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EF509675.1 gg_id:226514 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5096
FM873785.1 gg_id:370109 occupant source house mattress dust clone MA04F09 FM873
GQ087754.1 gg_id:423895 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
AJ251987.1 gg_id:45265 Gemella sp. str. M60449/99/1 T AJ2519
GQ006874.1 gg_id:502790 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g11c GQ006
GQ023356.1 gg_id:486313 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317d07 GQ023
EU427463.1 gg_id:258882 Gemella sp. str. WAL 1945J EU4274
GQ006635.1 gg_id:503029 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85h02c GQ006
Y13365.1 gg_id:14920 Gemella bergeri str. 617-93 Y13365
DQ113771.1 gg_id:129485 dog jejunum clone J5-76 DQ113
AM420049.1 gg_id:236798 Noma subgingival plaque clone 202F06(oral) AM420
EF999972.1 gg_id:278692 Haloplasma contractile str. SSD-17B EF9999
EF586062.1 gg_id:245842 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EF585995.1 gg_id:240344 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_F EF5859
GU455254.1 gg_id:519748 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
EF586039.1 gg_id:248439 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
DQ431898.1 gg_id:204684 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
NZ_ACIL02000016.1 gg_id:469920 Catonella morbi str. ATCC 51271 NZ_AC
DQ113697.1 gg_id:129773 dog duodenum clone D5-23 DQ113
DQ113716.1 gg_id:130850 dog jejunum clone J1-18 DQ113
AF318316.1 gg_id:35088 Aerococcus sanguinicola str. BBMML 01 AF3183
U64456.1 gg_id:15070 Aerococcus urinae str. F1-84 U64456
U64457.1 gg_id:15071 Aerococcus urinae str. G1-84 U64457
U64460.1 gg_id:15074 Aerococcus urinae str. 998-93 U64460
AY707773.1 gg_id:136245 Aerococcus viridans str. 37R AY7077
EU289060.1 gg_id:254233 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
EU289078.1 gg_id:237214 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
Y17318.1 gg_id:15076 Aerococcus christensenii str. CCUG 28826 Y17318
AJ278341.2 gg_id:23513 Aerococcus urinaehominis str. CCUG 42038b AJ2783
EU075039.1 gg_id:238621 Aerococcus viridans str. 15MS EU0750
AM230658.1 gg_id:196766 Aerococcus suis str. 1821-02 AM230
AM292063.1 gg_id:250567 Aerococcus viridans zf-68-I AM292
GQ161096.1 gg_id:412780 Aerococcus viridans str. GDQY-1 GQ161
NR_029351.1 gg_id:593109 Facklamia sourekii str. SS 1019; CCUG 28783; ATCC 700629 NR_029
Y15716.1 gg_id:52354 Facklamia ignava Y15716
GQ071953.1 gg_id:425055 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190d01 GQ071
Y18053.1 gg_id:15053 Facklamia languida str. 1144-97 Y18053
FM873282.1 gg_id:366119 occupant source house floor dust clone FD01A09 FM873
GQ497941.1 gg_id:561734 Facklamia sp. str. KO_PS21 GQ497
Y16426.1 gg_id:15060 Ignavigranum ruoffiae str. CCUG 37658 Y16426

3692.6	7889.6	6585.1	7622.8	6278.7	6762.2	6424.2	6127.6	8834.5	7525.7	9717.2
1558.1	1330.4	1284.8	1627.1	1715.1	1447.5	1305.9	1249.5	1705.6	803.2	2132.3
4262.3	2041.3	2108.1	2342.2	1964.5	1912.0	2232.2	1973.7	3418.4	3349.9	2855.8
9064.4	6576.4	7150.5	8401.6	8191.9	6849.0	9078.3	7064.7	9211.5	10041.4	9081.6
36.3	76.3	76.0	69.6	70.8	53.4	82.1	77.1	46.8	46.8	43.1
44.1	56.4	109.0	92.4	99.4	69.5	54.2	96.6	55.8	91.2	73.9
1210.6	21.7	1228.0	1186.5	955.1	1029.7	1600.6	950.8	1431.9	898.1	1889.0
37.1	1259.5	1275.5	1358.1	965.2	1347.2	961.0	1466.8	434.5	1893.0	68.5
5677.3	6823.5	7151.5	7468.1	6244.9	6209.2	6359.3	6290.5	10077.9	8782.4	8023.7
29.1	119.0	221.5	228.2	228.9	166.3	84.6	203.0	116.5	2333.1	118.0
51.8	38.2	45.4	53.0	44.7	29.2	34.2	58.9	26.5	47.5	32.4
13990.2	5720.5	5072.8	6388.8	4947.7	4992.6	6303.4	4439.9	9027.2	6632.4	8082.5
6023.0	4842.5	5317.1	4765.6	5254.7	5020.9	5655.8	4837.8	4838.7	5619.2	5756.6
1132.5	5123.9	4345.4	4735.8	4229.6	4804.0	4465.2	4077.6	5072.9	2825.6	3987.9
1575.6	4225.3	5122.0	4692.4	5502.0	4879.0	5414.1	5830.3	3291.7	3539.6	5260.9
2293.7	4068.9	3836.6	4593.5	3962.0	4478.4	4311.8	3933.2	3341.9	2125.2	3549.9
4638.7	4749.5	4654.6	4763.4	4881.6	4746.9	5128.8	4611.9	4725.3	4732.5	5257.0
80.9	313.6	756.5	552.7	383.4	444.7	333.4	603.2	231.5	86.6	253.5
994.9	4435.5	4879.5	3518.1	3522.5	5173.0	3920.4	5464.2	2392.9	5558.1	2934.7
5836.5	5142.1	5149.5	3848.0	4265.1	5285.0	4013.9	5776.5	3735.6	6672.4	3913.4
195.8	2348.5	2762.6	2275.2	2171.5	2853.3	1825.6	3323.9	1531.4	3406.6	2293.3
1068.4	1464.4	1943.9	2027.7	2123.7	1987.2	2059.3	1976.7	1040.1	986.5	1565.8
289.4	1438.3	1797.5	1636.4	1720.6	2336.4	1559.5	1544.9	1298.7	2785.9	1347.9
353.3	3293.3	4571.8	2969.0	3986.5	4882.1	2966.5	4459.2	2177.1	5596.4	2861.2
693.5	3821.8	6080.4	4149.5	2891.5	4467.3	2745.6	3961.2	2490.4	2654.8	4375.0
8236.9	2865.0	2485.3	2334.7	3100.3	2836.3	2819.6	3616.3	1806.0	2826.5	2465.8
112.6	380.0	590.6	514.7	437.1	452.0	328.2	526.1	221.1	128.0	341.8
233.8	3472.7	4321.8	4082.7	3249.1	3691.8	4237.2	4336.1	2023.9	2517.8	2859.2
416.1	4270.5	3518.4	2828.3	2879.7	4265.9	2496.1	3781.9	5052.9	4426.6	1996.2
51.3	38.1	34.9	51.0	52.7	38.9	37.6	55.5	37.7	80.4	38.2
51.2	1005.0	974.0	1007.5	1143.0	1487.8	732.3	1486.7	460.6	1262.1	996.1
75.2	977.6	2035.3	1940.0	1329.3	1134.2	1510.7	1960.8	618.5	1303.9	1339.2
14908.1	5288.2	7199.6	5119.7	5512.3	5397.7	5228.1	5980.5	4204.7	5857.5	6461.1
52.2	726.7	683.8	817.0	952.8	1202.6	618.9	1181.7	310.8	1189.5	669.7
36.9	370.4	712.2	577.1	686.5	637.0	574.4	1496.0	441.4	199.8	298.0
76.6	80.6	142.9	122.1	86.3	64.8	92.3	137.3	62.5	59.7	85.2
9102.5	5202.5	4891.0	5035.6	5244.1	5267.6	5516.6	5414.7	5953.8	5035.5	7382.6
259.9	480.5	538.8	410.6	628.2	542.6	436.8	554.5	225.3	413.4	235.1
314.1	2516.4	2459.6	1701.1	2456.5	2707.4	1996.6	2945.1	2873.0	2833.5	1137.4
50.7	463.8	639.9	438.2	262.8	730.7	215.8	422.2	404.7	2170.8	123.9
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6091.0	6608.4	5818.5
1059.7	1654.7	1173.4
1836.0	2983.2	1737.5
7927.3	8130.4	8256.1
66.6	106.9	373.8
70.3	144.3	186.6
798.4	1318.0	870.7
1418.8	1372.3	1723.3
5965.4	7335.0	6690.8
165.2	286.9	170.5
48.2	55.5	42.4
4349.9	5869.6	4865.5
4778.2	5581.2	6916.2
4221.7	3947.9	7465.7
6422.4	6221.3	8705.0
3835.8	3916.3	5804.5
4605.4	5162.7	7618.1
471.6	628.5	790.7
4392.6	4287.7	7330.2
5359.0	5709.2	8637.7
2771.7	3030.9	4174.9
2849.5	3113.9	4287.6
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3597.9	4239.9	7348.4
632.6	490.0	465.3
4079.1	4177.3	6826.2
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42.0	45.8	57.5
1632.9	1975.6	4424.3
1343.1	2040.3	3335.2
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1315.6	1642.4	4302.1
1281.3	643.9	1220.7
87.5	111.5	129.9
4590.5	6536.6	6951.9
553.5	993.9	1163.0
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876.7	314.3	591.4
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s__Alloiococcus otitis	43590
s__Carnobacterium divergens	72531
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s__Carnobacterium viridans	71817
s__Carnobacterium viridans	71908
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s__Carnobacterium viridans	72357

NR_025307.1 gg_id:537370 Dolosicoccus paucivorans str. 2992-95; CCUG 39307 NR_02
GQ071986.1 gg_id:390110 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190g07 GQ071
FJ671853.1 gg_id:520766 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ674961.1 gg_id:517319 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
GQ002938.1 gg_id:506724 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu182e09 GQ002
GQ060659.1 gg_id:463917 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g08 GQ060
FM873468.1 gg_id:369668 occupant source house floor dust clone FD04B03 FM873
EU341289.1 gg_id:240694 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
FJ672272.1 gg_id:515704 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
Y17780.1 gg_id:74511 Eremococcus coleocola str. M1832/95/2 Y17780
GQ068237.1 gg_id:399188 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
AJ279038.1 gg_id:16600 Aerosphaera taetra str. CCUG 43036T AJ2790
AY959019.1 gg_id:132717 Microbes on human vaginal epithelium clone rRNA246 AY9590
GQ020706.1 gg_id:488962 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
FJ672416.1 gg_id:527548 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
GQ024094.1 gg_id:485575 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ024
FJ672485.1 gg_id:531811 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
AF124041.1 gg_id:15240 sheep scab mite clone #1 AF1240
AB188091.1 gg_id:104418 Alkalibacterium iburiensis str. M3 AB1880
AB268550.1 gg_id:186973 Alkalibacterium polygonumreducens str. F11 AB2685
AB294173.1 gg_id:368743 Alkalibacterium kapii str. T82-5-1 AB2941
EU845714.1 gg_id:349078 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8457
GQ351352.1 gg_id:542881 Alkalibacterium sp. str. G4 GQ351
AF143512.2 gg_id:15252 Alkalibacterium olivapovliticus str. WW2-SN4c AF1435
AB294176.1 gg_id:361292 Alkalibacterium psychrotolerans str. JCM 12281 AB2941
AB294169.1 gg_id:364463 Alkalibacterium putridalgicola str. O26-12-2 AB2941
X92169.1 gg_id:27088 Lake Nakuru isolate WN16 X92169
GQ848212.1 gg_id:556700 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
X59765.1 gg_id:15237 Alloiococcus otitis str. NCFB 2890 X59765
AY543021.1 gg_id:103243 Carnobacterium divergens MF 156 AY5430
AY543036.1 gg_id:100049 Carnobacterium divergens MF 66 AY5430
AY543031.1 gg_id:99269 Carnobacterium maltaromaticum MF 204 AY5430
GQ304934.1 gg_id:568366 Carnobacterium maltaromaticum str. MMF-26 GQ304
GQ304938.1 gg_id:581552 Carnobacterium maltaromaticum str. MMF-30 GQ304
GQ304920.1 gg_id:559437 Carnobacterium maltaromaticum str. MMF-12 GQ304
AM179873.1 gg_id:150460 Carnobacterium maltaromaticum B26 AM179
DQ027061.1 gg_id:134675 Carnobacterium sp. str. AT7 DQ027
EU845619.1 gg_id:312732 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456
EU845247.1 gg_id:313812 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8457
L08623.1 gg_id:15257 Carnobacterium alterfunditum L08623
EU845677.1 gg_id:309286 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456

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6202.2	2898.3	3247.8	2750.6	2602.2	2975.6	2913.4	2841.1	4065.8	4490.5	2994.4
809.0	1784.1	1474.7	1364.8	1565.2	1400.1	1395.2	2228.6	587.9	502.7	1002.0
71.0	1149.0	2048.0	855.6	1110.3	1111.8	890.5	1510.3	497.1	1772.6	1035.6
423.6	3533.9	4108.2	3945.2	4010.0	3477.1	3961.4	3801.9	2708.1	1744.7	3510.1
61.9	1528.2	1687.7	1425.1	1604.5	1834.8	1336.6	1784.2	920.6	1202.4	991.5
2669.5	1359.4	2255.6	1420.2	1752.2	1741.9	1599.3	2080.8	798.1	662.4	1297.5
14053.2	3476.8	3489.2	3472.4	3142.5	3778.3	3481.4	3151.4	5195.1	5723.2	4584.8
5323.1	1151.1	1793.1	1500.5	1480.1	1177.3	1513.6	1758.8	627.2	496.4	941.3
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47.2	24.5	23.4	20.0	30.9	18.8	23.7	24.8	21.4	18.3	16.0
1609.4	3708.2	4564.0	3849.8	4130.6	3766.7	3990.6	4565.9	2888.5	5242.6	3990.3
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13848.5	2611.7	3756.4	3317.6	4181.8	3274.1	3879.8	4086.8	1722.3	1728.3	2509.9
53.5	205.0	447.3	439.2	215.9	491.4	212.3	433.2	174.2	365.8	192.3
165.2	2074.1	2816.2	2362.4	2226.0	2689.1	1738.5	3580.8	1355.7	3583.0	2488.8
900.7	2832.9	2958.1	3143.1	3717.2	2581.1	3706.5	2825.2	2918.7	2585.7	3791.7
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1313.9	4572.7	4823.8	4808.9	3475.7	4331.2	5990.0	5220.3	4194.8	4753.4	5047.8
413.0	3084.2	4626.5	4934.9	3919.6	3510.9	3727.5	4703.7	4617.4	4347.0	4083.3
2018.7	3678.2	4381.1	4637.5	4288.0	4472.8	4413.3	5498.6	4416.8	3114.5	3282.5
1307.0	4895.1	5635.1	4922.9	4057.9	4716.2	6415.6	4860.9	4993.4	4289.7	4700.0
1426.1	1402.0	2187.1	2702.2	1717.4	1663.4	1372.2	1908.0	1170.8	1403.9	2851.6
3017.4	5648.9	7261.8	7530.8	7355.4	5926.2	7341.9	7331.0	10188.6	4671.3	6766.1
155.4	1449.9	1920.1	1807.4	1874.8	1578.8	1463.5	2440.9	940.1	952.2	1022.5
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218.7	2835.6	3573.2	2407.2	2098.1	2939.7	2878.9	2796.2	1622.5	2182.1	1920.2
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3491.7	4585.3	4730.2	4446.4	4728.8	4757.1	4497.7	5490.0	4237.4	5303.3	5992.8
3491.7	4798.6	4854.2	4512.1	4442.4	4928.8	4621.1	5755.9	4435.6	5735.3	5689.3
9851.2	7708.7	6224.6	6520.0	6391.9	6491.9	6937.3	6046.6	8526.3	7153.0	9537.5
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1026.2	2456.7	2917.1	2496.5	2795.2	2655.2	2444.9	3084.8	1797.1	2433.3	2473.7
269.8	1506.0	1617.6	1615.9	1512.4	2232.4	1542.0	1748.4	1107.6	2087.5	1283.6
13856.9	7063.1	6723.6	7713.8	9453.0	7203.7	7517.7	6673.5	6655.1	5498.9	9861.1

676.5	1002.5	1766.0
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1553.5	1674.1	979.9
1251.4	1443.4	3150.2
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1598.6	2206.8	3530.1
2768.5	4358.0	3329.5
1368.4	2067.4	2054.2
4592.3	6512.3	6012.1
16.7	25.3	46.7
3825.3	4865.1	7385.3
5742.9	6566.3	9979.1
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2375.8	3122.4	5379.6
3660.8	6537.5	5661.5
2584.5	3221.2	4224.8
4229.3	5233.0	6179.7
4442.1	5125.1	5279.0
3720.4	4716.3	4375.5
4843.6	5900.2	8037.7
4823.1	5693.2	7060.3
1512.3	2514.5	3403.9
6235.9	8208.9	6299.2
1635.7	1908.6	2576.1
8668.6	9302.9	10697.3
3784.8	4313.8	6217.2
4589.1	5489.4	6194.8
4713.9	5122.7	6901.6
4891.0	5633.2	7483.4
6031.3	7194.8	6726.0
5078.8	6209.1	6908.0
2768.6	3881.7	6935.8
1163.5	1448.7	2603.4
2629.1	3173.5	4184.7
2627.9	2347.5	3748.6
7019.8	7742.5	8359.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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o__Lactobacillales	f__Carnobacteriaceae
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EU845485.1 gg_id:325830 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
NR_025197.1 gg_id:566585 Carnobacterium viridans str. MPL-11; ATCC BAA-336 NR_02
AM111051.1 gg_id:140940 Carnobacterium sp. str. 7196 AM111
DQ778093.1 gg_id:166840 Carnobacterium sp. str. LIV10 DQ778
EU817500.1 gg_id:332765 Carnobacterium sp. str. MS3 EU817
EU845027.1 gg_id:353898 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AF184247.1 gg_id:36062 Carnobacterium maltaromaticum str. BA AF184
S86170.1 gg_id:15243 Carnobacterium funditum str. pf3 (DSM 5970) S86170
AJ387905.1 gg_id:16452 Carnobacterium gallinarum str. DSM 4847(T) NCFB 2766(T) AJ3879
AM179875.1 gg_id:146934 Carnobacterium divergens B33 AM179
GQ008057.1 gg_id:501608 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
EU773383.1 gg_id:326100 BigHorn sheep feces clone BH2_aao23f01 EU773
GQ008163.1 gg_id:501503 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
FJ674675.1 gg_id:522048 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
Y17300.1 gg_id:15259 Desemzia incerta str. DSM 20581 Y17300
FJ674414.1 gg_id:512638 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
FJ674411.1 gg_id:522459 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
FJ674427.1 gg_id:515642 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6744
FJ675581.1 gg_id:530569 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6755
FJ675028.1 gg_id:509443 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6750
FJ671781.1 gg_id:525552 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6717
FJ674863.1 gg_id:520714 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6748
FJ674821.1 gg_id:525603 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6748
FJ674822.1 gg_id:526054 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6748
FJ672402.1 gg_id:516922 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6724
FJ674570.1 gg_id:524856 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6745
FJ671977.1 gg_id:516168 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6719
FJ674634.1 gg_id:527071 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6746
FJ194014.1 gg_id:353870 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1940
AY879299.1 gg_id:141939 Granulicatella adiacens str. 03252090 AY879
AF016390.1 gg_id:15054 Granulicatella elegans str. DSM 11693; B1333 AF016
AB022026.1 gg_id:15057 Granulicatella elegans str. HHC5 AB022
AB252689.1 gg_id:216513 Granulicatella elegans str. PAGU 792 AB252
AJ312375.1 gg_id:70105 Granulicatella adiacens str. 10/833 AJ3123
AY879298.1 gg_id:143622 Granulicatella paradiacens str. 04401102 AY879
Y15408.1 gg_id:15055 Granulicatella elegans str. 2640-91 Y15408
FJ558447.1 gg_id:521851 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
GU374018.1 gg_id:532021 normal teeth clone SRC_DSC5 GU374
AB247277.1 gg_id:147894 Marinilactibacillus piezotolerans str. JCM 12337 AB247
AB159717.1 gg_id:103175 Marinilactibacillus psychrotolerans str. INCT119 AB159
AY485792.1 gg_id:99434 Marinilactibacillus piezotolerans str. LT20 AY485

8513.9	5601.8	6706.7	6226.2	4896.3	5884.6	5517.8	4989.2	9570.1	6558.6	7105.0
5588.7	4476.2	4950.2	4587.7	4999.0	5046.3	5494.6	5322.4	4135.4	6099.2	4450.6
1829.3	3566.2	3618.7	4705.5	4006.9	3885.3	4126.8	4670.4	3168.2	6168.6	4737.6
1837.2	2518.8	2775.4	3020.1	2799.5	2505.8	2810.2	2782.1	2289.9	2514.7	3415.7
51.6	1199.9	1906.6	750.6	1531.0	1750.4	960.4	1968.1	556.1	1184.3	807.4
724.5	2476.4	3023.0	2309.6	2650.5	3141.1	2509.9	3439.7	1837.1	2322.6	2254.6
2440.2	3665.6	3878.8	3681.9	5076.1	4066.0	3732.8	3849.6	3694.8	5152.5	4756.5
621.0	3328.2	3967.7	2839.6	4233.8	3546.7	3445.9	4446.1	2107.7	3851.2	3152.8
424.6	2935.2	3985.1	4671.4	3273.7	4245.7	3328.4	5032.4	3888.5	5755.2	4044.0
247.8	4563.4	5114.2	4385.8	4860.1	4955.3	5884.6	5391.8	3920.2	5169.8	3918.4
1067.7	5879.1	4855.4	4530.4	3302.2	4088.9	4094.2	4124.9	4142.9	4691.3	4106.6
1355.0	5417.3	6282.5	4909.1	5442.6	5680.5	5949.6	6588.9	4889.9	6950.5	5867.6
1451.7	3525.3	3819.4	3579.5	3465.7	4155.4	4235.4	3593.3	3423.7	3658.3	3706.3
32.5	406.9	408.5	221.0	549.4	829.7	313.2	741.5	189.3	1124.2	155.4
923.4	1830.4	1479.1	1089.6	1603.8	1855.5	1073.9	2011.7	1857.1	2645.9	1397.5
4367.5	4686.6	5979.9	4310.1	4779.8	5023.1	4439.3	6112.6	3959.1	5936.8	5779.0
18646.7	9338.5	8676.7	9621.1	9229.3	8541.7	9432.0	8686.4	13555.3	11063.2	12915.0
6719.1	4832.6	6131.2	3962.1	4555.5	5361.5	4245.8	6312.6	4276.8	6539.1	5515.4
733.2	4320.1	5350.9	3441.2	4493.7	4872.0	3721.1	6373.6	2799.6	6208.2	4360.1
321.0	4465.1	5835.8	4509.9	4464.7	4690.0	4240.9	5433.7	2816.3	5235.7	4230.9
2966.5	3913.5	4207.1	3323.8	3377.6	3935.3	3034.7	4009.5	3221.1	4760.3	4396.4
2756.6	4147.7	5192.3	3597.3	4283.1	4830.9	3653.1	5947.6	3331.1	6750.7	4768.9
10436.4	6559.9	6606.8	5554.1	5698.6	6120.9	5370.4	6266.4	7377.3	9125.4	6768.9
1371.9	2650.7	3671.8	2452.5	2249.0	2505.6	2655.2	2739.5	2369.1	3214.2	2981.9
1446.6	3463.3	3555.3	2698.5	3421.9	3835.4	3548.3	3049.6	3865.5	4888.6	2109.8
4147.3	6570.8	7386.1	6805.5	7266.5	7185.9	8163.9	8463.8	5959.5	7860.8	7195.9
127.2	2911.8	3717.3	2502.3	2383.8	3008.8	2145.0	3287.6	1754.1	3777.3	3284.1
7870.7	3958.3	5058.3	2643.7	4568.8	4307.0	4601.2	4659.8	5274.2	6904.2	4340.3
4288.1	2504.6	4013.2	2931.5	2347.6	3051.2	2267.1	3332.9	1507.5	3765.7	2009.5
33.4	1282.6	2633.7	871.2	2014.2	1954.2	866.3	1994.8	415.5	2821.7	682.4
46.6	867.9	1327.8	707.3	706.8	727.7	502.9	1295.3	270.0	746.9	509.6
46.4	579.0	708.0	542.6	626.2	515.6	437.1	773.4	242.9	714.2	372.0
41.8	618.5	1623.6	459.0	622.5	741.9	241.2	1010.4	177.8	607.1	549.6
30.3	236.7	485.0	293.5	249.9	202.3	219.4	252.8	88.0	293.4	126.8
39.0	274.6	1833.7	526.6	428.1	1136.6	561.6	1187.1	300.0	1867.5	599.3
51.2	476.6	895.8	361.2	463.1	479.3	274.8	914.8	198.6	466.1	415.4
661.7	1150.3	1601.7	1126.6	1318.1	1163.5	1126.7	1523.5	1764.1	2210.8	1229.5
19564.1	6282.9	6043.6	6146.2	7625.8	5569.3	6166.6	5069.1	8616.8	7188.5	10444.0
2759.8	4857.3	5772.7	5871.3	4918.1	5175.9	5868.6	6239.2	3554.0	6754.1	4478.6
2750.4	4372.7	6035.2	5271.1	4446.6	4714.4	5267.0	5784.9	8479.2	4606.6	4849.4
1110.8	5783.6	6540.7	6464.0	5873.8	5598.4	6335.1	6452.7	7010.0	4458.2	5844.7

5087.3	7052.0	8041.1
5263.1	6228.9	7073.9
4180.9	4637.9	4901.5
2695.2	3376.9	3220.4
2294.1	2593.3	6475.2
3575.8	3824.8	6943.2
4600.2	4851.9	5613.1
3959.9	4185.2	6692.2
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5960.7	5381.3	8354.2
4702.3	4370.8	7106.9
6198.2	6393.0	10067.0
3908.6	4160.8	6023.0
654.9	752.6	2240.4
1914.6	2747.4	4277.2
4888.2	5346.9	7805.7
8404.3	10171.1	8842.4
5010.1	5634.5	7825.8
5014.7	5359.8	7863.5
4798.3	5647.1	6607.9
4314.7	5115.7	5163.0
5012.0	5285.6	7958.1
5294.4	8141.7	8320.7
2187.3	3246.1	3028.0
3462.6	3748.3	6740.6
7122.6	7190.5	10660.9
3233.6	3215.0	5205.2
4681.4	5513.0	6469.1
3190.4	3576.6	4631.5
2425.4	2344.3	3979.7
926.5	1160.2	1619.8
772.9	887.4	987.3
884.0	835.8	916.5
238.6	383.3	261.8
1506.5	1246.9	1904.3
529.6	664.0	816.3
1525.3	1574.5	2027.8
5319.9	7084.6	5469.2
5394.9	5977.0	8442.4
4218.8	6178.2	6509.4
5035.9	6884.3	7798.3

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

o__Lactobacillales	f__Carnobacteriaceae
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g__Trichococcus
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s__Trichococcus collinsii	71938
s__Trichococcus collinsii	71969
s__Trichococcus collinsii	72123
s__Trichococcus collinsii	72361
s__Trichococcus collinsii	72469
s__Trichococcus collinsii	72474
s__Trichococcus collinsii	72887
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s__Trichococcus collinsii	73069
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s__unclassified	71818
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s__unclassified	42706
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s__unclassified	42880
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s__unclassified	43076
s__unclassified	43080
s__unclassified	43192

EU434573.1 gg_id:277322 Trichococcus collinsii str. b73 EU4345
EU434534.1 gg_id:266599 Trichococcus collinsii str. b258 EU4345
EU434512.1 gg_id:264683 Trichococcus collinsii str. b239 EU4345
EU434551.1 gg_id:268210 Trichococcus collinsii str. b140 EU4345
EU434537.1 gg_id:275949 Trichococcus collinsii str. b253 EU4345
EU434536.1 gg_id:274539 Trichococcus collinsii str. b255 EU4345
EU434554.1 gg_id:259750 Trichococcus collinsii str. b205 EU4345
EU434507.1 gg_id:275512 Trichococcus collinsii str. b354 EU4345
EU434495.1 gg_id:277597 Trichococcus collinsii str. b362 EU4344
EU434510.1 gg_id:266846 Trichococcus collinsii str. b237 EU4345
NR_025435.1 gg_id:572224 Trichococcus palustris str. DSM 9172 NR_025
EU434478.1 gg_id:265112 Trichococcus collinsii str. b279 EU4344
FJ672147.1 gg_id:529854 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
AJ306612.1 gg_id:47658 Trichococcus collinsii str. 37AN3 AJ3066
AB186878.1 gg_id:101202 polychlorinated dioxin dechlorinating microcosm clone TSBX03 AB1868
L76599.1 gg_id:15246 Trichococcus pasteurii str. ATCC 35945 L76599
EU844884.1 gg_id:327706 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU434522.1 gg_id:263346 Trichococcus flocculiformis str. b328 EU4345
FJ675543.1 gg_id:509026 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
Y17301.1 gg_id:15254 Trichococcus flocculiformis str. DSM 2094 Y17301
FJ672105.1 gg_id:527794 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
DQ337518.1 gg_id:145184 tetracycline and tylosin resistance genes impacted swine effluent holding pit DQ337
EU434437.1 gg_id:272157 Trichococcus flocculiformis str. a209 EU4344
FJ674344.1 gg_id:527737 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
FJ672700.1 gg_id:527399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
EU434501.1 gg_id:265834 Trichococcus flocculiformis str. b319 EU4345
FJ671856.1 gg_id:511164 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ671301.1 gg_id:526709 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
GQ080732.1 gg_id:409174 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
NR_026454.1 gg_id:552567 Granulicatella balaenopterae str. M1975/96/1; CCUG 37380 NR_026
FJ764779.1 gg_id:565642 Marinilactibacillus sp. str. E-109 FJ7647
FJ671733.1 gg_id:514230 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
FJ671721.1 gg_id:518863 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
FJ672820.1 gg_id:513562 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ671872.1 gg_id:532281 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
X70907.1 gg_id:15241 Dolosigranulum pigrum str. NCFB 2975 X70907
GU395995.1 gg_id:526359 Dolosigranulum pigrum str. 33929-06 GU395
FJ670957.1 gg_id:516363 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6709
FJ672814.1 gg_id:520671 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
FJ675030.1 gg_id:515465 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
FJ674957.1 gg_id:519350 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749

81.5	2154.2	2641.0	1648.8	2952.2	2396.6	3325.7	2934.0	924.5	4048.9	2117.7
5884.1	2534.4	3870.6	2700.9	2560.5	3138.3	2979.6	3825.6	2014.6	5664.6	2586.2
135.7	2149.3	3658.4	2533.5	2938.2	2342.2	3181.7	2582.2	1393.5	3341.5	2532.5
2284.9	4801.0	5418.6	5420.6	4821.9	4727.0	5440.1	5602.5	6549.2	7125.5	5371.3
1683.7	4116.4	5135.0	3978.3	4397.7	4168.9	4563.4	4904.3	3951.7	5037.5	4478.4
15125.2	5607.4	5928.1	4924.8	5271.3	5548.1	5520.2	6365.1	6105.4	7598.4	6838.5
57.6	1420.8	1529.9	877.6	2644.4	1656.5	3217.8	1998.4	398.4	3007.1	1163.4
416.6	1385.1	1293.6	913.2	2385.9	1495.2	2996.3	1518.1	707.9	2615.6	1110.6
80.8	1791.9	2414.2	1522.3	2508.4	2050.1	2945.7	2577.7	875.4	3561.6	1981.7
6295.1	5014.7	5545.7	4863.6	4634.8	4935.6	5100.0	5667.2	5389.6	6876.6	5141.8
1147.6	5755.4	6763.8	4198.6	5821.6	5976.9	5251.6	6920.2	4656.0	9579.1	5522.5
61.4	1640.4	1845.2	1084.9	2819.7	1762.2	3262.5	2391.4	465.5	3205.4	1282.9
814.1	1670.3	3533.8	1231.0	1297.6	2102.0	757.0	2982.3	694.3	3647.2	1900.7
83.9	2115.5	2574.8	1593.7	2814.5	2364.4	3186.8	2905.1	927.5	3997.7	2079.4
55.7	1554.2	1239.6	909.1	1941.5	1545.5	1282.1	1691.6	446.2	1652.7	507.2
57.7	1637.5	1837.9	1076.8	2813.7	1757.6	3041.1	2389.2	466.0	3094.9	1280.4
87.0	1347.0	1818.3	1253.0	1352.8	1352.8	1483.8	1740.0	512.7	1666.1	1050.2
11680.3	6967.2	7856.1	7097.7	6477.2	6808.7	6901.4	7273.9	8390.5	10046.9	9545.8
4729.6	2579.9	3965.3	2436.2	1848.3	2569.2	1738.9	2953.8	1313.8	2683.8	2490.0
62.0	2946.0	2496.9	1981.3	2874.7	2972.9	2333.0	3918.0	1322.3	5039.7	1604.2
18942.0	4592.9	5431.6	5282.4	4453.3	4760.2	4619.4	5126.0	4776.1	5998.5	6165.6
94.5	32.8	33.4	30.3	34.3	45.8	22.0	25.6	24.8	26.9	16.4
5555.2	5344.2	4620.6	4693.5	5441.3	4858.8	5348.0	5776.4	4521.6	7734.8	5259.8
29297.4	6955.5	7869.7	7809.4	7199.1	7211.3	8117.1	7132.6	6882.5	8405.6	7960.9
17302.1	7540.0	7717.7	9388.8	7506.3	7609.5	7975.8	7478.1	8658.4	6095.4	8891.7
406.6	4142.0	5268.2	3686.9	3895.0	3965.0	4657.5	3898.8	5250.0	6614.9	4341.1
11213.8	4935.5	4713.5	4870.9	4389.3	7087.3	5329.5	4892.9	7860.7	6259.8	7091.7
1645.3	3003.3	3418.2	2693.7	3581.5	3659.1	3013.9	4054.5	2397.3	6234.3	2798.7
6634.2	4240.8	5526.5	4902.4	5118.5	4463.6	5808.4	4878.6	5687.1	5250.9	4995.0
39.0	173.6	225.2	196.0	206.3	230.7	208.5	196.2	67.1	174.1	124.6
991.2	2328.6	3989.5	3331.1	2693.3	2588.8	2829.3	3447.6	1443.4	2706.7	2756.4
16431.0	7146.8	6785.3	6922.1	6901.5	6685.9	8487.5	6397.0	8749.1	7476.0	9230.2
13300.2	4467.1	4663.3	4421.4	4703.1	4729.7	4503.8	4944.3	5279.6	6188.0	4631.7
172.4	1267.7	1408.6	1384.4	1165.2	1413.2	1638.7	1266.2	1021.7	323.5	923.4
1287.3	2294.5	3207.2	2980.3	2823.4	3473.4	2787.8	2242.7	3382.8	5517.7	3406.7
954.0	3779.0	5765.6	3872.6	2824.9	4219.4	2502.9	4416.2	3572.2	4265.2	3809.8
308.5	1585.1	1833.9	2139.0	1282.5	1543.9	1218.6	1379.3	1890.4	617.3	1288.7
1193.0	5518.3	5960.2	5907.4	4948.2	5530.7	5909.0	5439.2	5472.1	5576.9	6243.5
1011.0	1211.3	1405.6	1342.9	1549.0	1745.9	1639.8	2333.1	1464.7	1669.1	1528.0
6415.9	5613.7	5445.3	4816.5	4706.0	5113.0	4869.8	5545.0	6063.1	8023.4	5940.8
2694.3	2720.1	3182.2	3297.0	3082.1	3080.4	3402.8	3449.7	2269.3	3358.0	2917.9

2721.1	3484.6	12927.0
3712.2	3880.4	8528.0
2645.3	3045.6	8487.4
5140.2	6116.4	9636.9
3972.8	5179.9	8078.6
5819.8	6964.4	10226.0
1852.2	2834.7	13308.4
1396.6	2362.8	11181.4
2396.6	2933.4	11969.0
5164.8	5384.6	9995.5
6174.6	6188.5	12571.8
1965.3	3062.5	13538.6
2181.6	2483.0	3623.8
2703.0	3405.3	12432.6
1493.8	2127.2	4548.7
1964.7	2982.3	12709.0
1245.1	2140.9	8086.6
7324.4	8156.0	11472.3
2741.0	2788.2	4611.4
3558.6	3898.2	10189.0
5254.7	5082.3	5302.1
43.1	26.2	27.3
5394.1	6410.6	11236.9
7483.2	7033.7	7821.5
7256.8	8636.8	8116.3
3747.0	4810.9	8967.1
4073.7	6311.7	5115.9
4231.3	4458.5	5906.0
4453.0	5470.0	5899.0
190.6	334.1	791.7
3014.8	4877.9	8060.0
6441.3	8586.2	7650.3
4791.2	5278.3	5315.4
1200.3	1256.0	2211.7
2930.0	3462.3	2714.7
3853.8	4385.8	5626.5
1195.1	1719.0	1217.9
5420.5	5427.1	5568.5
2070.2	3783.9	2125.0
5147.4	7073.5	7019.6
2953.2	3201.1	6204.6

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FJ674400.1 gg_id:529137 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ671686.1 gg_id:515359 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
AJ458446.1 gg_id:111266 Allofustis seminis str. CCUG 45438 AJ4584
FJ825559.1 gg_id:559774 Microbial during start-up mesophilic biogas plant clone 46_BS5_10 FJ8255
FJ672294.1 gg_id:517005 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
FJ672544.1 gg_id:525845 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6725
FJ671690.1 gg_id:530430 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ672168.1 gg_id:514023 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
GQ080691.1 gg_id:466222 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
GQ085654.1 gg_id:407470 Topographical and Temporal Human Skin Microbiome skin palm clone nbw278f11c1 GQ085
FJ674468.1 gg_id:520088 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ672461.1 gg_id:509077 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
FJ675572.1 gg_id:516872 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ672927.1 gg_id:514848 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729
FJ893130.1 gg_id:545089 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8931
GQ079378.1 gg_id:445962 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1129f(GQ079
FJ672013.1 gg_id:509420 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
FJ671894.1 gg_id:523062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
FJ671904.1 gg_id:530966 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
FJ674889.1 gg_id:511294 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
DQ376550.1 gg_id:154459 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin DQ376
AY581816.1 gg_id:106773 feces clone 1D3 AY5818
AJ302648.1 gg_id:20210 Isobaculum melis CCUG 37660T AJ3026
FM875568.1 gg_id:365920 occupant source house dust skin surface swab clone SD01E05 FM875
FJ672609.1 gg_id:513204 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6726
AJ576362.1 gg_id:102730 hindgut homogenate Pachnoda ephippiata larva clone PeH49 AJ5763
GU166170.1 gg_id:561594 intestinal tract larvae (Musca domestica) direct cloning and sequencing genes whea GU166
Y11621.1 gg_id:15298 Enterococcus asini str. AS2 Y11621
GQ155330.1 gg_id:581895 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155347.1 gg_id:592273 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
NR_028748.1 gg_id:586815 Enterococcus avium str. E6844; CIP 103019 NR_02
AJ301825.1 gg_id:45325 Enterococcus avium str. LMG 10744 AJ3018
EF199997.1 gg_id:183702 Enterococcus casseliflavus str. ELS3 EF1999
X76177.1 gg_id:15285 Enterococcus sp str. LMG12316 X76177
AF367977.1 gg_id:37079 Enterococcus casseliflavus str. CCM 4869 AF3679
FJ538215.1 gg_id:536036 Enterococcus casseliflavus str. BPSr32 FJ5382
GQ337020.1 gg_id:544389 Enterococcus casseliflavus str. SS1229 GQ337
AJ420804.1 gg_id:42419 Enterococcus casseliflavus str. CECT969T AJ4208
AB547326.1 gg_id:515778 Enterococcus casseliflavus str. NCCP-53 AB5473
DQ395285.1 gg_id:156436 Enterococcus casseliflavus F00186 DQ395
FJ915804.1 gg_id:561364 Enterococcus casseliflavus str. IMAU10148; WH15-3-3 FJ9158

996.3	4582.4	5667.1	5773.7	5409.1	5167.0	5423.0	5670.6	5377.7	3207.4	5026.2
9755.9	6621.2	7728.0	6882.1	7090.3	7070.6	7926.3	7045.7	6871.6	9160.7	8664.4
61.2	106.0	125.2	112.7	56.3	87.5	51.0	200.8	59.4	98.7	101.2
2634.5	2870.8	3970.7	2649.8	2905.7	3208.0	2568.4	3260.8	2013.1	2917.5	2871.0
473.4	2423.1	3497.1	3236.3	3007.0	2781.1	3097.9	3603.4	2962.5	2848.7	3100.6
1485.2	4630.1	5351.2	5292.6	6324.8	5115.6	6922.5	5367.6	3973.2	3740.2	4336.0
1528.9	1446.3	1619.3	1428.6	1317.3	1322.7	1336.0	1514.9	1442.3	1418.5	1759.5
2269.6	3106.0	3762.7	4097.6	3156.8	3089.2	3944.1	3861.9	3051.6	5434.2	2920.3
2386.0	4031.2	4926.0	3791.9	4013.0	3909.0	3767.2	4683.6	3299.8	4794.6	3660.2
4100.6	5965.9	6841.4	6556.5	5806.1	7537.2	5962.9	6013.9	7810.0	12311.4	7376.1
1010.6	3185.7	3599.2	3702.2	2690.2	2880.3	3198.7	3315.1	3626.9	2742.3	3170.5
1607.4	2600.6	2999.5	3334.8	2967.8	2455.0	2962.6	3188.4	3071.1	3162.9	3390.2
2998.8	2596.8	2795.0	2788.8	2769.4	2693.7	3197.5	2963.7	4203.4	3122.3	2865.0
5974.6	3641.6	4146.6	4514.0	4413.3	3820.0	6427.4	4774.6	3844.1	2867.0	4557.4
6773.1	10310.2	7802.7	8385.3	8944.3	8315.4	10905.9	9849.7	11158.5	9500.3	11519.3
907.5	2487.6	2086.9	1804.6	1954.8	2175.1	2433.3	2913.6	1506.5	3874.8	1466.8
4136.3	4468.0	4730.3	5843.7	5905.2	4932.6	6921.8	6870.9	4047.9	4884.5	5310.0
5792.8	3892.3	4462.2	4727.3	4461.9	4806.5	5310.6	4674.8	4650.8	4657.7	5118.3
10561.7	5624.7	5576.7	5437.5	5571.2	6026.6	7039.3	5723.0	6554.2	6915.2	6041.8
8416.5	2245.0	2090.9	2061.1	2009.1	2080.6	1881.6	1859.9	2783.8	3753.0	2997.4
47.2	879.6	1055.8	646.0	997.1	837.6	1241.0	1720.7	266.9	1364.9	814.7
390.3	719.3	886.0	1018.9	644.8	878.7	979.0	616.2	787.7	385.7	1282.6
2292.5	4376.6	7335.5	4906.2	4168.8	5551.9	4303.7	6985.1	3389.7	7526.3	6434.0
108.3	2475.1	3354.5	2561.4	2007.1	2665.2	3408.0	3029.4	1649.3	2521.5	2534.8
556.8	940.3	1033.1	1155.9	1193.2	1245.9	926.1	1508.8	862.4	2904.5	779.0
38.6	1707.5	1701.0	636.0	2907.7	2080.2	2222.5	1862.7	409.5	2943.4	707.1
506.5	4170.7	3939.7	3621.3	4060.2	3570.5	3604.2	4416.4	3120.1	5242.9	3343.9
216.1	4693.9	6555.4	3484.0	3763.9	4703.1	3380.3	5946.2	2561.0	6790.6	4432.7
329.7	3356.8	3713.8	2714.1	4492.0	4225.9	3625.5	4670.1	2145.4	3582.0	3290.0
61.3	2058.7	2417.2	2022.1	2429.6	3136.5	1623.5	3194.5	1518.2	3196.2	1728.9
292.3	3664.3	4494.3	2691.0	5007.3	4725.5	3621.4	5004.3	2301.7	3570.8	3504.7
53.0	2966.6	3243.8	2006.1	3866.4	4145.3	2377.3	4320.4	1695.2	4201.6	2447.4
8495.3	7293.6	8012.8	7583.7	8172.2	7254.2	8465.1	7826.1	7443.1	7537.1	8341.5
245.5	1865.7	2316.3	1027.3	1405.2	1646.7	1027.9	1810.7	1160.8	1414.6	1859.9
62.1	872.9	1131.4	888.4	892.6	2102.0	527.0	1449.6	361.1	3412.2	480.3
4452.6	5770.5	6405.2	5135.1	5316.7	6361.6	4410.4	6842.7	5682.8	10419.3	5835.2
54.1	1029.3	1317.4	890.3	1067.1	2382.7	579.1	1452.0	453.6	3964.4	551.9
3356.2	6124.3	6382.8	5992.0	7127.3	6648.1	6505.0	6343.1	6286.1	8760.3	6178.9
51.8	706.9	1176.3	685.9	1009.9	2269.6	353.7	1282.2	269.3	2442.4	391.8
88.0	1510.2	1925.9	1463.1	1344.5	2853.4	1017.3	2100.5	647.9	4129.2	1164.2
53.5	1052.4	1361.7	946.6	1059.1	2586.7	581.7	1509.2	460.3	3871.2	571.9

5340.4	6062.9	6198.4
6947.3	8603.0	8163.5
116.6	177.3	111.1
2880.1	4337.0	5141.3
3322.8	3866.9	4397.1
5302.5	6512.1	6840.1
1398.8	2421.7	1587.9
3494.9	4233.1	3529.4
4265.3	4956.8	4905.3
7345.4	7089.4	5825.5
3429.6	3417.2	4036.1
2846.0	4338.3	3936.5
3295.9	4013.1	3639.2
3465.5	4482.9	6871.3
7974.6	7794.9	8630.8
2268.0	2672.8	3063.0
5468.2	5486.4	6489.1
4379.5	5815.0	6981.0
5679.3	6525.9	7840.7
1990.8	3582.2	3039.7
1034.2	1704.2	3083.1
718.8	825.5	1268.2
5718.0	5553.5	7815.6
2172.3	2966.0	5589.9
1452.9	2048.6	2816.5
2623.0	3334.6	10039.1
4082.1	5218.2	7159.7
4458.1	4533.7	6586.3
5199.3	3804.6	6160.8
3895.0	2774.8	4070.4
5728.9	4142.2	6050.2
5274.9	3478.3	5313.5
7096.3	8428.7	11379.7
1529.6	1399.3	1746.9
3051.5	1251.8	2250.5
7053.2	6247.4	9540.3
3308.7	1297.6	2539.6
6703.8	6792.3	8623.1
3433.8	1309.5	2387.0
3923.8	1758.2	3246.1
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GQ995669.1 gg_id:584241 Enterococcus casseliflavus str. C1 GQ995
EU075075.1 gg_id:241365 Enterococcus gallinarum str. 22-19BAM EU075
U30931.1 gg_id:15301 Enterococcus saccharolyticus U3093
DQ683079.1 gg_id:160884 Vibrio fluvialis str. CIFAMVIFL01 DQ683
EU075043.1 gg_id:239422 Enterococcus casseliflavus str. thirtyfourmpalpha EU075
EU459407.1 gg_id:294670 cheetah feces clone CE3_aai07e07 EU459
Y18355.1 gg_id:15280 Enterococcus cecorum str. NCDO 2674T Y18355
DQ057437.1 gg_id:132661 str. ii1209 DQ057
AJ301828.1 gg_id:17976 Enterococcus columbae str. LMG 11740 AJ3018
Y18358.1 gg_id:15330 Enterococcus dispar str. NCIMB 13000T Y18358
EF197994.1 gg_id:193264 Enterococcus carnosus str. 933 EF1979
FJ749767.1 gg_id:539955 Enterococcus durans str. IMAU60041; XZ12301 FJ7497
EU717964.1 gg_id:355906 Enterococcus durans str. Hx05 EU717
GU177630.1 gg_id:556032 Enterococcus durans str. 6-2 GU177
FJ607264.1 gg_id:548980 Enterococcus durans str. KLDS6.0618 FJ6072
FJ917730.1 gg_id:573141 Enterococcus durans str. IMAU60177; ZLG3-3 FJ9177
FJ749805.1 gg_id:537200 Enterococcus durans str. IMAU60084; XZ22301 FJ7498
FJ378680.1 gg_id:358790 Enterococcus faecium str. HN-N25 FJ3786
AJ420801.1 gg_id:47779 Enterococcus durans str. CECT411T AJ4208
FJ917736.1 gg_id:555337 Enterococcus durans str. IMAU60185; ZLG6-3 FJ9177
FJ917735.1 gg_id:561625 Enterococcus durans str. IMAU60184; ZLG6-2 FJ9177
FJ555518.1 gg_id:573791 Enterococcus pernyi str. CS1 FJ5555
DQ239692.1 gg_id:144178 Enterococcus durans str. D1 DQ239
AF070224.1 gg_id:15273 Enterococcus faecalis str. JH2-2 AF0702
GU299085.1 gg_id:534960 Enterococcus faecalis str. 3-12 GU299
DQ295035.1 gg_id:144018 Lactobacillus plantarum str. PFK2 DQ295
GQ155859.1 gg_id:510957 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ603646.1 gg_id:533585 Enterococcus faecalis str. XJ-1 FJ6036
AB092693.1 gg_id:58583 Enterococcus faecalis str. K-4 AB092
DQ983196.1 gg_id:182752 Enterococcus faecalis str. ABPL 007 DQ983
FN377815.1 gg_id:574542 Enterococcus faecalis str. S5 FN3778
DQ340074.1 gg_id:145783 Enterococcus faecalis str. KLDS 6.0319 DQ340
DQ340071.1 gg_id:145866 Enterococcus faecalis str. KLDS 6.0317 DQ340
FJ378704.1 gg_id:358683 Enterococcus faecalis str. HN-S7 FJ3787
FJ378698.1 gg_id:362655 Enterococcus faecalis str. HN-S1 FJ3786
GQ155862.1 gg_id:542841 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ378685.1 gg_id:359449 Enterococcus faecalis str. HN-N30 FJ3786
AJ276460.1 gg_id:50297 Enterococcus faecalis str. P7812 AJ2764
AY942558.1 gg_id:113485 Enterococcus faecalis str. ChDC YE2 AY9425
AB362599.1 gg_id:250917 Enterococcus faecalis str. NRIC 0110 AB3625

9798.1	10603.0	9862.8	8388.3	9336.3	9992.9	8885.2	13381.9	15638.1	15259.0	10345.0
91.5	1704.7	2082.6	1555.3	1475.1	3090.3	949.4	1621.2	1146.5	4045.8	1567.4
1898.5	7098.1	6243.5	5158.3	5255.5	6631.6	4397.8	5503.4	9651.2	9584.9	5772.3
6546.3	4560.9	5600.8	3975.8	5670.8	5530.3	5119.9	4878.0	6663.5	8032.1	4149.2
66.2	1727.7	2847.7	1549.8	1674.5	3354.1	1200.0	2600.5	982.6	4470.3	1530.6
54.7	837.8	1216.2	979.8	805.8	2429.5	526.0	1125.7	540.4	2514.9	532.1
554.6	2226.0	2972.8	2832.7	3692.4	2710.1	3064.9	3458.3	1892.1	2315.8	2609.2
50.0	869.7	1013.3	1290.6	1106.7	1209.1	961.5	1082.1	453.2	1524.8	1010.2
52.4	669.1	1021.5	716.1	865.4	995.6	484.1	957.5	427.1	1252.4	694.6
47.9	948.6	1533.4	510.5	1015.2	1254.1	563.4	1182.4	438.9	1747.2	411.3
72.7	2779.7	3442.9	2477.0	3146.3	3103.7	2777.3	3074.7	1558.8	3220.6	1785.0
302.2	2710.4	3448.9	2509.2	2716.5	4052.9	1977.7	3838.6	1898.2	5236.6	3359.0
170.3	3361.0	5075.3	2721.8	4103.5	4587.8	3234.6	4500.5	2924.6	6335.2	3038.7
147.4	3333.6	4627.1	2935.7	3291.0	4132.7	3026.8	4530.4	2830.2	6204.5	3599.3
991.7	5097.8	5950.1	5457.7	5750.6	5920.5	5738.9	5889.2	5412.7	8165.5	6056.1
83.3	2887.1	4429.2	2591.1	3054.9	4269.9	2642.0	4345.1	1997.9	6740.1	3243.7
1222.8	5642.2	6332.7	6262.0	5953.5	6077.9	6650.2	5699.6	6038.6	8386.7	7300.7
83.8	2960.8	4501.6	2642.6	3287.5	4302.9	2532.8	4407.4	2022.8	6676.1	3292.2
138.4	3690.0	5226.0	3036.4	3995.4	4690.3	3262.9	4862.5	2972.8	6743.0	3787.2
1159.5	3917.2	5009.1	5717.7	4113.6	4552.0	4765.8	4796.5	3830.7	4978.2	4823.7
79.7	2611.9	3570.3	2477.9	3029.6	3964.0	2421.6	3629.8	1828.2	5698.2	2878.2
169.2	3476.2	4995.7	3091.0	3771.7	4597.3	3239.4	4929.6	3012.5	7402.9	3771.6
1012.9	3164.5	4610.7	4211.2	3117.6	3661.8	2621.0	4678.9	2651.6	2297.4	3701.5
165.0	3105.9	4675.4	2366.3	3715.9	4439.1	2838.9	4764.0	2542.7	7290.9	3188.1
321.5	1837.9	2472.9	1889.6	2200.2	2553.3	2628.2	2331.0	1142.1	2634.5	1903.7
283.2	1910.1	2701.4	1719.9	2821.1	2634.1	2318.3	2688.5	1381.9	3656.0	1731.3
318.9	1729.9	2276.5	1858.1	2271.6	2418.7	2368.8	2217.3	1152.3	2577.8	1883.3
376.0	2858.0	3445.9	2619.1	3701.8	3671.0	2921.9	3317.7	1400.9	4371.7	2497.5
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8455.3	4514.3	5257.8	4089.0	4844.8	5569.7	4966.2	5038.0	5421.0	10086.6	1338.2
302.0	1829.8	2468.8	2016.3	2194.5	2532.6	2438.4	2326.5	1217.5	2618.4	1896.0
1690.4	3753.0	4312.7	3906.7	4036.0	3804.1	5391.5	4112.1	5254.4	5795.8	4383.6
148.6	381.3	465.4	444.3	398.0	572.7	540.3	378.0	301.4	384.1	459.5
285.6	2018.0	2897.9	1761.1	2676.4	2760.3	2577.5	2802.1	1354.6	3712.7	1761.2
126.7	4747.2	4656.3	2631.2	3272.0	5297.3	3130.9	4876.2	2866.8	6695.0	3111.7
16160.6	6869.0	6393.4	6615.5	6685.2	7572.2	6402.3	6369.2	7659.2	6707.4	8368.0
30902.1	11493.3	10699.1	11728.5	12317.8	11362.3	14124.4	10474.0	12744.8	15601.9	15084.1
320.3	1844.6	2475.8	2021.1	2200.7	2399.8	2631.2	2335.0	1219.8	2638.9	1900.0
322.3	1845.8	2480.3	2022.6	2199.2	2557.8	2447.0	2184.2	1221.8	2641.7	1903.3
161.1	1284.0	1356.5	682.5	1380.4	2422.9	898.2	1678.0	608.8	3953.2	737.9
283.1	1970.6	2676.9	1729.6	2491.8	2688.7	2372.1	2580.4	1342.7	3687.9	1716.6

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4192.8	1912.7	3149.1
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5979.5	6064.1	6170.6
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3188.6	1275.7	1677.3
3145.1	3880.7	3551.9
1586.8	1612.6	2376.6
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6430.6	5437.6	6260.4
4466.5	3613.6	4837.8
6467.3	5598.1	6068.1
4638.0	3734.1	5497.1
5420.8	4085.0	6485.5
3645.7	4809.4	5466.7
4481.6	3243.9	4941.2
4886.5	4262.8	5520.0
4087.2	4247.1	6583.8
4899.7	4154.6	5902.4
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3126.7	2522.0	3370.7
2716.3	2061.3	2909.8
4411.0	3661.5	6913.0
1590.5	2292.0	1334.5
5954.5	5579.5	7476.5
2993.9	2332.1	3068.1
4027.2	4981.3	5479.1
618.2	722.8	521.9
3432.5	2831.2	3533.1
4813.0	4440.8	6969.0
6907.1	6871.1	7299.9
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3053.5	2370.1	3070.7
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GQ156001.1 gg_id:591089 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
FJ378696.1 gg_id:364518 Enterococcus faecalis str. HN-N41 FJ3786
FJ378703.1 gg_id:367986 Enterococcus faecalis str. HN-S6 FJ3787
GQ156058.1 gg_id:585011 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
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FJ607298.1 gg_id:539417 Enterococcus faecalis str. KLDS6.0610 FJ6072
GQ155908.1 gg_id:552462 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ337019.1 gg_id:586597 Enterococcus canis str. SS1724 GQ337
Y18160.1 gg_id:15321 Enterococcus gallinarum str. NCFB 2314 Y18160
EF025905.1 gg_id:253248 Enterococcus gallinarum str. B2 EF0259
AJ420805.1 gg_id:19924 Enterococcus gallinarum str. CECT970T AJ4208
EU477410.1 gg_id:563672 Enterococcus saccharolyticus str. SD1 EU4774
AF286831.1 gg_id:70378 Enterococcus moraviensis str. CCM 4856T AF2868
GQ337032.1 gg_id:586775 Enterococcus moraviensis str. SS1689 GQ337
AF286832.1 gg_id:28186 Enterococcus haemoperoxidus str. CCM 4851T AF2868
GQ337028.1 gg_id:549794 Enterococcus hermanniensis str. SS1760 GQ337
FJ851687.1 gg_id:592320 Enterococcus faecium str. HS3 FJ8516
AB186307.1 gg_id:136967 Enterococcus hirae str. DST 2010 AB186

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32.0	1557.8	2036.1	1567.2	2128.9	2532.7	1367.7	2155.5	1349.4	5056.2	1124.2
512.7	2482.7	3259.7	2469.1	2992.7	2934.3	3402.4	2384.3	1851.6	2793.5	2766.6
9589.3	4721.7	5137.4	4414.1	4278.3	4727.7	3826.2	5181.9	4197.3	5998.3	5229.2
18701.0	5982.0	5541.4	5641.5	5840.6	6096.8	6268.9	5569.8	6116.7	8248.5	6690.7
48.0	1861.8	1968.3	1744.2	1842.0	2981.3	1654.4	1934.4	1153.5	1980.4	1800.9
3568.6	5546.8	6726.5	6106.7	5747.3	7325.1	6193.8	6117.1	6965.6	8445.1	8206.2
30480.5	10242.4	9232.4	10297.9	9115.2	10336.6	10306.0	8139.9	14656.5	11772.0	13514.5
3412.0	2555.4	3081.8	2654.2	2569.1	4444.2	2208.4	2731.9	2659.3	4846.9	3243.9
318.8	1790.4	2278.5	1858.6	2045.3	2477.0	2419.1	2140.7	1131.0	2609.7	1859.0
28802.9	9300.1	8812.4	9598.3	9641.6	8974.1	10262.8	8978.2	12799.3	10579.3	12755.2
40.1	841.2	1725.0	525.6	1138.0	1989.0	630.9	1628.7	437.1	3067.7	573.4
198.2	1100.5	2092.2	443.5	1162.6	1333.7	607.2	1934.0	678.4	2267.6	911.5
13513.8	5538.6	5901.0	5218.3	5210.4	5975.4	6044.5	5318.5	6351.9	8865.1	6843.3
49.8	656.3	1021.6	375.0	945.7	1264.2	542.6	1198.4	312.7	1325.4	375.0
314.6	1771.3	2424.3	1813.5	1911.7	2799.1	1628.8	2314.5	1760.0	3176.2	1350.5
73.4	550.6	529.1	501.3	523.6	843.4	331.8	936.2	76.0	1180.3	330.4
22254.1	6043.9	5867.8	6110.4	6209.5	5567.6	6491.0	5086.9	9628.0	6614.7	9015.5
20443.5	6594.4	5557.3	6522.6	5121.4	6465.1	6147.6	5832.8	9737.7	6484.4	9550.4
2681.3	5579.1	5516.4	5739.0	5752.5	6014.1	4342.5	5510.6	5009.9	6762.8	4616.8
59.4	1194.6	1808.5	917.0	1314.7	2007.6	982.6	1737.0	821.6	3419.6	909.7
17935.1	4845.4	4688.6	5254.9	4489.8	5649.9	5316.3	4988.6	6498.2	5301.1	5460.0
77.9	1058.8	1398.9	910.2	1348.3	1478.2	1165.7	1556.2	782.3	1314.0	823.8
106.3	1186.0	1463.4	1211.5	1170.6	1517.5	938.0	1870.7	384.5	2590.0	807.2
9570.1	4835.7	4597.7	4804.5	5104.2	6314.3	4892.5	4745.3	5286.4	8178.1	4926.0
17273.2	6209.7	5818.0	5992.1	5831.6	7203.7	5753.6	5782.4	7981.4	8951.1	7785.0
426.7	2868.0	3416.1	2580.3	3008.4	3765.4	3077.6	3402.7	1416.5	4398.8	2319.0
78.8	1066.7	1405.8	968.5	1347.4	1483.0	1098.5	1467.0	841.7	1321.2	823.3
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71.3	610.2	847.6	483.8	514.5	1091.0	397.3	893.7	144.0	1541.3	389.0
41.0	1649.8	1089.0	976.6	1973.6	1760.3	1104.1	2168.5	620.6	2025.4	603.1
58.6	1483.0	2063.7	1320.2	1657.7	3061.1	1192.4	1916.3	936.7	4162.1	934.5
73.5	1443.4	1961.3	1339.3	1284.0	2806.6	1311.1	1709.9	933.2	3775.3	1198.6
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37.5	683.5	991.5	465.3	1002.3	1446.1	395.1	1391.1	323.3	2247.6	530.9
93.0	654.4	1003.8	710.9	1025.2	1496.2	492.3	1232.0	465.9	2039.5	573.8
1343.7	2735.2	3411.0	3110.1	4193.5	3410.1	2979.2	3817.1	2217.2	3657.5	3784.4
188.0	3745.5	4750.0	4194.2	3777.2	4985.7	2949.4	5218.3	2526.9	7473.4	4405.1
71.8	2410.6	2904.8	2078.3	2359.1	2705.9	1988.5	3299.0	1513.4	3570.1	2815.4
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3452.4	2927.4	3989.2
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6587.0	6732.5	6425.7
2910.2	2096.1	2407.4
6406.7	6249.6	6839.8
9021.7	10223.0	9505.4
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9231.4	10112.9	9552.6
2500.6	1733.6	2946.5
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5958.0	6897.8	6820.7
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4557.3	8004.3	5329.1
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5575.5	5889.9	6625.3
2420.8	1682.1	2638.8
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5526.5	6401.9	5461.4
6303.2	6623.5	5696.5
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1824.7	1612.3	1970.0
3693.8	2893.0	4466.5
1693.2	1051.6	1873.4
2818.4	2530.8	5433.2
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9590.2	8490.3	11178.0
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1758.5	1709.1	1991.8
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4033.6	4070.9	4742.3
5018.2	4213.9	6392.1
2789.5	2422.3	3737.9
5788.7	5356.0	7262.8

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Y18354.1 gg_id:15327 Enterococcus hirae str. NCFB 1258T Y18354
AJ301837.1 gg_id:40545 Enterococcus pseudoavium str. LMG 11426 AJ3018
EF591816.1 gg_id:232955 Enterococcus mundtii str. CWBI-B1431\(A2-17) EF5918
GU213907.1 gg_id:564647 Enterococcus hirae str. -12 GU213
GU255468.1 gg_id:583493 Enterococcus hirae str. ST3 GU255
AJ301834.1 gg_id:37447 Enterococcus hirae str. LMG 6399 AJ3018
AM050562.1 gg_id:138572 Enterococcus inusitatus str. E2ET29 AM050
AB507170.1 gg_id:393887 Enterococcus faecalis str. JCM 20313 AB507
EU717955.1 gg_id:340166 Enterococcus faecium str. wh05 EU7179
GQ267520.1 gg_id:594212 Enterococcus faecium str. Linex GQ267
AB018210.1 gg_id:25976 Enterococcus faecium str. E 26 AB0182
EU857635.1 gg_id:367979 Enterococcus faecium EU8576
EF533988.1 gg_id:222834 Enterococcus faecium str. IDCC 2102 EF5339
AY692451.1 gg_id:100464 Enterococcus faecium str. SL2 AY6924
EU857636.1 gg_id:366313 Enterococcus lactis EU8576
EU717965.1 gg_id:327400 Enterococcus faecalis str. Zy05 EU7179
GQ493354.1 gg_id:590982 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU337116.1 gg_id:513300 Enterococcus lactis str. SK12 EU3371
NZ_ACHL01000045.1 gg_id:470321 Enterococcus faecium str. TX1330 NZ_AC
FJ743438.1 gg_id:553522 Enterococcus faecium str. VIT EF FJ7434
DQ403193.2 gg_id:153252 Enterococcus faecium DQ403
FJ982664.1 gg_id:429448 Enterococcus faecium str. JBE0015 FJ9826
EU887827.1 gg_id:341145 Enterococcus faecalis str. H13 EU8878
GQ337034.1 gg_id:533020 Enterococcus phoeniculicola str. SS1721 GQ337
AJ301839.1 gg_id:43998 Enterococcus saccharolyticus str. LMG 11427 AJ3018
Y18341.1 gg_id:15283 Enterococcus sulfureus str. NCIMB 13117T Y18341
FJ378684.1 gg_id:359101 Enterococcus faecium str. HN-N29 FJ3786
AF070223.1 gg_id:15287 Enterococcus faecium str. GUCR AF0702
Y18294.1 gg_id:15290 Enterococcus faecium str. NCFB 942T Y18294
AJ459875.1 gg_id:62639 larval intestine clone E AJ4598
AJ301838.1 gg_id:20443 Enterococcus raffinosus str. LMG 12999 AJ3018
GQ155811.1 gg_id:566795 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU560859.1 gg_id:557059 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
AJ301827.1 gg_id:37798 Enterococcus cecorum str. LMG 12902 AJ3018
DQ239693.1 gg_id:142719 Enterococcus durans str. D2 DQ239
AJ877015.1 gg_id:139088 Enterococcus aquimarinus str. LMG 16607 AJ8770
FJ378700.1 gg_id:358320 Enterococcus avium str. HN-S3 FJ3787
FJ870986.1 gg_id:555272 Enterococcus faecium str. EF1 FJ8709
GQ156077.1 gg_id:578964 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
FN600541.1 gg_id:554755 Enterococcus raffinosus Raj FN600

601.9	3960.1	5117.6	4042.8	3824.5	5083.2	3586.7	5421.1	3470.7	6673.5	5255.9
103.1	3287.8	4632.1	2568.4	2935.1	3878.3	2543.2	4073.8	2151.5	5434.9	3272.9
312.5	4921.7	7152.1	5707.3	5590.6	6023.9	4992.0	6293.9	3686.0	7042.3	5191.0
345.3	2083.2	2688.6	2021.8	2458.0	2586.1	1995.4	2284.2	1704.0	2572.3	2121.5
3174.3	4759.2	5142.9	3440.5	4881.5	5594.8	3285.0	5746.1	3798.7	7625.3	4080.9
13332.9	7474.0	7114.0	7204.0	6223.6	6552.3	6360.4	6189.4	8414.3	9604.3	9926.8
6099.2	6662.1	6937.2	5872.2	5699.7	6568.2	5945.9	6327.8	6630.5	9397.8	7475.2
38.4	2047.7	2161.0	1518.9	2907.9	2352.2	1553.1	3699.4	1217.2	2850.1	2316.9
376.3	4537.9	5697.6	2925.9	4188.8	5066.2	3014.4	5276.5	2994.7	8790.8	4380.5
100.0	1969.8	3037.8	1397.9	2528.0	3369.6	1368.1	3335.1	1073.6	5710.8	1802.5
668.2	6262.3	5912.3	4421.9	5910.8	5780.3	5381.1	6461.0	5549.8	6877.3	4725.4
118.4	1167.8	2245.5	730.5	1223.4	1811.4	691.0	1707.2	772.0	3334.3	924.7
366.8	4107.1	5216.8	2484.8	3841.7	4594.8	2774.7	4275.5	2766.4	7306.6	3462.7
386.9	3230.8	4240.3	2560.8	3805.8	4093.0	2858.0	4447.1	2523.3	6373.7	3210.6
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13320.2	6225.2	5047.1	5329.6	5162.3	4754.0	5249.1	4916.6	7591.9	5815.0	6391.4
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372.2	5062.9	4896.5	4067.8	5562.6	4833.7	5175.1	5243.4	4226.6	7399.2	2971.6
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46.8	1343.6	2218.1	707.8	1601.6	2194.5	1123.7	1955.0	575.7	2482.3	990.6
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87.3	2084.9	2728.6	2303.2	2380.3	2491.1	2506.7	2437.2	1528.5	3315.3	1903.3
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4259.3	3117.6	5034.8
4117.7	2882.0	4803.8
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FJ481129.1 gg_id:552330 Enterococcus faecalis str. RSCQ0
AJ420800.1 gg_id:50018 Enterococcus faecium str. CECT410T
AY953149.1 gg_id:114861 anaerobic swine lagoon clone B-1A
Y18274.1 gg_id:15332 Enterococcus avium str. NCFB 2369T
FJ378672.1 gg_id:359990 Enterococcus faecium str. HN-N17
AY971749.1 gg_id:115294 Enterococcus faecium
EU081012.1 gg_id:238193 Enterococcus devriesei str. BMG 128
EU074827.1 gg_id:256245 Enterococcus mundtii str. MC6
AM157434.1 gg_id:141429 Enterococcus faecium mother C4
FJ378686.1 gg_id:357324 Enterococcus faecium str. HN-N31
AB012213.1 gg_id:15286 Enterococcus faecium str. JCM 5804
GQ337035.1 gg_id:584752 Enterococcus raffinosus str. SS1278
FJ378682.1 gg_id:367316 Enterococcus faecium str. HN-N27
AY057055.1 gg_id:49707 Enterococcus faecium str. ID9201
FJ749344.1 gg_id:539586 Enterococcus durans str. IMAU40069; QH27-4
AJ301826.1 gg_id:44126 Enterococcus casseliflavus str. LMG 10745
EU459193.1 gg_id:294816 hedgehog feces clone HH_aai33f05
AF335596.2 gg_id:74276 Enterococcus villorum str. ATCC 700913
AY098492.1 gg_id:72595 Enterococcus sp. AK61
FJ378693.1 gg_id:366369 Enterococcus faecium str. HN-N38
EU714899.1 gg_id:322682 Enterococcus mundtii str. SRDIPC3
FJ378706.1 gg_id:361210 Enterococcus faecium str. HN-F21
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AY653231.1 gg_id:111218 Enterococcus faecium str. MLG856-2
FJ861091.1 gg_id:554398 Enterococcus faecium str. KLDS 6.0640
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AF326472.1 gg_id:57509 Enterococcus ratti
FJ915701.1 gg_id:569577 Enterococcus faecium str. IMAU40164; QH25-2
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FJ378689.1 gg_id:363778 Enterococcus faecium str. HN-N34
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EF428252.2 gg_id:221584 Enterococcus mundtii str. HDYM-33
EU878169.1 gg_id:346951 Enterococcus faecium str. SH 528
GQ337037.1 gg_id:592016 Enterococcus termitis str. SS1793
DQ223885.1 gg_id:169662 Enterococcus raffinosus str. P6
GU384204.1 gg_id:516700 Enterococcus sp. str. CJ-1
EU428012.1 gg_id:263573 Enterococcus faecium str. SM21
FJ378676.1 gg_id:361678 Enterococcus faecium str. HN-N21

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AM157
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FJ7493
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GU084
EF4282
EU8781
GQ337
DQ223
GU384
EU4280
FJ3786

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42.5	631.3	1254.4	535.0	671.4	1508.3	608.0	1096.1	348.3	2557.4	455.4
97.9	2400.7	2115.8	1601.7	2076.6	2795.7	1410.3	3377.1	2209.2	2730.5	2079.0
379.9	4281.9	4416.0	3336.2	5257.3	4899.8	3871.9	5655.7	3129.1	4734.0	4293.9
52.6	2860.0	4232.1	1738.5	3246.9	4045.4	1947.8	4035.3	1276.1	6102.1	2329.9
81.4	1522.4	1693.5	1267.9	1288.8	1834.3	1054.6	2383.6	626.6	2972.3	1820.1
53.6	1233.7	1458.2	1136.4	1373.7	2408.8	754.4	2211.6	786.1	2534.7	1140.4
2807.8	1871.3	2141.0	2536.0	1876.5	2203.0	2336.3	1892.6	1791.1	1779.3	1800.9
83.8	1590.8	2569.0	866.8	1975.9	2396.1	1274.2	2344.0	737.6	2652.6	1304.9
40.9	1119.5	2012.9	754.0	1416.2	2600.4	858.7	1834.7	541.1	3576.7	647.0
1285.5	1928.7	1679.5	1625.6	2383.7	1891.4	2192.7	1533.0	1434.0	1294.7	1384.6
54.1	1649.2	2392.4	1359.4	1723.5	3262.4	1182.3	3080.8	1100.4	4238.3	1693.6
100.9	1193.2	2511.3	1222.9	1599.5	2405.1	2100.8	2149.7	1025.2	2255.3	1218.3
53.1	1139.9	1296.2	625.2	1237.0	1346.9	971.5	1346.0	453.2	1842.6	568.9
992.5	5912.2	6865.0	5920.0	6619.6	6254.3	6730.1	5929.4	6665.0	9024.2	6122.0
90.4	1693.4	2080.1	1563.3	1469.2	3067.8	946.3	1620.5	1146.2	4081.5	1566.8
51.3	1667.4	1914.5	1282.2	1759.2	2628.5	839.7	2821.4	1017.7	3028.1	1437.9
832.2	3370.7	3624.6	2586.0	2600.1	3813.0	2371.7	3469.8	2476.2	5200.2	2692.5
87.0	1459.0	1794.0	1334.9	1183.7	2499.0	871.6	2368.4	634.1	3874.3	1674.8
48.4	588.0	819.4	391.8	697.9	1036.8	472.1	998.6	295.2	1412.8	376.9
4519.7	3361.5	4302.4	2883.2	3582.8	3731.8	3060.6	3869.9	3310.1	3978.1	3592.6
10936.6	3631.8	4514.8	3083.2	4281.8	4123.0	3450.6	3916.0	4015.1	6879.0	4177.4
400.9	4242.9	5681.0	3010.4	3561.1	4980.9	2834.7	5721.6	2476.9	7897.5	4937.7
76.5	1611.6	2599.3	890.2	1984.6	2478.6	1280.3	2349.6	746.5	2905.9	1225.7
41.9	1234.7	2224.1	693.6	1490.2	2538.1	859.8	2184.9	576.8	2934.4	887.1
37.5	1071.3	2068.3	503.2	916.6	1595.6	383.1	1541.5	548.6	2563.9	866.2
167.0	1531.4	2721.8	2588.9	1402.3	3006.7	912.8	3327.2	1267.0	6015.4	1914.5
2459.5	5177.1	4802.4	2828.7	3835.9	5228.0	3288.5	4570.9	4824.3	8869.2	3300.8
67.1	2447.9	2753.8	1746.4	2915.4	3443.8	1419.9	3847.4	1179.9	5013.2	2299.6
40.0	1731.9	2947.9	848.5	2243.3	2670.5	1295.9	2074.5	726.2	3668.2	1130.2
87.2	1855.0	2117.6	1045.9	1728.8	2023.3	1255.4	2345.9	744.7	3384.9	1189.3
53.5	587.4	685.6	391.0	779.7	982.9	552.6	602.1	196.7	1242.0	218.5
49.8	1042.4	1428.2	858.8	1317.8	1531.9	934.1	1237.5	789.1	1819.6	742.5
600.4	3294.6	5032.3	3326.1	4001.3	3810.2	2874.6	3912.2	3015.7	4221.2	3949.2
83.7	1135.0	1397.2	886.7	983.5	1796.7	830.0	1401.4	446.2	1803.8	818.0
93.6	1362.5	2409.2	1078.4	1609.3	2480.8	1166.5	3010.7	879.7	3277.7	1520.8
58.4	2322.4	2661.8	1871.6	2474.9	3040.3	1453.5	3500.2	1512.2	3523.0	2151.7
203.1	1965.9	3280.3	1587.2	1379.6	3205.4	1003.0	3191.7	1018.3	3475.2	2299.6
73.6	1827.5	2341.5	1159.4	1790.4	2165.5	1453.6	2398.1	733.4	3313.8	1345.0
3197.5	2821.9	2502.6	1690.4	2661.9	3019.7	2629.6	3081.2	3491.5	4576.7	1884.7

3063.7	2287.3	3288.7
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1875.1	1207.3	1671.5
2809.9	3222.4	4661.9
5955.7	4617.0	6631.9
4873.5	3348.5	6442.5
2071.5	1445.1	2453.8
3692.0	1879.1	2383.3
2816.4	2853.2	1944.3
3170.0	2286.4	4618.2
3462.0	2133.6	3309.8
2205.4	2087.5	2804.1
4497.1	2501.5	3627.3
2503.5	2520.7	3408.3
1879.1	1257.7	2572.8
7174.2	6193.3	7462.5
4197.0	1924.9	3168.5
3976.0	2361.1	3320.5
4530.9	3424.0	4478.6
3115.7	1582.5	2649.8
1446.3	851.9	1947.1
3329.1	4599.6	5833.0
4561.5	6049.6	6108.8
5285.0	4001.9	6302.6
3311.6	2295.5	4644.5
3595.7	2153.1	4009.5
1810.6	2109.4	3073.3
3464.2	3028.0	3596.6
5327.5	6212.6	5448.1
4177.2	3102.3	6025.7
3500.7	2332.3	4613.8
2622.5	1935.3	3978.7
1474.4	801.7	1161.2
1871.4	1550.7	1873.6
3659.6	4592.0	5606.8
2447.0	1382.6	2303.3
2946.8	2772.4	3999.0
4253.9	3079.1	4370.1
3216.9	2773.0	3171.0
2913.2	1949.3	3750.4
3140.4	4449.9	4231.8

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FJ674559.1 gg_id:516797 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6745
FJ751788.1 gg_id:553011 Enterococcus hirae str. DSPV 346T FJ7517
AB066266.1 gg_id:62895 Enterococcus mundtii str. NFRI 7393 AB066
EU888524.1 gg_id:313899 Enterococcus faecium str. ES_MS1c EU888
FJ378683.1 gg_id:366505 Enterococcus faecium str. HN-N28 FJ3786
FJ917737.1 gg_id:556893 Enterococcus durans str. IMAU60186; ZLG7-1 FJ9177
GQ155710.1 gg_id:581919 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155106.1 gg_id:572042 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ378691.1 gg_id:359087 Enterococcus faecium str. HN-N36 FJ3786
GU139738.1 gg_id:590537 Enterococcus durans str. 2-4 GU139
AM039967.1 gg_id:146606 Enterococcus silesiacus str. LMG 23084 = R-23708 AM039
EU418442.1 gg_id:558319 Enterococcus faecium str. 133 EU418
FJ378678.1 gg_id:362310 Enterococcus faecium str. HN-N23 FJ3786
FJ378669.1 gg_id:366456 Enterococcus faecium str. HN-N14 FJ3786
AF395325.1 gg_id:37654 isopod gut clone RKPsBA AF3953
AJ276352.1 gg_id:30497 Enterococcus rottae str. CCM4629 AJ2763
FJ378681.1 gg_id:362734 Enterococcus faecium str. HN-N26 FJ3786
NZ_ACIY01000209.1 gg_id:470292 Enterococcus faecium str. DO NZ_AC
GQ337018.1 gg_id:582529 Enterococcus canintestini str. SS1787 GQ337
AB470234.1 gg_id:367959 Enterococcus pseudoavium str. h50 AB470
DQ985159.1 gg_id:223992 Enterococcus faecium str. R0026 DQ985
AJ301830.1 gg_id:39621 Enterococcus faecium str. LMG 11423 AJ3018
EU003448.1 gg_id:241772 Enterococcus faecium str. IDCC 2104 EU003
GQ155230.1 gg_id:549024 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ378670.1 gg_id:368923 Enterococcus faecium str. HN-N15 FJ3786
EU528257.1 gg_id:287252 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
FJ378668.1 gg_id:359756 Enterococcus faecium str. HN-N13 FJ3786
EU717963.1 gg_id:309491 Enterococcus faecium str. Lyws05 EU717
FJ378661.2 gg_id:362596 Enterococcus faecium str. HN-N6 FJ3786
GU369800.1 gg_id:529160 Enterococcus faecalis str. YH-10-3 GU369
FJ378692.1 gg_id:362577 Enterococcus faecium str. HN-N37 FJ3786
AJ301836.1 gg_id:74813 Enterococcus mundtii str. LMG 10748 AJ3018
EU845466.1 gg_id:316840 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ378675.1 gg_id:361670 Enterococcus faecium str. HN-N20 FJ3786
AJ271856.1 gg_id:73318 Enterococcus faecalis str. UK873 traditional fermented milk AJ2718
FJ378707.1 gg_id:369245 Enterococcus faecium str. HN-F22 FJ3787
GQ155748.1 gg_id:557151 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
DQ199665.1 gg_id:140065 Enterococcus durans DQ199
FJ672209.1 gg_id:515601 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6722
FJ845008.1 gg_id:559785 Enterococcus faecium str. IMAU20109; ML11-2-2 FJ8450
EU459323.1 gg_id:294649 hedgehog feces clone HH_aai36d01 EU459

562.7	2106.4	2715.1	2193.8	2652.4	3212.0	2437.2	2391.7	1939.3	3496.6	2337.7
520.0	3901.4	5097.4	4020.5	3803.8	5149.2	3721.5	4992.7	3696.0	6817.7	5214.0
51.6	1050.8	1438.8	861.1	1323.9	1552.7	996.2	1240.6	787.9	1869.1	743.2
154.2	2835.6	4130.1	2010.6	2280.5	4123.8	1585.1	4571.9	1172.8	7656.1	3415.2
48.1	1258.8	2191.1	683.1	1661.1	2050.3	1072.8	1935.3	585.4	2342.7	995.2
8763.5	10008.0	8431.5	8439.1	7968.6	8960.6	8123.1	8947.6	12309.1	9232.2	9148.9
293.1	3296.6	4156.3	4029.3	3735.9	4111.4	3162.0	5125.7	2377.7	4543.3	3900.6
5133.5	4366.2	5177.6	4385.8	3915.7	4943.1	3899.8	5496.9	4999.1	7570.9	5380.9
33.4	2422.6	4022.9	1572.1	2292.9	3318.3	1550.2	4887.1	1089.4	5193.0	2630.6
1065.8	4790.3	5348.5	5347.8	5095.6	5344.5	5490.6	5624.7	5269.2	7627.6	5868.4
117.6	1655.0	2319.0	1714.0	1986.7	2264.1	1376.2	2786.1	1154.7	2757.5	1790.4
55.9	2735.7	3991.6	1553.5	2967.7	3581.5	1720.8	3999.0	1176.7	5829.0	2370.0
301.0	1577.6	2495.1	1531.3	1715.1	2274.4	1981.3	2209.2	1217.0	1927.3	1417.0
44.0	1330.9	1460.5	1203.0	1275.2	1815.0	1216.6	1216.9	397.8	2538.5	455.0
903.2	2519.2	3100.4	2228.5	2511.4	3783.9	1956.2	3547.0	1707.7	4998.6	2352.1
93.3	1257.6	1994.8	1257.4	1732.8	2169.1	1076.4	2901.5	865.9	2741.0	1730.7
40.7	1259.2	2272.0	757.9	1696.5	2347.8	1060.8	2009.5	585.8	2765.2	941.8
46.8	2257.6	3517.2	1106.9	2607.8	3136.4	1580.7	2685.7	944.1	4426.6	1592.5
35.1	904.8	1858.2	1048.4	563.3	1493.5	962.5	1455.1	417.2	1511.8	658.4
54.6	1464.0	1945.6	1161.8	1923.9	2848.6	944.6	2752.6	912.9	2940.9	1274.5
394.9	4936.1	6223.1	3011.2	4457.1	5384.8	3259.5	5509.3	2845.3	8634.1	4467.3
3834.6	3076.5	3887.0	3479.9	2874.5	3522.0	2814.6	4103.4	1968.6	5561.7	3526.0
52.7	705.8	1022.9	515.4	921.1	1243.7	702.2	1118.6	352.2	1460.8	433.4
72.0	1994.4	2185.9	1373.0	1876.3	3210.7	1402.5	2850.3	899.1	4940.2	1356.8
47.6	744.7	962.6	516.7	921.1	1176.6	699.9	1117.6	349.7	1468.7	459.0
2174.6	5103.6	6494.6	4645.7	4980.5	4849.0	5243.5	7074.5	2970.8	8064.0	5748.7
52.1	646.9	1494.9	434.0	1091.0	1475.4	689.0	1336.6	333.3	1426.6	492.1
66.7	3011.4	4070.1	2438.6	2797.4	3479.4	2466.6	3758.7	1859.8	4929.9	3346.9
69.7	919.9	1599.8	566.4	989.0	1470.1	848.6	1328.8	447.9	1682.5	799.2
363.6	3610.5	4566.5	2633.8	2768.4	4628.2	2256.1	4647.0	1815.1	6703.8	4151.2
42.0	1385.3	2310.3	773.4	1631.9	2495.9	1065.8	2122.5	624.9	2712.0	954.9
62.8	1418.7	1932.5	1241.7	1703.5	2111.8	1193.4	2329.4	1072.1	3668.4	1652.5
1485.7	2377.6	3039.5	2440.2	2554.3	3677.7	2208.0	3663.6	1809.8	4103.5	2656.2
1493.8	2336.9	2843.1	1814.5	3767.7	2919.1	2676.2	2740.7	1740.1	2129.3	1759.4
975.9	5663.8	6457.8	5597.1	6291.2	6115.2	6296.6	6295.3	6437.0	9290.2	6128.6
11681.8	5594.8	5915.0	3789.8	4736.7	5486.6	3905.9	5103.2	6108.0	6968.2	5762.1
396.9	2510.5	3339.4	2272.8	2599.0	4055.7	2615.8	3044.9	1464.4	5819.5	2333.6
984.5	6580.0	7894.6	6454.8	7557.7	7198.4	6760.8	7635.5	7022.9	10880.3	7214.5
656.8	1750.2	2612.9	1629.2	1417.6	2753.9	1236.2	2813.1	977.1	2807.1	1709.9
107.4	1623.2	3039.4	954.9	1899.0	2959.4	1323.9	2547.2	832.5	4593.5	1314.4
88.6	2244.6	2440.7	1834.8	2322.1	3242.3	1965.9	3882.1	1436.3	3335.6	2640.1

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4265.7	3577.4	4845.3
4514.8	5006.2	5731.6
5108.1	3748.6	11361.6
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2594.8	2298.0	3712.4
2629.3	1403.5	2628.4
3834.4	4169.0	4879.5
2895.1	2802.5	3745.9
3379.0	2059.9	4131.7
4030.8	2708.3	5741.8
2171.1	1570.3	3039.3
4166.7	2424.4	3466.4
6051.7	4792.8	8274.6
3360.4	3453.1	4209.3
1685.0	1058.4	2168.0
3915.7	2672.8	4725.4
1689.4	995.9	2033.3
5316.8	6028.8	8246.7
2167.0	1494.9	2591.4
3675.2	2912.3	4505.2
2086.8	1370.3	2518.0
4606.3	3429.4	4641.9
3527.7	2175.8	4171.0
2208.7	1846.4	2277.3
3689.8	4075.5	4303.2
3697.3	3494.1	5520.2
6674.6	5848.2	6373.4
5631.5	6707.2	6875.8
4298.9	3141.3	4742.8
8020.7	7093.7	9496.6
2398.6	3310.5	4257.0
3527.3	2324.3	3690.6
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FJ015055.1 gg_id:350606 Enterococcus lactis str. GA4 FJ0150
GQ131184.1 gg_id:424771 Enterococcus italicus str. IMAU70068; HS2301 GQ131
AF349930.1 gg_id:67810 Enterococcus sp. str. CR-303S AF3499
EU717957.1 gg_id:355438 Enterococcus faecium str. Yl05 EU7179
GU255467.1 gg_id:555823 Enterococcus faecium str. ST2 GU255
EU789396.1 gg_id:325104 Enterococcus faecium str. M0138 EU7893
FJ378697.1 gg_id:357775 Enterococcus faecium str. HN-N42 FJ3786
DQ411812.1 gg_id:155933 Enterococcus pallens str. ATCC BAA-351 DQ411
AB189709.1 gg_id:114014 alkaline-enriched termite gut homogenate clone Pl-9.2e-20 AB1897
EF428246.2 gg_id:226289 Enterococcus mundtii str. HDYM-22 EF4282
AJ301832.1 gg_id:28797 Enterococcus flavescens str. LMG 13518 AJ3018
FJ378694.1 gg_id:368401 Enterococcus faecium str. HN-N39 FJ3786
EU459175.1 gg_id:288293 hedgehog feces clone HH_aai33c04 EU4591
FJ378674.1 gg_id:361558 Enterococcus faecium str. HN-N19 FJ3786
EU844974.1 gg_id:352189 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
AJ420806.1 gg_id:44890 Enterococcus mundtii str. CECT972T AJ4208
AJ301835.1 gg_id:48898 Enterococcus malodoratus str. LMG 10747 AJ3018
EU807757.1 gg_id:322616 Enterococcus faecalis str. NR1 EU8077
EU878170.1 gg_id:315043 Enterococcus faecium str. SH 632 EU8781
AY862507.1 gg_id:109837 Melissococcus plutonius str. ATCC 35311 AY8625
EU689058.1 gg_id:352407 Tetragenococcus halophilus str. JCM 2015; T19 EU6890
EU522084.1 gg_id:305691 Tetragenococcus halophilus str. T2 EU5220
EU522090.1 gg_id:315186 Tetragenococcus halophilus str. T9 EU5220
D88824.1 gg_id:15292 Tetragenococcus muriaticus D88824
AJ301840.1 gg_id:20568 Enterococcus solitarius str. DSM 5634 AJ3018
Y18338.1 gg_id:15294 Enterococcus solitarius str. NCIMB 12902T Y18338
AY690334.1 gg_id:106000 Tetragenococcus koreensis str. Wan-Taek Im AY6903
GQ502552.1 gg_id:553330 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ675076.1 gg_id:519677 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
AJ576414.1 gg_id:101516 midgut homogenate Pachnoda ephippiata larva clone PeM56 AJ5764
AJ854484.1 gg_id:145696 Catellicoccus marimammalium str. M34/04/3 AJ8544
GQ156063.1 gg_id:565384 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AJ576356.1 gg_id:107176 hindgut homogenate Pachnoda ephippiata larva clone PeH40 AJ5763
FJ672320.1 gg_id:512239 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
FJ675223.1 gg_id:524674 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ192638.1 gg_id:330592 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
AJ576341.1 gg_id:101355 hindgut homogenate Pachnoda ephippiata larva clone PeH24 AJ5763
AY571409.1 gg_id:114659 termite gut clone RsaHf388 AY5714
Y16546.1 gg_id:43965 Atopobacter phocae str. m1590/94/2 Y16546
EU560817.1 gg_id:571665 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608

1068.2	5730.5	6736.9	5833.2	6278.7	6250.8	5787.3	6852.4	5881.4	9575.0	6504.7
72.0	2888.6	3274.7	1520.0	2812.7	3059.7	1906.0	2963.7	1278.5	5582.3	1742.9
1292.0	2579.0	3141.7	2819.0	3634.5	2692.2	4263.6	3090.8	1525.1	2603.1	2013.1
14372.4	2219.2	2749.6	1926.6	2313.2	2510.3	2430.0	2483.2	2637.6	3993.1	2594.4
121.5	2310.3	4417.9	1267.7	2776.4	3061.8	1696.2	3446.1	1490.3	5297.4	2137.0
87.3	1626.2	1761.2	1291.1	1142.5	2243.9	959.8	2561.9	638.4	3412.4	1816.7
53.5	2758.0	4039.6	1599.6	2967.0	3726.2	1724.1	4028.9	1183.4	6054.9	2230.8
53.1	1243.7	1551.4	664.5	1385.9	1565.3	949.4	1733.4	522.2	2632.3	688.6
364.4	3829.8	5358.8	3279.7	4492.8	4993.1	3137.5	4994.7	2555.8	5729.3	3525.7
329.7	2267.5	2691.4	2214.9	2495.3	3631.3	2045.4	3374.7	1623.4	3537.9	2561.6
3145.8	4022.3	4912.7	3936.8	5787.1	4637.1	4226.1	4645.1	3592.1	5571.3	3358.5
54.8	1039.6	1337.8	931.7	1059.9	2506.3	548.8	1497.9	468.5	3948.8	571.7
3000.2	4303.2	3904.6	3356.7	3324.8	4114.8	3230.9	3319.2	4508.6	5011.8	3066.2
1093.5	3877.0	3423.2	3463.4	3733.1	4083.9	3400.2	4890.9	2527.9	4485.0	3316.9
73.4	1273.2	2205.8	681.5	1690.6	2075.9	1084.6	1947.3	592.8	2240.4	997.6
204.0	2872.8	3894.8	2856.9	3140.2	3896.3	2523.0	5446.1	1974.4	3855.2	3755.8
19132.0	7045.6	6493.2	7218.6	6918.0	6591.3	7329.3	6310.1	11952.4	9089.9	9087.3
6551.0	5820.2	6968.7	4304.4	5934.8	6447.4	4572.4	6477.6	6428.0	8644.8	5422.8
115.3	1510.4	2028.1	1003.5	1734.4	2120.7	1050.5	2262.9	649.7	2441.6	1277.0
47.9	469.9	639.1	395.1	528.9	783.5	505.1	774.3	249.1	790.4	388.9
2772.8	2714.8	3135.6	2184.0	2559.0	2742.5	153.0	3127.4	4137.5	2822.2	3555.0
5251.3	4546.3	4853.7	4326.5	4903.2	4728.5	4452.1	4627.7	4888.5	4480.3	5339.0
142.5	2322.4	2951.6	2067.3	3126.7	2691.6	2500.4	3114.6	1315.1	3089.1	1997.8
21573.6	7224.1	6912.6	7400.4	7749.9	7156.2	7953.6	6830.0	9561.4	6741.3	12167.1
43.6	26.7	23.8	25.0	26.3	21.8	25.5	25.6	22.4	22.9	20.8
2898.5	3218.7	3648.3	2715.7	3458.4	3291.3	2928.4	3523.8	3085.0	3506.7	4199.3
1601.9	1921.6	2321.7	2000.5	3105.7	2227.6	2095.3	3304.7	992.5	1287.7	2105.2
1079.0	2989.0	4299.8	2895.9	4034.6	4206.8	2507.5	6723.5	1764.2	5669.5	4632.4
41.5	45.2	59.3	59.9	32.7	88.9	33.7	48.8	24.9	139.9	33.6
1639.0	3349.0	3969.3	4146.2	3900.9	4003.2	4690.8	4664.4	3288.1	4001.6	4023.5
706.0	4511.6	3291.5	3397.0	3372.4	3904.3	3884.0	4107.8	4005.8	2821.3	3531.3
36.8	14.0	16.7	18.5	16.7	11.7	26.2	13.5	13.5	14.5	14.4
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5531.5	5008.0	3225.8	3583.6	3426.2	4031.2	3780.7	3548.4	4529.1	3827.4	3938.3
59.5	638.0	891.8	578.3	534.9	1428.7	526.8	1005.3	409.8	1813.5	535.5
48.6	1032.0	1377.3	1135.3	1276.7	1734.1	866.3	1372.7	759.8	1077.2	1026.2
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39.3	1005.9	1787.2	835.1	1653.0	1253.4	1340.9	1702.1	419.3	1050.1	556.1
37.0	19.4	22.5	20.0	31.3	16.0	31.9	15.1	18.1	10.4	16.9
5149.4	3028.0	2895.7	2334.2	2459.5	2682.7	2602.3	2477.5	2361.3	2398.9	3277.0

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3012.0	3289.9	3675.9
3623.2	3922.0	5430.4
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2105.0	1531.4	2772.5
6112.6	4840.9	7259.6
4716.0	2832.7	3668.6
4625.1	5113.6	6838.2
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7218.8	8797.1	8026.5
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3617.1	5239.1	4416.8
1550.8	1321.2	1321.4
2454.1	1696.6	2333.8
1543.1	1387.2	1377.0
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1363.1	1888.6	3120.5
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EF608535.1 gg_id:230114 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
NR_025689.1 gg_id:566186 Vagococcus carniphilus str. 1843-02; ATCC BAA-640 NR_02
AY669387.1 gg_id:110054 Vagococcus carniphilus 12J AY6693
GU166171.1 gg_id:570199 wheat bran (Musca domestica) direct cloning and sequencing genes intestinal tract GU166
NR_025360.1 gg_id:533589 Vagococcus fessus str. m2661/98/1; CCUG 41755 NR_02
DQ860043.1 gg_id:240763 anchovy intestinal microflora clone F2G DQ860
FJ211190.1 gg_id:334656 Vagococcus sp. str. AC-1 FJ2111
FJ360897.1 gg_id:590532 Vagococcus penaei str. CD 276 FJ3608
AM490371.1 gg_id:200615 Vagococcus carniphilus str. JIP 14-01 AM490
EU660371.1 gg_id:301246 Vagococcus fluvialis str. CT21 EU6603
Y17152.2 gg_id:15276 Vagococcus lutrae str. m1134/97/1; CCUG 39187 Y17152
AM490375.1 gg_id:202657 Vagococcus salmoninarum str. JIP 20-00 AM490
AB326357.1 gg_id:250831 Lactobacillus acidipiscis str. NBRC 102164 AB3263
NC_006814.3 gg_id:128961 Lactobacillus acidophilus str. NCFM NC_00
EF533992.1 gg_id:224532 Lactobacillus acidophilus str. IDCC 3301 EF5339
DQ057474.1 gg_id:137026 str. ii1369 DQ057
EU460840.1 gg_id:301883 short-beaked echidna feces clone ECH_aai39a11 EU4608
EU774899.1 gg_id:322737 Short-beaked Echidna feces clone ECH_aai39c02 EU7748
AB175732.1 gg_id:221299 Lactobacillus aviarius str. LAV7 AB1757
EU177639.1 gg_id:334767 Lactobacillus brevis str. NS125 EU1776
EF412979.1 gg_id:209868 Lactobacillus brevis str. I12 EF4129
AF515219.1 gg_id:64389 Lactobacillus brevis str. RO97 AF5152
GQ900602.1 gg_id:574944 Lactobacillus brevis str. E37 GQ900
GU116478.1 gg_id:542716 Lactobacillus brevis str. TCCC13007 GU116
GQ289387.1 gg_id:572012 Lactobacillus plantarum str. TJ2 GQ289
FJ532359.1 gg_id:552133 Lactobacillus brevis str. TJ7 FJ5323
GU125543.1 gg_id:556178 Lactobacillus brevis str. IMAU80121 GU125
DQ974207.1 gg_id:184047 Lactobacillus brevis str. BH2 DQ974
AF090328.1 gg_id:15172 Lactobacillus brevis str. K9 AF0903
GQ900600.1 gg_id:591412 Lactobacillus brevis str. E6 GQ900
GQ900601.1 gg_id:579148 Lactobacillus brevis str. E36 GQ900
EF412983.1 gg_id:212390 Lactobacillus brevis str. I218 EF4129
GQ900599.1 gg_id:573530 Lactobacillus brevis str. D13 GQ900
D37785.1 gg_id:15173 Lactobacillus brevis L63 D37785
FJ405226.1 gg_id:360833 Lactobacillus brevis str. ZJ2 FJ4052
AJ937772.1 gg_id:126840 Lactobacillus brevis str. TKS8 AJ9377
EU147304.1 gg_id:236581 Lactobacillus brevis str. BFE 8359 EU1473
EU626007.1 gg_id:277794 Lactobacillus brevis str. KLDS 1.0722 EU6260
FJ532360.1 gg_id:562473 Lactobacillus brevis str. 14G FJ5323
EF412982.1 gg_id:204678 Lactobacillus brevis str. I211 EF4129
EU194344.1 gg_id:335435 Lactobacillus brevis str. LMG 11992 EU1943

38.6	40.7	37.7	35.9	28.5	38.0	42.0	30.2	22.5	34.1	29.7
3876.8	2641.1	4379.9	2617.5	3351.7	3071.1	3022.8	3410.2	1368.7	3355.6	2690.9
678.8	4747.7	4377.1	4312.2	3277.2	4207.8	3828.7	3768.9	5919.8	6607.5	4558.9
208.7	2160.2	3357.5	1621.0	1849.8	2825.1	1559.4	3970.8	1057.5	5525.9	2529.7
398.4	1502.7	1678.7	1881.5	962.5	1993.8	1667.2	1922.0	1232.2	1636.4	1284.9
274.0	2852.5	3990.9	2806.0	3268.9	3235.8	2858.6	3996.4	3996.5	3654.3	2558.1
8290.6	3431.0	5273.7	2944.0	3390.9	3597.1	3396.3	5295.6	1772.0	3159.0	4693.2
676.5	2627.5	3391.5	2643.9	2587.3	2501.6	2165.9	3104.6	1584.9	2187.5	2758.8
9614.4	2384.2	4298.7	1867.4	3898.0	3442.8	2693.9	3380.7	1817.2	2360.9	2432.8
785.9	1698.7	2183.6	1886.3	2837.8	2227.0	2251.0	2093.0	1499.3	1523.1	2260.4
320.4	949.4	1337.5	988.5	804.8	981.2	857.3	1347.6	439.0	1218.4	696.6
2432.9	3766.9	5440.6	5190.3	3666.6	4438.1	4484.2	5061.1	2671.9	3160.7	3594.8
1458.0	1891.9	2345.5	1651.4	1893.0	1879.5	1966.7	2708.1	2324.9	910.4	3103.4
2689.8	4021.8	4131.3	4379.2	4981.5	3940.9	4436.9	3941.2	4084.7	2120.1	4190.8
50.3	3214.4	3308.1	2766.7	2440.1	2763.8	2983.6	3506.3	1139.4	2661.8	4881.9
281.2	2484.2	2908.4	3234.3	2789.3	3359.6	2803.7	3608.1	1296.2	3210.8	1935.2
13331.4	3042.6	2800.9	3154.7	3824.7	3217.4	3730.1	3688.4	2434.4	2089.7	2302.4
1764.6	1732.3	1918.8	1513.0	2190.5	2309.2	1687.3	2472.7	1450.9	1727.2	1427.5
83.5	169.2	355.8	346.8	334.7	483.0	165.6	403.1	205.1	791.5	208.2
863.5	3013.1	3945.0	2425.7	3542.9	2948.9	2586.4	3575.7	2021.8	4114.9	3440.0
376.9	1608.1	1612.5	1403.4	1789.3	1419.6	1215.5	1586.7	1057.6	1904.7	1708.3
414.6	1952.7	2825.2	1961.0	3098.9	2186.0	2426.0	1316.5	1040.0	2488.6	3615.8
90.3	899.8	1580.1	664.4	1072.5	669.9	519.0	1386.9	390.0	739.7	1573.2
1332.6	2826.6	3912.1	2029.3	3145.3	2879.3	2337.0	3306.4	1891.5	5328.5	3585.5
1903.3	3297.5	4641.9	2753.0	3276.0	3442.5	2838.1	4319.6	3148.2	4922.2	4314.2
3804.6	2550.9	2841.1	2855.0	3158.0	2275.6	2828.7	2495.8	2341.1	2353.5	2758.0
1247.7	2861.9	3947.7	2061.7	3193.0	2927.3	2344.9	3372.6	1900.8	5392.9	3842.4
1325.3	2544.0	3712.5	1771.9	2768.7	2687.5	2152.7	3104.8	1734.8	5051.1	3727.8
2043.3	3157.0	4373.1	2645.0	3013.7	3228.7	2468.3	3777.3	3002.9	5072.4	4085.8
2149.0	2621.9	3162.3	2746.8	3224.9	2731.9	2680.6	2719.6	2908.7	3216.2	3645.2
2249.0	4244.4	6124.1	3487.5	4713.0	4236.5	2973.9	4933.0	3178.3	3353.0	7966.0
1218.5	2130.8	2595.0	1896.0	2835.7	2253.1	2265.4	2548.9	1795.4	3901.9	2772.6
289.0	2829.1	3026.4	1791.4	3561.9	2459.4	1651.6	3864.2	1812.6	2582.7	2147.4
686.9	2191.6	3209.6	1665.0	2495.9	2286.5	1613.8	2717.7	1289.5	4320.6	3058.2
2491.7	4003.4	5515.2	3629.8	4714.7	4266.4	4168.8	4901.6	3712.3	6264.1	5532.2
514.5	3996.4	6201.4	3515.3	5236.1	4041.9	3242.7	5180.9	4233.3	5113.8	7306.4
2179.9	3521.3	4795.6	2856.9	3734.0	3601.8	2899.1	3889.7	3160.4	4860.4	4966.1
1920.4	4156.6	5435.7	3596.3	3766.0	4349.0	3693.7	5552.4	3553.9	6522.3	5049.9
1340.8	3319.9	4239.8	2436.5	3521.0	3207.4	2913.0	3903.3	2469.1	5251.2	3344.2
322.4	1757.4	2352.9	1150.1	1948.8	1727.3	1066.5	2049.0	652.2	3001.8	2428.7
544.3	1968.4	3035.1	1380.4	1952.4	2117.9	1376.1	2878.5	1270.8	4384.5	2399.9

67.0	76.8	71.0
3063.6	3324.0	5284.9
3908.8	3689.3	5956.1
2356.1	2076.7	3668.1
2160.7	2693.5	2776.5
3420.9	3768.6	6023.6
3545.8	3766.8	5847.1
2291.7	3251.0	4835.6
3923.3	3548.9	5991.6
2509.5	2261.8	3241.7
1149.8	1336.6	2337.9
4431.9	5085.9	9282.1
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3122.0	4065.4	4209.4
3387.4	2631.1	2949.4
3308.2	4055.7	5488.5
3241.5	4466.7	4127.5
2048.6	3030.3	4250.8
370.0	294.8	437.7
2783.9	3145.2	4865.6
1300.3	1976.1	2855.9
2495.9	2575.4	4239.7
876.9	1280.9	1397.7
2633.8	2977.7	4706.0
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3150.6	3468.3	3619.3
2685.2	3121.3	4895.2
2422.2	2677.6	4198.7
2992.9	3266.9	4724.9
2551.8	2995.2	3961.5
3409.6	4067.3	4058.5
2173.9	2701.1	4760.1
3323.7	3104.9	4192.1
2059.6	2442.1	4109.5
4219.0	4968.9	7864.2
3784.9	4245.4	5098.0
3275.4	3646.9	5028.8
4177.2	4396.6	6663.9
3141.0	3452.8	5337.5
1553.5	2014.4	3378.6
1979.3	2170.7	4074.7

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s__Lactobacillus coleohominis	72985
s__Lactobacillus crispatus	71791
s__Lactobacillus crispatus	71820
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s__Lactobacillus curvatus	71821
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s__Lactobacillus delbrueckii	71824
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s__Lactobacillus diolivorans	72994
s__Lactobacillus farraginis	72094
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s__Lactobacillus fermentum	72036
s__Lactobacillus fermentum	72209
s__Lactobacillus fermentum	72620
s__Lactobacillus fermentum	72645

AY929284.1 gg_id:113742 Lactobacillus brevis str. BFE 6673 AY9292
EU626006.1 gg_id:277822 Lactobacillus brevis str. KLDS 1.0721 EU6260
EF412980.1 gg_id:205080 Lactobacillus brevis str. I23 EF4129
FJ377713.1 gg_id:368916 Lactobacillus brevis str. RSD42 FJ3777
GU220024.1 gg_id:581930 Lactobacillus brevis str. SC2A GU220
CP000416.1 gg_id:187895 Lactobacillus brevis str. ATCC 367 CP0004
AB365977.1 gg_id:351825 Lactobacillus capillatus str. YIT 11317 AB3659
AB425925.1 gg_id:580392 Lactobacillus coleohominis str. TB-C19 AB4259
AJ292530.2 gg_id:23477 Lactobacillus coleohominis AJ2925
EU559595.1 gg_id:276632 Lactobacillus crispatus str. ZDY35b EU5595
AF243141.1 gg_id:41700 Lactobacillus crispatus str. BLB2 AF2431
GQ074725.1 gg_id:452720 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ074
GQ070874.1 gg_id:455412 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
GQ074133.1 gg_id:371731 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ074601.1 gg_id:402842 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ074192.1 gg_id:391592 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ074160.1 gg_id:427907 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ011573.1 gg_id:498091 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw793f10 GQ011
AJ242969.1 gg_id:15129 Lactobacillus crispatus str. NCTC 4 AJ2429
DQ317604.1 gg_id:149002 Lactobacillus crispatus str. 15L08 DQ317
GQ070816.1 gg_id:441240 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
DQ057450.1 gg_id:133039 str. ii1269 DQ057
DQ057440.1 gg_id:131154 str. ii1225 DQ057
AF243171.1 gg_id:33386 Lactobacillus crispatus str. TL23a AF2431
GQ010914.1 gg_id:498752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
GQ078614.1 gg_id:422527 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ078
AM285451.1 gg_id:199536 Lactobacillus crustorum str. LMG 23702 R-19087 AM285
AY204891.1 gg_id:81329 Lactobacillus curvatus str. YMRS3a AY2048
AY204890.1 gg_id:82190 Lactobacillus curvatus str. PSTJA3a AY2048
AF349922.1 gg_id:67818 derived cheese sample clone 51CR AF3499
EU722745.1 gg_id:326330 Lactobacillus delbrueckii str. L4 EU7227
FJ749581.1 gg_id:548624 Lactobacillus diolivorans str. IMAU10018; SY5-2 FJ7495
AB262731.1 gg_id:180597 Lactobacillus farraginis str. NRIC 0676 AB2627
AM266587.1 gg_id:161232 Lactobacillus faeni str. TMW 1.1303 = DSM 180 AM266
EU419594.1 gg_id:260994 Lactobacillus fermentum str. KLDS 1.0617 EU4195
EF535257.1 gg_id:220122 Lactobacillus fermentum str. KLB 261 EF5352
AF302116.1 gg_id:52471 Lactobacillus fermentum str. KLD AF3021
EU547297.1 gg_id:557918 Lactobacillus fermentum str. BCS25 EU5472
EU469860.1 gg_id:302890 western lowland gorilla feces clone GOR_aag72g08 EU4698
U62624.1 gg_id:15140 Lactobacillus fermentum str. KRM U62624
EF460496.1 gg_id:214156 Lactobacillus fermentum str. SR2 EF4604

687.2	2509.9	3412.3	1751.5	2818.4	2572.8	1826.5	3026.6	1281.2	3952.7	3056.6
2036.4	3520.6	4816.4	3056.6	3731.2	3611.0	2893.1	4148.1	3166.9	4858.3	4972.6
693.5	2209.8	2615.6	2192.4	2485.3	2183.6	1895.9	2601.6	2008.6	3256.8	2595.4
393.5	1352.0	1181.6	1241.7	1696.6	1176.3	1331.1	1350.1	971.6	1433.0	842.9
855.7	2696.0	3721.1	2150.1	3323.5	2730.6	2738.2	3299.6	1856.0	3458.0	3336.0
1198.2	2498.3	3504.4	1675.8	2475.4	2545.0	1920.1	3024.9	1736.8	5631.7	2955.6
52.5	884.8	1272.8	856.4	818.7	1159.2	740.5	1289.0	402.7	1457.0	974.3
43.7	917.0	1514.4	1595.7	498.6	421.5	696.8	1350.3	210.4	348.5	524.3
6979.9	2583.0	2502.4	3229.2	2858.6	2229.2	2879.0	2698.8	2502.1	237.5	2430.6
224.4	992.0	1379.8	904.3	473.9	653.9	686.2	1505.3	379.5	324.6	980.7
1075.4	4070.8	4896.8	4043.4	4745.4	3656.8	4098.8	4832.2	4290.3	5317.2	3801.9
91.9	1083.0	2016.1	1531.0	1577.4	1183.3	1702.8	1588.0	622.9	2254.4	1053.4
1425.0	2205.9	3103.0	2829.6	1623.7	2268.7	1468.5	1584.1	2926.1	2798.2	1422.6
1343.0	3469.6	4759.7	5173.7	3546.7	4131.6	3563.5	4257.5	2604.4	380.3	3880.3
8208.6	3330.9	4102.6	4566.7	4090.8	3264.7	2313.9	3870.7	3278.6	3579.2	3681.1
2702.3	1499.9	2537.9	2394.0	2021.2	2260.5	1854.2	2008.0	1618.5	6893.7	1420.3
4652.3	5679.3	5930.8	6668.2	5709.2	5193.7	6108.5	4994.9	10949.7	6987.4	7942.3
25456.3	9730.7	8923.8	9642.0	11939.2	8642.8	10709.0	8175.7	11771.1	8530.6	13250.0
4189.5	3093.8	5235.8	5598.5	2811.0	2229.2	2671.3	2123.4	2974.1	928.2	3648.1
137.6	2068.8	2422.3	2126.9	1843.6	1584.7	2227.4	1784.5	992.7	862.4	2234.8
24885.6	7086.2	6857.2	7203.5	6377.7	6287.6	6812.9	5840.4	9254.2	7770.7	9316.2
44.0	206.0	515.5	481.9	247.5	181.8	333.8	192.0	59.6	58.3	104.6
2541.0	4656.4	4781.0	4926.5	6322.7	4291.3	4981.6	4595.8	4431.1	4505.0	4939.4
1274.0	1056.8	1081.4	1343.4	1104.3	912.8	1453.4	786.9	746.6	451.6	907.3
27.9	632.1	1288.1	1380.5	707.6	733.1	651.5	657.6	276.8	1077.5	481.1
8354.8	7350.7	7397.3	7691.2	6954.9	7652.6	7842.9	6838.6	7494.2	8525.6	8731.3
52.6	1428.9	1725.6	1266.0	481.2	1374.2	1806.2	2060.2	1270.8	1432.4	1681.9
335.9	1227.7	1682.5	1556.6	1537.7	1348.6	1251.0	1677.1	955.6	1229.8	1023.5
336.4	1232.2	1440.5	1307.0	1509.7	1396.3	1184.4	1727.5	954.4	1335.4	1011.4
1844.2	1235.6	1278.3	1414.7	1145.2	1147.5	1901.9	1533.8	1752.3	1849.9	1600.3
27.8	708.1	1207.9	1376.1	753.1	771.2	1423.4	960.7	204.1	322.4	509.5
279.4	1576.0	1549.5	1389.3	1203.8	1604.0	1424.5	1385.2	1010.0	820.9	1505.6
274.1	3628.1	4606.1	5237.5	4230.0	3879.0	4340.4	4288.7	3811.2	4343.3	3415.0
1556.7	3500.1	4214.5	4556.8	4311.0	4314.7	4645.7	4533.1	4332.1	6346.8	4052.3
173.0	1527.7	2084.1	1344.1	1542.6	1640.9	1809.5	1647.6	851.3	2646.0	1415.2
9338.0	7076.9	6175.8	6342.1	6700.0	6117.4	7348.5	5749.0	6607.3	7821.8	7440.5
25523.6	6342.6	4047.4	5764.6	5597.2	5861.0	6780.3	5587.6	8149.2	6200.6	9596.7
867.1	1758.1	2884.5	1636.2	2681.3	2853.8	1955.9	2623.5	1352.3	7671.2	876.6
2056.6	4720.9	6296.8	5218.2	5080.7	5345.7	5995.0	6028.0	4557.5	9473.2	6273.2
8069.1	5070.4	4966.9	5731.5	4900.7	5720.6	5899.8	4795.1	6170.6	4728.8	6948.9
1394.8	1468.4	1742.7	1688.5	1447.8	1460.1	1252.9	1321.4	1188.8	564.5	2174.0

2289.5	2622.4	4475.6
3283.8	3657.7	5038.6
2027.1	2646.2	4528.9
1207.9	1718.6	2933.0
2506.3	2684.1	4450.4
2394.3	2730.5	4581.4
1174.7	1668.4	4005.7
839.7	870.6	822.0
2044.2	2683.3	2403.4
724.9	925.2	787.7
3780.4	5669.3	6190.5
1318.6	1438.8	1824.2
1795.1	2455.5	1477.6
3147.8	3756.9	4015.8
3740.0	4504.5	4659.2
2173.8	2630.6	1575.2
5249.2	5411.3	5927.3
8186.7	9976.6	8445.3
2768.9	2865.0	2733.4
2141.8	2121.1	2005.6
6323.1	7942.5	6750.0
193.4	212.9	556.5
3417.0	5100.6	6345.5
928.2	1092.1	1304.1
739.5	765.1	1036.1
6535.7	7866.4	7559.9
1329.5	1819.8	3070.6
1572.0	1675.1	1953.0
1660.8	1766.8	2214.9
882.6	1610.8	1153.8
748.9	954.1	1152.7
1165.9	1673.9	2611.8
4020.1	4831.9	6843.4
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1724.0	2381.2	3351.7
5419.9	7535.1	6332.1
5079.7	6444.3	5653.4
2887.3	2834.2	3074.2
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4702.5	6030.9	5066.4
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s__Lactobacillus jensenii	73025
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s__Lactobacillus kefiranofaciens	72412
s__Lactobacillus kefiri	72108
s__Lactobacillus kefiri	72550
s__Lactobacillus lindneri	72028
s__Lactobacillus mali	73021
s__Lactobacillus manihotivorans	72716
s__Lactobacillus manihotivorans	72756

EF535258.1 gg_id:222909 Lactobacillus fermentum str. KLB 231 EF5352
AB370875.1 gg_id:276599 Lactobacillus fuchuensis str. B5M10 (=JCM 11249 =DSM 14340) AB3708
Y17361.1 gg_id:15125 Lactobacillus amylolyticus str. LA 5 Y17361
AB368915.1 gg_id:281310 Lactobacillus harbinensis str. T9-8 AB3689
AB196123.1 gg_id:140719 Lactobacillus harbinensis str. SBT10908 AB1961
FJ749416.1 gg_id:588829 Lactobacillus helveticus str. IMAU50013; YN15-4-1-2 FJ7494
FJ749434.1 gg_id:562265 Lactobacillus helveticus str. IMAU50033; YN17-1-2-3-1 FJ7494
EF533989.1 gg_id:225190 Lactobacillus suntoryeus str. IDCC 3101 EF5339
FJ749689.1 gg_id:556337 Lactobacillus helveticus str. IMAU30123; F1402 FJ7496
EU419585.1 gg_id:267753 Lactobacillus helveticus str. KLDS 1.0601 EU4195
FJ861099.1 gg_id:548478 Lactobacillus helveticus str. KLDS 1.0356 FJ8610
FJ749644.1 gg_id:549081 Lactobacillus helveticus str. IMAU30052; C6203 FJ7496
FJ861108.1 gg_id:541176 Lactobacillus helveticus str. KLDS 1.0647 FJ8611
AY675248.1 gg_id:105631 Lactobacillus suntoryeus str. LH AY6752
FJ861102.1 gg_id:540215 Lactobacillus helveticus str. KLDS 1.0635 FJ8611
FJ861100.1 gg_id:568817 Lactobacillus helveticus str. KLDS 1.0633 FJ8611
EU124655.1 gg_id:242121 Lactobacillus helveticus str. C7303 EU1246
FJ749412.1 gg_id:564090 Lactobacillus helveticus str. IMAU50009; YN1-4-2 FJ7494
GQ155447.1 gg_id:580616 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155579.1 gg_id:572925 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GU138582.1 gg_id:544201 Lactobacillus helveticus str. LSYM7-1 GU138
AY763429.1 gg_id:100251 Lactobacillus acidophilus str. LH4 AY7634
FJ749714.1 gg_id:568800 Lactobacillus helveticus str. IMAU30155; XC1-2 FJ7497
AB368911.1 gg_id:285740 Lactobacillus hilgardii str. T3-12 AB3689
EU177634.1 gg_id:336162 Lactobacillus hilgardii str. NS13 EU1776
NZ_ACLN01000018.1 gg_id:470599 Lactobacillus iners str. DSM 13335 NZ_AC
AF333975.1 gg_id:52162 Lactobacillus ingluviei str. KR3 AF3339
AF317703.1 gg_id:40447 Lactobacillus thermotolerans str. G 43 AF3177
AF317702.1 gg_id:44614 Lactobacillus thermotolerans str. G 35 AF3177
EU510751.1 gg_id:266445 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40f06 EU5107
DQ015194.1 gg_id:202045 Obesity alters gut microbial ecology mouse cecum clone M2_g10_2 DQ015
AF243143.1 gg_id:31979 Lactobacillus jensenii str. BLB1a AF2431
EU559597.1 gg_id:265038 Lactobacillus jensenii str. ZDY46a EU5595
FJ749487.1 gg_id:553705 Lactobacillus kefiranofaciens subsp. kefirgranum str. IMAU50089; YN37-1-1 FJ7494
AJ575259.1 gg_id:95575 Lactobacillus subsp. kefiranofaciens str. LMG 19149 AJ5752
AB362681.1 gg_id:239687 Lactobacillus kefiri str. NRIC 0586 AB3626
EU688976.1 gg_id:286983 Lactobacillus kefiri str. F3201 EU6889
D37784.1 gg_id:15194 Lactobacillus lindneri DA1 D37784
FM878596.1 gg_id:550949 Lactobacillus mali str. LA214 FM878
EU460788.1 gg_id:294550 short-beaked echidna feces clone ECH_aai38b03 EU4607
AF000163.1 gg_id:15212 Lactobacillus manihotivorans str. YAM I; LMG 18011 AF0001

2382.3	2997.1	2732.6	2501.7	2573.2	3249.7	3118.2	2257.5	3354.1	1906.4	3247.1
833.8	2179.0	2692.7	2588.7	1600.8	1798.9	1923.6	1953.3	1312.6	2288.7	1550.7
231.8	4486.8	4780.5	3847.5	3901.9	4097.9	4309.2	4721.7	3545.6	1906.6	4953.5
545.4	921.3	1239.6	865.4	1157.2	1131.4	1089.7	1481.0	540.3	1542.5	1222.8
616.7	898.4	1327.2	884.6	1182.1	1155.5	1103.9	1720.3	558.1	1369.6	1339.4
39.0	578.5	798.1	745.8	305.8	171.3	246.1	1111.1	72.7	101.2	453.2
28.8	821.3	1752.0	1834.8	757.0	1291.9	872.9	926.0	452.3	937.7	602.4
737.5	1759.1	2341.6	2269.7	1620.2	2367.1	1828.1	2796.7	1548.3	3114.6	2138.8
1180.6	1596.6	2085.0	1864.0	1164.1	1715.8	1290.9	2326.3	1115.9	1086.9	1501.8
814.4	3386.3	4280.2	3927.8	2665.6	3727.2	2732.1	4085.7	3886.2	4445.9	3558.2
761.7	3554.5	4331.5	3974.4	2707.3	3769.4	2787.3	4471.7	3916.7	4147.8	3399.6
47.3	1536.5	2263.9	1825.3	1243.2	1358.0	1215.2	2725.6	1184.7	1263.4	1264.2
756.9	3104.4	3706.8	3548.9	2848.8	3273.2	2757.6	3620.4	4046.7	3755.6	3169.3
87.5	694.8	1254.8	1320.2	700.8	1052.5	826.3	1433.7	699.3	356.2	693.2
709.5	2680.9	3216.7	3231.9	2259.6	2516.3	2179.2	3209.5	3166.3	3071.8	2682.0
760.7	2942.3	3222.2	3254.1	2453.6	3241.2	2284.2	3219.2	4076.0	3159.5	2662.8
46.0	2509.8	3022.4	2372.7	2289.1	2940.2	2374.0	2991.2	3165.4	4281.4	2014.4
2373.0	2658.2	3229.5	2996.9	2570.5	3354.6	2500.1	2783.0	3602.2	3039.3	2800.1
25692.1	7934.4	8037.9	10233.7	7637.0	8916.4	8389.0	7731.6	11985.4	8666.7	12008.0
42.4	964.6	1767.0	1838.2	972.0	1371.2	931.3	1390.8	717.6	1445.4	807.1
36.2	247.9	743.3	895.3	179.2	335.3	243.8	360.8	89.0	90.3	238.8
315.1	1460.9	2226.0	2141.1	1876.2	1765.4	1580.6	2169.7	1673.0	1371.6	1637.5
36.7	323.1	564.2	498.0	309.1	546.4	243.4	535.4	492.8	1085.9	223.2
2579.6	1814.6	3308.0	2820.0	2567.5	3068.2	3328.1	3395.8	2791.0	3427.8	3206.2
1356.7	839.5	1859.0	1768.8	1344.1	1618.7	1890.3	1798.9	1514.4	1469.5	1727.5
116.6	88.7	125.2	110.3	250.2	99.7	132.2	107.6	59.5	154.1	77.8
71.7	1182.6	1609.4	1352.6	1248.3	1438.1	1326.5	1713.0	695.7	1466.6	1217.8
5721.6	2775.9	4013.7	2577.1	2989.8	3251.8	2677.8	3358.5	2660.0	4480.6	3301.1
58.2	1087.1	2028.7	1038.6	1207.1	1667.3	1367.1	1753.0	719.9	1735.8	1198.0
36.0	26.7	42.5	44.0	33.4	32.7	18.9	29.5	20.3	12.4	23.7
46.7	331.5	456.7	625.7	461.1	265.6	334.9	329.1	55.0	121.0	140.2
27.0	581.2	1032.5	1241.8	43.1	17.8	172.4	107.0	27.0	23.7	151.7
7829.0	3564.6	3579.7	3470.8	3261.5	3737.5	3977.9	3315.2	4055.1	4009.6	2717.1
501.0	1569.5	2402.3	2037.7	1438.4	1949.9	1639.6	2013.3	711.7	436.3	1850.7
1652.1	1358.7	2123.9	1889.2	1822.8	1744.7	1365.3	1855.3	938.1	578.7	1463.5
13854.5	8883.3	8322.9	9700.2	9102.6	8165.1	10070.7	7714.5	13229.5	8315.5	11256.5
310.3	7986.3	7870.4	8689.0	7475.4	8284.0	8759.4	8745.5	6833.0	12095.4	10009.5
2373.9	4061.2	3656.1	4118.1	3749.0	3854.5	3631.3	3673.5	5514.2	3240.9	4245.6
1585.0	382.7	625.9	456.1	381.6	568.5	376.2	532.7	295.0	216.5	404.3
966.7	1155.9	1349.0	1323.5	1566.5	1328.0	1302.4	1331.7	593.4	1243.3	742.3
92.4	1028.1	1214.9	1089.2	1191.0	1048.3	944.9	1061.1	680.1	1609.8	1004.6

2244.6	2890.7	2410.1
2404.1	3623.8	4605.8
4228.0	3847.3	4718.8
1233.8	1598.1	2562.9
1273.8	1544.5	2967.4
403.8	527.1	1153.4
985.2	1072.2	1506.8
2197.6	2154.1	2734.3
2366.8	2805.9	3718.5
3763.9	4119.1	5645.4
3884.5	4162.8	5681.5
2019.9	2155.5	3694.2
3221.5	3743.3	4856.3
1018.2	943.4	1577.9
2934.5	3044.3	4256.5
2755.0	2925.4	3143.4
3633.6	3192.2	4179.3
2834.9	3002.8	2906.1
7156.6	9829.2	7419.3
1246.5	1153.8	1292.7
480.8	421.6	476.8
1789.6	2263.0	1947.5
920.3	816.2	350.2
2646.1	3533.2	4486.3
1444.5	1968.9	2518.5
130.9	191.0	139.5
1568.8	1769.6	3415.8
3435.0	3536.6	5931.9
1808.0	1834.2	3806.9
19.1	29.8	24.1
384.7	380.1	1143.3
882.8	785.3	46.7
3286.4	4180.5	3390.8
1944.3	2050.5	3074.7
1599.6	2035.3	1939.3
8043.5	10021.9	12071.6
8529.8	8563.1	11382.0
3548.9	4436.0	4327.6
460.0	802.8	445.3
1679.7	2105.9	3421.7
1055.1	1423.1	2415.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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o__Lactobacillales	f__Lactobacillaceae
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s__Lactobacillus manihotivorans	72897
s__Lactobacillus mindensis	72882
s__Lactobacillus mucosae	71815
s__Lactobacillus oeni	72158
s__Lactobacillus oligofermentans	72421
s__Lactobacillus panis	72019
s__Lactobacillus pantheris	72251
s__Lactobacillus pantheris	72730
s__Lactobacillus parabrevis	72239
s__Lactobacillus parabrevis	72447
s__Lactobacillus paracollinoides	71932
s__Lactobacillus parakefiri	72467
s__Lactobacillus paralimentarius	73052
s__Lactobacillus paraplantarum	72089
s__Lactobacillus paraplantarum	72355
s__Lactobacillus paraplantarum	72893
s__Lactobacillus paraplantarum	72920
s__Lactobacillus pentosus	71825
s__Lactobacillus pentosus	72229
s__Lactobacillus pentosus	73043
s__Lactobacillus pobuzihii	72272
s__Lactobacillus pontis	71961
s__Lactobacillus pontis	71981
s__Lactobacillus reuteri	71819
s__Lactobacillus reuteri	71829
s__Lactobacillus reuteri	71944
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s__Lactobacillus reuteri	72139
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s__Lactobacillus reuteri	72668
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s__Lactobacillus reuteri	72719
s__Lactobacillus reuteri	72747
s__Lactobacillus reuteri	72778
s__Lactobacillus reuteri	72804
s__Lactobacillus reuteri	72915

NR_024835.1 gg_id:575000 Lactobacillus manihotivorans str. OND 32; LMG 18010 NR_02
GU138543.1 gg_id:569931 Lactobacillus mindensis str. LSWM2-4 GU138
AF243145.1 gg_id:18857 Lactobacillus mucosae str. BLB1c AF243
EU821350.1 gg_id:538942 Lactobacillus oeni str. 103 EU8213
AY733083.1 gg_id:104517 Lactobacillus oligofermentans str. MARL13 AY733
X94230.1 gg_id:15148 Lactobacillus panis str. DSM 6035T X94230
AB257867.1 gg_id:158349 Lactobacillus pantheris FP37-1 AB2578
NR_025189.1 gg_id:573944 Lactobacillus pantheris str. LMG 21017 NR_02
AB512779.1 gg_id:580959 Lactobacillus parabrevis str. YIT 12113 AB512
AB297927.1 gg_id:253940 Lactobacillus senmaizukensis str. L13 AB297
AB473626.1 gg_id:528967 Lactobacillus paracollinoides str. JCM 15729 AB473
NR_029039.1 gg_id:566740 Lactobacillus parakefiri str. GCL 1731; LMG 15133 NR_02
NR_025045.1 gg_id:550403 Lactobacillus kimchii str. MT-1077; AP1077; JCM 10707 NR_02
AB191250.1 gg_id:107631 Lactobacillus paraplantarum str. II 32 AB191
AY383631.1 gg_id:95489 Lactobacillus plantarum str. MiLAB14 AY383
DQ486145.1 gg_id:158659 Lactobacillus plantarum str. SFCB2-7c DQ486
GU138564.1 gg_id:557831 Lactobacillus plantarum str. LSBM6-5 GU138
AB362711.1 gg_id:249730 Lactobacillus pentosus str. NRIC 1554 AB362
AB362739.1 gg_id:238712 Lactobacillus plantarum str. NRIC 1739 AB362
EU559599.1 gg_id:264917 Lactobacillus plantarum str. ZDY128 EU559
AB326363.1 gg_id:588823 Lactobacillus pobuzihi str. NBRC 103224 E100326 AB326
X76329.1 gg_id:15142 Lactobacillus pontis str. LTH 2587 X76329
AJ422032.1 gg_id:76876 Lactobacillus pontis str. LMG 14187T = R-1465 AJ4220
GQ155597.1 gg_id:511199 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
CP000705.1 gg_id:231242 Lactobacillus reuteri F275 str. DSM 20016 CP000
CP000705.1 gg_id:231245 Lactobacillus reuteri F275 str. DSM 20016 CP000
EF412975.1 gg_id:214229 Lactobacillus reuteri str. C1 EF4129
GQ155514.1 gg_id:510643 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ156435.1 gg_id:591239 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ155466.1 gg_id:556287 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF412977.1 gg_id:203814 Lactobacillus reuteri str. C16 EF4129
EF097168.1 gg_id:185432 mouse cecum clone SWPT18_aaa02d05 EF0971
GQ155469.1 gg_id:585860 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155455.1 gg_id:575693 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155615.1 gg_id:579207 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ155669.1 gg_id:558815 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF412976.1 gg_id:216761 Lactobacillus reuteri str. C10 EF4129
GQ155573.1 gg_id:538440 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY735406.1 gg_id:108135 Lactobacillus reuteri str. LU3 AY7354
GQ448922.1 gg_id:585264 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
GQ155509.1 gg_id:540888 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155

111.1	2188.1	2289.2	2058.0	2082.6	2109.3	1595.1	2680.3	1553.9	2750.5	2062.9
437.1	3474.7	3522.8	3809.8	2742.0	2997.4	4659.4	3753.7	3163.0	2382.0	2679.3
46.8	246.1	410.2	472.7	191.4	364.5	521.0	558.5	96.0	175.1	248.2
52.4	512.9	443.1	458.7	525.3	643.8	495.1	771.9	241.7	1666.4	218.7
46.4	352.6	473.6	516.3	522.7	433.1	530.6	267.4	195.0	360.1	340.3
105.0	2868.2	4687.7	4379.0	3793.2	2699.6	3977.8	3404.8	2149.8	1880.0	2774.7
36010.4	10303.0	9444.5	11182.4	9916.8	9578.1	11170.7	9625.6	15078.4	10993.0	15136.3
322.2	991.9	743.7	960.6	1320.1	878.8	746.6	1173.9	478.6	1417.9	461.2
398.2	2343.8	3193.6	2241.5	2487.1	2682.9	3030.2	3149.6	1247.5	3826.0	2162.9
226.1	2338.7	2758.7	3176.0	2327.5	2610.3	2967.7	2700.0	1435.5	4301.8	2576.9
114.7	1119.4	1490.7	672.5	637.3	923.8	903.4	885.1	258.2	363.7	458.5
1403.4	2901.0	3345.3	3134.2	3058.5	3327.4	3146.3	3807.2	4056.7	3745.9	3522.6
4905.2	7551.3	7838.1	8114.9	6116.9	7208.4	8356.6	7488.4	6902.9	11818.0	8035.5
292.6	2320.0	2743.0	2512.9	2181.8	2418.8	1996.9	3261.7	1487.1	2847.0	2115.1
315.7	2520.7	2968.9	2829.3	2533.7	2422.6	2100.7	3528.2	1661.6	3066.6	2240.3
324.0	2364.7	2607.5	2514.0	2517.2	2442.0	2101.6	3324.9	1604.7	2783.0	2135.5
296.3	3113.1	3602.1	3495.9	3098.9	3027.6	2681.6	4237.5	1896.0	4457.1	2964.2
323.1	2407.0	2825.0	2574.1	2401.9	2490.3	2072.5	3337.2	1515.7	3041.1	2175.9
51.9	1243.9	1886.5	1475.4	1581.9	1168.4	985.1	2010.1	585.8	872.8	953.7
49.8	2283.8	3243.7	1184.3	3312.8	3321.7	1762.3	3089.0	1004.3	5619.5	1036.6
12825.5	5925.2	7259.1	5249.6	6183.7	5711.7	5478.1	6212.9	6733.7	7737.9	8290.1
95.1	680.3	741.9	489.6	599.2	686.2	726.5	623.3	418.0	1097.6	471.2
70.4	1123.9	2106.2	1006.4	1304.2	1390.1	744.2	1887.1	425.1	1358.5	980.4
23410.2	4936.9	5089.5	6289.4	4952.7	4365.4	5972.6	4659.4	8746.0	5443.9	7050.5
82.9	627.0	794.1	566.3	438.3	544.5	425.2	691.5	1018.8	964.1	219.6
71.2	572.1	758.4	524.1	354.9	575.3	412.3	639.9	845.4	901.4	220.5
246.4	962.3	2055.8	2092.5	1637.3	1679.0	2133.8	1965.0	2920.6	2268.2	1622.3
316.1	2923.7	3629.7	3687.7	3054.4	2924.3	3673.8	3448.6	4498.5	3017.7	3721.8
329.3	3069.3	3830.7	3836.8	3253.1	3108.7	4033.1	3604.8	4597.4	3435.4	3864.5
963.6	5205.8	5130.9	6481.7	7675.6	4708.9	7445.8	6074.1	5392.8	3882.9	4242.3
233.5	1003.4	2451.3	2900.8	1750.1	1697.3	1871.7	2098.2	2879.2	2126.5	1564.1
61.3	317.6	430.3	483.6	167.9	515.9	273.2	456.4	143.8	270.2	193.4
481.9	1383.8	859.8	1114.4	878.7	1001.9	1019.0	1125.9	2039.1	1168.7	799.6
672.2	1120.5	1710.2	1524.9	1261.8	1441.3	1424.5	1654.7	1003.6	1993.5	1145.8
7104.8	3040.5	3405.9	4005.2	4009.4	2879.0	4550.4	3465.7	2435.3	872.9	2786.3
2874.0	2459.0	2754.2	3311.3	2662.1	2468.3	2644.4	2605.2	2527.3	941.1	3638.4
577.4	766.1	1119.5	841.5	829.1	766.6	956.4	671.4	1290.6	1622.2	223.4
6449.8	2921.5	2824.4	3522.8	3180.2	2581.1	3591.9	3180.5	4237.2	2891.9	2940.0
10918.1	3988.1	4438.8	4063.1	4629.6	3760.0	4343.8	3985.9	9629.1	4982.5	3852.7
2978.0	2460.8	2959.8	3242.0	2633.8	2742.5	2401.6	2977.8	2439.0	6047.7	2315.3
745.0	2170.3	3023.0	2650.9	2525.9	2529.0	2698.9	2715.2	3145.0	3304.7	2367.6

2421.9	3450.2	4217.8
3437.2	4202.4	4431.1
419.2	551.9	477.4
811.3	683.4	609.1
250.2	199.2	300.6
2859.6	3606.9	4146.9
9153.9	10417.7	9101.3
1032.5	1565.7	2066.4
2818.4	3411.3	5257.8
2523.0	3357.4	3541.3
770.5	1263.9	954.9
3256.4	3336.3	4485.9
7181.9	7990.5	8531.2
2620.5	2458.4	3819.5
2860.9	2684.1	3975.9
2684.5	2400.1	3689.3
3510.6	3527.2	4928.8
2717.4	2528.4	3850.8
1600.6	1560.0	2284.5
3406.0	3182.7	6153.4
4740.5	7826.6	5768.3
382.1	695.4	1126.3
1482.5	1848.7	2482.7
4150.7	6045.5	4641.1
777.8	596.8	909.9
701.4	568.8	901.0
1449.2	1535.6	2165.9
2848.1	3754.3	3279.9
3022.3	4000.2	3573.6
5212.0	7095.5	6542.3
1673.9	1753.4	2527.8
318.6	393.2	559.0
875.7	1426.2	1052.0
1342.3	1615.2	2252.3
3906.1	2706.3	4697.0
2059.7	2631.1	2632.9
837.3	928.6	833.0
2653.9	3388.0	3544.5
4013.1	5272.3	5403.8
2702.2	4062.7	3821.3
2433.2	2801.7	3638.6

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AP007281.1 gg_id:269738 Lactobacillus reuteri F275 str. JCM 1112 AP007
AB425927.1 gg_id:555024 Lactobacillus reuteri str. TB-D21 AB425
AB370880.1 gg_id:268385 Lactobacillus rossiae str. DSM 15814 AB370
EU180606.1 gg_id:307389 Lactobacillus reuteri str. NS98 EU180
GU138515.1 gg_id:587018 Lactobacillus rossiae str. LSWM2-5 GU138
GU138561.1 gg_id:544158 Lactobacillus rossiae str. LSAM1-2 GU138
AB034088.1 gg_id:26075 rumen clone 3C3d-2 AB034
AB425942.1 gg_id:551940 Lactobacillus saerimneri str. TB-I37 AB425
AB186340.1 gg_id:137150 Lactobacillus salivarius str. DLS 0811 AB186
FJ751781.1 gg_id:593337 Lactobacillus salivarius str. 325T FJ7517
AJ422037.1 gg_id:76839 Lactobacillus sanfranciscensis str. C57 = R-15351 AJ422
NR_028658.1 gg_id:585770 Lactobacillus satsumensis str. NRIC 0604 NR_02
AB370882.1 gg_id:276238 Lactobacillus siligionis str. NBRC 101315 AB370
AB458681.1 gg_id:591269 Lactobacillus sucicola str. NRIC 0735 AB458
AJ621556.2 gg_id:132461 Lactobacillus vaccinostercus str. LMG 9215 AJ6215
AB218799.1 gg_id:159914 Lactobacillus vaccinostercus str. YIT 10316 AB218
AJ315640.1 gg_id:74107 Lactobacillus durianis str. LMG 19193 AJ3156
AB218797.1 gg_id:160167 Lactobacillus vaccinostercus str. YIT 10300 AB218
EF460497.1 gg_id:215674 Lactobacillus vaginalis str. SR8 EF4604
NR_025371.1 gg_id:536754 Lactobacillus frumenti str. TMW 1.666; DSM 13145 NR_02
AB242320.1 gg_id:142448 Lactobacillus mobilis str. SIID2227-1-3b AB242
AY699577.1 gg_id:106143 Lactobacillus casei str. LC2 AY699
AF243146.1 gg_id:48136 Lactobacillus rhamnosus str. F11 AF243
AY735405.2 gg_id:108112 Lactobacillus paracasei str. LPC4 AY7354
EU825659.1 gg_id:445624 Lactobacillus rhamnosus EU825
AY852248.1 gg_id:110589 Lactobacillus rhamnosus str. P15 AY852
AJ558112.1 gg_id:83495 Lactobacillus casei str. CWBI-B623 AJ5581
EF495247.1 gg_id:218969 Lactobacillus rhamnosus str. L60 EF4952
AY773957.1 gg_id:107860 Lactobacillus rhamnosus 5D AY773
AB362692.1 gg_id:249164 Lactobacillus paracasei str. NRIC 0625 AB362
AY773945.1 gg_id:108736 Lactobacillus casei str. BCRC10697 AY773
AY773958.1 gg_id:107861 Lactobacillus rhamnosus 11D AY773
AY675253.1 gg_id:100985 Lactobacillus rhamnosus str. LR3 AY675
NZ_ABWJ01000068.1 gg_id:335393 Lactobacillus rhamnosus str. HN001 NZ_AB
EU456340.1 gg_id:329446 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU456
EU454546.1 gg_id:325815 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU453007.1 gg_id:331646 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EF097456.1 gg_id:181526 mouse cecum clone SWPT19_aaa02h04 EF0974
EF096822.1 gg_id:181275 mouse cecum clone SWPT13_aaa01c03 EF0968
EU621849.1 gg_id:278869 Lactobacillus plantarum str. K2 EU621
GU125607.1 gg_id:563127 Lactobacillus alimentarius str. IMAU80187 GU125

828.5	3384.0	3399.2	3131.5	4063.4	2761.8	4351.8	3270.4	3787.8	1969.1	2515.6
60.5	568.3	765.3	529.1	352.9	572.8	410.2	649.0	790.0	962.1	216.3
64.1	1467.5	3176.9	2641.9	2042.7	1601.2	2282.5	2363.9	1732.6	2137.0	2367.2
875.0	4659.4	7311.6	4506.8	4248.3	5900.8	4263.3	6333.0	3846.3	9812.3	5223.6
41.7	727.6	1419.2	1193.0	781.3	988.7	866.6	1251.9	340.5	920.9	946.2
305.1	1254.1	1890.6	1668.7	1347.1	1744.7	1214.0	1710.8	1106.7	1218.3	1535.4
35.1	43.7	62.1	47.8	47.7	58.5	32.5	79.5	25.2	47.8	40.7
49.1	24.8	27.2	23.0	28.8	27.7	27.2	23.1	20.3	23.3	19.5
40.1	76.8	110.1	66.5	69.7	111.0	55.3	192.6	25.2	48.7	33.9
196.0	2870.6	3975.5	3363.1	3856.9	4417.3	3870.5	3829.8	2598.6	6208.3	3136.3
2524.3	6738.3	6812.4	7631.2	7890.7	6682.3	8383.4	7006.7	7843.0	4445.9	6967.8
594.8	3230.1	5505.3	2823.8	2553.2	3556.4	2157.2	4271.1	1786.6	3606.2	4998.9
344.8	4822.7	5916.0	4474.1	5716.2	5236.4	4766.8	5397.9	3529.4	5765.9	4644.4
2154.7	4047.2	4943.7	3726.3	4646.0	4613.1	4059.8	4935.2	4092.3	4841.1	4484.1
254.0	3162.5	2745.6	2238.5	2684.5	2736.4	2316.2	2898.1	1001.7	1673.7	2373.8
94.9	1156.5	1188.6	947.5	1144.9	1313.1	861.0	1542.7	395.2	1888.1	900.3
109.4	882.1	987.4	592.3	710.6	1052.6	459.4	1263.6	431.6	1508.4	627.6
105.2	1038.0	1411.9	1559.9	1246.8	1264.5	1264.4	1340.1	454.8	1690.7	916.8
38.1	296.6	403.4	493.0	311.0	356.2	194.4	371.8	108.3	191.2	143.5
70.7	403.9	548.9	477.0	424.8	402.1	696.4	450.5	184.9	468.7	370.0
37.3	102.2	161.7	82.2	91.2	136.1	176.8	223.6	68.1	64.2	107.4
7056.0	4814.5	4024.5	3155.6	1656.4	3328.2	2929.7	4363.6	3400.8	3294.7	4495.8
217.8	3663.5	3266.4	3286.6	2711.4	3106.9	3939.5	3094.6	2818.9	2338.3	3825.7
1425.0	2207.1	2734.8	2248.7	2109.0	2201.9	2425.0	2435.2	2283.7	1920.1	2018.0
52.9	1241.4	796.0	857.4	736.8	1016.9	677.3	1421.5	536.4	459.1	853.7
475.9	2832.7	2902.1	2793.5	2387.5	2305.6	3118.0	2618.4	2610.8	3351.5	2801.8
957.1	3275.7	4284.1	3885.6	3850.6	3827.0	4059.3	3854.0	1952.1	3559.4	3021.0
109.4	2361.3	1832.3	2007.6	1469.7	1947.1	2248.1	2039.8	846.3	1022.3	1906.4
112.1	2540.3	2257.4	2265.7	1930.5	2046.9	2739.8	2211.2	2250.4	1604.0	2353.6
1328.9	2264.0	2625.0	2307.2	2283.5	2323.5	2524.4	2467.8	2304.8	1935.5	2063.4
4716.4	4667.7	6513.6	5448.6	4591.6	4503.8	5338.7	4864.4	4374.0	4942.6	5082.9
9127.8	6883.3	5859.7	6541.7	5690.2	5553.8	6615.1	5497.2	8126.1	4612.4	8880.0
50.7	889.8	684.4	704.6	436.8	642.6	491.5	946.2	306.5	257.6	591.7
98.5	2379.9	1775.4	1857.1	1092.2	1489.7	1830.2	1886.0	699.2	451.1	1376.2
83.6	1428.3	2547.5	2102.0	1822.4	1950.7	2406.0	2129.5	2434.1	1400.8	1654.5
1323.2	3449.9	3907.2	3693.9	3086.6	2870.7	4173.7	3077.4	3182.4	2774.1	2927.9
113.0	1667.3	4037.7	4046.5	1205.1	1351.1	958.2	1960.3	681.0	2143.5	1074.0
6487.8	1561.6	2425.7	2442.3	1785.8	1463.8	2153.4	1872.7	4403.6	2757.5	2130.4
4598.3	2769.9	3131.4	2854.5	3254.8	2685.7	4615.6	2753.7	3774.2	3721.0	2415.7
611.4	2953.9	3284.4	2633.2	3473.8	3033.1	2488.2	3495.4	2504.7	2985.1	2511.8
1998.1	6657.5	6507.2	7280.6	6098.8	6776.2	7774.2	7272.0	5420.8	7451.0	6429.0

2451.8	3133.3	2996.2
701.1	575.4	899.3
1727.8	3377.1	6163.5
5985.5	5523.6	5570.8
832.3	1315.6	2072.7
1523.4	2047.4	1697.3
76.6	17.9	11.8
30.4	32.8	21.3
217.6	280.3	198.4
3033.5	3716.3	4273.9
7658.9	8664.7	8067.7
3067.5	3587.4	4481.2
5226.9	5480.3	7796.7
5093.5	5023.0	7579.9
2266.4	3122.5	3874.4
1407.0	1544.5	2186.3
1145.1	1303.0	1727.7
1151.9	1428.5	1618.5
209.1	296.4	677.3
265.7	627.0	540.8
92.8	231.4	420.3
3262.5	3682.4	5453.2
2425.8	3004.3	3613.9
2188.3	2607.9	3199.4
919.3	1182.6	1538.7
2045.4	2787.9	5137.3
3370.9	3773.3	5078.6
1464.1	1998.9	2276.9
1677.0	2145.8	2694.6
2239.0	2675.5	3025.0
4652.4	5406.2	7520.1
5240.6	5531.7	7627.7
574.1	817.6	1142.0
1011.3	1492.5	2115.4
2780.7	2243.6	3073.2
2784.2	3770.6	2360.7
2387.3	1951.9	1220.9
1479.3	2390.7	1860.3
2617.2	3155.5	3411.0
3155.2	3340.9	4192.0
6589.7	7725.7	7823.3

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EU381122.1 gg_id:271366 Lactobacillus reuteri str. ls21 EU381
FJ480209.1 gg_id:582919 Lactobacillus plantarum str. WCP931 FJ4802
EU453133.1 gg_id:323257 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU453
EF614861.1 gg_id:232078 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU456847.1 gg_id:316572 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4568
EU453072.1 gg_id:330003 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU453
EF097553.1 gg_id:182410 mouse cecum clone SWPT19_aaa04c08 EF0975
EU450981.1 gg_id:310929 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU450
AB362726.1 gg_id:250627 Lactobacillus plantarum str. NRIC 1592 AB3627
EU455101.1 gg_id:304585 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
AY445127.1 gg_id:107784 Lactobacillus sp. str. RA2113 AY445
AY204896.1 gg_id:82312 Lactobacillus sakei str. HNSL5a AY2048
EU526815.1 gg_id:263646 Lactobacillus paracasei str. L7 EU5268
EU509472.1 gg_id:261492 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h09 EU5094
GQ155657.1 gg_id:583427 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB186322.1 gg_id:136262 Lactobacillus johnsonii str. DLM 1701 AB1863
AM113780.1 gg_id:140659 Lactobacillus homohiochii str. DSM 20571 AM113
AY667698.1 gg_id:112026 Lactobacillus alvei str. 1G2 AY6676
AB262735.1 gg_id:190397 Lactobacillus parafarraginis str. NRIC 0680 AB2627
AB008209.1 gg_id:257632 Lactobacillus gasseri DSM 20243 AB0082
AY590777.1 gg_id:106640 Lactobacillus plantarum str. lp-onlly AY5907
AM113785.1 gg_id:139929 Lactobacillus suebicus str. DSM 5007 AM113
EU451093.1 gg_id:337269 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU451
EU456268.1 gg_id:336900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU4562
EU455863.1 gg_id:318335 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4558
EU457595.1 gg_id:352447 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4575
AJ417737.1 gg_id:61751 Lactobacillus gallinarum str. ATCC 33199 AJ4177
EU451738.1 gg_id:332402 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4517
EU455031.1 gg_id:311151 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4550
EU455929.1 gg_id:333597 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4559
EU722746.1 gg_id:322818 Lactobacillus reuteri str. L7 EU7227
EU451068.1 gg_id:324226 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
EU773885.1 gg_id:320037 Cheetah feces clone CE2_b07 EU7738
EU455600.1 gg_id:353888 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4556
EU463871.1 gg_id:293298 Seba's short-tailed bat feces clone bat_aaj06b09 EU4638
EU468211.1 gg_id:300202 lion feces clone LI1_f05_1 EU4682
DQ399354.1 gg_id:153558 Lactobacillus paracasei str. SFCB2-5 DQ399
AB366389.1 gg_id:553644 Lactobacillus rapi str. YIT 11204 (= NRIC 0743 = JCM 15 AB3663
EU457577.1 gg_id:320463 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4575
FJ749595.1 gg_id:561759 Lactobacillus reuteri str. IMAU10037; ZL12-1-1 FJ7495
AB257866.1 gg_id:157489 Lactobacillus suebicus MCH2-2 AB2578

81.2	625.5	796.1	536.0	622.2	670.9	737.9	695.6	315.2	1028.4	465.0
897.6	3657.3	4382.0	4146.6	4318.8	3615.1	3277.7	4251.3	2130.3	3272.3	3677.6
2192.7	3955.8	5452.2	5010.0	4973.0	4104.6	5905.4	4655.3	4721.0	4540.2	4257.2
7961.6	2750.3	2626.5	2755.9	2864.8	3114.4	2769.3	2714.9	3027.8	2870.8	4590.0
28.8	280.4	677.6	735.9	94.9	99.1	169.5	188.1	24.2	43.8	118.8
316.7	1608.2	2676.7	2620.9	1462.1	1393.7	1516.9	1777.2	2058.2	1718.6	1780.1
693.4	1388.4	3859.6	3372.0	1229.7	1442.8	841.4	1879.8	920.2	2461.3	1166.1
2502.8	2253.9	3798.0	3548.4	2408.2	2302.9	2430.5	2553.3	1894.3	2722.8	1900.6
1187.0	4446.9	4633.4	4552.9	5144.1	4518.5	4614.6	4794.6	4444.0	3560.5	5336.1
13909.1	5361.0	5361.4	6402.2	5718.0	6028.8	7457.5	5337.3	10336.5	3914.7	8639.5
518.9	1482.7	1641.9	1877.6	1871.9	1537.1	2163.5	1611.5	1409.8	1436.7	995.3
92.3	1155.4	1073.4	1018.1	687.7	1059.3	594.8	1027.2	847.7	470.7	824.5
1866.7	4373.1	5218.6	4580.9	4430.4	4788.7	4728.2	5086.5	3089.5	4050.9	4115.4
18530.7	9430.6	8979.4	11458.9	9741.0	9077.1	10232.2	8265.7	12993.3	10519.4	13352.5
556.7	2297.1	2595.4	2443.2	3116.4	2101.3	3480.2	2769.6	2289.3	1173.5	2118.9
56.5	766.4	912.8	1052.4	653.8	540.0	865.5	675.8	222.2	115.6	297.7
2459.5	2790.1	2231.7	2416.0	2931.3	2668.9	3233.6	2438.3	2772.4	2101.9	4803.0
64.8	830.8	1130.5	915.7	1124.3	1158.1	688.5	1223.0	415.9	1540.2	592.0
286.5	2240.7	1734.7	2834.0	2573.5	2106.6	2555.0	2522.3	3580.7	3601.2	2281.5
136.4	970.8	2835.5	3053.2	321.0	425.3	341.3	666.6	251.9	1215.5	608.1
2058.4	3693.1	3733.1	3617.9	4112.8	4272.7	4633.9	3821.7	4480.2	5185.9	3610.8
71.2	2314.3	3008.0	993.8	1653.2	2282.5	1177.2	2972.3	742.8	4600.8	1829.0
360.7	839.3	1538.7	1264.6	1021.0	1136.3	895.1	1639.4	773.1	1533.3	809.9
1309.3	1491.9	1680.3	1517.8	1274.5	1308.6	1483.9	1448.8	1231.2	1293.0	1571.9
2190.1	3571.8	5618.0	5422.1	3408.0	3840.8	3458.2	4313.3	3550.6	3649.8	4402.5
1853.4	1836.7	2806.0	2770.8	1756.6	1979.6	2196.6	2647.7	2223.0	1467.9	1919.9
36.3	723.7	1054.5	1110.2	512.9	976.9	683.6	986.9	296.4	561.7	547.1
8194.4	3182.4	4033.8	3704.4	3447.2	4329.2	3616.7	3717.7	4612.3	4537.3	3905.1
358.9	1178.5	1358.4	1329.4	1204.0	1184.6	1237.6	1311.8	734.5	1198.4	804.6
2568.1	2731.5	3384.6	3426.4	3448.7	2712.3	3246.5	2994.0	3031.7	3669.0	3025.1
53.4	360.3	544.3	263.6	271.5	243.0	222.2	336.6	762.8	805.1	83.7
328.6	1053.2	1693.6	1404.9	1142.2	1341.1	1361.0	1655.6	803.0	1810.8	1009.9
5762.0	4580.9	4686.2	4264.4	4154.1	4381.3	4114.5	4389.7	4067.1	3312.4	4142.1
3996.5	3561.3	5947.0	5436.7	5944.8	4354.5	5713.7	4756.4	3719.2	8474.7	3467.9
589.1	4589.9	4832.9	3730.6	3208.4	3892.1	3140.9	4067.0	6742.2	3019.4	3940.6
12438.7	5528.6	5639.9	5726.7	5359.5	5515.8	5713.1	5140.8	5290.5	4845.9	7521.0
1096.2	4678.7	5825.3	5169.9	5032.5	5612.6	5871.0	6171.6	1698.0	5536.0	4360.6
1353.8	3385.1	3459.4	3157.3	2944.4	3199.3	3188.3	3265.8	3499.1	1896.9	3583.6
1540.6	2944.5	4673.7	5148.9	1837.1	2221.9	1992.3	2401.2	4191.8	1783.9	3740.6
6622.1	1659.4	1683.2	1633.8	1326.5	1246.3	1379.1	1306.7	2848.8	2193.4	1875.3
2710.4	4362.4	5324.5	3770.4	4431.3	4483.0	4675.5	5296.8	2073.6	7862.0	4615.4

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3564.6	3527.0	5281.6
4279.1	5698.9	5441.5
2441.8	3115.1	3159.6
226.6	294.6	92.8
1915.3	2093.5	2023.4
1947.2	1835.8	2679.1
2686.4	2971.3	2964.1
3115.6	4536.3	5871.2
4756.0	6903.3	5232.6
2094.1	1965.2	3154.4
888.7	977.5	956.0
4355.7	4900.9	6160.3
8391.5	9594.8	9289.5
1991.2	2562.9	2302.6
963.8	999.5	1384.7
2505.7	2586.0	2932.2
1060.3	1403.5	2405.8
2430.2	2649.9	3071.0
1138.2	1153.3	463.6
4066.0	4276.8	5355.1
2386.8	2351.9	5019.0
1445.3	2195.6	1778.3
1191.0	1683.9	1684.8
4065.7	3923.4	4537.9
2035.1	2622.7	2386.3
709.0	766.9	1013.5
3099.3	5155.2	3722.9
1141.3	1891.8	1600.8
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407.4	335.4	467.9
1429.2	2249.6	1767.2
4065.0	4697.7	4490.8
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3514.9	4758.9	4786.4
5159.6	5503.0	5964.3
4696.7	6234.1	8021.1
3110.4	3469.8	4564.3
2536.5	2849.6	2295.6
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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EU081010.1 gg_id:246945 Lactobacillus plantarum str. BMG 114 EU081
EU456750.1 gg_id:334574 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU456
FJ975803.1 gg_id:509149 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9758
EU006413.1 gg_id:251090 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AY675252.1 gg_id:100824 Lactobacillus casei str. LC3 AY675
NZ_ACGU01000081.1 gg_id:470670 Lactobacillus ultunensis str. DSM 16047 NZ_AC
AY253659.1 gg_id:85511 Lactobacillus antri str. Kx146A4; LMG 22111T; DSM 16041T; CCUG 48456T AY253
GU138587.1 gg_id:568871 Lactobacillus plantarum str. LSYM4-5 GU138
EF098449.1 gg_id:187083 mouse cecum clone SWPT15_aaa03c12 EF0984
DQ057469.1 gg_id:137125 str. ii1348 DQ057
AB366391.1 gg_id:565657 Lactobacillus otakiensis str. YIT 11452 AB366
EU455899.1 gg_id:319136 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
FJ645924.1 gg_id:536462 Lactobacillus crustorum str. 90 FJ6459
DQ141558.2 gg_id:138504 Lactobacillus plantarum str. HDRS1 DQ141
EU456125.1 gg_id:315311 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU456
GU292563.1 gg_id:569336 Lactobacillus reuteri str. Probio-16 GU292
EU074833.1 gg_id:238687 Lactobacillus plantarum str. TC110 EU074
AB326356.1 gg_id:236816 Lactobacillus acidipiscis str. NBRC 102163 AB326
EU452791.1 gg_id:345369 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
GQ900607.1 gg_id:549064 Lactobacillus plantarum str. F35 GQ900
EU510744.1 gg_id:272882 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40e08 EU510
EU509523.1 gg_id:265707 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60b05 EU509
EU474981.1 gg_id:302975 red river hog feces clone RRH_aaa01h07 EU474
AB267406.1 gg_id:257071 Lactobacillus hayakitensis KBL13 AB267
AM113777.1 gg_id:140651 Lactobacillus curvatus str. DSM 20019 AM113
DQ837634.1 gg_id:170784 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
DQ837632.1 gg_id:166998 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
FJ861114.1 gg_id:545513 Lactobacillus plantarum str. KLDS 1.0630 FJ8611
EF412984.1 gg_id:210733 Lactobacillus gallinarum str. I16 EF4129
EU457730.1 gg_id:356383 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU504703.1 gg_id:259372 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04g05 EU504
EU454829.1 gg_id:346005 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU454
AY992212.1 gg_id:130575 mouse cecum clone C16_F15 AY992
EU452351.1 gg_id:356305 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
GQ900605.1 gg_id:583868 Lactobacillus plantarum str. F33 GQ900
EU510741.1 gg_id:272748 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40e01 EU510
EU510975.1 gg_id:266415 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak52f08 EU510
Y19167.1 gg_id:15232 Lactobacillus perolens str. L532 Y19167
EF097249.1 gg_id:198443 mouse cecum clone SWPT18_aaa03g06 EF0972
GQ289389.1 gg_id:561949 Lactobacillus brevis str. YJ10 GQ289
EU505416.1 gg_id:274138 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04b07 EU505

241.4	2417.7	2770.0	2584.8	3397.9	2415.8	3044.4	2917.1	1022.4	3429.5	1735.3
190.7	993.3	1573.1	1142.5	1130.6	1009.1	894.3	1830.2	655.1	662.0	716.1
19784.8	6145.1	6612.4	7202.5	6523.4	5458.0	7388.3	6322.2	9072.7	6727.9	9079.7
5623.3	2977.9	3888.8	3239.4	3315.7	4869.2	3258.3	4602.4	2210.5	6968.3	3741.2
2047.9	3332.4	5147.1	4504.2	3337.6	3609.4	3750.2	4367.3	3900.1	3094.8	3444.9
650.7	1208.4	1766.0	1797.0	1485.6	1155.4	1377.1	1190.8	534.6	639.6	888.4
172.8	2859.2	2989.9	3764.2	3342.2	3083.9	3515.2	3427.5	1922.6	1875.3	2445.6
333.0	1790.7	2488.6	1295.2	1869.0	1853.5	1123.0	2593.8	870.3	2053.5	2142.7
1919.8	1449.2	2052.7	1358.8	1451.1	1396.9	1323.4	1590.2	1707.0	1383.6	2051.6
1584.6	715.3	815.4	493.6	556.6	577.3	596.3	461.5	1678.8	2110.8	413.1
1410.7	2918.2	3423.4	3164.4	3086.3	3371.8	3165.1	3861.1	4081.8	3781.1	3335.8
13538.8	3932.3	5221.2	5577.7	5280.7	4049.5	4738.8	4240.0	4227.9	5376.1	4783.9
72.5	981.7	1699.6	1079.4	740.2	1031.2	723.7	1526.4	577.4	1062.2	983.3
545.8	2588.6	3716.8	1824.4	2524.3	3101.6	1609.0	3887.6	1483.1	3381.6	3186.1
49.6	671.9	1578.8	1453.6	589.0	534.9	619.1	716.6	277.6	731.9	527.1
587.2	671.6	1057.3	1017.9	930.6	825.7	1230.9	796.0	472.0	1209.1	385.8
2099.3	2684.4	2574.2	2457.5	2916.9	2756.5	2278.8	2655.5	2361.9	3429.9	2654.8
3026.9	3417.7	3253.0	3221.8	4029.6	3355.3	3621.6	3103.7	4130.2	2134.3	4789.6
52.8	194.3	618.6	658.4	33.3	33.4	49.4	230.8	133.2	118.8	173.2
2382.6	3275.5	3600.2	3913.8	3451.8	3433.2	3528.4	4082.8	2588.2	3497.3	3142.3
35.2	148.4	235.8	447.3	325.6	145.3	281.4	204.6	78.7	47.2	96.7
69.5	3264.7	3168.7	1512.1	1956.5	3554.2	1942.1	3642.4	3558.9	6150.8	3044.6
2831.5	3257.0	4893.6	3952.1	3911.8	3801.1	4299.5	4257.5	3739.7	6913.7	3255.4
186.0	2965.8	3137.4	2807.4	3172.6	3133.9	3767.4	2928.4	3431.4	1730.9	2640.9
110.2	1556.9	1931.3	1952.2	1130.0	1366.6	947.3	1431.9	1069.8	1355.3	1001.7
522.3	1938.9	2572.9	2418.9	2000.3	2577.3	2061.1	2707.4	1653.1	4091.4	1547.0
33.8	88.6	83.3	76.1	97.9	107.4	52.9	127.6	38.3	195.1	45.5
326.0	2368.5	2678.5	2737.2	2560.3	2390.0	2107.4	2988.9	1485.5	2823.8	2007.3
107.2	1010.0	936.3	684.2	662.1	697.9	792.5	1304.9	365.9	314.4	1035.7
162.8	624.2	2155.1	971.8	547.8	739.3	310.8	993.2	329.3	825.6	789.1
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122.8	1042.2	1775.2	1084.9	807.3	1054.5	887.8	1716.8	879.8	1407.7	1729.7
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3912.6	2306.2	2648.3	2562.6	2541.1	2424.6	2571.6	2640.2	2664.2	2601.1	3494.8
105.0	1243.0	2647.4	2549.0	1413.7	1065.1	1509.9	1445.1	1830.2	1677.9	1249.7
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1769.0	3880.4	4764.3	4928.3	4133.2	3618.5	4466.3	4290.8	6474.2	5562.8	5118.7
99.7	1142.3	2428.7	2501.3	1292.6	953.7	1491.9	1248.7	1802.2	1446.9	1166.5
99.6	2244.8	3503.2	773.7	1799.6	2494.5	672.6	4307.6	1080.8	4269.4	3119.3
138.6	1050.1	2209.1	2471.4	763.8	942.8	987.1	1163.4	408.1	560.6	742.2

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4013.0	3755.6	4921.6
3671.9	5187.4	5990.7
1202.8	1421.3	2004.5
2516.7	3101.1	4152.7
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4167.3	5160.7	5731.2
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AF316585.1 gg_id:50977 Lactobacillus sp. str. YE06 AF316
AY253657.1 gg_id:84126 Lactobacillus kalixensis str. Kx127A2; LMG 22115T; DSM 16043T; CCUG 48459T AY253
GQ156506.1 gg_id:536680 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU453934.1 gg_id:312564 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU460844.1 gg_id:300935 short-beaked echidna feces clone ECH_aai39b05 EU460
NC_009513.1 gg_id:232292 Lactobacillus reuteri F275 str. DSM 20016 NC_00
FM177140.1 gg_id:338587 Lactobacillus casei str. BL23 FM177
AM113783.1 gg_id:140595 Lactobacillus malefermentans str. DSM 5705 AM113
AB425933.1 gg_id:576004 Lactobacillus equigenerosi str. TB-F27 AB425
AB330933.1 gg_id:240133 Lactobacillus paracasei str. 1532 AB330
FJ532361.1 gg_id:585123 Lactobacillus plantarum str. 14W FJ5323
AJ272031.1 gg_id:73879 Lactobacillus plantarum str. HSW36 AJ2720
GQ900597.1 gg_id:590725 Lactobacillus plantarum str. A15 GQ900
AJ417499.1 gg_id:70957 Lactobacillus farciminis str. DSM 20185 AJ4174
AB018528.1 gg_id:18684 Lactobacillus paralimentarius str. TB 1 AB018
EU457235.1 gg_id:336661 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU457
EU453395.1 gg_id:326168 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
GU177629.1 gg_id:582937 Lactobacillus casei str. 3-2 GU177
EU776515.1 gg_id:314385 Lion feces clone LI1_d02 EU776
EU460828.1 gg_id:288584 short-beaked echidna feces clone ECH_aai38h04 EU460
EF187245.1 gg_id:348593 Lactobacillus sp. str. Bin4 EF1872
EU504694.1 gg_id:259726 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04f04 EU504
AF243163.1 gg_id:43142 Lactobacillus sp. str. KC45a AF243
GQ030443.1 gg_id:446566 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878c09c GQ030
GQ155448.1 gg_id:591100 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB268119.1 gg_id:192776 Lactobacillus composti str. NRIC 0690 AB268
EU454159.1 gg_id:323205 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU510722.1 gg_id:265346 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40a07 EU510
EU454340.1 gg_id:323666 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU454
EU505289.1 gg_id:263903 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01h10 EU505
EU460768.1 gg_id:301085 short-beaked echidna feces clone ECH_aai37g02 EU460
DQ815603.1 gg_id:171781 mouse cecum clone aab43d12 DQ815
EF097628.1 gg_id:177863 mouse cecum clone SWPT20_aaa01e05 EF0976
FN185731.1 gg_id:578837 Lactobacillus sp. 1.1424 FN185
EU453153.1 gg_id:324998 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
EU454019.1 gg_id:313356 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU454
AM500777.1 gg_id:534519 proof spatial heterogeneity hot composting clone E12 AM500
FJ751792.1 gg_id:568482 Lactobacillus farciminis str. DSPV 353T FJ7517
AB512778.1 gg_id:559510 Lactobacillus lindneri str. YIT 10387 AB512
EU505411.1 gg_id:271014 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04a08 EU505
GQ131124.1 gg_id:436188 Lactobacillus casei str. IMAU70007; BM2302 GQ131

2538.4	3352.9	4737.8	2213.0	2827.5	3509.0	2432.2	5147.5	3965.2	6535.7	4900.8
122.1	2581.6	4331.5	4349.6	1999.6	3058.6	2209.5	3229.5	987.8	2789.5	2714.5
945.7	3105.5	4459.8	4000.3	3346.5	3448.6	3595.8	3903.1	2833.0	4307.4	3885.0
445.1	1724.3	3997.7	3760.7	2039.8	1613.7	1627.2	2020.9	1998.3	1981.4	1423.1
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1174.7	2532.5	2896.4	2593.3	3143.5	2299.1	3285.8	2447.6	3039.8	2169.9	1899.7
1208.6	3465.8	4254.9	3688.2	3881.9	3984.0	3782.1	4299.1	2118.3	3183.7	2992.7
55.3	32.6	41.7	42.6	45.9	68.9	30.3	31.1	36.3	25.9	39.4
46.4	2618.7	4440.6	2493.8	2852.1	2860.6	2260.6	3318.2	1001.7	4600.8	1502.7
694.9	3109.3	3944.8	3336.6	3262.0	3564.6	3262.3	4091.1	2084.0	2813.7	2742.8
2564.4	3439.9	4989.7	2773.9	4475.1	3623.9	2928.3	4606.2	2066.3	3933.4	4955.1
1624.3	2963.0	3298.3	3026.4	3787.9	3278.8	3153.2	3569.3	2261.9	3340.8	2966.5
82.7	1724.2	2041.3	1961.3	1778.7	1692.6	1363.1	2335.2	716.7	2352.8	1161.6
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2178.9	2751.3	3192.6	3250.6	3386.1	3352.2	3202.4	3544.2	2384.5	2351.0	2368.3
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1669.2	2327.6	3624.1	2517.8	2586.0	3006.8	2103.3	3134.7	1274.3	1367.3	2414.0
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23701.9	7071.4	8707.4	9271.6	9008.3	10700.7	7419.9	11930.6	8564.2	6037.9	13900.4
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6532.5	2961.7	4248.0	3705.0	3918.3	3475.8	4227.1	3867.8	3469.2	4838.9	3931.2
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6961.8	4518.4	5728.7	5767.3	3505.5	4796.4	4338.3	3903.8	3978.3	4499.1	4654.9
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5981.8	6093.2	6794.7	6879.7	6807.4	5939.7	6738.8	5956.6	6291.5	4544.2	6497.3
4850.3	6732.7	8531.4	6687.9	6716.3	6849.4	6833.4	7639.1	7604.6	9483.3	7505.6
301.1	2744.9	2532.4	3219.4	3423.5	2660.6	3045.0	2942.5	3008.9	1549.7	2102.8
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1262.5	1566.6	1405.1
8710.1	10140.8	8303.7
2511.8	4188.4	3528.4
3682.7	4251.7	4286.0
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3335.8	3566.3	3793.1
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EU505126.1 gg_id:268866 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03c02 EU505
EU453151.1 gg_id:332855 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
AY212750.1 gg_id:100041 equine manure clone wet199 AY212
AB048833.1 gg_id:74053 Lactobacillus equi str. YIT 0455 AB048
DQ014569.1 gg_id:133995 mouse cecum clone M1_b08 DQ014
EU776667.1 gg_id:351922 Lion feces clone LI2_aae47g12 EU776
EU728754.1 gg_id:340933 Lactobacillus reuteri str. DJF_RP45 EU728
FJ192637.1 gg_id:356529 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1926
EF098373.1 gg_id:192635 mouse cecum clone SWPT15_aaa01g09 EF0983
EF096254.1 gg_id:189201 mouse cecum clone obob1_aaa03e05 EF0962
AM279150.1 gg_id:185189 Lactobacillus secaliphilus str. TMW 1.1309 AM279
EU457030.1 gg_id:353708 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
Y11374.1 gg_id:15179 Lactobacillus kunkeei str. YH-15 Y11374
EU454221.1 gg_id:326198 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N EU454
AF197125.1 gg_id:15202 Lactobacillus sp. str. C33LV5 AF197
EU419599.1 gg_id:275265 Lactobacillus plantarum str. KLDS 1.0623 EU419
EU463024.1 gg_id:297096 southern three-banded armadillo feces clone arma_aaj56f06 EU463
AB284944.1 gg_id:177366 Lactobacillus sp. str. TS1 AB284
DQ015596.1 gg_id:130744 mouse cecum clone M3_a03_3 DQ015
GQ202837.1 gg_id:551236 Lactobacillus plantarum str. C06 GQ202
EF096361.1 gg_id:174939 mouse cecum clone obob2_aaa01f01 EF0963
EU504983.1 gg_id:260003 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b10 EU504
AY281292.1 gg_id:105149 Lactobacillus curvatus str. KNUC04 AY281
X76330.1 gg_id:15190 Lactobacillus fructivorans str. DSM 20203 T X7633
AAPZ02000002.1 gg_id:325109 Lactobacillus reuteri str. 100-23 AAPZ0
AY735409.1 gg_id:108246 Lactobacillus plantarum str. LP2 AY735
EU507666.1 gg_id:270372 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02g07 EU507
EU451014.1 gg_id:316980 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU451
DQ239699.1 gg_id:144704 Lactobacillus plantarum str. L6 DQ239
EU460890.1 gg_id:302821 short-beaked echidna feces clone ECH_aai40a07 EU460
EU455582.1 gg_id:335842 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
GQ155531.1 gg_id:594070 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU453262.1 gg_id:311179 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
AB498046.1 gg_id:590362 Lactobacillus sp. str. F9-2 AB498
EF096134.1 gg_id:191524 mouse cecum clone obob1_aaa01b04 EF0961
AJ417738.1 gg_id:56512 Lactobacillus letivazi str. JCL3994 AJ4177
EU453171.1 gg_id:337918 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU453
NC_009513.1 gg_id:232290 Lactobacillus reuteri F275 str. DSM 20016 NC_00
NR_028617.1 gg_id:577716 Lactobacillus algidus str. M 6 A9; JCM 10491 NR_02
DQ015578.1 gg_id:133239 mouse cecum clone M3_g04_2 DQ015
EU451147.1 gg_id:340145 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451

12241.5	3120.2	3043.5	2366.8	3186.2	3660.0	3247.4	3585.3	4245.7	4853.8	3646.3
49.8	669.6	1559.7	1541.1	587.1	532.1	616.9	707.8	272.1	727.2	518.3
53.3	744.1	1208.4	1151.8	1129.8	750.8	1012.1	696.0	1345.8	1138.5	796.1
115.9	1066.0	1940.1	1216.5	1198.7	1371.5	1594.9	2192.4	1555.6	940.0	932.3
219.7	1393.4	2417.9	2585.5	1395.7	1550.3	1599.4	1669.6	504.1	673.0	1423.7
290.9	2020.2	2422.2	2301.2	2006.2	2184.2	2057.6	2324.1	2801.9	988.4	1762.5
752.3	451.3	561.9	590.6	462.4	513.6	809.0	634.1	285.6	566.1	454.9
55.2	1543.0	3517.2	3987.4	731.4	706.3	1024.2	1092.8	378.0	574.3	1011.7
8520.2	5640.8	7254.3	6709.4	6185.4	6363.8	6599.4	5931.8	11227.2	6503.3	6853.5
9596.9	4029.6	4531.3	4902.3	3432.7	3696.3	3701.5	4522.0	5302.3	2737.1	7429.4
694.8	2713.9	3329.8	3225.4	4643.9	2823.4	4538.4	2723.6	2759.5	972.0	2485.9
137.2	1508.9	1549.3	2012.2	654.0	1472.0	871.3	2127.7	2303.8	1802.3	1161.2
30.8	20.8	29.6	32.2	28.8	19.1	32.3	24.1	19.1	17.8	23.3
260.8	6596.0	4934.9	4835.7	4530.8	5899.6	5527.7	4816.9	5893.5	5333.5	3938.3
771.0	4630.9	5977.2	5415.4	4759.5	5567.3	5387.3	5831.3	4389.4	5489.1	4990.0
1321.8	2900.6	3176.3	3065.3	3595.3	3318.2	2697.6	3891.0	1987.1	3617.3	2680.3
1976.1	4813.7	6218.2	4552.4	4667.9	4590.6	3972.4	5645.5	5859.8	5152.0	4396.6
136.6	1595.1	2325.8	2424.7	2232.3	1585.3	2797.7	1848.0	1102.2	1546.2	1075.6
6312.0	3826.3	3817.3	3118.0	4185.9	4171.0	4091.4	3542.9	3813.3	2956.6	6264.4
163.0	4548.6	3648.4	2112.0	2401.8	3156.9	1613.8	3223.3	2398.2	4798.8	2434.4
2679.8	3513.3	4277.6	4329.0	3730.8	2647.8	3692.8	3152.4	2915.9	3320.5	2703.5
3674.4	4031.2	3726.3	3634.3	3538.3	3994.9	3467.9	3076.6	4904.1	4111.6	5730.4
505.0	1622.3	2193.4	1880.1	2061.1	1964.8	1746.4	2260.7	1136.9	3054.3	1590.3
203.4	1370.8	1666.0	1521.4	1466.3	1373.4	1865.9	1600.8	1633.8	554.2	1498.7
42.4	322.6	490.0	161.6	174.1	199.0	165.1	131.5	1235.4	781.2	64.3
6212.6	3207.5	3645.4	3638.3	4045.8	3621.8	3153.2	4166.7	2197.7	3360.9	2901.2
8566.1	7234.9	7368.5	7490.5	7181.0	6876.0	7023.9	7547.0	6449.5	7102.1	7864.7
2367.1	4145.8	6534.0	5803.7	6006.1	4336.8	6365.3	5172.8	6109.7	7826.2	4429.2
661.4	3085.2	3732.8	3010.4	3146.5	3479.0	2935.7	4103.1	3036.9	3551.6	2824.3
6447.1	5280.4	5425.9	5416.2	5599.1	5781.7	4618.7	4573.7	4396.9	4198.5	4557.9
11354.2	6274.2	5711.0	6157.7	5664.6	6805.1	6859.5	5372.7	11297.0	7608.5	7795.8
561.8	2389.5	2808.0	2314.9	3229.1	2198.7	3499.2	2767.7	2309.4	1331.6	2194.8
6310.5	2675.3	3614.1	3376.0	2647.0	3413.2	3955.8	2963.0	1672.1	3301.8	3971.6
55.6	45.1	48.5	50.7	69.0	69.5	63.5	42.2	30.4	38.9	37.0
34119.4	9036.6	9740.4	11257.3	10266.6	8772.0	9658.5	8457.3	17238.2	9711.3	13193.7
333.1	1621.9	2332.1	2004.1	1944.9	1665.6	2305.9	1974.9	1152.5	1024.5	1406.0
827.0	2485.1	4108.3	3943.5	3150.3	3010.0	3050.2	2797.2	3462.1	3148.7	2190.4
677.9	1510.6	2429.4	2064.4	1352.5	1632.2	1418.3	1423.7	1728.3	2176.8	789.7
80.4	1356.4	1904.8	2178.8	1334.3	1775.8	1426.4	2225.3	734.6	4132.8	1136.1
19379.9	6601.4	7235.5	6673.5	7313.2	8080.0	7729.8	6145.0	8736.4	6489.8	9249.8
25704.1	6697.9	7320.7	8324.1	7411.4	6983.4	7594.3	6798.1	9505.2	9851.4	9774.2

3189.9	4702.2	4005.3
731.8	848.7	620.2
1077.3	1128.6	1140.4
2272.2	2104.0	4173.8
1516.2	1535.9	2018.8
1801.3	2809.0	2245.0
664.2	837.7	562.2
1846.5	1659.0	1576.9
5663.8	7515.3	6212.2
3396.6	4010.6	3120.1
2373.8	3525.0	2870.3
750.8	1584.7	894.7
22.1	29.9	28.7
4190.9	5503.9	5966.1
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4366.1	6782.5	7727.6
1855.0	2134.3	2512.7
3272.0	4012.4	4266.4
3033.7	2823.9	5120.4
2977.2	4366.9	3161.0
3172.5	3802.5	3784.2
2294.2	2249.3	3453.3
1191.5	1341.0	2501.0
253.6	247.7	373.5
4122.8	4005.8	5007.6
5980.9	7628.8	9707.3
5560.6	5723.6	6884.0
3591.6	4187.1	5223.8
4725.9	5705.5	7796.3
5529.1	7047.5	5661.3
2066.5	2748.1	2639.9
2510.3	3562.3	2621.7
74.2	71.8	69.6
8190.1	11288.7	9745.0
2049.8	1881.9	2698.7
2590.5	3658.0	3134.8
1666.8	1711.7	1481.1
1734.9	1605.6	2597.9
5763.5	8581.5	6134.8
6898.5	8442.6	7867.1

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EU457651.1 gg_id:318419 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU457
EU454579.1 gg_id:324926 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU454
AY675255.1 gg_id:101305 Lactobacillus paracasei str. LPC1 AY675
EU457692.1 gg_id:336522 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU457
EU460769.1 gg_id:301721 short-beaked echidna feces clone ECH_aai37g03 EU460
AM113778.1 gg_id:140432 Lactobacillus graminis str. DSM 20719 AM113
NR_024885.1 gg_id:538781 Paralactobacillus selangorensis str. LMG 17710 NR_02
GQ131183.1 gg_id:426143 Lactobacillus reuteri str. IMAU70067; HS1302 GQ131
EU456756.1 gg_id:335169 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU456
GU125459.1 gg_id:569558 Lactobacillus alimentarius str. IMAU80037 GU125
EU452409.1 gg_id:306780 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
DQ815922.1 gg_id:168412 mouse cecum clone aab24c08 DQ815
EU455875.1 gg_id:342787 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU455
AM905389.1 gg_id:275385 Lactobacillus cacaonum str. LMG 24285 AM905
AB257864.1 gg_id:158959 Lactobacillus camelliae MCH3-1 AB257
EU461951.1 gg_id:292302 white-faced saki feces clone Saki_aaj64c05 EU461
AY773954.1 gg_id:107854 Lactobacillus paracasei 4C AY773
EU454930.1 gg_id:338011 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU454
EU511492.1 gg_id:273320 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak05e02 EU511
DQ103575.1 gg_id:134244 Lactobacillus casei str. AK16 DQ103
EU454940.1 gg_id:340982 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU454
EU456468.1 gg_id:322647 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
AB362730.1 gg_id:251080 Lactobacillus sakei str. NRIC 1600 AB362
L23507.1 gg_id:15143 Lactobacillus reuteri L23507
AB362735.1 gg_id:247913 Lactobacillus pentosus str. NRIC 1732 AB362
AY690834.1 gg_id:123663 Lactobacillus nantesii str. Lp33 AY690
EU454131.1 gg_id:316490 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU454
EU456036.1 gg_id:319309 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU456
EU456289.1 gg_id:316723 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU455211.1 gg_id:326968 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
AB512775.1 gg_id:562275 Lactobacillus similis str. YIT 12117 AB512
EU456989.1 gg_id:314305 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU456
AF049743.1 gg_id:15206 Lactobacillus sp. str. LMG 17676 AF049
EU457691.1 gg_id:318641 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU457
AM905388.1 gg_id:268188 Lactobacillus fabifermentans str. LMG 24284 AM905
GQ030571.1 gg_id:428757 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw880a05c GQ030
EU508681.1 gg_id:270597 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49d02 EU508
EU509957.1 gg_id:261239 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c10 EU509
EU776728.1 gg_id:333200 Lion feces clone LI2_aae49c06 EU776
EF536364.1 gg_id:219489 Lactobacillus casei str. Zhang EF536
EU450898.1 gg_id:344695 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU450

569.8	1609.5	2268.9	1972.2	1786.2	1737.2	1652.0	2166.8	1452.2	2677.2	1827.1
34.9	140.3	713.3	745.0	110.9	45.9	80.2	148.6	29.9	42.5	120.4
1553.1	3559.1	6332.6	4742.9	3699.9	4138.2	3734.5	5348.9	3431.9	3065.9	3175.2
796.3	3244.2	4871.3	4808.6	5165.2	3075.9	4722.5	3987.8	6153.2	3208.0	3185.2
46.9	662.5	777.5	400.2	761.4	850.2	466.9	1039.8	353.7	607.3	546.1
76.6	1343.7	1580.8	1586.0	944.5	1132.4	794.0	1215.9	833.8	780.7	931.9
8759.6	2457.8	2468.7	2654.8	2740.0	2331.1	3049.4	2533.4	2327.8	2757.8	3119.4
6114.5	1645.5	1996.6	1966.6	1375.0	1257.9	1552.5	1380.3	3004.5	1955.8	2048.3
5662.2	3855.1	3999.7	4425.7	3960.3	4008.1	3764.6	4394.5	3836.2	4971.2	4068.9
1952.4	6495.7	7034.7	7502.1	6170.1	6277.7	7645.9	6428.8	5975.9	7554.4	6799.5
57.4	507.2	1771.9	1811.0	293.2	541.4	596.0	532.6	123.9	209.3	385.0
11203.1	7313.1	8178.2	7505.3	7254.0	7340.1	6608.0	7340.3	7463.0	7872.2	9586.5
13439.0	7023.1	7375.2	7051.8	6545.5	8274.1	6930.2	6551.7	11051.4	7992.9	9667.8
2923.8	2450.8	3246.8	1288.8	2524.9	2394.5	2497.3	3136.3	2416.2	1623.4	2272.2
12604.0	4499.6	4193.3	4220.0	4444.3	4470.5	5194.7	4138.0	4353.4	4950.8	5469.1
22756.5	4317.3	3968.0	4559.6	5150.6	4743.9	4461.0	5745.2	4122.4	3983.7	5328.1
1969.9	2825.7	3130.0	3358.3	2192.7	2735.5	2666.4	3212.4	2019.5	1412.9	2788.1
809.3	3299.8	4840.8	4691.8	4311.9	4307.9	4877.2	4251.9	3818.1	5440.8	2948.2
4276.1	4744.1	5823.2	5242.2	5264.3	5023.5	5749.7	5435.7	4636.4	7595.6	5235.5
2180.4	3282.2	3621.9	3250.9	3922.2	3835.8	3409.0	4077.9	2665.5	2946.8	2744.7
6146.2	3876.9	4418.9	4944.6	4384.3	4103.3	5012.3	4148.3	3106.0	3528.7	3809.9
16037.1	3002.5	3461.4	4041.1	2732.8	3457.5	3044.7	3278.6	4927.6	5073.5	4229.1
83.2	1387.7	1602.9	1492.6	929.6	1256.8	703.5	1170.0	894.7	1118.3	842.3
50.4	106.8	220.1	168.3	108.7	115.3	111.5	214.2	58.7	94.7	68.0
280.0	2405.9	2846.7	2726.3	2187.7	2335.7	1923.9	3575.1	1516.9	3254.3	2314.9
1263.8	4569.4	6010.5	5283.2	3077.5	4667.1	5785.7	4844.8	6588.8	6725.4	5887.8
28507.6	9475.0	9709.0	10821.0	8755.9	9603.0	9087.1	8903.4	11977.1	10452.1	13203.9
6300.6	5622.8	6205.2	6167.7	6622.9	7835.0	7953.1	5493.3	11812.6	8166.5	6199.1
44.4	1520.7	3257.7	3551.7	607.4	891.5	851.4	1403.9	532.9	1454.5	929.5
9372.5	3826.8	5521.5	5051.3	3947.4	4726.1	4174.3	4380.8	5020.2	4146.9	4226.5
72.7	1371.2	1745.5	2005.2	1950.3	1312.3	2107.8	1300.6	1191.3	1952.3	894.1
1253.9	2419.6	4669.5	4129.8	2344.1	2664.1	2400.2	3312.0	2233.7	3057.3	2624.4
12514.7	2399.2	3098.9	2126.1	2745.0	2192.2	2377.4	3082.6	2866.6	3937.9	3113.9
9254.7	6154.6	6429.2	6138.0	6194.0	6718.0	6241.3	6133.6	6764.4	10256.4	6384.9
458.4	3464.7	4265.9	2813.8	3324.6	3507.5	2240.5	5173.2	2093.1	4645.1	3337.2
2995.3	3554.0	3579.8	2567.9	2439.2	4154.3	2162.3	2720.7	3544.4	3260.8	2895.8
104.1	369.4	594.6	501.1	373.2	410.5	426.1	886.8	242.4	770.1	484.1
492.1	1580.8	3329.3	3078.9	1775.5	1412.3	1622.9	1642.2	1840.5	1472.3	1099.1
476.4	3162.4	4118.6	2610.0	2020.8	2736.1	1913.8	2690.9	2097.0	1670.0	2755.2
707.2	3647.7	4378.6	3923.6	3564.6	3813.5	4021.0	4017.7	2281.2	3260.3	3510.1
333.5	1124.5	1709.9	1351.0	1219.6	1408.4	1305.5	1759.7	903.4	1845.9	1027.2

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939.6	903.4	1624.8
1162.4	1376.0	1117.2
2986.8	3710.4	3280.8
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3998.2	4960.6	5528.3
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3877.6	4568.6	5323.1
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3413.8	4936.4	3389.4
1454.4	1724.0	1444.0
253.7	134.4	196.0
2718.1	2526.5	3837.1
3951.4	5175.7	5264.9
7167.3	9525.2	9339.2
5336.5	6528.0	6085.3
1574.1	1314.4	1067.7
3893.0	5262.4	4881.2
1956.6	2222.9	5726.6
3225.2	3107.9	3435.2
2643.8	4387.4	3912.4
6331.6	6606.3	7600.4
3623.3	3855.6	6909.1
2618.9	2834.6	4051.8
407.5	1046.1	1222.9
1691.7	2082.9	1881.0
2783.9	3757.1	3310.8
3466.6	4358.8	5171.1
1491.4	2391.0	1898.6

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EU511587.1 gg_id:258972 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak07a10 EU511
EU451452.1 gg_id:316790 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU451
AY773955.1 gg_id:107855 Lactobacillus paracasei 9C AY773
EU381123.1 gg_id:262517 Lactobacillus reuteri str. ls23 EU381
EU453529.1 gg_id:313523 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU453
GU458924.1 gg_id:561670 microbiota human male female forehead forearm and influence make-up skin clone GU458
GQ421851.1 gg_id:578242 Lactobacillus buchneri str. L225 GQ421
EU455189.1 gg_id:322892 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU455
GQ155609.1 gg_id:587513 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
X76328.1 gg_id:15144 Lactobacillus reuteri str. DSM 20016 T X76328
AY349383.1 gg_id:92041 human oral cavity clone HT070 AY349
GU125550.1 gg_id:576646 Lactobacillus plantarum str. IMAU80128 GU125
DQ815338.1 gg_id:162668 mouse cecum clone aab46a06 DQ815
EF096511.1 gg_id:180677 mouse cecum clone obob2_aaa04a10 EF0965
EU456758.1 gg_id:328141 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU456
EU457050.1 gg_id:321592 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
EU074832.1 gg_id:251568 Lactobacillus plantarum str. TC97 EU074
EU456918.1 gg_id:340234 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU508703.1 gg_id:259236 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49f06 EU508
AB362982.1 gg_id:247174 Lactobacillus plantarum str. LQ80 AB362
EU453721.1 gg_id:316608 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU453
E17066.1 gg_id:36168 Lactobacillus sp E17066
EU474925.1 gg_id:299491 red river hog feces clone RRH_aaa04e04 EU474
FJ861112.1 gg_id:554107 Lactobacillus plantarum str. KLDS 1.0628 FJ8611
DQ057436.1 gg_id:133363 str. ii1204 DQ057
AB290830.1 gg_id:514694 Lactobacillus equicursoris str. DI70 AB290
AB362657.1 gg_id:245705 Lactobacillus pentosus str. NRIC 0390 AB362
EU509821.1 gg_id:274002 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21f01 EU509
DQ815684.1 gg_id:169512 mouse cecum clone aab44g09 DQ815
EU452068.1 gg_id:332130 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU452
EF097607.1 gg_id:189318 mouse cecum clone SWPT20_aaa01b09 EF0976
EU451715.1 gg_id:342038 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU451
GQ275139.1 gg_id:590798 gut symbionts are tightly linked herbivory ants extract single ant clone #163 GQ275
EU507448.1 gg_id:275991 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03d04 EU507
EU456851.1 gg_id:306115 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU456
AM697058.1 gg_id:226751 sequencing libraries indoor dust clone BF0002B008 AM697
EU465427.1 gg_id:300717 lion feces clone LI3_aah77b08 EU465
EU451859.1 gg_id:328253 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU451
EU507501.1 gg_id:259734 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b10 EU507
EU381121.1 gg_id:267051 Lactobacillus reuteri str. ls4 EU381

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436.9	1911.3	1767.9	2075.5	1694.8	3200.1	1773.4	2591.2	902.4	1533.1	1389.1
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2561.9	3422.9	5261.8	4870.8	4816.4	4312.4	5137.2	4875.1	3624.9	8537.1	3571.8
4932.1	5064.0	5309.0	4869.4	4597.4	5031.6	4913.2	5266.5	4413.7	4004.3	5052.4
1406.3	3075.5	3822.4	3688.1	3089.8	3400.0	3183.3	3918.6	4098.8	3990.9	3698.7
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212.7	2691.4	2960.3	2522.5	2452.6	2649.1	2561.5	2379.1	2365.1	1878.3	2465.0
108.1	950.1	1608.1	730.4	1215.1	997.8	555.3	1643.9	421.8	1008.3	1215.5
40.7	590.1	1841.8	1794.4	162.5	200.6	221.7	383.1	200.5	342.6	293.1
461.1	3643.0	5475.3	4832.4	3925.2	3642.5	4060.3	4101.2	6171.6	4327.6	3697.2
2114.7	1886.3	2558.2	2447.0	1907.0	2067.6	2158.1	2472.1	2377.2	3100.9	1870.5
162.1	1767.3	3329.3	2951.6	1908.3	1649.6	1977.4	2043.6	2206.5	2268.9	2037.3
282.6	2523.8	2967.6	2848.6	2537.0	2600.3	2250.6	3535.2	1650.1	3069.1	2229.8
814.6	2554.8	4668.7	3726.4	3087.2	3693.2	3181.1	2940.1	3243.6	2895.7	3854.1
121.8	1579.0	2097.3	1524.7	1626.0	2509.4	1628.6	2863.4	1416.5	3798.6	2688.0
282.6	2369.0	2791.4	2669.6	2537.0	2436.2	2106.3	3316.3	1443.9	3070.2	2107.6
3153.5	4557.8	4861.2	4916.0	5028.6	4633.2	4970.7	4484.3	5755.6	6033.4	4777.6
11253.0	3109.9	2997.9	3072.2	3172.9	3550.3	3307.2	4028.9	5459.9	3714.1	4615.1
2402.4	2141.6	2735.6	2478.8	2405.8	2189.0	2608.7	2456.8	1939.7	2409.5	2293.2
119.0	1742.5	2001.5	1720.1	1881.5	1797.5	1468.9	2672.7	917.1	2087.4	1373.3
11191.6	3630.3	2797.4	3417.1	2980.6	3224.7	2781.8	2923.6	4342.7	3132.2	4106.7
206.0	1738.9	3725.8	4553.4	1628.4	1452.6	1693.2	2733.9	1423.3	784.1	1693.3
2888.3	3757.5	4071.3	3881.0	4053.8	3917.1	3538.0	4242.4	2802.4	4525.2	3704.7
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13312.5	7597.0	6802.5	7241.7	6889.6	8356.9	7426.9	6531.3	8989.3	10206.0	10820.9
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611.8	1272.5	1969.7	1689.0	1434.1	1518.8	1656.7	1630.6	1198.3	2115.9	1660.7
1558.8	1744.6	2418.7	2805.9	2183.8	1647.8	2364.6	1829.9	2760.1	996.4	1557.4
4750.7	7125.3	6085.9	6923.6	6546.9	5982.4	6591.6	5892.8	5696.0	5206.3	5499.9
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6847.2	4434.4	3689.9	3835.6	4157.2	3863.9	3715.7	4040.6	4103.4	3095.2	3322.6
816.1	1252.7	2371.6	2090.1	1195.3	1304.3	1181.0	1730.5	1205.5	1574.1	1249.4
4239.8	2993.9	3067.2	3345.1	3356.7	2872.8	3076.3	3149.8	2804.5	1252.3	3271.6
12654.3	6048.7	5232.3	5435.9	6511.2	5279.9	5596.5	5091.4	7017.5	6808.5	6028.6

627.6	437.5	867.7
5459.0	5785.8	5932.0
1588.0	2573.6	2037.1
2394.4	4156.5	4388.8
1270.2	1563.7	1305.7
4919.7	4855.5	6266.1
4925.7	5178.3	6067.7
3441.1	3546.1	4489.5
1422.5	2226.0	1771.1
1123.8	1032.0	987.6
6400.6	8008.0	7165.2
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2971.0	4539.1	4185.3
2250.8	3059.4	3251.2
1971.1	1985.3	3113.5
2593.2	4614.0	3202.2
3065.8	1478.5	1747.7
3776.8	3905.3	4696.4
1272.0	1635.4	1879.2
6380.3	7770.0	7540.2
3743.0	5432.7	4376.8
1509.3	1910.7	2343.3
1808.6	2166.9	2727.0
5352.3	6853.7	7497.0
3401.8	4420.0	4440.5
1698.2	1323.3	2097.2
1517.8	1629.0	2566.8
4150.6	4571.8	3536.1
1546.3	2294.6	2545.9
3014.2	3470.1	3702.4
5676.4	8538.9	6482.5

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AL935261.1 gg_id:80366 Lactobacillus plantarum str. WCFS1 AL9352
FM177140.1 gg_id:338585 Lactobacillus casei str. BL23 FM177
EF098024.1 gg_id:182758 mouse cecum clone SWPT12_aaa04c03 EF0980
EU507563.1 gg_id:267604 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01b05 EU5075
EU455156.1 gg_id:339840 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4551
DQ239695.1 gg_id:141655 Lactobacillus plantarum str. L2 DQ239
AB470237.1 gg_id:363520 Lactobacillus sakei str. S2 AB4702
EU460915.1 gg_id:296432 short-beaked echidna feces clone ECH_aai40d09 EU4609
EF097172.1 gg_id:182972 mouse cecum clone SWPT18_aaa02d10 EF0971
EF097176.1 gg_id:190167 mouse cecum clone SWPT18_aaa02e05 EF0971
EU454503.1 gg_id:326900 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4545
EU510255.1 gg_id:266771 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03f06 EU5102
AY204897.1 gg_id:81036 Lactobacillus sakei str. HNSL5c AY2048
EU455625.1 gg_id:315788 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4556
EU451160.1 gg_id:335029 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4511
EF412985.1 gg_id:208876 Lactobacillus gallinarum str. I26 EF4129
EU507280.1 gg_id:272684 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01a06 EU5072
FJ405227.1 gg_id:359669 Lactobacillus casei str. ZJ3 FJ4052
AB368904.1 gg_id:282265 Lactobacillus plantarum str. T8-7 AB3689
AF308146.1 gg_id:72717 Lactobacillus thermotolerans str. G 12 AF3081
EU474952.1 gg_id:299475 red river hog feces clone RRH_aaa04g03 EU4749
EU508709.1 gg_id:264123 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g05 EU5087
AB362741.1 gg_id:249746 Lactobacillus pentosus str. NRIC 1753 AB3627
AY735404.1 gg_id:108108 Lactobacillus plantarum str. LP1 AY7354
GQ131182.1 gg_id:376168 Lactobacillus reuteri str. IMAU70066; HS1301 GQ131
DQ015426.1 gg_id:130724 mouse cecum clone M3_h10 DQ015
AB368903.1 gg_id:282170 Lactobacillus plantarum str. T4-5 AB3689
EU074828.1 gg_id:243630 Lactobacillus plantarum str. TC41 EU0748
AB162131.1 gg_id:106519 Lactobacillus nagelii str. NRIC 0559 AB1621
EU457936.1 gg_id:323012 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4579
DQ399353.1 gg_id:154984 Lactobacillus paracasei str. SFCB2-4 DQ399
EU453809.1 gg_id:318211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4538
GQ461596.1 gg_id:593464 Lactobacillus plantarum str. K25 GQ461
EU457051.1 gg_id:317830 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4570
EU451427.1 gg_id:354114 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4514
GQ156407.1 gg_id:537937 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU456062.1 gg_id:308210 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4560
AB362731.1 gg_id:255682 Lactobacillus sakei str. NRIC 1609 AB3627
GU177634.1 gg_id:578809 Lactobacillus casei str. C-1 GU177
EU474892.1 gg_id:287698 red river hog feces clone RRH_aaa04e08 EU4748

1039.8	3692.7	4512.2	3243.8	2744.1	3222.7	3074.5	3451.5	5966.5	3108.3	3465.9
325.9	2055.1	2422.2	2566.2	2251.0	2175.7	2111.2	2867.8	1411.7	2280.2	1924.3
2200.7	3299.7	4167.0	3477.0	3931.1	3849.5	3415.7	4362.4	2502.5	2965.2	2748.2
9502.0	4939.2	5710.3	6208.0	6596.8	5206.5	6258.3	5182.0	5436.0	4635.8	6228.4
1696.6	2834.9	3339.7	3123.9	3282.6	2869.7	3157.5	2893.4	2718.1	1835.6	2956.1
338.1	714.2	1163.3	938.4	796.6	909.4	909.6	1003.9	590.3	1561.7	651.8
543.2	3169.7	4830.2	1814.4	3206.0	3924.3	1819.4	4521.5	1561.0	4589.0	3612.5
108.5	1598.2	1918.9	2002.6	1147.9	1431.2	1013.8	1431.1	1077.1	1304.4	1120.4
48.1	733.8	684.0	270.9	753.7	640.4	741.4	1043.2	424.4	408.6	453.5
9162.4	3454.5	4058.5	3903.7	3593.7	3385.1	3488.5	3817.0	3735.5	5320.5	4256.6
47.9	765.0	2607.4	2557.9	497.2	415.7	398.7	779.8	435.6	721.4	680.0
228.7	823.1	1754.9	1668.3	598.6	615.2	524.3	866.9	439.2	580.2	697.8
16992.3	3245.5	3011.4	3220.5	4598.3	3271.0	3942.4	3142.9	4041.9	3753.5	2818.5
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452.6	3219.9	5316.2	5565.5	3306.8	3169.9	2540.7	3294.3	2717.2	3781.7	2391.9
464.4	2325.4	4567.6	4465.8	2977.0	2357.1	2695.0	3306.5	2266.8	3141.0	2757.1
64.1	453.4	251.2	216.6	216.1	192.2	373.1	610.8	103.7	69.8	229.1
84.9	1722.2	2349.1	2202.4	2167.5	1904.7	2178.1	2551.0	1019.6	731.7	1676.8
894.7	2872.0	4205.3	4211.9	3280.9	3576.3	3240.6	4392.7	2397.3	5136.8	2375.0
281.4	2363.2	2619.7	2689.4	2322.8	2442.8	2096.6	3558.0	1600.4	2979.2	2123.7
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57.4	169.2	234.2	186.8	154.0	111.3	361.6	154.7	61.8	45.6	71.2
13772.4	8693.4	9366.0	9061.1	7222.1	8810.1	8579.3	8982.4	12503.6	9941.9	11380.7
4980.0	2035.5	2163.9	1972.9	2660.5	2581.9	1603.9	2373.4	1632.9	1678.1	1993.0
7030.4	7066.8	6617.5	6535.4	6258.7	6835.2	6213.4	5779.8	8525.7	9188.2	7540.4
1338.7	3233.5	3490.9	3115.3	4050.8	2857.8	4048.0	3190.2	3730.1	2350.9	2397.7
692.0	1073.6	1317.5	1151.4	1251.1	1396.0	1372.7	1383.2	747.8	1330.8	1079.7
222.6	2265.3	2720.9	2794.4	2219.8	2451.0	2068.9	3517.8	1580.5	3053.5	2052.3
8760.0	4548.7	4903.4	4894.7	4411.8	4621.0	3429.7	4813.7	4173.1	4526.8	5341.0
175.4	93.5	94.3	169.3	164.5	74.2	110.6	119.3	27.1	30.9	82.8
1990.0	3247.3	5332.4	5075.8	5354.6	3833.0	5209.2	4262.4	3193.4	6979.4	3507.1
17940.3	10005.9	12109.7	11821.3	8178.7	10403.8	10281.5	10752.0	12883.0	10315.8	14404.9
63.4	968.9	1885.8	2060.8	748.0	1110.2	990.2	1373.1	604.9	1086.1	803.3
473.1	1422.9	1831.6	1400.7	1841.6	1851.6	1395.0	2500.5	1135.9	1383.3	1412.8
894.3	1519.8	3966.2	3217.9	1643.3	2182.4	1928.0	1929.3	2985.6	2389.1	1659.4
65.1	947.2	2268.5	2057.7	857.0	761.4	818.7	1035.4	511.7	1127.1	1003.4
988.9	3948.5	5498.5	4892.2	4478.8	4411.1	4926.9	4954.3	5594.0	5592.2	5566.5
3679.2	996.4	1468.0	1134.8	947.8	1079.4	1157.6	1452.0	1058.5	1706.1	1208.4
820.4	4066.0	5049.7	4850.2	3704.6	3782.2	4106.1	4108.8	3315.1	4846.7	3912.8
1404.3	2229.0	2438.0	2134.6	2254.5	2294.6	2505.8	2291.7	2287.3	1902.8	2049.6
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1338.6	1380.1	648.3
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EU460885.1 gg_id:302664 short-beaked echidna feces clone ECH_aai39h11 EU460
EF605142.1 gg_id:229845 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EU453930.1 gg_id:328325 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU453867.1 gg_id:313722 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU457601.1 gg_id:337406 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU457
EU455334.1 gg_id:317894 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
NR_029084.1 gg_id:576663 Lactobacillus gastricus str. Kx156A7; LMG 22113T; DSM 16045T NR_02
AB362607.1 gg_id:244469 Lactobacillus sakei str. NRIC 0126 AB362
EU510005.1 gg_id:274605 cecal contents Mus musculus strain C57BL/6J; WD1 clone WD1_aaf15e11 EU510
GU369759.1 gg_id:524305 Lactobacillus plantarum str. YM-4-5 GU369
EU452893.1 gg_id:303591 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
GQ155548.1 gg_id:512953 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AB362667.1 gg_id:258139 Lactobacillus pentosus str. NRIC 0403 AB362
GQ231436.1 gg_id:588182 Lactobacillus reuteri str. DSPV 002C GQ231
GU299083.1 gg_id:534440 Lactobacillus casei str. NQ2-2 GU299
DQ815681.1 gg_id:166336 mouse cecum clone aab44g06 DQ815
AJ965487.1 gg_id:126988 Lactobacillus arizonensis str. DSM 13273 AJ9654
AB239468.1 gg_id:141834 Lactobacillus casei str. CP1-13 AB239
EU457018.1 gg_id:330111 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
GQ030377.1 gg_id:467257 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw877c08 GQ030
EF095994.1 gg_id:186522 mouse cecum clone lean2_aaa01f03 EF0959
FJ682870.1 gg_id:530798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
EU454755.1 gg_id:356144 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU454
EU460235.1 gg_id:295058 polar bear feces clone PB1_aai25b05 EU460
GQ155587.1 gg_id:513479 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF096038.1 gg_id:187066 mouse cecum clone lean2_aaa02e07 EF0960
AB303848.1 gg_id:257805 Monitoring Pickling Bed Fermented Rice Bran Which Dominated S-Growing Lactobac AB3038
EU439433.1 gg_id:267700 Lactobacillus plantarum str. 1L48P35 EU439
EF097557.1 gg_id:196803 mouse cecum clone SWPT19_aaa04c12 EF0975
DQ815682.1 gg_id:167719 mouse cecum clone aab44g07 DQ815
DQ015553.1 gg_id:135934 mouse cecum clone M3_e03_2 DQ015
EU460783.1 gg_id:296454 short-beaked echidna feces clone ECH_aai37h09 EU460
EU454204.1 gg_id:347044 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74 EU454
FJ678780.1 gg_id:521424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
EU465367.1 gg_id:302089 lion feces clone LI3_aah76b05 EU465
AB332024.2 gg_id:246232 Lactobacillus nodaensis str. IZ4B AB332
EU526816.1 gg_id:276202 Lactobacillus plantarum str. Z6 EU526
GQ900606.1 gg_id:550314 Lactobacillus plantarum str. F34 GQ900
EU505359.1 gg_id:276978 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03b09 EU505
GQ131153.1 gg_id:385174 Lactobacillus casei str. IMAU70037; BM10307 GQ131
AJ242968.1 gg_id:15128 Lactobacillus gallinarum str. ATCC 33199 AJ2429

43.7	1509.4	2220.7	2293.2	1235.3	1249.9	1585.0	1611.8	772.6	1287.8	855.2
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19906.2	5389.8	5791.0	6434.1	5555.2	6552.1	7662.5	3764.2	10902.7	6816.8	8252.8
4363.3	2561.3	4163.5	4105.7	3008.1	2757.8	3057.8	3392.5	2403.1	1626.3	2449.5
94.6	1095.7	2514.1	2416.7	1269.9	921.7	1234.8	1302.4	1756.9	1477.2	1106.1
78.7	640.6	1422.6	1025.0	508.7	779.2	1005.0	829.5	376.6	774.2	939.7
70.2	2114.8	3439.9	1551.4	2464.8	2764.4	1682.9	3264.4	2536.0	3390.6	1506.4
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4275.5	2137.1	2259.2	2178.8	2066.3	2264.0	2349.4	2357.6	3502.7	3365.8	3055.0
324.6	2284.5	2589.0	2497.5	2269.8	2305.6	1957.0	2932.6	1387.5	2802.1	2014.1
2875.3	4309.8	5948.6	5854.3	4479.0	4151.0	5004.5	4394.2	4105.9	4853.1	4438.4
706.2	3238.1	4900.9	4250.3	3723.3	4016.6	3881.1	4557.1	4242.6	5677.5	4503.5
325.6	1851.8	2640.3	2216.8	2101.5	1768.4	1473.3	2690.5	1058.4	1765.7	1455.9
6129.3	1636.1	1724.7	1725.2	1434.4	1340.9	1409.0	1585.6	1789.6	1928.7	2081.5
84.1	1013.0	1579.3	1001.5	856.0	1227.1	577.8	1767.9	435.2	1281.4	761.1
285.7	2027.8	2384.6	2181.5	2200.1	2369.1	1890.1	3173.0	1028.8	3643.3	2238.4
1432.0	4924.3	5459.8	7246.8	8397.0	5266.0	5531.6	6872.6	3887.7	5874.2	5123.1
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6842.4	3239.2	4286.1	4423.4	3875.7	3917.4	3700.6	3461.5	4615.2	3272.7	3474.6
26394.1	5071.6	5546.9	5777.0	7639.4	6213.5	5928.3	6115.2	7015.0	6780.2	5139.1
34.5	113.5	111.9	136.2	253.8	197.8	168.0	177.1	47.3	47.3	67.5
1525.8	3111.5	4333.0	4599.2	2776.5	3301.5	3067.5	3272.8	2454.0	5238.5	3237.0
3806.0	2534.2	2282.8	2117.5	1881.9	2257.6	2662.5	1852.2	3320.2	2950.0	2117.0
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108.5	262.6	774.0	774.7	157.0	181.7	174.6	213.2	173.4	243.8	248.6
335.8	2550.2	4641.8	4457.0	3713.6	2946.8	3787.5	3392.1	3045.8	2283.3	2019.9
109.6	2336.1	3034.9	2068.4	2153.7	2569.6	1684.2	3202.4	1479.4	3096.3	2520.9
180.8	933.6	1570.5	1615.9	1193.1	995.9	1268.0	1367.8	642.2	1367.9	911.3
4916.4	4482.5	5461.5	5844.8	4843.4	4982.2	5181.6	5502.7	6942.2	5894.4	5387.4
9983.8	4876.8	5186.3	4500.0	3871.9	4557.7	4628.8	4475.0	5294.9	5305.4	5827.3
105.2	3470.2	5820.9	5457.6	4154.9	3712.7	5699.7	5186.8	1860.8	2360.6	3247.1
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229.1	108.4	118.9	118.3	152.0	81.5	127.9	120.5	71.1	84.0	80.4

1841.1	1996.3	3018.5
5729.7	6626.6	7581.5
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AF243151.1 gg_id:22892 Lactobacillus gasseri str. KC36a AF2431
DQ815389.1 gg_id:164758 mouse cecum clone aab47d05 DQ815
EU451364.1 gg_id:346613 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4513
GQ156345.1 gg_id:575537 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
AM292799.1 gg_id:187763 Lactobacillus ceti str. 142 AM292
AY253660.1 gg_id:84798 Lactobacillus ultunensis str. Kx146C1; LMG 22117T; DSM 16047T; CCUG 48460T AY2536
EU451966.1 gg_id:333408 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4519
EU161635.1 gg_id:239571 Lactobacillus murinus str. LR EU1616
GU191837.1 gg_id:581162 Lactobacillus reuteri str. BR11 GU191
AB303841.1 gg_id:236486 Lactobacillus acetotolerans str. JCM 3825 AB3038
EU511690.1 gg_id:263080 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07a08 EU5116
EU504504.1 gg_id:276180 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01e09 EU5045
EU547306.1 gg_id:545371 Lactobacillus delbrueckii subsp. bulgaricus str. BCS113 EU5473
EU505043.1 gg_id:263220 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02a11 EU5050
GQ155476.1 gg_id:593810 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM236150.1 gg_id:177499 Lactobacillus amylotrophicus str. NRRL B-4435 AM236
EU455693.1 gg_id:305429 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4556
AF515229.1 gg_id:56475 Pediococcus acidilactici str. RO17 AF5152
AB018214.1 gg_id:15157 Pediococcus acidilactici str. LA 35 AB0182
FJ915623.1 gg_id:538273 Pediococcus acidilactici str. IMAU20090; mgh10-7-2 FJ9156
AB018212.1 gg_id:27815 Pediococcus acidilactici str. E 7 AB0182
EU331307.1 gg_id:244766 Pediococcus damnosus str. Bpe233 EU3313
AB258357.1 gg_id:158048 Pediococcus siamensis MCH3-2 AB2583
GU125433.1 gg_id:560139 Pediococcus ethanolidurans str. IMAU80011 GU125
AJ271383.1 gg_id:19307 Pediococcus inopinatus str. DSM 20285 AJ2713
EU331259.1 gg_id:239673 Pediococcus parvulus str. Bpe301 EU3312
FM878597.1 gg_id:589816 Pediococcus parvulus str. LA1110 FM878
AY675245.1 gg_id:105170 Pediococcus pentosaceus str. LM2632 AY6752
AB018215.1 gg_id:15152 Pediococcus pentosaceus str. LS 5 AB0182
AJ305321.1 gg_id:38120 Pediococcus pentosaceus str. DSM 20336 (T) AJ3053
EU080993.1 gg_id:245909 Pediococcus pentosaceus str. BMG 74 EU0809
AB362987.1 gg_id:242063 Pediococcus pentosaceus str. NGRI 0305 AB3629
EU483113.1 gg_id:265290 Pediococcus pentosaceus str. MY-800 EU4831
EU878171.1 gg_id:328309 Pediococcus pentosaceus str. SH 740 EU8781
AJ973157.1 gg_id:147407 Pediococcus stilesii str. LMG 23082 = FAIR-E AJ9731
FJ378890.1 gg_id:359769 Pediococcus pentosaceus str. B-38 FJ3788
AJ621555.1 gg_id:113414 Pediococcus claussenii str. DSM 14800 AJ6215
FJ405228.1 gg_id:366574 Pediococcus claussenii str. ZJ5 FJ4052
AY675243.1 gg_id:104878 Pediococcus pentosaceus str. SL4 AY6752
AM279764.2 gg_id:161185 Lactobacillus plantarum 7.8.2 AM279

320.5	1662.2	2178.1	1719.7	2012.8	1679.1	1389.0	2459.9	1067.0	1701.6	1384.0
37.2	489.7	1821.6	1874.9	78.0	32.9	117.0	378.1	25.5	52.1	359.3
7811.3	2690.3	2749.2	3069.7	2367.9	3325.7	2747.2	2738.6	4083.4	5594.8	4569.5
714.2	1905.2	3888.8	3530.0	2092.1	2101.1	1921.8	2556.2	1473.4	2447.8	1760.7
2820.0	2846.8	3540.9	2274.7	3533.5	2841.8	4043.8	3328.3	3801.7	2013.6	2849.2
1981.0	3212.6	2626.8	2461.0	2588.8	3279.8	2876.6	3141.1	4280.6	2334.5	3449.5
11121.0	5895.9	5677.3	6322.5	5812.1	5862.4	6490.0	5278.2	7077.5	5930.9	6650.6
3107.3	2364.1	2985.1	2674.2	2781.3	2731.9	2283.3	2279.0	1510.7	2403.3	1654.2
11383.5	5993.4	6444.0	6080.0	7032.6	6436.4	6343.7	6237.0	6421.2	5253.1	6235.3
106.8	706.9	992.8	567.0	617.7	893.2	386.6	1132.2	504.8	1034.3	722.8
150.3	2241.9	3393.2	3636.4	2926.8	2582.9	3446.3	2899.0	2199.2	1060.5	1802.0
53.1	204.0	340.0	309.5	289.2	254.7	302.3	405.6	145.9	73.9	179.7
40.9	357.6	1484.6	1354.5	35.0	40.1	82.8	351.2	91.5	129.6	244.7
35.0	23.7	37.3	41.3	37.6	34.2	58.5	32.4	17.8	16.0	19.4
678.7	5772.0	5646.4	6393.6	7036.8	6787.4	7356.9	6019.8	9590.2	8445.1	8410.1
69.4	744.7	778.3	769.9	633.1	984.0	761.4	974.4	261.0	861.7	511.0
30.0	24.0	83.6	83.5	24.7	15.7	16.7	19.1	77.6	13.0	31.1
2674.6	3045.3	3933.2	3494.1	3714.5	3211.2	3533.9	3883.0	3327.9	3999.2	4053.9
18442.9	5989.7	6168.2	8214.4	6042.9	7123.8	6323.0	5659.0	8601.3	5102.7	7726.7
702.1	4348.1	6168.0	4180.5	4452.7	4841.9	3721.1	5701.4	3635.4	5809.5	5118.8
829.7	1575.5	2019.9	1837.9	1951.7	2067.0	1752.3	1829.0	3498.7	1581.4	1942.1
189.1	593.6	694.5	554.9	495.8	708.4	558.5	792.3	394.0	957.2	706.6
2948.5	5484.9	6523.8	5457.0	6241.4	5080.0	5247.1	6158.1	7646.4	5824.2	6465.4
1416.8	5650.0	5788.6	5188.2	4981.3	5273.1	5908.4	5152.2	4873.0	7151.4	4968.8
758.9	6461.6	8762.0	7441.5	7280.8	6765.6	7621.9	7555.3	6718.8	3874.2	6558.4
1005.3	3550.8	4251.9	4093.4	3979.8	3574.9	4441.1	3931.4	4114.9	3401.3	3884.0
321.9	1456.1	2085.7	1639.7	1959.5	1346.1	1786.4	2133.0	2383.7	1113.3	1746.5
176.4	1279.4	2390.9	949.7	1373.3	957.8	1233.0	1998.3	2477.2	1729.0	1627.3
608.0	776.2	1310.8	1202.5	673.6	854.9	464.2	1080.5	604.6	289.4	992.0
18227.5	8806.8	8633.5	9617.6	8310.9	7674.8	8782.3	8144.4	11176.6	10786.8	12384.7
812.1	1530.5	2267.3	2237.3	1808.7	1939.2	1281.7	2094.9	888.3	2184.3	1263.3
817.1	1333.0	2114.9	2004.5	1570.1	1782.1	1361.2	1906.9	753.0	1551.9	1195.8
1367.2	5130.5	5815.2	5786.1	4495.7	6038.5	4469.5	5818.1	3199.9	9057.6	5581.3
556.8	1558.2	1830.1	1939.9	1883.3	1432.2	1245.2	1858.0	960.2	824.2	1193.7
863.7	2078.9	3673.3	2366.0	2167.8	2634.6	1945.1	2912.9	936.4	2033.2	2284.5
51.0	592.4	942.6	591.7	497.4	826.5	389.1	1143.2	335.3	458.5	497.5
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67.9	2874.0	3027.8	3164.3	2796.8	2812.7	2629.6	3612.9	2052.8	4507.8	2703.0
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64.5	1129.5	1276.4	636.0	1152.0	961.0	920.0	1463.2	628.9	548.1	1049.8

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2245.9	2747.0	3196.5
2635.9	4464.9	4295.1
2363.7	2990.2	2927.8
5442.7	6516.0	6662.7
2442.2	2771.7	2991.1
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865.6	918.7	1853.4
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20.6	44.5	60.5
5533.7	6010.7	8642.9
834.7	1202.9	1511.6
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3302.5	4055.9	4369.5
5952.5	6545.4	6524.4
4666.9	4397.1	6773.4
1856.3	2074.6	2377.4
825.7	954.7	893.0
6537.8	6223.7	7193.7
4942.3	5729.4	5940.2
6106.1	6534.3	7487.5
4285.1	4285.7	4889.5
1547.1	2171.8	2359.0
1143.8	1647.0	2148.8
1324.2	947.7	822.0
7203.3	11123.6	6998.9
2393.7	2092.2	2139.6
2187.4	1750.9	1575.7
5807.5	5797.8	5711.1
1839.7	2440.2	2233.0
2908.5	1990.7	2008.9
1157.9	1393.9	1364.8
2462.1	2215.1	2312.0
3703.4	4024.5	5088.6
3253.6	3368.9	5301.0
2184.8	1666.3	1854.9
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EU460868.1 gg_id:296482 short-beaked echidna feces clone ECH_aai39f03 EU460
AB240455.1 gg_id:145715 Lactobacillus halophilus str. KG34 AB240
EU460734.1 gg_id:303093 short-beaked echidna feces clone ECH_aai37b12 EU460
EU460924.1 gg_id:300991 short-beaked echidna feces clone ECH_aai40e11 EU460
EU626008.1 gg_id:277639 Lactobacillus coryniformis str. KLDS 1.0723 EU626
EU460820.1 gg_id:297646 short-beaked echidna feces clone ECH_aai38g03 EU460
AF360737.1 gg_id:67685 Leuconostoc fructosum str. DSM 20349 AF360
DQ837629.1 gg_id:163654 structures honeybee intestines and their response insecticidal proteins gut clone HB DQ837
AY169967.1 gg_id:101369 Leuconostoc pseudoficulneum str. LC51 AY169
AM157423.1 gg_id:141780 Leuconostoc citreum mother C3 AM157
AM157430.1 gg_id:143322 Leuconostoc citreum mother C4 AM157
GQ392137.1 gg_id:553432 Leuconostoc citreum str. CJGN34 GQ392
FJ040200.1 gg_id:535439 Leuconostoc citreum str. C16 FJ0402
EU074846.1 gg_id:245787 Leuconostoc citreum str. TM319 EU074
AM157444.1 gg_id:141773 Leuconostoc citreum mother V4 AM157
AM600682.1 gg_id:226092 Leuconostoc holzapfelii str. LMG 23990 = BFE 700 AM600
AY929286.1 gg_id:113747 Leuconostoc fallax str. BFE 6749 AY929
EU074837.1 gg_id:240308 Leuconostoc mesenteroides str. CM160 EU074
GQ351321.1 gg_id:533637 Leuconostoc mesenteroides str. OR2P-2 GQ351
EU074843.1 gg_id:249310 Leuconostoc mesenteroides str. AC318 EU074
FJ040199.1 gg_id:550853 Leuconostoc mesenteroides str. C12 FJ0401
GQ915096.1 gg_id:539665 Leuconostoc mesenteroides str. AaD8 GQ915
FJ215674.1 gg_id:312330 Leuconostoc mesenteroides str. IMAU60052 FJ2156
EU074838.1 gg_id:238676 Leuconostoc mesenteroides str. PC216 EU074
EU074836.1 gg_id:252222 Leuconostoc mesenteroides str. CM135 EU074
EU074841.1 gg_id:247929 Leuconostoc mesenteroides str. CC317 EU074
EU177638.1 gg_id:341233 Leuconostoc mesenteroides str. ANN12 EU177
EU074839.1 gg_id:248008 Leuconostoc mesenteroides str. PM249 EU074
AF515228.1 gg_id:64385 Leuconostoc pseudomesenteroides str. RO1 AF515
EU177631.1 gg_id:337944 Leuconostoc pseudomesenteroides str. NS28 EU177
EU074840.1 gg_id:253688 Leuconostoc mesenteroides str. PM141 EU074
EU177632.1 gg_id:345546 Leuconostoc pseudomesenteroides str. NS33 EU177
FJ015056.1 gg_id:315407 Leuconostoc pseudomesenteroides str. FL6 FJ0150
EU337117.1 gg_id:546379 Leuconostoc pseudomesenteroides str. MC EU337
EF121354.2 gg_id:249922 Leuconostoc citreum str. GJ7 EF1213
EU574896.1 gg_id:267454 Leuconostoc mesenteroides str. NRRL B-1355 EU574
FJ749310.1 gg_id:547101 Leuconostoc lactis str. IMAU40034; QH4-6-2 FJ7493
FJ480207.1 gg_id:592022 Leuconostoc mesenteroides str. WCP907 FJ4802
AB362723.1 gg_id:238348 Leuconostoc citreum str. NRIC 1581 AB362
AB362719.1 gg_id:244448 Leuconostoc garlicum str. NRIC 1577 AB362
AB470239.1 gg_id:365285 Leuconostoc gelidum str. GD AB470

70.5	3217.4	3599.2	2844.4	2363.6	3127.1	2688.6	3571.6	1643.5	5744.0	3675.3
48.2	39.6	36.0	44.1	37.5	38.2	36.6	32.3	28.7	24.8	28.9
988.1	5113.0	5676.6	4410.0	3957.1	4405.5	2767.9	4588.3	3901.6	4861.5	5370.3
2584.0	4835.8	5314.8	4933.2	4668.5	4796.5	5028.6	4976.1	3771.8	7104.3	5325.9
72.1	481.0	720.4	521.7	757.1	713.4	504.5	829.9	196.7	507.0	478.4
260.9	5249.0	6260.3	5092.0	4591.5	4611.4	5354.6	5488.9	8283.8	6181.4	6039.3
412.4	975.7	1940.5	1993.6	1192.2	1074.5	1233.1	1692.6	592.1	428.5	773.0
286.8	5825.5	7016.1	6436.7	4836.1	5386.1	6120.7	6110.9	4769.6	4938.6	6181.3
388.9	3699.0	5087.8	5327.3	3877.1	4029.1	5696.6	5870.3	4093.9	1395.7	3684.3
1878.6	3717.3	4700.4	4818.6	4692.0	3473.6	4660.7	4120.5	4076.7	2903.2	4800.5
879.2	2962.7	3966.7	3934.4	3503.4	2356.9	3477.4	3084.3	2965.7	2285.2	3136.9
2008.2	4433.7	5677.6	5703.9	5301.7	3688.1	5475.7	4688.8	4690.0	3448.8	5456.0
16959.3	7566.2	7144.3	8236.7	7963.2	6876.5	8034.0	8332.9	12042.8	5254.6	8100.3
1871.8	3220.6	4307.1	4477.7	3744.9	2481.2	3810.8	3620.2	3689.1	2545.7	4083.4
929.6	2675.9	2691.2	2900.5	3208.9	2539.5	3205.1	2854.1	3655.2	1856.9	2657.1
1880.8	3763.9	4893.4	5021.9	4409.4	3053.6	4605.3	4090.7	4074.5	2858.8	4808.0
82.8	677.7	687.5	847.8	269.8	239.3	231.9	244.9	111.9	67.4	183.7
80.9	1268.7	2295.4	2377.8	1703.2	1526.4	1339.2	2876.8	1154.2	256.8	1195.5
277.5	2198.3	3415.8	3313.0	3187.6	2673.0	3592.6	4036.1	2011.4	1273.4	2201.6
404.1	3703.4	4695.3	4630.7	4225.7	4462.9	4797.5	5139.5	2550.1	2922.7	4591.1
291.7	2413.7	3739.3	3731.6	3289.6	2828.2	3769.1	4332.0	2056.5	1369.5	2318.9
261.9	2313.2	3641.1	3508.5	3092.1	2666.7	3486.7	4076.7	2031.6	1325.6	2269.5
278.1	3137.1	4916.9	4506.3	3602.3	3913.5	4328.1	5724.6	2337.6	1008.1	3511.8
171.3	1656.4	2798.6	2822.7	1706.9	1917.8	1635.2	3133.6	1390.2	407.3	1467.4
1061.9	2305.5	3477.9	3970.9	2886.9	2871.3	3515.7	4200.3	2365.0	1131.5	3364.0
168.3	2187.9	3517.4	3750.6	2642.4	2470.8	2504.4	4098.5	1939.4	609.7	1949.7
274.3	1740.0	2508.8	2393.4	2234.1	2181.4	2646.1	2854.7	1203.3	1177.6	1505.9
76.1	1732.9	2972.6	3122.3	2350.7	2017.0	1957.6	3737.7	1675.5	368.4	1608.6
450.1	3221.2	4112.6	3290.0	4220.3	3781.4	4838.1	3635.3	2324.7	3645.5	3439.9
471.1	3953.1	4746.0	4646.9	4457.3	4088.5	5092.7	4498.1	2512.9	3332.5	4008.9
1609.6	3327.5	3913.3	4800.0	1817.2	3903.8	2759.6	5325.8	1976.5	816.7	3227.0
519.0	4177.9	5337.4	5259.5	4690.8	4736.6	5733.0	5646.7	2729.8	3363.4	4613.1
437.6	2757.9	3692.0	3816.8	2324.1	3126.3	3092.0	4159.9	1772.3	1767.5	3212.1
170.6	2349.1	2914.4	2780.5	2505.0	2419.9	3108.3	2926.7	1412.3	2238.4	2015.6
1884.1	4032.4	5085.7	5355.4	4561.2	3329.0	4773.7	4181.3	3750.1	3358.3	4978.7
1820.6	2805.5	3592.1	3887.8	2607.4	3444.2	3099.8	4538.1	3633.8	1622.3	4463.5
1018.1	4785.2	5222.3	5462.2	5792.7	4331.2	5881.6	4945.8	4428.0	3910.5	5483.8
14840.6	5182.0	7419.4	7460.8	7842.6	6600.4	9668.5	8452.3	8500.2	7739.4	7926.6
705.9	2285.1	2713.9	2489.4	2957.7	2206.4	2688.5	2483.8	2914.1	1493.0	2464.0
4069.1	3106.2	3695.4	3528.1	3169.4	2482.2	3438.0	3791.0	3233.7	4079.9	4312.4
16808.1	7251.7	7507.2	8323.7	8017.7	7629.9	8855.6	7324.8	8879.2	6130.9	9213.8

3455.7	3335.8	4441.3
33.4	46.2	38.5
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699.8	993.6	1561.9
5218.7	5791.6	6259.5
2024.7	1855.6	2080.9
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4503.9	4159.8	6311.3
3824.4	4195.2	5050.7
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4376.9	4921.7	6485.0
7424.8	8340.5	10172.6
3534.7	3650.3	3898.4
2477.5	3488.9	4313.9
3885.9	4226.1	4996.3
163.8	262.3	228.8
2613.5	2071.2	2951.9
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3958.2	3571.9	3737.3
3890.7	3625.9	5187.8
3674.2	3414.8	4873.9
4505.2	4743.3	4884.2
2991.0	2539.3	3429.9
3657.3	3734.8	3384.3
4031.2	3346.5	4839.3
2267.0	2563.1	3021.7
3488.7	2649.8	4135.8
3389.7	3546.7	4629.7
4501.4	3873.1	4769.8
4458.7	3322.9	3047.7
4972.0	4365.2	5054.9
3722.9	3130.0	2617.0
2948.8	2734.4	2829.6
4200.0	4543.9	5465.0
2998.1	4503.2	3443.4
4548.5	5244.4	6353.4
7231.1	7778.1	8922.1
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3308.5	4258.2	4727.2
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AM940225.1 gg_id:349734 Leuconostoc palmae str. TMW 2.694 AM940
AB362720.1 gg_id:252701 Leuconostoc garlicum str. NRIC 1578 AB3627
AF111948.1 gg_id:15110 Leuconostoc citreum str. ATCC49370; KCTC3526 AF1119
AB362722.1 gg_id:256844 Leuconostoc garlicum str. NRIC 1580 AB3627
EU463822.1 gg_id:290159 Seba's short-tailed bat feces clone bat_aaj05d07 EU4638
AY165007.4 gg_id:75964 Leuconostoc citreum str. CY2 AY1650
AB022921.1 gg_id:24935 Leuconostoc gelidum str. NRIC 1778 AB0229
AB362682.1 gg_id:246692 Leuconostoc mesenteroides str. NRIC 0587 AB3626
AB470240.1 gg_id:363305 Leuconostoc gasicomitatum str. GC AB4702
AB054806.1 gg_id:43827 Oenococcus oeni str. 95 St.Mer-2-4 AB0548
CP000411.1 gg_id:175948 Oenococcus oeni str. PSU-1 CP0004
FM878590.1 gg_id:571983 Oenococcus oeni str. LA126 FM878
AB221475.1 gg_id:159865 Oenococcus kitaharae str. NRIC 0645 AB2214
GU138518.1 gg_id:568005 Weissella confusa str. LSBM3-1 GU138
AB022926.1 gg_id:45087 Weissella halotolerans str. NRIC 1627 AB0229
EU465515.1 gg_id:292431 lion feces clone LI3_aah78f11 EU4655
AB022922.1 gg_id:43687 Weissella kandleri str. NRIC 1628 AB0229
AM157446.1 gg_id:144619 Weissella confusa mother V4 AM157
EU855224.1 gg_id:352468 Weissella paramesenteroides str. CTSPL5 EU8552
FJ193714.1 gg_id:346360 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1937
AM157435.1 gg_id:142903 Weissella cibaria mother C4 AM157
AB015642.1 gg_id:15084 Weissella hellenica str. DS-12 AB0156
EU439435.2 gg_id:560064 Weissella sp. str. 2L24P13 EU4394
AM882997.1 gg_id:241383 Weissella ghanensis str. LMG 24286 AM882
EU177641.1 gg_id:320990 Weissella paramesenteroides str. NS74 EU1776
EU869290.1 gg_id:331921 Weissella sp. str. JZ-1L EU8692
DQ294962.1 gg_id:143027 Weissella cibaria str. Uga57 DQ294
EU074829.1 gg_id:251397 Weissella cibaria str. BC48 EU0748
DQ294964.1 gg_id:142786 Weissella cibaria str. Uga69 DQ294
AF477495.1 gg_id:23573 Weissella confusa str. PL9001 AF4774
AF477498.1 gg_id:36439 Lactobacillus fermentum str. PL9005 AF4774
AF312874.1 gg_id:22775 Weissella cibaria str. CHJ3 AF3128
FJ429974.1 gg_id:565622 Weissella confusa str. C3-7 FJ4299
GU369772.1 gg_id:530233 Weissella confusa str. JS-7-1 GU369
FJ263453.1 gg_id:366705 Weissella confusa str. XW1 FJ2634
AB257595.1 gg_id:158275 Weissella salipiscis str. FS55-1 AB2575
X95981.1 gg_id:15090 Weissella hellenica str. NCFB 2973 X95981
FJ654456.1 gg_id:537058 Weissella hellenica str. 138 FJ6544
FJ654465.1 gg_id:511014 Weissella hellenica str. 1507 FJ6544
DQ883229.1 gg_id:163888 Weissella koreensis str. 405 DQ883
EU180607.1 gg_id:335281 Weissella soli str. NS26 EU1806

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1532.2	4526.5	5086.7	5293.5	4400.0	4433.0	5486.2	5480.9	4047.9	4047.1	5566.7
901.0	3161.9	3617.7	3411.0	4266.4	2783.3	4647.2	3315.3	2895.7	3161.6	3221.2
22663.9	7456.7	7594.0	9161.5	7532.8	7288.8	9096.8	7874.7	9310.4	8811.5	9562.4
5865.8	4400.0	4955.1	5053.4	5745.2	5553.8	5460.9	5488.3	4616.8	2734.5	5370.3
5606.4	5193.8	6912.5	6892.9	4575.0	4786.8	5270.8	5226.5	5978.7	4564.4	6164.1
932.5	3365.9	4678.6	4529.8	3231.3	3153.2	3599.4	5036.1	2587.8	2797.5	4102.0
11039.9	6359.1	7365.8	8003.9	8104.3	6807.6	11552.4	8947.3	7715.5	6589.6	9545.9
30363.5	10611.0	10309.4	11404.9	11610.7	10001.1	12139.4	9546.0	13195.9	10285.2	13049.9
160.1	1659.2	1869.3	1795.3	1555.1	1721.5	1829.7	2104.2	2293.5	2369.8	1476.5
207.6	1760.8	1794.4	1565.2	1084.4	1397.7	1414.5	1990.4	1592.8	1388.3	1232.2
17026.1	5431.6	6393.2	6694.2	5565.1	6242.2	6344.0	6505.1	9660.8	5549.8	7972.2
11552.1	3504.8	3721.4	4321.0	3400.2	4118.5	3447.0	3882.3	4172.4	4006.2	4791.1
487.5	3042.2	3503.3	2565.0	4216.0	2997.3	4263.1	3734.8	2921.9	4461.2	2807.3
150.9	330.5	362.1	292.9	388.5	352.5	208.8	674.3	232.0	118.1	140.5
8347.2	6058.8	5597.3	6229.8	5406.8	4974.6	5199.8	7262.4	6702.1	5687.2	6957.1
45.1	571.5	1218.0	977.1	491.5	497.0	379.4	581.0	129.0	508.3	245.9
3005.4	1800.5	2986.6	2809.8	2147.8	2112.1	2094.1	2448.6	2350.9	2425.0	2233.5
494.3	2556.2	3210.6	2505.8	3587.1	2853.9	3655.5	3414.7	2470.2	1187.9	2423.9
1664.1	1769.4	2270.2	2180.1	1313.9	1286.1	1197.8	1548.8	1328.0	1618.1	1989.4
144.8	1074.1	1831.3	1963.3	1329.3	872.7	971.7	1225.3	679.7	618.7	741.0
2553.0	3288.3	3762.4	3811.1	3496.3	2749.0	3280.3	3962.7	3592.5	1957.7	4198.6
412.7	2077.9	2330.0	1513.6	2268.5	2438.6	1779.0	2585.0	1110.9	2142.5	873.5
5543.8	6360.8	6278.4	6453.5	6353.1	5891.8	5968.5	5225.0	6275.4	4377.8	7307.8
57.6	922.3	1217.2	1385.4	1008.1	1248.2	824.1	1092.6	550.1	1559.2	745.1
46.7	28.5	28.0	34.1	33.7	48.4	19.0	28.3	21.7	25.4	18.6
169.7	1254.0	1072.6	1634.1	1347.2	1385.0	852.4	1292.2	606.7	1443.7	613.7
6274.1	3123.0	2962.8	3237.3	2955.7	3124.5	3205.3	3011.4	2903.9	2663.6	3642.3
692.3	1825.1	2286.7	1842.1	1528.1	2094.9	1376.4	2516.7	1474.0	2091.3	1705.8
208.2	1687.5	1737.4	1775.4	1843.9	1680.1	1601.0	1945.8	1356.4	1534.0	2231.5
5298.1	2760.1	3535.0	2884.8	2363.3	3028.8	2680.5	3911.8	3346.0	3790.6	3235.6
100.8	979.6	886.1	1262.3	771.0	965.2	642.2	944.6	448.5	528.7	444.1
1227.5	1537.4	2406.4	1817.0	2109.7	2061.8	1898.2	2599.6	1666.7	2613.8	1323.4
1219.4	1111.7	1900.3	1125.6	1638.7	1362.3	1564.5	1821.0	1478.3	989.6	1077.1
1124.9	1160.4	2105.8	1334.3	1676.3	1665.1	1558.6	2026.2	1535.9	1883.0	1116.1
2554.9	2874.3	3495.8	2972.0	3040.5	2720.3	3474.9	3533.5	3265.0	1989.1	2604.3
205.7	718.0	1106.4	1290.0	774.7	747.8	651.9	715.0	491.4	542.2	603.0
194.6	1067.4	1648.8	1869.5	1117.7	1173.8	987.7	1211.9	683.1	993.8	981.0
188.5	1061.8	1643.4	1875.5	1052.7	1147.1	1003.5	1131.5	682.6	1110.5	1039.9
55.4	2116.5	3008.2	2718.8	2322.3	1696.0	1664.6	2554.0	1349.4	1828.0	1039.2
659.7	1518.5	1990.8	1887.2	2144.4	2154.7	2059.3	1858.0	1251.6	1367.3	2068.1

4119.4	4875.7	5896.4
3989.0	5473.7	7318.9
3012.7	3492.0	4648.7
7978.8	10671.8	8683.8
4281.1	5527.7	6205.4
4807.9	6804.7	7376.7
3945.3	3924.6	3858.7
7404.3	6997.1	9302.1
9442.7	9678.6	11471.6
1674.6	2124.0	1853.9
1267.8	1891.4	2138.0
5916.8	7419.5	6596.0
4411.6	3823.8	3658.7
2822.5	3548.3	4903.1
609.5	596.5	928.1
4858.3	5729.6	5711.2
857.4	920.5	879.0
2294.3	2186.0	2264.2
2566.1	3087.8	5100.9
2055.9	2278.7	2042.2
1089.2	1167.7	1079.5
1377.0	3769.7	4544.0
3145.6	3209.5	3980.7
5607.0	5881.4	7178.2
1105.9	1498.0	1685.1
64.7	59.0	61.8
1159.2	1862.8	2132.1
3317.6	4195.6	3098.8
1903.3	2264.8	2582.7
1563.0	1928.7	1869.9
3036.2	5066.0	3984.7
745.8	1190.0	1259.8
2069.0	2609.0	2583.4
1410.6	1706.5	1664.5
1614.1	1936.5	1664.6
3166.1	4049.0	3172.0
830.5	796.4	794.9
1428.5	1432.0	1577.2
1403.0	1427.0	1474.2
2744.8	2279.9	4308.2
1668.4	1623.7	1840.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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o__Lactobacillales	f__Leuconostocaceae
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o__Lactobacillales	f__Streptococcaceae

g__Weissella
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s__Weissella viridescens	71967
s__Lactococcus garvieae	42650
s__Lactococcus garvieae	42815
s__Lactococcus garvieae	42882
s__Lactococcus garvieae	42914
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s__Lactococcus lactis	43335
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AB023236.1 gg_id:33970 Weissella viridescens str. NRIC 1536 AB023
EU775634.1 gg_id:315664 Hedgehog feces clone HH_d06 EU775
EU777721.1 gg_id:330069 Polar bear feces clone PB1_aai28f10 EU777
EU460570.1 gg_id:298506 polar bear feces clone PB2_aai22g09 EU460
EU460926.1 gg_id:299075 short-beaked echidna feces clone ECH_aai40f04 EU460
EU791208.1 gg_id:455671 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou EU791
AB018211.1 gg_id:42931 Lactococcus garvieae str. E 1 AB018
EU460718.1 gg_id:302924 polar bear feces clone PB2_aai24h07 EU460
EU467542.1 gg_id:296207 southern three-banded armadillo feces clone arma_f03 EU467
EU775705.1 gg_id:333803 Hedgehog feces clone HH_aai36e07 EU775
EU460397.1 gg_id:302882 polar bear feces clone PB1_aai28a07 EU460
AF283499.1 gg_id:45250 Lactococcus garvieae AF283
EU775674.1 gg_id:336969 Hedgehog feces clone HH_d10 EU775
EU460462.1 gg_id:293407 polar bear feces clone PB2_aai21b11 EU460
EU458153.1 gg_id:297489 North American black bear feces clone BB2_f02 EU458
AB244446.1 gg_id:257338 Lactococcus garvieae str. An10-2 AB244
EU460864.1 gg_id:292600 short-beaked echidna feces clone ECH_aai39e07 EU460
DQ223877.1 gg_id:173259 Lactococcus sp. str. RT5 DQ223
DQ223876.1 gg_id:167936 Lactococcus lactis str. RT4 DQ223
AM490366.1 gg_id:203331 Lactococcus lactis str. C22 AM490
AM157445.1 gg_id:141784 Lactococcus lactis mother V4 AM157
AJ488176.1 gg_id:66046 Lactococcus lactis str. 04 AJ488
AY348313.1 gg_id:93048 Lactococcus lactis str. Akira2 AY348
AM157424.1 gg_id:141720 Lactococcus lactis mother C3 AM157
EU203156.1 gg_id:251182 Lactococcus lactis str. WH11-1 EU203
GQ337889.1 gg_id:594031 Lactococcus lactis str. KLDS4.0352 GQ337
AY762104.1 gg_id:108349 Lactococcus sp. str. MKRL19 AY762
AJ133479.1 gg_id:69992 Lactococcus sp. TmLO5 AJ1334
EU073957.2 gg_id:240865 Lactococcus sp. Da-18 EU073
AB234513.1 gg_id:150304 termite gut homogenate clone MgMjW-44 AB234
AJ439543.2 gg_id:110020 Lactovum miscens str. anNAG3 AJ4395
DQ856510.1 gg_id:253776 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1N DQ856
AB089063.1 gg_id:78015 termite gut homogenate clone Rs-C68 sp. AB089
DQ343754.1 gg_id:146404 Lactococcus piscium str. CCUG 32732 DQ343
EF204369.1 gg_id:201186 Lactococcus sp. G23 EF2043
EU460490.1 gg_id:294254 polar bear feces clone PB2_aai21f02 EU460
AB089061.2 gg_id:78223 termite gut homogenate clone Rs-B70 AB089
AY571411.1 gg_id:114538 termite gut clone RsaM9 AY5714
EF694029.1 gg_id:256029 Lactococcus plantarum str. DSM 20686 EF6940
GQ502570.1 gg_id:555286 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AM944736.1 gg_id:270649 Enterococcus sp. str. UNK1 AM944

29.5	37.7	74.4	115.8	50.5	35.7	38.8	54.4	22.9	58.6	25.9
14103.8	7236.9	6908.5	7625.7	6808.3	7675.4	7317.5	6334.6	8441.9	8807.4	10749.4
5864.4	4015.4	4164.9	4150.6	4138.9	4397.5	3952.2	3931.0	3101.8	4964.8	4426.7
5058.5	5045.2	5056.7	5524.8	4578.3	5397.2	4841.2	4294.1	4966.2	6716.6	7311.4
10005.9	6147.0	5733.9	6276.2	6135.2	6522.4	6244.9	5973.8	6012.9	7073.1	8810.3
750.9	4118.8	4647.5	4884.5	4646.5	5222.6	4772.3	6119.6	3264.2	4547.6	3997.3
4451.2	5599.4	6233.0	5071.7	3635.5	6239.2	4561.0	5180.7	6729.4	7966.7	7035.7
1476.7	3292.8	3316.5	3321.3	2837.3	4094.9	2709.9	3196.8	2038.6	4439.8	3030.1
12683.5	4358.7	4607.1	4576.9	4332.4	4842.0	4402.6	4305.4	4666.8	5518.9	5537.0
2285.0	3390.7	3315.3	3634.5	2717.7	4010.2	2775.5	3129.7	2484.3	4427.9	3428.6
1285.7	2506.5	2428.0	2845.7	2297.4	3158.7	2069.9	2618.9	1542.9	4218.8	2267.9
17503.6	9160.9	8510.7	9762.1	8972.3	8939.8	9508.3	7695.5	13899.7	12697.1	13067.1
664.0	2103.6	2629.6	2511.5	1974.2	2890.2	1868.6	2546.7	1432.3	4001.3	1977.0
10568.1	8227.5	6306.3	6668.0	7100.2	7273.9	5975.8	6810.5	8874.4	9552.9	7203.3
2100.7	2285.7	2916.9	2992.3	3245.9	3313.8	2708.6	3116.3	1255.0	2494.6	2203.0
30426.9	8687.3	8447.8	9119.7	9403.8	8357.3	8941.7	7788.4	10005.0	8769.5	13913.9
503.2	1937.0	2535.0	1829.6	1431.0	3156.5	1282.9	1927.8	663.4	4721.4	1273.0
190.3	2760.5	3074.2	2279.3	1955.4	2735.8	2192.5	3040.4	1534.5	2059.0	2165.7
381.7	2829.2	3420.2	2882.1	2516.4	3306.5	2726.4	5283.7	1507.9	2708.7	4570.1
5549.0	3259.5	3224.3	3112.3	2626.4	2983.5	2826.7	3042.8	3299.6	4215.5	3633.1
6916.5	3409.6	3281.4	2739.2	2836.8	3536.8	2842.6	4144.9	3571.1	3754.3	3401.2
3504.5	3890.3	4582.7	4150.5	3766.6	4614.3	3572.2	5424.1	2131.8	3006.2	4418.6
146.7	1992.8	1791.0	1467.3	849.8	2340.1	858.2	1861.2	391.2	1593.8	567.5
476.3	3336.5	4301.0	4104.5	3649.6	4232.7	3815.8	5195.8	2195.5	2369.5	4408.1
12281.2	5309.8	5006.9	4898.2	4760.8	5526.0	4872.6	5738.8	5509.4	5545.4	6969.3
7944.5	4674.1	5126.9	4894.0	4519.8	5277.4	3404.8	6038.1	3069.4	3582.5	5505.5
58.1	463.3	650.9	646.5	441.6	899.2	524.8	977.8	201.2	607.4	407.0
56.2	85.0	127.9	83.5	87.8	100.2	110.5	157.9	53.3	53.7	79.7
1377.1	3213.5	3175.9	3482.5	2974.3	3286.8	3174.6	3366.6	2639.0	1932.4	3500.5
523.9	2989.2	3921.2	3786.2	3004.2	3611.1	3267.3	4225.4	2835.2	3156.3	2244.2
633.4	5105.1	4413.3	2671.5	1505.6	3170.5	1722.9	3683.1	8180.6	5587.6	3177.7
1469.6	3146.1	4441.2	4480.6	4630.9	3489.0	3927.8	4349.0	2882.0	3567.8	3955.1
79.4	453.6	856.2	833.1	882.0	626.0	488.5	916.3	263.0	221.2	300.6
171.7	3034.8	3883.7	3363.1	3457.9	3428.6	3346.2	3695.2	1769.1	1186.6	2910.6
223.3	1588.4	1531.9	1232.0	818.3	1581.6	789.2	1685.2	1239.9	1187.5	848.7
637.3	5145.1	6949.5	4771.4	5151.1	5621.9	5359.7	6416.2	2945.1	6981.3	5963.4
214.3	1927.3	1782.3	1735.2	2201.4	2470.0	2104.3	2736.8	1532.2	2064.1	1731.6
97.0	1323.0	2019.9	1515.0	1417.0	1590.9	1108.3	2795.6	674.9	1733.4	1608.0
47.9	251.8	344.5	318.2	161.1	589.5	295.6	338.3	116.6	92.8	119.4
38.0	207.8	354.9	294.9	256.1	449.4	184.7	434.7	138.1	87.5	149.4
16044.7	9166.9	8491.0	9341.9	8796.1	8613.9	9433.8	6841.8	11623.7	7087.1	11601.5

66.3	119.3	62.5
7712.5	6987.9	7624.4
4973.4	4093.1	5016.7
6074.5	5123.5	5024.6
6875.7	6791.1	6917.6
6239.1	4758.4	4775.5
5929.9	5507.5	6433.9
5082.7	2952.1	3022.4
4796.3	5179.8	4886.4
4919.0	2868.4	3053.2
4129.7	3237.2	3070.3
9411.4	9565.6	9618.2
3878.6	2434.3	3485.5
7721.8	8056.0	9690.2
3861.3	4521.6	5609.9
7989.4	8677.0	8566.6
4552.6	1290.0	1393.4
4021.7	2532.9	3707.6
4952.3	3523.0	3718.6
3569.4	3671.9	3397.6
4403.2	4134.3	3569.8
5168.1	4469.9	4759.5
3512.3	1068.0	1201.3
5347.8	4034.8	4248.2
5956.4	6269.9	5587.8
5975.7	5187.6	5376.3
1153.1	620.0	929.2
143.1	160.3	266.3
3175.8	3300.5	2943.7
4460.3	4096.4	5044.1
1943.9	2800.6	2393.7
4211.8	4921.6	4636.6
880.6	735.8	1562.0
3595.4	2980.1	3782.4
1973.2	1808.9	1966.1
5368.5	5073.3	6093.6
2682.2	2371.5	3111.1
2259.5	2178.8	4134.7
305.4	400.5	670.2
329.0	523.7	346.5
9285.8	8767.7	8201.7

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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EU689104.1 gg_id:564529 Lactococcus sp. str. YM05290 EU689
NZ_AAJO01000148.1 gg_id:140424 Streptococcus agalactiae str. 18RS21 NZ_AA
AAJO01000006.1 gg_id:139711 Streptococcus agalactiae str. 18RS21 AAJO0
EU473184.1 gg_id:300948 giant panda feces clone GP_1aaa04g12 EU473
AB002519.1 gg_id:15456 Streptococcus alactolyticus str. ATCC 43492 AB002
EU473340.1 gg_id:289833 giant panda feces clone GP_1aaa04h11 EU473
AB355611.1 gg_id:240886 Streptococcus anginosus str. IMU103 AB355
AY691534.1 gg_id:107288 Streptococcus anginosus str. ChDC YA1 AY691
AY986761.1 gg_id:115190 Streptococcus anginosus str. ChDC YA2 AY986
EU075058.1 gg_id:239570 Streptococcus canis str. 3-35MP EU075
FJ557869.1 gg_id:525128 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
FJ557854.1 gg_id:527756 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
AB182324.1 gg_id:169991 Streptococcus orisuis str. NUM 1001 AB182
AJ853835.1 gg_id:108737 Streptococcus cristatus str. PD01A5 AJ8538
AY281090.1 gg_id:90588 Streptococcus cristatus str. ATCC 49999 AY281
AB008313.1 gg_id:15567 Streptococcus cristatus str. NCTC12479 AB008
NR_029015.1 gg_id:589575 Streptococcus devriesei str. CCUG 47156 NR_02
DQ303185.1 gg_id:167230 Streptococcus didelphis str. ATCC 700828 DQ303
AF176107.1 gg_id:15363 Streptococcus didelphis str. 95-3349-1 AF176
AY942561.1 gg_id:133561 Streptococcus downei str. ChDC YD1 AY9425
AY942564.1 gg_id:137388 Streptococcus downei str. ChDC YD4 AY9425
EF405993.1 gg_id:219796 Streptococcus subsp. equi str. Bd 5895/99 EF4059
AB002516.1 gg_id:15355 Streptococcus equi subsp. zooepidemicus str. ATCC 43079 AB002
AB002515.1 gg_id:15354 Streptococcus subsp. equi str. ATCC 33398 NCTC 9682 AB002
AJ420197.1 gg_id:39498 Streptococcus ferus str. 8S1 AJ4201
U87827.1 gg_id:15564 aortic heart valve patient with endocarditis clone v2 U8782
AJ427479.1 gg_id:36023 Streptococcus gordonii str. DL1 AJ4274
AB355602.1 gg_id:243837 Streptococcus gordonii str. NUK38 AB355
AB002518.1 gg_id:15428 Streptococcus hyointestinalis str. ATCC 49169 DSM 20770 AB002
DQ462420.1 gg_id:203615 Streptococcus icataluri LS0706-05 DQ462
GQ050656.1 gg_id:398932 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488f1 GQ050
GQ115486.1 gg_id:393307 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686c07 GQ115
EU156759.1 gg_id:331335 Streptococcus infantis str. CCUG 39817 EU156
AB008315.1 gg_id:15551 Streptococcus infantis str. GTC849 AB008
GQ077246.1 gg_id:395569 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
EU620580.1 gg_id:279591 Streptococcus iniae str. CMS003 EU620
EU467794.1 gg_id:287876 North American black bear feces clone BB1_b04 EU467
AB002482.1 gg_id:15458 Streptococcus bovis str.ATCC 33317 AB002
AJ297214.1 gg_id:30971 Streptococcus luteciae str. NEM 760 AJ2972
EU461863.1 gg_id:299806 white-faced saki feces clone Saki_aaj62e05 EU461
EU467738.1 gg_id:295347 North American black bear feces clone BB1_a07 EU467

145.4	1746.8	2084.6	1612.4	2062.0	2539.4	2115.5	2560.7	966.9	2048.0	1392.7
3533.8	3181.6	3915.7	3916.0	3623.8	3429.9	3973.7	3916.4	3364.2	6702.0	2951.9
48.0	224.4	354.9	214.8	458.9	333.9	185.1	606.9	154.8	241.1	249.5
90.3	1959.3	2469.7	2052.8	2282.4	2073.5	2128.1	2601.1	1085.9	1035.6	1632.0
3432.2	4279.1	3751.5	3894.4	4369.3	3502.9	4835.4	3712.4	2493.6	2028.2	3933.5
1974.6	4421.3	4129.7	3416.1	3919.1	3879.5	3463.9	4208.5	3576.2	4311.8	3296.9
264.3	1568.1	1657.2	1545.8	1545.8	1904.9	1562.1	1928.3	730.9	1059.2	1306.0
39390.0	11401.8	10326.2	12062.5	11072.5	11059.2	11635.7	10914.7	14464.9	11830.6	15485.5
12770.4	3902.6	3691.7	3993.7	3987.4	3958.5	4110.7	3781.8	5619.9	5102.8	5610.2
90.1	1446.9	2166.0	1973.7	1814.4	1746.8	2243.9	1799.4	947.6	807.1	1182.7
432.5	1711.4	1229.4	1411.9	1369.9	1753.5	987.7	1967.0	1454.7	1985.8	1838.3
92.5	238.0	278.2	371.4	489.8	499.6	292.2	923.9	168.3	508.5	288.7
676.2	2806.6	3227.2	3273.3	2444.1	2720.8	2597.8	2538.5	2474.7	3506.6	3925.4
30.9	32.7	64.9	43.3	73.7	29.7	27.7	45.7	32.7	8.3	24.0
86.8	270.0	419.5	481.2	352.2	351.4	363.7	426.8	297.7	362.4	308.0
40.0	377.2	577.8	333.8	472.0	440.6	405.4	590.2	133.4	288.8	208.4
78.7	669.1	919.6	696.2	403.8	900.7	479.4	983.4	195.6	726.5	444.8
52.8	986.7	1860.3	776.0	1171.6	1511.9	685.5	1644.9	460.7	1465.1	715.7
2742.1	1276.1	2080.1	985.6	1357.3	1730.2	1134.5	1654.2	1368.8	2668.3	1195.5
587.6	1471.9	1927.2	1274.5	1403.4	1427.5	1258.1	1791.6	2184.2	2648.7	947.5
461.5	1494.8	2556.3	1701.2	1437.0	1781.2	1387.3	1881.7	1155.3	2528.6	1596.1
1512.9	925.2	1272.0	1052.2	1065.9	1320.7	1022.6	1334.3	1230.0	2844.6	936.9
1519.5	1127.1	1510.5	1278.5	1395.0	1450.7	1379.1	1495.3	1334.3	2881.7	1054.6
13299.7	3790.8	3945.1	3374.7	3759.1	3774.0	3591.4	3896.5	4315.4	2735.1	3680.8
51.1	746.5	1168.1	547.6	909.7	929.0	674.4	1145.3	476.8	555.6	783.1
489.1	256.6	285.8	358.7	293.3	263.4	315.0	283.3	321.6	127.5	122.7
7352.4	3456.9	3893.2	3843.1	3564.8	3904.0	4244.1	3348.6	4104.1	4897.1	4201.9
716.5	1541.2	2431.3	1652.2	1875.2	2269.8	1442.8	2918.8	1271.6	3252.3	1814.7
114.4	287.2	659.4	582.1	587.7	395.6	434.2	548.1	418.4	230.1	266.1
122.3	538.4	842.7	793.0	609.8	862.4	591.8	841.0	533.1	1689.7	601.1
264.7	769.2	625.3	688.7	496.1	685.1	511.4	757.8	810.5	273.8	854.2
6138.0	4550.3	4092.4	4032.2	3513.9	4146.4	3848.0	3994.3	4895.8	4596.0	4212.7
35.2	281.4	560.0	402.2	548.1	499.5	288.4	430.7	114.8	134.7	104.8
65.1	636.9	941.5	811.5	681.6	973.4	782.6	1179.6	323.8	149.3	485.0
44.4	128.6	243.5	180.5	82.6	189.5	124.4	193.6	64.3	35.1	51.9
105.1	974.2	1084.9	914.8	857.7	1522.3	626.0	1742.0	384.1	965.9	924.7
1091.1	3899.9	3711.7	3483.1	3915.7	3184.5	4665.1	4458.2	2994.7	4468.8	3532.0
6935.6	3146.1	2888.4	2946.4	3036.0	3059.4	2538.3	2999.4	2866.9	2977.8	2430.0
35.2	1515.3	2135.1	827.0	1687.0	2012.6	1031.2	2226.1	649.5	3730.0	651.6
872.3	6079.8	6020.1	6768.9	7733.2	6252.1	7629.6	8133.2	9970.6	8262.7	7303.9
44.3	1417.5	1521.8	1585.8	1326.3	1390.0	1879.2	1849.4	646.3	602.2	928.9

2989.9	2133.3	2443.8
3973.8	4182.0	5147.3
480.8	605.9	1331.6
2298.3	2674.5	3626.8
3836.3	4268.1	5631.2
4574.2	4127.4	5581.1
1943.6	2094.8	2197.2
10497.8	12600.9	11227.9
3369.8	3971.1	3392.2
1511.2	1846.4	2820.1
2013.5	1606.6	1865.6
624.6	600.5	258.8
897.1	2442.8	2997.9
208.9	41.1	55.6
448.2	529.0	416.3
783.8	766.4	1211.4
1360.7	1417.2	1551.8
1584.0	1768.8	2141.2
2040.7	2905.8	2745.8
1947.2	2446.5	2860.5
1779.3	2388.4	2482.8
1461.8	1554.8	1474.7
1492.9	1731.8	1993.7
3845.1	4365.1	5050.3
775.7	1291.3	2087.1
225.1	451.0	369.4
3466.3	4018.4	3839.9
2597.7	2328.2	3465.0
950.6	718.4	495.6
930.7	1439.0	878.8
907.0	613.7	703.6
4359.2	4411.4	5762.8
1149.8	419.2	685.4
1266.1	1035.1	905.9
666.1	261.1	45.1
2040.0	1525.8	1949.7
2958.9	6765.8	6883.4
3199.5	3371.0	4645.9
2266.7	2348.4	3811.2
6079.0	8374.7	7007.6
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s__Streptococcus luteciae	44919
s__Streptococcus luteciae	44953
s__Streptococcus luteciae	45256
s__Streptococcus luteciae	45387
s__Streptococcus luteciae	45703
s__Streptococcus luteciae	45869
s__Streptococcus lutetiensis	45825
s__Streptococcus macedonicus	44256
s__Streptococcus minor	44366
s__Streptococcus minor	45019
s__Streptococcus minor	45538
s__Streptococcus minor	45639
s__Streptococcus mutans	44395
s__Streptococcus mutans	44413
s__Streptococcus mutans	44508
s__Streptococcus mutans	44560
s__Streptococcus mutans	44701
s__Streptococcus mutans	44779
s__Streptococcus mutans	44811
s__Streptococcus mutans	44856
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s__Streptococcus mutans	45150
s__Streptococcus mutans	45165
s__Streptococcus mutans	45168
s__Streptococcus mutans	45173
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s__Streptococcus mutans	45336
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s__Streptococcus mutans	45415
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s__Streptococcus mutans	45451
s__Streptococcus mutans	45469
s__Streptococcus mutans	45554
s__Streptococcus mutans	45579
s__Streptococcus mutans	45651
s__Streptococcus mutans	45686

EU467837.1 gg_id:290948 North American black bear feces clone BB1_b03_1 EU467
EU458240.1 gg_id:295954 North American black bear feces clone BB2_e04 EU458
EU467796.1 gg_id:298722 North American black bear feces clone BB1_b07_1 EU467
EU467742.1 gg_id:291695 North American black bear feces clone BB1_b06 EU467
AJ297218.1 gg_id:21570 Streptococcus luteciae str. NEM1603 AJ2972
EU461969.1 gg_id:291625 white-faced saki feces clone Saki_aaj64e12 EU461
EU163444.1 gg_id:253732 Streptococcus lutetiensis str. 644 EU163
EU163501.1 gg_id:251131 Streptococcus macedonicus str. 905 EU163
EU075079.1 gg_id:246776 Streptococcus minor str. 26-59MP EU075
AF227836.1 gg_id:70091 str. 37236 AF227
AJ409287.1 gg_id:55342 Streptococcus entericus str. CECT 5353 AJ4092
FJ769470.1 gg_id:545996 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7694
DQ677768.1 gg_id:162458 Streptococcus mutans str. ChDC YM53; 32111 DQ677
DQ677712.1 gg_id:170656 Streptococcus mutans str. ChDC YM230; PD1163-1 DQ677
DQ677734.1 gg_id:173377 Streptococcus mutans str. ChDC YM204; PD32 DQ677
DQ677782.1 gg_id:169174 Streptococcus mutans str. ChDC YM26; 16235 DQ677
DQ677717.1 gg_id:169011 Streptococcus mutans str. ChDC YM223; PD1063 DQ677
DQ677727.1 gg_id:170005 Streptococcus mutans str. ChDC YM212; PD1026 DQ677
AF139600.1 gg_id:55433 Streptococcus mutans str. UA96 AF139
DQ677716.1 gg_id:164384 Streptococcus mutans str. ChDC YM225; PD1111 DQ677
DQ677783.1 gg_id:170638 Streptococcus mutans str. ChDC YM29; 17135 DQ677
DQ677733.1 gg_id:169266 Streptococcus mutans str. ChDC YM205; PD59 DQ677
AF077835.1 gg_id:81591 Streptococcus mutans str. UA96 AF077
DQ677769.1 gg_id:171585 Streptococcus mutans str. ChDC YM51; 31125 DQ677
DQ677755.1 gg_id:172601 Streptococcus mutans str. ChDC YM14; 9211 DQ677
DQ677736.1 gg_id:164353 Streptococcus mutans str. ChDC YM202; PD9 DQ677
DQ677787.1 gg_id:172359 Streptococcus mutans str. ChDC YM16; 9226 DQ677
DQ677750.1 gg_id:166980 Streptococcus mutans str. ChDC YM79; 49215 DQ677
DQ677777.1 gg_id:172519 Streptococcus mutans str. ChDC YM6; 3217 DQ677
DQ677765.1 gg_id:169834 Streptococcus mutans str. ChDC YM57; 33211 DQ677
DQ677737.1 gg_id:162868 Streptococcus mutans str. ChDC YM201; PD4 DQ677
AY691526.1 gg_id:102599 Streptococcus mutans str. ChDC YM3 AY691
DQ677753.1 gg_id:164446 Streptococcus mutans str. ChDC YM72; 44211 DQ677
DQ677786.1 gg_id:171168 Streptococcus mutans str. ChDC YM20; 10115 DQ677
DQ677779.1 gg_id:167840 Streptococcus mutans str. ChDC YM34; 20235 DQ677
DQ677761.1 gg_id:167048 Streptococcus mutans str. ChDC YM63; 37121 DQ677
DQ677741.1 gg_id:170415 Streptococcus mutans str. ChDC YM96; 62211 DQ677
DQ677758.1 gg_id:163887 Streptococcus mutans str. ChDC YM1; 1211 DQ677
DQ677722.1 gg_id:171075 Streptococcus mutans str. ChDC YM217; PD1047 DQ677
AF139599.1 gg_id:69287 Streptococcus mutans str. UA140 AF139
DQ677718.1 gg_id:162408 Streptococcus mutans str. ChDC YM222; PD1062 DQ677

354.4	1696.4	1677.9	1738.6	1681.7	1513.7	1942.1	1756.6	940.9	927.6	939.1
28288.3	6364.0	6768.0	7273.8	6544.4	6527.4	7728.1	7465.2	9764.1	11487.5	9649.1
105.4	1575.6	2098.8	2306.8	1835.7	1696.2	2210.5	2027.6	808.0	622.4	1134.5
1636.8	1964.6	2010.8	2007.1	1552.2	1889.8	1879.4	1135.9	657.0	1836.4	2136.5
34.6	1649.2	2274.4	962.6	1733.7	2121.8	1083.4	2293.6	652.6	3741.5	693.2
10236.1	6963.7	6019.1	6626.0	6792.8	6337.3	7323.8	7607.3	7045.7	4862.0	6324.4
52.6	2070.6	2908.3	1408.3	2310.4	2496.8	1762.4	2791.3	793.6	3568.5	991.7
283.7	2152.1	2498.3	2170.5	1427.6	2563.5	2086.1	2766.0	1184.0	3600.9	1629.2
48.1	495.6	1067.8	412.7	474.1	640.6	342.4	1234.9	206.2	1521.2	298.6
50.3	540.0	1041.5	245.8	537.2	721.4	266.2	1241.1	233.5	1138.7	619.8
280.1	210.4	218.3	231.8	166.0	215.5	182.7	207.0	80.2	64.6	130.2
64.8	2548.4	3870.2	2382.1	2685.7	2324.3	3800.5	2337.9	867.4	1610.3	1575.6
275.3	2801.0	3570.3	3279.6	3455.6	3487.6	3492.8	3671.3	3020.5	4476.3	3935.0
10456.6	12984.4	11297.7	11804.8	10373.2	13056.6	12401.5	14915.3	19282.2	15669.0	15148.4
717.6	3667.1	4474.6	4015.1	4001.1	4145.5	4370.7	4466.7	4112.0	5299.8	4522.3
1525.1	7429.2	6956.4	7405.2	8211.0	6818.6	8524.5	6820.3	7988.5	11350.7	10986.4
790.0	3934.3	4852.8	4339.4	4218.8	4593.2	4450.8	4870.8	4592.3	5949.4	4738.5
34999.9	9050.4	8108.1	8964.9	8484.2	10618.6	9460.3	7389.7	12954.2	10006.6	13423.3
763.4	3217.4	3915.8	3543.0	3776.5	3715.1	4031.7	4194.6	4164.6	4810.4	3826.7
412.4	2297.4	3184.0	2695.5	2781.9	2950.8	2779.5	3372.7	2092.7	3825.5	2353.7
778.4	3454.0	4307.6	3833.3	4038.3	3952.2	4110.4	4209.7	4345.7	6186.1	4329.3
4640.8	7313.5	7270.5	6774.0	6707.0	7322.5	7330.1	6977.7	11005.4	9390.4	7494.8
1738.2	5941.8	6304.7	6199.4	6269.9	5572.9	6730.5	5800.8	7526.1	7776.0	7149.2
3353.9	6885.3	8164.1	7200.8	7273.0	7956.7	8348.8	7813.6	9038.0	9734.0	8073.0
10312.9	5997.0	6624.6	5749.9	6158.6	6784.0	6515.2	6267.9	7294.8	8395.0	5093.7
8318.9	7270.2	7425.2	7637.7	7446.9	8129.6	8216.2	6739.1	11691.7	9081.3	10716.7
150.2	1931.5	2307.1	2377.9	1651.9	2398.8	2108.1	2644.3	1098.6	1556.7	1847.4
749.4	3710.0	4815.4	4478.6	4165.7	3988.8	4888.4	4875.8	7040.7	5256.8	4490.7
1120.5	5031.6	6055.2	4924.1	4909.1	5956.4	5417.1	5896.7	4221.2	6884.0	4638.4
9404.6	9166.4	9475.2	9224.2	9075.8	9550.1	9813.5	8763.8	13582.0	11721.7	11951.9
5957.2	5939.1	7031.9	6106.3	6052.1	7228.7	5840.7	6324.0	5284.4	7362.4	6015.6
3861.7	7288.9	7462.2	7346.6	7053.0	7922.7	7902.9	6961.8	10397.6	10522.2	9199.0
1591.4	5678.3	6524.8	6180.6	6396.3	6131.2	6741.8	6502.4	6344.3	8990.8	7625.0
1909.2	4026.8	4546.5	4239.9	3773.2	5547.0	4454.7	4869.4	4006.8	4588.6	3700.6
1255.8	4182.9	5222.4	4691.9	4395.2	4798.8	4707.2	4770.6	5945.1	5522.2	5575.1
696.2	3494.3	4315.2	4182.1	3935.4	3907.9	4284.6	3932.2	4339.6	5544.7	4315.9
3893.5	8117.1	8880.6	8794.8	8087.4	9147.7	8795.1	7908.0	10697.9	11117.6	10806.9
790.0	3900.7	4787.0	4298.4	4463.2	4287.0	4649.7	4821.2	4567.8	6323.7	4689.5
763.7	3939.1	5134.2	4749.3	4318.4	4565.9	4961.0	4613.2	4520.0	5619.3	4393.1
739.6	3516.1	4370.3	3979.7	3943.0	3923.2	4310.2	3948.4	4341.0	5933.6	4057.2
992.9	5583.3	6482.9	6458.3	6242.9	6526.3	6832.7	5994.9	5854.7	5477.8	7140.3

1537.8	1891.7	2025.9
6143.7	10663.1	7059.8
1824.4	1935.1	2416.9
1776.2	1897.0	2184.9
2343.5	2432.6	3864.6
5987.7	8463.0	8373.6
2826.1	2566.0	4517.5
2545.9	2711.3	3621.4
834.1	1030.9	1998.4
817.0	1020.9	2028.6
154.3	297.7	180.3
1661.8	2417.6	3568.3
3609.4	3570.5	4612.7
10037.9	12333.2	12895.5
4365.4	4307.3	6020.6
5458.7	6911.9	7196.2
4841.0	4891.5	6562.3
7176.9	9043.6	8180.5
3912.6	4221.7	4995.7
3323.0	3233.5	4348.9
4404.5	4318.1	5895.2
6603.0	9046.3	8114.9
5038.2	5834.1	7519.4
7443.8	8276.1	10432.8
6419.7	7316.6	8216.9
6448.6	8299.1	6773.6
2282.0	2810.7	4036.6
4230.1	4293.8	5693.4
5701.7	6041.3	8164.9
8620.6	10197.2	10359.1
7073.9	5851.2	8433.8
6960.8	8588.9	8846.6
6000.8	6417.6	8567.2
4246.6	5029.6	5304.0
4499.2	4918.0	6512.6
4008.2	4593.9	5237.9
8388.7	8706.2	10700.4
4796.2	4836.9	6525.4
4566.6	4822.7	6411.5
4010.0	4318.5	5612.1
5923.6	6336.7	8924.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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o__Lactobacillales	f__Streptococcaceae
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s__Streptococcus mutans	45760
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s__Streptococcus oralis	44321
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s__Streptococcus parasanguinis	45778
s__Streptococcus parauberis	45793
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s__Streptococcus phocae	45284
s__Streptococcus pluranimalium	45539
s__Streptococcus pneumoniae	44178
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s__Streptococcus pneumoniae	45496
s__Streptococcus pneumoniae	45756
s__Streptococcus porcinus	44975
s__Streptococcus pseudopneumoniae	44153
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s__Streptococcus pseudopneumoniae	44654

AF077836.1 gg_id:82224 Streptococcus mutans str. UA140 AF077
DQ677732.1 gg_id:167860 Streptococcus mutans str. ChDC YM206; PD65 DQ677
GQ112239.1 gg_id:426772 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
GQ073529.1 gg_id:430079 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ011465.1 gg_id:498201 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792c07 GQ011
FJ557749.1 gg_id:518996 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
GQ111665.1 gg_id:428868 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
AY281080.1 gg_id:90116 Streptococcus oralis str. ATCC 700233 AY281
AY880050.1 gg_id:112132 Streptococcus sp. S16-08 AY880
GQ111693.1 gg_id:410090 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
AY281087.1 gg_id:90242 Streptococcus parasanguinis str. ATCC 15909 AY281
EU156771.1 gg_id:356452 Streptococcus parasanguinis str. ATCC 15912 EU156
AY485605.1 gg_id:102231 Streptococcus parasanguinis str. ATCC 15912 AY485
AF543299.1 gg_id:58281 Streptococcus parasanguinis str. ChDC OS49 AF5432
EU081009.1 gg_id:253153 Streptococcus parauberis str. BMG 149 EU081
AY584477.1 gg_id:99803 Streptococcus parauberis str. DSM 6631 AY5844
AJ621053.1 gg_id:102460 Streptococcus phocae str. CCUG 35103 AJ6210
EU391530.1 gg_id:534876 Streptococcus pluranimalium str. 219 EU3915
NC_011072.1 gg_id:318252 Streptococcus pneumoniae str. G54 NC_01
CP000920.1 gg_id:517593 Streptococcus pneumoniae str. P1031 CP0009
NC_010582.1 gg_id:260561 Streptococcus pneumoniae str. CGSP14 NC_01
CP000936.1 gg_id:266609 Streptococcus pneumoniae str. Hungary19A-6 CP0009
NC_010582.1 gg_id:260560 Streptococcus pneumoniae str. CGSP14 NC_01
CP000919.1 gg_id:530213 Streptococcus pneumoniae str. JJA CP0009
AF003930.1 gg_id:15572 Streptococcus pneumoniae str. ATCC 33400 AF0039
DQ303207.1 gg_id:173018 Streptococcus pseudoporcinus str. LQ 559-98 DQ303
GQ011626.1 gg_id:498040 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794d09 GQ011
GQ019354.1 gg_id:490312 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189a GQ019
GQ040213.1 gg_id:458178 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw95 GQ040
GQ021941.1 gg_id:487727 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ073432.1 gg_id:374596 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ000271.1 gg_id:468836 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11 GQ000
GQ016796.1 gg_id:492871 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825f03 GQ016
GQ073552.1 gg_id:376487 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ114404.1 gg_id:374477 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ007970.1 gg_id:501695 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
GQ018379.1 gg_id:491290 Topographical and Temporal Human Skin Microbiome skin back clone nbu138d03c1 GQ018
GQ111622.1 gg_id:465964 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
GQ103077.1 gg_id:403395 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
GQ021669.1 gg_id:487999 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ043832.1 gg_id:392907 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043

1049.6	5551.3	5959.3	5936.1	5948.9	5360.5	6227.5	5277.5	6382.0	7416.2	7257.5
4678.0	9682.3	9245.3	9456.5	11717.1	10334.8	12059.3	8418.5	9637.0	8890.1	8895.7
29641.2	7692.6	8346.6	9058.7	7363.2	6866.6	9536.1	7077.8	11443.4	8288.8	10800.6
52.2	389.6	660.9	608.6	833.2	631.2	574.7	548.0	177.3	88.6	189.8
92.8	610.2	1127.2	1039.4	914.8	784.7	850.7	985.4	474.4	728.3	531.4
428.5	1860.4	1603.5	1651.5	1814.2	2014.1	1426.9	2370.6	1462.2	1638.4	1989.0
693.3	2728.7	2992.6	3319.9	3051.6	3096.6	2827.7	3554.7	2010.2	2723.6	2434.1
58.4	172.2	247.8	263.9	238.6	253.5	213.5	293.3	113.3	126.2	121.1
189.8	2703.4	2947.2	2813.0	2905.7	2737.5	2369.5	3001.3	1966.8	2018.7	2629.6
101.5	397.1	603.5	669.7	458.0	664.6	383.4	695.3	313.8	561.6	361.2
152.5	910.0	1269.0	1455.0	2556.5	1817.5	1419.0	1883.4	819.2	889.1	1039.9
107.8	1936.7	3704.0	1506.2	2799.3	3132.4	1874.0	3196.5	914.0	3204.6	1627.5
94.0	1177.0	1895.5	859.6	1535.7	2158.0	1129.5	1991.7	575.9	1694.1	1038.1
6047.2	4217.0	4204.3	3793.1	4754.6	4863.5	3866.8	4265.6	5077.4	8196.9	4128.6
821.5	3733.0	3952.4	3860.5	3671.1	3562.6	3969.9	4787.0	3570.1	4331.0	4135.0
211.4	673.2	979.1	622.3	654.9	693.6	866.0	938.1	491.3	505.5	534.5
74.3	378.3	392.1	356.8	372.1	694.5	338.0	837.4	218.4	254.5	260.7
49.4	856.3	1566.9	284.6	771.9	1079.0	623.1	1351.5	404.7	1843.0	573.5
805.3	5939.1	6566.2	5169.6	5365.6	5532.5	5220.1	6778.7	4999.8	8188.8	6210.0
861.9	6690.3	7037.9	6224.1	5930.5	6191.0	5884.1	7209.7	5685.4	9346.0	7060.9
783.7	4766.3	5345.0	4496.4	4547.3	4418.1	4379.6	5645.1	4104.2	7000.1	4588.6
753.7	5110.8	5682.0	4593.7	4973.7	4713.0	5136.6	5944.3	4169.7	6756.2	4750.3
227.5	3726.0	4186.5	3394.7	3489.3	3360.8	3555.5	4381.4	2672.3	5639.1	3461.8
981.5	5357.0	5958.8	5534.5	5222.0	5047.3	5065.8	6395.5	4666.2	6845.2	5282.4
988.1	6483.1	7325.7	6097.9	5998.9	6175.6	5933.5	7625.0	5579.9	8662.3	6901.3
49.9	908.1	1192.4	1130.1	1164.9	1049.5	1473.6	1011.9	541.7	264.1	579.7
107.7	760.5	1065.6	984.5	1077.6	1006.0	1261.6	1358.0	481.2	809.5	819.5
24802.3	7445.0	6270.3	8520.6	6736.9	7313.6	7782.1	6376.6	10390.8	10169.9	8144.7
1405.2	2225.2	2713.3	2661.4	2700.8	2548.4	2514.4	3048.1	2046.0	1477.2	2629.9
19285.9	6089.1	5331.4	7051.7	6085.6	5408.9	6261.1	5460.0	7496.7	5742.3	7560.7
49.4	482.6	630.7	232.0	609.8	794.7	483.3	1052.6	228.6	299.5	480.9
586.4	1982.4	3051.4	3205.4	2650.1	2823.2	2348.0	4018.6	1755.0	2855.6	2924.1
108.9	457.8	757.9	775.1	621.6	583.2	670.8	787.9	397.2	485.7	505.1
25892.4	6347.8	4945.2	6910.1	5811.8	5916.1	6181.8	5583.2	9408.3	7760.6	8699.1
22784.5	6185.5	6665.3	7400.6	6899.6	5626.1	6447.5	6086.7	8358.0	8111.1	6719.2
54.4	175.3	419.2	248.4	432.1	274.2	255.8	606.7	142.0	358.8	115.2
73.7	886.0	1190.4	1316.1	1252.3	1340.5	1085.5	1568.7	464.0	344.5	779.4
376.7	4739.6	4392.8	4751.8	3334.7	4157.1	3177.3	4092.3	4383.0	4684.7	3626.3
55.0	395.3	575.2	488.1	796.4	580.9	320.4	1018.1	228.0	129.8	325.7
9188.2	6976.4	7248.1	6341.9	5756.5	6061.5	6241.1	5695.5	8701.0	7307.6	7867.0
1312.0	1944.8	2215.5	3163.4	2483.9	2180.7	2364.4	2835.6	1572.3	1542.5	2014.3

4714.7	5182.9	7168.0
8849.6	9663.8	12333.8
6811.3	8342.2	7119.0
990.9	599.4	776.8
1058.4	1110.4	1212.8
2096.2	2065.0	2550.6
3136.3	3773.0	3201.3
364.6	479.1	254.2
3009.9	2948.6	3544.1
785.8	833.4	552.8
1717.4	1707.5	2889.4
2888.4	2954.9	4248.9
1820.3	1909.7	2730.8
1995.5	4317.4	6539.7
3812.7	4112.1	6081.7
858.0	1120.6	1067.2
716.1	573.3	655.2
1068.4	1366.6	2538.2
7339.4	6030.6	10244.5
7300.1	6386.7	10736.9
5546.2	4936.1	7989.9
5980.3	5182.8	8731.8
4287.7	3825.3	7055.7
6672.6	5798.5	8786.4
7954.4	6865.1	10380.7
1200.0	1272.1	1761.8
1407.2	1062.0	1941.6
6211.9	8502.6	8152.2
3119.7	2809.7	3430.7
6345.2	5577.8	6318.5
1159.9	720.8	931.6
3698.3	3430.4	4870.8
776.8	752.2	905.0
6145.5	7141.0	6053.9
5846.6	5745.3	6075.3
670.0	297.7	478.5
1561.6	1205.2	1715.7
4266.0	4065.2	5309.8
1061.3	645.9	485.9
6167.7	7962.1	7153.9
2719.3	2794.0	2975.4

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

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s__Streptococcus pseudopneumoniae	45887
s__Streptococcus pyogenes	44634
s__Streptococcus pyogenes	45224
s__Streptococcus salivarius	44274

GQ032099.1 gg_id:459269 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ116212.1 gg_id:459597 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw689c06 GQ116
GQ011481.1 gg_id:498186 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792e03 GQ011
GQ012738.1 gg_id:496928 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8 GQ012
GQ043722.1 gg_id:454796 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
D38483.1 gg_id:15561 Streptococcus gordonii str. NCTC7865 D3848
GQ000709.1 gg_id:469274 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ101353.1 gg_id:442140 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw494b GQ101
GQ011011.1 gg_id:498655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ011
GQ114954.1 gg_id:375288 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685f02 GQ114
GQ060409.1 gg_id:401159 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ060
GQ037331.1 gg_id:431806 Topographical and Temporal Human Skin Microbiome skin palm clone nbu392a07c1 GQ037
GQ068281.1 gg_id:440575 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
GQ060662.1 gg_id:421166 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03h01 GQ060
GQ032327.1 gg_id:433199 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu541a04 GQ032
GQ095830.1 gg_id:438226 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
AY053482.1 gg_id:17851 gas hydrate clone AT425_EubB10 AY053
AY281076.1 gg_id:88205 Streptococcus mitis str. ATCC 15914 AY281
GQ073532.1 gg_id:453009 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ088993.1 gg_id:454354 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3 GQ088
GQ076920.1 gg_id:399933 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
GQ026845.1 gg_id:425917 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ088086.1 gg_id:375021 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ088
GQ074626.1 gg_id:444906 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164c GQ074
GQ000464.1 gg_id:469029 Topographical and Temporal Human Skin Microbiome skin palm clone nbu103h07c1 GQ000
GQ032155.1 gg_id:434917 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ012673.1 gg_id:496994 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8 GQ012
GQ071973.1 gg_id:386691 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190f02 GQ071
GQ038042.1 gg_id:454223 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu37 GQ038
GQ060519.1 gg_id:378178 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02g04 GQ060
GQ043355.1 gg_id:419060 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
GQ074070.1 gg_id:443358 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ074
GQ012816.1 gg_id:496851 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8 GQ012
GQ029799.1 gg_id:410188 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw927e12 GQ029
GQ091881.1 gg_id:455224 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ074369.1 gg_id:392384 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162b GQ074
GQ026868.1 gg_id:426596 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ074391.1 gg_id:392084 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
NC_011375.1 gg_id:314875 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 NC_01
CP000829.1 gg_id:319062 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 CP000
AM157451.1 gg_id:143051 Streptococcus salivarius mother V5 AM157

1482.3	1272.6	1324.1	1365.7	1996.5	1594.2	1983.2	1729.2	1174.1	503.1	1720.0
54.7	1359.3	1939.2	1775.7	2003.1	1796.0	2113.7	3195.7	994.6	958.9	2258.6
104.6	923.0	1143.5	1294.5	1186.5	1260.6	893.9	1687.5	659.5	651.4	1066.8
10815.7	7625.8	7976.9	7203.0	6524.1	7122.5	6745.7	6748.9	10192.3	8697.1	8081.9
99.9	911.5	1220.7	1272.3	1116.5	1231.3	913.4	1730.7	666.5	819.7	1091.0
9418.8	4357.0	4704.9	4086.4	4606.2	4255.7	4579.5	4558.5	4619.7	4941.1	6233.1
103.6	383.6	800.6	711.4	809.0	608.9	528.0	1101.6	374.0	751.3	463.7
57.3	425.8	576.3	495.0	825.6	683.3	322.6	1046.0	226.9	137.6	326.6
136.4	922.5	1146.0	1155.3	959.1	905.2	1201.9	1231.7	446.5	816.3	811.8
1347.6	2355.0	2898.8	3012.4	2675.2	2514.4	3129.3	2829.6	2014.8	1537.1	2770.2
3701.4	3117.5	3252.4	4960.0	3103.7	3151.7	3534.0	3584.9	3690.6	4552.9	4678.4
28615.9	8469.3	8160.4	10777.2	8539.5	8271.2	8907.7	8457.1	8505.7	8862.8	10419.9
1400.4	1782.1	2138.4	2287.1	2272.7	1994.3	2052.3	2400.5	1810.5	1303.5	2332.3
101.9	932.0	1170.8	1211.3	1267.8	1336.6	901.3	1708.5	693.0	646.6	990.1
1503.9	2345.9	2516.7	2820.3	2698.8	2861.5	2472.9	3038.8	2043.6	1482.4	2613.9
48.4	509.1	765.0	261.3	663.1	794.7	537.9	1143.0	248.0	316.1	553.2
74.4	575.9	833.9	986.3	1072.6	799.4	782.3	1507.5	560.1	250.2	936.5
43.5	79.2	118.8	70.4	183.2	88.9	119.8	445.0	88.4	42.9	57.7
1235.2	1608.9	1972.1	2064.8	2184.0	2018.8	2158.5	2169.6	1394.8	875.1	1736.5
57.7	238.7	203.1	264.3	376.6	306.0	160.2	455.8	110.7	133.9	148.3
13126.6	3818.7	3894.8	4151.8	3999.1	3949.2	3938.7	3289.6	3999.1	4990.3	5274.6
14432.3	4444.9	4851.0	4347.4	4328.0	4156.7	4444.3	4378.6	5924.4	5167.7	5932.1
98.1	506.1	610.8	709.5	780.0	791.6	526.1	1062.1	418.7	467.8	599.8
9347.2	4901.3	5972.0	5734.8	5167.6	4948.1	5339.3	5529.8	4797.5	4371.1	5875.7
45.9	1094.9	2067.3	1467.8	2191.0	1869.8	1509.1	3548.3	864.6	1516.9	1934.5
877.2	3153.5	4010.1	4120.4	3165.5	3111.8	3046.4	3649.8	3453.2	3306.8	3931.5
1409.5	2227.2	2544.1	2840.3	2698.9	2553.5	2517.1	3048.7	2052.2	1483.1	2637.6
2588.2	2012.3	2315.6	2890.3	2112.5	2030.1	1952.0	1806.0	1951.2	1989.0	2522.8
66.5	45.7	143.9	31.7	112.5	61.2	72.0	107.8	91.1	18.3	28.8
93.4	268.7	569.0	477.4	365.0	400.5	334.2	569.7	319.9	422.1	364.0
11951.9	4412.1	4136.9	5137.8	4213.0	4193.8	4292.8	4371.7	6485.6	4233.4	5644.2
2437.5	2866.1	3136.8	2779.8	3359.5	2695.5	2900.9	3065.4	2490.4	1471.7	3201.4
123.2	969.7	1241.9	1297.2	1364.6	1232.0	1660.0	1628.8	569.3	897.7	960.6
64.9	488.8	651.0	729.9	846.1	756.8	715.2	1067.0	291.8	181.3	484.3
297.5	1755.0	2524.2	2357.8	2641.4	2233.1	2090.8	3395.1	2295.5	2683.4	2255.4
109.5	934.7	1358.0	1135.0	1237.1	1128.1	1337.3	1544.7	525.0	1011.2	883.7
49.8	279.5	637.7	373.5	510.4	431.3	300.2	722.1	179.5	367.3	216.8
71.9	649.1	814.4	647.3	811.9	761.0	750.1	1173.4	281.9	564.0	542.7
57.8	433.5	457.4	562.9	540.4	474.8	758.7	427.7	452.3	183.2	357.0
81.4	1013.8	1157.4	1221.5	1220.4	1093.9	1500.3	1039.7	832.0	505.4	768.5
48.7	1951.0	3277.8	1155.2	2520.9	2765.0	1565.9	2640.5	1263.8	4109.0	1653.5

1335.3	1718.0	2083.8
3225.3	2311.4	2949.1
1506.8	1427.0	1646.1
6107.6	8676.0	7470.0
1532.0	1465.6	1622.7
4117.8	5148.3	4373.8
929.9	763.1	830.3
1105.0	660.7	522.5
1175.5	926.9	1297.1
2943.1	2723.9	3272.6
3301.3	3600.7	3557.4
7893.0	8427.6	8438.3
2664.4	2245.4	2971.1
1673.0	1431.7	1646.5
2954.1	2802.3	3224.5
1251.9	777.0	1032.0
849.7	660.8	861.6
513.6	185.3	100.3
2425.5	1874.0	2789.8
499.6	355.9	509.6
3463.3	4486.4	3931.4
4345.0	5025.3	4313.1
1156.1	871.5	1336.2
5353.8	5629.2	5362.3
2749.9	2089.4	2943.7
3413.8	3665.5	3826.6
3011.9	2814.7	3427.0
2091.2	2745.3	2147.8
885.7	77.9	30.8
646.8	525.5	453.8
3969.1	5798.3	4055.9
1988.6	3209.4	3561.1
1587.9	1322.9	2491.9
1145.8	700.4	1373.8
3551.5	3183.7	4295.8
1683.4	1318.0	2275.2
842.6	445.6	626.1
1144.8	637.0	1335.3
514.1	560.6	805.3
1196.3	1292.2	1889.9
3396.4	3269.7	5374.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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s__Streptococcus salivarius	44289
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GQ067898.1 gg_id:411450 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw144a0 GQ067
GQ041746.1 gg_id:399498 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932a0 GQ041
GQ037788.1 gg_id:398562 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ037
GQ032436.1 gg_id:433098 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ073305.1 gg_id:405731 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207e04c1 GQ073
GQ073284.1 gg_id:395657 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c05c1 GQ073
EU767000.1 gg_id:352345 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
GQ056935.1 gg_id:413299 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1038e GQ056
GQ012076.1 gg_id:497590 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw796h1 GQ012
DQ327158.1 gg_id:146000 Metagenomic gut microbiome healthy human stool clone E679 DQ327
GQ073122.1 gg_id:445048 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205d01c GQ073
GQ073243.1 gg_id:443817 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g05c1 GQ073
GQ156099.1 gg_id:545941 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ076917.1 gg_id:450079 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
GQ027306.1 gg_id:436913 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ016818.1 gg_id:492852 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825h0 GQ016
GQ015172.1 gg_id:494494 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765c11c1 GQ015
GQ073290.1 gg_id:408634 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c11c1 GQ073
GQ048766.1 gg_id:405294 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5 GQ048
GQ027709.1 gg_id:450712 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
EU766977.1 gg_id:346736 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ154798.1 gg_id:585857 Streptococcus salivarius str. CCRI 17344 FJ1547
GQ022123.1 gg_id:487545 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GQ102628.1 gg_id:413657 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ102
GQ032182.1 gg_id:445687 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ032967.1 gg_id:401843 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ057589.1 gg_id:393274 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ073120.1 gg_id:419730 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c11c1 GQ073
GQ009438.1 gg_id:500227 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ082412.1 gg_id:402163 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11 GQ082
GQ032928.1 gg_id:403958 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ076841.1 gg_id:447628 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ073193.1 gg_id:465072 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206b09c GQ073
GQ027336.1 gg_id:374888 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ073296.1 gg_id:401949 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207d07c GQ073
GQ076874.1 gg_id:398881 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ027284.1 gg_id:415774 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ073188.1 gg_id:377770 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206b04c GQ073
GQ074060.1 gg_id:438313 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ074
GQ032208.1 gg_id:468347 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ086295.1 gg_id:448788 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086

631.7	832.0	1419.5	911.9	1106.0	1048.4	1059.4	1501.9	820.3	2893.2	825.2
71.6	41.0	1338.8	1550.9	50.9	1210.5	1665.1	1585.8	1742.1	832.7	53.7
124.2	1452.4	1763.7	1958.9	1648.8	1644.4	1994.7	2184.2	1248.9	804.3	1701.2
898.6	1326.2	1438.6	1585.4	1569.0	45.0	1832.4	1903.4	35.7	1988.0	1830.6
9408.7	3981.0	3881.6	4026.5	4150.8	3691.2	4797.0	3466.7	5610.5	2753.2	4953.5
130.6	1480.1	1804.9	1983.1	1662.0	1671.6	2019.9	1922.3	1269.2	764.9	1595.8
56.5	700.5	835.2	805.5	676.0	901.6	726.9	966.3	551.3	360.0	734.6
116.8	1680.4	1835.0	1924.4	1923.5	1780.3	2228.1	2271.8	1469.2	1036.5	1750.8
259.4	2275.1	2641.5	2920.3	2630.0	2484.2	3097.3	3227.3	2094.5	1550.2	2498.3
336.8	2032.1	1640.2	1897.7	1672.9	1197.4	2095.0	1907.7	2837.4	1960.0	2245.5
293.2	2891.7	3434.0	3468.9	3827.7	2950.4	4161.8	3458.1	3599.7	1471.9	3666.1
128.3	2156.0	2126.3	2418.5	2181.0	2047.5	2406.7	2353.6	2233.4	977.4	2822.8
124.1	1645.1	2021.1	2081.0	1911.2	1883.2	2194.8	2121.9	1358.4	787.9	1523.6
124.3	1480.3	1805.6	1860.2	1663.3	1672.3	1887.3	1922.9	1374.1	813.5	1595.8
124.0	1461.1	1788.0	1968.9	1655.9	1656.5	2007.2	2046.2	1255.1	760.0	1585.6
259.1	2273.3	2635.5	2919.3	2630.5	2484.7	3094.9	3224.5	2093.2	1550.2	2497.3
38.3	1420.7	1689.5	1698.0	1424.8	1279.1	1625.5	1873.0	1656.8	1141.8	1971.5
185.7	2081.1	2379.5	2604.4	2164.4	2309.3	2743.8	2517.3	1886.1	1250.3	2314.2
233.5	1833.8	2101.5	2230.8	2204.2	1929.2	2398.7	2252.3	1937.5	1369.8	1993.9
22746.9	9912.6	9143.3	11704.9	9609.5	9181.6	11938.7	11985.1	13266.6	11290.6	15664.9
862.3	5372.4	5685.8	5283.1	3277.3	4746.4	4823.8	5453.2	6297.7	6403.7	6759.7
49.4	1949.7	3274.1	1229.5	2519.2	2763.5	1666.4	2842.0	1262.9	4109.9	1771.2
857.7	1520.2	2106.9	2024.1	1609.6	1785.6	1966.1	2883.4	1201.5	1833.9	1773.0
521.8	1917.5	2318.3	2728.8	2402.8	2012.4	3150.9	2931.2	1711.6	1724.4	1909.9
243.8	2287.1	2654.4	2749.7	2637.4	2495.4	2899.8	2810.8	2098.4	1453.6	2324.4
6203.7	8417.6	7031.2	7428.9	5713.4	7174.0	6417.6	8350.2	9274.0	8416.7	8490.3
4437.3	1756.1	1625.5	1753.1	1488.7	1655.0	1852.8	1633.5	2473.4	2041.5	2618.2
90.3	1458.6	1580.7	1702.1	1443.0	1586.4	1775.0	1682.1	1139.3	790.3	1431.4
2583.3	9438.5	8403.9	8673.0	6427.1	7993.5	7814.7	9055.0	11685.8	11708.1	10375.4
260.2	2268.1	2618.2	2911.2	2625.7	2473.3	3087.6	3210.3	2088.5	1545.5	2691.1
360.7	3083.1	2993.4	2990.2	2366.3	2713.5	2693.5	3207.4	1892.2	2176.0	2730.4
260.0	2276.2	2636.9	2917.9	2626.8	2484.1	3093.5	2999.0	2264.9	1551.2	2704.2
1486.0	4663.6	4359.1	3911.6	3453.9	3966.2	3535.8	4375.6	6090.2	5340.7	4164.5
259.9	2276.8	2642.5	2921.2	2632.9	2485.4	3100.0	2999.0	2094.8	1454.8	2499.4
43.5	215.7	330.8	219.0	272.8	220.3	297.7	284.1	175.3	225.1	187.9
84.3	1781.0	2101.0	2321.5	2659.8	1817.0	3251.5	2023.1	1262.6	545.1	1652.6
1801.1	2768.2	3204.5	3441.4	3049.0	2710.6	3747.4	3972.4	4131.4	3454.8	3100.1
1109.8	5651.4	5628.4	5597.4	5215.0	4686.8	5418.5	5948.2	7254.5	4983.5	8002.2
6230.2	2796.3	2717.7	2994.3	2706.4	2684.1	3162.0	2782.8	2888.1	2629.6	3971.7
119.0	1018.5	1232.9	1422.6	1226.8	1094.5	1538.5	1380.9	956.9	629.2	1163.3
2883.7	2077.7	1924.1	2212.5	1928.0	2024.8	2103.3	2081.0	2867.8	2585.1	2950.1

1253.9	1609.1	1844.1
1455.0	957.3	1166.7
1706.9	2065.3	1932.4
1867.4	1851.2	1728.2
4170.9	4320.2	2954.7
1819.3	2102.5	1965.9
900.0	1167.9	694.4
1907.2	2096.4	2164.7
2685.6	2842.3	3089.3
1405.2	2007.5	1963.5
3060.3	3417.4	4179.2
1926.4	1957.1	2272.9
1946.7	2229.6	2511.3
1821.9	2102.4	1967.0
1820.7	2084.0	1962.4
2662.0	3023.2	3088.4
1877.8	1437.9	2143.9
2231.6	2839.9	2810.7
2283.2	2593.9	2857.0
8743.5	10402.8	9553.3
4721.2	4765.6	5720.1
3386.5	3270.3	5373.8
1919.1	2297.5	2937.5
2330.1	2476.9	3682.2
2739.4	3253.3	3313.1
4432.6	5835.6	8061.0
1665.2	2228.8	888.8
1596.1	1956.4	1775.9
7207.4	8748.1	9156.0
2517.5	3014.9	3062.2
2204.7	2331.4	3412.6
2641.7	3031.7	3086.6
3757.3	5430.0	6143.8
2685.3	3032.4	3090.2
413.3	345.1	557.3
1775.8	1542.2	2746.2
3001.1	3458.9	3705.3
3905.4	4874.7	6369.4
2585.7	3526.7	3148.4
1318.9	1425.1	1575.4
803.6	2268.1	2311.5

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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GQ076786.1 gg_id:376508 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ012122.1 gg_id:497544 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw797e05 GQ012
FJ154797.1 gg_id:547030 Streptococcus salivarius str. ATCC 25975 FJ1547
GQ032902.1 gg_id:379571 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ076850.1 gg_id:445671 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ043267.1 gg_id:448280 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ043
GQ074824.1 gg_id:399219 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ074
FJ363284.1 gg_id:367277 feces adult twins and mothers; TS149 clone TS149_a01d10 FJ3632
GQ019319.1 gg_id:490350 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ019
GQ041356.1 gg_id:452091 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
FJ154805.1 gg_id:545804 Streptococcus vestibularis str. CCRI 17387 FJ1548
GQ076777.1 gg_id:376055 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ073340.1 gg_id:405098 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h04c1 GQ073
EF463056.1 gg_id:219466 Streptococcus salivarius str. RKA2 EF463C
GQ073226.1 gg_id:417324 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e07c1 GQ073
GQ076892.1 gg_id:379619 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
EF463059.1 gg_id:224298 Streptococcus salivarius str. RKA5 EF463C
GQ078835.1 gg_id:428382 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ078
GQ073204.1 gg_id:424160 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206c08c1 GQ073
GQ073389.1 gg_id:452062 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208e03c1 GQ073
GQ032174.1 gg_id:418733 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ073349.1 gg_id:468290 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a01c1 GQ073
GQ057898.1 gg_id:393890 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ057
GQ027365.1 gg_id:396642 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ027
GQ007920.1 gg_id:501744 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ007
AM157419.1 gg_id:141989 Streptococcus salivarius mother C3 AM157
GQ032472.1 gg_id:384506 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ032
GQ019505.1 gg_id:490163 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190g GQ019
GQ073065.1 gg_id:378696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204f09c GQ073
GQ088234.1 gg_id:440158 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1 GQ088
GQ076935.1 gg_id:386247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
DQ801238.1 gg_id:190678 human fecal clone RL116_aaf02c02 DQ801
GQ073241.1 gg_id:451593 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206g03c1 GQ073
GQ019428.1 gg_id:490239 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h GQ019
GQ073128.1 gg_id:374338 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205d10c1 GQ073
GQ073291.1 gg_id:376264 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c12c1 GQ073
GQ057595.1 gg_id:413021 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
FJ154803.1 gg_id:549813 Streptococcus salivarius str. CCUG 7215 FJ1548
GQ041484.1 gg_id:426958 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
FJ363912.1 gg_id:358274 feces adult twins and mothers; TS14 clone TS14_a04g10 FJ3639
GQ019436.1 gg_id:490234 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu190a GQ019

124.5	1472.2	1786.9	1853.9	1662.2	1661.5	1881.8	2042.2	1266.3	807.6	1583.7
123.4	1459.4	1786.9	1968.0	1653.1	1655.4	2004.4	2201.2	1254.9	809.0	1584.5
30.6	866.7	2395.0	532.6	1526.5	2345.3	965.7	2161.4	467.2	2144.4	944.8
3277.9	1910.2	1642.1	1988.7	1636.0	1701.4	2251.3	1776.1	3901.1	2456.6	3311.0
86.0	694.1	940.8	997.4	700.9	893.2	763.7	1283.6	666.4	429.4	879.7
248.9	1823.2	2089.2	2367.3	2198.8	1919.0	2552.1	2412.0	1933.3	1371.1	2155.3
8086.0	3869.2	4174.0	3921.1	3510.7	3698.7	4048.8	3923.4	4402.4	4009.5	5335.0
90.0	2933.3	2644.0	2024.2	1726.8	2458.1	1766.0	1934.6	2995.8	2870.6	1818.8
130.9	1471.4	1780.6	1973.2	1654.8	1659.5	2007.4	2041.6	1262.9	809.5	1712.2
86.4	668.5	893.2	964.0	676.7	848.6	662.3	1193.8	610.9	424.8	905.7
46.6	1949.5	3270.3	1228.9	2690.9	2762.5	1661.8	2643.5	1350.1	4110.6	1770.8
243.1	2127.4	2633.6	2934.5	2737.6	2317.2	3004.6	2934.6	4601.2	2009.6	2838.2
174.9	1636.3	1850.6	2060.5	1737.4	1755.1	2231.3	1825.4	1714.0	1076.0	1819.7
45.1	1589.9	2635.7	1088.2	1798.7	2121.9	1401.4	2063.5	1102.0	3534.9	1542.3
3764.4	2842.1	2833.7	3627.6	2625.0	2813.1	3325.2	3701.3	3258.2	1468.7	5128.3
59.5	803.6	571.5	442.0	367.3	596.2	466.2	651.3	1025.6	630.2	570.2
48.4	1930.1	3255.0	1213.9	2506.6	2748.1	1650.2	2827.8	1248.3	4105.9	1759.3
7121.7	2366.2	2686.5	2120.8	2634.7	2445.5	2522.2	2540.8	4301.2	3699.9	2703.7
181.6	2051.6	2357.0	2572.5	2139.6	2271.4	2645.2	2458.6	1875.9	1251.1	2286.7
161.4	3519.6	2764.6	1870.0	1572.8	2796.7	1002.2	2230.6	3296.5	3052.7	2090.5
2026.8	1586.8	1281.9	1464.9	1383.8	1527.1	1544.2	1516.4	1587.4	1090.7	2141.1
187.0	2087.1	2410.4	2613.5	2199.8	2474.8	2789.4	2547.5	1897.5	1257.4	2168.6
47.3	688.2	861.4	915.3	749.4	733.9	1298.3	70.6	636.1	106.9	962.7
16477.8	6460.9	6136.2	7696.2	6792.5	6072.5	8851.6	7784.7	5594.8	5047.9	9751.7
3325.5	2578.5	2448.8	2591.0	2366.4	2667.3	2137.4	2460.4	3491.6	1149.3	4327.5
1810.8	3392.5	4536.0	2570.0	3830.1	4288.5	2958.6	4818.7	2589.8	3422.5	4229.9
1788.0	1450.1	1503.2	1592.9	1267.2	1345.0	1408.2	1616.9	1614.4	878.1	2771.8
118.8	1026.6	1251.6	1429.3	1227.9	1105.3	1544.0	1300.3	1038.9	635.1	1176.5
75.3	655.3	892.5	896.4	668.3	843.5	614.9	1111.3	601.5	422.9	838.5
120.8	1470.5	1784.2	1852.9	1658.1	1659.8	1880.6	2040.0	1176.0	806.6	1470.4
92.1	1493.4	1622.6	1739.8	1462.2	1631.6	1884.4	1751.8	1249.8	741.4	1470.0
6995.7	3290.8	3168.3	3693.3	3473.1	2971.9	4732.6	3588.0	2974.7	1500.9	3223.6
830.7	1943.8	2211.5	2327.1	3522.5	2064.8	3091.1	2600.2	1833.0	2618.9	2250.8
3666.5	3150.0	2938.6	3923.2	2710.2	2959.1	3555.3	4197.8	5563.3	1898.4	5169.2
5106.9	2896.0	2617.6	2787.6	2534.2	2531.8	2525.9	2991.2	3995.7	1644.5	5476.6
13252.6	6035.5	6007.2	6333.1	6577.2	5724.9	7221.8	6214.5	6038.9	4478.7	8003.3
221.2	2335.1	3377.9	3267.2	3823.5	2541.1	4207.8	3612.9	4682.2	2327.2	3149.2
42.0	1928.2	3246.1	1211.0	2675.4	2745.2	1645.2	2629.4	1333.1	4105.9	1759.2
46.8	1298.2	1686.9	1727.9	1849.6	1600.1	1613.5	2423.2	1570.2	228.8	1319.8
10563.6	6485.2	5444.8	6076.6	5677.9	5637.4	6461.3	6359.3	8536.4	7814.1	6445.8
1865.1	3868.1	4808.7	5145.9	4493.0	4120.5	5716.9	5163.9	3228.9	6564.1	4222.0

1748.9	2084.7	1940.9
1821.0	1944.5	1961.4
2856.8	2102.3	4948.1
2079.6	2064.0	1853.4
963.4	1183.7	675.3
2229.1	2416.9	2676.6
3457.4	4993.5	4741.7
2428.7	2531.7	3035.1
1705.7	2083.8	1935.9
902.4	1160.9	576.8
3344.2	3269.4	5372.5
2134.4	2288.7	2917.6
1924.2	2241.9	2416.1
2487.7	2462.1	4144.5
2421.3	3303.9	2858.9
597.3	691.2	678.5
3354.4	3250.3	5365.8
2226.9	3399.8	2589.3
2337.5	2756.1	2763.7
2350.1	1955.8	3310.9
1696.1	1861.0	1779.0
2330.9	2693.2	2856.0
713.1	856.7	1657.7
6020.1	6857.0	7091.5
1896.2	3609.9	2520.3
4410.9	4294.7	6191.0
1131.9	1778.4	1035.7
1363.2	1443.1	1599.7
922.9	1083.1	643.2
1747.5	1945.1	2087.6
1629.6	1921.4	1849.0
3401.6	3246.2	3724.3
2128.8	2480.2	3118.5
2421.9	3525.4	2494.6
2202.7	2549.6	2471.2
5509.0	6542.2	6593.8
2806.9	3169.6	4456.4
3303.7	3250.1	5747.2
1683.3	1976.6	2468.6
5104.6	5893.4	5365.0
3868.1	5444.2	7458.8

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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s__Streptococcus salivarius	45886
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s__Streptococcus sanguinis	45595
s__Streptococcus sinensis	44665
s__Streptococcus sobrinus	44428
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s__Streptococcus sobrinus	45454
s__Streptococcus suis	44388
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GQ041461.1 gg_id:464018 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ041
GQ027302.1 gg_id:380914 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
FJ365649.1 gg_id:367692 feces adult twins and mothers; TS21 clone TS21_a01d05 FJ3656
GQ995676.1 gg_id:548391 Streptococcus sanguinis str. Hanzhong-A2 GQ995
CP000387.1 gg_id:210400 Streptococcus sanguinis str. SK36 CP000
AB002524.1 gg_id:38234 Streptococcus sanguinis str. ATCC 10556 AB002
U87828.1 gg_id:15570 aortic heart valve patient with endocarditis clone v3 U87828
U87829.1 gg_id:15571 aortic heart valve patient with endocarditis clone v5 U87829
NC_009009.1 gg_id:205756 Streptococcus sanguinis str. SK36 NC_00
NR_028833.1 gg_id:593803 Streptococcus sinensis str. HKU4; DSM 14990 NR_02
AY691533.1 gg_id:107142 Streptococcus sobrinus str. ChDC YS1 AY691
DQ677799.1 gg_id:170824 Streptococcus sobrinus str. ChDC YS13; 40125 DQ677
DQ677794.1 gg_id:167103 Streptococcus sobrinus str. ChDC YS206; PD1017 DQ677
AJ871181.1 gg_id:110876 Streptococcus sp. 1040-02B AJ8711
AF009484.1 gg_id:15515 Streptococcus suis str. 22083 AF009
DQ113766.1 gg_id:136603 dog jejunum clone J5-01 DQ113
GQ101022.1 gg_id:380857 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48 GQ101
GQ007632.1 gg_id:502032 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
X68418.1 gg_id:15434 Streptococcus thermophilus str. DSM 20617 X68418
GQ104143.1 gg_id:374288 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw563g1 GQ104
GQ058136.1 gg_id:376543 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ155489.1 gg_id:577395 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ033163.1 gg_id:406397 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ033
GQ101185.1 gg_id:408208 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ031863.1 gg_id:372703 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ021918.1 gg_id:487750 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ058145.1 gg_id:416754 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ054754.1 gg_id:386599 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1100h GQ054
GQ052795.1 gg_id:404186 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
GQ057721.1 gg_id:447223 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ031888.1 gg_id:374845 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ045675.1 gg_id:449085 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ045
GQ052810.1 gg_id:451499 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
FJ363751.1 gg_id:357648 feces adult twins and mothers; TS14 clone TS14_a02h07 FJ3637
DQ327131.1 gg_id:148345 Metagenomic gut microbiome healthy human stool clone E649 DQ327
DQ176426.1 gg_id:139353 Streptococcus thermophilus DQ176
GU195648.1 gg_id:578630 Streptococcus thermophilus str. M4 GU195
GQ058082.1 gg_id:392901 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ069727.1 gg_id:406513 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
NC_008532.1 gg_id:197884 Streptococcus thermophilus str. LMD-9 NC_00
GQ052788.1 gg_id:423913 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052

25189.1	6672.0	6296.7	7427.5	6036.1	6267.7	7486.6	7741.2	9967.4	7539.4	10394.4
14025.3	12018.3	13023.9	14147.9	13335.8	12639.6	13560.2	12273.9	19785.3	13434.8	15997.9
170.5	1194.4	1898.6	1321.6	985.7	1372.5	1072.5	2662.6	990.0	1962.3	1660.9
2279.7	3644.8	3497.9	2638.0	4751.9	3038.3	2950.6	4035.9	3202.7	4900.1	3565.4
2352.9	4350.5	4602.8	4637.3	4672.4	4463.1	4036.4	5020.2	3291.4	3375.6	3910.7
3880.7	1310.7	1395.8	1162.4	933.0	1175.1	956.7	1548.1	1018.9	1624.3	1268.6
2662.5	5217.5	5285.6	4502.8	5714.9	4833.8	4820.3	4296.2	6474.3	5952.1	5333.6
20887.2	10397.4	9120.7	8968.7	10035.4	9622.9	9305.4	11048.8	11040.7	11867.3	13913.6
13928.0	7488.8	8232.5	6694.3	9201.7	7035.2	6608.3	7108.8	8963.0	10734.6	10674.4
178.5	1848.6	1567.6	1271.7	1516.2	1928.5	1461.3	1643.2	1221.9	4058.2	1197.7
4011.1	1992.2	2497.0	2059.9	2980.6	2427.7	2340.1	3337.7	1798.9	2404.5	2495.7
9761.9	4943.6	4722.8	5639.0	6107.6	5624.3	5296.0	5724.6	4814.7	4770.3	5789.3
16322.0	7964.1	7805.2	8987.1	8945.6	8687.1	8598.2	8546.3	11450.5	10005.2	8473.9
2005.9	1483.1	1925.4	1990.5	1863.4	2111.2	3529.1	2668.2	1384.9	912.3	1754.2
45.8	1202.6	1345.9	1480.1	1541.5	1166.6	2650.0	1209.6	1103.4	454.4	908.1
744.1	3105.0	3133.5	3780.6	3771.7	3227.9	4076.3	3501.4	4823.2	2739.6	2943.0
1969.3	1666.9	1756.4	1864.6	1797.3	1765.9	2020.6	1801.6	1988.3	1315.5	1430.9
128.4	2727.1	2188.7	1468.4	1164.6	2075.3	1300.0	1730.9	3490.7	2663.9	1753.5
1169.7	2990.0	3614.7	3973.0	4451.5	3871.6	4188.3	4086.6	4221.1	6804.1	2368.6
9404.4	3940.3	3891.8	3909.6	3389.5	3537.4	3910.4	3503.2	7185.4	3424.1	6421.4
7728.9	3771.1	4530.2	3702.3	5128.4	3954.4	4661.3	4060.8	8503.6	5293.3	4281.0
2719.6	2687.9	2715.8	2891.3	2155.1	2720.9	2594.3	2734.3	2858.8	3149.6	2226.4
19445.0	10161.0	9442.0	10194.7	10537.3	9559.4	9229.7	8740.8	14684.2	11231.7	13156.2
78.2	387.6	409.2	462.8	352.6	457.3	395.6	659.5	313.0	380.1	347.1
82.6	157.7	202.3	150.2	195.7	191.5	167.5	217.2	94.1	106.4	97.4
159.8	269.1	379.3	368.0	491.1	384.4	435.1	428.8	256.0	251.8	186.2
6218.6	1659.5	1545.3	1739.4	1763.4	1614.0	1683.7	1540.9	3550.6	1098.4	2515.9
1967.9	1669.5	1755.6	1865.3	1794.9	1766.5	2022.9	1803.4	1987.5	1314.7	1431.0
41.0	95.8	164.9	256.5	98.3	69.1	383.1	131.8	35.4	24.5	67.1
1988.7	1391.4	1625.2	1869.3	1473.0	1610.0	1502.7	1790.7	2066.9	1433.9	1620.3
293.6	489.0	606.7	652.3	692.0	544.6	638.4	731.7	368.3	169.3	466.4
18364.2	8081.7	8230.7	8695.2	8025.0	7670.4	8965.8	7446.8	17069.4	8882.4	11143.2
360.7	91.2	392.8	253.5	257.5	250.1	108.7	280.6	300.6	158.4	383.4
11376.4	5020.5	4746.1	5001.1	5093.2	5116.4	5231.1	5401.8	7444.2	5671.7	5101.8
1838.2	1614.2	1695.2	1811.8	1755.7	1701.3	1913.5	1725.3	2144.9	1308.4	1598.0
3272.8	4049.6	4731.4	4338.0	4345.3	4403.3	4442.4	4553.0	5200.0	3501.6	4636.7
52.2	611.7	694.3	252.6	1409.1	956.8	401.6	1005.1	498.3	772.2	311.9
1970.4	1659.8	1733.2	1856.3	1792.6	1755.0	2012.1	1787.8	1981.5	1311.1	1519.9
3829.0	1940.9	1862.3	2012.0	1669.6	2293.4	1495.8	2291.3	2832.9	3033.6	1850.5
12508.4	7410.4	7434.8	5820.5	7173.5	7345.6	6071.8	7137.0	8533.7	8253.5	8294.8
1837.1	1612.0	1689.0	1814.7	1755.6	1703.9	1916.0	1723.6	2145.5	1308.0	1484.9

5720.4	7274.2	6073.4
11927.5	12607.3	13151.8
1804.0	1917.2	3210.8
3720.8	3934.4	5426.5
4956.2	5385.5	5501.5
1292.9	1806.5	2290.2
4670.1	5261.6	5218.6
9338.4	10620.0	11812.3
7263.9	8302.8	8166.2
1830.8	2289.6	2934.2
2939.2	2397.2	4062.8
4800.3	5111.0	6114.2
7512.1	8514.2	8238.9
2312.9	2964.8	3596.1
1392.8	1158.1	2056.8
3918.8	4231.5	5625.7
2016.3	1959.8	1973.2
1788.8	2111.7	2463.7
4444.1	5383.7	4597.1
3239.6	4782.7	3504.6
3894.9	3319.1	4867.2
2907.8	2904.0	2482.2
9225.8	10520.6	10462.7
693.3	782.8	487.0
333.6	343.5	264.9
665.9	562.3	748.7
1803.1	2138.5	1692.8
1982.9	2090.7	1974.5
86.4	94.4	91.6
1850.9	1897.8	1581.7
547.0	837.1	701.0
7345.9	9066.8	8100.0
381.6	461.0	225.0
4755.4	6316.1	4933.6
1954.3	1981.1	1901.9
4001.0	5356.8	5425.0
1629.4	1343.2	3071.0
1890.1	2073.6	1947.8
2491.1	2403.3	2415.8
6939.0	6988.8	8137.3
1940.7	1977.3	1900.2

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GQ155655.1 gg_id:549850 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
FJ558254.1 gg_id:517963 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5582
FJ749314.1 gg_id:537395 Streptococcus thermophilus str. IMAU40038; QH31-3-2 FJ7493
GQ031954.1 gg_id:397216 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ031
GQ073080.1 gg_id:443273 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw204h03 GQ073
DQ804818.1 gg_id:185602 human fecal clone RL385_aao81b02 DQ804
DQ805013.1 gg_id:198675 human fecal clone RL385_aao84a10 DQ805
GQ106050.1 gg_id:398015 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ106
GQ101210.1 gg_id:411772 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
FJ364706.1 gg_id:358192 feces adult twins and mothers; TS19 clone TS19_a02a11 FJ3647
GQ155517.1 gg_id:557282 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ058019.1 gg_id:372435 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
GQ048271.1 gg_id:377521 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
GQ155829.1 gg_id:584000 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ007512.1 gg_id:502151 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GQ101087.1 gg_id:387080 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ155483.1 gg_id:579474 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AY675258.1 gg_id:101812 Streptococcus thermophilus str. ST3 AY675
DQ804809.1 gg_id:190074 human fecal clone RL385_aao81a02 DQ804
AF429765.1 gg_id:71159 Streptococcus equinus str. NCDO1037T; ATCC9812 AF429
GQ074419.1 gg_id:371556 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162f GQ074
GQ032260.1 gg_id:431839 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
EU473988.1 gg_id:291047 giant panda feces clone GP_2aaa03g07 EU473
FJ557752.1 gg_id:519951 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
GQ041684.1 gg_id:467380 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw931b1 GQ041
GU045381.1 gg_id:587346 Streptococcus oralis str. KCOM 1408 GU045
EU458225.1 gg_id:296232 North American black bear feces clone BB2_b03_2 EU458
EU458269.1 gg_id:292189 North American black bear feces clone BB2_b03_3 EU458
FJ678567.1 gg_id:526324 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
AF396922.1 gg_id:46196 Streptococcus bovis str. NCFB 2476 AF396
GQ076772.1 gg_id:459838 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
EU458273.1 gg_id:292624 North American black bear feces clone BB2_b09_2 EU458
GQ073147.1 gg_id:404881 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f05c1 GQ073
EU470279.1 gg_id:294884 Grevy's zebra feces clone GZ_aaa03a08 EU470
AY858648.1 gg_id:148448 Streptococcus gallolyticus str. 329 AY858
EU460756.1 gg_id:289494 short-beaked echidna feces clone ECH_aai37e12 EU460
DQ824742.1 gg_id:187029 human fecal clone RL185_aaj72e07 DQ824
AY769997.1 gg_id:113900 Streptococcus massiliensis str. 4401825 AY769
EU467782.1 gg_id:297236 North American black bear feces clone BB1_h02 EU467
EU467863.1 gg_id:289201 North American black bear feces clone BB1_g04_1 EU467
FJ684768.1 gg_id:529028 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847

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109.0	1599.2	1777.7	1490.0	1278.3	1685.3	1396.0	1451.0	1326.2	2495.4	1638.6
1802.3	1703.6	2669.1	1294.0	1950.8	2606.8	1545.8	2950.4	1557.2	3607.6	1490.9
1966.0	1630.4	1710.7	1826.4	1766.2	1717.1	1925.8	1732.8	1969.5	1311.9	1494.4
367.2	685.1	743.7	848.6	798.6	694.8	1022.8	544.8	674.9	162.6	856.9
1966.8	1520.8	1562.2	1664.4	1457.2	1587.9	1811.4	1640.2	2067.9	1375.7	1516.5
3801.5	2997.4	3196.7	2793.7	3384.7	3056.9	3470.0	2883.2	2929.5	3222.2	3066.7
4908.8	4669.0	4249.3	4435.1	3146.4	4519.3	4323.1	3947.8	8783.3	4771.6	5379.8
1963.8	1632.6	1712.1	1827.8	1761.6	1717.5	1927.5	1733.4	1806.2	1310.9	1395.2
3848.9	4609.4	4085.3	3475.9	2812.5	4077.8	2833.0	3488.7	4709.5	4429.4	2896.2
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8520.0	2694.2	2941.6	2865.0	2705.3	2843.7	2961.6	3075.7	5466.2	3794.5	2961.5
6249.0	12023.1	10864.9	10228.2	8226.7	10848.1	8904.5	9226.5	17449.7	16713.8	11772.9
993.2	3441.6	3655.2	3601.4	3328.8	3688.8	3657.4	3293.1	2897.7	5848.3	3761.7
2175.5	1893.5	1812.1	1700.3	1675.8	1658.5	1556.2	1668.5	2354.5	800.9	2775.7
544.3	3849.4	3453.3	2705.7	2165.2	3246.3	2195.0	2845.5	5620.4	4196.1	3562.6
2185.5	3379.0	3767.2	3764.9	3303.7	3687.7	3851.7	4048.5	3770.4	3542.3	3494.6
302.0	2614.5	4518.4	2552.9	2827.3	3423.1	2701.6	3316.4	2287.1	4884.2	4530.9
16238.3	7198.4	6037.2	6868.1	7153.0	6768.9	7473.8	6857.4	10890.7	7718.3	12086.2
47.6	2239.0	3548.5	1608.2	2525.5	2885.8	1612.8	2927.0	893.7	3500.4	1473.3
288.5	1433.9	1898.7	2055.7	2006.9	2009.6	2376.2	1831.4	1184.8	1460.8	1386.3
48.6	580.6	934.1	660.4	814.1	734.2	633.6	968.1	340.5	515.1	399.0
78.5	3292.2	3053.0	1738.5	1611.6	2912.0	1499.2	2409.0	2981.7	3331.8	1773.2
140.0	472.7	472.4	444.8	365.5	568.3	413.9	593.9	243.7	188.3	335.2
48.0	875.7	1004.9	1101.9	951.5	970.9	1142.1	1295.9	659.8	339.2	972.9
126.9	2703.4	3265.1	2605.3	2827.1	3231.6	2555.2	3569.7	1414.4	3468.6	2028.1
189.3	4028.5	3653.9	2895.6	2822.3	3445.9	2897.1	3812.6	3101.6	3848.6	2321.0
240.9	3061.3	3611.9	3825.3	2600.3	3271.6	3131.8	4933.9	2915.4	3782.1	3056.9
4595.2	2512.8	2408.4	2666.2	2110.2	2061.8	2352.0	2192.8	2397.8	2240.9	2561.9
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603.0	718.1	808.2	938.8	949.0	759.5	943.7	1257.9	670.5	667.9	1143.5
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67.7	985.4	1188.6	1097.7	847.5	1058.7	1032.4	1285.5	331.1	537.3	725.6
839.9	1667.9	2393.6	2139.2	1993.3	1905.1	2251.2	2666.1	1765.3	3075.3	1434.8
135.7	967.4	1287.8	1174.1	1204.7	1381.7	1088.5	1545.4	415.2	450.8	585.1
7121.9	4517.0	4534.5	4948.0	4743.8	4139.6	5366.6	4825.7	4393.1	5169.4	5611.0
1334.2	2576.8	2614.2	2454.6	2937.0	2422.1	3178.7	3377.7	1449.0	1218.3	1822.7
8627.9	4138.8	5226.7	4979.3	5997.9	4928.0	5645.6	5157.1	4254.0	3178.0	4276.6

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1702.8	2609.6	2768.9
3272.9	2706.0	3709.2
1973.2	1989.8	1906.7
559.3	999.6	1152.8
1891.9	1906.3	1711.2
3069.3	4176.1	3756.5
3998.9	5053.5	4784.5
1948.1	1988.8	1906.9
3661.8	3493.8	4121.5
4111.2	4225.2	4351.2
3036.9	2638.1	3006.2
10036.2	11515.4	11178.2
3885.0	3734.0	5264.5
1323.0	1831.6	1401.4
2614.6	4164.7	3671.1
4165.8	4058.4	4429.2
3439.8	4358.0	5116.1
6348.2	9128.6	6994.5
3357.4	2783.1	4978.2
1860.0	2294.9	2359.2
1269.6	781.3	1403.7
2394.1	2677.2	4397.6
971.4	747.9	500.8
1042.7	1081.7	948.2
3458.7	3554.6	6861.4
2991.4	3555.9	4535.8
2365.7	5024.7	5045.3
1824.7	3266.3	2068.8
3296.9	3174.0	4946.4
1242.3	1497.0	947.7
2709.6	2848.3	3627.3
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4786.4	5716.2	6982.7

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FJ675372.1 gg_id:509952 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
GQ156114.1 gg_id:542895 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU156788.1 gg_id:349229 Streptococcus pseudopneumoniae str. CCUG 50870 EU156
EU458191.1 gg_id:288025 North American black bear feces clone BB2_d10_1 EU458
AJ871184.1 gg_id:110043 Streptococcus sp. 1606-02B AJ8711
GQ156276.1 gg_id:511755 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU458233.1 gg_id:300876 North American black bear feces clone BB2_c02_2 EU458
EU463426.1 gg_id:295495 domesticated horse feces clone horsem_aai93f11 EU463
GQ072611.1 gg_id:398533 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
GQ069087.1 gg_id:426030 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
GQ032546.1 gg_id:458384 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
EU458204.1 gg_id:291703 North American black bear feces clone BB2_f09 EU458
FJ892877.1 gg_id:574304 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8928
EU460889.1 gg_id:296865 short-beaked echidna feces clone ECH_aai40a06 EU460
GQ156133.1 gg_id:509836 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU475773.1 gg_id:297422 white-faced saki feces clone Saki_aaj63a10 EU475
EU461988.1 gg_id:300951 white-faced saki feces clone Saki_aaj64h04 EU461
EU474053.1 gg_id:296602 giant panda feces clone GP_2aaa02b11 EU474
EU779059.1 gg_id:316587 Prevost's squirrel feces clone SQ_aah81a03 EU779
EU471387.1 gg_id:303161 spectacled bear feces clone SB_2aaa01e06 EU471
EU772598.1 gg_id:326464 North American Black Bear feces clone BB1_c09_1 EU772
FJ679343.1 gg_id:517628 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU475742.1 gg_id:290829 white-faced saki feces clone Saki_aaj62d04 EU475
AJ305257.1 gg_id:36122 Streptococcus bovis str. NCTC11436 AJ3052
GQ019432.1 gg_id:490235 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189h GQ019
GQ057697.1 gg_id:447655 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ072785.1 gg_id:440026 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201b07 GQ072
NR_029025.1 gg_id:590801 Streptococcus halichoeri str. M512/02/1; CCUG 48324 NR_02
FJ558186.1 gg_id:519809 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
GQ072303.1 gg_id:392871 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw194f05 GQ072
AY525794.1 gg_id:111799 Streptococcus pneumoniae str. VN_O27 AY525
EU461851.1 gg_id:289861 white-faced saki feces clone Saki_aaj62c04 EU461
EU458245.1 gg_id:288170 North American black bear feces clone BB2_f04_2 EU458
EU467179.1 gg_id:297263 white-faced saki feces clone Saki_b01 EU467
GQ105172.1 gg_id:446697 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ105
GQ110037.1 gg_id:465867 Topographical and Temporal Human Skin Microbiome skin back clone nbw658a08c1 GQ110
EU458137.1 gg_id:299774 North American black bear feces clone BB2_c11 EU458
GQ032551.1 gg_id:392746 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
AF124350.1 gg_id:22640 Streptococcus orisratti str. ATCC700640; A63 AF1243
FJ154804.1 gg_id:561563 Streptococcus salivarius str. K12 FJ1548

2919.1	2158.3	3016.6	2840.4	2554.3	2931.4	2571.8	3245.0	2205.0	7800.6	1913.0
24695.1	7543.9	6837.7	7707.0	7191.9	7031.4	7447.1	6762.5	7317.5	7798.5	9066.4
227.3	2444.3	2687.2	2590.9	2690.0	3632.6	2700.2	3420.0	2016.8	3737.5	2352.7
108.6	933.1	1354.8	1134.3	1237.1	1197.6	1333.8	1546.1	523.1	1011.0	880.9
1350.6	1591.8	1523.0	1488.5	1033.1	1552.5	1318.1	1689.0	1133.9	769.0	1227.4
42.1	691.3	1449.7	418.7	786.2	1032.4	645.5	1210.7	284.9	498.1	472.8
248.0	5156.2	4911.2	3795.4	3466.4	4549.3	3611.2	4354.7	4638.1	6627.9	4046.9
72884.1	12774.6	12057.1	13377.8	11379.6	11928.5	14715.5	13573.3	18086.5	15471.6	18508.5
127.1	1821.0	2393.3	2724.8	2176.9	1944.8	2675.9	2401.4	922.0	686.5	1314.8
30.6	98.5	119.9	59.5	52.4	114.3	48.6	83.0	36.9	208.8	35.7
8772.9	4490.9	6469.1	5311.7	4678.5	5110.5	5088.3	5865.4	5688.2	6586.8	6345.6
38.3	1361.6	1582.5	1422.5	1230.4	1205.4	2017.9	1811.1	1528.7	1388.4	2006.2
4001.0	3369.9	3380.1	3855.9	3899.1	3461.7	4429.5	4846.9	2428.1	2401.7	3017.4
144.1	1772.4	1844.8	1663.4	1010.1	1816.3	1266.8	1921.0	2318.6	1835.9	1247.9
186.4	1086.5	1766.5	1536.0	1759.0	1575.7	2063.5	2563.7	753.3	1582.0	1410.0
2234.6	5655.1	5647.0	5496.2	5731.6	5428.7	5722.2	6042.1	6244.5	4171.3	5132.8
19763.0	3681.8	3380.1	3852.6	2980.3	2797.9	3608.8	3782.1	4437.1	6330.6	4796.2
7550.9	7245.8	7113.1	7494.9	5321.8	6349.9	6087.5	6010.1	10224.6	9450.6	8194.8
91.8	1949.8	2460.6	2044.7	2309.1	2206.0	2158.8	2621.4	1088.3	1033.7	1623.7
221.1	304.8	510.2	342.2	269.4	350.4	320.5	399.4	350.0	389.0	257.2
5765.2	2272.5	2472.4	2657.9	2409.4	2332.1	2564.8	2230.2	2817.6	2812.5	2140.7
5990.3	5380.4	5774.0	5563.2	6241.8	5301.9	5573.9	7122.8	5121.0	9191.3	4799.3
2577.9	2223.8	2039.1	2166.2	2074.2	2260.3	2384.8	2430.5	2192.0	1803.4	2650.4
14199.2	6425.4	5036.7	4675.3	5315.0	4867.6	6022.6	5709.5	3654.5	5326.5	6369.3
1760.7	6511.1	6835.1	6583.0	7567.6	6555.8	7565.8	8408.5	4510.8	11581.6	6786.0
348.5	1276.8	1523.9	2188.8	1535.3	1255.1	1893.7	1505.0	723.7	606.3	943.9
179.1	716.9	915.0	1218.8	906.7	759.5	1062.2	1398.0	725.0	762.9	606.8
127.5	490.2	785.1	838.3	701.2	624.8	667.5	718.4	504.2	286.8	493.5
52.2	1577.6	1846.8	1217.3	2609.4	1886.9	1602.3	2568.5	733.8	1029.0	1514.7
7779.7	4747.3	4538.7	4695.2	3940.0	4403.6	4726.5	3951.6	4643.9	4571.0	6374.8
44.8	506.4	1342.2	1977.7	827.2	977.6	655.0	1412.2	2063.0	197.2	501.7
183.1	2240.9	2737.0	2199.9	2418.5	2245.5	2056.3	3013.7	2318.4	2250.6	2163.9
3072.3	2796.9	2948.2	3103.4	2701.9	2508.3	3553.4	3287.3	1653.4	1606.0	1954.8
4406.4	2816.8	2594.9	2161.8	2267.9	2484.5	2180.2	3327.4	2569.7	1652.2	3681.8
16912.5	5833.4	5553.0	6284.3	6154.0	6118.7	6612.2	5842.6	6765.9	6019.3	8082.6
70.9	1027.2	1537.7	1296.7	1246.4	1439.9	1220.8	1818.0	485.6	2334.8	686.7
37.2	50.7	50.9	44.7	41.5	61.5	30.6	66.9	28.5	41.8	54.5
19192.6	5901.4	5526.3	6127.1	5557.3	5530.0	5788.8	7888.2	8148.3	8334.7	8407.7
196.7	2043.6	2352.6	2565.0	2143.9	2263.2	2650.8	2623.1	1875.7	1174.0	2286.5
9449.3	4044.4	4470.8	4758.6	4299.1	3919.9	4199.6	4035.5	5527.4	5787.9	4774.7
48.3	1930.0	3252.4	1217.0	2508.7	2750.3	1655.9	2830.7	1338.1	4106.0	1761.7

3934.1	3992.5	4734.8
6584.1	6764.6	6776.8
2774.0	3222.4	4290.5
1679.5	1316.4	2272.4
1080.4	1751.4	913.3
1241.8	1169.1	1059.2
4104.2	5016.2	6991.4
11789.4	17587.7	13293.3
2125.5	2337.6	3000.8
208.0	308.4	591.1
5485.5	6763.4	6958.3
1493.3	1392.1	1807.1
3418.9	5698.9	4740.9
1411.9	1982.9	1593.5
1914.9	2572.7	3869.5
6165.8	6152.7	6732.3
2954.0	5867.4	2884.7
5932.4	7465.3	7893.2
2307.0	2695.6	3884.0
469.3	801.5	355.0
2426.2	3562.9	2944.8
5981.8	7992.2	7192.1
1698.5	3381.1	2739.5
4536.5	7248.1	4562.5
6535.1	8542.1	9803.4
1551.8	1827.2	2093.6
1495.7	1120.2	953.2
1207.8	762.9	881.8
2210.3	2168.7	3272.0
4078.5	5169.9	3935.5
3529.3	819.9	701.8
2586.2	2980.6	4042.4
2589.3	4242.5	3485.0
1857.1	3678.1	2007.6
5294.1	6788.0	6077.1
1739.8	1725.8	1927.5
66.0	98.6	70.8
5228.7	9698.0	5345.4
2331.2	2754.6	2582.8
3929.9	5291.7	4436.2
3356.0	3256.8	5366.7

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GQ091903.1 gg_id:378478 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ074386.1 gg_id:465792 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
AY134901.1 gg_id:59566 oral periodontitis clone FX003 AY1349
GQ076806.1 gg_id:421906 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
EU467824.1 gg_id:302874 North American black bear feces clone BB1_g09_1 EU4678
EU458201.1 gg_id:296761 North American black bear feces clone BB2_f04_1 EU4582
AJ617805.1 gg_id:105608 Streptococcus mitis str. B6 AJ6178
GQ073665.1 gg_id:407180 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ073117.1 gg_id:372638 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c08c1 GQ073
GQ091708.1 gg_id:432165 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
EU458275.1 gg_id:294190 North American black bear feces clone BB2_c04_2 EU4582
GQ076774.1 gg_id:419654 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
EU471392.1 gg_id:294794 spectacled bear feces clone SB_2aaa03c03 EU4713
EU467785.1 gg_id:297386 North American black bear feces clone BB1_h05 EU4677
EU471507.1 gg_id:301767 spectacled bear feces clone SB_2aaa04f06 EU4715
EU461831.1 gg_id:296458 white-faced saki feces clone Saki_aaj61g11 EU4618
EU467834.1 gg_id:288953 North American black bear feces clone BB1_a10_2 EU4678
EU475853.1 gg_id:295993 white-faced saki feces clone Saki_aaj62e08 EU4758
GQ114957.1 gg_id:414368 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
FJ558178.1 gg_id:528842 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
EU467902.1 gg_id:302209 North American black bear feces clone BB1_f02_2 EU4679
EU461802.1 gg_id:294888 white-faced saki feces clone Saki_aaj61c11 EU4618
AY281084.1 gg_id:88494 Streptococcus pneumoniae str. ATCC 6303 AY2810
GQ082014.1 gg_id:413510 Topographical and Temporal Human Skin Microbiome skin back clone nbw1199a11c GQ082
FJ677072.1 gg_id:523529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
EU156778.1 gg_id:339761 Streptococcus pneumoniae str. CCRI-14666 EU1567
EU467758.1 gg_id:291579 North American black bear feces clone BB1_d10 EU4677
EU458258.1 gg_id:299395 North American black bear feces clone BB2_h04_1 EU4582
GQ086143.1 gg_id:389175 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
EU458150.1 gg_id:289299 North American black bear feces clone BB2_e08 EU4581
FJ673591.1 gg_id:518062 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
CP000262.1 gg_id:157784 Streptococcus pyogenes str. MGAS10750 CP0002
EU467778.1 gg_id:294914 North American black bear feces clone BB1_g03 EU4677
FJ679590.1 gg_id:525580 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
EU483251.1 gg_id:265868 Streptococcus sp. str. 24180-02 EU4832
EU467842.1 gg_id:291050 North American black bear feces clone BB1_c02 EU4678
GQ074394.1 gg_id:395063 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
FJ558046.1 gg_id:525966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EU470264.1 gg_id:290919 Grevy's zebra feces clone GZ_aaa01e07 EU4702
GQ155707.1 gg_id:562565 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU461911.1 gg_id:303202 white-faced saki feces clone Saki_aaj63e11 EU4619

18145.5	5796.9	5136.6	6557.0	5255.2	5296.6	5792.4	4745.0	8434.5	8538.7	7827.0
335.6	2393.9	2762.8	2691.7	2406.9	2455.6	2415.6	2713.6	1913.4	2121.2	2675.2
41.2	43.2	79.2	47.1	48.9	51.5	81.0	51.4	33.8	15.6	32.4
136.2	1650.4	2556.3	2734.1	2039.4	2022.0	2313.7	2253.0	1095.7	964.6	1575.0
3809.9	2581.7	2448.5	2728.3	2420.8	2405.2	2140.3	3675.9	2987.6	1911.5	3493.3
172.4	2548.1	3366.1	3224.9	2948.4	2803.9	3199.6	3486.9	1354.5	2459.1	2307.2
216.0	3312.6	3833.3	2519.1	2644.2	2971.0	2014.8	4096.9	2252.1	6475.5	4625.2
134.7	491.0	772.6	900.7	691.9	625.6	667.4	716.7	474.3	305.4	494.8
449.3	4592.5	3612.0	3443.9	2649.6	3575.1	3469.8	3631.9	6089.1	4730.9	4680.6
4047.5	2610.8	2338.2	2173.2	2495.9	2108.6	2420.8	2221.9	3591.7	2674.2	2347.5
3722.6	4972.6	3925.8	4221.4	2906.7	4080.4	4505.5	4718.7	4890.1	6900.6	5172.2
119.0	1496.8	1827.6	2007.1	1679.4	1705.2	2107.9	1984.6	1372.7	814.1	1624.2
4824.0	3927.2	4019.7	4798.4	4082.0	3658.3	5304.7	3598.1	3312.5	2679.3	3616.4
1855.2	3589.9	4410.4	4288.9	4482.8	3788.1	5053.8	5406.4	2787.4	4819.9	3061.9
38.0	439.1	530.8	386.2	157.8	291.0	184.2	312.3	42.6	73.8	141.9
17296.5	7940.6	7519.1	7619.1	7982.3	7407.4	7979.3	9320.5	10441.0	7791.6	9034.6
14531.4	6610.4	6262.5	7008.4	6794.5	6739.2	8064.3	5736.5	6987.5	5304.7	9017.1
126.6	1551.4	1638.8	1886.8	1724.6	1387.9	2248.0	1935.3	794.1	634.7	1045.6
5736.2	3154.6	3882.6	3342.3	3208.6	2935.9	3398.9	3165.7	4100.7	4127.7	4816.8
77.7	976.6	922.0	916.6	1191.1	1080.4	986.0	1105.1	1099.4	1086.7	920.1
1842.4	1733.4	1629.5	1812.2	1572.0	1583.0	2049.0	1708.0	998.8	809.5	1145.7
77.7	1216.2	1853.0	1721.5	1228.9	1913.4	1522.4	2504.7	2448.1	2289.1	1493.1
2387.0	4979.0	5404.3	5733.6	6304.0	5440.2	6483.7	5417.4	5234.8	4778.5	4017.3
24505.8	6431.9	5797.6	7416.1	5411.8	5562.8	6014.3	5599.3	6942.5	7574.2	8635.6
474.4	7845.9	6023.7	6561.0	6628.8	5814.0	7255.1	7592.9	8404.7	5255.0	4934.8
1766.5	4662.0	4899.3	6008.6	5431.5	5207.0	5932.5	4992.6	4696.5	4218.2	3878.2
10537.3	6965.1	5701.7	6131.3	5759.8	5534.9	7276.3	4041.3	4948.5	6273.8	7987.8
49.6	277.6	427.5	326.5	210.4	377.6	257.4	694.7	225.1	738.3	242.7
49.5	189.6	461.1	439.6	263.2	506.2	359.9	829.8	250.5	244.7	431.1
75.2	1746.1	1898.1	2213.7	2211.8	2055.8	2975.5	1940.2	1284.4	503.9	1328.7
114.1	1413.8	2030.9	2195.7	1524.4	1682.5	1902.0	2214.3	622.1	450.7	1108.7
156.6	3040.7	3993.0	3587.9	3621.5	3504.9	4014.0	3784.2	1760.8	2328.0	2770.2
17520.6	6888.2	6542.3	7686.0	6529.0	6644.5	6861.2	6861.4	8193.7	8243.9	9474.8
122.9	1753.6	2348.9	2441.9	2170.8	1925.8	2680.8	2399.5	934.2	635.4	1303.0
103.5	2954.7	4553.3	2879.1	3432.1	3762.7	3244.3	4637.0	1474.1	5171.0	2235.6
14531.9	6625.7	6295.2	7023.9	6798.1	6301.2	8072.0	5742.2	6526.8	5309.6	9029.8
333.2	2451.4	2828.7	2567.0	2446.8	2531.2	2466.8	2773.8	1923.2	2126.1	2533.1
88.7	658.0	685.4	680.9	1101.7	520.8	1057.3	538.6	163.2	274.7	281.5
5017.4	2495.0	2342.4	2693.3	1838.0	1981.9	1973.8	1990.0	2181.7	1262.4	3010.3
71.8	885.9	1020.0	810.5	725.3	992.6	864.3	846.6	747.6	1304.6	822.1
860.8	4213.8	4024.7	4277.8	3792.1	3579.9	4321.2	4356.5	3485.3	2944.5	3705.4

4938.5	6200.7	6030.0
2625.8	2575.6	3063.7
54.1	66.8	105.1
2315.5	2202.1	2923.9
1970.6	4607.2	2261.4
3159.1	3439.5	4516.1
3768.4	3479.5	6203.7
1069.7	765.7	882.8
2960.1	3956.9	3812.7
1969.0	2330.9	2584.3
3546.3	5873.4	4300.8
1818.3	2043.9	2034.7
3733.9	4283.5	5214.0
4127.0	5849.7	5895.9
418.6	324.8	194.2
7413.8	10003.3	7711.1
5832.9	6386.4	6825.9
1711.9	1870.0	2409.5
2579.0	3920.5	2843.8
881.1	1256.1	1159.9
1152.8	1760.8	1869.1
1532.4	2292.7	1785.3
7068.8	4756.1	6501.2
4741.9	6960.5	5292.0
5690.5	7552.9	7564.3
6163.8	4420.2	6063.0
5084.7	5779.7	5861.0
603.8	949.9	755.5
749.9	602.9	886.4
1907.0	2034.0	3250.5
1681.2	2022.1	2029.6
3855.4	3861.5	5765.3
6089.6	7762.2	6626.7
2236.5	2341.1	3015.3
4342.5	4031.6	7248.1
5853.2	6390.7	6829.5
2873.0	2635.5	3321.7
758.9	595.2	1375.7
1696.3	2209.6	1804.1
1063.7	1360.9	1879.9
2891.4	4029.1	4543.4

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GQ034460.1 gg_id:455356 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ034
EU473383.1 gg_id:294502 giant panda feces clone GP_1aaa04f12 EU473
EU467774.1 gg_id:302237 North American black bear feces clone BB1_f09 EU467
FJ673292.1 gg_id:520118 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU458129.1 gg_id:299791 North American black bear feces clone BB2_c01 EU458
EU775692.1 gg_id:343045 Hedgehog feces clone HH_d11 EU775
EU461849.1 gg_id:294466 white-faced saki feces clone Saki_aaj62b10 EU461
EU467158.1 gg_id:297683 white-faced saki feces clone Saki_c09 EU467
EU458133.1 gg_id:302604 North American black bear feces clone BB2_c05 EU458
GQ058671.1 gg_id:465504 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58 GQ058
EU458141.1 gg_id:294837 North American black bear feces clone BB2_d06 EU458
EU461875.1 gg_id:291824 white-faced saki feces clone Saki_aaj62g04 EU461
EU461834.1 gg_id:301274 white-faced saki feces clone Saki_aaj61h04 EU461
FJ680001.1 gg_id:521890 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
AB038371.1 gg_id:42006 Streptococcus sp. str. PSH2 AB038
AY525792.1 gg_id:111812 Streptococcus pneumoniae str. SI_P7 AY525
EU458282.1 gg_id:295664 North American black bear feces clone BB2_d02_2 EU458
GQ081650.1 gg_id:437407 Topographical and Temporal Human Skin Microbiome skin back clone nbw1197g04c GQ081
EU458172.1 gg_id:289129 North American black bear feces clone BB2_h11 EU458
AJ608938.1 gg_id:107158 Streptococcus pneumoniae str. 101 AJ6089
FJ823146.1 gg_id:548508 Streptococcus infantis str. ToTI FJ8231
EU458250.1 gg_id:288235 North American black bear feces clone BB2_g02_2 EU458
EU461821.1 gg_id:288580 white-faced saki feces clone Saki_aaj61f03 EU461
EU774846.1 gg_id:304567 Short-beaked Echidna feces clone ECH_aai39a01 EU774
GQ073297.1 gg_id:451731 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207d08c GQ073
EU467802.1 gg_id:299936 North American black bear feces clone BB1_d04_1 EU467
FJ679627.1 gg_id:522003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU458256.1 gg_id:295491 North American black bear feces clone BB2_h01_1 EU458
AM774229.1 gg_id:256872 Streptococcus sp. str. 1355-03 AM774
EU461915.1 gg_id:300834 white-faced saki feces clone Saki_aaj63f06 EU461
EU461938.1 gg_id:295646 white-faced saki feces clone Saki_aaj64b02 EU461
EU458276.1 gg_id:294389 North American black bear feces clone BB2_c06_2 EU458
GQ101337.1 gg_id:461282 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493h GQ101
EU467854.1 gg_id:293702 North American black bear feces clone BB1_d12_2 EU467
EU458163.1 gg_id:288669 North American black bear feces clone BB2_g05 EU458
EU779414.1 gg_id:333660 Grevy's Zebra feces clone GZ_aaa01g10 EU779
GQ154714.1 gg_id:578309 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
FJ675847.1 gg_id:518137 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
EU458305.1 gg_id:290994 North American black bear feces clone BB2_g04_2 EU458
GQ057676.1 gg_id:414752 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AY976601.1 gg_id:124166 human cecum mucosal biopsy clone K155 AY976

23151.1	6455.9	6841.4	7139.4	6481.9	6180.7	6963.7	6511.3	9613.8	6236.6	9601.9
11388.9	4992.0	5066.1	4641.2	5210.5	4412.8	4883.0	4742.0	4554.3	6097.1	4589.1
5064.6	4350.0	5070.7	5830.8	5446.5	4478.8	5859.2	7798.5	6222.9	4011.7	4344.5
298.6	2724.3	2726.4	3252.7	2914.0	2457.4	3201.2	3416.9	1967.3	1890.5	2105.9
104.8	1327.6	1889.6	2023.3	1277.8	1727.2	2202.8	1879.6	1283.5	928.9	774.5
404.4	796.0	1595.8	899.4	1704.7	1444.7	831.9	1348.2	664.8	473.6	843.0
394.2	2556.6	2750.1	3155.6	2897.7	2495.5	3441.2	3299.2	2717.7	1436.8	1978.6
24569.8	8763.1	7991.7	8676.7	8219.9	8414.6	8975.9	9767.5	10241.0	10420.7	11394.3
8184.3	3116.0	4581.7	3724.8	3884.9	3596.6	4079.1	4091.0	3800.8	5174.3	3982.7
5586.6	3800.7	3715.3	3574.1	3920.0	3364.9	4600.3	3276.0	4529.5	4787.9	4912.4
34.8	778.2	793.2	840.6	603.4	721.0	803.8	649.2	328.1	506.1	435.5
115.4	1602.7	1704.2	1844.0	1535.5	1421.2	1813.2	1623.7	787.9	600.7	949.8
5271.0	6885.2	6023.9	5423.4	4675.5	6511.1	5189.5	4958.4	9618.4	8429.8	6466.5
54.8	539.2	635.4	516.6	216.4	428.5	223.7	600.2	168.4	217.5	221.5
42.1	142.8	261.5	186.8	392.7	255.3	237.2	692.8	119.4	168.3	96.4
199.7	2535.8	3264.2	2038.7	2014.2	2428.7	1677.3	3295.1	1714.1	4847.5	3660.6
111.3	1883.9	2161.1	2185.0	2026.7	1949.1	2060.0	2655.9	970.8	888.8	1426.4
5641.2	5393.0	4747.8	3838.7	3881.4	4616.8	4055.8	5725.2	5801.9	9582.8	4388.4
3252.6	2869.0	2870.7	2916.7	2971.7	2730.2	3174.8	2911.1	2919.1	2289.4	1962.8
156.4	2348.0	2600.7	1356.3	1695.5	1906.4	1205.4	2777.4	1849.4	6045.2	2884.2
56.2	332.6	457.3	451.8	371.3	387.3	357.0	514.6	138.0	82.5	180.4
41096.1	8483.0	7877.0	8510.0	7651.8	7920.6	8755.7	9230.0	12177.8	12455.3	11767.7
11111.9	5359.2	5789.7	5431.5	4643.8	5848.9	4850.6	8082.9	5855.5	9251.2	8338.1
150.8	3084.0	4348.1	3447.2	3852.4	3805.4	4058.4	6274.1	2122.1	6519.1	3758.7
4907.0	5544.6	5236.0	5843.2	5296.8	5848.8	6135.3	5815.7	8547.3	9127.9	10170.1
16684.8	5855.2	5980.0	5950.5	6744.2	5638.1	7209.2	6898.1	6193.5	6349.4	6030.4
2188.3	1459.7	2500.1	2416.0	1005.8	2224.3	2362.8	2742.6	2456.6	2496.9	1355.9
141.1	1296.7	1646.8	1773.1	1291.3	1220.6	1451.0	1969.1	1288.2	614.2	983.0
12291.4	4766.5	4851.5	4802.0	4171.9	4495.7	5338.5	4603.4	5100.1	4972.1	4801.0
92.1	1228.8	1682.9	1985.1	1456.8	1309.8	1996.7	1657.2	564.9	325.2	870.0
31443.2	5561.4	5030.6	6461.1	5447.7	5510.1	5642.9	6937.5	5540.2	5814.9	9383.3
2575.2	4570.0	5158.1	5735.5	5388.8	4755.4	5990.8	5776.9	5406.2	5259.4	3926.9
58.1	406.6	552.2	464.4	732.4	612.6	245.4	1009.3	227.3	136.3	309.1
1285.9	2242.9	2441.8	2446.8	1971.1	2029.7	2302.9	2608.7	1469.3	1021.2	2024.2
371.8	3036.3	4278.2	3597.0	2857.9	3225.8	3263.3	4774.0	3853.8	4960.1	3489.0
2062.9	3283.6	3195.5	4069.7	3664.2	3148.1	4014.3	3259.7	1888.0	2619.8	2285.3
803.0	2659.6	3080.7	3358.0	3016.6	3046.1	3265.1	3273.3	2541.4	2277.3	2665.9
2689.5	2323.4	2326.9	2481.4	1762.8	2117.3	1796.5	2351.4	1815.6	1088.6	2948.1
28256.8	5602.4	5701.4	5743.1	5598.2	5867.9	6091.9	7305.2	9489.7	11225.7	6794.0
56.0	653.5	770.4	755.2	617.7	787.7	583.2	995.2	526.0	352.8	740.7
14393.7	11919.7	11744.7	12012.1	9932.9	11287.6	11909.9	10750.4	15249.0	11421.8	13691.2

6164.7	8146.5	6346.4
5044.2	5638.3	6255.3
6829.5	7068.6	5866.6
2477.8	4023.2	3353.7
1635.7	1629.5	1859.7
1154.7	1259.2	1747.8
3290.5	2715.8	3161.5
7679.5	12476.6	8205.6
3818.6	4967.0	5738.1
3123.4	3544.2	3444.0
694.4	712.0	748.6
1461.5	1529.3	1934.4
4957.9	7283.5	6741.3
486.2	545.9	358.2
354.9	235.1	315.8
3185.1	2563.3	4271.4
2066.2	2640.6	2712.6
4569.6	6012.3	5441.0
2622.3	3044.7	2860.3
2384.4	2602.2	4899.4
550.0	578.1	440.2
7098.0	12342.5	7446.6
4707.8	6868.5	5105.3
4038.7	5657.6	6779.8
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5631.8	8342.5	7029.0
2010.9	3468.3	1960.6
1341.6	1926.4	2182.5
4512.5	5774.0	5421.1
1426.8	1446.4	1922.1
5704.6	7804.5	6015.7
6108.1	5037.9	5687.5
1104.5	610.9	426.4
1778.4	2912.0	2150.4
3097.7	4283.2	4212.2
3273.0	4238.0	4413.5
3374.6	3579.8	4125.6
1505.6	2676.6	1701.1
5293.7	10044.7	6139.4
877.0	1115.0	554.1
10222.5	12013.6	13164.0

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EU467161.1 gg_id:288666 white-faced saki feces clone Saki_e03 EU467
EU473954.1 gg_id:301968 giant panda feces clone GP_2aaa01a05 EU473
EU458115.1 gg_id:292424 North American black bear feces clone BB2_a03 EU458
FJ675711.1 gg_id:529778 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
GQ051339.1 gg_id:422100 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ051
EU467772.1 gg_id:295379 North American black bear feces clone BB1_f07 EU467
EU772573.1 gg_id:343721 North American Black Bear feces clone BB2_g11_1 EU772
GQ030437.1 gg_id:440962 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878c02c GQ030
EU461836.1 gg_id:292510 white-faced saki feces clone Saki_aaj61h07 EU461
GQ156121.1 gg_id:569797 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ043851.1 gg_id:396351 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EU467836.1 gg_id:299093 North American black bear feces clone BB1_b02_1 EU467
EU467810.1 gg_id:288003 North American black bear feces clone BB1_e09_1 EU467
EU467768.1 gg_id:291502 North American black bear feces clone BB1_e12 EU467
GQ016664.1 gg_id:493003 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824b0 GQ016
GQ022888.1 gg_id:486781 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GU470907.1 gg_id:549026 Streptococcus mitis bv. 2 str. F0392 GU470
EU458155.1 gg_id:287652 North American black bear feces clone BB2_f04 EU458
EU458251.1 gg_id:293413 North American black bear feces clone BB2_g04_1 EU458
GU045386.1 gg_id:558644 Streptococcus oralis str. DSMZ 20395 GU045
GQ072839.1 gg_id:408605 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201g11c GQ072
FJ679770.1 gg_id:524800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
EU458207.1 gg_id:301617 North American black bear feces clone BB2_g02_1 EU458
FJ673446.1 gg_id:527638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
GQ112397.1 gg_id:449675 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
FJ558181.1 gg_id:526804 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ678184.1 gg_id:527125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU461987.1 gg_id:297081 white-faced saki feces clone Saki_aaj64h03 EU461
AY485604.1 gg_id:102076 Streptococcus australis str. ATCC 700641 AY485
EU458221.1 gg_id:292142 North American black bear feces clone BB2_a07_1 EU458
EU458291.1 gg_id:302636 North American black bear feces clone BB2_e02_3 EU458
EU473431.1 gg_id:301627 giant panda feces clone GP_1aaa02c05 EU473
EU467885.1 gg_id:293888 North American black bear feces clone BB1_c08_3 EU467
FJ684898.1 gg_id:518374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ558211.1 gg_id:525410 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5582
FJ678668.1 gg_id:523145 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
GQ116366.1 gg_id:403611 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692b0 GQ116
EU458192.1 gg_id:302661 North American black bear feces clone BB2_d12 EU458
GQ032269.1 gg_id:391176 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ038600.1 gg_id:432587 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ032521.1 gg_id:396059 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032

2093.2	3012.6	3446.5	3236.1	3105.9	2865.6	3328.0	4051.9	4138.7	4631.2	2729.7
168.7	2102.1	2714.8	2390.8	2584.4	2354.0	2487.4	2869.7	1459.6	1347.4	1947.3
11053.2	4848.9	5637.9	5485.5	5033.3	4568.2	5509.1	4697.6	6472.8	7548.7	6981.7
378.5	710.7	708.7	657.6	485.0	493.5	654.7	572.4	205.8	129.9	358.6
150.8	1239.5	1459.6	1552.6	1159.7	1451.0	1299.1	1820.1	1321.2	867.1	1667.1
2854.5	4074.9	3809.2	4035.8	3313.0	3786.8	4172.4	2322.5	1873.4	2901.2	4179.4
31566.2	10088.2	8681.0	9423.7	8558.3	8746.3	9508.4	10478.3	14135.2	15295.2	12753.8
268.3	2968.7	3353.2	3229.2	2836.5	2974.4	4954.6	3484.6	1647.1	2201.5	2915.4
209.6	1822.0	2324.6	2769.5	2419.9	2155.8	2832.7	2905.0	2192.1	1416.4	1567.8
10628.7	8126.9	7698.3	7912.0	7641.0	7751.3	7968.5	8174.9	8985.9	7439.8	10143.4
485.1	2457.1	2203.2	2492.3	2190.4	1920.5	2502.0	1809.6	3225.7	4197.1	4117.6
4660.9	4390.6	3897.5	4509.1	4367.4	3922.0	4589.0	4823.9	3316.3	2080.5	4344.0
21488.8	4437.5	4373.0	5367.6	4488.0	4019.9	4922.6	3741.0	4161.4	5696.5	6172.0
13570.3	4738.1	5064.8	4029.5	4971.9	4991.0	5648.1	6360.4	4975.4	6410.3	5395.9
132.4	1470.3	1798.9	1975.3	1664.0	1663.4	2021.7	2047.6	1268.7	764.3	1594.6
47.0	218.3	248.8	212.9	205.3	296.7	218.6	283.5	191.9	673.2	198.8
84.2	1483.1	2349.9	1084.6	2065.2	2050.0	1279.4	2473.2	858.1	2973.7	921.7
334.6	653.6	780.4	665.5	525.1	429.2	461.9	484.3	277.1	463.3	642.4
129.9	2355.4	2875.2	3250.3	2619.6	2488.2	3464.6	2686.5	1205.5	784.7	1864.5
53.9	1603.6	2013.5	1362.4	2057.0	2118.8	1664.2	2380.6	728.3	3213.8	757.2
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1855.2	2111.9	3471.6	2804.7	3056.1	2677.4	2922.6	3181.1	2067.7	4614.7	1942.7
1132.5	1516.5	1572.7	1407.2	1039.0	1575.0	1235.1	1642.1	1142.0	779.3	1247.8
1996.5	1056.9	1129.7	1123.7	1050.5	971.7	1035.2	1028.5	1363.3	503.9	746.0
112.7	618.3	830.1	724.5	560.4	556.3	454.7	929.3	383.6	561.3	619.7
18586.6	6018.4	5672.9	6445.1	6320.0	8052.6	6461.9	6200.6	7305.8	6881.6	7279.7
124.2	1404.7	1406.1	1461.1	1276.6	1264.9	1524.1	1426.9	708.7	509.2	791.8
18490.4	7066.3	6325.7	7228.6	6677.5	6772.5	6967.7	8276.9	7745.7	10397.1	10324.0
105.8	2247.7	2202.9	1257.6	2503.4	2413.7	1652.1	2474.2	990.6	3362.8	1112.4
18956.3	5211.3	5065.8	5249.3	5137.5	4726.2	5742.7	5798.2	5964.0	6089.6	5885.7
17446.0	6308.9	5283.4	5439.6	4912.5	5036.2	6372.0	5755.6	8513.3	6906.1	10422.5
127.8	1613.3	2282.1	1865.8	1727.7	1977.0	1471.7	2590.4	1080.8	1138.3	1706.1
2964.9	4902.4	3969.5	3635.2	3303.4	4191.1	2721.6	4658.2	4592.5	4324.9	3596.1
249.8	2636.0	4000.5	3483.4	2924.6	2801.7	3282.9	4097.2	1814.9	1603.0	2177.7
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3684.5	2383.1	2233.4	2364.2	2615.7	2333.8	2511.2	2817.6	2201.5	1200.6	2739.6
94.5	866.1	977.8	1059.9	906.4	901.3	1195.5	1028.9	1541.9	326.8	1030.9
51.9	713.2	921.2	995.1	567.7	801.9	585.8	1545.7	331.9	653.5	520.4
149.2	1249.9	1471.2	1563.6	1163.9	1460.5	1303.8	1702.0	1224.1	813.9	1543.3

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2608.9	2996.0	4315.5
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571.0	657.9	657.5
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8051.5	13077.6	9113.8
2769.0	3147.6	4522.9
2215.3	3186.7	3115.6
7201.8	9366.7	9060.1
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1811.4	1959.1	1837.5
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5989.9	7286.0	7752.9
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2719.6	3065.4	4236.8
4433.4	8188.9	5200.7
4154.4	7152.8	4661.2
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3560.5	4308.6	4306.0
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1127.6	1048.2	1471.5
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FJ682967.1 gg_id:517809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ662826.1 gg_id:551205 Streptococcus pyogenes str. Sp4 FJ6628
EU460892.1 gg_id:302391 short-beaked echidna feces clone ECH_aai40b02 EU460
EU467908.1 gg_id:292450 North American black bear feces clone BB1_g03_1 EU467
GQ068224.1 gg_id:458497 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw148 GQ068
EU458149.1 gg_id:289551 North American black bear feces clone BB2_e07 EU458
GQ076119.1 gg_id:372054 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ076
EU458116.1 gg_id:296356 North American black bear feces clone BB2_a05 EU458
GQ013235.1 gg_id:496431 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ013
GQ073338.1 gg_id:418360 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h02c GQ073
GQ057439.1 gg_id:371684 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ057
NC_003485.1 gg_id:129068 Streptococcus pyogenes str. MGAS8232 NC_00
EU535969.1 gg_id:281999 profile human microbiota antecubital fossa (inner elbow) skin clone nbt06g07 EU535
FJ676264.1 gg_id:525392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6762
EF509615.1 gg_id:225348 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5096
GQ101509.1 gg_id:465878 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495 GQ101
EU467763.1 gg_id:294288 North American black bear feces clone BB1_e06 EU467
EU461902.1 gg_id:295919 white-faced saki feces clone Saki_aaj63d11 EU461
EU156782.1 gg_id:350039 Streptococcus pneumoniae str. CCRI-15796 EU156
FJ678537.1 gg_id:526366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
EU461866.1 gg_id:298094 white-faced saki feces clone Saki_aaj62e09 EU461
EU458187.1 gg_id:302971 North American black bear feces clone BB2_c08_1 EU458
GQ074067.1 gg_id:404983 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ074
EU458210.1 gg_id:292277 North American black bear feces clone BB2_g09_1 EU458
EU458286.1 gg_id:295358 North American black bear feces clone BB2_d06_1 EU458
GQ028155.1 gg_id:406593 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ028
GQ018843.1 gg_id:490825 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191d GQ018
EU458252.1 gg_id:296907 North American black bear feces clone BB2_g05_1 EU458
GQ018860.1 gg_id:490807 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f GQ018
EU458292.1 gg_id:302364 North American black bear feces clone BB2_e03_1 EU458
GQ010556.1 gg_id:499109 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
FJ679324.1 gg_id:509856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU774903.1 gg_id:319192 Short-beaked Echidna feces clone ECH_aai38d02 EU774
GQ000869.1 gg_id:469434 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ000
EU461949.1 gg_id:297276 white-faced saki feces clone Saki_aaj64c03 EU461
EU467748.1 gg_id:289224 North American black bear feces clone BB1_c07 EU467
AM157421.1 gg_id:141768 Streptococcus parasanguinis mother C3 AM157
GQ058009.1 gg_id:449776 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ058
EU458304.1 gg_id:297241 North American black bear feces clone BB2_f10_2 EU458
FJ894952.1 gg_id:555959 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8949
EU471452.1 gg_id:295151 spectacled bear feces clone SB_2aaa01f05 EU471

5519.4	2324.9	2463.9	2738.7	2924.1	2423.7	3238.5	2649.1	1692.0	1734.5	1896.9
79.0	1002.4	1223.0	1280.9	1280.0	1160.2	1595.1	1029.6	826.0	495.5	811.8
286.1	1731.5	1989.7	1935.7	1815.2	1901.5	2080.6	3085.3	702.1	1213.3	1826.0
1487.0	1588.5	1745.2	1658.0	1239.7	1620.5	1342.6	903.3	528.1	1676.2	1769.5
95.5	946.2	1690.6	1688.1	1327.3	1236.4	1577.1	1434.9	497.5	641.9	742.0
7264.4	2669.5	2693.1	2930.1	2496.5	2448.4	2753.6	2379.4	2633.4	2503.8	3047.3
865.5	1762.0	2186.9	3087.0	2314.0	2074.5	2224.6	2651.7	1707.9	1705.1	2198.5
5381.2	4832.8	5155.6	4482.3	4794.2	4666.6	4646.8	5021.7	5081.9	5546.8	5287.6
10250.2	3563.0	4397.6	5494.3	4299.0	4346.6	4495.1	4481.4	4284.5	6629.8	5133.0
145.3	1286.5	1524.4	1603.0	1218.0	1609.2	1442.8	1681.2	1346.5	874.2	1589.8
12807.5	5958.4	5744.6	7003.2	5773.2	5805.5	7135.1	6837.8	9317.3	6434.6	11976.0
67.5	178.7	264.6	209.4	174.1	243.2	166.0	224.1	144.4	120.5	172.8
154.9	1113.0	1072.0	857.1	834.2	920.7	1087.9	1041.4	1310.0	1421.8	943.2
265.0	5197.7	5348.7	5829.3	5540.4	4935.0	6316.9	6475.2	5813.9	5511.1	5700.3
1585.8	4085.2	3640.4	4196.3	4444.2	3581.4	4111.5	4773.9	6184.7	4228.8	5392.7
483.3	1905.5	1620.1	1747.9	1830.7	2154.3	1537.0	2429.9	1590.4	1594.0	2128.8
3369.8	3471.4	3451.7	3142.2	3133.2	3187.8	2619.4	3621.9	3366.4	2430.4	3479.3
15316.7	5130.3	4485.0	4777.0	4589.8	5036.2	4883.8	6869.6	5609.9	7927.2	8112.7
104.8	666.9	930.0	1212.6	1311.4	986.3	891.8	821.2	468.2	324.7	514.1
14508.2	4092.1	3976.0	2575.8	3740.8	3433.0	3880.2	4206.2	5166.5	6265.2	7012.8
265.0	2819.4	2826.9	3000.4	2709.4	2583.7	3847.8	3428.7	1613.2	1588.8	2022.8
126.6	2199.6	2879.2	3242.6	2608.6	2480.3	3213.0	2749.4	1189.2	771.8	1738.3
58.4	467.9	529.2	521.9	694.6	714.5	344.4	1021.0	290.7	277.6	452.9
1350.4	1494.2	1550.9	1494.6	1035.0	1559.1	1221.1	1640.2	1135.1	769.2	1231.3
3576.4	3749.9	3807.9	3547.4	3705.8	3621.9	3692.1	4307.5	3657.7	3955.0	3061.9
10003.0	3239.2	3551.9	4760.1	3485.3	3470.2	3510.7	3729.0	4025.1	3508.4	5046.1
61.4	595.5	763.2	890.4	813.0	563.6	944.0	638.9	237.8	182.8	318.8
9398.1	4625.0	4038.3	4731.9	3865.5	4628.3	4496.0	6214.5	5723.9	7084.4	5484.2
13735.9	5465.8	5585.2	6435.0	4583.7	5149.4	5437.0	5340.5	7959.6	6347.8	6832.4
107.6	395.9	428.7	449.0	136.5	282.8	202.9	250.6	130.3	74.4	151.3
8114.8	5089.2	5158.2	6519.2	5716.4	4807.8	5781.9	5508.8	6554.6	8133.9	6456.9
666.6	1951.8	2843.8	2926.4	2560.3	2303.0	3156.0	3577.4	1765.6	1340.4	1923.0
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326.7	2066.0	1395.6	1359.9	1652.4	2018.1	1228.1	2442.3	1503.2	1815.9	2359.7
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103.5	2424.2	2519.2	1467.3	2202.6	1974.1	1704.0	2956.5	1351.2	3957.4	2335.4
271.3	699.0	902.0	931.7	716.0	717.4	1295.8	1198.4	553.3	455.0	747.3
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1807.3	5647.1	5593.5	5762.8	4883.9	5160.6	5112.9	5460.7	6331.0	5427.5	5111.1
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1507.0	1663.7	1648.8
1463.0	1194.8	2004.6
2277.8	3647.6	2652.0
2376.8	2526.9	2572.7
5297.9	5400.7	5878.9
4671.8	4705.5	4559.5
1453.8	1893.7	1494.9
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2397.9	4273.5	3619.0
2539.3	2618.6	3432.6
1057.6	726.3	918.6
1116.3	1912.6	948.8
3659.6	3986.3	4243.0
3879.0	4126.0	3992.1
985.2	654.3	1241.0
4050.3	8177.5	4288.0
4496.9	6489.0	5202.6
402.0	473.9	289.8
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2187.8	4420.1	3518.5
1102.5	1158.5	2052.3
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EU458127.1 gg_id:295594 North American black bear feces clone BB2_b09 EU458
U87830.1 gg_id:15387 aortic heart valve patient with endocarditis clone v6 U8783
AB259061.1 gg_id:192739 Streptococcus dentirousetti str. NUM 1303 AB259
EU473378.1 gg_id:303070 giant panda feces clone GP_1aaa03e07 EU473
EU660341.1 gg_id:293142 Streptococcus pyogenes str. Sp30 EU660
GQ060712.1 gg_id:431280 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e07 GQ060
EU467898.1 gg_id:291675 North American black bear feces clone BB1_e07_1 EU467
EU460848.1 gg_id:288152 short-beaked echidna feces clone ECH_aai39c04 EU460
AB002510.1 gg_id:15413 Streptococcus dysgalactiae V24 AB002
GU045379.1 gg_id:578793 Streptococcus oralis str. KCOM 1401 GU045
EU458169.1 gg_id:288654 North American black bear feces clone BB2_h04 EU458
EU774892.1 gg_id:353416 Short-beaked Echidna feces clone ECH_aai38e06 EU774
AF184974.1 gg_id:42170 Streptococcus australis str. AI1; ATCC 700641 AF184
GQ074435.1 gg_id:377602 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162 GQ074
EU534731.1 gg_id:286668 profile human skin microbiota ear punch biopsy female C57BL/6J mouse clone nbt18 EU534
GQ073325.1 gg_id:409438 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207g01c GQ073
GQ032481.1 gg_id:407929 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ156288.1 gg_id:582512 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ043370.1 gg_id:446121 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw9 GQ043
EU467891.1 gg_id:290897 North American black bear feces clone BB1_d09_2 EU467
GQ010627.1 gg_id:499038 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
EU475847.1 gg_id:298266 white-faced saki feces clone Saki_g03 EU475
GQ088816.1 gg_id:422570 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
EU458230.1 gg_id:294980 North American black bear feces clone BB2_b08_2 EU458
GQ073229.1 gg_id:452542 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206e10c GQ073
AF335573.1 gg_id:33357 Streptococcus iniae str. Dan 1 AF335
EU461941.1 gg_id:297117 white-faced saki feces clone Saki_aaj64b06 EU461
GQ092789.1 gg_id:374841 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ092
EU461957.1 gg_id:303168 white-faced saki feces clone Saki_aaj64d06 EU461
GQ003166.1 gg_id:506496 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu19 GQ003
EU470337.1 gg_id:292055 Grevy's zebra feces clone GZ_aaa03c12 EU470
DQ148957.1 gg_id:139480 Streptococcus bovis SbH8.11 DQ148
GQ156147.1 gg_id:580333 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ096744.1 gg_id:446169 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ096
EU458211.1 gg_id:300882 North American black bear feces clone BB2_g10_1 EU458
EU467816.1 gg_id:298015 North American black bear feces clone BB1_f06_1 EU467
GQ069073.1 gg_id:404627 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EU156767.1 gg_id:325913 Streptococcus oligofermentans str. CCUG 48365 EU156
GQ076979.1 gg_id:425421 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ076
EU156773.1 gg_id:342992 Streptococcus pneumoniae str. ATCC 49619 EU156
GQ101197.1 gg_id:419981 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101

23139.8	6398.3	6596.9	6943.2	6788.7	6189.5	6853.3	8179.9	10132.1	8904.1	8453.8
11246.1	3977.2	4790.0	4487.2	4764.3	4688.6	4251.7	4951.2	5841.6	6569.9	4677.5
609.1	2023.7	2923.7	2413.4	2117.8	2560.2	2085.5	2859.3	2871.7	4034.9	2132.3
242.3	3841.4	5614.4	4142.5	3524.8	4541.7	4002.9	4524.6	2530.0	1601.0	4593.8
4547.9	3758.4	3442.0	4190.9	4111.4	4048.9	3842.1	3477.3	3115.0	2915.3	4538.9
166.9	697.5	859.1	1193.4	952.1	865.4	712.2	1101.4	625.8	1410.1	736.8
12848.6	6184.1	6377.4	6722.7	7269.9	6208.0	7215.0	5985.3	6286.0	8292.6	8891.6
608.1	2355.5	2689.9	2459.4	2155.1	2489.2	2532.3	4044.4	1227.5	2511.8	1972.0
45.1	258.2	416.2	355.6	327.5	605.3	260.2	891.3	158.8	276.6	344.4
423.1	2808.6	3037.9	1951.2	2856.6	3457.7	2110.2	3729.9	1884.7	4163.3	2336.0
223.6	6015.4	4875.3	3469.2	2724.4	4448.2	2771.7	4819.4	5415.7	6880.5	3395.8
67.4	824.6	1016.0	934.8	794.3	925.8	965.0	1304.0	324.3	559.2	710.3
107.4	1239.7	1403.7	1076.0	1604.1	1469.0	987.0	1554.9	846.4	994.8	1397.0
127.1	2956.5	3477.4	4098.0	3090.1	2990.9	3035.2	3344.1	2357.0	2430.8	3599.1
1487.3	2326.0	2723.3	2626.4	2613.1	2612.9	1998.4	2715.7	948.2	2641.0	1747.0
2028.8	1768.5	1739.4	1969.0	1596.8	1729.8	1624.2	1804.6	2393.9	867.1	3688.5
142.4	1721.6	2084.8	2346.5	1980.9	1915.6	2527.0	2426.3	1436.7	891.3	1866.7
52.8	128.0	249.9	182.2	326.6	162.1	210.4	187.1	91.0	59.8	126.0
109.0	810.7	1010.2	1154.2	909.1	1125.0	716.1	1231.5	565.5	481.1	828.5
3178.5	6408.0	6014.8	6459.5	6667.8	5837.2	7459.2	5725.9	5801.4	6529.0	6345.2
66.5	1696.1	2477.0	2512.0	2261.9	1869.6	2512.5	2163.4	1044.7	1293.4	1356.0
93.1	1393.4	1606.3	1782.0	1517.0	1311.3	1746.5	1589.1	731.6	597.7	970.1
64.7	181.3	421.8	295.6	348.1	261.2	294.7	335.2	182.3	62.1	129.0
32991.0	9867.1	8671.2	9897.8	8944.8	9101.0	9792.0	10398.6	13315.1	11065.6	13206.8
43.0	186.4	197.7	190.1	174.8	223.2	191.6	275.2	170.8	171.8	158.3
51.2	597.8	1025.4	676.1	538.6	946.0	403.0	1250.8	230.9	414.4	518.0
142.7	3326.2	2599.1	1578.5	1426.8	2288.7	1225.9	2571.9	2703.5	2630.2	1756.3
2725.1	3008.6	3426.0	3772.0	3471.7	3294.5	3340.6	3754.2	2487.5	2123.4	3493.6
34.1	1302.2	1543.2	1158.0	1068.6	1153.0	1142.4	1358.7	652.5	914.6	640.3
3317.2	5385.3	5919.2	6398.8	5506.6	4470.6	6065.8	4986.9	11488.3	9152.7	7583.4
1135.5	1757.9	1573.9	1507.4	1048.2	1464.5	1451.7	1526.0	1074.1	728.3	1332.1
51.3	591.7	755.5	670.9	412.8	529.2	561.9	546.1	150.4	123.3	311.5
461.5	2221.1	2725.3	2314.0	1494.1	2261.5	2306.9	2863.5	2988.6	2070.6	2190.9
69.8	624.0	815.6	890.4	919.9	858.8	764.4	1177.0	328.2	213.6	579.4
24574.7	5777.4	5240.8	5231.6	5206.6	5230.2	4965.3	6671.4	7629.7	8418.1	6295.7
9450.5	7719.1	7495.6	7304.4	7738.5	7067.8	7958.7	7095.1	8662.1	9878.6	7941.7
73.9	525.0	928.1	796.4	751.3	634.7	706.2	782.4	325.4	591.7	380.2
1237.6	2027.5	2642.0	2427.1	2592.2	2565.4	2588.2	2784.3	1620.0	1039.7	2172.1
2443.1	2914.3	2871.7	3355.1	3240.5	2784.6	3445.6	3196.0	3480.4	1142.9	3729.2
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111.7	694.5	968.8	1233.6	1338.3	1037.8	943.6	862.3	485.2	334.1	542.2

5981.8	10646.6	5972.8
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4410.6	3294.8	5904.5
3463.7	4593.5	4192.7
1026.5	1369.9	1470.3
5669.6	6622.1	7474.8
2560.6	3133.6	4160.8
689.5	955.5	1566.5
3549.3	3446.3	4928.2
3770.0	4891.8	5387.1
1029.3	1153.8	1992.6
1331.8	1406.7	1437.8
3695.6	3709.8	4386.5
3658.4	3424.7	5956.1
1248.8	1806.1	1517.8
2088.7	2461.8	2601.5
251.5	220.1	343.9
1238.0	1152.5	866.8
5281.1	6665.2	7354.4
2134.8	2041.5	4085.7
1557.3	1667.3	2255.0
917.1	222.3	333.8
7988.1	12854.3	8980.8
331.5	468.6	273.9
968.0	1523.8	1742.8
1912.7	2656.1	2865.7
3864.3	3466.9	4327.9
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5286.9	7454.2	5663.7
1141.0	1632.6	989.2
583.6	451.0	543.0
3024.2	3599.8	4683.8
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4841.9	8289.3	5228.8
6356.6	7995.0	8271.7
916.0	695.3	1251.4
2826.3	2412.0	3019.4
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5488.9	3521.8	5249.7
1256.2	928.5	1251.8

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EU460730.1 gg_id:295580 short-beaked echidna feces clone ECH_aai37b08 EU460
EU458283.1 gg_id:293073 North American black bear feces clone BB2_d03_1 EU458
EU465122.1 gg_id:300671 African elephant feces clone AFYEL_aaj68d04 EU465
GQ101296.1 gg_id:419123 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493c GQ101
EU467176.1 gg_id:301477 white-faced saki feces clone Saki_a08 EU467
GQ071872.1 gg_id:459330 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw189d0 GQ071
EU458234.1 gg_id:292953 North American black bear feces clone BB2_c04_1 EU458
EU458200.1 gg_id:289631 North American black bear feces clone BB2_f03_1 EU458
FJ975977.1 gg_id:571637 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9759
GQ077262.1 gg_id:406562 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
EU458131.1 gg_id:298527 North American black bear feces clone BB2_c03 EU458
FJ662835.1 gg_id:565491 Streptococcus pyogenes str. Sp19 FJ6628
GQ072817.1 gg_id:454091 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201e08 GQ072
GQ060504.1 gg_id:466552 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02e10 GQ060
EU467877.1 gg_id:297939 North American black bear feces clone BB1_b06_2 EU467
EU458146.1 gg_id:300972 North American black bear feces clone BB2_e03 EU458
GQ073546.1 gg_id:459692 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073
FJ662836.1 gg_id:557233 Streptococcus pyogenes str. Sp21 FJ6628
EU458242.1 gg_id:298551 North American black bear feces clone BB2_f01_2 EU458
EU772612.1 gg_id:329630 North American Black Bear feces clone BB1_g02_1 EU772
EU160562.1 gg_id:332405 diagnosis central-venous infections cultivation-dependent and techniques biofilm sc EU160
FJ672424.1 gg_id:519177 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6724
CU917914.1 gg_id:568929 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
EU458167.1 gg_id:291884 North American black bear feces clone BB2_g11 EU458
EU467806.1 gg_id:291430 North American black bear feces clone BB1_d10_1 EU467
DQ824669.1 gg_id:193137 human fecal clone RL185_aaj71d09 DQ824
GQ113281.1 gg_id:456797 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ113
EU475811.1 gg_id:295833 white-faced saki feces clone Saki_a01_1 EU475
X89237.1 gg_id:135882 Streptococcus pyogenes str. serotype M49 CS101 X89237
EU467843.1 gg_id:297229 North American black bear feces clone BB1_c04_1 EU467
EU473927.1 gg_id:295065 giant panda feces clone GP_2aaa01a01 EU473
EU467830.1 gg_id:299221 North American black bear feces clone BB1_h10 EU467
DQ232533.1 gg_id:179010 Streptococcus mitis str. CIP 104996 DQ232
GQ091667.1 gg_id:417572 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ057669.1 gg_id:375780 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AF003933.1 gg_id:15555 Streptococcus parasanguinis str. ATCC 15912 AF003
FJ673895.1 gg_id:518670 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
AY691525.1 gg_id:102441 Streptococcus mutans str. ChDC YM2 AY691
FJ558016.1 gg_id:517987 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EU467856.1 gg_id:298009 North American black bear feces clone BB1_e05 EU467
EU458177.1 gg_id:296799 North American black bear feces clone BB2_a07 EU458

36.1	632.0	721.3	697.7	450.4	588.8	601.9	747.7	157.8	143.5	397.4
9486.0	2609.2	2937.3	2344.9	2375.9	2600.5	2577.2	3455.4	3767.2	4961.5	2766.2
4586.7	11148.9	10699.2	12079.7	10884.2	10494.1	11909.2	12703.8	13592.7	13732.1	12109.2
108.8	979.0	1255.6	1401.8	1173.0	1201.3	1294.3	1435.7	782.4	553.2	1193.7
38834.5	8533.5	8587.1	8701.5	8233.4	8233.2	9111.6	10736.9	12501.9	11918.0	11642.3
82.7	546.2	743.7	740.6	433.9	545.9	441.4	585.9	525.9	167.0	418.9
99.8	3306.7	4284.7	3853.0	2967.2	3621.7	3783.1	5134.3	1501.9	2433.7	2558.1
129.4	1717.0	2294.7	2604.1	2144.9	1876.0	2653.6	2352.8	921.0	633.4	1297.8
65.1	209.2	254.3	172.9	239.0	412.6	304.1	466.1	109.4	65.2	169.0
197.6	4059.6	3430.2	2868.6	2830.6	2870.6	3344.3	3088.3	1946.9	3867.2	2262.4
17548.0	8303.5	7298.9	8360.3	7101.4	7990.6	8307.3	7070.5	8201.1	9462.7	8967.9
43.1	736.6	1117.3	1046.9	2078.7	920.0	1883.7	1042.3	419.8	998.6	472.1
21245.3	6961.2	6739.2	8412.7	7845.0	7034.8	7563.9	6168.1	11925.9	8222.2	7902.9
1407.1	2289.3	2649.6	2722.3	2544.3	2781.3	2458.0	3004.6	2036.6	1475.4	2802.6
164.1	3903.9	2841.1	1826.3	1421.4	2525.7	1397.8	2684.3	1919.4	4485.7	1778.4
51657.0	12688.5	11243.4	12568.5	11949.1	11465.0	13430.9	14273.3	17912.8	15884.0	17372.2
494.9	1120.4	1297.1	1681.1	1398.7	1008.2	1976.8	1057.4	1000.5	755.0	1500.3
8445.9	3050.8	2729.5	3206.3	3119.5	3205.7	3084.8	2864.0	4400.5	2764.2	4312.9
4317.3	3210.0	2848.7	3150.2	2169.4	3049.1	3254.2	3229.9	2928.9	2320.3	3256.5
149.1	2150.2	2907.0	2870.4	2526.9	2426.0	2674.5	2987.0	1213.6	2105.4	2034.2
53.4	882.1	896.5	770.9	732.1	896.2	882.3	976.3	957.7	786.0	1165.2
3962.4	3173.5	3137.1	3153.1	2739.4	2826.8	2584.6	3669.8	2812.3	1688.9	4190.7
268.4	1068.0	2323.1	1654.5	2241.4	1428.8	1603.7	2365.4	1060.6	1606.9	1134.3
25757.7	8243.1	7121.2	8056.9	7435.1	8075.1	8011.4	9071.4	6900.2	8084.1	8875.4
149.1	2260.6	3009.8	2996.2	2560.4	2499.3	2704.9	2964.1	1218.6	2267.6	2064.0
37547.6	7004.2	6834.6	7606.0	7148.7	6844.4	7319.3	8759.1	9679.0	9926.1	10536.6
46.3	716.8	1073.6	624.0	905.0	870.8	863.3	1243.1	350.0	439.7	599.2
14526.9	6288.6	6377.4	7119.1	6819.3	6814.5	7555.2	5777.9	6975.7	5681.6	8445.8
57.6	683.4	805.4	866.3	886.7	744.7	1213.7	685.9	605.4	213.4	497.0
2564.0	2891.4	4100.2	3368.9	4321.6	3287.0	4545.3	4025.6	3072.8	7511.3	2947.9
80.1	1493.1	1941.6	1544.9	1883.1	1617.1	1685.1	1921.5	827.0	873.0	1200.9
545.2	1194.6	1716.3	1375.7	1028.3	1234.8	1132.3	1900.2	1356.3	2208.0	1101.7
118.3	1379.4	1646.8	1030.0	1200.8	1288.1	1004.5	1862.0	927.2	1886.3	1433.1
489.8	1660.1	1402.0	1635.5	1609.0	1854.8	1355.8	2228.7	1401.1	1590.8	1850.6
212.5	1543.4	1876.7	2030.9	1744.1	1795.0	1894.2	2200.8	1576.4	1119.9	1814.2
58.3	229.5	941.8	407.2	540.1	766.0	539.9	791.3	188.1	837.9	275.4
14769.0	4722.1	5148.2	6135.8	4508.0	4579.2	5547.9	4127.6	6332.2	5620.2	5350.1
10362.5	9036.6	9219.9	9296.0	9246.6	9764.4	9865.8	9069.9	13012.6	10689.1	12064.3
4256.7	1862.4	1705.0	1551.9	1754.4	1919.0	1771.4	2048.2	1967.9	2762.5	1288.6
47489.3	9066.8	8540.7	9236.9	8980.7	8117.6	10090.1	10777.8	10835.2	11907.5	11784.3
15143.6	6118.5	6535.7	7030.3	6457.1	6479.4	6537.7	8623.2	7814.6	7420.8	8561.7

623.9	684.2	1017.2
2346.5	4615.4	2654.0
10260.0	13452.3	11333.3
1188.9	1716.8	1306.0
8290.1	12219.5	10109.3
1160.8	744.3	715.7
3649.0	5081.3	4151.3
2073.7	2281.7	2969.1
501.0	439.7	319.1
3653.8	3365.3	5706.4
6618.1	8309.1	8066.4
853.5	1405.1	1673.2
6234.3	6651.2	7790.5
2810.9	2751.6	3008.5
2113.5	2464.0	3478.3
11049.6	17540.9	12042.8
1540.3	1199.3	1417.6
2908.4	3594.2	3202.5
2579.1	3656.8	2901.4
2778.5	2897.5	3830.4
1163.3	1094.5	904.6
2118.9	3952.7	2363.0
2199.6	2319.7	2266.8
6973.3	9919.5	7544.4
2822.2	2744.6	3837.6
6669.6	11102.0	6867.3
1656.5	1100.9	1556.0
5890.3	6427.7	6830.2
666.4	903.1	1352.5
4322.2	4720.9	5509.2
1894.5	2124.1	3408.8
1331.6	2371.5	2132.4
2042.3	1505.5	3154.0
2094.9	1756.8	2211.4
1913.2	2383.9	2015.5
835.3	688.1	1417.6
4364.1	4835.2	4235.7
8418.6	10334.2	10605.0
2053.9	2816.2	2326.3
7979.6	12503.1	8935.8
6411.6	10270.4	7121.1

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EU467865.1 gg_id:293109 North American black bear feces clone BB1_g07_1 EU467
EU458255.1 gg_id:292733 North American black bear feces clone BB2_g11_2 EU458
AY500370.1 gg_id:104134 Streptococcus bovis Sb5 AY500
AB264619.1 gg_id:164145 Streptococcus sp. bSSV21 AB264
EU461840.1 gg_id:294868 white-faced saki feces clone Saki_aaj62a02 EU461
AY485603.1 gg_id:101921 Streptococcus infantis str. ATCC 700779 AY485
EU461967.1 gg_id:297953 white-faced saki feces clone Saki_aaj64e08 EU461
EU467779.1 gg_id:298188 North American black bear feces clone BB1_g08 EU467
AY324611.1 gg_id:90414 Streptococcus bovis str. MPR2 AY324
GQ073778.1 gg_id:391010 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ073
GQ100994.1 gg_id:451940 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48 GQ100
GQ011458.1 gg_id:498208 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792b1: GQ011
AJ634751.1 gg_id:111084 Streptococcus marimammalium str. M54/01/1 AJ634
EU458212.1 gg_id:291889 North American black bear feces clone BB2_h01 EU458
GQ018924.1 gg_id:490744 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d GQ018
GQ023586.1 gg_id:486084 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320c12 GQ023
FJ677566.1 gg_id:530906 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ677
AM183037.1 gg_id:253441 and its spatial composts compost clone SMB52 AM183
GQ072181.1 gg_id:391890 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193b1(GQ072
EU467826.1 gg_id:301858 North American black bear feces clone BB1_h03_1 EU467
NR_027214.1 gg_id:535803 Streptococcus pseudopneumoniae str. 108; ATCC BAA-960 NR_02
EU458243.1 gg_id:296265 North American black bear feces clone BB2_f02_2 EU458
GQ155808.1 gg_id:588046 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ074087.1 gg_id:401778 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
FJ673496.1 gg_id:527788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ673
GQ155734.1 gg_id:592904 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU467871.1 gg_id:303225 North American black bear feces clone BB1_h05_2 EU467
FJ678041.1 gg_id:518979 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ678
GU045388.1 gg_id:541157 Streptococcus mitis str. KCOM 1350 GU045
AY324610.1 gg_id:89376 Streptococcus bovis str. MPR1 AY324
EU458295.1 gg_id:295303 North American black bear feces clone BB2_e07_2 EU458
EU772625.1 gg_id:349233 North American Black Bear feces clone BB1_a08_1 EU772
GQ051010.1 gg_id:373888 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ051
GQ018662.1 gg_id:491006 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu141e05 GQ018
FJ673875.1 gg_id:528552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ673
GQ027253.1 gg_id:388019 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
EU772603.1 gg_id:349682 North American Black Bear feces clone BB2_c10 EU772
EU772567.1 gg_id:350483 North American Black Bear feces clone BB2_d03 EU772
EU473235.1 gg_id:296749 giant panda feces clone GP_1aaa01e12 EU473
GQ019637.1 gg_id:490031 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu205c03 GQ019
EU458213.1 gg_id:302190 North American black bear feces clone BB2_h05_1 EU458

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6234.1	4472.7	4523.6	4719.4	4165.5	4077.7	5079.1	4701.6	4762.0	1344.6	5650.0
1751.1	8331.5	10031.6	6457.6	9079.2	8124.5	6869.3	10807.1	6342.7	10556.8	7597.3
5344.3	4261.1	4096.8	3440.0	3959.8	3959.9	3582.5	4507.0	4954.9	4151.8	4767.5
216.6	5440.8	4562.0	4013.9	2782.5	3969.1	3065.5	3521.2	4955.4	5095.2	3279.0
48.5	1140.3	2499.4	614.3	1666.6	2017.4	826.5	2209.0	453.5	3623.6	771.6
1204.7	1619.6	2330.8	1976.8	1684.9	2169.4	1963.3	3109.1	1652.6	3517.8	1678.9
5368.6	2739.0	2700.5	2819.3	2235.7	2546.0	2768.9	1710.8	1363.0	2935.6	3197.3
6025.7	4400.9	4988.2	3511.6	4920.1	4649.2	4116.3	5911.4	3141.6	5696.7	3606.7
672.7	814.3	1019.8	861.5	1078.1	1061.0	923.6	1363.9	866.9	250.9	1655.0
66.9	582.5	775.0	662.7	856.3	776.2	676.0	1235.4	300.7	164.4	489.4
47.2	277.6	308.1	211.1	207.3	269.6	204.6	284.0	172.6	345.2	171.7
195.4	1486.1	2770.2	2105.0	1847.1	1824.1	2248.9	2229.6	1247.2	1012.8	1422.3
287.7	1564.6	2082.8	1514.5	1222.5	1498.7	1377.7	2454.9	999.1	2971.8	1309.7
277.1	2326.5	2714.3	2950.0	2663.6	2549.6	3138.7	3061.3	1965.0	1554.4	2502.4
536.6	1722.5	1467.9	1485.0	1494.5	1669.6	1112.5	2063.5	1527.3	2801.3	1847.2
108.7	1276.5	1341.8	1293.0	1863.5	1372.0	1755.4	2074.6	815.4	1882.3	772.7
39.2	922.7	2405.0	905.4	442.4	1281.6	587.8	1292.3	378.5	132.0	843.8
210.8	1545.3	1943.3	2319.0	1672.9	1874.2	2693.8	1604.1	1156.5	1966.0	1711.7
113.6	1717.1	2294.1	2604.9	2145.4	2009.6	2654.1	2042.7	986.1	591.8	1298.2
302.4	4071.1	4838.6	3692.8	3430.9	3825.0	3086.1	4997.6	2956.8	7244.7	4823.1
16455.6	6388.8	7015.7	7025.7	7961.0	6199.1	8247.3	8573.6	9538.1	6132.9	5900.0
1869.1	3892.8	4777.5	4411.8	5889.6	4486.4	5912.6	4815.8	3794.1	5859.6	3704.9
8935.3	4164.8	4560.8	4724.7	4512.3	4237.2	5156.0	4809.5	8081.6	5269.4	6088.3
34187.4	6964.7	6835.5	7614.0	6457.3	7829.0	7494.4	8614.4	12778.9	10052.4	11102.6
108.8	1328.2	1125.7	1348.9	1160.3	1525.2	2130.0	1970.7	681.8	404.6	828.0
282.8	2798.3	2999.5	3268.2	3784.8	2777.2	4111.0	4644.5	1558.9	1590.4	1987.4
184.0	992.8	1133.6	1274.3	1061.8	844.8	1184.1	1788.8	874.4	554.1	734.0
280.4	3897.1	4695.9	3193.9	3348.9	3665.2	2765.1	4985.9	2841.6	6556.8	5072.8
1513.6	5855.6	7232.8	5095.5	7039.4	6678.7	5614.7	7302.8	5827.6	9488.7	5299.4
8904.1	4719.2	4545.4	3923.9	4549.4	4380.8	4139.7	5491.4	4388.2	5173.5	4246.8
12495.4	6853.8	7402.5	7364.7	6606.7	6735.1	6719.6	6414.8	8248.6	5467.0	9827.1
147.5	643.2	884.0	1242.8	1150.0	1021.8	704.2	1264.3	597.8	1117.3	823.8
75.1	726.2	1050.4	1174.6	975.2	1068.0	917.8	1194.2	369.8	189.6	598.0
40.4	807.1	834.5	842.9	631.4	680.8	810.1	713.1	361.8	234.0	492.4
10623.1	4533.9	3948.0	4061.8	3876.7	3790.7	4917.1	3671.7	4172.9	4329.5	4037.9
152.5	2840.8	2810.6	2600.8	2279.7	2493.3	2834.3	2953.3	1577.1	1967.1	1690.3
108.1	1831.2	2404.9	2550.0	2179.7	2096.0	2682.8	2087.9	985.9	646.7	1330.9
12727.4	5281.9	5460.4	5837.4	5569.0	5027.4	5884.6	4941.1	5506.1	3546.5	6652.9
548.3	1622.4	1046.4	1282.2	1152.5	1417.3	923.0	1717.8	1914.7	2792.8	1807.2
116.1	1309.8	1932.3	2075.0	1492.4	1613.8	1878.1	2165.7	621.1	414.4	1091.7

1806.9	1799.1	2413.9
3071.4	4699.1	4062.2
8671.7	10086.6	12986.4
3881.4	5595.4	4484.1
3683.6	3260.7	4985.4
2648.7	2146.1	3417.6
2064.8	2987.2	3242.7
2235.7	4306.6	2454.1
5092.9	6097.0	6231.7
1519.7	823.5	764.4
1255.7	800.3	476.3
455.2	663.9	753.7
2209.1	2069.6	2926.8
1438.3	2663.5	2629.8
2825.8	3086.4	3155.0
1729.3	1389.2	2299.2
1384.9	2665.7	2548.6
1507.5	931.0	1348.7
1485.4	2250.4	1998.6
2073.3	1958.5	2969.5
4363.1	4494.1	7396.2
6686.6	10882.9	8896.6
6294.3	4285.7	6087.6
4161.4	4717.4	4960.1
5975.2	11589.5	6665.6
1830.4	1771.5	2766.3
3299.3	6403.6	4727.9
1132.4	2178.1	1717.7
4721.5	4348.8	7066.3
7046.0	7312.2	9039.6
3984.6	6440.0	5215.7
6243.6	8154.5	6229.8
1188.1	1451.7	1197.0
1227.6	938.0	926.4
711.1	699.7	809.2
3644.7	4480.1	3949.1
2394.8	2874.7	3923.4
2089.1	2009.4	2977.0
4913.9	5787.2	6744.0
1611.5	1320.1	1844.3
1629.4	1966.2	1995.6

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GU470899.1 gg_id:558469 Streptococcus cristatus str. F0329 GU470
GQ032924.1 gg_id:416414 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
EU458218.1 gg_id:299212 North American black bear feces clone BB2_a03_2 EU458
GQ027310.1 gg_id:434159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ006598.1 gg_id:503066 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85d08c GQ006
GQ010315.1 gg_id:499348 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw736b1 GQ010
GQ104022.1 gg_id:456295 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562a0 GQ104
EU458216.1 gg_id:293266 North American black bear feces clone BB2_h10 EU458
EU458302.1 gg_id:299685 North American black bear feces clone BB2_f07_1 EU458
EU475848.1 gg_id:293772 white-faced saki feces clone Saki_aaj62b04 EU475
EU460835.1 gg_id:288716 short-beaked echidna feces clone ECH_aai39a03 EU460
DQ294302.1 gg_id:160607 Streptococcus equi Hyena M149 DQ294
AF084832.1 gg_id:15483 Streptococcus sp. str. KN1 AF084
GQ091850.1 gg_id:416768 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
AM157428.1 gg_id:142502 Streptococcus mitis mother C4 AM157
FJ678391.1 gg_id:513075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
GQ155781.1 gg_id:550710 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU473460.1 gg_id:297804 Somali wild ass feces clone WA_aaa03b08 EU473
GQ030486.1 gg_id:407093 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878h11 GQ030
EU473991.1 gg_id:299801 giant panda feces clone GP_2aaa04a03 EU473
GQ074320.1 gg_id:386466 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161 GQ074
FJ367135.1 gg_id:361983 feces adult twins and mothers; TS28 clone TS28_a03h09 FJ3671
GQ073355.1 gg_id:434919 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208a09c GQ073
EU467888.1 gg_id:294779 North American black bear feces clone BB1_c11_2 EU467
EU458114.1 gg_id:302527 North American black bear feces clone BB2_a02 EU458
FJ679191.1 gg_id:519599 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
GQ021841.1 gg_id:487827 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
AB469560.1 gg_id:359502 Streptococcus sp. str. NUM 1529 AB469
EU474107.1 gg_id:290522 giant panda feces clone GP_2aaa03a05 EU474
GQ102163.1 gg_id:457320 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561g1 GQ102
EU467809.1 gg_id:288523 North American black bear feces clone BB1_e06_1 EU467
EU474171.1 gg_id:289475 western lowland gorilla feces clone GORSD_2aaa04h03 EU474
EU473228.1 gg_id:294997 giant panda feces clone GP_1aaa04d08 EU473
AY442818.1 gg_id:104405 Streptococcus sp. YE54 AY442
GU045389.1 gg_id:578175 Streptococcus mitis str. KCOM 1379 GU045
GU045392.1 gg_id:512763 Streptococcus mitis str. KCOM 1286 GU045
EU458209.1 gg_id:302903 North American black bear feces clone BB2_g06_1 EU458
EU458287.1 gg_id:296176 North American black bear feces clone BB2_d09_2 EU458
FJ675732.1 gg_id:509993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
GQ073629.1 gg_id:413473 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073

13048.6	6290.6	5483.5	6976.2	4853.6	5938.5	5350.0	6017.0	7527.0	6332.9	8139.7
40.3	231.1	242.8	133.6	283.0	292.2	229.3	348.4	134.1	506.2	87.2
16749.5	3794.2	3777.1	4523.1	3441.0	3511.3	4523.1	4411.8	5705.3	5026.8	6849.6
2554.2	2442.2	3085.5	3032.6	2887.1	2859.4	2779.7	4428.8	2584.8	4038.3	2891.5
312.5	1394.8	2003.1	1804.1	2025.2	1448.8	2255.8	2524.2	6053.9	1907.6	2202.4
54.9	132.7	287.3	179.6	389.9	250.1	236.2	673.0	132.3	179.0	93.6
666.3	3683.8	4713.6	5501.1	4398.6	3836.4	4570.1	4886.7	8048.9	3565.3	4315.5
452.4	2092.4	3277.7	2450.7	2745.8	2583.2	2587.6	3928.2	4247.2	4043.9	2399.6
2784.3	2120.6	2432.8	2310.6	2201.4	2287.8	2289.7	2743.7	2040.8	3301.3	1791.6
8139.9	4464.0	4089.0	4429.8	3839.3	3720.0	4410.6	3470.4	4817.4	3816.0	4586.5
436.4	2778.4	3027.7	3159.2	3139.5	2640.2	3833.5	3681.7	1651.1	1674.2	1971.0
10344.2	3300.7	3453.1	3655.4	3011.3	3678.7	3541.6	5953.5	4133.8	6328.5	5166.8
1452.2	1858.8	2360.9	2112.5	2363.5	2252.6	2562.1	2327.6	1899.7	3094.3	1635.5
3273.4	1226.1	245.7	1438.8	1289.6	944.9	1156.2	1268.2	955.1	877.7	848.7
2208.9	3667.1	4328.3	5615.4	6027.0	4414.6	5254.9	4410.0	2672.0	3244.6	4014.8
2406.3	2353.0	3056.7	1941.7	2783.2	2481.1	2197.3	4100.1	2888.6	3204.6	3691.2
101.3	957.1	1477.3	1577.2	1066.1	1093.6	1443.5	1406.6	359.6	252.8	685.9
128.6	382.1	470.4	250.7	325.0	330.4	423.1	357.6	183.7	478.7	192.9
7654.8	5316.9	4657.4	4403.8	4378.1	4560.1	4486.9	4163.1	5444.2	4455.7	5278.6
1748.5	1538.9	1403.7	1813.5	2210.4	2050.1	1760.5	1835.2	1210.0	839.1	1516.1
61.0	1085.9	1601.8	1115.0	1223.4	1354.8	967.6	1759.3	527.1	681.3	994.8
95.5	3075.8	3697.5	4090.7	2699.5	3089.2	3075.8	3270.5	2040.9	3183.3	3604.1
100.6	412.4	622.5	708.4	1113.2	738.7	664.1	567.1	306.9	299.1	357.0
94.5	1592.1	1622.9	1632.2	1462.9	1738.8	1761.0	1751.4	1249.9	739.4	1472.3
16283.7	8272.9	7819.0	8332.9	8223.5	7810.7	8612.2	8647.8	8694.8	9698.9	11597.8
30834.4	7501.5	6317.4	7048.2	6498.6	6682.5	7720.4	8810.2	10454.1	11558.9	7317.3
12233.0	8175.7	7332.6	7769.5	6895.1	8010.1	8071.0	6851.7	10934.4	6878.8	10640.6
95.4	565.1	1024.2	959.3	801.5	708.4	793.8	899.2	476.1	708.5	475.6
906.3	2139.1	2493.0	2904.7	2386.0	2777.4	3045.8	2623.1	2221.8	2203.4	3197.8
61.0	1333.9	1804.9	1501.6	1591.6	1534.0	1606.6	1755.0	754.4	671.8	1161.1
125.5	469.0	890.2	815.9	677.3	643.5	696.8	779.5	514.1	373.8	477.5
192.3	3649.3	2858.6	2393.5	1815.1	2872.6	2112.7	2925.5	3366.0	3281.8	2253.4
1744.5	3692.0	3361.1	3521.4	2652.8	3223.9	2790.6	3374.4	2852.6	3063.3	2852.9
124.4	1717.3	2374.5	1961.1	1754.1	2045.7	1493.5	2632.5	1081.8	1218.0	1723.1
125.6	629.3	876.4	858.8	377.7	949.0	332.9	821.4	147.2	1180.6	299.1
113.5	1102.2	1313.4	584.7	827.4	1005.0	619.3	1661.9	842.3	1976.3	1383.6
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411.8	2442.7	2279.0	2500.9	2379.5	2056.0	2877.1	2772.4	1579.3	1074.5	1760.1
20715.2	6660.9	6665.8	8204.1	7862.8	6913.6	7519.7	6599.7	7259.4	6887.3	7228.7
9648.7	6821.6	6354.9	5986.9	6624.6	6778.1	5050.7	9264.5	6890.4	9731.6	7484.4
214.3	5875.5	5303.2	3872.1	3016.7	4469.5	2898.8	4078.1	5472.8	5932.6	3487.3

5662.0	6855.0	6636.2
581.3	357.5	641.0
3190.2	5407.6	4047.3
2787.9	5689.6	4812.8
1770.3	2836.1	2297.2
534.0	239.7	314.3
4981.0	5203.0	5346.2
2879.3	3922.2	5255.7
2447.6	2944.5	2648.3
3564.4	4509.1	4113.0
2781.1	4454.6	4023.0
3551.9	6304.7	4579.7
2448.3	2741.4	2980.7
1299.7	1511.4	1421.3
4745.2	4597.1	6424.2
2774.2	3405.7	3984.8
1241.2	1259.4	1665.0
541.5	881.5	1121.0
4144.3	4542.8	4780.8
1873.1	1975.6	2752.2
1478.0	1853.3	2466.8
3054.8	3380.2	5552.5
638.5	716.6	921.1
1634.9	1922.6	1990.9
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6454.4	11282.4	7646.2
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1264.0	739.8	794.1
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1516.9	1235.2	1139.6
1832.7	1211.1	2580.1
1234.4	985.0	1427.2
2108.2	2980.6	3004.0
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7005.0	9270.5	8868.1
3846.7	3821.5	5461.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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GQ111651.1 gg_id:461851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
GQ156134.1 gg_id:581022 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU774840.1 gg_id:319809 Short-beaked Echidna feces clone ECH_aai38g08 EU774
EU772577.1 gg_id:308943 North American Black Bear feces clone BB2_g09 EU772
EU461937.1 gg_id:289435 white-faced saki feces clone Saki_aaj64a10 EU461
EU458220.1 gg_id:291672 North American black bear feces clone BB2_a06_2 EU458
EU156779.1 gg_id:334078 Streptococcus pneumoniae str. CCRI-14734 EU156
EU461935.1 gg_id:301946 white-faced saki feces clone Saki_aaj64a07 EU461
EU289129.1 gg_id:245916 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
FJ893225.1 gg_id:571456 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM3; ear p FJ8932
FJ676607.1 gg_id:526041 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
GQ079517.1 gg_id:393671 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
EU467801.1 gg_id:297452 North American black bear feces clone BB1_d02_1 EU467
EU458173.1 gg_id:301800 North American black bear feces clone BB2_h12 EU458
AY281085.1 gg_id:90432 Streptococcus sanguinis str. ATCC 29667 AY281
EU467151.1 gg_id:298042 white-faced saki feces clone Saki_a06 EU467
EU461955.1 gg_id:301020 white-faced saki feces clone Saki_aaj64c10 EU461
FJ678419.1 gg_id:516100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
GQ032429.1 gg_id:384627 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542h04 GQ032
FJ677709.1 gg_id:519382 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
AJ420199.1 gg_id:27408 Streptococcus macacae str. NCTC11558 AJ4201
EU775424.1 gg_id:336695 Western lowland gorilla feces clone GORSD_2aaa04d03 EU775
EU467754.1 gg_id:299092 North American black bear feces clone BB1_d05 EU467
GQ067186.1 gg_id:394313 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ067
AB501126.1 gg_id:515853 Streptococcus ursoris str. NUM 1615 AB501
GQ019375.1 gg_id:490293 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189c GQ019
AY273147.1 gg_id:84371 Streptococcus pyogenes AY273
EU467739.1 gg_id:287916 North American black bear feces clone BB1_a08 EU467
GQ023335.1 gg_id:486334 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu317a0 GQ023
GQ076817.1 gg_id:395887 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153 GQ076
GQ073289.1 gg_id:421921 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207c10c1 GQ073
GQ018889.1 gg_id:490779 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192a GQ018
AM420093.1 gg_id:240905 Noma subgingival plaque clone 302F04(oral) AM420
GQ154900.1 gg_id:557859 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ154
AY324612.1 gg_id:88822 Streptococcus bovis str. MPR4 AY3246
GQ040793.1 gg_id:374127 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958g01 GQ040
DQ232536.1 gg_id:199646 Streptococcus oralis str. CIP 104985 DQ232
EU461824.1 gg_id:297884 white-faced saki feces clone Saki_aaj61f09 EU461
GQ155776.1 gg_id:585008 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EF364097.1 gg_id:226980 Streptococcus henryi str. 126 EF364
FJ682683.1 gg_id:514572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826

67.1	340.3	518.9	403.9	296.1	571.3	298.1	704.3	171.4	410.5	234.3
472.2	2502.9	2464.4	2371.5	2348.5	2743.4	2346.6	2598.4	2007.3	2052.4	2447.4
6050.1	3504.9	3894.7	3889.9	4432.7	3603.1	4730.8	5282.5	4136.1	2364.3	3057.0
19543.5	4687.4	4518.1	4524.1	4005.9	4188.9	4441.1	5323.1	5941.6	7074.8	5949.9
12775.7	3839.0	4247.7	4208.8	3836.1	4044.9	4053.7	5165.3	3055.1	4598.4	4654.0
6538.6	6271.9	6099.0	6524.9	6231.6	5890.2	7140.5	7117.5	8297.0	5520.4	6842.2
2602.4	5561.8	6088.0	6652.6	6921.0	6181.1	7202.0	6221.0	5811.2	5106.8	4702.4
12220.5	5710.8	4884.1	5360.4	4872.6	4783.6	6415.9	5298.4	7260.7	6113.6	7908.4
38.6	418.6	762.0	267.1	531.2	547.6	485.9	658.7	127.7	131.3	269.9
1234.8	5132.7	4633.6	4570.6	4827.7	4337.6	5496.5	3625.1	4212.3	3836.4	2409.5
2367.2	4425.9	6311.2	6006.5	6050.2	5243.5	7505.4	5927.3	3968.8	7937.4	4649.0
86.9	683.4	986.3	969.9	682.9	864.7	679.6	1142.8	624.8	429.5	919.4
1375.9	1709.9	1765.1	1659.1	1241.5	1522.5	1435.9	844.3	529.7	1567.3	1771.1
13505.3	7225.3	6092.9	6910.3	6760.4	5917.0	8151.4	6201.0	9068.2	7016.0	10570.3
86.0	369.9	431.9	480.9	758.8	573.3	412.2	443.9	107.4	69.9	183.6
15583.1	8660.3	7854.8	8660.7	7121.4	8130.2	8319.0	9592.8	12124.0	13018.7	11072.6
114.8	1328.1	1367.5	1609.0	1136.5	1514.6	1832.7	1971.9	533.8	361.5	720.7
13205.1	6067.9	5826.3	6088.8	6098.2	5685.8	6904.4	7070.0	6053.6	6884.7	6472.2
3681.7	4355.1	4102.4	4004.1	6111.4	4264.2	5579.3	3616.8	1969.7	2415.2	2751.7
9908.2	6980.4	5834.6	5615.5	4804.3	5997.5	5209.8	6948.7	8878.9	10459.3	6563.7
57.3	619.6	935.7	704.5	1263.0	678.0	836.5	772.6	286.3	239.9	287.3
10459.0	5766.6	5427.4	5556.9	4106.3	4896.8	4592.8	4328.2	5064.9	5856.8	5387.0
32.6	270.8	310.4	238.2	109.3	194.3	132.1	210.5	36.3	46.8	98.1
3655.3	2211.4	2565.7	2208.4	2617.8	2365.8	2136.5	2988.0	1800.8	2688.5	1851.9
193.9	716.8	1214.7	1141.0	1102.9	876.5	1204.3	1361.7	456.9	715.5	792.8
66.0	625.2	793.4	919.8	840.5	614.1	995.2	679.1	247.4	191.6	345.2
80.7	1032.8	1194.5	1160.5	1262.8	1137.7	1508.2	1133.5	1002.7	684.2	838.8
194.5	586.6	614.8	604.6	368.5	440.6	518.0	484.0	122.7	100.4	269.4
95.4	918.4	1652.2	1661.2	1386.3	1194.7	1537.1	1401.6	489.7	679.6	715.8
501.4	872.5	1178.9	1138.9	854.3	1020.8	1146.0	1442.9	782.8	1649.6	1126.5
185.2	2089.8	2403.8	2613.8	2171.4	2321.4	2756.9	2375.7	1892.3	1178.2	2163.1
70.3	653.3	773.6	894.2	777.8	645.9	930.8	670.3	246.6	198.1	329.8
60.6	461.1	653.7	586.7	548.0	591.3	806.7	491.8	123.2	290.9	254.7
48.7	941.4	969.7	1023.7	775.1	788.3	1073.2	761.9	814.1	270.3	575.2
349.0	1762.6	3428.2	1233.4	2589.0	2788.9	1640.7	3860.8	1025.7	3164.3	1750.2
66.9	202.5	316.7	319.6	370.4	242.5	265.4	274.2	172.4	41.8	118.2
61.5	981.2	2249.5	453.8	1531.8	1710.2	627.9	1615.3	443.5	3063.7	686.5
17164.0	7054.6	7077.6	6487.6	7090.9	6870.1	7058.6	8088.0	6503.6	7702.0	7772.0
811.1	2697.1	2681.8	2714.3	2689.2	2910.9	2770.4	2511.9	2681.6	4276.8	2651.2
601.0	1206.4	1442.2	1470.1	1883.3	1331.4	1689.0	1455.1	1496.6	1100.8	783.0
7807.0	4037.3	3562.4	4237.5	2019.2	3852.2	3473.7	4618.2	4414.3	4387.9	5173.1

691.6	791.9	509.4
2393.9	2908.0	3051.3
3857.9	6729.6	6035.0
4117.7	6858.9	4934.2
3695.2	5435.1	4527.9
5487.0	8442.3	7007.8
7655.1	5536.5	7179.6
4800.7	6369.4	6571.7
1025.1	741.4	485.4
4916.0	3130.2	4557.0
5940.7	6286.4	7866.5
1027.9	1106.5	610.2
1541.9	1551.9	1653.3
5920.8	7262.0	6165.1
504.3	439.5	466.4
7306.7	11524.2	8151.6
1622.0	1698.6	1971.8
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5036.7	9573.1	7160.2
897.3	1286.7	2106.5
4257.6	4806.0	5025.2
243.4	154.9	134.5
2744.0	2938.2	3268.4
1143.7	1809.8	1851.9
1087.6	684.4	1351.6
1255.1	1568.4	2113.6
486.2	550.3	583.7
1310.9	1169.1	1869.4
1134.8	1134.5	1739.8
2380.3	2857.3	2840.7
1127.7	646.8	1287.1
683.0	693.2	849.9
788.3	817.7	957.3
3660.0	3890.7	5082.2
837.1	245.4	421.5
1653.6	1714.2	2952.4
6318.5	8588.9	7857.9
2972.2	3183.2	3669.2
1198.5	1660.1	2284.2
3324.8	5727.6	3207.4

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AJ617796.1 gg_id:100642 Streptococcus pneumoniae str. HER 1055 = Hu-o8 AJ6177
EU471428.1 gg_id:301608 spectacled bear feces clone SB_2aaa02d04 EU4714
NC_006086.1 gg_id:128611 Streptococcus pyogenes str. MGAS10394 NC_00
GQ115642.1 gg_id:373633 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688h07 GQ115
GQ073111.1 gg_id:429959 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c02c1 GQ073
EU458224.1 gg_id:293705 North American black bear feces clone BB2_a12_1 EU458
EU467860.1 gg_id:296641 North American black bear feces clone BB1_f04_1 EU467
EU467199.1 gg_id:299664 white-faced saki feces clone Saki_g09 EU467
EU779062.1 gg_id:311993 Prevost's squirrel feces clone SQ_aah79h08 EU779
AF396920.1 gg_id:39742 Streptococcus bovis str. B315 AF396
GQ115601.1 gg_id:400616 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688b1 GQ115
FJ558308.1 gg_id:516966 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5583
EU458307.1 gg_id:289803 North American black bear feces clone BB2_h08_3 EU458
AB002522.1 gg_id:15573 Streptococcus pneumoniae str. MAFF 911410 AB002
GQ156243.1 gg_id:561883 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
GQ076853.1 gg_id:464954 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ021817.1 gg_id:487851 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU467781.1 gg_id:299667 North American black bear feces clone BB1_g10 EU467
GQ023571.1 gg_id:486098 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320b09 GQ023
EU458196.1 gg_id:292217 North American black bear feces clone BB2_e11 EU458
DQ318881.1 gg_id:150451 -DGGE and sequencing piglet stomachs stomach clone SY6 DQ318
GQ095863.1 gg_id:435368 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
EU467163.1 gg_id:301619 white-faced saki feces clone Saki_f02 EU467
GQ102584.1 gg_id:390165 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ102
EU471514.1 gg_id:294127 spectacled bear feces clone SB_2aaa01d12 EU471
EU467165.1 gg_id:300974 white-faced saki feces clone Saki_f06 EU467
EU474059.1 gg_id:302396 giant panda feces clone GP_2aaa01c07 EU474
GQ074646.1 gg_id:464930 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164f GQ074
AM157442.1 gg_id:142694 Streptococcus pneumoniae mother V4 AM157
GQ021904.1 gg_id:487765 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
EU458151.1 gg_id:291631 North American black bear feces clone BB2_e12 EU458
GQ032381.1 gg_id:399032 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542a07 GQ032
GQ156168.1 gg_id:590723 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
EU460825.1 gg_id:295866 short-beaked echidna feces clone ECH_aai38g10 EU460
AJ307888.1 gg_id:63461 Streptococcus gallinaceus str. CCUG 42692 AJ3078
AF009507.1 gg_id:15367 Streptococcus suis str. EA1172.91 AF009
EU772622.1 gg_id:314465 North American Black Bear feces clone BB2_c10_1 EU772
EU467845.1 gg_id:287347 North American black bear feces clone BB1_c06_2 EU467
EU775569.1 gg_id:324468 Giant Panda feces clone GP_2aaa01h07 EU775
GU045397.1 gg_id:586088 Streptococcus pneumoniae str. CCARM 4033 GU045
EU473918.1 gg_id:293540 giant panda feces clone GP_2aaa04e06 EU473

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9660.1	3360.0	4177.7	4762.8	3287.2	3605.3	3997.5	3660.3	3836.9	2788.8	4619.6
49.8	167.0	293.6	126.5	204.5	236.1	135.6	264.6	72.7	95.0	107.6
174.7	423.1	780.5	499.7	508.9	489.6	436.6	924.9	263.8	712.8	352.1
206.3	673.0	782.4	1021.9	769.4	1032.4	958.1	71.1	528.4	1026.2	735.2
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600.0	4040.0	4427.9	4610.8	5228.2	4042.7	4305.4	4636.8	4060.0	4568.1	4326.4
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26129.2	8686.3	8700.6	9062.8	8335.4	7927.9	9582.2	7612.0	11165.9	10007.0	12110.7
1411.5	2269.6	2890.3	2912.3	2851.3	2621.3	2598.7	3190.7	2070.2	1416.4	2713.9
77.5	792.4	1032.4	949.0	606.6	1062.1	578.9	1673.5	428.8	627.7	743.6
3287.1	3471.7	4115.3	3802.9	3706.5	3747.3	4116.7	4169.3	2502.1	4072.6	3295.6
68.4	530.8	620.5	695.7	628.7	526.9	866.4	582.9	223.2	188.7	295.4
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103.0	3174.4	3125.2	2647.6	2874.6	2571.3	2404.7	3511.0	2333.4	2641.5	3248.9
87.1	443.7	747.4	581.6	690.0	688.8	510.8	1062.3	414.1	574.8	622.0
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47.3	731.1	1038.6	719.1	1247.7	1071.0	919.9	895.6	277.7	160.9	390.5
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999.9	816.0	1166.7
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EU467869.1 gg_id:296719 North American black bear feces clone BB1_h03_2 EU467
GQ073370.1 gg_id:442986 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208c05c1 GQ073
EU461864.1 gg_id:300903 white-faced saki feces clone Saki_aaj62e06 EU461
GQ040889.1 gg_id:457333 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw959g10c GQ040
AY281079.1 gg_id:89930 Streptococcus oralis str. ATCC 9811 AY281
GQ010954.1 gg_id:498711 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
DQ232534.1 gg_id:190717 Streptococcus mitis str. CIP 104997 DQ232
EU475873.1 gg_id:302995 white-faced saki feces clone Saki_aaj62f09 EU475
GQ073509.1 gg_id:431778 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ113226.1 gg_id:461942 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ155674.1 gg_id:512915 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
GQ073236.1 gg_id:420071 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f09c1 GQ073
EU467847.1 gg_id:288218 North American black bear feces clone BB1_c09_2 EU467
FJ677289.1 gg_id:509161 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
EU660342.1 gg_id:299977 Streptococcus pyogenes str. Sp32 EU660
EU461896.1 gg_id:290594 white-faced saki feces clone Saki_aaj63c10 EU461
EU458288.1 gg_id:295039 North American black bear feces clone BB2_d11 EU458
EU156784.1 gg_id:331800 Streptococcus pseudopneumoniae str. CCRI-8984 EU156
FJ679815.1 gg_id:531369 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
GQ082003.1 gg_id:446773 Topographical and Temporal Human Skin Microbiome skin back clone nbw1198h10c GQ082
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DQ232537.1 gg_id:196966 Streptococcus oralis str. CIP 105158 DQ232
FJ674207.1 gg_id:527106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
AM941160.1 gg_id:259084 Streptococcus sp. 2923-03 AM941
GQ102114.1 gg_id:374555 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw561c0 GQ102
GU045383.1 gg_id:550425 Streptococcus oralis str. KCOM 1416 GU045
NR_029052.1 gg_id:538185 Streptococcus oligofermentans str. 2-4; LMG 21535 NR_02
FJ674309.1 gg_id:509855 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
GQ054576.1 gg_id:456757 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092a07c GQ054
EU458193.1 gg_id:294978 North American black bear feces clone BB2_e02_1 EU458
GQ019723.1 gg_id:489945 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu206c09 GQ019
FJ672838.1 gg_id:515480 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
GQ011178.1 gg_id:498488 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ011
GQ155339.1 gg_id:546051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458183.1 gg_id:296971 North American black bear feces clone BB2_b12_1 EU458
EU461976.1 gg_id:300448 white-faced saki feces clone Saki_aaj64f08 EU461
EU471475.1 gg_id:302979 spectacled bear feces clone SB_2aaa03d08 EU471
EU458160.1 gg_id:287785 North American black bear feces clone BB2_g02 EU458
GQ073238.1 gg_id:377455 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206f11c1 GQ073
AB008314.1 gg_id:15560 Streptococcus peroris str. GTC848 AB008

15409.3	5406.3	5554.2	5395.7	5506.4	5339.2	5863.7	6910.4	9100.9	7959.6	5894.0
95.2	1193.8	1759.1	1815.5	1224.0	1450.3	1457.1	1853.9	526.8	403.3	941.3
128.7	1395.0	1518.9	1666.4	2180.5	1551.9	2480.7	1553.5	1558.0	848.1	1166.4
927.9	3985.0	4211.9	3923.1	4384.0	3987.8	5133.9	4772.3	2856.7	2857.0	2519.6
257.1	1342.6	1979.2	2785.5	1845.1	1598.4	1538.6	2106.0	1425.6	1094.3	1580.2
580.0	1600.5	1169.8	1243.8	1156.9	1565.7	1027.0	1926.6	1652.9	1951.0	2377.2
108.9	580.5	782.9	719.0	528.7	586.7	444.0	932.9	383.8	553.8	612.3
287.7	3847.4	4644.9	3547.2	3191.1	3598.8	2751.3	4943.7	2835.3	7019.0	5432.4
28838.8	7082.3	7133.6	7765.1	7371.0	6519.3	7208.3	8698.6	9409.6	8507.9	8782.0
193.4	1543.9	2835.2	2054.1	2793.5	1889.3	2461.9	2577.0	3230.7	1947.5	1739.8
5622.5	4702.7	5103.9	5805.3	4909.5	4797.8	5146.3	5111.3	5304.1	4185.3	5402.4
9298.3	7112.6	7227.9	7341.3	7712.8	8606.8	7692.7	7364.1	7591.6	8130.0	8225.3
261.7	2349.2	2741.2	2979.6	2679.3	2581.5	3221.9	2917.7	2120.9	1556.3	2364.3
1273.3	3045.5	3838.6	4396.0	3967.7	3182.2	4608.9	3491.0	2108.1	3480.1	2442.1
35191.7	7829.4	7395.5	7768.7	6973.4	6965.9	7580.4	8888.1	11450.7	10971.6	10801.5
50.3	362.8	413.7	311.1	401.6	509.6	256.2	522.5	126.1	105.6	198.9
1133.0	1126.0	1242.9	1280.2	1077.8	1284.2	1146.6	1671.7	1283.2	1455.5	1610.5
3490.6	5350.8	4329.6	3970.3	3488.6	4322.0	5133.6	4340.8	5200.6	4868.5	5057.8
1345.5	2532.0	3122.8	3199.5	3039.5	2781.8	3302.7	3357.9	2112.0	1858.7	3034.5
454.6	1506.9	1464.3	1608.3	1280.1	1412.0	1442.6	1417.5	940.6	569.5	1263.8
27307.2	7459.7	7459.4	7384.4	6938.4	6595.6	7606.2	7860.6	10512.7	11039.7	10659.6
404.7	4495.2	3935.6	3610.8	4421.8	3959.7	2914.8	3619.0	3372.7	4645.1	3040.5
36.2	2522.8	4626.7	1822.3	4127.6	3626.3	2191.8	3654.9	1549.2	4081.7	2001.1
8103.9	4423.0	5529.6	4677.5	3864.7	4259.3	4392.4	5143.8	5991.7	8382.3	5276.7
32.7	709.4	1251.8	702.6	728.7	738.4	436.3	936.0	308.3	931.5	549.0
59.0	753.6	1350.3	1056.6	109.4	372.7	677.9	924.1	85.9	50.7	1004.3
7441.1	2861.9	2911.9	2922.1	3050.6	3127.9	2846.6	3039.0	2504.8	4344.8	2870.3
1217.0	1999.7	1778.2	1932.3	2069.2	2653.1	1542.1	2575.3	1745.5	3748.5	1852.3
39.4	774.7	787.1	770.8	595.7	682.6	792.7	565.6	345.5	255.7	445.5
32.8	95.9	155.7	81.2	76.4	108.6	112.3	112.2	72.0	126.0	68.1
127.0	2245.9	2061.4	1131.2	817.0	1699.5	769.8	1964.7	1666.9	2627.7	1039.1
77.1	889.4	1187.6	1321.6	1275.5	1274.2	1106.2	1675.0	465.1	368.2	840.2
458.8	3417.4	3004.0	3329.8	3234.6	2878.0	3723.2	4221.9	2213.1	1904.2	2229.6
106.3	725.1	1325.7	1202.7	945.7	950.8	975.9	1185.2	559.3	950.3	727.1
11362.7	7687.4	6406.3	5296.9	4843.6	6100.7	5216.0	5698.0	8310.4	7223.9	7088.3
6955.9	3966.6	4650.7	4119.8	4188.3	4468.2	4537.3	6303.8	3687.6	6244.8	4266.2
201.4	1260.3	1464.6	1564.7	1058.1	1123.7	1085.0	1842.3	565.0	1074.7	615.7
1213.2	798.8	1090.9	751.7	650.0	843.4	676.7	844.1	362.4	1151.1	366.6
265.0	4079.8	4477.8	4310.6	4427.5	3703.8	5595.5	5417.0	2667.6	3452.9	3415.1
2134.8	2741.9	2563.3	2580.8	2948.3	2778.0	2707.7	2429.1	2419.0	1029.9	3044.5
114.0	633.0	600.2	573.8	796.4	733.6	571.4	1305.3	247.9	193.2	507.0

5068.5	8153.3	5895.4
1407.9	1643.9	1471.5
2375.6	1718.9	2155.6
3774.8	5311.3	5315.0
2957.1	1952.0	2858.9
1963.7	1254.4	1744.0
809.9	678.8	518.1
4201.8	4298.6	6861.7
6439.7	9346.1	6620.4
1943.6	2251.3	3135.1
2765.6	5157.8	5847.0
6734.5	7745.3	8535.8
2821.0	2973.6	3205.2
3785.4	3366.2	5387.6
6206.2	11361.4	6795.4
654.1	902.4	528.3
1249.0	2587.0	1051.8
4112.4	5245.6	6005.6
3257.6	3075.3	4005.2
1137.0	1441.4	1340.4
6873.0	10755.6	6308.0
4258.1	3582.0	4286.2
3476.0	3986.3	5909.3
4990.3	5746.3	6666.0
957.3	1378.3	2629.8
832.8	248.1	1566.3
3297.5	3587.3	3557.0
2696.1	2518.3	3250.2
650.9	585.3	726.9
267.0	271.2	288.5
1361.3	1897.3	2200.1
1538.4	1228.0	1724.4
2721.2	4069.3	3787.9
1171.5	1198.4	1945.3
5173.1	5659.6	8021.6
4531.3	6030.4	6194.7
1611.3	1553.8	1086.8
968.0	1279.1	858.2
3884.3	5670.2	5869.1
1733.1	2995.0	3630.9
1077.5	941.0	557.5

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GQ057678.1 gg_id:389049 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ019801.1 gg_id:489867 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu207c04 GQ019
AB023576.1 gg_id:15371 Streptococcus uberis str. HN1 AB0235
FJ679289.1 gg_id:526351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
AF135453.1 gg_id:25587 Streptococcus bovis str. 1276 AF1354
AY525790.1 gg_id:111444 Streptococcus pneumoniae str. HK_P55 AY5257
FJ672957.1 gg_id:511682 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
AJ853836.1 gg_id:108738 Streptococcus cristatus str. 0109 93830B AJ8538
FJ677170.1 gg_id:525204 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
EU458274.1 gg_id:296367 North American black bear feces clone BB2_c02_3 EU4582
EU458257.1 gg_id:301824 North American black bear feces clone BB2_h02_1 EU4582
EU458189.1 gg_id:303194 North American black bear feces clone BB2_d05_1 EU4581
EF364098.1 gg_id:219115 Streptococcus caballi str. 151 EF3640
EU467867.1 gg_id:288591 North American black bear feces clone BB1_g10_1 EU4678
GQ060702.1 gg_id:420623 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d06 GQ060
FJ557366.1 gg_id:524022 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5573
FJ679360.1 gg_id:524008 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
AY525791.1 gg_id:111760 Streptococcus pneumoniae str. HK_P116 AY5257
FJ558253.1 gg_id:526846 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5582
DQ303188.1 gg_id:168087 Streptococcus mitis str. ATCC 49456 DQ303
GQ111270.1 gg_id:383764 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
FJ676643.1 gg_id:520991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
EU458226.1 gg_id:290193 North American black bear feces clone BB2_b04_2 EU4582
GQ043319.1 gg_id:439032 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ043
EU775741.1 gg_id:309550 Horse feces clone horsem_aai93e09 EU7757
FJ558487.1 gg_id:530902 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
DQ303190.1 gg_id:170102 Streptococcus oralis str. CCUG 24891 DQ303
GQ019394.1 gg_id:490274 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189e GQ019
GQ032401.1 gg_id:406741 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542d06 GQ032
EU458208.1 gg_id:303353 North American black bear feces clone BB2_g03_1 EU4582
EU774894.1 gg_id:345575 Short-beaked Echidna feces clone ECH_aai40c10 EU7748
EU460725.1 gg_id:302963 short-beaked echidna feces clone ECH_aai37b01 EU4607
EU475871.1 gg_id:298472 white-faced saki feces clone Saki_e02_1 EU4758
EU467833.1 gg_id:301583 North American black bear feces clone BB1_a07_2 EU4678
GQ086202.1 gg_id:388839 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
NC_011375.1 gg_id:314877 Streptococcus pyogenes NZ131 str. NZ131; ATCC BAA-1633 NC_011
EU467904.1 gg_id:298775 North American black bear feces clone BB1_f06_2 EU4679
GQ048268.1 gg_id:451556 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
EU458272.1 gg_id:293401 North American black bear feces clone BB2_b08_3 EU4582
GQ156135.1 gg_id:591692 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
Y17358.1 gg_id:26896 Streptococcus ovis str. S369-98-1 Y17358

239.4	1752.5	2117.5	2349.8	2041.4	2027.1	2313.3	2393.1	1614.2	1214.5	2020.7
4152.5	2200.0	2687.9	3441.0	2998.8	2532.1	2548.0	3025.0	2077.8	1515.4	2503.3
1945.3	2950.7	3910.4	3925.7	5254.6	2938.1	5734.7	3462.8	7282.9	3180.7	2658.1
447.6	893.1	1026.6	1045.8	873.1	793.8	1061.1	1329.2	378.2	411.6	550.5
44.2	846.4	1168.1	652.4	846.8	1121.3	401.5	1238.3	272.3	418.2	412.8
67.4	260.5	437.3	384.9	354.0	301.6	435.7	370.4	266.4	101.3	215.5
19853.8	8454.5	8102.0	8665.2	8330.1	8340.6	9288.2	8663.0	8414.2	7542.4	11757.4
1175.8	3043.5	3086.8	3648.1	3516.1	3076.9	4008.4	3148.0	4116.2	3463.2	2853.6
14679.6	5172.7	4981.5	4837.0	4545.5	3750.7	5145.1	6145.6	7035.4	8954.7	5833.9
113.1	1846.9	2424.1	2744.8	2182.2	1960.2	2689.3	2091.5	927.7	647.3	1332.5
109.4	1599.1	2106.0	1859.8	1550.6	1827.5	1436.5	2435.2	864.4	1969.4	1723.6
8505.7	4439.1	3864.8	4353.0	3563.2	4009.1	4285.4	4780.2	5262.5	6509.1	5517.3
1195.6	3550.6	3814.9	3818.0	3029.0	4102.6	3503.8	3904.7	3716.9	2661.3	4249.1
37685.8	12026.3	11120.0	12046.0	10547.5	10931.3	11329.1	13111.7	16223.0	18136.2	17514.9
3917.9	3321.7	3404.8	3684.8	3826.3	3588.2	3790.0	3724.7	3629.7	3244.4	4343.4
616.4	3295.4	3986.9	4093.8	3098.7	3537.5	3381.0	3855.4	2847.6	3918.2	3558.2
25.0	860.3	791.5	765.7	395.2	579.6	253.8	1071.3	233.1	856.7	503.8
162.8	1851.5	2792.5	3081.5	2023.3	2211.3	2459.1	2681.7	1205.1	1889.4	1981.8
707.1	3608.2	3103.5	2962.0	2596.5	3274.4	3281.2	2904.4	2951.7	2506.6	2961.4
52.2	362.6	485.8	361.6	708.9	565.8	382.8	759.1	183.2	237.1	230.1
135.0	4469.2	3427.7	2690.4	2217.5	2098.2	2309.4	2916.6	3316.5	4349.4	2962.4
101.1	1048.9	1588.7	1595.4	1282.3	1220.3	1645.2	1545.4	392.5	283.5	736.6
97.7	353.8	353.4	339.5	127.3	310.0	188.1	303.0	133.3	84.7	142.7
385.6	1955.8	2238.7	2347.5	2223.1	2270.0	2442.3	2490.3	1683.4	1714.8	1911.3
874.7	2775.4	2755.9	3025.6	2660.4	2629.4	3073.5	3423.9	1842.0	1445.0	2605.5
153.5	850.3	1238.6	1333.2	1469.0	1431.3	1022.1	1513.6	705.8	1520.6	810.0
95.2	1730.1	2684.4	1257.0	2139.2	2677.0	1365.7	2664.4	907.6	2905.9	1262.9
217.0	1588.0	2143.6	2536.0	2857.6	1949.6	1959.3	2280.3	1370.8	1107.3	1910.2
45.8	735.5	1032.7	729.8	1247.2	1074.2	919.4	893.9	270.1	160.7	388.9
137.8	2110.3	2566.9	2509.6	2286.3	2158.5	2263.8	2671.0	1165.3	2361.1	1946.8
3588.3	6610.6	6263.7	5798.9	5405.1	5592.9	6978.0	5458.0	6763.0	3095.4	8512.9
1694.2	1780.8	1684.3	1831.5	1579.1	1501.6	2067.9	1495.3	1005.5	765.7	1165.7
11524.2	7003.2	6605.5	6641.1	6209.3	6348.4	7256.1	6056.7	8191.1	5769.4	7106.7
2982.1	6395.0	6868.9	7220.7	7333.3	6173.7	8226.2	6043.2	8478.4	5001.0	7291.0
2670.6	2975.0	3109.2	3237.5	3605.9	2968.8	3697.3	3152.1	3784.5	2989.3	2835.1
82.4	1010.5	1153.4	1213.4	1213.2	1165.8	1484.2	1036.0	988.8	499.9	815.2
33.7	707.5	807.3	925.5	609.0	556.5	837.8	829.3	190.8	178.6	405.3
1404.7	2211.7	2706.5	2640.2	2859.9	2672.0	2485.1	3035.9	2168.1	1469.6	2602.9
18604.6	8004.8	7727.7	7937.1	7335.9	7172.1	7625.7	9762.4	10898.5	6678.7	11224.9
689.4	7513.7	8874.8	8266.2	8035.8	7757.8	8746.3	7683.9	11732.1	6630.7	9318.2
117.1	128.4	286.2	185.8	197.8	171.5	313.6	228.5	73.3	59.1	152.4

2134.0	2667.1	2432.8
2973.3	3138.8	2990.7
3585.2	3691.0	3920.5
1011.1	1836.9	1396.6
1116.6	1169.3	1018.1
730.5	370.2	447.1
7927.2	9364.5	8872.0
3468.0	3492.6	3752.1
4386.4	8885.6	5004.4
2151.1	2012.8	3006.2
2130.7	2348.8	2846.0
3867.4	7206.3	3816.6
3529.9	4869.2	4923.8
10626.3	15596.0	11169.4
4041.8	3696.3	4401.3
3438.2	3956.4	3852.9
871.6	1907.2	1010.0
2763.4	2690.6	4024.1
2537.2	3013.3	2714.8
997.5	547.5	863.9
2833.1	2633.1	3975.6
1317.4	1551.6	1901.8
266.3	611.6	226.5
2517.6	2488.4	2497.9
2291.1	3324.0	3114.7
1692.5	1647.4	1995.0
2729.5	2443.7	3771.6
2399.5	2207.8	2619.6
1567.3	877.1	1148.0
2626.8	2765.7	3794.5
4775.0	5213.2	5477.3
1218.4	1657.3	1879.8
5993.8	7946.8	8924.5
6103.9	6953.1	7727.7
3053.0	3520.7	3700.5
1190.4	1384.1	1882.5
699.0	1058.8	1054.7
3120.1	2793.2	3197.6
5341.8	9918.2	6642.6
6885.7	8488.4	10342.5
207.5	219.2	288.6

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DQ805392.1 gg_id:184376 human fecal clone RL203_aai62a07 DQ805
FJ892760.1 gg_id:550176 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota HM1; ear p FJ8927
FJ678216.1 gg_id:521294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU458184.1 gg_id:296435 North American black bear feces clone BB2_c02_1 EU458
EU467771.1 gg_id:291232 North American black bear feces clone BB1_f05 EU467
EU772601.1 gg_id:322567 North American Black Bear feces clone BB2_b10 EU772
GQ078830.1 gg_id:423740 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ078
GQ056825.1 gg_id:374781 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ056
EU461930.1 gg_id:299204 white-faced saki feces clone Saki_aaj63h11 EU461
GQ070655.1 gg_id:395351 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
EU460784.1 gg_id:287545 short-beaked echidna feces clone ECH_aai37h10 EU460
EU660340.1 gg_id:290080 Streptococcus pyogenes str. Sp12 EU660
GQ077236.1 gg_id:386987 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115 GQ077
EU467798.1 gg_id:294395 North American black bear feces clone BB1_c05 EU467
EU467191.1 gg_id:289185 white-faced saki feces clone Saki_e06 EU467
FJ675610.1 gg_id:518399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6756
EU473899.1 gg_id:289643 giant panda feces clone GP_2aaa02a01 EU473
EU475801.1 gg_id:287600 white-faced saki feces clone Saki_aaj64e04 EU475
EU473322.1 gg_id:295789 giant panda feces clone GP_1aaa03a08 EU473
EU458277.1 gg_id:295281 North American black bear feces clone BB2_c07_1 EU458
EU467864.1 gg_id:293154 North American black bear feces clone BB1_g05_1 EU467
FJ683535.1 gg_id:518286 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
FJ676479.1 gg_id:521992 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
GQ072667.1 gg_id:411298 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
EU779050.1 gg_id:333155 Prevost's squirrel feces clone SQ_aah82f11 EU779
AY525789.1 gg_id:112327 Streptococcus pneumoniae str. HK_P47 AY525
GQ076939.1 gg_id:377312 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
AF543291.1 gg_id:58287 Streptococcus mitis str. ChDC OS41 AF543
GQ115448.1 gg_id:425877 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685g05 GQ115
EU467812.1 gg_id:303216 North American black bear feces clone BB1_e11_1 EU467
GQ155692.1 gg_id:589905 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
AM396401.1 gg_id:165104 Streptococcus sp. str. DT2005WUE_IHM AM396
EU458148.1 gg_id:298590 North American black bear feces clone BB2_e06 EU458
EU467827.1 gg_id:302755 North American black bear feces clone BB1_h05_1 EU467
EU779446.1 gg_id:309732 Grevy's Zebra feces clone GZ_aaa04g04 EU779
AF323911.1 gg_id:31706 Streptococcus gallolyticus AF323
EU475852.1 gg_id:296662 white-faced saki feces clone Saki_e08 EU475
GQ101164.1 gg_id:430460 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ073361.1 gg_id:378214 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208b05c GQ073
DQ303194.1 gg_id:167724 Streptococcus urinalis str. CCUG 41590 DQ303
EU475777.1 gg_id:292482 white-faced saki feces clone Saki_aaj61g03 EU475

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132.5	1146.6	1124.0	1047.7	695.4	1156.9	845.1	1187.5	869.3	907.0	857.6
10693.0	6603.5	5450.1	4951.9	5886.8	4953.3	6135.3	4921.6	7887.4	6467.9	6367.5
3336.6	3758.9	4429.7	3868.3	2690.4	4083.8	3639.9	5468.7	2756.7	5253.4	3878.6
23462.4	8655.5	8065.2	7831.1	7217.8	8185.5	8176.1	7586.0	13453.8	11278.3	10517.5
53.1	1534.6	1840.9	1721.0	1178.0	1597.1	1602.0	1709.6	558.3	734.5	1043.0
132.3	1775.0	1582.3	1678.3	1620.8	1631.8	1965.8	1704.8	1566.5	1092.2	1663.7
283.1	1105.0	746.3	861.7	1089.4	1141.8	717.2	1502.1	821.4	983.4	1260.9
408.6	1283.4	1784.9	1774.7	1311.9	1435.5	1319.2	1808.3	1430.0	1913.6	1183.0
747.8	1225.8	1376.6	1349.1	1882.7	1474.3	1521.1	1204.9	1003.9	485.6	210.2
56.7	537.0	667.5	632.0	429.6	720.2	418.4	1200.0	216.1	378.7	449.8
8987.2	3989.1	3633.2	4342.7	3791.8	4640.6	3874.8	4055.8	4687.8	4471.2	5566.4
41.8	328.9	394.1	306.0	367.6	433.6	291.6	646.5	103.9	51.2	200.3
3206.7	2943.9	3235.9	3564.9	3378.7	2949.3	4543.0	3938.5	2619.7	1284.5	3181.6
229.9	6478.6	5392.1	4139.4	3104.5	5041.2	3216.9	4177.1	5774.2	7076.8	4103.6
19435.9	9251.4	9030.4	10016.6	9484.2	8876.5	10367.3	10694.2	12079.1	9312.7	13330.2
639.0	905.4	1181.0	933.1	1006.6	1101.5	877.5	1173.4	393.9	586.7	829.7
101.7	1996.5	2350.4	2385.5	2323.7	2380.0	2699.3	3153.3	1256.6	873.0	1531.0
89.7	1841.9	2468.2	2053.1	2306.0	2206.3	2023.1	2620.8	1077.4	1028.4	1534.2
11489.6	5114.0	4245.5	4370.3	3825.4	5131.4	4630.4	5597.8	7500.5	5429.4	4913.8
17535.4	4373.7	4170.4	4497.7	4448.7	4037.2	4785.2	5420.6	3664.4	3882.4	4826.5
11904.0	3671.8	3836.3	4481.3	4665.3	4050.5	4983.0	4227.7	3678.3	3472.0	3674.0
5910.9	2862.5	2748.1	3046.9	2442.0	2404.7	2725.5	2527.4	2999.1	2780.2	3208.7
107.6	981.1	1150.2	1295.6	1186.2	1417.0	883.8	1606.0	659.7	616.5	994.6
65.9	1867.3	1943.4	1903.0	2261.7	1674.6	2882.2	1666.0	1616.4	1103.2	1394.6
135.4	1672.3	2521.1	2721.5	2264.6	2138.7	2434.1	2614.2	1146.9	1161.1	1602.7
38.3	469.9	827.1	843.8	352.6	676.5	682.2	944.6	336.8	571.3	652.2
983.4	3198.4	3534.1	2895.4	3567.7	3402.5	2771.6	4229.0	2733.2	3454.2	3334.2
105.9	954.8	1116.1	1273.1	1186.4	1383.9	849.7	1677.5	650.7	650.7	1043.1
24260.9	5562.0	5366.6	5652.0	4721.6	5061.1	5596.4	6370.2	6451.9	7038.3	6961.8
3806.8	4510.9	4859.6	4792.1	4888.6	4806.9	4849.3	4432.4	5711.6	5747.8	4631.1
1495.9	5659.4	6178.3	6391.3	6952.7	5882.4	6454.1	5554.0	6741.3	7220.7	9226.9
3820.9	2396.8	2263.2	2441.4	1907.6	2607.1	2334.8	2567.3	2494.2	2351.5	2273.8
6753.4	4512.4	4224.4	5390.7	4203.7	3897.9	5027.8	4151.8	5210.6	4259.7	6454.9
165.3	3220.0	4217.1	4926.2	2802.3	3461.8	4242.9	3846.3	2102.2	1791.0	2976.8
145.1	4514.4	4217.6	3901.0	4006.7	3614.8	3226.0	4184.6	4375.5	4172.3	4171.5
115.7	2099.3	2228.8	2564.1	2317.6	1880.3	3071.4	3027.4	1045.8	891.8	1422.6
46.8	1267.4	1685.1	2002.6	1131.0	1669.1	1397.3	1945.9	580.4	752.2	1007.9
151.9	2415.1	2706.0	2959.1	2799.0	2357.8	3566.2	3035.4	2126.2	811.3	2161.2
55.8	515.6	1111.9	901.9	336.6	1168.5	268.7	1799.8	194.2	1414.1	801.5
444.3	3125.1	3792.2	3561.4	3493.8	2908.2	4221.8	4190.1	2033.6	1891.2	2581.5

3155.9	3456.3	3646.0
1096.4	1171.6	1054.1
4983.2	7510.5	6358.6
3567.2	6197.8	4047.0
6845.5	10659.8	8183.9
1518.3	1578.0	1464.4
1538.2	1453.0	2135.0
1467.0	922.0	1297.8
1594.4	1745.9	2197.5
1872.9	1327.1	1817.0
781.9	1406.4	1646.6
3786.1	5425.1	3977.8
706.3	636.4	402.5
3054.9	3732.8	3822.8
4214.3	3971.1	5972.1
8098.2	12228.6	9758.4
1054.0	1849.6	2308.9
2332.7	2961.2	3070.1
2307.1	2692.9	3868.6
3666.3	7728.0	5384.0
3455.6	6133.8	4691.8
3824.0	4721.8	4869.3
2136.6	3858.5	2341.8
1571.9	1419.7	1675.4
1484.5	2428.2	2322.7
2506.4	2314.1	3526.2
862.8	1028.5	733.7
4093.4	3631.9	4815.0
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4789.7	8789.8	5578.3
5302.5	5184.2	6224.4
4757.2	5904.4	6969.7
1943.8	3059.6	2122.6
4099.2	4328.6	4236.6
3749.3	3893.7	4656.1
4094.1	5075.0	10225.2
2048.1	2884.9	3272.1
1729.4	2797.8	3314.8
3257.0	2535.9	3968.5
1033.2	2357.7	2331.8
3319.0	5089.4	4424.5

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AY005040.1 gg_id:28885 Streptococcus sp. oral strain str. 7A AY005
GQ076078.1 gg_id:431953 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ076
EU341148.1 gg_id:243231 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
AJ295853.1 gg_id:46365 Streptococcus mitis str. 209 AJ2958
GQ076899.1 gg_id:409566 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
EU461789.1 gg_id:298208 white-faced saki feces clone Saki_aaj61b04 EU461
GQ043419.1 gg_id:429551 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
EU467196.1 gg_id:299158 white-faced saki feces clone Saki_g01 EU467
EU458284.1 gg_id:297654 North American black bear feces clone BB2_d04_1 EU458
EU467823.1 gg_id:301071 North American black bear feces clone BB1_g07 EU467
FJ678805.1 gg_id:525261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
GQ081009.1 gg_id:395948 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ081
EU458246.1 gg_id:299675 North American black bear feces clone BB2_f06_2 EU458
EU467808.1 gg_id:298882 North American black bear feces clone BB1_e02_1 EU467
EU458139.1 gg_id:298862 North American black bear feces clone BB2_d04 EU458
GQ155683.1 gg_id:551174 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ155
EU458171.1 gg_id:292100 North American black bear feces clone BB2_h08 EU458
FJ680107.1 gg_id:518559 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6801
EU660336.1 gg_id:298908 Streptococcus pyogenes str. Sp8 EU660
EU778418.1 gg_id:323518 Red Panda feces clone RP_2aaa01c07 EU778
EU458198.1 gg_id:288649 North American black bear feces clone BB2_f01_1 EU458
EU458202.1 gg_id:287473 North American black bear feces clone BB2_f06_1 EU458
EU461971.1 gg_id:299458 white-faced saki feces clone Saki_aaj64f02 EU461
Y07601.1 gg_id:15430 Streptococcus sp. str. SHV515 Y07601
EU458117.1 gg_id:294121 North American black bear feces clone BB2_a06 EU458
EU772619.1 gg_id:345747 North American Black Bear feces clone BB2_c03_2 EU772
EU467750.1 gg_id:291931 North American black bear feces clone BB1_c10 EU467
AJ606047.1 gg_id:114860 Streptococcus castoreus str. M60581/03/2 AJ6060
FJ677268.1 gg_id:531460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
GQ069167.1 gg_id:442582 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
FJ673358.1 gg_id:520177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU458124.1 gg_id:302904 North American black bear feces clone BB2_b05 EU458
GQ073148.1 gg_id:406688 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f06c1 GQ073
EU458223.1 gg_id:295170 North American black bear feces clone BB2_a10_1 EU458
EU467903.1 gg_id:301865 North American black bear feces clone BB1_f05_2 EU467
GQ101429.1 gg_id:407688 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495a GQ101
GQ073121.1 gg_id:397965 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c12c1 GQ073
DQ798234.1 gg_id:194026 human fecal clone RL181_aah39c03 DQ798
EU156776.1 gg_id:325399 Streptococcus pneumoniae str. CCRI-14589 EU156
EU467878.1 gg_id:297820 North American black bear feces clone BB1_b07_3 EU467
EU458244.1 gg_id:289054 North American black bear feces clone BB2_f03_2 EU458

41.2	1086.4	2690.6	730.7	2067.1	1852.4	807.8	2453.2	433.6	2700.7	786.7
110.2	982.6	1144.5	1299.5	1208.7	1430.8	897.5	1715.2	659.0	659.5	1067.6
4217.3	2295.0	3494.8	2313.0	3081.6	2966.8	2591.6	3291.7	2253.6	4363.4	2224.9
299.8	3898.5	4679.4	3407.2	3347.5	3663.9	2762.7	4978.3	2835.7	7020.1	5073.8
6390.2	1606.1	1493.3	1515.9	1305.7	1483.9	2103.9	1330.7	2713.6	1124.6	3049.8
34929.3	9546.7	7687.8	9757.1	9687.9	7563.7	10045.6	11107.2	10815.1	10359.2	12544.4
104.5	924.3	1117.5	1197.2	1051.6	1350.5	874.3	1676.2	653.9	652.8	1060.3
84.6	1759.3	2036.5	1992.7	1991.4	1528.4	2294.7	2125.1	814.8	716.3	1162.6
20281.3	5947.5	5729.0	5548.5	5919.0	5756.4	6121.2	8242.2	5978.9	10884.5	7559.6
9473.9	5182.5	5660.1	5548.0	5193.6	6628.4	5173.0	7408.5	4874.4	10530.9	9873.2
385.8	3643.4	3642.8	4003.8	2941.3	3236.4	3848.8	5843.6	2945.6	4176.6	3855.1
18041.1	6756.5	6198.2	6801.6	6122.3	6184.6	6834.1	5939.1	10744.7	8734.3	8345.9
407.1	2924.9	3848.8	4126.1	4124.5	3321.7	3804.3	4970.5	2207.6	2014.7	2614.5
229.6	2241.6	2854.9	2724.2	2321.6	2710.9	2225.9	3873.8	1475.3	3105.3	1892.1
89.4	1890.3	2609.8	1812.9	2168.7	1844.8	1861.1	1906.0	1205.3	1478.0	1455.8
15068.0	6598.1	6393.0	6521.6	5918.5	6019.5	6705.2	5850.6	6689.0	6999.4	7756.1
2946.8	2343.7	2418.0	2707.3	2074.9	2115.9	2566.5	3028.2	2071.5	1321.6	3038.6
96.7	1007.5	1545.1	1497.7	1100.3	1161.4	1487.0	1469.8	379.1	277.7	735.7
292.8	732.4	1004.9	1112.4	860.4	820.8	1263.4	936.3	566.4	556.4	571.3
129.4	1834.8	2404.4	2739.6	2180.7	1954.1	2686.1	2328.0	926.3	694.9	1329.5
5273.0	2525.6	4251.0	3207.8	3004.4	3399.7	2817.7	5732.9	2950.1	7435.1	3143.1
33799.3	7312.8	6693.6	8528.3	6285.8	6705.9	7344.6	8468.0	10987.8	8494.0	10843.8
7506.1	4594.8	4737.5	5536.7	5378.3	4881.2	4805.7	4550.0	4316.2	3748.5	4845.5
77.7	834.1	1127.6	1319.3	1548.8	1281.7	1527.1	1867.4	538.9	502.9	1027.4
10572.1	4375.1	3820.3	4479.7	4036.9	3861.1	4724.2	4304.3	4552.8	2688.4	3994.8
148.4	2653.8	2859.6	3021.1	3221.4	2501.2	3736.2	3543.6	1399.3	1386.9	1766.4
113.1	1841.8	2413.6	2549.5	2180.6	1958.5	2688.1	2402.3	928.0	695.8	1330.2
615.1	1371.5	1965.7	1792.3	2916.1	1940.1	2405.4	2124.0	1446.0	942.9	1056.7
127.5	1602.6	2391.2	2280.1	1532.3	2126.6	1793.8	2021.4	1450.0	1474.2	1896.5
331.4	1642.2	1829.7	1996.3	1907.5	1496.3	2268.4	1481.3	1581.7	836.7	1607.7
8218.0	5163.3	5688.9	6150.4	6755.5	5419.7	6901.8	5781.8	4541.3	3908.1	5718.5
37.7	406.4	483.5	379.4	154.0	301.8	176.2	266.0	39.9	76.0	136.5
142.9	1285.6	1510.8	1601.9	1187.3	1509.2	1404.5	1663.3	1339.1	871.6	1581.9
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383.6	2085.5	2298.5	2351.1	2532.4	1967.2	2703.3	2817.9	1162.5	1206.8	1409.6
97.6	686.6	1139.4	1034.6	570.5	1508.4	450.4	1790.0	334.1	932.2	643.4
283.5	1821.9	2086.0	2368.7	2199.8	1923.2	2729.9	2415.5	1786.7	1370.7	2154.3
18195.7	8303.6	7239.7	8737.1	8984.2	7801.6	8527.3	7797.6	11817.9	9422.0	10889.0
1421.4	3384.1	4156.8	4392.5	4223.2	3478.2	4593.3	4050.8	3606.9	4081.0	2812.1
1487.2	1679.4	1720.7	1652.8	1238.0	1614.7	1428.4	886.6	527.0	1676.1	1766.1
120.5	1726.7	2298.5	2420.2	2145.5	1876.2	2657.0	2351.2	987.6	634.1	1296.8

2331.7	2077.6	3508.4
1544.6	1440.9	1680.1
2987.4	3827.7	5017.6
4549.1	4344.2	7067.4
1313.1	2028.9	1264.5
8887.0	13794.0	9745.2
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1663.1	2399.1	2792.6
5843.9	9296.5	6913.4
5119.8	4753.7	5444.6
3201.0	4202.1	3607.5
5737.9	7439.1	6353.4
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4369.4	7758.4	5508.8
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1483.4	1444.5	2054.4
3704.7	4337.0	4301.4
2733.7	3848.6	4094.5
2143.1	2341.4	3003.5
1291.0	1716.2	2452.4
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347.9	315.5	158.7
1479.9	1995.4	1477.6
1565.8	1626.9	2449.6
2178.2	4172.1	2847.5
1577.4	3109.7	2586.2
2232.0	2415.6	2677.9
7759.2	9366.1	9050.9
4809.0	3505.5	4815.7
1475.6	1543.3	1620.0
2100.0	2490.0	2968.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Bacilli
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EU461828.1 gg_id:301841 white-faced saki feces clone Saki_aaj61g06 EU461
EU777768.1 gg_id:349666 Polar bear feces clone PB1_aai27f03 EU777
EU461813.1 gg_id:294792 white-faced saki feces clone Saki_aaj61e02 EU461
FJ678126.1 gg_id:520301 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
GQ267979.1 gg_id:563263 Surveys lactic acid yak Tibet China method fermented milk product clone IMAU 462 GQ267
GQ087792.1 gg_id:375084 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
EU458219.1 gg_id:291040 North American black bear feces clone BB2_a04_1 EU458
AF009508.1 gg_id:15540 Streptococcus suis str. EA1832.92 AF009
AM157420.1 gg_id:142116 Streptococcus mitis mother C3 AM157
EU289036.1 gg_id:238994 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
GQ018929.1 gg_id:490737 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu192d GQ018
EU461983.1 gg_id:296189 white-faced saki feces clone Saki_aaj64g06 EU461
GQ030493.1 gg_id:459696 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw879a10 GQ030
AM157441.1 gg_id:142633 Streptococcus parasanguinis mother V4 AM157
EF509782.1 gg_id:219258 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5097
EU458152.1 gg_id:292449 North American black bear feces clone BB2_f01 EU458
EU467884.1 gg_id:299150 North American black bear feces clone BB1_c06_3 EU467
GQ018857.1 gg_id:490812 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu191f GQ018
EU458161.1 gg_id:293794 North American black bear feces clone BB2_g03 EU458
GQ060042.1 gg_id:441561 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ060
EU461878.1 gg_id:301061 white-faced saki feces clone Saki_aaj62h01 EU461
GQ074530.1 gg_id:394032 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw164c GQ074
AM157443.1 gg_id:143690 Origen y potencial probiotico microbiota de la leche materna breast milk clone 5V4 AM157
EU638618.1 gg_id:337396 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638858.1 gg_id:316255 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638622.1 gg_id:319590 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638451.1 gg_id:334625 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
NR_025355.1 gg_id:534827 Thermicanus aegyptius str. ET-5b; DSM 12793 NR_02
GQ079892.1 gg_id:439457 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
EU638737.1 gg_id:333346 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638544.1 gg_id:354384 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638577.1 gg_id:340110 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638576.1 gg_id:333359 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638435.1 gg_id:336118 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638466.1 gg_id:340259 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638734.1 gg_id:355173 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638336.1 gg_id:339047 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638556.1 gg_id:303923 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638526.1 gg_id:328129 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU638732.1 gg_id:336395 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
AY518549.1 gg_id:107665 Bacillus solfatarensis str. Sol1 AY518

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124.3	1831.2	2405.5	2549.3	2179.1	1956.7	2682.3	2405.0	920.7	695.7	1330.5
10435.1	3934.5	3490.8	3354.2	2869.5	3195.4	3411.3	3939.0	4562.7	5286.5	3600.0
95.4	1643.2	1915.9	1817.6	2055.8	1832.8	1903.3	2202.7	1347.2	718.9	1411.6
1103.8	3670.1	4447.8	4255.0	4511.4	3701.8	4809.5	4521.4	3975.3	4110.3	3097.5
483.5	2426.3	2308.3	2683.7	2431.3	2014.7	2831.9	2036.9	1242.0	1668.0	1441.0
1906.4	1806.6	1340.6	1494.6	1686.0	1857.1	1454.8	2259.8	1034.1	2709.0	1614.7
6483.7	8245.5	7886.7	8260.6	9006.1	8067.2	9030.1	8403.7	10222.3	10433.8	8504.2
56.0	291.0	278.9	309.2	456.5	432.2	271.3	673.2	178.6	251.3	279.2
74.3	587.1	1053.3	1054.5	943.7	728.6	1004.1	932.7	352.4	469.1	406.4
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152.6	3727.1	4182.9	3506.6	2631.8	3425.4	4978.7	4078.0	1826.2	2836.8	3436.3
87.8	1607.0	1455.0	1091.3	1917.2	1635.0	1231.8	1655.2	1134.2	1501.9	1372.2
54.7	117.5	208.9	134.4	231.9	141.9	153.5	330.4	129.2	130.3	109.5
1730.8	5239.3	5234.6	5248.4	6182.1	5363.0	6158.1	5267.9	4814.3	4756.4	4031.7
19478.0	5551.9	6166.4	6000.2	5854.2	5871.7	5996.7	8222.7	6884.6	11148.7	5596.5
3296.8	1351.8	1471.3	2398.7	1598.4	1480.7	1684.0	1515.3	1058.6	786.9	1164.6
1496.4	857.6	941.5	879.2	413.0	790.6	385.6	1139.6	345.8	895.7	456.4
11842.9	3553.5	3729.3	2856.4	3875.4	3354.8	4083.0	3318.9	2707.1	3199.5	4859.1
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279.5	3689.0	4836.0	4520.9	4834.1	4233.0	6011.8	4605.1	2083.8	4308.4	3199.5
58.5	33.4	42.2	36.1	36.0	27.8	39.2	31.9	39.0	25.3	20.1
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906.4	5188.7	6402.3	4571.2	4659.6	5359.4	4832.4	6104.7	3797.3	6962.4	6611.7
5921.6	6476.7	6595.0	3851.5	4054.6	5305.2	5434.4	5638.1	7329.9	8258.7	6478.6
1980.0	3664.3	4236.0	2637.1	4202.6	3614.0	3301.4	3525.5	2116.2	6716.2	3141.5
54.8	370.8	654.0	523.2	603.6	568.7	732.9	735.4	207.0	552.7	293.8
2222.4	2711.1	3710.8	2830.8	2773.6	3024.4	2700.4	3432.8	2343.2	2727.8	2776.2
2614.4	5251.6	6390.6	4094.6	4338.9	5098.0	4993.6	6152.9	3736.1	5418.9	6174.2
25707.8	7664.6	7177.8	6578.9	6481.5	6684.7	8004.1	7520.5	10866.0	10899.5	9117.0
8284.8	5883.8	6329.9	5119.4	5922.5	5509.3	5859.3	6191.0	4939.7	7168.4	6645.7
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416.6	3174.0	4477.6	3307.0	2181.0	3118.3	4368.1	3733.4	2050.3	3330.4	3041.7
549.3	4056.8	4419.0	3830.7	4300.1	3724.5	4959.6	4308.5	4001.7	4605.8	3855.0
790.2	4444.1	4738.4	4045.2	3636.8	3170.8	4833.6	4538.1	2548.4	3479.8	5280.2
475.7	2164.5	2886.6	2422.5	2052.5	2259.2	2196.3	2740.0	1060.9	1539.6	2448.1
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3981.9	5562.5	5777.8
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2997.1	6163.6	4203.4
1935.4	2167.9	2410.3
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2140.2	2663.8	3171.6
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4683.7	7715.9	6217.6
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909.3	210.2	192.7
5007.2	5782.4	6908.6
6087.3	9451.3	7219.8
847.3	1637.0	2055.8
1112.2	1481.3	1247.2
3399.0	3509.7	3115.1
4063.2	5312.7	5206.6
4421.6	4593.9	6303.4
23.6	48.9	61.8
5899.9	6774.7	10565.1
5487.3	5982.4	8382.8
5759.9	5341.3	7539.1
3094.6	5193.6	6973.3
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4474.2	6218.1	5313.5
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AB042060.1 gg_id:83619 Bacillus schlegelii str. ATCC 43741T AB042
EU638752.1 gg_id:352598 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
AF349724.1 gg_id:20396 Turicibacter sanguinis AF349
DQ015579.1 gg_id:202097 Obesity alters gut microbial ecology mouse cecum clone M3_g05_2 DQ015
DQ015594.1 gg_id:202509 Obesity alters gut microbial ecology mouse cecum clone M3_h11_2 DQ015
DQ015619.1 gg_id:201528 Obesity alters gut microbial ecology mouse cecum clone M3_c07_3 DQ015
DQ815845.1 gg_id:171268 mouse cecum clone aab23b04 DQ815
AJ400262.1 gg_id:41555 intestine clone S24-10 AJ4002
DQ815366.1 gg_id:171609 mouse cecum clone aab46f09 DQ815
DQ015045.1 gg_id:134601 mouse cecum clone M2_d06 DQ015
DQ015416.1 gg_id:201837 Obesity alters gut microbial ecology mouse cecum clone M3_g11 DQ015
EU509845.1 gg_id:272578 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d03 EU5098
DQ015488.1 gg_id:201366 Obesity alters gut microbial ecology mouse cecum clone M3_f09_1 DQ015
FJ880353.1 gg_id:379703 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
DQ815843.1 gg_id:172983 mouse cecum clone aab23b01 DQ815
DQ815565.1 gg_id:165315 mouse cecum clone aab42g09 DQ815
DQ015666.1 gg_id:200054 Obesity alters gut microbial ecology mouse cecum clone M3_h01_1 DQ015
DQ015508.1 gg_id:202862 Obesity alters gut microbial ecology mouse cecum clone M3_a02_2 DQ015
DQ015025.1 gg_id:200030 Obesity alters gut microbial ecology mouse cecum clone M2_b01 DQ015
EU509846.1 gg_id:268098 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22d04 EU5098
DQ015420.1 gg_id:202998 Obesity alters gut microbial ecology mouse cecum clone M3_h03 DQ015
EU369151.1 gg_id:334937 libraries oyster shell clone MBHOS-02 EU369
AM500764.1 gg_id:536014 proof spatial heterogeneity hot composting clone E2 AM500
GU136560.1 gg_id:588822 Bacillus sp. str. S130(6)-2 GU136
AB308475.1 gg_id:240826 Caldaterra yamamurae str. YMO722 AB3084
DQ346500.1 gg_id:153225 during composting libraries compost clone 2B16 DQ346
AB233999.1 gg_id:151965 anaerobic reactor clone B-6 AB2339
EU194835.1 gg_id:267680 Electricity generation thermophilic microorganisms marine Charleston harbor sedim EU1948
EF559058.1 gg_id:248820 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
AB175380.1 gg_id:103425 mesophilic anaerobic BSA digester clone BSA2B-08 AB1753
EU358728.1 gg_id:354523 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
DQ887928.1 gg_id:167272 thermophilic anaerobic solid waste bioreactor clone GHB3F05 DQ887
AM947553.1 gg_id:275685 Minor changes detected microbial structure and after three week thermophilic dige AM947
DQ887961.1 gg_id:169373 thermophilic anaerobic solid waste bioreactor clone TIBG11 DQ887
AB486136.1 gg_id:559728 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4861
AJ229198.1 gg_id:34224 anoxic bulk soil flooded rice microcosm clone BSV43 clone AJ2291
DQ129364.1 gg_id:138439 microarray level air two cities Texas urban aerosol clone AKIW782 DQ129
FJ196298.1 gg_id:351034 Microbiological floras Cambrian Period Feicheng Shandong edgewise conglomerate cl FJ1962
EF092457.2 gg_id:187815 Carboxydocella ferrireducens str. 019 EF0924
FJ367045.1 gg_id:368252 feces adult twins and mothers; TS28 clone TS28_a02h01 FJ3670
DQ815751.1 gg_id:165529 mouse cecum clone aab21g12 DQ815

255.6	3882.6	4010.6	4078.0	6372.8	4063.6	5519.8	4134.2	3047.8	3323.0	3125.2
5105.4	4817.2	5537.7	4712.8	3736.1	4650.1	4114.3	5034.6	6096.8	7645.3	5914.6
68.0	994.9	1320.8	1217.6	2219.9	1064.3	891.6	1523.4	522.1	991.7	548.8
66.7	760.0	550.0	703.6	1740.9	1286.9	551.0	1805.7	502.8	570.3	381.0
1643.7	2488.7	2621.2	2321.5	3560.7	2855.2	2185.1	3374.8	3318.6	1256.5	2784.2
559.4	3599.7	2913.6	2573.0	3206.7	3462.7	2026.7	3119.3	2984.8	2354.9	2130.7
650.3	3308.4	2479.3	2130.6	2271.5	2558.2	2830.0	2545.4	4700.9	1706.9	1692.5
103.9	5224.1	3591.0	2552.0	3005.5	3292.0	2657.5	3490.3	6883.1	4076.6	2310.7
1555.8	3526.9	4506.1	3659.3	5312.5	4038.4	4424.3	4659.7	3997.8	5525.3	3067.0
118.1	296.3	540.6	360.3	524.0	452.9	332.0	570.6	244.8	418.8	279.0
43.1	1231.2	1359.3	1040.2	2890.8	1741.9	679.7	3074.1	967.0	1926.3	1265.3
1801.8	1258.2	1355.4	1230.4	895.2	1309.9	1095.7	1590.5	475.1	428.3	663.5
927.3	1297.6	1447.5	1381.0	1768.2	1734.2	1172.9	1982.5	1724.2	1654.6	910.3
153.5	3046.1	3220.8	2572.4	2795.1	3452.7	2615.9	4449.1	1805.9	4067.6	3686.6
76.6	135.7	283.7	113.0	122.6	199.0	78.7	329.0	89.5	242.5	153.8
218.4	2085.9	2641.9	1969.6	1637.9	1513.5	1968.8	1897.6	3867.6	779.3	1588.5
40.7	986.9	1209.7	1293.6	978.6	1065.9	784.2	1738.2	443.4	391.3	679.0
13011.9	4936.2	4363.4	4424.5	5027.5	5267.0	4673.2	5037.4	5135.2	5965.4	6551.3
5842.1	2041.0	1759.6	1967.2	2842.9	1901.2	1539.2	2568.2	3313.8	1983.2	2116.4
607.6	1788.1	2344.3	1997.1	2248.0	2089.2	1906.2	2649.0	1509.9	2551.6	1863.5
2619.1	5952.8	6132.5	6061.7	6500.7	5853.5	6175.7	6478.7	7019.0	6036.9	7827.3
1978.9	4471.8	5402.4	3909.2	3815.9	4969.8	3289.4	5622.1	4343.1	6251.9	3740.8
187.8	5546.7	5439.3	4955.0	3641.0	6420.5	4079.4	5228.9	6029.0	4162.6	3067.5
3282.3	1562.0	1888.7	1617.7	1829.4	1612.5	1660.7	1977.4	959.8	613.1	1927.0
435.7	1205.9	1379.0	1370.9	1811.4	1410.1	1983.6	1207.0	558.8	1646.9	827.1
52.1	845.9	1122.1	1057.5	720.3	1130.1	934.1	693.8	607.9	308.8	945.0
4659.3	4173.6	4323.1	3622.9	4033.3	4046.0	4094.1	4132.6	3872.7	3330.6	3746.7
72.1	655.3	1758.7	1927.1	1227.3	1019.1	2062.7	1344.6	686.1	210.5	616.4
2303.1	6173.7	6561.4	7009.3	6341.7	6024.9	6768.7	6986.5	4849.0	5662.0	5544.4
74.5	382.3	493.9	478.0	543.5	405.4	427.1	427.7	171.1	106.4	486.0
8239.6	7350.7	7428.1	6740.7	6225.3	7405.5	6694.6	7273.5	8114.8	7443.0	7108.1
34.5	104.4	188.0	192.0	369.1	121.3	216.4	132.0	62.3	28.0	89.7
9444.2	7487.7	8013.3	8470.6	7994.6	7859.1	8728.1	6954.2	8951.5	5175.2	9357.3
1763.9	6468.3	7798.2	7397.2	6114.9	6344.4	7197.1	7562.4	6048.7	3340.7	6753.0
3699.5	6714.4	7813.9	6883.4	6704.5	6209.5	8024.3	6237.9	6500.1	5177.2	7775.9
4667.6	2802.5	3189.5	2900.8	2867.6	2512.0	3078.9	2946.4	4023.5	2404.9	2761.1
3392.3	3673.3	5626.4	3956.2	3859.4	4055.6	3765.0	4319.2	5648.4	4659.5	3594.0
491.4	1988.9	2713.2	2031.2	2463.7	1864.1	2692.1	2169.5	2362.6	1336.6	2281.8
52.4	97.3	110.4	100.9	64.9	97.0	118.4	93.6	58.7	27.4	70.7
133.6	2831.2	2831.4	2386.0	2279.7	2129.8	2253.0	2578.3	2276.6	3812.0	2401.3
53.2	457.1	623.8	551.4	599.8	785.3	611.1	686.5	154.9	90.3	118.0

4226.0	4471.9	5360.1
5041.7	5243.5	6714.8
1677.2	1932.1	5789.7
1731.7	1490.1	4573.1
3150.8	3290.9	7468.7
3343.2	3081.3	4514.3
2644.4	2522.8	3232.3
3713.1	3384.0	6842.8
3590.6	4574.6	5263.7
680.0	585.2	1036.2
2748.3	2522.2	8733.9
1245.5	1510.8	1639.7
1947.1	2376.7	3982.1
3370.5	3944.3	4826.8
176.3	213.5	484.5
1595.3	2191.2	2675.4
1784.8	1393.0	3300.2
4664.8	6330.6	7087.8
2611.2	2736.8	6277.0
2246.9	2795.5	3308.0
6153.5	6627.3	8890.3
5013.6	5200.8	8667.2
5606.6	5253.8	7512.4
1976.1	3322.5	6502.9
1105.5	1236.8	2234.8
861.0	1167.5	1621.8
4194.1	5241.6	5153.0
1090.4	1543.8	1994.6
6738.5	6969.7	8800.9
417.6	544.6	1223.2
6562.6	7828.0	9625.3
87.3	166.6	389.4
7482.9	7583.9	9715.5
7244.7	6686.7	9454.4
4796.2	7227.2	9050.8
2633.7	2949.8	3335.4
4135.3	5629.5	5403.4
1798.5	2634.5	3003.2
54.2	120.9	119.7
1884.7	2546.9	1586.7
345.3	521.8	1280.9

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EU778320.1 gg_id:324015 feces clone RL387_aao91c02 EU778
DQ815454.1 gg_id:164595 mouse cecum clone aab48f09 DQ815
GQ175436.1 gg_id:592913 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EF445143.1 gg_id:205846 rabbit cecum clone NED2A2 EF4451
AB192047.1 gg_id:142288 termite gut homogenate clone M2PT2-06 AB192
DQ015494.1 gg_id:133077 mouse cecum clone M3_g04_1 DQ015
AY426451.1 gg_id:101401 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B7 AY4264
AB234456.1 gg_id:146392 termite gut homogenate clone MgMjD-038 AB2344
EF604609.1 gg_id:227821 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
DQ800941.1 gg_id:197539 human fecal clone RL387_aao89f10 DQ800
AB062822.1 gg_id:18245 termite gut homogenate clone BCf4-09 AB0628
EU472310.1 gg_id:291318 francois langur feces clone FL_2aaa03d08 EU4723
EF454103.1 gg_id:221121 termite hindgut clone 290cost002-P3L-1640 EF4541
FJ881172.1 gg_id:416837 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
AB243284.1 gg_id:148219 acetone-preserved termite gut clone M2PB4a-024 AB2432
AB299541.1 gg_id:237802 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
DQ815908.1 gg_id:161771 mouse cecum clone aab24b02 DQ815
DQ456434.1 gg_id:157545 pre-adolescent turkey cecum clone CFT214E5 DQ456
FJ681080.1 gg_id:528434 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
DQ815614.1 gg_id:166791 mouse cecum clone aab43f01 DQ815
EF445166.1 gg_id:216356 rabbit cecum clone NED1H7 EF4451
FJ881210.1 gg_id:418334 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EF604503.1 gg_id:232085 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
FJ681260.1 gg_id:525729 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ681301.1 gg_id:511624 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EF454637.1 gg_id:220301 termite hindgut clone 290cost002-P3L-2450 EF4546
EF098915.1 gg_id:197478 mouse cecum clone SWPT1_aaa03b11 EF0989
FJ367654.1 gg_id:365731 feces adult twins and mothers; TS2 clone TS2_a02a06 FJ3676
GQ422712.1 gg_id:552928 Human Oral Microbiome dental plaque clone CK059 GQ422
AF371714.1 gg_id:69942 swine intestine clone p-4154-6Wa5 AF3717
DQ456425.1 gg_id:157989 pre-adolescent turkey cecum clone CFT214F4 DQ456
EU508608.1 gg_id:276402 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36b11 EU5086
AB243285.1 gg_id:149668 acetone-preserved termite gut clone M2PB4a-031 AB2432
DQ815372.1 gg_id:161993 mouse cecum clone aab47b03 DQ815
EF604607.1 gg_id:234054 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
DQ015370.1 gg_id:135193 mouse cecum clone M3_c05 DQ015
GQ175384.1 gg_id:554511 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
GQ175467.1 gg_id:585880 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AB009208.1 gg_id:16273 rumen clone RFN54 bacterium AB0092
EU458602.1 gg_id:299565 European rabbit feces clone RA_c03 EU4586
DQ905244.1 gg_id:172163 human fecal clone 013-e8 DQ905

1083.7	3218.6	3404.6	3541.6	4128.7	3440.6	4683.0	4015.9	2265.5	2553.1	2571.8
528.4	2012.8	2518.0	2987.9	1965.4	2522.4	2051.4	3317.8	2390.7	777.7	1598.8
183.6	2831.5	2777.2	3415.4	2718.0	2269.1	2627.6	2833.1	1468.8	584.7	1932.4
1140.1	870.2	1108.4	1605.8	1003.7	1018.0	1289.7	1201.5	1196.9	759.7	938.5
49.0	39.5	71.2	56.7	32.2	31.8	39.8	31.8	36.1	29.9	30.2
1850.1	4299.1	5300.5	4203.7	4997.0	4613.0	4841.2	4464.4	5087.3	4927.9	4745.8
41.0	1004.1	677.1	277.8	250.8	705.3	367.9	672.8	804.4	63.1	294.1
42.9	74.9	62.5	109.3	41.0	57.5	46.3	128.5	38.6	31.0	51.5
64.2	774.6	1205.9	1642.9	591.6	672.3	470.2	1277.4	410.4	141.6	821.6
68.9	1351.7	1080.2	1061.3	1268.0	1477.3	1051.3	1397.3	609.2	367.6	630.1
28.3	58.4	67.6	117.8	49.6	55.7	86.7	92.0	53.1	23.4	42.5
629.2	353.1	555.6	677.0	434.7	460.2	458.9	541.5	133.4	116.6	252.2
3504.5	4593.4	4334.0	3925.8	4186.6	3869.6	3990.2	4952.1	3412.1	2886.0	3534.0
7043.7	4250.8	4048.5	3860.4	3565.2	3777.8	3791.4	3988.6	5781.9	3621.6	5860.9
785.5	2295.4	2223.1	2282.5	3147.9	2817.5	3371.3	2415.5	2750.6	1639.7	1917.9
249.8	1312.7	1698.6	1397.9	1195.3	1237.6	1694.2	1291.8	1265.8	1833.4	1310.1
2005.4	1912.2	1837.0	1988.5	1411.8	1422.9	1726.0	1578.1	1786.8	1820.2	1817.1
93.3	700.9	891.9	1103.6	999.5	923.0	1110.7	1039.2	497.4	145.2	762.4
12136.5	7484.4	7140.4	7494.3	7093.5	6825.6	6987.9	6391.3	8109.1	7891.1	6701.1
2237.7	1337.1	1432.0	1220.7	857.0	1107.6	1201.7	1212.4	1023.4	669.2	1092.8
112.7	1512.7	1638.1	1793.3	1679.7	1604.1	2857.7	2634.8	3019.3	516.0	992.9
338.7	3355.2	3196.2	2771.9	3188.1	2658.8	4034.5	2968.8	4904.7	1856.9	2030.8
5750.1	2115.0	2448.6	2609.3	2233.4	1865.0	2210.5	1902.9	2287.3	392.4	3400.0
12266.2	5471.9	4984.1	4946.6	5105.4	4805.7	5458.1	5330.3	4376.6	5113.1	5643.3
15938.4	11744.1	10576.9	11480.3	10217.3	11125.0	11203.6	9342.4	19075.5	10916.8	13751.8
1629.2	1724.2	2572.7	2853.5	2832.7	2326.1	3082.9	2782.6	2537.5	2021.7	2684.4
56.1	732.1	822.4	926.5	1330.4	687.8	1287.4	1190.2	493.5	161.0	487.1
275.6	855.7	1371.6	868.1	833.4	843.1	857.5	917.3	622.9	1319.3	731.0
28.5	48.2	57.4	67.1	49.0	35.9	36.1	38.4	51.4	41.7	65.1
188.5	2535.8	2684.9	2576.1	3533.9	2771.6	2664.8	2502.7	2614.3	1315.3	2306.2
4549.8	1566.8	1891.2	1755.2	1462.4	1607.9	1425.6	1433.9	1826.7	2651.1	2198.7
6937.4	4592.2	3855.5	3864.4	3813.8	3726.2	3770.4	3903.4	4724.8	3415.9	4327.2
60.8	310.2	595.6	413.8	543.9	318.6	604.8	299.7	74.0	65.3	96.0
3144.1	3156.0	2696.4	2808.4	2380.0	2693.1	2905.0	2577.8	3244.2	3351.7	3392.7
7949.3	3570.5	4229.4	5033.6	3772.2	3664.3	3638.0	4256.8	4124.3	2609.0	3162.9
94.6	540.1	715.9	637.1	259.7	444.4	269.2	577.0	255.2	51.7	346.8
1332.2	5745.4	5428.3	4624.9	3858.3	4575.5	4774.2	4970.9	4764.8	4527.1	3933.8
3144.5	5319.1	6191.9	5925.6	5434.9	5335.7	5979.7	5658.9	4589.0	3633.9	5437.3
86.6	960.9	1006.0	911.1	1086.1	866.0	1016.1	881.1	474.6	254.5	937.7
566.5	2775.0	3136.2	3228.9	2589.7	2857.3	3353.9	3304.9	2465.0	2746.7	2604.5
716.6	1162.1	1333.7	1470.0	1398.5	1200.6	1177.6	1850.8	932.2	894.7	3031.6

4069.3	4509.4	5160.2
3524.1	3694.5	4017.9
2645.2	2793.5	3025.8
1023.7	1664.9	1915.0
37.2	67.4	38.7
3349.7	4025.8	6749.2
231.7	323.4	508.0
140.7	121.7	794.1
1113.2	2187.1	2305.1
1948.6	1429.0	2129.1
80.8	79.0	95.5
421.7	594.7	679.4
4296.7	4085.6	4734.4
3283.4	4751.1	4457.9
2333.5	3283.0	3423.3
1157.3	1619.9	1805.7
1658.7	2030.3	2302.8
848.2	946.4	1235.0
7412.3	8689.9	7130.9
1110.5	1780.5	1554.8
1696.0	1770.2	1149.0
2761.8	2933.8	3715.1
1856.1	3159.2	4064.0
4467.7	5815.2	5774.7
9507.8	11179.6	10513.7
2708.5	2248.6	3004.0
870.6	1044.3	1423.0
809.0	1018.8	1281.9
32.4	68.7	65.6
1935.3	2385.5	4511.9
1251.4	2393.7	1805.1
3711.5	5281.2	4830.8
168.0	195.1	543.3
2415.3	2680.3	2482.7
4082.8	4402.9	5085.6
447.2	946.4	1286.1
4207.2	4599.9	6237.2
5507.3	6413.8	6648.1
972.1	1214.5	892.0
2928.2	4441.9	4331.1
1322.1	1733.8	1517.7

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EF602917.1 gg_id:228798 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
EF436324.1 gg_id:204369 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC38 EF4363
GQ897552.1 gg_id:555547 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU845633.1 gg_id:346636 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8456
AJ009493.1 gg_id:16086 anaerobic TCB-transforming consortium clone SJA-136 AJ0094
AB487703.1 gg_id:538197 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4877
EF436352.1 gg_id:208802 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC66 EF4363
GU303307.1 gg_id:576911 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU474551.1 gg_id:288952 bighorn sheep feces clone BHSD_aaa03g05 EU4745
EF063613.1 gg_id:174127 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
AY858451.2 gg_id:110439 gastrointestinal tract zebra clone ZEBRA_12 AY8584
EF603775.1 gg_id:230542 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
EU842417.1 gg_id:327471 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
CU925649.1 gg_id:569463 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EU843209.1 gg_id:351235 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
EF401880.1 gg_id:217109 human fecal clone SJTU_D_15_78 EF4018
EU778048.1 gg_id:344860 Black rhinoceros feces clone RH_aaj90h01 EU778
GU302617.1 gg_id:538833 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ416096.1 gg_id:359349 sediments sediment station NEC5 Northern Bering Sea clone 056M55 FJ4160
AB486406.1 gg_id:549867 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
CU924768.1 gg_id:550433 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AM278890.2 gg_id:231376 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
CU927708.1 gg_id:571884 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
FJ517038.1 gg_id:513057 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AF275916.1 gg_id:72230 anaerobic digester clone AA05 AF2759
AY692049.1 gg_id:99789 UASB reactor clone M77 AY6920
EU844816.1 gg_id:315276 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
DQ800959.1 gg_id:178394 human fecal clone RL387_aao89h10 DQ800
EU842554.1 gg_id:346151 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
EU844348.1 gg_id:330515 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
AB062820.1 gg_id:33347 termite gut homogenate clone BCf4-07 AB0628
AY574991.1 gg_id:102360 Catabacter hongkongensis str. HKU16 AY5749
EF434372.1 gg_id:215573 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
AB486418.1 gg_id:584437 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
EF688248.1 gg_id:317224 Detection microbial sludge anaerobic wastewater treatment system clone 6D9_cons EF6882
AY985462.1 gg_id:116947 human stool clone C418 AY9854
CU923982.1 gg_id:551149 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9239
EU774614.1 gg_id:331966 Angola Colobus feces clone EAC_1aaa02d10 EU7746
CU927863.1 gg_id:557576 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9278
DQ326341.1 gg_id:145236 Metagenomic gut microbiome healthy human stool clone C332 DQ326
FJ535031.1 gg_id:592702 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350

40.7	479.0	906.6	978.0	867.9	436.5	667.6	522.9	251.5	35.0	350.2
37.9	110.4	128.2	204.4	103.9	152.8	117.6	205.5	48.6	45.9	171.4
52.6	730.1	1264.8	1013.4	586.1	931.0	883.1	1045.5	418.4	162.6	402.1
45.5	585.1	760.8	666.2	517.0	511.5	847.7	486.5	259.9	132.5	454.7
119.0	1599.9	2376.3	2574.6	1913.8	1815.3	1883.7	3091.5	1040.0	1261.4	2005.7
195.3	4085.7	4927.6	4694.0	4403.2	4016.2	5474.2	4162.6	2990.2	2079.3	5634.7
5291.7	1896.8	2180.2	2603.0	3147.2	1845.4	2497.5	2269.7	1882.9	1081.0	2427.0
38.0	1363.8	1475.6	618.7	243.5	541.3	281.0	548.8	453.3	133.1	429.6
66.1	1057.5	1816.2	1544.0	759.5	1364.6	993.5	1854.3	836.5	538.5	1327.9
46.3	1848.6	2222.4	2104.5	2630.5	1572.1	2779.1	2214.0	813.2	367.0	1091.1
29.7	33.8	56.5	136.5	47.4	39.2	84.3	40.5	28.7	39.2	25.3
40.3	190.5	139.9	91.6	299.0	141.6	205.9	275.8	135.7	47.9	129.5
55.3	2854.8	3185.2	2209.5	3514.4	3230.5	3430.9	2731.2	2095.9	1273.0	2959.1
50.2	2063.1	2696.2	2491.5	1699.3	2187.8	3205.8	2299.0	854.4	1089.5	1621.2
211.1	4284.7	3913.9	4023.2	4567.8	3556.7	4868.6	4446.9	4220.4	2504.5	5144.2
42.9	47.8	164.0	156.8	155.1	70.0	149.4	218.5	30.9	56.1	91.3
409.2	2591.2	2530.1	2837.6	2569.1	2533.4	2666.3	3381.0	1751.5	1261.7	2075.2
61.9	500.7	1235.6	986.0	742.5	746.9	605.6	714.3	310.8	97.9	711.1
261.6	4683.8	4581.4	4033.1	4253.1	4469.4	5454.6	4096.0	4775.8	3090.4	2764.8
29.0	2713.4	3678.7	3194.2	3365.9	2739.3	3666.0	3204.1	1774.9	1185.5	2968.9
27.4	106.3	268.6	244.7	111.7	205.6	272.7	190.0	102.6	37.3	183.4
47.0	1561.6	1757.1	1615.1	1169.6	1058.7	1702.1	1469.2	620.7	251.9	1094.8
192.5	3132.6	3799.4	3485.8	3279.4	2614.7	4449.3	3328.9	1818.9	2219.3	2992.7
2399.4	2369.3	3607.8	3290.5	2507.8	3226.5	3957.9	3271.6	2404.2	1970.5	2360.4
19987.8	8067.7	7616.8	8223.5	9083.5	7815.4	9458.5	7842.9	10717.9	10515.8	10815.8
129.4	560.8	976.5	813.3	753.0	723.5	1325.6	599.0	485.9	271.2	447.8
535.7	3886.3	4382.6	4488.9	3858.7	4284.9	5130.9	4069.1	2322.5	3707.2	4196.9
45.5	268.9	478.9	533.6	163.6	213.6	368.4	499.3	154.7	98.3	222.5
2486.8	4723.2	5392.4	4982.9	3711.6	4373.8	4501.4	4586.9	2736.5	1694.8	5639.5
71.0	1108.3	1728.5	1282.0	650.3	1113.5	1254.9	1452.2	583.8	261.8	959.5
4841.8	2048.5	3303.2	2924.8	1750.7	1707.7	2430.2	2930.5	1819.6	1791.2	2837.6
76.9	2278.1	2900.2	2934.1	2564.0	2161.2	4419.9	3342.5	1122.6	1033.4	2436.1
48.5	56.3	155.9	196.0	93.1	52.0	63.6	83.6	60.2	23.6	75.7
211.3	3723.4	4667.4	4907.5	3370.6	4254.3	5486.3	4062.9	4002.9	2749.6	3992.8
443.4	4175.1	4067.2	3898.8	3803.9	4264.3	4614.1	4760.6	3354.3	1888.9	2788.6
1681.8	6267.6	5719.1	5069.1	4304.4	5331.2	4778.2	4603.1	7622.0	8726.9	6191.9
209.4	5240.9	5096.7	2929.1	3448.9	4205.8	3386.6	3657.7	4640.7	4401.4	1755.5
10677.8	3341.1	3314.8	3387.6	3727.7	3949.3	3992.5	3407.1	3377.8	3282.4	3209.1
1462.9	3582.8	3727.1	3581.0	2559.1	2967.3	4251.1	3431.1	3385.6	3692.6	2973.4
42.4	485.8	842.5	717.3	306.3	616.0	551.8	413.5	261.3	68.1	308.4
24.1	581.0	850.6	1323.3	112.3	82.3	1529.8	452.3	95.1	68.1	738.2

470.7	843.7	2049.5
107.3	44.5	146.1
726.9	777.9	2652.1
442.7	596.7	3240.5
2783.5	2078.4	4098.3
3526.6	4115.9	5432.6
2231.8	2281.0	2481.2
350.1	526.3	1053.1
1326.3	1390.6	2287.0
2191.1	2217.7	3057.8
39.8	95.1	464.4
208.3	203.1	252.9
2684.0	2579.7	4053.5
2048.9	2328.3	1922.0
3679.8	4381.9	5550.0
100.4	123.7	339.0
2449.2	2776.7	4766.0
732.3	754.3	1751.3
3574.6	4160.2	6660.8
2806.3	3266.2	6709.0
133.2	135.2	1786.7
1000.4	1412.0	3052.6
2853.3	2843.9	4787.0
2932.0	3074.6	4532.6
7798.4	8359.5	8268.3
682.4	871.6	2130.5
4023.3	3530.1	5945.5
226.1	370.0	660.0
4209.4	4451.9	9859.7
1456.4	1238.1	2277.6
2777.4	2526.9	3739.9
1790.6	2370.5	5389.9
57.3	104.7	243.6
4496.2	4515.3	6336.3
4697.5	3997.2	6128.0
4810.5	6666.5	8680.2
4112.8	2591.1	4308.1
2886.0	3771.6	4002.7
2583.4	4082.7	4191.2
250.9	714.1	1278.4
252.6	77.8	258.8

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EU843730.1 gg_id:321463 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ366077.1 gg_id:361711 feces adult twins and mothers; TS25 clone TS25_a02d10 FJ3660
AY854309.1 gg_id:110388 herbivore gastrointestinal tract clone Thompsons14 AY8543
EU259437.1 gg_id:255950 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC61 EU2594
DQ797645.1 gg_id:189301 human fecal clone RL206_aaj14b09 DQ797
AJ576334.1 gg_id:105672 hindgut homogenate Pachnoda ephippiata larva clone PeH17 AJ5763
AF129865.1 gg_id:16131 anaerobic digestor clone HA16 AF1298
EU844475.1 gg_id:338166 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8444
AM275604.2 gg_id:231952 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
FN563365.1 gg_id:582043 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
AF129867.1 gg_id:16130 anaerobic digestor clone HB69 AF1298
DQ805386.1 gg_id:177600 human fecal clone RL203_aai62a01 DQ805
EU508399.1 gg_id:274619 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33a04 EU5083
DQ800020.1 gg_id:188183 human fecal clone RL247_aaj23b09 DQ800
AB175358.1 gg_id:107322 mesophilic anaerobic BSA digester clone BSA1B-04 AB1753
AB185741.1 gg_id:107464 rumen clone U29-A02 AB1857
AB486816.1 gg_id:578501 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4868
EU844677.1 gg_id:338831 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8446
EU771507.1 gg_id:320073 Hamadryas Baboon feces clone AFBAB_aai01h10 EU7715
EU475386.1 gg_id:290991 rock hyrax feces clone RHSD_aaa02g08 EU4753
AB294304.1 gg_id:205022 Microbial structure deep coal seem groundwater clone YWB35 AB2943
EU844902.1 gg_id:350834 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
EF434357.1 gg_id:213762 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
U81761.2 gg_id:14133 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinBB35 U81761
DQ809166.1 gg_id:180585 human fecal clone RL308_aal82f10 DQ809
EU844060.1 gg_id:339645 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8440
EU774645.1 gg_id:322962 Angola Colobus feces clone EAC_2_aaa02f05 EU7746
AB486582.1 gg_id:571348 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4865
DQ798367.1 gg_id:177179 human fecal clone RL181_aah41f03 DQ798
EU466370.1 gg_id:302115 bighorn sheep feces clone BH2_aao22f06 EU4663
EU509200.1 gg_id:270441 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g05 EU5092
FJ366040.1 gg_id:368527 feces adult twins and mothers; TS25 clone TS25_a02a06 FJ3660
AB192038.1 gg_id:142190 termite gut homogenate clone M2PB4-86 AB1920
AB089007.1 gg_id:78174 termite gut homogenate clone Rs-G06 AB0890
AB243282.1 gg_id:149631 acetone-preserved termite gut clone M2PB4a-013 AB2432
AB192021.1 gg_id:143863 termite gut homogenate clone M2PB4-35 AB1920
AB192048.1 gg_id:144142 termite gut homogenate clone M2PT2-23 AB1920
AB255919.1 gg_id:169989 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
CP000853.1 gg_id:239100 Alkaliphilus oremlandii str. OhILAs CP0008
DQ128252.1 gg_id:137817 Unique Microbial Fluids Chinese Continental Scientific Drilling drilling fluid clone CCS DQ128
EF125434.1 gg_id:176156 mangrove soil clone MSB-2D5 EF1254

11857.2	6338.2	6242.6	6949.7	6097.6	7381.4	7093.3	5924.1	9277.3	6846.2	9482.2
156.3	312.1	659.7	514.2	262.0	527.1	427.8	447.1	238.8	572.2	286.3
51.8	446.6	533.9	542.2	528.8	505.9	411.0	434.8	350.7	129.4	444.9
706.2	1042.3	1469.7	1957.1	1717.4	1237.0	1407.1	1801.3	804.8	211.5	823.6
48.3	591.3	890.7	646.7	384.5	660.7	549.2	387.9	290.2	98.9	319.0
81.9	1257.9	1696.2	2212.1	978.8	1091.6	1893.8	768.2	904.6	951.5	796.7
498.7	3761.9	4230.6	4372.6	4573.0	4167.3	5676.9	4588.7	2531.8	3652.3	2774.5
750.7	3829.9	3937.0	4060.0	5291.4	4032.1	6023.5	3351.1	2812.5	2976.0	2971.8
4226.2	7529.4	8067.8	8986.3	6977.0	7266.2	8025.7	7494.9	6747.9	4315.7	9580.6
2791.8	6459.6	7833.7	7387.1	6762.4	6622.2	8055.1	7239.5	6235.3	3446.7	8299.6
34.0	268.6	342.7	322.1	225.2	126.4	433.9	309.1	35.9	42.4	103.4
5306.0	7178.8	7311.3	7759.9	6393.5	6699.9	6922.1	6505.8	10245.6	8111.0	7624.3
1660.1	6534.4	7363.8	7814.6	6399.5	6223.6	7337.4	6213.1	4814.4	3013.1	7191.9
4724.2	2034.5	2290.1	2403.3	1732.1	853.5	2589.1	1912.4	2137.0	2851.9	2707.6
62.3	607.5	1100.9	647.1	490.1	622.2	1300.5	640.1	374.7	128.0	398.3
614.3	2506.7	2366.1	2567.6	3204.8	2384.5	3811.2	2508.2	1818.8	911.0	2009.3
94.0	3496.2	4237.1	3927.7	3624.1	3343.9	4389.9	4510.6	2623.6	1370.3	2979.1
354.9	3251.2	3705.0	3190.5	3672.4	4180.1	3009.3	3576.3	1565.0	4020.5	2283.1
499.6	2540.2	4069.9	3714.4	3060.0	2622.9	3080.1	3735.9	2548.9	1322.8	2898.7
1953.4	2139.9	1827.7	1251.4	1702.9	1760.2	2041.6	1746.2	2297.3	1068.7	3290.1
49.6	164.6	353.9	356.4	120.2	184.8	456.3	243.5	87.1	84.3	151.7
327.8	4274.5	3522.9	3428.1	4048.2	3589.4	2941.8	3615.8	2966.6	1735.4	2073.2
33.9	156.5	337.7	251.6	160.7	145.1	139.5	199.5	79.3	38.4	127.4
65.8	990.3	1366.3	1228.7	1662.6	1188.4	1611.4	1422.1	1196.7	791.9	1346.6
84.3	151.0	286.0	172.3	742.1	144.6	239.4	191.6	290.6	159.7	133.2
485.6	4161.0	5208.7	5433.4	4537.3	4762.1	5675.5	4857.5	2815.5	2557.7	4558.7
3199.3	2227.0	3137.0	2657.2	2999.5	3094.9	2887.1	3170.1	1843.2	1537.9	2625.6
3963.0	2336.2	3049.6	2598.1	3015.1	2605.0	3462.6	2770.8	1882.2	978.7	2001.4
247.8	1800.9	1783.5	1906.2	1577.3	1944.8	1586.2	2193.0	1008.8	1112.1	759.4
779.4	3567.2	3624.1	3489.8	2568.6	3906.5	3430.0	3068.3	3217.0	2696.9	2912.6
22053.8	9285.3	10037.7	10384.0	9062.4	8901.9	10929.2	8981.5	10615.2	8285.8	14797.4
3284.5	2303.8	2776.5	2631.3	1804.2	2284.4	2552.6	2304.0	2103.5	1884.0	2964.7
163.9	1540.1	2276.3	1638.1	953.7	2084.3	1255.4	1769.7	628.1	213.1	1283.8
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95.6	244.2	238.1	291.5	430.6	269.0	380.7	314.4	136.5	58.1	157.3
185.0	266.3	264.2	305.0	387.4	292.4	325.2	380.0	179.7	92.4	264.1
33.6	161.2	239.3	133.1	174.9	92.5	167.9	109.6	65.0	47.3	55.7
740.0	2934.5	3187.2	3915.5	3997.9	2938.8	6203.3	4183.9	2386.3	853.8	2288.4
4512.2	1428.2	1438.8	1541.4	1874.8	1543.2	1371.5	1655.5	1174.7	2452.3	1408.2
71.8	1336.3	1195.2	853.8	588.6	1251.7	620.9	757.0	590.3	991.5	569.3
923.1	4852.5	3863.4	2974.7	2556.8	4312.5	3380.6	2938.8	2693.5	1699.6	3300.8

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447.8	932.7	452.2
454.8	738.6	541.0
1627.7	2236.9	2175.4
357.1	867.2	962.8
1327.2	1502.8	3817.8
4351.0	4914.3	6991.1
3470.7	3478.9	5570.9
7118.9	6516.6	9061.3
6315.7	7094.8	10599.9
174.8	228.1	954.7
6021.5	8981.4	8651.0
5678.5	6088.1	8743.9
2000.1	2986.9	2295.7
445.1	700.8	1902.4
3919.6	2628.3	4359.5
3749.2	3426.7	5719.4
3690.8	2136.0	4554.4
2516.6	3824.1	5380.4
1515.4	2750.4	966.7
222.1	419.9	1724.5
3700.7	3464.8	5011.4
143.3	383.6	579.1
1172.7	1939.9	1275.6
179.5	287.5	361.1
5156.5	4120.8	7184.2
2800.3	3934.7	4782.2
2049.1	2576.5	5261.9
1775.7	2315.7	2554.9
3485.0	2902.0	4439.8
8261.4	9925.6	10059.9
2273.5	3326.6	2381.2
1260.7	2346.7	1557.1
189.6	328.0	416.1
232.5	358.8	564.4
245.3	477.7	351.5
106.4	206.7	458.3
3647.4	3978.5	3620.2
1676.3	1927.2	1604.4
332.4	722.9	870.5
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g__Alkaliphilus
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g__Caloramator
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s__Alkaliphilus transvaalensis	70581
s__unclassified	70314
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s__unclassified	73048
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s__unclassified	70451
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s__Clostridium baratii	44362
s__Clostridium baratii	45139
s__Clostridium bifermentans	71017
s__Clostridium bifermentans	71133
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s__Clostridium bowmanii	71878
s__Clostridium bowmanii	72070
s__Clostridium bowmanii	72323
s__Clostridium bowmanii	72621
s__Clostridium bowmanii	72760
s__Clostridium butyricum	44423
s__Clostridium butyricum	44938
s__Clostridium butyricum	45218
s__Clostridium butyricum	45831
s__Clostridium cellulolyticum	27653

AY569285.1 gg_id:101611 pink microbial mat clone YJQ-8 AY569
EF559033.1 gg_id:235642 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF559
AM183354.1 gg_id:169422 genetic physiological d deep-biosphere Equatorial Pacific and Peru Margin marine s AM183
X75788.1 gg_id:16108 Caloramator indicus str. IndiB4 X75788
NR_026265.1 gg_id:564401 Caloramator proteoclasticus str. Uruguayensis; DSM 10124 NR_02
AF104215.1 gg_id:16110 Caloramator coolhaasii str. Z AF1042
L09187.1 gg_id:16111 Caloramator fervidus str. RT4. B1 L09187
AF489534.1 gg_id:68459 Caloramator uzoniensis str. JW/VK-KU2 AF4895
AF181848.1 gg_id:34407 Caloramator viterbiensis str. JW/MS-VS5 AF1818
DQ676295.1 gg_id:220054 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
GQ906581.1 gg_id:584933 Clostridium sp. str. SW003 GQ906
AB486915.1 gg_id:558768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB486702.1 gg_id:575035 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB487603.1 gg_id:536237 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR AB487
GQ906580.1 gg_id:558972 Clostridium sp. str. SW002 GQ906
AB488197.1 gg_id:548100 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR AB488
DQ129398.1 gg_id:151986 microarray level air two cities Texas urban aerosol clone AKIW1006 DQ129
AB486298.1 gg_id:554614 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
Y18179.1 gg_id:32182 Clostridium cylindrosporum str. DSM 605 Y18179
DQ129395.1 gg_id:138500 microarray level air two cities Texas urban aerosol clone AKIW981 DQ129
AJ431243.1 gg_id:102801 Clostridium sp. str. Dex60-61 AJ4312
FN356335.1 gg_id:590922 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
AJ431244.1 gg_id:79318 Clostridium sp. str. Dex60-75 AJ4312
FN356332.1 gg_id:563046 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
FN356242.1 gg_id:583876 Prokaryotic structure sulfate reducer activity -temperature reservoirs and without ni FN356
AM231183.1 gg_id:151509 Clostridium acetobutylicum str. 7 MSU AM231
AB240207.1 gg_id:141357 Clostridium baratii str. T8 AB240
AB240209.1 gg_id:142276 Clostridium baratii str. T10 AB240
EU547723.1 gg_id:271569 Clostridium bifermentans str. SL186 EU547
EU460327.1 gg_id:299386 polar bear feces clone PB1_aai26f05 EU460
AB539899.1 gg_id:535555 Clostridium sp. str. C5S3 AB5398
EF589987.2 gg_id:227564 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5899
AJ506120.1 gg_id:60735 Clostridium bowmanii str. DSM 14206 AJ5061
EF063634.1 gg_id:191245 Microbial ecology autotrophic anaerobic denitrifying UASB reactor clone R1Cb41 EF0636
EF570920.1 gg_id:231269 Clostridium frigoriphilum str. 14F EF5709
AJ297443.1 gg_id:29618 Clostridium psychrophilum str. -1/C-/I AJ2974
DQ831126.1 gg_id:170961 Clostridium butyricum str. W4 DQ831
ABDT01000025.2 gg_id:262123 Clostridium butyricum str. 5521 ABDT0
AJ289705.1 gg_id:21382 Clostridium butyricum str. IBUN 125C AJ2897
AM930366.1 gg_id:541328 gradual cooling stage mass and its spatial composting clone SMR62 AM930
NC_011898.1 gg_id:471235 Clostridium cellulolyticum H10 str. H10; ATCC 35319 NC_01

5816.6	1562.7	1409.3	1415.2	1505.9	1295.7	1246.0	1112.7	1445.5	907.3	1278.4
56.2	1404.0	2081.3	1894.8	1245.5	1731.6	1596.7	2907.5	1392.8	1584.6	1981.8
1004.6	4714.7	5015.0	4712.7	5411.2	3848.4	7727.4	6080.7	3566.5	2489.0	5039.1
346.1	5795.5	7540.0	6597.7	5848.9	5334.9	6192.6	6308.8	4372.2	4593.0	6348.5
71.3	118.1	63.4	78.8	63.5	55.0	180.9	132.1	76.3	58.9	76.3
28.2	240.7	432.2	390.9	395.7	280.8	342.9	451.3	133.0	69.5	182.7
42.8	145.7	337.0	209.6	175.6	163.3	187.1	228.2	98.9	87.3	109.9
124.8	716.6	1157.7	1038.7	973.5	1063.6	935.4	2111.4	993.5	3698.2	1281.8
41.1	77.1	156.9	122.9	67.6	78.7	82.0	131.7	33.3	27.2	63.5
8471.9	9877.5	11868.1	8604.5	7626.5	8978.5	7447.8	9511.8	12157.4	8139.4	9132.4
3852.4	6765.8	8858.8	7162.2	7215.2	6971.3	8258.6	6906.8	7060.3	4324.8	7082.1
1397.2	5777.7	6575.9	6273.9	5106.3	6215.4	6109.1	5838.0	5831.2	4325.3	5576.9
63.1	276.2	710.2	748.7	1076.7	373.5	386.5	730.9	752.6	88.7	346.5
6265.8	4457.7	9029.6	4179.9	3057.6	5244.1	3627.8	4899.2	4099.1	1954.5	4602.2
19716.3	10703.3	9858.6	9248.0	8914.3	9166.4	9512.6	9538.0	15130.2	11394.4	13356.2
125.0	3017.8	7808.5	2780.6	1983.5	3865.3	2092.5	3689.5	2107.2	1463.2	3016.8
57.1	1941.0	2287.9	1480.0	1826.3	1773.6	1266.5	2105.7	1509.7	1233.5	1349.5
108.2	3547.0	5534.5	3756.0	2165.2	3894.9	2493.6	5296.7	2294.4	905.8	3677.8
41.2	1932.6	4273.4	2207.4	1532.9	2791.6	2483.4	2858.5	1140.6	127.4	1246.1
84.4	703.0	1469.2	929.2	922.5	1111.9	1267.5	1183.3	527.3	207.6	728.5
40.0	31.3	43.1	26.5	36.2	23.8	34.2	28.4	24.5	17.0	19.2
10975.2	7133.4	7796.5	7832.4	9064.9	6858.5	7306.9	6804.9	6405.9	8401.5	7371.4
1263.6	4624.1	4777.8	4202.0	4040.0	5126.8	4351.9	4703.0	3774.6	2634.0	4186.9
3248.1	5565.5	6119.3	7293.8	6164.8	5353.4	5885.8	6757.2	6348.2	5473.7	5233.6
1165.9	5081.9	7313.7	5984.8	5946.1	4739.3	4877.0	5758.6	4713.7	4692.2	5573.5
258.6	4450.7	6057.1	4415.2	4331.9	4293.7	4945.8	5058.9	3060.0	1940.1	4195.4
68.4	1845.6	2552.1	1754.9	1364.9	1836.8	1238.3	3203.4	848.3	493.0	1772.6
8044.1	2690.9	3520.3	2509.5	2960.0	2233.9	2517.5	3881.0	2740.0	1233.9	1999.1
31.2	1275.5	843.3	718.5	660.7	607.5	590.0	1973.8	1286.4	188.2	798.3
395.3	2813.1	2097.4	2021.0	3444.5	1923.2	2162.6	5128.2	2396.5	904.0	1997.7
102.9	2349.7	3501.6	2172.9	2001.2	2672.6	3693.7	3328.8	1093.9	189.6	2476.6
1082.5	4677.0	6244.3	4430.0	4953.7	5453.5	6665.8	5976.9	3521.8	1396.0	4612.8
362.5	3461.6	4676.2	2861.5	3737.0	4016.9	6395.2	5219.0	2244.9	1813.7	3820.7
1441.2	7336.2	8306.8	8200.3	7724.6	7918.0	9752.1	8337.9	7479.1	5530.3	7932.2
2346.3	6173.7	8539.9	6380.4	6061.5	6801.0	7846.0	7192.0	5742.1	3382.0	7358.9
88.4	2995.4	4086.3	2977.8	2386.7	3002.2	4998.7	4581.5	1812.3	891.7	3208.0
917.6	3564.4	5014.4	3677.4	2933.4	4015.1	3282.6	4613.3	2555.7	1435.3	3345.5
136.6	4611.4	7054.9	4487.7	2847.7	4933.9	3519.0	5117.8	2547.0	1497.7	4764.9
556.7	3041.4	4338.0	3225.1	2776.9	3838.9	2968.7	3905.6	2189.5	1369.8	2649.8
59.8	1043.9	1910.7	1079.9	764.4	1218.0	700.8	1898.6	1137.3	462.6	1183.3
638.7	3995.3	4555.6	3928.4	3195.4	3695.2	3915.3	3792.3	3265.5	2807.0	3333.8

1263.4	1574.7	1592.8
1766.1	1381.0	2709.5
3862.4	3739.5	6089.7
5191.5	5303.9	8612.5
49.6	58.4	69.4
257.2	313.0	698.5
190.1	335.9	520.8
1030.7	1925.4	1308.6
71.6	76.4	64.5
9193.3	9453.0	9031.8
6616.5	6901.1	9174.9
5075.3	5418.9	6480.6
368.0	714.0	3752.6
3835.9	5160.1	6817.7
8297.8	10591.4	10419.9
2574.6	3274.1	4287.6
1787.8	1965.8	2366.3
3980.7	3455.6	3531.4
1874.5	1791.6	2801.3
1026.8	154.6	1741.8
23.8	32.4	45.5
7184.1	8546.9	8334.5
3541.5	3952.5	5711.3
6343.8	7547.4	8006.0
5429.4	5960.3	7059.9
4583.4	4493.0	6032.3
2686.7	1568.3	3584.6
3683.9	2428.6	3928.1
1295.2	527.4	806.0
3018.8	1862.4	2638.7
2155.0	2175.3	3041.9
4792.8	4227.2	5434.8
3058.7	2889.1	4786.8
7319.3	7866.9	8425.2
5760.8	5339.9	7252.1
2839.6	2593.3	3222.6
4390.8	4070.9	3945.8
5681.4	3862.2	5087.5
3644.2	3336.8	3689.8
1551.8	899.9	1139.5
3735.7	3200.1	4597.4

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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s__Clostridium cellulovorans	72712
s__Clostridium colicanis	45774
s__Clostridium difficile	70879
s__Clostridium glycolicum	70664
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X73438.1 gg_id:16231 Clostridium cellulovorans str. DSM 3052
FJ957870.1 gg_id:454680 Clostridium colicanis str. JPL_15
NZ_ABHE02000055.1 gg_id:559187 Clostridium difficile QCD-76w55
AY007244.1 gg_id:40074 Clostridium glycolicum str. CIN5
FJ384385.1 gg_id:359641 Clostridium glycolicum str. BG-C128
EU887819.1 gg_id:340525 Clostridium glycolicum str. SN10
L37590.1 gg_id:16126 Clostridium botulinum
AB035087.3 gg_id:22235 Clostridium novyi str. ATCC25758
EU458365.1 gg_id:288771 spotted hyena feces clone HY1_e01
FJ978743.1 gg_id:414789 feces clone CL_F_446
EU772684.1 gg_id:319770 Bush dog feces clone bdog1_aai77a07
EU776210.1 gg_id:308823 Spotted hyena feces clone HY1_d03_1
EU776124.1 gg_id:345246 Spotted hyena feces clone HY1_h10
EU772930.1 gg_id:326430 Bush dog feces clone bdog1_aai78c05
DQ800516.1 gg_id:197510 human fecal clone RL183_aah27g08
DQ800626.1 gg_id:185590 human fecal clone RL183_aao01c05
EU468360.1 gg_id:299843 lion feces clone LI2_aae48c06
EU465520.1 gg_id:287479 lion feces clone LI3_aah78g11
EU772771.1 gg_id:318578 Bush dog feces clone bdog1_d07
EU465499.1 gg_id:302610 lion feces clone LI3_aah78d08
EU772822.1 gg_id:319652 Bush dog feces clone bdog1_aai77f11
EU772713.1 gg_id:344553 Bush dog feces clone bdog1_aai80g01
EU458402.1 gg_id:290404 spotted hyena feces clone HY1_d09_2
EU776059.1 gg_id:306891 Spotted hyena feces clone HY1_f06
EU468383.1 gg_id:295187 lion feces clone LI2_aae49a09
EU467616.1 gg_id:297934 southern three-banded armadillo feces clone arma_g12_1
EU459388.1 gg_id:289373 cheetah feces clone CE3_aai06g06
EU776726.1 gg_id:305526 Lion feces clone LI1_c05_1
EU778549.1 gg_id:312781 Ring-tailed lemur feces clone RT_aai09b05
EU468210.1 gg_id:288094 lion feces clone LI1_f02_2
EU463367.1 gg_id:300475 bush dog feces clone bdog1_aai80b06
EU772883.1 gg_id:320308 Bush dog feces clone bdog1_aai79c02
EU458351.1 gg_id:301967 spotted hyena feces clone HY1_b05_1
EU773971.1 gg_id:322366 Cheetah feces clone CE3_aai06a11
EU465484.1 gg_id:293823 lion feces clone LI3_aah78b07
EU772860.1 gg_id:347235 Bush dog feces clone bdog1_aai77b09
EU772796.1 gg_id:355548 Bush dog feces clone bdog1_aai79e10
EU774859.1 gg_id:324938 Short-beaked Echidna feces clone ECH_aai37g08
EU772948.1 gg_id:310880 Bush dog feces clone bdog1_aai80a09
EU773973.1 gg_id:341829 Cheetah feces clone CE3_aai07f08
EU458412.1 gg_id:295090 spotted hyena feces clone HY1_g02_2

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AY0072
FJ3843
EU8878
L37590
AB0350
EU4583
FJ9787
EU7726
EU7762
EU7761
EU7729
DQ800
DQ800
EU4683
EU4655
EU7727
EU4654
EU7728
EU7727
EU4584
EU7760
EU4683
EU4676
EU4593
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EU4682
EU4633
EU7728
EU4583
EU7739
EU4654
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EU7748
EU7729
EU7739
EU4584

72.3	622.5	1279.8	546.0	594.0	529.0	506.7	1103.3	193.7	166.4	489.2
1795.8	4338.3	5673.9	5339.3	3805.6	5420.4	3986.4	5886.2	3908.4	2170.2	4823.7
64.5	674.6	528.9	354.0	644.7	429.4	424.3	771.1	339.3	150.9	299.2
2966.9	1951.2	2482.6	2339.3	2288.1	1836.5	2150.6	2636.3	2396.8	1027.0	1952.1
65.2	753.2	675.6	585.1	638.5	696.3	507.0	1148.5	490.4	319.4	518.3
378.5	527.9	657.6	588.8	516.2	564.6	448.7	895.2	460.3	282.0	476.3
19314.8	6753.1	6327.3	6790.4	6168.9	6437.2	7027.3	6244.1	9491.1	7574.5	7515.6
99.1	2909.1	4198.5	3771.0	2624.9	3206.9	3112.9	3917.4	1671.4	1510.7	2693.1
10467.6	3919.1	3964.2	4231.9	4202.5	3633.9	4917.7	4047.2	4611.8	4193.7	5133.1
6849.8	5542.1	5469.7	5200.7	5673.0	4856.6	5921.7	6063.1	5097.4	3325.4	4622.6
2504.2	2469.3	2176.2	2051.9	1940.9	2007.7	1948.9	2798.1	1644.3	887.3	2209.0
19068.2	5710.5	5489.3	5241.6	5293.0	5091.1	5575.1	6183.2	7012.3	6212.2	7342.9
17287.1	6825.6	6316.8	7515.1	7078.2	7068.7	7802.9	6719.0	9105.9	7703.5	10962.2
41.3	1356.1	999.9	967.1	1510.0	924.2	857.5	1916.5	509.2	301.7	843.6
55.3	553.0	115.4	55.7	1385.5	656.7	165.7	608.0	504.6	207.8	229.6
6291.7	5383.6	5109.9	5434.7	4851.1	4899.0	6463.5	4778.0	6654.4	5326.2	7620.5
22738.1	5722.2	5341.8	5803.1	5401.3	5955.1	6847.3	4630.1	8347.6	5931.0	8362.8
13673.4	10227.9	9877.9	9030.2	8243.2	8353.0	9310.5	7578.7	12851.5	9488.6	10701.0
9392.3	5677.9	5226.1	5457.6	4984.0	4579.0	5429.9	5473.8	5510.6	2162.0	4238.8
14771.4	7078.5	6481.8	6959.6	5853.9	7115.5	7139.8	6064.3	9941.3	9289.4	8871.5
27623.9	7571.0	6753.1	7130.4	7146.2	6392.6	7087.0	7834.7	8921.6	7703.5	9263.7
165.5	3045.1	3939.2	3836.4	2861.4	3113.1	2957.9	3907.9	2836.6	1242.9	3025.4
3026.7	3841.2	4153.9	4051.7	3015.4	3790.4	4129.5	4196.6	3715.3	2918.3	3836.1
5615.3	6375.6	8161.1	6594.5	6560.4	6077.2	7580.2	6372.0	5389.7	4076.6	7984.0
48.2	1804.5	1174.0	1108.8	2084.7	1223.7	930.4	3310.4	967.9	610.9	1110.2
65.3	1429.9	1660.8	1477.6	1808.8	1177.6	1314.9	2005.8	1547.0	1659.1	1048.1
240.3	2456.6	3195.1	3335.0	2181.4	2357.3	3339.7	2966.6	1143.4	510.8	2853.5
34.9	3319.3	3148.4	1619.8	1381.2	2040.9	1788.3	1458.1	415.0	1157.6	778.6
56.4	780.0	832.9	689.0	747.2	700.0	528.3	919.2	247.5	980.5	348.3
10722.4	8595.0	7367.6	8785.8	7822.3	8051.8	8031.8	7835.3	8496.1	6762.0	10641.4
1921.0	2755.3	2754.0	2477.5	2365.8	2296.6	2342.7	2964.0	2670.4	1556.0	3496.0
83.9	1946.6	2267.1	3101.1	1984.1	2043.4	1263.7	3553.4	1796.0	979.2	1439.8
14466.3	3908.6	3542.4	3861.2	3550.8	3184.1	3617.9	3935.7	4001.3	4220.4	4932.7
2693.2	2312.1	2057.9	2142.4	2812.3	2650.2	1763.2	3091.8	1753.7	3333.3	2564.3
358.8	4422.7	4884.0	4419.4	4691.6	3878.3	4722.6	5991.7	8110.7	4006.0	4733.2
64.2	1044.4	817.0	590.7	763.2	1350.1	493.1	1734.6	640.3	410.2	678.1
31.9	393.0	332.9	242.6	510.9	326.6	255.3	780.7	205.4	107.7	235.4
235.7	2346.0	2267.3	1790.0	1225.2	2052.4	1526.5	2121.9	2197.5	2780.6	2596.0
2298.8	6497.2	5584.7	5882.5	6497.2	5236.3	6799.5	6256.3	6252.7	2549.7	5270.7
694.7	4126.2	4721.5	5618.2	2741.5	4093.4	2992.7	5993.8	2671.6	462.9	5462.9
52.0	1174.0	957.9	607.2	1521.9	940.4	1047.2	1830.1	632.8	469.7	682.5

719.6	638.2	779.8
5293.7	4655.6	5143.0
458.3	597.2	1000.6
2187.4	1861.0	2612.7
553.4	621.9	836.0
562.8	684.7	727.2
5945.1	7497.6	5999.1
3511.5	3965.0	5097.9
3933.0	5490.9	4389.3
5193.6	5592.5	7342.4
2253.5	2454.3	2548.0
5196.3	6661.8	6080.7
5545.9	8116.6	6034.2
1415.2	1222.5	2073.6
630.9	220.3	1323.7
4524.0	4696.8	4642.4
4855.8	6367.5	5658.6
7307.6	9242.4	10047.0
5599.8	5909.7	5997.7
5269.9	8951.4	6860.3
6797.3	7497.0	7601.4
3848.4	3324.5	4553.1
3562.5	5044.4	4027.2
5152.6	7982.2	7620.3
2004.5	1483.2	2543.0
1778.5	2322.8	4609.0
2631.7	2791.6	5942.2
1699.6	1733.5	1899.9
889.0	945.9	1165.4
7054.7	8311.4	7966.4
2335.3	3166.9	2453.7
3868.0	3161.1	3340.2
3527.2	5432.7	4111.5
3305.0	3770.9	2957.5
4991.7	5445.1	6147.1
1414.5	1963.5	2166.0
485.5	546.9	983.1
1892.5	2216.8	1924.4
5785.2	6299.1	7085.8
4657.6	3026.9	2271.3
1306.9	1169.6	1755.1

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

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

EU467710.1 gg_id:290179 bush dog feces clone bdog1_g09 EU467
EU772864.1 gg_id:306149 Bush dog feces clone bdog1_aai78h05 EU772
EU773792.1 gg_id:326083 Cheetah feces clone CE3_aai06h01 EU773
EU773797.1 gg_id:339350 Cheetah feces clone CE3_aai05c02 EU773
AY781385.1 gg_id:108384 Clostridium intestinale AY781
NR_029263.1 gg_id:578541 Clostridium intestinale str. Catt39; DSM 6191 NR_02
EU887817.1 gg_id:303972 Clostridium irregulare str. SN8 EU887
X73447.1 gg_id:14214 Clostridium irregulare str. DSM 2635 X7344
CP000673.1 gg_id:254073 Clostridium kluyveri str. DSM 555 CP000
ABAJ01000001.1 gg_id:219164 Clostridium kluyveri str. DSM 555 ABAJ0
EU828402.1 gg_id:560739 Microbial effects changeover without CO2 sparging two-stage biological and methan EU828
EU887818.1 gg_id:342268 Clostridium metallolevans str. SN9 EU887
DQ133569.1 gg_id:138329 Clostridium metallolevans str. ASI1 DQ133
EU887815.1 gg_id:324891 Clostridium metallolevans str. SN1 EU887
EU887823.1 gg_id:338957 Clostridium metallolevans str. SN16 EU887
EU887820.1 gg_id:315305 Clostridium glycolicum str. SN12 EU887
AF275949.1 gg_id:73000 Clostridium neonatale str. LCDC no.99--005 AF275
EU869244.1 gg_id:349217 Clostridium neonatale str. CM-C98 EU869
AB045606.1 gg_id:29673 Clostridium novyi str. JCM1406 AB045
Z69928.1 gg_id:14186 Clostridium paradoxum str. DSM 7308T Z69928
Z69933.1 gg_id:14196 Clostridium paradoxum str. DSM 7308T Z69933
X75907.1 gg_id:16215 Clostridium paraputrificum str. ATCC 25780 X7590
EF656616.1 gg_id:248740 Clostridium pasteurianum str. AFBR-G EF656
EF140980.1 gg_id:175357 Clostridium pasteurianum str. CH1 EF140
AB536773.1 gg_id:572490 Clostridium pasteurianum str. JCM 1408 AB536
EU459335.1 gg_id:294957 hedgehog feces clone HH_aai36f06 EU459
AM889034.1 gg_id:237367 Clostridium perfringens JS9 AM889
FJ215327.1 gg_id:577392 Clostridium perfringens str. MOTB3 FJ2153
ABDU01000051.2 gg_id:270573 Clostridium perfringens C str. JGS1495 ABDU0
NC_003366.1 gg_id:128673 Clostridium perfringens str. 13 NC_00
EU773814.1 gg_id:323142 Cheetah feces clone CE2_c01 EU773
NZ_ABOO01000021.1 gg_id:267792 Clostridium perfringens D str. JGS1721 NZ_AB
FJ215350.1 gg_id:559845 Clostridium perfringens str. ME1 FJ2153
EU775668.1 gg_id:304779 Hedgehog feces clone HH_aai35d06 EU775
EU772738.1 gg_id:315982 Bush dog feces clone bdog1_aai80b01 EU772
FJ424478.1 gg_id:363985 Clostridium septicum str. SH-C24 FJ4244
FJ375896.1 gg_id:308996 and prevalence blaTEM genes polar bear feces clone PBF_d34 FJ3758
FJ375897.1 gg_id:334569 and prevalence blaTEM genes polar bear feces clone PBF_d35 FJ3758
FJ375892.1 gg_id:325217 and prevalence blaTEM genes polar bear feces clone PBF_d30 FJ3758
FJ375783.1 gg_id:354513 and prevalence blaTEM genes polar bear feces clone PBF_b12 FJ3757
FJ375820.1 gg_id:320883 and prevalence blaTEM genes polar bear feces clone PBF_c1 FJ3758

1731.6	3535.4	3662.3	3393.0	4232.5	3737.2	3713.4	4050.2	2336.8	2262.3	2580.7
6119.8	3794.3	3001.6	3566.8	3096.1	2813.0	2901.3	3408.4	3322.0	1039.1	2540.2
3936.9	4371.6	5492.1	4841.6	4168.5	4422.0	4038.3	5033.3	2176.2	1725.5	3680.7
656.8	4521.8	4760.5	5251.9	4124.8	3934.9	4338.4	5617.0	3574.6	4362.5	4646.3
442.7	3115.9	3838.2	3523.2	2978.2	3549.3	3454.4	4256.3	3249.4	2857.1	3000.2
3384.0	5223.2	5579.4	4872.1	4348.7	5599.0	5902.2	5136.8	6108.6	5727.1	5336.8
11284.0	5127.4	4081.9	4243.4	4254.2	4248.0	4040.7	4796.7	6211.6	4501.0	5393.6
150.4	2821.8	2543.5	2403.1	2757.7	2769.8	2841.4	3206.3	1941.9	1319.1	1889.0
322.9	5621.9	6802.8	6041.1	5476.3	6132.7	6065.8	6505.8	3284.9	2102.1	5248.8
181.4	4934.0	5670.8	5554.2	4971.3	5516.1	5618.7	5942.8	1743.6	1629.6	4031.0
48.4	985.7	2272.4	955.8	471.6	860.1	423.2	1161.3	325.8	558.5	623.4
7874.4	3563.2	3611.7	3823.9	3450.3	3806.1	3338.8	4198.0	4418.6	1874.4	4343.6
2976.7	1234.6	1420.5	1338.8	1726.3	1159.4	1242.3	1971.9	1660.4	585.9	1142.1
7126.1	4436.0	5126.1	4682.5	5973.0	4939.6	5243.6	4578.8	7117.9	4121.3	4971.9
14584.3	3759.2	7626.4	6322.9	5568.5	5221.8	5989.1	5338.8	8719.8	5435.4	8613.2
1675.4	3489.0	4152.6	3798.0	3028.0	3322.2	3797.9	3711.9	3965.0	1961.8	3702.5
47.3	190.4	418.2	43.5	28.5	129.0	32.2	160.5	42.8	18.4	54.0
44.4	4775.1	6265.7	5271.7	3019.9	4843.8	3465.8	5642.3	3041.3	1448.0	5415.7
275.9	2517.2	3202.4	2973.0	2483.6	2626.8	2409.6	3327.8	1473.8	5783.3	2310.6
222.8	1380.1	1846.9	1536.9	1404.0	1361.0	1654.1	1887.4	918.0	362.0	1623.8
66.2	1244.6	2247.9	1260.8	1105.3	1410.3	1165.7	2184.5	734.6	373.5	1410.4
123.3	2282.6	2839.7	2258.3	1471.3	1891.8	1940.7	2958.1	893.5	383.1	1627.3
70.1	2110.5	2964.6	1930.9	1162.2	2365.7	1975.9	2839.6	861.1	241.1	1636.0
1489.3	5530.8	6495.4	6752.6	5939.1	6663.4	7036.9	6356.5	9837.8	5036.7	7625.8
139.0	3113.2	3977.8	3030.9	2513.1	3167.4	3559.0	3523.5	2747.6	742.7	2770.8
261.6	2899.9	3656.1	3647.6	2266.5	3450.6	2703.7	4271.1	1852.6	2460.1	2928.4
8380.2	5774.2	6569.9	5043.6	4242.1	5163.9	4492.5	7133.7	5724.1	4107.4	6416.2
12200.3	5033.9	4582.5	4617.4	4039.6	4613.1	3621.0	5478.9	4627.1	4479.8	6098.5
1145.5	3552.4	4541.4	3661.1	3876.9	4130.3	3365.5	4939.8	2887.3	4472.9	3556.0
866.8	4905.8	5866.8	4228.0	3649.8	4225.8	3575.3	6362.4	3809.4	3798.3	4848.0
1518.9	3905.3	4124.9	3383.0	3975.9	4234.3	2921.9	3381.5	2944.0	2519.0	2776.7
12633.5	7185.4	7851.6	6308.6	5975.6	6206.6	6182.2	7905.4	7310.6	5851.7	6828.2
11071.9	4115.2	4933.9	4228.9	3868.5	3945.4	3956.5	5000.5	4212.5	2847.6	5268.2
2584.0	2984.0	3802.0	2846.0	3251.3	3508.1	2676.4	3150.0	3095.6	1359.5	3160.3
2837.2	5663.8	6417.2	5734.1	5224.6	5143.9	4779.9	6030.8	5279.2	3835.1	5702.7
40.0	1391.3	2078.8	1691.4	905.8	1380.4	991.0	2478.1	901.5	400.8	981.4
1788.2	6151.2	6014.7	5691.3	7472.6	5355.7	6304.9	7565.4	6090.6	4771.4	5521.9
162.4	5178.9	3619.7	3154.3	3870.4	3472.1	3308.0	4827.8	2442.7	3919.8	2815.5
1476.3	3356.8	2821.3	3089.3	4128.0	2686.8	3279.0	4403.8	2381.4	2846.7	2602.9
284.4	5253.0	5094.9	6023.8	5678.1	4227.5	5299.3	6676.5	5148.4	2803.0	5375.1
49.4	1167.4	778.0	634.0	1480.8	833.1	692.3	3488.2	979.6	388.2	858.5

3178.7	3745.7	4963.7
3760.5	3348.7	4204.8
3878.8	4306.5	6082.0
4635.8	6103.3	7139.8
4455.2	3281.0	4787.5
5557.0	5463.5	6488.9
3866.2	5553.6	5562.5
2563.8	2336.4	3843.2
4889.8	4806.8	8274.5
3856.1	3845.2	7891.2
852.1	713.1	1225.8
4054.4	4668.3	5205.0
1178.1	1108.0	1513.5
4041.0	4863.3	5307.6
5143.4	4259.0	5726.3
3701.6	4245.2	5356.8
50.5	83.6	121.8
5655.1	3286.2	4958.3
3310.9	3536.5	4830.1
1453.5	1192.9	2983.2
1617.8	1420.1	1827.8
3486.1	1220.9	2901.0
1733.4	1771.2	3347.6
5568.1	7368.2	6689.2
2870.0	3078.8	4376.6
3859.3	4034.6	4588.5
5202.4	5121.0	5515.0
4457.3	5345.2	5254.6
4517.3	4277.8	5907.6
5101.4	4176.3	6414.2
4154.4	3540.0	3872.5
6607.6	6658.9	8187.6
4202.9	4899.0	4650.7
3134.6	2476.6	2842.0
5564.5	5038.6	6478.2
1832.4	1344.5	2007.7
6047.4	5913.1	7521.1
3686.5	3049.8	3381.7
3697.9	3736.9	3278.3
5068.7	5035.6	5523.3
1302.3	795.6	1826.9

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s__Clostridium subterminale	72366
s__Clostridium tetani	72553
s__Clostridium thermocellum	27879
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FJ375886.1 gg_id:318634 and prevalence blaTEM genes polar bear feces clone PBF_d24 FJ3758
FJ375781.1 gg_id:312800 and prevalence blaTEM genes polar bear feces clone PBF_b10 FJ3757
FJ375891.1 gg_id:304496 and prevalence blaTEM genes polar bear feces clone PBF_d29 FJ3758
FJ375832.1 gg_id:337750 and prevalence blaTEM genes polar bear feces clone PBF_c14 FJ3758
FJ375879.1 gg_id:304036 and prevalence blaTEM genes polar bear feces clone PBF_d17 FJ3758
AJ310082.1 gg_id:31278 Clostridium stercorarium str. DSM 8532T AJ3100
EF030542.1 gg_id:190008 Clostridium botulinum str. G196 EF0305
NC_004557.1 gg_id:471257 Clostridium tetani E88 str. Massachusetts NC_00
AABG04000051.1 gg_id:130271 Clostridium thermocellum str. ATCC 27405 AABG0
FJ599513.1 gg_id:545541 Clostridium thermocellum str. CTL-6 FJ5995
NR_026112.1 gg_id:569919 Clostridium thermopalmarium str. BVP; ATCC 51427 NR_02
DQ887919.1 gg_id:164481 thermophilic anaerobic solid waste bioreactor clone GHB3A06 DQ887
X71856.1 gg_id:15980 Clostridium cellobioparum str. DSM 1351 X71856
AB307636.1 gg_id:271652 clay wall used Japanese traditional buildings clone B46 AB3076
EF559080.1 gg_id:218474 mesophilic anaerobic digester clone B35_F_B_A02 EF5590
AJ863357.1 gg_id:122896 poplar tree microcosm rhizosphere flooded clone 17RHF8 AJ8633
EU753611.1 gg_id:315396 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
AY959944.2 gg_id:114917 Clostridium alkalicellum str. Z-7026 AY9599
AB240379.1 gg_id:142282 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AF280831.1 gg_id:41245 bioreactor clone tbr4-15 AF2808
AF482449.1 gg_id:77496 granular sludge clone R6b7 AF4824
AB486179.1 gg_id:577580 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB198481.1 gg_id:135577 termite gut wall fraction clone RsW01-052 AB1984
AB294296.1 gg_id:216349 Microbial structure deep coal seem groundwater clone YWB27 AB2942
AM982551.2 gg_id:278657 microbial and slurry pig straw spent bedding clone PIST-AGE08 AM982
EU703284.1 gg_id:538658 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
AB486460.1 gg_id:574342 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
X71852.1 gg_id:15957 Clostridium papyrosolvens str. DSM 2782 X71852
AY684073.1 gg_id:130444 methanogenic enrichment 'MRE50' clone MRE50b28 AY6840
CU918823.1 gg_id:556438 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AB486564.1 gg_id:560650 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4865
FJ502269.1 gg_id:578409 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak FJ5022
EU753609.1 gg_id:353886 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
AB374114.1 gg_id:245904 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
GQ921436.1 gg_id:590008 Worms hell: presence Nematoda terrestrial deep subsurface (0.9-3.6 km) fracture w GQ921
AF407388.1 gg_id:68943 MCB-contaminated groundwater-treating reactor clone RA9C1 AF4073
AB488016.1 gg_id:579868 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC AB4880
L35517.1 gg_id:15955 Bacteroides cellulosolvens L35517
AJ229249.1 gg_id:15960 Clostridium sp. str. FCB90-1 AJ2292
AB240232.1 gg_id:144522 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB2402

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2132.4	6456.0	7166.9	7095.0	7576.6	6505.8	7400.1	7276.0	6451.7	5021.4	6326.0
1542.2	6224.7	5892.2	5863.5	6889.5	5212.7	5998.7	7245.1	5850.9	4172.9	5495.6
158.9	3444.7	2521.4	1594.7	4220.6	2498.3	2295.4	5907.5	2341.1	3299.8	2322.7
5819.9	7039.8	6443.4	5664.4	6131.2	6637.9	5579.2	6879.2	4276.1	8569.6	5024.9
1443.7	5045.5	4521.2	4641.3	6010.4	4124.9	4940.8	6192.9	4763.0	3174.8	4174.0
102.6	261.0	528.8	443.2	462.5	368.3	735.7	529.4	285.4	88.7	389.6
62.0	2289.9	2699.7	2186.2	1894.2	2217.1	2974.0	3193.8	2090.5	857.3	2499.1
33.1	633.8	1281.6	604.0	357.7	750.1	529.4	849.8	359.6	45.6	613.6
1533.3	1461.2	2767.3	2220.5	1414.5	1804.5	1584.6	2403.5	1455.2	607.0	2051.5
107.0	2930.0	3492.0	2897.0	2607.3	3712.7	3345.1	4047.2	1940.1	1406.9	3002.7
40.4	247.8	444.3	156.5	198.7	135.6	100.8	226.8	76.8	33.6	78.0
40.7	500.0	1183.6	1012.4	546.4	738.2	935.5	836.4	641.2	79.4	454.6
124.8	1606.0	2833.9	2334.8	1359.8	1775.4	2181.2	2446.1	1126.0	685.3	1374.5
1075.3	5091.0	4830.1	4443.0	4503.5	4399.5	4914.2	4536.8	5288.6	3635.7	3855.9
36.7	1397.4	1773.5	1420.8	1143.4	1429.5	1549.1	1413.5	936.7	563.6	1547.3
503.4	5620.4	9134.5	7288.8	5111.6	7509.5	7506.6	7600.9	5125.8	1950.3	5867.8
969.7	3735.0	5870.8	4439.0	3648.6	4040.8	4539.3	4176.2	2467.7	1427.2	2629.2
43.4	205.3	642.6	224.6	145.4	246.2	164.5	369.0	90.3	70.2	113.1
1665.1	2106.3	3511.8	3526.8	1801.4	2350.1	3688.2	2731.9	2353.9	784.4	2097.2
96.6	1795.6	2559.8	2125.2	2507.2	2185.5	2284.0	1753.8	1456.0	2039.9	1154.1
67.3	138.9	233.8	133.7	232.0	187.9	294.1	218.8	131.6	54.5	79.3
216.6	2441.0	3514.9	3652.4	1732.8	2352.7	2181.0	2989.7	1398.2	490.1	2141.6
311.1	3411.3	4490.2	3733.9	2840.6	3634.3	3481.5	3447.1	1930.1	1360.0	3028.0
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3895.3	4142.9	4672.9	3996.8	3133.0	4575.5	4127.3	4412.6	5263.4	5453.9	4061.3
750.7	4399.7	5418.8	4399.3	4288.3	5131.0	5805.6	6108.6	2984.1	3223.4	4199.1
1296.3	2737.7	3091.5	2721.3	3649.1	3049.0	3154.8	2915.8	2492.5	2444.9	3605.9
230.6	3399.6	4878.1	3964.5	3157.6	4014.1	4121.8	4343.4	1860.5	1052.2	2883.1
44.0	74.4	181.4	65.4	73.3	91.7	62.0	176.9	40.2	143.2	95.6
4952.8	10270.9	9641.1	10765.6	9934.5	9365.3	10995.1	9971.3	9559.9	6655.1	10851.3
7757.7	3136.4	3938.6	3642.2	2857.6	3334.2	3538.2	3407.5	3683.6	2726.8	4206.0
2595.2	3194.0	4863.4	4601.4	3301.4	4153.3	3717.1	4569.1	5257.2	1102.8	4300.3
4036.3	8429.7	8756.7	8808.9	9336.6	8425.8	9616.4	7839.5	10472.7	7640.5	9251.0
2557.7	3167.3	3648.0	2978.5	2710.3	3096.4	3069.7	3710.5	2311.7	4452.7	3389.1
951.7	1662.1	2675.5	2083.4	1671.5	2750.7	1701.0	2808.4	1154.0	646.3	1574.7
983.1	3373.9	3953.2	4197.9	3624.7	3028.5	3976.3	3312.3	4590.0	3027.3	4324.2
11364.5	7363.6	7103.5	7097.4	5965.5	6547.0	6694.9	6325.5	9322.9	6953.8	8245.8
783.8	5938.7	7427.5	5833.9	4867.1	6063.0	6191.7	5315.5	6008.5	6805.0	7308.7
17269.7	4856.0	5147.8	5210.7	5502.2	5229.8	5116.5	5486.9	5171.1	4984.3	6501.6
39.3	206.7	669.8	378.2	183.1	437.4	325.3	536.2	156.8	48.0	142.8

5280.8	5057.2	6456.0
5948.1	7032.2	7213.1
5846.0	5798.4	7351.5
3949.6	2340.7	4814.1
6633.2	5233.8	7073.1
4691.4	4832.9	5785.0
744.2	358.3	1059.5
3068.1	2345.5	2961.3
508.7	683.6	767.2
1839.0	1599.3	2187.0
3337.2	3038.3	4263.0
161.8	179.3	262.2
813.1	648.2	1580.3
2927.1	2248.5	4049.4
3469.9	4914.5	6692.8
880.2	1201.2	3073.4
5526.9	6162.1	10932.7
3201.6	3140.8	6394.5
207.7	448.4	330.7
2245.0	2278.1	3738.9
1639.9	1364.5	2754.5
175.0	234.9	612.4
2635.1	2181.7	5929.1
2486.6	3281.3	3720.3
6420.2	6196.2	11708.9
3326.7	4915.9	4980.2
5301.2	5545.7	7002.0
2405.3	2867.9	3041.9
4667.4	2877.4	4998.5
102.8	57.5	96.4
8721.6	9609.6	12395.4
3363.2	3853.8	4777.7
2252.9	2826.4	3193.9
6679.3	8716.6	9325.8
2538.1	3844.8	5055.9
1550.5	2723.0	5066.3
3141.6	3635.4	4056.1
5527.6	6922.6	7285.4
4629.0	4763.8	5750.5
5658.2	6383.6	7267.7
257.1	340.8	1328.5

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FJ825485.1 gg_id:540295 Microbial during start-up mesophilic biogas plant clone 175_BE3_2 FJ8254
FN436024.1 gg_id:547395 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
DQ125722.1 gg_id:136404 uranium contaminated soil clone AKAU3820 DQ125
DQ125755.1 gg_id:132457 uranium contaminated soil clone AKAU3868 DQ125
AB274495.1 gg_id:213313 packed-bed reactor clone CFB-6 AB274
EF586065.1 gg_id:245011 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF586
DQ887967.1 gg_id:161992 thermophilic anaerobic solid waste bioreactor clone TIBE03 DQ887
CR933129.1 gg_id:109994 Evry municipal wastewater treatment plant clone 013B04_B_SD_P15 CR933
DQ125655.1 gg_id:134002 uranium contaminated soil clone AKAU3717 DQ125
AF050580.1 gg_id:16001 contaminated aquifer clone WCHB1-21 AF050
GQ487969.1 gg_id:550979 Microbial metal soil polluted heavy metals clone G10-80 GQ487
EU250962.1 gg_id:360102 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU250
AF407399.1 gg_id:48313 MCB-contaminated groundwater-treating reactor clone RA13C2 AF407
EF205577.1 gg_id:205562 among geographically regions central Tibet geothermal spring mat clone TP20 EF2055
AJ318164.1 gg_id:16925 Waste-gas biofilter clone BIri47 AJ3181
AB011057.1 gg_id:15977 Clostridium josui str. FERM P-9684 AB011
FJ815191.2 gg_id:554015 Clostridium sp. str. A6 FJ8151
GU214168.1 gg_id:585365 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
X71854.1 gg_id:15963 Clostridium termitidis str. DSM 5396 X71854
AB487128.1 gg_id:587360 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
AJ229248.1 gg_id:15959 Clostridium sp. str. FCB45 AJ2292
EF559108.1 gg_id:219192 mesophilic anaerobic digester clone C35_D7_H_B_G09 EF5591
AB486913.1 gg_id:572847 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AY330128.1 gg_id:97132 methanogenic landfill leachate bioreactor clone AC065 AY330
GQ502575.1 gg_id:564645 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
NC_011898.1 gg_id:471233 Clostridium cellulolyticum H10 str. H10; ATCC 35319 NC_01
DQ069224.1 gg_id:128200 gold mine clone SRB16 DQ069
AY642570.1 gg_id:153096 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY642
X71847.1 gg_id:15998 Clostridium cellulolyticum str. ATCC 35319 X71847
FM994911.1 gg_id:534331 springs Velingrad region Bulgaria hot spring Mizinka clone VS-7 FM994
AB486893.1 gg_id:532875 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB486146.1 gg_id:561133 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
AJ229216.1 gg_id:50120 anoxic bulk soil flooded rice microcosm clone BSV72 clone AJ2292
AB294749.1 gg_id:211979 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobact AB294
GQ406191.1 gg_id:509371 Benthic submerged sinkhole ecosystems sediment clone -39-11 GQ406
AB240269.1 gg_id:142277 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU057605.1 gg_id:252234 Clostridium sp. str. CJT-3 EU057
EU772520.1 gg_id:306873 Hamadryas Baboon feces clone BAZ_aah92f09 EU772
AY337519.1 gg_id:91168 Clostridium sp. str. L15 AY337
EU459349.1 gg_id:288632 cheetah feces clone CE3_aai05a07 EU459
FJ672914.1 gg_id:523511 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6729

158.7	2327.3	2166.7	1835.3	887.8	1470.2	1321.5	1735.2	1627.2	307.8	1340.9
40.9	2481.3	3949.4	3002.9	1938.1	3250.9	4000.3	3376.0	2144.2	750.2	1981.4
89.8	494.7	5165.2	757.3	524.1	3843.2	930.5	2576.2	626.1	104.5	257.8
51.7	54.6	220.4	130.6	29.1	81.2	58.3	117.4	48.7	17.4	61.7
60.9	127.3	318.4	295.7	173.8	237.0	311.9	257.8	58.5	28.4	97.2
62.1	178.2	334.5	297.1	214.4	170.5	267.9	322.2	132.2	54.4	178.2
493.8	4688.0	7884.8	6017.0	3854.2	5503.4	6199.2	5921.5	3914.0	1183.5	4945.6
44.9	1810.7	2844.6	2341.8	1289.5	1835.7	1788.2	2497.6	1152.8	512.1	1781.5
67.8	317.9	500.7	397.8	262.6	330.3	474.4	395.9	140.8	141.2	234.6
32.2	164.0	697.6	267.5	180.3	373.9	258.2	553.6	214.2	39.7	99.8
1376.5	2009.0	3914.2	2678.2	1360.1	2937.6	2969.4	3016.6	1855.8	769.3	1814.0
433.1	3636.0	4627.8	4246.1	3636.7	4259.6	4447.7	4391.6	2656.4	1818.7	3863.8
187.7	1820.0	1297.3	1509.5	1439.6	1864.3	2390.5	2147.7	956.9	1008.3	1780.8
688.7	1081.6	1311.7	1295.0	1816.0	1003.1	1547.5	941.1	666.4	411.1	951.3
39.7	130.9	481.1	138.7	40.9	151.2	95.2	171.0	68.6	18.2	67.1
237.0	2707.6	2413.6	1545.0	1867.7	2267.8	2572.0	3058.9	1576.2	1134.0	2024.7
44.7	150.2	455.5	253.2	87.7	277.6	167.4	341.2	99.9	21.0	91.8
973.3	2704.4	3725.5	3240.1	2551.5	2622.7	3303.7	3225.9	2044.0	952.8	2338.9
423.6	4085.7	5162.2	5220.1	4462.0	4821.3	5847.4	5583.8	3118.9	1517.3	3671.2
242.4	5300.0	8431.8	6804.0	4137.4	6103.1	6626.1	6622.8	4269.5	1913.9	4869.5
74.1	1683.5	2502.5	2000.3	971.6	1799.5	1444.0	1926.5	1015.6	259.6	1152.6
35.9	886.7	1926.0	1245.1	377.9	1046.9	966.2	1468.4	494.2	49.1	706.1
284.0	4830.1	7151.0	5448.1	4536.4	5984.8	5818.4	5729.3	3633.1	3742.7	5272.7
48.2	544.9	1859.0	847.9	318.0	979.4	1037.1	855.0	537.0	29.0	120.1
3113.6	5173.0	5131.4	5232.3	4796.2	5013.1	5760.8	4756.3	5172.6	2792.8	6105.9
618.6	3253.9	3858.0	2996.6	2824.1	2821.4	3286.8	3557.1	2498.8	2046.3	3483.5
45.8	1029.0	2003.3	1973.5	538.2	1385.6	1101.4	1740.3	390.7	117.9	984.4
38.9	123.0	1208.6	495.9	148.7	429.1	216.0	898.6	146.7	22.6	373.7
683.6	4277.4	4599.3	3990.6	3625.4	3830.4	4009.7	4359.1	3621.9	2790.1	3840.4
977.6	1819.5	2479.6	2789.8	2517.2	2165.6	2468.5	2083.9	1552.5	613.1	677.0
399.2	4186.8	6282.1	5157.2	4785.9	5352.7	4916.9	5547.4	3046.9	2709.2	4824.5
36.0	2630.9	5243.3	3460.0	1771.2	2982.6	3710.9	3029.7	1651.6	150.3	2080.3
1518.4	1715.3	3182.5	2800.0	1679.7	2366.2	2773.8	2459.1	2445.7	1117.7	2208.4
69.9	31.5	54.4	63.4	50.2	49.9	48.4	58.0	26.0	19.9	42.7
875.2	4693.8	6214.4	5497.4	4034.7	5123.2	5170.3	5304.9	3738.1	1331.5	4498.4
26.2	1064.3	2865.0	2243.1	739.9	1805.1	1322.7	1338.0	847.0	124.3	749.0
135.4	3171.3	4055.8	3528.3	2668.6	3031.0	2760.9	3218.6	2050.6	1110.4	2141.8
75.0	1829.3	2270.5	1780.5	1319.3	1687.4	1771.8	2432.1	1119.8	673.1	1695.3
102.4	2659.7	3606.7	1995.4	1695.3	2706.3	1660.2	3705.5	1111.6	1513.9	2306.7
699.0	1715.1	2828.3	1737.6	1565.9	1997.4	1594.5	2425.3	1510.5	1456.9	1838.8
143.6	2303.2	3522.8	2625.3	1350.2	2747.9	1551.8	4026.6	1158.0	1295.6	2842.6

1385.0	2006.0	3657.7
3109.2	2664.0	4547.7
692.0	661.7	2655.8
34.1	68.1	101.5
136.2	225.9	425.0
123.1	328.6	1124.0
5910.5	4021.8	8579.5
2141.3	1668.3	3216.7
270.9	404.0	358.2
231.9	481.4	1722.4
2478.2	2172.9	3458.2
4195.3	4030.2	7114.9
1835.3	1960.5	2482.2
822.6	1274.4	1930.5
70.9	184.1	797.8
3356.8	2193.9	3542.5
140.5	272.5	631.8
3031.6	3103.9	4912.3
6480.4	4767.4	6887.8
6094.6	4782.6	9052.2
2391.3	1170.1	3719.3
757.4	902.7	881.1
4462.6	5643.6	7861.6
516.2	358.2	1302.9
4635.7	4995.6	6600.9
3881.1	2684.4	4165.0
1159.8	1251.3	3516.4
386.3	196.1	874.2
4004.9	3801.2	4561.4
2045.6	2023.8	3459.2
4057.1	3939.9	4243.0
1610.4	1609.3	5020.7
1686.9	1797.6	2737.2
32.2	50.4	367.1
4493.7	4891.7	6878.2
1372.2	754.4	3468.5
3795.0	2716.7	3479.1
1888.2	1774.8	2791.9
3644.5	1723.0	3185.7
2176.5	2688.4	1918.8
3355.3	1765.9	2700.5

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FJ683489.1 gg_id:519525 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU473709.1 gg_id:287502 banteng feces clone BG_aaa04c08.Contig1 EU473
EU473983.1 gg_id:288648 giant panda feces clone GP_2aaa03h01 EU473
GQ458239.1 gg_id:547433 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
EU467045.1 gg_id:291305 hedgehog feces clone HH_b05 EU467
EU459232.1 gg_id:288088 hedgehog feces clone HH_aai34e01 EU459
FJ674874.1 gg_id:531852 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
AM183095.1 gg_id:241843 and its spatial composts compost clone SMC146 AM183
EU473956.1 gg_id:301835 giant panda feces clone GP_2aaa04d05 EU473
EU473643.1 gg_id:302631 banteng feces clone BG_aaa01c06.Contig1 EU473
FJ682017.1 gg_id:512879 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU459171.1 gg_id:299102 hedgehog feces clone HH_aai33b11 EU459
EU467934.1 gg_id:299336 cheetah feces clone CE2_e04 EU467
DQ196630.2 gg_id:172362 Clostridium sp. str. BL-26 DQ196
FJ960229.1 gg_id:564094 bottlenose dolphin upper respiratory tract blowhole clone D9A4_121 FJ9602
FJ370179.1 gg_id:356848 feces adult twins and mothers; TS56 clone TS56_a01d05 FJ3701
EU775688.1 gg_id:315362 Hedgehog feces clone HH_aai33h06 EU775
GQ868440.1 gg_id:582630 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC518 GQ868
FJ375881.1 gg_id:328969 and prevalence blaTEM genes polar bear feces clone PBF_d19 FJ3758
FJ683394.1 gg_id:530072 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
DQ238608.1 gg_id:145018 Effect daidzein on piglets piglet gastrointestinal tract clone 8 DQ238
EU468026.1 gg_id:294154 cheetah feces clone CE2_d12_2 EU468
EU777813.1 gg_id:322174 Polar bear feces clone PB2_aai23a05 EU777
EU474114.1 gg_id:301771 giant panda feces clone GP_2aaa02g05 EU474
EU459181.1 gg_id:291701 hedgehog feces clone HH_aai33d07 EU459
EU475570.1 gg_id:288446 babirusa feces clone BARB_aaa03g08 EU475
DQ817233.1 gg_id:172276 mouse cecum clone aaa70d07 DQ817
AJ245413.1 gg_id:16236 Clostridium tertium str. ATCC 14573 AJ2454
EU474799.1 gg_id:292527 takin feces clone TAK_aaa01g04 EU474
DQ238613.1 gg_id:142447 Effect daidzein on piglets piglet gastrointestinal tract clone 6 DQ238
FJ670668.1 gg_id:528824 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
EU473968.1 gg_id:295254 giant panda feces clone GP_2aaa03d03 EU473
DQ800540.1 gg_id:199214 human fecal clone RL183_aah29d02 DQ800
GQ129976.1 gg_id:403839 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
FM874206.1 gg_id:356785 occupant source house mattress dust clone MC03A02 FM874
AF371844.1 gg_id:33176 swine intestine clone p-1965-s959-5 AF371
FJ679483.1 gg_id:527748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
AB332117.1 gg_id:247793 Continuous cultivation and structure thermophilc propionate-degrading microbial co AB332
EU474794.1 gg_id:293733 takin feces clone TAK_aaa03c02 EU474
AB540985.1 gg_id:572196 Eubacterium moniliforme str. JCM 9990 AB540

7916.7	4429.2	4120.2	4402.1	3407.7	3153.5	3703.6	4154.1	4646.1	3317.1	4973.1
348.4	4940.5	7168.3	4847.3	3522.3	5065.6	3867.8	5608.6	3126.5	2210.3	5088.0
1769.6	8232.8	9606.9	9610.7	9952.1	9004.7	11096.5	9560.4	5469.4	10986.4	9048.5
314.1	1355.2	1805.6	1693.0	1338.4	1426.8	1433.9	1774.8	881.8	609.4	1051.1
3057.4	4816.3	6500.3	5313.6	5144.1	5339.8	5219.5	5840.6	4287.7	3923.0	4824.6
153.0	1560.3	2562.8	1502.9	1253.4	2101.2	1416.0	2291.1	1111.3	839.2	1851.8
12779.9	5842.9	6563.5	6835.9	7250.5	5988.9	6037.8	6226.2	6382.6	5286.9	10019.6
176.2	4192.0	6230.2	4085.3	3519.8	4527.1	2942.7	5409.0	3078.1	1388.2	4148.7
35.4	1154.2	2850.6	1239.0	405.8	1616.7	714.9	2221.2	340.9	155.9	1031.1
12324.3	7095.7	5535.1	5696.5	5238.1	4469.2	4992.3	4970.4	5560.9	5023.1	7026.1
331.3	3587.8	5056.9	2825.9	2708.3	3893.6	2790.1	4672.8	2344.6	2457.6	4115.4
697.6	3504.8	4149.9	3267.2	3232.6	3294.3	2770.9	4442.8	2738.7	2431.1	2806.7
53.2	3499.7	4668.2	3036.1	2583.9	3364.3	2297.5	4672.8	2097.0	1195.0	3044.9
440.3	4645.2	6890.5	5992.8	5055.9	6975.7	5571.6	7587.5	5026.9	4225.0	6632.8
125.1	6896.5	9137.0	7037.9	3645.5	6903.9	4377.6	7678.2	3919.8	1823.1	8194.9
471.8	3630.3	4827.3	3564.7	2131.4	3773.2	2945.7	4661.2	2520.8	1176.0	3281.8
13448.4	3546.1	3776.9	3150.5	3616.0	3838.8	3336.8	3697.2	3294.6	3180.1	3381.7
5176.5	4939.6	6623.2	5070.4	5499.9	5418.9	6071.8	5887.0	4421.4	3558.3	5692.1
12736.4	3205.5	3047.8	2995.2	2931.3	2570.4	3250.9	3002.4	3570.5	2990.0	3599.8
1086.9	3618.3	5293.2	4734.1	2986.8	4878.6	3421.6	5464.5	3109.7	1516.1	4444.9
3818.2	1622.0	2040.0	1671.9	1249.5	1588.8	1210.8	2085.1	1231.0	1205.6	1335.3
60.5	2407.2	3654.0	2345.3	1802.1	2480.0	1845.3	3438.6	2267.5	1230.6	2691.9
203.6	2337.1	3177.0	2475.6	1892.6	2520.2	2809.9	3670.9	1770.7	757.6	2839.1
4048.9	8216.5	9962.6	7335.7	6982.2	8420.3	6043.6	8224.3	10611.1	3409.8	11085.2
2338.3	2450.1	2767.1	2720.7	2152.5	2134.4	2064.1	2572.6	1789.8	1164.7	2424.6
367.6	4913.3	5878.2	4691.6	3985.6	5649.8	4763.9	5237.0	5468.5	4299.8	4787.5
159.1	3445.5	5341.6	3410.4	3073.5	3851.6	2677.9	4609.8	2520.7	1120.7	3457.5
36.8	357.0	687.3	487.6	176.8	481.0	242.6	725.7	218.9	123.0	115.1
219.1	2662.0	3842.9	3216.8	2142.1	2812.7	2183.6	3862.5	1758.0	1964.1	2780.1
3197.4	4524.5	5745.3	4501.6	3735.4	4179.9	4318.1	5312.6	3789.5	2818.0	5030.8
9739.1	3790.6	4034.0	3619.8	3142.8	3705.0	3628.4	3926.7	4992.1	4016.3	3843.6
1412.1	4337.5	6411.5	4124.7	3527.7	4884.6	3103.3	5692.1	3492.5	1824.2	4532.2
6626.6	4803.6	5542.5	4004.5	3648.5	4251.2	3355.2	5010.1	3818.8	2475.2	4461.7
1447.8	4139.3	4439.8	4016.7	3873.5	4060.0	4172.8	3930.1	3834.1	2329.0	3907.4
4714.8	2682.6	3353.0	2888.7	3308.0	3345.9	3352.5	3381.5	1973.7	961.5	2796.1
757.3	4136.6	5574.9	5605.1	4435.3	5298.3	4907.5	6008.7	3354.5	1880.0	6108.4
948.7	5935.2	6910.9	5583.8	5096.3	5961.1	6297.2	6567.6	4703.5	2878.9	6168.2
2216.0	7716.1	9170.0	8767.2	7155.6	7738.1	7354.8	8032.1	6529.2	6563.8	8550.2
47.5	3912.3	4925.3	3564.6	2575.5	3787.3	2923.3	4889.1	2236.7	1776.1	3113.6
11343.1	7262.9	6888.2	6030.8	5178.4	5860.1	5477.5	6928.1	8652.3	7293.5	7254.8
78.6	1813.7	3088.4	1619.9	1073.2	1901.0	1001.3	3457.2	965.0	585.2	1739.7

2491.4	3898.6	4069.1
5608.7	4515.2	5412.5
8298.0	8360.6	12979.2
1245.9	1882.3	2080.3
6440.0	5225.5	6909.3
1599.8	2130.3	2721.4
6170.9	6941.6	7640.6
4684.8	2774.8	4694.0
2253.8	856.7	1679.5
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4004.4	3424.1	4557.5
4149.6	2727.1	4392.4
4465.3	2344.4	3493.0
5724.0	5690.5	6743.6
7683.3	5100.1	6602.4
4298.2	3590.8	4061.6
3348.5	4233.8	2797.7
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2621.6	1897.5	2744.6
4402.2	5036.7	6200.6
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590.2	347.8	473.0
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5061.0	3671.3	4948.7
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6441.8	5033.3	8361.6
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FJ375788.1 gg_id:331828 and prevalence blaTEM genes polar bear feces clone PBF_b17 FJ3757
X68174.1 gg_id:16213 Clostridium baratii str. ATCC27638 X68174
AM183061.1 gg_id:248563 and its spatial composts compost clone SMB82 AM183
EU464172.1 gg_id:289404 reticulated giraffe feces clone gir_aah95e03 EU464
EU473287.1 gg_id:296539 giant panda feces clone GP_1aaa04b12 EU473
EU773016.1 gg_id:333228 Banteng feces clone BG_aaa01d12.Contig1 EU773
EU473216.1 gg_id:287467 giant panda feces clone GP_1aaa01d05 EU473
AB018184.1 gg_id:40062 Eubacterium multiforme str. JCM 6484 AB018
EF559177.1 gg_id:223161 mesophilic anaerobic digester clone G35_D8_H_B_B06 EF5591
EU474087.1 gg_id:295458 giant panda feces clone GP_2aaa02h06 EU474
GQ492949.1 gg_id:569263 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ881333.1 gg_id:433124 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU473365.1 gg_id:290438 giant panda feces clone GP_1aaa02b03 EU473
EU459334.1 gg_id:287565 hedgehog feces clone HH_aai36f05 EU459
DQ015563.1 gg_id:133360 mouse cecum clone M3_f01_1 DQ015
EU471447.1 gg_id:291025 spectacled bear feces clone SB_2aaa03f07 EU471
EU462622.1 gg_id:302041 Sumatran orangutan feces clone orang2_aai66c04 EU462
EU472577.1 gg_id:289501 Angola colobus feces clone EAC_2_aaa03a09 EU472
EU473337.1 gg_id:292010 giant panda feces clone GP_1aaa01h01 EU473
FJ682831.1 gg_id:530824 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FM873505.1 gg_id:359728 occupant source house floor dust clone FD04G02 FM873
GQ007726.1 gg_id:501938 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ007
FJ681425.1 gg_id:525936 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
EU473883.1 gg_id:301102 giant panda feces clone GP_2aaa04c03 EU473
EU762963.1 gg_id:329216 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
DQ793454.1 gg_id:187953 human fecal clone RL199_aaj43h11 DQ793
EU460613.1 gg_id:295137 polar bear feces clone PB2_aai23d09 EU460
EU473225.1 gg_id:288164 giant panda feces clone GP_1aaa01d11 EU473
EU763600.1 gg_id:340717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ683685.1 gg_id:531765 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
EU474080.1 gg_id:290462 giant panda feces clone GP_2aaa03d09 EU474
DQ325781.1 gg_id:149036 Metagenomic gut microbiome healthy human stool clone B469 DQ325
EU473304.1 gg_id:289102 giant panda feces clone GP_1aaa04a09 EU473
FJ684155.1 gg_id:524467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ680008.1 gg_id:525078 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
EU459342.1 gg_id:293771 hedgehog feces clone HH_aai36g12 EU459
EU473952.1 gg_id:294441 giant panda feces clone GP_2aaa01e11 EU473
EU473891.1 gg_id:289769 giant panda feces clone GP_2aaa01h11 EU473
EU474127.1 gg_id:295740 giant panda feces clone GP_2aaa01b01 EU474
EU772351.1 gg_id:313142 Babirusa feces clone BARB_aaa01b09 EU772
GQ898543.1 gg_id:541594 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898

3644.0	3235.5	4788.0	3703.9	3069.0	4147.4	3208.7	4096.2	2555.8	1363.4	3405.5
273.3	2445.8	3637.6	2498.4	1686.0	2522.7	1906.3	3368.4	1640.2	1429.0	2987.5
46.9	1485.0	2778.8	2215.2	1492.7	2024.7	2168.2	2607.1	713.0	705.3	1665.9
149.8	2224.5	2951.6	2037.9	1570.5	2186.6	1451.7	3191.8	1548.0	816.1	2082.0
20817.7	6665.5	5517.9	5554.3	5943.2	5448.3	5452.8	5049.5	7270.8	6441.8	7065.9
2665.7	5338.8	5786.8	5743.6	4606.6	5454.9	5158.9	5452.3	5031.9	4405.5	5924.7
77.7	3443.2	3479.5	3004.4	2699.2	2830.6	2288.3	3794.7	2110.7	979.8	2770.2
7989.9	4034.6	4631.2	3965.3	3342.7	3911.2	3906.0	4749.1	4315.7	3221.4	4334.2
32.9	184.3	258.7	142.0	253.7	148.0	220.8	264.3	84.9	24.8	69.8
254.0	6231.2	5562.9	5866.3	7467.1	5356.7	5968.2	5943.6	3635.7	2476.9	5059.4
7992.4	6287.7	7237.0	5631.7	5222.8	5618.3	5358.3	5732.2	6099.0	4143.9	6789.3
2668.0	1847.2	2260.2	2149.1	2137.7	2253.6	1961.7	2766.4	1345.7	566.5	1564.0
3596.8	3394.3	4654.4	4138.3	2848.6	3669.9	2613.9	5352.6	2601.5	2089.8	4295.2
49.2	1618.8	1944.0	1652.7	942.3	1499.0	1323.6	2342.3	955.7	510.4	1288.1
577.1	2249.8	2617.6	2565.2	2655.2	2337.3	1944.4	3591.5	1420.3	711.2	1230.5
530.3	4114.9	5702.9	5036.3	3972.2	4722.1	4125.8	6237.2	3240.0	1829.3	5976.1
772.3	3478.0	5978.6	3106.8	2219.9	3806.9	1765.3	3958.3	1916.1	1095.8	3570.5
2417.0	3089.3	2913.4	3058.2	2833.3	2469.7	2541.9	3199.2	3160.2	2301.8	2832.1
4217.6	4494.0	4239.8	3810.1	3787.3	3676.5	3475.1	4382.9	4726.6	2488.5	3781.7
371.5	3423.3	3545.5	3062.1	3750.2	2962.1	3763.9	3475.1	2804.4	4416.2	2687.3
64.7	1744.6	2997.5	1600.9	1104.7	1814.9	1192.7	797.4	1114.6	159.4	1693.3
3399.4	5271.8	4612.5	4100.4	4071.0	4092.8	3656.0	4682.2	4083.5	1553.7	4649.6
10743.8	6090.0	6375.4	5902.5	5926.7	5185.7	5339.7	6358.0	6364.2	4974.4	8146.3
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4450.5	3420.9	3858.1	3788.0	3161.0	3751.4	3303.1	3902.4	2887.0	2238.9	2885.8
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8742.7	4652.0	6456.9	4887.9	3729.3	4307.2	4334.4	4435.8	4722.3	3876.5	6328.7
51.0	2878.9	3796.3	2545.1	2105.3	2607.4	1822.3	3613.3	1554.9	859.7	2163.3
1857.0	4478.1	5821.7	5537.8	2824.3	4642.9	4269.2	5485.4	4367.7	2647.0	5499.1
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3501.3	7743.9	8690.7	6714.8	5348.9	7182.9	5430.5	6966.6	7777.5	8817.7	10606.7

3691.8	3416.4	3838.2
3052.2	2422.0	2899.8
2856.4	1691.4	2569.7
2733.0	2654.0	3518.6
4943.8	6284.0	5376.8
4995.4	4536.8	4680.5
3153.3	2067.4	3851.4
3990.5	4496.7	4453.6
359.9	156.2	334.0
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3867.4	3216.9	3535.2
3603.4	3963.2	5519.1
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EU475622.1 gg_id:301597 babirusa feces clone BARB_aaa03f01 EU475
FJ681136.1 gg_id:512574 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
DQ801475.1 gg_id:193154 human fecal clone RL388_aao96a07 DQ801
X77842.1 gg_id:16234 Clostridium sardiniense str. DSM 599 X7784
GQ458227.1 gg_id:512965 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
DQ808504.1 gg_id:182358 human fecal clone RL239_aaj09d12 DQ808
EU460604.1 gg_id:290233 polar bear feces clone PB2_aai23c07 EU460
EU774647.1 gg_id:324893 Angola Colobus feces clone EAC_1aaa02a10 EU774
FJ683095.1 gg_id:514947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
GQ249583.1 gg_id:509782 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
EU473255.1 gg_id:290901 giant panda feces clone GP_1aaa01f11 EU473
DQ817220.1 gg_id:169629 mouse cecum clone aaa70b08 DQ817
GQ359970.1 gg_id:582866 Microbial intestinal contents and mucus yel catfish (Pelteobagrus fulvidraco) intestir GQ359
FJ682482.1 gg_id:524162 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EU473352.1 gg_id:287684 giant panda feces clone GP_1aaa02h03 EU473
AB018185.1 gg_id:31869 Eubacterium nitritogenes str. JCM 6485 AB018
DQ796773.1 gg_id:182452 human fecal clone RL179_aao54c09 DQ796
EU772391.1 gg_id:315755 Hamadryas Baboon feces clone BAZ_e03 EU772
EU869238.1 gg_id:306622 Clostridium sp. str. CM-C81 EU869
DQ129391.1 gg_id:138056 microarray level air two cities Texas urban aerosol clone AKIW654 DQ129
EU777055.1 gg_id:348224 Okapi feces clone OK2_b02_1 EU777
DQ815970.1 gg_id:164332 mouse cecum clone aaa85a09 DQ815
FJ678772.1 gg_id:525918 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ800727.1 gg_id:190296 human fecal clone RL183_aao02f08 DQ800
EU473932.1 gg_id:301964 giant panda feces clone GP_2aaa03b11 EU473
EU459282.1 gg_id:290241 hedgehog feces clone HH_aai35e07 EU459
GU293208.1 gg_id:538968 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EU474817.1 gg_id:297379 takin feces clone TAK_aaa02d10 EU474
DQ815984.1 gg_id:171437 mouse cecum clone aaa85c02 DQ815
EU474090.1 gg_id:295920 giant panda feces clone GP_2aaa01c04 EU474
FJ678171.1 gg_id:518018 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU761992.1 gg_id:333674 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
NR_026149.1 gg_id:534306 Clostridium quinii str. DSM 6736 NR_02
GQ492067.1 gg_id:574003 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU473929.1 gg_id:288858 giant panda feces clone GP_2aaa01h06 EU473
DQ807486.1 gg_id:180069 human fecal clone RL307_aam07b11 DQ807
EU777067.1 gg_id:338591 Okapi feces clone OK2_d10 EU777
FM873847.1 gg_id:359116 occupant source house mattress dust clone MB01G06 FM873
EU779088.1 gg_id:317926 Takin feces clone TAK_aaa02h01 EU779
FJ679435.1 gg_id:517527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6794
FJ685390.1 gg_id:512217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853

5028.0	5845.2	6313.8	6480.4	6075.1	5858.1	6132.5	6289.8	5850.8	6287.9	7119.9
4193.6	3199.7	2705.4	2567.8	2579.8	2186.8	2283.4	2856.7	2506.4	2125.2	2303.5
3319.4	3698.9	5693.3	5013.1	3717.6	5541.0	5438.8	4993.0	4058.0	2300.1	7348.7
78.0	533.5	665.6	519.9	279.2	544.9	403.7	997.0	235.5	141.1	320.8
3464.2	4627.7	4300.4	4346.8	5237.7	5155.1	4789.9	4803.4	4822.7	4481.0	4999.3
158.3	3995.5	5390.6	4353.8	3128.9	3763.9	3844.7	4935.7	4527.2	3585.8	4762.4
368.5	2547.4	3042.4	2656.9	2011.5	2807.7	2052.2	3430.8	1474.3	646.9	2529.9
1121.1	3665.6	3704.9	2607.9	3374.3	2962.1	2883.1	3439.5	3856.8	3357.3	2561.4
3557.9	4696.6	4767.5	4372.7	4486.1	3936.2	4671.3	4047.2	4372.5	3034.2	5977.7
356.0	2149.7	3922.8	2668.0	1911.4	2827.2	1972.4	3419.1	1654.5	1488.6	2660.0
10496.2	5502.7	6215.0	6480.8	5630.6	5413.7	5299.3	6317.2	4433.3	3645.0	6555.4
231.0	988.5	1422.1	1046.3	851.9	979.6	821.7	1881.5	731.3	409.5	862.8
91.2	3540.0	5213.4	3751.8	2902.3	3860.6	3431.4	4986.0	2381.0	1814.3	3050.8
4104.7	6736.5	6422.1	5877.8	6202.4	6175.5	7704.3	7344.7	6242.1	4373.3	9023.0
5735.9	2993.8	4045.7	3293.8	2300.5	2835.9	3125.8	3502.2	2497.2	1976.8	3126.5
909.3	3173.7	3485.6	3710.0	4423.9	3403.8	4069.0	4001.2	4411.1	1301.9	4082.5
366.7	4333.6	5139.1	4352.5	3788.6	4681.6	5059.8	5206.8	2736.2	3012.3	4358.0
2325.7	6602.5	7384.8	5930.9	4665.9	6311.6	5157.8	6295.3	5399.6	4232.1	7337.9
42.3	1804.3	2468.5	2253.1	1268.0	1948.1	1183.8	3260.5	977.6	491.6	1663.8
778.2	4214.8	5593.8	3768.6	3940.7	4331.0	4184.9	4857.9	3222.4	1835.3	3679.6
438.3	3030.8	2918.6	2646.1	3519.8	2777.5	2481.0	3946.7	2594.4	1513.2	2377.2
4225.2	4122.5	5565.7	3868.5	3201.6	3979.6	3938.7	4988.9	4674.3	3688.1	3944.2
131.2	1367.0	2185.7	1334.0	1474.0	1533.3	1588.9	1731.5	838.2	425.4	1524.5
2280.9	3254.7	4449.0	3808.1	2185.1	3425.3	3492.4	2736.6	2802.8	1330.6	3785.6
10164.7	6051.2	5289.3	6204.4	6370.1	5398.6	5129.2	5904.7	6343.6	4519.7	7673.4
57.1	1779.6	2775.7	1458.3	1078.6	1644.6	1163.1	2506.9	859.1	447.8	1529.3
80.9	3309.4	5132.9	3214.5	2956.9	3852.8	2753.8	5271.1	2439.1	1331.9	3575.8
196.4	5876.1	7330.2	4751.1	4519.4	5798.2	3943.0	7497.1	5230.3	5975.6	6052.8
43.1	72.1	63.5	41.0	60.0	36.3	56.6	135.4	35.8	28.7	53.7
6201.5	6446.6	6454.3	6307.1	6224.1	6031.0	5803.9	6353.3	5805.8	4904.0	7178.0
925.3	6917.6	8694.7	6994.6	5735.4	6976.4	4807.0	7588.5	4706.6	5411.5	8370.4
885.1	1816.9	2811.1	2092.6	1683.2	2204.3	1826.1	2435.2	1200.5	1293.2	1861.7
162.5	1699.6	2678.5	1715.7	1581.9	1828.8	1280.8	2811.4	1075.5	542.6	1579.1
10402.8	6450.9	6562.9	7372.9	6340.8	6415.0	7076.2	6466.4	7236.8	5349.9	8012.8
81.1	2869.1	4856.8	2787.1	2039.3	2996.8	2444.5	3478.3	1532.3	835.6	3312.5
201.2	6049.4	7213.1	5713.6	3767.2	5722.8	4345.8	5716.0	5341.0	4319.7	6205.2
6613.0	2550.5	3505.9	2997.5	2635.9	2704.2	2921.9	3292.5	3472.8	2250.8	2829.8
97.0	1960.1	3094.7	1646.4	2543.2	3694.9	1397.1	1868.2	1596.3	406.7	1765.1
81.8	2346.2	3224.0	2587.3	1905.7	2958.0	2157.5	3271.4	1569.6	751.2	2832.7
2027.0	4216.6	6184.8	4291.7	3421.8	4418.5	2777.4	4945.2	2700.6	1578.5	4886.1
2210.7	4826.4	6448.4	4977.9	3728.8	5096.4	3390.5	5640.4	3133.2	2974.4	5691.6

6395.8	6898.4	6441.8
2040.4	2707.5	2486.9
4538.0	5243.2	4583.7
733.7	677.4	1171.1
4447.5	4192.5	5571.1
4393.4	3938.8	4714.3
3025.2	2951.1	2862.2
2936.4	3408.3	3487.9
2939.2	5075.9	4076.2
3040.6	2097.8	2682.8
5610.2	6716.3	6698.8
1268.7	1055.9	1280.2
4676.5	3343.8	4665.9
6753.6	5721.5	8975.2
2767.8	4036.5	3901.0
3710.6	4231.9	4413.0
5026.2	5911.5	6338.9
6069.7	5664.8	6551.4
2290.7	1563.5	2062.5
4772.2	4262.7	5031.4
3606.1	3030.9	5311.0
4176.0	4739.5	4813.5
1186.8	1384.8	2051.8
2937.7	3625.9	3874.4
6206.0	6179.4	5977.7
2024.4	1344.7	1632.6
3915.8	3462.1	4682.2
6130.5	5043.6	7673.1
61.1	70.0	63.4
5854.5	6491.5	6587.0
8009.1	5544.0	7186.5
2433.4	1655.8	2595.2
2642.1	1877.0	2116.2
5993.3	7598.0	6900.1
3128.4	2733.4	3575.3
4837.2	4865.1	4955.7
3337.3	3162.6	3759.8
2076.0	1402.6	2523.4
2742.6	2123.8	3566.7
4990.1	3962.1	4586.2
5856.1	4304.8	5413.7

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FJ957496.1 gg_id:426638 Microbial Anaerobes Spacecraft Clean Rooms spacecraft clean room clone JPL-S2_C1: FJ9574
AB020189.1 gg_id:34846 Clostridium beijerinckii str. JCM 7844 AB0201
X77843.1 gg_id:16243 Clostridium caliptrosporum str. DSM 5905 X77843
NR_026013.1 gg_id:565322 Clostridium chauvoei str. 2585; ATCC 10092 NR_02
EU474076.1 gg_id:287515 giant panda feces clone GP_2aaa03a12 EU474
EU777692.1 gg_id:307341 Polar bear feces clone PB2_aai22c01 EU777
DQ796807.1 gg_id:184442 human fecal clone RL179_aao54g10 DQ796
FJ673626.1 gg_id:529116 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ817225.1 gg_id:168712 mouse cecum clone aaa70c01 DQ817
EU474705.1 gg_id:297093 Indian rhinoceros feces clone IR_aaa03b10 EU474
EU473278.1 gg_id:289356 giant panda feces clone GP_1aaa04e09 EU473
FJ681715.1 gg_id:529490 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ679026.1 gg_id:514689 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
DQ808581.1 gg_id:195664 human fecal clone RL239_aaj10d07 DQ808
EU777219.1 gg_id:319567 Okapi feces clone OK2_b04 EU777
EU473193.1 gg_id:290998 giant panda feces clone GP_1aaa01f06 EU473
EU473368.1 gg_id:287591 giant panda feces clone GP_1aaa01h05 EU473
EU777716.1 gg_id:338956 Polar bear feces clone PB1_aai28h01 EU777
AM183092.1 gg_id:252144 and its spatial composts compost clone SMC120 AM183
EU459246.1 gg_id:289622 hedgehog feces clone HH_aai34f09 EU459
AM998793.1 gg_id:283776 Clostridium saccharobutylicum str. Ox29 AM998
CP001056.1 gg_id:286203 Clostridium botulinum B str. Eklund 17B CP001
DQ326262.1 gg_id:150131 Metagenomic gut microbiome healthy human stool clone C203 DQ326
EU473286.1 gg_id:289372 giant panda feces clone GP_1aaa03c01 EU473
EU473395.1 gg_id:298080 giant panda feces clone GP_1aaa01d09 EU473
DQ810116.1 gg_id:196719 human fecal clone RL184_aao68c04 DQ810
FJ678592.1 gg_id:519790 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ808820.1 gg_id:194032 human fecal clone RL243_aai85f11 DQ808
FJ680093.1 gg_id:515102 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
DQ793612.1 gg_id:197786 human fecal clone RL246_aai74d08 DQ793
EU775619.1 gg_id:330962 Hedgehog feces clone HH_aai35b03 EU775
X68175.1 gg_id:16232 Clostridium baratii str. ATCC43756 X68175
X97432.1 gg_id:16227 Clostridium vincentii X97432
FJ682951.1 gg_id:526262 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GU060306.1 gg_id:564332 Clostridium saccharobutylicum str. BS2 GU060
FJ880242.1 gg_id:429210 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ685096.1 gg_id:514508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
AY133085.1 gg_id:59906 TCE-contaminated site clone ccslm2120 AY133
EU473145.1 gg_id:295777 giant panda feces clone GP_1aaa01b06 EU473
DQ326540.1 gg_id:147920 Metagenomic gut microbiome healthy human stool clone C693 DQ326
FJ683485.1 gg_id:522966 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834

3040.3	4424.1	4882.5	4588.4	4092.7	5232.3	4577.9	4628.6	5964.8	3158.8	4427.1
1496.1	7139.0	9096.4	6996.4	5122.9	6598.0	5369.3	7298.0	5771.8	3352.9	8372.8
956.8	5080.2	8152.4	5623.9	3042.5	5503.8	3494.3	6311.9	2892.6	1170.4	6227.3
172.2	2660.8	4739.4	2430.7	2463.0	3171.4	1706.5	3875.7	2403.0	847.3	2399.3
53.0	1977.9	2960.8	1721.4	1618.1	1878.3	1256.5	2710.1	1253.0	610.9	1341.2
12093.9	5452.1	5664.8	5473.4	5753.4	5248.2	5951.9	5471.8	6182.0	5490.2	6230.1
665.8	2462.7	4784.2	3750.3	2205.9	2973.3	2596.4	3820.6	1557.8	2339.7	3510.3
3948.6	6185.7	7680.0	6413.2	4669.6	6173.2	4390.0	6793.9	5005.3	3061.8	6981.5
7001.1	5811.0	7073.3	6778.2	6034.4	5999.5	6308.0	6519.2	8025.9	6713.7	7513.7
121.1	5521.4	7313.9	5497.4	3845.6	5450.2	4272.4	6569.8	3130.5	1616.3	6150.9
63.3	2365.0	3370.9	2103.2	1693.3	2201.2	1534.0	3087.9	1480.9	701.0	1839.5
5892.4	4295.7	4563.2	4823.8	4605.4	4187.1	4474.7	4654.0	5767.3	3988.3	5247.7
833.4	5044.2	7494.6	5697.5	3524.0	5756.7	4194.3	6085.9	3894.4	4296.2	6840.4
89.2	2181.0	3115.5	2486.3	2348.7	2418.1	3093.6	2634.5	1260.4	1135.7	1502.7
39.8	2830.3	3223.9	2610.7	2552.2	2688.2	2110.4	3929.5	2064.3	1132.1	2620.9
208.8	3136.8	4427.4	2822.8	3300.2	3155.4	2467.0	3824.7	2264.6	1263.3	2946.8
279.0	2033.5	3104.6	1677.3	1808.6	2038.8	1093.5	2852.2	1655.6	547.8	1828.0
272.8	2700.5	4367.9	2941.7	2536.3	3484.5	2531.8	4554.2	1965.3	1309.3	3430.0
757.2	4049.0	4623.2	3817.0	4508.6	3702.3	4524.8	4794.1	3339.8	3934.5	4612.7
258.9	2534.4	4719.6	2642.1	1726.2	2812.5	1402.8	3742.6	1483.1	602.5	2970.6
49.8	2851.3	5714.5	2987.8	1581.5	3490.7	1830.2	4207.2	1244.3	545.7	3780.6
321.6	4041.4	5603.8	4166.5	3099.8	4157.4	3373.1	5682.3	2683.4	2930.8	4794.2
854.9	949.1	1513.1	969.6	1094.6	1108.1	763.2	1765.2	587.6	263.3	465.9
3983.5	5544.3	5106.7	5324.8	5130.7	4477.8	4614.9	4897.3	4694.6	4008.4	6623.8
6277.1	4317.8	4615.3	4177.6	3979.0	4413.2	4312.8	4354.4	6025.4	4364.6	4605.5
2201.6	2149.5	2144.3	433.2	1925.6	1875.2	2507.7	2139.4	2318.5	949.6	2775.1
22208.0	8756.5	10459.9	9703.8	7397.7	8960.4	8220.3	8977.6	9608.1	7100.8	12112.3
8580.5	2202.9	2587.3	2310.5	2224.6	2657.2	671.3	2697.5	1785.8	1439.6	1951.1
1909.3	5387.3	7258.5	5989.4	4077.5	5773.0	3844.8	6484.0	3687.2	4617.9	7090.0
139.5	626.8	1094.9	747.8	714.6	887.9	568.1	889.1	427.0	146.8	663.5
514.0	5505.7	8079.3	6933.4	4612.8	6849.4	5459.4	7111.7	4766.8	2568.9	7364.3
10344.2	5914.1	6450.7	6446.4	5032.1	5897.5	5912.7	6600.1	7332.7	5891.1	8113.9
520.4	3965.9	4899.3	5074.0	5475.4	4643.9	5810.1	5318.6	3632.8	1532.8	3514.8
396.8	7850.4	8942.2	9906.6	6308.9	8436.5	8267.7	8272.6	6936.9	7444.1	9865.5
757.9	4380.0	7525.3	4994.2	2135.5	5172.8	3171.8	6146.9	2104.0	742.4	5969.4
1699.9	3708.5	5067.1	4460.2	3513.2	4389.5	3519.8	5052.0	3292.6	1810.3	4622.9
69.5	3006.1	4347.9	2564.4	1487.0	2818.8	2213.2	3537.7	1901.2	997.2	2585.1
134.0	8212.7	10739.4	9103.3	5064.7	8468.6	5875.7	9213.1	5418.6	3437.6	10710.1
121.9	3799.0	4104.0	2705.6	2495.3	2844.7	2435.2	4243.4	3287.3	2457.8	2305.7
10117.6	5096.5	6768.1	5760.1	5251.1	6729.0	5453.9	6083.4	4378.2	7729.1	6207.5
1816.2	3521.6	4571.0	3362.7	2928.1	3553.1	3148.6	3789.9	3086.5	2480.0	3393.4

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5860.4	3725.4	5239.6
3219.1	1984.4	2976.2
2505.0	1234.8	2347.9
5558.8	5880.2	5903.7
3317.6	4066.0	3884.6
6565.2	5403.8	6275.4
6547.0	3869.2	8381.8
7478.4	3919.9	5949.4
2768.4	1312.2	2655.9
4070.9	4930.9	4924.4
6359.9	5243.7	6681.8
2424.6	2319.9	3454.7
3493.3	1949.3	4175.4
3099.5	2358.3	3453.6
1907.1	1364.7	1817.6
3317.6	3068.2	3775.7
5000.6	3742.9	4767.8
3247.9	2008.3	2925.2
3925.6	2688.1	3238.7
4901.0	3784.8	5576.5
1301.0	888.4	847.0
5220.9	4676.4	4762.2
4228.6	4723.2	5173.3
1921.1	1783.7	2073.9
9797.7	9938.1	10165.9
2274.3	2963.1	2422.0
6387.3	4634.4	6028.6
634.3	800.7	838.9
6059.6	4931.0	5485.6
5890.6	6587.0	6373.8
5715.4	4667.9	5690.4
8092.2	7689.9	8663.3
5178.6	3335.1	4715.3
5367.2	4061.6	5286.2
3012.1	2710.9	3760.2
9350.3	6154.2	8621.9
3668.1	2649.0	3303.7
5641.9	5974.3	7369.1
3816.6	4167.4	3561.9

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AB020191.1 gg_id:49549 Clostridium beijerinckii str. JCM 7847 AB020
EU463601.1 gg_id:297513 domesticated horse feces clone horsej_aai89e09 EU463
EU775687.1 gg_id:312729 Hedgehog feces clone HH_aai33b04 EU775
DQ800651.1 gg_id:179521 human fecal clone RL183_aao01e12 DQ800
FJ682021.1 gg_id:529108 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU474123.1 gg_id:295402 giant panda feces clone GP_2aaa03d05 EU474
EU474687.1 gg_id:294960 Indian rhinoceros feces clone IR_aaa04a12 EU474
FJ683569.1 gg_id:526389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
GQ868434.1 gg_id:558476 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC512 GQ868
FJ684781.1 gg_id:524895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ196631.1 gg_id:166896 Clostridium sp. str. BL-24 DQ196
AJ420008.1 gg_id:76200 Clostridium colicanis str. DSM 13634 AJ420
DQ808612.1 gg_id:196359 human fecal clone RL239_aaj10h09 DQ808
FJ678831.1 gg_id:518772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EU459179.1 gg_id:299482 hedgehog feces clone HH_aai33d05 EU459
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EU473204.1 gg_id:288298 giant panda feces clone GP_1aaa04a04 EU473
EU460605.1 gg_id:296166 polar bear feces clone PB2_aai23c08 EU460
AM183065.1 gg_id:237935 and its spatial composts compost clone SMB112 AM183
FJ681311.1 gg_id:530465 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EU473935.1 gg_id:291622 giant panda feces clone GP_2aaa04g05 EU473
FM873828.1 gg_id:361822 occupant source house mattress dust clone MB01D07 FM873
DQ800217.1 gg_id:191808 human fecal clone RL303_aal69g05 DQ800
DQ800538.1 gg_id:184824 human fecal clone RL183_aah29c10 DQ800
EU474813.1 gg_id:297938 takin feces clone TAK_aaa04g11 EU474
EU773874.1 gg_id:326918 Cheetah feces clone CE3_aai05f04 EU773
FJ960326.1 gg_id:571221 bottlenose dolphin upper respiratory tract blowhole clone D9A4_224 FJ9603
EU470820.1 gg_id:295850 red panda feces clone RP_2aaa01e02 EU470
DQ015110.1 gg_id:130878 mouse cecum clone M2_e05_1 DQ015
FJ680768.1 gg_id:511288 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
AJ810554.1 gg_id:104410 superficial sediments clone AJ8105
EU475686.1 gg_id:303104 babirusa feces clone BARB_aaa03c12 EU475
EU459347.1 gg_id:296403 hedgehog feces clone HH_aai36h12 EU459
EU766580.1 gg_id:348914 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU468766.1 gg_id:298784 okapi feces clone OK3_c11_1 EU468
GQ867474.1 gg_id:582379 and prevalence blaTEM genes Arctic seals colon content clone CSG45 GQ867
EU460716.1 gg_id:299954 polar bear feces clone PB2_aai24h05 EU460
AB198536.1 gg_id:135311 termite gut wall fraction clone RsW02-061 AB198
FJ375811.1 gg_id:332200 and prevalence blaTEM genes polar bear feces clone PBF_b42 FJ3758

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117.3	2017.6	3155.1	1894.7	1429.8	2151.9	1736.8	2722.8	1219.3	487.5	2325.5
5394.8	3891.9	5298.4	4233.9	4010.2	4497.9	4125.1	5613.2	3026.0	4747.8	4640.3
1155.7	5158.1	6028.2	5147.1	4921.2	5017.8	5642.5	5035.8	3177.7	4797.9	5291.4
7917.7	2782.8	3759.1	2769.7	3003.4	3289.0	2643.8	3747.2	2759.2	1222.6	2743.1
228.5	2850.5	3858.5	3431.3	3258.2	3304.3	3518.1	4482.4	3184.3	1961.0	3016.3
394.5	5886.8	7801.5	5644.9	5355.3	6356.3	6040.2	7125.9	4782.9	6402.1	6394.9
10866.0	4292.1	5018.6	4682.8	4368.9	4646.4	4827.8	4285.2	4931.4	4155.4	6023.7
3641.5	3446.5	3038.9	3401.1	3298.3	3834.6	3718.4	3211.8	3655.6	2592.4	3701.1
5076.4	7703.1	8999.1	6824.6	5884.6	7468.8	5996.6	7962.1	8322.0	6690.1	8596.4
101.5	2598.5	3366.7	2140.7	1747.4	2126.4	1685.2	3480.9	1208.9	692.2	1808.7
255.1	2223.5	3104.2	2588.5	1476.2	2815.0	1824.5	2844.5	1365.8	480.2	2461.2
260.9	3463.6	4464.5	3559.7	2817.8	3543.8	3122.9	4180.0	2544.7	2201.9	3312.5
2884.9	2681.3	2922.7	3048.8	2262.4	2232.4	2299.7	2601.2	2299.4	1509.4	3001.1
358.0	2693.0	3308.8	2022.9	1614.7	2508.0	1680.5	2792.9	2583.2	3730.1	4460.8
562.0	2978.3	4015.8	2653.9	1770.1	2760.9	2187.1	3360.9	1627.4	792.7	2871.9
15528.0	4679.0	4608.8	4151.5	4383.5	3629.8	3524.8	4283.2	4264.1	3970.1	4782.4
7088.4	3904.3	4734.4	4081.7	3834.7	3558.6	3717.5	4132.6	3954.3	5841.1	5125.5
240.7	5668.8	5835.3	4339.2	3298.2	4264.6	2884.0	4492.1	4714.2	6071.7	5493.1
46.4	923.2	1708.2	995.2	430.5	1133.8	644.3	1337.9	482.0	137.3	813.0
56.5	2087.5	3167.4	2296.5	1042.6	2405.2	1250.3	2788.8	663.3	881.4	2888.2
2888.7	3324.8	4397.9	3779.0	3066.9	3636.8	2945.6	4264.5	3183.4	3692.4	3627.0
9513.1	5619.7	3873.0	5330.9	4667.0	4051.5	5086.0	4375.8	5678.8	4981.7	6673.3
278.6	4098.8	6850.8	3608.0	3495.0	4491.7	2607.5	5658.8	2433.2	4005.2	4859.1
2043.2	4310.2	4827.2	3315.1	3398.3	4210.0	3254.8	4499.9	3031.7	4809.9	3219.1
4627.8	2032.4	3151.2	2375.4	2795.7	3095.2	2329.4	2761.6	2141.5	2561.0	2838.9
2428.3	6216.1	6533.5	5023.7	4344.1	5822.4	4974.1	6820.3	5320.5	5067.7	5439.6
510.1	3176.1	4801.0	3259.1	2171.7	3351.1	2433.1	4795.1	1861.2	905.5	3471.4
528.9	3963.6	5144.7	3852.4	2471.7	3912.6	3048.5	5196.4	2534.7	1274.9	3820.9
190.1	3825.1	5847.2	3806.9	3244.9	4165.0	2252.1	4857.7	2666.7	1251.9	3855.0
6386.8	4539.9	5756.3	4942.5	4326.2	4894.4	4115.4	5607.3	4016.3	3111.2	5554.1
10285.6	8176.7	7891.2	6775.5	5753.5	7301.1	6315.3	6816.4	9455.8	7879.5	8264.0
59.8	319.7	789.6	454.2	200.8	404.6	174.1	543.3	154.4	96.4	374.3
156.7	2150.8	1637.4	1276.1	2257.0	1673.0	1373.4	3253.5	1292.1	882.5	1226.9
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3203.3	5183.2	5180.7	5655.1	5373.1	5431.6	5812.2	5883.5	4700.1	3688.7	5834.9
111.7	1771.1	1569.0	1387.3	2017.9	1267.3	1304.0	2433.6	1194.8	1133.3	1169.2
37.5	95.1	136.6	92.5	80.4	135.4	102.6	101.7	63.7	45.4	57.8
1649.5	4678.6	5331.7	5141.2	5320.3	4839.3	5821.6	6308.3	4836.5	2829.4	4530.9

7982.7	7666.9	7414.3
2622.1	2299.5	2563.8
4205.1	5410.1	5361.0
4707.8	6556.9	6012.7
2835.7	2779.1	2489.2
3950.9	3451.7	3491.6
4644.8	5885.2	8058.8
4102.0	5396.4	4996.1
2799.9	4332.8	3061.5
7470.4	6618.7	8293.8
3864.6	1699.1	2824.1
2803.1	2029.6	2463.2
3945.9	2928.3	3745.8
2227.0	3194.7	2350.5
2344.8	2622.6	3349.0
3354.7	2482.1	3145.2
4397.0	4169.6	3828.7
3750.4	4153.0	4784.9
5037.5	3608.6	3689.3
910.2	827.8	991.9
2581.2	2180.5	3593.7
3495.2	4157.6	4574.4
4597.2	5190.7	4533.9
5311.7	4201.2	6562.3
4062.9	4212.6	5748.7
2523.0	4116.1	3835.7
5407.8	6422.4	8702.1
4309.7	2905.6	3596.5
4632.9	3787.0	4143.6
5002.6	2592.0	3759.0
4845.0	5239.5	5478.4
6909.4	8186.7	8088.7
179.2	358.5	498.5
1995.5	1587.7	2549.0
1985.5	2208.7	2467.4
674.6	461.9	793.7
4441.3	3750.4	5479.3
5402.4	5375.8	6615.6
1743.8	1526.6	3634.1
106.4	152.8	188.4
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EU468283.1 gg_id:299186 domesticated horse feces clone horsej_f05_2 EU468
EU475598.1 gg_id:302926 babirusa feces clone BARB_aaa04d08.Contig2 EU475
EU766310.1 gg_id:344545 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU475640.1 gg_id:302964 babirusa feces clone BARB_aaa01h01 EU475
GQ491217.1 gg_id:553388 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU460543.1 gg_id:300919 polar bear feces clone PB2_aai22d08 EU460
DQ796870.1 gg_id:184692 human fecal clone RL179_aao55f12 DQ796
EU472395.1 gg_id:288493 Angola colobus feces clone EAC_1aaa01b08 EU472
EU767428.1 gg_id:351406 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ672948.1 gg_id:508872 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
EU459194.1 gg_id:295462 hedgehog feces clone HH_aai33f07 EU459
FJ681981.1 gg_id:526708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU467719.1 gg_id:303332 bush dog feces clone bdog1_d08 EU467
EU528192.1 gg_id:287156 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
FJ366771.1 gg_id:359041 feces adult twins and mothers; TS27 clone TS27_a03f08 FJ3667
EU460503.1 gg_id:287887 polar bear feces clone PB2_aai21g09 EU460
DQ809722.1 gg_id:176126 human fecal clone RL184_aan83c03 DQ809
FJ375922.1 gg_id:309747 and prevalence blaTEM genes polar bear feces clone PBM_b9 FJ3759
AB075771.1 gg_id:46716 Clostridium sordellii str. ATCC 9714 AB075
DQ113681.1 gg_id:130854 dog colon clone C5-09 DQ113
FJ366569.1 gg_id:368997 feces adult twins and mothers; TS27 clone TS27_a01c06 FJ3665
GQ458231.1 gg_id:594005 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
FJ978707.1 gg_id:384411 feces clone CL_F_403 FJ9787
EU775276.1 gg_id:308502 Reticulated giraffe feces clone gir_aah94h12 EU775
FJ673530.1 gg_id:528464 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
EU468826.1 gg_id:291183 okapi feces clone OK3_c04_1 EU468
DQ445857.1 gg_id:156623 Clostridium sp. C01-2409 DQ445
DQ810015.1 gg_id:185149 human fecal clone RL184_aao67a12 DQ810
EU460560.1 gg_id:299990 polar bear feces clone PB2_aai22f08 EU460
EU775664.1 gg_id:337083 Hedgehog feces clone HH_aai35f05 EU775
FJ366714.1 gg_id:357630 feces adult twins and mothers; TS27 clone TS27_a03a04 FJ3667
EF682951.1 gg_id:247473 Eastern Mediterranean atmosphere clone F13_9D_FL EF6829
GQ868388.1 gg_id:541925 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC65 GQ868
FJ366695.1 gg_id:369406 feces adult twins and mothers; TS27 clone TS27_a02g04 FJ3666
EU463306.1 gg_id:291844 bush dog feces clone bdog1_aai77e10 EU463
FJ375874.1 gg_id:316634 and prevalence blaTEM genes polar bear feces clone PBF_d11 FJ3758
EU459287.1 gg_id:288071 hedgehog feces clone HH_aai35f07 EU459
EU475638.1 gg_id:295162 babirusa feces clone BARB_aaa02d07 EU475
EU763479.1 gg_id:349439 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ375912.1 gg_id:306812 and prevalence blaTEM genes polar bear feces clone PBM_a4 FJ3759
DQ798320.1 gg_id:179306 human fecal clone RL181_aah40f08 DQ798

729.5	4197.8	5097.6	4751.9	3923.1	4543.7	4490.3	4657.6	3686.4	2356.3	4494.1
700.4	3129.6	2921.0	2927.5	3256.7	2521.4	2648.6	3324.9	2249.9	2088.1	2592.7
66.3	243.6	360.8	210.3	281.7	296.7	187.1	662.2	192.5	240.4	272.0
9438.8	2800.6	2165.9	2010.4	2694.4	2042.8	1928.8	3292.2	2748.6	2256.1	3110.3
66.3	2217.0	2062.9	1086.2	1359.3	1543.5	945.2	1927.8	1868.8	1726.3	1127.1
31.0	1035.0	1043.8	543.4	1492.6	936.1	724.1	1424.6	826.8	495.7	546.1
34.4	126.2	60.1	26.6	127.2	58.3	41.3	271.2	62.4	37.9	79.0
74.2	1108.6	978.6	798.2	937.5	897.9	683.3	1653.3	641.2	421.6	716.3
13458.9	5499.3	5826.7	5694.5	5029.7	4866.5	4595.7	5014.7	5234.4	8635.2	6155.6
14221.2	7229.1	6581.6	7004.7	7261.9	6641.7	7167.0	6785.5	6833.1	7996.5	7883.7
293.3	2257.2	3842.5	2568.1	1692.9	2463.1	1490.6	3104.9	1812.5	967.0	3048.2
51.4	1875.9	2197.5	1691.8	1944.3	1347.0	1319.7	3086.1	1142.1	551.6	1455.9
128.9	2377.4	2182.4	1554.5	1864.6	2269.5	1766.9	1823.6	1554.1	1418.7	1228.6
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9485.9	4159.0	4530.3	4810.1	4453.5	4194.4	5215.9	4463.8	7350.3	4163.8	5333.9
288.0	1585.9	1521.1	1704.8	1193.4	1474.9	2025.1	1643.6	1865.9	1644.6	1478.0
241.8	1141.0	2220.3	1118.5	1030.9	938.5	1189.0	1367.8	854.6	749.3	864.1
608.4	7447.3	8528.4	7714.6	7552.3	6913.1	7810.4	8068.5	5686.8	5397.4	8018.5
115.3	2321.3	1511.9	1155.1	2824.9	1623.8	1556.5	4373.4	1632.5	877.0	1312.3
167.4	1944.0	1257.9	970.1	1923.8	1122.1	955.8	3602.9	1210.3	822.2	1129.0
7415.1	2344.8	2502.8	2522.7	3367.1	2127.5	2829.8	2554.0	4781.2	1614.8	2780.3
1235.0	2600.2	2676.3	2778.0	3053.0	3301.0	2774.0	2686.6	2513.4	2868.3	1757.1
5418.2	4310.0	4638.7	4448.3	4172.9	4429.5	4075.2	5101.7	6527.2	4311.3	4841.6
856.0	3296.1	3254.3	2935.7	3534.3	3088.0	3390.9	4013.5	2814.6	2774.1	2765.7
10803.6	4858.4	4754.5	4960.9	4365.3	4473.1	4713.8	4437.0	5969.5	5333.9	6626.2
2577.2	2728.2	3343.0	3835.9	3833.6	2911.7	3067.0	2788.4	2332.2	912.4	2404.9
73.7	1539.0	1178.2	867.4	1807.7	1069.0	911.2	3555.8	1119.0	487.8	1018.4
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5897.6	3594.7	3524.0	3385.4	3142.9	3477.1	3471.9	3058.9	4112.2	3607.9	4668.0
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98.4	2041.4	1191.8	845.4	2620.6	1291.3	1216.7	4219.5	1505.7	850.4	1098.6
493.0	3820.0	4313.3	4308.1	4414.4	3888.8	5682.5	3662.3	4346.2	2269.9	4228.5

4287.5	4244.3	6047.5
3069.7	3014.5	5554.7
347.2	527.6	453.9
2486.1	2854.2	2730.2
1542.9	1323.4	2153.9
1010.7	813.6	2080.1
111.5	90.9	142.1
886.1	877.3	1316.7
4822.1	5436.0	5310.0
6533.7	8003.2	8720.6
2876.0	2420.1	4290.3
2788.4	1561.5	2522.7
1614.7	2034.1	3468.9
3552.2	2838.1	3652.2
4768.3	5375.0	5414.0
817.3	2144.6	3233.8
1180.5	1525.3	941.1
7188.4	7500.6	10226.0
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1959.8	2829.2	2244.5
3475.0	3372.8	3522.5
3974.6	4800.9	4749.6
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4373.0	5061.6	4869.5
2928.9	3401.1	6056.2
1810.4	1099.0	1647.6
2935.2	2468.6	2493.0
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1455.5	1108.1	2281.7
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3149.0	3385.8	3699.4
4590.8	5551.5	5209.7
3961.1	4139.1	5614.1
1481.1	1988.9	2758.9
6019.5	5952.2	7491.9
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FJ375865.1 gg_id:355523 and prevalence blaTEM genes polar bear feces clone PBF_d2 FJ3758
EU475172.1 gg_id:303077 visayam warty pig feces clone VWP_aaa02h09 EU4751
EU773258.1 gg_id:333378 BigHorn sheep feces clone BH1_aao27f08 EU7732
EU459247.1 gg_id:299625 hedgehog feces clone HH_aai34f12 EU4592
DQ809435.1 gg_id:191709 human fecal clone RL184_aah20h04 DQ809
EU475653.1 gg_id:297403 babirusa feces clone BARB_aaa04f06 EU4756
EU488411.1 gg_id:534957 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU475631.1 gg_id:297994 babirusa feces clone BARB_aaa02f02 EU4756
EU777293.1 gg_id:318173 Okapi feces clone OK3_b09_2 EU7772
EU475627.1 gg_id:295791 babirusa feces clone BARB_aaa02b09 EU4756
DQ113713.1 gg_id:136214 dog ileum clone I5-47 DQ113
EU467066.1 gg_id:288435 hedgehog feces clone HH_b11_1 EU4670
GQ867290.1 gg_id:591762 and prevalence blaTEM genes Arctic seals colon content clone WSp20 GQ867
EU475100.1 gg_id:290125 visayam warty pig feces clone VWP_aaa01h04 EU4751
FJ678801.1 gg_id:514611 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ366693.1 gg_id:366425 feces adult twins and mothers; TS27 clone TS27_a02g02 FJ3666
EU475586.1 gg_id:292078 babirusa feces clone BARB_aaa03g02 EU4755
EU773916.1 gg_id:332962 Cheetah feces clone CE3_aai05g07 EU7739
FJ681620.1 gg_id:511228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU460520.1 gg_id:290323 polar bear feces clone PB2_aai22a08 EU4605
GQ359984.1 gg_id:577153 Microbial intestinal contents and mucus yel catfish (Pelteobagrus fulvidraco) intestir GQ359
DQ799856.1 gg_id:193066 human fecal clone RL247_aaj21a04 DQ799
FJ366818.1 gg_id:365641 feces adult twins and mothers; TS27 clone TS27_a04c03 FJ3668
EU560842.1 gg_id:534075 Assessment genetic Apriona germari (Hope) larvae normalization techniques intestir EU5608
AM697422.1 gg_id:218452 sequencing libraries indoor dust clone BF0001D037 AM697
EU468628.1 gg_id:291564 okapi feces clone OK2_f08 EU4686
AM982558.1 gg_id:279235 microbial and slurry pig saw dust spent bedding clone PISD-AIH04 AM982
FJ375835.1 gg_id:348777 and prevalence blaTEM genes polar bear feces clone PBF_c17 FJ3758
EU465318.1 gg_id:299076 lion feces clone LI3_aah75b10 EU4653
AJ810555.1 gg_id:104561 superficial sediments clone AJ8105
GQ868411.1 gg_id:561998 Fungal and Structure Bioaerosols Pig Stable pig stable bioaerosols clone BBC812 GQ868
FJ363465.1 gg_id:362524 feces adult twins and mothers; TS149 clone TS149_a03e09 FJ3634
DQ113746.2 gg_id:136804 dog duodenum clone D1-17 DQ113
GQ492355.1 gg_id:547714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ680320.1 gg_id:526583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU475618.1 gg_id:298176 babirusa feces clone BARB_aaa01b01 EU4756
EU475575.1 gg_id:293486 babirusa feces clone BARB_aaa02f04 EU4755
FJ679600.1 gg_id:516687 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU462544.1 gg_id:295449 Sumatran orangutan feces clone orang1_aai56g06 EU4625
FJ673752.1 gg_id:526864 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737

49.6	249.6	52.0	56.5	376.7	65.3	111.6	1584.2	137.4	116.6	101.2
3147.2	6236.1	5742.6	5803.2	7920.4	5305.2	5780.2	8538.3	7977.8	3585.3	5668.0
12504.1	3248.5	2812.7	3073.3	2713.9	2581.1	2608.3	2812.6	3971.0	3214.4	3733.2
50.8	949.7	1204.8	1038.5	852.3	882.1	683.2	1928.2	617.4	235.5	848.1
18515.1	5613.4	4881.3	5179.2	5651.1	5113.3	5777.0	5323.1	7036.8	4789.7	7382.2
318.6	1024.0	886.9	612.6	891.4	903.4	742.6	1772.6	704.6	527.2	879.0
1318.5	2593.3	1296.5	1857.9	2947.4	1784.3	1502.6	3528.3	1598.8	563.0	1206.8
4001.5	1930.6	1730.8	1567.1	1758.2	1608.9	1537.8	2091.0	2012.8	1782.8	2248.7
961.1	3156.6	3516.2	3334.6	3537.8	2918.5	3509.1	3978.1	2744.7	1827.9	2763.4
3772.0	6317.3	5185.3	4827.8	3956.3	5427.1	4622.2	4472.7	6354.3	4081.3	5852.0
263.1	2904.3	3481.6	3090.9	3702.2	3021.9	3347.3	3720.3	2724.0	882.3	2812.4
46.6	2072.2	1281.8	852.2	2205.8	1214.4	848.1	3283.4	1172.9	567.4	1054.0
14763.5	6492.8	7367.1	7024.6	6882.4	6064.9	7413.7	5459.4	8908.8	6251.5	10032.6
14.8	2230.0	1797.9	1682.1	2464.3	1942.6	1998.3	3615.9	1725.3	1320.5	1424.1
199.4	3226.8	3282.7	3262.8	3220.1	3062.8	3062.6	3961.5	4473.3	3523.0	4617.9
4732.0	5228.9	3677.2	4187.3	4865.0	4089.1	4553.2	5311.1	5133.8	3191.0	4738.0
219.3	1528.7	2331.5	2564.9	2131.4	1832.1	3450.4	2510.2	2595.0	404.5	1770.8
65.3	2193.7	1730.5	1181.0	1269.0	1471.4	979.0	1700.2	1599.6	1739.6	938.7
54.9	2524.1	2626.2	2951.4	1813.0	2400.2	1924.8	3704.8	1772.4	1121.2	2317.2
125.5	3085.8	4384.5	3081.7	2955.3	3613.6	2704.8	4267.8	4349.8	2841.5	3307.7
6040.5	3606.8	3365.7	3567.7	3761.2	2410.3	3683.5	3451.6	4153.8	4708.1	4063.3
3481.9	5207.6	5737.8	7374.9	6046.6	4909.2	5152.6	6532.8	6826.7	1886.9	5917.5
66.2	1445.3	1918.9	1429.4	1308.5	1745.4	1723.6	2015.7	1001.5	402.1	1579.3
13373.3	5551.2	6347.0	5990.9	6553.9	5684.4	8510.8	5733.0	10803.2	5332.8	8839.6
45.1	1889.7	2647.6	2085.2	1768.5	2279.7	1816.8	2696.5	1206.0	1665.4	2318.0
6879.8	3291.9	4203.4	3934.6	4697.1	4480.4	4197.2	4134.5	5938.3	2103.8	3381.1
470.0	2114.3	2173.9	1986.9	2888.0	1803.3	1877.6	2598.9	1153.9	1881.4	1292.1
84.3	1118.2	977.6	1025.2	1611.6	1031.9	1142.2	2052.0	685.5	264.7	758.1
150.6	2063.8	1834.0	1788.9	2237.7	1894.1	1870.7	2234.0	2364.0	2234.0	1185.1
55.7	1897.8	1913.4	1856.2	2023.8	1804.6	1576.4	3018.4	1076.4	989.2	1447.9
1144.1	1263.3	2244.4	1727.1	2068.6	1645.2	2328.5	2263.4	1087.0	2355.8	959.9
7241.7	2601.5	2515.7	2455.6	2278.5	2291.2	2338.3	2789.9	3783.6	2377.3	3566.3
1241.2	1090.9	1213.0	872.5	1177.9	1027.6	1011.5	1434.8	1523.0	598.2	1040.7
7002.4	5244.6	4009.3	4670.6	5702.5	4211.6	4944.9	6174.7	6887.7	4910.0	5313.2
71.3	2612.2	2201.9	1233.8	1697.1	1765.4	1075.5	2072.7	1815.8	1829.5	1081.3
9858.4	8637.3	6667.0	6019.5	5886.1	6353.6	6257.6	7143.5	9281.6	7888.1	6716.4
47.4	798.0	417.2	205.2	743.9	426.8	218.8	1498.3	421.0	200.1	342.1
2876.6	2300.3	2448.9	2398.4	2159.9	2052.9	1789.1	3321.8	1782.0	1167.8	1939.5
109.6	4005.1	2811.6	2223.1	1954.6	1598.3	1952.0	3683.3	1598.1	2712.5	2183.3
257.7	2512.2	3608.4	3273.9	3370.6	2782.3	4558.2	3707.8	2937.3	628.0	2167.8
16163.7	8354.5	7500.1	7662.6	8705.0	7991.5	7994.8	7740.3	9874.2	8657.8	10142.9

315.9	79.5	449.4
6446.5	5504.0	6987.6
2685.1	3486.0	2944.3
1305.9	1296.3	1848.8
5041.3	6032.7	5883.2
687.0	884.8	1368.4
2436.0	1773.1	3533.4
1542.5	2468.6	2257.1
3402.0	3633.4	5023.1
4565.6	5552.9	4919.5
3237.3	2970.2	4068.4
2243.3	1270.8	3428.0
5785.2	6672.7	6606.9
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3239.9	3271.6	3904.7
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1540.7	1911.1	2002.5
1394.1	1323.5	2269.3
3724.8	2886.4	2959.4
3755.4	3862.9	4030.8
3177.0	4568.3	4416.4
5955.0	5437.4	6453.8
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2439.8	2774.8	4157.4
1741.5	1174.9	1310.1
2842.1	2075.8	2019.7
2366.7	1900.8	2786.0
1999.4	1772.9	2874.4
2126.7	3368.6	2646.7
1159.2	1231.9	1269.1
4726.5	4976.0	7076.1
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659.3	334.8	1083.3
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2823.0	3336.8	4255.5
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AJ409003.1 gg_id:21834 human colonic clone HuCB31 AJ409
FJ975999.1 gg_id:586027 Human gut microbiome adopts alternative state bowel transplantation ileum effluent FJ9759
EU475604.1 gg_id:288181 babirusa feces clone BARB_aaa02d12 EU475
EF644506.1 gg_id:255177 Structure and performance microbial involved reductive dechlorination 1122-tetrach EF6445
AB218295.1 gg_id:147444 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-7 AB218
EU828373.1 gg_id:562096 Microbial effects changeover without CO2 sparging two-stage biological and methan EU828
EU236399.1 gg_id:295330 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92C10 EU236
DQ126679.1 gg_id:138256 Clostridium dongmakense str. HY-45-18; IMSNU 40129; KCTC 5147 DQ126
L37589.1 gg_id:16150 Clostridium botulinum B str. B3 L37589
AJ810553.1 gg_id:104248 superficial sediments clone AJ8105
NR_028898.1 gg_id:594284 Clostridium acidisoli str. CK74; DSM 12555 NR_02
EU535463.1 gg_id:281510 profile human microbiota antecubital fossa (inner elbow) skin clone nbt25f11 EU535
NZ_ABDQ01000035.1 gg_id:263445 Clostridium botulinum C str. Eklund NZ_AB
EU468033.1 gg_id:291999 cheetah feces clone CE2_f03_2 EU468
GU227151.1 gg_id:574341 Clostridium tyrobutyricum str. B6-2 GU227
AB186864.1 gg_id:104466 polychlorinated dioxin dechlorinating microcosm clone TSAF01 AB186
AB486908.1 gg_id:541432 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
AB081585.1 gg_id:71518 Clostridiaceae str. A4d AB081
NZ_ABDQ01000017.1 gg_id:264222 Clostridium botulinum C str. Eklund NZ_AB
AY742899.1 gg_id:106253 Clostridium crotonatovorans str. R6B AY742
AJ229185.1 gg_id:36004 anoxic bulk soil flooded rice microcosm clone BSV20 clone AJ2291
AB486626.1 gg_id:566529 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU474720.1 gg_id:297378 takin feces clone TAK_aaa03e09 EU474
GU476608.1 gg_id:525790 microbial biogas fermentation enrichment clone BBMC-8 GU476
AJ222546.1 gg_id:16199 Anaerobacter polyendosporus AJ2225
AB486197.1 gg_id:563918 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
AY395437.1 gg_id:107326 pasture soil clone EB1118 AY3954
L08062.1 gg_id:16144 Clostridium tyrobutyricum str. NIZO 51 L08062
AB487095.1 gg_id:589921 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR AB487
EU467918.1 gg_id:298719 cheetah feces clone CE2_a09 EU467
AB509218.1 gg_id:543607 Microbial reservior produced water oil reservoir clone HNB-13 AB509
AJ427628.1 gg_id:64232 Clostridium scatologenes str. FP AJ4276
NR_029250.1 gg_id:591228 Clostridium proteolyticum str. CG; DSM 3090 NR_02
AB470964.1 gg_id:535657 Clostridium sp. str. r13 AB470
AB470961.1 gg_id:571639 Clostridium sp. str. r53 AB470
EU536517.1 gg_id:279856 profile human microbiota antecubital fossa (inner elbow) skin clone nbt215c07 EU536
DQ129397.1 gg_id:137941 microarray level air two cities Texas urban aerosol clone AKIW662 DQ129
EU467972.1 gg_id:297029 cheetah feces clone CE2_c12_1 EU467
EF088329.1 gg_id:177051 Clostridium hveragerdense str. AK14 EF0883
AB264078.1 gg_id:190766 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-151 AB264
AY167950.1 gg_id:75821 Isolation and identification hyper-ammonia producing swine storage pits manure AY167

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2997.1	4193.8	4194.7	3237.0	3532.4	3845.0	3630.0	4007.6	5335.6	4423.4	3816.5
51.0	4095.3	6121.2	3510.1	2780.3	3838.3	3979.0	5300.5	2482.7	2549.7	4562.4
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71.5	1991.9	2962.0	2083.3	1784.5	2125.2	2327.8	2434.4	1494.7	723.8	1557.5
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8958.6	4309.3	3819.8	3546.4	3753.6	3832.7	3574.4	4182.7	3914.6	4016.1	3210.1
115.4	3247.2	5047.6	3825.2	3822.5	3878.4	3937.5	4679.2	2573.3	2232.5	3958.5
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2023.0	1754.7	2121.7
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EU536029.1 gg_id:287039 profile human microbiota antecubital fossa (inner elbow) skin clone nbt07c07 EU536
DQ196621.2 gg_id:167430 Clostridium sp. str. BL-28 DQ196
AB470965.1 gg_id:533504 Clostridium sp. str. r22 AB470
AY858804.1 gg_id:137989 Clostridium lundensis str. DSM 17049 AY858
AY581269.1 gg_id:114950 Clostridium sp. str. HY-34-8 AY581
L37585.1 gg_id:16148 Clostridium botulinum type A L37585
AY548785.1 gg_id:104893 Clostridium sp. str. PPf35E10 AY548
DQ680019.1 gg_id:173147 Clostridium sporogenes str. IBUN 182 DQ680
DQ125892.1 gg_id:134335 uranium contaminated soil clone AKAU4146 DQ125
AJ229230.1 gg_id:35306 anoxic bulk soil flooded rice microcosm clone BSV86 clone AJ2292
AF407686.1 gg_id:60611 Great Artesian Basin clone R10 AF407
AB487192.1 gg_id:572576 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIRO AB487
AY551086.1 gg_id:102321 Clostridium sp. 17cr1 AY551
AB486869.1 gg_id:558685 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB486
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GQ503831.1 gg_id:588312 Taptapani hot water spring clone tpsrb003 GQ503
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AF092548.1 gg_id:16239 Clostridium gasigenes str. DSM 12272 AF0925
EF197795.1 gg_id:192526 Clostridium tepidiprofundum str. SG508 EF1977
AF317650.1 gg_id:31985 Clostridium thiosulfatireducens str. Lup21 AF3176
NR_029246.1 gg_id:578922 Clostridium collagenovorans str. SG; DSM 3089 NR_02
AB488292.1 gg_id:591402 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB488
FJ269106.1 gg_id:308659 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2691
GQ461617.1 gg_id:581078 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial TCE Bioren GQ461
AB487999.1 gg_id:563768 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB487
GU118536.1 gg_id:574100 Threatened Corals Provide Microbial Habitats clone Mfav_O15 GU118
AB218319.1 gg_id:148431 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-84 AB2183
FJ384387.1 gg_id:368281 Clostridium sp. str. BG-C131 FJ3843
AB486212.1 gg_id:554530 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB479046.1 gg_id:571847 SSU sequences Alps Cadagno di Fuori submerged biofilm mats montane wetland ma AB479
DQ129267.1 gg_id:137771 microarray level air two cities Texas urban aerosol clone AKIW1140 DQ129
FJ167457.1 gg_id:310070 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
EU376532.1 gg_id:275993 Clostridium sp. str. SL149 EU376
AB486270.1 gg_id:586263 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU540396.1 gg_id:280295 profile human microbiota antecubital fossa (inner elbow) skin clone nbt114d04 EU540
EF515406.1 gg_id:224769 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24a07 EF5154
AB488015.1 gg_id:587690 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURO AB488

1374.9	4152.3	5337.4	4118.7	5165.4	4488.0	5537.7	4873.0	3996.4	2130.1	3235.1
5487.4	5166.6	6393.6	6205.4	5957.6	5109.8	6443.0	5563.7	10628.1	7250.5	8387.4
31.4	1700.2	1925.0	1354.0	911.6	1282.4	575.0	2955.7	723.2	536.2	913.8
8472.6	3007.1	3374.0	3682.3	2882.7	2780.6	3436.9	3112.2	3902.6	2774.8	4038.1
45.8	426.2	619.4	520.8	500.4	450.1	619.9	576.9	201.7	108.1	282.7
95.2	2847.5	4104.3	2429.8	1815.8	2435.6	2375.3	3558.5	1927.2	810.7	2372.3
1819.7	2770.6	3915.4	2681.7	2418.7	2994.6	2219.3	3175.6	2583.0	1609.1	3317.7
52.9	753.7	1651.1	1216.4	491.2	1020.2	1530.7	1034.5	459.2	127.6	555.4
2617.0	2366.5	3002.0	3174.4	2422.6	1895.9	3249.2	2669.2	1119.4	1517.9	2062.2
445.2	4236.5	6386.4	5246.9	2920.8	5929.8	4635.7	4955.6	3399.0	731.8	5612.5
123.3	1442.4	2906.9	2034.6	635.7	2045.9	1175.3	2158.8	951.7	247.0	1685.8
3702.9	4146.5	5239.7	4038.9	4659.3	3739.8	5145.7	3931.6	4275.2	2632.9	4417.5
2401.8	5805.9	7134.4	5413.1	4601.2	5567.0	4951.3	6822.8	5029.5	3195.1	6091.6
102.1	1707.5	3120.4	1968.6	1276.0	1814.8	1475.1	2368.5	838.3	310.6	1185.6
326.5	3489.9	5891.3	2916.7	2348.7	3776.8	2687.7	4295.7	2342.3	461.5	3038.2
66.9	1415.6	1811.8	928.0	798.1	1285.2	635.0	1665.2	966.4	656.4	952.8
1600.7	4244.2	4457.7	3632.2	3051.4	4238.3	3573.7	5122.7	3109.7	2529.8	3201.5
1526.8	7644.2	8080.3	6616.9	6043.5	6575.8	6048.2	6646.6	6926.6	5319.0	8492.2
87.5	616.5	1353.7	1167.6	564.8	551.7	552.2	876.9	384.0	203.9	377.5
180.5	1199.7	1812.6	1516.0	1409.9	1355.5	1448.8	1576.4	897.3	201.8	1175.5
539.3	6510.8	7075.1	7270.7	6434.8	6738.7	7712.6	6911.6	5110.6	4184.0	7222.3
26.4	231.9	236.6	378.0	185.4	173.9	350.6	591.5	158.2	80.7	127.2
55.5	464.1	974.9	368.8	396.2	554.6	339.5	611.0	260.0	210.1	388.7
277.2	2824.7	4634.3	3175.1	2517.2	3169.7	3738.7	3876.7	1713.7	1794.7	2784.1
72.5	351.0	798.0	198.0	354.8	369.8	195.5	482.5	215.1	139.3	251.3
653.7	4335.8	4442.6	4355.4	4285.6	4366.6	4448.4	5114.1	3448.8	2423.1	3579.3
606.6	5613.1	7736.5	5133.3	3398.0	5816.3	5658.8	6803.6	4675.7	3827.2	6357.4
18560.7	7534.8	8237.0	8165.6	7249.0	8079.7	7110.2	7381.7	10274.8	6498.3	10218.9
3951.7	6829.2	6588.1	5628.6	4341.6	5738.2	5747.3	5487.8	7669.6	6604.7	6363.1
69.6	1393.8	1917.8	1348.9	1036.6	1367.0	2186.9	1817.1	684.2	277.6	1715.4
299.0	3205.6	4439.3	3102.4	2226.2	3491.6	3152.6	3679.2	1963.3	798.0	3185.5
54.7	361.7	747.6	351.2	237.2	292.0	228.9	817.9	109.4	31.0	221.2
1543.7	4748.5	5870.3	4830.6	4099.6	4786.2	4024.3	5044.8	3622.3	3440.3	4936.6
575.8	3305.6	5417.0	2909.8	1475.9	4553.1	2479.6	3987.0	2972.1	323.3	3713.6
370.5	3524.8	4454.5	4127.8	3646.6	3723.9	4421.8	3628.7	2875.3	2443.6	4087.5
884.8	6416.9	7287.0	5526.2	4919.7	5791.3	6479.6	7350.3	4758.0	4101.9	7531.7
174.2	2864.0	4235.2	2566.4	2452.2	3000.7	2794.9	3230.6	2493.6	755.0	2599.1
997.7	5608.2	6180.8	4853.4	4520.0	5482.8	5379.4	5705.2	3963.7	2302.6	4535.0
2318.2	6049.8	6322.0	5946.4	4914.8	5559.0	5266.7	5411.9	6872.0	3541.0	6530.3
7616.3	7493.6	8280.8	7545.7	6017.4	7093.3	7340.2	6909.9	7465.2	5970.1	8673.8
1320.7	5286.8	6229.5	4482.9	4058.7	5469.4	3753.0	6098.0	3778.0	7034.6	5588.2

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5269.7	7735.0	6672.0
2167.0	1298.8	2719.9
3094.2	4492.2	3347.7
332.6	410.4	622.2
3453.0	2399.2	3216.2
2830.2	2534.9	3390.9
667.0	1056.7	1210.9
2534.1	2856.0	4603.9
3119.2	3259.6	5911.9
1523.9	1380.7	1917.9
3605.1	4431.4	5098.9
5423.7	5899.5	6241.4
2172.6	2057.4	3252.9
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4243.8	3515.8	3317.6
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924.8	702.4	655.6
1403.5	1278.7	1675.9
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356.6	223.4	327.9
500.0	422.8	493.6
3136.4	3104.9	4246.9
549.1	434.0	670.9
3764.0	4050.6	4048.4
5228.2	4577.2	6999.5
7443.5	7669.6	7435.4
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771.4	936.2	1341.6
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196.5	257.1	367.6
4231.8	5371.8	4014.1
2022.6	2935.9	3783.4
3357.2	3559.0	4595.5
6190.0	5776.1	9237.5
2466.7	2517.2	3643.5
5208.2	5073.8	6305.1
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6538.3	7245.5	6871.8
5841.8	5296.9	6908.1

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AY217406.1 gg_id:81138 TCE-dechlorinating microbial community clone 7H AY2174
AB487423.1 gg_id:535222 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4874
EU468070.1 gg_id:300313 cheetah feces clone CE2_c07_2 EU4680
AB487443.1 gg_id:551963 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4874
AB486434.1 gg_id:587168 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
EU037903.1 gg_id:240095 Clostridium mesophilum str. SW408 EU0379
FJ957871.1 gg_id:417891 Clostridium sporogenes str. JPL_17 FJ9578
AB488261.1 gg_id:578160 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4882
DQ196626.2 gg_id:167821 Clostridium sp. str. BL-22 DQ196
AY667266.1 gg_id:102839 TCE-dechlorinating groundwater clone TANB101 AY6672
EU073771.1 gg_id:248695 Microbial subsurface beds and methanogenic s coal enrichment clone ObedB-8G EU0737
NR_025352.1 gg_id:542995 Clostridium akagii str. CK58; DSM 12554 NR_025
AB239189.1 gg_id:220242 Clone acidigenic anaerobic enriched starch thermophilic methanogenic sludge clone AB2391
AB237714.1 gg_id:139836 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB2377
AY548784.1 gg_id:104736 Clostridium sp. str. PPf35E8 AY5487
FJ455907.1 gg_id:513952 Variations archaeal and sulfate-methane transition zone continental margin sedimen FJ4559
DQ196619.1 gg_id:168422 Clostridium sp. str. BL-14 DQ196
DQ675453.1 gg_id:172040 Clostridium sp. str. Z-0511 DQ675
EF586022.1 gg_id:246053 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_ EF5860
EU878275.1 gg_id:305185 Clostridium sp. Z-0511 str. Z-0511; DSM 18346; VKM B-2402 EU8782
EU471390.1 gg_id:300773 spectacled bear feces clone SB_2aaa03a02 EU4713
EU470899.1 gg_id:299498 red panda feces clone RP_2aaa01g08 EU4708
EU470928.1 gg_id:295858 red panda feces clone RP_2aaa02b04 EU4709
EU776817.1 gg_id:327397 Mongoose lemur feces clone ML_aaj25b03 EU7768
EU778467.1 gg_id:331973 Red Panda feces clone RP_2aaa03f09 EU7784
EU470764.1 gg_id:290811 red panda feces clone RP_2aaa04g03 EU4707
EU777367.1 gg_id:353163 Sumatran orangutan feces clone orang1_d07_1 EU7773
EU470993.1 gg_id:300606 red panda feces clone RP_2aaa01h06 EU4709
EU469919.1 gg_id:289211 western lowland gorilla feces clone GOR_aag74c06 EU4699
EU471360.1 gg_id:294343 spectacled bear feces clone SB_2aaa04b03 EU4713
EU471368.1 gg_id:288826 spectacled bear feces clone SB_2aaa01c02 EU4713
EU462444.1 gg_id:288082 Sumatran orangutan feces clone orang1_aai54g01 EU4624
EU469616.1 gg_id:298985 flying fox feces clone FF_h02 EU4696
EU471421.1 gg_id:303385 spectacled bear feces clone SB_2aaa03a07 EU4714
EU470768.1 gg_id:298193 red panda feces clone RP_2aaa01h02 EU4707
EU470933.1 gg_id:297215 red panda feces clone RP_2aaa02d08 EU4709
EU462038.1 gg_id:298407 black-handed spider monkey feces clone SPIM_aaj33g03 EU4620
EU470866.1 gg_id:300995 red panda feces clone RP_2aaa03g06 EU4708
EU467216.1 gg_id:296163 black-handed spider monkey feces clone SPIM_c12 EU4672
EU469939.1 gg_id:293118 western lowland gorilla feces clone GOR_aag74h05 EU4699
EU471395.1 gg_id:295548 spectacled bear feces clone SB_2aaa01f09 EU4713

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15838.3	7581.4	8449.8	7643.4	7336.6	7193.7	7329.5	8639.5	7617.0	6678.6	9097.3
1155.4	4430.5	5623.1	4669.5	3335.8	4526.5	4006.9	4744.6	7996.1	4886.7	5035.5
569.2	6866.4	8888.4	5873.4	4927.3	6680.6	6017.6	7080.9	4565.7	2635.4	6417.0
2718.0	5277.8	5791.7	4497.0	4625.3	6258.0	5574.4	7074.9	4438.6	4528.6	5505.9
548.2	4137.8	6117.4	3709.7	3055.0	4715.5	3955.2	5272.1	3210.2	1601.3	3753.4
1808.3	2491.8	3601.2	2363.2	2113.6	2639.0	2227.6	2787.7	2464.8	1092.5	2987.4
2850.1	7288.2	9481.4	7453.2	7169.5	7311.2	8218.9	8070.1	6016.3	3198.0	8245.0
744.1	3319.2	4375.6	3754.2	3585.7	3715.4	4200.4	3859.3	3938.2	2997.4	3367.8
82.3	3083.2	5148.4	3962.9	2501.6	3389.7	3288.6	3626.6	2009.8	1021.0	2640.4
1869.1	2958.3	3718.1	3055.0	2312.9	2647.0	2326.9	3501.5	2874.7	1061.4	3273.7
49.2	1077.0	1620.8	808.4	812.1	1118.8	1294.2	1459.9	546.3	279.4	913.2
41.6	524.2	1135.4	398.5	558.3	846.4	793.7	1246.6	359.1	52.4	341.7
109.0	2520.2	4392.9	2328.3	1729.2	3099.9	2192.0	3199.1	1855.8	2042.8	2710.2
54.8	839.6	1213.6	728.8	616.4	749.0	683.9	931.2	557.9	228.7	665.1
2547.8	5636.9	7745.5	5721.7	5475.2	6218.1	7388.5	6956.0	4601.9	1759.0	6735.6
41.9	442.8	628.9	441.1	409.3	438.1	810.9	777.9	164.0	72.0	369.6
132.1	2170.7	2584.7	1789.2	1475.3	1685.0	1684.7	2157.9	1948.7	1414.7	1490.1
40.6	252.1	385.0	264.7	230.7	395.1	214.5	323.7	238.4	98.9	162.1
3483.7	9498.6	8874.2	8007.7	7449.0	7813.6	8066.5	7604.6	9160.9	7737.8	9167.5
91.7	2487.3	3927.0	2322.7	2090.6	2601.5	1897.5	3301.3	3310.4	1622.9	2268.0
629.4	4873.1	5007.4	4229.0	4340.8	3936.2	5684.7	4028.2	2671.9	2765.3	4273.3
237.7	4255.6	4416.3	3924.1	3426.4	3954.4	4435.0	4293.3	3249.2	4427.3	5412.7
264.8	5109.8	5748.3	4671.6	4711.9	5648.2	3687.9	6114.0	3133.6	3445.9	4454.7
3053.1	4551.9	5570.2	4703.6	3147.0	4336.6	3448.5	4270.7	3696.8	2979.9	5745.2
5249.5	5837.4	5181.2	5042.3	3746.9	4945.8	4560.7	4832.9	4932.4	2382.8	5381.3
1560.7	6781.3	7525.9	6391.8	5443.6	6138.6	6041.2	6463.9	4370.3	2469.7	7169.4
2849.9	6494.1	7869.4	6389.3	4499.5	6031.0	5486.1	6086.9	4376.9	2537.7	7186.1
85.9	3355.0	3257.9	2109.9	1707.4	2557.2	1776.6	2478.6	1726.0	1110.2	1977.3
6246.4	3555.5	3961.7	3227.6	2869.2	3081.1	3208.5	3616.0	3000.2	3875.1	2952.8
260.9	3740.6	4694.1	3587.8	3487.0	4260.5	2910.0	5108.6	2521.6	2217.2	3296.5
412.9	5979.9	5753.2	4460.9	4397.9	5527.6	3716.2	5343.6	2829.3	7325.5	3578.0
665.1	6299.0	6744.1	5840.7	4117.8	5514.7	4300.2	5907.4	3886.5	2035.5	5812.8
9751.8	6000.0	7126.2	6651.7	4964.1	6024.9	6024.7	5502.8	8377.8	5836.7	6793.9
1489.6	5080.8	6027.4	4593.5	3627.9	4568.3	3929.7	5216.7	3178.1	1892.6	4971.2
733.7	4374.9	3941.5	3407.5	2691.4	3462.2	2916.3	3279.8	4517.4	2271.4	3167.9
2109.0	7955.2	7003.8	6234.8	5410.2	6542.3	5257.1	6153.3	5695.7	4540.4	7122.7
80.7	1227.3	2652.7	1401.6	934.3	1511.8	932.9	2110.2	1088.0	342.1	1278.0
214.0	4052.4	5328.7	4368.2	3010.7	4015.8	3779.4	4185.9	3498.7	2449.0	4061.0
1866.9	3667.3	4342.0	3887.0	3111.6	3747.5	3511.4	4811.5	2490.0	1156.9	3503.3
2246.8	1952.1	2613.1	2027.2	1699.8	1937.3	1960.0	2505.1	1787.6	1824.9	2066.5

7340.2	8775.8	8436.7
7172.3	7572.2	7813.2
4232.0	6243.3	5942.7
6173.4	5872.9	7703.1
5359.4	4517.1	5142.0
3791.1	3392.5	5034.4
2213.7	2009.5	2362.8
6650.5	6478.3	8157.1
3791.9	4046.8	4456.2
3400.8	3495.4	5718.2
2780.8	2528.8	3454.6
991.3	995.9	1256.0
544.1	423.1	706.3
2500.6	2286.2	4027.5
634.8	915.3	995.5
4494.2	4552.4	6911.2
325.1	465.0	699.4
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191.4	290.6	247.9
7037.2	7510.4	10091.1
2852.5	2943.9	2862.5
3176.1	4933.5	6880.8
3577.8	3962.0	4351.5
5827.6	4348.6	4998.8
4628.3	4184.5	3898.8
4715.9	4844.5	4980.6
6424.4	5619.5	6909.6
6410.7	4677.3	6251.4
2377.0	2393.2	2419.1
3816.8	3162.4	3341.0
4991.5	2918.1	4446.6
5778.4	3338.4	5054.9
5724.6	4864.0	5980.1
5399.8	6749.2	5214.2
5300.1	4185.8	5202.0
2861.8	3681.8	2790.6
6268.1	5140.6	5910.8
1613.2	1855.6	1512.0
3757.1	4082.9	4400.1
4129.0	3575.5	4513.3
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EU470864.1 gg_id:289965 red panda feces clone RP_2aaa04e09
EU461261.1 gg_id:302605 hamadryas baboon feces clone BAZ_aah91f12
EU471394.1 gg_id:302208 spectacled bear feces clone SB_2aaa02c08
EU775362.1 gg_id:304758 Western lowland gorilla feces clone GOR_aag74d03
EU777443.1 gg_id:322847 Sumatran orangutan feces clone orang1_aai53a11
EU461293.1 gg_id:295126 hamadryas baboon feces clone BAZ_aah92d06
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EU470975.1 gg_id:299372 red panda feces clone RP_2aaa03c10
EU777525.1 gg_id:341642 Sumatran orangutan feces clone orang1_aai55h09
EU470815.1 gg_id:289711 red panda feces clone RP_2aaa04b05
EU471455.1 gg_id:290626 spectacled bear feces clone SB_2aaa01c04
EU462037.1 gg_id:301778 black-handed spider monkey feces clone SPIM_aaj33g02
EU778647.1 gg_id:349573 Spectacled bear feces clone SB_2aaa03d12
EU773056.1 gg_id:336187 Banteng feces clone BG_aaa03e12.Contig1
EU470735.1 gg_id:292631 red panda feces clone RP_2aaa01a07
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EU471476.1 gg_id:293333 spectacled bear feces clone SB_2aaa03c12
EU470843.1 gg_id:292525 red panda feces clone RP_2aaa02c06
EU467479.1 gg_id:289409 Sumatran orangutan feces clone orang1_f07_1
EU778399.1 gg_id:312733 Red Panda feces clone RP_2aaa02h11
EU469758.1 gg_id:293303 flying fox feces clone FF_d05
EU470773.1 gg_id:302078 red panda feces clone RP_2aaa04h10
EU467437.1 gg_id:292461 Sumatran orangutan feces clone orang1_b03
EU471327.1 gg_id:300582 spectacled bear feces clone SB_2aaa01b12
EU774131.1 gg_id:344202 Chimpanzee feces clone CHIMP12_h06
EU773439.1 gg_id:332920 Black lemur feces clone BKLE_e08_1
EU471402.1 gg_id:300228 spectacled bear feces clone SB_2aaa04h09
EU470984.1 gg_id:295643 red panda feces clone RP_2aaa01a08
EU467293.1 gg_id:288118 hamadryas baboon feces clone BAZ_f08
EU776880.1 gg_id:352379 Mongoose lemur feces clone ML_aaj26c04
EU471517.1 gg_id:290669 spectacled bear feces clone SB_2aaa01h09
AJ271455.1 gg_id:40951 Clostridium aminovorans B7FT-
AF373919.2 gg_id:28874 Tindallia californiensis str. APO
AJ271456.1 gg_id:71603 Clostridium alcaliphilum B8NS1-

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AF3739
AJ2714

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1008.7	5723.8	6712.0	5160.7	3936.6	4873.6	4338.3	5643.3	3240.8	1876.7	5267.7
1328.8	6128.3	5129.7	4393.4	3139.9	4697.7	3382.9	4267.6	4101.4	2117.4	5206.3
4708.6	4681.1	4877.2	4635.9	4575.9	4311.8	4557.6	3903.1	3573.8	2571.6	6209.5
2843.5	8586.5	9344.8	8163.9	6561.9	7492.3	7600.1	7325.6	6595.9	4157.1	8506.7
279.4	1958.6	3114.9	2387.2	1654.5	2140.1	1859.7	2558.0	1571.7	747.1	2125.8
1245.7	6126.6	5380.1	4424.3	3423.4	4657.8	3229.9	4217.1	3496.0	2469.5	4187.7
8193.1	6063.5	6461.9	6565.3	6722.4	6065.8	6827.2	7511.3	6117.2	4068.7	6645.7
1099.6	5036.3	6766.8	5038.9	2460.6	4246.6	3254.8	4204.9	2322.7	1135.9	5493.6
6350.2	5940.5	5836.5	5433.5	3587.0	4469.9	3931.8	4825.2	4779.8	3078.5	5594.6
259.4	1960.2	2154.0	1865.9	2810.5	1931.3	3637.6	2056.4	1233.3	1762.8	1721.4
338.6	6466.3	7252.2	6060.0	4925.2	5824.9	5063.1	6609.2	4174.1	2443.4	5847.3
1466.3	6819.6	7218.1	6205.9	4820.6	6017.7	5462.3	6238.7	4577.7	2961.6	6932.5
124.1	2961.2	4676.9	3040.8	2002.7	2974.9	2176.7	3927.3	1898.4	1058.9	2723.3
621.5	4636.0	5713.8	4617.3	3258.9	4205.0	3969.1	4438.9	2596.5	1369.3	4997.9
199.9	3149.1	4836.0	2272.7	2278.5	2905.7	1725.8	3305.7	2104.7	923.9	2984.9
711.9	5847.8	8154.1	6055.0	5294.3	5883.5	6365.2	7823.9	5984.8	2551.5	6718.9
112.4	4401.5	5716.4	4028.6	3573.4	4284.8	3943.4	4908.1	2611.2	2643.2	4099.3
231.5	3617.3	5351.1	3981.7	3473.2	4171.3	4194.0	5305.5	2903.1	4871.2	4770.6
4844.7	6145.4	6304.3	5610.0	4133.5	5572.5	4746.4	4544.6	5261.8	5038.2	6992.7
119.2	3996.4	4931.4	3671.1	2527.9	3559.3	2868.9	4673.0	2150.9	1372.8	3820.8
11386.0	7203.5	6964.6	7162.5	6014.9	6215.7	6199.2	6252.3	6464.7	5003.9	9154.1
2054.0	3198.7	4153.7	3317.5	2654.7	3761.0	3132.6	3806.6	2254.5	2645.1	2859.9
6742.7	5088.7	5249.3	4560.0	4410.0	4871.0	4484.2	4639.6	3074.2	2354.1	3550.1
17931.8	9234.9	7177.7	7544.4	6803.4	7405.1	7522.4	7311.0	10166.5	8736.4	9788.5
122.2	1782.0	2005.1	1472.6	1057.5	1595.7	1316.1	1444.9	1106.1	532.0	1673.3
18389.9	11220.0	9635.9	9880.2	8386.7	9434.7	9717.0	8839.6	13021.3	9756.3	12661.8
3465.7	7367.5	6350.0	6504.4	5616.6	6010.4	6336.1	6701.9	6560.2	5054.8	7756.9
112.7	6892.1	7672.8	5636.7	5274.6	6377.2	5422.6	6647.9	4699.6	2804.3	6485.0
397.9	2558.1	2559.9	2401.6	2004.2	2276.5	2098.4	2516.3	1984.6	1086.3	2091.2
555.7	4514.0	5501.7	4127.3	4220.0	3828.3	5974.4	4033.4	2655.0	2836.9	3964.8
3905.4	8030.5	8376.9	8649.4	6679.5	6801.1	8247.3	7182.3	8984.2	4672.2	9497.7
314.6	1356.1	2279.8	1253.4	920.1	1291.6	1030.5	1660.2	798.0	245.1	1234.4
1397.6	4672.5	5616.4	6165.9	3579.0	5036.7	3738.2	5624.2	4026.2	6194.9	4882.9
381.8	3560.5	4849.3	3981.4	2630.5	3745.6	3224.1	4500.8	3092.7	3147.5	4105.9
38.6	616.4	1042.5	734.3	345.2	751.1	551.8	728.3	328.4	169.2	648.2
1161.3	2125.4	2783.8	2307.2	1662.4	2225.9	1710.6	2718.6	1487.8	1909.3	2026.3
10297.5	7799.6	8105.9	7983.1	7563.5	7526.9	8695.5	7414.5	7844.5	8732.8	9565.9
1201.1	4701.8	4455.6	4039.0	4424.6	4178.4	4964.3	4338.1	3806.0	4403.6	3731.8
1249.8	4131.7	4865.6	4010.5	3411.2	4164.6	3948.9	4358.1	3126.1	4920.5	3499.6

1025.8	714.3	943.0
6399.7	7469.7	6623.8
5548.0	4590.1	5589.8
4007.5	4560.8	3379.5
3493.3	4869.8	4147.2
7841.0	6493.0	7228.3
2533.5	2282.2	2778.3
4545.8	3862.4	4441.8
6594.9	5976.5	6922.7
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3917.5	3514.1	5647.1
3534.4	2167.5	2523.9
6738.1	5781.1	8174.7
5184.6	3958.5	5957.8
4273.6	4688.2	6575.4
4903.3	5534.3	5296.0
4281.0	3048.9	4014.2
6670.4	7724.4	6568.4
3151.1	3165.9	4259.6
4706.9	4845.0	5287.2
7305.6	8216.2	7077.0
1271.6	1730.7	1157.1
8504.9	9353.1	9120.1
6383.3	7005.1	6245.4
6936.7	5446.7	6861.3
2484.8	1753.9	2401.9
3242.7	4800.7	6789.0
6967.1	7998.7	7511.7
1226.2	1456.7	1186.6
5207.6	5333.4	4151.6
4155.5	3852.7	5894.2
718.7	570.3	789.3
2504.9	2838.2	2593.9
6994.3	9135.4	11051.8
4397.9	4655.5	7960.5
4532.7	5217.5	7058.1

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FJ424474.1 gg_id:364085 Clostridium sp. str. SH-C10 FJ4244
EU775653.1 gg_id:356516 Hedgehog feces clone HH_aai34d11 EU775
EU467043.1 gg_id:288286 hedgehog feces clone HH_a10_1 EU467
AF458779.1 gg_id:67640 Clostridium caminithermale str. DVird3 AF458
EU573106.1 gg_id:279224 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c EU573
AB294306.1 gg_id:216573 Microbial structure deep coal seem groundwater clone YWB37 AB294
AF507894.1 gg_id:62667 Mono Lake at depth 23m station 6 July 2000 clone ML623J-36 AF507
EU443727.1 gg_id:442217 Thermotalea metallivorans str. B2-1 EU443
DQ234642.1 gg_id:141863 subsurface water clone DR546BH1103001SAD18 DQ234
Y16716.1 gg_id:43181 Natronincola histidinovorans str. Z-7940T (DSM 11416) Y16716
DQ206418.1 gg_id:140290 microbial mediates arsenate reduction soda lake water clone ML-S-1 DQ206
DQ643978.1 gg_id:170026 Geosporobacter subterrenus str. VNs68 DQ643
DQ234901.1 gg_id:141051 Tindallia texcocoense str. IMP-300 DQ234
AJ271453.1 gg_id:19154 Clostridium elmenteitii E2SE1-B AJ2714
AY464940.1 gg_id:104179 Caldanaerocella colombiensis str. P4.4 AY464
GQ848202.1 gg_id:582632 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
FM178809.1 gg_id:337073 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
AF407695.1 gg_id:60603 Great Artesian Basin clone R82 AF407
EU458270.1 gg_id:288703 North American black bear feces clone BB2_b06_2 EU458
EU775654.1 gg_id:310410 Hedgehog feces clone HH_aai36a02 EU775
AF069742.1 gg_id:16220 Clostridium frigidicarnis str. SPL77A AF069
EF420221.1 gg_id:208357 Mature fine processing harbour methanogenic oil sands tailings pond clone 12-10F EF4202
EU775663.1 gg_id:311928 Hedgehog feces clone HH_aai33c11 EU775
EF614838.1 gg_id:227851 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU471505.1 gg_id:300929 spectacled bear feces clone SB_2aaa01c11 EU471
DQ015091.1 gg_id:133265 mouse cecum clone M2_c01 DQ015
X77676.1 gg_id:16200 Clostridium algidicarnis str. NCFB 2931 X77676
EU470498.1 gg_id:290076 red panda feces clone RP_1aaa01f09 EU470
EU775623.1 gg_id:321747 Hedgehog feces clone HH_d12 EU775
EU458271.1 gg_id:298041 North American black bear feces clone BB2_b07_3 EU458
EF687331.1 gg_id:282549 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
EU470672.1 gg_id:295461 red panda feces clone RP_1aaa04f06 EU470
EU471456.1 gg_id:288039 spectacled bear feces clone SB_2aaa01f07 EU471
AJ229222.1 gg_id:31072 anoxic bulk soil flooded rice microcosm clone BSV78 clone AJ2292
EU458119.1 gg_id:296563 North American black bear feces clone BB2_a10 EU458
EU776900.1 gg_id:306522 Mongoose lemur feces clone ML_aae89h03 EU776
EU459248.1 gg_id:295190 hedgehog feces clone HH_aai34g01 EU459
FJ671124.1 gg_id:519851 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6711
EF174499.1 gg_id:180489 Clostridium sp. str. R6T EF1744
AB487300.1 gg_id:555862 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
EU471302.1 gg_id:289222 red panda feces clone RP_3aaa03a04 EU471

37.2	146.6	273.7	117.5	187.7	196.6	309.3	200.9	63.0	70.3	109.0
11733.8	4929.1	5680.9	4681.0	3678.1	4364.2	4051.2	5168.7	5285.4	4912.9	6118.8
105.8	3096.3	5155.6	3430.5	2586.7	3197.3	3058.8	4243.8	1789.7	1518.7	3112.1
185.8	3431.5	3424.4	3453.9	3189.0	3131.6	2780.9	3122.1	2829.6	2173.2	3626.6
36.3	180.4	767.8	513.3	359.1	307.0	1934.9	1635.3	1129.4	151.0	287.6
379.4	3304.5	3709.1	3445.0	2852.9	3199.6	4178.6	3225.1	1596.0	1223.2	2822.8
188.4	1379.8	1520.7	1453.2	629.5	1183.0	1326.4	971.2	800.0	51.6	841.4
38.8	65.9	109.6	72.1	61.3	67.6	82.5	129.6	49.9	38.9	190.9
52.9	58.9	111.9	58.0	47.3	54.6	48.3	84.2	42.8	100.5	45.7
2531.2	3210.7	4458.0	3719.6	3749.0	3614.0	4225.4	4062.4	3104.9	4272.5	4540.7
1495.3	3686.8	3718.4	3821.8	3345.8	3302.7	4699.8	4015.3	3461.5	3182.8	2509.9
221.6	1855.9	2972.3	2324.9	2076.2	2216.3	2058.1	1876.4	920.5	688.5	2581.3
1146.7	4181.1	4180.9	4585.8	2930.7	3155.8	3366.2	3538.5	4066.4	4308.3	3976.8
323.4	1960.7	2048.1	1716.2	1574.1	1904.2	2397.3	2104.7	1099.2	1937.6	1612.6
50.1	28.2	26.6	33.6	45.5	26.9	36.9	33.2	16.9	26.0	25.7
200.1	1821.3	2676.0	2251.8	2140.9	2169.7	2436.6	2386.8	1202.2	1158.9	1755.2
1147.3	2811.9	3371.4	2955.4	2927.4	2719.5	3321.3	3015.2	2727.6	2249.4	3425.4
56.1	29.4	36.1	31.8	51.6	102.9	35.3	22.9	101.9	22.0	37.5
524.7	2696.1	3368.0	2895.8	2397.5	2976.0	2105.6	4036.3	1795.2	1799.3	3082.5
6763.3	3822.5	3679.7	3101.2	2945.4	3618.2	2278.3	3656.0	1899.5	2039.9	2702.3
52.5	1330.7	1013.9	774.6	436.2	880.1	489.1	2765.3	532.0	201.3	671.4
3081.0	1214.6	1542.6	1220.2	765.0	1543.3	927.0	1786.6	1006.9	688.8	1406.2
2189.0	6324.8	8167.4	6626.3	6192.1	6259.1	6155.2	7696.7	5741.1	6780.4	7241.5
6366.1	5831.8	5943.1	5442.7	4278.0	5230.6	5500.7	5799.0	6618.7	4822.3	6349.4
1191.3	7402.0	8069.4	6060.5	5375.4	6725.0	6199.5	6750.0	5423.9	4937.7	7745.7
2579.8	3871.0	3514.2	3839.5	3496.8	3654.9	3953.3	3604.8	3662.9	3429.4	4361.4
36.0	434.8	709.0	292.9	295.7	473.1	279.9	675.5	219.6	156.7	230.2
9691.3	9011.6	8587.1	9387.2	8640.1	8285.8	10024.7	8886.9	11019.8	8566.6	10091.6
169.7	2392.6	3637.8	2764.2	1884.4	2491.8	1939.5	3537.8	1492.0	1449.7	2680.8
2812.2	4163.7	5621.2	5156.6	2562.8	4474.7	3456.8	5098.2	2745.2	1815.5	4665.5
441.5	2334.8	4686.0	2168.0	2164.8	1993.3	2079.1	3130.0	1561.4	1172.3	1574.4
1011.6	3114.2	3675.7	3331.1	2489.5	3020.1	2683.5	3952.6	2741.6	2995.4	2918.3
8680.4	7879.0	8743.1	7928.6	7053.7	7533.1	8446.1	7328.9	7098.9	5963.0	11314.6
58.7	421.9	986.6	440.3	213.6	603.2	279.6	667.7	353.8	696.0	353.8
10519.3	10000.7	10460.3	9124.0	8095.8	9324.1	8602.9	9914.0	13918.7	9580.6	11593.2
220.0	2693.6	3773.0	2813.5	2405.3	2769.6	3838.5	4090.2	2648.4	1294.0	2147.7
9391.8	5041.9	5434.1	5494.0	4295.3	5209.6	3315.0	5660.1	4546.3	7794.0	5870.5
1556.1	5818.3	6675.1	5792.0	4775.8	5236.5	5166.6	6468.8	6127.4	4398.9	5508.4
54.4	143.7	299.0	181.5	91.8	125.6	99.6	250.5	81.4	33.8	149.1
3408.8	5267.5	8393.7	5804.2	3554.6	5649.0	5177.6	5805.5	4488.0	3018.3	5463.8
6802.5	7699.0	8817.6	8517.7	8125.9	7574.7	8215.4	8898.4	9355.8	5467.3	8693.8

141.8	157.4	264.6
4229.8	5533.9	4759.0
2799.8	3234.0	4571.5
2554.9	3129.4	4352.6
2261.9	164.8	75.2
3255.3	2807.0	4709.4
684.3	758.7	1558.4
45.8	109.5	176.1
79.8	118.7	107.6
3726.9	4269.6	5484.8
4546.7	3312.8	5394.7
1716.4	2368.0	2409.2
3182.2	3413.2	4725.1
1743.3	1686.0	2156.9
27.4	21.7	31.9
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2805.6	3910.0	3931.6
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7169.3	6182.1	7970.3
5225.9	6340.1	5476.6
4944.0	6651.6	6178.7
3814.5	4624.0	4043.5
598.6	346.9	553.4
8240.4	8822.5	12200.4
2721.4	3546.1	4429.9
4868.9	5692.8	7686.8
2849.7	2232.4	2948.3
3508.3	3386.9	5828.0
5882.1	7808.7	8150.4
454.5	766.7	648.8
9321.1	9057.2	10305.4
2787.4	3124.8	4020.4
5418.9	6164.3	5772.0
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s__Anaerococcus hydrogenalis	70861

EU334518.1 gg_id:268609 Hexahydro-135-trinitro-135-triazine (RDX) mediated microbial shift under sulfate-rec EU3345
AB487835.1 gg_id:573564 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4878
EU459314.1 gg_id:302597 hedgehog feces clone HH_aai36b12 EU4593
EU791182.1 gg_id:583383 Enteric defensins are essential regulators intestinal microbial ecology MMP7++ mou: EU7911
EU467034.1 gg_id:297538 hedgehog feces clone HH_b12 EU4670
EU459211.1 gg_id:290495 hedgehog feces clone HH_aai34a09 EU4592
DQ113757.1 gg_id:133349 dog duodenum clone D1-79 DQ113
EU471060.1 gg_id:295623 red panda feces clone RP_3aaa03e04 EU4710
GU370097.1 gg_id:530236 Clostridium sp. str. P530(2) GU370
FJ671035.1 gg_id:530294 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
AB487325.1 gg_id:570714 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4873
EU471294.1 gg_id:298559 red panda feces clone RP_3aaa02e09 EU4712
EU471296.1 gg_id:295884 red panda feces clone RP_3aaa01b07 EU4712
GU370092.1 gg_id:531462 Clostridium sp. str. P410(2) GU370
AM179918.1 gg_id:147513 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G15-: AM179
DQ378249.1 gg_id:155706 oil-polluted soil clone M29_Pitesti DQ378
AJ229181.1 gg_id:49771 unidentified eubacterium clone BSV07 AJ2291
EF614827.1 gg_id:228319 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
AY188850.1 gg_id:100886 Clostridium sp. str. C4/1 AY1888
X80834.1 gg_id:16195 long segmented filamentous organism X80834
EU471048.1 gg_id:298484 red panda feces clone RP_3aaa04c09 EU4710
FJ672742.1 gg_id:515811 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
EU458241.1 gg_id:302475 North American black bear feces clone BB2_e07_1 EU4582
EU470690.1 gg_id:300663 red panda feces clone RP_1aaa01a07 EU4706
EU471212.1 gg_id:301163 red panda feces clone RP_3aaa03e11 EU4712
DQ339713.1 gg_id:207741 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
AB486591.1 gg_id:535624 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR0 AB4865
EU459196.1 gg_id:299207 hedgehog feces clone HH_aai33f09 EU4591
EF512134.1 gg_id:275472 Clostridium bovipellis str. B30 EF5121
AB487343.1 gg_id:586332 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4873
FJ675375.1 gg_id:524340 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
EU459197.1 gg_id:303389 hedgehog feces clone HH_aai33f10 EU4591
EU471292.1 gg_id:293132 red panda feces clone RP_3aaa04d12 EU4712
EU470539.1 gg_id:296716 red panda feces clone RP_1aaa02d04 EU4705
AB487691.1 gg_id:541232 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4876
FJ670764.1 gg_id:514451 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6707
EF614891.1 gg_id:230025 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF614886.1 gg_id:232991 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU471288.1 gg_id:288145 red panda feces clone RP_3aaa04h03 EU4712
EU458168.1 gg_id:294391 North American black bear feces clone BB2_h02 EU4581
GQ014753.1 gg_id:494913 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763g GQ014

690.5	4226.6	5371.5	4917.6	5360.5	4601.5	6404.9	4808.8	3187.1	5120.2	4605.7
4535.7	8254.3	8302.6	7412.2	6746.8	6974.2	7620.7	7428.4	7108.9	4842.6	9925.5
865.6	2264.7	4737.6	4349.6	3665.3	4093.7	3994.8	4739.1	2623.0	3837.9	2602.1
464.8	3975.1	4363.8	3389.2	2954.4	3501.8	3365.5	4089.7	2226.4	1358.8	2107.6
326.5	4048.5	5932.8	4949.0	4172.7	4222.9	4334.6	5286.9	2163.3	3278.8	4007.8
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1973.5	3102.1	3668.9	2929.7	2362.7	3223.3	2460.3	3659.9	2751.5	1370.8	1809.2
7334.5	6113.7	5802.6	5652.8	5208.0	5438.6	6536.5	5773.4	5101.6	4508.1	6667.9
783.4	2772.0	4061.4	2871.5	2509.3	2684.4	572.2	3586.3	2695.8	2246.4	2780.6
3903.9	13034.3	10993.8	10887.9	9404.8	10534.4	11049.2	10238.8	13903.8	12603.1	14602.6
56.7	664.4	1094.7	1030.9	995.6	688.2	965.4	1124.0	431.3	182.8	553.3
349.6	6969.6	9603.3	8445.1	6007.5	7235.8	6277.5	7221.4	5530.2	5768.5	8135.4
4643.2	4298.4	4187.4	4749.3	4282.6	4358.2	4730.0	5423.5	2779.5	2257.2	3736.6
269.4	4487.7	6890.0	4593.7	3173.0	4743.3	4191.1	5507.6	2694.3	3389.9	4022.2
305.4	3672.0	4706.7	3372.6	3540.5	4136.7	3523.3	4959.0	3008.6	2161.2	3761.5
522.7	7576.9	9827.8	7713.8	6321.4	7573.4	7178.4	8841.8	6381.6	4943.2	7935.9
141.6	2278.3	2549.3	2209.0	2810.3	2197.5	3279.2	2163.4	1621.7	835.4	1741.3
610.7	4844.9	4681.5	4632.3	4231.5	4526.2	4021.0	4655.4	4209.0	2451.7	4440.9
62.3	2668.0	4810.6	986.2	899.9	1816.3	656.6	3904.5	824.5	1694.3	1046.8
662.1	4127.4	4836.7	4647.8	3871.5	4592.6	4334.8	4444.5	3601.8	2467.2	4696.9
321.1	4230.4	2975.5	4164.0	4409.2	3821.9	2681.4	4993.6	2882.4	4676.6	3866.3
218.4	2860.8	4653.5	2803.9	2418.2	3476.1	2276.5	4476.0	1799.1	4133.8	3583.2
178.5	4824.3	6346.0	5150.1	4612.8	4931.6	5756.4	6152.5	3645.0	2266.3	5083.3
4451.0	9006.5	9315.6	8398.8	6555.9	8146.0	8160.5	8322.5	11445.2	8864.8	9195.4
521.4	3174.8	3992.0	2755.2	2223.2	3116.6	2861.6	3424.0	2437.2	1492.3	3065.0
1473.0	4551.4	5877.3	5340.3	4123.8	4448.1	4062.3	5268.2	3615.0	2063.3	5064.5
151.9	4814.9	7424.0	4542.1	2773.4	5301.2	4134.7	5078.7	3313.6	1241.3	4238.0
85.5	507.5	773.2	688.3	699.8	517.0	493.6	989.1	396.9	314.7	238.1
246.2	4442.8	6996.1	3946.6	3051.4	4836.4	3324.7	6959.9	3216.3	2159.2	4404.4
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94.6	1951.0	2940.0	2616.9	1059.0	2189.3	1594.4	2530.6	1552.7	847.0	2667.7
2136.6	5849.3	7166.7	5316.8	4353.3	5880.1	4322.2	7943.5	3782.5	8283.1	6828.7
65.3	1112.4	1521.4	1026.0	500.9	1062.2	473.7	2168.9	385.5	320.8	927.8
83.8	4477.0	4129.1	3935.5	3309.9	4074.1	3541.1	4151.0	4173.8	2512.0	2712.5
2134.0	6407.0	7792.7	6887.2	6365.7	6241.3	6473.3	6878.1	5940.4	4329.6	7014.4
159.8	1371.2	3530.0	3619.8	1995.8	2026.6	1568.8	3336.5	2299.1	789.6	2102.4
612.7	4654.0	3265.4	4019.1	4725.3	4567.8	3463.5	4593.8	3315.5	3634.7	2909.1
346.8	3039.4	5088.8	3431.2	2306.4	2923.5	2243.9	3110.2	2034.7	4485.3	3227.4
3469.2	3292.1	3807.2	3101.6	3212.9	3472.9	3342.8	4029.5	2119.2	1952.1	3283.0
5206.3	2297.5	2546.3	2042.2	1976.0	2118.6	2074.4	2813.9	2134.4	1818.0	2098.3
139.4	1683.7	1312.2	1399.1	1392.7	1127.6	1375.6	1043.2	1221.7	986.6	839.8

4452.9	5646.1	6882.3
6289.8	6858.0	7204.2
4266.4	4589.2	5706.9
4248.0	4591.3	4610.2
4063.6	4854.7	6749.2
4897.6	6262.3	6416.8
3561.2	3965.6	4130.9
4519.9	5141.0	7060.7
2916.8	2926.4	3429.5
10376.1	11081.7	13244.2
777.8	1172.5	1377.7
6995.5	7102.3	7010.5
4753.9	4650.8	9190.9
4542.5	4076.8	5924.0
3983.6	3868.7	4411.4
8601.0	6797.6	9137.9
1745.4	2646.0	3596.9
4739.4	4969.2	5195.5
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3647.6	4410.6	5442.9
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GQ014582.1 gg_id:495084 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw761e GQ014
GQ082223.1 gg_id:408144 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
GQ069902.1 gg_id:436277 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw243b0 GQ069
GQ001575.1 gg_id:508087 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu174f11 GQ001
GQ006366.1 gg_id:503298 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu8 GQ006
GQ031456.1 gg_id:414909 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw874b GQ031
GQ055843.1 gg_id:457745 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1120h: GQ055
GQ016171.1 gg_id:493496 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
AF542234.1 gg_id:85988 Anaerococcus tetradius str. CCUG 46590 AF542
GQ052076.1 gg_id:384301 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu5 GQ052
GQ069413.1 gg_id:387057 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069
GQ081501.1 gg_id:437020 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ047199.1 gg_id:468042 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009h GQ047
GQ029523.1 gg_id:455796 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862e08 GQ029
GQ081506.1 gg_id:390253 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ081494.1 gg_id:428347 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ041827.1 gg_id:380722 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw933 GQ041
GQ085212.1 gg_id:413797 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw272c GQ085
GQ094136.1 gg_id:438590 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw37(GQ094
AM183108.1 gg_id:239292 and its spatial composts compost clone SMC65 AM183
GQ016235.1 gg_id:493432 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
GQ004504.1 gg_id:505157 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59c09c1 GQ004
GQ016624.1 gg_id:493043 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
GQ031395.1 gg_id:453253 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873b GQ031
EF419346.1 gg_id:212397 Substantial alterations cutaneous biota psoriatic lesions human skin clone 1P1-44 EF4193
GQ092919.1 gg_id:400531 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ092
GQ068683.1 gg_id:419268 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ068
GQ094219.1 gg_id:411988 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw371 GQ094
AM176528.1 gg_id:180355 Anaerococcus sp. gpac104 AM176
GQ075874.1 gg_id:427322 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ075
GQ069446.1 gg_id:464288 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069
GQ091453.1 gg_id:401886 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw346c0! GQ091
GQ082563.1 gg_id:390980 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
GQ112151.1 gg_id:453052 Topographical and Temporal Human Skin Microbiome skin nare clone nbw585b08c1 GQ112
GQ077289.1 gg_id:406725 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ077
GQ070900.1 gg_id:452977 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ070
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GQ075849.1 gg_id:415537 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ075

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174.8	2425.0	1699.5	1619.7	1736.9	1528.4	1584.7	2221.9	1826.7	1903.3	2041.1
685.1	2512.1	2923.0	2566.4	3408.0	2295.5	3231.4	2543.1	2392.2	1336.7	2336.5
1119.9	3853.3	2981.4	3191.2	3813.2	2975.6	3003.2	3873.9	1990.8	2433.9	2954.0
16864.1	6046.7	5326.2	6629.8	7213.6	5590.8	6591.6	5633.9	5659.4	6149.3	8354.9
2040.6	3260.8	3267.2	4437.1	4461.4	3174.3	3522.9	3441.1	1800.9	2661.9	3855.5
940.9	1792.7	2702.3	3192.9	2508.0	2112.7	2301.3	2660.0	1522.3	422.1	1768.3
13333.0	6561.7	5895.8	5895.0	7314.0	5870.9	7125.2	6255.2	6592.0	7729.4	7067.5
4560.8	6053.3	4497.9	4822.7	5015.2	4722.1	4443.5	5212.7	4595.3	6477.1	5744.4
3854.1	3664.2	4579.3	4812.6	6782.7	4245.5	5688.0	4658.6	2796.9	2349.6	3476.4
17433.5	9071.0	6501.5	7563.5	8589.7	7270.6	8200.1	6779.9	8259.2	8032.0	8996.4
584.9	4309.4	4817.4	4780.9	4855.8	3846.5	4985.6	5121.9	3222.4	3651.9	4518.9
12345.7	8033.5	7617.8	7619.3	6816.8	7976.6	7673.0	7366.2	9340.0	9005.8	10702.7
1710.9	4327.3	3172.7	3037.0	4915.3	2916.5	4207.1	3415.5	2903.8	3072.7	3299.1
114.3	1093.4	1240.1	1325.5	1239.4	1107.9	1924.7	1267.4	631.4	558.6	670.2
5282.9	3254.1	3771.2	3734.7	3915.2	3662.8	4021.4	4096.4	2851.2	2953.2	3627.2
5480.5	7957.6	7432.2	7298.3	6650.5	6245.2	8150.8	7025.0	7027.5	6247.0	9163.2
10627.1	5408.3	4955.5	5514.9	4775.4	5287.1	4996.4	4981.0	6469.7	6331.1	7355.0
1322.4	2249.0	2662.8	2493.4	2763.3	2557.1	2742.8	2575.6	1855.3	2765.4	1866.5
5599.5	7970.4	7324.3	6509.9	6233.1	6442.7	6758.9	6739.6	9349.9	7923.8	8662.7
2588.3	5858.9	5247.4	5043.8	4695.1	4736.7	5437.2	4327.2	7084.7	3804.8	9488.1
2090.2	4452.0	4823.9	4895.6	3313.4	4491.7	4226.6	4888.5	2444.2	2921.2	3981.9
3539.3	2947.3	3117.3	2944.1	3038.3	2964.2	2673.4	3216.5	2431.2	4347.9	2980.9
2260.4	3101.7	3975.2	3092.6	3457.4	3350.1	3746.7	3774.1	2004.1	3416.2	2805.9
294.3	2340.7	2347.9	2586.7	1852.2	1926.8	2229.8	2622.7	1478.7	1056.3	1742.7
1004.8	1743.5	2268.7	2090.0	1606.9	1759.2	1800.5	2644.5	1305.0	1213.7	2162.2
1120.7	5940.7	3145.9	3222.1	2799.5	3077.5	3185.3	3477.4	2363.5	693.1	4472.9
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5538.2	3071.5	3259.9	2746.9	3094.9	3289.2	2856.6	3648.8	2476.6	4469.6	2382.9
24875.9	8588.4	7650.0	8120.2	8306.6	7967.4	8277.6	7796.5	9873.2	8607.7	11914.7
584.5	7651.7	6644.7	5114.5	4407.4	6281.6	4504.7	5625.1	7886.5	7444.6	5043.8
5899.8	7205.4	6817.4	5584.6	5596.7	6160.3	5520.5	5408.6	10749.6	8266.4	6156.6
787.9	3457.7	4143.8	3737.6	2785.3	3173.3	3058.3	3509.9	2661.8	3136.2	3347.6
645.3	2121.7	2878.4	1978.8	1956.6	1884.6	2150.0	1991.6	1709.0	1715.1	2298.2
5013.4	5847.7	5324.9	4615.9	4429.1	5116.3	4423.6	5345.6	5623.4	5811.0	4890.2
826.6	1791.7	1919.8	1624.7	1380.5	1808.1	1428.6	2146.8	1370.6	2193.2	1171.3
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2613.6	2625.4	3869.3
3276.5	3716.7	7001.5
5410.3	7100.2	7199.0
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5159.9	8238.3	7396.7
4938.4	5446.6	4987.1
5080.3	4197.0	6935.8
6911.5	7512.7	10296.5
5523.3	5884.3	5003.4
6837.6	8280.7	7280.0
3319.0	3644.0	3485.5
996.6	1314.7	1690.6
4221.8	4593.3	5114.7
6152.9	7113.2	6737.7
4763.1	5975.1	5200.5
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3934.0	4763.2	5504.2
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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GQ422749.1 gg_id:574384 Anaerococcus tetradius str. F0127 GQ422
GQ094326.1 gg_id:383714 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372 GQ094
GQ094616.1 gg_id:415471 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372 GQ094
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GQ016193.1 gg_id:493475 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
GQ081492.1 gg_id:464987 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
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EU931448.1 gg_id:524113 examined methods chronic venous leg ulcer clone CONR87 EU931
AM176536.1 gg_id:185333 Anaerococcus sp. gpac155 AM176
GQ040106.1 gg_id:377658 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw95 GQ040
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GQ094232.1 gg_id:394565 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw371 GQ094
GQ011147.1 gg_id:498519 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ011
GQ076559.1 gg_id:464143 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ076
GQ070343.1 gg_id:371710 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ070
GQ069466.1 gg_id:484565 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069
GQ046817.1 gg_id:395478 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ046
GQ085051.1 gg_id:419213 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw270e GQ085
GQ031380.1 gg_id:451739 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873a GQ031
GQ094289.1 gg_id:424831 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw372 GQ094
GQ081218.1 gg_id:380367 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ004351.1 gg_id:505311 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu GQ004
GQ020017.1 gg_id:489650 Topographical and Temporal Human Skin Microbiome skin nare clone nbu202a01c1 GQ020
GQ016875.1 gg_id:492792 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826e0 GQ016
FM872849.1 gg_id:363159 occupant source house floor dust clone FB03F12 FM872
GQ081577.1 gg_id:384208 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ086109.1 gg_id:441795 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
GQ044012.1 gg_id:389592 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017g GQ044
GQ093207.1 gg_id:379387 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42 GQ093
GQ070149.1 gg_id:449513 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ070
GQ081583.1 gg_id:383839 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081
GQ069472.1 gg_id:463391 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ069
GQ082189.1 gg_id:457901 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
GQ080759.1 gg_id:410475 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
GQ004581.1 gg_id:505083 Topographical and Temporal Human Skin Microbiome skin nare clone nbu60b07c1 GQ004
FJ670693.1 gg_id:514078 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
GQ089736.1 gg_id:461914 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3 GQ089
GQ042145.1 gg_id:455500 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw93e GQ042
GQ081175.1 gg_id:462037 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ081

12112.0	9205.7	8120.8	8625.8	7979.8	7517.0	8864.8	7855.7	8191.8	8804.4	11283.4
3336.5	5044.4	4013.5	4812.2	5506.3	4328.5	4747.4	4329.5	2755.0	2945.7	4425.2
1103.7	4076.3	4567.0	3924.5	3382.2	4979.8	3369.7	3723.1	4771.6	5614.6	3245.2
4276.4	6087.2	5957.7	6236.3	5079.1	4636.6	5795.5	5425.4	4811.1	5511.7	6044.7
201.6	2919.7	5499.9	3336.6	2760.4	3209.1	2634.4	3734.8	2523.3	3323.8	2882.9
7240.2	3373.4	3231.3	3031.9	2774.9	2606.8	3039.0	3140.3	2405.5	2079.0	3153.0
1233.6	2730.9	3286.0	3308.5	4311.2	3160.9	4791.3	3787.5	1891.2	1464.0	2452.9
1318.3	3536.9	3079.6	4139.4	3931.7	2710.9	3366.6	3916.3	1720.2	1060.3	2351.5
39.2	310.6	454.9	592.3	430.7	262.1	533.6	656.6	113.0	162.8	210.3
1723.9	1193.8	1628.6	1719.1	2541.0	1257.0	1997.1	1564.4	1221.1	857.2	2064.1
4708.3	4460.8	4463.2	4785.0	4807.6	4247.6	4408.1	4798.3	3063.6	3614.3	3570.1
2023.5	3461.9	4761.2	4849.3	4703.3	3992.0	5388.0	4979.2	2637.2	2887.4	3162.5
2525.1	5965.3	4889.8	5070.8	4726.6	4334.0	5308.8	5441.3	4487.5	5608.4	4886.9
756.0	6601.1	8195.8	6299.4	4047.8	5885.4	4880.4	5938.3	5983.3	5230.3	6692.9
343.4	2058.1	2084.3	1834.3	1744.5	1387.4	1657.3	2144.3	1667.9	985.8	1022.9
12898.0	8435.3	7880.9	8042.5	8582.9	7166.0	8918.7	8135.5	9477.9	5873.1	9496.9
3490.6	4146.5	4261.3	3857.3	3550.3	3953.5	3826.8	4088.0	3791.0	4161.3	4767.5
6656.5	3887.3	4485.3	3751.7	4056.6	4051.5	4112.3	4352.6	3560.2	5968.9	3495.2
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1739.0	6147.0	5612.0	5823.5	6016.9	5177.5	7529.7	5957.3	5499.2	4400.1	9824.2
1749.0	6986.7	7143.1	7360.5	5748.6	6303.3	7194.6	6843.1	7593.9	4816.4	8661.1
876.8	1938.5	1462.4	1276.6	1299.5	1363.3	1177.5	1743.3	1442.6	539.5	1619.9
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4920.6	6158.0	5772.1	5800.8	4978.9	6047.4	5470.3	5793.0	7642.4	7051.4	6354.2
9712.8	8773.2	7766.4	7555.6	8516.6	7241.1	8913.0	7610.3	7210.7	6435.8	10016.5
5028.7	7597.5	7201.7	7692.7	8668.8	6936.3	8361.2	7164.0	7834.6	8565.8	7843.2
9707.1	4584.5	4179.3	4276.3	3873.6	4284.5	3996.1	4193.9	3244.6	4384.3	4567.3
6136.6	6097.9	5808.0	6060.1	5629.7	4444.3	6253.0	5177.2	5639.4	5747.8	6941.4
2217.9	5748.5	5097.1	5192.0	4711.3	5196.7	4648.6	5487.8	5288.6	3599.9	3916.6
10946.2	9831.1	8023.6	8712.9	7786.5	7540.6	7903.3	8060.3	9915.5	8518.0	11916.9
2463.8	9542.2	6532.4	5655.3	5140.0	6497.5	5082.8	6507.9	8145.6	6487.4	7877.9
1937.2	4960.3	5194.3	4200.6	4148.9	4419.6	4161.5	4636.6	5134.3	4998.3	3923.7
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1856.3	4522.5	5366.7	5117.3	5898.0	3931.6	5848.7	5453.3	3546.2	3727.7	4654.0
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3603.2	3879.0	3399.1
3526.0	4027.9	4267.6
4108.1	3202.9	5004.4
3475.0	3560.3	2827.6
361.7	529.4	522.5
1252.6	2171.8	1600.0
4357.2	4921.6	5588.6
5214.2	5040.4	6657.3
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5056.2	5812.6	6187.9
1931.6	2020.3	1416.6
7888.2	8135.0	9712.2
3582.7	4890.4	4185.8
4493.4	5166.7	5366.6
5264.2	6561.7	6560.0
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6972.4	7198.8	7049.2
1907.8	1736.1	1561.7
5612.9	6254.4	7254.9
5613.2	6692.3	6800.1
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7205.7	7609.4	9324.9
4177.9	4749.5	6894.9
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5291.4	5545.9	6172.4
7743.4	7892.1	9315.4
6199.4	6396.2	7780.6
4518.9	4962.2	5210.0
8477.1	9497.1	9859.7
3620.2	3909.9	4892.6
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2331.7	2649.7	5404.9
5224.7	5769.0	6909.0
5626.8	6441.0	6937.5
5850.1	6058.6	7549.8

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

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GQ060761.1 gg_id:378168 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw05b GQ060
GQ016761.1 gg_id:492904 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825c0 GQ016
GQ077116.1 gg_id:375675 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1207c GQ077
FM872962.1 gg_id:367842 occupant source house floor dust clone FB02C01 FM872
GQ035694.1 gg_id:395882 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu GQ035
GQ113910.1 gg_id:375438 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ035734.1 gg_id:402899 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu GQ035
GQ085245.1 gg_id:420172 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw272b GQ085
GQ080712.1 gg_id:399798 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
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GQ076712.1 gg_id:384708 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ076
GQ076602.1 gg_id:392493 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ076
GQ040340.1 gg_id:373833 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw953c GQ040
GQ082554.1 gg_id:465922 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
FM872684.1 gg_id:360880 occupant source house floor dust clone FA02D08 FM872
GQ052405.1 gg_id:397258 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu535f03 GQ052
GQ082580.1 gg_id:443192 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
GQ029488.1 gg_id:394661 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862b0 GQ029
GQ050431.1 gg_id:437176 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu485g GQ050
GQ089886.1 gg_id:396465 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3 GQ089
GQ030344.1 gg_id:408492 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw876g GQ030
GQ080678.1 gg_id:458386 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ080
NR_026531.1 gg_id:550421 Clostridium ultunense str. BS; DSM 10521 NR_02
EF586060.1 gg_id:241189 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF586
EU369163.1 gg_id:314592 libraries oyster shell clone MBFOS-04 EU369
AF550609.1 gg_id:84656 Peptostreptococcaceae bacterium 19gly3 AF550
EF586042.1 gg_id:246996 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF586
AB109772.2 gg_id:87971 Finegoldia magna str. ATCC 29328 AB109
NZ_ACHM01000169.1 gg_id:470400 Finegoldia magna str. ATCC 53516 NZ_AC
NC_010376.1 gg_id:471282 Finegoldia magna str. ATCC 29328 NC_01
GQ030213.1 gg_id:446471 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw875a GQ030
NR_029237.1 gg_id:590651 Helcococcus kunzii str. 22; NCFB 2900 NR_02
EU931445.1 gg_id:523124 examined methods chronic venous leg ulcer clone CONR27 EU931
AB542081.1 gg_id:541571 Helcococcus ovis str. H10-Yamagata-990517 AB542
GQ047161.1 gg_id:393130 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1009d GQ047
FJ671232.1 gg_id:524188 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6712
DQ532264.1 gg_id:162924 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
FJ959755.1 gg_id:537785 bottlenose dolphin upper respiratory tract blowhole clone D8A8_086 FJ9597
FJ671016.1 gg_id:512501 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
FJ959635.1 gg_id:570400 bottlenose dolphin upper respiratory tract blowhole clone D896_235 FJ9596

955.2	1777.9	1678.4	1839.7	1922.1	1403.9	1799.2	1803.8	995.7	663.3	1688.1
9707.2	7763.6	6283.6	6825.4	6528.4	5637.2	6613.3	6420.4	7308.9	2958.2	7391.6
1934.5	3087.2	4001.9	3964.9	3841.2	3373.0	4248.3	4382.9	2561.0	2026.7	3987.4
8416.5	5281.1	5474.6	5268.5	4598.3	5269.5	5182.5	5925.0	6554.8	6815.2	5970.0
2613.8	2600.3	2173.9	2099.4	3037.0	2082.2	2473.1	2291.6	1706.2	2487.9	1742.9
176.8	1274.3	1193.9	856.3	664.5	1071.6	677.1	1151.5	1275.6	999.2	734.7
5400.1	8340.0	7004.9	7323.0	6648.2	6445.0	7572.3	6786.4	7864.7	7520.3	9281.9
1983.5	5593.5	6002.5	6122.8	6516.4	5541.4	6848.7	6390.8	4694.8	5216.6	6045.7
1685.9	3470.3	3309.5	2926.9	2789.1	3059.0	2642.5	3753.6	3555.7	3699.2	2925.5
17078.9	8888.2	8591.0	8352.0	8203.4	8008.9	8105.3	7969.3	9564.7	8748.1	10302.1
7906.2	4024.8	5105.9	5550.2	4451.8	5314.9	4850.0	4406.4	3186.2	3346.0	4218.5
4794.4	7659.8	6577.4	6469.5	6014.5	6377.2	5860.4	6460.2	6143.5	5041.3	7238.6
1538.7	5231.2	5565.7	4264.9	3929.4	4599.3	4306.9	4205.8	5477.3	4495.8	4641.4
1508.6	2456.7	2168.5	1814.4	2369.1	1998.9	2022.4	2452.0	1468.4	2998.7	1643.3
4871.0	6907.1	5976.7	6303.6	6315.6	5528.8	6345.6	4986.2	6500.8	4053.0	6966.1
2036.5	2079.7	2106.0	2227.0	2345.9	1952.6	3134.7	2200.6	1478.9	1323.8	1414.7
3436.5	4098.4	3963.0	3866.9	3551.2	3342.9	3674.8	4156.5	3099.5	2350.3	3719.2
706.9	4962.3	4629.8	5578.9	5666.4	4544.8	5938.0	4996.9	3373.0	2786.4	3978.7
5425.2	4483.1	4574.4	4168.9	4264.6	4011.2	4971.0	3753.3	5753.9	5274.9	8755.6
9694.8	6411.5	5932.8	5800.2	5820.9	5226.6	5664.6	5297.1	7965.9	5721.5	6602.8
650.1	3481.8	3740.7	3183.6	2458.6	3520.0	3155.9	3320.4	2796.7	3228.5	2697.5
4837.0	4216.8	5000.1	4203.3	3958.6	4095.3	4494.9	4420.3	3061.2	3563.3	3893.9
10828.9	9067.3	8220.2	7682.7	6975.0	7835.4	7648.4	7718.5	11074.4	9586.9	11212.3
149.9	3977.7	3631.1	3415.8	2601.1	3712.6	3962.6	3275.2	2560.5	1660.9	2654.9
11690.5	7644.9	7165.3	8233.5	7016.1	6809.8	8867.6	6441.8	6775.2	6584.9	11255.7
11436.6	9149.9	6844.8	7953.9	6071.5	6928.9	8631.3	7425.3	8763.5	5848.8	10172.7
4217.1	2893.0	3086.8	3383.2	2033.5	2897.4	3319.1	3079.1	2008.2	1575.7	3584.5
11565.5	7242.5	5313.0	5748.5	4863.0	5157.8	6262.2	5503.3	7993.2	5722.5	8177.5
52.7	809.9	1208.9	1079.9	893.2	1142.4	934.0	1543.5	305.8	203.5	657.8
1981.0	1526.1	1843.1	2033.0	2313.2	1859.9	1913.5	2329.0	1017.2	537.0	1329.0
59.6	262.2	408.3	500.0	268.1	302.9	401.2	561.0	193.6	93.9	226.5
3986.7	5326.2	5249.5	5790.9	5124.7	5233.4	6344.2	5083.7	6746.3	5621.4	8221.1
4180.8	6771.7	6771.1	6468.2	6931.1	6289.1	7389.1	6923.3	4362.2	4389.2	5351.1
1415.4	2891.5	2914.5	2599.8	2632.2	2931.0	2515.1	2716.0	2931.5	2403.2	1876.3
91.0	1571.5	1576.6	1317.6	1515.4	1340.9	2052.4	1307.6	860.1	639.8	1044.8
87.2	2907.3	4052.7	3128.3	2434.9	3593.9	2799.3	4194.4	2992.8	958.0	2304.5
1257.0	1568.2	2806.4	1991.1	2105.0	2005.9	2158.4	2753.2	1636.6	3226.7	1565.5
57.5	746.5	1254.0	1036.7	2946.6	2098.4	874.8	1199.5	96.5	141.5	300.2
7422.9	2585.6	2907.3	2980.9	2384.4	2764.1	2613.2	4175.0	3060.4	912.5	3068.4
4018.4	4042.4	4917.6	4732.3	4877.8	4500.3	5249.7	4421.1	3678.7	3697.2	4075.4
109.6	3625.2	3489.4	3764.9	4092.5	3320.1	4250.3	3628.1	2482.6	2586.6	2711.3

1746.8	2100.1	1424.0
6262.7	6402.4	6843.2
3519.1	4519.3	4633.4
4626.4	7147.5	5999.6
2443.3	2579.9	2721.4
1341.7	1163.0	1339.6
6213.1	6527.0	6031.1
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3562.2	3520.2	4402.9
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4944.9	4388.1	6355.3
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4005.9	4818.2	5430.2
2166.9	2620.5	2784.4
5572.2	5399.1	5973.6
1921.9	2179.6	3721.3
3431.8	4357.0	2707.8
4783.2	5339.9	6389.5
4407.9	4409.7	4237.2
4822.7	6995.2	5718.4
3497.5	4034.7	4003.1
4267.9	4058.3	5580.1
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6470.9	7716.8	9509.9
2282.3	3413.2	4726.7
4914.3	6653.4	6226.0
1021.0	1098.0	1140.7
1825.2	1860.3	1978.0
379.9	460.5	485.4
4892.2	5453.5	5282.6
6977.9	6531.0	9148.6
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1197.3	1857.0	2577.3
5084.0	2755.3	4334.9
2562.4	2498.4	3889.1
595.7	676.7	714.0
4436.3	4119.8	3219.2
4620.5	4313.0	6237.6
3258.2	3820.5	5292.3

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FJ670651.1 gg_id:523741 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6706
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FJ960145.1 gg_id:556060 bottlenose dolphin upper respiratory tract blowhole clone D9A4_031 FJ9601
AM176521.1 gg_id:183658 Peptostreptococcus micros gpac022 AM176
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AY349390.1 gg_id:92862 human oral cavity clone FJ023 AY3493
AF542231.1 gg_id:83408 Peptostreptococcus micros str. ATCC 33270 AF5422
GQ016336.1 gg_id:493331 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
FJ577254.2 gg_id:567933 Peptoniphilus sp. 'Oral Taxon 386' str. F0131 FJ5772
GQ069670.1 gg_id:437159 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw7 GQ069
FJ557799.1 gg_id:524282 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
GQ004943.1 gg_id:504719 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65a1 GQ004
GQ101711.1 gg_id:392255 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw498d03c GQ101
AY153431.1 gg_id:86504 Peptoniphilus indolicus str. CCUG 46591 AY1534
GQ014236.1 gg_id:495429 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760e GQ014
GQ087341.1 gg_id:448805 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ087
AB538435.1 gg_id:583324 Peptoniphilus sp. str. JCM 8143 AB5384
GQ031426.1 gg_id:387138 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873g GQ031
GQ043038.1 gg_id:405497 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012d GQ043
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GQ004003.1 gg_id:505659 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67d0 GQ004
GQ033299.1 gg_id:381665 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ033
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GQ076958.1 gg_id:415523 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
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EU526289.1 gg_id:269603 Peptoniphilus sp. str. WAL 1768N EU5262
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GQ031247.1 gg_id:464237 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ031
AF481225.1 gg_id:68341 Peptostreptococcus sp. str. E3_32 AF4812

2716.6	2464.4	2664.6	2427.3	2623.9	2254.6	2767.2	2615.0	2883.7	2328.3	2071.6
11075.8	4782.5	4444.2	5162.9	5326.2	4868.0	5583.0	5255.6	5538.2	4044.4	4593.0
8239.1	7600.6	7716.0	8127.5	7415.5	7795.5	8026.9	7174.9	9701.9	7146.3	10986.7
3982.2	4795.1	5853.8	5118.0	5578.8	4729.3	5240.4	5511.4	5002.6	6291.2	4338.5
2119.8	3622.4	3982.6	4269.3	4084.9	4065.9	4014.5	4587.6	5499.5	3632.8	3681.3
148.3	2687.4	2280.3	1999.6	1771.7	2335.7	2022.7	2374.7	3021.6	2716.8	1800.7
15104.4	4582.5	5121.1	5282.3	4391.6	4640.5	4923.7	6384.7	6710.0	5834.5	6507.3
508.0	2827.8	2990.5	3471.2	2577.1	2567.7	2862.0	4007.7	2542.6	1657.9	3337.8
2821.0	1871.0	1979.8	1967.4	1675.8	1851.7	1946.7	2056.4	2183.8	1819.6	2174.9
8342.0	4778.9	4811.8	4968.8	4901.9	4214.6	5149.0	4605.7	5942.5	4998.6	5327.2
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3667.0	2816.8	3740.4	3190.3	2660.2	3032.3	3074.3	4471.1	3776.0	3035.2	3532.5
6040.6	5293.6	6065.9	5891.0	6148.7	5350.2	6734.9	6400.9	5263.5	4264.4	4865.5
1692.5	4204.0	5286.4	4227.0	3382.8	3835.1	3619.8	5276.2	3528.2	2323.9	3706.6
1837.6	4501.0	6420.1	4767.2	4195.5	4959.1	4677.4	5655.0	3916.7	3211.6	4816.3
928.7	3896.6	5535.6	3819.6	2935.3	3789.8	3528.2	4047.0	3873.9	2294.4	3635.8
1714.9	4800.4	6755.5	5142.4	4547.1	5280.7	5026.2	6225.9	4152.8	3882.1	4739.6
12274.2	3489.2	4146.6	4321.3	3583.3	3484.8	3984.2	3705.4	4329.5	5071.9	4635.7
35.4	130.5	158.0	197.3	169.6	139.2	432.3	196.8	59.2	25.8	93.4
13001.3	5037.8	4665.5	5267.8	5540.3	4994.0	5565.1	5134.8	4540.2	3790.3	3808.1
2364.0	3652.4	4430.8	3722.7	3238.9	3276.7	3737.7	3770.3	3824.6	1971.2	3860.9
2914.9	4522.9	4930.1	5070.9	5227.0	4532.3	4849.6	5110.5	4490.7	5803.9	4168.0
147.1	1476.7	2274.0	2178.7	1768.1	1848.5	1927.8	2474.3	1552.4	1829.2	1145.2
58.9	408.6	852.2	661.5	1155.4	800.2	336.0	1652.9	284.1	296.2	653.3
14867.4	7282.7	8030.8	7756.9	6561.3	7142.3	7053.0	7194.8	9017.4	7647.7	9639.4
1044.9	2823.4	2451.9	2311.8	2728.4	2422.8	2251.4	2109.9	2414.9	1860.9	1823.6
43.5	589.8	375.4	155.6	118.1	228.8	91.4	352.8	548.8	94.3	187.2
2111.8	5916.0	5991.9	5697.7	4523.1	5069.0	5056.0	6203.9	3892.2	3150.2	5981.8
186.6	1269.7	2124.0	1811.1	1638.7	1649.7	2634.4	1823.7	1550.4	1259.4	1238.8
191.9	2283.7	2975.9	3220.2	2594.5	2738.6	3361.0	3498.3	2326.2	2887.6	1815.5
9720.8	6058.3	6351.6	6619.7	6147.6	6325.5	6775.7	5951.7	7621.1	7428.9	8197.6
3337.8	3045.6	3526.1	2953.8	3304.7	3010.9	3724.2	3455.7	2455.2	3491.5	2342.7
2967.5	1877.5	2278.8	2122.2	1776.5	1853.8	2506.6	1888.8	2214.5	1876.0	1933.4
737.2	4888.3	5828.2	4488.5	3280.2	4260.6	3939.7	5316.9	2820.7	2775.3	3357.6
1972.4	3249.2	4012.2	4203.7	4167.3	3508.7	4359.7	4629.7	2903.9	3264.2	2345.2
72.4	1042.3	1669.2	2122.9	2261.2	1379.8	2694.8	1231.0	496.3	145.4	645.8
5447.8	2484.8	3457.4	3046.2	3632.3	2937.6	2934.6	3801.6	2366.3	3381.5	2013.4
5612.7	5022.9	4797.9	4843.3	4874.2	4963.9	4950.6	5296.3	3801.9	3449.7	7225.8
6965.1	4979.3	7380.6	6191.2	5432.5	6398.2	5846.3	6860.5	5533.4	6426.2	5192.8
138.5	1168.9	1712.2	1738.7	1933.0	1411.5	1996.7	1478.0	793.7	1196.3	1021.2
115.3	2975.2	2618.9	2727.9	2411.8	2453.8	2608.1	2951.7	1621.9	2164.7	1651.8

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6791.2	9716.4	7509.8
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4410.7	5453.4	4306.0
2224.2	2253.4	3110.9
6678.3	6574.5	5309.7
3181.6	3782.0	3297.5
1760.8	3105.3	2357.4
4934.3	4989.8	4705.1
3650.3	5204.5	3958.5
4127.6	4214.0	3371.4
6781.0	5388.2	7723.5
4659.2	5071.2	7487.4
4768.6	5601.7	7248.9
3431.1	3804.1	6351.4
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3901.8	5114.7	4294.2
164.2	200.0	318.6
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3305.9	4061.6	4725.2
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2667.0	2255.0	2748.5
710.4	1151.7	1148.3
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1307.7	2668.4	4124.4
3775.8	3213.3	4431.8
4683.0	6295.9	6818.0
3069.4	3867.3	4798.6
1431.3	3452.7	3889.9
5244.5	5490.2	9959.3
4691.0	4039.8	5270.7
1288.2	1446.8	2784.8
3021.7	5312.2	5779.8
4885.1	4056.3	4976.0
5660.0	8102.6	10303.5
1492.8	2063.7	3490.0
2819.5	2320.8	3281.8

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GQ082187.1 gg_id:426785 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
Y07840.1 gg_id:14275 Peptoniphilus ivorii str. DSM 10022; SBH093 Y07840
EU289040.1 gg_id:249152 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
X90471.1 gg_id:14281 Peptostreptococcus sp str. 9succ1 X90471
FJ671194.1 gg_id:521628 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6711
AY167967.1 gg_id:75475 Isolation and identification hyper-ammonia producing swine storage pits manure AY1679
FJ675039.1 gg_id:528981 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
CU919308.1 gg_id:540944 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AY754832.1 gg_id:108707 Hudson river sediment clone Z35 AY7548
FJ674316.1 gg_id:518267 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
FJ825558.1 gg_id:535477 Microbial during start-up mesophilic biogas plant clone 45_BS4_8 FJ8255
FJ675649.1 gg_id:529080 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6756
DQ168650.1 gg_id:157172 sediment-free PCB-dechlorinating enrichment culture clone JN18_A14_H DQ168
FJ671648.1 gg_id:528290 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
NR_025498.1 gg_id:569679 Sedimentibacter saalensis str. ZF2; DSM 13558 NR_02
FJ674650.1 gg_id:513014 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
EF059533.1 gg_id:221904 Sedimentibacter sp. JN18_V27_I EF0595
CU927625.1 gg_id:567949 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
FJ825486.1 gg_id:568699 Microbial during start-up mesophilic biogas plant clone 178_BE2_28 FJ8254
AF427155.1 gg_id:34493 Clostridium sp. LTR1 AF4271
AY913838.1 gg_id:136382 fixed-film bioreactor clone MBR283-55 AY9138
AB294744.1 gg_id:207626 Dechlorination biphenyl polychlorinated dibenzo-p-dioxin species genus Dehalobacte AB2947
AY353956.1 gg_id:103341 Soehngenia saccharolytica str. BOR-Y AY3539
NR_025151.1 gg_id:553089 Sporanaerobacter acetigenes str. Lup33; DSM 13106 NR_02
GQ461820.1 gg_id:585584 Tissierella sp. str. LBN 299 GQ461
AB175360.1 gg_id:102260 mesophilic anaerobic BSA digester clone BSA1B-06 AB1753
AB332034.1 gg_id:312984 Tepidimicrobium sp. str. HUT8119 AB3320
AY466712.1 gg_id:101098 Clostridiales NS4-1 AY4667
AB436741.1 gg_id:284303 Clostridium sp. str. AAN13 AB4367
AF280824.1 gg_id:72660 bioreactor clone tbr1-9 AF2808
GQ461826.1 gg_id:587283 Tepidimicrobium ferriphilum str. DSM 16624 GQ461
X80833.1 gg_id:14261 Tissierella praeacuta str. ATCC 25539 X80833
GQ461802.1 gg_id:544735 Tissierella praeacuta str. AIP 224.02 GQ461
FN436079.1 gg_id:567822 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN4360
FJ675493.1 gg_id:517458 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
DQ378266.2 gg_id:151594 oil-polluted soil clone M50_Pitesti DQ378
FJ825564.1 gg_id:561089 Microbial during start-up mesophilic biogas plant clone 62_BS5_26 FJ8255
AM500851.1 gg_id:560842 proof spatial heterogeneity hot composting clone F132 AM500
EU887816.1 gg_id:321681 Tissierella praeacuta str. SN5 EU8878
FJ672701.1 gg_id:510178 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
GQ461818.1 gg_id:579451 Tissierella sp. str. LBN 291 GQ461

107.7	1434.1	1556.8	1707.0	1858.6	1543.4	2137.3	1524.8	1548.8	411.5	1473.0
6165.2	4908.9	5696.7	5488.4	5133.1	4777.2	6053.4	4958.6	4228.5	3284.4	5978.5
1315.1	3883.9	5777.2	4696.7	3786.5	4673.2	4115.4	5508.8	2786.3	1570.6	5630.6
130.7	117.9	208.4	191.2	270.8	164.7	74.6	1499.4	136.3	57.4	284.7
678.1	4078.2	4967.7	5084.4	5005.6	4122.0	5542.7	5878.8	3003.8	2934.4	4528.6
41.4	59.0	101.0	48.1	37.2	23.3	33.4	36.2	50.9	23.6	39.7
2836.0	2473.2	2531.0	2378.0	1820.2	2323.7	2086.2	2496.4	2020.7	1237.0	2164.9
1670.4	6642.5	7085.9	7304.6	8081.7	7025.6	8696.5	7466.7	6255.4	5732.6	5747.3
9520.5	4921.3	4709.2	5490.1	4886.4	4375.4	4857.2	4542.5	6464.0	4924.4	6238.8
359.0	1974.5	2550.8	2554.8	2067.2	1790.4	2120.6	4042.1	4911.2	451.7	2064.6
3462.7	2248.5	2824.9	2690.1	2596.4	2357.2	2632.5	3335.3	1652.6	2236.7	2206.4
118.4	2244.0	2596.1	2555.1	1978.8	2245.6	2384.5	2583.1	1793.1	1098.9	1716.2
312.4	2621.1	3454.3	3286.5	2657.4	2994.4	2747.6	3959.1	1597.5	1003.7	3549.4
4119.5	3443.9	4265.9	4408.9	4234.2	3722.2	4428.6	4347.1	3139.9	1941.7	4545.8
140.3	523.2	936.8	696.9	562.2	654.3	669.2	622.9	1111.6	586.0	458.5
333.1	1603.4	1991.3	1799.9	994.3	1648.3	1616.7	1858.5	954.5	360.5	1309.2
1376.9	3365.1	4165.9	3683.3	2900.8	2983.3	3788.5	4053.6	1872.1	2807.4	4496.1
1790.8	3992.7	3499.3	4178.4	3579.8	3295.8	3634.6	3626.1	2424.4	2735.0	2941.6
12481.6	3545.6	3851.6	5246.0	3553.7	3709.0	3894.2	4683.7	2705.2	2671.0	4095.6
9607.1	3944.4	4014.2	3886.5	3617.7	3682.4	3811.5	3562.9	5475.1	4226.1	5376.4
127.9	2169.8	2586.0	2177.9	1374.5	2102.7	1505.3	2008.3	1118.0	1698.7	2210.1
175.9	2099.3	2312.6	2403.7	2148.7	2413.8	2852.9	2192.6	2014.2	2007.9	3483.3
156.5	847.5	1241.5	1351.4	1094.8	895.5	972.4	2754.8	383.8	228.5	1972.9
45.9	66.9	125.6	120.1	89.7	259.4	75.3	85.5	48.6	54.1	53.1
578.6	3477.8	4495.2	4673.8	4357.7	4144.7	4600.7	4536.2	3388.3	5732.7	4080.6
212.9	1752.8	2758.4	2568.2	1304.0	1915.4	1788.6	2908.9	906.6	526.3	2444.7
51.9	53.1	57.4	258.4	78.2	205.9	116.1	267.1	31.6	162.6	118.8
13929.7	3865.8	3292.1	4597.4	4204.7	3123.3	3728.2	3667.3	4685.0	6234.8	5081.1
2267.3	9295.4	7431.7	6054.2	5481.3	6955.7	4237.9	5915.1	9195.8	7524.9	6277.7
30.9	303.4	381.8	521.9	1024.5	403.0	1639.0	452.0	116.0	75.4	149.2
638.1	1566.4	2700.0	2649.2	2515.7	2402.2	3026.9	2278.6	1222.3	2259.9	3634.8
3829.8	998.2	1722.5	1674.2	1369.3	1264.7	1822.7	1615.3	1196.2	771.7	1660.1
1598.5	1244.1	2173.0	1643.5	1342.8	1439.3	1648.6	2324.7	1035.8	399.3	1530.2
14244.6	6094.9	6157.7	7476.5	6819.2	7412.1	6813.8	6294.3	5785.9	9622.8	6412.3
283.8	1896.4	2048.6	2036.9	2304.5	2280.1	2258.8	2432.5	1813.4	1039.2	1578.3
4792.6	3458.6	3509.1	2643.6	2976.7	3442.4	3328.8	3070.8	5106.6	2709.7	2885.3
2829.7	3433.0	4296.8	3688.0	3383.0	3680.5	3780.0	4567.3	3336.3	3926.7	2664.7
178.4	3905.1	4804.0	4824.9	4676.6	4473.0	5308.2	4575.5	3402.1	4984.2	4417.0
1030.3	6821.1	7712.9	8116.4	4922.9	6988.7	7126.3	6512.1	5746.8	6130.8	8021.4
147.3	1473.7	1424.6	1943.6	2006.6	1501.8	2302.2	1502.6	1467.7	731.4	1286.8
72.9	787.5	1356.6	1360.7	742.0	1000.8	1407.8	1126.4	606.5	123.4	454.5

1670.7	1628.0	2221.4
4904.4	5522.9	6921.6
4921.5	5024.1	5835.0
721.3	470.7	645.1
4556.2	3881.1	7518.0
43.6	107.4	51.3
2549.0	3765.0	3857.8
8072.1	6471.8	11633.5
4572.3	6044.5	9189.3
2502.4	2386.3	4896.6
3880.5	2960.1	7645.8
3032.1	2639.9	4998.1
4199.3	3040.6	5863.7
3421.8	4931.5	5241.9
539.6	1057.0	505.4
2056.6	2233.7	4522.9
4084.7	4133.6	10385.1
3199.7	4011.0	6654.8
3628.1	4013.6	8864.4
3681.5	4506.7	5131.4
1755.2	1981.0	4209.8
2316.9	2619.5	3809.6
803.3	1106.9	1192.4
69.8	90.6	28.2
4310.4	5188.8	5798.8
1675.4	2218.7	2817.7
194.4	354.9	405.7
3311.6	5070.1	4626.6
5694.2	5963.7	7343.3
382.2	477.7	914.5
2231.1	2868.1	3018.0
1055.9	1925.3	3375.6
1465.6	2235.7	3269.3
6425.5	7483.5	11093.3
2205.5	2364.6	4256.6
2977.4	3606.2	3677.3
3948.6	4019.1	6696.8
4233.3	4625.7	9116.7
5580.9	5242.4	7636.1
1099.2	1297.7	4624.7
707.1	1174.8	2598.9

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FJ825528.1 gg_id:543440 Microbial during start-up mesophilic biogas plant clone 66_BS1_7 FJ8255
X75909.1 gg_id:14266 Clostridium sp str. BN II X75909
AF443595.1 gg_id:88113 Clostridium sp. str. ArC6 AF4435
FJ674955.1 gg_id:516090 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
GU112188.1 gg_id:551545 library biogas slurry anaerobic fermentation pig manure clone 52 GU112
GU455356.1 gg_id:528917 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
GQ054096.1 gg_id:465377 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1098e GQ054
AJ002593.1 gg_id:14269 Clostridium sp.PO AJ0025
GU455275.1 gg_id:530269 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
GQ028320.1 gg_id:460097 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ028
EF174267.1 gg_id:184280 direct activated sludge compost maturation stage clone H1-814 EF1742
GQ006814.1 gg_id:502850 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88a10c GQ006
EU037326.2 gg_id:265875 structure landfill sediments receiving long-term augmentations wastes chromium co EU0373
DQ447178.1 gg_id:156727 Coexistence homoacetogens and heterotrophic sulfate-reducing synthesis gas fed la DQ447
GU455358.1 gg_id:521864 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AB222052.1 gg_id:132531 Clostridium sp. str. EBR-02E-0599 AB222
GQ077044.1 gg_id:394722 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1206b GQ077
GQ027206.1 gg_id:434668 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ027
EU289106.1 gg_id:242578 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2891
DQ887923.1 gg_id:163666 thermophilic anaerobic solid waste bioreactor clone GHB3D11 DQ887
GQ461816.1 gg_id:541364 Tissierella sp. str. AIP 285.00 GQ461
GU455269.1 gg_id:532271 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
DQ532342.1 gg_id:172183 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
GQ004946.1 gg_id:504716 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65b0 GQ004
GQ026805.1 gg_id:447236 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ029521.1 gg_id:436394 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw862e05 GQ029
GU455219.1 gg_id:515391 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
DQ887969.1 gg_id:164133 thermophilic anaerobic solid waste bioreactor clone TIBG06 DQ887
AY169425.1 gg_id:81585 Finegoldia magna AY1694
AM500724.1 gg_id:548585 proof spatial heterogeneity hot composting clone D18 AM500
AB294307.1 gg_id:210515 Microbial structure deep coal seem groundwater clone YWB38 AB2943
EF586050.1 gg_id:240034 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
GQ015365.1 gg_id:494301 Topographical and Temporal Human Skin Microbiome skin palm clone nbw767e08c1 GQ015
GQ079937.1 gg_id:406655 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
GQ016716.1 gg_id:492950 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw824g0 GQ016
EU523731.1 gg_id:261418 methanogenic microbial consortia mature oil sands tailings clone 12-2A EU5237
EU289047.1 gg_id:236547 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
FJ674639.1 gg_id:526334 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
CU919210.1 gg_id:560673 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
FM873737.1 gg_id:364028 occupant source house mattress dust clone MA03H02 FM873
GQ004012.1 gg_id:505653 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67e0 GQ004

41.4	1859.6	1961.1	2505.9	1580.5	1593.2	2154.7	2146.2	740.9	692.3	1581.8
27.3	82.7	157.0	172.5	61.6	207.7	80.1	179.3	100.3	269.8	105.9
349.3	10898.9	7353.9	7562.0	4909.3	6440.0	6549.7	6175.3	4453.7	2013.4	7898.3
136.4	3503.6	3582.7	3441.8	2777.7	3690.4	2725.3	3925.8	2806.6	2027.3	2875.4
46.8	1415.3	1908.0	2046.7	1305.8	1665.1	1799.2	1801.3	586.9	405.2	1275.3
172.4	2212.0	3161.5	2932.1	2252.4	2200.7	2314.4	2918.2	1466.5	1432.1	2526.4
10759.6	7498.8	8530.6	7581.6	7117.7	7629.2	8704.6	7952.6	9801.1	7333.7	9419.2
44.1	37.8	87.8	70.9	50.7	40.4	66.0	49.9	35.2	42.3	47.9
3298.7	9446.3	7366.6	5169.6	6653.3	7707.8	6825.7	4603.1	10628.1	6811.7	6302.4
2932.2	3819.7	5358.5	4300.6	3899.2	4313.3	5344.0	5204.1	3836.3	6252.7	3846.3
212.4	1108.0	1603.3	1586.1	1897.1	1133.5	3482.8	1406.4	641.4	193.6	1390.6
4043.1	5590.4	6012.5	5129.7	4421.9	5653.8	6884.1	6149.0	4784.1	5829.0	5527.7
9171.8	4036.2	3786.1	3738.9	3464.2	3702.9	4599.8	3468.3	5100.3	3402.8	5318.2
1748.6	3346.8	2949.0	2853.0	2739.3	2594.5	3268.1	2666.4	3114.5	1239.4	2977.9
5247.5	8815.4	9090.4	9069.5	9740.9	8129.1	10631.4	7885.6	6464.0	4941.8	9768.5
10707.8	5831.4	5308.8	4826.3	6191.5	5097.1	6143.2	4451.2	3727.7	5571.6	5759.1
93.4	757.3	908.0	1004.4	610.7	622.5	653.3	857.5	343.7	152.4	432.5
10370.9	7783.6	7280.5	7449.5	6238.4	7760.3	10600.5	7385.2	8570.9	7313.3	10177.2
6394.2	8247.3	7369.8	6349.4	5303.5	6639.1	5889.3	5719.2	8663.0	7242.4	6843.6
1201.2	1151.1	2010.3	1206.2	1197.9	1316.6	1644.5	2052.7	883.4	671.3	1538.2
1560.6	5355.0	4867.1	4817.9	4783.5	4408.8	4810.7	4931.0	3999.7	6857.0	4652.0
7139.6	4944.0	4995.1	5127.0	5803.4	5037.0	6156.7	4890.9	5220.7	5055.4	5080.4
16349.2	5658.1	5699.0	6068.3	5489.7	5424.3	6854.0	5561.6	8052.8	8113.0	7804.7
114.2	2717.3	3540.8	2594.9	1908.6	2484.5	2759.7	3279.5	2153.1	1877.6	3083.0
1749.4	5382.6	5370.7	5149.7	3603.3	4374.4	5840.9	5639.5	4302.4	3628.9	5563.4
4338.7	6818.7	6588.3	5019.8	4289.6	4288.3	6394.9	6905.5	6554.5	7101.5	5810.9
3209.5	4232.4	5256.5	4959.8	4674.1	4605.9	4607.3	5097.0	3786.8	3601.2	4865.7
56.0	33.7	34.8	28.0	39.3	22.5	27.6	21.7	26.0	38.0	36.1
443.4	2420.8	2763.5	2865.9	2144.2	2361.3	3600.8	2386.1	1586.8	1206.9	1717.7
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36.1	66.2	40.4	54.3	32.3	48.6	38.6	37.6	33.3	13.0	33.7
607.6	3997.7	3904.9	3956.0	3452.7	3683.3	4087.8	2824.8	2782.2	2070.5	2977.4
7613.7	4736.9	4799.2	4489.6	3478.6	4037.7	6032.3	5273.8	5377.9	3876.7	5268.3
8138.7	4017.7	4932.2	4302.7	4201.6	4368.3	5952.3	5062.5	4277.6	6517.7	4028.3
14756.6	6102.3	6557.8	6044.3	4984.1	6598.8	8145.2	6294.7	7173.4	5663.6	7435.6
146.4	1267.6	1481.3	1104.3	1385.7	1415.1	1875.5	1390.3	781.5	527.4	1128.6
4660.7	6381.8	6754.7	6287.8	6170.3	6111.9	6385.4	6371.1	5908.5	3971.3	6114.0
71.5	1179.4	2065.9	1728.1	970.2	1263.7	1743.0	1745.6	811.1	389.3	1419.1
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13628.8	5792.9	5208.3	5908.7	5116.4	5540.9	7745.2	6475.4	5728.9	6804.7	7601.5

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175.8	174.0	510.2
5655.2	5702.1	7127.3
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1133.2	1608.8	3003.8
2635.3	3297.4	3980.4
7768.7	7910.7	7315.1
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4696.0	5710.9	6207.4
1029.4	1038.1	2551.6
5325.0	6330.4	7456.8
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2473.9	2917.5	4442.8
8033.1	9162.5	11112.7
4627.5	4878.7	5219.2
668.8	832.5	1159.4
6336.1	8243.7	6593.0
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1579.3	2022.9	2580.2
4376.1	4460.6	8472.5
5430.9	6211.8	5429.9
5580.7	6857.3	6447.2
2119.2	2826.6	2654.5
3931.6	4972.2	4935.0
4870.3	8253.5	8145.9
4559.1	4814.5	7336.1
19.6	27.3	63.4
2381.5	2827.8	3914.1
1557.2	1364.4	2726.5
47.8	69.9	319.9
2832.9	3860.8	4885.7
3392.2	5894.0	4451.2
4564.3	6236.6	5853.0
5151.2	8183.4	6984.1
1043.3	1277.8	4189.2
6115.9	5793.6	7670.5
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4743.5	6778.8	6583.6
3073.4	4070.1	5043.4
5280.6	7151.5	5909.1

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GU455253.1 gg_id:520156 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
FJ672003.1 gg_id:527552 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
GQ032132.1 gg_id:453352 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
EF586044.1 gg_id:239034 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
FM873179.1 gg_id:367696 occupant source house floor dust clone FC02H05 FM873
EF559008.1 gg_id:256589 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
GU455217.1 gg_id:514459 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
FJ674852.1 gg_id:522075 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
EU842984.1 gg_id:325610 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8429
GQ179692.1 gg_id:451042 Heterogeneity vaginal microbial within individuals vagina clone VE58A09 GQ179
EU289054.1 gg_id:254577 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2890
AY207059.1 gg_id:83665 Peptostreptococcus sp. P3 str. P4P_31 AY2070
GQ077578.1 gg_id:432408 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1210e0 GQ077
EU289126.1 gg_id:236687 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU2891
FJ672085.1 gg_id:524642 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6720
GQ037136.1 gg_id:402486 Topographical and Temporal Human Skin Microbiome skin palm clone nbu389c09c1 GQ037
GQ003924.1 gg_id:505737 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu66c09 GQ003
GQ082499.1 gg_id:408773 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
GQ032012.1 gg_id:379026 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ009384.1 gg_id:500281 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ009
EU931446.1 gg_id:523577 examined methods chronic venous leg ulcer clone CONR40 EU9314
AM500842.1 gg_id:561616 proof spatial heterogeneity hot composting clone F68 AM500
GQ047234.1 gg_id:464149 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010c GQ047
GQ033406.1 gg_id:464209 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ033
EU407217.1 gg_id:259078 household biogas digester clone GW-34 EU407
AF016691.1 gg_id:14132 Acidaminobacter hydrogenoformans str. glu 65 AF0166
EU591652.1 gg_id:275236 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic EU5916
EU517558.1 gg_id:267846 methanogenic microbial consortia mature oil sands tailings clone 22-7A EU5175
AF491333.1 gg_id:85424 Fusibacter sp. str. SA1 AF4913

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243.1	467.0	989.4	1065.9	1363.5	1264.9	1263.0	1086.4	1191.8	1142.7	1377.6
199.1	3935.7	6099.5	4102.2	3631.5	4323.4	4119.8	4458.4	3040.5	1411.6	2982.4
41.3	693.2	946.3	877.6	949.6	571.7	602.3	851.9	221.4	355.2	427.5
1541.7	4460.4	5800.8	5483.8	3593.1	5228.4	4474.2	5435.3	2600.5	1133.2	5285.9
211.3	2779.3	2779.1	2296.7	2028.3	2921.7	2529.6	2907.0	1466.7	1505.8	2180.5
3155.3	4382.7	4523.1	4201.6	3097.2	4349.2	4871.7	4282.0	4004.8	3666.6	4371.6
68.6	2773.4	3770.8	4011.3	2609.4	3144.5	2690.8	3511.6	2508.9	1595.6	2638.0
1294.4	4310.9	5110.1	4141.2	3682.3	4524.9	4424.1	5593.4	3283.9	3584.2	3856.7
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327.9	3433.7	4503.8	3018.4	1688.6	2891.8	3345.0	3650.8	3114.6	4315.8	3939.0
2119.8	3806.3	4051.6	4011.4	3891.2	4960.9	5098.9	4129.9	3306.8	4233.4	5697.1
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2740.5	6442.7	6235.3	6219.5	6967.1	6075.1	6846.0	6210.6	4803.8	6887.3	5856.0
16625.3	5630.2	6004.6	6791.8	6486.4	5854.2	7944.9	5488.8	8732.7	6804.0	6464.1
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14748.9	6975.4	6484.6	6509.4	5617.9	5513.8	5943.2	5898.8	6335.2	5043.4	8287.2
311.4	5148.1	4247.1	3948.3	3419.1	4457.5	3562.2	4213.5	2800.0	1887.3	3070.6
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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Clostridiales Family XII. Incertae Sedis
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AY570635.1 gg_id:108512 biodegraded Canadian oil reservoir clone PL-5B6 AY570
FJ167488.1 gg_id:342752 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
GQ355042.1 gg_id:583445 structure between two geochemically distinct springs Alum Rock Park spring clone M GQ355
EU662607.1 gg_id:561558 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
AB243990.1 gg_id:245248 Methods Investigate Microbial Niigata oil well clone Niigata-22 AB243
DQ378233.1 gg_id:155716 oil-polluted soil clone M13_Pitesti DQ378
FM205000.1 gg_id:534793 Prokaryote shifts and reductive dehalogenase redundancy response electron donor FM205
GU208315.1 gg_id:584294 Study on Sediment Dongping Lake sediment clone Sef3-12 GU208
AF255644.1 gg_id:41951 EBPR sludge clone Ebpr14 AF255
GQ054198.1 gg_id:422335 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099g GQ054
GQ014246.1 gg_id:495420 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760f GQ014
EF562251.1 gg_id:241088 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum EF5622
GQ014194.1 gg_id:495473 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760a GQ014
GQ054010.1 gg_id:426893 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1097e GQ054
EF419415.1 gg_id:213421 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6PN20 EF4194
GQ009336.1 gg_id:500329 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ009
AJ005636.1 gg_id:14151 Eubacterium minutum str. ATCC 700079 AJ0056
AJ006963.1 gg_id:14160 Eubacterium sulci str. ATCC 35585 AJ0069
GQ502514.1 gg_id:552342 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
FJ880553.1 gg_id:426130 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EF099448.1 gg_id:178412 mouse cecum clone SWPT3_aaa03d03 EF0994
DQ793597.1 gg_id:191389 human fecal clone RL246_aai74b05 DQ793
EU844897.1 gg_id:344416 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
GU303039.1 gg_id:576991 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842953.1 gg_id:332719 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
FJ880679.1 gg_id:420891 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8806
FJ879943.1 gg_id:380842 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
EU773171.1 gg_id:324364 BigHorn sheep feces clone BH1_aao26e07 EU773
GU304138.1 gg_id:583497 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU304385.1 gg_id:553278 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
U13041.1 gg_id:14155 Eubacterium nodatum str. ATCC 33099 U1304
GQ458236.1 gg_id:579985 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
EU842678.1 gg_id:340989 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ687606.2 gg_id:552238 Eubacterium sp. str. WAL 14571 FJ6876
AF044945.1 gg_id:14152 Eubacterium sp. str. C2 AF044
EF099332.1 gg_id:181305 mouse cecum clone SWPT3_aaa01h03 EF0993
EU452756.1 gg_id:318652 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
EU469216.1 gg_id:294038 Speke's gazelle feces clone SP3_c03_2 EU469
AB034093.1 gg_id:39613 rumen clone 4C3d-12 AB034
FJ879878.1 gg_id:409369 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
GU304486.1 gg_id:592803 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304

1780.0	5017.3	5196.5	5524.2	5009.0	4178.1	5412.1	5506.1	3427.7	3609.1	5559.7
77.9	877.2	1200.8	1344.4	627.9	880.0	991.7	1398.7	351.8	359.8	1256.3
670.7	7503.4	7059.3	7421.8	7098.4	6507.2	7199.2	7000.0	6957.5	6846.1	7610.5
580.7	2021.5	2134.7	2026.5	2085.4	1968.4	2297.4	2517.4	1174.6	1598.6	1848.0
103.7	1357.3	2588.6	2916.8	1099.6	1256.5	898.7	3319.8	617.9	371.9	2724.6
42.2	820.0	1095.2	1183.0	1278.7	1030.5	935.3	1801.8	422.9	497.1	1293.0
3177.8	7773.0	8844.8	9182.1	7170.5	6967.4	7970.3	9244.7	6957.9	6124.9	10131.2
83.4	2117.7	2335.5	3085.3	2135.2	2016.2	2999.7	2486.6	652.4	723.5	2499.5
37.1	1085.3	696.6	515.9	70.5	425.5	158.7	1707.9	494.6	298.0	695.7
236.7	1385.9	1551.1	1402.1	1179.0	1244.9	1312.6	1664.0	1395.5	459.9	1152.4
2209.5	5819.0	5043.1	4889.5	4626.8	5041.6	5646.3	5598.4	6806.8	4245.0	5302.3
11638.5	5540.6	6140.9	5791.3	5706.4	5350.1	6040.1	5960.7	7990.5	3932.5	7698.6
241.8	3434.2	4039.2	3627.0	3607.0	3071.4	3970.6	3851.7	3592.3	2108.4	3150.9
5278.3	3362.1	3598.8	3330.6	3630.6	3304.8	3659.7	4239.5	3938.6	1118.6	2250.0
7801.8	5780.6	6057.8	5817.4	6075.1	5398.9	7213.0	6466.5	9187.8	3872.0	7639.8
2504.3	6024.1	6764.0	6230.2	6090.1	5600.0	6431.6	6816.3	8032.8	4512.5	6847.9
42.3	17.6	14.6	22.6	14.5	15.4	16.5	17.3	17.3	15.5	14.1
28.3	44.0	46.8	48.4	20.7	41.2	42.1	25.8	25.5	13.3	47.4
33.9	221.6	291.2	241.5	218.9	213.5	388.3	256.7	121.4	81.1	161.0
1517.5	4321.5	4312.2	5532.2	3935.0	4160.2	4512.4	3981.5	5529.8	2116.7	4428.0
502.7	1272.6	1736.5	1633.2	1274.1	1310.4	1209.7	2337.2	2073.0	803.3	1441.0
887.4	1098.6	1440.2	1613.6	743.6	1021.8	997.9	1220.6	1347.1	658.0	1196.5
13694.3	8550.4	8974.9	9245.2	8326.3	8410.2	9413.8	8763.3	8068.3	9270.7	9658.3
10449.4	8868.6	10196.5	9810.9	9751.4	8808.2	10727.5	9160.5	7783.2	7277.5	10579.0
938.9	1691.7	2265.4	2210.6	858.1	1849.4	2120.8	1525.7	1416.7	764.7	1548.1
106.7	998.0	1299.0	1270.5	1194.4	1512.2	832.7	1788.3	620.1	963.7	666.4
4060.7	5057.4	6866.1	6227.1	6161.8	5308.8	7137.2	6070.0	4789.2	2392.4	5636.6
1727.2	3647.0	3315.1	3693.8	2944.3	3630.7	4240.0	4036.7	2571.1	4030.5	3390.4
119.9	711.2	1125.0	933.2	526.1	728.8	820.5	1138.3	209.0	191.5	618.7
21755.2	7480.2	7986.4	8290.1	7729.4	7454.3	9209.2	7422.7	9827.1	6278.5	9648.0
57.0	38.1	61.5	59.3	47.2	47.7	34.6	50.0	43.5	35.8	57.1
6624.5	3189.9	3814.8	4321.5	3631.0	3079.0	4999.1	3262.4	3403.2	2244.0	3382.8
651.2	4103.2	4198.8	4275.2	3531.8	3353.7	3720.1	3891.5	3544.6	2374.6	3294.3
338.4	4353.2	5033.1	5163.2	4365.7	4014.6	5002.8	4740.3	3243.0	2366.3	3932.3
274.9	667.7	1101.1	936.0	982.4	1031.0	1382.9	1205.8	769.9	345.2	569.6
85.4	957.4	1515.2	1149.2	751.1	1083.7	951.8	1260.3	582.9	176.3	953.8
2655.5	520.7	525.4	574.3	134.9	365.9	469.9	548.7	493.7	365.3	434.6
372.8	670.6	1413.1	953.5	664.0	737.6	959.9	1138.6	368.8	192.3	496.4
36.6	274.5	427.3	483.8	210.4	310.3	307.4	506.9	162.3	83.8	264.3
49.8	1643.9	2446.9	1874.2	1562.8	1892.7	1874.0	2339.7	1097.6	521.5	1697.8
2008.0	2624.4	2863.1	3404.4	2212.4	2595.7	3103.1	2904.4	1882.6	1069.6	1948.6

4380.9	5338.8	5462.7
710.5	812.0	839.7
5716.3	7436.5	7247.6
2389.0	2704.5	3549.3
2186.9	1772.2	2193.6
1202.4	1399.3	2273.8
7978.6	7359.8	7937.8
1968.3	605.4	818.6
808.6	152.7	84.7
1997.0	1850.4	2206.1
5682.0	4579.8	7359.6
5838.9	5774.8	7612.3
3723.8	3475.8	6793.8
3900.2	4063.7	6094.2
6496.5	5966.4	8155.8
6662.2	6449.8	7214.0
14.9	16.6	20.1
36.9	57.2	124.4
376.8	363.9	506.2
4328.2	4916.3	5578.6
1371.0	2596.0	2052.7
1097.8	1683.5	1605.2
8839.9	9273.5	11969.5
8622.2	8843.5	14011.9
2156.7	2874.7	3364.9
1566.5	1155.5	2085.8
5105.2	5647.4	8949.7
3440.0	3907.6	4349.9
1729.0	893.4	4212.4
6922.1	8093.9	10592.2
42.0	48.2	40.9
2869.8	4163.8	4727.9
3290.9	4410.9	5390.0
4864.5	5791.8	5870.6
1417.9	1150.3	1181.3
1258.6	1269.5	1937.0
451.2	1048.6	971.5
689.1	989.9	1721.9
586.6	379.8	527.7
1946.2	1629.1	3098.0
3406.7	3627.1	6111.2

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

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g__Eubacterium
g__Mogibacterium
g__Mogibacterium
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FJ983009.1 gg_id:451218 Aspects Oral Microbiome root canal clone FJ9830
EU777969.1 gg_id:342539 Black rhinoceros feces clone RH_aaj90f11 EU777
Z36296.1 gg_id:14163 Mogibacterium timidum str. ATCC 33093 Z36296
AB037875.1 gg_id:46159 Mogibacterium neglectum str. ATCC 700924 (=P9a-h) AB0378
AF371681.1 gg_id:36226 swine intestine clone p-3263-42A2 AF3716
EU794083.1 gg_id:304402 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E28 EU7940
FJ680355.1 gg_id:525024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
DQ797373.1 gg_id:189641 human fecal clone RL248_aai98e08 DQ797
EU771238.1 gg_id:309179 Asiatic elephant feces clone AE1_aaa03b04 EU7712
GU303467.1 gg_id:588896 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU234217.1 gg_id:239736 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
EU457038.1 gg_id:342368 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4570
GU304097.1 gg_id:584897 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GQ014713.1 gg_id:494953 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763c GQ014
FJ833233.1 gg_id:508773 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q202_47G06 FJ8332
GU303409.1 gg_id:583010 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842915.1 gg_id:335229 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8429
EU470097.1 gg_id:289968 trancaspain urial feces clone TU1_aaa01h04 EU4700
AY858404.3 gg_id:112328 gastrointestinal tract Grant's gazelle clone GRANT32 AY8584
EU469300.1 gg_id:301283 Speke's gazelle feces clone SP3_f08_3 EU4693
EU462515.1 gg_id:302242 Sumatran orangutan feces clone orang1_aai56b09 EU4625
EU468647.1 gg_id:295362 okapi feces clone OK2_d11_1 EU4686
DQ353910.1 gg_id:150089 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z23 DQ353
GU303120.1 gg_id:580364 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
DQ325886.1 gg_id:148168 Metagenomic gut microbiome healthy human stool clone B691 DQ325
GU304081.1 gg_id:577079 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU234134.1 gg_id:236437 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU2341
EU776276.1 gg_id:319547 Red Kangaroo feces clone KO1_aai42d10 EU7762
DQ325813.1 gg_id:147447 Metagenomic gut microbiome healthy human stool clone B543 DQ325
EU344320.1 gg_id:276794 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
GU304446.1 gg_id:586769 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
GU302749.1 gg_id:589680 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ801393.1 gg_id:196828 human fecal clone RL388_aao94h07 DQ801
EU463611.1 gg_id:288422 domesticated horse feces clone horsej_aai89g02 EU4636
EU748523.1 gg_id:341085 neotropical folivorous flying bird adult hoatzin crop clone hoa61_11e08 EU7485
EU748100.1 gg_id:307485 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42b01 EU7481
DQ325766.1 gg_id:147449 Metagenomic gut microbiome healthy human stool clone B444 DQ325
AF371687.1 gg_id:28381 swine intestine clone p-1032-a5 AF3716
DQ394650.1 gg_id:151714 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
AY854283.1 gg_id:109624 herbivore gastrointestinal tract clone CATTLE_21 AY8542
GU303390.1 gg_id:535500 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303

42.9	86.4	168.9	229.7	176.7	190.8	126.8	249.2	80.9	55.2	112.2
5313.6	6146.5	7444.5	7786.1	7541.1	6552.4	8314.8	6558.3	6816.0	3620.2	7110.3
207.1	1056.2	2083.8	1049.2	1057.8	1173.8	1684.3	1202.5	757.1	356.8	1069.4
269.7	1213.9	1525.4	1748.1	750.2	1200.9	1457.4	1617.8	567.7	224.7	1318.6
123.9	1994.1	2685.5	2667.4	2070.2	2171.0	2468.4	3314.0	1411.0	406.9	1641.7
86.0	2843.1	4154.7	3300.1	2459.0	3160.4	3107.5	3498.6	2780.2	1988.8	3211.9
8012.5	5083.1	5105.0	4207.0	3053.7	4451.7	4062.7	4674.3	5608.3	4513.0	5621.1
347.2	2585.9	3492.8	3014.7	3161.8	2621.1	3486.6	3813.9	6869.5	2935.5	3025.4
7068.6	6305.3	7025.8	6796.2	6163.5	5884.4	6723.5	6395.0	5411.5	3200.9	7272.6
5290.0	3690.4	4346.5	4360.6	4607.5	4326.2	4964.0	4993.9	3841.1	1571.6	4616.7
6645.3	4331.9	3976.5	3414.9	3651.6	3979.1	4064.1	4130.4	5507.3	4505.3	2927.2
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1191.6	5316.7	5423.7	5917.1	5611.9	5546.7	6287.1	5615.9	4946.2	8666.7	5539.0
486.7	1872.9	1746.6	1813.4	1799.6	1594.9	1515.5	2281.8	1717.5	425.7	1248.3
113.7	3932.8	4425.2	4427.1	3850.5	3739.3	4339.5	3823.1	3131.6	3469.5	3795.3
6052.7	2912.6	2985.1	3002.7	3173.7	3144.6	3411.8	2984.9	3258.0	1513.8	3292.1
82.0	1348.3	1936.5	2216.6	1489.7	1463.6	1816.2	2383.2	659.0	544.7	1821.9
2127.1	2261.4	2424.2	2565.5	3346.9	2663.3	3287.0	2587.5	2156.0	2884.4	1941.0
33.7	42.2	48.6	34.8	40.2	45.8	38.8	31.0	30.6	29.5	31.0
248.7	2914.8	2273.5	3546.9	3564.7	3127.9	3934.7	3238.7	3060.6	3715.8	3043.3
3943.6	4633.7	4693.5	4142.7	4860.8	4993.7	4031.5	4962.1	3855.2	9273.5	3566.3
1084.3	4826.2	6289.9	5991.4	4716.6	5029.9	5996.0	5574.8	4037.2	2309.0	4932.4
2762.6	4935.5	7299.9	5951.8	5523.6	5450.5	5949.1	5211.6	4021.8	1932.8	5378.6
1174.3	5918.3	6461.3	5855.6	7038.3	4864.6	6379.5	5994.7	8935.5	4902.3	5082.2
277.3	490.4	668.0	595.6	1087.4	557.7	805.0	830.7	313.2	1795.6	560.6
272.0	3429.6	4129.3	4046.4	4006.0	3500.2	4372.4	3858.3	2039.0	3038.1	4120.4
1413.3	3878.1	2279.8	3565.9	2782.7	4055.3	4381.0	3855.6	3790.7	2993.4	3266.0
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562.4	3030.3	3378.7	2847.0	2854.5	3084.0	3283.9	2899.5	2608.7	1122.2	2151.1
803.8	3420.1	3830.2	4130.4	3914.4	3503.3	4807.7	3298.8	2916.5	2364.6	3992.1
30.4	69.5	82.1	87.7	40.7	64.7	57.3	76.9	31.1	25.0	78.9
1186.9	1578.2	2097.8	2057.3	1305.3	1547.6	1937.4	1634.8	1045.3	465.7	1499.6
3787.6	5165.8	6894.8	6588.5	7751.8	5266.1	7400.7	5692.4	3872.0	2500.3	4742.2
6204.7	6742.0	6059.7	6508.5	4164.2	5543.8	5119.9	6670.2	11791.7	6787.4	7079.4
294.2	1864.2	2839.2	1757.1	1329.0	1889.3	2117.0	2309.9	1535.8	979.7	1753.8
7698.1	5500.9	5860.0	6364.9	7135.9	5630.3	6588.7	6895.8	6481.1	6869.2	6695.9
6156.4	4813.2	5028.9	5111.5	4672.4	4996.6	5462.9	5211.9	5333.8	5208.3	4300.0
5241.9	2258.4	3023.7	2605.8	2590.8	2190.2	3287.8	2617.2	2445.0	2724.6	2481.3
1418.4	2899.6	2952.4	2963.1	2598.2	2712.8	3099.1	3417.2	1725.5	2381.5	3298.1

210.8	466.6	224.7
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878.0	1228.8	2893.0
1475.5	1609.7	1769.2
2668.1	3180.1	3748.1
3401.2	3717.1	4727.4
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2861.1	4066.2	3596.4
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43.2	42.9	85.2
3137.7	3151.6	4663.2
4254.6	4391.4	4709.6
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3074.3	4252.0	5029.7
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1488.2	2532.8	3376.2
5548.7	6501.6	6741.3
6551.7	6953.5	5885.1
1948.5	2596.0	3282.5
5687.6	6495.7	6569.9
5534.3	4675.0	7383.9
2226.2	3142.3	4060.4
2947.5	3680.3	3523.5

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o__Clostridiales	f__Clostridiales Family XIII. Incertae Sedis
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GQ088939.1 gg_id:461939 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
AB218305.1 gg_id:148228 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-3 AB2183
EU775736.1 gg_id:320853 Horse feces clone horsej_aai91a05 EU7757
DQ797955.1 gg_id:184240 human fecal clone RL302_aal93g12 DQ797
EF586058.1 gg_id:249539 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EU878314.1 gg_id:510808 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
EF559085.1 gg_id:223604 mesophilic anaerobic digester clone B35_F_B_E05 EF5590
EU639283.1 gg_id:324728 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6392
EU591634.1 gg_id:271468 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic : EU5916
AB274505.1 gg_id:203717 packed-bed reactor clone CFB-16 AB2745
AY684094.1 gg_id:137161 first genome data rice I methanogens combination cultivation and techniques metha AY6840
FN563391.1 gg_id:572575 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
EU639029.1 gg_id:316446 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6390
EU358732.1 gg_id:304420 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EF603619.1 gg_id:229057 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
X86690.1 gg_id:13929 Dehalobacterium formicoaceticum str. DMC X86690
AB486500.1 gg_id:568326 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4865
EF603618.1 gg_id:230762 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
AM943569.1 gg_id:258502 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hyper AM943
EU259468.1 gg_id:238635 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC92 EU2594
EU469050.1 gg_id:296184 Speke's gazelle feces clone SP2_e04_3 EU4690
AY426448.1 gg_id:106335 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B35 AY4264
EF614786.1 gg_id:229827 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EF515659.1 gg_id:227372 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5156
AY991064.1 gg_id:130311 mouse cecum clone C13_I13 AY9910
FJ879326.1 gg_id:449353 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EF614689.1 gg_id:231836 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
GU303484.1 gg_id:575101 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU134643.1 gg_id:244028 tallgrass prarie soil clone FFCH13041 EU1346
EF559162.1 gg_id:221790 mesophilic anaerobic digester clone G35_D8_L_B_E01 EF5591
EU474249.1 gg_id:288109 western lowland gorilla feces clone GORSD_aaa02b06 EU4742
AY990091.1 gg_id:135305 mouse cecum clone C12_E08 AY9900
EF602919.1 gg_id:228772 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
CU918616.1 gg_id:545232 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9186
DQ015163.1 gg_id:131268 mouse cecum clone M2_d06_2 DQ015
AB546238.1 gg_id:532064 Acetobacterium carbinolicum str. Mic2c03 AB5462
AB546237.1 gg_id:523930 Acetobacterium carbinolicum str. Mic2c01 AB5462
AB294288.1 gg_id:213453 Microbial structure deep coal seem groundwater clone YWB19 AB2942
FM178819.1 gg_id:354559 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
X96960.1 gg_id:14231 Acetobacterium bakii str. DSM 8239 X96960
AY185326.1 gg_id:79463 Acetobacterium sp. clone AKS48 AY1853

42.7	67.7	74.5	103.3	165.5	128.2	220.8	62.7	38.2	59.4	48.0
190.6	1260.5	2110.2	1812.3	1544.3	1340.9	1985.2	1773.2	851.9	447.7	1280.3
4046.7	6350.0	8214.2	6548.8	7046.1	6185.1	8062.9	6755.9	5205.5	3186.0	6675.4
1103.1	7549.6	5839.7	4224.5	4537.8	6327.2	5671.7	3761.9	6064.2	4179.1	3687.1
151.6	2016.0	2168.2	2548.7	2542.4	1995.7	2733.8	2075.0	3153.4	976.9	1880.6
8194.6	5983.7	5635.6	5963.5	6174.3	5260.5	7607.0	6102.7	4756.0	3120.1	5354.0
94.6	424.2	160.0	66.8	115.3	374.9	93.1	95.9	254.7	90.7	62.9
1684.5	1604.0	1316.1	1418.9	1173.8	1228.1	1898.7	1103.4	2148.9	1628.6	2114.6
6719.2	3443.5	4076.2	4610.7	3594.8	4085.9	4808.2	4689.9	4028.8	2024.1	3878.7
629.0	1966.2	2103.6	2187.7	2508.3	1926.8	3052.5	1841.8	2725.3	2632.9	2495.2
1400.8	3097.5	3088.4	3260.1	3853.9	3221.5	3850.6	3474.7	2570.2	2636.6	2681.8
2545.2	5516.8	6472.1	6462.4	7866.3	6095.1	7865.9	6117.0	4123.2	6076.2	5418.2
56.6	578.0	566.8	750.1	665.0	498.6	1104.9	646.7	230.0	115.2	503.4
61.2	1304.8	2549.0	2279.7	2372.3	1541.8	2558.8	2078.9	1226.2	240.3	1831.9
2376.2	1599.1	1919.2	1758.9	2194.8	2106.9	2227.2	2434.8	1335.6	444.1	1845.6
88.2	4938.1	6534.5	6366.8	4485.8	5044.3	5232.6	6818.5	3516.6	2949.4	5884.7
5246.0	5425.5	6926.2	6249.9	5959.0	5648.3	5612.1	5851.9	4424.5	2014.2	4491.1
23109.0	6476.6	7473.2	7275.1	7766.2	6929.2	8334.4	7410.0	8901.1	6140.4	8497.8
1622.4	6114.5	6490.2	6483.1	5706.0	5755.4	6424.3	6546.9	5924.9	3718.4	5470.9
9039.9	11184.8	10577.5	11181.5	10630.7	10539.7	12333.7	9817.2	12468.1	10433.3	17093.5
446.0	3098.2	4605.3	4160.0	4934.5	3832.0	4302.6	4981.7	3381.3	929.6	3126.2
42.2	25.3	29.7	42.6	36.3	24.2	29.8	24.3	28.9	25.4	21.4
538.8	2477.7	3243.4	3322.5	3202.1	3022.0	4244.7	3161.4	2666.2	2127.7	3020.2
73.2	81.1	107.2	80.2	92.1	138.5	204.3	131.8	37.1	52.6	58.6
133.3	1470.0	2123.6	2040.7	1599.5	1647.0	2421.6	1717.5	951.5	585.2	1598.3
1207.7	3156.5	3507.5	3399.1	3443.4	3506.7	3871.7	3642.8	3205.6	3157.3	3535.7
4018.2	3419.7	3736.5	3923.6	4068.2	3516.7	3878.3	4047.3	3571.4	1444.5	3047.5
802.4	4699.8	7422.3	5324.5	5024.5	4374.1	5484.8	5431.7	2991.3	2242.9	3993.2
259.5	3670.0	6011.3	5318.5	4120.9	4213.4	4756.4	5592.0	6495.3	2246.4	3250.3
49.9	147.5	246.7	210.5	144.6	137.4	172.1	226.9	81.5	46.3	101.4
6362.6	7261.0	6315.0	6562.8	6635.8	6690.8	6574.2	5703.0	8377.5	7063.7	7240.0
40.1	894.6	765.8	1074.7	1307.3	1446.2	1521.1	1083.0	688.8	430.3	693.6
47.2	31.1	51.3	28.6	20.9	36.6	22.1	26.6	21.4	9.1	36.9
3671.2	3928.4	4063.4	4104.2	3626.7	4268.6	3037.8	4576.3	3506.7	2207.0	2955.8
73.2	395.7	394.5	443.7	601.2	932.7	528.4	603.8	580.8	70.5	296.3
2995.5	5969.0	6563.8	5556.8	5960.2	4885.1	7256.9	6454.2	5158.3	3885.8	6448.8
3663.8	4959.3	5556.5	5873.6	5625.2	4112.7	5636.2	6335.0	5317.3	5159.5	5006.6
1376.7	1874.8	2236.2	2292.2	2129.0	1152.5	2451.1	2712.9	2158.9	2180.2	1349.1
20571.5	6648.1	7149.3	7083.6	7278.4	6827.6	8370.4	7378.8	9759.6	7605.9	7732.0
666.5	2946.7	3312.2	3633.9	3637.4	3115.5	4139.5	3947.4	3210.7	2279.5	2226.5
7774.1	4883.3	4906.6	5143.1	4316.4	4654.7	5322.8	5419.0	7558.6	5047.4	6200.8

114.3	181.4	101.2
1707.4	1761.1	2359.2
6919.0	7292.2	8606.4
4458.1	3947.2	6781.9
1767.8	2613.5	2904.5
7003.9	8863.3	7314.8
73.0	74.5	115.9
1283.8	2148.0	2261.8
5279.2	4553.1	5401.0
2259.7	2472.8	2204.7
3213.0	3874.1	3941.0
6084.3	5538.1	9536.1
407.9	926.7	1240.3
1384.3	1309.8	2197.1
1645.7	2448.0	2847.8
7737.8	5529.4	7356.5
6374.1	6146.3	9248.0
6799.3	8236.9	7901.8
6823.6	6355.0	9321.8
10216.8	10393.0	11052.0
4644.4	4601.9	5134.5
39.4	32.7	29.9
2551.2	3947.2	4068.5
65.1	186.5	489.0
1790.3	2511.8	3073.6
3422.7	3301.4	4210.9
4180.3	4771.5	4679.9
5681.2	5858.5	6911.3
4578.5	6042.2	7643.3
152.0	293.3	712.8
6352.6	6063.6	6331.3
1156.2	1093.9	1593.7
20.2	27.6	64.1
4950.1	4925.2	5408.2
459.7	525.3	599.5
5894.9	6125.0	7756.7
5241.6	5562.0	7112.9
2122.8	2364.4	3292.8
6711.6	7932.3	10632.7
3280.3	3880.4	5824.8
4478.8	6196.7	5653.3

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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s__Eubacterium limosum	69489
s__Eubacterium yurii	70921
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s__unclassified	69628
s__unclassified	71061
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s__Pseudoramibacter alactolyticus	69750
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AY185330.1 gg_id:79459 Acetobacterium sp. clone AKS70 AY1853
X96954.1 gg_id:14237 Acetobacterium woodii str. DSM 1030 X96954
AY185325.1 gg_id:79549 Acetobacterium sp. clone AKS42 AY1853
AB546245.1 gg_id:522312 Acetobacterium sp. str. Mic7c05 AB5462
AY185319.1 gg_id:79098 Acetobacterium sp. clone AKS04 AY1853
X96958.1 gg_id:14249 Acetobacterium paludosum str. DSM 8237 X96958
DQ447180.1 gg_id:156581 Coexistence homoacetogens and heterotrophic sulfate-reducing synthesis gas fed la DQ447
AF132739.1 gg_id:14234 Acetobacterium psammolithicum str. CN-E AF1327
AY185318.1 gg_id:79515 Acetobacterium sp. clone AKS02 AY1853
X96959.1 gg_id:14257 Acetobacterium fimetarium str. DSM 8238 X96959
AY185323.1 gg_id:79093 Acetobacterium sp. clone AKS29 AY1853
AJ518871.2 gg_id:104008 Anaerofustis stercorihominis str. wal 14563 AJ5188
DQ353902.1 gg_id:148988 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z4 DQ353
AB198513.1 gg_id:135410 termite gut wall fraction clone RsW01-091 AB1985
EU843431.1 gg_id:319993 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
FJ833673.1 gg_id:543902 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_77E10 FJ8336
DQ353937.1 gg_id:149723 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z105 DQ353
EU462735.1 gg_id:291786 Sumatran orangutan feces clone orang2_aai68b12 EU4627
EU844993.1 gg_id:323946 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8449
AB088988.1 gg_id:77821 termite gut homogenate clone Rs-H81 bacterium AB0889
AM691886.2 gg_id:527988 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar AM691
AB298910.1 gg_id:275347 Eubacterium limosum str. #5 AB2989
AY533381.1 gg_id:106035 Eubacterium yurii subsp. margaretiae str. ATCC 43715 AY5333
EU463292.1 gg_id:294324 naked mole-rat feces clone molerat_aai72h11 EU4632
AJ518868.1 gg_id:109633 Eubacterium sp. str. CS1 Van AJ5188
AY533382.1 gg_id:106183 Eubacterium yurii subsp. schtitka str. ATCC 43716 AY5333
AM419991.1 gg_id:247984 Noma subgingival plaque clone 102C12(oral) AM419
AB036759.1 gg_id:46867 Pseudoramibacter alactolyticus str. 23263T AB0367
EU474929.1 gg_id:296092 red river hog feces clone RRH_aaa02e07 EU4749
AF073898.1 gg_id:14253 Eubacterium aggregans str. SR12; DSM 12183 AF0738
EU845579.1 gg_id:335896 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8455
EU468268.1 gg_id:302875 domesticated horse feces clone horsej_g07 EU4682
DQ478748.1 gg_id:157142 UASB reactor treating brewery wastewater clone CLONG19 DQ478
DQ339707.1 gg_id:214750 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
FJ672150.1 gg_id:514900 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
GU180172.1 gg_id:554177 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AY312403.2 gg_id:89746 Alkalibacter saccharofermentans str. Z-79820 AY3124
EU843219.1 gg_id:311974 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
FJ672463.1 gg_id:524649 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU344196.1 gg_id:274259 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3441
FJ672328.1 gg_id:532190 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723

243.3	2058.4	2015.6	1915.7	1920.1	1541.8	2610.8	1973.0	1256.3	833.1	1431.8
86.4	1470.3	1631.5	1713.9	1893.5	1087.0	3374.8	1633.0	458.2	419.3	767.5
1802.0	4099.0	3990.5	4164.3	4028.6	3444.5	4757.0	4448.3	4411.3	3689.6	3264.2
159.7	2115.1	2595.4	2282.5	3032.0	2778.8	2746.0	2347.6	1373.3	1727.8	2163.2
3916.3	1625.3	2059.3	1214.3	1437.0	1291.4	2100.5	1673.9	2125.2	2019.1	1611.7
150.8	2414.9	3147.6	3097.1	1956.1	2603.9	3342.0	3308.8	1121.6	477.8	2612.4
7370.3	8952.5	8131.2	7803.9	6503.2	7333.0	7735.0	6567.9	11606.7	14117.5	8936.2
3872.5	7826.6	9280.8	9028.5	8861.6	7857.1	9390.7	8964.6	8991.7	8779.3	9183.0
787.3	2201.7	2977.0	2207.7	1965.2	2192.2	3073.8	3045.1	1570.5	2050.6	1871.4
3543.1	4452.0	4884.4	4259.6	3935.2	4131.7	5478.4	3857.1	3904.7	4844.1	4523.7
523.5	2635.4	3191.6	2651.9	2455.3	2220.3	3248.9	3251.3	2198.5	2497.4	2495.6
608.4	2012.2	1837.3	1826.6	1558.7	2208.7	1347.8	1905.1	1926.3	904.0	1315.6
32.1	62.3	95.0	117.7	84.1	121.0	59.5	91.5	56.0	131.1	64.6
6802.9	7361.2	6886.4	6974.4	7256.0	7102.3	7216.3	6629.7	7127.7	6968.4	6534.5
1369.9	2285.6	2496.2	2637.1	2844.3	2261.4	2914.2	2570.5	3018.7	2531.4	4439.8
14380.5	6326.1	6891.9	4803.5	5790.0	5749.6	6016.6	5488.1	6646.4	4221.9	6602.6
81.4	1528.0	2811.8	1520.8	1097.5	1895.7	1906.9	1682.5	626.8	285.9	1058.7
1310.1	1699.9	1566.5	2160.2	1991.1	1754.0	1868.7	2393.8	1165.4	563.6	1304.4
846.1	3979.0	5733.3	5004.6	2945.6	3945.3	4018.6	4224.9	1962.7	763.7	2962.7
1913.1	2793.1	3474.6	3408.7	3377.5	3145.5	4237.8	3168.8	1992.1	1769.1	3278.8
877.2	4878.6	4516.2	3545.1	3816.6	4198.4	4112.1	3777.5	5528.9	3198.5	5415.7
888.2	2996.8	3240.0	4393.8	3743.7	2206.5	3290.5	5190.0	2890.7	1238.7	2826.6
1311.4	1913.4	2412.4	2256.1	2116.3	2209.5	2253.8	2594.4	1948.5	1809.1	2150.0
909.6	3204.7	3637.2	4338.6	4378.4	2676.7	3819.0	4709.0	2929.3	1204.5	2961.5
43.9	440.1	443.3	389.4	288.7	163.3	593.7	475.3	121.5	78.0	187.8
32.7	151.4	218.7	216.0	98.6	192.4	200.4	165.0	84.0	29.2	100.1
533.0	5091.6	5012.0	4845.8	3935.5	4297.4	3936.4	5334.9	2738.1	1026.5	3946.9
44.8	31.3	35.3	24.8	33.6	34.4	31.7	40.4	29.7	24.4	34.9
45.5	254.4	321.9	325.9	196.7	203.2	373.4	233.6	153.8	105.0	188.9
39.3	591.8	182.4	160.3	74.3	128.7	231.9	167.7	39.2	60.5	80.1
223.3	2779.5	3929.3	2602.6	2093.7	2913.8	2904.1	3119.6	1842.2	1374.1	2357.1
291.2	1974.4	2474.6	2317.0	2381.7	2116.5	3155.0	2111.4	1341.2	1354.9	2697.6
3161.4	5315.6	6430.7	5878.7	5201.5	6484.8	5893.2	6166.7	4701.0	5800.2	6647.2
12281.7	4846.0	4757.1	4701.4	4005.9	4840.2	4899.0	4131.2	5713.9	4893.2	4596.0
1283.1	6493.5	6353.7	6509.4	7627.0	6109.2	8746.0	6043.9	5246.1	4379.6	5061.6
668.1	3070.1	4709.1	3582.8	3194.9	3341.1	3960.6	3609.4	3321.5	976.3	3172.1
59.2	556.1	1617.0	716.4	377.3	502.5	629.9	933.2	294.7	81.8	494.5
929.3	5516.9	5861.3	5881.5	5182.6	5198.0	6520.5	5754.6	3365.6	3108.0	4830.1
22575.4	5751.0	5493.0	5779.1	5238.1	5173.9	6091.8	7065.8	9043.2	5716.0	8161.4
4021.2	4886.1	5161.2	4782.8	3943.4	4214.5	4282.5	4752.2	5968.4	5479.2	6748.7
10919.6	6595.9	7492.3	7349.7	7323.6	6655.9	7982.5	6680.4	5654.4	8001.8	7659.3

1506.1	1597.1	2011.4
1498.8	1628.5	1995.4
3830.7	4028.5	5404.5
2338.7	2545.4	3990.9
1280.6	2162.1	1481.4
3059.5	2630.7	3729.1
7073.8	8388.6	11426.1
8221.7	9826.4	11767.4
2322.5	2582.0	3479.5
3403.0	4074.5	4764.1
2467.9	2642.8	3384.9
1726.6	2197.2	3778.3
118.5	246.5	92.4
5851.3	6642.3	7757.5
2349.6	3275.5	2763.5
5929.7	6254.7	6832.8
1240.9	2045.3	4140.4
1938.4	2656.8	3864.8
3854.4	4590.4	7630.7
2721.9	4439.7	3819.9
2656.3	3682.9	3313.3
4198.1	3633.2	5168.1
2121.9	2297.6	2102.2
4486.8	4497.8	5628.0
366.2	386.6	446.4
87.1	73.7	118.4
4306.7	5009.2	6394.6
25.0	36.7	103.1
175.6	373.5	942.9
154.9	160.1	354.4
2581.6	3211.5	5204.8
1824.1	2577.5	3900.8
5884.1	5499.2	7086.0
3649.3	5410.8	4554.8
6013.9	6915.0	9227.1
3324.3	4025.2	5664.1
659.6	1041.4	1574.9
5343.8	5308.9	7547.1
4710.1	5796.1	5291.1
4314.5	5012.2	7180.1
6680.5	7184.9	10113.1

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s__Anaerostipes caccae	20423
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s__unclassified	19222
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s__Bacteroides pectinophilus	20485
s__Blautia producta	20633
s__Blautia producta	20641
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AY554414.1 gg_id:103303 Alkalibacterium sp. 8B AY5544
CP000930.2 gg_id:262344 Heliobacterium modesticaldum Ice1 str. Ice1; ATCC 51547 CP0009
NC_010337.1 gg_id:268302 Heliobacterium modesticaldum Ice1 str. Ice1; ATCC 51547 NC_01
AB100837.1 gg_id:110646 Heliobacterium gestii str. DSM 11169 AB1008
AF249678.1 gg_id:73860 Heliobacterium sulfidophilum str. BR4 (T) AF2496
NR_028721.1 gg_id:571373 Heliorestis daurensis str. BT-H1; ATCC 700798 NR_02
NR_025932.1 gg_id:548015 Heliobacterium chlorum str. ATCC 35205 NR_02
AF028351.1 gg_id:14069 Clostridium indolis CM971 AF0283
NR_024993.1 gg_id:555445 Clostridium fimetarium str. Z-2189; DSM 9179 NR_02
DQ513077.1 gg_id:161135 Microbial life fluids ridge flank crustal fluid clone FS266-27B-03 DQ513
EF559143.1 gg_id:221028 mesophilic anaerobic digester clone G35_D8_L_B_A11 EF5591
FJ672313.1 gg_id:524287 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
AF275914.2 gg_id:72606 anaerobic digester clone AA02 AF2759
ABVQ01000036.1 gg_id:561391 Bacteroides pectinophilus str. ATCC 43243 ABVQ0
GQ493997.1 gg_id:594268 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ369932.1 gg_id:360069 feces adult twins and mothers; TS55 clone TS55_a02d10 FJ3699
FJ978689.1 gg_id:458990 feces clone CL_F_376 FJ9786
EU463007.1 gg_id:293490 southern three-banded armadillo feces clone arma_aaj56d10 EU463
FJ678747.1 gg_id:512569 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
DQ804305.1 gg_id:195563 human fecal clone RL187_aan77g02 DQ804
FJ364622.1 gg_id:368535 feces adult twins and mothers; TS19 clone TS19_a01b05 FJ3646
FJ978518.1 gg_id:412390 feces clone CL_F_049 FJ9785
DQ804223.1 gg_id:183849 human fecal clone RL187_aah70e06 DQ804
EU465331.1 gg_id:290362 lion feces clone LI3_aah75d08 EU465
GQ867449.1 gg_id:578056 and prevalence blaTEM genes Arctic seals colon content clone CSG14 GQ867
EU772751.1 gg_id:318444 Bush dog feces clone bdog3_aad67f09 EU772
EU468418.1 gg_id:298896 lion feces clone LI2_aae50b09 EU468
GQ491687.1 gg_id:571472 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU465525.1 gg_id:288367 lion feces clone LI3_aah78h10 EU465
AY977095.1 gg_id:119459 human cecum mucosal biopsy clone K786 AY977
FJ677562.1 gg_id:532487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
AY975491.1 gg_id:120281 human ascending colon mucosal biopsy clone N930 AY9754
GQ491473.1 gg_id:562403 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ368564.1 gg_id:365763 feces adult twins and mothers; TS49 clone TS49_a01g11 FJ3685
EU462872.1 gg_id:291656 southern three-banded armadillo feces clone arma_aaj54c07 EU462
FJ364917.1 gg_id:369814 feces adult twins and mothers; TS19 clone TS19_a04g02 FJ3649
EU467598.1 gg_id:297131 southern three-banded armadillo feces clone arma_h05_1 EU467
FJ368665.1 gg_id:365150 feces adult twins and mothers; TS49 clone TS49_a03a07 FJ3686
EU465383.1 gg_id:287495 lion feces clone LI3_aah76d08 EU465
DQ803632.1 gg_id:179340 human fecal clone RL251_aaj88d11 DQ803
EU458570.1 gg_id:302128 spotted hyena feces clone HY2_h05_1 EU458

68.5	3359.8	4874.4	3697.2	3872.5	3467.2	5294.6	4464.6	1636.7	893.9	2512.7
8260.1	7496.8	6506.7	6974.5	6879.4	6040.0	6273.8	5328.2	6189.6	4008.1	7698.3
8782.2	3803.1	3395.0	4161.5	6176.0	4301.5	5771.2	3747.6	2078.0	1476.9	3226.6
37.4	986.4	1120.6	1080.4	1410.3	867.1	1481.0	1138.9	410.0	192.3	777.7
678.0	2165.3	1578.1	1298.4	1472.7	1715.0	2308.9	1588.6	2378.1	1362.3	1407.2
40.7	109.1	115.6	127.5	90.3	87.4	56.8	147.2	42.6	34.9	76.2
56.8	473.7	798.2	627.2	498.9	627.2	565.1	729.6	356.5	324.7	269.1
30.2	244.4	279.4	379.9	318.8	159.9	367.9	237.1	62.7	25.6	108.9
38.4	287.1	552.4	1017.7	140.7	83.4	120.0	421.4	59.0	20.3	261.4
51.0	271.7	422.8	280.4	86.1	257.7	151.2	186.7	77.8	40.4	185.1
34.5	3090.5	5927.3	4448.4	2056.7	3466.2	3401.7	4097.0	1693.1	1772.6	3358.0
148.5	2425.5	3515.8	2150.4	1711.8	1931.1	2407.9	2455.1	1111.6	671.1	2592.6
41.5	21.5	25.2	31.7	27.0	30.7	31.3	20.1	36.7	15.0	21.0
55.6	890.4	1327.3	1430.6	1386.6	1151.0	3149.9	1237.4	390.8	171.9	561.5
57.0	654.7	910.8	701.7	663.5	646.1	1016.6	844.7	420.4	770.1	520.6
332.3	2407.9	3134.0	2565.8	2995.5	3082.9	2829.8	3113.4	1595.0	1681.4	2939.2
1498.3	3358.7	3494.1	3832.2	4242.4	3604.1	4386.0	3547.1	2810.4	3760.4	4184.6
195.4	2466.2	3025.1	3230.0	2700.2	2094.1	2864.1	2442.6	1556.8	1094.2	1993.3
33.7	717.3	1056.9	1175.3	291.7	695.6	596.5	1314.5	552.6	209.7	936.2
63.0	559.0	892.6	658.8	183.3	484.7	256.3	1076.0	188.3	105.5	650.3
45.4	498.2	814.6	990.1	278.2	353.5	459.6	470.6	141.5	143.1	427.9
99.7	1025.0	1609.6	1845.4	2023.0	1127.7	2273.0	1155.1	484.3	297.2	785.7
57.3	1129.4	1725.6	1418.6	1013.1	1260.6	881.2	1874.0	640.2	409.0	1131.9
40.2	411.9	207.0	327.8	73.7	111.9	175.2	372.0	40.0	78.6	76.1
5278.5	3647.0	3709.4	3777.7	3073.7	3139.4	2999.0	4216.5	3933.3	3732.1	4502.0
104.6	1104.4	705.1	1184.5	1138.4	1425.2	1009.4	1652.7	1104.7	634.9	1119.2
163.8	1848.3	2798.7	2711.3	1878.6	2678.8	1521.1	4420.3	2064.9	5079.0	3124.3
43.2	671.0	1252.6	1006.6	631.7	731.4	644.1	1080.7	370.3	190.5	711.0
228.9	1589.6	1941.2	2283.8	1046.6	1789.7	1394.2	2559.9	1059.9	577.7	1744.8
50.1	747.4	1291.2	1194.4	307.1	1038.8	635.5	1235.2	204.9	156.0	1044.9
16953.8	6957.0	5773.0	6297.5	6099.5	6383.2	5534.1	5472.0	7469.8	7520.8	6072.1
3040.6	4419.0	4762.7	5052.4	4100.0	4389.0	4303.2	4234.1	6700.8	5529.5	4132.4
41.8	463.9	694.8	799.3	336.2	471.9	731.4	460.7	116.6	55.8	249.0
266.1	498.1	570.3	484.1	456.4	467.8	309.9	525.5	367.7	67.3	726.8
68.3	602.5	1177.7	951.4	230.6	421.3	290.2	606.6	114.6	57.2	285.7
70.8	742.5	1307.2	1174.2	584.1	717.7	762.8	941.4	734.6	544.3	720.1
202.9	1559.7	1523.8	1082.4	1771.6	1574.3	1083.2	1486.7	1432.6	48.1	960.2
7186.3	4629.4	4013.6	5078.4	3417.4	4097.6	3924.1	3541.0	4257.6	3093.9	5355.1
46.9	1040.6	1020.8	1181.7	477.8	673.1	504.3	1081.8	437.7	99.6	487.3
6043.7	2396.1	3125.2	3020.9	2169.4	2725.8	2459.3	3194.4	2016.0	2458.3	2709.4
134.1	668.8	1095.4	1212.1	1266.6	841.5	991.1	911.1	455.0	415.7	590.6

3941.1	4642.4	6552.5
6400.1	5180.9	7295.5
3815.2	3131.1	5611.6
1115.9	1345.6	1491.9
1589.6	2014.5	1763.3
111.7	189.5	140.1
498.0	748.5	948.2
188.9	191.9	249.7
102.3	144.9	130.3
426.9	277.2	160.4
3606.1	3255.2	4102.0
2362.7	1541.5	1757.2
27.4	27.5	29.0
1066.5	1390.8	5124.3
743.1	794.1	554.1
3041.6	3698.5	3439.1
3522.9	3601.8	5422.3
2602.2	2399.3	3346.4
1553.3	514.7	841.3
948.6	475.7	420.3
553.2	394.8	619.7
1307.4	1277.3	2125.8
2041.8	1606.1	1893.5
646.7	312.0	381.7
921.4	3352.3	4197.1
1305.7	1093.4	683.2
3449.3	2523.3	4225.8
1301.4	716.8	994.2
2651.7	1330.7	1757.9
2040.6	668.1	978.7
5458.0	6750.6	5372.1
4259.2	4871.6	5150.6
472.2	320.7	613.8
391.5	726.3	351.9
768.8	556.8	858.4
995.3	1057.9	1217.1
1852.1	1345.0	1345.2
3848.9	4532.6	4034.1
1030.1	870.8	546.5
2992.7	3109.2	3982.2
1516.3	1110.2	1412.0

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s__Ruminococcus obeum	20710

DQ795717.1 gg_id:191316 human fecal clone RL245_aai81b10 DQ795
EU772730.1 gg_id:304309 Bush dog feces clone bdog1_aai80c10 EU772
EU463036.1 gg_id:301318 southern three-banded armadillo feces clone arma_aaj56g11 EU463
EU467565.1 gg_id:296174 southern three-banded armadillo feces clone arma_e09 EU467
DQ456327.1 gg_id:158939 pre-adolescent turkey cecum clone CFT212A8 DQ456
AY980578.1 gg_id:115563 human rectum mucosal biopsy clone X564 AY980
DQ804061.1 gg_id:194041 human fecal clone RL187_aah67h08 DQ804
DQ804970.1 gg_id:192897 human fecal clone RL385_aao83d06 DQ804
EU465381.1 gg_id:295456 lion feces clone LI3_aah76d06 EU465
AY984413.1 gg_id:115474 human stool clone B322 AY984
FJ370721.1 gg_id:363714 feces adult twins and mothers; TS57 clone TS57_a04d11 FJ3707
EF403112.1 gg_id:205138 human fecal clone SJTU_B_15_05 EF4031
EU462960.1 gg_id:289142 southern three-banded armadillo feces clone arma_aaj55g02 EU462
EU462816.1 gg_id:301634 southern three-banded armadillo feces clone arma_aaj53e06 EU462
GQ491355.1 gg_id:585006 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY858537.2 gg_id:109545 gastrointestinal tract eland clone ELAND_90 AY858
EU462957.1 gg_id:287601 southern three-banded armadillo feces clone arma_aaj55f09 EU462
EU771926.1 gg_id:304393 Southern three-banded armadillo feces clone arma_aaj55d07 EU771
EU465322.1 gg_id:291815 lion feces clone LI3_aah75c06 EU465
EU462823.1 gg_id:299390 southern three-banded armadillo feces clone arma_aaj53f04 EU462
EU467568.1 gg_id:292964 southern three-banded armadillo feces clone arma_f10 EU467
EU467548.1 gg_id:301090 southern three-banded armadillo feces clone arma_h01 EU467
DQ807651.1 gg_id:192025 human fecal clone RL180_aah35e03 DQ807
EU467605.1 gg_id:288469 southern three-banded armadillo feces clone arma_c03_1 EU467
DQ804131.1 gg_id:181706 human fecal clone RL187_aah69a12 DQ804
AM276759.2 gg_id:231704 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM276
GQ491435.1 gg_id:566739 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ793721.1 gg_id:194494 human fecal clone RL246_aai76b10 DQ793
EU771867.1 gg_id:311777 Southern three-banded armadillo feces clone arma_h08 EU771
DQ803436.1 gg_id:176107 human fecal clone RL251_aaj85g06 DQ803
AB534168.1 gg_id:537101 Blautia hansenii DSM 20583 str. JCM 14655 AB534
GQ492373.1 gg_id:564101 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU773903.1 gg_id:310173 Cheetah feces clone CE3_aai06h09 EU773
EU771961.1 gg_id:337246 Southern three-banded armadillo feces clone arma_aaj56h08 EU771
DQ804247.1 gg_id:183955 human fecal clone RL187_aah70h02 DQ804
EU772709.1 gg_id:311712 Bush dog feces clone bdog1_aai79g01 EU772
EF399220.1 gg_id:211999 human fecal clone SJTU_F_13_18 EF3992
FJ368791.1 gg_id:357004 feces adult twins and mothers; TS49 clone TS49_a04f03 FJ3687
DQ905190.1 gg_id:163706 human fecal clone 013-a11 DQ905
GQ079651.1 gg_id:433152 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232g(GQ079
EF402578.1 gg_id:214316 human fecal clone SJTU_B_09_74 EF4025

42.9	37.3	62.0	65.9	18.1	32.0	21.2	50.6	29.6	21.6	33.0
33.6	347.2	703.5	531.0	253.5	282.0	237.8	665.6	165.0	297.6	245.8
29.3	921.3	1532.2	2107.0	126.6	436.0	320.1	731.6	83.8	48.6	550.3
3348.2	4949.8	5246.6	5061.8	4902.9	4236.4	4321.3	5845.1	4784.0	3496.6	5380.7
51.9	51.0	48.7	62.3	38.0	35.1	44.7	52.2	35.6	25.8	45.3
39.8	343.7	637.3	607.2	44.2	162.2	135.2	248.0	28.2	16.3	271.5
36.8	595.9	965.1	765.2	415.6	640.5	812.6	988.5	338.9	125.7	987.7
143.7	1018.3	1371.6	1338.9	635.3	642.7	888.4	1373.3	445.7	436.8	688.3
66.2	221.5	331.9	404.3	203.4	195.5	191.3	268.6	102.2	93.1	141.6
43.0	1905.1	2680.4	2463.5	1941.0	2671.1	2045.9	2610.9	1100.8	820.3	2033.0
59.3	701.6	1219.0	1257.2	469.8	958.9	614.4	1675.7	315.9	178.6	741.2
187.2	3044.0	3180.9	2078.5	3250.8	2404.9	2917.4	2716.5	2864.4	2549.2	1971.0
71.2	1367.7	2130.1	2002.9	1246.6	1272.1	1303.3	1863.8	546.1	383.0	1045.1
620.1	1009.4	1556.5	1463.8	790.7	987.7	772.3	1395.3	447.2	539.1	994.0
127.5	549.6	709.6	824.6	382.9	558.2	557.8	763.3	607.3	211.6	392.6
31.0	19.1	17.2	20.3	30.7	18.8	24.6	52.1	12.1	18.3	25.0
88.0	1967.4	3619.9	3266.0	1384.3	2264.4	1693.9	3050.8	836.1	901.2	1935.2
50.6	2049.4	2060.8	2321.8	2308.5	1752.9	2177.1	2361.6	774.7	291.6	1322.1
14435.9	9086.9	8705.4	9082.4	8883.6	8505.3	10468.1	7779.2	11150.0	8290.7	12778.4
435.9	1891.1	2804.6	3164.3	2236.6	2751.3	2385.2	3052.7	1045.3	535.5	1998.4
206.3	1668.0	316.3	1546.6	2267.0	1940.6	1136.1	1779.3	951.9	1549.9	1107.2
31.7	368.1	503.1	616.9	117.0	407.2	154.4	549.8	73.8	84.2	198.6
29.1	22.2	20.1	20.8	23.0	17.6	19.6	20.5	10.0	15.1	20.1
133.5	1245.4	1283.6	1556.1	840.5	1111.2	1050.3	1401.8	338.7	177.8	588.6
191.0	2352.4	2424.9	2786.6	1768.1	3118.9	1030.5	2940.1	2805.1	4602.1	1623.7
49.0	1199.0	1778.9	997.3	759.2	1085.3	1282.5	1430.9	542.5	331.1	748.5
707.2	3132.9	3062.7	2891.7	3716.4	3571.3	3466.1	3637.2	1824.9	2356.8	2600.3
108.4	658.2	960.2	875.5	1397.3	653.5	1414.9	631.0	417.8	367.4	618.6
118.1	458.6	498.2	567.1	499.1	348.2	289.2	365.1	214.6	146.5	284.2
236.9	1019.6	1236.8	1206.9	621.5	920.4	831.7	728.2	519.4	337.9	610.9
68.8	764.0	763.7	806.1	346.2	566.0	397.9	694.7	584.4	239.0	391.4
46.3	1339.6	1986.6	1728.2	536.9	1446.5	1189.7	2164.1	597.9	385.7	1457.4
1332.7	8193.1	7101.9	7970.8	8164.3	9537.5	7591.0	8007.7	8996.3	5449.6	9298.6
111.5	723.3	1434.9	746.2	912.4	1464.0	474.8	999.7	526.6	929.9	694.6
2801.8	926.6	1015.0	770.0	617.7	858.1	677.5	1090.0	591.9	903.3	1130.0
30.1	101.2	227.7	216.2	41.5	86.6	74.4	103.0	35.6	46.0	29.5
51.5	445.5	624.5	735.1	580.3	770.6	703.7	705.3	268.3	646.9	390.0
4372.2	1586.9	1919.2	1712.5	2071.6	1876.9	1913.5	1428.7	2050.0	2123.4	3220.5
823.1	2471.1	3032.9	2843.0	1933.0	1410.2	2952.7	3392.8	2436.2	1717.8	3725.6
46.0	378.7	647.0	649.5	247.0	439.7	244.3	685.2	109.7	121.0	212.8
27.8	268.1	392.2	456.3	54.6	158.3	168.1	198.1	53.3	22.0	125.0

69.2	47.7	32.9
742.8	725.2	687.4
1064.0	742.0	763.8
4879.2	4569.7	4457.1
41.9	52.8	52.5
394.0	231.8	471.6
774.3	502.9	550.4
1379.0	940.4	1061.9
494.4	416.7	209.9
3108.0	2276.6	3338.6
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2552.2	1992.2	4084.2
1906.0	1485.0	2077.8
1234.7	1917.4	1191.3
663.8	1243.5	994.0
15.7	21.9	22.4
3455.4	2694.5	3008.2
2181.4	2314.7	2141.1
7879.1	9068.1	8494.7
2919.1	2807.5	3716.0
2026.8	1296.9	1858.4
664.2	535.9	787.6
24.0	20.7	26.6
1613.9	1118.8	1410.1
2905.9	3235.4	2788.6
1181.6	941.3	1485.7
3666.1	3249.9	5539.8
609.8	1219.1	1062.0
381.3	797.6	387.5
974.6	1292.2	1001.3
649.2	486.6	678.0
2371.8	1268.6	1475.7
8129.7	6493.5	6803.9
1091.5	838.7	1086.6
873.1	1546.4	884.6
108.0	195.4	97.2
458.6	1117.6	697.0
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934.0	570.2	834.4
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AY985501.1 gg_id:121327 human stool clone C466 AY9855
FJ363787.1 gg_id:364910 feces adult twins and mothers; TS14 clone TS14_a03d01 FJ3637
EU530199.1 gg_id:268713 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU5301
GQ897170.1 gg_id:564568 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ367882.1 gg_id:360376 feces adult twins and mothers; TS2 clone TS2_a04f09 FJ3678
AY978324.1 gg_id:120310 human transverse colon mucosal biopsy clone F221 AY9783
FJ366070.1 gg_id:366070 feces adult twins and mothers; TS25 clone TS25_a02d03 FJ3660
DQ804337.1 gg_id:176335 human fecal clone RL187_aan78c04 DQ804
DQ804193.1 gg_id:180310 human fecal clone RL187_aah70b05 DQ804
FJ368690.1 gg_id:360794 feces adult twins and mothers; TS49 clone TS49_a03d02 FJ3686
FJ367559.1 gg_id:362330 feces adult twins and mothers; TS2 clone TS2_a01a03 FJ3675
EU762964.1 gg_id:330799 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7629
FJ368669.1 gg_id:366222 feces adult twins and mothers; TS49 clone TS49_a03b03 FJ3686
DQ326724.1 gg_id:146107 Metagenomic gut microbiome healthy human stool clone E179 DQ326
GQ077133.1 gg_id:436257 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1207e GQ077
X85101.1 gg_id:13989 Ruminococcus obeum X85101
EF404046.1 gg_id:206980 human fecal clone SJTU_C_03_91 EF4040
NZ_AAVO02000010.1 gg_id:254715 Ruminococcus obeum str. ATCC 29174 NZ_AA
DQ804388.1 gg_id:180845 human fecal clone RL187_aan79b02 DQ804
FJ371930.1 gg_id:363437 feces adult twins and mothers; TS8 clone TS8_a03h01 FJ3719
EF402596.1 gg_id:215785 human fecal clone SJTU_B_10_02 EF4025
FJ363590.1 gg_id:361362 feces adult twins and mothers; TS14 clone TS14_a01b02 FJ3635
FJ363622.1 gg_id:358484 feces adult twins and mothers; TS14 clone TS14_a01d10 FJ3636
FJ369679.1 gg_id:362541 feces adult twins and mothers; TS51 clone TS51_a03e08 FJ3696
AY976610.1 gg_id:122356 human cecum mucosal biopsy clone K164 AY9766
FJ368962.1 gg_id:365261 feces adult twins and mothers; TS4 clone TS4_a02f04 FJ3689
FJ364994.1 gg_id:366762 feces adult twins and mothers; TS1 clone TS1_a01f02 FJ3649
GQ897939.1 gg_id:546581 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ363819.1 gg_id:362428 feces adult twins and mothers; TS14 clone TS14_a03g02 FJ3638
FJ366168.1 gg_id:364536 feces adult twins and mothers; TS25 clone TS25_a03e05 FJ3661
AY982558.1 gg_id:118219 human descending colon mucosal biopsy clone KW23 AY9825
EU728790.1 gg_id:346709 Ruminococcus sp. str. DJF_VR66 EU7287
FJ363623.1 gg_id:362465 feces adult twins and mothers; TS14 clone TS14_a01d11 FJ3636
FJ367436.1 gg_id:368938 feces adult twins and mothers; TS29 clone TS29_a03e06 FJ3674
FJ366601.1 gg_id:368132 feces adult twins and mothers; TS27 clone TS27_a01f03 FJ3666
FJ366452.1 gg_id:366345 feces adult twins and mothers; TS26 clone TS26_a03d10 FJ3664
FJ368714.1 gg_id:360328 feces adult twins and mothers; TS49 clone TS49_a03f04 FJ3687
AY978747.1 gg_id:118593 human transverse colon mucosal biopsy clone KU92 AY9787
DQ806775.1 gg_id:176537 human fecal clone RL186_aao48e10 DQ806
FJ363900.1 gg_id:359930 feces adult twins and mothers; TS14 clone TS14_a04f10 FJ3639
DQ807635.1 gg_id:187021 human fecal clone RL180_aah35c04 DQ807

93.2	1306.0	1502.3	1221.3	824.2	1068.4	1049.9	1320.6	1361.0	860.0	823.4
35.0	430.8	872.7	462.9	365.6	523.2	557.6	556.4	455.3	672.1	325.5
49.4	627.1	1084.5	874.6	421.4	617.2	440.9	843.5	387.7	416.8	422.0
36.4	456.7	1010.6	729.0	354.7	635.2	814.8	793.9	439.3	122.6	431.9
30.7	317.0	658.5	441.6	244.8	441.1	246.8	512.2	119.9	143.3	252.4
1104.8	2238.0	2714.2	2463.7	1452.5	2050.6	2928.2	2061.8	2333.1	1358.2	2940.2
98.7	2855.7	2927.1	2251.0	1417.8	2440.7	2269.9	2508.8	2195.3	2032.5	1950.9
59.3	972.4	813.6	642.0	647.8	746.6	920.0	923.6	904.2	742.4	1038.1
10775.0	6337.8	7294.9	7455.4	6244.3	5860.7	7990.8	6091.8	8460.5	8675.1	8159.4
4964.1	2403.9	2647.2	2337.4	2106.5	2229.5	3093.1	2225.5	3034.6	3043.0	3152.8
31.9	633.1	1178.8	1051.7	394.5	656.5	752.5	826.5	371.7	194.9	466.1
314.4	2509.6	3342.8	2508.4	2018.5	2323.2	2566.0	2609.4	2494.2	1142.3	2837.0
14598.7	3755.2	4169.8	4362.7	4631.1	4099.4	4712.5	5196.6	5076.9	3767.1	5683.3
7188.6	2664.1	3152.1	3381.1	1960.6	2320.3	2582.9	2306.3	3500.8	1997.5	4217.4
30.8	1489.4	2153.2	2300.6	670.1	1451.6	1492.3	2384.1	649.2	1125.1	1557.9
33.1	898.3	1472.9	1106.5	383.8	758.9	745.9	1086.4	424.1	143.7	705.6
73.7	3186.6	3189.2	2331.7	1797.4	2623.3	2740.4	3262.2	3340.7	2091.2	2282.3
35.8	487.2	1141.6	669.7	488.2	668.4	826.9	1167.9	370.9	277.3	472.5
322.0	477.8	429.6	597.1	540.1	476.9	466.9	731.6	445.9	434.9	425.9
5941.8	2791.0	3206.6	3656.8	2412.2	2886.8	4064.5	3884.4	2872.5	731.6	3697.6
35.6	173.9	308.6	244.6	128.4	204.0	133.5	166.8	112.5	46.8	91.1
36.7	215.4	409.2	283.2	95.6	494.4	222.6	637.4	157.1	116.1	138.4
33.9	1194.0	1528.6	1566.5	441.9	1318.0	768.0	1913.2	417.9	514.3	947.1
105.9	1716.1	2711.4	2238.3	2231.9	1905.5	2677.9	2048.5	1315.7	1373.5	1545.9
36.6	187.1	263.1	216.2	93.8	268.1	132.7	310.5	87.1	106.8	115.3
5739.6	3748.6	3787.4	4095.5	2924.3	3403.6	4352.8	3712.8	3694.0	2867.7	5011.8
174.2	2219.6	3702.0	2897.8	1489.4	2473.8	3317.0	2892.1	1658.6	2998.4	2772.8
148.6	970.1	1484.2	1320.5	1385.8	1289.3	2033.7	1398.7	1011.9	409.5	528.1
10158.0	2576.0	2809.9	3579.5	2260.6	3144.4	3257.6	3533.3	2400.5	2055.7	2856.7
10278.0	4881.2	4807.1	4744.8	4178.4	4227.5	5709.1	4544.6	7147.1	5657.9	6241.2
48.8	837.1	1561.3	1168.7	531.7	825.1	668.4	1128.7	554.9	322.6	754.8
33.7	387.4	656.6	498.5	127.1	347.2	249.4	376.5	120.5	144.8	197.2
885.3	1553.1	1625.1	1358.7	1066.8	1440.7	1259.4	1400.8	807.9	1443.9	1072.4
30.8	491.2	910.1	738.3	388.6	524.3	476.8	670.3	228.6	180.3	406.3
43.1	515.1	971.8	549.2	420.9	720.1	612.5	1323.1	446.8	726.4	310.5
27.5	677.1	1268.5	995.6	218.7	799.1	427.9	1108.7	223.0	455.8	392.9
37.4	522.6	862.4	642.4	339.2	729.2	795.8	1017.0	472.7	389.8	288.2
46.9	872.9	1832.9	1074.8	961.3	1144.9	1376.0	1788.7	836.9	1098.1	884.6
43.1	444.5	878.8	737.1	288.0	539.5	437.8	705.6	261.4	209.6	263.1
719.2	918.1	1343.6	1091.0	1075.1	972.3	1302.8	1432.5	1195.6	1399.0	772.9
37.7	677.8	652.8	779.9	882.0	585.8	650.6	358.3	113.5	71.1	172.7

1340.9	1151.1	1789.1
795.4	663.1	1626.8
1191.7	733.5	1387.3
478.8	587.6	1115.2
832.1	351.4	977.9
1949.7	2819.4	3796.1
2367.8	1898.9	3865.1
856.4	943.0	685.5
6432.0	7508.7	8369.6
2384.8	2793.8	3490.7
853.0	683.1	1674.6
2344.3	2611.3	3852.5
5661.1	5081.1	6367.7
2304.6	3232.0	3412.1
2589.4	1415.0	1990.7
881.6	519.5	1233.7
3223.0	2668.1	3825.4
1161.6	652.1	1734.2
525.1	802.6	513.2
3677.4	2654.0	4125.8
243.2	91.2	437.5
910.8	235.8	856.7
2545.9	839.3	1470.4
1794.2	2345.4	3273.8
408.5	170.8	597.5
3579.7	3752.1	4287.6
2961.1	3302.0	4632.5
1049.1	2211.6	1880.2
3613.0	4292.4	3665.5
4071.4	5642.5	5292.4
1312.7	1197.3	1866.8
605.8	326.2	646.8
1161.1	1730.1	1345.4
949.9	497.6	1272.4
1703.3	741.6	2302.5
1940.7	648.3	1763.9
1080.9	702.3	1626.3
1972.2	1020.9	3674.5
955.5	623.7	1590.4
1141.6	1383.4	1571.7
481.1	984.2	1437.5

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DQ795429.1 gg_id:193842 human fecal clone RL178_aah54c06 DQ795
DQ326454.1 gg_id:146226 Metagenomic gut microbiome healthy human stool clone C529 DQ326
EU466824.1 gg_id:289535 African elephant feces clone AFEL2_aao29h11 EU466
DQ808076.1 gg_id:183267 human fecal clone RL180_aan72a03 DQ808
DQ825011.1 gg_id:198532 human fecal clone RL185_aao72c02 DQ825
DQ807333.1 gg_id:196082 human fecal clone RL307_aam05c04 DQ807
DQ808105.1 gg_id:187385 human fecal clone RL180_aan72e11 DQ808
DQ801994.1 gg_id:194896 human fecal clone RL241_aaj01e12 DQ801
DQ807015.1 gg_id:185563 human fecal clone RL244_aaj45b06 DQ807
DQ808195.1 gg_id:183824 human fecal clone RL180_aao73g05 DQ808
DQ810151.1 gg_id:186621 human fecal clone RL184_aao68f05 DQ810
DQ794894.1 gg_id:174093 human fecal clone RL310_aam37f07 DQ794
EU779348.1 gg_id:303897 Somali Wild Ass feces clone WA_aaa02e07 EU779
DQ825110.1 gg_id:197657 human fecal clone RL185_aan85e05 DQ825
DQ808200.1 gg_id:179609 human fecal clone RL180_aao73g10 DQ808
DQ799237.1 gg_id:191132 human fecal clone RL205_aaj19e10 DQ799
DQ800722.1 gg_id:178016 human fecal clone RL183_aao02f03 DQ800
DQ802815.1 gg_id:184861 human fecal clone RL188_aan96h07 DQ802
DQ795471.1 gg_id:197050 human fecal clone RL178_aah54g05 DQ795
EU771766.1 gg_id:336948 African elephant feces clone AFEL2_aao31g05 EU771
DQ326114.1 gg_id:148619 Metagenomic gut microbiome healthy human stool clone BB74 DQ326
DQ802802.1 gg_id:173917 human fecal clone RL188_aan96g04 DQ802
DQ800314.1 gg_id:181003 human fecal clone RL303_aal71c11 DQ800
DQ808280.1 gg_id:193210 human fecal clone RL180_aao74g04 DQ808
DQ823693.1 gg_id:191950 human fecal clone RL250_aaj77g04 DQ823
FJ370624.1 gg_id:359520 feces adult twins and mothers; TS57 clone TS57_a03c09 FJ3706
DQ803440.1 gg_id:188945 human fecal clone RL251_aaj85g11 DQ803
DQ803485.1 gg_id:181226 human fecal clone RL251_aaj86d09 DQ803
EU460987.1 gg_id:293389 red kangaroo feces clone KO1_aai41f04 EU460
EU771800.1 gg_id:356581 African elephant feces clone AFEL2_aao29b06 EU771
DQ057459.1 gg_id:130214 str. ic1296 DQ057
DQ805983.1 gg_id:186994 human fecal clone RL186_aah59e06 DQ805
DQ797262.1 gg_id:198626 human fecal clone RL248_aai97a11 DQ797
DQ799354.1 gg_id:193868 human fecal clone RL305aal85c08 DQ799
DQ799334.1 gg_id:176070 human fecal clone RL305aal85a09 DQ799
FJ674172.1 gg_id:510818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ800278.1 gg_id:179866 human fecal clone RL303_aal70g01 DQ800
DQ801693.1 gg_id:183940 human fecal clone RL201_aai45e12 DQ801
DQ804358.1 gg_id:189998 human fecal clone RL187_aan78e11 DQ804
DQ801564.1 gg_id:198752 human fecal clone RL117_aae91d03 DQ801
DQ808168.1 gg_id:187796 human fecal clone RL180_aao73d11 DQ808

60.0	150.1	184.3	212.2	135.0	95.0	149.0	101.2	40.9	27.9	52.5
51.7	318.9	412.1	747.0	190.6	211.5	151.5	442.6	54.5	73.8	210.0
44.1	116.2	290.9	336.2	83.1	138.1	78.8	155.0	41.2	30.7	70.0
111.6	378.4	518.7	529.8	131.8	289.6	265.1	343.5	59.8	70.7	381.9
5168.1	4499.9	4263.1	3996.9	3613.3	3797.5	3512.4	4203.5	3883.0	3586.1	3670.1
46.9	126.6	195.5	272.4	37.8	111.6	54.1	210.6	28.8	42.1	59.4
4461.0	2947.6	2719.7	3055.8	2712.6	2938.6	2844.2	3069.6	3405.4	3128.5	3762.5
911.5	712.1	964.4	714.6	535.2	877.0	782.7	920.3	584.0	1478.2	582.2
99.7	28.0	33.8	40.3	19.8	27.0	22.7	63.2	23.3	17.5	27.9
58.3	1753.9	2186.6	2321.9	1766.2	2498.3	2100.4	2929.0	1807.3	2521.5	3590.3
896.2	711.3	1015.2	1198.2	605.8	740.7	754.8	828.8	415.9	231.9	620.9
37.4	124.1	248.4	207.5	111.6	186.8	154.3	295.1	66.6	51.7	177.9
179.1	1226.9	1930.2	2279.8	1620.1	1448.3	1841.5	1937.2	666.5	689.2	1745.9
41.2	166.0	304.6	318.3	130.3	170.9	172.0	256.0	45.5	45.5	112.0
52.9	414.6	673.7	631.9	369.4	362.1	424.3	676.6	257.8	211.1	478.1
80.7	448.5	682.5	438.4	578.3	406.5	456.1	663.5	469.9	451.6	337.5
8168.4	3513.1	3651.0	3461.3	2584.6	3086.4	3289.1	3272.5	4198.9	4848.6	4782.8
144.8	747.5	1291.9	1166.1	600.8	614.0	690.9	1287.0	466.3	479.2	687.2
3282.5	3185.4	1886.1	2097.1	1759.2	2075.1	2093.7	1926.1	2554.8	4028.8	2219.2
79.7	347.8	606.6	546.5	360.4	268.6	149.5	502.1	79.6	171.0	299.2
38.8	1025.1	1787.5	1498.5	561.1	1622.6	927.5	2122.8	657.4	321.3	1257.5
42.3	34.2	46.5	45.7	60.1	27.1	51.5	29.1	28.4	23.8	32.0
287.1	1826.4	1879.4	2857.6	1623.2	2052.7	2000.4	2223.2	1369.9	1747.4	1600.5
168.4	1298.1	1279.9	795.5	874.9	1085.9	844.0	1308.5	564.7	190.0	837.3
709.9	3442.8	2995.8	2329.1	2330.5	2765.3	2760.3	2550.8	2364.8	1356.1	3015.3
1432.7	2493.0	2185.9	2195.5	2455.0	1712.5	2158.6	2363.8	1858.1	1160.4	1532.4
5664.3	3068.7	3415.1	3776.4	2570.2	2890.3	2503.0	3427.0	3661.0	4354.6	3900.3
43.5	207.8	318.9	399.0	345.9	296.7	212.7	531.3	226.5	336.9	241.3
29.7	578.9	988.7	946.2	726.9	490.2	719.0	708.9	221.5	276.3	448.6
126.2	674.6	1093.2	768.1	926.2	697.0	1096.6	1296.5	1360.7	577.0	490.5
31.8	422.6	394.3	560.9	321.4	387.5	419.3	684.0	191.0	144.8	251.2
259.2	686.4	233.9	935.6	1456.8	721.1	783.7	1217.2	493.7	234.0	651.6
81.0	507.9	713.2	787.9	446.9	507.2	580.3	637.4	316.7	169.9	272.6
104.4	368.5	991.2	675.9	279.2	488.7	444.6	702.1	252.9	80.2	334.5
38.5	1098.3	1006.5	1187.5	1385.3	1416.8	1033.4	1082.4	908.3	709.9	1074.6
42.6	916.2	1349.3	1799.2	431.2	838.1	567.2	1174.3	250.2	234.1	707.4
50.5	25.5	26.9	35.5	33.7	26.7	28.3	37.7	20.8	39.7	27.9
10392.3	7115.3	6368.1	6840.7	4261.6	5377.2	5704.6	6729.7	8239.2	8696.6	7055.7
1102.3	1493.0	1652.0	1576.3	819.1	1340.1	786.3	2484.9	920.1	290.9	1549.4
78.9	2153.1	2292.6	3042.7	1408.3	1943.1	1756.2	2862.3	879.7	489.1	1646.7
178.4	389.4	379.0	507.2	287.5	317.5	460.8	415.3	221.2	160.1	369.7

136.4	195.3	283.6
372.6	378.3	382.3
326.9	277.1	201.0
350.4	584.8	361.9
4949.2	3409.1	5079.6
144.0	164.6	132.6
2731.5	3744.4	2702.8
845.9	1377.0	1221.0
81.4	51.4	51.8
2424.2	2830.9	2860.4
956.0	874.1	1199.8
209.6	249.7	223.6
1466.0	1377.4	2590.5
565.8	173.9	509.0
340.5	366.7	347.1
751.2	704.4	389.7
2595.9	4193.0	3519.1
1107.8	810.7	564.9
2302.5	2049.0	2362.3
313.4	347.7	973.8
3160.0	1467.4	2028.7
32.4	38.9	60.4
2631.6	2986.0	2221.7
1326.8	1398.4	1268.6
2176.9	3421.7	2443.8
1959.5	2358.7	2848.2
3391.2	3472.0	2828.9
581.3	418.2	430.9
834.5	1121.3	2000.0
902.9	1627.0	660.2
536.5	536.5	554.3
1352.4	1337.5	1476.0
786.5	614.9	714.8
569.5	881.3	1415.5
1110.5	1066.3	1186.6
1912.2	802.5	1132.3
24.0	20.4	25.4
4385.9	8625.7	7525.4
1306.9	1803.4	1406.9
3059.8	1887.0	3949.7
435.4	347.7	634.4

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

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EF404604.1 gg_id:208025 human fecal clone SJTU_C_13_39 EF4046
FJ681567.1 gg_id:509707 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
DQ795306.1 gg_id:187002 human fecal clone RL178_aah52g06 DQ795
DQ794954.1 gg_id:189588 human fecal clone RL310_aam38d06 DQ794
GQ492255.1 gg_id:570706 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ800660.1 gg_id:185400 human fecal clone RL183_aao01g01 DQ800
EU778183.1 gg_id:342468 feces clone RL388_aao94c02 EU778
EU766659.1 gg_id:332436 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EF403475.1 gg_id:214725 human fecal clone SJTU_A2_01_70 EF4034
FJ369341.1 gg_id:359787 feces adult twins and mothers; TS50 clone TS50_a03c12 FJ3693
EU462921.1 gg_id:302090 southern three-banded armadillo feces clone arma_aaj55a07 EU462
GQ492965.1 gg_id:587062 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ796740.1 gg_id:177714 human fecal clone RL179_aao53h03 DQ796
GQ493873.1 gg_id:571081 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ804656.1 gg_id:199135 human fecal clone RL187_aao71a01 DQ804
DQ801910.1 gg_id:190027 human fecal clone RL201_aai48d05 DQ801
FJ370830.1 gg_id:366957 feces adult twins and mothers; TS5 clone TS5_a01g05 FJ3708
FJ368442.1 gg_id:361708 feces adult twins and mothers; TS3 clone TS3_a04d06 FJ3684
DQ327155.1 gg_id:150223 Metagenomic gut microbiome healthy human stool clone E676 DQ327
DQ808062.1 gg_id:176424 human fecal clone RL180_aan71f05 DQ808
DQ808152.1 gg_id:198845 human fecal clone RL180_aao73c07 DQ808
DQ808775.1 gg_id:188753 human fecal clone RL243_aai85b01 DQ808
FJ365594.1 gg_id:360717 feces adult twins and mothers; TS20 clone TS20_a04g01 FJ3655
FJ367376.1 gg_id:359034 feces adult twins and mothers; TS29 clone TS29_a02g04 FJ3673
FJ673633.1 gg_id:519730 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EF398335.1 gg_id:209425 human fecal clone SJTU_F_01_26 EF3983
DQ824458.1 gg_id:188557 human fecal clone RL304_aal76c05 DQ824
DQ795572.1 gg_id:193771 human fecal clone RL178_aan66d07 DQ795
FJ365831.1 gg_id:363623 feces adult twins and mothers; TS21 clone TS21_a03e10 FJ3658
DQ809636.1 gg_id:179734 human fecal clone RL184_aan81h06 DQ809
EU462008.1 gg_id:296699 black-handed spider monkey feces clone SPIM_aaj33c03 EU462
FJ363818.1 gg_id:362676 feces adult twins and mothers; TS14 clone TS14_a03g01 FJ3638
DQ804899.1 gg_id:179597 human fecal clone RL385_aao82c04 DQ804
EU461755.1 gg_id:292588 mongoose lemur feces clone ML_aaj28c11 EU461
GQ046085.1 gg_id:408619 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ046
AF371545.1 gg_id:71965 swine intestine clone p-2624-9F5 AF3715
FJ368685.1 gg_id:368329 feces adult twins and mothers; TS49 clone TS49_a03c09 FJ3686
DQ805105.1 gg_id:188292 human fecal clone RL249_aaj81c09 DQ805
DQ327067.1 gg_id:150231 Metagenomic gut microbiome healthy human stool clone E575 DQ327
DQ796291.1 gg_id:185492 human fecal clone RL179_aah25c11 DQ796

3109.2	1272.8	1253.1	1245.8	1021.2	1388.3	1380.6	1622.6	1546.5	2180.9	1136.6
42.8	1705.0	2556.9	1827.6	826.0	1859.6	1087.4	2425.4	670.1	353.9	1535.7
8730.9	5833.9	5292.8	6083.0	5275.3	4878.8	7066.7	5715.6	5786.8	4298.5	6830.3
39.7	61.4	72.2	59.4	34.8	18.0	24.9	42.4	22.1	19.0	31.2
2566.0	4287.7	3150.0	3200.2	3694.3	3121.8	3848.2	3193.1	3822.2	3891.1	3057.7
4876.9	4456.3	3731.6	4157.4	3525.0	3791.4	4377.2	3860.1	4576.9	3156.7	7814.0
1993.7	3007.2	3542.5	3172.8	2737.3	2771.5	2893.9	3043.6	3894.0	3296.2	3986.9
216.9	614.4	946.3	916.3	439.2	786.0	695.3	1190.9	358.3	472.1	576.5
36.7	251.4	470.3	393.4	156.4	323.3	257.7	726.2	112.5	181.2	251.5
42.4	83.1	190.6	226.1	35.2	80.9	53.6	162.1	31.7	22.5	52.3
461.6	1123.3	646.9	1283.8	1457.7	1020.8	1084.3	995.8	819.5	573.8	1329.0
57.9	405.1	892.4	480.1	262.9	516.0	264.9	1137.3	222.2	290.0	640.5
782.7	2509.4	2914.6	2474.1	2398.3	3512.9	2177.3	2845.4	4550.2	3653.7	3104.4
4505.1	5528.5	5933.6	6059.6	4987.8	5486.3	6531.2	5568.9	7479.8	8018.6	7622.6
30.6	136.5	200.0	194.2	138.5	126.1	173.0	393.3	65.6	42.2	61.8
14318.6	6465.9	6447.1	6323.8	6257.8	6270.6	6627.0	6410.7	7178.8	8159.8	8057.6
16836.1	5523.6	5993.0	6110.4	5440.0	5320.8	6094.2	5395.8	8198.9	6936.9	7583.9
2877.5	4524.2	4230.3	5378.2	5445.4	4379.6	5098.5	4915.4	4276.5	4106.4	5959.1
15312.5	5532.6	4253.2	4985.5	6440.6	5584.5	4885.7	5093.7	5217.1	4770.6	6781.4
38.6	141.4	186.5	246.8	199.9	144.2	292.5	284.5	92.8	66.9	79.4
14618.0	6158.8	5525.8	6866.3	6097.5	5684.6	7275.4	5974.9	7981.1	5066.3	9261.5
31.9	237.9	474.8	355.2	149.7	437.0	130.0	896.6	85.8	323.6	197.0
1768.0	2190.3	2860.8	2510.2	2451.0	1989.8	2530.1	2306.2	2852.2	3385.1	2220.0
45.6	343.2	470.1	597.9	167.5	328.2	280.2	442.0	89.4	86.5	144.4
8044.5	3267.9	3670.0	3594.1	2979.9	3195.6	3662.3	3581.8	3948.9	3589.0	3720.4
227.7	2119.5	2326.7	2299.2	2534.2	2085.7	2419.0	2609.6	2282.7	1648.8	1940.6
4108.3	2504.7	2598.5	2353.5	2754.5	2215.1	2804.7	2205.5	3937.8	2779.1	2532.1
44.0	306.2	437.5	773.3	105.0	172.3	265.2	410.5	53.1	38.1	181.1
2406.7	1068.3	1478.6	1568.1	695.2	1147.7	1057.0	1300.9	1352.3	487.2	2337.9
100.3	1315.6	1350.7	1207.2	1342.4	1379.0	1239.4	1370.1	1084.8	1017.5	912.4
47.6	170.2	256.7	258.3	185.2	150.9	159.0	251.8	91.6	50.2	101.8
859.0	2350.2	4230.6	2579.1	2153.9	2173.8	2121.8	2475.8	2280.4	3722.5	5304.3
7477.8	2220.7	1869.6	2565.5	2102.7	2031.3	2852.6	2355.5	2410.6	1145.4	2453.9
159.4	1137.8	1906.8	1862.4	1298.1	1522.3	1300.3	2378.4	1938.8	1167.6	1425.5
38.0	1042.3	1184.6	1225.9	438.8	771.2	1038.6	920.1	165.0	74.0	640.8
2187.4	1450.2	1519.6	1358.1	954.4	1499.0	1410.7	1565.2	1531.3	1189.7	1458.7
57.6	577.2	1003.3	1090.5	410.9	527.5	700.5	695.2	135.2	84.6	351.2
37.7	631.3	1100.7	763.3	275.3	618.4	356.5	1096.7	267.3	290.0	582.7
89.4	597.4	954.2	1085.5	223.6	715.8	502.3	1486.0	247.0	171.1	583.3
220.7	553.1	940.3	582.1	290.2	444.9	334.8	474.7	278.2	190.5	596.9
251.7	1234.6	1989.1	1265.6	1118.1	1657.7	1240.4	1447.4	578.6	1127.5	809.7

2217.7	2139.8	1706.0
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5654.8	6013.4	8094.6
34.9	29.1	24.5
3904.5	4421.4	3162.7
3714.9	3728.6	3570.5
3170.8	3495.6	3353.0
1418.5	847.8	1672.9
1189.3	283.1	618.1
100.5	106.8	97.1
1132.1	1601.1	1015.5
1134.1	676.2	920.0
2534.2	2766.9	3011.4
4901.1	6275.3	6584.0
187.6	149.1	161.4
7087.4	7516.7	6662.0
5324.0	7901.0	6595.7
5114.7	5348.3	5035.0
5009.3	7285.7	5402.3
387.0	142.8	115.7
6402.0	6987.8	5953.7
1417.6	542.2	1358.2
2656.8	3744.5	3584.9
557.0	424.3	494.3
3880.9	3723.6	3776.1
2638.2	2693.7	3039.1
2111.0	3187.4	2574.3
502.4	208.2	342.7
1411.2	1399.9	1039.5
1782.5	1095.7	701.5
197.3	207.8	127.4
2476.9	3291.4	2522.0
2402.1	2859.2	2734.7
2220.9	1821.7	2587.4
1124.9	781.9	2160.7
1578.3	1711.0	2150.1
909.0	656.1	635.0
1358.0	780.0	1437.1
1799.7	904.5	1774.4
590.4	578.3	562.9
1508.6	1844.8	1830.7

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DQ803581.1 gg_id:192013 human fecal clone RL251_aaj87g01 DQ803
DQ802572.1 gg_id:182035 human fecal clone RL188_aan93e09 DQ802
DQ803467.1 gg_id:178303 human fecal clone RL251_aaj86b08 DQ803
DQ803488.1 gg_id:194155 human fecal clone RL251_aaj86e01 DQ803
FJ834020.1 gg_id:540096 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q301_49A07 FJ8340
GQ491945.1 gg_id:560070 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ793395.1 gg_id:181678 human fecal clone RL199_aaj43b10 DQ793
FJ365331.1 gg_id:358442 feces adult twins and mothers; TS20 clone TS20_a01f04 FJ3653
FJ367717.1 gg_id:357170 feces adult twins and mothers; TS2 clone TS2_a02g06 FJ3677
DQ823900.1 gg_id:178122 human fecal clone RL250_aaj80f07 DQ823
DQ808806.1 gg_id:176621 human fecal clone RL243_aai85e04 DQ808
DQ807520.1 gg_id:193431 human fecal clone RL307_aam07f07 DQ807
FJ370181.1 gg_id:368835 feces adult twins and mothers; TS56 clone TS56_a01d07 FJ3701
DQ804460.1 gg_id:175586 human fecal clone RL187_aan80b09 DQ804
EF398689.1 gg_id:204315 human fecal clone SJTU_F_05_07 EF3986
FJ679312.1 gg_id:524376 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ368258.1 gg_id:367873 feces adult twins and mothers; TS3 clone TS3_a02b04 FJ3682
DQ808355.1 gg_id:187289 human fecal clone RL180_aao75f07 DQ808
FJ833986.1 gg_id:589328 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_82B11 FJ8339
DQ804066.1 gg_id:184882 human fecal clone RL187_aah68a02 DQ804
GQ090418.1 gg_id:449524 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
FJ682063.1 gg_id:523934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
DQ808292.1 gg_id:187565 human fecal clone RL180_aao74h05 DQ808
FJ368724.1 gg_id:358242 feces adult twins and mothers; TS49 clone TS49_a03g02 FJ3687
EU779376.1 gg_id:341433 Somali Wild Ass feces clone WA_aaa01e03 EU779
DQ807930.1 gg_id:194523 human fecal clone RL180_aan69c06 DQ807
DQ807157.1 gg_id:177252 human fecal clone RL244_aaj47a02 DQ807
DQ803367.1 gg_id:178494 human fecal clone RL311_aam24f12 DQ803
FJ369515.1 gg_id:361740 feces adult twins and mothers; TS51 clone TS51_a01e03 FJ3695
FJ674140.1 gg_id:532103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
AY960566.1 gg_id:115149 Clostridium sp. str. IE5 AY9605
FJ364769.1 gg_id:364891 feces adult twins and mothers; TS19 clone TS19_a02h04 FJ3647
DQ804868.1 gg_id:188830 human fecal clone RL385_aao81g08 DQ804
DQ804978.1 gg_id:185255 human fecal clone RL385_aao83e08 DQ804
DQ797797.1 gg_id:184290 human fecal clone RL206_aaj16a02 DQ797
FJ368622.1 gg_id:369716 feces adult twins and mothers; TS49 clone TS49_a02e03 FJ3686
DQ905909.1 gg_id:169429 human fecal clone 29c-e10 DQ905
EU842917.1 gg_id:351299 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ673517.1 gg_id:521392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
DQ807843.1 gg_id:180481 human fecal clone RL180_aah37h04 DQ807
FJ372363.1 gg_id:364213 feces adult twins and mothers; TS9 clone TS9_a04g03 FJ3723

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50.6	251.2	318.6	201.8	195.1	269.3	121.8	241.0	88.5	150.1	132.4
44.7	169.0	280.6	219.4	53.8	187.3	125.6	448.8	64.3	201.1	104.9
43.0	181.1	365.2	345.6	90.6	109.4	82.9	227.0	54.0	37.3	97.3
93.6	376.7	765.2	600.0	204.9	435.5	355.8	845.4	119.3	291.0	334.4
476.9	1647.8	1564.4	1329.7	1235.5	1368.3	1358.8	2047.7	1408.6	2332.7	1803.5
27.6	276.0	744.3	506.8	193.2	351.2	242.1	512.3	157.5	77.6	130.2
3341.0	2268.2	1786.1	2571.8	2088.3	1979.6	2277.5	1933.5	2398.3	2002.6	3138.5
27.8	344.3	507.9	576.8	167.7	362.5	229.9	446.4	90.6	56.4	347.2
67.9	1194.3	725.9	394.8	926.6	608.1	421.1	1918.4	522.1	109.6	453.7
51.5	196.6	347.0	412.5	46.3	152.4	147.4	165.8	31.9	22.5	158.9
87.4	233.2	377.4	472.5	101.5	156.6	84.0	221.4	50.1	58.8	94.5
158.2	259.5	398.0	376.7	244.2	265.8	545.1	513.2	366.3	128.4	190.4
2445.2	7420.7	6844.9	6823.7	6925.8	7250.8	5951.8	6302.6	10227.2	9152.8	8452.1
48.8	418.6	940.0	908.6	117.6	548.7	148.3	607.7	89.2	133.0	319.8
50.5	1173.2	1498.0	1730.4	154.8	640.3	530.5	1057.1	168.4	107.3	827.0
3978.9	2427.3	3032.0	2894.9	2574.4	2270.5	2753.2	3179.9	4184.2	2124.5	2643.0
2326.4	2682.4	1757.3	3079.5	2951.3	2928.9	3914.6	2709.5	2817.9	1948.9	3811.0
177.7	1208.0	1479.9	1826.1	1879.8	1276.5	1508.5	1921.7	623.0	652.4	982.5
51.0	78.6	141.2	107.6	64.9	115.1	91.9	168.4	40.8	87.8	79.7
2610.0	2765.6	2903.4	3412.0	2095.4	2955.5	2790.7	2903.0	1888.9	1585.4	2894.0
49.0	144.8	187.8	146.5	119.0	117.4	167.4	94.8	102.0	33.3	96.6
48.8	51.0	107.9	104.7	45.0	50.7	32.6	87.4	29.3	19.4	62.5
9259.3	2232.3	1969.5	2315.6	1711.2	2241.5	2311.4	1938.2	2644.8	2297.8	3296.6
618.2	256.0	1579.9	1617.6	1559.7	1332.8	1641.6	1581.2	99.5	235.4	1619.8
46.6	377.5	322.3	408.9	170.6	206.5	241.3	357.5	524.0	555.6	214.5
1449.3	2011.6	1716.2	1521.1	1778.6	1596.7	2138.6	1726.4	1749.5	2535.3	1462.6
38.4	239.7	627.5	562.4	352.2	273.1	500.2	625.3	65.3	36.8	376.6
51.0	292.4	356.4	357.0	154.7	204.7	259.9	367.5	84.0	75.8	161.7
9557.5	2370.2	2728.7	2899.1	3151.4	2419.0	2955.1	3047.9	3889.9	2262.2	3686.9
110.9	618.4	795.9	1053.8	14.3	857.9	1066.4	742.3	225.7	98.0	748.2
34591.2	9097.8	8413.9	9315.4	8850.8	8051.5	9183.7	9117.7	14145.7	10021.3	12734.5
36.3	231.8	548.7	503.4	66.1	143.3	92.1	220.6	46.0	27.4	120.7
89.9	776.5	1180.3	1138.3	747.3	861.9	820.1	959.0	297.9	311.5	716.8
697.0	849.2	1289.9	1262.0	752.5	797.2	1504.7	950.9	424.0	763.3	564.7
45.3	18.5	15.4	19.5	18.6	16.1	21.1	15.2	15.7	14.3	16.5
52.9	406.6	415.5	510.6	291.5	316.4	540.4	104.2	92.6	128.9	114.4
1264.3	4630.1	5496.1	5925.8	3913.0	4363.5	5144.8	4929.5	4203.5	4161.7	4750.0
52.1	1167.3	1544.4	1585.1	327.1	768.7	706.9	1102.1	265.9	124.2	886.5
97.3	1147.7	1732.4	1646.4	882.1	1043.8	1299.7	1383.5	1257.8	976.9	1342.1
28.0	20.1	27.1	32.4	15.5	14.6	18.3	30.8	12.2	15.1	28.2

1639.4	1262.0	1908.0
328.2	367.5	450.9
655.5	224.4	346.1
319.9	189.2	277.1
767.4	695.5	647.2
1487.9	1894.2	1905.4
478.5	399.3	559.8
1992.2	3554.4	2052.0
605.8	421.3	698.2
1103.7	711.8	1291.7
232.3	194.3	276.4
428.8	489.7	245.9
610.3	749.8	1121.3
6467.8	6862.4	7407.1
841.5	469.6	409.3
1333.4	660.5	1052.0
3077.6	3372.1	2352.2
2541.6	3105.6	3154.2
2026.6	1844.8	2093.2
150.2	327.6	171.3
3559.5	2656.5	3519.0
78.9	140.1	222.9
81.4	115.8	128.7
2185.8	2652.8	1977.8
1443.9	1893.1	1573.0
281.8	464.7	257.9
1566.4	2085.6	1478.8
506.6	483.1	601.7
378.9	231.2	415.1
2672.2	3511.9	3256.2
900.0	985.4	970.8
9343.1	8368.7	9806.2
333.3	203.0	163.3
1110.7	980.5	1414.7
1100.0	1064.9	1847.2
15.7	18.9	20.1
205.3	425.0	115.4
4543.1	5997.7	6155.0
1184.0	1127.0	1149.4
1269.3	1580.6	2081.6
27.9	43.8	8.9

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DQ800760.1 gg_id:184185 human fecal clone RL183_aao03b04 DQ800
DQ807941.1 gg_id:197208 human fecal clone RL180_aan69e04 DQ807
FJ673378.1 gg_id:515300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ800119.1 gg_id:192899 human fecal clone RL247_aaj24d07 DQ800
GQ493994.1 gg_id:583043 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ804040.1 gg_id:194148 human fecal clone RL187_aah67e08 DQ804
FJ369151.1 gg_id:362193 feces adult twins and mothers; TS4 clone TS4_a04h05 FJ3691
AF371547.1 gg_id:22923 swine intestine clone p-2465-18B5 AF3715
FJ680876.1 gg_id:518515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
DQ794465.1 gg_id:175434 human fecal clone RL197_aah88c03 DQ794
DQ795202.1 gg_id:179436 human fecal clone RL178_aah51e01 DQ795
DQ794420.1 gg_id:181675 human fecal clone RL197_aah87e07 DQ794
FJ363299.1 gg_id:358542 feces adult twins and mothers; TS149 clone TS149_a01f02 FJ3632
EU466833.1 gg_id:299620 African elephant feces clone AFEL2_aao30b02 EU4668
EU469499.1 gg_id:288896 black lemur feces clone BKLE_a01_2 EU4694
FJ680899.1 gg_id:531159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
DQ799771.1 gg_id:184890 human fecal clone RL182_aah33c01 DQ799
EU462827.1 gg_id:290477 southern three-banded armadillo feces clone arma_aaj53f10 EU4628
DQ799073.1 gg_id:192246 human fecal clone RL205_aaj17c03 DQ799
GQ896789.1 gg_id:574406 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ804493.1 gg_id:188479 human fecal clone RL187_aan80g04 DQ804
AY983069.1 gg_id:122341 human descending colon mucosal biopsy clone L312 AY9830
DQ801581.1 gg_id:173802 human fecal clone RL117_aae91h12 DQ801
DQ326186.1 gg_id:148423 Metagenomic gut microbiome healthy human stool clone C092 DQ326
FJ677211.1 gg_id:514970 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6772
FJ367463.1 gg_id:363302 feces adult twins and mothers; TS29 clone TS29_a03h04 FJ3674
FJ365713.1 gg_id:359758 feces adult twins and mothers; TS21 clone TS21_a02b04 FJ3657
FJ369196.1 gg_id:357975 feces adult twins and mothers; TS50 clone TS50_a01d06 FJ3691
EF398925.1 gg_id:204830 human fecal clone SJTU_F_09_12 EF3989
EU462231.1 gg_id:294476 chimpanzee feces clone CHIMP1_aaj38a07 EU4622
FJ367949.1 gg_id:356869 feces adult twins and mothers; TS30 clone TS30_a01f03 FJ3679
DQ804026.1 gg_id:186234 human fecal clone RL187_aah67c08 DQ804
DQ794963.1 gg_id:178221 human fecal clone RL310_aam38e05 DQ794
FJ681816.1 gg_id:516988 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ682724.1 gg_id:511020 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ369965.1 gg_id:366165 feces adult twins and mothers; TS55 clone TS55_a02g10 FJ3699
EF398293.1 gg_id:208184 human fecal clone SJTU_F_01_72 EF3982
DQ805689.1 gg_id:178495 human fecal clone RL306aal89g12 DQ805
DQ804024.1 gg_id:179715 human fecal clone RL187_aah67c06 DQ804
FJ879925.1 gg_id:413935 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8799
DQ806925.1 gg_id:195679 human fecal clone RL198_aaj75e07 DQ806

195.6	1252.3	983.0	1321.6	2006.1	816.1	1688.3	1065.6	267.0	93.9	532.8
58.7	242.1	403.0	369.4	165.0	238.0	159.8	212.4	220.2	575.8	202.6
6892.6	5654.5	6116.6	6260.4	4377.6	5191.4	5158.6	5679.0	5530.3	4226.9	7402.7
161.6	2502.2	2789.4	1919.7	1117.5	2219.7	1637.0	2233.9	2435.3	4243.7	1773.3
6333.9	5911.6	5833.3	4510.8	4732.2	4270.9	5015.8	5832.0	4863.8	4590.1	5833.4
34.4	431.4	459.2	708.3	138.1	273.6	201.7	497.2	205.0	65.2	296.2
318.6	1094.5	1162.0	1753.4	1184.1	1202.3	1237.0	1959.0	801.9	328.0	1079.0
31.4	13.6	12.9	11.7	14.4	12.0	12.0	11.8	13.8	10.8	11.3
417.7	1521.0	1647.5	2335.4	1844.9	1412.8	2050.0	2094.6	895.7	250.7	2513.0
8709.3	4544.8	4397.8	4833.2	5054.2	4559.0	5084.9	4854.1	4722.3	5417.5	4387.1
47.8	183.5	386.5	552.8	97.5	125.1	111.9	248.0	38.9	28.2	125.4
35.2	22.5	55.2	40.1	28.8	27.1	43.8	36.2	19.8	13.1	25.8
100.3	377.4	508.0	549.9	495.0	448.8	411.2	720.3	140.3	132.8	204.4
48.7	164.6	267.8	168.9	123.7	174.9	123.8	217.0	63.2	131.9	82.9
26047.4	7882.5	7463.3	8417.1	7741.3	7008.1	9814.7	7114.9	13202.9	7447.0	10930.8
19464.0	6084.3	6162.5	5470.7	5590.7	6167.9	6018.5	5646.6	8109.9	6984.4	6328.7
49.1	60.1	77.9	82.6	83.1	86.8	86.1	62.4	39.1	38.1	60.0
43.4	784.7	1370.7	974.1	430.7	708.6	457.6	1094.3	382.1	144.1	1428.3
34.5	125.9	408.8	388.3	100.0	143.8	78.3	195.0	43.7	74.7	117.8
7445.2	4941.8	4691.1	4923.9	3821.6	4157.9	3487.1	4087.1	3547.3	3073.0	4559.0
2157.3	1804.7	1940.4	2368.1	1813.9	1807.3	1959.5	2032.5	2536.8	1772.3	2573.4
80.4	623.3	951.0	970.3	803.1	608.3	1729.7	595.7	251.3	161.3	328.7
921.3	1092.7	1270.0	1111.3	1542.1	1062.8	1120.3	1334.5	1448.4	987.6	1021.0
594.6	531.5	793.4	497.7	467.8	874.5	504.1	484.1	260.9	193.4	347.9
40.4	518.4	837.8	921.8	362.4	465.7	479.2	575.1	150.3	72.3	234.5
2963.6	2752.7	2915.9	3080.8	2605.8	2630.6	2652.1	3036.9	2191.6	2572.2	2393.3
354.8	2897.5	2659.4	2953.1	1373.4	2089.7	1522.8	2837.1	2383.8	1778.7	2259.1
7531.8	4326.8	3958.4	4382.8	3086.4	4232.5	3922.4	3480.0	4878.3	3524.0	5544.6
4549.5	4005.8	4141.8	4206.4	3093.7	3690.8	3682.6	3842.4	4670.3	5013.2	5456.1
49.7	209.5	315.9	236.9	151.0	237.2	250.6	307.5	100.2	148.0	131.1
20665.5	6692.1	6521.5	7098.4	6703.7	5951.6	5343.4	5536.9	9324.4	7256.9	11243.6
177.5	1054.7	1102.0	1000.4	901.9	749.4	1207.8	1021.2	957.8	502.1	983.1
50.1	117.5	266.4	292.0	135.1	177.6	140.0	241.0	73.2	28.2	163.8
1870.8	783.0	1600.5	820.6	575.2	663.4	644.2	786.4	727.1	216.8	577.0
34.3	147.9	178.3	190.6	82.8	144.4	90.4	314.7	51.8	44.2	92.2
477.3	1147.5	1330.0	1797.8	1026.2	1075.6	1044.8	1129.5	790.4	919.4	655.7
80.5	1424.9	1912.8	1972.6	799.9	1687.4	1605.2	1351.8	1322.1	326.6	1441.4
3376.9	3145.2	2967.7	2817.9	2636.7	2760.2	2628.8	3584.1	3491.7	2693.1	3084.7
429.9	4185.7	5280.8	4896.3	3954.2	4004.1	1602.1	3251.3	9972.7	3035.9	4490.7
39.9	374.4	688.5	817.7	134.2	283.9	383.5	537.5	110.1	48.5	230.6
38.5	318.8	319.4	309.8	133.0	266.9	153.8	408.6	268.3	116.0	267.5

848.0	1096.2	1971.4
277.8	423.8	297.1
5322.0	6191.5	5518.7
2699.6	1785.4	1815.9
4810.2	5711.9	6394.1
479.3	354.6	352.5
2689.5	1832.7	1818.1
10.6	14.7	11.0
1587.2	2262.7	2105.3
5744.4	5634.8	5551.2
180.2	263.2	215.1
24.9	51.6	33.0
726.0	486.9	1027.5
334.8	262.7	253.4
6803.9	8849.2	7409.7
5427.7	7344.1	6231.1
40.4	89.6	89.8
1006.2	1371.7	1413.6
208.1	335.2	335.4
3819.4	3824.8	3453.2
1697.7	2333.6	1646.6
652.3	555.3	1308.7
1032.5	2049.6	1048.3
720.1	758.3	818.7
906.9	484.7	855.6
3360.3	2851.5	3352.5
3637.9	1844.8	2817.6
3543.1	4078.5	3642.3
3178.3	4935.0	3282.3
380.4	311.3	441.4
5569.9	7301.4	6192.2
954.9	1139.9	1274.1
230.8	296.8	345.8
827.6	1380.0	919.9
217.4	244.2	335.5
1153.9	2039.4	1421.7
717.5	797.1	1099.7
4687.8	3492.0	3217.8
2414.8	3831.7	3339.7
584.8	484.3	471.8
309.8	227.9	481.9

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EU779326.1 gg_id:342613 Visayam Warty Pig feces clone VWP_aaa04e07 EU779
EU762797.1 gg_id:305632 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU465456.1 gg_id:295217 lion feces clone LI3_aah77f05 EU465
DQ824386.1 gg_id:198143 human fecal clone RL304_aal75d10 DQ824
FJ366844.1 gg_id:365869 feces adult twins and mothers; TS27 clone TS27_a04e06 FJ3668
EU472527.1 gg_id:292228 Angola colobus feces clone EAC_2_aaa01b11 EU472
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FJ679798.1 gg_id:524019 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
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EU458491.1 gg_id:299304 spotted hyena feces clone HY2_a04_1 EU458
FJ678819.1 gg_id:517547 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ368482.1 gg_id:367763 feces adult twins and mothers; TS3 clone TS3_a04h07 FJ3684
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DQ805632.1 gg_id:187239 human fecal clone RL306aal89b12 DQ805
EU778834.1 gg_id:333694 Black-handed Spider Monkey feces clone SPIM_aaj35b11 EU778
FJ678972.1 gg_id:524202 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ794571.1 gg_id:192840 human fecal clone RL240_aaj29g04 DQ794
FJ367473.1 gg_id:366237 feces adult twins and mothers; TS29 clone TS29_a04a02 FJ3674
FJ368067.1 gg_id:362389 feces adult twins and mothers; TS30 clone TS30_a03f01 FJ3680
DQ808129.1 gg_id:191317 human fecal clone RL180_aao73a06 DQ808
DQ798248.1 gg_id:195606 human fecal clone RL181_aah39e05 DQ798
DQ803705.1 gg_id:199487 human fecal clone RL200_aai57d05 DQ803
FJ369569.1 gg_id:361208 feces adult twins and mothers; TS51 clone TS51_a02b04 FJ3695
DQ804787.1 gg_id:174796 human fecal clone RL187_aao72f12 DQ804
DQ809680.1 gg_id:190956 human fecal clone RL184_aan82e07 DQ809
DQ800120.1 gg_id:174967 human fecal clone RL247_aaj24d08 DQ800
EU467144.1 gg_id:292859 mongoose lemur feces clone ML_aae89e06 EU467
GQ492618.1 gg_id:572387 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ799584.1 gg_id:198805 human fecal clone RL305aal88a01 DQ799
EU462126.1 gg_id:300629 black-handed spider monkey feces clone SPIM_aaj35d04 EU462
EU778853.1 gg_id:343716 Black-handed Spider Monkey feces clone SPIM_aaj34h02 EU778
FJ368580.1 gg_id:364581 feces adult twins and mothers; TS49 clone TS49_a02a03 FJ3685
EU778515.1 gg_id:317113 Red river hog feces clone RRH_aaa03d05 EU778
DQ801893.1 gg_id:176898 human fecal clone RL201_aai48b10 DQ801
GQ002337.1 gg_id:507325 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176c02 GQ002
EU764414.1 gg_id:334570 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ680085.1 gg_id:516004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
DQ824108.1 gg_id:184288 human fecal clone RL204_aaj59d11 DQ824
EU776698.1 gg_id:303452 Lion feces clone LI3_aah78h03 EU776

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48.6	354.6	667.2	630.8	51.2	438.7	242.0	512.1	72.9	61.0	289.0
156.4	724.6	689.5	1047.6	682.3	606.5	761.0	704.5	489.8	148.3	526.9
53.2	133.6	230.8	296.0	92.5	120.2	113.5	169.9	25.4	26.2	126.6
64.8	688.6	975.1	895.3	771.8	677.2	630.0	1151.6	1149.4	413.4	390.6
2096.6	2148.8	2276.6	2716.9	3515.8	1894.9	2684.0	2402.8	1987.7	1126.2	2068.2
2921.6	1591.2	1746.6	1448.4	1488.1	1566.3	1361.5	1610.6	943.2	908.3	1261.6
32.9	6030.0	4528.4	1149.5	537.0	4685.4	400.9	1632.8	4070.2	2686.2	675.0
515.6	1517.0	2061.9	2086.7	1662.7	1244.9	1582.9	1271.0	710.8	232.1	1117.4
4703.8	2434.4	2303.4	2408.6	2251.6	2312.4	2416.5	2101.3	1927.8	2178.3	2701.4
3548.6	904.6	1036.1	901.2	948.5	919.5	1345.1	987.3	1132.8	513.3	1119.5
34.9	304.2	575.3	794.4	92.4	313.4	186.7	566.9	57.6	44.9	171.5
2837.9	2920.1	3422.2	3753.7	2954.4	3046.6	3353.4	3026.0	3018.1	2841.9	3379.0
41.6	142.5	259.7	182.8	81.5	116.3	82.0	248.2	38.9	23.1	124.7
889.8	2192.4	2837.8	3062.0	1282.7	2353.5	1877.0	3439.9	669.4	542.5	1614.8
3731.5	5958.1	6217.1	5946.5	4431.3	4833.5	4818.5	6227.0	5534.5	4292.4	7509.7
50.1	572.3	1062.3	981.0	335.2	597.3	517.2	896.3	164.5	84.8	461.0
4515.7	2560.1	2013.0	1563.5	1340.6	1874.2	1579.5	1922.7	2094.0	2496.0	1559.7
160.4	1466.0	1817.5	1594.3	1019.0	1500.7	1536.8	1661.5	637.7	183.5	1000.8
1142.8	3787.5	3712.7	4679.7	6000.3	4225.3	5601.8	4690.2	3469.1	2202.7	4031.7
21747.4	6805.6	6638.7	7218.5	7070.6	6762.8	7461.4	7619.4	10300.0	8245.5	10026.2
612.7	1037.6	1505.3	1246.5	1450.7	1078.3	1251.1	1738.0	1110.1	1120.7	998.8
108.4	258.8	390.9	424.1	314.3	360.0	427.5	418.0	153.6	189.3	191.3
9969.2	5544.5	6822.3	5606.7	5366.3	5406.6	5745.1	5286.6	7821.0	5979.4	7479.7
65.7	458.1	676.0	537.9	290.6	378.1	428.6	758.3	157.9	340.2	298.4
45.2	316.0	460.2	399.5	88.0	232.2	145.6	343.8	76.4	81.4	232.0
3335.1	3395.6	4051.2	4386.0	4127.1	3853.4	4947.8	5190.2	4270.3	4280.4	4084.0
34.1	65.2	127.5	28.6	29.7	47.0	99.3	68.1	16.8	21.5	48.8
493.0	1500.2	1812.5	2026.5	1467.0	1720.1	1773.9	1773.2	1066.6	939.2	1113.8
1120.4	4203.2	4376.1	3959.2	4211.2	3503.6	3997.3	5517.9	2509.6	1454.4	3088.4
2238.7	5287.6	4626.2	4844.5	4314.3	4764.9	5083.9	4626.5	6360.8	4545.5	5375.5
66.5	1398.5	2481.4	2358.2	557.0	1095.9	711.6	2303.5	715.9	184.4	1957.9
45.7	520.8	681.6	614.9	294.1	349.9	308.2	646.3	258.5	148.8	358.8
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398.7	555.3	742.5	864.8	422.8	536.9	475.9	596.7	322.6	453.1	289.0
76.6	568.0	558.8	653.9	221.9	397.9	329.1	772.9	573.5	47.3	288.5
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39.7	177.8	254.2	250.5	143.9	185.1	147.3	277.5	73.3	139.7	99.0
1035.6	4160.3	5403.9	4278.9	4070.2	4093.0	4553.4	4865.9	5015.5	3632.5	5502.6
246.2	1434.3	1615.8	1874.0	1814.8	1199.8	1749.7	2265.7	745.2	938.3	1156.7
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555.4	564.5	292.7
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988.3	1206.9	657.3
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1386.4	2353.5	2661.4
2066.8	2831.4	2062.5
818.9	1048.3	1491.2
486.1	511.0	548.6
3089.5	3337.7	4019.7
312.4	225.5	218.2
4521.2	2200.1	3083.8
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960.6	717.2	616.4
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873.7	987.4	799.5
981.7	691.8	419.4
686.4	969.4	851.1
598.9	250.3	523.2
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DQ809417.1 gg_id:188472 human fecal clone RL184_aah20f03 DQ809
DQ805441.1 gg_id:184344 human fecal clone RL203_aai62f08 DQ805
AF357567.1 gg_id:73388 mpn-isolate group 19 AF3575
FJ676500.1 gg_id:510563 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
AF132274.1 gg_id:72420 adult human fecal matter clone adhufec52 AF1322
DQ804933.1 gg_id:196581 human fecal clone RL385_aao82g10 DQ804
DQ804952.1 gg_id:187432 human fecal clone RL385_aao83b03 DQ804
EU462096.1 gg_id:287668 black-handed spider monkey feces clone SPIM_aaj34h11 EU462
FJ673623.1 gg_id:509645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ801879.1 gg_id:174348 human fecal clone RL201_aai48a04 DQ801
AF153853.1 gg_id:13992 faecal clone adhufec35.25 AF1538
DQ796760.1 gg_id:194745 human fecal clone RL179_aao54b03 DQ796
FJ363676.1 gg_id:362514 feces adult twins and mothers; TS14 clone TS14_a02a05 FJ3636
FJ366409.1 gg_id:358537 feces adult twins and mothers; TS26 clone TS26_a02g06 FJ3664
DQ808220.1 gg_id:197652 human fecal clone RL180_aao74a10 DQ808
FJ682086.1 gg_id:531472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
DQ904728.1 gg_id:166362 human fecal clone 001-h6 DQ904
DQ804935.1 gg_id:182308 human fecal clone RL385_aao82h01 DQ804
DQ796155.1 gg_id:178646 human fecal clone RL202_aai52d05 DQ796
GQ492609.1 gg_id:553609 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ326200.1 gg_id:145758 Metagenomic gut microbiome healthy human stool clone C115 DQ326
DQ798716.1 gg_id:198766 human fecal clone RL181_aao00e02 DQ798
FJ371877.1 gg_id:365497 feces adult twins and mothers; TS8 clone TS8_a03c04 FJ3718
NZ_AAVO02000004.1 gg_id:470971 Ruminococcus obeum str. ATCC 29174 NZ_AA
EU776277.1 gg_id:340251 Red Kangaroo feces clone KO1_aai41g04 EU776
FJ364807.1 gg_id:358558 feces adult twins and mothers; TS19 clone TS19_a03d03 FJ3648
AY981223.1 gg_id:126425 human sigmoid colon mucosal biopsy clone G186 AY9812
DQ807835.1 gg_id:198325 human fecal clone RL180_aah37g06 DQ807
FJ368592.1 gg_id:368630 feces adult twins and mothers; TS49 clone TS49_a02b05 FJ3685
EF401712.1 gg_id:208349 human fecal clone SJTU_D_14_18 EF4017
EU468139.1 gg_id:290228 lion feces clone LI1_c04 EU468
DQ807766.1 gg_id:193852 human fecal clone RL180_aah37a01 DQ807
FJ366613.1 gg_id:364141 feces adult twins and mothers; TS27 clone TS27_a01g04 FJ3666
DQ799635.1 gg_id:192476 human fecal clone RL305aal88e08 DQ799
DQ795414.1 gg_id:174625 human fecal clone RL178_aah54a12 DQ795
DQ808431.1 gg_id:176519 human fecal clone RL180_aao76e04 DQ808
FJ364646.1 gg_id:364097 feces adult twins and mothers; TS19 clone TS19_a01d06 FJ3646
DQ796801.1 gg_id:191021 human fecal clone RL179_aao54f11 DQ796
FJ678562.1 gg_id:517282 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
AY983064.1 gg_id:125001 human descending colon mucosal biopsy clone L306 AY983

317.7	761.9	1213.8	1263.1	915.4	660.3	876.3	944.6	375.6	311.0	435.2
516.5	1595.8	1237.5	1917.2	2270.3	1578.5	1792.6	2193.4	1477.6	1253.6	1587.1
206.5	858.2	1069.5	1335.4	1005.0	965.0	1505.4	1438.2	545.0	378.4	536.8
30.7	1139.8	1288.6	1137.9	382.1	580.7	477.0	712.1	138.9	489.6	324.6
272.2	1237.6	633.7	1289.5	1044.2	834.2	876.7	1006.5	846.3	267.8	726.4
5541.3	3367.6	3474.1	4413.1	2750.6	3727.0	3553.0	2904.5	4561.6	2638.7	5183.0
40.9	207.9	329.5	436.7	49.2	130.1	84.9	211.8	37.8	20.2	116.8
577.8	1256.0	1544.1	1600.8	1542.2	1181.7	1639.4	1350.9	967.4	794.6	884.4
162.6	1313.6	2183.1	1999.9	1174.2	1577.5	1248.4	2298.2	850.0	693.7	1178.8
654.2	2756.5	2223.1	3239.3	2976.5	2308.1	3279.5	2822.9	2716.1	1457.9	3104.1
97.1	91.9	167.6	137.1	136.3	108.9	133.5	135.7	67.7	168.7	120.6
341.2	739.8	701.9	763.2	738.1	534.8	737.5	841.1	365.2	626.4	530.8
82.8	990.8	1253.9	1285.7	785.9	693.5	611.0	1212.3	521.1	663.6	658.2
5322.2	3299.9	2761.1	3148.0	3057.0	2941.1	3046.3	2460.3	3838.2	2766.9	4137.7
4477.7	1778.7	1943.2	2652.3	2198.0	2055.6	1704.2	1039.2	2582.2	1462.7	2331.3
68.4	635.2	701.4	632.8	957.7	618.8	984.3	885.0	534.4	603.9	654.5
378.5	1478.4	2048.7	2495.4	2109.5	1351.5	3743.0	2283.6	826.9	352.4	1622.2
65.8	1249.8	1125.0	660.8	562.4	801.1	810.5	1239.3	1641.9	1273.7	907.8
28.2	46.0	72.8	59.0	36.9	27.0	35.1	52.9	17.3	13.5	24.5
36.5	106.9	263.6	286.9	353.4	250.5	651.4	237.7	80.6	24.1	132.0
10349.2	3833.2	3900.6	3397.4	2939.0	3681.7	3428.4	4238.6	4051.1	6131.5	2915.9
249.0	850.8	779.9	1078.2	1577.4	1001.7	1062.2	1440.5	873.9	314.0	659.5
360.8	1666.5	1443.8	1364.2	1062.5	1161.0	1359.9	1126.3	1508.0	811.0	346.2
7953.6	4824.8	4863.3	4937.0	4185.2	4103.7	4288.7	4272.0	6144.0	5430.7	5318.3
36.4	208.8	375.3	239.6	147.7	213.2	97.5	328.7	114.0	189.9	113.6
82.6	621.9	904.9	965.1	611.3	578.1	910.9	849.2	194.9	600.6	533.2
16005.0	5692.6	4371.9	4977.4	4976.6	4944.0	5563.2	4796.7	7777.9	7834.7	6903.9
59.1	379.4	422.5	535.9	295.7	477.0	287.4	657.0	202.8	176.6	424.3
98.2	324.3	519.3	615.4	385.4	565.4	534.6	582.6	283.8	204.4	175.1
27.4	244.9	423.7	519.7	155.2	139.4	205.1	221.2	86.6	14.9	113.1
3713.8	3665.7	3393.0	3847.7	3649.0	3594.4	3487.1	3972.0	2165.9	1565.4	2779.9
246.6	3769.3	4333.7	4192.7	3933.8	3414.0	4320.0	4076.2	3139.4	2061.7	3640.9
149.1	2762.9	2787.4	3146.7	2065.0	2705.0	1492.4	3117.3	3981.5	3376.2	1844.7
407.1	2827.0	3802.8	3709.6	3760.1	3671.6	4285.2	3541.1	3229.7	2397.0	3625.7
268.3	1073.5	1894.0	1512.4	1275.4	1211.9	1175.5	1875.7	1612.8	1681.3	944.0
66.2	784.0	1307.4	1132.8	1132.5	561.5	626.8	940.2	457.3	233.3	391.0
330.5	1467.0	1361.3	1246.6	1050.0	1163.5	1140.7	1263.2	732.1	2042.1	858.8
445.6	1693.9	1622.7	1388.5	1638.4	1641.6	1504.5	1996.7	2458.4	2040.6	1127.8
946.4	3978.2	3860.9	3422.6	1150.4	3169.6	3833.4	3897.3	4909.2	3539.0	4550.2
213.7	1181.8	1382.3	2055.8	886.1	839.7	891.2	1017.1	389.6	151.7	651.2
6331.3	1956.3	1988.9	1975.8	1585.8	1973.4	2143.1	1644.5	1465.4	773.6	1833.1

1847.2	1185.2	1270.3
2761.6	2414.6	971.4
1103.8	1074.9	2423.1
1049.6	973.1	1073.1
1047.1	1816.3	1522.8
3031.8	3991.0	2844.9
319.5	126.6	122.5
1237.0	1902.4	1959.7
2254.1	1759.0	2402.4
2572.7	3475.7	3473.4
163.1	274.5	131.5
882.4	927.1	984.7
1330.3	1207.1	1399.0
3140.7	3164.1	3029.9
1911.3	2699.5	2344.4
1642.1	193.6	281.6
2397.4	2050.9	1464.4
1246.0	952.3	1378.0
58.0	58.3	59.3
225.2	274.6	221.8
3531.5	4155.2	3688.1
2589.8	1430.3	2391.4
1051.3	1605.7	1171.9
4193.5	4825.7	4100.0
596.3	264.3	527.2
995.5	624.4	909.9
4658.5	6516.9	5022.8
711.9	598.3	876.1
693.3	873.0	640.1
288.4	158.7	212.1
3943.1	4250.1	6576.3
4114.1	3967.1	5022.7
3007.6	2685.6	3118.7
2704.2	3256.0	3061.2
2198.0	2217.7	1464.2
998.9	1112.8	1139.5
1491.4	772.7	946.0
1935.3	2552.6	1345.2
2889.9	2869.3	2982.1
1358.7	1282.2	1289.6
1366.5	2092.4	2207.9

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DQ796784.1 gg_id:196862 human fecal clone RL179_aao54d10	DQ796
FJ366261.1 gg_id:358843 feces adult twins and mothers; TS25 clone TS25_a04f01	FJ3662
FJ369162.1 gg_id:357114 feces adult twins and mothers; TS50 clone TS50_a01a06	FJ3691
DQ802535.1 gg_id:197244 human fecal clone RL188_aan93b03	DQ802
DQ804262.1 gg_id:196986 human fecal clone RL187_aan77b05	DQ804
DQ805430.1 gg_id:185521 human fecal clone RL203_aai62e04	DQ805
FJ367768.1 gg_id:362466 feces adult twins and mothers; TS2 clone TS2_a03d05	FJ3677
FJ369199.1 gg_id:370044 feces adult twins and mothers; TS50 clone TS50_a01d09	FJ3691
DQ805300.1 gg_id:199508 human fecal clone RL249_aaj84g06	DQ805
AJ133124.1 gg_id:22899 Ruminococcus luti str. bln9	AJ1331
DQ801236.1 gg_id:182962 human fecal clone RL116_aaf02b10	DQ801
FJ362873.1 gg_id:368307 feces adult twins and mothers; TS13 clone TS13_a04c03	FJ3628
DQ825010.1 gg_id:187491 human fecal clone RL185_aao72c01	DQ825
DQ806646.1 gg_id:188588 human fecal clone RL186_aao47b05	DQ806
DQ905659.1 gg_id:163685 human fecal clone 014C-D5	DQ905
DQ057417.1 gg_id:134268 chicken ileum/cecum clone oc44	DQ057
DQ807155.1 gg_id:181330 human fecal clone RL244_aaj46h12	DQ807
DQ797201.1 gg_id:187271 human fecal clone RL386_aao88c09	DQ797
DQ804499.1 gg_id:185360 human fecal clone RL187_aan80h04	DQ804
FJ367409.1 gg_id:361412 feces adult twins and mothers; TS29 clone TS29_a03b08	FJ3674
FJ363998.1 gg_id:358181 feces adult twins and mothers; TS150 clone TS150_a01g10	FJ3639
DQ801129.1 gg_id:183212 human fecal clone RL387_aao92f11	DQ801
DQ802249.1 gg_id:189871 human fecal clone RL188_aah15a10	DQ802
FJ370034.1 gg_id:368166 feces adult twins and mothers; TS55 clone TS55_a03f10	FJ3700
DQ805353.1 gg_id:196792 human fecal clone RL203_aai61e09	DQ805
GQ493491.1 gg_id:545944 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ493
EU774067.1 gg_id:324163 Chimpanzee feces clone CHIMP1_c12	EU774
DQ798308.1 gg_id:188852 human fecal clone RL181_aah40e02	DQ798
FJ363960.1 gg_id:369883 feces adult twins and mothers; TS150 clone TS150_a01d04	FJ3639
DQ802328.1 gg_id:182581 human fecal clone RL188_aah16b05	DQ802
FJ366920.1 gg_id:360553 feces adult twins and mothers; TS28 clone TS28_a01d05	FJ3669
DQ803447.1 gg_id:196353 human fecal clone RL251_aaj85h09	DQ803
DQ825323.1 gg_id:176089 human fecal clone RL185_aan88e07	DQ825
DQ808188.1 gg_id:186103 human fecal clone RL180_aao73f09	DQ808
DQ800214.1 gg_id:184636 human fecal clone RL303_aal69g02	DQ800
FJ368971.1 gg_id:366601 feces adult twins and mothers; TS4 clone TS4_a02g01	FJ3689
EU475728.1 gg_id:300551 white-faced saki feces clone Saki_aaj63c03	EU475
FJ678854.1 gg_id:515724 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee	FJ6788
FJ364216.1 gg_id:359342 feces adult twins and mothers; TS150 clone TS150_a04c10	FJ3642
DQ799793.1 gg_id:197502 human fecal clone RL182_aah33f10	DQ799
FJ368939.1 gg_id:363739 feces adult twins and mothers; TS4 clone TS4_a02c12	FJ3689

4274.3	4164.4	4407.9	4420.0	6205.2	4455.8	3984.2	4617.2	4555.6	2691.7	4487.5
24995.7	9267.4	10391.2	9730.0	9253.7	8496.9	10139.4	8774.1	13573.1	10871.5	13606.1
126.6	388.4	485.9	497.0	319.2	393.0	425.1	442.1	144.9	97.9	320.8
87.3	1624.8	2309.0	2107.2	1233.5	1654.1	1693.6	1338.9	1250.7	2009.3	1526.5
2938.6	2001.2	2002.9	1965.7	1877.4	1778.4	1846.2	2416.2	2982.2	1874.6	2026.7
1536.3	1404.5	1445.0	1321.3	2041.0	1170.3	1544.8	1327.9	682.0	1166.1	626.2
127.2	1234.7	1816.6	1819.2	919.0	1196.9	1192.2	1498.5	1734.2	1200.0	1479.4
308.6	1384.1	1995.0	1892.7	1816.3	1597.2	2066.6	1999.2	1441.1	1429.4	1263.9
43.0	1174.1	1221.1	1756.2	507.3	918.2	470.5	1335.6	207.6	111.6	283.7
58.3	686.6	1439.1	1187.1	423.3	750.9	809.3	1448.3	593.0	118.7	536.7
939.5	945.8	1001.7	1179.0	742.4	820.0	657.9	928.9	482.8	387.9	604.1
72.0	373.4	597.7	740.9	76.9	274.6	203.8	416.3	62.2	48.8	243.2
3571.8	4563.9	4966.4	4690.9	3504.8	4424.1	4921.9	4549.6	4328.8	3933.2	3689.4
149.8	946.8	1243.3	1161.8	831.1	789.2	761.4	872.9	463.1	297.5	704.1
21191.2	5753.6	6043.6	5109.2	6392.3	5430.4	6575.7	6231.0	2343.6	5364.4	5127.0
4977.5	1704.0	2157.8	2589.3	1135.6	1489.8	1759.2	1761.8	1962.8	1490.7	2337.0
24.6	130.3	46.9	90.2	32.7	40.0	54.3	50.1	16.2	20.3	33.4
44.3	400.5	611.1	692.9	304.5	290.5	257.6	594.6	62.4	61.3	144.8
887.6	360.3	479.3	441.1	258.7	280.5	193.4	383.3	248.5	434.3	230.6
5444.6	1840.1	1714.0	1423.5	1386.0	1581.2	1464.5	1610.8	2699.3	1466.4	2553.5
2970.2	2401.3	2509.8	2608.8	2430.6	2395.4	2328.3	2543.9	2552.8	2263.3	2576.1
6900.3	3732.7	3451.9	3565.9	3055.5	3411.8	3315.5	3293.5	4302.9	2952.2	5680.7
219.8	1387.2	1864.7	1759.9	1682.0	1635.4	2258.8	2019.7	808.2	1381.7	1065.9
2859.9	2679.9	3153.9	3635.7	2604.5	2898.3	2764.4	3578.7	2652.4	2235.3	2168.3
730.9	2878.4	3738.6	4518.3	2307.2	3060.7	3453.5	4502.2	1524.6	837.1	2736.3
347.1	787.5	797.2	956.2	1029.9	781.8	1040.1	1101.4	678.2	346.4	146.6
30.0	331.5	337.2	422.6	249.6	180.8	167.9	345.6	97.2	48.8	191.0
3900.6	2889.9	2372.4	2030.0	2059.4	2253.5	1645.5	2655.7	3049.3	2291.9	2175.9
72.8	210.0	281.2	361.3	173.3	155.9	247.9	251.5	72.2	88.7	82.8
4422.1	4092.7	4042.6	4348.5	3707.3	4174.1	4050.9	3774.2	6053.8	4449.7	4221.1
438.3	1302.9	2252.7	2078.0	1053.9	1315.9	1070.1	1667.2	1733.3	797.8	1240.1
595.0	481.2	525.5	410.9	358.1	438.3	248.1	671.6	264.0	496.2	532.6
623.4	1664.5	2193.9	2343.2	1621.3	2083.3	2343.2	2070.2	1121.2	1260.0	1845.3
32.1	22.2	21.5	30.6	38.1	18.9	20.4	25.4	23.0	17.1	20.3
1609.5	1949.9	2176.3	2070.4	2096.1	2131.9	2264.4	2104.2	2803.1	2458.8	2722.5
7322.7	3707.2	3196.1	4532.3	4553.5	3346.4	4850.7	3382.8	4252.2	3335.8	6163.4
361.7	330.7	347.5	516.0	428.7	297.0	332.2	365.7	210.5	111.8	259.4
2221.6	2540.6	2703.5	2532.0	3668.5	2941.1	2879.4	2980.7	2725.5	1239.7	2406.0
60.6	538.7	1201.0	854.4	428.2	675.3	722.3	873.7	462.0	867.2	428.6
6820.6	3741.4	3587.1	3284.4	2905.9	2804.9	2665.1	3211.0	5272.8	3469.8	3455.1
172.8	1664.4	1691.7	1710.2	1317.0	1606.2	1373.3	2356.7	3206.0	2241.1	2018.8

4334.0	4515.6	4510.1
8468.7	10003.4	9093.4
464.1	564.3	584.1
2021.8	2385.5	2382.1
1903.2	3129.3	2182.6
1214.9	1551.2	1756.5
1511.1	1586.8	1681.7
2032.6	2231.9	2300.9
1763.1	1284.3	2363.5
1060.1	904.0	1561.9
946.9	1180.0	1245.5
565.7	338.7	347.2
4754.6	4183.5	6222.3
1142.1	1307.8	1576.5
6947.0	6199.0	5210.5
2130.3	2412.9	1877.2
57.6	49.2	42.7
620.0	698.4	510.2
547.3	1103.9	361.3
1358.3	2450.1	1627.4
3132.4	2712.7	2581.0
3002.8	3937.9	3040.4
2266.2	2178.7	1720.4
3992.7	3132.2	3709.5
4011.3	3169.3	5145.9
1063.4	1326.3	1241.3
133.3	469.6	309.2
1968.9	3105.1	2490.1
394.1	241.8	322.9
3794.4	4575.1	3856.9
1797.2	1735.5	1733.0
623.8	680.1	385.2
2226.0	2207.9	2969.7
20.3	47.4	41.1
2025.3	2236.3	2777.4
3402.6	4925.6	3961.1
413.2	841.1	500.5
2677.2	3380.9	2911.5
1245.1	847.6	2053.8
3668.0	3608.9	3776.5
1942.7	2392.9	1779.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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DQ800094.1 gg_id:193828 human fecal clone RL247_aaj24b02 DQ800
DQ806736.1 gg_id:198868 human fecal clone RL186_aao48b04 DQ806
FJ679989.1 gg_id:530488 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ802544.1 gg_id:177692 human fecal clone RL188_aan93c02 DQ802
DQ807801.1 gg_id:181955 human fecal clone RL180_aah37d03 DQ807
EU461651.1 gg_id:294606 mongoose lemur feces clone ML_aaj26c12 EU461
FJ369921.1 gg_id:361609 feces adult twins and mothers; TS55 clone TS55_a02c11 FJ3699
DQ824342.1 gg_id:188584 human fecal clone RL304_aal74g05 DQ824
DQ825086.1 gg_id:194112 human fecal clone RL185_aan85c02 DQ825
DQ796199.1 gg_id:189049 human fecal clone RL179_aah23a09 DQ796
EU774977.1 gg_id:308504 Flying Fox feces clone FF_-aag84a06 EU774
DQ798974.1 gg_id:198990 human fecal clone RL242_aaj99h04 DQ798
EU466825.1 gg_id:297983 African elephant feces clone AFEL2_aao30a03 EU466
EU466972.1 gg_id:296298 African elephant feces clone AFEL2_aao32b02 EU466
FJ363105.1 gg_id:359560 feces adult twins and mothers; TS148 clone TS148_a03b04 FJ3631
DQ795166.1 gg_id:199748 human fecal clone RL178_aah51a02 DQ795
DQ796431.1 gg_id:193150 human fecal clone RL179_aah28c03 DQ796
DQ805262.1 gg_id:183936 human fecal clone RL249_aaj84a03 DQ805
FJ369915.1 gg_id:367583 feces adult twins and mothers; TS55 clone TS55_a02c05 FJ3699
EU764574.1 gg_id:324741 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ679697.1 gg_id:516792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
DQ795521.1 gg_id:188166 human fecal clone RL178_aan65f02 DQ795
FJ679919.1 gg_id:516653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU469802.1 gg_id:300479 western lowland gorilla feces clone GOR_aag71c05 EU469
AY442822.1 gg_id:99566 Ruminococcus sp. YE58 AY442
FJ370524.1 gg_id:368808 feces adult twins and mothers; TS57 clone TS57_a02a12 FJ3705
FJ365661.1 gg_id:365684 feces adult twins and mothers; TS21 clone TS21_a01e06 FJ3656
AM696975.1 gg_id:218995 sequencing libraries indoor dust clone BF0001B001 AM696
FJ363916.1 gg_id:370410 feces adult twins and mothers; TS14 clone TS14_a04h04 FJ3639
DQ800834.1 gg_id:188686 human fecal clone RL183_aao04a10 DQ800
DQ806459.1 gg_id:174163 human fecal clone RL186_aan92h02 DQ806
DQ801767.1 gg_id:189357 human fecal clone RL201_aai46e09 DQ801
DQ803372.1 gg_id:191062 human fecal clone RL311_aam24g08 DQ803
FJ681121.1 gg_id:519761 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU728792.1 gg_id:344947 Ruminococcus sp. str. DJF_VR70k1 EU728
FJ364765.1 gg_id:361855 feces adult twins and mothers; TS19 clone TS19_a02g10 FJ3647
DQ799858.1 gg_id:176933 human fecal clone RL247_aaj21a07 DQ799
FJ365546.1 gg_id:369247 feces adult twins and mothers; TS20 clone TS20_a04b07 FJ3655
EU763193.1 gg_id:334957 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ367161.1 gg_id:361308 feces adult twins and mothers; TS28 clone TS28_a04c03 FJ3671
GQ492131.1 gg_id:578713 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492

1709.4	993.2	1155.8	1168.0	1024.1	898.4	946.2	1245.7	501.5	314.3	783.4
42.2	318.7	523.9	610.0	553.0	314.1	379.2	525.5	113.5	72.1	137.9
37.2	780.8	955.0	1090.8	134.7	556.6	339.8	959.9	88.8	110.4	301.7
20813.1	6887.4	6571.3	6760.7	6220.1	6079.7	6316.9	6650.6	7519.8	6675.4	9162.2
45.8	424.6	701.3	882.0	466.0	734.4	605.9	1098.3	219.6	206.8	355.3
41.6	282.6	298.0	347.5	571.4	264.2	608.2	321.4	101.3	108.6	145.4
1701.1	1639.4	2001.0	2213.9	2079.2	1988.9	2355.0	2090.9	1975.6	1079.6	1857.4
11646.1	3082.6	3373.9	2957.7	3268.9	3164.8	3278.6	3752.7	4587.1	3902.2	2873.3
60.6	848.9	1438.2	1227.5	872.4	834.4	623.4	1022.8	818.0	172.4	652.3
49.6	504.7	973.8	959.4	184.4	478.4	266.3	1027.6	187.0	89.0	470.3
11046.4	4985.6	4449.1	4776.6	4683.0	4853.8	5236.6	4851.4	6131.0	6587.0	5547.3
485.5	1700.7	2258.3	2058.1	1791.2	1721.2	1522.3	2137.9	1973.4	1689.5	1414.0
10311.4	3652.0	3264.1	4135.9	3089.3	3166.9	3254.1	3693.5	3235.8	2152.4	4607.6
1563.0	1956.9	1836.7	1994.0	1845.6	1645.4	1727.6	1905.8	1307.9	665.2	1901.8
65.7	1042.4	885.3	1261.7	341.3	790.6	342.7	907.0	230.7	406.4	296.5
60.3	244.2	485.0	494.2	105.3	249.6	110.8	468.3	92.4	102.6	214.4
150.0	702.5	721.8	1100.4	692.2	672.9	552.5	1010.0	622.5	602.6	543.3
50.5	223.8	277.5	287.3	214.1	210.8	188.1	269.0	84.0	49.8	151.2
49.5	45.3	37.1	87.9	95.8	60.4	118.8	77.4	31.0	25.6	21.0
35.5	885.1	1524.1	1210.5	310.3	998.9	814.9	1346.3	336.2	190.1	593.0
731.1	1959.6	2856.3	2568.0	2189.6	1985.1	2719.2	2235.5	2034.5	2419.6	1900.6
58.6	309.8	623.6	419.2	166.1	268.4	206.0	417.2	188.0	77.0	481.7
14892.7	6112.9	5888.4	5561.2	5431.0	5640.0	5596.2	5742.9	9407.4	6044.3	7600.4
344.7	574.3	814.8	935.6	511.7	405.9	585.1	666.6	191.8	256.9	216.5
37.9	305.9	556.7	833.6	317.1	475.5	312.3	682.9	83.9	73.7	366.7
80.6	832.7	1285.9	1816.5	395.4	764.9	568.1	1215.5	182.4	132.0	465.7
4042.5	5002.1	5475.5	4808.0	4114.3	4419.5	5140.9	4667.1	5535.2	5208.8	6056.6
8051.8	4021.4	3919.9	3957.5	4049.8	4530.7	4086.0	5343.2	4327.6	4383.5	5860.6
64.4	544.1	861.9	838.1	195.0	441.2	333.1	789.3	152.5	73.7	440.2
352.6	4903.9	4554.0	3334.8	3110.6	3799.3	3046.6	3444.6	4570.6	4164.3	3434.4
5807.3	4225.6	4201.7	4336.0	4427.7	3843.8	5190.5	4245.9	4052.4	5623.0	3551.0
982.4	2733.2	2569.6	2195.7	1940.3	2313.7	2207.9	2352.3	2783.4	2678.9	1891.4
2688.9	1752.2	2177.2	2087.3	1800.7	2018.0	2419.6	2877.8	1215.9	2397.8	1347.4
85.2	316.9	510.5	603.1	513.0	418.4	565.5	661.7	365.4	81.2	171.2
438.6	1586.1	2106.6	2252.6	1110.5	1659.7	1289.6	3049.6	866.3	354.3	1799.3
9521.8	4322.4	3964.3	4431.7	3563.5	3770.5	3436.2	2909.7	2999.6	2680.6	3960.4
796.1	1302.7	1177.6	1636.9	1230.3	1253.0	1328.0	1787.3	963.7	557.3	980.2
326.2	892.7	1304.1	1275.7	864.7	875.8	1088.9	1209.7	706.2	686.8	768.6
33.2	269.4	457.0	415.5	269.3	258.8	227.3	516.0	93.2	209.2	130.9
275.0	738.6	164.0	725.1	888.5	649.8	803.8	827.0	645.7	262.7	554.4
79.7	845.6	972.8	945.1	926.7	1028.4	1083.6	1406.2	750.3	1623.0	953.2

1026.5	1478.2	1388.1
655.2	639.0	471.6
1680.0	356.5	955.1
8242.7	6348.5	5553.4
1524.2	637.2	2443.3
491.6	294.8	405.7
1874.9	2852.5	2212.0
4034.5	4767.5	3542.2
1547.8	1097.1	1287.0
1424.2	651.7	641.9
5021.3	5124.0	4907.7
1988.5	2577.6	2464.4
4110.5	3831.8	3074.9
2090.1	2735.8	1630.1
1168.7	1078.9	1534.9
378.1	461.9	493.9
1302.9	1153.1	1172.3
331.5	233.5	269.0
65.1	87.2	40.8
1896.1	1075.8	1885.9
2012.2	2406.5	2618.3
465.2	440.8	527.4
5480.9	6647.8	6794.0
1233.3	673.0	838.5
684.3	492.4	804.3
1525.8	938.5	1063.8
4130.2	5526.0	4672.4
4744.5	4440.5	5319.8
681.4	640.5	565.0
3261.7	3752.2	4992.6
3874.3	5273.9	6250.2
2035.4	2636.7	3287.7
2062.8	2374.5	3950.5
621.3	1272.1	484.1
3466.5	1435.8	2026.8
3290.3	4154.7	3283.0
2614.0	2195.0	2630.7
1305.9	1112.1	1271.4
1004.2	414.3	870.2
940.2	1316.4	824.6
1328.3	1247.8	1701.7

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EU778140.1 gg_id:323778 feces clone RL388_aao95c12 EU778
FJ682155.1 gg_id:519441 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
DQ797815.1 gg_id:173975 human fecal clone RL206_aaj16b08 DQ797
GQ492839.1 gg_id:585610 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ799779.1 gg_id:189842 human fecal clone RL182_aah33d09 DQ799
DQ326493.1 gg_id:148279 Metagenomic gut microbiome healthy human stool clone C591 DQ326
DQ326406.1 gg_id:149236 Metagenomic gut microbiome healthy human stool clone C448 DQ326
FJ677824.1 gg_id:529004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
DQ327590.1 gg_id:145858 Metagenomic gut microbiome healthy human stool clone EB76 DQ327
GQ491902.1 gg_id:576504 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU773407.1 gg_id:311080 Black lemur feces clone BKLE_c10_3 EU773
DQ804121.1 gg_id:175988 human fecal clone RL187_aah68h08 DQ804
DQ808356.1 gg_id:181831 human fecal clone RL180_aao75f08 DQ808
DQ795593.1 gg_id:194234 human fecal clone RL178_aan66g03 DQ795
DQ803639.1 gg_id:187496 human fecal clone RL251_aaj88e10 DQ803
DQ800645.1 gg_id:180900 human fecal clone RL183_aao01e03 DQ800
DQ825047.1 gg_id:191384 human fecal clone RL185_aao72f11 DQ825
DQ808011.1 gg_id:174599 human fecal clone RL180_aan70f05 DQ808
FJ367398.1 gg_id:368950 feces adult twins and mothers; TS29 clone TS29_a03a08 FJ3673
FJ370628.1 gg_id:362215 feces adult twins and mothers; TS57 clone TS57_a03d01 FJ3706
EU773503.1 gg_id:312986 Bonobo feces clone BNO_aaa01a01 EU773
GQ052306.1 gg_id:429460 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu534a05 GQ052
DQ805014.1 gg_id:194889 human fecal clone RL385_aao84a11 DQ805
DQ825038.1 gg_id:187583 human fecal clone RL185_aao72e12 DQ825
EU344383.1 gg_id:258461 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EF403780.1 gg_id:204996 human fecal clone SJTU_A2_02_06 EF4037
DQ808990.1 gg_id:184545 human fecal clone RL243_aai87h08 DQ808
DQ807910.1 gg_id:180777 human fecal clone RL180_aah38h03 DQ807
FJ363776.1 gg_id:362510 feces adult twins and mothers; TS14 clone TS14_a03c02 FJ3637
FJ674058.1 gg_id:531865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
DQ806218.1 gg_id:190648 human fecal clone RL186_aah62g11 DQ806
FJ683556.1 gg_id:521865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ798341.1 gg_id:175589 human fecal clone RL181_aah41b11 DQ798
EU467251.1 gg_id:296692 black-handed spider monkey feces clone SPIM_a03_1 EU467
DQ804949.1 gg_id:195941 human fecal clone RL385_aao83a10 DQ804
FJ684827.1 gg_id:513226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ370430.1 gg_id:358419 feces adult twins and mothers; TS57 clone TS57_a01a05 FJ3704
DQ795634.1 gg_id:199010 human fecal clone RL178_aan67d07 DQ795
DQ802591.1 gg_id:195295 human fecal clone RL188_aan93g08 DQ802
FJ364772.1 gg_id:357464 feces adult twins and mothers; TS19 clone TS19_a02h08 FJ3647
DQ804278.1 gg_id:187591 human fecal clone RL187_aan77c12 DQ804

42.0	126.1	196.3	89.4	57.3	77.6	48.2	93.2	33.2	18.9	31.1
42.7	35.7	113.0	105.5	70.6	105.4	116.8	161.6	31.9	15.9	70.1
48.5	22.1	35.8	26.6	28.1	41.0	17.9	30.5	24.4	25.1	30.8
3097.2	4969.1	3908.6	3620.9	4371.6	4453.3	3585.4	4492.3	3184.9	4445.2	4573.4
60.9	1090.3	1592.9	2032.4	452.7	776.9	814.8	1561.0	235.0	161.9	590.5
43.1	532.6	782.5	796.8	103.2	324.0	262.5	547.5	164.5	64.7	410.2
1183.4	1638.1	2262.5	1498.8	1781.6	1532.3	1920.9	1964.1	2498.6	2319.4	2345.6
48.1	430.5	610.1	689.0	164.2	263.1	476.9	328.2	200.8	50.9	225.4
63.9	436.3	800.1	1127.8	274.2	331.0	350.4	613.8	135.5	61.0	220.8
1558.5	487.6	531.8	756.1	486.6	597.7	564.6	745.0	408.9	478.8	552.3
34.2	410.4	1103.1	1582.8	130.3	315.5	260.1	758.1	66.3	46.2	319.1
503.5	859.4	1112.2	1004.5	772.0	726.7	713.0	924.8	775.5	684.6	470.2
609.2	1848.2	1599.4	2525.6	1843.7	1491.3	1429.5	1731.8	1164.6	1253.2	1395.5
103.6	1325.5	1381.7	1473.9	2682.2	1514.5	1864.3	1893.2	844.1	562.8	1112.7
1429.5	5067.6	6754.7	6361.5	6263.8	5446.7	6970.0	6538.8	6597.8	8900.7	4786.2
1914.4	1633.8	1747.4	1885.8	1687.3	1627.1	1577.8	1794.9	1116.0	805.6	1867.4
4111.5	4421.9	5018.0	4533.0	3084.5	3654.3	3835.3	3856.9	5814.8	4132.7	5327.6
292.8	928.6	1650.9	1552.5	859.3	1007.1	1192.5	1232.7	564.2	541.4	932.8
344.0	1283.7	1188.7	1026.3	1162.9	1111.9	1086.8	2417.7	555.0	954.9	833.4
232.7	2150.8	2013.6	2179.8	1397.9	1714.0	1455.1	2083.7	1803.5	1246.7	1346.8
95.7	614.3	742.0	817.8	684.3	787.4	647.4	1398.4	243.2	203.2	525.6
4082.4	2134.2	1883.7	2195.4	2699.4	1984.2	1978.9	2128.2	1856.4	1290.5	2498.1
8270.7	3812.3	3742.7	3694.6	2998.9	3204.0	4039.8	2777.7	4450.0	2586.9	5905.8
74.5	442.9	719.4	450.1	647.9	511.4	418.6	683.9	423.0	503.2	376.0
733.7	1871.9	2460.4	2768.1	2092.2	1739.3	2235.5	1931.9	900.2	1268.3	995.5
39.7	236.8	335.2	246.4	258.5	222.9	478.5	253.2	83.5	88.6	137.2
53.2	373.1	324.2	623.2	309.9	536.6	331.8	1262.8	153.5	146.3	420.1
1297.4	1417.6	1273.6	1054.4	1132.4	1253.9	1014.1	1327.2	875.4	4490.9	743.5
4223.5	2108.3	2013.5	2551.5	2458.8	1830.3	2547.1	2944.3	1624.6	791.4	1846.1
81.3	799.9	1051.4	1212.4	921.8	1029.1	1302.4	1083.2	348.1	180.8	710.0
416.3	1541.0	2532.9	1845.8	1805.7	1783.9	1376.0	2296.8	1585.9	2362.6	1179.7
102.1	2185.7	2623.4	2476.8	1334.8	2061.2	2067.1	2547.3	1162.5	1986.1	2328.6
31.7	193.2	303.5	235.0	98.5	227.7	185.1	287.7	73.9	157.6	125.1
31.3	453.7	761.0	691.5	161.3	387.1	300.9	543.9	110.3	102.3	292.3
43.1	193.6	320.8	382.6	38.3	133.8	79.6	209.1	36.8	31.3	65.4
9998.0	4436.8	3607.9	4711.5	4459.0	4065.6	4853.8	4046.1	4793.3	2638.0	6315.1
9114.5	4402.5	4222.5	4547.3	4741.9	4316.2	4561.5	4056.4	5877.8	5701.0	6348.9
102.7	423.4	221.4	281.4	837.2	392.6	513.1	407.4	239.4	273.5	113.7
55.0	187.0	252.3	294.4	233.6	133.6	264.4	274.1	82.2	47.1	228.0
886.6	4081.2	4215.6	4158.7	1298.6	3380.5	3675.2	3827.1	5088.2	3322.1	4680.2
650.9	621.2	847.5	961.1	774.0	862.8	757.5	800.0	612.4	955.4	1044.3

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170.0	143.4	184.3
18.9	24.2	20.6
4405.4	4687.8	5489.6
1775.2	1172.6	922.9
684.9	570.1	469.8
2163.9	2493.6	2234.1
532.7	345.7	617.9
870.8	636.0	1902.8
1075.4	843.0	889.4
890.6	666.9	1129.1
930.1	1187.9	1106.3
2366.3	2847.4	2149.4
2172.1	1013.3	1081.2
6250.7	7146.6	8355.6
1702.2	2013.6	2749.7
3153.9	4512.4	3762.1
1153.9	1700.6	2192.1
1387.8	1190.0	1238.4
1819.7	2057.4	2551.5
1700.7	851.1	1938.6
2151.0	3655.4	2405.1
2887.4	3723.0	4028.8
713.5	749.0	606.0
2394.5	2372.1	2477.5
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1299.2	992.8	1811.4
2043.3	2443.1	1596.3
2516.0	2556.2	2350.0
344.9	329.4	585.0
1201.7	494.0	911.9
391.2	184.4	96.9
3965.6	4766.9	4516.2
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3539.3	2472.7	1064.8
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DQ824793.1 gg_id:179080 human fecal clone RL185_aao69d02 DQ824
FJ366169.1 gg_id:357289 feces adult twins and mothers; TS25 clone TS25_a03e06 FJ3661
FJ678441.1 gg_id:519063 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU467416.1 gg_id:296514 chimpanzee feces clone CHIMP12_c03 EU467
GQ491331.1 gg_id:575263 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ492790.1 gg_id:580891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ364998.1 gg_id:362334 feces adult twins and mothers; TS1 clone TS1_a01f06 FJ3649
AF349421.1 gg_id:77371 pig feces clone AF3494
FJ364211.1 gg_id:366259 feces adult twins and mothers; TS150 clone TS150_a04c05 FJ3642
FJ677875.1 gg_id:514708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
FJ370381.1 gg_id:360033 feces adult twins and mothers; TS56 clone TS56_a04c02 FJ3703
DQ798463.1 gg_id:191746 human fecal clone RL181_aan97a06 DQ798
FJ678829.1 gg_id:528093 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
GQ491285.1 gg_id:587632 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ370535.1 gg_id:365441 feces adult twins and mothers; TS57 clone TS57_a02b11 FJ3705
FJ367412.1 gg_id:365431 feces adult twins and mothers; TS29 clone TS29_a03c02 FJ3674
DQ809682.1 gg_id:195537 human fecal clone RL184_aan82e09 DQ809
DQ804413.1 gg_id:173896 human fecal clone RL187_aan79e02 DQ804
X95624.1 gg_id:13997 Ruminococcus hydrogenotrophicus str. S5a36 X95624
FJ366380.1 gg_id:360776 feces adult twins and mothers; TS26 clone TS26_a02c11 FJ3663
FJ365881.1 gg_id:364310 feces adult twins and mothers; TS21 clone TS21_a04b07 FJ3658
AY982924.1 gg_id:122998 human descending colon mucosal biopsy clone L118 AY9829
FJ369197.1 gg_id:357853 feces adult twins and mothers; TS50 clone TS50_a01d07 FJ3691
AY974849.1 gg_id:118782 human ascending colon mucosal biopsy clone KG89 AY9748
EU462164.1 gg_id:302830 black-handed spider monkey feces clone SPIM_aaj36c04 EU4621
DQ801948.1 gg_id:193284 human fecal clone RL201_aai48h05 DQ801
GQ898643.1 gg_id:569010 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ802277.1 gg_id:198083 human fecal clone RL188_aah15e06 DQ802
DQ802736.1 gg_id:180297 human fecal clone RL188_aan95h08 DQ802
EU462179.1 gg_id:303169 black-handed spider monkey feces clone SPIM_aaj36f06 EU4621
DQ801357.1 gg_id:193389 human fecal clone RL388_aao94d11 DQ801
FJ678267.1 gg_id:529473 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AB218345.1 gg_id:150230 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-129 AB2183
DQ799789.1 gg_id:180169 human fecal clone RL182_aah33f04 DQ799
AY977739.1 gg_id:121304 human cecum mucosal biopsy clone LE08 AY9777
DQ799700.1 gg_id:188200 human fecal clone RL182_aah31f10 DQ799
EU768469.1 gg_id:336275 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7684
DQ807542.1 gg_id:197222 human fecal clone RL307_aam07h12 DQ807
GQ491581.1 gg_id:567715 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801753.1 gg_id:196693 human fecal clone RL201_aai46d04 DQ801
FJ363021.1 gg_id:367919 feces adult twins and mothers; TS148 clone TS148_a02a07 FJ3630

29.6	98.0	124.5	170.3	61.5	84.9	74.5	94.8	47.3	31.9	93.3
19717.2	5718.5	4874.6	4976.0	4488.1	4781.5	5151.5	4568.2	6283.5	5209.8	7569.4
58.1	165.4	255.7	278.7	301.5	230.3	304.3	248.5	103.9	69.3	155.7
3799.6	1753.6	2282.8	1955.1	1937.5	2271.7	1794.7	3268.4	1161.0	1433.8	1375.0
581.0	1941.3	2406.1	1935.3	1209.2	1595.6	1161.9	1707.6	2771.0	2938.3	2859.7
2761.0	2607.7	2903.4	2437.0	2089.0	2017.4	2184.6	3194.3	2203.2	1493.6	1823.6
184.8	2308.8	1921.0	1840.8	1783.0	2023.1	2093.7	2206.4	1463.3	2062.2	1446.6
64.9	276.9	525.6	601.0	294.5	440.1	503.5	436.3	145.6	85.8	289.1
2352.0	1917.6	3020.0	2851.2	1666.7	2504.8	2139.2	2791.0	1199.6	635.4	2549.3
1395.5	1954.1	1627.7	1693.5	1583.0	1753.8	1545.3	2399.0	1795.9	1965.8	1374.2
295.8	1296.3	985.1	1926.5	1571.1	1445.1	2040.1	1590.8	968.0	1317.6	1095.9
9614.9	4352.1	4205.5	4085.0	4737.7	4450.1	5041.4	5445.8	3950.2	6207.0	3658.8
3899.0	2190.7	1968.1	2271.5	1675.8	1934.8	2310.9	1811.0	2323.8	2202.2	3522.8
94.6	473.6	790.9	940.8	116.4	368.1	250.2	518.7	123.9	56.2	322.1
1303.7	1286.3	1402.6	1241.8	1221.9	907.8	1112.9	1164.8	975.3	1134.2	1140.8
45.6	44.6	109.7	57.0	39.3	42.2	41.8	53.5	36.7	20.2	61.6
43.3	201.8	352.1	448.6	47.5	280.2	109.8	631.7	76.7	40.8	122.6
316.9	929.7	1401.5	1688.7	489.9	921.9	547.6	1987.3	399.8	197.1	741.8
55.7	2005.8	3219.6	2490.1	772.6	2560.3	1402.6	3321.7	760.5	548.2	2238.1
6573.9	1972.0	2699.2	2260.3	2095.2	2079.1	2315.7	2255.9	2654.4	2685.8	2287.3
173.5	2162.4	3000.3	2967.8	2971.2	2142.9	2979.9	2842.9	1671.7	1707.7	1949.4
136.9	1048.4	1775.0	1770.1	359.1	990.2	404.3	2050.3	412.9	213.1	900.2
49.7	306.8	513.6	426.3	254.9	298.8	465.9	518.9	126.2	130.4	208.7
34.6	196.4	322.9	249.1	151.8	206.7	107.0	256.6	83.6	182.9	121.0
50.2	995.1	1401.9	1585.9	437.3	675.8	607.6	1056.0	271.5	133.8	562.4
2940.8	1534.3	1727.2	1459.1	1177.6	1309.7	1577.1	1584.5	1777.4	2266.7	2148.8
95.9	1862.6	2053.0	1770.2	900.0	1185.7	1316.3	1797.1	1272.3	1285.9	1284.6
1769.5	715.4	641.2	665.6	506.7	577.5	468.4	623.7	184.7	148.9	459.3
7075.3	2840.2	3324.4	3757.2	2639.8	3039.9	3325.0	3040.1	2569.4	1260.1	3560.0
97.3	1029.9	1509.7	1144.1	1186.4	1119.6	1409.5	1213.1	652.5	467.6	1026.2
34.8	435.6	783.2	939.8	159.6	287.1	202.6	421.8	69.1	96.5	173.7
125.6	309.2	609.2	485.3	311.4	318.6	351.9	346.0	185.8	106.0	204.5
41.7	29.8	63.9	45.4	28.8	48.5	42.9	75.1	25.2	35.9	47.7
7248.4	5761.9	5479.5	5814.7	5050.9	5495.4	5578.4	5571.2	6833.5	6230.5	7223.3
28.0	16.2	19.7	18.2	13.7	10.0	18.1	14.2	13.5	11.2	12.4
52.3	158.7	174.4	220.6	145.5	68.3	96.4	107.2	64.0	33.0	95.8
47.4	1464.2	1832.2	2419.0	1491.0	1239.1	1606.8	2954.8	552.5	402.6	1376.0
52.3	667.9	431.0	457.3	896.7	617.6	553.1	2493.9	265.8	138.1	744.0
7351.2	2939.9	2710.8	2762.1	2766.6	2922.7	3614.6	1524.1	2202.5	3218.8	2877.7
43.0	300.0	409.5	341.9	384.8	456.5	407.8	538.5	87.3	64.1	146.7
9826.6	4450.8	4590.5	5352.6	4341.2	5375.7	5133.1	4666.4	6540.4	3716.1	6067.7

97.4	85.2	103.6
5399.1	5640.1	5031.8
317.7	424.5	887.6
4067.9	2654.5	4002.4
2001.0	1833.1	1230.5
2487.0	3085.4	3297.5
2646.5	2505.9	3511.9
481.4	484.2	592.7
2923.5	2986.7	3427.6
3106.4	2646.2	2561.1
1741.1	1979.6	2102.1
5276.6	5322.2	5093.7
1638.3	2050.6	1695.1
600.7	435.0	459.0
1254.6	1910.7	1447.1
50.9	47.1	71.4
840.6	278.8	404.7
2118.9	1571.6	1914.8
2818.5	2493.7	3016.1
2377.3	2637.9	2518.2
2879.1	3513.8	2890.0
517.6	742.1	1103.6
440.6	554.6	1084.7
542.6	283.2	433.3
1249.3	1253.6	1081.1
1495.9	2488.6	1322.4
1317.9	1173.6	2004.2
878.6	800.0	660.4
3262.1	3362.0	2652.9
1117.8	1309.1	1259.3
685.9	425.1	296.1
322.5	623.6	826.9
121.1	42.6	99.4
5539.5	6318.8	5166.1
14.8	19.0	26.0
134.3	145.9	203.8
2057.7	1788.3	2315.8
905.7	706.6	1281.8
2506.6	3453.0	2604.0
656.1	383.8	940.8
3683.9	6466.8	4638.3

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FJ369206.1 gg_id:364996 feces adult twins and mothers; TS50 clone TS50_a01e07 FJ3692
FJ880511.1 gg_id:384505 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
FJ683509.1 gg_id:531675 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ803719.1 gg_id:177307 human fecal clone RL200_aai57e08 DQ803
DQ809757.1 gg_id:183040 human fecal clone RL184_aan83g05 DQ809
DQ796661.1 gg_id:193951 human fecal clone RL179aan76g10 DQ796
DQ794215.1 gg_id:194994 human fecal clone RL176_aan59e11 DQ794
EU530217.1 gg_id:262919 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M1 EU530
DQ807936.1 gg_id:193031 human fecal clone RL180_aan69d10 DQ807
DQ801248.1 gg_id:180078 human fecal clone RL116_aaf02h09 DQ801
FJ674092.1 gg_id:517703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
GQ079643.1 gg_id:392131 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1232e GQ079
EU772296.1 gg_id:310490 Argali sheep feces clone AS1_aao37b06.Contig1 EU772
DQ326182.1 gg_id:148131 Metagenomic gut microbiome healthy human stool clone C085 DQ326
EU766231.1 gg_id:351847 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ365593.1 gg_id:365207 feces adult twins and mothers; TS20 clone TS20_a04f12 FJ3655
DQ799673.1 gg_id:196932 human fecal clone RL305aal88h11 DQ799
DQ804111.1 gg_id:174535 human fecal clone RL187_aah68f11 DQ804
DQ794385.1 gg_id:184488 human fecal clone RL197_aah87a12 DQ794
GQ493579.1 gg_id:580685 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ675878.1 gg_id:524722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
DQ799473.1 gg_id:194586 human fecal clone RL305aal86f12 DQ799
EF399628.1 gg_id:205950 human fecal clone SJTU_E_01_40 EF3996
FJ364795.1 gg_id:365988 feces adult twins and mothers; TS19 clone TS19_a03c02 FJ3647
EF403194.1 gg_id:215270 human fecal clone SJTU_A1_6_25 EF4031
EU468183.1 gg_id:295586 lion feces clone LI1_e03_1 EU468
DQ804318.1 gg_id:183528 human fecal clone RL187_aan77h08 DQ804
DQ804781.1 gg_id:189687 human fecal clone RL187_aao72f05 DQ804
DQ800464.1 gg_id:183252 human fecal clone RL183_aah24h07 DQ800
FJ369439.1 gg_id:359096 feces adult twins and mothers; TS50 clone TS50_a04e06 FJ3694
DQ801547.1 gg_id:183577 human fecal clone RL388_aao96h06 DQ801
DQ804005.1 gg_id:198999 human fecal clone RL187_aah67a02 DQ804
DQ057397.1 gg_id:131559 chicken ileum/cecum clone cc361 DQ057
DQ803204.1 gg_id:191545 human fecal clone RL311_aam22b01 DQ803
EU459628.1 gg_id:292800 ring-tailed lemur feces clone RT_aai09e08 EU459
FJ673676.1 gg_id:531582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ368296.1 gg_id:359143 feces adult twins and mothers; TS3 clone TS3_a02f02 FJ3682
AY976522.1 gg_id:124583 human cecum mucosal biopsy clone K047 AY9765
FJ368201.1 gg_id:370186 feces adult twins and mothers; TS3 clone TS3_a01d08 FJ3682
DQ795062.1 gg_id:194595 human fecal clone RL310_aam39g01 DQ795
DQ807718.1 gg_id:175548 human fecal clone RL180_aah36d05 DQ807

382.7	1218.1	1655.8	1728.5	856.1	1294.7	1425.3	2039.7	531.5	388.7	751.6
31.4	663.8	1163.6	1325.5	448.3	727.0	515.1	1148.0	372.0	128.1	505.4
11465.5	5422.6	4742.4	5818.5	6301.2	5057.0	6466.5	4676.1	6382.9	5812.3	6593.8
51.2	162.3	368.6	381.3	93.9	240.5	62.3	275.0	66.8	66.9	44.4
809.5	646.6	887.8	728.6	504.0	658.4	570.9	1123.4	907.1	652.5	1037.6
533.7	196.7	257.8	208.5	172.6	184.9	155.4	419.6	149.2	81.3	156.2
2545.1	1694.5	2432.2	2051.3	1469.8	1957.1	1958.6	2422.1	1885.8	2834.7	1790.8
341.9	1123.8	1186.6	1109.2	731.9	888.0	938.8	1127.5	1013.0	625.4	745.0
4421.7	3714.5	3841.1	4322.4	3130.2	3265.4	3444.1	3718.9	3553.8	3270.9	4987.8
196.6	1052.7	1606.8	1492.2	1041.2	1179.3	1479.9	1291.1	812.8	1199.8	1173.2
59.4	1149.5	1693.1	1657.6	802.1	751.6	1633.1	1191.4	342.8	207.0	1123.1
1124.4	1191.2	2127.0	1747.2	1171.3	1290.7	1630.1	1654.3	941.1	1150.5	1448.0
510.6	2403.3	2810.5	2798.1	1589.7	2179.4	1491.9	2523.8	1608.8	1147.5	2371.1
720.2	1066.4	1501.8	1794.2	916.7	1189.0	1183.4	1339.3	438.5	270.1	760.7
3588.1	2558.8	2408.5	2059.0	1622.7	2085.3	1819.6	1999.5	2604.4	1629.9	2384.9
1835.1	3110.4	4327.3	4218.4	3130.7	3202.6	3718.8	3170.0	2945.4	3393.7	3746.7
54.1	1898.1	1984.7	1841.7	1791.3	1812.4	2005.8	1639.6	1502.7	2211.1	1441.9
169.7	1351.3	1473.9	1283.3	1166.3	1509.7	1012.4	1587.5	905.0	1528.2	986.8
287.7	1088.7	1681.7	1500.7	1383.3	1170.3	1663.2	1874.8	1533.7	1552.0	881.7
48.6	339.7	414.1	460.8	99.6	244.2	187.5	265.7	65.7	46.5	193.5
1939.2	5593.0	5511.8	5092.9	5644.6	5166.2	4898.7	4472.1	6997.5	4660.5	5394.6
949.9	479.0	650.5	763.5	393.6	388.9	503.3	438.7	393.9	185.3	155.9
78.9	1710.3	2256.2	2038.3	1711.3	2125.0	1797.1	3496.1	1795.7	877.5	1433.2
74.4	846.3	877.1	903.9	453.5	690.4	498.9	828.7	286.3	507.3	301.1
41.3	139.5	313.3	232.7	79.5	236.0	93.4	239.3	62.6	97.1	150.6
728.4	1526.5	1721.0	1720.4	1195.4	1355.7	772.3	2180.0	896.2	345.8	964.6
6007.7	3525.7	3689.7	4607.9	4882.5	3976.4	3640.6	3453.9	3707.8	4270.2	4542.6
58.1	911.1	1376.7	1256.0	837.8	850.9	1090.3	1392.5	627.5	660.8	833.2
32.3	281.5	478.8	488.2	291.1	303.9	249.3	529.8	122.8	298.5	206.7
1200.0	1781.9	3020.6	2779.9	1671.4	2007.4	1804.3	2534.2	1429.5	3098.9	1957.7
425.7	1455.2	1763.2	1957.2	985.8	1207.9	985.4	2702.9	618.4	196.2	1183.3
30.6	301.5	788.2	528.5	442.6	344.8	267.9	355.5	290.2	94.9	197.0
185.2	686.7	961.9	1806.3	435.1	729.6	478.5	626.8	1220.5	348.9	310.7
1935.7	2703.0	3511.2	3543.1	2733.9	2947.0	3039.6	3621.6	1931.0	2359.8	2603.9
145.7	1440.9	2358.9	2824.2	798.7	1436.8	1123.7	2116.5	490.5	264.2	1099.1
15072.2	3355.8	3835.4	4126.5	3140.3	3438.0	3089.3	3749.1	5065.4	4539.6	4728.2
64.3	453.2	758.0	806.5	12.6	570.1	472.2	1004.3	9.7	633.8	548.4
41.6	148.3	201.8	210.6	91.6	115.7	172.2	254.7	56.5	29.1	68.0
878.2	801.4	1067.8	1017.5	529.9	1017.7	452.4	1893.0	265.2	372.9	662.4
67.2	470.1	665.1	641.6	266.2	517.9	320.4	1160.8	206.8	282.8	383.7
5140.4	5085.8	5859.4	5561.7	4621.1	5133.5	4702.9	6352.7	5285.8	7626.2	5154.3

1961.3	1372.6	2070.1
1551.7	949.6	1442.2
4807.7	5748.9	5987.2
439.0	277.1	126.6
666.8	1150.7	667.5
443.9	666.7	921.2
1609.4	2846.1	2506.8
1062.8	1252.6	1581.4
3312.5	4165.2	4126.1
1334.3	1817.0	2020.6
878.9	762.2	1025.2
1595.8	1401.4	2610.8
2579.9	2274.4	2743.1
1281.9	1338.2	1748.4
1783.8	3121.8	2738.5
3412.9	4521.1	4169.1
1804.0	2028.7	2650.0
1722.2	1733.6	1844.6
1639.2	2386.8	1763.2
368.2	361.4	512.8
5827.8	6211.7	6554.4
492.0	1061.1	844.3
3702.0	2053.7	3748.2
834.9	827.7	818.1
235.0	194.8	250.8
2295.0	2019.2	1740.1
3470.6	4262.6	3924.5
2025.2	462.6	970.5
517.6	368.1	552.2
2518.1	2270.0	2839.5
2206.2	1638.0	1392.4
290.4	425.8	1296.8
852.7	934.7	1007.7
4184.1	3813.9	2419.3
2717.6	1648.0	3080.2
3325.6	4466.1	3608.3
491.3	12.7	728.6
333.3	152.2	306.6
2836.8	1076.8	2601.2
1082.0	621.9	777.8
4964.9	5780.0	5336.0

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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

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GQ175480.1 gg_id:579563 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ673048.1 gg_id:522463 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ367338.1 gg_id:359066 feces adult twins and mothers; TS29 clone TS29_a02c11 FJ3673
DQ802497.1 gg_id:178768 human fecal clone RL188_aah18e07 DQ802
EU776600.1 gg_id:331271 Lion feces clone LI2_aae50f03 EU776
EU777561.1 gg_id:337080 Sumatran orangutan feces clone orang1_aai55e12 EU777
DQ824090.1 gg_id:176724 human fecal clone RL204_aaj59b12 DQ824
FJ370157.1 gg_id:367719 feces adult twins and mothers; TS56 clone TS56_a01b02 FJ3701
FJ364096.1 gg_id:365980 feces adult twins and mothers; TS150 clone TS150_a02h11 FJ3640
FJ367236.1 gg_id:360886 feces adult twins and mothers; TS29 clone TS29_a01b07 FJ3672
FJ674006.1 gg_id:531328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
DQ793750.1 gg_id:181927 human fecal clone RL246_aai76f11 DQ793
FJ678797.1 gg_id:529608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
GQ175502.1 gg_id:544532 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
FJ673697.1 gg_id:518146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ807587.1 gg_id:188805 human fecal clone RL307_aam08f01 DQ807
DQ804414.1 gg_id:198951 human fecal clone RL187_aan79e03 DQ804
FJ879848.1 gg_id:464311 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
DQ824766.1 gg_id:176450 human fecal clone RL185_aao69a01 DQ824
FJ370129.1 gg_id:365387 feces adult twins and mothers; TS55 clone TS55_a04g02 FJ3701
DQ824815.1 gg_id:197379 human fecal clone RL185_aao69f03 DQ824
FJ679957.1 gg_id:520155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
DQ798965.1 gg_id:193337 human fecal clone RL242_aaj99g03 DQ798
FJ372063.1 gg_id:361345 feces adult twins and mothers; TS9 clone TS9_a01d02 FJ3720
DQ806358.1 gg_id:176330 human fecal clone RL186_aan91b11 DQ806
GQ896722.1 gg_id:585057 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EF405003.1 gg_id:216807 human fecal clone SJTU_G_05_74 EF405
DQ823723.1 gg_id:177005 human fecal clone RL250_aaj78b10 DQ823
DQ806093.1 gg_id:183145 human fecal clone RL186_aah61a12 DQ806
GQ493166.1 gg_id:583059 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ367354.1 gg_id:363558 feces adult twins and mothers; TS29 clone TS29_a02e05 FJ3673
FJ680513.1 gg_id:514809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
GQ493777.1 gg_id:587010 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ798694.1 gg_id:190120 human fecal clone RL181_aao00b12 DQ798
FJ369874.1 gg_id:358576 feces adult twins and mothers; TS55 clone TS55_a01g07 FJ3698
DQ825195.1 gg_id:185845 human fecal clone RL185_aan86e08 DQ825
EF399515.1 gg_id:204058 human fecal clone SJTU_F_11_92 EF3995
GQ493460.1 gg_id:539851 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU462101.1 gg_id:288684 black-handed spider monkey feces clone SPIM_aaj35a05 EU462
EU344285.1 gg_id:264113 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU469501.1 gg_id:292310 black lemur feces clone BKLE_a03_2 EU469

93.2	607.0	942.7	1088.3	687.6	730.6	712.0	849.4	369.9	396.6	422.5
1575.7	1268.1	1648.7	1680.7	1045.9	1093.7	1432.8	1001.1	756.9	689.5	1103.6
477.3	2777.7	2468.2	2279.7	1759.6	2420.8	1868.2	2353.8	2648.3	2162.5	1720.4
424.6	806.0	1353.1	1344.8	453.7	897.4	760.9	1641.1	470.4	326.0	819.2
40.9	414.6	638.8	573.4	35.2	148.5	105.7	289.7	54.2	22.5	255.1
83.9	1221.1	1409.4	1306.0	756.6	1074.1	2393.0	1879.5	3268.1	740.5	760.7
75.6	665.5	1457.1	757.0	345.5	740.8	446.1	655.7	597.5	104.9	619.5
9457.3	2838.0	2582.7	2579.8	2534.5	2525.6	2697.0	2642.7	4635.0	3722.7	2550.6
91.1	1193.3	2160.1	2425.9	792.9	1439.3	1694.3	2310.4	941.8	379.7	1687.4
5675.4	4756.8	4710.8	4829.2	4207.2	4071.9	4658.1	4217.7	5078.5	4815.6	6151.1
89.8	517.3	863.0	825.1	328.5	339.4	350.2	545.4	154.3	330.4	297.5
64.6	308.6	392.2	384.2	144.7	271.3	239.5	393.7	129.8	157.1	234.7
530.4	1457.0	2091.6	1936.4	1027.5	1240.9	1200.4	1530.2	1296.0	805.1	1769.1
4205.5	1571.4	1586.7	1962.9	1299.7	1623.9	1792.9	304.8	1565.8	616.9	1906.5
94.1	719.0	1213.7	1291.7	410.2	480.0	527.8	643.0	160.4	130.5	393.9
2692.3	3299.0	4317.2	4756.5	3583.9	3728.5	4090.3	4361.5	3165.3	3908.8	3674.5
60.4	1685.9	1588.1	1526.4	1478.9	1337.4	1438.8	1389.8	1495.6	2949.5	1304.4
71.3	558.4	1168.7	1122.3	551.6	561.9	504.9	606.9	203.3	162.1	320.0
823.5	1573.9	2801.1	2786.6	4237.1	3012.9	3592.7	2254.6	972.5	605.5	1935.3
501.2	1722.7	3207.5	1409.8	1115.5	1104.2	952.8	1877.6	1401.0	531.3	2405.2
1412.9	1230.3	1279.4	1396.2	1131.0	1424.0	1463.2	1379.9	1640.2	1111.3	1286.1
82.4	245.8	412.1	310.8	212.8	253.2	212.1	295.8	163.9	167.2	181.8
263.7	1249.2	1236.0	1880.1	1139.6	1029.0	1064.1	1386.9	767.5	304.7	1047.3
732.1	2886.6	3011.2	3345.3	3057.1	2614.4	2901.4	3919.8	1956.0	2920.3	2128.5
59.8	640.3	768.9	669.7	584.0	551.8	636.7	878.3	1129.4	829.5	610.3
60.8	1526.3	1319.7	1485.9	905.5	923.7	661.1	1479.7	606.3	364.3	733.2
74.1	1590.8	1388.9	846.3	861.7	830.0	1475.3	1288.9	1551.3	806.1	986.1
54.1	96.0	87.5	100.8	140.0	48.4	80.5	127.7	34.4	25.1	39.3
8328.2	2998.7	3481.1	3077.0	2488.4	2913.7	2685.5	2943.8	3660.8	3472.9	3308.1
294.4	748.3	1179.1	871.3	480.1	708.7	719.7	880.2	343.5	201.1	605.9
270.2	1750.4	2216.9	2421.2	1430.6	1790.0	2042.4	2238.1	921.8	638.7	1742.9
1256.7	2053.7	2495.7	2579.8	2601.3	2303.4	2802.7	2127.4	3090.0	1649.8	2092.9
126.8	1265.4	1914.7	2195.5	574.0	1216.2	1721.0	1855.2	1253.7	590.5	1524.2
55.4	252.7	336.3	344.0	293.1	388.0	355.6	922.3	117.8	106.8	159.2
43029.8	13297.9	12539.9	13491.6	12723.2	12369.6	14110.4	11838.2	20051.0	14299.2	19265.2
61.6	84.5	88.8	101.5	31.6	37.7	33.7	109.3	26.4	28.0	50.7
59.9	503.5	719.5	466.9	448.5	521.2	514.2	595.7	433.9	1184.3	404.2
59.8	4090.4	2793.8	1499.8	1373.0	2313.0	1445.2	3077.3	2626.6	2401.6	1904.7
2281.8	3945.7	3794.2	3713.9	3897.2	2901.2	3830.3	3395.8	4202.4	2847.8	5335.7
2201.4	4860.2	4557.7	4640.7	5420.6	4262.4	4792.8	5409.7	2201.9	1442.7	3858.8
3452.7	3746.5	3228.8	3205.5	3058.3	3005.3	3500.5	3462.3	2684.0	3746.7	2188.0

933.8	956.4	868.9
957.9	1979.7	1379.2
2215.6	2568.3	3357.0
1643.4	1247.3	2066.8
340.1	351.5	343.7
2363.3	2013.2	1724.4
554.6	749.9	533.5
2726.8	3884.8	2630.4
2018.3	1621.3	2645.4
4811.3	4891.8	4890.4
496.2	761.9	559.4
559.1	387.4	444.4
1277.0	1219.7	1153.0
1468.8	2012.0	1590.4
868.4	919.3	524.4
4185.8	4729.9	3582.1
522.0	1599.8	1426.5
820.7	1190.7	750.2
2599.0	3165.4	3285.8
1361.0	2127.3	1183.8
1177.5	1915.7	1370.0
387.0	447.6	265.7
1424.9	1947.8	1308.0
5481.5	3775.5	3271.7
625.9	1418.0	555.6
1642.5	1132.1	1506.0
758.6	808.2	1501.3
108.8	65.4	67.8
2981.7	3438.4	2934.2
922.6	863.9	1204.9
2121.3	2010.4	2240.1
2608.9	2921.0	3469.1
1810.7	1533.2	2065.8
1456.0	270.4	640.9
9563.3	13896.4	12008.9
141.9	57.0	47.4
548.6	606.0	965.4
2176.4	2054.9	3491.8
2934.5	3833.9	3182.7
6227.3	4185.0	5489.7
2751.8	3149.4	4182.7

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FJ678020.1 gg_id:528103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
DQ824491.1 gg_id:178952 human fecal clone RL304_aal76f09 DQ824
GQ897401.1 gg_id:562918 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU467434.1 gg_id:302049 chimpanzee feces clone CHIMP12_h05_2 EU467
DQ803247.1 gg_id:182728 human fecal clone RL311_aam22h02 DQ803
GQ492415.1 gg_id:580087 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ325573.1 gg_id:146093 Metagenomic gut microbiome healthy human stool clone B068 DQ325
FJ368900.1 gg_id:361009 feces adult twins and mothers; TS4 clone TS4_a01h05 FJ3689
FJ679103.1 gg_id:527140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
EU467241.1 gg_id:287583 black-handed spider monkey feces clone SPIM_d07 EU467
DQ326151.1 gg_id:150033 Metagenomic gut microbiome healthy human stool clone C045 DQ326
DQ806462.1 gg_id:195972 human fecal clone RL186_aao45a02 DQ806
DQ798304.1 gg_id:184228 human fecal clone RL181_aah40d07 DQ798
GQ493558.1 gg_id:539526 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ365989.1 gg_id:361245 feces adult twins and mothers; TS25 clone TS25_a01d12 FJ3659
DQ793371.1 gg_id:192937 human fecal clone RL199_aaj42h06 DQ793
FJ362957.1 gg_id:365345 feces adult twins and mothers; TS148 clone TS148_a01c04 FJ3629
FJ880700.1 gg_id:420661 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
DQ805900.1 gg_id:184238 human fecal clone RL306aal92d10 DQ805
EF398596.1 gg_id:217110 human fecal clone SJTU_F_04_21 EF3985
DQ805654.1 gg_id:198983 human fecal clone RL306aal89d10 DQ805
FJ370553.1 gg_id:358066 feces adult twins and mothers; TS57 clone TS57_a02d09 FJ3705
AY977207.1 gg_id:115602 human cecum mucosal biopsy clone MT17 AY977
EF401997.1 gg_id:206178 human fecal clone SJTU_B_02_27 EF4019
EU459666.1 gg_id:300510 ring-tailed lemur feces clone RT_aai10d12 EU459
FJ683591.1 gg_id:528355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ802605.1 gg_id:174714 human fecal clone RL188_aan94a06 DQ802
DQ793844.1 gg_id:192433 human fecal clone RL176_aah44c02 DQ793
FJ362761.1 gg_id:357683 feces adult twins and mothers; TS13 clone TS13_a02g10 FJ3627
DQ804255.1 gg_id:186416 human fecal clone RL187_aan77a07 DQ804
DQ800776.1 gg_id:193211 human fecal clone RL183_aao03c12 DQ800
DQ795338.1 gg_id:182672 human fecal clone RL178_aah53b06 DQ795
DQ801899.1 gg_id:185135 human fecal clone RL201_aai48c04 DQ801
FJ880520.1 gg_id:436032 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
DQ809688.1 gg_id:187533 human fecal clone RL184_aan82f07 DQ809
DQ810008.1 gg_id:174624 human fecal clone RL184_aao67a03 DQ810
DQ804959.1 gg_id:186381 human fecal clone RL385_aao83c01 DQ804
FJ363959.1 gg_id:362856 feces adult twins and mothers; TS150 clone TS150_a01d03 FJ3639
DQ804062.1 gg_id:177461 human fecal clone RL187_aah67h09 DQ804
FJ367854.1 gg_id:369480 feces adult twins and mothers; TS2 clone TS2_a04d03 FJ3678
DQ905094.1 gg_id:170387 human fecal clone 2-002-h6 DQ905

15346.2	5241.8	5365.0	5278.4	4739.3	4654.3	5202.3	4149.8	6845.4	5512.2	6994.4
1532.0	1616.0	1311.5	1552.8	939.9	1021.1	985.4	1341.3	716.1	283.3	936.2
39.4	335.8	517.6	488.1	102.6	457.1	404.4	756.2	82.6	61.1	157.4
4449.9	5168.3	5634.4	5360.4	4183.1	4436.8	4792.3	5280.6	6284.5	5169.6	6607.2
297.8	1486.8	2406.5	2403.3	1795.9	1812.9	2353.2	1718.5	1115.4	530.3	1400.9
7101.8	3792.3	3906.9	3585.7	3235.7	4032.2	3862.8	4123.6	9080.7	3875.5	5198.4
84.6	3227.5	3315.6	2933.8	3270.6	3184.4	3464.6	3617.2	4271.0	3761.1	2942.7
2223.5	3840.9	4941.8	4784.0	4144.1	4001.6	5164.4	4007.8	5743.1	3544.9	8566.5
47.3	933.3	1253.0	1345.6	946.1	665.3	1735.0	1114.8	544.3	149.9	450.4
40.7	172.4	299.7	102.5	96.0	83.9	186.5	113.8	107.4	31.5	172.7
50.9	371.2	592.1	660.8	781.6	13.2	630.3	538.0	226.9	110.7	351.5
6279.8	5596.4	6975.2	6129.0	5624.6	5632.8	5869.0	5495.0	5335.1	7432.6	6717.8
3696.6	3620.9	3608.5	3591.4	3967.4	3765.1	4038.5	3697.9	4241.2	4452.5	4176.9
1227.7	3034.8	3141.6	3236.3	2365.3	2677.8	2331.6	3674.4	2140.2	1435.6	3085.4
6492.7	3719.9	3616.3	3439.0	3724.6	3384.7	3506.1	4364.4	4567.2	4341.4	3153.4
36.8	327.4	273.7	220.6	23.1	78.0	43.3	71.5	113.5	24.8	36.8
131.7	1021.0	1154.5	1083.4	665.3	946.2	806.0	914.0	635.8	328.2	805.9
924.3	1754.4	2571.1	2900.7	2262.8	1577.1	2173.5	2061.9	1647.8	1587.3	2090.4
26.4	21.6	20.5	17.8	19.9	19.8	19.7	17.2	19.4	14.9	21.3
1573.8	1255.3	1322.7	1128.3	1093.4	1077.9	1085.4	1312.6	695.2	1249.2	898.3
78.3	225.1	483.9	407.5	256.2	343.7	314.7	430.8	122.1	104.4	235.2
2705.9	903.6	1100.6	996.3	1044.7	986.8	1007.9	931.0	1332.0	1019.1	844.8
38.5	119.1	204.5	154.9	56.9	111.3	67.9	225.3	33.6	26.0	52.7
31.4	596.8	943.5	877.3	150.3	411.1	224.7	638.3	162.0	186.7	445.6
2824.5	3133.2	3805.3	3740.8	2458.4	3078.4	2627.6	3662.3	3435.7	3031.5	4289.8
1926.8	1968.9	2258.6	2388.5	2177.2	2207.0	2546.5	2886.8	2283.7	3656.3	2513.8
11836.7	5303.8	5753.3	5665.1	5320.7	4440.6	5494.3	4526.0	6087.4	6069.0	7237.0
44.5	315.0	832.0	613.2	395.0	394.5	764.9	962.4	350.8	209.3	469.1
1967.0	2396.5	2444.5	2735.6	3007.4	2502.6	2913.8	3359.5	2023.3	1256.5	3253.6
27.5	368.8	301.1	580.6	113.2	274.5	197.1	604.2	97.8	99.3	156.0
227.7	169.5	197.3	179.2	160.1	149.5	165.2	244.4	89.5	81.9	142.0
1870.7	1102.8	1198.6	1117.6	738.8	839.3	756.5	1097.8	790.9	706.5	948.4
797.2	3361.4	2941.8	3297.9	2265.2	2738.4	2315.7	2986.7	3476.1	3229.8	5056.1
32.8	230.2	347.3	356.8	125.4	127.9	197.4	235.1	74.0	46.6	116.1
2185.7	773.0	934.0	825.4	756.7	799.1	1010.4	787.7	1511.3	1511.6	769.9
2779.1	2300.1	2378.9	2928.3	3482.0	2508.6	3015.7	2727.6	1633.6	1737.5	4311.5
53.3	369.6	692.5	718.2	141.0	274.9	210.7	477.6	154.3	45.9	395.4
35.6	556.6	845.3	903.3	645.6	653.3	657.8	810.2	393.1	427.7	552.6
79.0	523.8	943.8	772.1	144.4	404.3	197.0	560.9	100.3	90.9	582.8
61.2	139.8	160.5	201.0	113.5	107.3	110.3	132.3	73.0	38.9	103.9
5952.3	5179.2	6044.8	5441.8	4659.8	4103.7	6918.4	4980.1	6826.4	5148.6	8042.2

3880.7	6411.5	4806.1
1667.7	1188.6	1457.5
818.1	565.0	681.5
4932.8	4959.6	4393.6
2156.6	2079.1	3425.9
3417.7	3908.7	4201.3
2739.0	3282.0	3687.6
3843.2	4538.5	3998.4
991.9	931.1	1258.7
96.6	228.4	94.4
409.7	799.2	581.2
5809.1	7020.1	6031.9
3838.2	3980.4	4049.6
3123.5	3209.7	3726.9
5135.0	4549.8	3897.7
129.2	176.6	53.9
766.5	921.0	971.2
2121.7	3104.3	2626.9
21.6	22.5	17.8
1244.9	1431.2	1382.0
338.3	426.6	627.8
874.8	1814.3	1789.9
280.8	167.9	221.8
903.7	443.2	644.6
3291.3	4621.0	3711.9
2474.4	2608.0	3554.2
5916.4	6342.4	5297.0
702.2	897.6	538.3
3923.6	3202.5	3029.3
784.3	479.7	610.9
136.8	434.5	198.6
1116.4	1427.4	837.2
3109.4	3777.1	2755.0
280.3	350.3	322.8
797.3	1540.4	888.8
2408.4	2746.3	2903.4
719.2	491.0	396.2
812.7	1013.3	962.1
437.4	438.0	189.5
109.4	103.0	125.6
4141.2	5687.8	6274.8

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DQ801655.1 gg_id:179531 human fecal clone RL201_aai45a12 DQ801
DQ327198.1 gg_id:149658 Metagenomic gut microbiome healthy human stool clone E729 DQ327
DQ802779.1 gg_id:187866 human fecal clone RL188_aan96e01 DQ802
FJ368606.1 gg_id:362131 feces adult twins and mothers; TS49 clone TS49_a02c08 FJ3686
DQ805395.1 gg_id:198771 human fecal clone RL203_aai62a11 DQ805
DQ794663.1 gg_id:190108 human fecal clone RL240_aaj30g12 DQ794
GQ492387.1 gg_id:587729 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ799186.1 gg_id:186828 human fecal clone RL205_aaj18g10 DQ799
DQ805683.1 gg_id:181869 human fecal clone RL306aal89g06 DQ805
DQ808174.1 gg_id:195511 human fecal clone RL180_aao73e06 DQ808
FJ370752.1 gg_id:360353 feces adult twins and mothers; TS57 clone TS57_a04h02 FJ3707
GQ492049.1 gg_id:537067 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ833196.1 gg_id:589215 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_21E03 FJ8331
DQ905209.1 gg_id:166627 human fecal clone 013-b6 DQ905
DQ806393.1 gg_id:185655 human fecal clone RL186_aan91f10 DQ806
FJ673686.1 gg_id:526313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ805059.1 gg_id:187040 human fecal clone RL385_aao84f06 DQ805
EU776195.1 gg_id:338657 Spotted hyena feces clone HY2_c05 EU776
DQ802126.1 gg_id:185798 human fecal clone RL241_aaj03d06 DQ802
FJ367229.1 gg_id:367427 feces adult twins and mothers; TS29 clone TS29_a01a09 FJ3672
DQ824785.1 gg_id:184926 human fecal clone RL185_aao69c04 DQ824
FJ684853.1 gg_id:526044 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ370795.1 gg_id:359557 feces adult twins and mothers; TS5 clone TS5_a01d03 FJ3707
EU763793.1 gg_id:318944 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
FJ370583.1 gg_id:359794 feces adult twins and mothers; TS57 clone TS57_a02g05 FJ3705
EU469566.1 gg_id:289089 flying fox feces clone FF_a05 EU469
FJ370920.1 gg_id:370338 feces adult twins and mothers; TS5 clone TS5_a02g10 FJ3709
DQ795286.1 gg_id:199065 human fecal clone RL178_aah52e04 DQ795
DQ806583.1 gg_id:194217 human fecal clone RL186_aao46d03 DQ806
DQ803474.1 gg_id:176483 human fecal clone RL251_aaj86c05 DQ803
DQ823702.1 gg_id:196262 human fecal clone RL250_aaj77h05 DQ823
FJ363706.1 gg_id:365327 feces adult twins and mothers; TS14 clone TS14_a02c11 FJ3637
EU463322.1 gg_id:302321 bush dog feces clone bdog1_aai78c06 EU463
DQ804117.1 gg_id:189289 human fecal clone RL187_aah68g09 DQ804
GQ491877.1 gg_id:551761 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ057452.1 gg_id:131571 str. ic1272 DQ057
FJ673904.1 gg_id:516385 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
DQ325682.1 gg_id:149909 Metagenomic gut microbiome healthy human stool clone B281 DQ325
EU774663.1 gg_id:347115 Angola Colobus feces clone EAC_1aaa03b04 EU774
FJ676585.1 gg_id:525814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
DQ798720.1 gg_id:192200 human fecal clone RL181_aao00e06 DQ798

7208.2	4680.8	4680.5	4432.0	5164.2	4306.5	5351.3	4489.1	4433.6	5322.8	4652.8
56.9	120.5	182.8	251.7	90.3	112.8	102.4	205.3	47.3	77.6	105.1
496.5	3301.7	3574.9	3331.4	2635.4	3257.5	3372.4	3724.8	7853.6	4711.4	4344.6
15383.5	3696.1	4028.6	3472.7	3541.3	4391.4	4245.1	3856.5	5504.5	4818.0	5308.0
4197.7	1803.4	2163.5	2325.5	2180.1	1843.9	2131.1	2578.9	1568.8	1353.9	2117.5
3508.1	11517.4	9723.3	10058.3	8309.4	8782.5	8843.1	10374.0	11238.7	8971.3	11157.6
8651.2	2502.4	2627.2	2543.3	3197.5	2833.2	3852.8	2394.1	2382.8	4028.1	2297.1
123.3	584.2	891.5	765.7	857.1	713.7	864.6	728.0	387.2	657.8	469.6
2684.1	2005.7	1599.9	1893.5	1633.7	1450.8	1726.4	1325.0	1687.2	1871.1	2218.9
32.2	34.8	41.8	39.1	24.1	32.4	20.7	35.3	26.9	15.1	28.0
961.4	866.1	1436.8	1629.9	433.0	793.8	420.5	1522.1	336.6	505.4	808.7
2689.4	6635.3	6365.4	5514.3	5080.6	5273.1	4909.2	7070.1	6986.1	6702.3	6011.2
60.3	1243.7	1606.4	1919.7	1438.4	1323.1	1292.2	2207.2	493.3	370.7	1136.6
117.2	779.8	1156.6	1279.0	964.2	974.3	1770.1	1043.9	423.0	301.8	691.6
40.4	108.3	143.3	190.1	62.2	78.6	56.9	114.9	35.4	26.2	91.8
326.4	1877.4	2317.1	2685.6	2026.3	1972.9	2325.3	2060.7	985.5	1219.9	1750.1
41.8	527.6	837.2	1023.9	173.0	390.1	303.7	906.5	92.9	130.0	171.2
47.4	277.6	487.9	472.1	120.8	243.0	260.0	537.7	110.8	79.5	232.6
440.7	1311.9	1768.1	1472.2	936.7	1483.9	1660.0	1414.3	1434.4	861.4	1700.9
112.8	1325.7	1298.5	1197.6	702.4	1216.4	790.0	1276.7	902.9	946.9	855.6
35.5	179.1	537.0	513.5	251.3	242.5	242.8	358.0	48.8	44.7	83.0
248.6	1050.4	1572.2	1545.0	1116.3	845.3	1166.0	1256.4	1198.5	987.5	924.6
921.0	1651.2	1866.2	1616.0	1049.3	1171.6	1784.7	1446.7	797.2	952.9	1092.1
20859.6	5404.4	5048.6	5435.6	5569.6	3018.4	5258.4	4380.3	7842.3	6170.0	6975.7
2812.9	1966.6	2195.2	2128.9	1902.0	1555.4	1920.9	1853.8	2024.7	1589.6	2631.5
3782.8	2816.7	3562.6	3363.0	3422.0	2640.2	3112.7	3701.4	3811.7	3153.1	2667.4
634.0	686.5	844.3	861.8	585.6	556.2	749.2	554.5	538.7	398.9	688.0
42.9	223.6	435.5	625.8	125.1	240.7	194.3	392.6	67.5	57.6	197.4
345.2	1418.0	1572.9	3053.7	1181.6	1406.6	1669.0	1609.7	731.6	278.6	1044.3
48.2	244.4	455.6	440.2	102.6	286.6	109.8	530.7	73.8	169.0	153.2
35.1	71.7	128.1	118.1	152.2	71.2	179.5	162.9	31.4	26.2	91.9
44.1	1064.2	1211.4	997.2	937.2	839.6	1018.7	976.9	380.6	1111.4	450.9
348.1	1601.8	1734.3	1604.4	1261.3	1286.0	2021.8	2126.6	736.4	317.7	542.6
39.4	231.1	417.1	432.6	246.3	376.3	201.8	335.6	94.1	63.7	156.2
2475.4	3104.5	3038.3	2727.6	2714.3	2450.5	2964.5	3673.7	2874.8	4235.3	4257.6
36.0	83.0	95.9	129.1	78.2	94.9	54.3	139.2	80.9	37.1	44.1
4701.4	2847.6	2624.0	2615.5	2808.5	2638.3	3251.9	3751.0	3276.2	2164.0	2670.6
38.3	490.8	717.5	1002.5	276.7	628.9	298.8	833.4	197.2	133.2	359.5
55.7	905.9	1486.9	1429.0	515.3	967.6	830.2	1214.5	287.8	100.9	846.6
6721.7	4741.1	4857.9	4708.6	4332.5	4139.0	4522.9	4182.5	6508.8	4706.6	5556.5
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2445.4	1826.9	2219.4
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2847.0	3539.8	3745.6
694.8	855.0	1077.5
1561.8	2320.6	1504.9
27.1	33.3	40.7
2101.1	888.3	1098.5
5204.3	5851.0	7096.8
2847.7	1392.4	2481.5
1236.3	1039.6	1723.2
126.3	74.8	164.3
1903.7	2912.9	3452.2
1304.8	535.7	890.1
781.0	277.3	378.4
1246.2	2087.9	1659.3
1391.5	1386.4	2225.9
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1199.0	1493.8	2477.9
4548.8	6064.1	4827.6
1712.5	2915.3	2402.2
3692.6	3953.7	2763.4
560.9	988.6	931.7
655.0	420.1	627.5
3406.6	2044.7	1731.7
836.4	456.9	517.8
191.5	94.5	209.2
997.9	744.0	804.1
1764.1	1734.2	2337.7
317.6	362.2	689.6
3067.9	3259.5	4091.7
147.0	179.1	234.0
2657.7	3537.0	3459.7
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DQ805035.1 gg_id:182850 human fecal clone RL385_aao84c12 DQ805
FJ370620.1 gg_id:366727 feces adult twins and mothers; TS57 clone TS57_a03c04 FJ3706
DQ796687.1 gg_id:197500 human fecal clone RL179_aao53b09 DQ796
DQ796582.1 gg_id:197670 human fecal clone RL179aan75c08 DQ796
FJ368118.1 gg_id:367639 feces adult twins and mothers; TS30 clone TS30_a04c07 FJ3681
DQ809130.1 gg_id:183564 human fecal clone RL308_aal82b02 DQ809
GQ077072.1 gg_id:415735 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1206e GQ077
DQ799157.1 gg_id:194125 human fecal clone RL205_aaj18d04 DQ799
FJ676799.1 gg_id:520380 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
DQ804486.1 gg_id:183159 human fecal clone RL187_aan80f05 DQ804
AY960563.1 gg_id:115104 Clostridium sp. str. CE6 AY9605
FJ364732.1 gg_id:369530 feces adult twins and mothers; TS19 clone TS19_a02d04 FJ3647
DQ804248.1 gg_id:194327 human fecal clone RL187_aah70h04 DQ804
DQ808467.1 gg_id:185180 human fecal clone RL180_aao76h06 DQ808
DQ801496.1 gg_id:181942 human fecal clone RL388_aao96c10 DQ801
FJ367468.1 gg_id:363767 feces adult twins and mothers; TS29 clone TS29_a03h09 FJ3674
DQ804281.1 gg_id:192533 human fecal clone RL187_aan77d07 DQ804
FJ682467.1 gg_id:524374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AJ408999.1 gg_id:16475 human colonic clone HuCB25 AJ4089
AY981581.1 gg_id:126684 human sigmoid colon mucosal biopsy clone L764 AY9815
EF404178.1 gg_id:207790 human fecal clone SJTU_C_05_79 EF4041
EU459398.1 gg_id:294439 cheetah feces clone CE3_aai07c06 EU4593
FJ369208.1 gg_id:369619 feces adult twins and mothers; TS50 clone TS50_a01e09 FJ3692
FJ681290.1 gg_id:528650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
DQ806327.1 gg_id:174763 human fecal clone RL186_aan90f07 DQ806
FJ833830.1 gg_id:543708 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_07G01 FJ8338
EU776912.1 gg_id:321453 Mongoose lemur feces clone ML_aaj28d01 EU7769
GQ077026.1 gg_id:409732 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1205h GQ077
GQ491288.1 gg_id:583454 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ683504.1 gg_id:531001 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
DQ803389.1 gg_id:186324 human fecal clone RL251_aaj85a10 DQ803
FJ673117.1 gg_id:517348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ673669.1 gg_id:515203 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU764302.1 gg_id:336328 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7643
FJ674047.1 gg_id:517387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
DQ797638.1 gg_id:181387 human fecal clone RL206_aaj14a12 DQ797
DQ905829.2 gg_id:165922 human fecal clone 29E-d8 DQ905
DQ805269.1 gg_id:189310 human fecal clone RL249_aaj84b03 DQ805
GQ897352.1 gg_id:566202 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ897
DQ824909.1 gg_id:190610 human fecal clone RL185_aao70h05 DQ824

118.5	690.8	811.4	848.5	768.2	742.8	766.3	950.1	238.7	137.0	342.0
70.7	996.1	1238.3	1383.8	592.7	1151.9	1026.4	1615.8	389.3	296.5	956.3
108.8	971.5	1396.0	1401.8	724.2	678.3	985.9	1287.7	287.6	576.1	909.6
126.3	629.6	671.7	774.8	819.0	616.7	559.9	1114.0	369.2	290.4	617.2
474.9	604.2	768.6	880.0	504.1	574.6	637.4	708.2	560.6	404.5	561.7
11600.3	4769.1	4274.0	5182.9	5226.9	5179.5	4682.3	5804.7	4352.0	3248.0	5887.6
42.8	289.2	639.8	632.4	295.6	371.8	339.3	455.6	135.2	37.5	293.4
8804.0	3810.8	3875.1	3579.2	2969.8	3498.7	3707.1	3799.1	2379.7	3605.6	3255.1
46.1	163.3	191.2	231.3	90.3	57.7	118.2	122.4	35.3	25.8	65.8
558.8	1259.0	1429.3	1160.8	1070.0	1004.7	1072.1	1099.2	815.7	2870.7	749.8
169.1	640.2	995.5	449.3	315.0	600.8	403.4	1010.4	59.1	262.1	772.8
1104.7	1113.9	1361.8	1335.4	1402.9	1180.4	2041.3	1129.7	932.0	912.7	2136.8
24976.4	6524.3	5944.9	6193.1	4574.7	6593.8	6409.4	5343.3	7936.8	10191.5	8563.8
9836.9	3948.3	4424.3	4323.6	3802.2	4067.6	5296.6	3419.6	4206.3	4581.0	6050.6
21192.2	11943.1	12627.8	12061.8	10885.5	10876.5	11906.8	11190.1	14635.1	11017.9	15644.2
6202.3	3790.8	3295.4	3307.5	2344.9	3282.2	3527.8	3974.3	3626.1	2430.7	3964.9
2789.3	2517.4	2883.5	2871.1	2833.5	2264.8	2781.5	2699.1	2837.5	2708.5	2823.9
11860.8	7593.2	7179.0	7756.0	6516.5	6694.6	7225.7	6503.5	9931.7	8052.8	12172.7
13222.3	6936.9	6607.9	7151.7	5570.0	6117.9	6874.5	6173.6	8103.3	6571.4	8199.7
40.9	285.1	424.1	395.8	344.9	292.3	229.9	415.0	243.0	73.7	194.8
21.4	820.7	1295.8	1536.5	268.7	613.7	646.9	1172.5	203.7	391.6	558.5
38.5	318.8	601.2	705.3	275.4	334.5	233.4	582.7	170.3	251.6	413.5
106.0	807.8	1544.9	1504.9	617.1	787.0	648.7	1282.5	336.3	328.5	793.2
11166.8	4534.1	4496.3	4325.7	3919.0	5018.6	4919.1	4158.2	6222.8	5066.7	5591.4
12280.8	5663.3	5978.9	6945.4	6475.6	5938.8	6727.1	6234.3	9324.9	5936.2	7831.3
1424.3	1553.8	1575.5	1630.4	1573.4	1661.8	679.3	2062.6	962.9	1288.1	362.4
59.6	625.0	864.1	1036.2	430.8	454.2	466.7	744.3	148.4	194.3	270.5
512.1	1578.1	1879.3	1898.5	1713.7	1363.1	1389.2	1916.6	1256.5	1360.5	1465.8
3014.1	2273.6	3004.4	3134.8	1670.4	2095.2	2232.7	2771.5	3190.4	4207.6	2690.7
2753.2	2179.7	2159.6	2290.5	2027.1	2124.1	2100.1	2366.5	2688.6	2664.5	2882.4
3595.1	3801.9	3656.7	3549.8	2878.6	3505.8	2866.2	3595.6	4381.3	4058.5	4756.3
73.4	790.8	973.1	975.6	454.3	572.3	499.7	843.0	271.6	224.2	539.9
68.1	723.1	953.9	988.8	126.8	286.5	337.1	528.6	94.5	79.0	219.2
726.2	2384.2	2540.7	2973.7	2871.6	2327.0	3671.5	2349.1	1494.4	1578.8	2230.1
42.3	368.1	563.7	720.0	102.7	226.5	191.2	415.4	77.7	46.3	117.4
323.1	1943.7	2093.8	1571.7	1195.1	1614.2	1277.6	1633.3	2212.2	2899.5	2728.9
3068.3	1667.0	1687.8	1695.9	1526.7	1344.0	3121.8	1508.6	3370.3	924.5	2414.6
1692.3	4685.7	5085.5	4355.3	4482.6	4238.8	5169.7	4358.1	5544.7	3995.1	6739.8
299.8	722.2	888.8	932.6	592.7	586.4	431.2	794.3	159.2	60.6	265.8
47.0	1266.4	1722.4	1680.5	556.5	1320.0	897.3	2056.7	368.8	331.9	865.6
69.7	388.1	493.3	510.7	313.4	361.2	400.1	508.7	182.9	89.3	360.9

835.1	730.2	1549.3
1576.2	1147.0	2909.2
1184.4	858.4	845.8
797.1	916.4	1102.0
628.1	746.4	1330.0
6568.5	7183.4	7112.5
590.3	755.2	964.2
3602.2	3276.7	2963.5
88.1	126.5	144.7
927.7	1153.7	885.5
1737.0	487.0	691.4
1044.9	2105.9	1499.8
5336.5	6878.0	5723.8
3851.0	5350.1	5300.7
12333.4	11050.2	12203.7
3665.0	3115.4	3212.5
3133.7	3275.6	2636.9
6509.0	7861.1	6538.6
6444.6	6932.0	5362.5
316.6	581.1	367.3
1609.2	788.7	975.3
640.0	460.8	496.6
1467.7	1082.4	1699.4
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5422.3	7830.0	6866.6
2076.5	1672.4	1118.7
1004.3	585.9	707.9
2616.9	2175.1	1356.6
2887.9	3322.0	2986.4
2543.2	2577.9	2098.5
2932.3	3920.8	4308.1
858.9	1009.5	975.5
694.9	539.0	639.9
2231.2	3828.9	3659.8
455.4	339.4	328.3
1552.5	1737.4	1977.7
1186.2	2730.5	1336.4
3439.1	3808.1	4281.3
1253.3	561.0	836.7
2987.5	1291.8	2519.6
559.0	639.6	549.6

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DQ825227.1 gg_id:194540 human fecal clone RL185_aan86h11	DQ825
FM872529.1 gg_id:358675 occupant source house floor dust clone FA01F10	FM872
EU469676.1 gg_id:292633 flying fox feces clone FF_-aag84h04	EU469
FJ364608.1 gg_id:369728 feces adult twins and mothers; TS19 clone TS19_a01a03	FJ3646
DQ807273.1 gg_id:175296 human fecal clone RL244_aaj48d10	DQ807
FJ363614.1 gg_id:365076 feces adult twins and mothers; TS14 clone TS14_a01d02	FJ3636
DQ824897.1 gg_id:181054 human fecal clone RL185_aao70f09	DQ824
DQ806731.1 gg_id:174501 human fecal clone RL186_aao48a10	DQ806
DQ905045.1 gg_id:165102 human fecal clone 2-002-d3	DQ905
FJ364581.1 gg_id:366418 feces adult twins and mothers; TS15 clone TS15_a04f07	FJ3645
EU459631.1 gg_id:292864 ring-tailed lemur feces clone RT_aai09f02	EU459
DQ799731.1 gg_id:189522 human fecal clone RL182_aah32c08	DQ799
DQ325939.1 gg_id:149178 Metagenomic gut microbiome healthy human stool clone B807	DQ325
EU469413.1 gg_id:296007 black lemur feces clone BKLE_d08	EU469
FJ369499.1 gg_id:361773 feces adult twins and mothers; TS51 clone TS51_a01c10	FJ3694
EF401262.1 gg_id:211501 human fecal clone SJTU_D_08_02	EF4012
FJ370165.1 gg_id:361226 feces adult twins and mothers; TS56 clone TS56_a01b10	FJ3701
GQ492725.1 gg_id:560281 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ492
GQ493627.1 gg_id:569232 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ493
FJ364178.1 gg_id:359500 feces adult twins and mothers; TS150 clone TS150_a03h05	FJ3641
DQ799855.1 gg_id:179980 human fecal clone RL247_aaj21a03	DQ799
DQ802334.1 gg_id:183044 human fecal clone RL188_aah16c05	DQ802
EU778311.1 gg_id:355874 feces clone RL387_aao91d11	EU778
DQ905629.1 gg_id:168527 human fecal clone 014C-A4	DQ905
AB185576.1 gg_id:102704 rumen clone F24-A02	AB185
FJ680469.1 gg_id:528843 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee	FJ6804
DQ796458.1 gg_id:177101 human fecal clone RL179_aah28f09	DQ796
FJ369472.1 gg_id:365941 feces adult twins and mothers; TS50 clone TS50_a04h10	FJ3694
FJ370160.1 gg_id:370278 feces adult twins and mothers; TS56 clone TS56_a01b05	FJ3701
EU774103.1 gg_id:336133 Chimpanzee feces clone CHIMP1_f08	EU774
DQ795672.1 gg_id:174801 human fecal clone RL178_aan68b10	DQ795
EU773420.1 gg_id:340910 Black lemur feces clone BKLE_f01_1	EU773
FJ975983.1 gg_id:572109 Human gut microbiome adopts alternative state bowel transplantation ileum effluent	FJ9759
DQ825217.1 gg_id:190683 human fecal clone RL185_aan86g10	DQ825
DQ794691.1 gg_id:186166 human fecal clone RL240_aaj31b11	DQ794
FJ367085.1 gg_id:356822 feces adult twins and mothers; TS28 clone TS28_a03d04	FJ3670
DQ805508.1 gg_id:188525 human fecal clone RL203_aai63e10	DQ805
DQ806426.1 gg_id:187597 human fecal clone RL186_aan92c03	DQ806
GQ491899.1 gg_id:534865 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice	GQ491
FJ367501.1 gg_id:364982 feces adult twins and mothers; TS29 clone TS29_a04c08	FJ3675
AY169424.1 gg_id:81152 Ruminococcus obeum	AY169

61.5	210.8	358.9	110.3	97.9	174.9	117.0	354.7	141.5	219.6	155.8
90.8	2253.0	2942.4	2924.3	2676.3	2415.1	3856.9	3660.0	2300.5	1314.7	2481.5
174.8	2092.5	2313.5	2497.9	975.7	1708.9	1279.8	2395.3	1106.1	365.1	2603.6
6160.3	4944.1	5062.4	5388.0	5278.7	4848.5	6304.9	4608.9	5498.6	6977.9	7101.6
68.3	371.1	522.7	409.9	229.7	292.5	253.5	467.7	235.0	109.8	378.4
1714.4	1675.8	1384.1	1623.1	1200.2	1463.4	986.6	1522.4	1369.7	982.8	788.6
56.9	554.6	692.4	795.4	346.7	464.8	652.3	517.6	132.8	52.0	474.8
645.7	1056.9	1763.1	1507.8	819.7	887.0	904.2	1226.1	617.7	540.9	1082.6
13884.2	8775.5	7981.8	9328.3	10559.9	8305.4	8394.9	7483.9	8428.9	9391.7	9146.0
4569.5	3525.6	4750.9	5226.6	5606.5	4828.1	6991.5	4511.6	6109.9	4995.9	6771.9
1153.0	3093.2	3462.2	2408.4	1248.1	2803.2	1982.9	2981.7	2399.2	3913.7	2179.3
21131.1	5991.5	5790.9	6304.6	5703.7	5457.6	6348.6	5534.1	7410.4	7285.9	7805.5
269.9	1719.4	1752.3	2140.1	1570.0	1427.7	1459.7	1836.8	743.2	943.0	1149.8
41.9	372.1	458.6	795.4	347.0	291.5	485.9	352.3	116.0	358.3	138.5
3099.2	1966.1	2001.0	2222.7	1886.9	2019.2	1478.7	2158.4	1249.5	1992.2	1425.4
40.3	343.1	485.8	318.5	353.8	250.7	440.3	378.2	114.2	319.0	168.6
36924.9	6667.8	6394.3	6682.2	6540.6	6190.2	7309.1	6158.7	9271.4	7543.1	8988.9
5017.4	3237.2	2886.7	2489.6	2257.2	2441.4	2547.5	3658.2	2948.0	2687.1	3463.7
46.7	693.2	705.3	795.7	1000.6	599.0	1222.9	601.8	229.2	91.3	384.0
36516.7	8169.2	7728.5	9743.0	7050.4	7408.2	10121.1	7054.3	14302.9	9192.8	12012.1
17222.5	5639.7	5672.5	5864.1	5845.1	5315.0	8338.5	6198.0	9372.2	5848.8	8568.5
226.7	1129.2	1281.1	1580.3	604.0	827.7	936.4	1406.4	388.6	218.1	837.0
1415.5	2740.5	2390.2	2725.0	3444.8	2529.1	2401.4	3137.2	2324.8	2874.4	2282.6
10758.7	6094.2	6102.9	5327.3	7179.1	6780.1	7158.0	5579.7	7828.6	5461.1	6822.8
34.0	257.3	246.5	420.7	316.6	238.7	615.6	337.3	81.8	38.7	125.5
7192.1	3422.6	3289.8	3057.4	3127.0	3160.1	3184.4	3187.3	3041.3	4279.0	2689.9
8107.6	2827.5	3406.9	3492.7	2343.9	3057.5	3488.6	3450.4	3486.4	2664.0	4275.7
1157.4	2913.9	3306.4	3642.2	2094.4	2776.0	3322.7	2912.6	2410.3	1672.6	3469.9
40.2	252.4	648.1	188.3	170.3	394.4	203.6	594.9	102.4	646.6	265.0
403.6	496.0	481.5	558.9	502.4	462.6	352.1	638.2	34.5	127.6	268.7
285.9	3179.7	2437.7	2036.2	1881.7	2568.2	1897.1	2645.6	4059.5	1853.2	1785.2
58.5	785.0	607.9	977.9	941.6	829.4	741.3	838.8	476.1	397.3	482.7
39.6	253.6	626.4	626.6	115.0	202.9	229.2	408.7	60.1	44.4	249.9
374.7	1016.1	873.7	1334.6	1030.4	939.9	1035.5	1250.0	682.9	358.2	973.5
11321.3	6445.2	6721.0	7278.9	6419.9	5929.6	9257.3	7548.4	9014.3	5022.1	11296.5
2349.0	3590.4	3516.4	3640.2	2661.7	3246.6	3229.1	3376.9	3318.7	4560.5	3637.3
188.4	470.5	678.1	769.2	585.6	510.3	713.6	800.3	270.4	151.0	452.7
687.4	2070.3	3143.7	2930.9	1514.9	2041.3	1794.8	2748.3	1172.9	938.2	1608.1
2412.6	1771.1	1999.3	2281.7	1422.8	1652.3	1524.2	2148.5	2318.5	1065.6	2866.1
8905.2	4081.0	2940.0	4603.7	4867.3	4379.0	3930.0	3849.1	5237.9	3803.1	6066.5
216.3	495.1	680.7	793.8	237.2	378.1	287.0	744.0	192.0	108.8	320.3

257.4	385.3	388.2
3618.1	3019.0	4183.1
2895.8	1499.4	1803.1
4844.2	5253.3	5799.9
510.2	489.4	634.8
1428.8	2097.0	1978.6
465.0	456.2	772.6
973.6	1215.2	1550.5
8049.6	8513.7	9864.0
5039.5	5189.9	5106.0
3073.1	3060.6	3516.4
5418.2	6475.5	6130.2
2262.0	1188.0	1777.7
396.2	553.3	370.7
2104.1	2917.6	1991.2
391.5	431.6	635.4
6005.5	6878.7	6419.0
2606.6	2914.8	2945.8
846.7	988.8	1074.8
7488.1	9450.9	8526.7
5416.1	9650.1	5078.4
1487.9	860.9	1992.4
2658.0	2625.6	2639.0
4638.0	7165.4	5567.4
132.0	189.4	215.6
2945.5	4313.4	3977.1
3517.8	3245.2	3397.4
3330.4	3758.9	3489.5
573.7	471.6	1153.2
546.2	755.7	961.2
2098.4	2392.9	1369.1
704.0	986.6	1533.5
436.2	394.7	717.9
1329.0	1850.8	1405.3
5919.2	7832.7	7072.4
2861.7	3975.3	4018.4
636.6	698.6	1126.7
2762.3	2800.8	3706.4
2379.1	2116.2	2194.5
4135.7	6022.9	4499.0
861.6	659.8	495.7

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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k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia

o__Clostridiales	f__Lachnospiraceae
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FJ364389.1 gg_id:368235 feces adult twins and mothers; TS15 clone TS15_a02d01 FJ3643
GQ898361.1 gg_id:581094 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ794403.1 gg_id:191306 human fecal clone RL197_aah87c10 DQ794
DQ808364.1 gg_id:176416 human fecal clone RL180_aao75g04 DQ808
DQ807968.1 gg_id:181844 human fecal clone RL180_aan69h11 DQ807
FJ365929.1 gg_id:369888 feces adult twins and mothers; TS21 clone TS21_a04g07 FJ3659
DQ804897.1 gg_id:180401 human fecal clone RL385_aao82c02 DQ804
EU463335.1 gg_id:289863 bush dog feces clone bdog1_aai78h02 EU463
DQ796672.1 gg_id:190370 human fecal clone RL179_aao53a06 DQ796
FJ362616.1 gg_id:365574 feces adult twins and mothers; TS13 clone TS13_a01b04 FJ3626
DQ905859.2 gg_id:167403 human fecal clone 29E-g4 DQ905
DQ803223.1 gg_id:177941 human fecal clone RL311_aam22d08 DQ803
FJ879477.1 gg_id:449983 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
GQ898276.1 gg_id:549857 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ898
DQ806568.1 gg_id:181584 human fecal clone RL186_aao46b10 DQ806
DQ905381.1 gg_id:162651 human fecal clone 013C-A12 DQ905
DQ802069.1 gg_id:175754 human fecal clone RL241_aaj02f11 DQ802
EU776809.1 gg_id:354131 Mongoose lemur feces clone ML_aae88d12 EU776
EF399954.1 gg_id:211432 human fecal clone SJTU_E_06_47 EF3999
FJ366059.1 gg_id:362157 feces adult twins and mothers; TS25 clone TS25_a02c02 FJ3660
DQ807356.1 gg_id:190415 human fecal clone RL307_aam05e05 DQ807
FJ368244.1 gg_id:359889 feces adult twins and mothers; TS3 clone TS3_a01h09 FJ3682
FJ673226.1 gg_id:519792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ673404.1 gg_id:516361 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
AY981104.1 gg_id:123256 human sigmoid colon mucosal biopsy clone G018 AY981
DQ809635.1 gg_id:190191 human fecal clone RL184_aan81h05 DQ809
DQ804289.1 gg_id:175766 human fecal clone RL187_aan77e06 DQ804
DQ805215.1 gg_id:179077 human fecal clone RL249_aaj83b11 DQ805
EU728791.1 gg_id:328717 Ruminococcus sp. str. DJF_VR67 EU728
FJ679970.1 gg_id:523939 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU530242.1 gg_id:262753 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
DQ806890.1 gg_id:185969 human fecal clone RL198_aaj74g10 DQ806
FJ369700.1 gg_id:367283 feces adult twins and mothers; TS51 clone TS51_a03g05 FJ3697
GQ492798.1 gg_id:557714 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU774068.1 gg_id:304108 Chimpanzee feces clone CHIMP1_g12 EU774
DQ806715.1 gg_id:184849 human fecal clone RL186_aao47h05 DQ806
FJ364854.1 gg_id:362009 feces adult twins and mothers; TS19 clone TS19_a03h11 FJ3648
GQ491341.1 gg_id:563161 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ674265.1 gg_id:530490 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ674119.1 gg_id:519474 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ673319.1 gg_id:518746 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733

1970.4	655.6	768.1	659.3	329.0	593.4	509.9	694.5	345.7	346.4	618.0
12856.1	4420.1	4019.0	4581.9	4965.6	4497.9	5185.2	4824.4	5604.6	5076.3	6605.8
300.0	533.5	1059.0	746.4	531.0	898.2	810.8	1052.3	366.1	362.8	484.4
43.3	623.9	849.4	711.6	351.1	491.9	566.3	725.4	476.9	250.3	544.9
4615.4	3837.5	3545.9	3966.7	4588.3	3225.0	3567.0	3740.5	3951.6	1574.4	3111.5
29753.6	7765.8	7446.0	7872.5	7376.2	7154.9	8266.6	6285.5	11238.7	8859.0	11863.0
6726.4	2170.6	1797.5	2146.8	1986.0	1898.2	2064.8	2051.1	1699.1	1434.0	401.0
390.4	1040.7	1283.2	1107.0	893.2	870.5	977.2	1163.4	728.5	1226.8	809.6
76.8	274.3	356.8	252.8	132.1	178.7	182.4	235.3	77.2	310.8	136.6
40.1	415.0	702.2	258.7	235.5	458.1	325.2	541.7	133.1	829.5	263.4
4877.3	5679.8	5001.1	4827.4	3654.6	4910.2	5204.8	4902.0	7605.6	7497.0	7734.1
1603.2	1326.4	2073.5	1615.5	1741.1	1484.7	4484.3	1773.9	4817.6	1759.4	983.0
2022.5	988.4	1157.4	1103.2	791.0	168.6	706.5	1035.2	813.0	865.4	1178.3
383.3	1712.4	1528.4	2081.6	1320.4	1631.0	2259.9	2495.5	1827.4	714.3	1586.1
86.7	2073.4	2358.2	2953.5	1572.4	2159.1	1808.4	3330.3	967.0	660.0	1266.2
2298.2	2344.9	2334.0	2660.7	2470.3	1777.3	2641.3	2083.4	1657.8	1197.9	1981.8
180.1	1699.8	1534.3	2099.1	2603.2	1339.7	1956.4	1649.1	1660.5	481.3	938.4
2071.7	4313.1	4470.9	3642.7	3597.2	4014.9	3553.4	3991.9	4313.4	5325.0	3180.2
36.5	319.2	517.0	646.3	247.1	250.0	287.4	380.1	100.1	184.1	166.8
293.0	812.4	1233.2	1195.2	261.2	564.4	541.5	1378.6	327.0	402.1	456.8
2835.7	2401.8	2604.1	2773.8	3649.8	2661.5	3705.2	2242.1	3049.6	2700.7	2861.8
12342.8	8077.3	7514.3	7482.8	6581.8	7198.8	8150.3	6471.3	11108.4	9784.0	9939.0
8112.2	4272.7	6108.2	5604.4	3893.8	4711.3	5037.5	4828.0	3940.7	4875.6	5477.9
51.7	530.8	931.2	989.9	517.5	492.7	785.3	586.7	104.1	70.9	379.1
50.1	137.7	165.0	165.8	150.4	163.4	132.6	255.0	92.2	62.3	115.4
60.1	174.3	289.0	455.3	206.0	208.6	419.0	283.8	65.8	41.7	161.9
47.4	408.2	965.7	905.0	265.6	434.9	343.2	674.9	297.4	82.9	235.2
51.7	313.1	602.8	433.9	315.2	289.6	420.5	635.9	86.1	131.9	237.2
809.8	1674.9	1862.9	1900.1	2019.1	1781.7	1336.8	2089.8	1510.5	594.2	1360.3
8989.1	5953.3	6020.6	5557.9	5999.1	5546.6	6745.3	5730.5	5626.0	9739.3	5240.5
787.9	3034.6	3506.3	2872.6	2762.5	2700.1	5009.7	3487.5	5273.4	2208.4	3630.3
2359.2	440.0	509.1	442.4	480.8	452.2	373.8	758.1	631.4	488.5	445.0
613.1	1272.5	1437.8	1315.5	1376.7	1099.7	1500.0	1416.1	819.5	596.0	1447.5
1111.9	239.7	271.1	219.4	191.3	209.3	202.1	287.7	288.5	139.0	62.7
7508.3	6172.8	7418.4	6712.9	4378.0	5939.2	5595.9	6166.8	5769.4	5228.1	6859.8
5862.2	2956.9	3470.6	2960.8	2558.2	2580.4	3231.2	2925.0	5620.1	3185.2	4021.8
61.6	791.5	1289.7	1411.1	590.6	663.0	484.7	868.8	403.7	520.2	283.5
42.4	335.6	847.6	828.3	233.5	544.2	362.6	874.6	159.9	536.4	389.6
1460.4	2702.3	4053.2	4043.8	3501.6	4065.1	3848.3	3709.9	4298.8	2828.5	5195.8
15743.4	5709.7	5010.4	6491.9	3828.9	4303.7	4388.9	4295.4	6894.8	4948.2	7168.0
1852.7	2206.2	2324.9	3076.0	1361.5	1748.7	1799.0	1777.6	1859.2	1712.0	2822.3

706.4	1354.5	775.7
4670.0	5765.7	4641.0
1124.3	802.9	1292.7
584.2	790.4	919.9
4543.0	3820.5	3122.1
6875.6	7814.2	7123.7
1993.5	2410.1	1892.9
1380.3	1155.9	1495.6
333.2	335.6	270.0
546.6	420.2	830.6
4197.3	5360.1	5677.1
1639.7	3037.8	2034.1
1065.0	1133.6	810.2
1389.3	2042.4	1638.8
4157.1	2106.0	4822.9
2276.9	2541.8	2602.2
1710.2	1560.5	1739.5
3643.8	4013.4	3935.7
395.3	682.3	1136.5
2076.9	1128.3	1360.8
2756.8	3193.5	2905.6
6898.0	8009.2	7987.3
5146.4	6720.5	5843.0
328.2	575.4	894.5
427.1	244.1	127.3
369.4	497.5	461.4
500.9	703.4	1157.0
664.9	347.7	668.9
2138.4	1998.7	2123.6
5444.9	6027.3	6631.0
2543.4	3834.8	3003.4
336.0	1320.2	340.3
1311.3	1659.5	1357.0
230.2	721.9	221.1
5660.2	7585.1	8089.8
2404.6	3316.6	2646.6
1139.3	1143.0	767.6
990.7	737.3	1288.0
3732.7	4444.7	4177.2
4269.2	5522.8	5202.2
2005.8	2214.7	1681.3

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s__Butyrivibrio hungatei	23005
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s__Clostridium proteoclasticum	22615
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FJ680842.1 gg_id:530175 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
FJ673287.1 gg_id:511533 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ674209.1 gg_id:510222 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ674009.1 gg_id:522634 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ680897.1 gg_id:514482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
FJ684208.1 gg_id:521014 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ673372.1 gg_id:517174 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ673461.1 gg_id:528243 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ680913.1 gg_id:510622 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ680874.1 gg_id:531676 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
FJ673170.1 gg_id:513764 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ672955.1 gg_id:515356 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
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FJ673550.1 gg_id:524819 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
AY858435.2 gg_id:111427 gastrointestinal tract Grant's gazelle clone GRANT16 AY8584
EU381909.1 gg_id:267626 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ673495.1 gg_id:164906 rumen fluid clone GRC30 DQ673
AB270010.1 gg_id:172308 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU844557.1 gg_id:310999 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU844013.1 gg_id:322677 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU468887.1 gg_id:290501 Speke's gazelle feces clone SP2_f07 EU468
DQ810011.1 gg_id:195034 human fecal clone RL184_aao67a08 DQ810
DQ799482.1 gg_id:193685 human fecal clone RL305aal86g09 DQ799
EU771915.1 gg_id:312589 Southern three-banded armadillo feces clone arma_g06_1 EU771
EU462163.1 gg_id:291179 black-handed spider monkey feces clone SPIM_aaj36c02 EU462
DQ804800.1 gg_id:184327 human fecal clone RL187_aao72h04 DQ804
FJ369853.1 gg_id:360784 feces adult twins and mothers; TS55 clone TS55_a01e09 FJ3698
AJ318527.2 gg_id:94718 Bryantella formatexigens I-52 AJ3185
FJ794074.1 gg_id:576531 Butyrivibrio hungatei str. AR10 FJ7940
X89972.1 gg_id:13946 Butyrivibrio fibrisolvens str. NCDO 2398 X89972
AJ428553.1 gg_id:41384 Butyrivibrio hungatei str. JK 615 AJ4285
AF001772.1 gg_id:13940 rumen clone RFP4 AF001
EU844037.1 gg_id:303813 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EF436377.1 gg_id:217025 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC91 EF4363
EF686628.1 gg_id:247786 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EU842438.1 gg_id:312418 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
GU174088.1 gg_id:569196 Microbial Bactrian camel estimated rumen clone XJC46 GU174
DQ518911.1 gg_id:227475 Butyrivibrio hungatei str. OV109 DQ518
DQ392992.1 gg_id:154939 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ392
AY178635.1 gg_id:98638 Butyrivibrio hungatei str. Su6 AY1786

501.2	1479.6	1582.9	1976.7	1314.1	1348.6	1407.3	1211.5	1345.9	411.6	1350.1
846.6	1498.6	1761.8	1983.4	982.4	1109.1	1026.3	1566.9	817.4	1285.6	839.0
44.9	1222.4	1460.5	2485.3	345.0	582.8	693.4	898.2	182.3	447.1	678.2
65.8	1279.2	1710.7	2347.3	331.5	636.7	521.4	1360.5	228.1	101.3	722.0
163.8	2242.0	2786.6	2856.8	947.6	1783.5	1136.2	2733.8	1685.3	502.1	1044.0
4955.3	2532.1	2289.9	2856.4	1612.2	1805.7	1861.6	1576.9	2679.0	2845.5	2838.2
11074.7	4971.2	3920.7	5094.6	3868.9	3754.1	4336.9	3821.9	5071.3	4897.4	4247.2
3694.9	845.8	755.8	781.0	471.1	554.4	547.3	744.1	650.7	591.6	585.5
9676.4	5513.6	4864.2	6053.8	5243.5	4615.5	5469.4	4564.7	3977.7	2790.6	4469.7
3402.8	2996.5	3590.7	3680.1	3369.4	3371.3	4188.6	3795.2	2272.1	2093.9	2929.3
6210.5	5324.2	4051.8	4772.1	5475.8	4059.6	4555.6	4709.1	5855.7	5670.1	5360.8
1348.1	1339.3	1298.2	1373.6	703.3	994.1	836.8	935.0	701.0	693.6	983.1
864.0	745.2	966.9	1262.0	443.2	523.6	527.3	424.5	306.2	1007.2	398.4
4344.3	4857.4	4245.4	5147.2	3206.0	3709.1	3718.3	3862.0	5604.0	5604.2	5325.9
37.4	356.8	436.5	579.7	207.9	295.7	282.1	431.3	97.6	27.8	178.3
857.3	2740.7	3379.0	3696.2	4133.3	3223.4	5209.1	3627.6	1860.1	3658.3	2664.1
3539.6	5231.4	5880.5	5627.2	5175.0	4995.2	5248.8	5006.2	5089.7	5241.4	6738.5
39.6	28.5	36.1	36.0	34.8	16.5	28.9	29.7	38.2	15.8	26.1
99.7	1259.4	1771.0	2218.1	1327.8	1696.4	1634.0	1637.4	612.8	250.7	885.7
103.6	826.4	1389.9	1500.4	579.1	643.3	795.8	1358.1	356.2	277.2	801.5
53.9	503.9	807.6	1195.6	395.6	418.3	427.6	707.1	114.9	64.9	269.5
1152.2	2255.6	2302.3	2763.2	2483.1	2116.0	2831.3	2168.2	2365.8	841.7	2155.9
909.3	1317.0	1620.2	1864.1	1226.5	1262.7	1353.3	1696.7	759.7	460.2	892.6
236.5	677.5	890.8	1210.4	723.1	707.0	737.6	981.8	264.4	170.5	507.7
140.6	938.6	1644.8	1218.9	649.3	964.5	640.1	2127.9	564.9	278.8	668.9
370.9	2391.7	2198.2	2370.5	1635.6	2285.4	2168.8	2003.7	2352.8	1870.4	1836.2
34.0	120.5	299.2	202.2	123.4	133.9	174.4	183.3	47.8	35.2	76.7
39.9	709.5	778.5	960.4	527.6	794.9	786.7	1102.7	490.2	740.7	703.9
67.0	265.9	400.3	485.3	439.7	245.0	303.9	247.6	86.6	51.7	161.4
1163.6	2976.9	4248.6	4723.6	2686.6	2774.5	2814.0	3430.2	1724.9	2957.2	3614.0
27.8	121.6	161.3	290.9	31.2	64.9	41.8	110.4	100.2	11.4	56.1
5398.8	5150.1	5558.1	6432.5	5322.0	4917.9	5380.8	4689.9	5445.8	8787.9	8990.9
32.3	335.4	321.4	418.3	89.5	225.0	104.2	322.0	92.1	53.4	171.0
50.6	610.1	817.0	1068.8	257.3	537.4	277.3	940.1	109.4	138.5	294.4
232.6	1118.9	1222.0	1193.2	1121.5	1155.7	716.0	1015.9	524.1	960.9	1014.8
211.2	1327.9	1191.3	1172.8	816.4	933.2	871.8	1062.6	501.2	746.7	823.2
1068.9	2450.1	3230.1	3216.9	1930.2	2318.0	1984.0	2956.9	1655.3	1617.6	1942.8
224.2	1269.1	1809.1	1878.0	1323.6	1605.2	1093.0	1842.2	733.2	985.6	1341.9
9716.4	3544.0	3562.0	4404.2	3600.5	3428.6	3666.9	3411.2	4073.5	4295.3	4900.6
315.4	1437.1	1818.1	2003.3	1364.9	1577.2	1078.2	1633.7	900.9	1513.4	1368.5
1151.6	1486.8	1830.7	2154.7	1356.1	1501.6	1394.2	1952.3	1412.2	862.8	973.0

1375.1	1304.1	1512.1
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1600.8	1206.1	1647.8
3288.8	1791.2	2835.9
1962.7	2402.9	1978.4
3741.1	5206.2	4735.1
790.0	1189.4	1029.2
4637.0	5236.3	5008.5
4118.1	3786.8	4616.2
4397.2	4519.3	4903.9
811.7	1513.5	870.4
544.4	683.4	720.1
3818.5	4943.0	3431.8
405.2	321.4	272.5
4042.2	3687.3	4879.7
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38.1	44.5	47.7
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1406.9	1246.6	1197.4
967.6	894.0	1514.5
2590.0	2250.7	2674.4
1929.3	1790.4	1885.7
1334.9	1093.6	1851.1
2333.6	1858.9	1567.2
2917.7	1885.5	2614.6
238.2	190.4	488.1
1143.1	1061.9	1582.8
267.9	396.3	823.2
3515.9	3948.9	3277.5
176.5	150.8	140.0
4755.6	5836.6	4362.5
322.8	285.7	442.8
1429.4	628.7	917.9
1094.0	1101.2	960.3
1185.2	1325.7	2137.3
2727.4	3395.9	3410.2
1677.6	1630.6	1581.7
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EF686558.1 gg_id:255035 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC4 EF6865
FJ172816.1 gg_id:333793 Qinghai Yak Ruminal and Fungi China rumen clone RB-4H4 FJ1728
EU381489.1 gg_id:270511 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU3814
FJ833606.1 gg_id:572615 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_15G02 FJ8336
EF686606.1 gg_id:248567 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9 EF6866
EU259429.1 gg_id:244932 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC53 EU2594
AB034043.1 gg_id:42145 rumen clone 5C0d-10 AB0340
DQ393009.1 gg_id:154018 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ393
EU843345.1 gg_id:321214 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
EU843378.1 gg_id:313437 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
EU842593.1 gg_id:317110 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
AY699274.1 gg_id:105823 Butyrivibrio fibrisolvens L8 AY6992
AB494757.1 gg_id:559488 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
FJ832859.1 gg_id:576482 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_86F11 FJ8328
GU303840.1 gg_id:548476 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AB270154.1 gg_id:166087 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2701
FJ833278.1 gg_id:510595 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_79G10 FJ8332
EF445246.1 gg_id:212281 dairy cow rumen clone NED4C4 EF4452
AB185815.1 gg_id:107748 rumen clone U29-H10 AB1858
AB494789.1 gg_id:554405 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4947
AB494805.1 gg_id:589848 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
FJ833585.1 gg_id:560025 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q401_59C08 FJ8335
EU748391.1 gg_id:334520 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07c03 EU7483
EU382023.1 gg_id:263296 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3820
AB494829.1 gg_id:562425 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB4948
AB185609.1 gg_id:100426 rumen clone F24-D09 AB1856
AB034111.1 gg_id:45716 rumen clone 4C28d-22 AB0341
FJ685127.1 gg_id:529667 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EF686550.1 gg_id:237534 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC3 EF6865
AY858397.2 gg_id:111923 gastrointestinal tract Grant's gazelle clone GRANT63 AY8583
AB185548.1 gg_id:105647 rumen clone F23-E11 AB1855
EU845063.1 gg_id:330080 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8450
FJ832174.1 gg_id:593439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q101_33A05 FJ8321
DQ393006.1 gg_id:155107 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ393
FJ673134.1 gg_id:518548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
DQ673488.1 gg_id:171181 rumen fluid clone GRC23 DQ673
AM039826.1 gg_id:151973 Butyrivibrio hungatei str. JK684 AM039
EU998648.1 gg_id:344220 Anaerobic bio-energy process study on bioreactor fermentative hydrogen productio EU9986
AF018563.1 gg_id:13983 rumen fluid clone 12-116 AF0185
EU259455.1 gg_id:250378 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC79 EU2594
AF396927.1 gg_id:46567 Butyrivibrio fibrisolvens str. WV1 AF3969

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524.9	1327.4	2008.7	2152.0	965.5	1306.7	1382.6	1771.4	957.6	459.9	1135.4
123.9	3031.3	3351.8	3420.1	3267.2	2814.9	4108.8	3041.1	1710.8	1228.1	2000.5
1373.4	1154.6	1355.3	1577.9	1230.0	1212.6	1647.7	1537.4	1255.8	694.6	889.2
287.8	1538.8	2418.7	2181.3	1585.7	1599.6	1968.8	1890.6	766.3	1274.2	1251.6
1633.8	1726.2	1914.4	1592.4	1299.3	1983.3	1355.7	1645.5	1574.1	1567.7	1102.9
142.1	1352.0	1500.1	1078.9	671.5	1109.3	725.5	1061.2	1782.1	1521.2	885.4
37.1	559.1	816.0	996.9	65.1	469.5	306.0	859.6	128.6	66.7	373.9
4911.7	3356.9	4535.4	4958.4	2611.6	3211.8	4092.2	3989.7	3289.8	2793.8	3830.9
3285.2	2984.2	3560.9	3867.9	3532.0	3010.2	3511.7	3873.1	2314.1	2253.3	2540.1
748.2	4660.8	4164.3	4327.2	4267.0	3773.1	4340.9	4216.9	6324.6	3665.8	4535.0
864.2	688.0	959.1	1362.9	635.6	808.3	814.3	1076.5	590.6	183.9	1236.1
563.9	2709.3	3002.3	3060.7	3006.8	3226.2	3118.8	3881.0	1632.7	942.1	1843.0
3975.4	3794.2	4370.9	4875.4	3455.0	3445.4	4505.3	4377.3	2706.1	1614.0	4767.1
7258.9	4101.1	4180.9	4228.2	3656.8	3465.6	3876.7	3812.6	3649.8	3235.5	4643.2
41.6	101.9	140.4	200.0	26.1	63.6	25.8	104.1	41.8	25.3	50.4
50.4	1690.0	2589.0	3010.6	961.7	1749.7	1476.2	2925.1	844.8	304.9	2446.8
45.0	268.7	281.0	389.3	40.4	141.5	63.7	617.6	47.5	17.4	160.2
599.9	876.6	1127.3	1593.9	849.6	767.1	799.8	1229.9	515.5	432.5	601.3
3192.3	2395.0	2364.9	3155.9	2386.9	2176.9	2770.0	2779.2	1110.7	690.9	1530.9
211.4	777.1	1191.7	1598.6	540.6	698.7	611.4	1247.4	357.4	186.4	837.3
108.3	2763.9	3609.3	4280.6	1687.0	2286.4	2683.4	3868.7	890.5	411.7	2408.6
5378.5	10677.0	10690.1	9518.6	7930.7	8706.1	8835.3	8371.3	11165.6	9979.6	10546.7
730.5	799.4	1128.0	1164.4	1044.5	634.3	809.5	1252.1	317.4	135.2	503.2
199.3	1185.5	1210.9	1321.0	1182.3	1167.4	810.3	1176.8	946.7	1135.8	1361.3
2856.0	4035.6	4198.3	4971.4	4158.8	4051.5	5642.3	4457.4	3850.4	3795.2	4228.3
34.2	52.2	62.9	115.6	46.4	43.5	39.3	63.3	23.0	15.8	29.7
426.9	1671.8	1588.3	1888.8	1969.4	1227.2	1968.2	1593.1	986.1	683.2	1420.3
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494.6	1411.6	1626.9	1893.7	1208.1	1326.6	241.5	1866.9	813.6	288.1	1233.9
30.3	847.7	1351.6	1549.5	678.1	976.5	948.9	1732.0	398.9	173.6	524.7
39.3	118.4	275.8	246.9	58.5	97.6	58.0	130.7	50.3	31.0	96.6
53.7	459.5	879.9	768.8	354.1	411.0	543.2	495.8	123.4	54.3	341.7
133.4	902.1	1492.3	1459.9	691.5	814.5	843.4	1328.5	382.8	339.2	718.1
5457.1	1476.4	1901.1	2257.2	1276.4	1287.2	1248.9	1353.7	2307.5	1455.9	2075.6
115.1	4034.2	3707.8	2867.0	2273.3	3242.7	2534.8	3495.7	2735.2	2046.9	3230.5
9580.0	3785.9	3511.4	3629.4	3374.7	3303.4	3915.7	3452.0	3405.8	4309.2	3739.9
1866.7	3789.9	4575.2	5971.1	3138.3	3181.1	4120.8	3609.1	2224.8	1360.9	2724.4
10899.9	3116.7	4509.0	4732.3	3877.2	4254.1	4521.3	3738.0	10533.7	5330.8	6552.8

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1957.1	1989.6	1757.6
2500.3	2489.4	4046.1
1552.7	1632.9	1672.2
1800.2	2220.1	3247.4
2223.9	2451.0	1869.7
1136.4	1257.4	1264.1
442.7	501.8	475.4
3455.0	5396.6	5686.6
4019.0	3746.2	3429.8
4300.1	4417.9	4372.7
1065.9	891.4	1605.7
3526.3	3516.5	6328.0
4429.8	3829.5	4400.7
3709.5	5188.9	4460.4
150.3	128.0	98.5
2900.8	2262.4	3203.4
260.0	213.7	700.5
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2822.6	2393.6	2585.6
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898.2	872.9	978.1
1044.8	1150.8	716.5
4147.2	5554.1	6016.4
41.8	65.7	128.0
1436.3	1698.3	2041.4
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53.7	65.8	59.6
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1950.8	1609.2	1773.5
1700.3	1235.8	1441.0
172.7	158.3	99.8
532.6	610.5	1752.5
1184.2	1544.6	1559.1
1627.8	1902.2	1447.8
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FJ172856.1 gg_id:352708 Qinghai Yak Ruminal and Fungi China rumen clone RB-3H4 FJ1728
EU475426.1 gg_id:292105 springbok feces clone SBSD_aaa04h10 EU475
AF001728.1 gg_id:13939 rumen clone RCP17 AF001
EU748328.1 gg_id:353814 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05b05 EU748
FJ832996.1 gg_id:571152 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q102_35C05 FJ8329
NR_025981.1 gg_id:554698 Butyrivibrio fibrisolvens str. ATCC 19171 NR_02
GU303265.1 gg_id:544781 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU381935.1 gg_id:272045 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU887842.1 gg_id:313349 Butyrivibrio fibrisolvens str. H15 EU887
GU303723.1 gg_id:583937 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU845522.1 gg_id:317020 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU259488.1 gg_id:251666 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC112 EU259
FJ832546.1 gg_id:551295 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q301_19C03 FJ8325
EU344292.1 gg_id:273016 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
X89973.1 gg_id:13947 Butyrivibrio fibrisolvens str. NCDO 2432 X89973
GQ402115.1 gg_id:572392 alpacas and sheep forestomach clone ALP7 GQ402
FJ833317.1 gg_id:508957 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q401_47G06 FJ8333
EU845719.1 gg_id:329343 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EF686570.1 gg_id:257136 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC5 EF6865
EU845411.1 gg_id:355326 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU468953.1 gg_id:303390 Speke's gazelle feces clone SP2_h03_1 EU468
FJ832450.1 gg_id:590844 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_35C05 FJ8324
GU303299.1 gg_id:562486 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU344321.1 gg_id:266983 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ172805.1 gg_id:310869 Qinghai Yak Ruminal and Fungi China rumen clone RB-2E2 FJ1728
AB185626.1 gg_id:101165 rumen clone F24-F04 AB185
AB034057.1 gg_id:53486 rumen clone 4C3d-2 AB034
AF084837.1 gg_id:13951 Eubacterium sp. str. TW2 AF084
EU843480.1 gg_id:333462 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ832235.1 gg_id:538459 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q102_57A08 FJ8322
EU469799.1 gg_id:295622 western lowland gorilla feces clone GOR_aag71b07 EU469
AY699275.1 gg_id:105974 Butyrivibrio fibrisolvens L10 AY699
DQ673500.1 gg_id:173319 rumen fluid clone GRC35 DQ673
FJ684664.1 gg_id:515496 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
EU844205.1 gg_id:350862 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AB494756.1 gg_id:550436 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone A AB494
X89976.1 gg_id:13950 Butyrivibrio fibrisolvens str. Bu 43 X89976
FJ678988.1 gg_id:511462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ832270.1 gg_id:587175 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q201_33A05 FJ8322
EU748148.1 gg_id:313865 neotropical folivorous flying bird adult hoatzin crop clone hoa32_08H01.F EU748
EU844744.1 gg_id:324284 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844

39.5	288.4	602.8	625.2	286.4	320.1	335.0	742.0	193.8	65.4	355.7
38.8	86.4	102.0	154.1	25.5	85.6	79.0	99.6	29.2	14.2	87.7
16192.8	2155.7	2492.7	3176.8	2521.7	2109.4	2820.6	2457.2	2778.6	3038.7	3067.1
2920.0	2694.6	3481.5	3766.4	3205.8	2681.2	3503.3	3484.4	1847.9	2145.6	2113.8
21615.2	5563.8	5309.6	6184.3	5036.2	4266.4	5867.4	5088.7	3960.8	4857.0	6750.4
5477.1	2043.7	2656.1	3038.3	1293.4	1675.7	1505.6	2057.1	2482.3	1338.5	2742.6
125.6	762.8	970.0	1028.3	801.0	857.3	660.6	1011.6	527.7	639.2	777.5
27.9	265.1	561.4	334.4	290.9	323.6	177.2	559.6	151.0	86.9	325.9
4275.1	3285.2	3260.6	3363.7	2776.0	3172.5	2827.8	3836.7	2453.0	2960.3	4262.5
1702.9	2508.0	2642.9	2797.4	1853.1	2060.3	2397.5	2084.9	2563.6	2016.2	2781.5
137.5	1427.3	1497.6	1398.9	872.7	1493.2	975.8	1203.4	658.5	722.2	540.1
43.2	1056.4	1701.8	1450.1	453.1	1211.7	832.0	1067.3	618.8	178.3	542.9
78.9	1060.0	1536.8	1538.7	1366.2	1319.2	1276.5	1674.6	667.2	665.7	772.5
7315.9	4344.3	5126.0	5377.6	4238.8	3753.3	5407.3	5007.8	3439.5	2836.2	5356.9
2216.0	2287.7	2743.0	3247.8	2539.1	2079.0	2312.7	2972.7	1281.6	809.6	1457.8
2087.0	2254.5	2719.2	2887.3	2055.5	2289.5	2257.7	2317.4	2438.3	2095.8	2099.2
824.7	1927.6	2151.4	2049.9	1582.8	1603.9	1681.4	2317.9	1174.3	982.4	1844.7
274.4	1375.0	2144.3	2073.2	1131.2	1357.8	1691.1	1931.7	572.7	372.5	1064.7
1138.5	2377.7	2658.1	3393.6	2132.3	2220.3	2058.3	2478.1	957.1	947.6	1429.5
4833.0	6215.2	7212.8	8210.8	6380.0	5922.9	6706.3	6122.3	4329.0	4020.0	6387.8
2628.3	3702.9	4078.2	4108.7	3936.5	3833.3	4109.6	4022.8	3509.6	2755.2	3681.4
49.0	788.1	1022.9	843.7	711.5	663.1	1172.3	1297.9	334.2	177.1	566.5
80.8	1180.9	1481.4	1673.1	1036.2	906.8	1187.1	1244.4	582.2	343.3	612.6
68.6	2291.2	2349.1	2797.7	1693.2	1397.0	2132.2	2123.4	1205.0	501.5	1148.2
199.5	1377.0	1789.2	1934.4	1653.3	1444.4	2056.9	1407.4	851.7	1674.4	1296.7
41.2	1048.7	1256.5	1596.7	974.3	1256.3	961.1	1349.3	269.0	143.6	660.4
3055.6	6931.0	7136.1	7749.1	7195.1	6676.8	7854.5	6595.0	7575.0	8425.6	8071.5
109.5	241.0	402.0	498.2	191.1	189.7	196.6	167.9	125.6	77.9	271.8
116.0	1457.2	964.4	825.3	868.7	865.1	690.8	1082.9	281.2	366.0	421.3
317.1	1984.4	2731.2	2629.5	1725.1	1779.7	2459.8	2463.1	973.7	826.8	1603.2
29.7	16.6	14.1	20.6	19.0	11.3	15.3	16.1	13.4	10.7	20.7
119.7	1190.6	1608.5	1681.9	605.9	1178.3	729.6	1464.1	659.1	201.4	565.2
3023.7	1576.9	1955.8	2202.6	1198.9	1913.9	1632.3	2819.8	948.9	538.1	1114.3
12181.5	6166.6	5649.6	6348.5	5949.6	6542.4	6528.0	6342.5	6201.4	5468.2	7976.0
273.5	2525.1	3545.3	2883.3	2662.0	3197.3	3043.1	3672.6	1699.0	4389.6	2028.4
111.8	2690.4	3585.2	4316.4	2542.5	2455.2	2957.3	2551.0	1529.8	598.2	1666.6
43.3	950.9	1899.8	1354.2	499.4	1172.9	793.5	1510.9	688.2	247.3	785.4
7764.0	5316.8	5467.9	6513.3	5744.4	5363.1	5880.0	5265.5	4393.2	4500.1	6762.8
662.8	1938.3	2235.4	2646.5	1620.5	1425.7	1519.8	1862.2	635.6	649.3	1258.0
75.4	2559.7	3228.2	2696.7	3267.2	2722.9	2519.4	2753.6	3255.8	1819.9	1610.7
9825.8	3171.1	3031.3	2710.4	3008.0	2915.7	3881.0	3164.0	3654.2	5230.1	3355.6

537.4	389.7	534.7
176.8	118.0	303.0
2953.8	3947.3	1784.8
3560.7	3483.6	4868.6
4133.6	5089.1	5595.7
2388.9	2712.8	3365.6
792.7	1257.1	1603.1
394.2	465.0	627.9
2845.8	5060.2	3779.1
2102.1	2447.9	2805.3
1320.2	1689.8	1655.1
1123.7	1004.2	2054.7
1598.6	1893.7	2262.8
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2878.4	2966.5	3363.3
2357.7	2744.9	3085.2
2668.2	2252.7	2765.4
2161.2	2138.7	2847.8
2342.1	2839.9	3230.1
6490.4	6744.6	8079.4
3852.2	4156.1	4673.9
1210.8	1028.9	1077.2
1282.4	1167.9	2277.6
1744.9	1723.8	3377.8
1565.5	2067.5	1661.0
1010.2	975.2	1844.6
7122.1	7323.5	8374.4
286.4	469.1	317.6
1324.4	930.8	1965.9
2415.6	2112.5	3760.9
16.9	20.0	17.3
1692.4	1239.8	2033.0
2977.0	2171.5	2519.7
6008.2	7512.1	6884.4
2982.0	2844.9	4419.0
2995.1	3220.9	4909.4
1424.7	1035.4	1698.9
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2166.2	1892.3	2207.5
2149.4	3221.0	6212.2
2964.7	3931.2	3125.4

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s__Clostridium scindens	18677

NR_029185.1 gg_id:582636 Clostridium proteoclasticum str. B316; ATCC 51982 NR_02
EF436289.1 gg_id:212460 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC03 EF4362
EU458792.1 gg_id:288228 Goeldi's marmoset feces clone CAL_g01_1 EU458
AJ428552.1 gg_id:29965 Clostridium proteoclasticum str. UC 142 AJ4285
X89975.1 gg_id:13949 Butyrivibrio fibrisolvens str. NCDO 2435 X89975
DQ256289.1 gg_id:142613 Rumen fermentation and dynamics during stepwise adaptation -concentrate diet gc DQ256
EF436453.1 gg_id:208144 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC167 EF4364
EU344334.1 gg_id:260128 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
AF396926.1 gg_id:37898 Butyrivibrio fibrisolvens str. C211 AF3969
EU468849.1 gg_id:287834 Speke's gazelle feces clone SP2_a02 EU4688
GU302641.1 gg_id:535265 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ833856.1 gg_id:578507 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_60D08 FJ8338
AB034049.1 gg_id:52499 rumen clone 5C0d-19 AB034
GU303019.1 gg_id:556604 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
FJ833619.1 gg_id:591679 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_08H01 FJ8336
GU303967.1 gg_id:544678 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ834274.1 gg_id:584208 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_73A10 FJ8342
EU843301.1 gg_id:306119 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
DQ278862.1 gg_id:155730 Clostridium aminophilum 152R-1b DQ278
FJ833697.1 gg_id:551575 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q101_44D06 FJ8336
EU998650.1 gg_id:304850 Anaerobic bio-energy process study on bioreactor fermentative hydrogen productio EU998
GU302568.1 gg_id:557599 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ115584.1 gg_id:382807 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687h1 GQ115
AM420037.1 gg_id:239814 Noma subgingival plaque clone 202A08(oral) AM420
GU407024.1 gg_id:571776 Human Oral Microbiome oral cavity GU407
X87151.1 gg_id:14096 Catonella morbi str. ATCC 51271 X87151
AF385556.1 gg_id:48583 crevicular epithelial cells clone BR063 AF3855
NZ_ACIN02000016.1 gg_id:469479 Abiotrophia defectiva str. ATCC 49176 NZ_AC
NZ_ABCC02000039.1 gg_id:469991 Clostridium bolteae str. ATCC BAA-613 NZ_AB
FJ371143.1 gg_id:360723 feces adult twins and mothers; TS6 clone TS6_a01d12 FJ3711
AJ508452.1 gg_id:83226 Clostridium bolteae str. 16351 AJ5084
DQ479412.1 gg_id:157999 Clostridium sp. CYP2 DQ479
FM994938.1 gg_id:537456 Clostridium celerecrescens str. HP2 FM994
AB117568.1 gg_id:111552 Clostridium hylemonae str. CT-30 AB117
D14638.1 gg_id:14113 Clostridium piliforme str. RJ D14638
DQ352808.1 gg_id:151298 Clostridium piliforme CRL-K DQ352
DQ352807.1 gg_id:155362 Clostridium piliforme 7MTS DQ352
DQ352806.1 gg_id:153965 Clostridium piliforme DQ352
DQ352811.1 gg_id:153952 Clostridium piliforme R1 DQ352
DQ352810.1 gg_id:153713 Clostridium piliforme CRL DQ352
AY244789.1 gg_id:86360 Clostridium scindens str. 2002-69680 AY2447

10979.1	3735.3	4342.4	5573.9	4745.6	3891.7	5513.6	4269.0	4446.2	3846.2	3941.8
40.0	108.9	113.9	241.6	103.6	198.6	87.3	123.3	112.6	150.2	108.0
479.1	3453.7	3725.8	3620.6	3298.9	3269.8	4683.0	3528.1	2295.8	1496.7	4171.5
18352.5	5627.7	6119.8	6418.9	5897.4	5886.9	6678.6	4986.7	7304.5	6260.5	8060.9
152.0	1254.2	1641.8	2511.3	1117.4	1364.7	1570.7	1536.9	604.8	227.8	990.4
62.0	35.9	52.7	38.6	160.5	23.1	35.7	31.4	106.1	81.1	33.8
4972.8	4451.4	2545.9	5745.4	6351.7	4533.7	6082.2	4615.7	4075.6	4104.2	4955.7
16725.3	5929.3	5883.0	6423.0	5872.2	6320.9	6377.6	5442.3	8651.4	6232.2	8094.0
2077.8	4056.5	3927.2	4251.2	4251.8	3970.6	4635.3	3991.4	3789.5	2704.4	5149.0
13607.7	5988.8	7930.0	6620.0	6095.8	6321.1	6651.2	5900.5	6317.7	4489.9	7281.5
2969.7	2307.8	3067.4	3362.3	1847.5	2264.0	2399.1	2717.7	2113.3	1554.0	3045.5
72.9	2298.7	3425.4	4238.6	2587.8	2038.7	2941.9	2573.9	743.5	317.9	1897.8
40.8	82.1	139.5	136.9	113.5	115.8	105.3	148.4	65.1	36.0	79.6
264.4	2293.9	2925.4	2939.3	2298.6	2296.5	2518.6	2397.9	1435.8	840.0	1276.2
173.4	3586.0	3799.4	4369.2	3454.5	3240.3	4616.4	3774.5	2854.3	1651.5	3389.3
3782.3	3043.3	3467.9	3640.2	3071.8	2810.9	3402.4	2964.7	2764.2	2234.0	2912.7
170.9	1173.8	1799.4	1785.9	1559.5	1353.0	1564.4	1959.7	596.7	334.1	915.1
49.3	87.7	197.5	224.8	90.9	95.1	115.7	223.4	52.9	40.5	58.1
307.8	49.2	46.9	52.1	608.9	33.0	609.5	46.8	22.4	17.7	432.1
565.2	1630.9	2061.4	2167.4	1630.5	1560.5	2136.5	2218.9	1283.7	1010.3	1332.3
214.5	677.8	1037.0	1063.7	634.7	510.9	725.9	923.1	532.3	151.3	352.1
22867.9	7468.8	6887.1	7170.6	6520.0	7849.8	7261.7	6392.9	9727.1	8111.1	11023.5
11983.3	2523.3	3120.9	3952.0	3441.1	2804.3	3149.5	3179.7	2821.4	2740.2	2943.5
653.7	4225.4	4584.5	5531.7	4165.5	4685.8	3504.9	5293.6	6639.2	7717.9	4139.9
11563.1	5252.4	4633.8	6723.1	5991.6	5081.2	5154.4	5180.5	4848.2	3713.0	6733.7
106.7	715.2	921.5	1096.8	656.8	593.4	736.6	801.9	190.4	86.4	399.0
940.2	4254.1	4858.2	6179.7	5054.8	4756.7	4103.0	5323.6	4426.5	6519.8	3177.6
2657.8	2527.5	2948.8	3892.9	2224.2	2353.7	1993.8	2827.1	1841.0	1607.2	2357.6
41.2	873.4	2215.3	1216.8	228.9	1156.1	343.5	1212.4	285.5	79.4	477.3
89.2	1532.6	2423.1	2166.4	1737.1	1335.8	1686.0	1490.8	1262.5	1971.2	1368.3
54.3	505.9	669.0	949.7	401.3	450.9	400.7	736.9	183.3	110.4	261.7
40.6	622.6	1109.3	1064.7	204.5	1115.3	457.6	3464.5	264.9	1180.8	586.7
2859.8	5293.1	6388.2	4593.3	4642.8	5456.6	5195.4	5974.5	5180.6	5711.6	7703.8
49.2	210.0	458.9	105.9	115.2	252.7	141.6	139.8	212.8	31.9	306.5
3247.8	3502.3	4283.8	4216.6	3270.5	3267.4	4455.4	4088.0	2751.7	2584.7	3145.8
1969.1	4707.8	3247.1	3066.5	2192.8	3284.0	2523.7	3188.3	3528.9	3790.5	2266.7
2846.7	3706.5	4137.6	4099.0	2879.9	3500.3	3895.4	3172.8	4090.6	2545.0	6203.2
6967.9	2386.8	2516.2	2602.1	2255.2	2241.5	3292.5	1274.2	3198.7	1837.6	3373.0
12527.7	7323.4	7108.3	6571.5	5669.1	5909.2	7421.1	6151.3	9021.9	8066.3	7905.2
8782.7	4380.5	5416.9	4717.9	4272.4	4365.8	5429.3	5005.1	5007.2	3890.6	5969.2
29.4	174.1	335.6	325.5	36.7	124.1	79.3	307.3	31.8	20.4	162.6

5156.0	5619.3	5218.0
254.1	476.1	200.6
3165.3	3520.2	5273.2
5074.6	6711.3	7494.9
1748.8	1607.8	1650.3
225.3	169.5	179.3
4670.3	5346.5	6360.5
5476.0	7108.9	5688.6
4255.2	4400.2	5367.7
4987.9	6144.4	6548.8
1894.9	3019.2	2435.3
3188.1	2401.6	5343.2
107.0	151.1	221.7
2381.0	2994.7	2673.4
3640.3	3040.0	4882.1
3291.4	3031.7	3697.0
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322.1	163.2	229.3
457.4	612.1	569.2
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4854.0	5455.2	5187.1
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702.0	869.9	1081.9
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917.5	745.1	1271.9
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106.4	190.8	202.8
3824.0	3524.8	4447.2
2561.1	3042.8	3458.0
2654.5	3102.3	2840.6
2070.4	3345.5	4371.9
5640.3	7347.0	6797.5
4710.5	5618.6	6041.7
179.8	194.6	147.4

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FJ370593.1 gg_id:368214 feces adult twins and mothers; TS57 clone TS57_a02h04 FJ3705
DQ799592.1 gg_id:191476 human fecal clone RL305aal88a10 DQ799
DQ806965.1 gg_id:193601 human fecal clone RL198_aaj76c02 DQ806
DQ801189.1 gg_id:179381 human fecal clone RL116_aaf00c04 DQ801
FJ678914.1 gg_id:522609 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
EU451069.1 gg_id:322062 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
AY984751.1 gg_id:122545 human stool clone B711 AY9847
GQ492488.1 gg_id:584140 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU462089.1 gg_id:292294 black-handed spider monkey feces clone SPIM_aaj34g08 EU462
EU504811.1 gg_id:273376 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02e11 EU5048
DQ823839.1 gg_id:185281 human fecal clone RL250_aaj79g08 DQ823
DQ456402.1 gg_id:157112 pre-adolescent turkey cecum clone CFT214H8 DQ456
DQ801439.1 gg_id:185174 human fecal clone RL388_aao95e09 DQ801
DQ799332.1 gg_id:179876 human fecal clone RL305aal85a06 DQ799
EU455444.1 gg_id:342887 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU455
EU778887.1 gg_id:306692 Black-handed Spider Monkey feces clone SPIM_f10 EU778
FJ685196.1 gg_id:531394 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
DQ799688.1 gg_id:189413 human fecal clone RL182_aah31c11 DQ799
FJ879747.1 gg_id:419244 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8797
EU779009.1 gg_id:341752 Prevost's squirrel feces clone SQ_aah80e08 EU779
FJ371024.1 gg_id:360061 feces adult twins and mothers; TS5 clone TS5_a04a08 FJ3710
GQ156416.1 gg_id:558831 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
FJ683057.1 gg_id:528893 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
EU509444.1 gg_id:267886 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e03 EU509
DQ805861.1 gg_id:184155 human fecal clone RL306aal92a04 DQ805
GQ491719.1 gg_id:560908 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ369253.1 gg_id:363341 feces adult twins and mothers; TS50 clone TS50_a02b02 FJ3692
EU510715.1 gg_id:269586 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39g09 EU510
DQ801354.1 gg_id:188674 human fecal clone RL388_aao94d08 DQ801
DQ057375.1 gg_id:130277 chicken ileum/cecum clone cc152 DQ057
DQ805819.1 gg_id:182430 human fecal clone RL306aal91e02 DQ805
EU451541.1 gg_id:349757 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU451
EU508869.1 gg_id:270015 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap37d12 EU5088
EU766372.1 gg_id:328667 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
DQ825256.1 gg_id:182940 human fecal clone RL185_aan87d04 DQ825
EU470204.1 gg_id:297920 trancaspain urial feces clone TU2_aaa04b02 EU470
FJ367980.1 gg_id:358986 feces adult twins and mothers; TS30 clone TS30_a02b03 FJ3679
FJ678396.1 gg_id:513429 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
EU455270.1 gg_id:340600 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU455
EU763188.1 gg_id:323777 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7631
EF399125.1 gg_id:205476 human fecal clone SJTU_F_12_07 EF3991

54.3	108.6	158.8	196.1	61.0	118.2	69.1	211.1	37.1	22.6	106.9
44.0	32.9	36.5	48.4	41.7	34.0	37.3	52.1	43.9	16.0	29.1
3951.0	1607.2	1560.8	1664.3	1103.7	1332.4	1163.0	1511.0	1075.8	2188.4	1705.0
96.5	429.3	774.8	919.1	67.2	644.1	213.0	2037.3	116.4	197.8	142.4
35.7	223.5	345.2	507.3	35.1	112.7	41.4	204.6	29.1	24.5	56.3
62.9	1150.4	1610.5	1267.2	774.3	973.7	950.4	1078.9	652.1	591.9	954.5
305.7	2351.7	2500.1	3076.3	2677.6	2283.9	2848.6	2647.0	2959.8	1341.5	2100.3
38.8	178.4	431.7	584.4	57.7	94.6	79.8	142.3	41.3	58.4	160.5
72.6	471.8	633.0	707.4	344.2	318.1	484.3	364.6	163.1	58.2	158.7
169.2	945.5	1811.2	2057.3	611.7	1330.2	934.6	1600.2	640.6	280.2	803.4
53.8	671.2	848.4	834.0	380.2	349.8	356.7	532.1	113.8	51.9	173.7
318.7	926.1	1121.3	1581.3	473.5	917.4	771.5	1095.9	242.6	218.9	463.0
4936.4	3499.0	2783.4	3355.2	2645.2	2787.6	3045.9	3072.7	3748.8	2827.9	4147.1
46.6	244.7	348.4	476.0	34.9	95.2	66.5	279.0	47.2	45.8	49.1
329.9	2116.2	2081.1	2209.3	2212.6	2032.1	2297.4	2972.3	1335.6	790.5	2771.2
2219.3	5897.4	6181.0	7005.9	8124.9	5808.0	7734.5	7128.0	5245.1	4288.3	8162.0
308.1	1834.2	2212.9	2470.8	2023.5	1922.3	2442.1	2395.2	959.8	1034.0	1200.6
49.3	492.2	862.8	1030.4	474.5	517.1	572.4	1048.1	250.6	110.3	451.7
83.7	1483.7	2228.4	2546.3	1160.2	1350.5	1010.1	1126.4	1314.1	384.5	828.0
1049.3	3192.5	2583.7	2308.6	1973.1	1239.5	2161.8	2024.5	4399.3	2946.2	2893.4
2678.7	785.9	540.2	569.2	498.1	628.4	575.5	630.3	1619.9	816.8	530.6
76.5	660.8	1332.6	1509.8	210.7	573.8	423.2	733.5	186.5	67.8	379.9
527.9	1895.1	1562.1	1736.6	1525.1	1682.5	1259.0	1374.1	965.6	2604.2	1285.4
1177.8	1643.1	1696.6	2181.4	1849.4	1575.4	1933.3	1746.4	1040.6	1236.3	1413.6
37.4	207.3	281.2	386.4	98.8	106.0	96.9	185.8	48.0	44.9	89.8
96.7	818.2	906.0	1007.4	996.5	930.1	1066.5	798.9	424.0	422.4	517.2
405.2	2794.8	2574.0	2640.6	2623.5	2367.0	2201.9	2970.7	2018.2	1270.1	2667.9
3021.9	2829.0	3214.1	2797.1	2555.9	3017.9	3599.8	3012.8	5628.3	2796.8	3016.8
75.4	693.7	762.3	1042.8	1082.1	700.8	1060.2	935.7	313.1	393.4	337.6
32.9	134.5	259.6	461.9	92.7	66.9	50.8	245.9	24.8	19.4	84.9
4517.1	2966.6	3270.8	3092.3	3603.0	2887.8	3098.4	3843.0	3346.4	2966.8	3150.7
1310.9	4780.1	4083.0	3179.2	2850.0	4021.2	3026.0	3205.3	6176.4	5038.7	4596.3
61.9	66.9	96.6	97.7	51.0	72.7	70.9	74.4	48.5	37.7	63.8
46.9	199.2	214.9	101.7	108.0	144.7	68.5	151.4	62.4	26.4	138.6
34.4	100.5	275.2	232.3	38.0	139.8	148.1	151.0	43.0	29.1	132.0
105.6	2157.2	3006.4	2932.8	2351.6	2308.6	2864.5	3262.0	1053.9	563.6	1957.9
5359.1	2821.8	2182.0	2863.6	2222.7	2588.1	2404.7	2801.6	3270.3	3036.2	2242.4
10229.9	3300.2	3320.3	3292.1	3486.6	2934.6	3481.1	3206.9	4288.4	2920.5	5102.9
49.7	127.0	260.0	394.9	86.2	117.9	95.4	203.9	41.5	33.4	149.4
12908.7	5396.4	5019.4	5674.5	5195.1	5369.5	5444.6	4902.1	6938.9	6528.0	7348.7
33.2	169.5	339.1	350.9	89.4	236.2	115.7	308.6	95.7	70.6	260.9

99.2	105.1	156.0
26.8	30.8	37.2
1505.1	1828.1	1051.0
2353.8	702.3	1628.2
360.1	116.0	146.6
1123.8	1866.8	1857.0
2761.7	2181.9	2713.9
327.0	316.1	295.2
829.4	495.3	994.2
2380.6	1294.0	1504.7
539.1	517.6	549.9
1643.0	1207.4	1326.8
2572.5	3376.2	2582.2
418.2	234.2	226.6
912.1	1882.6	1834.1
7004.4	6382.2	8189.4
2368.0	1843.7	2710.6
1098.8	753.4	876.1
2283.4	1706.8	1908.5
2048.1	1992.3	2582.3
539.0	1137.2	528.5
1017.2	900.3	1061.9
1890.4	2283.2	1957.6
2300.4	1836.1	2722.4
242.8	206.6	127.3
973.0	976.8	2021.3
3200.3	2468.9	2226.2
2760.6	3456.4	3218.5
878.5	637.6	1311.3
180.6	155.4	224.0
3190.5	4213.6	3620.6
3235.3	3988.5	4365.0
70.3	146.1	77.1
120.8	106.9	85.1
221.2	118.9	212.0
3040.2	2587.2	3138.7
2876.0	2803.9	3714.3
2859.1	3911.5	3061.3
131.3	103.0	59.3
5073.8	6422.5	5309.2
291.8	374.8	256.6

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
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DQ802257.1 gg_id:183438 human fecal clone RL188_aah15b10 DQ802
EU510626.1 gg_id:260811 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38d06 EU510
GQ492126.1 gg_id:573110 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ832608.1 gg_id:545139 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_31G04 FJ8326
DQ799840.1 gg_id:191687 human fecal clone RL182_aah34g05 DQ799
DQ806982.1 gg_id:179726 human fecal clone RL198_aaj76f07 DQ806
EU468527.1 gg_id:290934 okapi feces clone OK1_a07_2 EU468
EU451201.1 gg_id:329571 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
GQ491160.1 gg_id:544635 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ681675.1 gg_id:513440 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
DQ800343.1 gg_id:173900 human fecal clone RL303_aal71h03 DQ800
GQ492164.1 gg_id:534016 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ326040.1 gg_id:202839 Metagenomic distal gut microbiome healthy human stool clone BA08 DQ326
DQ801933.1 gg_id:190188 human fecal clone RL201_aai48f09 DQ801
GQ493000.1 gg_id:537661 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ905665.1 gg_id:164419 human fecal clone 014C-D11 DQ905
FJ681847.1 gg_id:523064 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ368654.1 gg_id:368572 feces adult twins and mothers; TS49 clone TS49_a02h04 FJ3686
FJ680491.1 gg_id:519396 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ366657.1 gg_id:362539 feces adult twins and mothers; TS27 clone TS27_a02c07 FJ3666
EU459642.1 gg_id:288103 ring-tailed lemur feces clone RT_aai09h02 EU459
EF404404.1 gg_id:209847 human fecal clone SJTU_C_09_53 EF4044
FJ679391.1 gg_id:518431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU508804.1 gg_id:269313 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51c11 EU508
EU462022.1 gg_id:291771 black-handed spider monkey feces clone SPIM_aaj33d11 EU462
AB234508.1 gg_id:147442 termite gut homogenate clone MgMjW-19 AB2345
EU463310.1 gg_id:291477 bush dog feces clone bdog1_aai77g06 EU463
FJ676399.1 gg_id:522177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
FJ364631.1 gg_id:366411 feces adult twins and mothers; TS19 clone TS19_a01c03 FJ3646
FJ677673.1 gg_id:517081 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6776
EF398872.1 gg_id:205862 human fecal clone SJTU_F_08_42 EF3988
DQ905410.1 gg_id:163456 human fecal clone 013C-D7 DQ905
GQ016102.1 gg_id:493565 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
DQ795830.1 gg_id:189334 human fecal clone RL245_aai83a11 DQ795
EU459637.1 gg_id:298788 ring-tailed lemur feces clone RT_aai09g03 EU459
GQ493802.1 gg_id:566459 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU459728.1 gg_id:292544 ring-tailed lemur feces clone RT_aai11f10 EU459
EU462186.1 gg_id:295683 black-handed spider monkey feces clone SPIM_aaj36g03 EU462
EF398675.1 gg_id:207959 human fecal clone SJTU_F_05_23 EF3986
DQ808211.1 gg_id:193699 human fecal clone RL180_aao73h09 DQ808
EF401865.1 gg_id:210965 human fecal clone SJTU_D_04_32 EF4018

63.8	250.0	383.9	458.7	218.8	245.1	264.0	511.4	125.7	187.9	256.4
8135.3	5446.6	5465.2	6630.2	4305.1	5936.6	5592.3	6195.6	4879.2	3184.3	7014.7
37.8	222.7	208.3	305.0	104.8	204.4	113.5	254.4	389.5	373.7	147.6
290.3	944.2	1078.4	915.2	821.1	943.3	1083.9	1013.8	402.2	319.7	615.3
42.4	336.3	662.9	663.4	84.6	208.1	138.4	395.8	60.7	56.2	181.9
903.4	1637.3	1560.6	1598.7	1866.3	1615.8	1571.2	1668.3	1363.0	3141.5	1152.5
72.7	2569.2	3812.2	4081.0	1432.1	2629.5	2126.4	3883.1	740.8	814.6	2448.9
4338.3	1245.2	1503.8	1530.0	1033.2	1137.6	1442.4	1285.8	2161.2	1586.5	2010.2
69.6	986.1	1338.1	1440.9	864.6	825.3	1272.3	1110.7	335.2	227.2	733.9
39.0	615.8	1014.5	1196.2	497.5	612.8	675.7	1098.1	405.9	146.3	322.7
40.1	309.4	592.1	654.4	230.0	524.2	186.1	1155.7	76.2	99.0	212.4
117.4	858.8	974.5	874.8	826.2	770.3	666.3	770.2	525.3	196.7	1155.2
53.7	109.7	463.7	678.9	261.5	386.3	241.6	449.3	230.5	198.6	81.2
7000.9	2941.7	2749.6	2998.2	2827.0	2800.3	2741.5	2599.1	4366.4	3125.4	3654.5
19024.0	7166.4	6412.5	7031.3	6504.4	7041.1	7186.9	6106.7	9568.9	10923.2	8513.2
71.0	752.8	1344.1	1371.2	321.0	909.1	969.8	1393.4	314.1	147.1	632.0
678.0	2583.5	3043.1	2796.3	2185.5	2257.5	2643.1	2699.0	1647.2	737.7	3040.2
1121.3	5911.4	4915.3	5535.0	6750.9	5820.3	5914.6	6667.1	6792.9	3646.5	5629.2
16263.1	6216.5	6879.1	7461.5	5436.5	6453.4	6470.2	5961.2	8638.1	7672.6	8095.5
38.4	90.3	333.1	186.8	78.8	186.9	90.5	290.5	141.0	42.6	122.9
2282.2	1553.2	961.7	818.5	758.2	1253.2	856.0	854.0	1478.9	758.1	603.8
111.9	924.7	1002.7	1191.6	664.0	891.9	1485.1	1378.0	705.0	478.3	777.0
1163.9	2172.9	2319.8	2542.0	2669.4	2252.3	2214.6	2260.9	2726.8	1985.2	1910.7
10835.8	4891.9	4944.0	5077.0	4773.4	5346.7	5146.8	4645.7	5376.7	3976.8	5542.0
61.3	959.6	1253.5	1646.2	715.9	883.4	807.7	1402.2	294.2	212.3	440.6
56.8	97.3	201.9	218.8	98.9	102.9	107.4	211.9	35.4	58.8	71.7
51.2	463.5	588.6	670.4	618.5	681.7	614.9	724.0	203.6	160.2	232.6
79.0	491.1	707.1	1037.6	565.9	602.9	451.4	669.7	327.6	378.6	307.1
1869.3	2532.7	3195.3	2971.5	2205.0	2247.3	1793.8	2567.5	1860.5	1088.1	2796.6
1052.1	1284.6	1327.4	1539.1	1560.2	1089.6	2200.5	1043.6	449.4	2444.1	885.3
1018.7	2689.1	3106.8	3458.2	2699.1	2609.5	3237.9	2757.6	2027.2	1095.2	2011.5
17663.7	3762.6	3136.9	3023.7	2671.2	3206.5	2962.5	3076.7	4733.3	3140.9	4874.8
119.7	787.1	1143.5	1131.5	1146.5	959.8	1287.3	1773.0	533.8	463.7	642.2
1012.7	2280.7	3135.1	3070.0	2969.8	2573.7	3723.3	3561.0	1831.8	1159.3	2898.8
5228.4	3916.4	4466.4	5106.3	5203.6	4267.6	5437.4	4619.9	2675.7	3085.3	5897.0
256.6	769.2	935.0	1355.0	568.1	764.2	485.1	649.1	286.9	308.5	441.1
74.9	1120.7	1679.6	1821.3	1191.8	1123.6	1594.3	1772.6	514.7	452.0	550.3
104.5	872.8	1068.1	1129.5	553.0	771.7	707.8	921.2	1622.3	728.1	593.8
56.7	776.3	557.6	648.0	161.8	319.4	368.0	534.4	909.7	199.6	373.2
45.3	1622.3	1659.4	2463.0	629.7	1694.2	1010.0	1196.3	902.5	1543.1	2325.4
61.0	633.4	968.0	1008.2	574.6	667.7	877.4	928.4	514.0	311.3	671.6

367.6	563.0	805.5
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241.4	568.3	186.1
1455.4	1766.4	1382.1
439.1	373.1	552.4
2032.8	2739.0	2399.3
4359.8	3519.4	5779.5
1060.4	1956.4	1122.6
1029.5	1082.8	1438.4
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1422.2	672.3	2214.5
680.7	815.0	597.7
500.3	355.5	276.1
49.2	2770.3	3010.4
6133.1	7034.6	7834.0
1255.7	1056.3	1303.1
2681.0	2523.0	3137.2
7566.5	5190.0	6242.0
7089.0	8607.9	7121.6
155.3	253.3	186.3
744.6	1203.9	1127.4
1368.6	1267.1	1530.3
2484.2	2853.2	2887.8
4935.4	5101.9	5485.0
1730.8	1252.6	1662.1
239.6	246.2	147.3
1080.5	642.0	879.4
829.9	1128.0	738.5
2109.8	2702.6	2466.2
1042.7	1463.0	857.6
3309.8	3053.0	3326.4
3320.3	3654.6	3309.8
2461.4	1032.2	1580.0
3386.5	3660.5	4140.1
4565.6	5517.8	5654.4
880.4	981.2	833.3
2115.2	1497.0	2071.2
1471.3	1236.3	1842.4
218.6	358.4	396.1
1151.8	1151.4	694.6
802.5	783.6	955.4

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AY916317.1 gg_id:113422 human stool clone B395 AY9163
EU510296.1 gg_id:259056 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04c08 EU5102
FJ368701.1 gg_id:368980 feces adult twins and mothers; TS49 clone TS49_a03e03 FJ3687
AM405126.2 gg_id:573969 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.76 AM405
EU456172.1 gg_id:311674 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4561
AY984289.1 gg_id:117903 human stool clone B182 AY9842
DQ808725.1 gg_id:198434 human fecal clone RL239_aaj12d08 DQ808
FJ676459.1 gg_id:531723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU510783.1 gg_id:259781 cecal contents Mus musculus strain C57BL/6J; WD6 clone WD6_aak49c02 EU5107
EU761737.1 gg_id:349087 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7617
EU009784.1 gg_id:256807 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_R38 EU0097
EU463311.1 gg_id:298468 bush dog feces clone bdog1_aai77g08 EU4633
EU771786.1 gg_id:313144 African elephant feces clone AFYEL_aaj65g01 EU7717
EF096345.1 gg_id:185355 mouse cecum clone obob2_aaa01c07 EF0963
DQ809008.1 gg_id:187682 human fecal clone RL243_aai88b05 DQ809
DQ799785.1 gg_id:178610 human fecal clone RL182_aah33e05 DQ799
DQ342332.1 gg_id:174153 Effect probiotics and synbiotics on gastrointestinal broilers broiler chicken intestine DQ342
GQ492903.1 gg_id:593444 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF399415.1 gg_id:207651 human fecal clone SJTU_F_15_57 EF3994
DQ809996.1 gg_id:198555 human fecal clone RL184_aao66h02 DQ809
FJ364704.1 gg_id:358447 feces adult twins and mothers; TS19 clone TS19_a02a09 FJ3647
FJ680441.1 gg_id:527271 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ362631.1 gg_id:361732 feces adult twins and mothers; TS13 clone TS13_a01c08 FJ3626
EU459643.1 gg_id:293128 ring-tailed lemur feces clone RT_aai09h03 EU4596
FJ680851.1 gg_id:521515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EU778329.1 gg_id:313557 feces clone RL116_aaf01d03 EU7783
EU459610.1 gg_id:301862 ring-tailed lemur feces clone RT_aai09c01 EU4596
EU009777.1 gg_id:239053 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_I27 EU0097
FJ367490.1 gg_id:359444 feces adult twins and mothers; TS29 clone TS29_a04b09 FJ3674
NZ_AAXB02000032.1 gg_id:470236 Dorea longicatena str. DSM 13814 NZ_AA
FJ371029.1 gg_id:356903 feces adult twins and mothers; TS5 clone TS5_a04b02 FJ3710
EF604799.1 gg_id:234097 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
DQ798501.1 gg_id:181434 human fecal clone RL181_aan97e05 DQ798
DQ796631.1 gg_id:199154 human fecal clone RL179aan76c06 DQ796
DQ803468.1 gg_id:188970 human fecal clone RL251_aaj86b09 DQ803
DQ014717.1 gg_id:130551 mouse cecum clone M1_h04_1 DQ014
EU767921.1 gg_id:306209 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7679
DQ809818.1 gg_id:188194 human fecal clone RL184_aan84f06 DQ809
EU453069.1 gg_id:355468 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4530
FJ680448.1 gg_id:515629 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
NZ_ACCJ01000522.1 gg_id:469972 Clostridium asparagiforme str. DSM 15981 NZ_AC

41.0	253.2	528.6	643.0	122.5	197.2	99.4	551.5	93.0	80.3	175.4
2084.0	932.6	995.4	571.2	612.3	1069.6	793.0	534.6	959.2	533.7	956.1
114.1	1112.1	1887.9	1883.4	685.8	1297.3	1450.9	1925.2	623.9	241.6	1335.3
67.9	739.9	953.6	1430.7	722.5	651.3	1126.7	900.0	269.4	202.3	486.7
23919.1	6255.4	6152.1	6721.9	6127.5	6731.1	7038.8	5459.9	11148.8	8241.2	13155.1
16901.0	3338.2	3226.4	3489.4	3191.1	3153.1	3415.7	3078.0	5764.2	3882.5	4654.5
47.2	194.3	345.2	315.7	65.5	209.6	42.8	427.1	117.5	52.7	54.5
20837.4	8736.2	6504.3	7836.1	8941.8	7334.8	7675.1	5744.0	7820.7	7204.1	5823.1
1677.6	2918.7	3637.6	3126.3	2446.9	2458.3	2337.9	3035.3	1759.1	1738.9	1746.9
169.1	1019.2	1636.1	1905.8	888.9	1412.4	1694.7	1781.6	555.3	1886.0	685.7
46.0	207.1	349.9	376.2	96.3	286.5	186.6	417.2	108.4	44.3	268.8
433.3	983.4	1175.0	1313.2	1305.0	1090.2	1257.3	1228.7	625.0	988.4	1105.4
700.0	3982.0	4547.6	5578.5	3269.5	3783.0	3961.0	4780.9	5457.0	5194.4	4534.4
66.6	200.0	259.3	158.6	162.9	118.8	185.9	349.3	137.6	71.3	299.2
2421.7	1811.8	1936.1	1697.5	1718.1	1997.9	1881.8	2188.4	2212.6	2146.2	1426.4
3478.3	3393.3	4622.3	3232.8	3333.9	3673.8	3750.5	3996.6	3671.3	5284.1	3336.6
39.4	35.2	79.3	111.9	59.0	54.3	46.7	197.3	24.7	22.9	39.0
222.9	1086.8	1886.5	1720.4	674.8	894.2	816.3	986.5	883.8	811.6	1097.5
70.4	1650.2	1951.4	2154.9	1177.7	1478.6	1759.0	1715.5	1913.3	304.5	1067.1
39.1	252.6	668.1	574.3	591.6	370.5	600.9	1002.7	248.5	146.3	444.8
231.7	1809.5	1733.5	1707.3	1283.8	1699.1	1350.9	2608.7	2332.5	2075.7	1257.1
82.9	409.2	464.6	486.2	363.6	390.3	432.5	553.4	228.4	300.3	319.9
108.8	418.6	545.0	647.2	168.2	439.7	369.4	799.3	190.7	145.2	253.5
4825.1	2231.9	2024.3	2215.5	2815.9	2535.5	2792.4	3294.3	933.3	1284.9	1697.3
1480.8	3629.3	3294.5	3992.0	4340.1	3841.0	5057.4	4222.5	4456.5	2604.1	3075.6
7039.2	3582.7	3458.6	2911.9	2912.2	3099.1	2765.2	3111.3	4337.8	3706.3	3399.5
14215.3	3848.0	3916.0	4079.1	3281.2	3416.0	4256.3	3529.5	5626.2	4149.2	5102.1
37.5	1135.8	2003.3	2659.5	213.7	1212.2	459.4	2316.8	234.3	188.4	631.9
301.0	1802.4	2141.5	2092.6	1133.5	1639.8	1340.8	2343.0	1498.5	1387.9	1421.1
68.2	1372.7	2541.8	2438.4	744.6	1744.2	2008.9	1875.7	727.0	275.5	1634.7
88.4	2092.6	1809.5	2575.1	1191.4	1670.5	1374.8	1668.8	732.4	184.2	1690.5
17155.3	6571.9	6278.7	6334.6	6425.9	6178.6	8603.6	5763.0	8402.0	5196.4	9712.7
3986.7	3255.8	2895.2	1756.4	3168.2	2659.0	3037.3	2635.2	3135.0	2309.1	3525.7
3633.5	4182.4	2783.2	3654.5	2609.8	3331.8	2609.5	2624.7	2281.6	4687.0	2969.4
251.1	875.8	1069.6	1748.5	988.1	1062.8	1160.0	1459.2	1431.7	951.1	1585.4
119.2	1753.4	1468.8	2172.3	1075.1	1585.7	1567.3	1423.9	1083.7	1652.9	1053.8
2935.9	983.4	1431.8	1795.8	905.0	1015.8	906.5	1648.5	636.1	538.2	781.4
61.7	1625.1	2010.0	2226.2	1871.0	1452.1	1592.6	1896.2	808.8	432.4	1288.2
91.0	415.3	814.8	841.6	487.9	735.6	425.2	880.3	193.2	405.6	333.2
9949.6	4096.9	3470.5	3483.5	3138.0	3401.6	3483.9	4012.1	5711.3	4841.5	3500.2
78.0	1168.4	1448.4	1797.2	1162.4	1205.0	1388.8	1838.8	630.2	340.6	773.8

405.1	413.8	466.0
423.6	1400.1	704.0
1729.5	1111.4	1763.0
881.6	634.7	928.6
5531.4	6703.4	6331.2
2757.4	4326.4	3199.2
265.3	371.4	76.9
6731.7	9881.5	7141.6
3187.6	2976.9	3716.6
1918.8	1659.8	1595.6
503.3	258.0	350.0
1179.9	1005.4	1333.0
4706.9	4515.4	4675.1
120.5	302.4	215.8
1774.8	2760.9	1909.1
4041.3	4530.5	4784.4
307.4	46.6	35.8
1293.6	1330.0	1120.3
2175.3	1256.4	2392.8
708.3	686.1	999.7
2939.4	1898.0	2643.3
701.4	610.1	467.4
1041.5	572.9	845.9
3929.0	2352.0	3483.8
4100.2	3894.1	4564.0
2930.0	4044.5	3312.3
4009.0	4245.5	3384.3
3449.6	1563.9	1781.9
2744.2	1935.8	2208.7
1390.0	1388.9	1688.9
1355.3	1123.0	1558.9
5735.8	8118.3	6222.8
2791.4	3052.2	2837.5
3217.5	4339.9	2910.5
857.2	1777.0	1505.5
2306.4	1874.2	1322.2
1755.0	1841.4	1636.8
1871.0	1169.3	2180.7
869.2	862.3	1030.2
4699.0	4246.7	4725.2
2147.9	1413.9	3179.5

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FJ365573.1 gg_id:369227 feces adult twins and mothers; TS20 clone TS20_a04e01 FJ3655
DQ905776.1 gg_id:167098 human fecal clone 29A-g7 DQ905
DQ807951.1 gg_id:196160 human fecal clone RL180_aan69f04 DQ807
FJ676983.1 gg_id:525798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ681024.1 gg_id:515999 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EU456668.1 gg_id:335149 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU456
EU767879.1 gg_id:350481 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ364032.1 gg_id:364034 feces adult twins and mothers; TS150 clone TS150_a02b10 FJ3640
DQ796690.1 gg_id:198124 human fecal clone RL179_aao53c04 DQ796
EU509687.1 gg_id:261368 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak47b05 EU509
EU463375.1 gg_id:298858 bush dog feces clone bdog1_aai80e02 EU463
FJ367507.1 gg_id:358064 feces adult twins and mothers; TS29 clone TS29_a04d03 FJ3675
DQ805157.1 gg_id:193769 human fecal clone RL249_aaj82b11 DQ805
FJ370811.1 gg_id:362280 feces adult twins and mothers; TS5 clone TS5_a01e09 FJ3708
EU510136.1 gg_id:261334 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01h03 EU510
EF098609.1 gg_id:197240 mouse cecum clone SWPT16_aaa02b03 EF0986
EF098496.1 gg_id:189905 mouse cecum clone SWPT15_aaa04c05 EF0984
EU461086.1 gg_id:297708 red kangaroo feces clone KO1_aai43h08 EU461
EF098635.1 gg_id:191772 mouse cecum clone SWPT16_aaa02e02 EF0986
EU467257.1 gg_id:299536 black-handed spider monkey feces clone SPIM_d12_1 EU467
FJ363999.1 gg_id:370424 feces adult twins and mothers; TS150 clone TS150_a01g11 FJ3639
DQ799835.1 gg_id:197134 human fecal clone RL182_aah34f05 DQ799
GQ492902.1 gg_id:550531 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF025255.1 gg_id:177762 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F17 EF0252
DQ456162.1 gg_id:158542 pre-adolescent turkey cecum clone CFT29B5 DQ456
EU767769.1 gg_id:352786 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
AF499906.1 gg_id:83271 human colonic mucosal biopsy clone ABLCf11 AF499
EU794106.1 gg_id:334661 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_U22 EU794
FJ678586.1 gg_id:522277 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ057365.1 gg_id:132892 chicken ileum/cecum clone cc112 DQ057
DQ325863.1 gg_id:149131 Metagenomic gut microbiome healthy human stool clone B647 DQ325
EU768387.1 gg_id:322204 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ673162.1 gg_id:522205 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ370677.1 gg_id:356832 feces adult twins and mothers; TS57 clone TS57_a03h07 FJ3706
EU459600.1 gg_id:294988 ring-tailed lemur feces clone RT_aai09a08 EU459
GQ491319.1 gg_id:542096 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU459747.1 gg_id:296770 ring-tailed lemur feces clone RT_aai12b05 EU459
EF098200.1 gg_id:183362 mouse cecum clone SWPT14_aaa02h11 EF0982
FJ685226.1 gg_id:512257 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
EU503833.1 gg_id:269103 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01c06 EU503
DQ799122.1 gg_id:197783 human fecal clone RL205_aaj17h06 DQ799

489.1	3330.1	2449.7	2752.7	1257.9	2212.3	1688.1	2487.6	1804.8	1980.6	1592.3
406.0	3072.3	3414.3	3597.5	2460.6	3053.4	3159.6	4604.8	2721.5	1458.2	2512.3
41.2	149.1	274.5	323.7	136.2	300.0	92.9	290.2	204.9	257.4	47.2
1199.3	2529.0	3979.3	4000.7	1676.4	2727.0	2383.8	3174.9	1987.4	1072.6	2732.9
19421.6	9710.7	7513.0	7358.2	6895.7	7646.6	7120.5	7729.7	8163.8	6379.6	8684.0
102.3	1600.9	2222.3	2871.4	1818.9	1830.7	2423.3	2111.3	517.7	220.1	899.2
51.3	668.6	1170.3	1406.6	285.3	692.7	705.1	1020.6	303.9	137.4	723.0
52.2	1319.3	1782.0	2258.4	771.9	1099.9	1274.6	1493.5	1359.1	646.0	1150.6
1226.3	2033.2	2304.4	2144.9	2147.4	2238.5	1911.4	2654.4	1894.4	3332.3	1402.6
4169.2	1326.1	1769.8	2459.2	2091.1	1461.1	2007.2	2355.7	1583.2	842.1	1162.7
51.1	402.0	602.0	739.4	545.2	450.7	567.7	485.6	198.6	86.4	235.8
21240.2	4705.1	4787.7	4784.0	4859.0	4406.3	4995.5	4341.4	5520.5	6339.0	6185.6
3181.5	1738.9	2180.5	1857.3	1348.5	1518.7	1597.3	1987.7	917.2	1773.4	1664.4
54.7	992.6	1709.8	1710.7	614.5	1710.8	709.2	1712.7	433.8	1827.5	1178.3
44.2	961.8	1555.8	1468.8	685.0	569.3	735.4	666.8	314.7	206.2	452.9
347.9	585.5	664.5	565.1	642.0	741.2	782.7	781.2	424.0	649.5	528.3
12534.2	6891.8	7074.6	7028.4	7236.7	6737.3	7410.6	6916.7	6977.4	5420.5	8991.4
1800.6	2808.4	3738.7	3344.8	2007.6	2769.0	2564.1	3684.7	2227.2	1720.9	3575.4
49.4	261.5	330.6	444.1	150.8	216.4	188.7	331.4	80.4	72.3	124.9
96.7	639.3	851.0	874.4	288.1	786.5	491.0	1501.8	308.6	380.8	353.5
53.8	471.8	787.3	784.9	167.5	500.4	384.9	876.1	297.9	221.4	393.8
337.9	1471.9	1863.7	1731.2	1310.3	1642.4	1503.7	1959.2	1612.7	2900.7	1309.8
78.4	209.5	296.9	243.4	126.5	219.5	127.0	310.0	61.3	219.8	175.3
96.0	1763.9	2727.5	2622.6	1515.1	2023.9	2026.2	2967.7	887.1	612.8	1552.4
24919.8	7656.8	6779.6	6887.2	6434.5	6446.0	6377.2	5518.0	7445.6	6642.8	6999.6
54.0	296.2	392.3	517.6	134.0	227.2	142.1	344.2	123.5	267.6	169.6
59.8	763.0	611.5	549.7	345.2	512.3	400.5	914.1	975.8	198.0	489.1
726.0	3353.3	4072.8	4757.8	3544.2	3305.0	3541.8	4328.9	3588.6	2329.5	2938.3
419.1	822.2	1022.3	1078.3	842.6	1071.8	1116.3	1710.2	564.2	865.9	541.3
63.3	350.4	607.7	602.9	125.7	439.7	264.4	614.9	122.0	104.1	331.5
36.3	306.0	488.7	505.7	159.8	318.2	383.6	220.9	167.2	308.9	299.9
2853.5	1216.7	1554.5	1358.3	876.8	1124.3	898.8	1125.3	1122.6	1025.8	1291.2
9145.3	3761.1	3395.3	3466.4	3228.5	3166.3	3845.3	3000.0	5178.5	2071.0	4388.1
47.7	191.5	340.4	406.0	123.9	176.9	213.7	245.0	46.3	54.2	128.9
41.2	771.9	1076.9	1548.6	547.8	704.2	714.5	947.8	282.9	100.0	184.3
1743.0	1391.0	1708.5	1437.4	1196.5	1758.0	1414.2	2354.8	771.5	1268.7	1008.1
1295.5	3762.6	3440.0	3299.2	3246.2	3192.2	3409.7	3889.8	3087.8	2393.0	3398.5
114.0	1482.5	1985.0	2244.8	1710.8	1671.8	1682.0	2144.8	1132.6	356.1	1396.1
78.6	3265.3	3676.0	4055.6	3053.4	2784.2	3961.4	3039.9	2569.8	1996.0	3233.3
67.5	1535.8	2049.1	2167.8	1019.6	1679.5	1152.4	1989.8	1735.9	1882.4	1066.9
41.3	331.7	234.3	248.1	78.3	251.6	88.4	823.6	43.3	68.6	123.4

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372.3	462.7	142.4
3314.9	3480.0	4415.2
8474.8	7009.2	8902.4
3771.1	2085.6	2167.3
1103.9	1026.8	1137.2
1937.0	1486.0	1477.3
3134.3	2649.5	3874.0
3833.2	2449.2	3080.1
606.9	618.8	330.7
4731.3	6579.7	5002.2
1671.9	2569.1	2083.6
1355.9	1528.5	2927.5
1379.0	1085.3	2000.5
688.4	679.7	929.4
6447.5	8134.2	6990.6
2862.8	3810.2	3013.8
311.2	311.2	743.7
1393.9	1339.3	1998.2
1060.5	291.8	857.5
2112.6	2081.3	421.1
214.3	193.2	420.5
3307.7	2311.3	3730.0
6823.3	5365.8	6235.9
256.4	305.0	179.3
739.9	892.6	606.1
4965.9	3824.2	5184.0
2266.0	1288.2	2306.6
630.3	406.5	289.5
368.8	475.2	715.4
1341.5	1577.9	1302.4
2785.4	3974.8	3348.2
218.1	360.1	164.4
1125.3	520.7	1017.5
2478.9	1436.2	2166.3
4220.2	3609.3	3963.8
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2607.8	1904.0	2934.0
897.8	242.4	322.4

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EF098375.1 gg_id:195470 mouse cecum clone SWPT15_aaa01h03 EF0983
EU510719.1 gg_id:269618 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39h10 EU5107
EU768430.1 gg_id:326928 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7684
FJ675705.1 gg_id:517846 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ824939.1 gg_id:180216 human fecal clone RL185_aao71c05 DQ824
EU775513.1 gg_id:323595 Western lowland gorilla feces clone GORSD_aaa01c09 EU7755
EU778621.1 gg_id:316740 Ring-tailed lemur feces clone RT_aai10e02 EU7786
EF095977.1 gg_id:181683 mouse cecum clone lean2_aaa01c05 EF0959
DQ797241.1 gg_id:184394 human fecal clone RL386_aao88g09 DQ797
GQ896927.1 gg_id:554259 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU772874.1 gg_id:316781 Bush dog feces clone bdog1_aai79d12 EU7728
AY978223.1 gg_id:117538 human transverse colon mucosal biopsy clone F032 AY9782
EU451143.1 gg_id:351734 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4511
DQ798482.1 gg_id:180957 human fecal clone RL181_aan97c07 DQ798
DQ806976.1 gg_id:197405 human fecal clone RL198_aaj76d11 DQ806
EF614705.1 gg_id:231146 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
EU454651.1 gg_id:352861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75M EU4546
AY984335.1 gg_id:125016 human stool clone B234 AY9843
EF098022.1 gg_id:199550 mouse cecum clone SWPT12_aaa04b11 EF0980
EU454185.1 gg_id:335430 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4541
DQ794783.1 gg_id:187360 human fecal clone RL240_aaj32c10 DQ794
DQ279737.1 gg_id:141412 Clostridium citroniae str. RMA 16102 DQ279
EF098354.1 gg_id:190273 mouse cecum clone SWPT15_aaa01d07 EF0983
AB234505.1 gg_id:149725 termite gut homogenate clone MgMjW-36 AB2345
GQ047220.1 gg_id:424615 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010b GQ047
DQ353932.1 gg_id:146448 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z86 DQ353
DQ456197.1 gg_id:157470 pre-adolescent turkey cecum clone CFT29E6 DQ456
GQ867559.1 gg_id:573341 and prevalence blaTEM genes Arctic seals colon content clone CSH64 GQ867
EU531926.1 gg_id:258392 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5319
EF025272.1 gg_id:175640 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N3 EF0252
EU452062.1 gg_id:352160 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4520
DQ014807.1 gg_id:132092 mouse cecum clone M1_h08_2 DQ014
AY978473.1 gg_id:119101 human transverse colon mucosal biopsy clone KP30 AY9784
EF097959.1 gg_id:180717 mouse cecum clone SWPT12_aaa02h07 EF0979
EF098965.1 gg_id:181568 mouse cecum clone SWPT1_aaa04a07 EF0989
DQ797248.1 gg_id:198490 human fecal clone RL386_aao88h07 DQ797
EF614514.1 gg_id:230096 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EF614857.1 gg_id:232638 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
DQ815496.1 gg_id:171989 mouse cecum clone aab41f05 DQ815
GQ491971.1 gg_id:559976 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AY975738.1 gg_id:125725 human ascending colon mucosal biopsy clone Y188 AY9757

38.4	32.8	43.1	37.9	30.3	38.0	22.7	29.5	24.2	19.4	23.4
38.4	761.4	1405.6	1999.5	71.1	228.5	150.4	516.7	63.6	31.9	304.2
64.1	2471.5	2494.4	2513.7	3019.1	2215.3	3042.7	2111.0	2211.9	1502.8	2057.5
299.1	1079.3	1407.6	1477.8	491.1	842.4	733.3	1304.2	782.7	808.7	1080.5
109.0	1422.1	1734.9	1712.2	2132.6	1579.0	1482.5	2431.1	1227.9	1631.9	1410.6
7253.5	5641.7	5576.3	6380.5	4863.6	5462.1	6622.1	4872.6	6731.7	5346.9	7723.9
255.9	561.6	843.4	1183.0	347.8	678.8	708.1	660.6	208.6	1019.6	396.1
1016.0	3314.7	3178.9	3193.7	2880.9	3006.4	2717.9	2977.6	4186.1	2973.6	2551.0
37.5	402.6	611.3	725.1	421.4	485.9	502.7	528.1	306.0	212.6	207.3
4737.8	3214.1	3302.5	3483.1	3883.1	3224.6	3605.1	3243.1	2636.8	2990.1	2842.8
54.1	639.7	644.3	282.6	357.5	397.5	339.5	402.7	208.4	105.0	187.4
149.8	2231.2	2588.7	2114.0	256.9	1955.7	1222.1	2548.9	2204.2	2854.6	2313.3
68.8	1365.3	1866.2	1944.9	765.9	1111.1	1206.9	1519.7	680.7	218.6	1054.1
42.9	54.3	99.1	81.9	45.2	52.2	43.1	47.5	17.8	20.4	50.8
38.0	343.5	572.5	259.8	280.7	669.8	264.2	738.9	203.1	143.9	273.1
830.3	2813.8	3531.3	2535.6	1418.7	2477.5	2010.7	2595.3	3621.5	3448.4	2871.7
170.9	671.4	883.3	966.0	898.3	865.3	822.3	1033.1	554.3	1010.0	436.0
568.2	2733.5	3959.7	3849.7	3954.7	3138.1	4175.1	5400.3	8165.5	4306.0	2706.9
34.3	16.3	20.0	25.9	14.7	14.2	14.5	16.9	13.3	14.9	13.0
1052.5	1626.4	1569.9	1118.0	1167.3	1540.1	1225.6	1267.3	1059.7	3012.5	862.8
27.6	442.3	506.3	572.3	87.1	522.5	276.1	599.6	44.5	77.1	222.8
215.5	498.5	766.0	999.8	471.3	601.3	574.7	884.2	270.8	153.1	301.9
42.7	530.2	662.4	564.4	470.1	421.9	571.8	537.7	286.5	146.9	512.2
55.8	3016.5	3827.0	3775.1	942.7	2699.2	2069.5	4037.2	1702.6	645.3	3113.3
22954.8	7037.0	6450.2	7073.2	8307.9	6936.0	8422.6	6493.9	6612.0	5895.7	7949.2
40.5	54.1	128.7	158.7	40.4	106.2	36.9	85.3	60.0	26.0	37.3
61.3	401.3	661.5	662.6	475.8	446.3	501.3	595.4	154.7	196.7	316.6
11166.6	6396.0	6261.3	5367.0	5312.6	5191.4	6051.3	5468.7	8810.7	10265.5	5282.9
271.5	2276.1	2942.9	2653.0	1474.5	2012.0	1430.5	2392.3	1907.9	2254.8	1492.8
2441.8	2488.9	2840.0	1960.5	1542.7	2373.5	2188.2	2662.1	2076.4	1526.6	3242.1
3010.8	1798.1	1553.2	1611.5	1722.1	1610.5	1497.1	1634.1	1422.7	1257.4	1481.4
44.0	48.0	203.5	263.7	56.2	67.0	19.6	486.8	40.7	24.1	101.2
1118.2	4614.3	4122.0	4339.3	2415.6	3807.7	2780.1	3595.9	4906.6	3666.6	3398.7
11909.7	4329.3	4387.7	4479.4	4670.0	4190.4	4509.9	3867.3	7267.5	5063.5	6078.7
144.1	1457.3	2028.0	2230.5	1296.8	1559.8	1249.6	2263.9	789.9	1114.1	1061.6
2738.8	686.6	828.4	814.1	625.3	634.2	876.9	849.0	704.0	476.9	760.6
75.0	416.6	698.8	808.4	297.8	440.5	553.6	609.1	84.1	58.0	344.8
10747.2	5560.0	5430.2	6250.8	5903.9	6010.7	5951.5	5643.0	6074.0	4193.8	7069.3
3858.8	2000.7	2324.6	2267.9	1838.9	1954.3	1922.5	2157.9	1718.2	2147.9	1698.5
655.1	2592.1	2308.1	2387.2	2007.3	2301.5	2174.1	2702.7	4898.5	2752.5	2500.5
35.4	235.2	495.7	429.1	123.5	494.2	208.9	491.9	159.8	75.2	289.3

38.9	52.2	51.0
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2108.7	2135.1	3277.3
1392.3	1314.1	1282.3
2753.2	2260.8	1368.0
4579.2	5040.5	5870.4
1640.1	1344.2	1537.0
3130.1	3996.4	3872.5
409.6	634.2	1403.1
3545.6	4483.5	3714.9
330.3	333.5	473.4
2525.8	2072.2	2225.7
1682.3	1438.6	2187.3
52.2	91.4	47.9
620.5	767.6	962.8
3173.8	2952.6	2321.5
1324.3	958.3	1260.1
2595.8	4263.1	4132.8
16.1	15.6	15.3
1338.6	1426.3	1029.4
1215.3	411.9	858.4
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360.2	514.8	685.9
4648.9	2257.6	3266.3
7158.0	7645.1	8864.1
128.9	165.8	45.8
653.3	743.5	905.7
5135.8	6775.8	5724.7
2538.5	2243.2	2995.4
2508.0	2484.9	2103.5
1336.7	2105.5	1913.7
192.2	188.1	61.9
4156.0	4515.4	4262.7
3729.4	4995.9	3632.5
2187.6	2298.2	2269.9
691.7	1384.6	759.0
643.9	452.0	594.6
5497.3	6249.2	5788.4
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2486.5	2763.7	2538.1
779.0	340.6	546.2

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FJ365651.1 gg_id:369032 feces adult twins and mothers; TS21 clone TS21_a01d07 FJ3656
FJ440041.1 gg_id:510813 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
EF096677.1 gg_id:192991 mouse cecum clone SWPT11_aaa03a03 EF0966
EU452637.1 gg_id:314945 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4526
EU457171.1 gg_id:311466 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4571
EU508167.1 gg_id:276240 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02c06 EU5081
NR_026409.1 gg_id:559837 Desulfotomaculum guttoideum str. DSM 4024 NR_026
AY977745.1 gg_id:123816 human cecum mucosal biopsy clone LE16 AY9777
FJ880789.1 gg_id:458831 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU776090.1 gg_id:346658 Spotted hyena feces clone HY1_e08_2 EU7760
EF614550.1 gg_id:229302 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6145
EU767569.1 gg_id:311176 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7675
EU510621.1 gg_id:263896 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38d01 EU5106
AF092549.1 gg_id:52289 Clostridium algidixylanolyticum str. SPL73 AF0925
EU457056.1 gg_id:318912 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4570
EU776542.1 gg_id:319417 Lion feces clone LI3_aah77g11 EU7765
DQ798202.1 gg_id:182631 human fecal clone RL302_aal96g08 DQ798
EU511054.1 gg_id:264774 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal02a07 EU5110
GQ493516.1 gg_id:542055 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY992804.1 gg_id:131095 mouse cecum clone C22_c07 AY9928
AY991713.1 gg_id:135440 mouse cecum clone C20_a06 AY9917
GQ492799.1 gg_id:583974 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF099655.1 gg_id:177473 mouse cecum clone SWPT4_aaa02e04 EF0996
EF096370.1 gg_id:183391 mouse cecum clone obob2_aaa01f11 EF0963
FJ680759.1 gg_id:514398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
GQ867532.1 gg_id:587724 and prevalence blaTEM genes Arctic seals colon content clone CSH36 GQ867
AY353957.1 gg_id:103489 Clostridium amygdalinum str. BR-10 AY3539
EF098651.1 gg_id:197167 mouse cecum clone SWPT16_aaa02g06 EF0986
EU451387.1 gg_id:351209 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4513
EF097514.1 gg_id:189187 mouse cecum clone SWPT19_aaa03f12 EF0975
EF098106.1 gg_id:174540 mouse cecum clone SWPT14_aaa01e12 EF0981
EU507818.1 gg_id:272778 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01d02 EU5078
EF614747.1 gg_id:233250 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6147
FJ365805.1 gg_id:361998 feces adult twins and mothers; TS21 clone TS21_a03c06 FJ3658
AY984860.1 gg_id:119032 human stool clone B831 AY9848
DQ015443.1 gg_id:135545 mouse cecum clone M3_b07_1 DQ015
AB234506.1 gg_id:146502 termite gut homogenate clone MgMjW-10 AB2345
EU509027.1 gg_id:261702 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42c01 EU5090
FJ370740.1 gg_id:357463 feces adult twins and mothers; TS57 clone TS57_a04f09 FJ3707
EU457966.1 gg_id:330827 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU4579
DQ800914.1 gg_id:187219 human fecal clone RL387_aao89c01 DQ800

40.8	483.7	927.4	1005.2	108.9	474.4	233.1	856.1	166.0	72.0	366.0
881.0	2150.2	2890.4	3383.5	1477.4	2078.2	1769.5	3368.4	756.6	421.6	1478.2
355.2	2875.2	2378.6	1826.9	1766.1	2087.6	1693.8	2151.3	2176.4	2538.9	1574.0
32.3	28.9	27.7	31.2	35.0	26.8	30.1	24.8	27.0	27.0	29.4
37.5	602.7	982.2	1655.9	72.4	306.5	149.9	583.8	70.4	63.5	176.6
4295.9	3395.6	3968.9	4037.5	4258.6	3429.8	4097.1	4025.4	2153.6	1763.7	2804.8
93.2	1016.7	1655.6	1619.0	468.9	1377.8	1125.4	2488.2	426.4	269.7	1729.5
6433.8	1259.6	1441.2	1299.9	1040.9	1216.7	1610.5	1157.4	1155.0	1259.3	1285.0
87.0	639.3	850.8	787.1	389.8	418.7	384.8	798.1	358.5	128.9	438.5
203.1	1032.5	1319.6	1447.2	1328.1	912.3	1206.9	1410.2	1410.3	1865.3	1365.9
59.0	1475.8	2177.2	3025.8	978.7	934.3	974.4	1330.3	387.6	294.6	1154.2
287.1	1290.2	1224.1	1059.4	1097.2	1185.8	1245.7	1342.5	1612.7	1555.4	908.2
630.7	1001.2	1214.2	791.4	649.0	794.8	1105.5	1459.4	1171.3	982.1	1027.2
118.9	2128.1	3038.0	3657.0	1615.9	2681.4	2400.8	5575.6	861.3	531.8	2444.6
19318.5	6325.9	6277.7	6851.1	5878.6	6261.6	6552.4	6200.3	9478.7	7403.8	9156.2
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452.0	1718.9	1520.7	1675.8	2038.7	1415.2	1363.7	2815.5	1266.8	589.4	1380.3
43.9	53.6	137.8	153.7	19.1	41.1	51.8	128.7	25.2	30.1	61.0
13046.1	6215.1	5618.1	6155.6	6728.9	5504.3	6171.8	5895.1	7039.0	9432.3	6693.4
190.6	1870.3	2348.4	2237.6	2116.7	2541.1	1753.2	2392.9	1261.2	1701.4	1415.8
157.3	69.0	88.7	121.0	129.7	76.3	113.8	67.9	30.2	56.3	47.1
13303.4	6466.4	6478.4	6412.6	6926.5	5904.5	7377.0	6482.6	10249.2	6321.4	7580.5
56.3	213.8	249.6	269.9	77.4	231.0	114.3	279.6	60.4	63.3	73.3
57.5	283.8	478.4	364.1	192.6	317.2	240.8	340.4	212.9	70.2	270.1
630.8	3717.1	4432.1	4857.8	4179.6	3574.8	5044.2	4166.2	2847.3	2493.7	4205.9
94.3	5384.3	4114.1	2296.8	1870.5	2509.9	3333.5	3962.5	6832.2	4514.6	3407.3
122.2	1262.9	1785.8	2147.4	665.1	1558.4	1245.3	4077.6	494.3	513.1	1438.7
1450.7	1750.9	1929.2	1773.4	1444.3	2049.9	2179.9	1787.4	1115.5	1399.7	2414.2
11217.6	3665.4	3398.1	3497.1	3266.0	3489.1	3430.0	3849.2	5636.0	4570.9	4303.0
9165.9	4426.3	4165.4	4457.6	3407.6	4664.4	4573.2	4796.3	5024.5	4435.9	4992.0
301.8	2386.9	3036.9	3055.9	3154.0	3087.2	2700.1	3369.9	2507.6	3509.1	2140.1
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2699.1	2327.7	2166.6	1923.6	1721.3	1958.4	1490.8	2175.9	1972.7	1285.8	1987.8
529.5	219.0	512.5	614.3	154.9	330.2	150.3	415.2	59.3	176.2	152.8
352.7	1375.1	2253.6	1943.8	1308.6	1793.3	1385.9	2534.0	901.7	424.9	1490.2
668.3	1512.5	1685.8	1294.8	855.6	1113.5	1114.5	1324.5	1466.1	810.9	1376.3
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246.8	2872.9	3891.8	3577.0	1993.3	2817.0	2099.6	3490.3	1688.1	1399.7	1935.9
1901.6	2693.7	2660.6	2399.2	2415.2	2494.6	1973.9	3279.1	1669.1	4120.2	2012.1
1922.6	2955.6	3406.2	3239.9	2588.9	2564.3	3293.9	2982.7	2519.7	1338.2	3122.8

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4257.3	2372.6	3501.2
2189.8	2647.4	2619.1
28.8	27.8	35.5
1082.4	584.3	399.0
4834.5	3458.7	5300.2
3791.7	1063.9	1869.9
1225.2	1582.7	1298.5
627.9	572.9	596.8
1085.9	1457.5	1894.6
1087.8	1231.3	1565.5
1182.0	1597.7	1084.5
845.1	1403.1	914.2
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73.2	68.8	126.2
7369.7	7199.8	6836.2
2773.8	2156.9	2863.6
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516.7	580.7	465.5
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2332.5	1753.9	2895.0
5965.0	1326.5	3677.7
1245.1	2488.1	1421.3
3542.7	4391.6	3427.6
3658.2	4786.7	4961.9
3622.2	2686.0	3391.9
7058.3	8367.9	8583.6
1998.7	2602.2	1816.2
460.5	547.9	225.4
3233.0	2430.3	2818.2
1027.4	1448.4	980.1
20.0	24.5	32.3
4292.2	6241.9	4033.1
4595.9	2763.6	4473.1
2595.9	2587.0	2408.9
3649.5	2466.5	3655.3

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EU768688.1 gg_id:353667 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
GQ491558.1 gg_id:586550 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801140.1 gg_id:195881 human fecal clone RL387_aao92h01 DQ801
FJ370445.1 gg_id:365964 feces adult twins and mothers; TS57 clone TS57_a01b09 FJ3704
EU773398.1 gg_id:336380 Black lemur feces clone BKLE_a10_2 EU773
EU509201.1 gg_id:263138 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45g06 EU509
DQ905099.1 gg_id:161968 human fecal clone 002C-a12 DQ905
EU778925.1 gg_id:320055 Black-handed Spider Monkey feces clone SPIM_f09 EU778
AY993032.1 gg_id:129499 mouse cecum clone C22_p16 AY993
EU455030.1 gg_id:348772 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU455
DQ326829.1 gg_id:146345 Metagenomic gut microbiome healthy human stool clone E306 DQ326
EU509143.1 gg_id:259818 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44g03 EU509
EF096881.1 gg_id:187921 mouse cecum clone SWPT13_aaa02b10 EF0968
EU474306.1 gg_id:301475 western lowland gorilla feces clone GORSD_aaa02a05 EU4743
EU457851.1 gg_id:308032 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4578
EF096575.1 gg_id:173922 mouse cecum clone SWPT11_aaa01c11 EF0965
EU508162.1 gg_id:261380 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02b10 EU508
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EU455805.1 gg_id:346278 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4558
EU510123.1 gg_id:272390 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01f11 EU510
EU457007.1 gg_id:346275 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75M EU457
EU459640.1 gg_id:296042 ring-tailed lemur feces clone RT_aai09g10 EU459
EF098240.1 gg_id:196497 mouse cecum clone SWPT14_aaa03e03 EF0982
EU508949.1 gg_id:259909 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap40a10 EU508
GQ493246.1 gg_id:545473 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
Y18184.1 gg_id:26602 Clostridium indolis str. DSM 755 Y18184
EU506499.1 gg_id:259653 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03a06 EU506
FJ369112.1 gg_id:367707 feces adult twins and mothers; TS4 clone TS4_a04d05 FJ3691
EF096597.1 gg_id:178199 mouse cecum clone SWPT11_aaa01f04 EF0965
EU511885.1 gg_id:261220 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10e04 EU511
EU454984.1 gg_id:328536 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
FJ370230.1 gg_id:359949 feces adult twins and mothers; TS56 clone TS56_a02b02 FJ3702
EF098306.1 gg_id:181133 mouse cecum clone SWPT14_aaa04e07 EF0983
AY993145.1 gg_id:135431 mouse cecum clone C21_g02 AY993
EU458073.1 gg_id:315358 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU458
GQ491281.1 gg_id:583045 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU509952.1 gg_id:269949 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24c03 EU509
EU504399.1 gg_id:266896 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03f03 EU504
EU457908.1 gg_id:309360 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
EU450910.1 gg_id:333069 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU450

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821.1	1302.0	1557.5	1934.4	2017.4	1167.2	1715.7	1484.4	301.0	387.6	845.1
8925.9	8815.2	7077.4	7577.6	7241.3	6890.1	7481.3	7175.8	9016.7	6969.6	9258.1
1900.7	1966.2	2702.9	3591.9	2187.3	2277.0	2446.7	3011.1	1465.2	1004.5	1816.2
2933.1	2898.3	2539.3	2770.2	2330.1	2408.4	2324.5	2502.5	3052.2	1749.0	1753.1
163.6	1046.7	1709.5	1446.4	719.3	1083.9	1263.7	1279.5	609.1	271.9	874.1
37.9	940.8	1545.0	1828.2	716.4	1058.7	1107.8	2940.9	386.5	369.4	553.7
5358.4	2651.7	3229.7	3711.2	2676.6	2884.5	3748.0	3431.9	2733.1	2561.9	3576.9
46.6	1171.7	1713.4	2155.3	302.3	890.3	559.4	1473.3	232.7	129.0	754.6
4874.7	3837.3	3882.9	3316.0	3544.2	3330.9	3814.6	3736.1	6071.4	4355.5	3737.6
84.6	1795.3	2405.5	1748.8	1722.5	2254.4	1530.7	1869.7	2668.6	2047.4	1676.1
36.3	51.7	87.8	87.5	22.6	38.6	27.9	66.7	38.2	32.2	53.7
4205.8	1655.3	2040.8	2006.4	1518.1	2202.3	2291.7	2100.2	1318.2	124.8	1680.5
48.6	152.0	287.7	313.7	208.8	204.7	348.9	391.9	54.3	113.7	262.3
2035.9	1664.8	2129.2	1950.8	1086.9	1516.9	1202.7	2667.0	972.9	462.4	1365.1
3640.0	2223.9	2461.1	2664.9	2369.7	2445.2	3022.9	2597.8	2228.0	1640.8	2715.6
653.8	1479.5	1489.9	1725.5	2013.7	1299.7	1612.0	1445.0	1302.3	484.6	1308.4
7443.8	2478.7	3069.7	3398.2	2278.2	2899.7	2605.2	2685.6	3270.9	3180.4	3500.3
7875.7	3640.1	3615.7	3701.2	3212.0	3789.2	3838.7	3407.7	3037.5	2869.3	3941.1
1665.1	1545.2	1493.5	1430.6	1495.4	1473.2	1446.7	1170.8	2757.6	2347.5	1931.4
42.0	107.0	124.1	142.4	34.2	86.1	42.8	99.0	40.0	27.3	95.8
61.1	1355.7	1556.9	2481.6	695.2	843.5	575.3	1165.9	367.0	250.5	637.5
188.0	1262.4	1670.0	1767.6	899.0	1168.3	1104.4	1757.4	699.8	431.1	909.5
1400.2	1813.2	2367.0	2657.3	1785.0	2440.5	3034.4	2815.3	989.9	892.0	1981.5
66.6	63.2	63.1	64.7	65.8	50.9	56.3	71.1	32.6	24.8	43.1
3144.7	1175.5	1338.3	1356.7	1365.2	1383.4	1195.4	1362.7	1009.1	1723.3	813.7
28.4	961.1	1486.5	1999.4	255.7	1322.8	939.5	3749.7	345.8	1543.2	817.1
151.2	1861.2	1826.0	2264.5	1683.9	1678.1	1275.9	2897.6	1160.4	335.6	2238.5
4827.9	4135.0	4408.2	4535.2	3717.1	3809.3	3806.0	4135.2	4148.5	3127.7	3674.7
7306.8	2313.8	2937.3	2131.3	1836.5	1996.8	2375.5	1662.2	2425.4	3503.8	2362.1
609.6	2334.2	2390.8	1982.1	1607.3	1788.7	2414.8	2371.3	2308.5	1740.1	2913.5
610.9	1331.0	2167.8	1944.1	1008.4	996.7	834.6	1343.9	545.7	733.6	814.4
1525.7	3401.5	3372.3	3720.6	2374.7	2967.8	2903.7	3622.8	3435.6	2334.2	3780.7
773.5	1014.8	1140.9	1295.8	1242.8	1114.6	1164.3	1352.9	656.9	1042.2	974.4
937.1	1252.6	1717.2	1816.7	1810.8	1409.9	1728.8	1714.7	992.5	1465.8	896.2
56.2	184.8	417.8	438.8	66.7	153.5	70.8	333.0	64.4	31.7	87.4
1020.1	1568.2	1477.9	1378.4	1174.3	1257.9	828.7	1703.8	699.3	410.8	972.6
31.1	545.1	1060.0	1023.5	150.3	388.7	262.6	559.0	167.6	79.3	379.6
890.9	1867.8	2568.9	2221.6	2257.2	1824.3	2331.1	3168.4	1351.1	1117.6	2653.6
608.9	3137.0	5215.9	4513.2	2368.1	4943.9	3117.3	4954.8	2501.3	1435.2	4328.4
323.0	1177.9	1367.7	1389.9	1444.4	1473.0	1611.4	1156.5	1185.4	1115.2	763.1

9194.8	8787.9	9014.8
1456.7	1575.2	2064.5
7918.4	7137.1	7797.4
5150.3	3058.0	2264.9
2681.4	2837.7	2815.1
1284.7	1271.5	1869.8
3569.7	1233.6	3938.0
3331.1	3576.6	4104.7
2097.6	1117.9	1406.7
4358.2	4542.2	3517.1
1875.0	2016.0	2043.1
44.7	50.8	39.2
1471.4	2513.4	3172.4
185.5	868.5	591.0
2728.5	2417.2	2259.9
2270.5	3063.6	2978.8
1388.3	1222.2	1835.6
2808.9	3061.8	3426.2
3213.4	4385.1	3552.4
1299.5	1364.5	1229.4
147.8	150.8	160.0
1692.8	1334.0	1063.7
2010.2	1473.3	1856.4
2107.9	2147.6	2923.5
49.6	116.6	59.7
1736.0	2156.1	1306.4
4586.8	1007.9	2101.0
846.9	1709.7	934.5
4801.3	4952.3	3920.7
1711.1	2996.7	2015.2
1442.4	1519.5	1623.5
2047.7	2090.2	1500.7
3398.9	3764.7	3738.8
1252.6	1258.1	1599.3
1807.0	2362.1	2268.3
518.5	381.2	214.4
1511.5	1438.0	1527.8
754.0	1170.1	570.8
2956.8	2100.4	2898.2
3928.2	5204.4	5845.0
1346.6	2122.7	1580.6

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EU767855.1 gg_id:332308 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU7678
EF403444.1 gg_id:211174 human fecal clone SJTU_A2_01_30 EF4034
EU508356.1 gg_id:259998 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03f08 EU5083
AY992008.1 gg_id:134549 mouse cecum clone C20_p10 AY9920
EF096052.1 gg_id:180458 mouse cecum clone lean2_aaa03a05 EF0960
EF096277.1 gg_id:199341 mouse cecum clone obob1_aaa04a05 EF0962
EU452590.1 gg_id:312205 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4525
EF099536.1 gg_id:186085 mouse cecum clone SWPT3_aaa04f01 EF0995
EF604514.1 gg_id:234516 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EF614877.1 gg_id:233595 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
DQ815426.1 gg_id:166609 mouse cecum clone aab48b10 DQ815
GQ492112.1 gg_id:593369 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ957873.1 gg_id:461989 Clostridium saccharolyticum str. JPL_21 FJ9578
EF404438.1 gg_id:209193 human fecal clone SJTU_C_10_05 EF4044
FJ370463.1 gg_id:362460 feces adult twins and mothers; TS57 clone TS57_a01d06 FJ3704
FJ370529.1 gg_id:357221 feces adult twins and mothers; TS57 clone TS57_a02b05 FJ3705
FJ680978.1 gg_id:527327 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
AJ311620.2 gg_id:90431 Clostridium hathewayi str. DSM 13479 = CCUG 43 AJ3116
AJ408971.1 gg_id:69958 human colonic clone HuCA19 AJ4089
EU463123.1 gg_id:296872 naked mole-rat feces clone molerat_aai70c02 EU4631
EU509115.1 gg_id:276941 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44a08 EU5091
EF099826.1 gg_id:193023 mouse cecum clone SWPT4_aaa04h05 EF0998
EU510090.1 gg_id:270627 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01b12 EU5100
DQ815622.1 gg_id:169045 mouse cecum clone aab43f10 DQ815
DQ801685.1 gg_id:181521 human fecal clone RL201_aai45e03 DQ801
FJ370676.1 gg_id:361375 feces adult twins and mothers; TS57 clone TS57_a03h06 FJ3706
DQ904855.1 gg_id:173777 human fecal clone 001C-c6 DQ904
EU452655.1 gg_id:321921 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4526
EU511980.1 gg_id:267783 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12c04 EU5119
EF406450.1 gg_id:211001 mouse colon clone control_14days-A1 EF4064
EF095970.1 gg_id:178026 mouse cecum clone lean2_aaa01b07 EF0959
EU450991.1 gg_id:350064 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74M EU4509
DQ815701.1 gg_id:164638 mouse cecum clone aab21b07 DQ815
EF604630.1 gg_id:231997 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EU511917.1 gg_id:274132 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11c02 EU5119
FJ370659.1 gg_id:367027 feces adult twins and mothers; TS57 clone TS57_a03f09 FJ3706
EF096886.1 gg_id:175986 mouse cecum clone SWPT13_aaa02c04 EF0968
DQ015121.1 gg_id:131793 mouse cecum clone M2_f12_1 DQ015
AY993011.1 gg_id:130465 mouse cecum clone C22_o10 AY9930
EF098094.1 gg_id:184695 mouse cecum clone SWPT14_aaa01d09 EF0980
FJ880800.1 gg_id:429698 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808

42.2	104.9	196.7	236.7	102.0	214.2	156.7	478.1	70.9	83.2	96.8
49.8	754.0	1141.5	1449.3	416.7	794.0	575.0	1052.4	291.4	162.9	862.8
779.8	1606.5	1690.5	1700.9	1235.6	1272.1	1456.1	532.3	1250.3	1162.3	1676.1
404.3	887.0	2085.2	2796.2	1214.1	1034.6	1245.8	2218.3	865.7	364.7	1038.9
734.4	1302.1	1740.8	1646.1	1026.8	1611.8	1340.1	1500.4	1264.8	1707.2	1050.6
52.0	73.4	82.4	90.8	46.6	31.1	43.7	60.8	43.2	20.8	44.8
4280.7	2923.8	3180.4	3193.6	2843.6	2732.2	3622.2	3540.9	1899.6	3158.8	2646.5
22153.9	9969.1	9126.9	9419.5	9240.9	10716.8	11050.5	8715.1	8649.0	9998.0	10831.8
40.3	984.0	1132.3	1524.2	1172.7	668.1	1249.4	779.8	180.8	84.3	351.8
9431.1	5275.6	5215.4	5959.4	5351.3	5054.4	7108.8	5458.8	6832.8	7265.3	7755.3
29.4	91.9	94.6	97.1	34.3	76.3	52.2	112.6	49.4	14.9	80.1
16963.1	4149.7	4252.2	4604.2	4180.2	5526.1	5352.3	3939.6	5579.8	7018.7	7002.8
3251.8	3813.3	5443.6	6212.0	3159.0	4341.5	4221.7	6990.9	2893.0	1790.0	5196.5
473.5	1374.5	1143.0	1392.3	546.2	1142.7	750.7	1206.5	457.5	303.2	2046.4
8086.5	3607.5	3965.4	4151.3	3178.2	3539.1	3692.4	3458.6	6011.1	3769.0	5539.6
81.5	714.4	800.4	608.5	305.5	479.6	352.1	421.7	598.1	934.7	380.6
76.1	1130.0	901.8	872.3	510.3	626.5	665.7	886.5	973.0	278.1	492.1
2035.9	7717.8	6976.3	8643.1	8413.4	6980.1	8517.1	8715.4	6492.9	3990.4	7830.0
6760.2	3459.4	3733.4	3310.7	3996.6	3380.1	4396.9	3845.3	3350.6	4452.3	3183.1
134.1	368.3	656.5	513.3	88.0	311.0	222.1	783.0	229.9	402.0	452.2
730.7	1525.3	2122.3	2390.3	1448.1	1621.9	1609.4	2115.8	742.9	551.4	1198.3
665.9	5161.5	5483.2	4810.6	4841.0	4728.9	4133.0	4337.7	11749.5	2670.4	4116.8
96.4	1706.3	1239.0	1512.0	2038.3	1372.2	2574.7	1577.1	1212.2	280.4	1139.8
417.8	1074.7	972.5	1164.1	1474.2	1114.6	1596.2	1003.1	682.0	525.2	830.4
139.6	1749.9	2618.3	2603.1	1584.3	2021.4	1880.5	2691.2	1242.4	1650.2	1754.6
2035.0	3081.0	3830.2	4794.3	3159.9	2711.6	2924.9	3187.1	2286.8	1837.1	2929.7
4683.6	2347.1	2933.0	3049.1	1982.3	2475.7	2238.1	2635.0	1431.8	1118.8	2442.5
33.1	81.0	112.9	161.4	51.6	35.8	41.1	78.8	30.7	15.0	27.2
55.8	570.0	800.7	784.2	154.7	528.6	320.6	943.0	217.3	82.4	609.0
1948.3	1014.3	1643.4	1918.2	1057.2	811.3	1193.2	1087.0	417.2	326.0	518.5
163.4	1033.6	785.1	253.3	674.1	812.1	701.4	834.1	582.6	280.8	797.9
227.2	1308.2	1567.8	1524.4	1014.1	1211.7	1243.3	1725.8	2425.8	1954.9	1521.3
3716.0	2314.2	2361.6	2938.5	2822.6	2603.0	2736.1	2719.0	1525.7	1642.6	2114.1
206.2	971.3	1335.6	1358.3	1300.4	1029.2	1454.0	1326.4	3174.6	786.4	1346.4
1511.5	1006.6	1477.8	1747.4	1044.8	1244.7	1265.9	1561.6	524.7	320.0	1107.2
8522.0	4045.0	4382.2	4678.2	3886.8	3837.2	4289.5	3827.8	6386.0	5172.9	5052.2
21624.5	7577.3	7030.7	8012.1	6732.7	6526.3	8026.4	6542.8	7660.5	6647.5	7493.5
2925.5	3051.3	2575.2	2392.3	2350.1	2535.3	1934.4	1344.5	2623.0	1568.6	1659.2
63.9	231.8	465.9	442.6	272.3	193.5	385.7	271.8	77.0	63.3	174.9
349.7	400.8	423.8	448.7	427.7	313.2	342.3	316.4	347.4	195.9	299.9
1353.5	3175.6	3143.1	2941.5	2619.4	2882.3	2754.5	2913.3	2579.0	1785.9	2323.8

816.1	279.4	260.8
628.7	982.3	1200.5
1415.2	1926.6	1387.7
1189.7	1986.2	1896.7
1661.8	2438.3	1417.0
64.9	76.2	113.8
2674.1	3423.1	4450.5
8598.9	9181.6	8909.3
662.7	983.2	1266.0
4582.2	6238.5	4838.1
122.0	149.7	105.1
4352.6	5645.2	4627.0
8627.3	3655.1	6662.3
568.8	1277.1	1220.4
3465.4	4887.9	3439.4
469.8	606.1	611.9
863.2	729.9	886.4
9470.5	6688.8	8482.1
4331.1	4659.0	5174.4
833.0	620.8	964.1
2225.9	2007.0	2435.9
5149.3	5964.6	4576.3
1386.1	1570.7	1396.9
1035.0	1040.3	1815.8
2533.8	2976.2	2569.5
3521.0	3149.1	4042.6
2708.6	2945.7	3766.8
106.5	135.9	97.8
1201.7	705.9	901.0
1438.7	1557.6	1235.7
576.7	1697.3	828.0
1377.2	1817.5	1283.2
3749.0	3469.1	3149.1
1344.0	1433.8	1411.1
1775.9	1621.0	1882.9
4011.0	4712.6	4320.3
8262.7	7571.2	7342.5
2203.1	2779.7	2130.9
384.9	351.0	454.3
400.7	496.0	433.5
2560.8	2718.8	2826.0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Lachnospiraceae
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