	1580.7	670.0	2358.4	971.4
156.9	1316.7	1923.2	1812.4	1819.0	1753.7	1758.1	1886.0	387.9	332.3	766.5
33.5	658.3	679.3	795.4	65.4	151.8	128.7	609.5	54.6	46.2	57.4
42.6	1327.9	1623.2	1912.0	978.2	1175.3	908.3	1740.7	923.7	424.2	922.2
48.1	136.0	151.4	192.2	125.1	123.1	129.2	168.5	86.0	49.9	147.6
10586.6	2075.8	2301.9	2091.5	2630.4	2251.0	2774.3	2456.4	2460.2	2258.2	1897.0
28.4	56.3	139.9	162.8	42.7	50.1	42.1	109.8	24.6	22.9	47.3
33.8	241.2	389.0	308.5	149.4	234.4	191.8	274.6	73.4	54.8	161.1
36.0	710.5	1368.8	1177.3	1195.7	896.7	1209.8	1045.4	1356.8	1160.4	943.3
40.2	24.2	44.2	36.2	22.8	26.3	20.2	53.5	18.7	14.5	28.3
58.6	388.1	539.1	601.4	441.6	398.3	452.0	544.6	177.6	64.1	217.2
40.6	1891.0	3389.2	2481.9	788.5	1473.7	1050.8	2107.1	585.2	216.7	1733.9
2711.3	4841.0	4499.2	5009.8	4105.7	4295.4	4995.4	4465.4	8675.1	3711.7	4820.7
40.9	99.6	145.5	215.8	72.6	79.0	81.5	130.1	35.2	23.6	55.0
88.1	1345.5	2312.6	2566.2	1318.8	1782.4	1317.6	2145.3	752.3	482.4	1186.7
226.7	2733.4	2749.1	2177.5	1728.4	2682.4	1712.4	2070.2	2934.6	3373.5	1919.7
186.8	514.1	711.9	921.4	605.3	640.1	573.9	1029.9	356.9	191.7	567.9
46.2	163.7	96.0	191.8	109.6	162.0	109.9	179.0	42.1	21.5	62.4
26.8	246.3	749.4	614.7	122.1	348.1	161.3	326.1	121.7	46.8	144.4
47.7	1313.0	1469.8	1831.5	1657.2	1729.3	1768.9	1620.7	622.3	304.4	874.4
46.2	81.3	816.4	650.1	487.7	401.3	398.5	743.0	313.2	215.1	609.1
51.3	590.6	1018.6	851.1	737.7	641.3	921.0	715.2	345.4	241.7	756.8
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46.7	633.9	1046.9	898.7	533.5	700.4	803.0	754.7	309.3	88.1	476.3
34.2	353.7	558.9	183.4	516.2	280.4	675.7	388.3	115.0	73.1	239.4
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3987.6	4751.9	4629.8
721.2	715.4	954.1
473.0	715.3	767.3
1613.7	1651.6	1783.4
5.8	10.0	6.0
3082.9	2690.9	3626.9
577.6	450.3	540.0
2020.4	1769.4	1992.2
498.4	585.9	639.8
549.9	827.4	1097.8
1501.0	2263.8	1483.2
1210.4	1165.0	1435.8
2199.6	1735.4	3001.6
3747.2	4501.5	4323.8
1877.9	1503.4	1220.1
1472.2	1386.8	1958.2
968.1	358.3	278.2
1854.9	1502.0	1515.3
113.5	143.2	130.3
2383.7	2653.5	2570.2
108.0	98.1	164.4
392.4	403.5	362.5
1121.3	1348.1	1602.3
67.6	45.7	47.2
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1783.8	1852.6	1179.0
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106.6	155.5	104.0
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2243.5	2350.4	2160.8
927.6	997.6	928.2
108.3	225.9	254.3
276.7	385.8	422.6
1673.4	1940.9	1123.0
701.3	779.1	669.0
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FJ368247.1 gg_id:360519 feces adult twins and mothers; TS3 clone TS3_a02a04 FJ3682
FJ673138.1 gg_id:523606 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU843729.1 gg_id:327420 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU773511.1 gg_id:347200 Bonobo feces clone BNO_aaa02d08 EU773
FJ684021.1 gg_id:522696 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
FJ833395.1 gg_id:537491 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_45E06 FJ8333
DQ799462.1 gg_id:174709 human fecal clone RL305aal86e11 DQ799
DQ797183.1 gg_id:192513 human fecal clone RL386_aao88a10 DQ797
EF403388.1 gg_id:207390 human fecal clone SJTU_A1_7_6 EF4033
DQ800938.1 gg_id:180562 human fecal clone RL387_aao89f04 DQ800
EU771222.1 gg_id:317818 Asiatic elephant feces clone AE3_aaa01a12 EU771
EU771954.1 gg_id:337465 Southern three-banded armadillo feces clone arma_aaj54f04 EU771
DQ327113.1 gg_id:145966 Metagenomic gut microbiome healthy human stool clone E631 DQ327
EU381587.1 gg_id:268183 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU777129.1 gg_id:324917 Okapi feces clone OK1_g06 EU777
FJ832328.1 gg_id:509226 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_31G04 FJ8323
DQ801476.1 gg_id:178774 human fecal clone RL388_aao96a08 DQ801
FJ833622.1 gg_id:594255 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_11C02 FJ8336
EU850599.1 gg_id:328553 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF431 EU850
DQ804798.1 gg_id:185925 human fecal clone RL187_aao72g12 DQ804
GQ492365.1 gg_id:536336 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU462282.1 gg_id:293511 chimpanzee feces clone CHIMP1_aaj39b12 EU462
DQ673545.1 gg_id:166637 rumen fluid clone GRC80 DQ673
FJ681633.1 gg_id:513474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU762110.1 gg_id:323071 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
AY984165.1 gg_id:120309 human stool clone B049 AY984
FJ367874.1 gg_id:360592 feces adult twins and mothers; TS2 clone TS2_a04e11 FJ3678
FJ673360.1 gg_id:526301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ805079.1 gg_id:175959 human fecal clone RL385_aao84h09 DQ805
AB494795.1 gg_id:559499 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
EU844564.1 gg_id:333139 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AY979556.1 gg_id:124784 human transverse colon mucosal biopsy clone M217 AY979
EU457230.1 gg_id:308224 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
DQ803572.1 gg_id:183436 human fecal clone RL251_aaj87f01 DQ803
EU764773.1 gg_id:324574 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
FJ672986.1 gg_id:527972 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
EU474741.1 gg_id:289636 takin feces clone TAK_aaa01a05 EU474
EU777239.1 gg_id:350732 Okapi feces clone OK3_f07 EU777
DQ326920.1 gg_id:148694 Metagenomic gut microbiome healthy human stool clone E411 DQ326
EU843498.1 gg_id:330352 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ493359.1 gg_id:566623 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493

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67.2	898.5	1184.8	1375.9	601.0	801.2	1007.1	1101.7	282.7	199.4	568.3
383.1	2127.7	2434.0	3204.0	1228.0	1578.8	1593.8	1776.4	418.6	350.1	988.5
510.8	2391.9	2757.4	2868.4	1787.8	2122.6	2498.0	2459.4	2240.7	1642.0	2855.2
149.2	4191.7	5932.3	5927.0	2821.0	5142.0	3079.8	4992.4	3693.7	2417.0	5208.3
2591.3	3731.9	4223.6	6012.3	5803.4	3448.4	5583.4	3754.6	3499.7	1294.2	3504.2
4443.3	5697.5	6758.7	5963.9	6487.1	5407.0	6792.8	6402.9	5507.7	4129.7	7594.2
3681.5	2855.1	2839.1	3331.9	2683.5	2681.2	3496.1	2808.4	3445.1	3379.8	3129.8
4917.2	2047.5	2803.7	1384.1	3104.0	2749.0	2757.6	2983.8	1723.0	2639.2	2201.3
63.9	1018.5	1531.0	1926.3	789.8	1018.0	870.3	1953.9	450.4	458.6	1176.5
574.8	1191.7	1405.2	1641.5	714.7	1127.0	1194.9	1407.2	744.4	440.1	877.2
82.0	752.0	1312.2	1395.5	468.4	621.7	520.8	799.6	268.3	131.6	515.7
66.3	828.2	970.2	1350.6	630.5	783.8	1086.5	813.0	168.2	129.3	339.8
42.6	339.9	710.4	499.9	143.3	336.3	333.9	641.3	206.2	83.1	522.6
71.1	2775.9	3936.7	4246.7	1740.9	2670.6	1909.5	3236.2	1501.3	1775.7	2262.5
4315.6	3893.6	4285.7	4639.5	4724.7	3975.9	5236.8	4204.6	4219.9	4160.3	4708.9
239.4	1612.7	2439.3	2547.2	1258.7	1286.6	1392.9	2084.5	823.4	210.0	2451.1
46.4	692.7	889.7	1033.5	458.7	583.3	497.1	648.3	244.4	737.9	352.9
47.6	846.4	1146.3	1123.9	864.3	694.9	1037.4	1024.0	284.9	128.5	531.1
597.4	1609.6	1762.2	1723.6	1134.7	1630.1	1445.0	1924.1	1261.6	413.8	834.4
113.5	487.2	1003.3	676.6	500.1	487.0	663.6	752.3	223.7	284.0	488.0
131.4	918.4	1156.8	980.3	754.9	961.9	910.5	1475.7	549.3	213.3	1584.7
6150.0	1666.6	3781.4	4341.5	4109.7	2860.4	3282.9	3148.7	2824.8	1864.1	2742.8
308.1	3026.3	2738.8	3235.6	2395.0	2706.2	2948.4	3272.3	1630.8	1867.0	2382.1
209.6	566.5	965.4	1040.1	880.7	599.2	1047.6	720.2	248.5	1044.0	576.9
8667.6	3716.3	3586.8	3680.0	3065.7	3473.4	3387.8	4322.1	3605.8	3665.2	4920.2
1456.3	1438.2	1668.7	2060.9	1645.8	1397.7	2198.1	1425.0	1890.3	1743.0	1610.6
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95.6	1716.1	1038.7	676.1	650.4	914.4	600.7	582.6	1971.7	1506.8	698.9
1809.3	731.5	819.5	818.2	628.1	591.6	692.6	587.9	826.5	886.6	1242.5
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49.7	458.4	665.9	886.6	526.1	368.5	909.8	492.1	99.0	47.6	167.4
24.6	77.2	209.0	190.4	49.8	84.6	39.0	149.3	50.7	24.6	51.2
1901.3	2223.4	2122.4	2665.0	1637.6	1838.3	2497.7	2217.6	1442.0	999.3	1768.6
11906.1	3797.4	3472.7	3402.0	3267.7	2936.9	4545.6	2929.1	4925.1	2793.4	4523.6

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1369.5	1234.4	2599.0
2206.2	1425.3	2299.3
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4064.9	4064.1	5852.5
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2916.5	3892.6	2982.2
1788.5	1665.5	2367.2
1737.1	1610.4	1575.7
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624.0	703.0	840.1
1560.2	1053.7	1206.0
3270.9	4060.9	3722.2
3424.6	3296.2	5817.4
605.9	805.1	681.3
3802.3	4721.5	4931.1
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1901.2	2079.6	3402.6
820.5	449.0	489.1
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1592.0	1985.0	1884.6
557.1	783.0	691.0
690.6	1170.3	623.6
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4868.1	2642.3	4047.6
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AY858459.2 gg_id:110682 gastrointestinal tract zebra clone ZEBRA_20 AY8584
FJ370755.1 gg_id:368416 feces adult twins and mothers; TS57 clone TS57_a04h06 FJ3707
EU748068.1 gg_id:353775 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43g03 EU748
AM697398.1 gg_id:225076 sequencing libraries indoor dust clone BF0001D013 AM697
EU779441.1 gg_id:336542 Grevy's Zebra feces clone GZ_aaa03g03 EU779
GQ897199.1 gg_id:589713 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EF404929.1 gg_id:204981 human fecal clone SJTU_G_08_37 EF4049
EU779444.1 gg_id:336656 Grevy's Zebra feces clone GZ_aaa04b09 EU779
DQ326787.1 gg_id:149313 Metagenomic gut microbiome healthy human stool clone E254 DQ326
EU779344.1 gg_id:334956 Somali Wild Ass feces clone WA_aaa03a06 EU779
DQ796666.1 gg_id:184565 human fecal clone RL179aan76h06 DQ796
AB288925.1 gg_id:202310 termite gut homogenate clone BOf12-06 AB288
EU762975.1 gg_id:316156 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
AF371582.1 gg_id:29205 swine intestine clone p-57-a5 AF3715
AY985812.1 gg_id:116723 human stool clone D067 AY9858
DQ057364.1 gg_id:128392 chicken ileum/cecum clone cc110 DQ057
GQ493363.1 gg_id:564583 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
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EF403348.1 gg_id:211205 human fecal clone SJTU_A1_6_69 EF4033
EF404635.1 gg_id:214825 human fecal clone SJTU_C_13_82 EF4046
EU459681.1 gg_id:291997 ring-tailed lemur feces clone RT_aai10g06 EU459
FJ367841.1 gg_id:360727 feces adult twins and mothers; TS2 clone TS2_a04c01 FJ3678
DQ794467.1 gg_id:180911 human fecal clone RL197_aah88c06 DQ794
DQ800571.1 gg_id:195449 human fecal clone RL183_aah30a09 DQ800
EU461161.1 gg_id:291713 hamadryas baboon feces clone BAZ_aah89e06 EU461
DQ796881.1 gg_id:195675 human fecal clone RL179_aao55h07 DQ796
EU778721.1 gg_id:327266 Springbok feces clone SBSD_aaa03e05 EU778
EU462798.1 gg_id:289181 southern three-banded armadillo feces clone arma_aaj53c08 EU462
DQ815735.1 gg_id:172857 mouse cecum clone aab21f03 DQ815
DQ326745.1 gg_id:147644 Metagenomic gut microbiome healthy human stool clone E205 DQ326
FJ675975.1 gg_id:530740 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
DQ805223.1 gg_id:197121 human fecal clone RL249_aaj83c09 DQ805
EU452521.1 gg_id:320141 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
FJ363748.1 gg_id:366612 feces adult twins and mothers; TS14 clone TS14_a02g11 FJ3637
EU748519.1 gg_id:345339 neotropical folivorous flying bird adult hoatzin crop clone hoa61_11d02 EU748
DQ809238.1 gg_id:186237 human fecal clone RL308_aal83g11 DQ809
EU844853.1 gg_id:305726 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AF371573.1 gg_id:21881 swine intestine clone p-1616-c5 AF3715
GQ493531.1 gg_id:552681 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF436378.1 gg_id:207610 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC92 EF4363

129.8	428.7	640.6	655.2	521.5	347.7	494.3	616.4	218.5	64.8	356.7
305.4	923.5	1075.3	970.3	690.1	1023.7	581.8	1257.4	523.7	221.4	552.3
37.5	470.5	818.9	1107.2	311.6	391.3	307.4	828.6	75.0	105.3	199.7
1728.6	2580.1	3330.1	3670.7	1754.5	2438.1	2455.1	3260.7	1357.5	2213.5	2684.6
36.1	454.1	827.9	1241.8	367.2	380.5	446.4	971.4	135.5	72.7	417.7
12730.4	6287.6	6050.5	6575.7	7861.1	5811.3	6383.5	6433.0	9177.8	7428.1	8527.3
3567.9	1235.2	1342.4	1659.8	1046.2	1164.7	1085.6	1502.2	1092.6	1208.8	1865.2
1246.6	4672.3	5134.7	5919.2	6250.6	4862.0	6415.9	5608.4	2666.4	2506.6	3768.2
1673.7	1767.0	1907.0	2145.1	1663.0	1850.4	1932.4	1889.4	2087.3	1670.6	2047.9
29.4	257.5	34.9	215.4	145.9	294.6	176.7	476.8	167.1	64.1	228.8
31.3	419.7	868.3	927.3	270.1	322.5	275.6	476.1	169.4	93.6	204.8
1563.9	762.2	983.2	1379.4	786.8	893.5	689.9	1355.5	2085.7	361.5	541.7
41.9	36.8	39.8	33.5	37.3	26.3	26.7	25.9	16.8	23.2	25.8
15853.7	6809.2	5598.3	5821.0	4266.4	5312.3	4801.7	5477.6	6821.3	4727.8	7340.5
34.2	29.4	25.4	40.0	13.9	19.7	15.4	22.8	16.6	9.7	20.3
584.5	1092.0	1118.9	963.4	1071.8	896.5	906.4	1194.0	552.6	54.6	683.0
53.4	18.0	19.0	20.8	20.5	12.0	25.3	14.4	24.6	15.9	21.4
189.9	306.1	460.8	424.5	415.2	307.4	491.6	261.5	162.3	188.8	175.9
43.5	724.6	1171.9	973.5	693.1	884.6	476.5	1224.6	458.9	393.8	572.1
22.1	14.8	14.7	16.9	10.4	8.1	15.2	8.8	11.3	12.6	13.5
30.4	713.4	1226.6	1834.7	196.3	183.8	127.1	926.8	98.1	51.6	511.1
46.1	607.0	1064.3	1329.8	131.2	274.0	291.3	627.3	98.0	70.7	202.0
746.6	4448.7	5330.2	2293.9	1972.0	4034.0	1800.8	3971.1	5712.9	7128.0	3018.1
5154.3	792.1	1011.8	1065.5	656.0	1390.4	718.9	992.8	1029.9	576.0	1196.3
61.4	549.3	1003.7	809.9	721.4	666.4	750.6	937.9	260.6	959.6	441.8
558.6	2966.9	3595.5	4068.4	2134.8	2917.7	2560.7	3270.7	1250.4	707.2	2068.4
1135.3	1232.9	1463.6	1511.9	803.5	1327.1	1074.3	1723.5	485.3	809.7	1063.4
207.6	3231.6	2863.1	3516.4	4288.8	2812.7	3866.0	3405.6	1944.6	2250.7	1869.6
28.4	131.2	301.5	358.3	125.0	222.8	189.9	271.4	57.9	331.4	156.4
39.4	55.6	126.6	186.3	93.9	70.2	69.9	61.8	34.0	23.3	58.1
52.7	729.1	1220.4	1240.7	566.7	765.1	442.8	1288.9	690.9	169.8	831.7
3672.6	4793.9	4784.9	4909.8	7853.9	4999.5	6604.5	4473.6	1912.2	2571.6	3204.3
4483.0	1956.1	2006.7	2219.4	2118.0	1996.4	2288.2	1824.5	1658.6	1904.9	2175.1
630.9	4782.0	5468.7	5809.0	5081.1	4471.2	4887.7	5595.4	5080.1	3544.0	7659.7
2119.1	1436.3	1065.1	847.0	1055.1	1171.9	914.4	1141.1	680.6	1409.1	1214.4
2979.4	2379.2	2866.9	3705.2	1984.3	1939.6	2807.5	2473.3	1625.8	1223.8	2464.9
35.2	61.4	102.5	115.7	40.6	45.1	52.5	105.0	44.5	23.3	51.8
72.9	769.1	1351.8	2116.6	227.6	867.1	735.9	2641.0	182.9	268.5	453.5
102.3	479.9	840.6	741.9	319.1	371.2	66.9	948.0	283.0	180.7	501.2
51.2	399.8	706.3	489.3	231.4	626.7	289.4	965.3	312.5	89.2	458.6
37.5	21.3	25.0	15.9	23.2	17.9	18.5	13.8	16.3	9.2	17.4

519.7	445.3	452.0
1197.7	1238.7	1418.3
1158.7	686.0	702.5
3052.4	3414.8	2726.6
728.8	714.0	502.1
5645.1	6156.2	5842.5
1058.2	2013.5	934.2
6993.7	5042.1	9666.4
2029.4	2985.0	2239.0
379.4	264.4	290.3
792.8	713.4	882.6
1236.6	1495.3	807.7
30.4	49.4	53.8
5480.1	5921.9	4436.3
17.0	20.3	13.7
1416.8	1405.5	1021.2
20.6	19.8	14.8
359.6	486.3	335.6
999.9	1106.1	788.9
11.2	11.8	11.9
959.4	1032.8	1335.8
1184.1	813.4	605.9
3820.5	3906.8	3427.8
685.9	1870.1	1033.1
1188.4	1181.6	1092.1
2785.0	3240.4	2490.6
1534.7	1684.4	1682.6
3493.3	2882.5	4329.1
263.5	284.3	536.2
126.0	201.3	71.2
1416.9	778.6	1203.1
4485.5	4465.9	6152.5
1538.7	3045.0	1606.6
4253.1	4067.8	3602.6
1086.4	1308.6	1335.7
2089.4	2676.0	2737.5
171.1	136.7	121.1
3061.8	1170.7	1760.5
1087.0	173.2	1168.6
1122.2	498.4	783.0
21.9	27.5	29.2

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU771261.1 gg_id:325199 Asiatic elephant feces clone AE3_aaa02f02 EU771
EU510839.1 gg_id:269731 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak50a07 EU510
DQ796444.1 gg_id:197556 human fecal clone RL179_aah28e03 DQ796
GQ491903.1 gg_id:541554 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ175376.1 gg_id:513132 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ681212.1 gg_id:526436 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
AY854272.2 gg_id:110046 herbivore gastrointestinal tract clone CATTLE_10 AY854
DQ798787.1 gg_id:195294 human fecal clone RL242_aaj97d04 DQ798
EF402362.1 gg_id:207819 human fecal clone SJTU_B_06_88 EF4023
GU302776.1 gg_id:564138 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU259384.1 gg_id:236097 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC8 EU259
EU766228.1 gg_id:316136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ804133.1 gg_id:186334 human fecal clone RL187_aah69b06 DQ804
GQ493885.1 gg_id:570496 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU765927.1 gg_id:320147 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
AF371568.1 gg_id:49141 swine intestine clone p-355-a3 AF371
FJ680379.1 gg_id:530243 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
DQ796324.1 gg_id:178474 human fecal clone RL179_aah25g07 DQ796
EU779375.1 gg_id:352840 Somali Wild Ass feces clone WA_aaa01h05 EU779
EU765704.1 gg_id:342929 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ801320.1 gg_id:195032 human fecal clone RL388_aao93h07 DQ801
EU767358.1 gg_id:352792 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU472571.1 gg_id:298701 Angola colobus feces clone EAC_2_aaa02h11 EU472
FJ833576.1 gg_id:579126 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_47G06 FJ8335
EU778532.1 gg_id:318470 Red river hog feces clone RRH_aaa01c10 EU778
EU464334.1 gg_id:299814 hamadryas baboon feces clone AFBAB_aai02h08 EU464
EU681990.1 gg_id:293330 microflora imbalances intestine dogs inflammatory bowel disease duodenum health EU681
AM276768.2 gg_id:230741 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM276
DQ801456.1 gg_id:190280 human fecal clone RL388_aao95g05 DQ801
EU767534.1 gg_id:339790 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU771984.1 gg_id:329662 Southern three-banded armadillo feces clone arma_aaj54g06 EU771
DQ799971.1 gg_id:190961 human fecal clone RL247_aaj22e07 DQ799
EU765750.1 gg_id:322377 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ797780.1 gg_id:195509 human fecal clone RL206_aaj15g06 DQ797
EU767434.1 gg_id:352852 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
AY983070.1 gg_id:119344 human descending colon mucosal biopsy clone L313 AY983
DQ804852.1 gg_id:177986 human fecal clone RL385_aao81f01 DQ804
EU778831.1 gg_id:317041 Black-handed Spider Monkey feces clone SPIM_aaj33f01 EU778
FJ682817.1 gg_id:525948 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ370121.1 gg_id:363780 feces adult twins and mothers; TS55 clone TS55_a04f06 FJ3701
DQ798059.1 gg_id:194648 human fecal clone RL302_aal95a11 DQ798

483.1	1520.4	2214.4	2214.0	1232.2	1564.2	1560.3	2112.7	994.1	1354.6	2160.3
325.7	3018.1	2679.1	4324.9	3323.8	4249.5	2940.0	3276.5	2322.5	8061.2	2790.0
294.4	211.0	543.5	607.2	120.8	215.2	142.8	497.8	67.8	61.1	158.3
543.3	1201.0	1453.2	1247.6	1658.1	1505.8	1368.9	1531.1	626.1	1099.2	1043.4
532.7	3380.1	3600.4	4191.0	3046.1	3785.4	3739.8	3616.9	2274.2	1388.6	4649.0
140.9	3298.6	2808.6	2794.4	1022.1	2143.3	1664.3	3089.0	3571.4	861.3	2401.7
162.2	1679.4	1850.3	2245.3	2532.7	1763.5	3875.4	1957.1	1495.4	826.6	1670.7
119.9	491.4	644.3	1075.1	155.5	169.5	103.1	278.7	94.5	36.9	116.7
7666.6	5469.9	4949.6	5278.1	4361.8	4891.2	4925.3	4392.2	7003.3	6156.0	7197.2
1139.7	2352.9	3610.4	4034.1	2885.3	2343.4	3421.5	3233.0	1314.6	1245.8	2928.7
68.1	750.4	837.5	722.5	526.4	584.3	753.1	1040.9	192.5	578.8	376.8
3299.3	3831.6	4038.9	3635.2	2980.6	3716.1	3090.2	2978.4	4456.6	4333.5	5141.2
508.8	1772.1	2139.5	1499.4	1403.0	1725.5	1289.6	1387.6	3841.9	2837.2	3122.7
138.4	742.2	1341.6	1171.9	763.8	902.3	1060.0	1112.6	476.6	163.6	616.8
6228.4	4712.6	6704.0	4514.0	3514.0	5045.3	3375.6	4171.0	4714.8	7364.1	4227.5
7460.9	3551.0	4079.4	4759.2	3900.6	3831.3	3468.4	3751.7	3388.7	3855.6	4110.0
3369.7	4123.3	4107.0	3890.4	4851.2	3712.7	4238.1	4391.9	5369.9	4897.0	3502.0
31.6	162.1	270.6	362.8	61.1	130.8	86.2	227.4	33.2	38.1	79.4
94.6	1430.0	1798.1	1829.0	1535.3	1388.0	1654.0	1851.2	1662.2	650.3	1323.5
9403.7	4658.5	3771.0	3990.9	3711.3	4331.8	4210.7	4529.1	5544.3	4618.3	7275.7
7462.4	3551.5	3832.8	3761.1	3168.2	3639.6	3619.9	3663.1	3892.6	3508.4	5461.1
5819.8	6227.3	5815.4	5012.4	4889.0	5159.4	5664.3	4934.0	7773.6	5509.4	7497.5
3840.0	3663.0	3445.3	3550.0	3946.1	3160.6	3860.9	3481.0	4405.9	3870.6	5198.5
15916.0	5780.4	6083.5	7083.0	4823.2	6319.2	4854.0	5800.3	7234.4	8623.7	7038.7
54.5	2111.2	2702.6	3007.6	1570.4	1637.3	2104.0	2259.6	550.8	485.0	1471.1
452.0	3186.8	5212.4	2928.3	2215.9	2683.1	2412.2	2839.3	3116.1	1529.5	4282.9
66.8	466.1	894.1	855.0	207.1	437.7	301.3	719.6	144.2	98.2	537.6
700.0	936.7	965.6	1101.6	782.1	1154.7	971.8	919.5	616.8	678.1	642.3
27.4	344.4	319.5	361.9	505.2	305.1	549.5	383.1	112.6	84.4	171.6
461.4	2150.5	2154.9	2606.9	2740.0	2215.0	2272.8	2834.1	1780.6	1448.2	1843.6
42.4	175.3	330.7	328.3	68.2	137.3	73.6	231.1	37.1	24.4	94.5
656.2	784.2	1002.4	1230.6	1069.3	822.6	968.6	1096.0	346.1	476.3	525.0
14145.8	3806.7	3753.6	3755.0	3297.6	4181.6	4043.3	3363.4	5599.4	4540.1	4459.5
35.6	110.2	174.1	139.7	27.6	61.2	56.1	171.1	37.5	34.4	91.2
291.5	3712.7	3255.4	3207.1	1898.8	2907.4	3126.9	2984.1	3530.9	2969.4	1854.4
1940.8	1810.8	2714.2	2050.5	2016.0	2081.5	2692.8	2251.9	2779.4	1934.1	1999.7
51.8	143.3	343.1	363.8	116.3	203.6	148.0	279.4	114.6	174.4	100.9
43.6	413.2	971.5	1286.7	250.7	407.5	389.3	834.3	115.1	61.4	235.8
12518.6	3802.2	5076.2	4527.6	4385.2	3942.5	4582.5	3420.6	6184.9	4254.3	5357.6
246.5	3905.7	3665.8	2626.1	2225.2	4215.3	2151.0	2455.5	3763.2	4525.4	3850.0
3697.8	4089.0	4080.5	3915.6	3430.6	3980.3	4455.3	3834.0	4096.2	3436.2	3572.3

2319.6	2469.7	2461.6
2969.0	3112.4	2279.0
414.9	494.1	245.3
1565.5	1495.6	2385.3
3366.0	4835.2	4270.7
2959.8	1847.0	2351.7
1528.5	1918.8	2851.4
578.8	424.0	215.9
5143.3	5807.8	5255.4
3224.5	3757.6	3193.3
804.8	744.5	1028.1
3118.1	4229.6	3064.1
1473.8	1687.5	1114.5
979.2	1418.4	1580.0
3903.1	4312.6	3619.9
4647.1	5583.3	4093.8
4702.7	4981.2	4411.5
241.5	209.3	133.8
1516.3	1857.8	1826.9
3496.0	5003.1	4706.1
2936.2	3729.0	3215.2
4842.4	4557.7	5060.6
3934.5	3501.8	3542.1
6128.8	7935.8	5322.3
2639.9	1959.6	2836.2
2986.6	3687.9	2784.7
673.4	489.9	482.7
988.0	1023.8	912.3
441.8	433.8	781.8
3193.4	3086.1	1611.8
224.6	372.2	1706.9
1094.0	1330.3	1403.0
3491.7	4634.5	4240.6
194.8	128.4	33.1
3421.1	3091.2	3972.4
1957.0	2631.7	2947.2
288.2	249.0	439.5
1047.3	697.9	636.0
3493.9	5359.5	4028.8
2687.1	3153.8	2523.3
3812.0	4590.7	4362.0

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DQ794409.1 gg_id:181367 human fecal clone RL197_aah87d04 DQ794
EU344663.1 gg_id:260855 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ679598.1 gg_id:527276 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
AY239462.1 gg_id:97679 Clostridium sp. cTPY-17 AY2394
DQ801352.1 gg_id:195793 human fecal clone RL388_aao94d06 DQ801
EU463470.1 gg_id:290514 domesticated horse feces clone horsem_aai94e11 EU463
FJ675753.1 gg_id:519815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ808253.1 gg_id:187425 human fecal clone RL180_aao74d10 DQ808
DQ802555.1 gg_id:196013 human fecal clone RL188_aan93d03 DQ802
FJ367734.1 gg_id:364859 feces adult twins and mothers; TS2 clone TS2_a03a03 FJ3677
FJ880611.1 gg_id:370809 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EU776530.1 gg_id:305881 Lion feces clone LI2_aae49b11 EU776
EU464984.1 gg_id:290079 African elephant feces clone AFYEL_aaj66c03 EU464
EU774288.1 gg_id:356410 Chimpanzee feces clone CHIMP1_b07_1 EU774
DQ795273.1 gg_id:187470 human fecal clone RL178_aah52d02 DQ795
EU467273.1 gg_id:293835 black-handed spider monkey feces clone SPIM_e02_1 EU467
DQ796977.1 gg_id:179115 human fecal clone RL386_aao85c06 DQ796
DQ824427.1 gg_id:199308 human fecal clone RL304_aal75h05 DQ824
AF371554.1 gg_id:22771 swine intestine clone p-214-o5 AF371
EU467600.1 gg_id:302443 southern three-banded armadillo feces clone arma_a10_2 EU467
EU774768.1 gg_id:336539 Angola Colobus feces clone EAC_2_aaa04g07 EU774
DQ327377.1 gg_id:146774 Metagenomic gut microbiome healthy human stool clone E934 DQ327
FJ370482.1 gg_id:363144 feces adult twins and mothers; TS57 clone TS57_a01f02 FJ3704
EU474994.1 gg_id:297271 red river hog feces clone RRH_aaa03a09 EU474
FJ684167.1 gg_id:509948 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU468918.1 gg_id:288160 Speke's gazelle feces clone SP2_c03_1 EU468
EU771676.1 gg_id:324696 African elephant feces clone AFEL3_aao14d08 EU771
FJ833377.1 gg_id:577323 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_06F01 FJ8333
DQ326550.1 gg_id:148288 Metagenomic gut microbiome healthy human stool clone C717 DQ326
FJ678967.1 gg_id:511702 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
EU467081.1 gg_id:290467 mongoose lemur feces clone ML_aae87f05 EU467
DQ806352.1 gg_id:183449 human fecal clone RL186_aan91b04 DQ806
DQ803435.1 gg_id:195336 human fecal clone RL251_aaj85g05 DQ803
EU464713.1 gg_id:297440 Hartmann's mountain zebra feces clone AFZEB_aaj69e12 EU464
EU766185.1 gg_id:319374 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ673541.1 gg_id:515133 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
EU773502.1 gg_id:351880 Bonobo feces clone BNO_aaa03h07 EU773
EU465395.1 gg_id:296257 lion feces clone LI3_aah76f05 EU465
EU344701.1 gg_id:274828 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ810001.1 gg_id:177820 human fecal clone RL184_aao66h07 DQ810
FJ366131.1 gg_id:362662 feces adult twins and mothers; TS25 clone TS25_a03b01 FJ3661

215.0	1490.5	1455.6	1463.4	2041.6	1611.2	1561.4	1770.8	882.6	1312.5	1038.1
809.9	1425.7	2256.2	2492.8	1299.6	1475.5	2063.1	1766.3	1005.0	520.9	1708.9
196.3	664.4	913.1	948.0	431.7	761.4	526.4	1888.0	274.1	106.5	674.9
49.7	190.1	379.7	408.4	73.5	270.5	202.2	426.1	87.1	24.2	416.1
942.3	3602.9	2958.7	3521.6	3237.2	2923.2	3262.4	2687.7	2363.9	3097.9	1837.4
51.9	176.5	317.7	243.8	159.5	165.6	149.8	252.3	56.1	78.3	121.9
3912.3	2830.2	3214.8	1888.2	3097.8	2867.3	3024.7	2969.3	3695.2	3294.3	3139.7
528.9	2711.2	3701.6	4006.9	1702.6	3076.0	2199.1	3845.9	1081.7	542.3	2614.0
56.4	840.9	898.1	950.0	1191.9	1022.7	1613.5	882.3	404.1	503.3	469.8
67.9	330.4	457.4	420.4	149.8	242.9	149.2	288.2	63.0	45.5	176.2
122.5	712.5	1080.3	1313.9	359.8	691.3	1103.0	855.1	135.8	135.4	498.0
110.2	1701.6	1949.8	2268.3	1824.5	1744.5	1538.9	2992.5	827.6	859.9	1250.3
56.4	898.6	1349.3	1338.1	322.3	752.4	732.7	1081.3	248.4	141.3	572.9
35.1	383.2	453.7	343.3	203.5	192.6	209.9	617.7	98.8	86.8	156.6
9329.7	3239.0	2363.4	2500.7	3140.0	2804.0	2776.7	1963.7	3604.1	2055.0	4176.7
44.1	352.7	482.7	564.4	127.1	198.9	227.1	304.1	186.9	79.1	160.5
3203.2	3772.8	3471.5	3385.6	2774.8	3914.6	3047.8	3747.5	5146.2	3785.2	4060.0
6100.8	3544.0	2609.5	3797.8	3639.5	3125.6	3911.0	3261.6	4502.9	2860.8	5294.5
48.1	680.0	962.9	1206.4	259.2	640.1	504.3	1054.4	185.2	81.9	486.7
50.2	818.4	1406.1	1448.6	312.5	922.4	781.0	1225.7	344.3	295.7	423.8
190.4	979.0	891.6	755.1	950.2	932.2	895.9	973.1	912.7	1036.1	728.3
45.6	936.2	1087.2	961.4	664.5	701.9	709.7	925.4	268.9	108.8	426.1
12386.4	4884.1	6238.1	6131.0	5350.1	5452.9	5178.0	4585.8	8492.8	6367.2	5840.3
3754.2	4500.0	6285.6	4973.4	4100.2	4258.0	4349.4	4525.0	5232.6	2092.5	5103.9
30.7	894.9	1061.9	1436.2	321.5	724.8	750.4	1181.9	53.2	82.2	452.1
1472.4	3149.3	3288.1	3896.1	3574.0	3300.7	3699.6	4384.9	2048.9	3071.2	3129.7
79.3	432.7	705.5	709.4	286.5	406.4	295.1	570.2	158.6	127.5	286.5
47.1	794.9	1113.5	1241.1	235.6	524.1	471.2	1159.3	204.0	100.3	354.6
42.2	14.7	13.7	22.6	25.2	15.5	23.7	19.7	13.1	15.6	21.8
663.1	263.2	424.0	366.9	158.8	245.1	192.4	411.4	152.5	121.6	206.3
93.1	1212.1	1424.5	1658.2	1146.3	1351.6	1384.1	2261.5	769.6	568.9	1047.9
1923.7	3053.8	3418.3	3683.9	3878.2	3689.5	4401.7	2994.8	2716.2	2732.5	2802.2
537.3	3358.4	4636.2	2288.4	4086.6	3566.9	4484.6	3905.8	5054.9	2204.8	3569.9
47.8	460.2	698.6	281.4	511.7	608.2	351.8	814.3	384.6	510.4	447.5
16347.9	5782.2	5306.0	6094.1	4660.5	5111.9	4456.4	5335.9	6828.6	5075.2	5391.7
85.3	783.7	1189.9	1142.2	843.2	1075.6	1021.0	1241.9	1056.4	1255.1	932.5
36.9	766.8	1103.4	831.3	176.1	675.0	485.1	913.1	203.6	58.7	803.0
212.9	1359.4	1886.9	2176.2	1291.9	1618.1	1468.1	2190.0	1875.2	1581.4	1563.7
99.4	689.0	1184.3	1322.1	413.0	818.6	524.8	935.2	824.7	549.1	555.4
38.9	470.5	693.6	502.6	491.9	402.0	701.7	471.9	145.8	117.7	291.9
9168.9	4004.3	3858.8	3861.9	3979.7	3269.6	3531.1	3579.0	4243.1	3844.0	4432.2

1665.1	1391.4	1705.8
1967.8	2064.2	2350.5
1665.9	744.6	1190.5
491.4	376.4	505.2
2957.9	2705.6	3354.7
378.0	335.9	398.9
3540.8	4203.2	3015.6
5226.2	3083.9	3843.6
985.5	1041.5	1411.6
372.3	305.5	309.4
604.6	744.7	1234.8
2623.2	2029.2	3389.7
1359.0	1247.5	1113.1
1073.5	325.4	520.0
2172.6	2859.7	256.1
394.7	406.8	244.8
3029.7	4444.4	3884.3
3117.9	5013.8	3342.7
1352.6	835.3	1081.3
2284.5	1044.7	2000.7
862.4	772.2	1360.3
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4861.7	6664.2	5725.7
5504.1	4676.2	5296.8
796.9	1103.2	957.8
4071.4	3282.3	4180.7
710.0	619.3	748.7
1569.1	683.6	824.5
18.5	26.0	12.3
602.8	743.8	578.9
2089.0	1658.0	1669.4
3685.0	2954.5	5232.4
3976.2	3700.0	4238.1
649.8	861.1	444.6
6484.5	5276.7	5051.0
922.4	1162.5	1168.2
990.2	514.9	717.5
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EU773448.1 gg_id:328357 Black lemur feces clone BKLE_c07_1 EU773
AF371556.1 gg_id:16853 swine intestine clone p-2593-9F5 AF371
DQ796727.1 gg_id:174911 human fecal clone RL179_aao53f12 DQ796
DQ804862.1 gg_id:198522 human fecal clone RL385_aao81g01 DQ804
EU471793.1 gg_id:288210 Asiatic elephant feces clone AE2_aaa04e03 EU471
DQ456135.1 gg_id:158566 pre-adolescent turkey cecum clone CFT114G12 DQ456
DQ057374.1 gg_id:130289 chicken ileum/cecum clone cc151 DQ057
FJ683028.1 gg_id:509752 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
EU842178.1 gg_id:341449 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ794881.1 gg_id:181807 human fecal clone RL310_aam37e03 DQ794
AF371561.1 gg_id:36330 swine intestine clone p-195-o5 AF371
EU777867.1 gg_id:337551 European rabbit feces clone RA_a03_1 EU777
FJ677862.1 gg_id:527800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ369295.1 gg_id:359255 feces adult twins and mothers; TS50 clone TS50_a02f06 FJ3692
FJ673384.1 gg_id:531690 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ326682.1 gg_id:149120 Metagenomic gut microbiome healthy human stool clone E129 DQ326
DQ326355.1 gg_id:146254 Metagenomic gut microbiome healthy human stool clone C358 DQ326
EU469410.1 gg_id:287978 black lemur feces clone BKLE_d05 EU469
EU467214.1 gg_id:291883 black-handed spider monkey feces clone SPIM_c05 EU467
EU771482.1 gg_id:321822 Hamadryas Baboon feces clone AFBAB_aai01h09 EU771
FJ683838.1 gg_id:526575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
DQ802212.1 gg_id:186717 human fecal clone RL241_aaj04e08 DQ802
DQ800765.1 gg_id:183368 human fecal clone RL183_aao03b10 DQ800
EU467078.1 gg_id:301579 mongoose lemur feces clone ML_aae87d07 EU467
FJ673350.1 gg_id:513767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU776792.1 gg_id:355905 Mongoose lemur feces clone ML_aaj25h01 EU776
AF371619.1 gg_id:103407 swine intestine clone p-1631-c5 AF371
DQ824461.1 gg_id:195946 human fecal clone RL304_aal76c08 DQ824
FJ679856.1 gg_id:527985 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
EU777917.1 gg_id:320009 European rabbit feces clone RA_f07_3 EU777
GQ896703.1 gg_id:593086 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ808139.1 gg_id:184983 human fecal clone RL180_aao73b05 DQ808
EU510056.1 gg_id:267797 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf11e10 EU510
EU774616.1 gg_id:318760 Angola Colobus feces clone EAC_2_aaa03g04 EU774
FJ370471.1 gg_id:369394 feces adult twins and mothers; TS57 clone TS57_a01e03 FJ3704
DQ801050.1 gg_id:197076 human fecal clone RL387_aao91d10 DQ801
DQ808546.1 gg_id:182513 human fecal clone RL239_aaj10a03 DQ808
DQ806797.1 gg_id:179807 human fecal clone RL186_aao48g11 DQ806
EU776227.1 gg_id:350447 Spotted hyena feces clone HY2_f11 EU776
DQ794523.1 gg_id:182428 human fecal clone RL240_aaj29b04 DQ794

295.9	730.1	1075.7	1078.8	542.8	671.7	607.2	853.6	702.0	755.2	874.6
50.3	631.6	468.9	1024.5	656.5	558.1	564.1	933.0	192.4	143.7	223.6
32.0	29.1	52.2	60.3	38.5	29.2	15.6	23.2	18.4	21.0	19.4
150.3	865.8	1156.5	1499.3	1003.7	979.7	1296.6	1346.9	388.9	1050.0	567.8
382.6	860.9	1185.7	1173.2	1313.2	762.5	1048.5	691.3	571.3	640.6	976.7
91.7	730.4	1026.8	509.6	518.0	799.0	685.2	1470.3	330.1	318.8	554.7
50.7	19.3	31.4	24.6	19.9	23.4	21.6	24.0	22.5	22.3	32.0
40.2	339.1	577.0	693.2	59.6	242.1	191.3	497.9	171.2	64.9	204.9
186.2	1900.4	2983.5	2544.3	2592.5	2453.8	2454.9	2574.9	1290.0	1069.1	2218.9
57.8	791.9	921.8	1139.2	402.4	496.9	634.8	885.3	107.7	78.7	358.4
53.7	51.8	59.1	63.9	50.2	58.8	49.1	125.5	35.8	43.8	44.4
68.8	48.7	45.8	47.6	59.5	47.5	40.3	70.0	33.0	29.1	45.6
238.8	1480.4	1621.9	1883.8	1194.4	1215.7	2139.5	1615.7	517.8	564.1	1424.1
2828.4	5181.5	6150.4	5630.9	3749.9	5127.9	4686.8	6148.6	4517.9	4507.0	5649.5
94.5	698.0	906.8	294.4	622.4	797.4	836.8	748.8	449.0	151.3	550.2
530.6	1902.9	2233.9	2350.7	2191.7	2245.0	2019.4	2439.0	1897.2	1177.0	1331.7
30.7	375.3	652.0	828.8	186.7	314.0	226.2	642.7	193.8	589.3	485.3
232.6	276.0	365.8	278.2	376.1	255.0	293.8	340.8	412.6	195.9	192.7
51.0	555.7	767.6	797.1	316.5	432.6	645.9	565.1	67.3	70.8	302.2
410.8	3322.4	4141.5	4417.5	2848.0	3294.2	2945.3	3813.2	2704.8	2551.9	4113.0
37.6	636.4	1131.4	1380.1	190.6	937.1	648.4	1175.5	369.3	116.3	419.5
2525.7	3329.0	3955.0	3738.7	4270.6	3509.6	4478.8	4150.5	3370.4	3459.8	3777.9
129.4	354.8	601.0	697.7	203.2	351.6	319.5	507.9	153.3	257.2	275.0
47.8	175.6	320.4	231.6	137.4	239.8	311.2	325.9	103.2	65.3	188.9
161.3	664.2	999.3	944.1	565.9	780.1	1136.6	1115.5	346.2	195.8	1275.3
688.7	1400.4	1572.6	1777.3	1783.8	1154.3	1673.7	1119.7	1209.0	1567.8	1223.4
105.8	1579.1	1660.1	1644.3	855.9	1406.7	1433.6	1887.5	431.6	392.5	1488.4
48.7	1264.4	1715.6	1858.7	625.9	1153.9	836.8	2022.9	703.0	293.5	883.6
36.7	113.6	151.3	188.2	61.0	127.7	97.4	142.9	48.0	28.9	33.3
2280.6	2898.3	3219.4	3684.5	3166.6	3154.9	2712.7	3775.0	2590.4	3180.3	3081.4
953.7	4434.0	5580.4	5967.9	5218.6	4362.1	5096.3	5041.5	5728.0	5779.9	4261.4
2199.2	2602.0	2807.2	2734.5	1866.7	2442.9	1908.9	2771.2	2259.1	1391.3	2452.2
76.1	519.1	680.8	742.2	492.5	488.7	513.6	995.6	327.3	156.6	640.0
291.6	84.7	470.3	323.5	359.8	387.1	199.2	358.7	366.8	67.6	1177.7
2249.6	3588.9	5374.6	4528.1	4258.8	4038.6	5319.3	4026.3	2854.4	2919.2	3763.1
2687.6	1063.2	1540.6	1847.2	706.6	1063.4	864.8	2097.9	2089.1	959.8	852.7
66.2	1214.6	1936.1	1207.6	933.5	1540.0	1464.0	1276.1	1023.3	417.1	1452.2
736.8	280.3	1027.1	855.1	378.0	513.9	602.9	602.2	751.6	596.9	423.8
42.6	156.1	388.0	321.6	134.0	156.3	163.5	183.4	127.6	41.0	115.0
12674.0	2880.3	3425.6	3731.9	2435.3	2995.2	2822.5	2931.2	2991.8	1659.5	3081.0
42.6	153.0	212.4	200.2	146.7	195.0	117.6	301.5	98.3	78.4	104.6

677.3	1242.1	646.3
1280.1	545.7	1306.4
37.6	70.4	66.4
1423.6	1278.7	1291.4
910.8	773.2	824.1
1314.3	1243.6	1359.9
26.8	31.1	19.9
427.3	417.0	255.9
2350.9	2874.4	3642.7
899.7	822.5	874.8
196.3	83.2	112.9
77.2	67.0	61.4
1246.5	1366.0	1883.7
5732.7	6105.8	7028.2
665.8	719.7	930.8
2225.3	2225.0	2909.7
534.6	441.1	371.0
301.9	656.8	603.7
996.1	464.2	840.1
3897.9	3752.2	3581.8
1789.8	935.2	1316.3
3454.8	4106.5	3984.8
604.5	590.1	788.0
355.8	347.9	362.9
1137.8	1326.0	1443.5
1482.9	2344.9	2393.3
1409.1	1919.2	2501.8
1545.7	1240.9	1781.3
81.6	164.1	47.6
4357.6	3106.9	2981.1
5261.0	5493.1	5365.9
2792.3	2511.5	2322.5
748.1	680.7	1115.2
332.0	375.3	225.5
4179.3	4804.5	4758.9
2237.2	1675.8	1326.4
1440.0	943.4	1453.3
711.0	1162.4	573.1
154.2	261.2	460.6
2988.4	2827.6	3608.0
260.3	396.7	563.3

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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FJ681993.1 gg_id:523823 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
DQ809906.1 gg_id:190092 human fecal clone RL184_aao65g07 DQ809
GQ896616.1 gg_id:557450 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ807661.1 gg_id:178609 human fecal clone RL180_aah35f04 DQ807
DQ796984.1 gg_id:179989 human fecal clone RL386_aao85d04 DQ796
EU778867.1 gg_id:329526 Black-handed Spider Monkey feces clone SPIM_f07_1 EU778
EU775452.1 gg_id:321589 Western lowland gorilla feces clone GORSD_2aaa03d01 EU775
FJ674257.1 gg_id:522727 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ682726.1 gg_id:527135 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
GQ864252.1 gg_id:592901 microbiota geese cecum lumen clone ML1 GQ864
EU530329.1 gg_id:274745 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU530
EU778076.1 gg_id:342933 feces clone RL116_aae99e06 EU778
DQ326564.1 gg_id:147799 Metagenomic gut microbiome healthy human stool clone C746 DQ326
DQ809460.1 gg_id:183866 human fecal clone RL184_aah21c06 DQ809
AY684376.2 gg_id:110457 mucosal biopsies human intestine clone HuRC75 AY6843
FJ673139.1 gg_id:519398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU459775.1 gg_id:299302 ring-tailed lemur feces clone RT_aai12e10 EU459
EF403824.1 gg_id:214980 human fecal clone SJTU_C_01_02 EF4038
EU467083.1 gg_id:290922 mongoose lemur feces clone ML_aae87f07 EU467
DQ327356.1 gg_id:149445 Metagenomic gut microbiome healthy human stool clone E911 DQ327
FJ681296.1 gg_id:525329 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ673124.1 gg_id:526780 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
DQ905375.1 gg_id:164113 human fecal clone 013C-A5 DQ905
EU774799.1 gg_id:311692 Angola Colobus feces clone EAC_2_aaa04g11 EU774
DQ794777.1 gg_id:174078 human fecal clone RL240_aaj32c02 DQ794
EU773433.1 gg_id:325586 Black lemur feces clone BKLE_b02 EU773
DQ777928.1 gg_id:161899 rat feces clone R-1319 DQ777
FJ682390.1 gg_id:520588 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
FJ678944.1 gg_id:519149 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ678858.1 gg_id:522624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EU508047.1 gg_id:260800 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa02f04 EU508
FJ677197.1 gg_id:514623 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
DQ806721.1 gg_id:186869 human fecal clone RL186_aao47h11 DQ806
FJ676370.1 gg_id:528050 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
DQ794600.1 gg_id:177977 human fecal clone RL240_aaj30b02 DQ794
FJ364246.1 gg_id:369450 feces adult twins and mothers; TS150 clone TS150_a04f09 FJ3642
DQ797980.1 gg_id:178994 human fecal clone RL302_aal94b03 DQ797
FJ978523.1 gg_id:453756 feces clone CL_F_054 FJ9785
DQ806841.1 gg_id:184514 human fecal clone RL198_aaj73g03 DQ806
FJ363309.1 gg_id:366333 feces adult twins and mothers; TS149 clone TS149_a01f12 FJ3633
FJ679241.1 gg_id:520841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792

7215.6	5103.6	4699.6	5274.9	3906.5	4371.1	5276.0	4954.7	9183.9	5045.4	6884.4
47.6	301.5	485.1	527.0	537.1	364.3	818.7	568.0	216.4	97.6	430.5
244.0	1684.5	1220.7	2153.9	3589.1	1762.4	3004.3	2375.9	1192.5	1131.3	2185.3
322.0	829.6	622.1	1051.5	1630.9	903.3	998.3	839.0	677.0	454.7	634.5
6127.4	5476.3	4482.7	4805.2	5176.5	4600.6	4774.1	4211.2	3310.5	5033.2	3590.5
2703.4	1703.3	1650.8	1904.2	1944.5	1687.9	1598.3	1689.8	1442.2	778.9	1647.3
249.2	1322.6	1698.7	1114.8	979.4	1447.3	1356.8	1030.7	916.4	1376.2	1940.9
378.5	3258.1	3349.2	3508.9	2652.8	2377.6	3669.7	3687.5	3258.5	2704.7	3207.0
184.4	875.7	1183.7	1555.1	766.2	886.6	1012.7	1386.6	737.9	548.0	928.4
48.4	460.1	914.7	770.0	388.0	530.2	480.8	725.6	237.0	69.4	245.9
76.1	899.3	1153.6	1481.2	700.7	1029.3	878.0	1542.0	583.2	381.0	678.1
42.2	315.1	667.3	609.8	370.4	443.1	343.6	480.7	108.5	84.8	224.9
37.8	262.0	452.8	711.3	94.8	287.4	138.8	598.3	64.0	71.8	223.3
43.9	146.9	264.8	307.3	64.8	73.9	56.4	118.7	38.1	17.7	70.1
40.6	107.9	161.4	125.6	68.4	82.2	72.8	177.2	66.5	38.3	60.3
91.4	2016.0	1541.6	1388.4	1439.1	1744.3	1413.9	1512.1	2042.3	2139.0	1167.1
3461.4	1830.7	2603.7	2459.3	1077.0	1779.1	1364.5	2267.6	1799.2	1093.6	3960.7
212.5	1496.9	2484.6	1814.1	1281.7	1465.1	2101.1	1951.7	850.5	579.2	1493.7
36.6	206.2	324.2	348.4	39.3	198.4	214.9	291.8	24.0	73.9	127.9
1900.1	1647.6	2092.9	1888.2	1485.0	1642.2	1794.4	1958.1	1688.3	1365.1	1695.5
887.4	4100.9	3824.4	3664.1	4789.9	3621.3	4123.4	3535.2	4864.0	1895.0	2814.1
825.1	3868.2	4657.5	3058.8	2982.1	3065.5	3009.2	3205.4	4072.9	2666.3	4900.2
37.3	868.2	1468.0	1546.0	679.5	906.4	542.6	1296.6	245.1	155.3	692.3
60.8	405.8	573.9	714.8	518.3	359.2	482.4	524.9	248.5	204.0	328.8
35.9	130.3	200.0	253.8	49.1	121.8	109.5	154.1	37.3	33.2	81.5
44.7	446.9	745.6	1008.9	143.6	723.6	402.6	990.1	183.7	131.1	315.0
55.6	331.6	789.7	977.2	403.9	700.1	425.3	793.1	331.0	284.0	373.3
9626.8	4142.6	4102.4	4511.7	3614.6	3511.7	4423.7	3735.8	5383.0	4714.5	4494.9
6903.0	4455.4	4117.6	4052.7	3789.1	4005.4	3750.6	4224.3	4464.4	4065.7	4301.6
38.5	966.2	1743.6	1589.2	623.3	824.2	657.2	1375.0	273.4	469.9	702.6
80.3	2527.1	2154.8	1660.8	1791.4	2625.9	1447.3	2392.1	1286.8	1123.9	1204.3
630.1	4986.9	6522.6	5935.6	4229.8	4963.8	4478.8	5530.1	7036.9	7699.4	6119.2
67.5	422.0	531.5	676.3	332.7	273.5	355.1	461.8	80.9	63.1	303.0
749.9	2415.2	1997.0	1415.1	1154.7	1852.9	485.9	1612.5	1709.1	2257.2	1283.2
466.5	2687.0	3114.4	2775.8	3556.0	2557.1	2617.0	2630.6	2506.7	1423.7	2810.9
582.2	1005.1	1523.0	1783.1	1263.0	1271.3	1370.2	1354.1	627.9	470.2	1216.2
67.0	1454.5	1153.8	900.8	210.3	1065.5	692.4	1210.5	642.0	1117.6	485.1
40.3	780.2	1630.2	1287.8	254.3	997.3	635.3	1187.8	376.3	118.8	1203.8
5818.2	1562.4	1858.4	1751.4	2743.6	2025.9	2132.2	2919.3	1588.3	1081.7	1630.6
5390.3	1455.6	1388.4	1599.8	1962.3	1388.8	3929.7	1580.7	3885.3	933.2	926.0
550.0	2943.6	4012.6	3984.4	4237.5	3325.5	4547.7	3603.2	2395.0	1475.0	2838.0

4315.8	5798.2	4144.1
866.1	477.0	791.9
2725.1	2292.9	2695.4
824.9	1526.0	1012.6
4865.8	5504.7	5047.8
1765.7	2591.3	2263.5
1199.3	1330.7	1301.6
3116.5	3391.8	4326.1
1529.5	1409.6	1740.0
800.2	839.8	575.7
1904.5	1736.9	1518.7
293.6	446.4	1041.8
844.8	343.8	375.1
265.5	176.1	65.6
180.1	136.5	142.1
1366.4	1584.8	2161.0
2052.9	2761.7	1940.9
1872.2	2413.2	2476.0
375.8	392.2	232.0
1555.3	2024.5	2081.6
3731.3	3495.7	4765.4
2621.9	2977.4	3003.9
1477.0	862.3	1270.4
570.7	569.7	589.1
265.0	159.8	153.6
1250.4	676.0	1036.4
837.7	968.5	821.5
3891.5	4415.0	4004.9
4580.3	5422.5	5050.8
1807.2	841.9	1027.4
2379.1	2396.9	1454.4
5418.9	5782.4	4803.4
550.1	489.3	785.2
1769.9	1976.1	2588.3
2827.6	3040.0	4199.4
1441.9	1419.3	2277.0
1337.9	748.5	1164.0
1377.6	1159.3	1688.5
2803.1	3085.8	2272.5
1411.9	3326.6	2102.7
4311.3	2726.4	4710.1

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU475069.1 gg_id:298031 visayam warty pig feces clone VWP_aaa04b01 EU475
EU773219.1 gg_id:352777 BigHorn sheep feces clone BH1_aao26b01 EU773
GQ493996.1 gg_id:557489 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY978904.1 gg_id:116192 human transverse colon mucosal biopsy clone NF83 AY978
AJ608222.1 gg_id:145181 human biopsies ulcerative colitis biopsy clone UC7-4 AJ6082
AF371562.1 gg_id:103782 swine intestine clone p-2565-9F5 AF371
DQ804819.1 gg_id:187384 human fecal clone RL385_aao81b03 DQ804
EU774109.1 gg_id:320898 Chimpanzee feces clone CHIMP1_d08 EU774
FJ679838.1 gg_id:527736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
FJ371321.1 gg_id:358483 feces adult twins and mothers; TS6 clone TS6_a03e12 FJ3713
FJ677257.1 gg_id:529683 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
DQ797030.1 gg_id:189685 human fecal clone RL386_aao86a10 DQ797
FJ880395.1 gg_id:377385 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
EU462840.1 gg_id:299884 southern three-banded armadillo feces clone arma_aaj53h01 EU462
DQ673522.1 gg_id:164569 rumen fluid clone GRC57 DQ673
GQ493042.1 gg_id:578960 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU474973.1 gg_id:289074 red river hog feces clone RRH_aaa04d09 EU474
DQ802768.1 gg_id:193704 human fecal clone RL188_aan96d02 DQ802
FJ370555.1 gg_id:361483 feces adult twins and mothers; TS57 clone TS57_a02d11 FJ3705
DQ798027.1 gg_id:178352 human fecal clone RL302_aal94f11 DQ798
EU475035.1 gg_id:297101 visayam warty pig feces clone VWP_aaa02a02 EU475
EU458658.1 gg_id:296606 European rabbit feces clone RA_b11 EU458
EU462117.1 gg_id:298632 black-handed spider monkey feces clone SPIM_aaj35c05 EU462
DQ804840.1 gg_id:185090 human fecal clone RL385_aao81d08 DQ804
FJ672578.1 gg_id:526064 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6725
EU468606.1 gg_id:300581 okapi feces clone OK1_h08_1 EU468
FJ680287.1 gg_id:520937 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EU773244.1 gg_id:316452 BigHorn sheep feces clone BH1_aao28g03 EU773
EU458517.1 gg_id:302666 spotted hyena feces clone HY2_a09 EU458
FJ879040.1 gg_id:391692 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
EU765088.1 gg_id:319438 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU772937.1 gg_id:306431 Bush dog feces clone bdog1_e11_1 EU772
EU765584.1 gg_id:353840 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU775824.1 gg_id:333807 Horse feces clone horsem_aai93b02 EU775
DQ803717.1 gg_id:195413 human fecal clone RL200_aai57e06 DQ803
EU461559.1 gg_id:300036 black rhinoceros feces clone RH_aaj92e04 EU461
EU469503.1 gg_id:290696 black lemur feces clone BKLE_a05_2 EU469
EU776796.1 gg_id:303866 Mongoose lemur feces clone ML_aaj26h09 EU776
FJ880217.1 gg_id:455746 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU466069.1 gg_id:299639 bighorn sheep feces clone BH1_aao25b10 EU466
EU766047.1 gg_id:352733 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766

51.6	1631.0	2115.5	2117.8	1000.0	2942.9	1012.3	2879.4	1139.0	524.2	1508.6
454.8	1745.4	2111.5	2297.5	1046.7	1740.5	1511.4	2421.6	1624.9	867.1	2247.3
621.4	2097.9	3062.7	1446.2	1522.5	2429.4	2082.6	2970.1	1369.7	1245.2	2260.9
284.4	2672.1	3178.2	2642.4	2781.0	3408.6	2200.2	3130.9	1770.6	3616.8	1883.3
84.9	687.1	1592.6	1237.7	866.2	1324.2	709.6	1249.9	349.4	533.5	593.0
30.6	31.1	54.2	39.1	33.8	38.9	32.3	20.0	26.7	16.3	35.1
39.5	145.5	228.1	285.4	40.6	85.1	82.1	222.8	44.7	44.6	131.3
39.4	352.7	403.9	386.9	299.0	359.2	576.5	582.8	108.7	389.3	157.9
6473.6	4803.9	4302.1	3839.4	3151.8	4145.2	3521.6	3710.8	4858.6	4310.3	4744.8
5721.6	3669.2	3189.7	3988.7	3986.5	3855.2	3870.7	3842.6	3206.2	2513.9	5843.9
3215.1	4116.4	4315.0	5745.7	4774.2	3955.7	5914.6	4578.0	3682.0	4102.0	5320.8
1697.6	5430.6	5008.3	4853.1	4610.7	4443.5	5013.1	4296.1	5388.1	3800.5	4978.5
72.6	339.8	613.5	617.1	240.6	305.8	534.2	610.7	116.9	86.3	377.4
206.6	1028.1	939.2	794.6	1181.9	688.1	941.6	978.3	792.5	247.3	285.8
47.3	32.1	67.2	52.6	23.4	37.8	22.5	37.6	19.5	14.1	26.7
7928.4	6406.5	7138.7	6470.4	6974.3	5534.3	7277.0	6898.7	8241.3	8033.6	7936.4
32.7	367.6	618.6	664.8	143.9	265.8	135.6	282.5	49.4	81.2	99.9
36.3	129.4	204.7	180.9	171.5	127.0	240.0	157.1	62.4	33.2	219.7
40.6	264.6	232.9	295.4	92.6	218.4	96.3	244.2	49.0	35.3	68.1
35.9	1171.4	1999.5	2180.4	1552.5	1346.8	2301.6	1696.7	585.1	209.4	1136.6
43.8	974.5	1603.8	1583.9	614.3	1155.4	536.1	1239.7	300.0	89.4	955.4
58.9	456.8	749.9	794.1	985.7	337.4	1150.8	990.4	323.4	199.6	400.9
61.2	635.2	734.5	658.5	385.1	468.5	533.5	674.9	386.7	125.1	354.6
71.2	587.8	869.8	1006.6	214.3	669.3	418.2	1425.3	250.0	117.3	814.3
313.3	1256.4	1788.0	1562.2	1507.4	1265.3	1076.4	1891.7	778.7	420.9	792.0
346.5	2107.5	1733.0	2342.8	1255.6	1294.2	1262.1	1561.0	502.1	685.7	1501.4
19119.9	5738.5	5303.1	5738.9	6826.0	6013.5	6591.9	6097.5	8324.0	6400.3	8055.8
127.1	1614.2	2385.9	2096.1	1209.3	1800.5	2168.8	2023.9	900.7	591.8	1835.1
5456.7	1499.6	1586.7	1456.8	1068.3	1330.2	1527.1	1489.9	2011.9	1688.0	2488.0
40.9	882.6	1409.9	1768.4	247.8	541.4	559.4	798.0	139.8	123.6	592.7
1162.0	4480.5	4467.9	5602.1	4802.2	4961.5	5267.3	2986.3	6088.2	3522.3	4911.8
36.1	1112.1	1458.5	1321.7	854.3	1237.1	1104.1	1406.6	541.9	244.0	738.9
100.1	32.6	31.8	29.3	31.9	27.0	21.4	23.9	32.9	31.7	25.5
7176.7	2866.5	3174.7	3231.9	2629.5	3279.0	2581.6	3059.3	1461.9	3922.3	3557.4
552.0	1132.3	1630.8	1461.6	1417.4	1158.2	1657.7	1821.8	747.1	545.8	498.4
57.7	609.3	905.7	361.2	424.1	594.4	441.4	528.9	294.0	150.5	348.2
472.6	1200.8	1522.1	1434.9	1248.1	1144.7	1330.7	1466.8	579.7	471.4	703.4
329.4	711.6	1068.6	1080.2	853.4	735.0	677.9	701.2	575.6	270.1	43.5
54.4	1708.1	1642.1	1901.1	1064.1	1456.8	1073.5	2182.3	831.5	376.5	1454.8
122.1	1623.9	2013.5	2099.2	1134.4	1529.8	1668.6	2217.9	955.6	564.7	1749.8
1339.3	1631.8	1793.1	2390.8	2154.6	1599.8	2563.2	1864.1	1198.7	925.7	1385.1

2675.4	2321.7	1722.8
1990.5	2135.2	1908.2
2311.5	2839.8	2495.4
3083.2	1998.8	3068.5
1081.0	568.7	363.8
26.0	37.2	97.3
38.9	85.2	112.4
602.8	456.6	592.5
3838.3	4754.8	3984.1
3631.3	4548.4	4475.1
5229.4	4478.6	5029.9
4518.2	4657.1	4818.9
643.5	404.4	695.5
1269.0	763.9	1259.5
40.2	46.6	41.0
5833.8	7534.4	6111.6
471.4	396.7	338.5
256.1	176.3	306.4
352.3	257.6	184.4
1892.6	1192.4	2620.0
1610.2	652.5	1275.8
596.2	743.7	939.2
763.3	908.8	1193.1
1549.0	353.2	767.8
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2013.5	1476.6	1621.2
5041.1	6419.3	5375.6
1484.4	2137.8	5164.0
1631.4	2273.8	1721.5
1126.9	925.9	1167.3
3971.6	4389.3	4591.6
1916.5	1579.0	1684.5
38.7	34.8	21.8
3326.3	3580.5	1935.6
2108.5	1571.7	3197.4
320.4	959.5	746.7
1784.6	1694.7	1912.6
807.5	1497.4	882.1
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2317.6	1746.8	1950.2
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU467533.1 gg_id:289451 southern three-banded armadillo feces clone arma_c07 EU467
AY974824.1 gg_id:120145 human ascending colon mucosal biopsy clone KG39 AY974
EU765285.1 gg_id:353980 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
DQ804490.1 gg_id:183045 human fecal clone RL187_aan80f09 DQ804
AY977050.1 gg_id:125501 human cecum mucosal biopsy clone K737 AY977
DQ057463.1 gg_id:130773 str. ic1311 DQ057
AF349429.1 gg_id:77514 pig feces clone AF349
FJ682459.1 gg_id:531092 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
DQ681227.1 gg_id:169077 Clostridium sp. str. CCUG 52336 DQ681
DQ804981.1 gg_id:183879 human fecal clone RL385_aao83e12.Contig2 DQ804
EU765646.1 gg_id:314952 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
FJ678196.1 gg_id:531800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU464411.1 gg_id:294003 hamadryas baboon feces clone AFBAB_aai04e09 EU464
DQ796899.1 gg_id:178063 human fecal clone RL179_aao56b05 DQ796
DQ810086.1 gg_id:173818 human fecal clone RL184_aao67h09 DQ810
FJ683201.1 gg_id:520429 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU458581.1 gg_id:296062 European rabbit feces clone RA_b10 EU458
DQ806698.1 gg_id:182568 human fecal clone RL186_aao47f11 DQ806
DQ326854.1 gg_id:145816 Metagenomic gut microbiome healthy human stool clone E333 DQ326
EU344424.1 gg_id:274536 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU764140.1 gg_id:334924 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU764
EU771275.1 gg_id:311521 Asiatic elephant feces clone AE2_aaa01a04 EU771
DQ904671.1 gg_id:166355 human fecal clone 001-c9 DQ904
FJ371836.1 gg_id:368489 feces adult twins and mothers; TS8 clone TS8_a02g04 FJ3718
EU779456.1 gg_id:350041 Grevy's Zebra feces clone GZ_aaa04d07 EU779
FJ677085.1 gg_id:508767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
EU462009.1 gg_id:301062 black-handed spider monkey feces clone SPIM_aaj33c04 EU462
DQ797205.1 gg_id:185589 human fecal clone RL386_aao88d02 DQ797
DQ794958.1 gg_id:174728 human fecal clone RL310_aam38d10 DQ794
EU767041.1 gg_id:308033 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU451719.1 gg_id:314332 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU455854.1 gg_id:309480 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU455
EF098809.1 gg_id:197007 mouse cecum clone SWPT1_aaa01c09 EF0988
EU451515.1 gg_id:340858 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU451
EF097803.1 gg_id:175899 mouse cecum clone SWPT20_aaa03h09 EF0978
EF099638.1 gg_id:185662 mouse cecum clone SWPT4_aaa02c07 EF0996
DQ801358.1 gg_id:192552 human fecal clone RL388_aao94d12 DQ801
EU655870.1 gg_id:285410 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EF686595.1 gg_id:239218 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6865
EU534682.1 gg_id:281927 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU534

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42.4	25.2	19.1	25.4	21.7	25.6	18.0	14.8	22.4	20.5	24.0
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32.5	1093.6	1386.1	1083.3	331.6	861.8	668.4	1098.5	261.2	153.4	454.0
4352.7	3376.4	3315.6	3305.0	2727.9	3130.9	3089.8	3611.8	5174.0	3597.5	3876.2
248.9	789.2	1924.7	2130.2	2169.2	1650.0	2039.7	2326.7	796.0	458.6	1380.6
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38.0	489.9	784.6	949.2	381.0	466.3	512.3	671.8	220.1	94.7	317.3
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2289.9	2374.3	3271.0	3574.4	2184.9	2427.0	3501.6	3858.4	2152.4	992.2	3273.9
3350.0	1354.6	1981.1	2064.1	1739.7	1309.2	1509.0	1453.4	800.5	755.9	762.8
582.5	949.5	1242.9	1103.5	1313.0	815.9	1066.6	1477.7	538.9	628.9	681.5
721.3	2669.9	3979.6	3003.4	2987.5	3157.6	2005.6	4518.4	2743.1	4442.3	2700.8
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5014.5	3760.1	3543.3	3824.9	3785.2	3303.9	3078.0	2984.8	2795.2	2517.8	2703.6
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8658.3	6205.0	5352.1	5763.2	6124.2	5134.5	6788.3	5503.4	4801.7	4165.0	5575.6
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62.8	891.4	1073.6	1146.7	1048.6	359.5	1385.8	805.3	805.1	170.2	701.8
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361.9	576.2	406.9
1032.5	918.4	1521.1
3165.3	4618.2	3049.0
2406.1	2150.7	2602.8
1503.1	719.8	1401.5
116.5	124.5	120.8
1554.6	1746.5	1643.8
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956.6	664.7	574.6
752.8	377.3	201.7
2829.4	3084.7	2739.0
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4081.2	2832.0	3748.2
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1005.8	1225.3	857.4
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2369.5	2503.7	2888.2
4553.5	6542.1	8656.0
4397.6	4885.9	7728.1
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DQ014559.1 gg_id:132561 mouse cecum clone M1_a10 DQ014
DQ015117.1 gg_id:134199 mouse cecum clone M2_f06 DQ015
EU455454.1 gg_id:343850 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
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EU455235.1 gg_id:322112 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
EU506174.1 gg_id:277104 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02b09 EU506
EF099371.1 gg_id:189691 mouse cecum clone SWPT3_aaa02d06 EF099
EU474253.1 gg_id:292385 western lowland gorilla feces clone GORSD_aaa02f03 EU474
EU773343.1 gg_id:350154 BigHorn sheep feces clone BH1_aao28b05 EU773
EU451567.1 gg_id:321007 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
EU381914.1 gg_id:265316 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
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EU450921.1 gg_id:337561 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU450
EU455730.1 gg_id:342015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
EF099372.1 gg_id:174704 mouse cecum clone SWPT3_aaa02d07 EF099
AY993109.1 gg_id:133763 mouse cecum clone C21_e12 AY993
EU474275.1 gg_id:291704 western lowland gorilla feces clone GORSD_aaa01c03 EU474
EF099245.1 gg_id:183700 mouse cecum clone SWPT2_aaa04e06 EF099
EU474231.1 gg_id:289177 western lowland gorilla feces clone GORSD_aaa02c10 EU474
EU505040.1 gg_id:266401 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02a06 EU505
EF096196.1 gg_id:181581 mouse cecum clone obob1_aaa02d02 EF096
EF098895.1 gg_id:197377 mouse cecum clone SWPT1_aaa02h09 EF098
EU455185.1 gg_id:330583 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
EU505171.1 gg_id:267850 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03h02 EU505
EU457977.1 gg_id:315158 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU457
EU453701.1 gg_id:315630 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU453
EF097503.1 gg_id:196243 mouse cecum clone SWPT19_aaa03e09 EF097
EF096852.1 gg_id:187520 mouse cecum clone SWPT13_aaa01f11 EF096
EU451453.1 gg_id:352892 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU503923.1 gg_id:260018 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02f08 EU503
EF099859.1 gg_id:197423 mouse cecum clone SWPT5_aaa01d07 EF099
AY992896.1 gg_id:134211 mouse cecum clone C22_h11 AY992
EU772813.1 gg_id:354258 Bush dog feces clone bdog1_aai80f06 EU772
EU451007.1 gg_id:321497 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EF097395.1 gg_id:197416 mouse cecum clone SWPT19_aaa02a08 EF097
EU451588.1 gg_id:322357 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
EU503986.1 gg_id:264289 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03f06 EU503
EF098956.1 gg_id:190962 mouse cecum clone SWPT1_aaa03h06 EF098
EU455856.1 gg_id:337586 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455

12218.4	3423.7	3319.3	3724.4	3715.0	3220.9	4126.4	3989.4	3491.9	3774.7	4984.1
39.2	109.9	196.1	166.0	149.3	105.2	206.9	150.8	76.5	84.1	98.9
2802.2	4485.5	3599.7	3512.3	2750.6	3218.3	3757.6	3055.6	4631.6	3025.6	4031.3
853.5	1592.8	2019.8	1552.5	1728.4	1586.5	1786.0	1783.9	1393.6	2237.7	1048.6
378.7	1954.5	2641.4	1947.3	1844.0	2022.7	2240.5	2177.5	1091.6	1146.9	2099.3
3312.2	1259.6	2006.1	2140.9	1160.7	1408.9	1329.6	2036.0	575.2	379.5	851.3
4517.5	1789.4	2190.1	2194.9	2236.1	2349.0	2880.0	2005.2	2145.0	3360.4	2130.4
71.3	1581.0	2019.5	2039.7	2614.1	2030.2	1964.1	1891.7	509.2	250.9	757.3
412.5	1976.5	2042.2	1326.7	1073.7	1370.4	1695.1	1400.8	2160.1	3024.9	1839.8
45.5	465.2	655.4	660.0	413.7	519.6	443.2	551.4	134.2	87.7	337.2
68.3	986.0	1373.5	1154.0	1351.1	1188.1	577.1	1954.6	856.3	2606.7	651.2
938.3	2007.3	2661.1	2393.7	1837.2	1617.0	2174.3	1724.4	1415.9	1139.0	2447.7
71.3	33.7	34.9	29.3	47.4	32.1	23.8	29.4	23.4	19.5	24.5
3545.6	2567.8	2230.2	2165.7	2143.5	2396.1	2752.0	2082.1	2722.9	3383.9	2455.3
38.9	383.0	508.4	497.4	286.0	475.7	401.8	691.4	105.3	40.7	256.1
8356.0	4093.9	5161.0	4611.8	3736.8	4001.6	4724.6	4294.3	4925.0	4567.7	4783.0
2446.2	775.9	934.3	993.1	768.3	1061.1	1034.4	1030.8	760.5	876.4	845.1
77.2	89.2	108.8	91.4	74.3	71.6	71.5	103.6	68.8	103.9	68.0
12077.5	4477.0	3885.2	4053.1	4412.2	4302.5	4469.0	3663.4	3713.6	5800.6	4033.3
7768.1	3681.6	3686.9	3851.5	4398.5	3542.5	4127.3	3743.1	4470.0	3266.8	3625.3
1120.8	1851.2	2659.2	2089.4	1168.6	1532.4	2561.6	2113.3	1053.0	997.9	1350.9
1841.5	938.6	791.4	600.9	672.3	814.8	625.3	768.4	750.5	874.2	1115.8
65.8	683.1	906.8	725.5	408.0	618.5	516.3	772.8	927.7	689.7	674.6
83.3	579.1	786.5	1101.3	682.2	893.1	778.8	721.4	90.4	285.4	299.1
44.6	412.7	608.1	511.5	317.8	403.3	391.3	524.0	40.0	125.2	343.7
419.6	2241.3	2308.9	1897.8	1936.0	1819.1	2578.7	1934.8	1418.2	1054.5	2107.6
2327.7	2800.9	3082.8	3416.6	3081.3	2865.2	3422.2	3086.0	2076.6	1583.1	2773.9
36.2	171.2	605.1	394.5	69.2	149.4	203.3	225.0	101.3	41.8	163.9
59.5	466.9	555.7	603.5	535.6	497.5	703.3	492.8	163.6	61.0	260.5
9225.0	6283.0	5054.1	6231.5	6345.5	5457.9	5537.3	6463.6	6405.1	6096.8	6402.4
17561.8	5381.1	4912.4	5331.1	4914.0	4889.8	6978.1	6191.2	7390.2	7105.2	7343.3
64.2	520.0	749.3	888.7	69.9	290.1	175.0	391.1	63.1	64.6	245.6
74.9	1199.2	1013.5	939.0	1337.4	839.2	1864.3	810.8	534.8	229.5	674.8
24.5	213.3	351.5	365.3	282.6	227.2	397.6	192.0	92.1	118.2	187.6
318.0	6417.2	6688.3	6544.9	5663.1	5572.8	4097.6	6589.7	5171.5	3218.0	6592.7
35.3	48.5	72.6	83.7	45.7	40.1	60.6	47.0	34.6	113.0	24.9
8298.2	2825.5	4131.3	3413.6	2922.4	2614.4	4621.8	2456.2	2937.2	3170.3	4117.0
10559.8	5488.7	6462.0	5341.6	6352.5	5377.5	6503.3	5288.7	8519.2	7042.0	6679.3
181.9	2253.4	3585.9	2873.7	2690.5	2367.4	6245.3	2686.7	2876.7	1789.6	2775.1
171.4	2827.4	3301.4	3168.5	2464.0	2993.9	2333.6	3386.9	2243.3	1724.3	2198.9
2523.5	2033.9	3258.4	2292.0	1641.9	2069.0	3014.1	2182.7	2209.5	1882.6	2156.8

3797.1	4802.4	4140.5
170.8	386.6	202.8
3043.5	3543.8	3455.9
1929.4	2141.6	2659.6
2120.0	2660.8	2541.4
2332.8	2257.0	2487.2
2479.9	2575.6	2946.2
1976.8	2530.2	2896.2
1153.4	1806.8	1552.4
534.5	512.3	612.4
1457.8	1598.7	3193.0
1611.6	3026.8	1826.1
25.4	59.7	165.2
2256.3	2586.3	2422.9
663.9	317.6	875.5
3739.4	4521.4	4767.7
61.8	1305.0	1135.9
62.3	171.0	76.3
4887.6	4744.3	3532.5
3303.7	4897.9	3787.9
2336.8	1973.2	2433.8
26.3	1106.6	507.3
704.8	1147.7	899.9
738.0	774.2	967.7
471.5	695.9	669.2
1779.8	2583.6	2305.3
4539.6	3863.9	2608.0
230.2	275.4	586.2
381.3	615.1	816.5
5331.1	6411.3	6116.0
4329.6	7343.9	4900.0
611.3	481.6	674.8
763.4	834.9	849.2
344.5	761.4	618.8
7045.8	5800.4	7720.6
65.6	101.1	73.6
2588.4	3770.6	3661.5
5670.2	7120.4	6629.5
1878.5	3381.3	2728.2
2757.5	3680.5	3500.7
1899.1	2997.3	3025.0

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EU457239.1 gg_id:307771 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
EF604509.1 gg_id:232645 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EU504979.1 gg_id:268552 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b03 EU504
EF100032.1 gg_id:175557 mouse cecum clone SWPT5_aaa03g03 EF100
AY993003.1 gg_id:130513 mouse cecum clone C22_n24 AY993
EF099410.1 gg_id:197215 mouse cecum clone SWPT3_aaa02h03 EF0994
EU457313.1 gg_id:344832 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
DQ793516.1 gg_id:202709 human fecal clone RL199_aaj44g09 DQ793
EU776954.1 gg_id:304097 Naked mole-rat feces clone molerat_2b12 EU776
EU456999.1 gg_id:324469 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
EU451921.1 gg_id:353922 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU451
EF096326.1 gg_id:185929 mouse cecum clone obob1_aaa04h11 EF0963
EF097332.1 gg_id:199333 mouse cecum clone SWPT19_aaa01c01 EF0973
EU474288.1 gg_id:289866 western lowland gorilla feces clone GORSD_aaa04e11 EU474
EU474220.1 gg_id:303184 western lowland gorilla feces clone GORSD_aaa02a10 EU474
EU453947.1 gg_id:333602 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU456021.1 gg_id:305896 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
EU453094.1 gg_id:313898 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU453
EU505189.1 gg_id:274627 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04b11 EU505
EU452853.1 gg_id:311225 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
EF097330.1 gg_id:191857 mouse cecum clone SWPT19_aaa01b08 EF0973
EU504478.1 gg_id:269893 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01b08 EU504
EU452157.1 gg_id:345604 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
EU510069.1 gg_id:267012 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf12b05 EU510
EF099469.1 gg_id:196740 mouse cecum clone SWPT3_aaa03e12 EF0994
EU778263.1 gg_id:352604 feces clone RL388_aao96c11 EU778
DQ014586.1 gg_id:132198 mouse cecum clone M1_d02 DQ014
EU505016.1 gg_id:263685 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f06 EU505
EU842518.1 gg_id:317517 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ881271.1 gg_id:381030 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EU503982.1 gg_id:268133 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03f02 EU503
EU468265.1 gg_id:292256 domesticated horse feces clone horsej_f07_2 EU468
EU457124.1 gg_id:331117 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU457
EU456402.1 gg_id:352955 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
EF099360.1 gg_id:186414 mouse cecum clone SWPT3_aaa02c04 EF0993
EF097660.1 gg_id:177443 mouse cecum clone SWPT20_aaa01h09 EF0976
FJ833939.1 gg_id:551915 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q201_72H09 FJ8339
AY992847.1 gg_id:135505 mouse cecum clone C22_e24 AY992
EF099375.1 gg_id:174597 mouse cecum clone SWPT3_aaa02d11 EF0993
EU451214.1 gg_id:350100 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU458083.1 gg_id:338652 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU458

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3392.7	5112.3	5365.2	4862.2	5169.0	4729.4	6464.3	4962.9	3586.0	4690.2	4345.2
73.3	1386.8	2225.5	1848.5	1513.9	1732.6	1406.5	1484.7	896.3	817.4	1182.7
6040.8	5849.0	5845.6	6181.3	5313.6	5500.2	5638.5	5573.1	5971.6	3770.3	3250.6
14308.3	5812.4	5800.1	6338.3	7340.3	5825.2	6263.1	5699.3	7296.3	6352.4	6340.0
34.8	115.1	125.2	117.0	108.9	133.2	100.2	161.6	271.9	209.6	141.0
6894.9	3002.6	3453.6	3475.5	2726.1	2989.2	3720.4	3916.0	3684.7	3223.8	4501.2
28.4	118.4	181.0	177.1	74.2	134.2	153.0	192.8	28.6	44.0	78.0
34.8	16.9	22.6	23.6	13.6	15.6	21.9	15.6	17.0	12.3	17.8
12141.1	5811.6	6928.7	5758.6	5368.6	5518.8	6917.0	5356.2	8722.1	7009.2	8046.4
65.5	813.7	1384.2	798.1	1054.2	1239.3	886.5	1056.1	385.8	203.6	656.4
7836.2	3743.8	4043.2	2398.4	3532.3	3331.0	4763.9	3345.3	4815.1	4077.3	4001.8
17108.3	4421.1	3744.2	3977.1	4646.3	3712.6	4620.5	2401.6	4909.4	4953.9	4834.7
2251.7	4774.8	3680.1	3549.1	3394.7	3509.9	3981.4	3402.6	4878.7	3887.4	3801.3
32.2	448.6	875.6	473.7	36.6	431.7	20.8	279.2	190.6	63.1	292.9
2516.8	5875.7	4150.5	4297.8	3379.7	4160.4	4818.9	5505.3	6929.4	5863.6	3693.8
330.2	2298.0	4414.6	3149.9	2196.0	2160.2	2624.4	2695.2	1181.7	2404.7	2081.0
2122.0	1293.5	1863.2	1989.5	1768.7	1451.8	2097.0	1693.7	943.1	627.5	1380.5
1213.7	1487.9	1682.9	2086.2	1241.8	1837.1	1861.6	844.8	734.9	268.3	1777.6
18499.6	5650.2	5384.5	5459.7	5436.0	5193.9	6628.0	6497.3	7793.1	9273.4	6134.9
4935.9	2383.0	3785.7	3425.2	3533.0	3387.4	4186.4	3061.9	4319.3	3426.1	5721.0
5302.6	2695.7	2509.3	2594.3	2252.3	2182.6	2777.6	1911.6	2154.8	2044.3	3056.3
62.8	201.8	558.0	349.3	163.4	200.4	280.8	421.3	168.6	113.4	199.9
6262.0	3159.4	3082.0	3092.8	2717.8	2872.5	2985.2	3028.0	3412.6	2906.7	3806.6
5856.0	2319.5	2293.6	2216.9	1663.0	2265.2	2603.4	2946.0	2738.3	3522.3	2903.4
59.7	188.9	397.0	232.2	77.9	190.7	101.0	285.9	70.9	49.8	164.9
82.7	144.3	349.1	228.7	410.9	202.1	321.5	230.0	258.4	119.5	138.7
1788.4	3705.2	3271.5	3525.7	3260.6	2884.5	3514.0	2728.8	2131.0	2466.3	2572.6
2386.8	3599.0	3660.9	4350.7	4393.8	4269.9	4502.7	5536.7	4835.8	4211.8	4009.6
14622.3	4709.3	4152.8	4396.9	4167.2	3993.9	4968.9	3682.3	6511.8	5329.4	6871.9
37.3	182.1	282.4	224.3	137.1	143.5	234.4	120.8	84.6	139.0	116.1
199.1	2063.5	2702.4	2858.0	1909.7	2587.1	2302.1	3374.0	2331.6	1224.6	2362.3
31.5	280.2	692.0	914.8	61.3	152.8	100.1	465.7	87.8	24.0	186.2
4512.7	1353.8	1247.4	1217.3	1181.3	1138.4	931.6	1910.2	546.2	303.3	603.6
5300.3	6834.8	4133.0	4524.8	3199.1	4047.0	5156.4	5358.2	6806.8	7034.5	6632.2
6939.7	3097.3	2529.9	3099.3	2674.9	3008.2	3435.1	2516.0	2769.1	589.5	2999.3
6025.1	3427.0	4300.1	3626.0	3527.5	3752.2	3424.7	4560.0	5126.6	2220.3	4397.1
48.0	1993.5	1610.5	1426.8	1540.8	1224.8	2046.1	1528.2	2311.4	2236.8	1261.4
46.9	74.6	111.9	118.3	66.4	67.0	97.8	109.0	37.5	66.8	26.1
3130.2	1871.3	3910.4	3116.1	2377.5	2659.4	4446.1	2554.0	3465.3	2915.2	1590.1
31.6	173.3	470.7	341.5	165.6	256.5	212.6	268.2	144.1	141.4	331.6

2203.0	2558.1	2852.3
5225.1	5752.8	6518.5
1623.1	1366.2	1950.0
5895.2	6016.6	7227.6
6966.7	7000.6	7660.5
115.4	474.1	151.6
3106.2	4310.2	4216.3
99.9	170.0	157.8
17.1	26.4	43.2
5395.2	7994.5	6834.5
778.3	763.0	882.9
3528.2	4802.3	3984.3
4488.8	4372.1	3999.7
3606.0	4700.2	4857.7
270.6	325.7	1052.9
4714.0	4510.0	5585.3
2456.4	3173.4	3120.8
1603.8	2165.5	1986.1
1528.2	1467.0	3372.2
5033.2	5096.1	6062.2
2952.3	4546.4	3447.4
2226.4	2882.1	2337.7
510.0	621.8	408.0
2553.1	3663.9	3646.6
2097.4	3176.2	2792.4
372.7	411.5	406.9
346.9	218.4	209.3
3753.0	3504.4	2762.6
5517.9	4777.2	7016.1
3875.5	5019.1	3645.4
142.3	249.5	310.4
2355.3	2938.0	2730.3
582.9	249.0	141.1
1566.0	2413.8	1525.7
3250.8	5008.9	3881.9
2517.0	2570.8	2825.8
3561.9	3648.5	4455.6
1315.9	1446.9	1326.2
147.7	160.5	144.6
2845.8	2937.7	2938.2
270.8	491.9	585.7

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EU452481.1 gg_id:311569 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU452
EF097653.1 gg_id:190116 mouse cecum clone SWPT20_aaa01h01 EF0976
EF096149.1 gg_id:180044 mouse cecum clone obob1_aaa01d01 EF0961
EU504954.1 gg_id:265135 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g05 EU504
EU467414.1 gg_id:296960 chimpanzee feces clone CHIMP12_a09_1 EU467
DQ015306.1 gg_id:130488 mouse cecum clone M2_1d06_2 DQ015
EU504093.1 gg_id:263621 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01b06 EU504
EU453452.1 gg_id:307074 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
EF099545.1 gg_id:176873 mouse cecum clone SWPT3_aaa04g02 EF0995
EU504080.1 gg_id:272205 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01a03 EU504
EF099034.1 gg_id:177397 mouse cecum clone SWPT2_aaa01d02 EF0990
EU455000.1 gg_id:303508 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
AY992844.1 gg_id:129614 mouse cecum clone C22_e21 AY9928
EU455363.1 gg_id:339952 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
EU453246.1 gg_id:334157 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU453
EU655813.1 gg_id:286236 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU504112.1 gg_id:264837 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01d10 EU504
EU451028.1 gg_id:307134 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU452732.1 gg_id:315731 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU452
DQ015394.1 gg_id:129484 mouse cecum clone M3_e11 DQ015
EF096795.1 gg_id:188148 mouse cecum clone SWPT11_aaa04g11 EF0967
AY991728.1 gg_id:129740 mouse cecum clone C20_b02 AY9917
EU454358.1 gg_id:329215 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454
EU505054.1 gg_id:259476 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02c04 EU505
EU453190.1 gg_id:307569 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU453
EU778338.1 gg_id:312707 feces clone RL388_aao93g07 EU778
EU474420.1 gg_id:297312 western lowland gorilla feces clone GORSD_aaa02d04 EU474
FJ880298.1 gg_id:423411 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
AY992981.1 gg_id:132309 mouse cecum clone C22_m13 AY9929
FJ881252.1 gg_id:372432 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EF099353.1 gg_id:197981 mouse cecum clone SWPT3_aaa02b08 EF0993
EU504577.1 gg_id:271311 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa02g01 EU504
AY916266.1 gg_id:113482 human rectum biopsy clone LP40 AY9162
EU457113.1 gg_id:308481 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
EU453390.1 gg_id:348679 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
EU455365.1 gg_id:307574 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EU457667.1 gg_id:352049 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
AY992938.1 gg_id:132015 mouse cecum clone C22_k01 AY9929
EU451335.1 gg_id:338609 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
AY992943.1 gg_id:129843 mouse cecum clone C22_k06 AY9929
EU457493.1 gg_id:348559 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU457

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131.9	482.9	552.4	638.4	414.3	330.2	471.3	446.2	477.3	91.0	179.2
1142.4	1655.0	2547.4	2733.5	1965.1	2062.7	2451.3	2724.5	1281.5	632.7	1735.5
1441.4	5669.2	5464.2	5888.5	5269.1	5194.3	6428.0	5993.6	6256.2	4604.0	5121.1
821.5	2240.5	2761.4	2696.2	1631.2	2282.1	2046.1	2693.7	1781.1	1863.8	2088.8
6598.5	4214.1	3519.2	3773.0	3802.7	2952.0	3991.1	2811.7	4105.1	4044.5	5367.0
7705.4	8105.7	7505.4	6203.4	6369.5	6347.5	8170.1	5459.4	10109.1	9930.7	8495.9
11121.0	3877.1	3858.9	3968.2	3417.4	4060.4	3999.4	4011.5	6077.5	6161.9	6739.5
469.0	1530.6	1561.4	1588.2	1286.8	1571.1	1704.0	1574.2	1211.1	1102.1	1107.4
11253.5	4717.5	5741.8	4665.8	4211.0	4365.9	5761.7	4126.1	4852.3	4998.1	6285.9
4617.9	2252.1	1928.1	1884.6	1790.0	1833.2	2344.5	1555.0	2657.1	2335.6	2467.2
501.1	1435.3	1735.1	1695.5	1700.6	1409.1	1906.9	1688.8	966.0	502.3	1230.0
16263.2	6605.0	6807.7	6807.1	6341.6	6099.5	7724.1	5778.5	8890.0	7053.0	9618.9
579.0	2961.8	3827.9	3346.7	2968.9	2646.0	4090.9	3577.5	1187.4	1896.3	3097.1
2252.8	1578.3	2290.0	2335.5	1291.6	1900.5	1965.1	1992.9	1362.3	718.2	3531.0
2880.6	2512.5	2605.5	2704.9	2975.8	2360.8	2619.5	2071.1	2054.4	1526.2	1507.9
5574.7	4014.7	4098.2	4291.8	4018.2	4022.7	5015.4	5236.5	5155.2	2849.2	3287.4
5238.3	2590.6	2198.3	2073.0	1866.1	2038.3	2497.0	2088.5	3148.9	2793.5	2983.7
35.1	124.7	267.1	213.2	100.8	149.8	147.2	275.9	86.3	193.4	97.3
1606.6	1126.4	1029.2	1356.2	1219.2	844.7	1146.8	1030.3	515.7	293.1	471.3
34.8	27.9	42.2	35.9	17.1	33.0	26.9	22.9	22.2	23.3	22.6
35.9	2043.6	2226.1	2008.7	1130.3	1976.2	2766.8	2208.9	3744.0	2641.4	2145.9
7366.7	7201.9	5220.8	5847.2	4726.8	5481.8	7188.8	6131.3	8243.9	7729.5	7868.4
10249.3	2967.8	3259.0	2945.4	2785.3	2609.6	3256.5	2631.1	3714.1	3628.1	4187.8
10760.6	4656.9	5808.0	5551.1	4000.8	4285.0	5505.6	4692.3	5163.0	4281.5	6137.9
47.4	97.3	119.7	146.6	135.4	116.3	147.1	150.3	64.0	30.0	83.3
5470.1	3152.8	2801.1	2839.3	2967.0	2589.5	3258.9	2663.8	2747.8	3566.1	3094.6
40.1	129.0	228.5	378.7	229.3	84.4	166.4	87.0	38.8	68.9	73.6
123.6	251.0	346.6	322.4	480.3	295.2	362.0	399.7	142.7	139.1	149.5
11170.2	5564.2	5779.9	6526.4	5395.1	5562.4	8210.3	6225.7	6664.0	4393.9	7855.0
284.6	3600.4	3890.8	2912.9	1706.3	2573.3	2599.7	2583.0	3105.3	2686.1	3318.4
658.0	191.3	301.2	288.6	178.6	237.5	177.9	408.6	78.9	119.6	124.8
46.2	999.3	1614.1	1977.8	478.9	961.4	613.9	1484.2	278.4	703.4	772.8
59.4	918.2	1729.1	1347.3	869.3	1038.9	1096.5	1327.9	470.9	595.3	1044.2
6366.5	5477.9	3219.1	3438.0	2790.3	1774.0	4182.6	3795.2	6058.6	7087.5	4091.2
8845.9	5732.3	4535.4	4925.4	6638.2	4350.2	5777.3	4547.1	4864.1	2226.5	3614.6
571.6	1883.7	2387.0	2307.7	1542.4	2619.8	1790.6	2648.5	1342.9	827.4	2102.7
3478.8	2692.9	3255.1	3149.4	2647.0	2689.9	3181.8	2876.4	1591.6	1578.9	1680.1
5861.9	2964.9	2935.6	2933.5	2953.9	2447.1	2987.7	2832.5	4438.9	3145.2	3149.2
641.5	3322.5	3958.2	2881.8	1956.9	3358.4	2458.1	2523.2	5290.1	7153.4	5225.1
83.2	1325.5	1524.4	1950.6	933.4	1056.7	975.9	1521.2	478.9	240.2	1163.0

1419.8	1715.7	1655.1
393.1	642.0	707.2
1961.8	3293.7	3200.3
6181.5	6086.1	5909.9
2757.0	2595.8	3307.9
3739.9	4429.5	2966.9
6643.1	6588.3	7034.5
3111.5	5219.7	3484.2
1420.8	1715.4	1588.5
3976.4	5684.3	4317.4
1316.7	2720.5	1513.9
1488.1	2329.4	2569.9
5690.1	8389.3	7251.1
2365.1	3410.0	3965.7
2030.3	2151.1	1790.0
2606.9	3332.2	2837.5
4026.5	4413.0	4768.9
2169.5	2862.2	2450.0
224.8	340.1	406.5
1305.1	1478.8	1497.5
39.4	58.0	41.1
1752.2	2167.7	1923.5
5059.5	5319.4	4934.2
2834.0	4075.9	3067.7
4164.5	5252.1	5231.7
101.9	407.1	400.3
3230.3	2649.4	2504.3
178.8	253.4	405.0
389.4	424.8	411.3
6589.9	6851.7	7454.8
2222.1	2970.2	2281.0
393.8	590.0	753.2
1640.7	1066.4	1237.5
1587.1	1587.8	1634.9
2444.3	3955.5	3123.6
4729.4	5134.6	6548.6
3376.8	2589.1	3034.7
3580.8	4492.8	2704.9
3063.1	3748.4	3184.9
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AY991757.1 gg_id:130270 mouse cecum clone C20_c18 AY991
EF097744.1 gg_id:183649 mouse cecum clone SWPT20_aaa03a10 EF0977
EU474227.1 gg_id:289283 western lowland gorilla feces clone GORSD_aaa02g03 EU474
EU456912.1 gg_id:309335 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU456
EF097562.1 gg_id:180476 mouse cecum clone SWPT19_aaa04d07 EF0975
EU455509.1 gg_id:313058 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
EU467652.1 gg_id:288325 naked mole-rat feces clone molerat_2b01_1 EU467
EU505125.1 gg_id:266288 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03b12 EU505
EF099346.1 gg_id:187648 mouse cecum clone SWPT3_aaa02a07 EF0993
EU503843.1 gg_id:273118 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01d07 EU503
EU452596.1 gg_id:345936 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU452
EF098890.1 gg_id:196119 mouse cecum clone SWPT1_aaa02g12 EF0988
EU475497.1 gg_id:293085 springbok feces clone SBSD_aaa02d11 EU475
EU778225.1 gg_id:311587 feces clone RL387_aao91b09 EU778
EU773290.1 gg_id:332742 BigHorn sheep feces clone BH1_aao26d03 EU773
DQ805491.1 gg_id:196494 human fecal clone RL203_aai63d02 DQ805
EU461402.1 gg_id:288950 red kangaroo feces clone KO2_aai20c04 EU461
EU778262.1 gg_id:347758 feces clone RL388_aao96h02 EU778
EU503709.1 gg_id:261132 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03e06 EU503
EU456193.1 gg_id:305753 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU456
EF098371.1 gg_id:202419 mouse cecum clone SWPT15_aaa01g04 EF0983
AB525414.1 gg_id:590169 Eubacterium saburreum str. JCM 11021 AB525
EF096517.1 gg_id:176243 mouse cecum clone obob2_aaa04b10 EF0965
EU451862.1 gg_id:304890 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU451
EU507682.1 gg_id:267982 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03b04 EU507
EU453519.1 gg_id:325047 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU455560.1 gg_id:317493 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
AJ272036.1 gg_id:30334 Parasporobacterium paucivorans str. SYR1 AJ272
EU504236.1 gg_id:267699 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04g05 EU504
EU469466.1 gg_id:288134 black lemur feces clone BKLE_d01_2 EU469
FJ677674.1 gg_id:521913 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
EU506582.1 gg_id:265839 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04g04 EU506
EU844109.1 gg_id:335527 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AF287769.1 gg_id:73894 human subgingival plaque clone AH153 AF287
DQ815607.1 gg_id:171088 mouse cecum clone aab43e06 DQ815
GU304514.1 gg_id:539098 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU843745.1 gg_id:346371 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU507725.1 gg_id:261007 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03g05 EU507
AB185642.1 gg_id:101771 rumen clone F24-G10 AB185
AM420119.1 gg_id:252100 Noma subgingival plaque clone 401E03(oral) AM420
EU465947.1 gg_id:295489 African elephant feces clone AFEL3_aao14f05 EU465

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5869.9	4812.2	6025.0	5406.6	5805.1	4828.7	5785.1	5520.4	4872.5	3532.9	5110.9
534.3	844.1	1044.3	835.4	900.4	897.2	1130.7	812.6	908.7	1690.2	776.0
47.2	594.1	864.2	878.0	399.2	686.6	628.6	1455.2	343.9	761.6	709.8
394.9	1102.7	1317.8	1170.9	922.8	1124.2	1439.4	1256.6	1212.8	1894.5	626.8
97.4	1680.3	2663.1	1909.0	1438.8	1620.7	1993.3	1792.8	1338.4	667.5	1265.5
1239.7	2229.1	2415.0	2868.0	3536.4	2403.4	3501.2	2383.8	1777.7	1719.4	1811.2
510.1	834.4	907.4	1007.6	781.5	832.0	992.6	881.0	645.6	873.1	509.6
6871.0	3165.6	3435.5	3799.2	3258.5	2578.0	3676.1	2854.1	1522.5	1809.8	1932.4
7516.2	5310.4	4432.7	4400.4	5596.2	4620.6	5243.1	4638.3	4236.2	3867.0	4003.5
9586.0	4921.6	5213.9	5142.3	5315.3	4762.7	5454.6	4543.1	7478.9	5938.1	5555.4
269.4	2309.4	2668.3	2769.7	2153.1	2048.4	2604.0	2082.0	2699.1	1672.2	1856.8
71.2	742.8	997.3	1255.6	816.2	930.9	898.9	1062.5	293.9	129.3	507.6
4159.0	4828.8	5113.5	6474.5	5297.6	4559.5	5750.4	4894.0	4823.7	4534.0	6536.3
7536.6	5621.2	6052.8	6146.9	6226.6	5894.1	6446.6	5837.7	6735.2	4947.4	5664.7
66.7	1637.5	2988.7	2293.7	1936.8	2187.6	1730.7	2256.8	1006.0	490.2	1436.1
36.0	130.1	197.9	288.0	130.2	52.7	216.8	228.8	70.2	14.8	77.4
50.1	217.6	326.3	398.4	154.6	297.1	245.6	662.3	117.0	95.8	198.6
11932.1	3939.3	4271.1	4345.8	3008.4	3580.5	4007.3	3596.9	4820.9	3111.0	5242.2
30.1	65.5	164.8	97.8	24.6	36.8	36.8	53.0	40.1	19.2	82.3
376.8	1507.7	1560.3	2530.9	2137.6	1298.9	2720.9	1578.5	780.7	364.1	788.7
3229.8	1107.2	1592.1	1785.3	1327.1	1250.7	1629.0	1645.7	3239.2	1871.2	1570.1
12507.0	3646.7	3116.7	3240.8	3819.0	4308.2	4503.3	3219.1	4033.3	2861.8	3305.4
1196.1	3095.1	5072.5	6719.8	3242.1	2937.0	3131.0	3533.0	988.9	674.3	3245.6
4392.3	4071.8	3304.6	4208.9	3846.8	3347.1	3367.8	3532.3	3216.6	1497.5	3047.6
3425.6	3317.7	2961.8	2803.7	2997.0	3374.2	2700.6	3231.9	3807.0	2807.0	2930.4
323.9	1981.3	2729.5	3059.9	2220.2	1438.4	2352.9	2528.4	751.0	924.8	1509.2
8476.0	5146.6	5200.0	5437.0	6015.2	5088.9	5468.0	5436.8	4621.1	2505.2	4548.8
607.4	2403.5	3504.2	2977.8	1993.3	1987.3	2166.1	2728.3	1362.2	517.7	2323.8
91.0	1089.7	1491.2	1534.1	736.2	1142.6	1313.7	1629.3	521.1	575.8	823.8
160.0	880.2	1248.7	1451.9	587.8	869.4	753.1	1394.2	380.9	361.9	868.7
328.4	1717.9	2471.3	2051.9	1948.6	2265.4	2275.6	2059.0	995.0	1054.2	1138.6
563.7	2433.0	2982.1	2866.6	3286.6	2410.3	2684.2	2653.6	1598.3	1291.5	1981.5
8685.2	5223.8	5127.4	5283.9	4888.8	4746.3	4717.8	5261.3	4073.2	3278.7	4722.9
3196.2	5638.6	5884.7	5739.9	5558.6	5383.2	5966.5	5836.6	5301.6	5084.0	5475.0
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425.5	989.4	962.0	869.3	737.5	687.8	699.9	891.0	637.1	927.0	959.0
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141.5	4504.7	5273.1	7698.7	5094.1	6359.7	2136.9	6526.3	7652.0	16159.8	4708.2
67.1	1612.3	2105.0	2297.4	842.0	1138.5	1537.0	1657.7	960.1	559.9	1011.2

2076.5	2407.2	2485.7
283.1	533.3	145.7
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628.0	847.6	1059.2
1542.4	1281.8	1321.4
1215.6	1863.8	1471.1
1531.9	2370.1	2060.8
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784.5	1218.4	1318.7
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2404.5	2741.4	2831.6
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5247.9	5318.9	6479.9
5849.6	6901.7	9079.8
1884.9	2134.7	4915.8
254.7	276.1	453.0
668.5	372.2	589.6
3491.0	4656.7	3870.3
82.7	94.8	42.6
1617.1	1801.7	2091.9
1822.9	1571.4	1617.2
3899.0	4224.2	4141.2
4359.0	5236.8	4743.0
3967.2	3575.5	4039.7
2690.9	3136.0	4114.9
2915.1	2847.3	3546.5
5493.6	6117.5	7009.6
2661.7	2833.1	3504.0
2402.8	1085.8	1346.1
1291.9	1398.1	990.4
2302.2	2161.5	2612.0
2166.0	3011.8	3940.5
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4073.3	6579.2	7687.4
4928.7	4202.6	4920.2
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EU507476.1 gg_id:258376 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03g07 EU507
AF481219.1 gg_id:73120 oral endodontic infection clone MCE9_104 AF481
EU451262.1 gg_id:356504 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EF096325.1 gg_id:192372 mouse cecum clone obob1_aaa04h10 EF0963
EF686587.1 gg_id:255980 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC7 EF6865
EU452564.1 gg_id:341005 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU452
FJ370255.1 gg_id:369685 feces adult twins and mothers; TS56 clone TS56_a02e02 FJ3702
EU508104.1 gg_id:261114 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa04a12 EU508
DQ015500.1 gg_id:134346 mouse cecum clone M3_g10_1 DQ015
FJ976266.1 gg_id:576638 Interindividual healthy human oral microbiota mouth clone 7BB311 FJ9762
EU452099.1 gg_id:323632 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU452
DQ803974.1 gg_id:191531 human fecal clone RL200_aai60e12 DQ803
EF099504.1 gg_id:180492 mouse cecum clone SWPT3_aaa04b01 EF0995
EF096289.1 gg_id:175444 mouse cecum clone obob1_aaa04b11 EF0962
EU461502.1 gg_id:300401 black rhinoceros feces clone RH_aaj91b02 EU461
EF097966.1 gg_id:185707 mouse cecum clone SWPT12_aaa03a11 EF0979
DQ815819.1 gg_id:162811 mouse cecum clone aab22g02 DQ815
EF099530.1 gg_id:185334 mouse cecum clone SWPT3_aaa04e05 EF0995
EU504732.1 gg_id:276204 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01c07 EU504
EU454681.1 gg_id:334577 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
GU303857.1 gg_id:588409 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
DQ805347.1 gg_id:185961 human fecal clone RL203_aai61e01 DQ805
EU455218.1 gg_id:335042 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
EU455007.1 gg_id:306262 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU455
EF096681.1 gg_id:191029 mouse cecum clone SWPT11_aaa03a07 EF0966
EF096515.1 gg_id:189280 mouse cecum clone obob2_aaa04b08 EF0965
FJ832990.1 gg_id:584152 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q102_26B04 FJ8329
EU504643.1 gg_id:260192 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa03f11 EU504
EU507674.1 gg_id:274979 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02h10 EU507
EU458018.1 gg_id:313725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU458
EU510414.1 gg_id:262884 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38b12 EU510
EU508262.1 gg_id:270992 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04g08 EU508
EU503934.1 gg_id:265562 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02h08 EU503
FJ879577.1 gg_id:453180 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
GU303201.1 gg_id:555977 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EF097908.1 gg_id:182622 mouse cecum clone SWPT12_aaa01g07 EF0979
EU505530.1 gg_id:258177 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02b08 EU505
EU506568.1 gg_id:262414 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04d08 EU506
EF099474.1 gg_id:174030 mouse cecum clone SWPT3_aaa03f05 EF0994
AB034114.1 gg_id:52043 rumen clone 3C28d-5 AB034
DQ015489.1 gg_id:129889 mouse cecum clone M3_f10_1 DQ015

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42.6	871.7	1020.4	1586.5	377.1	808.7	695.9	1300.8	380.9	137.7	642.0
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471.4	1347.7	1540.2	1581.1	1710.7	1377.9	1590.3	1167.4	1556.0	624.1	1137.6
1437.3	657.9	1068.5	808.0	935.4	870.4	1052.4	1001.6	942.1	510.7	415.0
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1478.7	3747.0	2712.6	3738.1	3875.5	3248.9	3606.4	3312.8	2531.0	1996.5	2209.2
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6587.2	3115.2	2722.3	2744.3	2789.5	2270.8	2694.8	2187.5	2977.8	2191.6	3853.0
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724.5	1002.0	1008.8	1016.3	1244.5	1488.7	991.5	1259.2	537.6	908.2	975.8
1860.3	3470.8	3566.1	3542.4	3066.6	2986.7	3654.8	3023.5	2992.2	975.4	2579.0
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36.1	86.2	112.6	137.2	38.4	94.0	53.8	71.3	71.2	17.9	98.6
23.4	398.1	702.7	794.0	758.5	328.1	541.7	516.2	219.0	286.5	320.1
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42.6	629.1	1082.7	1317.1	559.7	804.2	669.7	1037.9	552.8	585.3	748.2
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8559.8	3350.6	3096.8	3563.8	3108.4	3763.5	2966.2	2689.7	4598.8	3602.8	5060.4
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1314.6	799.1	1065.2
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4041.1	3631.1	3966.0
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257.3	808.1	521.5
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758.1	1283.1	1112.7
3888.5	5000.7	4035.4
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3823.9	3002.7	3930.5
164.6	27.1	84.7
379.3	389.0	367.7
3266.8	4131.6	3265.7
615.1	885.9	818.9
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121.5	188.7	183.0
1938.8	1883.9	1995.1
6708.0	8540.8	8097.7
372.1	530.8	365.9
5233.6	6845.5	5831.4
346.9	518.1	731.0
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1573.6	2435.3	2895.8
48.4	80.1	75.3
1246.0	1457.6	1683.2
3925.6	4411.5	4602.3
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o__Clostridiales	f__Lachnospiraceae
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EU452266.1 gg_id:326027 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
EU455117.1 gg_id:351465 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EU455148.1 gg_id:322240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU455
EU510426.1 gg_id:266246 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal38d12 EU510
EU452285.1 gg_id:317696 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU452
EF099856.1 gg_id:190047 mouse cecum clone SWPT5_aaa01d03 EF0998
AF287777.1 gg_id:72977 Eubacterium cf. saburreum oral strain str. C27KA AF287
EU511715.1 gg_id:277083 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07e05 EU511
GU303475.1 gg_id:540405 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
FJ834033.1 gg_id:587347 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q301_72H09 FJ8340
DQ825337.1 gg_id:187419 human fecal clone RL185_aan88g05 DQ825
DQ801639.1 gg_id:190464 human fecal clone RL117_aae93c07 DQ801
FJ362624.1 gg_id:368511 feces adult twins and mothers; TS13 clone TS13_a01c01 FJ3626
EU467624.1 gg_id:303028 naked mole-rat feces clone molerat_2c03 EU467
FJ172890.1 gg_id:319578 Qinghai Yak Ruminal and Fungi China rumen clone RB-136 FJ1728
EU451898.1 gg_id:356223 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
GQ175482.1 gg_id:548503 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EU451412.1 gg_id:339546 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU505103.1 gg_id:264965 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02h08 EU505
EF097313.1 gg_id:182323 mouse cecum clone SWPT18_aaa04h05 EF0973
EU506936.1 gg_id:264987 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08f03 EU506
EU475375.1 gg_id:295250 rock hyrax feces clone RHSD_aaa02b09 EU4753
EU505647.1 gg_id:268309 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a06 EU505
EF098421.1 gg_id:178817 mouse cecum clone SWPT15_aaa02g11 EF0984
EF096464.1 gg_id:192365 mouse cecum clone obob2_aaa03c06 EF0964
EU844657.1 gg_id:346195 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AY992581.1 gg_id:135307 mouse cecum clone C23_k01 AY9925
EU506457.1 gg_id:258757 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa02c02 EU506
EU454280.1 gg_id:331172 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU454
EF099400.1 gg_id:186162 mouse cecum clone SWPT3_aaa02g03 EF0994
AM420062.1 gg_id:256659 Noma subgingival plaque clone 301C11(oral) AM420
AY854354.1 gg_id:110678 herbivore gastrointestinal tract clone Thompsons76 AY8543
DQ795687.1 gg_id:175685 human fecal clone RL178_aan68f01 DQ795
AM420198.1 gg_id:236261 Noma subgingival plaque clone 502G12(oral) AM420
EU504938.1 gg_id:274146 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04e06 EU504
AY991885.1 gg_id:129741 mouse cecum clone C20_j09 AY9918
EF096321.1 gg_id:182712 mouse cecum clone obob1_aaa04h04 EF0963
EF097874.1 gg_id:182950 mouse cecum clone SWPT12_aaa01b07 EF0978
EU843319.1 gg_id:339293 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU843771.1 gg_id:333091 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU510601.1 gg_id:265569 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38a01 EU510

4326.7	3287.4	2851.1	3185.6	2087.4	2715.7	2323.3	3490.5	4435.4	3957.7	3271.8
7511.1	1416.0	1638.0	1502.4	1618.4	1280.1	1593.6	1762.4	994.1	671.6	1023.4
11915.8	5593.6	5562.2	5558.3	5728.2	4822.5	5883.9	4548.9	5989.8	5264.4	6652.3
234.5	4804.1	6168.3	7693.1	2451.5	3554.2	3418.1	5124.8	2373.4	968.5	4288.0
1400.0	4272.6	3168.1	3407.4	3912.3	3209.7	4211.1	3046.5	3963.2	2351.6	3001.7
60.8	315.1	487.4	606.9	136.5	157.6	126.3	255.8	71.4	95.9	147.3
51.5	1004.4	1449.4	1452.7	715.5	961.2	723.1	1180.3	569.2	157.0	610.8
816.2	6843.1	5785.7	5887.1	5616.6	5963.1	6386.1	5062.1	6754.6	7569.1	5488.3
62.7	1617.5	2436.5	1984.6	567.8	1227.8	1245.0	1703.8	518.0	217.1	1511.4
45.3	1088.7	1487.9	1671.7	605.4	588.6	604.7	1004.4	258.0	203.9	358.7
189.5	1991.6	1494.4	2246.3	2376.2	1592.0	2643.8	1756.4	655.6	437.5	867.9
479.0	651.1	811.6	808.9	455.6	425.9	473.0	715.2	293.9	134.8	356.1
2646.9	2200.1	3124.1	2476.1	1547.0	2456.3	1521.4	3372.8	1241.8	632.1	2145.4
201.5	2041.9	3032.2	3108.9	2338.5	2428.7	2652.0	3108.6	1596.5	650.1	2016.7
5250.3	6151.4	6374.1	7071.6	7719.7	5810.2	6287.0	6882.1	7186.4	5751.8	6791.0
224.2	1436.5	1743.0	2335.2	2253.8	1701.0	2882.6	2002.5	1088.4	1060.4	1617.9
525.9	2594.3	2341.6	2102.8	1492.8	1841.5	1658.2	2332.9	3665.8	1511.1	1752.3
378.3	1960.1	2831.7	3054.1	2049.3	2208.6	2560.4	3278.1	1272.2	2821.0	2592.1
373.9	2858.0	2973.0	2683.1	3542.7	2814.3	3272.7	2373.4	2286.2	772.0	1835.7
64.8	121.3	174.4	129.3	246.6	142.8	72.8	167.3	62.9	27.8	63.2
2774.1	2146.2	2084.4	2615.3	2076.4	2763.3	2860.1	2094.2	2029.9	3226.2	2864.1
614.7	1149.8	1736.9	1967.2	510.2	993.9	836.6	1586.8	786.9	447.4	1049.8
16559.6	6911.3	6056.2	7087.9	8032.9	6353.7	8717.5	5869.4	8999.9	7006.3	8703.8
74.2	151.5	178.9	263.3	32.4	66.6	43.9	80.0	29.8	20.4	30.2
2004.7	2504.3	2597.1	3065.6	2624.9	2619.3	2372.4	2663.6	1967.3	3480.1	2303.3
48.0	1917.4	2011.8	1624.6	1059.8	1430.0	1053.4	1973.7	1141.0	1219.1	1048.8
8978.7	2881.1	2229.4	2710.5	2284.8	2342.2	2990.8	2580.2	2828.7	1108.5	3409.8
493.9	1534.0	2064.0	2888.6	1130.4	1447.7	1100.6	1550.5	554.8	363.7	1378.0
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277.1	558.9	1002.8	1534.5	243.5	426.4	395.4	1061.3	61.8	74.2	306.2
124.9	1148.5	1569.4	1387.0	1223.5	1194.5	976.7	1527.1	967.4	311.0	760.2
56.0	389.7	672.3	391.4	324.6	377.1	250.8	621.4	126.6	595.3	291.5
51.4	179.2	257.9	259.8	287.7	219.6	270.0	252.2	28.7	29.8	113.1
886.6	2576.6	3172.9	2900.8	2879.7	2306.8	2145.1	3457.4	2255.0	848.1	3809.7
683.5	954.2	1226.4	678.0	1276.1	1126.3	951.2	1381.9	1065.5	488.8	851.5
149.5	943.5	1338.1	1165.4	964.1	844.4	1483.5	1325.1	1349.5	1534.1	851.5
88.4	623.2	1020.3	881.2	1269.4	700.2	713.5	1202.5	325.9	115.2	455.3
8276.6	2105.2	2319.3	2783.8	2333.6	2073.2	2624.6	2389.4	2883.7	1375.5	3969.8
163.3	1792.9	1915.8	1884.9	1496.7	1618.4	2008.5	1684.4	1216.4	976.6	1147.4
161.6	1794.0	1953.7	2257.9	1195.5	1399.8	1663.1	1676.1	986.8	598.9	987.4
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1497.7	1559.9	2829.6
5165.7	5861.6	5493.6
5800.8	4841.4	7453.5
2588.9	2803.5	3350.8
388.9	466.8	217.7
1352.8	1164.8	1830.7
6509.9	5553.0	7302.8
1700.9	1601.9	2425.2
1486.3	1214.1	2087.0
1893.8	1750.1	2633.7
1262.0	1087.1	931.6
4483.0	2935.7	3322.1
2914.4	2437.1	4387.1
6908.6	6488.2	6903.9
1663.5	2457.9	2242.0
1700.2	2060.9	2246.9
2264.8	2581.8	2475.8
2604.2	3585.2	4142.6
69.9	129.3	127.7
1691.0	2879.4	2730.3
1665.5	1529.6	1257.1
7305.0	6992.1	6820.0
104.8	202.8	72.4
2895.0	4501.0	2490.8
1670.3	1773.0	2641.9
2562.3	2556.2	2428.2
2026.7	1958.1	1776.8
2954.3	3960.8	3445.7
1326.1	575.8	848.6
994.4	1623.4	2012.6
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1009.3	1683.7	1611.7
614.0	1164.2	1079.7
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1741.5	1644.0	2586.1
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o__Clostridiales	f__Lachnospiraceae

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EU843391.1 gg_id:343290 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GU174079.1 gg_id:593301 Microbial Bactrian camel estimated rumen clone XJC35 GU174
EU509925.1 gg_id:264802 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak23g09 EU509
EU473502.1 gg_id:288364 Somali wild ass feces clone WA_aaa04b05 EU473
EU451344.1 gg_id:341750 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU451
EU504842.1 gg_id:263855 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03b07 EU504
EU508054.1 gg_id:274981 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa02g05 EU508
EU510189.1 gg_id:276193 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02f09 EU510
EU511858.1 gg_id:263310 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10a07.Contig2 EU511
AF157058.1 gg_id:14094 Eubacterium plexicaudatum str. ATCC 27514 AF157
EF096225.1 gg_id:177195 mouse cecum clone obob1_aaa03a01 EF0962
DQ798136.1 gg_id:183430 human fecal clone RL302_aal95h10 DQ798
GU304180.1 gg_id:552651 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU510381.1 gg_id:267043 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37f01 EU510
DQ015019.1 gg_id:130243 mouse cecum clone M1_1g09_1 DQ015
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AB185578.1 gg_id:102995 rumen clone F24-A05 AB185
EU510264.1 gg_id:273173 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03g07 EU510
EU470390.1 gg_id:293566 Grevy's zebra feces clone GZ_aaa01b09 EU470
EU505227.1 gg_id:274712 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04g07 EU505
EU508867.1 gg_id:268878 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37d08 EU508
EU453602.1 gg_id:307068 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU453
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EU454513.1 gg_id:341223 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU454
EU381766.1 gg_id:276783 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
AF116854.1 gg_id:14021 Sporobacterium olearium str. SR1; DSM 12504 AF116
DQ796512.1 gg_id:188077 human fecal clone RL179aan73f10 DQ796
EU457413.1 gg_id:318343 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU454125.1 gg_id:342786 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU454
EF686640.1 gg_id:249388 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EU452552.1 gg_id:328271 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78 EU452
DQ824188.1 gg_id:186505 human fecal clone RL204_aaj60f01 DQ824
DQ815495.1 gg_id:172161 mouse cecum clone aab41f02 DQ815
EU455531.1 gg_id:319352 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
EU344509.1 gg_id:262457 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU844745.1 gg_id:326985 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ801782.1 gg_id:182759 human fecal clone RL201_aai46g02 DQ801
EU381991.1 gg_id:275110 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ832961.1 gg_id:576473 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_95G12 FJ8329
EU474367.1 gg_id:296869 western lowland gorilla feces clone GORSD_aaa04d09 EU474

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133.0	2202.5	2768.3	3612.7	1856.5	2240.9	2614.3	3189.7	1343.3	516.1	1102.9
22094.1	6637.2	6382.6	6908.4	6560.5	6315.5	8089.6	7039.3	8765.3	9850.6	8378.1
980.8	849.3	996.9	955.3	1231.7	1149.5	946.7	1228.0	718.0	1576.0	769.6
3946.2	5437.5	4613.0	4980.9	4376.2	4717.9	3851.8	4371.0	5745.6	4641.7	5124.3
1833.7	4669.4	3667.9	3623.3	2760.9	3259.5	2443.9	2958.9	3742.7	2298.3	3379.8
8922.4	6634.6	6877.3	8022.4	6459.7	6100.9	8268.9	7030.5	8923.2	5980.3	8216.5
4335.6	3326.1	3900.0	3290.9	3778.4	3581.8	3914.7	4485.0	2659.7	3838.0	2904.0
1217.1	1396.6	1751.9	2050.1	2136.6	1307.9	2217.1	1635.5	352.7	559.4	802.8
2437.5	4208.9	4376.8	4680.5	4793.1	4835.9	4788.8	4260.0	5288.7	3557.9	4755.8
3191.3	5712.5	5086.8	4762.9	3617.8	4086.4	4326.1	4533.9	4267.6	2736.2	6052.8
2432.0	4110.0	4301.9	4278.4	4390.5	3730.6	4326.1	4122.5	3111.7	1533.0	3166.4
114.9	257.9	319.3	266.2	315.9	200.5	308.2	255.2	214.5	457.9	172.1
51.4	50.3	73.4	56.5	62.3	44.7	67.3	41.9	42.1	39.1	44.7
4693.0	4574.2	5051.4	5058.6	4108.7	6054.8	6212.8	6004.6	3506.0	3393.8	6127.4
17693.5	7310.0	6341.5	8182.3	6191.4	6636.7	6496.2	6655.9	7877.5	5172.3	9383.4
106.8	186.6	221.3	226.9	262.9	207.2	285.0	202.1	106.8	152.0	134.0
3934.8	4767.4	4034.8	5440.0	3862.6	4581.5	5728.2	4534.2	3453.2	2344.7	4100.4
562.7	1994.0	2927.2	3026.4	2182.9	2453.5	2451.8	3188.0	2049.8	2105.7	1970.5
152.8	1616.1	2724.4	2426.5	1198.3	1440.3	1294.3	1729.3	608.4	367.2	1510.5
13578.8	7327.4	7620.5	7974.9	6001.1	6854.4	7139.6	5987.9	7270.3	6848.8	9519.3
7078.7	7030.8	7429.9	5746.8	6040.8	5650.1	6812.9	5626.3	7978.3	6137.6	8068.2
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42.0	51.6	84.6	80.1	56.7	88.0	139.0	232.7	33.8	21.4	72.3
70.9	129.8	187.0	275.9	48.3	66.0	48.9	188.9	39.8	32.9	56.0
1982.0	379.1	728.3	725.8	919.4	622.0	637.1	886.4	319.3	342.1	319.2
90.1	638.4	1037.9	807.6	734.2	977.8	825.4	1020.2	748.1	398.4	937.5
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1464.2	1385.5	1923.2	2218.4	2228.2	1545.4	2590.5	1705.0	485.2	559.6	976.2
2012.0	4739.4	6177.2	7224.7	6333.3	6259.6	6161.8	6697.3	4250.7	4055.7	5406.7
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1485.6	8263.6	7200.9	4427.1	5155.6	7227.1	3818.4	4930.7	7584.8	4825.0	3880.9

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4686.3	4671.8	3867.9
4042.9	4192.6	5571.3
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EF098947.1 gg_id:177964 mouse cecum clone SWPT1_aaa03f11 EF0989
EU455846.1 gg_id:307194 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4558
DQ795505.1 gg_id:175704 human fecal clone RL178_aan65c08 DQ795
EU507521.1 gg_id:276702 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e04 EU5075
FJ833056.1 gg_id:557780 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_47G06 FJ8330
EU452541.1 gg_id:314032 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4525
EU504091.1 gg_id:270764 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01b04 EU5040
EF097896.1 gg_id:177802 mouse cecum clone SWPT12_aaa01e09 EF0978
GU304020.1 gg_id:583584 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
EF099869.1 gg_id:190998 mouse cecum clone SWPT5_aaa01e10.Contig2 EF0998
EU454954.1 gg_id:314134 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU4549
AF287774.1 gg_id:34466 human subgingival plaque clone CK051 AF2877
EU344721.1 gg_id:262716 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3447
EF100025.1 gg_id:182954 mouse cecum clone SWPT5_aaa03f07 EF1000
EF099731.1 gg_id:191411 mouse cecum clone SWPT4_aaa03e11 EF0997
DQ014709.1 gg_id:135344 mouse cecum clone M1_g06_1 DQ014
EU510229.1 gg_id:266639 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03c03 EU5102
EU453164.1 gg_id:324002 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4531
FJ671909.1 gg_id:515371 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
FJ676985.1 gg_id:517545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU456100.1 gg_id:332195 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4561
FJ879691.1 gg_id:456857 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
DQ071484.1 gg_id:227682 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc9 DQ071
EU622663.1 gg_id:279019 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6226
EF098355.1 gg_id:180944 mouse cecum clone SWPT15_aaa01d09 EF0983
EU510286.1 gg_id:261810 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04b06 EU5102
EF097493.1 gg_id:174860 mouse cecum clone SWPT19_aaa03d09 EF0974
EU509521.1 gg_id:276892 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60a08 EU5095
EU510230.1 gg_id:265116 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03c04 EU5102
EF602978.1 gg_id:231684 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
EU508184.1 gg_id:260627 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02g05 EU5081
DQ925472.1 gg_id:251561 Howardella ureilytica str. GPC589 DQ925
EU748032.1 gg_id:342251 neotropical folivorous flying bird adult hoatzin crop clone hoa14_50B07 EU7480
EU775421.1 gg_id:321778 Western lowland gorilla feces clone GOR_aag73a07 EU7754
AF385508.1 gg_id:71387 on Tongue Dorsa Halitosis Healthy Patients healthy and subjects halitosis clone DO008 AF3855
GU303527.1 gg_id:545236 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU450999.1 gg_id:348518 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4509
EU451727.1 gg_id:332854 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU4517
EU747925.1 gg_id:355742 neotropical folivorous flying bird adult hoatzin crop clone hoa11_74B10 EU7479
EU510553.1 gg_id:277176 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak37a10 EU5105
DQ795656.1 gg_id:199455 human fecal clone RL178_aan67h03 DQ795

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163.6	1897.1	1882.2	1501.7	1876.0	1712.7	1582.2	1620.0	1327.8	613.9	1115.4
164.8	501.4	577.2	633.7	463.5	586.1	538.1	708.8	329.6	323.4	390.9
14790.1	6015.4	6776.8	6729.6	5122.7	5641.5	6621.2	6046.5	8587.6	6866.4	7783.7
2725.0	7034.0	6329.0	5643.3	6360.6	6393.2	5321.4	5445.7	7906.7	7660.4	5414.7
7668.6	3447.5	3430.7	3663.7	3673.5	2845.0	3757.2	3371.0	3808.0	2442.0	2665.6
32.8	77.7	151.9	160.7	28.7	110.6	95.7	330.1	30.6	38.1	76.3
110.4	640.7	895.1	933.0	470.4	769.4	569.4	1698.6	438.0	487.2	318.2
8554.4	6737.3	6270.3	5306.3	4475.2	6516.7	4382.4	5504.5	7269.1	5520.5	5101.6
190.8	643.7	804.7	634.7	724.5	679.6	1060.5	702.4	712.4	388.0	632.9
45.9	33.4	35.0	32.9	31.5	19.1	32.8	26.5	28.1	16.7	34.8
49.0	714.6	929.2	1149.6	367.0	620.4	539.2	930.5	218.3	156.7	506.9
935.3	648.8	650.1	710.4	879.1	824.0	866.6	683.2	835.7	290.0	757.3
920.1	5097.8	4124.3	3600.1	3476.3	4417.4	3530.5	4103.6	3398.7	7704.0	3109.8
59.9	1057.1	1593.9	2621.4	665.7	691.8	368.4	1301.2	192.4	155.3	854.8
422.0	2376.3	1893.2	1959.4	1261.5	1257.8	2534.0	1492.0	2464.3	1390.4	1763.1
92.5	2164.5	2356.1	2796.3	1532.8	2025.9	1791.1	2059.9	2346.1	1041.5	1522.9
14291.8	4898.2	3898.6	4547.1	4021.5	4285.8	4352.0	4187.8	5141.2	3931.9	6335.4
64.6	90.1	139.5	150.5	148.1	93.9	129.2	120.0	57.3	94.6	101.8
37.5	119.6	192.3	251.9	24.3	48.1	35.7	105.4	27.5	26.0	46.7
66.7	193.2	236.5	346.6	210.7	193.4	263.4	396.5	67.8	54.6	131.0
46.9	341.6	610.6	654.7	108.2	327.3	201.6	569.6	126.8	75.0	80.8
666.2	327.1	1010.3	1057.4	1262.9	888.1	1477.8	946.7	248.5	128.4	1052.0
946.3	1558.6	1277.4	1453.6	1041.1	1476.6	1448.3	1202.9	1218.0	559.2	1354.0
2682.2	4258.5	3812.3	4090.8	4786.1	3894.2	5318.5	3706.4	4490.0	2901.0	3431.3
385.7	3383.5	4759.8	3335.4	3203.9	3526.2	3438.1	3216.7	2173.3	1720.8	3345.1
504.2	1750.4	1641.1	1747.3	1761.0	2203.2	1800.9	1865.9	1255.1	2268.9	1758.8
1842.2	6840.0	6029.5	5692.7	6152.5	5829.8	6517.9	5821.9	8817.8	5502.3	5574.3
170.0	1113.4	1631.6	1661.7	610.1	903.0	824.8	989.9	674.0	292.2	856.4
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38.0	386.9	629.8	659.0	114.2	330.5	247.2	723.9	291.3	86.6	478.5
267.6	2381.4	2401.9	2523.0	2096.2	2422.7	2046.2	2587.6	1658.0	738.7	1525.0
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34.5	216.5	352.8	221.6	225.5	330.8	166.4	321.7	99.9	61.8	187.8
3272.4	3728.8	3817.5	3044.2	3161.9	3037.9	4164.4	3990.7	3627.5	3289.1	2911.5
17456.5	8513.0	7897.3	8426.4	7954.3	8133.5	8350.5	8353.8	11220.2	8987.9	10869.7
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1223.0	4938.0	4529.8	4873.2	5094.2	3695.9	5085.0	4278.6	5019.4	3276.6	3465.4
830.7	1883.8	2323.0	2503.3	3459.0	2166.7	3748.8	2318.9	1619.6	554.4	1779.2
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1234.3	1077.3	1374.5
1264.5	2359.2	2841.8
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3807.1	4661.9	3834.5
91.5	138.9	350.8
120.2	145.6	38.3
810.9	283.3	492.6
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882.0	1333.8	1147.9
938.7	1710.3	1228.1
3492.4	3119.0	4121.8
2943.6	4204.5	4462.9
1774.6	2074.0	2142.5
4957.4	5674.4	6797.2
1199.2	1579.8	1095.5
4635.7	6604.9	5325.5
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182.3	244.9	363.6
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EU456793.1 gg_id:349351 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
DQ015012.1 gg_id:135647 mouse cecum clone M1_1f08_1 DQ015
EF097608.1 gg_id:193114 mouse cecum clone SWPT20_aaa01b10 EF0976
EU509474.1 gg_id:262863 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h11 EU509
EU473647.1 gg_id:295604 banteng feces clone BG_aaa04e01.Contig1 EU473
DQ807928.1 gg_id:196543 human fecal clone RL180_aan69b12 DQ807
DQ394701.1 gg_id:155423 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU455821.1 gg_id:311513 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU455
EU456217.1 gg_id:338554 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
EU461525.1 gg_id:295410 black rhinoceros feces clone RH_aaj91f05 EU461
EU463215.1 gg_id:295660 naked mole-rat feces clone molerat_aai71g09 EU463
EU455466.1 gg_id:336609 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EU508216.1 gg_id:261925 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03e03 EU508
EU473488.1 gg_id:298870 Somali wild ass feces clone WA_aaa04a09 EU473
EU504009.1 gg_id:260729 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04a01 EU504
EU454528.1 gg_id:317324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU457302.1 gg_id:344723 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU510167.1 gg_id:275142 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02c12 EU510
EU510763.1 gg_id:269872 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h05 EU510
EU509315.1 gg_id:263838 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47g07 EU509
EU504767.1 gg_id:265399 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g10 EU504
AY992587.1 gg_id:130556 mouse cecum clone C23_k07 AY992
EU456389.1 gg_id:318806 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU453873.1 gg_id:331530 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU453
DQ015498.1 gg_id:135682 mouse cecum clone M3_g08_1 DQ015
EU469974.1 gg_id:288611 trancaspain urial feces clone TU1_aaa01a01 EU469
EF096162.1 gg_id:186117 mouse cecum clone obob1_aaa01f05 EF0961
EF614468.1 gg_id:228521 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6144
AY992639.1 gg_id:134437 mouse cecum clone C23_m13 AY992
EF614694.1 gg_id:229965 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
EU504826.1 gg_id:262976 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02g09 EU504
AF287775.1 gg_id:52106 human subgingival plaque clone CH017 AF287
EU512012.1 gg_id:268423 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12f09 EU512
GU304107.1 gg_id:572067 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU468937.1 gg_id:292421 Speke's gazelle feces clone SP2_e10_1 EU468
EF099649.1 gg_id:199649 mouse cecum clone SWPT4_aaa02d09 EF0996
EU506486.1 gg_id:276566 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa02g03 EU506
EF096836.1 gg_id:181255 mouse cecum clone SWPT13_aaa01d10 EF0968
EU509508.1 gg_id:263860 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap59f11 EU509
EU466022.1 gg_id:297491 African elephant feces clone AFEL3_aao16a04 EU466

4474.7	2674.5	2342.0	2276.7	1974.6	3189.2	1578.9	2148.5	2421.2	2256.7	2622.9
7286.8	2624.8	2331.6	2040.3	1859.8	2070.2	2114.5	2136.8	2409.6	1457.4	2200.6
1541.9	3698.2	2854.9	2749.7	3227.2	2697.1	3211.8	2674.4	5975.9	4013.2	3751.7
129.5	721.4	944.0	1324.3	336.2	614.7	435.9	761.4	243.9	542.5	548.8
409.9	1306.5	1307.2	1174.6	1052.4	1145.5	1338.0	1017.8	1214.2	952.7	1071.2
110.8	1647.2	2446.3	2130.5	2076.2	1766.3	2304.9	2254.9	966.5	1594.2	1462.0
1615.3	3891.0	3950.3	3524.0	3594.6	3538.1	3937.9	3986.6	5324.3	3098.9	4088.9
63.3	686.6	835.6	1189.8	306.8	494.7	425.6	907.7	106.3	133.5	380.2
2817.4	926.6	985.7	1215.3	1016.3	957.9	1005.9	1407.1	1023.5	665.7	869.5
282.7	1203.4	2001.8	1607.6	1639.3	1523.7	1685.2	1670.3	1250.0	746.0	1448.2
1074.3	2778.1	4311.4	4006.8	3015.6	3184.8	2700.9	4230.6	2200.8	3155.8	3188.6
35.6	813.5	1408.7	1890.2	234.9	731.0	511.9	1758.7	275.0	120.9	648.3
26826.6	9617.2	9277.4	9653.9	9892.4	8750.9	10178.8	8519.9	13488.5	11002.1	11600.8
3572.5	4350.9	4530.1	4936.0	5412.1	5796.0	6283.8	4309.5	3598.3	3449.1	4119.0
3059.1	3097.5	3352.1	3568.1	2498.9	3406.3	3370.9	3678.9	3730.1	2484.5	2683.9
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4903.1	4515.9	4650.8	3885.6	3166.7	3801.8	3249.0	4402.2	3326.1	2491.3	3755.3
201.8	1027.8	1258.0	1626.6	1286.3	1001.7	1666.4	1516.6	632.7	1120.3	835.7
15802.1	9858.8	8277.2	8805.4	9868.2	8465.2	9744.0	7935.2	10579.9	9771.4	9864.1
4359.4	1860.8	2254.8	2973.9	1610.6	1235.1	1843.4	2250.5	3261.4	1508.0	2047.0
489.5	2034.8	3280.7	3266.9	1977.7	2595.7	2584.8	2807.7	2160.7	2005.2	2916.1
1097.9	1638.0	1702.6	1791.8	1644.6	1678.3	1315.6	1883.7	809.7	577.7	1750.1
228.4	2576.3	2093.7	2627.7	4242.5	2333.8	2407.7	2212.0	1684.0	1729.9	1664.2
8228.7	2761.2	3325.7	3460.8	3860.2	2950.2	3594.0	3297.7	1964.6	883.9	2522.1
740.3	6108.8	4432.5	4420.3	5620.5	4585.8	6017.7	5357.0	4214.1	2649.1	2972.1
116.6	257.7	419.3	395.1	78.0	144.6	93.8	299.5	98.0	53.4	123.6
531.5	1702.8	2153.9	2391.3	2061.9	1866.4	2715.6	2153.4	1835.2	792.0	1243.1
7993.2	2903.2	3434.9	3651.9	2983.4	3090.7	3169.2	3457.7	3572.6	5080.7	3224.5
1676.7	3139.5	3381.7	2864.4	3055.4	3286.2	2713.9	2685.5	3800.3	3885.1	2253.9
202.5	390.1	448.7	537.2	381.7	437.3	436.0	522.4	357.8	303.2	277.9
60.7	886.7	1424.9	1649.8	518.7	841.3	889.3	1531.3	341.7	79.5	660.9
176.6	876.0	1028.8	1166.3	792.5	748.4	803.6	894.9	628.3	765.9	1426.8
23.7	27.7	30.2	37.1	30.4	22.2	23.5	34.9	13.0	16.7	24.2
7051.3	6600.6	6211.8	6103.4	5237.8	5692.5	5646.7	5379.5	8331.8	7774.6	7478.7
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57.9	1109.9	1331.8	1839.6	842.1	614.5	785.1	1165.7	449.2	199.2	446.7
2124.2	3291.2	4383.2	4885.6	2542.4	2864.8	2987.0	2619.1	5913.7	3696.6	4719.6
47.4	415.3	774.4	728.0	241.6	470.1	356.3	485.9	161.2	162.5	621.4
582.7	4979.4	3408.6	3304.2	3034.4	3736.9	4143.1	3409.1	5787.9	4527.7	3105.3
238.6	613.3	971.3	1236.7	505.2	396.2	712.4	673.2	259.9	173.6	451.6
259.0	1280.8	1668.4	1487.3	1285.6	1232.2	1611.4	1382.9	763.1	535.2	1164.5

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872.6	795.6	1108.1
960.1	1741.8	1945.2
2077.5	2763.3	3348.3
3654.0	3820.9	4020.2
1263.8	1017.7	1247.1
951.8	2039.7	1380.6
1328.0	2546.6	2430.6
3989.7	4605.6	6122.1
2059.7	1072.9	2214.8
8854.9	10329.1	9427.3
4424.6	4611.7	6190.9
2881.8	3837.8	3780.2
3325.1	3828.4	5057.4
4137.5	3781.3	5265.5
1672.4	1304.6	1979.2
8353.5	8072.1	8107.4
1702.6	2835.7	2648.9
2322.4	3881.3	3005.8
1620.8	2233.9	2572.7
2774.7	1847.3	2860.5
4676.8	3968.6	4974.9
4047.1	4304.4	5137.9
306.3	358.5	197.2
2391.8	2323.7	3710.5
3526.7	4345.4	3569.2
2734.8	3241.2	4107.7
469.1	542.0	561.3
1659.5	1806.1	2932.9
894.9	998.9	1266.2
22.9	30.9	51.4
5155.4	6168.9	7821.5
4008.8	5131.0	5779.7
1463.8	1558.5	2173.8
3897.5	3167.0	2694.5
554.3	544.5	426.8
2768.0	2437.3	2925.8
582.0	946.4	810.1
1538.1	1553.5	1839.3

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EU344172.1 gg_id:262696 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EF025286.1 gg_id:189317 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N17 EF0252
FJ676934.1 gg_id:527024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU453854.1 gg_id:320751 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4538
GQ031254.1 gg_id:378428 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
EU453250.1 gg_id:341638 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4532
EU775955.1 gg_id:345806 Rock hyrax feces clone RHSD_aaa01f10 EU7759
EU507097.1 gg_id:262890 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01c09 EU5070
EU842748.1 gg_id:349546 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8427
DQ353936.1 gg_id:147987 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z101 DQ353
DQ825269.1 gg_id:194574 human fecal clone RL185_aan87e08 DQ825
EU509799.1 gg_id:260786 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b11 EU5097
EU508083.1 gg_id:263277 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa03e04 EU5080
EU747968.1 gg_id:324173 neotropical folivorous flying bird adult hoatzin crop clone hoa11_93E12 EU7479
FJ834062.1 gg_id:593393 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q401_60D08 FJ8340
EU748508.1 gg_id:334527 neotropical folivorous flying bird adult hoatzin crop clone hoa61_10g04 EU7485
EF686544.1 gg_id:255603 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC3 EF6865
EU455481.1 gg_id:317698 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU4554
EU505127.1 gg_id:270077 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03c03 EU5051
EU842663.1 gg_id:335786 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8426
EF099549.1 gg_id:181865 mouse cecum clone SWPT3_aaa04g08 EF0995
EF098163.1 gg_id:199316 mouse cecum clone SWPT14_aaa02e02 EF0981
EU456278.1 gg_id:338104 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4562
GU303152.1 gg_id:579509 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EF098202.1 gg_id:174847 mouse cecum clone SWPT14_aaa03a02 EF0982
GU304520.1 gg_id:579045 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU511987.1 gg_id:268611 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12d02 EU5119
DQ057370.1 gg_id:129783 chicken ileum/cecum clone cc129 DQ057
EF098143.1 gg_id:181392 mouse cecum clone SWPT14_aaa02b07 EF0981
EU771581.1 gg_id:317226 African elephant feces clone AFEL2_aao32f03 EU7715
DQ015472.1 gg_id:131415 mouse cecum clone M3_e03_1 DQ015
EF096536.1 gg_id:192418 mouse cecum clone obob2_aaa04e08 EF0965
EU451224.1 gg_id:329179 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4512
EU452061.1 gg_id:334921 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4520
EU452329.1 gg_id:351175 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4523
EU455127.1 gg_id:339117 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4551
EF099556.1 gg_id:195421 mouse cecum clone SWPT3_aaa04h12 EF0995
DQ794938.1 gg_id:188844 human fecal clone RL310_aam38b07 DQ794
AY992476.1 gg_id:135367 mouse cecum clone C23_f08 AY9924
EU451826.1 gg_id:322182 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4518
EU508898.1 gg_id:272770 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap38a10 EU5088

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283.6	1390.2	1532.9	1269.0	1064.3	1161.7	1086.1	1334.7	1529.3	607.7	2378.6
42.0	398.1	711.6	744.6	393.8	387.9	316.3	850.5	271.4	70.4	285.2
5261.6	5244.0	6042.2	5323.2	4909.8	4432.8	5367.8	4899.0	4441.9	2811.9	4591.7
14723.9	3945.2	3853.4	4200.0	4330.6	3568.1	3892.8	3478.7	4837.8	5406.8	4788.6
128.2	1204.3	1633.7	1977.0	1751.7	1434.8	1819.4	1827.8	769.2	1764.2	1061.3
1479.5	5154.9	5223.9	5774.6	4146.2	4648.5	4562.3	4906.8	4502.6	2706.3	4791.9
953.3	1345.9	1361.9	1674.9	1864.4	1366.4	1674.8	1541.3	1161.9	669.4	49.9
54.6	950.0	1504.6	1340.0	1324.6	1106.6	1616.5	1407.6	335.9	238.3	753.9
54.0	73.4	68.9	50.5	98.1	68.9	67.6	69.2	41.0	22.0	108.8
45.6	115.0	176.4	244.8	62.9	65.0	83.0	148.3	30.7	18.9	52.3
3392.0	1308.2	1633.7	1552.9	808.9	894.1	1135.4	845.5	843.7	1188.1	980.8
23417.1	11062.5	9025.4	10665.9	10078.5	10122.3	12159.7	8898.6	12922.5	9260.8	12984.3
60.7	140.7	197.6	170.7	144.4	141.9	103.5	163.3	74.3	67.4	117.7
398.3	2287.9	2911.7	2927.5	2998.9	2207.0	3497.8	2558.7	1072.8	605.2	2010.7
474.4	2418.9	2376.5	2277.9	4006.4	2171.5	3686.3	2743.9	2178.4	1234.6	1510.4
96.6	2832.7	2532.7	2163.6	2414.9	2528.3	2722.0	2482.6	3259.9	1903.7	1751.6
2868.1	2509.2	2902.7	3352.2	1899.2	2186.1	2233.0	2515.4	1657.7	1474.4	1908.4
176.6	2168.8	2250.4	2590.2	3733.9	2461.0	3443.6	2323.4	2232.2	524.8	2051.3
2047.0	2650.0	2206.8	2161.9	2168.5	2354.1	2279.4	2891.2	2496.9	1100.2	2159.6
2180.4	3792.9	4109.9	3410.0	4435.3	3552.0	4411.8	3705.1	6074.5	4157.5	3693.5
15711.4	4997.0	4795.1	4358.2	4648.6	4939.7	5252.4	5144.1	5604.6	7034.2	6427.1
106.4	1267.6	2180.2	2014.6	1228.3	1655.2	1777.4	1709.2	1008.9	416.2	1498.5
253.1	987.6	1290.8	1081.4	665.2	927.6	1042.5	1115.3	556.2	247.7	686.6
3969.3	2018.5	2165.0	2393.0	1546.8	1517.3	1531.4	1854.6	1295.2	1304.2	1831.1
1415.7	1718.8	2007.1	1803.6	2055.5	1719.4	2662.5	1769.4	1340.5	1483.3	1653.6
1691.1	1622.7	2039.0	2036.0	1682.4	1691.5	2089.2	2192.9	2494.9	1940.6	1676.5
47.0	122.3	235.1	261.8	81.8	106.1	117.5	279.5	38.5	40.7	61.8
1467.0	5460.0	4249.8	4134.0	4871.1	4661.7	3993.2	3859.8	4307.9	3329.9	5207.1
56.3	949.4	1329.4	1541.6	831.3	515.7	1120.1	996.3	348.7	262.7	546.2
2956.0	3150.1	2747.2	2522.2	2254.6	2680.6	2306.5	2590.4	4168.0	2126.3	2627.6
137.0	603.4	526.1	439.5	455.4	443.0	374.0	392.6	205.2	129.4	336.8
186.1	664.8	1056.9	1395.4	527.1	715.8	524.2	1363.1	291.6	233.3	507.8
2279.4	3719.9	3784.4	3997.5	3339.9	3261.8	3862.7	2919.1	4992.8	2770.6	3574.5
56.3	761.4	795.9	996.0	1255.9	1004.9	1355.8	1116.4	390.1	315.9	630.4
3673.1	2694.6	2242.9	2062.2	2360.4	2411.1	2708.8	2528.0	3291.0	2656.0	2591.7
6781.4	2667.7	2436.6	3044.7	2601.4	2489.8	2695.6	2450.5	2969.0	3357.8	2977.4
61.6	316.9	276.4	275.5	559.9	242.9	155.7	466.1	256.8	121.2	236.4
1153.0	2898.7	4083.7	4367.1	2733.7	3173.8	3004.0	3539.9	2011.3	2033.3	2679.1
5292.6	7737.6	7908.5	9122.5	8015.8	7158.1	7867.7	6453.4	8113.7	6008.8	7885.1
5693.1	2860.7	3251.1	2469.0	3118.5	2868.1	3080.4	2367.2	4238.6	3103.8	1259.9

5723.4	4298.3	4652.7
977.8	1152.1	1096.8
582.3	694.7	1462.6
5176.6	4640.1	6018.9
3385.6	4470.8	4287.2
2399.6	1642.0	2441.2
5347.8	4957.3	5801.5
1381.5	1524.9	2094.3
1332.4	1288.7	2187.8
68.5	106.9	306.9
135.6	160.0	123.9
925.2	1466.1	2221.7
9451.2	10254.4	10403.6
293.4	175.9	336.1
2349.0	2530.6	4172.1
2797.6	3124.3	3549.1
2264.2	2748.9	2985.9
2655.2	2886.1	2701.1
2423.4	2603.8	3185.2
2033.3	2364.8	2175.4
3071.6	4514.4	4384.1
4232.2	5628.9	4457.2
1501.2	1958.1	2787.5
1627.3	1298.1	1554.9
1938.3	2481.0	2254.4
2208.8	2468.2	2037.6
1718.5	2153.5	2310.5
313.5	199.9	235.5
3767.3	4255.7	7967.6
1222.0	750.3	661.6
2396.3	2667.5	3016.0
330.4	738.6	319.6
1011.1	1020.8	833.6
2860.8	3007.7	3562.3
1227.8	884.8	1461.1
2098.0	3590.5	2670.4
3390.6	2824.2	3112.7
412.7	330.9	260.7
3424.4	4283.9	4458.7
6312.0	7253.0	7982.8
2688.4	3517.8	3833.1

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU510991.1 gg_id:268138 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01a09 EU510
AY992665.1 gg_id:132681 mouse cecum clone C23_n18 AY992
EF602824.1 gg_id:230748 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF602
AF371669.1 gg_id:50208 swine intestine clone p-2169-s959-3 AF371
FJ881208.1 gg_id:451771 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
FJ680992.1 gg_id:515960 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU748082.1 gg_id:316388 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44b01 EU748
EU508303.1 gg_id:259395 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02b11 EU508
DQ824073.1 gg_id:185705 human fecal clone RL204_aaj59a05 DQ824
EU006427.1 gg_id:241287 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU452146.1 gg_id:331381 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU452
EU508800.1 gg_id:262443 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51c06 EU508
EU748045.1 gg_id:347653 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43e03 EU748
AY992553.1 gg_id:129913 mouse cecum clone C23_i21 AY992
EU505090.1 gg_id:268244 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02g04 EU505
DQ815411.1 gg_id:167204 mouse cecum clone aab47f11 DQ815
AB185722.1 gg_id:106444 rumen clone U28-G03 AB185
EU452106.1 gg_id:311187 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
AY992654.1 gg_id:133327 mouse cecum clone C23_n06 AY992
DQ015332.1 gg_id:129929 mouse cecum clone M2_1h08_2 DQ015
EU453747.1 gg_id:310479 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU510785.1 gg_id:264159 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49c04 EU510
EU508371.1 gg_id:275792 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04b05 EU508
EU451765.1 gg_id:355426 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU451
EU506702.1 gg_id:275914 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54g09 EU506
EU454328.1 gg_id:306215 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU454
EU451491.1 gg_id:335440 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EF096332.1 gg_id:181789 mouse cecum clone obob2_aaa01a09 EF0963
EF604682.1 gg_id:232262 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU451101.1 gg_id:333207 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU451
EU454602.1 gg_id:314786 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU454
EU843366.1 gg_id:309471 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
EF604679.1 gg_id:228595 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU454757.1 gg_id:337906 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU454
DQ015051.1 gg_id:131129 mouse cecum clone M2_d12 DQ015
EU456943.1 gg_id:319388 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU456
EU511944.1 gg_id:266981 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11f07 EU511
EU454080.1 gg_id:329617 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454
EU779464.1 gg_id:356407 Grevy's Zebra feces clone GZ_aaa01a11 EU779
EU503677.1 gg_id:266790 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03a02 EU503
EF098940.1 gg_id:184978 mouse cecum clone SWPT1_aaa03e11 EF0989

17271.7	6842.2	5793.6	6123.4	6256.1	5585.5	7206.9	6044.0	7457.7	6708.6	9118.8
16068.8	9346.4	7802.5	8506.1	8108.1	7698.3	9330.6	7968.0	10746.8	7953.1	11269.8
61.7	1047.7	1550.0	1183.5	1233.7	1230.4	1890.4	1668.3	694.0	368.6	1035.8
55.2	1675.1	3180.2	4248.4	1155.7	1563.0	1075.4	2177.0	960.2	206.2	1963.9
9269.1	5074.6	5720.9	5706.1	5484.1	4882.3	5715.7	4792.7	7096.5	6651.6	6046.3
5429.2	2612.9	3152.9	3089.0	3271.5	2587.1	3464.8	3562.8	2022.2	1037.6	2082.0
1218.6	1313.8	2023.9	1584.2	1604.5	1476.4	1703.2	1423.3	760.7	651.0	850.4
17127.4	7706.4	7200.7	9327.5	7798.4	7684.0	8480.8	7108.5	9685.0	6917.8	11848.0
24.7	149.7	280.7	238.2	42.7	110.7	99.5	178.2	37.6	38.4	96.5
114.2	293.0	452.0	523.2	148.1	196.0	232.4	299.9	103.2	145.1	228.8
256.1	823.4	1064.0	1514.7	578.7	557.6	636.7	762.4	422.1	238.2	747.3
530.5	3369.6	3748.5	4258.8	3821.2	3682.3	4863.3	4114.5	1859.2	974.5	3632.3
2510.6	3255.1	4176.0	4261.1	3871.7	3756.8	4059.5	3688.9	3414.3	1710.6	3367.8
43.8	1562.2	2263.6	3000.6	790.4	706.7	935.9	2045.7	287.5	155.6	1170.3
2894.8	4488.5	4724.4	4581.8	3914.4	3309.4	3873.3	3565.6	3281.4	2524.4	2818.8
837.7	1426.3	1778.9	2353.6	1144.3	1361.7	1249.5	1323.4	794.4	248.2	882.3
531.2	1173.7	1482.2	1766.6	1017.6	1158.0	1038.3	1637.4	438.8	588.5	916.3
31863.3	13266.2	11679.2	13739.2	12481.8	11909.8	12707.0	10197.9	16808.2	13566.3	16274.9
115.6	1105.0	1734.1	1419.1	969.0	1146.2	999.0	1364.4	503.6	709.6	1123.7
12899.2	5760.3	5482.0	5504.8	5136.4	5160.7	5676.9	5497.2	4901.5	5225.2	6532.8
410.0	3112.6	3801.0	4899.3	4253.3	2769.0	5308.5	3215.3	1324.3	1241.4	2531.8
254.5	1742.2	1538.3	2040.8	1317.6	1616.2	1747.8	1962.8	1653.6	983.8	1167.3
14667.0	7556.6	7427.2	8134.5	7107.5	7061.5	7475.7	7088.7	9648.4	7224.3	9764.1
11759.9	1298.8	1376.9	1990.5	1946.2	1633.5	1498.4	1624.7	1337.9	1748.5	1601.7
26977.2	11692.2	10136.4	12158.7	10323.1	11059.0	11403.3	9719.6	14954.8	11862.8	16107.0
367.7	2206.5	2459.6	2081.4	1640.3	2023.8	1835.3	2635.6	4091.2	2918.2	2536.7
18251.7	4904.4	4298.6	4738.8	5478.0	5147.5	5377.5	5157.2	6104.6	4067.6	5479.1
1665.3	2894.9	3040.8	3258.7	2073.6	2211.7	2353.5	3075.0	2649.4	809.8	2705.3
10117.6	3484.8	3925.1	3531.7	3039.0	2012.0	3388.9	3379.0	3474.8	3417.2	1826.1
567.8	1953.2	2035.0	2784.2	1713.6	2054.3	2669.2	2001.0	1397.8	3790.0	2031.4
4000.4	2727.1	2350.0	2588.1	3745.5	3552.2	3082.7	4046.9	2976.4	2151.1	1953.5
51.7	133.9	250.6	250.7	156.6	214.5	211.7	177.3	77.9	54.0	61.8
34.6	476.2	1139.9	1413.5	189.9	573.5	325.0	1446.4	197.8	141.9	449.7
12249.0	4654.8	5034.8	5855.8	5067.0	4804.2	5754.3	4907.5	7639.8	6289.5	6086.5
169.9	1754.2	2058.7	2065.2	1520.7	1531.2	1715.5	2297.2	1361.4	416.4	1641.7
1371.0	602.6	675.5	647.3	433.8	650.8	466.9	887.8	400.5	167.9	552.8
176.2	1330.3	2423.5	2618.2	952.3	1489.4	1092.8	2050.9	592.3	319.6	1116.1
7601.0	3442.4	3625.4	3268.9	3170.4	2844.7	3737.6	2923.1	3295.6	1672.7	2688.0
250.6	1084.1	1625.2	1086.4	781.5	1126.9	944.9	1804.5	575.2	315.3	1003.6
66.2	103.0	192.9	132.3	41.0	115.6	51.8	200.7	55.2	48.2	109.8
1829.2	3432.6	3772.6	5041.2	4199.0	2649.1	4330.3	3362.9	1536.9	793.9	2456.9

5799.7	7017.9	6188.0
7813.6	10516.6	10440.2
1633.5	1207.9	1416.6
1824.6	1797.3	1544.9
5940.9	6568.7	5671.2
2727.4	3175.5	4607.1
1474.4	1773.3	1933.4
6707.2	9100.8	8018.6
356.4	188.1	220.6
221.8	385.5	357.7
898.3	898.9	541.0
3962.3	4265.7	5154.9
3555.3	4411.8	4995.2
2150.6	1554.8	2351.6
3877.4	4348.5	2995.1
1792.0	1661.3	2470.4
1826.8	1532.7	1442.4
10579.3	11868.1	11852.7
1088.7	2058.8	2191.2
3916.4	4922.0	4943.8
3121.9	3486.5	4007.2
2445.9	2142.0	2853.1
6924.9	9551.7	7544.5
2074.9	2170.6	2343.9
9835.9	13019.0	10484.4
2209.8	2559.6	2047.5
4435.1	6151.6	6952.1
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1762.0	2186.2	1990.6
3205.3	4337.0	5483.0
263.5	352.6	623.1
1757.9	994.4	1189.3
4192.4	7458.8	6841.6
1776.3	1748.0	2449.9
527.6	1338.8	1074.1
2049.1	2099.5	1991.6
3158.6	4285.4	4182.1
1649.3	1412.2	1346.1
228.2	187.3	100.3
3435.0	3908.7	4617.5

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o__Clostridiales	f__Lachnospiraceae
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EF604619.1 gg_id:233894 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EF097752.1 gg_id:193180 mouse cecum clone SWPT20_aaa03b09 EF0977
EU511837.1 gg_id:260533 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09h02 EU5118
EF098562.1 gg_id:187222 mouse cecum clone SWPT16_aaa01d09 EF0985
EU451150.1 gg_id:339776 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4511
EU456175.1 gg_id:309702 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4561
DQ015076.1 gg_id:129833 mouse cecum clone M2_g09 DQ015
EU457597.1 gg_id:347293 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4575
DQ815590.1 gg_id:162898 mouse cecum clone aab43c10 DQ815
DQ014760.1 gg_id:129394 mouse cecum clone M1_d04_2 DQ014
EF097767.1 gg_id:188496 mouse cecum clone SWPT20_aaa03e01 EF0977
EF602872.1 gg_id:234789 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
EF100117.1 gg_id:193034 mouse cecum clone SWPT5_aaa04h10 EF1001
EF097616.1 gg_id:182470 mouse cecum clone SWPT20_aaa01c12 EF0976
EU842777.1 gg_id:312126 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8427
EU509273.1 gg_id:269277 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47a05 EU5092
EF604671.1 gg_id:230102 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EU451155.1 gg_id:306640 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU4511
EU457089.1 gg_id:346996 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4570
EU456190.1 gg_id:326286 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU4561
FJ678423.1 gg_id:523796 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU456873.1 gg_id:318445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4568
EU451180.1 gg_id:316261 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4511
FJ682440.1 gg_id:526888 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EF436447.1 gg_id:205859 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC161 EF4364
EF614812.1 gg_id:232911 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF097797.1 gg_id:193426 mouse cecum clone SWPT20_aaa03h02 EF0977
EU843542.1 gg_id:326862 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8435
DQ015222.1 gg_id:135715 mouse cecum clone M2_d08_3 DQ015
EU503739.1 gg_id:265374 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03h05 EU5037
EF096482.1 gg_id:183730 mouse cecum clone obob2_aaa03e11 EF0964
EU452611.1 gg_id:349197 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4526
EU454775.1 gg_id:309663 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4547
EU507387.1 gg_id:271326 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02e05 EU5073
EF098491.1 gg_id:182081 mouse cecum clone SWPT15_aaa04b08 EF0984
EU511974.1 gg_id:263834 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12b08 EU5119
EU509198.1 gg_id:275528 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g03 EU5091
DQ326528.1 gg_id:149441 Metagenomic gut microbiome healthy human stool clone C670 DQ326
AY992448.1 gg_id:132937 mouse cecum clone C23_e04 AY9924
EU507630.1 gg_id:264644 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02b11 EU5076
EU344316.1 gg_id:271681 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443

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87.6	168.3	349.8	706.5	92.9	88.1	154.2	123.8	58.9	30.1	63.6
202.0	1605.6	1743.1	2240.7	1671.2	1515.9	1587.2	1711.2	993.0	1121.7	894.9
817.9	770.9	998.8	1296.6	430.4	659.2	334.7	972.7	467.1	363.8	467.6
18682.8	7917.0	6955.0	7667.3	7651.3	7176.8	7679.8	7886.8	8332.2	6702.0	10278.8
506.4	2138.4	2375.0	2507.8	974.2	1347.8	1228.4	2177.1	1243.9	309.0	1078.9
621.9	1003.5	1289.4	1457.1	1540.3	1140.3	1960.1	1097.6	764.1	2994.6	854.7
589.3	1830.9	1788.6	1787.9	1207.9	1463.9	1374.4	1378.6	1476.5	405.9	966.9
47.9	1080.0	964.1	1269.9	2180.7	843.8	1928.6	1191.1	287.5	204.3	349.9
2242.8	1898.6	1880.0	2380.1	2423.3	2092.8	2570.6	2037.7	1337.6	1659.6	1754.9
1069.5	985.4	1398.7	1213.4	1498.5	1045.8	1177.1	1237.0	733.6	379.5	1294.9
3225.8	3995.9	4075.8	5524.3	4687.3	3631.3	5376.3	4014.9	3344.1	3390.4	4974.7
590.5	1573.4	1448.3	1803.9	1662.7	1519.3	1548.1	1610.5	673.3	361.8	1518.6
5711.2	2060.7	2612.1	2821.0	1633.6	1951.1	1867.2	2041.1	1992.1	1512.6	2560.4
207.0	1118.8	1680.1	1758.1	1031.4	1128.2	1098.6	1320.1	484.8	232.1	761.4
10772.2	3475.4	3343.0	3491.6	3870.0	3293.3	3312.4	3063.8	4175.9	3858.2	5065.8
11762.6	5405.8	6084.3	6316.7	4431.5	5153.7	5093.2	6200.7	6109.4	5520.6	7201.4
393.2	2493.9	2807.9	2614.3	1378.6	2055.1	2118.5	2943.8	2644.4	1134.6	1657.7
5583.3	4484.8	4351.1	4102.0	3144.3	4361.7	3277.5	3676.5	4242.8	5999.1	5775.2
20071.6	5617.2	6060.1	6681.4	5233.6	6056.6	5217.8	6597.0	5959.7	7321.8	6331.1
2750.7	2630.6	3022.1	3088.5	2974.1	2698.5	3075.3	3157.8	3811.4	3045.6	3220.3
57.8	436.0	768.9	942.6	379.2	656.4	590.4	746.3	273.3	97.6	494.9
1974.1	3824.4	3027.5	3635.6	3377.6	2890.3	2688.7	3167.8	2911.5	1268.5	2201.4
44.4	152.6	167.3	225.0	57.9	131.3	90.1	149.4	64.6	30.7	80.8
72.9	929.9	1289.6	1414.5	419.4	657.2	601.5	1072.5	290.1	456.3	538.7
13698.2	7663.8	6023.0	5036.2	5866.7	6212.8	6081.7	4983.5	9314.2	4156.9	7829.1
2625.3	2766.1	3112.1	3499.4	2923.3	2643.4	3231.0	2568.1	3823.6	2574.6	7202.5
63.2	1286.7	2172.0	1759.2	606.8	1208.4	764.2	1778.8	508.1	281.7	1169.2
3630.9	2860.9	3050.6	3689.1	2891.9	2755.4	3058.7	2780.9	2966.6	2596.3	3761.0
49.1	1380.3	1574.7	1057.0	724.1	1094.2	993.3	1139.1	3123.7	1523.0	419.0
62.0	148.0	321.1	287.2	256.0	118.0	185.2	145.2	64.2	53.1	119.5
6841.0	2649.3	2767.5	2543.1	1852.8	2276.4	2093.2	2911.2	1737.9	1279.4	1788.1
326.5	426.5	449.8	464.5	275.7	357.9	344.9	514.1	349.9	412.2	296.0
15268.1	6450.4	6189.5	6338.2	6156.7	6191.9	6515.8	5933.1	6343.8	6438.0	6018.5
32.6	199.3	352.5	357.7	97.5	111.0	245.1	171.0	40.3	34.6	103.3
54.5	205.6	426.7	944.6	40.9	102.1	45.6	248.4	34.0	22.0	41.2
5701.3	5141.9	5073.9	5333.5	5778.3	4772.2	5208.8	4393.6	6457.3	5664.7	7597.0
7161.9	3807.1	4453.5	4417.7	4238.3	4039.9	4639.8	4323.6	3585.9	3198.6	3758.6
220.6	1700.4	2860.7	2696.4	1784.1	1794.8	2060.6	2086.6	870.2	736.0	1572.7
9827.5	3469.3	3991.7	4830.3	4141.5	3612.9	3780.6	4097.6	3921.1	2879.1	3749.4
3576.8	1056.2	1496.8	1891.8	1182.0	1261.8	999.4	1402.4	770.3	397.9	748.0

3590.3	4426.9	3990.6
235.8	274.9	116.9
1608.1	2218.2	2328.5
1520.6	1245.9	1397.8
8196.0	9213.2	8109.0
2620.9	1734.0	1321.4
1222.5	1471.4	1167.0
1414.8	2163.6	1413.2
1140.7	620.6	1416.0
2140.7	2025.5	1968.5
1058.8	1531.8	1311.8
3678.1	4218.2	4317.1
1078.1	2072.8	1168.4
2111.6	3496.9	2429.6
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3128.5	4600.9	3386.6
5434.5	5709.7	7250.4
2937.6	2536.8	2289.2
3864.4	4249.2	3426.0
7068.2	6069.0	4878.8
2838.2	3146.4	3786.8
651.9	625.1	1472.9
3163.4	3083.1	2786.6
215.8	212.4	475.0
1292.7	1376.9	1289.2
4804.2	5049.6	4902.6
2752.4	3898.9	2994.3
1719.5	1293.4	1969.9
2646.1	4826.8	3005.5
886.6	1016.9	1757.5
173.6	263.7	258.5
2576.2	2778.3	2328.2
296.6	460.1	56.9
6348.8	6563.6	7354.1
205.9	234.3	508.1
335.9	229.5	133.9
4231.4	5921.3	4730.7
3891.8	4212.3	5121.4
2006.4	2854.8	3355.3
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU453802.1 gg_id:317167 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4538
EU463722.1 gg_id:292285 domesticated horse feces clone horsej_aai91f08 EU4637
EF100116.1 gg_id:180818 mouse cecum clone SWPT5_aaa04h07 EF1001
EU509445.1 gg_id:267418 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e04 EU5094
EU451822.1 gg_id:354878 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4518
EU452341.1 gg_id:307918 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4523
EF098388.1 gg_id:181733 mouse cecum clone SWPT15_aaa02b05 EF0983
EU509945.1 gg_id:259081 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b07 EU5099
EU457793.1 gg_id:337739 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4577
EU511827.1 gg_id:275180 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf09g02.Contig3 EU5118
EU456521.1 gg_id:327654 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4565
EU504059.1 gg_id:258202 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04f12 EU5040
EU457020.1 gg_id:311520 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4570
EU655949.1 gg_id:286453 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6559
EU452489.1 gg_id:308807 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4524
EU791075.1 gg_id:436881 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology HD5-- mouse EU7910
EU456820.1 gg_id:331669 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4568
EU453751.1 gg_id:345491 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4537
EU503966.1 gg_id:261937 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d01 EU5039
DQ809100.1 gg_id:190767 human fecal clone RL308_aal81d12 DQ809
DQ815386.1 gg_id:171769 mouse cecum clone aab47d01 DQ815
EU455278.1 gg_id:341516 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU4552
GQ896790.1 gg_id:565987 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ014561.1 gg_id:131869 mouse cecum clone M1_a12 DQ014
AY991945.1 gg_id:134421 mouse cecum clone C20_m08 AY9919
EU510036.1 gg_id:273116 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf16c05 EU5100
EU455292.1 gg_id:313025 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4552
EU508993.1 gg_id:265987 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41e02 EU5089
EU506679.1 gg_id:266956 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54d01 EU5066
EU452961.1 gg_id:308861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4529
DQ015060.1 gg_id:131736 mouse cecum clone M2_e09 DQ015
EU452038.1 gg_id:310743 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4520
EU456424.1 gg_id:321691 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4564
DQ015047.1 gg_id:129376 mouse cecum clone M2_d08 DQ015
AY992601.1 gg_id:135442 mouse cecum clone C23_k21 AY9926
FJ881265.1 gg_id:409829 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EF097620.1 gg_id:199574 mouse cecum clone SWPT20_aaa01d07 EF0976
EF603187.1 gg_id:234746 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
DQ015465.1 gg_id:134774 mouse cecum clone M3_d08_1 DQ015
EF096423.1 gg_id:191516 mouse cecum clone obob2_aaa02f03 EF0964

67.9	684.3	1051.3	1534.6	716.5	563.0	995.3	966.5	269.2	61.8	338.7
4201.8	5804.9	5281.4	5242.6	4009.3	4579.6	5325.5	4588.9	6264.1	3658.9	4768.7
875.8	1086.8	1460.6	1156.6	1507.7	1393.8	1661.0	1967.1	1070.8	671.3	1120.9
3790.4	1885.6	1634.7	1568.7	1718.0	1605.3	1755.8	1811.4	1964.9	1155.2	1439.5
891.1	1166.6	1075.2	1030.3	812.8	804.2	756.4	817.3	670.9	282.2	1210.4
5656.4	2232.1	2072.0	3127.3	1744.1	2087.9	1927.6	2264.4	2515.8	1330.6	2788.9
883.6	1975.7	2650.5	2279.2	2216.1	2136.9	2372.0	2255.9	1834.9	875.8	2776.8
3202.4	5570.8	5726.9	5431.4	5064.4	5506.1	4895.3	5277.8	5629.5	4668.4	6329.6
263.4	535.8	849.9	1084.6	514.3	680.4	482.7	1230.0	206.0	163.0	306.9
132.8	786.8	1392.8	1584.5	204.9	515.5	296.5	1000.6	192.7	103.3	597.6
229.9	634.0	649.5	681.3	695.2	615.1	920.4	668.7	511.3	219.2	647.1
602.4	2634.9	3490.4	3394.2	3182.1	2883.8	4419.4	3210.0	2634.3	1342.1	3240.6
107.4	482.8	749.0	735.7	295.3	512.5	417.4	970.1	215.3	130.2	382.4
541.9	4905.8	3700.8	3821.2	4023.2	3539.7	3280.2	3455.6	4893.0	2661.2	2936.7
2748.9	5441.7	4382.2	5394.3	4240.2	4170.7	4663.5	5272.9	4442.0	2759.8	5590.4
69.4	736.3	904.3	1220.8	1158.2	999.7	1169.6	768.6	384.6	820.6	476.0
34.5	371.0	597.4	762.4	358.7	293.2	374.4	645.5	173.8	60.5	200.5
1158.1	2856.1	3415.1	3595.7	2415.9	2949.3	2805.5	3344.6	1984.6	1523.1	2643.3
24306.7	12754.0	11332.1	12812.9	13466.4	11527.5	12375.6	10157.6	15373.5	12817.1	13731.4
514.9	2202.3	2346.0	2476.0	1619.5	1909.4	1834.0	2430.0	3474.7	2778.3	2484.3
59.1	1158.6	1323.4	1370.2	889.2	1014.2	786.7	1581.5	503.7	733.6	656.5
2028.0	2638.6	2578.5	2417.0	2406.4	3026.8	2714.5	3303.4	2490.2	2968.9	2234.2
3707.2	8487.9	7889.6	6538.4	5490.1	6603.4	6890.1	6386.7	8604.2	6117.1	5646.7
245.2	1522.5	2348.0	1760.2	835.3	1256.1	1490.1	1908.6	775.9	458.3	1197.1
476.5	4378.0	5644.7	5302.3	3766.6	4217.2	4851.3	6506.3	4107.7	1977.4	4844.0
44.8	1093.3	1146.0	1643.1	114.8	994.6	676.3	1389.5	302.3	178.4	629.8
4184.6	2080.8	2033.9	2649.1	2551.2	2226.1	3285.4	2417.1	1258.0	983.4	2033.6
4395.6	3051.4	3686.5	2907.1	3364.5	3042.9	3927.4	2894.3	2077.3	3215.5	2675.3
31.0	291.8	478.3	512.0	98.8	303.7	127.6	243.4	46.4	35.8	143.4
6071.2	1661.3	1571.5	1864.9	1378.3	1555.1	1653.5	1491.4	2409.5	1891.2	2019.8
10782.3	2722.3	3524.7	3452.1	2662.0	2893.3	2992.7	2769.3	3598.9	2493.8	3373.6
2067.0	2106.8	2862.7	2380.5	1971.4	2178.1	1975.9	2336.0	1713.8	1576.8	1294.7
844.5	4643.5	3874.1	3055.3	2859.7	4350.2	3006.4	3804.7	5012.1	4296.8	2801.9
100.8	529.1	746.8	960.2	617.8	557.0	604.9	734.4	184.5	60.7	272.9
53.7	118.5	207.6	231.7	139.1	178.0	107.7	343.8	70.9	46.7	145.1
26.7	15.5	18.0	22.5	19.5	13.7	17.4	14.1	13.2	17.0	16.3
13176.9	5994.1	5449.1	5939.7	5611.4	5152.2	5598.8	4954.2	8771.6	5606.8	6485.9
833.2	2663.8	2933.2	2773.8	2601.4	3244.5	3125.5	2634.4	2154.2	2496.6	3299.9
3031.0	6305.2	5529.5	6097.7	3772.5	5470.8	5290.3	6545.2	4420.2	3645.4	5656.4
28.4	58.8	95.6	99.1	48.7	45.3	85.7	62.1	22.3	24.1	41.7
5028.9	2597.4	3774.2	4098.4	3190.2	2854.6	4507.1	3054.9	2375.5	1924.3	3568.3

878.9	850.0	947.5
4416.7	4975.9	4199.9
1414.8	2001.4	1970.2
1809.4	2028.3	2214.2
698.3	1348.0	693.1
2320.6	2739.0	1976.6
1546.5	2578.0	2769.8
5062.1	5123.4	4774.0
1044.8	1142.8	1096.6
1285.3	661.7	577.0
756.0	715.7	957.2
2698.4	2958.9	3910.1
1284.8	771.2	1198.4
3259.2	3354.9	3455.6
5623.1	5018.0	5912.2
979.4	903.1	1686.1
428.5	616.4	1592.5
3150.9	3798.6	3729.8
9940.3	11070.6	11763.2
2116.6	2432.6	1985.5
2582.2	1397.4	1420.4
3242.3	2678.0	3424.2
6782.3	8076.9	7138.6
2374.0	1703.6	1940.0
5151.9	4383.3	7759.1
1433.5	1118.2	1595.5
2951.6	2741.1	3171.2
3015.9	4228.7	3811.2
296.3	355.4	153.1
1203.7	2840.2	1586.4
3829.8	3511.0	3154.1
2230.7	2797.6	3202.7
3275.2	3770.2	4514.3
557.2	982.5	1135.7
191.7	200.3	226.1
14.5	18.8	20.8
5406.7	6589.9	5454.7
2343.5	3297.9	3234.8
4857.7	5116.3	6930.7
58.8	96.8	58.3
3027.0	4063.9	4588.8

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
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EF097707.1 gg_id:180288 mouse cecum clone SWPT20_aaa02f01 EF0977
EU455936.1 gg_id:303799 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
EF602817.1 gg_id:234346 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
FJ833930.1 gg_id:547336 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q201_51C07 FJ8339
DQ015671.1 gg_id:133649 mouse cecum clone M3_h11_3 DQ015
EF099867.1 gg_id:175731 mouse cecum clone SWPT5_aaa01e07 EF0998
DQ808413.1 gg_id:186008 human fecal clone RL180_aao76c09 DQ808
AB218340.1 gg_id:149327 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-100 AB2183
EU504243.1 gg_id:273308 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04h10 EU504
EU506323.1 gg_id:266017 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63c06 EU5063
EU451871.1 gg_id:346750 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4518
EU762489.1 gg_id:343491 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7624
EF098532.1 gg_id:181688 mouse cecum clone SWPT16_aaa01a02 EF0985
EF097805.1 gg_id:190057 mouse cecum clone SWPT20_aaa04a01 EF0978
EF099875.1 gg_id:191762 mouse cecum clone SWPT5_aaa01f05 EF0998
EU510827.1 gg_id:261532 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49h03 EU5108
FJ833555.1 gg_id:582515 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_05E01 FJ8335
EU451866.1 gg_id:307719 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4518
EF099337.1 gg_id:179819 mouse cecum clone SWPT3_aaa01h08 EF0993
EF099450.1 gg_id:199453 mouse cecum clone SWPT3_aaa03d05 EF0994
EF434359.1 gg_id:204333 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
EU508086.1 gg_id:270995 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa03e08 EU5080
EU510977.1 gg_id:268951 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52g03 EU5109
AM932644.1 gg_id:541250 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ014938.1 gg_id:135493 mouse cecum clone M1_1h06 DQ014
DQ014739.1 gg_id:135448 mouse cecum clone M1_b06_2 DQ014
EF096263.1 gg_id:185989 mouse cecum clone obob1_aaa03f09 EF0962
EU775549.1 gg_id:330417 Western lowland gorilla feces clone GORSD_aaa02h04 EU7755
DQ015321.1 gg_id:129868 mouse cecum clone M2_1g05 DQ015
EF605072.1 gg_id:235136 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6050
EU454317.1 gg_id:354274 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU4543
EF097703.1 gg_id:181331 mouse cecum clone SWPT20_aaa02e09 EF0977
EU459675.1 gg_id:303191 ring-tailed lemur feces clone RT_aai10f10 EU4596
EU457914.1 gg_id:317740 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4579
AB192168.1 gg_id:142751 termite gut homogenate clone RsTz-49 AB192
EF614845.1 gg_id:229751 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF098701.1 gg_id:196922 mouse cecum clone SWPT16_aaa03f07 EF0987
EU504061.1 gg_id:266108 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04g02 EU5040
DQ015304.1 gg_id:133405 mouse cecum clone M2_1c11 DQ015
EU509118.1 gg_id:274236 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44b02 EU5091
AY992677.1 gg_id:135612 mouse cecum clone C23_o08 AY9926

385.7	843.6	994.8	1139.5	1338.1	1055.9	1387.2	1013.5	756.4	444.5	716.9
9322.5	3608.8	3068.7	3370.4	3012.8	3329.7	3853.7	3228.4	5552.3	4871.9	3197.6
177.9	1360.7	1861.0	2912.5	985.8	1189.4	1738.5	1466.1	827.7	329.9	1311.7
2795.2	4107.5	6176.8	6154.6	6784.4	6430.0	7013.2	6152.4	3119.2	1811.2	5353.3
1525.8	1596.1	1351.7	1200.4	1299.6	1418.4	1188.3	1224.1	1328.0	1454.3	1132.6
50.6	1183.0	1812.6	1920.2	857.9	1402.8	824.6	2307.7	723.3	536.3	1309.4
21014.6	6048.7	5546.4	5758.7	6655.5	5378.4	6290.4	5042.2	9687.6	7880.1	9774.7
39.0	192.4	313.8	249.1	280.2	198.3	244.1	165.0	34.0	18.7	174.7
687.8	4030.8	3916.3	3591.7	4241.8	4989.0	5107.2	4926.2	4438.2	2521.0	3572.9
1910.4	4482.8	6054.9	7545.6	5955.7	5490.9	5866.1	5500.0	3190.2	2478.8	4919.8
602.0	3198.2	3868.0	5006.0	5302.6	3196.9	5049.6	3204.1	2007.4	2005.7	2451.9
4616.3	3346.9	4105.5	3463.3	3246.1	3068.7	4613.8	3437.5	2460.7	1431.0	3015.4
55.4	306.0	652.2	712.4	133.4	257.7	158.6	468.7	97.3	122.8	134.8
280.1	301.9	446.5	523.5	70.9	218.5	208.6	228.2	181.1	217.5	499.7
491.6	932.7	1939.1	1527.5	1133.9	1123.4	764.3	1375.0	784.6	498.9	1806.6
1661.6	1034.8	837.5	1130.1	807.9	834.1	1167.4	711.9	1198.0	1131.4	1335.2
2406.6	2098.7	2706.2	2587.2	2599.2	2651.9	2108.4	2109.6	1675.0	2520.5	1513.0
6076.1	7849.2	6496.7	6644.7	6137.9	6587.6	6164.1	6445.3	9841.1	7838.9	7976.7
14473.9	7673.6	6779.6	6560.2	4696.9	6323.1	7265.4	5895.0	8598.8	8201.8	7735.7
53.9	31.6	129.8	115.7	125.9	102.1	145.4	117.5	55.3	34.0	51.3
1538.6	1887.0	3041.2	2343.7	700.7	1716.3	928.9	2000.7	809.9	443.5	1611.9
5953.3	2397.0	3066.1	2429.4	2699.1	2804.2	2579.7	2870.1	2522.2	4093.3	2009.3
510.1	1864.5	3215.3	3062.0	1935.9	2277.7	2380.3	3241.9	1564.6	505.5	2033.8
1155.2	448.8	526.0	536.5	235.0	484.4	291.6	717.4	261.6	289.5	524.6
4954.4	1315.7	1691.7	1365.2	489.1	1392.4	1302.1	2131.5	691.0	409.3	995.9
217.2	614.8	1299.0	1240.5	667.3	541.6	740.6	644.9	397.8	231.2	760.7
7525.8	3092.7	3077.1	3298.0	2351.6	2446.7	2812.5	2885.0	4893.3	1687.7	2864.3
37.2	277.2	482.0	410.4	163.9	248.9	245.8	444.2	151.4	74.6	283.4
100.9	566.7	726.3	851.3	434.7	621.6	915.0	765.4	226.8	152.9	360.3
4101.5	3210.1	3445.2	3883.3	3005.7	2488.4	3732.3	3106.2	2795.9	2873.5	3600.2
9517.8	3498.4	3469.2	3962.5	3034.7	3425.2	3840.5	3439.2	3573.2	3618.8	3413.2
2261.6	1671.5	1994.1	1892.8	1355.3	1568.4	1451.7	1550.5	2384.9	1415.5	1306.3
6406.8	5143.7	5791.4	6151.7	5299.7	5103.3	6517.6	5380.6	3155.6	3579.2	5239.8
10719.1	6165.5	5709.4	5802.1	5439.2	6388.7	6502.4	6600.1	6706.7	4430.4	7119.4
105.6	1157.2	1859.0	1955.2	985.6	1908.3	1477.2	1936.0	662.1	1301.1	758.9
3024.4	2130.2	2678.0	2181.4	1904.8	1527.8	2859.3	1543.5	2028.8	1456.7	3996.2
994.2	4231.3	4452.2	3879.5	3505.3	4111.6	3665.3	4110.1	4724.0	3007.5	5269.1
17235.2	5059.5	5000.1	5602.1	4832.6	4865.3	5415.6	5419.3	5643.5	4371.4	6569.5
8515.1	5686.2	5221.4	4307.0	4673.0	5540.2	4281.8	5093.9	8423.8	7404.9	5938.1
2221.4	5353.6	6261.1	6558.6	5838.2	5242.4	5882.0	6058.7	5265.4	3803.1	5038.6
13336.8	5562.4	7742.0	7100.3	5590.5	5586.3	6094.6	6293.2	7723.2	7467.7	6963.0

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3169.1	4142.6	3389.7
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1171.4	1809.7	1237.8
2268.4	1971.5	2135.6
5787.6	6556.9	5338.7
192.1	283.4	278.9
3783.6	4596.4	4217.7
5223.9	6765.4	7328.8
3287.3	4810.5	5692.3
3247.5	3393.0	3625.5
513.3	655.2	387.1
206.1	412.1	351.3
1097.9	1830.2	1290.8
770.1	1019.5	810.7
2539.1	3374.6	2369.4
6668.7	7613.5	5795.8
5167.5	7193.8	6390.9
99.8	98.3	144.8
2378.3	2064.2	2563.7
2886.2	4497.6	3417.7
4044.7	2451.7	3349.0
793.2	649.5	459.5
2526.1	2109.0	2396.4
766.3	1222.0	955.5
2648.7	2928.8	2756.8
419.9	491.5	412.2
756.6	450.5	875.1
2979.8	3871.6	3218.6
3223.0	4481.0	3490.6
1018.2	2087.3	1581.2
6496.3	5652.2	6307.1
5349.8	6168.2	5583.1
2680.4	2273.4	2015.6
1281.1	2055.2	1358.5
3810.9	3659.5	3330.5
5524.9	6133.0	5151.3
4432.8	5449.0	5431.0
6477.4	6042.9	6971.7
6054.2	9403.3	7495.9

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o__Clostridiales	f__Lachnospiraceae

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EU508676.1 gg_id:271662 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49c07 EU508
EU508491.1 gg_id:266933 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap34c10 EU508
EU471730.1 gg_id:289401 Asiatic elephant feces clone AE2_aaa01c04 EU471
EU748188.1 gg_id:353892 neotropical folivorous flying bird adult hoatzin crop clone hoa33_78F10.F EU748
EF099417.1 gg_id:188786 mouse cecum clone SWPT3_aaa02h10 EF0994
EU457885.1 gg_id:330606 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EU382068.1 gg_id:258566 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU474422.1 gg_id:293963 western lowland gorilla feces clone GORSD_aaa03h10 EU474
EU509750.1 gg_id:274752 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak48d02 EU509
EF406641.1 gg_id:209361 mouse colon clone infected_7days-C12 EF406
EU506251.1 gg_id:273127 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61d08 EU506
EF097905.1 gg_id:182808 mouse cecum clone SWPT12_aaa01g02 EF0979
EU509001.1 gg_id:274719 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41e12 EU509
EU508154.1 gg_id:270273 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01g04 EU508
EU457552.1 gg_id:350089 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EF099531.1 gg_id:176694 mouse cecum clone SWPT3_aaa04e06 EF0995
FJ682372.1 gg_id:525387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6823
EU503905.1 gg_id:263366 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02d07 EU503
EU455013.1 gg_id:337002 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU455
EU344186.1 gg_id:265676 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EF097204.1 gg_id:185576 mouse cecum clone SWPT18_aaa03b02 EF0972
EF095984.1 gg_id:194281 mouse cecum clone lean2_aaa01d06 EF0959
EU504772.1 gg_id:261755 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01h07 EU504
EU456684.1 gg_id:333576 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU456
EU508805.1 gg_id:264439 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51d02 EU508
EF096462.1 gg_id:183211 mouse cecum clone obob2_aaa03b12 EF0964
EU506793.1 gg_id:272787 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56d07 EU506
DQ801341.1 gg_id:179065 human fecal clone RL388_aao94c03 DQ801
EF096190.1 gg_id:181470 mouse cecum clone obob1_aaa02c05 EF0961
DQ799217.1 gg_id:181170 human fecal clone RL205_aaj19c10 DQ799
EU452204.1 gg_id:342519 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
EF603871.1 gg_id:232146 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
AY992508.1 gg_id:131139 mouse cecum clone C23_g22 AY9925
EF099749.1 gg_id:182095 mouse cecum clone SWPT4_aaa03g08 EF0997
EF614724.1 gg_id:230719 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EF098157.1 gg_id:193724 mouse cecum clone SWPT14_aaa02d03 EF0981
EU505182.1 gg_id:266389 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04a11 EU505
EF406746.1 gg_id:210149 mouse colon clone infected_14days-D8 EF4067
EF096844.1 gg_id:191951 mouse cecum clone SWPT13_aaa01e11 EF0968
EU457529.1 gg_id:325739 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
EF603088.1 gg_id:234218 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030

1087.6	4265.3	3973.5	3743.4	3569.3	3873.4	3520.7	4033.2	3935.4	4746.3	3464.5
1615.4	3103.9	4518.5	4658.2	4890.6	4416.1	5360.7	5022.8	2509.0	2471.5	4794.9
1806.3	2530.3	2579.7	2721.1	2047.0	2291.4	2032.5	2136.4	1842.3	2436.1	1657.5
24129.5	6778.9	5992.2	6756.6	6364.4	5934.8	6592.7	5483.8	8563.7	6503.8	6953.0
438.6	1913.0	1964.7	1985.0	1801.0	1906.3	2696.9	1671.3	1037.0	560.1	1989.3
4070.7	3288.6	3590.0	3372.7	2986.1	1367.7	3878.1	2684.7	3518.7	2570.2	4440.8
1522.3	884.9	1109.0	1164.6	828.7	720.5	904.6	1005.2	924.8	515.4	873.0
1021.4	3120.3	3321.5	3320.9	3757.6	3036.8	4018.0	2746.8	3454.1	1785.9	3089.6
918.5	2339.6	3822.3	3848.0	2788.1	3220.3	3500.1	4716.3	2378.6	694.9	2943.0
10590.6	4479.3	4364.6	4801.9	3834.9	4294.3	4009.1	3750.4	5992.6	1986.2	3844.2
60.7	927.5	1212.8	1494.3	937.0	1057.6	1293.9	1196.6	733.0	275.3	1156.0
4439.4	1441.1	1924.4	1013.8	1337.1	1422.8	1478.2	1556.7	2401.2	2078.2	2544.9
556.7	3925.5	4706.0	6126.4	4072.5	3932.9	4330.6	4175.8	2572.9	2040.3	3244.5
31744.2	8823.9	7928.4	9374.9	7864.4	8110.3	8823.7	8341.3	11376.6	9049.8	13004.3
4614.8	3283.0	2950.9	2865.1	2230.3	2320.7	2426.5	2398.1	2825.7	1734.8	2380.4
39.6	66.9	84.3	78.4	24.4	46.6	55.0	61.0	22.8	22.1	42.0
536.2	1890.3	2594.8	2110.5	2156.4	1260.8	2501.1	1925.2	1805.6	1715.4	2413.2
43.7	1257.6	1882.4	2272.5	1367.2	947.9	1371.2	1421.7	118.6	164.8	800.3
10385.7	3768.1	3799.5	4112.0	3656.8	3400.9	3379.6	3781.8	3871.2	2261.9	4755.0
187.8	2017.7	2599.8	2794.0	1722.0	2254.3	1732.2	3195.4	1309.9	2383.8	1844.4
36.7	111.7	119.1	249.4	46.7	32.6	36.8	54.1	29.1	22.1	22.4
4753.9	4781.9	5347.6	5692.8	4439.7	5038.5	5713.4	5339.6	4436.6	7538.4	7148.1
32.2	49.3	120.0	115.0	21.9	22.2	22.3	24.5	16.6	13.8	19.3
1754.8	4670.7	5337.0	5829.7	5196.6	4465.1	5477.8	4816.8	2956.3	4851.1	4008.6
350.1	3136.6	2771.6	2359.6	2513.5	2923.5	1761.6	3015.4	3276.5	3668.1	3182.7
1587.0	2399.1	2214.6	2396.8	1900.1	1719.2	2095.6	1605.5	2459.9	2035.2	3467.4
6471.0	4757.9	4235.7	6384.1	3967.0	3633.5	4590.4	3736.4	4502.0	2149.8	5144.0
6494.5	1628.2	2193.0	1433.5	1091.1	1333.7	1120.6	1606.9	1341.7	1510.2	1741.2
1691.9	2873.9	2925.3	3021.6	3392.2	1997.7	3127.6	2579.9	4512.1	1131.5	3514.9
44.4	1931.9	3025.3	2575.2	899.8	2393.0	1272.7	2503.3	1059.8	391.0	2147.7
10450.7	9673.6	7031.2	9698.9	6902.0	7586.1	6921.4	6261.8	8172.9	6593.5	9137.2
29.7	62.2	109.1	133.3	53.7	50.7	48.8	68.2	20.8	18.1	34.3
78.5	1358.5	2776.2	1722.0	1260.0	1526.2	1242.9	1808.0	1408.8	3102.4	1467.0
1827.2	2275.6	2303.5	1983.7	1882.6	2376.2	1865.9	1842.1	2762.9	1631.7	1543.9
2339.4	2587.7	3512.0	2408.3	1695.7	2340.5	1712.6	2629.1	1484.7	1082.1	2756.4
10174.1	4019.8	3370.7	2687.7	3538.4	3682.9	4458.9	3317.1	3154.8	4900.9	4117.7
1077.2	2909.4	2144.0	1736.2	2640.3	2336.8	2184.8	2124.0	1798.5	2103.7	1404.1
233.7	4030.0	3458.7	4446.9	4324.0	2947.7	4425.3	3780.5	1307.4	1837.8	2821.8
584.5	2432.0	3696.9	3669.6	3297.9	2509.1	4054.1	3082.0	1291.1	1362.3	2601.5
24103.5	10252.1	9188.3	10176.0	10179.8	9120.7	9918.8	8580.3	13602.5	10413.8	12574.2
1500.0	3361.9	4031.7	4757.7	2868.6	2983.7	3649.0	5148.2	2885.6	1837.1	5065.4

4047.3	4014.5	5074.2
4561.0	5914.1	5810.0
3018.2	3574.2	1812.5
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976.7	1705.0	1223.6
2830.4	3306.2	3744.8
5605.3	3140.5	4288.1
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1493.5	2158.4	2079.5
3954.2	4958.9	5943.8
7467.4	11354.5	8199.8
2476.8	3062.6	3512.5
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3973.9	4975.1	4799.6
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2580.8	2301.8	2068.8
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EU504387.1 gg_id:261446 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03d12 EU504
EU472601.1 gg_id:291380 Angola colobus feces clone EAC_2_aaa02e06 EU472
EU381522.1 gg_id:270410 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU457486.1 gg_id:346580 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU453821.1 gg_id:307296 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU454911.1 gg_id:310717 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EF097477.1 gg_id:180864 mouse cecum clone SWPT19_aaa03b06 EF097
EU771700.1 gg_id:341089 African elephant feces clone AFEL_aai30b06 EU771
EU507752.1 gg_id:262527 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04b10 EU507
DQ815934.1 gg_id:166664 mouse cecum clone aab24e02 DQ815
EF614558.1 gg_id:231854 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EF096019.1 gg_id:182878 mouse cecum clone lean2_aaa02b08 EF096
EU511067.1 gg_id:272594 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02b11 EU511
AF371670.1 gg_id:16766 swine intestine clone p-1807-c3 AF371
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EU508931.1 gg_id:262259 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39c10 EU508
EF603666.1 gg_id:227933 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EU453485.1 gg_id:308894 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU453
DQ015223.1 gg_id:132697 mouse cecum clone M2_d11_3 DQ015
EU508314.1 gg_id:266562 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa02d12 EU508
DQ015366.1 gg_id:130163 mouse cecum clone M3_c01 DQ015
EF098090.1 gg_id:174307 mouse cecum clone SWPT14_aaa01d03 EF098
EU655749.1 gg_id:280818 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU510201.1 gg_id:266443 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h02 EU510
EU775878.1 gg_id:323189 Horse feces clone horsej_aai91g01 EU775
EU504177.1 gg_id:267302 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03b05 EU504
EU453237.1 gg_id:344421 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU504232.1 gg_id:277443 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04f09 EU504
EU510718.1 gg_id:274056 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39h08 EU510
EU508170.1 gg_id:264643 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02d05 EU508
EF614731.1 gg_id:228805 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
AF371671.1 gg_id:50757 swine intestine clone p-3181-SwA3 AF371
EU452194.1 gg_id:310089 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU452
EF096027.1 gg_id:174272 mouse cecum clone lean2_aaa02c10 EF096
DQ815795.1 gg_id:167197 mouse cecum clone aab22d06 DQ815
EF603873.1 gg_id:228281 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EU451120.1 gg_id:303955 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451
EF098170.1 gg_id:179964 mouse cecum clone SWPT14_aaa02e09 EF098
DQ015660.1 gg_id:133505 mouse cecum clone M3_g07_3 DQ015
EU454413.1 gg_id:335832 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU457983.1 gg_id:303510 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU457

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4740.0	2445.0	2837.2	3106.7	2556.5	2484.1	3164.0	3048.8	2720.6	1595.2	2232.3
543.1	875.8	1250.1	1240.6	1745.9	1018.4	2203.7	1092.8	477.5	380.3	897.7
7686.6	6396.1	5494.5	6101.3	5253.9	5185.3	5034.5	5167.7	6137.1	4139.4	6558.5
37.8	29.8	42.9	77.7	48.7	44.1	48.0	24.5	44.4	22.9	25.4
1645.6	4006.4	4443.1	4151.6	3474.8	3553.7	4253.0	4136.2	6346.4	2632.2	4415.9
1306.9	2930.2	3019.9	3178.4	2966.8	3023.1	3394.9	3139.8	2162.3	2909.3	2247.6
737.1	2285.5	2492.5	2384.8	2348.0	2218.2	2246.4	2274.8	1673.2	2510.4	1601.0
681.4	1029.7	1300.2	1094.1	1095.8	1079.1	1541.2	1247.3	822.9	442.3	1092.7
291.1	2946.8	3049.6	2823.0	2628.3	2360.2	2402.2	2414.3	1678.4	1055.6	1874.1
4539.9	3011.9	2848.8	3510.9	2826.3	2888.7	3007.5	2987.3	2469.6	2527.4	4198.1
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58.3	1428.6	2423.7	1288.3	550.4	1327.6	489.1	1727.2	899.1	1514.1	1401.5
37.8	23.6	76.2	67.3	40.6	29.6	35.2	19.8	13.1	10.5	17.9
69.5	103.1	294.5	238.9	199.1	188.0	214.4	154.5	123.1	66.4	81.0
10617.9	6189.9	7380.6	6821.7	4584.6	7314.9	5356.3	7419.0	5747.3	4760.6	8202.1
4541.4	1696.9	2079.8	2143.6	1835.0	1638.0	1941.5	1799.0	1281.3	791.1	1339.1
49.4	702.0	1172.6	904.1	490.3	718.8	519.1	949.9	358.8	188.1	545.5
1416.8	2904.1	2204.7	2243.3	2060.4	2047.4	2179.6	1976.2	3624.9	2838.0	2345.2
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158.9	1492.3	963.4	506.8	877.2	970.5	981.3	974.7	1075.5	500.8	849.1
2867.5	5466.3	7590.9	6184.0	4821.4	4283.1	4256.7	5757.4	4802.5	3365.0	6145.5
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179.3	1374.1	1577.0	1949.6	2112.5	1634.8	2263.4	2286.5	1136.0	1057.9	1219.7
2429.8	3385.5	3992.7	4053.6	4469.7	3293.4	4429.8	3892.4	2490.5	1479.4	2952.7

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1658.0	1382.6	1306.5
31.1	40.7	32.8
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EU504026.1 gg_id:276937 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04b11 EU504
EU511868.1 gg_id:268130 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10b04 EU511
EU509552.1 gg_id:270545 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60f06 EU509
EF099819.1 gg_id:184463 mouse cecum clone SWPT4_aaa04g04 EF099
EF098904.1 gg_id:182079 mouse cecum clone SWPT1_aaa03a09 EF098
EF605077.1 gg_id:228860 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF605
EU455811.1 gg_id:341706 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU454169.1 gg_id:351220 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU454
EU503854.1 gg_id:265301 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01f01 EU503
EU454336.1 gg_id:355053 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU454
EU505201.1 gg_id:267215 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04d07 EU505
DQ673574.1 gg_id:166178 rumen fluid clone GRC109 DQ673
EU507887.1 gg_id:272764 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02g05 EU507
EU506551.1 gg_id:269966 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03g12 EU506
EU455724.1 gg_id:329290 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79 EU455
DQ815946.1 gg_id:163014 mouse cecum clone aab24f10 DQ815
EU455456.1 gg_id:329010 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79 EU455
EU761646.1 gg_id:328026 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU504019.1 gg_id:272454 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04b04 EU504
EU507347.1 gg_id:268466 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01h11 EU507
EU748047.1 gg_id:327000 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44d05 EU748
EU507456.1 gg_id:261848 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03e04 EU507
EU454439.1 gg_id:336426 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454
DQ237938.1 gg_id:142942 influence fumarate disodium on ruminal metabolism goats goat rumen clone M1 DQ237
EF098081.1 gg_id:179438 mouse cecum clone SWPT14_aaa01c03 EF098
EU510103.1 gg_id:264218 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01d09 EU510
AY916273.1 gg_id:113572 human rectum biopsy clone N322 AY916
EU506653.1 gg_id:264703 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54a02 EU506
EF603185.1 gg_id:231870 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
GQ502513.1 gg_id:572072 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU451680.1 gg_id:356109 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU451
AB088950.1 gg_id:77867 termite gut homogenate clone Rs-B88 bacterium AB088
EU455158.1 gg_id:316064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
EF603953.1 gg_id:230661 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EU457669.1 gg_id:336094 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU457
EU510908.1 gg_id:276935 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak51d03 EU510
EU510484.1 gg_id:269754 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal39e07 EU510
EU507594.1 gg_id:259172 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01e12 EU507
EF603952.1 gg_id:229562 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EU452303.1 gg_id:315527 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU452
EF098507.1 gg_id:195445 mouse cecum clone SWPT15_aaa04e06 EF098

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93.3	1632.9	1812.1	2009.0	2392.9	1673.5	2240.4	2114.4	1006.2	403.6	904.0
9553.3	5931.0	6078.3	6570.0	6511.2	5958.0	6985.5	5788.3	7739.6	6829.6	6672.4
124.6	1054.8	1341.7	1243.9	1118.8	1114.6	1551.2	1410.3	931.7	765.8	1202.0
515.0	913.6	1345.8	1295.0	796.1	977.1	1189.4	1470.3	862.8	791.9	1280.3
6161.2	3724.6	4377.1	3874.2	4445.3	3459.1	4098.9	3434.8	5108.5	5106.4	4422.3
980.7	2437.5	3419.7	3498.3	2380.0	2675.0	2921.1	3602.4	1766.8	2181.0	2680.0
104.5	174.8	270.6	268.5	150.1	173.6	234.8	365.6	197.0	66.4	192.8
4791.6	5477.1	5169.2	4537.5	4797.9	5466.7	4201.3	5750.6	5167.3	5413.8	4389.6
8673.2	4084.1	4352.2	5251.4	5964.8	6203.8	4704.6	4161.8	4149.5	3766.4	4471.7
6159.3	5449.1	5774.3	5201.5	5059.9	4547.3	6652.7	4969.0	5779.8	6171.2	4447.7
138.0	2197.9	2844.5	2973.0	1695.4	2182.3	2245.8	2636.6	932.9	382.0	1737.4
484.8	2054.2	1786.8	2329.6	2452.0	2128.4	1862.1	2466.5	1627.9	2260.2	1663.4
3227.2	4211.0	5097.8	6653.3	5528.2	4974.6	6074.9	5231.8	3269.7	1759.0	5233.2
3043.5	3478.7	3768.8	4046.5	3809.9	3896.4	4003.4	3362.2	4128.2	3065.2	4145.3
87.8	2775.9	2134.0	2113.9	875.6	1761.0	1387.8	1687.8	2354.0	2263.4	1670.3
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81.5	1241.9	1803.0	1590.3	1053.6	749.9	1167.3	978.2	501.2	1003.7	609.8
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3474.2	5583.1	5233.7	6148.9	6040.4	5764.8	6620.0	5913.2	4391.1	5251.1	4657.9
1205.9	2936.2	3015.8	3235.1	2155.6	2249.5	1886.8	2360.9	1854.4	1211.8	1754.3
82.3	468.0	816.3	794.0	451.6	499.2	369.1	570.4	191.8	181.1	450.9
34.1	297.7	590.0	794.2	133.1	251.6	180.0	423.0	53.2	30.8	177.9
736.0	1628.8	2014.7	2214.9	1570.5	1431.3	1487.6	1882.4	788.1	509.1	998.8
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703.0	7210.7	7817.8	7148.0	4312.3	6148.9	5020.6	6985.0	5950.9	5300.7	9661.7
656.3	448.3	761.5	818.9	852.1	818.5	428.0	906.3	558.2	1205.4	417.3
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507.7	2078.7	2927.8	3643.3	4546.3	2519.0	4791.7	2285.2	1168.9	410.4	1633.5
2192.5	3686.5	4985.2	6240.6	5351.0	4575.0	5041.9	4794.6	3216.7	2257.5	3768.4
638.7	1931.2	1635.5	1809.1	1723.8	1347.4	2450.9	1572.5	1645.2	1131.9	1188.0
1364.4	2424.4	1782.8	1500.0	1611.6	2048.7	1991.3	1541.0	3358.2	3364.2	1786.0
119.5	861.4	1447.8	1852.5	1014.5	993.2	1234.7	1179.8	313.3	170.6	879.2
205.9	137.5	154.2	254.3	122.3	133.7	115.7	286.7	109.2	47.4	250.7
161.7	720.6	1023.1	899.0	1077.5	885.7	748.6	1390.9	266.1	564.1	719.2

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5978.1	7485.0	8212.7
1198.6	1097.6	1320.3
1065.6	1513.5	1584.4
3557.4	5168.6	3966.9
3109.0	4295.7	4075.3
285.1	261.2	305.7
4972.6	4777.8	5654.3
6169.5	6242.3	6805.7
4602.3	4988.8	4581.4
2847.5	2350.4	3530.1
2442.4	2534.2	2797.8
5000.0	6631.2	6955.4
3804.2	4480.6	4786.5
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1870.0	2113.5	2914.1
6211.3	8560.7	6809.5
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978.7	1252.1	408.5

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EU504178.1 gg_id:264710 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03b07 EU504
EF603188.1 gg_id:233770 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6031
EF097774.1 gg_id:174773 mouse cecum clone SWPT20_aaa03e10 EF0977
FJ676625.1 gg_id:521311 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
EU504879.1 gg_id:273416 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03f11 EU5048
EF098804.1 gg_id:194682 mouse cecum clone SWPT1_aaa01c01 EF0988
EU510206.1 gg_id:262247 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02h08 EU510
EU508151.1 gg_id:271604 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01f05 EU508
EU508068.1 gg_id:263998 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa03b04 EU508
EU506413.1 gg_id:260208 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01d08 EU506
EU453966.1 gg_id:355377 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU453
EU508232.1 gg_id:259127 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03h09 EU508
EU507036.1 gg_id:266653 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10c02 EU507
EU506164.1 gg_id:264586 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa01g07 EU506
EU509958.1 gg_id:261999 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24d01 EU509
AY985863.1 gg_id:123051 human stool clone D139 AY985
EU452555.1 gg_id:306487 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU452
EU779413.1 gg_id:329742 Hartmann's Mountain Zebra feces clone AFZEB_aaj70d05 EU779
EU771195.1 gg_id:341737 Asiatic elephant feces clone AE3_aaa02d09 EU771
EU505013.1 gg_id:258435 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01f03 EU505
EF097384.1 gg_id:183060 mouse cecum clone SWPT19_aaa01h02 EF0973
EU655969.1 gg_id:283600 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU455052.1 gg_id:347910 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU504970.1 gg_id:277068 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h12 EU504
EU455813.1 gg_id:339351 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU455
AF371673.1 gg_id:33833 swine intestine clone p-1321-a5 AF371
EF604673.1 gg_id:230510 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EU451023.1 gg_id:305119 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU451
EU506314.1 gg_id:276253 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63b04 EU506
EU655863.1 gg_id:284578 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU504919.1 gg_id:277445 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04b10 EU504
EF097051.1 gg_id:187197 mouse cecum clone SWPT13_aaa04f12 EF097
EU455575.1 gg_id:308049 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU455
EU455793.1 gg_id:337999 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU455
EU505161.1 gg_id:262614 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03f12 EU505
EU509030.1 gg_id:260880 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42c09 EU509
EF096087.1 gg_id:182151 mouse cecum clone lean2_aaa03g01 EF096
EU511903.1 gg_id:268116 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak09e11 EU511
DQ815326.1 gg_id:169815 mouse cecum clone aab45e08 DQ815
EU511856.1 gg_id:264239 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10a06.Contig2 EU511
EF096163.1 gg_id:193879 mouse cecum clone obob1_aaa01f06 EF0961

372.9	1851.5	2308.6	2278.8	1050.3	1639.2	1332.1	1857.7	1180.3	957.9	1401.4
11656.1	5651.7	6157.0	7040.8	5597.5	6156.5	5937.0	8731.7	5113.2	5200.0	7201.1
20118.0	6626.4	5835.2	6581.8	6203.5	6136.7	9397.9	6589.3	9531.4	8397.2	9801.8
3313.1	6070.3	5849.1	5193.0	4439.7	5062.4	5497.6	4958.3	6978.0	4475.5	7387.7
4335.0	3612.6	3318.4	2773.2	2910.6	3315.2	3387.4	3012.9	4189.0	6507.5	3753.4
58.2	24.3	39.0	40.8	29.0	25.6	34.3	36.5	12.8	10.1	22.0
47.5	218.2	177.7	266.6	59.5	136.2	107.5	188.7	31.5	27.2	71.5
2657.9	3904.6	4001.6	4678.0	5162.9	3950.8	5609.4	4043.9	3860.2	3645.0	4166.5
4406.1	3004.2	3073.3	2224.3	3513.3	3066.1	3742.8	3154.4	3617.8	2695.3	4246.9
66.6	419.9	767.7	809.8	512.7	451.1	581.0	681.0	212.7	85.0	451.2
137.3	2045.8	1821.9	1907.2	1926.2	1604.9	2200.9	1742.3	1046.3	580.4	1159.0
18575.1	5737.3	5236.8	6186.6	5041.9	5059.2	5444.6	4820.3	8697.5	5941.3	6575.4
4997.7	4709.3	4311.3	4194.0	3651.2	4350.1	4011.8	3732.2	4915.6	3708.4	2941.5
13572.2	4961.1	4038.7	5122.1	4113.3	3870.7	5497.5	3930.7	5674.3	4318.1	6957.5
32.2	133.5	185.4	242.9	400.0	257.5	748.5	401.4	93.9	34.1	73.2
48.7	557.5	437.9	599.2	280.5	592.9	191.3	763.7	109.2	27.8	230.2
258.8	2076.0	3118.3	3207.3	1658.0	2571.4	3379.5	2924.5	1919.3	511.3	2421.9
5422.4	3375.2	3114.7	3094.2	2116.2	2875.5	2292.0	3728.5	2878.2	2389.7	2715.1
529.4	2117.1	2849.7	3089.3	2462.8	2260.8	2761.4	3227.4	1657.7	1184.0	2363.0
5569.8	2436.7	2589.6	2824.3	1672.4	2263.6	3540.5	2789.2	1649.1	1134.0	1427.9
13478.6	7038.5	6661.9	7288.5	6986.1	7376.2	9312.6	7505.2	8317.9	12049.3	11948.7
1923.7	5821.0	4974.4	4865.9	5191.0	4893.1	4196.9	4859.3	5202.5	3524.6	4433.1
3276.4	3174.5	3233.3	3381.2	3745.6	3947.4	4014.7	3805.0	3850.4	2538.5	2843.6
2987.2	2954.5	2985.9	3757.6	2765.7	2959.9	3124.2	2675.4	2941.8	3715.2	3186.5
5591.1	2760.4	2849.8	3579.1	3413.3	3770.8	3081.9	3079.7	3859.4	3402.6	2829.0
3148.4	3388.0	3366.2	3668.0	5246.0	3456.1	4617.2	3629.6	5410.9	2538.3	3496.7
15912.5	5219.2	5368.8	6538.2	4366.5	5014.5	4934.5	6439.4	5233.0	5296.2	7192.0
2990.4	8631.5	8480.5	7909.0	6741.9	7438.3	8269.7	8764.1	9903.7	10056.6	10702.2
24719.6	9892.7	8852.7	10802.1	9769.2	9923.0	10418.4	9753.7	12368.4	12406.5	14635.2
42.0	580.4	753.2	921.7	276.6	393.2	408.3	454.7	85.9	72.3	227.4
2282.0	2113.8	2642.5	2811.3	1602.4	1970.4	2259.7	2710.2	3558.5	774.6	2576.6
22773.5	5823.4	6425.5	6291.5	7020.9	5940.9	6644.9	6948.6	5664.5	4956.1	6666.5
5076.9	3683.4	3895.1	4250.7	3327.0	2984.1	4208.5	3624.7	1672.1	621.8	1955.1
21738.0	14438.4	12546.8	13785.7	14227.3	12854.6	12988.0	11077.0	17637.3	13872.0	16427.8
19593.4	5547.1	5758.5	6430.5	5949.5	5487.1	5746.2	5213.0	7117.9	6351.8	7015.2
628.6	5226.7	4766.8	4300.0	4283.3	4659.8	4439.9	4340.0	4805.2	6593.6	3539.5
37.0	1211.7	1747.4	1882.4	1614.3	936.2	1622.9	1305.7	363.3	266.9	729.8
51.1	2484.2	2531.8	2879.4	1364.8	1335.3	1896.2	2453.7	992.0	414.4	1152.1
41.9	99.0	141.9	205.9	38.2	78.0	118.7	112.2	54.8	25.7	69.7
875.1	1092.1	1517.8	1764.0	1290.1	1221.8	941.8	1340.9	1001.9	834.8	1692.6
6832.6	1997.1	2216.8	1905.3	1622.2	1969.4	1963.6	2207.5	3089.2	3648.6	3038.9

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5710.5	7099.0	6748.4
4698.9	5575.7	5525.6
3133.5	3647.9	2886.2
23.4	32.5	52.3
220.9	224.8	207.4
4575.0	4666.5	4756.2
2957.4	4347.6	4413.7
787.1	736.1	668.2
1459.8	2107.0	2742.2
4911.4	7728.3	5070.2
3939.3	4348.5	4199.4
3562.5	5873.9	3975.9
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493.5	386.2	848.1
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3627.1	2645.9	3507.6
2895.0	2930.4	4444.4
6490.1	8256.2	6058.1
4858.8	3822.4	4339.2
3432.7	3587.9	3992.8
2765.5	2855.0	3275.1
3174.9	3535.5	3823.3
3528.2	3739.5	4157.8
5374.3	6330.5	6402.6
6817.2	7514.3	6783.0
8854.8	12158.0	9899.0
649.0	745.4	645.6
2663.0	2420.9	2837.0
5877.7	6503.3	6208.7
4361.2	3316.4	3498.8
10902.8	13079.1	12000.1
4914.4	6733.7	5630.0
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1223.6	1341.3	1766.6
2118.6	1935.8	3399.9
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1472.6	2538.5	1212.9
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o__Clostridiales	f__Lachnospiraceae

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EU509936.1 gg_id:267590 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24a07 EU509
EU511605.1 gg_id:277486 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07d05 EU511
EU748097.1 gg_id:324079 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42d01 EU748
DQ815446.1 gg_id:162804 mouse cecum clone aab48e08 DQ815
FJ365425.1 gg_id:357471 feces adult twins and mothers; TS20 clone TS20_a02g02 FJ3654
EU455526.1 gg_id:308160 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU455
GQ897103.1 gg_id:545964 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU452423.1 gg_id:343002 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
EF602967.1 gg_id:230212 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF602
EU457703.1 gg_id:339505 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
EU843162.1 gg_id:325894 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU465634.1 gg_id:299985 argali sheep feces clone AS1_aao40c12.Contig1 EU465
EU510929.1 gg_id:264556 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak51g06 EU510
EU457265.1 gg_id:308291 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
EF099267.1 gg_id:194520 mouse cecum clone SWPT2_aaa04g10 EF0992
AY992528.1 gg_id:135672 mouse cecum clone C23_h19 AY992
EU453260.1 gg_id:321161 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
FJ364401.1 gg_id:363280 feces adult twins and mothers; TS15 clone TS15_a02e03 FJ3644
EF614600.1 gg_id:234794 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
EU457252.1 gg_id:353188 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
EU455732.1 gg_id:337572 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU455
EF603950.1 gg_id:234179 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EU453621.1 gg_id:333176 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU453
EU451529.1 gg_id:305718 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU451
EF096968.1 gg_id:175483 mouse cecum clone SWPT13_aaa03e04 EF0969
EU508528.1 gg_id:273169 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap34h10 EU508
FJ880080.1 gg_id:453405 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU451060.1 gg_id:316738 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
EF097677.1 gg_id:195885 mouse cecum clone SWPT20_aaa02b07 EF0976
EU511942.1 gg_id:271879 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11f04 EU511
AM932615.1 gg_id:575751 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ015082.1 gg_id:129641 mouse cecum clone M2_h07 DQ015
EU511099.1 gg_id:259148 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02f12 EU511
EU775850.1 gg_id:348919 Horse feces clone horsej_a10 EU775
EU454798.1 gg_id:355612 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
EU451537.1 gg_id:315395 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU508286.1 gg_id:259183 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa01f05 EU508
EU451665.1 gg_id:332587 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU451
EU451748.1 gg_id:322121 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451
DQ789123.1 gg_id:257328 Isolation Flagellated Crohn's Disease mouse cecum DQ789
DQ815888.1 gg_id:169242 mouse cecum clone aab23g06 DQ815

3377.8	1650.9	2273.2	2045.3	1243.1	1821.2	1789.1	2000.5	1516.8	684.3	2314.1
2687.1	3614.4	4170.1	4356.9	4498.4	4126.5	5108.0	4680.0	3760.1	1855.5	4223.6
2297.2	4164.8	3961.8	3447.1	3669.5	4584.9	3102.3	3247.0	4664.7	4632.2	2704.2
231.2	1216.2	1219.2	1500.7	1071.2	1068.8	587.4	1243.6	926.8	691.4	1013.8
5121.9	2816.8	3236.2	3094.1	4420.9	2877.5	3615.5	3057.1	3552.4	2995.6	2592.2
8769.6	6996.4	5632.1	8119.0	7571.8	6845.5	9167.6	6507.5	8180.2	6589.8	9447.7
120.0	1948.1	3610.5	2272.5	2303.5	2363.2	2878.8	2267.4	808.4	383.6	1891.8
16168.8	4919.5	4174.6	5310.1	4609.2	5386.7	4529.6	4765.6	5349.9	3224.1	7524.8
28481.6	8026.1	7448.5	8662.0	9314.7	7565.1	8987.8	8221.5	9703.4	7412.6	9722.1
315.2	3363.0	3461.2	2637.2	3200.3	3188.5	2095.1	2992.5	2504.4	966.1	1967.4
38.0	447.0	544.0	584.2	465.2	441.8	452.7	630.9	105.8	88.2	237.2
85.7	1247.1	1663.8	1828.3	1143.1	1099.8	1154.1	1498.2	1427.2	811.5	1024.5
26.1	2688.1	2880.4	3172.2	2383.6	2409.2	2965.6	2561.0	3923.3	3574.9	4890.2
3312.6	3401.2	5108.3	6454.3	5169.8	4325.9	5392.2	4504.3	2306.9	2002.1	4552.6
2836.2	4066.9	4522.8	4738.2	4373.6	4308.2	4560.5	3956.6	3188.8	2970.0	3974.3
9909.8	4795.4	5141.9	3206.9	4544.9	4621.2	4351.3	4016.4	5308.4	4678.5	5627.2
8371.8	3906.0	4338.5	4296.6	5884.3	4054.1	5743.5	4548.5	5416.3	4356.7	4441.1
2338.7	3229.6	4238.6	4435.6	3645.5	3764.0	4640.9	5212.2	2813.6	2194.2	4154.6
11398.5	6914.8	7501.6	8039.7	8127.7	7065.9	9212.7	6954.0	7972.9	6037.5	9380.7
1063.7	4705.6	4579.7	2684.9	2793.0	4144.5	2159.4	3384.6	4518.2	4743.4	4572.1
2770.2	2995.8	2825.4	2554.4	2996.5	2873.3	2635.8	2923.4	3364.6	4392.0	1950.3
3814.8	6790.1	7688.2	8969.0	6629.0	6548.3	7791.0	8011.5	7211.3	6882.7	8184.9
10170.6	5942.6	6114.4	6833.4	5321.6	5033.5	5252.5	5013.1	7346.3	5046.2	6977.0
1654.4	3396.5	4106.5	4789.6	2119.9	3169.8	2635.7	3503.1	1549.6	1361.3	3081.1
266.2	914.9	1229.8	1215.8	791.0	861.7	1141.9	915.1	323.7	14.8	630.6
9932.3	4368.0	4436.7	5902.3	4244.5	4176.0	4677.4	4156.5	4432.8	2984.1	5561.7
1672.5	5447.2	5637.9	5492.5	3179.6	4583.2	4239.5	5664.5	7510.5	6595.8	5756.9
26205.8	12426.2	10027.8	11130.6	10184.8	10169.0	9907.3	9670.1	15165.7	10928.6	15396.6
2779.0	615.7	677.0	803.7	615.4	715.2	612.6	21.6	388.0	213.8	437.8
11883.3	5988.8	5867.7	5889.9	5533.2	5782.9	6212.4	5684.1	7623.7	6285.8	5686.2
167.8	4069.4	5812.1	7348.7	1902.1	2652.2	2005.5	4095.7	741.2	301.3	2860.6
118.1	1713.0	2781.8	3074.3	907.2	2616.1	1655.8	4008.0	824.3	447.1	3204.0
695.2	1336.9	1810.3	1866.6	1563.5	1555.4	1848.9	2086.2	760.0	996.0	907.0
1013.1	3627.2	4554.2	3910.0	3147.4	3150.3	3548.5	4247.8	3154.5	1507.8	3992.1
57.6	47.3	60.2	55.8	32.7	29.3	33.7	37.0	13.7	25.7	31.4
2529.9	3878.6	3899.6	5110.5	3722.5	3253.4	3177.3	3133.8	3273.0	1949.5	2852.2
13972.7	5287.4	4932.6	5047.8	4677.8	4596.1	5151.7	4615.3	7573.2	5557.5	5119.3
7437.8	2347.7	2743.1	2175.9	2667.3	2689.6	2685.3	2319.8	3117.3	2978.0	2979.5
535.6	2470.3	2491.2	2598.5	2176.6	1936.0	2241.5	3224.9	1459.0	880.1	2395.1
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69.5	676.5	1204.4	1532.1	309.8	314.9	265.1	467.9	171.0	67.9	210.7

1975.6	1950.9	1923.1
5208.4	4650.7	5064.0
3837.0	4501.2	3979.4
1307.5	1389.4	1922.6
3756.5	5757.9	3663.1
6277.8	8336.1	7760.3
3235.1	2021.9	1840.7
4453.8	5512.6	5159.6
7294.5	9125.2	9372.9
2916.4	3113.9	3019.3
456.9	485.2	916.2
1791.2	1796.1	2121.1
2731.3	2739.7	2735.3
4725.1	6216.1	6257.7
3669.1	4488.2	5530.3
4628.7	6495.1	4412.1
3885.0	4851.0	6184.1
6372.6	4316.8	6135.8
6862.2	8163.9	8758.8
3108.4	3427.2	2525.4
3012.8	3562.4	3409.2
7284.8	7219.8	8724.2
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886.0	1038.4	991.2
3742.7	6325.2	4722.5
4486.1	5648.6	4605.1
9580.7	12481.9	12023.1
831.5	1175.8	1244.8
5880.5	6562.1	6200.8
5342.8	4361.8	6939.8
5151.7	1846.6	3232.8
1630.9	2300.0	2543.4
2129.3	4278.8	3984.5
38.5	59.7	38.8
3395.7	3321.3	3793.6
4629.0	6373.7	5069.3
2401.4	2917.3	2877.7
2267.4	2425.8	3710.0
2768.8	2617.7	2313.3
781.6	816.1	2524.9

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o__Clostridiales	f__Lachnospiraceae
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GU303078.1 gg_id:546585 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
GU304203.1 gg_id:585104 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU506630.1 gg_id:276637 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53f06 EU506
EU504958.1 gg_id:272111 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g10 EU504
EU471846.1 gg_id:293417 Asiatic elephant feces clone AE2_aaa01c10 EU471
EU510054.1 gg_id:276546 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf11e08 EU510
EU511233.1 gg_id:265917 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04g09 EU511
EU455557.1 gg_id:336092 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU455
DQ815838.1 gg_id:170131 mouse cecum clone aab23a05 DQ815
EU510984.1 gg_id:271528 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52g11 EU510
EF097986.1 gg_id:183225 mouse cecum clone SWPT12_aaa03f03 EF097
EU505646.1 gg_id:260752 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a04 EU505
EU507686.1 gg_id:270439 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03b11 EU507
DQ015437.1 gg_id:130806 mouse cecum clone M3_a11_1 DQ015
EU454933.1 gg_id:315559 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454
EU451455.1 gg_id:325386 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
FJ880885.1 gg_id:434795 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU452374.1 gg_id:324596 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU452
EU453705.1 gg_id:310281 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU453
EU451962.1 gg_id:348977 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
AY992605.1 gg_id:133748 mouse cecum clone C23_l02 AY992
EU452895.1 gg_id:303434 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU452
EU506399.1 gg_id:276681 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01b11 EU506
EU503588.1 gg_id:264252 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01f04 EU503
EU454860.1 gg_id:343879 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU506835.1 gg_id:275802 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07b02 EU506
EU503936.1 gg_id:275743 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03a01 EU503
EU511873.1 gg_id:264841 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_10b10.Contig2 EU511
FJ894710.1 gg_id:569581 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8947
EU510260.1 gg_id:265505 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03g01 EU510
EF097133.1 gg_id:177946 mouse cecum clone SWPT18_aaa01h01 EF097
EU451039.1 gg_id:347128 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
EU456612.1 gg_id:324754 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU456
EU454922.1 gg_id:350088 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
EU504263.1 gg_id:269057 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01c10 EU504
EF614840.1 gg_id:230379 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EF096403.1 gg_id:193921 mouse cecum clone obob2_aaa02c08 EF096
EF096997.1 gg_id:179928 mouse cecum clone SWPT13_aaa03h09 EF096
EU504310.1 gg_id:269809 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa02b08 EU504
DQ824834.1 gg_id:174571 human fecal clone RL185_aao69g11 DQ824
EU454845.1 gg_id:354667 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU454

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8720.1	3660.7	3527.0	3663.9	3064.6	3381.2	3527.6	2844.9	3865.4	3556.7	4584.8
2822.1	3105.6	1915.5	1899.1	1301.5	1550.6	3620.1	1740.2	4064.4	2925.4	1715.8
1543.8	2549.4	2861.4	2944.5	2608.8	2441.0	2647.3	2747.7	2305.7	939.7	2206.7
965.7	586.3	696.3	763.5	438.9	520.3	561.3	1476.8	283.1	220.9	376.3
9411.7	4737.7	2839.8	4023.5	3512.4	3379.3	4031.4	3391.5	5274.6	4504.8	5905.7
2172.2	805.4	1468.3	1553.2	1152.7	1443.5	1437.2	1290.1	738.7	419.9	1019.2
208.5	1511.7	2396.2	2584.3	1236.1	1850.9	1776.4	2181.1	562.3	439.2	2080.8
81.9	2086.6	1940.7	2490.1	1920.2	1772.3	1728.0	2178.6	1036.2	1273.1	1483.2
93.6	624.5	963.0	1062.1	364.1	579.6	495.9	693.1	473.8	1061.9	503.0
68.0	937.1	1251.6	1079.0	772.9	1003.0	809.7	1252.8	720.0	197.9	742.2
1449.7	4003.7	4630.1	3993.7	4137.1	4505.9	4513.5	4402.9	5865.1	6425.0	3767.7
255.8	1889.3	3264.9	1478.9	1975.2	1658.3	1804.4	1815.7	1126.4	782.1	3313.0
41.0	507.4	698.9	861.3	504.7	405.1	531.8	541.6	164.9	81.8	341.0
4540.8	2845.9	2934.3	2976.3	3031.9	3520.2	3841.8	2919.1	4093.4	2636.8	4051.9
49.4	320.6	532.6	598.5	135.1	297.6	383.5	614.8	52.5	68.9	197.0
48.0	769.5	885.7	1206.0	212.4	498.0	313.2	991.9	407.9	183.3	586.0
11402.7	9727.4	8779.9	8514.8	8118.3	8056.2	7774.1	7476.1	11003.6	6719.0	9274.0
57.0	1340.9	1551.6	2114.7	716.7	1346.2	788.6	1684.8	793.6	260.2	1344.1
54.9	1385.7	1807.3	1969.3	1630.2	1887.0	1957.0	1028.5	1001.3	618.7	1273.0
52.3	1351.5	1576.3	1724.5	2854.7	1512.5	1449.0	1636.4	747.8	489.5	788.9
36.3	567.7	1308.4	1204.3	277.1	598.1	295.6	807.3	70.0	56.0	273.0
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1954.8	5523.5	6062.0	5171.5	3285.4	5465.6	4818.1	4514.2	7195.2	7339.6	5827.3
14421.4	7625.3	6808.4	7546.1	7243.9	7143.6	7580.7	7267.6	8102.7	7476.4	9663.3
47.4	490.8	1012.0	1300.4	287.6	430.9	349.0	653.1	271.2	160.1	551.3
4483.2	2075.8	2174.6	2327.2	2768.8	1903.4	2179.7	2115.3	1687.4	1001.2	1589.8
245.9	2033.3	2803.4	3259.7	1259.3	1885.9	2061.3	2568.8	790.8	383.4	1615.3
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246.7	3763.8	4303.8	5287.4	3589.0	3666.1	4358.2	5692.3	2538.1	1021.3	3226.4
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82.9	504.1	375.2	291.8	391.1	380.8	263.5	400.9	172.8	66.3	191.9
53.2	950.0	2010.8	1588.1	1077.5	837.7	1150.7	1187.7	398.3	160.1	665.8
6448.7	3126.0	4009.6	4038.2	4144.2	4179.2	4400.2	3941.3	2701.4	2488.7	4217.4
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3674.7	4670.6	4394.1
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1591.1	2023.6	1515.7
696.8	750.0	557.8
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4851.6	5234.2	6389.8
191.9	137.6	66.9
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EU504233.1 gg_id:261142 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04f12 EU504
EF604803.1 gg_id:231563 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EU506340.1 gg_id:265356 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63e10 EU5063
EF098095.1 gg_id:189119 mouse cecum clone SWPT14_aaa01d10 EF0980
FJ680678.1 gg_id:527100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
AF371636.1 gg_id:104064 swine intestine clone p-4570-4Wb3 AF3716
EF603797.1 gg_id:233411 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
EU450915.1 gg_id:312822 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4509
EF603872.1 gg_id:227886 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
EU455616.1 gg_id:324807 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4556
EU457421.1 gg_id:347182 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4574
EF604676.1 gg_id:228048 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EF614887.1 gg_id:230111 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF096264.1 gg_id:183466 mouse cecum clone obob1_aaa03g03 EF0962
EU622706.1 gg_id:278440 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
EU456401.1 gg_id:329421 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4564
EU453753.1 gg_id:310227 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4537
EU454376.1 gg_id:322564 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80M EU4543
EU510396.1 gg_id:262556 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal37h09 EU5103
EF097716.1 gg_id:175859 mouse cecum clone SWPT20_aaa02f11 EF0977
EU622721.1 gg_id:278392 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
EU655773.1 gg_id:284761 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6557
FJ880662.1 gg_id:407782 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
EF098059.1 gg_id:186466 mouse cecum clone SWPT12_aaa04h08 EF0980
EU458068.1 gg_id:328433 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4580
AF371560.1 gg_id:40639 swine intestine clone p-2399-55G5 AF3715
EU452780.1 gg_id:329836 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74M EU4527
EU344354.1 gg_id:273480 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EU508661.1 gg_id:272449 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49a05 EU5086
EU509421.1 gg_id:271053 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap57h03 EU5094
EU455225.1 gg_id:319398 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74M EU4552
EU508200.1 gg_id:265997 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03a06 EU5082
EU503933.1 gg_id:263530 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02h06 EU5039
EU454836.1 gg_id:339886 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4548
EU451309.1 gg_id:337174 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4513
DQ014643.1 gg_id:135643 mouse cecum clone M1_a07_1 DQ014
EU508440.1 gg_id:258344 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33e08 EU5084
EU842297.1 gg_id:336994 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
FJ832588.1 gg_id:554490 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_04D01 FJ8325
EU507710.1 gg_id:264364 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03e06 EU5077

46.3	213.4	603.2	565.1	127.9	143.1	226.4	257.8	29.8	30.3	116.3
84.5	1558.9	1825.5	2279.1	1515.6	1194.6	1331.1	1511.7	787.4	569.3	806.6
2701.7	3528.3	4203.0	3046.5	2809.2	3100.9	3095.8	4432.5	3765.8	1891.2	3583.4
2845.5	4439.9	5407.1	7434.4	6137.1	5680.3	5493.9	5757.6	2684.2	1621.7	4353.4
6668.1	3880.5	3242.4	5277.9	5520.0	4080.8	4127.4	4558.9	4663.4	3435.6	6636.1
2228.1	2639.0	2795.2	3111.8	2374.4	2664.5	4013.5	3609.0	3923.7	2455.2	3261.4
209.6	501.9	1050.8	818.8	451.6	646.6	580.1	978.3	272.1	182.6	584.0
37.0	210.0	420.0	498.7	36.9	142.2	94.3	171.6	48.7	36.7	123.0
157.6	741.8	842.4	852.5	508.3	579.9	608.6	819.0	164.8	95.9	430.1
2168.5	3882.4	3903.3	3884.9	3800.7	3685.9	3824.0	4254.7	5951.7	4885.1	3619.3
240.1	1517.8	1843.9	2151.5	1340.2	1376.0	1821.3	1523.6	936.8	1573.9	1503.3
3627.3	8243.3	6633.5	6913.9	6387.7	6775.6	5600.5	5498.1	7837.2	6581.5	6518.8
15706.6	6396.8	5677.3	6281.4	6053.9	5623.6	6132.7	7775.8	5654.4	6928.1	7802.5
947.1	4625.8	4258.9	3834.1	2642.5	3563.6	2789.3	3358.4	3788.0	5229.0	3842.5
206.9	999.1	1257.1	1360.4	1216.6	1371.8	1671.5	1485.1	927.5	540.2	928.1
3902.4	2166.7	2087.4	2584.4	2091.8	2094.3	2005.4	2487.7	1458.9	1615.6	1580.2
27483.2	9919.9	8780.7	9854.9	9306.9	8348.6	8984.0	8274.5	12607.4	8535.6	12680.7
102.4	3282.0	3208.3	2858.2	2545.1	2675.8	2986.9	2331.5	1684.6	570.0	2605.9
2805.8	2327.8	2612.6	2545.5	2275.7	2170.6	3165.1	2433.4	2000.4	1204.9	1966.7
572.2	1376.9	2240.0	2403.1	1513.7	1393.4	2151.9	2012.2	610.8	237.7	1666.5
23196.1	9654.8	7614.7	7068.0	6500.2	6216.4	5079.6	6528.3	8782.3	6830.0	14645.4
71.6	1338.4	2605.0	2497.4	714.1	1051.3	1168.2	1893.8	492.6	266.3	1334.4
128.0	1571.3	2123.2	2298.7	1265.4	1522.8	1460.2	1771.3	740.8	429.8	1033.0
93.1	412.9	694.5	795.9	311.4	531.2	343.5	1193.4	176.2	179.6	398.4
378.3	2994.5	3455.4	4661.1	5939.6	4318.2	6143.2	3711.3	2426.0	2567.6	1985.9
14251.3	5723.3	5258.1	5930.3	5429.0	5296.1	5160.0	5046.4	5117.2	4074.3	6394.7
973.5	2428.2	2719.7	3645.5	2783.5	2220.9	2354.7	2975.2	3582.2	820.7	2471.9
1014.9	2359.3	3487.3	4348.3	1985.8	1710.8	2059.0	2314.3	849.9	534.1	1547.6
400.5	2483.2	3616.4	3027.4	2516.0	3409.2	2885.5	2623.8	1681.6	1354.6	2022.8
19887.6	8887.3	7556.4	9423.7	8809.7	7763.2	9327.7	7266.5	10336.9	5932.5	9265.9
177.0	2276.9	2684.1	3056.9	2783.0	2372.0	2699.6	2651.7	1505.3	1268.3	1432.0
546.4	946.2	1779.6	1278.9	1006.7	855.8	1207.5	990.5	400.5	1008.9	712.2
15707.8	5430.4	4984.9	5982.5	4886.9	5161.9	5329.8	4929.8	9350.1	6293.1	6790.3
27167.0	5789.8	7643.4	5919.9	5807.1	5350.3	9126.2	6676.8	9305.2	7425.2	6445.5
824.6	3715.4	3398.0	3000.1	2996.0	3142.4	2239.8	3466.9	2842.2	1727.8	2393.5
9584.4	7785.3	6586.1	6704.9	5521.4	6295.8	6567.5	5909.8	8637.2	6863.2	8692.2
2600.9	3429.2	5737.4	4125.8	3485.1	3358.1	3753.6	3503.5	2180.3	2038.7	3875.1
5081.7	3832.9	3124.1	3921.5	3792.9	3652.9	3066.4	3971.3	2995.6	2265.8	2607.4
38.4	208.3	346.5	536.4	218.1	317.2	559.1	493.7	119.8	37.2	263.4
1591.8	2321.5	2052.4	3286.3	2722.7	3688.4	2266.7	3191.2	1101.1	3768.6	1459.3
20274.7	4347.6	4168.1	3960.9	5975.3	5538.4	4981.7	5348.1	5267.4	4208.5	3916.5

369.7	195.6	640.7
1513.5	1475.4	1509.0
2863.6	3963.1	4029.8
5692.4	7483.3	6482.4
4793.2	5053.3	5508.1
3122.0	3833.3	3869.0
1342.0	726.0	926.3
267.9	217.6	87.5
646.5	693.1	736.1
3624.3	4153.1	4643.5
2069.6	2055.9	2792.9
5413.9	6479.8	5558.7
5081.9	6225.3	6988.9
2944.2	3369.6	3389.1
1550.9	1558.4	1826.3
3173.8	3346.0	3001.7
7712.2	9469.5	7938.1
2675.7	1999.0	2467.7
2492.0	2999.8	3069.9
1895.0	2067.5	2634.6
5159.5	7414.6	7214.2
2121.9	1642.6	1872.3
2063.0	2066.4	2142.6
1315.7	917.1	869.7
4066.1	3105.8	5458.1
5613.1	6698.4	5809.2
2260.6	3146.7	2686.7
2780.1	2986.9	3258.1
3266.6	2880.2	3537.4
7574.6	9746.0	8631.9
2554.9	3647.7	3736.2
846.5	1300.6	1226.2
4799.9	7371.9	5070.0
6001.4	10056.4	8393.1
4023.0	2664.9	3097.1
5737.0	9101.1	7575.8
2383.7	2976.6	3563.9
3249.6	3373.7	4460.5
329.7	262.4	538.5
2627.9	4373.5	2701.4
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EF097822.1 gg_id:194780 mouse cecum clone SWPT20_aaa04d03 EF0978
DQ014914.1 gg_id:133374 mouse cecum clone M1_1d05 DQ014
AY992811.1 gg_id:132748 mouse cecum clone C22_c21 AY9928
EU474235.1 gg_id:300219 western lowland gorilla feces clone GORSD_aaa01e06 EU474
EU452309.1 gg_id:349890 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4523
EU509303.1 gg_id:264933 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47e09 EU5093
EU453606.1 gg_id:356353 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4536
DQ015623.1 gg_id:135607 mouse cecum clone M3_c12_2 DQ015
EU455622.1 gg_id:313634 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4556
DQ815665.1 gg_id:165845 mouse cecum clone aab44e07 DQ815
EF604806.1 gg_id:229460 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EU508547.1 gg_id:267049 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35c01 EU5085
EU748004.1 gg_id:328729 neotropical folivorous flying bird adult hoatzin crop clone hoa14_30F04 EU7480
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EU505053.1 gg_id:260616 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02c03 EU5050
EU457612.1 gg_id:334547 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4576
EU455433.1 gg_id:332973 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4554
DQ015505.1 gg_id:132500 mouse cecum clone M3_h09_1 DQ015
EU511187.1 gg_id:264990 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04b02 EU5111
EU509940.1 gg_id:263077 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b01 EU5099
EU457596.1 gg_id:356404 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4575
DQ015207.1 gg_id:132275 mouse cecum clone M2_b08_3 DQ015
EF605063.1 gg_id:228930 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6050
EF098900.1 gg_id:181344 mouse cecum clone SWPT1_aaa03a05 EF0989
EU504120.1 gg_id:258750 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa01f11 EU5041
EU762169.1 gg_id:323459 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7621
EU504051.1 gg_id:258546 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04f01 EU5040
EU507552.1 gg_id:265268 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01a04 EU5075
EF099992.1 gg_id:173939 mouse cecum clone SWPT5_aaa03c07 EF0999
EF604540.1 gg_id:232969 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EU454548.1 gg_id:316031 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80M EU4545
EF096390.1 gg_id:195208 mouse cecum clone obob2_aaa02a09 EF0963
AY991835.1 gg_id:131998 mouse cecum clone C20_g17 AY9918
DQ456362.1 gg_id:158971 pre-adolescent turkey cecum clone CFT212E2 DQ456
EU457498.1 gg_id:315284 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75M EU4574
EU450902.1 gg_id:347778 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80M EU4509
EF097060.1 gg_id:188946 mouse cecum clone SWPT13_aaa04h03 EF0970
EU456745.1 gg_id:303890 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4567
EU511338.1 gg_id:263214 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18f03 EU5113
EF096673.1 gg_id:175893 mouse cecum clone SWPT11_aaa02h10 EF0966

297.0	1584.0	2071.9	2373.4	1167.8	1430.1	1490.1	2557.8	1069.9	680.8	1444.4
2809.3	3739.0	2900.2	4750.6	4940.9	3286.0	4199.7	3227.2	3615.7	2390.4	5645.8
2895.8	3308.2	3412.7	3967.5	2976.5	2848.8	3530.8	2651.5	2748.1	2042.6	3842.4
2988.4	2572.2	2480.1	2888.6	2378.0	2330.3	2467.6	2097.2	2881.3	2463.7	2516.3
4126.9	5894.8	5777.6	5818.4	6592.3	5626.6	6620.5	5088.0	7263.8	7618.3	5864.9
2459.4	3013.0	3482.5	3474.3	4343.0	3719.6	5136.7	3719.8	3873.3	3096.3	4051.1
13679.7	5431.4	5134.9	5270.0	5648.0	4749.2	2543.9	4552.7	5602.6	7141.3	6846.2
3860.8	1768.3	2115.6	2374.6	2230.7	1631.1	1753.2	1730.3	467.2	257.3	1022.1
42.1	2624.6	4173.5	4780.7	1346.8	3578.2	2241.3	4768.4	956.8	533.0	3594.0
4582.5	3481.5	3128.9	3693.7	3246.4	4199.0	3765.2	3295.7	3942.7	2506.5	4528.8
199.0	95.1	152.8	113.9	122.0	91.8	80.0	118.3	171.6	282.4	79.7
16564.5	5490.5	5826.6	6437.9	4546.9	4302.3	5480.1	7581.3	7087.0	5127.5	8249.1
40.9	1493.5	2773.6	3263.8	1258.4	1225.6	1626.5	2142.6	732.4	255.4	1107.8
310.6	3126.8	3630.8	3761.4	2681.5	3915.6	3164.2	4856.3	4668.2	2851.1	4472.5
4455.9	3401.8	3657.8	3199.0	2615.9	3271.6	3436.1	2926.1	5031.2	3937.4	3274.1
6590.1	3539.9	3633.8	2627.4	3271.8	3063.5	2804.4	2977.0	1418.9	7556.7	2400.7
18114.6	3737.8	3857.4	4862.7	4124.5	3574.7	4449.5	3943.2	3855.9	3690.2	3878.3
1881.7	529.5	1015.0	770.0	543.2	534.9	607.4	669.1	449.0	472.9	568.7
61.5	601.0	716.1	837.4	829.2	569.5	704.9	676.6	211.2	158.3	187.4
676.8	2281.5	2906.6	2267.8	1675.6	2054.8	2154.4	2099.3	2385.9	1822.7	1392.6
929.2	655.1	755.3	887.0	385.0	583.2	401.0	688.0	430.0	307.5	565.5
2962.9	5078.0	2726.0	5890.0	5106.0	4612.3	5771.7	4384.9	3631.9	5853.8	5432.0
2669.0	5358.6	5727.2	6482.8	7901.7	6276.7	7092.3	5987.7	4824.6	2743.3	4706.3
10223.7	4304.8	4507.3	5287.2	3909.1	4088.4	4370.4	4606.1	4281.2	4303.9	4739.7
1912.8	2227.9	2436.8	1978.2	2145.1	2338.7	1934.2	2741.3	1599.2	3194.5	1229.9
38.0	402.6	777.6	1308.8	254.5	322.4	344.7	586.8	238.1	28.2	532.3
7709.9	3120.4	2615.6	3245.2	3256.1	2156.0	3241.1	2882.3	3555.0	2973.3	3602.1
13246.9	4353.5	5391.9	8178.5	5062.2	6131.7	6905.6	6153.2	4737.6	4275.5	6052.0
258.3	3993.7	4558.1	5263.0	3377.2	3561.8	4385.3	4170.0	3318.7	2780.2	4515.1
43.5	303.9	390.4	455.6	409.8	288.8	359.2	238.3	158.3	69.8	252.7
3050.4	2217.6	2219.3	2037.2	2159.6	1770.2	2064.4	2203.6	1131.3	1977.8	1405.5
2436.9	5244.9	4549.2	6081.5	4937.1	4342.9	4889.5	3698.4	4112.6	3677.5	4109.0
2207.3	8650.1	8017.3	7759.6	7099.9	8026.3	7113.1	7461.0	9619.7	10502.6	8305.6
108.6	2735.1	3748.3	4207.7	2100.7	2764.4	2340.6	4372.5	1932.7	479.9	2702.1
132.8	1458.9	2193.5	2451.4	881.2	1519.8	1392.4	2898.1	499.8	442.6	1364.9
1606.7	6456.2	5784.2	6399.6	5878.4	5997.2	5264.9	5469.0	6329.2	5121.3	6297.1
838.9	977.7	1169.6	1496.5	1191.5	1046.5	926.7	1735.4	409.8	182.7	770.8
55.4	549.5	623.7	875.2	203.5	443.9	267.1	795.6	199.5	111.2	508.7
5287.8	6679.4	6533.0	6435.2	4889.2	6681.0	6376.1	5658.0	8363.6	9050.6	7260.0
603.7	845.8	835.5	1197.0	620.7	898.1	1124.4	961.0	754.8	539.1	543.4
280.8	766.9	1103.4	998.5	785.0	861.2	1027.2	1048.8	558.4	901.7	634.5

3005.4	1799.1	2262.6
3046.4	4318.9	3568.4
2646.7	3153.1	3765.6
1981.8	3244.5	2470.0
5124.1	6028.8	6605.9
3534.9	4455.3	4767.6
5104.7	5898.0	4727.8
2026.7	2521.7	2857.8
5719.2	2620.4	4906.1
2901.3	3596.2	3178.5
86.6	153.5	144.3
5449.2	6008.2	6821.9
1837.0	1563.5	2530.6
3888.4	4011.7	5415.6
2733.3	4061.1	4475.9
3141.8	3499.1	2704.0
4340.1	4592.0	5420.8
639.6	1401.6	798.1
993.3	863.7	1919.3
2329.3	1586.3	2033.5
721.6	2043.2	1014.3
4595.2	5266.4	6175.5
6238.3	6091.8	7890.1
4542.7	4826.9	4869.3
2135.6	1926.2	2355.4
496.0	530.8	381.2
2662.5	3919.9	2874.7
4944.5	4693.6	5799.5
5052.2	3706.9	5679.7
355.4	399.6	514.8
2353.6	2603.5	4152.5
4230.0	4236.2	4531.2
7896.4	7934.2	10307.3
4469.3	3695.8	4270.7
3789.7	1615.3	2636.2
5300.4	5982.1	7992.5
1051.4	1621.4	1435.6
684.7	547.1	626.4
5279.0	6380.2	7106.3
1184.5	1441.5	1308.9
1021.0	1086.4	1327.2

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o__Clostridiales	f__Lachnospiraceae
o__Clostridiales	f__Lachnospiraceae

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EF096425.1 gg_id:198098 mouse cecum clone obob2_aaa02f05 EF0964
EF602970.1 gg_id:230060 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6029
EU006430.1 gg_id:245693 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0064
EU455538.1 gg_id:326639 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4555
EF603630.1 gg_id:234601 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
EF098091.1 gg_id:191942 mouse cecum clone SWPT14_aaa01d04 EF0980
EU509591.1 gg_id:277550 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak45d08 EU5095
EF096942.1 gg_id:177095 mouse cecum clone SWPT13_aaa03b02 EF0969
EU508352.1 gg_id:276552 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03e06 EU5083
EU508155.1 gg_id:263923 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01g07 EU5081
DQ015134.1 gg_id:129951 mouse cecum clone M2_h07_1 DQ015
EU507687.1 gg_id:274805 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03c03 EU5076
EF099048.1 gg_id:195603 mouse cecum clone SWPT2_aaa01e08 EF0990
EF098359.1 gg_id:178043 mouse cecum clone SWPT15_aaa01e04 EF0983
EU509849.1 gg_id:270513 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d10 EU5098
EU509455.1 gg_id:270768 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58f06 EU5094
EU511589.1 gg_id:271918 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07a12 EU5115
AY854278.2 gg_id:109967 herbivore gastrointestinal tract clone CATTLE_16 AY8542
EF099955.1 gg_id:188052 mouse cecum clone SWPT5_aaa02g01 EF0999
AY992695.1 gg_id:135353 mouse cecum clone C23_p02 AY9926
EU457668.1 gg_id:338240 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU4576
EU507600.1 gg_id:274147 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01f11 EU5076
EU457464.1 gg_id:345956 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4574
EU509255.1 gg_id:268484 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46g02 EU5092
EU451423.1 gg_id:356499 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4514
EU453792.1 gg_id:307802 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4537
EF098014.1 gg_id:196251 mouse cecum clone SWPT12_aaa04a09 EF0980
EF614834.1 gg_id:229419 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU457495.1 gg_id:323383 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4574
EU453160.1 gg_id:304065 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4531
EU507400.1 gg_id:258325 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02f08 EU5074
DQ015131.1 gg_id:135515 mouse cecum clone M2_g12_1 DQ015
GQ897331.1 gg_id:591724 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ682910.1 gg_id:528582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ674029.1 gg_id:521228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ683574.1 gg_id:511181 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
EU878317.1 gg_id:547601 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
FJ682798.1 gg_id:522394 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ824455.1 gg_id:176312 human fecal clone RL304_aal76c01 DQ824
FJ674105.1 gg_id:530297 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU458763.1 gg_id:298607 Goeldi's marmoset feces clone CAL_h06_2 EU4587

40.8	102.3	142.3	118.2	210.6	81.0	178.8	98.7	134.5	83.3	105.2
7417.7	6741.9	6950.1	7953.2	5706.2	6461.0	6593.2	6330.5	7104.5	5348.7	10406.2
1547.0	3667.4	4418.6	4993.4	3416.5	3225.0	3889.0	3721.9	2166.1	1103.3	3786.9
5188.7	2698.8	2938.4	3001.1	3052.8	2545.0	2736.6	2579.1	3618.2	2909.3	4710.3
213.6	3828.0	3962.1	3612.6	3172.3	3943.5	2491.6	5080.7	1998.7	3181.0	2581.9
55.0	1359.8	1371.3	1625.5	551.5	926.7	739.7	1135.0	925.5	915.7	675.7
672.3	389.7	362.0	292.8	306.5	279.3	309.2	328.6	349.6	251.3	272.4
75.3	309.0	521.1	835.7	324.3	220.6	336.1	350.7	72.8	53.3	121.4
2422.7	2935.0	3178.6	3342.0	3503.7	2865.0	3922.8	3548.1	1950.8	1161.3	2092.2
8061.4	4529.0	5237.9	4664.4	4964.8	4484.1	4559.1	3933.1	5758.8	4630.5	5576.9
25787.8	8779.7	7620.5	8720.1	8302.2	7631.2	8925.6	7529.2	11285.3	9996.7	11723.4
3557.7	2448.7	2773.7	3285.2	2801.2	2586.8	3229.1	2572.2	1871.8	2148.2	2426.3
2685.4	4357.8	4922.3	4709.4	4561.3	4049.4	4237.3	5486.1	3480.1	3956.5	5956.3
42.4	647.5	958.0	1342.0	437.2	419.1	387.7	488.6	110.3	54.3	379.0
34.7	77.2	134.2	152.7	64.1	79.3	53.8	82.2	33.9	19.9	59.1
9765.1	3491.4	3456.6	3705.0	3892.6	3610.1	3742.1	3382.9	4179.0	4195.5	4580.7
572.1	1962.9	3362.3	3320.5	1449.9	2207.6	2066.6	3576.9	1205.7	729.7	2580.8
1974.6	4205.2	6801.3	7209.2	4301.0	4865.0	5793.3	5483.4	2700.5	1868.9	4733.4
3796.8	757.5	1379.5	1394.3	1235.7	1107.1	1427.2	1060.6	1485.7	1349.4	2084.1
32.7	37.7	50.7	65.8	23.7	18.1	45.7	79.5	36.9	17.2	29.1
149.0	932.0	1375.3	1948.0	895.8	1160.6	1175.6	1466.6	538.5	268.1	1057.4
910.1	5198.2	5084.7	5057.7	6515.0	4742.1	6131.1	5115.5	4943.8	4103.8	4240.6
3954.4	3440.1	4100.5	4954.0	3681.9	3264.8	3744.1	3575.5	2611.7	1282.6	4097.7
1198.3	4808.7	3718.4	4103.6	3901.1	3951.5	4219.6	4014.7	5094.0	6131.0	2774.3
2167.6	833.2	1105.8	1599.6	567.0	675.5	621.8	950.9	515.5	383.6	818.1
13774.2	6842.7	6628.8	6907.4	6900.0	6535.6	8712.1	6537.1	8672.9	6299.7	11464.0
46.7	165.2	272.6	328.4	228.7	149.9	187.3	343.3	90.7	52.5	125.8
250.3	1784.0	2112.3	2362.4	1799.7	1621.0	1892.5	1747.2	1367.8	817.3	1834.2
54.7	982.4	1458.2	1266.6	729.3	915.9	804.2	1212.2	288.0	299.0	643.5
630.7	1750.7	1794.5	2172.0	1856.0	1614.2	1493.5	1745.7	794.7	819.2	1568.9
53.5	1850.9	2493.9	2725.6	1476.4	1571.6	1989.9	2464.0	879.5	621.7	1680.8
965.5	1756.4	1891.5	1525.2	1418.5	1630.2	1226.2	1790.8	1237.3	1342.7	1207.8
12701.8	5986.0	5846.0	6295.3	4350.2	4341.8	4747.5	4908.6	5271.6	4891.3	4779.1
325.3	1456.9	1757.4	1737.0	1759.6	1209.2	1153.5	1207.8	474.9	1188.2	931.0
29864.1	8481.2	7848.7	8631.2	7786.8	7526.4	9084.3	7668.4	11537.4	9351.6	12805.4
2862.4	1509.6	1386.6	1478.2	1648.1	1385.1	1395.1	1560.2	1609.9	1352.8	1454.1
34.4	115.3	63.6	289.5	75.3	281.8	21.9	259.0	129.7	169.7	113.3
25497.7	5843.6	5761.9	7041.9	5514.0	5275.1	6310.1	4403.2	8603.7	6368.8	8534.9
148.5	496.1	667.1	839.4	327.5	480.4	453.2	598.2	189.1	134.4	205.2
5223.3	6021.6	5583.3	5872.0	5548.4	5377.6	6134.1	5629.4	8679.5	6632.7	7271.7
1050.8	4419.4	4941.7	5616.3	4450.3	4614.2	5267.8	5600.4	3202.5	1400.0	4339.8

91.5	224.3	358.7
6909.0	7579.6	7158.0
3927.6	3796.4	4827.0
2186.9	4218.6	2442.6
4764.5	2472.2	5080.1
1203.3	1269.0	1216.7
286.6	827.0	211.7
547.7	637.1	459.5
3100.4	4300.7	6077.8
4211.8	6067.3	4926.0
7424.8	8578.8	8019.0
2288.5	3157.1	3009.6
4053.4	4502.0	5577.3
536.2	564.1	675.5
88.4	141.7	80.3
3359.7	3741.1	3205.2
4257.7	2416.1	3457.8
5414.4	5891.9	7410.8
963.9	1934.6	1200.8
106.7	62.6	99.5
1604.0	2195.7	1531.2
5119.1	6231.9	5909.4
3822.8	4912.0	3884.2
4193.7	3992.6	4881.9
851.6	1158.1	774.6
5348.7	5999.7	4337.3
321.3	506.8	347.4
1719.0	1883.6	2292.7
1268.2	1425.9	1789.1
1995.2	1831.1	1655.1
2674.0	2338.0	4139.5
1477.1	2018.9	1628.9
5349.9	5831.9	4214.3
1531.2	1617.3	1446.0
9487.3	8733.1	7663.8
1718.6	2200.1	2421.8
325.0	425.0	157.9
6843.0	6065.9	5393.1
738.8	881.1	622.1
4841.2	6129.4	5692.7
6568.2	4753.0	5668.2

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FJ683156.1 gg_id:525294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU778295.1 gg_id:351009 feces clone RL117_aae92g08 EU778
EU748229.1 gg_id:325428 neotropical folivorous flying bird adult hoatzin crop clone hoa31_43C06.F EU748
EU776772.1 gg_id:355994 Mongoose lemur feces clone ML_aaj28d07 EU776
FJ683944.1 gg_id:516977 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
DQ796840.1 gg_id:193857 human fecal clone RL179_aao55c04 DQ796
DQ801499.1 gg_id:180881 human fecal clone RL388_aao96d01 DQ801
FJ682585.1 gg_id:521919 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
EU842502.1 gg_id:318015 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ673100.1 gg_id:509584 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
GQ897612.1 gg_id:549435 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ673236.1 gg_id:521060 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ678637.1 gg_id:527274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
EU765455.1 gg_id:305241 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ673604.1 gg_id:511676 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ683547.1 gg_id:523042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
EU766152.1 gg_id:318722 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EF400832.1 gg_id:207360 human fecal clone SJTU_D_02_16 EF4008
EU844606.1 gg_id:310033 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ807203.1 gg_id:199566 human fecal clone RL244_aaj47e06 DQ807
FJ684169.1 gg_id:521869 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU471640.1 gg_id:293892 Asiatic elephant feces clone AE1_aaa02e03 EU471
GQ897242.1 gg_id:592281 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU762076.1 gg_id:320832 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
EU344634.1 gg_id:267988 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU461587.1 gg_id:296506 mongoose lemur feces clone ML_aaj25a11 EU461
FJ369987.1 gg_id:362208 feces adult twins and mothers; TS55 clone TS55_a03b06 FJ3699
FJ678935.1 gg_id:526002 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ677628.1 gg_id:525254 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
FJ678824.1 gg_id:523139 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
AF371571.1 gg_id:39350 swine intestine clone p-2168-959-3 AF371
FJ676406.1 gg_id:519924 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
FJ365764.1 gg_id:362572 feces adult twins and mothers; TS21 clone TS21_a02g01 FJ3657
FJ365587.1 gg_id:365413 feces adult twins and mothers; TS20 clone TS20_a04f04 FJ3655
FJ673888.1 gg_id:521259 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ824009.1 gg_id:174940 human fecal clone RL204_aaj58b02 DQ824
EU768538.1 gg_id:326680 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
GQ493866.1 gg_id:575260 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ896748.1 gg_id:552047 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ678243.1 gg_id:529592 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ683038.1 gg_id:525861 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830

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4244.6	979.0	1129.2	927.4	774.8	1141.9	905.1	880.1	1973.8	2000.5	1825.8
176.5	1443.5	2456.2	2299.3	423.7	1234.0	1094.1	1677.8	885.7	296.9	1245.5
44.8	700.9	964.5	964.7	819.9	590.1	1013.1	702.8	316.3	151.1	480.0
8278.2	6955.8	6997.6	7128.3	6413.0	5637.9	7394.6	6249.2	8390.8	8621.7	9538.4
382.8	1114.3	1411.4	1404.5	894.8	1117.3	974.3	1829.6	819.3	1786.4	1013.4
32.7	130.1	84.3	168.6	40.9	50.1	20.8	88.7	27.2	19.7	30.1
834.6	435.1	617.4	519.0	221.0	403.0	189.2	484.7	290.2	182.8	286.9
93.1	808.0	1419.6	1322.0	734.2	1109.9	841.6	1598.6	570.7	357.3	708.0
2768.2	1913.3	2169.3	2621.4	1280.0	1481.7	1636.5	1704.3	1778.1	1405.8	1926.2
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310.4	1004.3	1775.1	1920.8	552.8	1254.5	707.6	1795.4	803.7	163.1	1097.9
14768.5	4255.7	4618.2	5145.7	5148.5	4351.3	5116.0	4974.3	5821.0	4060.6	6487.4
2613.2	1376.3	1565.4	1499.6	1017.5	1433.8	1379.7	1643.8	1640.4	1546.5	1842.2
33.5	299.1	961.6	913.3	122.6	334.5	172.1	720.5	103.3	33.6	632.7
23835.5	8446.6	6378.6	4533.0	6363.1	6797.3	4419.5	5077.5	10397.4	6068.4	5388.0
934.0	2291.8	2524.7	2467.2	1901.3	2275.2	2183.2	2457.6	2670.1	2220.7	2233.2
282.3	1775.6	2554.8	3342.6	1061.6	1767.8	1694.5	3202.6	1835.6	588.0	1857.1
570.6	2963.2	3765.7	2728.5	1398.8	2371.1	2271.6	2418.7	3100.5	1578.5	2562.6
6011.4	6095.9	6579.4	6210.1	5126.1	5903.4	5584.5	5738.7	8677.8	6641.7	7042.4
1165.2	5476.3	4948.9	4487.6	3404.4	5749.3	3614.3	4960.4	8097.1	6357.5	5098.1
6676.0	3819.8	3766.5	4150.8	3446.4	3337.6	4008.3	3821.5	4156.6	3159.8	4432.6
98.1	732.6	924.6	995.2	141.1	434.1	307.7	593.7	101.0	74.7	471.5
1004.3	256.4	908.4	371.6	1339.5	260.9	796.3	1144.2	48.8	220.2	582.3
376.4	2103.2	2175.0	2778.3	2342.8	2097.3	2361.0	2594.5	1408.2	2235.4	1691.6
4946.1	4086.7	3631.5	3859.1	2752.4	3355.6	3239.0	4023.0	4512.8	3942.1	3941.3
213.4	487.7	793.2	594.3	474.1	560.1	534.1	801.7	369.2	988.4	514.9
508.9	992.2	1062.8	1235.6	985.7	807.1	761.2	958.6	500.9	165.1	516.2
154.8	570.1	933.4	1221.1	266.1	342.6	418.3	837.9	127.4	141.5	177.8
1496.4	4806.4	4462.0	5322.7	4052.4	4528.5	3455.4	4585.4	4141.4	4191.5	4019.0
86.7	1028.9	1476.7	1987.0	320.5	658.4	793.1	998.8	165.0	95.7	859.3
201.8	2624.9	1678.9	1747.2	1907.9	960.3	2230.2	1223.9	2474.4	2695.2	1683.1
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1752.4	646.1	1226.0	1007.3	514.9	999.6	496.4	1696.3	478.5	391.0	748.2
2294.6	784.4	1298.1	1221.8	355.9	940.9	495.2	1495.6	545.3	316.7	761.5
5331.4	2868.0	2906.5	3383.7	3660.7	2681.8	3217.7	2823.1	4512.6	2311.3	3773.1
3008.4	6126.1	6146.6	6317.3	5009.1	4972.3	5330.4	6136.8	5754.9	4976.8	5804.4
398.4	5056.7	4941.9	4558.0	1895.5	4179.0	4276.6	4481.8	5314.9	3738.7	5621.8
536.8	2503.4	2795.9	2617.6	2744.1	2254.1	2763.1	2944.7	2023.4	2219.4	2066.7
60.4	541.4	809.1	620.9	389.6	688.6	382.4	554.3	387.7	699.7	363.3
18385.4	3710.5	3794.4	4727.8	4814.6	4211.0	5265.6	4093.7	4900.4	3580.9	5300.4

2772.0	4504.4	3296.4
760.4	1453.6	919.4
1669.7	1827.1	1200.5
660.3	640.1	812.7
5621.4	7269.1	6251.1
2663.4	1164.5	2295.3
115.2	104.4	87.2
505.0	1160.1	426.8
1193.5	1695.0	2136.0
1862.9	2637.9	1844.0
3387.2	2546.0	2378.8
1917.2	2184.9	1159.4
4387.2	5657.0	4988.1
2840.1	2043.3	1630.1
944.2	599.2	603.3
4607.5	4840.3	5204.4
3446.0	2632.4	2482.8
3137.4	2852.1	3713.7
1873.1	1922.7	2324.3
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4420.1	5534.1	5557.8
3626.4	3847.8	4303.6
1009.2	793.7	854.9
170.9	256.3	90.1
2185.9	2634.1	2632.3
4247.0	4607.1	4772.2
886.7	792.0	1134.5
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1405.1	631.3	935.7
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FJ683628.1 gg_id:518029 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
DQ793701.1 gg_id:188799 human fecal clone RL246_aai75h10 DQ793
EU471579.1 gg_id:289088 Asiatic elephant feces clone AE1_aaa02b09 EU471
EU842652.1 gg_id:335926 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ684990.1 gg_id:529224 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU843303.1 gg_id:333505 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU843314.1 gg_id:331449 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF402536.1 gg_id:212249 human fecal clone SJTU_B_09_22 EF4025
GQ491740.1 gg_id:539352 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU461879.1 gg_id:294773 white-faced saki feces clone Saki_aaj62h02 EU461
GQ493781.1 gg_id:559605 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ798491.1 gg_id:197983 human fecal clone RL181_aan97d06 DQ798
FJ678273.1 gg_id:515680 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
DQ797604.1 gg_id:186093 human fecal clone RL206_aaj13e12 DQ797
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EU843910.1 gg_id:342861 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ673106.1 gg_id:518482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU467223.1 gg_id:289139 black-handed spider monkey feces clone SPIM_f06 EU467
FJ674067.1 gg_id:514479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU766356.1 gg_id:342805 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
EU467254.1 gg_id:294800 black-handed spider monkey feces clone SPIM_b04_1 EU467
EU465864.1 gg_id:298108 African elephant feces clone AFEL3_aao13b07 EU465
DQ801572.1 gg_id:194536 human fecal clone RL117_aae91f06 DQ801
FJ364329.1 gg_id:357050 feces adult twins and mothers; TS15 clone TS15_a01f08 FJ3643
FJ673928.1 gg_id:526343 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
EF402856.1 gg_id:205712 human fecal clone SJTU_B_13_37 EF4028
FJ371802.1 gg_id:358665 feces adult twins and mothers; TS8 clone TS8_a02d03 FJ3718
DQ326236.1 gg_id:145868 Metagenomic gut microbiome healthy human stool clone C162 DQ326
FJ679447.1 gg_id:519381 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
FJ673719.1 gg_id:519898 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ673495.1 gg_id:521206 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ371748.1 gg_id:360201 feces adult twins and mothers; TS8 clone TS8_a01g05 FJ3717
DQ824233.1 gg_id:179128 human fecal clone RL304_aal73c09 DQ824
EU530197.1 gg_id:261328 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU5301
DQ802278.1 gg_id:175265 human fecal clone RL188_aah15e08 DQ802
GQ897602.1 gg_id:572883 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ683310.1 gg_id:528402 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
FJ679428.1 gg_id:524599 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
DQ796270.1 gg_id:188127 human fecal clone RL179_aah25a02 DQ796
FJ682859.1 gg_id:522528 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828