FJ371961.1	365148	45.0	59.0	128.8	119.7	66.0	27.8
EF402931.1	211189	963.9	967.6	846.6	1210.6	775.7	1110.0
FJ679195.1	521174	33.2	59.8	58.3	50.2	50.6	25.7
FJ682077.1	523004	930.6	1258.3	730.4	525.7	1689.9	1371.4
FJ679008.1	517327	3716.3	2926.3	3119.0	2403.8	6248.2	4065.9
AY981330.1	119373	205.3	361.0	846.5	358.6	933.4	530.0
DQ824177.1	179618	22.3	20.8	52.0	53.1	61.1	17.8
DQ455894.1	157039	3524.6	4015.3	1571.9	2160.9	3112.4	2970.5
FJ363424.1	362434	1238.1	982.5	1775.3	2004.5	350.5	637.0
EU765882.1	343729	466.1	357.9	1106.0	364.9	476.1	982.6
FJ673757.1	531957	7858.1	11695.2	5684.9	8545.2	11994.6	14237.2
DQ824273.1	182474	4368.3	3556.5	2359.2	1924.8	3825.5	3186.3
FJ673321.1	525934	128.1	124.4	482.8	130.8	237.1	87.5
DQ904869.1	165924	7341.3	6980.1	5408.0	6287.5	7700.6	8255.2
DQ326102.1	147918	2148.7	3473.5	3436.1	4245.8	4542.0	4118.1
FJ673706.1	515571	890.9	1522.0	5343.5	1040.1	908.2	1434.2
FJ365373.1	360869	2746.8	296.7	847.0	4108.1	2206.3	2144.0
FJ682702.1	511628	2579.3	2865.7	1906.4	2614.5	2597.0	3031.3
EF404926.1	208689	90.3	111.6	297.2	98.2	159.4	133.2
AY982292.1	120787	2091.7	1891.3	2249.8	4786.5	3503.5	3479.4
FJ365144.1	364153	2889.5	2775.5	3484.5	4103.6	3128.2	6936.1
FJ363150.1	366680	182.3	196.5	200.0	265.0	79.6	64.0
FJ673221.1	519426	26.0	25.2	150.9	55.3	58.0	7.8
DQ825336.1	180951	26.3	54.8	39.2	51.3	63.0	9.4
FJ362937.1	366344	3398.5	4206.5	2262.6	3315.5	4988.2	5513.1
FJ365109.1	369337	30.0	60.6	38.4	54.2	66.8	11.4
EF403511.1	209544	133.7	248.4	708.9	200.1	459.7	365.6
FJ676561.1	529243	9458.9	6142.7	4618.3	9332.1	5911.9	7439.2
FJ367175.1	363148	609.4	806.5	1389.4	399.7	387.1	632.0
DQ794121.1	187979	450.7	2316.8	645.1	184.8	190.1	139.0
FJ677399.1	513641	32.1	41.9	48.0	64.4	57.6	21.4
FJ680807.1	514436	2893.7	3313.4	3642.5	2647.3	4740.2	2557.1
FJ678672.1	513184	25.9	68.3	91.8	82.8	85.9	101.1
DQ325805.1	149722	540.9	703.7	1589.8	1365.3	712.3	1251.7
FJ372166.1	369577	21.6	47.6	50.7	46.5	59.9	47.0
FJ367110.1	362343	6298.1	4809.3	3182.9	4928.8	5408.4	3322.3
FJ680954.1	525656	4158.7	5504.9	2770.0	4055.0	3008.9	3853.0
FJ677126.1	528180	16037.4	15944.9	11466.0	13761.9	14651.8	16296.4
FJ369848.1	364242	40.3	52.5	55.7	60.9	48.9	58.1
FJ370300.1	363387	4964.6	4843.4	1862.1	1780.5	2150.3	1148.6
DQ825190.1	190661	35.2	47.4	34.9	51.1	54.9	30.6

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DQ798784.1 gg_id:190019 human fecal clone RL242_aaj97c12
EU764880.1 gg_id:346467 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
FJ364341.1 gg_id:369847 feces adult twins and mothers; TS15 clone TS15_a01g08
FJ367563.1 gg_id:365091 feces adult twins and mothers; TS2 clone TS2_a01a07
DQ797833.1 gg_id:176515 human fecal clone RL206_aaj16d04
FJ673732.1 gg_id:530736 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796920.1 gg_id:184733 human fecal clone RL179_aao56d09
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EF071181.1 gg_id:197944 library survey and quantitative measurement major mucosa- IBD human colonic muc
FJ371801.1 gg_id:370194 feces adult twins and mothers; TS8 clone TS8_a02d02
FJ673783.1 gg_id:516446 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ905052.1 gg_id:164808 human fecal clone 2-002-e10
EF403326.1 gg_id:204360 human fecal clone SJTU_A1_2_67
FJ673815.1 gg_id:528588 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673046.1 gg_id:526346 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796290.1 gg_id:198873 human fecal clone RL179_aah25c10
FJ362905.1 gg_id:366390 feces adult twins and mothers; TS13 clone TS13_a04f02
DQ801422.1 gg_id:178266 human fecal clone RL388_aao95c10
FJ365496.1 gg_id:357223 feces adult twins and mothers; TS20 clone TS20_a03e10
FJ370818.1 gg_id:364588 feces adult twins and mothers; TS5 clone TS5_a01f04
FJ367962.1 gg_id:358593 feces adult twins and mothers; TS30 clone TS30_a01g09
FJ372239.1 gg_id:362043 feces adult twins and mothers; TS9 clone TS9_a03c11
FJ679571.1 gg_id:515141 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ363627.1 gg_id:366946 feces adult twins and mothers; TS14 clone TS14_a01e03
FJ677044.1 gg_id:511855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802010.1 gg_id:184270 human fecal clone RL241_aaj01g09
EU774095.1 gg_id:308016 Chimpanzee feces clone CHIMP1_aaj37h01
DQ797810.1 gg_id:186215 human fecal clone RL206_aaj16b03
DQ795974.1 gg_id:198529 human fecal clone RL202_aai49f11
FJ363086.1 gg_id:361639 feces adult twins and mothers; TS148 clone TS148_a02g10
FJ678576.1 gg_id:520430 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU768009.1 gg_id:310054 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
FJ678764.1 gg_id:510485 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766847.1 gg_id:337990 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ676734.1 gg_id:528844 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ805199.1 gg_id:186809 human fecal clone RL249_aaj82h07
DQ809728.1 gg_id:183171 human fecal clone RL184_aan83c11
FJ365578.1 gg_id:367683 feces adult twins and mothers; TS20 clone TS20_a04e06
DQ805660.1 gg_id:192800 human fecal clone RL306aal89e05
DQ793292.1 gg_id:187426 human fecal clone RL199_aaj41h01

FJ367896.1	368633	30.9	41.8	103.7	69.7	59.7	34.6
DQ798784.1	190019	30.8	65.6	53.0	66.4	76.4	24.7
EU764880.1	346467	30.8	37.7	40.9	65.1	53.4	27.1
FJ364341.1	369847	4232.5	3977.1	2116.1	3888.8	4604.5	2749.6
FJ367563.1	365091	3985.9	2965.5	1869.0	7527.0	3675.7	4307.7
DQ797833.1	176515	5865.6	6154.7	8894.4	9948.1	7722.8	7870.3
FJ673732.1	530736	2972.9	2881.2	648.3	2787.2	2672.5	2711.3
DQ796920.1	184733	7113.8	6150.9	3936.8	2468.8	4289.4	3827.3
EF404253.1	207136	182.1	179.6	925.5	149.3	167.5	266.8
EF071181.1	197944	23.5	40.6	62.1	58.7	68.9	24.6
FJ371801.1	370194	1132.9	684.7	2259.9	4777.3	2093.1	2365.0
FJ673783.1	516446	44.5	42.5	41.1	61.8	60.4	30.8
DQ905052.1	164808	321.7	697.0	1688.4	525.0	1128.5	838.3
EF403326.1	204360	121.2	158.3	687.8	104.2	185.6	222.3
FJ673815.1	528588	1978.9	2461.1	3792.9	1778.0	764.9	1257.2
FJ673046.1	526346	1571.6	1235.3	1476.5	2823.6	642.0	1009.9
DQ796290.1	198873	2257.1	2027.6	2023.6	1324.6	1729.3	2704.7
FJ362905.1	366390	27.0	49.1	71.9	71.9	65.7	32.4
DQ801422.1	178266	35.9	55.0	65.0	80.5	74.3	33.9
FJ365496.1	357223	155.5	171.2	835.6	163.6	140.3	190.3
FJ370818.1	364588	3580.5	4117.0	3956.8	3651.9	3144.0	5141.1
FJ367962.1	358593	10037.5	9187.5	13314.9	9135.6	8070.7	8536.9
FJ372239.1	362043	8926.9	8648.7	8885.5	8829.8	7697.8	7902.0
FJ679571.1	515141	1282.5	2476.0	1363.0	1082.4	2878.6	2144.4
FJ363627.1	366946	803.5	2239.0	2741.3	914.9	1320.1	2580.3
FJ677044.1	511855	2426.9	3759.9	1885.9	1620.0	5168.9	4041.9
DQ802010.1	184270	532.5	1205.0	4004.7	1064.4	4850.3	3398.2
EU774095.1	308016	126.1	145.5	48.0	75.8	80.2	81.7
DQ797810.1	186215	41.0	59.4	174.5	1095.5	356.3	295.7
DQ795974.1	198529	980.5	1464.4	1187.6	608.8	1926.5	1640.6
FJ363086.1	361639	881.3	1855.5	2077.6	1313.7	4081.3	4303.1
FJ678576.1	520430	6174.6	6031.6	5579.9	6084.7	9153.6	5935.0
EU768009.1	310054	29.3	78.2	225.6	165.9	61.4	41.6
FJ678764.1	510485	7257.0	6733.5	3141.3	3826.5	4617.5	7029.4
EU766847.1	337990	427.0	771.9	727.2	392.6	547.7	608.8
FJ676734.1	528844	4499.1	5630.5	2804.3	3887.7	6818.3	5284.6
DQ805199.1	186809	2523.1	2347.3	2430.4	2440.0	3521.8	2168.1
DQ809728.1	183171	1406.2	960.2	1026.5	1166.3	2333.3	1228.1
FJ365578.1	367683	169.8	210.6	149.9	89.7	401.1	184.5
DQ805660.1	192800	2575.3	4240.4	3320.8	4164.0	4264.8	2080.8
DQ793292.1	187426	3997.8	2878.4	3621.3	5103.0	7305.6	6737.9

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EU776789.1 gg_id:327476 Mongoose lemur feces clone ML_aaj25f03
FJ367544.1 gg_id:363659 feces adult twins and mothers; TS29 clone TS29_a04g10
FJ674048.1 gg_id:516845 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683190.1 gg_id:512718 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ325841.1 gg_id:147654 Metagenomic gut microbiome healthy human stool clone B594
FJ679786.1 gg_id:518929 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372209.1 gg_id:359305 feces adult twins and mothers; TS9 clone TS9_a03a04
DQ801133.1 gg_id:183347 human fecal clone RL387_aao92g04
FJ673763.1 gg_id:526469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682837.1 gg_id:517363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766860.1 gg_id:316816 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ796611.1 gg_id:181620 human fecal clone RL179aan75g10
FJ677314.1 gg_id:522498 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ456290.1 gg_id:157756 pre-adolescent turkey cecum clone CFT211E12
DQ904670.1 gg_id:169786 human fecal clone 001-c8
EF402606.1 gg_id:215013 human fecal clone SJTU_B_10_14
FJ370336.1 gg_id:368289 feces adult twins and mothers; TS56 clone TS56_a03f05
FJ368299.1 gg_id:364051 feces adult twins and mothers; TS3 clone TS3_a02f05
FJ366958.1 gg_id:358048 feces adult twins and mothers; TS28 clone TS28_a01g07
FJ683641.1 gg_id:524114 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800981.1 gg_id:191715 human fecal clone RL387_aao90c08
GQ898224.1 gg_id:589684 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ683130.1 gg_id:529709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679304.1 gg_id:523216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU774255.1 gg_id:315391 Chimpanzee feces clone CHIMP1_aaj37h05
DQ326396.1 gg_id:147155 Metagenomic gut microbiome healthy human stool clone C433
FJ372294.1 gg_id:367632 feces adult twins and mothers; TS9 clone TS9_a03h12
EU767087.1 gg_id:327918 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ905091.1 gg_id:169975 human fecal clone 2-002-h3
FJ678239.1 gg_id:524423 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370406.1 gg_id:366038 feces adult twins and mothers; TS56 clone TS56_a04f04
DQ804705.1 gg_id:192118 human fecal clone RL187_aao71f07
EU777395.1 gg_id:314971 Sumatran orangutan feces clone orang2_aai68f02
DQ824046.1 gg_id:191356 human fecal clone RL204_aaj58f01
DQ456182.1 gg_id:157426 pre-adolescent turkey cecum clone CFT29D1
AY980880.1 gg_id:127786 human rectum mucosal biopsy clone LQ10
DQ798620.1 gg_id:175207 human fecal clone RL181_aan99b03
EU766848.1 gg_id:320759 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ798754.1 gg_id:198057 human fecal clone RL181_aao00h10
FJ684971.1 gg_id:529824 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679193.1 gg_id:521326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

EU776789.1	327476	2765.4	2454.9	2881.9	2873.8	944.8	1223.8
FJ367544.1	363659	209.0	257.6	1674.2	3242.5	2219.7	2860.3
FJ674048.1	516845	1660.8	1177.4	127.4	2628.7	3149.2	2106.1
FJ683190.1	512718	1981.8	2497.9	1091.3	2271.2	2148.4	1703.7
DQ325841.1	147654	2231.1	1843.5	1826.8	1780.2	3095.1	2705.7
FJ679786.1	518929	1370.2	2189.5	1258.8	1097.7	2899.6	2286.6
FJ372209.1	359305	512.5	438.8	782.6	344.8	310.6	1154.5
DQ801133.1	183347	1581.9	2498.8	1345.0	1079.6	3285.2	2623.0
FJ673763.1	526469	1487.5	1153.8	1576.3	2389.1	1364.0	1825.6
FJ682837.1	517363	5064.9	5244.9	3792.2	3272.1	7251.0	6810.8
EU766860.1	316816	705.5	1607.0	3913.5	1688.2	5969.8	4939.5
DQ796611.1	181620	171.2	306.3	286.6	236.1	155.3	233.6
FJ677314.1	522498	15821.9	10384.1	9301.8	13247.0	11139.0	11049.7
DQ456290.1	157756	895.1	1188.2	658.9	1289.6	204.7	152.5
DQ904670.1	169786	9235.8	7225.4	5774.8	8287.3	6907.1	5520.4
EF402606.1	215013	214.0	70.0	179.0	1274.6	191.1	250.4
FJ370336.1	368289	1965.1	2508.4	1621.2	3956.3	4343.3	3633.8
FJ368299.1	364051	5719.3	5592.3	3780.8	5538.0	2395.6	3974.6
FJ366958.1	358048	180.9	126.5	191.9	96.5	229.0	92.9
FJ683641.1	524114	22.9	42.8	38.8	64.7	61.0	31.7
DQ800981.1	191715	231.4	131.6	206.7	109.6	260.4	105.4
GQ898224.1	589684	2542.7	2287.2	3115.5	2376.5	996.8	2032.3
FJ683130.1	529709	1479.9	1144.1	1566.3	2224.7	1361.8	1582.3
FJ679304.1	523216	2394.4	3873.7	2090.5	1616.8	4696.3	3454.1
EU774255.1	315391	7065.5	7254.8	2965.1	4494.4	5681.7	6411.8
DQ326396.1	147155	274.2	240.2	1792.1	3243.7	2213.4	3174.7
FJ372294.1	367632	2854.2	2233.6	2489.0	1873.8	2260.8	4262.6
EU767087.1	327918	18.3	21.2	21.9	49.9	49.4	11.1
DQ905091.1	169975	49.0	55.0	174.5	68.6	92.5	47.7
FJ678239.1	524423	42.9	38.3	23.7	52.3	53.5	17.9
FJ370406.1	366038	8059.7	8203.6	9109.1	5906.4	7990.5	8037.9
DQ804705.1	192118	285.2	385.6	848.2	216.1	238.6	323.5
EU777395.1	314971	14.2	24.3	60.4	54.9	48.8	9.0
DQ824046.1	191356	623.4	774.9	1401.5	437.4	376.7	736.4
DQ456182.1	157426	3580.1	3313.5	4341.6	2365.2	1925.3	2265.1
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DQ798620.1	175207	22.1	33.9	31.6	40.3	61.2	14.5
EU766848.1	320759	12893.1	13226.9	11342.2	8625.3	13506.1	9911.5
DQ798754.1	198057	11496.4	11223.2	11652.7	9777.1	9040.6	7319.5
FJ684971.1	529824	516.9	746.8	1844.7	499.6	726.9	943.1
FJ679193.1	521326	274.0	368.6	676.7	135.5	853.1	582.4

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DQ809727.1 gg_id:175020 human fecal clone RL184_aan83c10
FJ680557.1 gg_id:515764 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ804517.1 gg_id:194362 human fecal clone RL187_aao69b05
EU762682.1 gg_id:325461 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
GQ175486.1 gg_id:588729 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
DQ806469.1 gg_id:191959 human fecal clone RL186_aao45a09
DQ801687.1 gg_id:197415 human fecal clone RL201_aai45e06
DQ904684.1 gg_id:166719 human fecal clone 001-e10
FJ677910.1 gg_id:530410 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU764731.1 gg_id:328591 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ682094.1 gg_id:528585 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ365268.1 gg_id:366317 feces adult twins and mothers; TS1 clone TS1_a04h02
FJ677326.1 gg_id:521282 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801338.1 gg_id:179248 human fecal clone RL388_aao94b10
DQ805970.1 gg_id:191547 human fecal clone RL186_aah59d04
FJ678720.1 gg_id:517184 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673068.1 gg_id:520389 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368316.1 gg_id:364708 feces adult twins and mothers; TS3 clone TS3_a02h02
DQ797877.1 gg_id:174294 human fecal clone RL206_aaj16h08
FJ676954.1 gg_id:525735 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ825031.1 gg_id:199007 human fecal clone RL185_aao72e03
FJ372253.1 gg_id:368567 feces adult twins and mothers; TS9 clone TS9_a03e02
FJ363363.1 gg_id:363925 feces adult twins and mothers; TS149 clone TS149_a02d03
FJ365444.1 gg_id:360470 feces adult twins and mothers; TS20 clone TS20_a03a01
FJ673804.1 gg_id:523203 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU530303.1 gg_id:260144 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
DQ794142.1 gg_id:184788 human fecal clone RL176_aan58f02
FJ676193.1 gg_id:522012 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371133.1 gg_id:367892 feces adult twins and mothers; TS6 clone TS6_a01d01
DQ824161.1 gg_id:183014 human fecal clone RL204_aaj60b08
EF403336.1 gg_id:210954 human fecal clone SJTU_A1_3_12
DQ797644.1 gg_id:194905 human fecal clone RL206_aaj14b08
EF405005.1 gg_id:211543 human fecal clone SJTU_G_05_78
FJ365576.1 gg_id:361467 feces adult twins and mothers; TS20 clone TS20_a04e04
FJ673788.1 gg_id:523374 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370164.1 gg_id:359647 feces adult twins and mothers; TS56 clone TS56_a01b09
FJ676910.1 gg_id:531618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF404154.1 gg_id:204944 human fecal clone SJTU_C_05_46
AY981009.1 gg_id:119750 human rectum mucosal biopsy clone V165
FJ366918.1 gg_id:360998 feces adult twins and mothers; TS28 clone TS28_a01d03

FJ683833.1	519061	1443.8	2365.8	1907.0	2477.8	4560.0	3563.5
DQ809727.1	175020	626.0	780.6	1925.3	463.1	804.4	1139.5
FJ680557.1	515764	2577.3	2826.4	910.0	1075.3	4419.1	1691.2
DQ804517.1	194362	16.2	16.5	25.2	44.1	49.6	9.9
EU762682.1	325461	2122.8	3754.0	5457.8	2897.6	5943.3	4201.6
GQ175486.1	588729	259.4	507.8	745.4	196.1	601.6	443.8
DQ806469.1	191959	460.6	468.5	754.4	287.2	524.3	276.7
DQ801687.1	197415	7916.1	8833.5	7182.7	6542.2	8986.8	10935.3
DQ904684.1	166719	2657.2	3033.1	439.3	397.1	511.1	640.6
FJ677910.1	530410	805.9	1291.6	992.1	579.4	1706.0	1228.4
EU764731.1	328591	86.2	70.3	48.3	122.9	72.2	35.8
FJ682094.1	528585	2288.2	2564.8	2483.9	3153.6	3205.2	2827.0
FJ365268.1	366317	1895.5	2485.2	4029.2	2341.9	2232.4	3383.3
FJ677326.1	521282	2674.5	1402.4	2372.6	2898.2	1408.1	2774.7
DQ801338.1	179248	62.7	75.3	213.1	117.6	122.2	81.8
DQ805970.1	191547	530.6	918.3	1368.2	427.9	572.7	570.0
FJ678720.1	517184	1875.8	1781.8	505.0	2803.3	3060.8	2504.1
FJ673068.1	520389	125.6	252.7	354.3	128.7	391.3	215.2
FJ368316.1	364708	2325.9	1310.3	1592.9	2039.8	948.6	2752.4
DQ797877.1	174294	1434.6	1168.9	166.5	1039.3	1538.7	902.3
FJ676954.1	525735	6779.7	6824.7	3103.8	6016.6	5122.0	4217.1
DQ825031.1	199007	1580.5	1431.0	450.2	4171.3	4808.2	3250.7
FJ372253.1	368567	2928.9	2113.3	1647.7	3583.9	1244.5	3484.5
FJ363363.1	363925	2266.7	2964.0	3386.2	2398.5	1528.3	3018.1
FJ365444.1	360470	5725.7	4659.7	1477.5	6489.5	2308.6	3502.4
FJ673804.1	523203	845.6	599.5	1125.3	342.7	1482.7	632.5
EU530303.1	260144	929.6	658.2	803.5	702.0	957.1	2234.2
DQ794142.1	184788	3424.5	6648.1	4259.6	4151.2	6095.9	6278.9
FJ676193.1	522012	79.1	184.4	345.8	108.9	45.2	54.2
FJ371133.1	367892	4627.3	4096.6	2693.2	2923.8	3017.2	3139.5
DQ824161.1	183014	80.2	120.3	684.0	118.6	275.6	327.8
EF403336.1	210954	18.9	23.2	17.1	34.2	40.1	6.8
DQ797644.1	194905	23.1	41.2	90.8	33.0	50.6	13.0
EF405005.1	211543	78.1	105.9	593.5	114.7	455.2	424.3
FJ365576.1	361467	1203.8	1087.1	585.3	753.9	253.0	1052.1
FJ673788.1	523374	1787.8	913.2	234.4	1646.5	1741.6	1155.1
FJ370164.1	359647	558.0	508.0	485.2	1187.4	598.0	520.2
FJ676910.1	531618	1729.5	2712.8	2262.3	2387.9	4735.2	3209.6
EF404154.1	204944	713.1	1191.9	1771.0	1925.8	2039.1	4896.4
AY981009.1	119750	36.4	55.0	63.7	95.2	73.7	32.6
FJ366918.1	360998	136.0	43.8	141.6	1063.0	140.0	115.6

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FJ674128.1 gg_id:531166 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ825301.1 gg_id:189448 human fecal clone RL185_aan88b03
DQ904647.1 gg_id:170586 human fecal clone 001-a8
FJ684991.1 gg_id:509638 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372202.1 gg_id:359005 feces adult twins and mothers; TS9 clone TS9_a02h06
FJ677611.1 gg_id:515866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364294.1 gg_id:357892 feces adult twins and mothers; TS15 clone TS15_a01c04
DQ796367.1 gg_id:182257 human fecal clone RL179_aah26c09
FJ372062.1 gg_id:368546 feces adult twins and mothers; TS9 clone TS9_a01d01
EU762631.1 gg_id:309490 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ364352.1 gg_id:368988 feces adult twins and mothers; TS15 clone TS15_a01h09
FJ678704.1 gg_id:527660 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF403596.1 gg_id:206288 human fecal clone SJTU_A2_04_13
DQ808661.1 gg_id:191202 human fecal clone RL239_aaj11e11
EU462241.1 gg_id:290630 chimpanzee feces clone CHIMP1_aaj38c05
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DQ808926.1 gg_id:195680 human fecal clone RL243_aai87a12
FJ362776.1 gg_id:366455 feces adult twins and mothers; TS13 clone TS13_a03a08
FJ680081.1 gg_id:518986 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683736.1 gg_id:530644 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ805791.1 gg_id:193043 human fecal clone RL306aal91b04
EF401601.1 gg_id:204061 human fecal clone SJTU_D_12_78
DQ800201.1 gg_id:192345 human fecal clone RL303_aal69e12
DQ823661.1 gg_id:190455 human fecal clone RL250_aaj77c05
DQ806386.1 gg_id:199397 human fecal clone RL186_aan91f02
AY979366.1 gg_id:119372 human transverse colon mucosal biopsy clone Z711
FJ372236.1 gg_id:367540 feces adult twins and mothers; TS9 clone TS9_a03c08
AY976211.1 gg_id:116392 human ascending colon mucosal biopsy clone LW36
DQ796461.1 gg_id:189599 human fecal clone RL179_aah28g02
DQ801227.1 gg_id:188144 human fecal clone RL116_aaf01h01
EU778090.1 gg_id:330103 feces clone RL117_aae91g07
FJ370097.1 gg_id:369940 feces adult twins and mothers; TS55 clone TS55_a04d05
FJ673826.1 gg_id:520993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ823824.1 gg_id:178396 human fecal clone RL250_aaj79f01
DQ797100.1 gg_id:182634 human fecal clone RL386_aao87a03
FJ682443.1 gg_id:517285 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673324.1 gg_id:515481 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ367239.1 gg_id:368259 feces adult twins and mothers; TS29 clone TS29_a01b10

EF399649.1	215230	1120.5	1501.4	1998.3	1558.1	1547.4	1899.1
DQ904696.1	163939	119.0	416.1	1680.9	161.7	393.8	523.7
FJ362742.1	362066	27.6	37.1	47.0	51.4	59.2	27.6
FJ674128.1	531166	4595.7	4322.2	3079.1	9813.7	9466.0	8289.5
DQ825301.1	189448	89.2	106.7	185.6	1130.1	355.2	460.7
DQ904647.1	170586	3757.1	4924.0	4885.1	3622.1	4240.7	6302.0
FJ684991.1	509638	1008.9	899.8	751.1	838.7	891.5	817.6
FJ372202.1	359005	1752.4	2476.1	3020.7	2038.5	2074.9	2770.0
FJ677611.1	515866	1361.3	1210.4	1979.9	2344.1	495.0	1071.0
FJ364294.1	357892	7988.0	8445.3	4927.2	6558.5	8170.0	6865.4
DQ796367.1	182257	2251.1	3509.6	1759.0	1529.4	4534.0	3835.4
FJ372062.1	368546	198.2	151.7	264.2	128.4	308.7	146.1
EU762631.1	309490	1526.5	112.8	391.8	1959.8	1101.2	1165.4
FJ364352.1	368988	840.4	817.3	1377.7	1268.8	347.0	538.3
FJ678704.1	527660	45.7	53.9	186.7	1086.1	308.3	285.7
EF403596.1	206288	550.0	627.0	1358.6	2152.0	793.6	1220.2
DQ808661.1	191202	292.0	388.7	747.8	229.3	236.8	322.8
EU462241.1	290630	43.0	80.6	98.8	109.2	106.4	118.3
EU763288.1	331854	66.9	108.7	281.0	72.2	222.1	216.5
DQ808926.1	195680	4716.6	6766.5	4186.6	4593.9	3486.4	4322.7
FJ362776.1	366455	2951.8	3611.0	2218.3	3058.6	5084.2	5066.2
FJ680081.1	518986	1273.9	956.6	531.8	3667.0	5945.8	3415.7
FJ683736.1	530644	40.3	46.1	40.4	55.7	44.3	31.3
DQ805791.1	193043	535.9	474.6	387.3	470.0	336.5	277.8
EF401601.1	204061	574.8	884.2	2294.4	336.4	351.5	601.0
DQ800201.1	192345	147.2	263.0	70.3	55.3	60.2	26.1
DQ823661.1	190455	4100.3	4934.8	3730.3	5122.1	7122.7	7532.5
DQ806386.1	199397	183.0	178.1	140.8	211.1	150.8	177.9
AY979366.1	119372	466.4	682.3	2570.5	2587.6	1947.1	1879.1
FJ372236.1	367540	2454.2	2079.8	3821.0	2511.9	2778.2	3371.3
AY976211.1	116392	122.2	402.2	346.6	221.7	272.0	124.1
DQ796461.1	189599	25.7	60.7	42.0	76.3	87.4	19.2
DQ801227.1	188144	365.0	506.9	1354.2	281.2	311.1	462.8
EU778090.1	330103	32.4	48.0	81.5	72.3	68.2	35.4
FJ370097.1	369940	24.1	41.5	43.1	72.2	65.4	34.9
FJ673826.1	520993	765.2	1202.3	752.6	560.6	1615.3	1284.5
DQ823824.1	178396	42.6	82.1	84.8	69.1	85.6	28.2
DQ797100.1	182634	44.8	63.6	32.5	70.8	65.4	29.1
FJ682443.1	517285	432.9	428.8	870.4	753.1	521.2	488.4
FJ673324.1	515481	5612.2	4756.5	3142.1	7504.3	4627.2	5422.2
FJ367239.1	368259	3281.4	2870.7	2548.9	6370.8	3131.8	4238.0

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DQ823987.1 gg_id:185491 human fecal clone RL204_aaj57g09
DQ904732.1 gg_id:163467 human fecal clone 001B-a10
FJ675779.1 gg_id:515438 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ365643.1 gg_id:369286 feces adult twins and mothers; TS21 clone TS21_a01c10
DQ796604.1 gg_id:178339 human fecal clone RL179aan75f11
DQ797136.1 gg_id:194708 human fecal clone RL386_aao87d10
EF400902.1 gg_id:208457 human fecal clone SJTU_D_03_19
EF404984.1 gg_id:209911 human fecal clone SJTU_G_05_50
FJ683493.1 gg_id:521773 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682763.1 gg_id:522043 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU763863.1 gg_id:346867 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
EF405285.1 gg_id:209137 human fecal clone SJTU_G_03_59
DQ796999.1 gg_id:192936 human fecal clone RL386_aao85e11
DQ793280.1 gg_id:177721 human fecal clone RL199_aaj41f11
EF403278.1 gg_id:205028 human fecal clone SJTU_A1_3_53
FJ367046.1 gg_id:357836 feces adult twins and mothers; TS28 clone TS28_a02h02
FJ682297.1 gg_id:524726 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU763421.1 gg_id:337991 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
FJ683916.1 gg_id:517515 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF402319.1 gg_id:215061 human fecal clone SJTU_B_06_36
DQ806205.1 gg_id:186576 human fecal clone RL186_aah62f05
FJ682383.1 gg_id:522784 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ363715.1 gg_id:367988 feces adult twins and mothers; TS14 clone TS14_a02d09
EF404396.1 gg_id:209672 human fecal clone SJTU_C_09_42
AY976064.1 gg_id:120976 human ascending colon mucosal biopsy clone LU21
FJ673310.1 gg_id:516016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ824877.1 gg_id:189055 human fecal clone RL185_aao70d10
FJ371414.1 gg_id:363722 feces adult twins and mothers; TS6 clone TS6_a04f09
DQ797226.1 gg_id:177587 human fecal clone RL386_aao88f04
FJ673952.1 gg_id:517339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ904701.1 gg_id:169896 human fecal clone 001-f3
EF400765.1 gg_id:207334 human fecal clone SJTU_D_01_26
DQ797659.1 gg_id:173956 human fecal clone RL206_aaj14c12
EF402703.1 gg_id:209510 human fecal clone SJTU_B_11_38
FJ677098.1 gg_id:531403 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ672949.1 gg_id:509934 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673009.1 gg_id:527460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801297.1 gg_id:194547 human fecal clone RL388_aao93e12
FJ365874.1 gg_id:358485 feces adult twins and mothers; TS21 clone TS21_a04a12
EF400079.1 gg_id:206506 human fecal clone SJTU_E_08_61

EF401203.1	209132	632.3	706.1	1945.4	2429.1	874.3	1406.1
DQ823987.1	185491	3099.8	2469.3	3073.7	1828.4	1351.7	1972.4
DQ904732.1	163467	987.4	545.7	1084.7	1885.8	875.4	1038.5
FJ675779.1	515438	1705.3	2331.9	1439.5	1077.7	3289.0	2448.5
FJ365643.1	369286	1494.3	1195.4	363.4	2752.3	454.1	438.6
DQ796604.1	178339	7600.0	8473.7	1472.6	10765.3	11441.8	10402.7
DQ797136.1	194708	7533.6	7150.2	4980.8	5465.6	6490.7	6037.8
EF400902.1	208457	748.6	1098.2	1799.0	748.1	1006.4	1790.9
EF404984.1	209911	32.6	36.0	28.9	59.9	59.6	27.1
FJ683493.1	521773	984.9	717.5	962.3	375.5	1266.4	858.5
FJ682763.1	522043	9407.2	7942.9	3985.7	7313.2	7491.9	5538.1
EU763863.1	346867	727.0	1156.1	2791.0	803.1	3973.6	3250.9
EF405285.1	209137	9515.3	9216.6	5225.6	7948.2	9614.4	8560.9
DQ796999.1	192936	2214.1	2841.8	4831.9	2261.7	2861.9	3179.8
DQ793280.1	177721	7723.4	7615.2	5939.6	6349.0	12253.1	10842.8
EF403278.1	205028	10353.2	10096.3	10027.4	7527.2	9920.8	9322.2
FJ367046.1	357836	3824.7	3640.6	6154.3	3137.4	3694.6	5199.3
FJ682297.1	524726	1291.0	1024.0	2054.3	3155.3	1729.7	2401.0
EU763421.1	337991	27.7	27.4	79.9	63.9	82.1	19.3
FJ683916.1	517515	40.9	115.4	224.7	102.1	68.9	70.6
EF402319.1	215061	2414.8	2497.3	1106.6	1559.4	276.0	653.9
DQ806205.1	186576	53.9	83.6	319.2	188.4	110.3	83.1
FJ682383.1	522784	1570.3	1971.9	1075.0	1031.0	2804.7	2778.7
FJ363715.1	367988	2019.5	2004.1	185.1	967.6	163.2	175.1
EF404396.1	209672	682.1	701.9	383.3	153.5	74.0	113.2
AY976064.1	120976	142.7	44.0	91.4	996.4	146.9	103.5
FJ673310.1	516016	4615.3	4489.4	3730.7	8531.8	7919.7	7201.7
DQ824877.1	189055	230.1	264.0	491.6	1388.9	591.3	551.4
FJ371414.1	363722	2330.8	2347.1	3952.9	3076.6	2185.0	3138.7
DQ797226.1	177587	149.0	98.3	124.7	110.4	95.3	135.4
FJ673952.1	517339	4004.8	2717.5	674.0	3423.6	4999.2	5970.6
DQ904701.1	169896	1950.0	2123.0	1206.2	1470.6	674.5	970.5
EF400765.1	207334	144.4	228.4	730.4	220.1	187.0	233.6
DQ797659.1	173956	270.5	120.8	284.5	1889.5	553.5	439.0
EF402703.1	209510	7644.8	6960.8	9852.2	8134.3	6285.9	6206.1
FJ677098.1	531403	2375.2	2974.9	4567.9	4826.2	2636.1	4080.3
FJ672949.1	509934	3175.0	2525.7	634.0	3119.1	691.6	1119.3
FJ673009.1	527460	3043.3	5033.0	2555.8	2410.0	5823.9	5142.2
DQ801297.1	194547	43.4	51.5	48.0	73.3	69.6	31.0
FJ365874.1	358485	113.6	205.0	146.1	101.6	85.4	75.7
EF400079.1	206506	138.8	186.4	338.2	189.9	129.5	152.6

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DQ824910.1 gg_id:174902 human fecal clone RL185_aao70h06
FJ682721.1 gg_id:530545 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU765972.1 gg_id:333253 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B
DQ455837.1 gg_id:158377 pre-adolescent turkey cecum clone CFT19B6
FJ364289.1 gg_id:364563 feces adult twins and mothers; TS15 clone TS15_a01b10
EF402831.1 gg_id:215016 human fecal clone SJTU_B_13_09
DQ801723.1 gg_id:186002 human fecal clone RL201_aai46a09
FJ675872.1 gg_id:526506 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683292.1 gg_id:516858 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU764935.1 gg_id:353272 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B
DQ905093.1 gg_id:167659 human fecal clone 2-002-h5
EU530424.1 gg_id:274738 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M
EU766146.1 gg_id:313430 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B
EF405024.1 gg_id:206629 human fecal clone SJTU_G_07_03
FJ673782.1 gg_id:519219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676929.1 gg_id:530715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674055.1 gg_id:519504 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF400703.1 gg_id:206334 human fecal clone SJTU_E_09_61
EF403393.1 gg_id:211843 human fecal clone SJTU_A1_7_65
AY982915.1 gg_id:121762 human descending colon mucosal biopsy clone L106
EU467322.1 gg_id:301906 chimpanzee feces clone CHIMP1_f05
DQ809123.1 gg_id:177872 human fecal clone RL308_aal81g11
DQ802345.1 gg_id:180178 human fecal clone RL188_aah16d10
DQ800008.1 gg_id:179287 human fecal clone RL247_aaj23a08
DQ905156.1 gg_id:170981 human fecal clone 002C-f10
FJ673481.1 gg_id:515674 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797371.1 gg_id:193574 human fecal clone RL248_aai98e03
DQ803312.1 gg_id:190701 human fecal clone RL311_aam23h03
FJ363156.1 gg_id:364468 feces adult twins and mothers; TS148 clone TS148_a03g05
FJ366455.1 gg_id:359333 feces adult twins and mothers; TS26 clone TS26_a03e03
DQ798245.1 gg_id:180281 human fecal clone RL181_aah39d09
FJ683213.1 gg_id:525431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683412.1 gg_id:527951 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY978428.1 gg_id:127100 human transverse colon mucosal biopsy clone KO36
FJ679905.1 gg_id:529329 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF403380.1 gg_id:205522 human fecal clone SJTU_A1_7_45
DQ807554.1 gg_id:198606 human fecal clone RL307_aam08b06
DQ804568.1 gg_id:176437 human fecal clone RL187_aao69g06
FJ675851.1 gg_id:519831 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801530.1 gg_id:183361 human fecal clone RL388_aao96f11

EU762453.1	320358	42.1	32.1	169.4	80.6	70.5	71.5
DQ824910.1	174902	27.4	35.1	76.8	53.9	49.7	17.3
FJ682721.1	530545	6353.5	7032.4	3930.3	5078.8	6769.8	5683.4
EU765972.1	333253	1463.5	1122.0	77.7	412.3	76.8	53.0
DQ455837.1	158377	148.0	278.1	389.3	148.3	131.8	119.8
FJ364289.1	364563	310.2	245.5	478.1	265.3	109.4	115.2
EF402831.1	215016	46.5	81.6	63.9	46.0	44.6	18.7
DQ801723.1	186002	1482.5	2564.2	7314.8	1902.0	4227.7	2133.9
FJ675872.1	526506	2167.6	2689.4	2604.9	3394.0	4296.7	3325.5
FJ683292.1	516858	14527.3	14709.2	10697.7	11982.9	12024.7	11374.6
EU764935.1	353272	23.5	17.6	26.6	55.0	58.9	21.3
DQ905093.1	167659	42.7	52.4	157.5	63.5	88.4	36.9
EU530424.1	274738	296.1	105.4	533.6	2259.5	639.4	421.1
EU766146.1	313430	300.3	636.0	875.0	282.9	253.4	356.0
EF405024.1	206629	2969.9	1964.5	1478.9	2775.8	1268.4	2585.4
FJ673782.1	519219	857.9	1543.8	3212.4	502.3	414.7	553.8
FJ676929.1	530715	1144.8	867.0	1006.0	1517.9	165.6	466.9
FJ674055.1	519504	695.3	829.9	2223.0	3116.5	2461.2	2331.0
EF400703.1	206334	2344.9	2531.7	3332.5	3122.6	2487.3	3898.7
EF403393.1	211843	1231.9	410.9	901.1	2153.1	1809.9	2188.6
AY982915.1	121762	32.5	94.6	41.6	80.6	77.7	35.3
EU467322.1	301906	680.9	745.1	270.7	2248.4	795.0	520.3
DQ809123.1	177872	1758.5	2308.9	3228.0	2056.8	2087.8	2936.6
DQ802345.1	180178	1883.9	2180.6	2178.7	3920.9	2591.1	1953.2
DQ800008.1	179287	2642.0	3184.0	2111.0	4303.9	2819.1	3107.7
DQ905156.1	170981	11136.3	11547.5	8484.3	8730.3	12274.7	8831.8
FJ673481.1	515674	6179.3	4519.5	1750.8	5895.0	8233.6	7739.4
DQ797371.1	193574	1998.6	2800.2	4466.9	2542.9	2687.6	3547.7
DQ803312.1	190701	357.9	494.8	1316.3	332.8	332.8	470.4
FJ363156.1	364468	1341.9	1583.9	128.3	356.3	270.0	428.2
FJ366455.1	359333	126.1	103.5	102.3	100.3	62.1	114.4
DQ798245.1	180281	2509.4	3027.1	2217.0	1483.2	1687.4	2615.8
FJ683213.1	525431	1288.0	1959.3	2841.8	4861.5	2903.1	2468.4
FJ683412.1	527951	1476.4	1051.3	1148.6	1256.7	1099.2	1280.2
AY978428.1	127100	8317.9	7209.2	3614.6	5143.4	9875.5	6696.5
FJ679905.1	529329	1942.6	2436.9	4699.2	4761.5	3825.7	4050.4
EF403380.1	205522	4685.2	5555.5	6695.4	5176.7	6401.4	5471.3
DQ807554.1	198606	1297.8	907.2	967.1	1115.1	2190.3	1038.8
DQ804568.1	176437	40.9	41.4	60.4	64.9	81.8	66.3
FJ675851.1	519831	27.0	39.2	46.7	60.8	62.7	31.1
DQ801530.1	183361	1982.6	1925.6	1556.7	990.5	2077.3	2522.6

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EU766002.1 gg_id:321282 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
FJ684419.1 gg_id:511583 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ363601.1 gg_id:366068 feces adult twins and mothers; TS14 clone TS14_a01c01
FJ371005.1 gg_id:359467 feces adult twins and mothers; TS5 clone TS5_a03h01
AY979529.1 gg_id:123479 human transverse colon mucosal biopsy clone M180
FJ370804.1 gg_id:366916 feces adult twins and mothers; TS5 clone TS5_a01e02
FJ673658.1 gg_id:515075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF399941.1 gg_id:210404 human fecal clone SJTU_E_05_96
FJ371804.1 gg_id:365075 feces adult twins and mothers; TS8 clone TS8_a02d05
FJ682112.1 gg_id:525703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797519.1 gg_id:191286 human fecal clone RL248_aaj00d12
FJ364478.1 gg_id:368957 feces adult twins and mothers; TS15 clone TS15_a03d10
DQ794259.1 gg_id:191088 human fecal clone RL176_aan60c06
AY978866.1 gg_id:117362 human transverse colon mucosal biopsy clone NE31
FJ371736.1 gg_id:363136 feces adult twins and mothers; TS8 clone TS8_a01f05
FJ679943.1 gg_id:523123 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ367279.1 gg_id:367728 feces adult twins and mothers; TS29 clone TS29_a01f05
FJ371386.1 gg_id:364979 feces adult twins and mothers; TS6 clone TS6_a04c11
GQ896640.1 gg_id:533914 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ364337.1 gg_id:369540 feces adult twins and mothers; TS15 clone TS15_a01g04
FJ368388.1 gg_id:368518 feces adult twins and mothers; TS3 clone TS3_a03g08
FM873463.1 gg_id:365347 occupant source house floor dust clone FD04A09
DQ796425.1 gg_id:180981 human fecal clone RL179_aah28b06
AY977092.1 gg_id:119801 human cecum mucosal biopsy clone K782
EF403170.1 gg_id:208332 human fecal clone SJTU_A1_1_05
DQ325722.1 gg_id:147313 Metagenomic gut microbiome healthy human stool clone B363
DQ801372.1 gg_id:187382 human fecal clone RL388_aao94f04
DQ800359.1 gg_id:175653 human fecal clone RL303_aal72b02
GQ038488.1 gg_id:461772 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
FJ678822.1 gg_id:528715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368086.1 gg_id:359840 feces adult twins and mothers; TS30 clone TS30_a03h01
FJ371394.1 gg_id:365787 feces adult twins and mothers; TS6 clone TS6_a04d09
FJ672996.1 gg_id:519087 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680690.1 gg_id:517251 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370369.1 gg_id:357768 feces adult twins and mothers; TS56 clone TS56_a04a09
EF402269.1 gg_id:211130 human fecal clone SJTU_B_05_74
FJ364321.1 gg_id:364093 feces adult twins and mothers; TS15 clone TS15_a01e11
FJ367945.1 gg_id:361901 feces adult twins and mothers; TS30 clone TS30_a01e06
DQ796342.1 gg_id:192023 human fecal clone RL179_aah26a05
FJ682336.1 gg_id:526850 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766815.1 gg_id:342863 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1

EU766002.1	321282	4848.9	2631.3	5174.4	4964.3	1123.5	4002.0
FJ684419.1	511583	3945.4	4461.8	8511.0	5305.2	9115.9	8623.1
FJ363601.1	366068	625.2	626.9	1139.3	409.1	1589.3	958.5
FJ371005.1	359467	62.2	95.4	210.3	1164.5	336.0	330.0
AY979529.1	123479	509.6	658.1	1270.4	727.4	476.9	767.3
FJ370804.1	366916	334.8	310.7	1021.3	805.0	183.4	228.2
FJ673658.1	515075	1823.3	2778.6	4589.1	2163.7	5574.8	4634.0
EF399941.1	210404	1781.1	1606.5	559.7	2247.1	3138.9	1853.8
FJ371804.1	365075	2175.7	2414.3	3361.7	818.2	818.1	1725.2
FJ682112.1	525703	47.0	43.5	35.9	57.1	60.3	24.7
DQ797519.1	191286	3104.0	147.1	503.3	3584.8	1395.1	1968.7
FJ364478.1	368957	1254.4	1728.2	1983.0	2610.4	2135.8	2203.8
DQ794259.1	191088	156.5	191.7	517.8	144.5	481.0	87.2
AY978866.1	117362	580.9	724.6	1645.0	659.9	663.2	1747.4
FJ371736.1	363136	21.0	35.1	71.2	60.6	165.4	228.1
FJ679943.1	523123	4653.6	5048.2	2403.5	6652.3	5681.9	5059.7
FJ367279.1	367728	1767.5	1490.9	1484.8	4490.3	3065.0	2839.9
FJ371386.1	364979	48.9	78.5	197.1	1103.8	319.1	293.5
GQ896640.1	533914	8544.9	9436.2	7910.1	7773.2	12450.4	11079.8
FJ364337.1	369540	1295.7	655.6	992.0	2290.0	110.4	280.3
FJ368388.1	368518	883.4	540.9	445.3	932.8	316.9	648.8
FM873463.1	365347	2667.8	1537.5	781.7	2149.0	2979.8	4257.9
DQ796425.1	180981	396.5	403.5	726.6	241.8	253.9	378.7
AY977092.1	119801	65.0	75.5	186.3	101.5	107.1	78.0
EF403170.1	208332	8066.7	8135.3	2040.1	4209.2	4479.5	3397.0
DQ325722.1	147313	1529.1	740.1	144.4	104.3	292.3	86.5
DQ801372.1	187382	1524.1	111.6	395.9	1947.6	1100.6	1167.3
DQ800359.1	175653	2441.1	2595.4	1556.4	1591.3	964.3	2351.6
GQ038488.1	461772	312.0	940.2	1411.3	615.5	2853.2	2142.2
FJ678822.1	528715	3539.3	3243.5	1993.2	5011.7	473.6	765.6
FJ368086.1	359840	2088.6	1924.2	1730.7	3143.1	2016.4	1726.5
FJ371394.1	365787	232.4	363.8	955.2	209.9	652.7	724.2
FJ672996.1	519087	2921.4	1919.8	2306.7	847.3	2654.2	2023.1
FJ680690.1	517251	948.7	2378.9	2376.9	2080.2	5505.7	4633.0
FJ370369.1	357768	3077.8	2847.0	2197.6	3226.3	2502.1	4214.2
EF402269.1	211130	10939.0	9952.3	7244.8	6385.1	6618.0	7660.4
FJ364321.1	364093	4081.6	7547.0	2573.9	2500.6	6073.8	4733.8
FJ367945.1	361901	1293.2	1042.6	1100.2	1105.5	2342.5	1039.6
DQ796342.1	192023	2184.0	3736.1	1683.1	1110.8	565.2	755.1
FJ682336.1	526850	30.9	52.1	46.0	93.1	103.2	18.2
EU766815.1	342863	8843.8	9450.3	1253.3	5387.0	6437.4	5575.5

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EU462258.1 gg_id:294922 chimpanzee feces clone CHIMP1_aaj38f03
FJ363396.1 gg_id:359501 feces adult twins and mothers; TS149 clone TS149_a02g02
FJ680071.1 gg_id:524461 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU761635.1 gg_id:329509 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
EF403807.1 gg_id:214604 human fecal clone SJTU_A3_11_28
EU774128.1 gg_id:310301 Chimpanzee feces clone CHIMP1_aaj38b03
FJ683496.1 gg_id:527743 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370925.1 gg_id:361734 feces adult twins and mothers; TS5 clone TS5_a02h04
FJ677019.1 gg_id:517142 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364613.1 gg_id:358324 feces adult twins and mothers; TS19 clone TS19_a01a08
FJ362730.1 gg_id:369611 feces adult twins and mothers; TS13 clone TS13_a02d11
DQ796897.1 gg_id:179291 human fecal clone RL179_aao56b02
FJ680023.1 gg_id:522639 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU761995.1 gg_id:334919 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ679977.1 gg_id:517083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677857.1 gg_id:521195 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681949.1 gg_id:513569 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF400356.1 gg_id:210432 human fecal clone SJTU_E_12_09
EF405201.1 gg_id:217164 human fecal clone SJTU_G_04_21
FJ680077.1 gg_id:516044 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY984867.1 gg_id:127621 human stool clone B841
EU763157.1 gg_id:309611 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ371159.1 gg_id:365400 feces adult twins and mothers; TS6 clone TS6_a01f05
FJ683410.1 gg_id:531453 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ794046.1 gg_id:185772 human fecal clone RL176_aan57b11
FJ682245.1 gg_id:521193 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673477.1 gg_id:520316 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ905741.2 gg_id:164241 human fecal clone 29A-d7
FJ372190.1 gg_id:359880 feces adult twins and mothers; TS9 clone TS9_a02g06
FJ685342.1 gg_id:515553 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368347.1 gg_id:366580 feces adult twins and mothers; TS3 clone TS3_a03c08
FJ365095.1 gg_id:368089 feces adult twins and mothers; TS1 clone TS1_a02g06
FJ366277.1 gg_id:358995 feces adult twins and mothers; TS25 clone TS25_a04g06
FJ371104.1 gg_id:365661 feces adult twins and mothers; TS6 clone TS6_a01a03
AY985216.1 gg_id:119095 human stool clone C080
FJ369891.1 gg_id:359736 feces adult twins and mothers; TS55 clone TS55_a02a02
FJ684085.1 gg_id:517705 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ325670.1 gg_id:145519 Metagenomic gut microbiome healthy human stool clone B262
EU766758.1 gg_id:322883 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ806563.1 gg_id:195758 human fecal clone RL186_aao46b05
FJ362646.1 gg_id:365822 feces adult twins and mothers; TS13 clone TS13_a01d12

EU462258.1	294922	9546.4	10532.8	6275.1	7273.2	10245.6	8091.0
FJ363396.1	359501	6686.5	5067.5	3074.0	5238.3	2839.0	3937.3
FJ680071.1	524461	1467.9	2492.6	1494.1	1098.2	3083.5	2451.3
EU761635.1	329509	36.6	53.9	64.5	91.9	76.7	32.1
EF403807.1	214604	627.6	789.6	2002.6	1433.7	715.0	1253.5
EU774128.1	310301	165.8	212.2	1059.7	212.5	331.7	538.0
FJ683496.1	527743	22.7	46.7	24.4	45.1	53.9	16.1
FJ370925.1	361734	4529.0	2217.4	2458.4	6381.9	2959.1	4963.3
FJ677019.1	517142	12905.1	10913.4	8985.7	12607.4	12170.6	10345.7
FJ364613.1	358324	885.9	668.5	1397.5	474.4	110.6	258.4
FJ362730.1	369611	1399.9	796.8	1281.3	2415.6	782.2	964.6
DQ796897.1	179291	3009.7	2024.8	612.2	524.0	335.1	488.8
FJ680023.1	522639	1953.7	2494.6	1723.0	1715.4	3982.0	3524.2
EU761995.1	334919	8437.6	7448.0	1713.5	5680.0	7834.2	6570.5
FJ679977.1	517083	46.2	55.1	186.4	96.0	110.5	123.3
FJ677857.1	521195	1468.0	2329.2	1586.0	1087.9	3079.1	2632.9
FJ681949.1	513569	2149.0	2980.3	2934.4	3198.8	3412.5	3080.8
EF400356.1	210432	477.9	115.3	482.3	2290.6	332.5	454.8
EF405201.1	217164	515.3	618.7	1051.3	1172.5	710.2	1071.8
FJ680077.1	516044	231.5	383.7	542.4	183.1	559.4	324.8
AY984867.1	127621	882.0	1218.2	502.4	230.5	286.1	358.5
EU763157.1	309611	1013.1	1867.2	3743.8	1130.5	2464.2	2497.0
FJ371159.1	365400	497.8	514.2	2415.6	2273.8	1824.3	1648.6
FJ683410.1	531453	2132.5	2573.6	1778.0	1019.8	1154.2	1874.7
DQ794046.1	185772	6077.1	5430.1	3586.4	7811.8	9973.4	10376.7
FJ682245.1	521193	4193.1	3762.8	1977.6	2118.9	3760.3	3418.1
FJ673477.1	520316	3896.3	3546.3	828.1	4211.1	1073.5	1008.2
DQ905741.2	164241	480.1	601.3	154.8	453.1	304.9	202.0
FJ372190.1	359880	3818.0	3193.2	980.7	6492.8	7014.9	5777.2
FJ685342.1	515553	3689.3	2956.4	2317.3	4703.0	4602.9	4318.1
FJ368347.1	366580	1904.6	1340.7	1692.2	2057.7	960.2	1534.5
FJ365095.1	368089	519.7	455.5	1699.9	2502.1	533.4	1015.4
FJ366277.1	358995	1177.0	1131.7	337.8	1714.8	1026.0	796.2
FJ371104.1	365661	2911.4	2551.7	1090.9	3225.8	3673.5	3264.2
AY985216.1	119095	18763.2	18675.8	13878.1	15479.1	17505.9	16963.7
FJ369891.1	359736	15562.2	13498.1	10490.3	11546.6	12685.7	12249.7
FJ684085.1	517705	1304.3	1002.3	1071.1	2217.5	1186.5	1445.4
DQ325670.1	145519	13.0	22.5	27.4	46.9	65.3	12.9
EU766758.1	322883	1365.5	1171.3	1664.3	1582.3	3428.9	2552.6
DQ806563.1	195758	2041.7	1636.6	1125.7	2384.4	2113.4	2208.3
FJ362646.1	365822	916.8	984.9	498.3	143.2	304.9	381.4

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FJ683725.1 gg_id:519688 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ904640.1 gg_id:171420 human fecal clone 001-a1
FJ370204.1 gg_id:362927 feces adult twins and mothers; TS56 clone TS56_a01g03
DQ802480.1 gg_id:193583 human fecal clone RL188_aah18c11
FJ683617.1 gg_id:524643 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678572.1 gg_id:527621 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801657.1 gg_id:178139 human fecal clone RL201_aai45b04
FJ673415.1 gg_id:532467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372244.1 gg_id:366729 feces adult twins and mothers; TS9 clone TS9_a03d04
FJ678365.1 gg_id:528634 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368893.1 gg_id:356750 feces adult twins and mothers; TS4 clone TS4_a01g09
EF405023.1 gg_id:215838 human fecal clone SJTU_G_07_02
FJ363642.1 gg_id:361321 feces adult twins and mothers; TS14 clone TS14_a01f07
DQ797286.1 gg_id:183033 human fecal clone RL248_aai97d04
FJ684341.1 gg_id:508990 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800968.1 gg_id:197811 human fecal clone RL387_aao90a10
DQ795769.1 gg_id:191005 human fecal clone RL245_aai82a11
FJ684460.1 gg_id:512202 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU778065.1 gg_id:332745 feces clone RL117_aae93c03
FJ679157.1 gg_id:525268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU761901.1 gg_id:336184 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ676393.1 gg_id:520110 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY985777.1 gg_id:122394 human stool clone D020
AY978413.1 gg_id:118037 human transverse colon mucosal biopsy clone KO12
DQ797125.1 gg_id:194262 human fecal clone RL386_aao87c10
FJ366217.1 gg_id:364840 feces adult twins and mothers; TS25 clone TS25_a04b02
FJ684396.1 gg_id:531731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676113.1 gg_id:527838 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800942.1 gg_id:184549 human fecal clone RL387_aao89f11
FJ363122.1 gg_id:360347 feces adult twins and mothers; TS148 clone TS148_a03d04
DQ797806.1 gg_id:184609 human fecal clone RL206_aaj16a11
FJ368088.1 gg_id:359308 feces adult twins and mothers; TS30 clone TS30_a03h03
FJ364489.1 gg_id:363784 feces adult twins and mothers; TS15 clone TS15_a03e10
AY982071.1 gg_id:127146 human sigmoid colon mucosal biopsy clone P522
FJ680054.1 gg_id:519260 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678075.1 gg_id:529865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371741.1 gg_id:370050 feces adult twins and mothers; TS8 clone TS8_a01f10
AY977065.1 gg_id:124585 human cecum mucosal biopsy clone K753
EU764123.1 gg_id:312088 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
FJ371415.1 gg_id:365951 feces adult twins and mothers; TS6 clone TS6_a04f10

AF376215.1	72853	21.3	48.6	23.2	45.5	64.6	10.9
FJ683725.1	519688	8617.6	8009.4	4070.1	8300.6	11086.8	8227.9
DQ904640.1	171420	486.0	636.5	1062.5	1106.5	609.8	1079.8
FJ370204.1	362927	5026.2	3823.7	2941.2	4500.3	2220.9	3274.0
DQ802480.1	193583	2954.6	4044.1	4300.6	3003.1	4524.5	5392.0
FJ683617.1	524643	2015.2	1675.0	2295.5	1255.9	858.6	2074.9
FJ678572.1	527621	1110.4	1094.1	1361.8	522.1	4419.1	2390.2
DQ801657.1	178139	1882.9	1509.4	944.5	2211.7	1823.5	1872.3
FJ673415.1	532467	1091.6	2901.5	3627.8	1522.6	6400.0	4731.4
FJ372244.1	366729	1226.0	1083.7	630.9	798.8	298.0	1352.4
FJ678365.1	528634	2970.7	4278.9	3010.8	5269.9	1734.8	1177.8
FJ368893.1	356750	6807.9	6752.7	2566.8	6092.5	5422.6	4781.5
EF405023.1	215838	384.8	220.9	1216.2	2127.3	352.1	485.5
FJ363642.1	361321	240.0	85.3	164.4	90.5	44.2	39.8
DQ797286.1	183033	31.1	44.4	35.6	56.7	55.9	33.4
FJ684341.1	508990	2351.7	2312.5	1228.8	2543.2	2941.0	2591.1
DQ800968.1	197811	432.1	850.3	1372.3	665.2	559.8	772.0
DQ795769.1	191005	158.9	198.3	518.2	46.7	167.7	163.7
FJ684460.1	512202	15.8	47.2	18.0	44.3	45.6	13.0
EU778065.1	332745	315.1	587.9	711.3	820.9	101.5	83.5
FJ679157.1	525268	9182.7	10494.3	7174.0	7943.4	9360.7	8329.3
EU761901.1	336184	1609.0	2511.5	4103.5	3003.1	2134.7	1723.8
FJ676393.1	520110	2595.4	1556.1	3705.7	2791.9	3233.9	3614.9
AY985777.1	122394	571.6	418.5	860.1	321.6	1611.4	1184.9
AY978413.1	118037	2484.5	1965.2	2759.9	6652.9	2621.6	2633.5
DQ797125.1	194262	27.4	51.3	68.9	74.1	66.9	15.6
FJ366217.1	364840	212.2	113.0	406.6	105.1	60.3	25.8
FJ684396.1	531731	537.8	166.0	634.6	149.9	204.3	473.9
FJ676113.1	527838	32.3	67.7	47.6	79.2	64.2	49.5
DQ800942.1	184549	2590.6	2541.0	3081.2	1940.6	2645.7	1529.7
FJ363122.1	360347	1515.3	649.0	785.0	1504.6	3459.6	3462.2
DQ797806.1	184609	274.9	230.3	332.6	187.3	440.7	158.5
FJ368088.1	359308	277.4	159.9	598.9	1325.6	208.2	330.4
FJ364489.1	363784	1429.2	1583.5	1064.2	2004.5	548.8	632.1
AY982071.1	127146	2697.6	4205.4	5001.5	4639.6	3996.6	4999.4
FJ680054.1	519260	35.6	74.1	256.3	83.4	52.6	25.0
FJ678075.1	529865	1641.8	2525.7	1832.4	2623.2	4857.8	4003.5
FJ371741.1	370050	10281.8	8796.1	9609.7	9261.0	8771.9	11728.5
AY977065.1	124585	2284.6	1647.9	1725.6	1515.6	2431.0	2188.8
EU764123.1	312088	6467.5	5660.7	5982.2	5117.4	6114.3	5981.2
FJ371415.1	365951	699.0	625.5	2076.0	549.0	818.6	3016.4

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FJ678352.1 gg_id:527741 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683259.1 gg_id:516155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
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DQ798035.1 gg_id:198457 human fecal clone RL302_aal94g09
FJ684131.1 gg_id:530157 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF402785.1 gg_id:212426 human fecal clone SJTU_B_12_44
EF071157.1 gg_id:199708 library survey and quantitative measurement major mucosa- IBD human colonic muc
FJ366888.1 gg_id:361634 feces adult twins and mothers; TS28 clone TS28_a01a08
DQ800979.1 gg_id:183465 human fecal clone RL387_aao90c06
FJ362639.1 gg_id:368154 feces adult twins and mothers; TS13 clone TS13_a01d04
FJ679858.1 gg_id:527207 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ904998.1 gg_id:170071 human fecal clone 002-h11
FJ683435.1 gg_id:529645 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ675792.1 gg_id:518214 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767181.1 gg_id:305562 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
FJ372286.1 gg_id:359224 feces adult twins and mothers; TS9 clone TS9_a03h02
EF402118.1 gg_id:204479 human fecal clone SJTU_B_03_85
FJ685348.1 gg_id:529021 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ326221.1 gg_id:150345 Metagenomic gut microbiome healthy human stool clone C143
FJ366949.1 gg_id:368858 feces adult twins and mothers; TS28 clone TS28_a01f10
DQ325799.1 gg_id:150495 Metagenomic gut microbiome healthy human stool clone B514
DQ798719.1 gg_id:198812 human fecal clone RL181_aao00e05
AY978564.1 gg_id:116677 human transverse colon mucosal biopsy clone KR30
FJ678164.1 gg_id:520304 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370309.1 gg_id:365868 feces adult twins and mothers; TS56 clone TS56_a03c05
EF405227.1 gg_id:212715 human fecal clone SJTU_G_04_56
FJ678642.1 gg_id:516541 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683970.1 gg_id:516455 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ809848.1 gg_id:195230 human fecal clone RL184_aao65b01
GQ898076.1 gg_id:543631 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ678782.1 gg_id:509694 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371649.1 gg_id:370248 feces adult twins and mothers; TS7 clone TS7_a04f04
DQ808981.1 gg_id:180285 human fecal clone RL243_aai87g06
GQ898670.1 gg_id:564850 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ680944.1 gg_id:527158 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798679.1 gg_id:180255 human fecal clone RL181_aao00a05
FJ673821.1 gg_id:517670 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798530.1 gg_id:189377 human fecal clone RL181_aan97h03
EF402819.1 gg_id:212119 human fecal clone SJTU_B_12_91
DQ799487.1 gg_id:186154 human fecal clone RL305aal86h04

FJ676206.1	509786	4462.7	4610.7	1915.3	5798.9	6816.1	6667.4
FJ678352.1	527741	503.6	679.5	263.8	325.2	1161.1	703.0
FJ683259.1	516155	13297.0	13447.0	10555.1	12525.9	12923.4	12000.0
DQ807398.1	198896	34.0	56.7	59.1	82.6	75.6	28.2
DQ798035.1	198457	31.6	52.3	46.0	56.5	74.4	34.7
FJ684131.1	530157	1745.5	1226.2	854.8	2079.7	1588.4	1530.5
EF402785.1	212426	685.7	1354.5	2478.0	372.6	604.2	1359.7
EF071157.1	199708	216.1	257.0	674.6	201.5	915.3	97.6
FJ366888.1	361634	241.4	197.6	245.9	882.6	560.3	648.7
DQ800979.1	183465	3510.9	3196.4	958.8	6567.4	8199.9	6616.7
FJ362639.1	368154	2104.6	3476.4	1975.6	1089.2	3005.3	2765.0
FJ679858.1	527207	2323.9	1869.3	291.8	4047.3	3258.7	3599.9
DQ904998.1	170071	7835.3	9494.6	4455.8	7538.6	8362.6	6656.2
FJ683435.1	529645	9737.3	10330.7	8105.9	8004.5	11183.0	9905.8
FJ675792.1	518214	26.4	58.0	47.1	73.6	72.5	35.1
EU767181.1	305562	3056.2	2798.1	1947.2	4656.6	1920.3	1831.5
FJ372286.1	359224	943.1	1098.6	2341.8	663.0	596.3	1158.2
EF402118.1	204479	1124.6	867.5	1649.6	3837.6	365.8	498.1
FJ685348.1	529021	3418.2	3083.8	618.6	6294.2	3983.5	3639.9
DQ326221.1	150345	2298.5	215.0	1251.9	4283.4	1521.8	1865.5
FJ366949.1	368858	10563.9	9921.1	7706.9	11562.5	9548.0	10835.4
DQ325799.1	150495	6217.3	7004.1	731.7	5058.4	2865.3	2867.6
DQ798719.1	198812	1334.7	1942.7	2790.7	3065.5	2901.2	3566.8
AY978564.1	116677	9225.5	9274.9	8170.0	6834.9	6568.9	5821.8
FJ678164.1	520304	1065.8	721.3	945.7	1044.9	1126.5	953.4
FJ370309.1	365868	2392.7	2751.1	638.9	1480.9	1148.5	1162.5
EF405227.1	212715	132.9	239.2	157.5	137.0	85.4	174.5
FJ678642.1	516541	2436.1	3842.6	2963.5	2027.5	4911.6	6290.3
FJ683970.1	516455	295.0	827.3	2629.9	700.7	1245.3	1923.8
DQ809848.1	195230	43.0	54.5	164.6	105.2	106.4	63.0
GQ898076.1	543631	633.0	747.2	1869.1	1449.8	731.6	1505.0
FJ678782.1	509694	1107.1	2111.3	1213.2	1633.1	1318.3	658.0
FJ371649.1	370248	4030.5	4982.6	4944.0	5153.6	1460.8	2902.4
DQ808981.1	180285	3170.7	1701.4	2416.0	2706.3	4512.3	3771.5
GQ898670.1	564850	5464.6	2687.2	3496.5	4968.3	2435.9	4962.4
FJ680944.1	527158	15.5	21.5	29.2	69.6	49.5	16.8
DQ798679.1	180255	3431.5	5207.9	868.3	2236.7	1755.5	2480.5
FJ673821.1	517670	2030.9	1510.3	873.7	2070.9	1952.3	2203.2
DQ798530.1	189377	1658.6	1019.4	781.5	1389.3	1777.3	1888.0
EF402819.1	212119	1527.9	1679.3	1697.5	1693.5	1371.6	1573.6
DQ799487.1	186154	27.3	30.3	117.0	67.2	69.1	35.4

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AY979514.1 gg_id:119264 human transverse colon mucosal biopsy clone M160
FJ676761.1 gg_id:526358 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682451.1 gg_id:526673 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673483.1 gg_id:527767 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ362814.1 gg_id:364795 feces adult twins and mothers; TS13 clone TS13_a03e05
FJ372156.1 gg_id:359874 feces adult twins and mothers; TS9 clone TS9_a02d04
DQ326201.1 gg_id:145226 Metagenomic gut microbiome healthy human stool clone C116
FJ680188.1 gg_id:528166 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ804764.1 gg_id:181116 human fecal clone RL187_aao72d08
FJ369823.1 gg_id:364058 feces adult twins and mothers; TS55 clone TS55_a01c02
FJ684742.1 gg_id:520441 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370273.1 gg_id:362326 feces adult twins and mothers; TS56 clone TS56_a02f11
EU765118.1 gg_id:309167 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
FJ362692.1 gg_id:366820 feces adult twins and mothers; TS13 clone TS13_a02a04
FJ367260.1 gg_id:369708 feces adult twins and mothers; TS29 clone TS29_a01d10
FJ363053.1 gg_id:370232 feces adult twins and mothers; TS148 clone TS148_a02d07
FJ371283.1 gg_id:360702 feces adult twins and mothers; TS6 clone TS6_a03b05
FJ365677.1 gg_id:367205 feces adult twins and mothers; TS21 clone TS21_a01g01
DQ799510.1 gg_id:186884 human fecal clone RL305aal87b07
GQ175373.1 gg_id:584966 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
EF402512.1 gg_id:203664 human fecal clone SJTU_B_08_92
FJ673240.1 gg_id:516744 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371180.1 gg_id:365540 feces adult twins and mothers; TS6 clone TS6_a01h03
FJ683865.1 gg_id:523118 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF401959.1 gg_id:212271 human fecal clone SJTU_B_01_85
FJ673944.1 gg_id:523733 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364604.1 gg_id:365932 feces adult twins and mothers; TS15 clone TS15_a04h10
AY983235.1 gg_id:122065 human descending colon mucosal biopsy clone A192
DQ804507.1 gg_id:186014 human fecal clone RL187_aao69a03
DQ808734.1 gg_id:199447 human fecal clone RL239_aaj12e07
FJ680784.1 gg_id:530524 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679029.1 gg_id:513799 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ808691.1 gg_id:190119 human fecal clone RL239_aaj11h08
FJ367381.1 gg_id:365214 feces adult twins and mothers; TS29 clone TS29_a02g09
EF402416.1 gg_id:206779 human fecal clone SJTU_B_07_64
FJ371107.1 gg_id:364493 feces adult twins and mothers; TS6 clone TS6_a01a08
DQ802576.1 gg_id:188600 human fecal clone RL188_aan93f02
FJ679591.1 gg_id:522278 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679377.1 gg_id:516690 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ825338.1 gg_id:192202 human fecal clone RL185_aan88g06
EF400945.1 gg_id:208336 human fecal clone SJTU_D_03_77

AY979514.1	119264	765.7	544.1	177.4	1136.0	1092.7	687.4
FJ676761.1	526358	5661.9	7282.8	6714.8	6694.0	10989.7	9731.1
FJ682451.1	526673	2544.4	2536.6	2795.8	4839.8	3861.8	3185.6
FJ673483.1	527767	948.7	1590.1	839.3	546.8	1763.3	1367.7
FJ362814.1	364795	3467.9	3397.4	2347.7	2476.1	3787.8	5071.4
FJ372156.1	359874	173.8	207.4	237.2	85.8	319.8	209.5
DQ326201.1	145226	1053.3	1720.2	1182.8	618.9	1746.5	1562.2
FJ680188.1	528166	3557.2	4716.5	2651.5	3251.2	6422.5	5002.7
DQ804764.1	181116	977.3	1243.5	2324.8	598.4	3230.9	1948.8
FJ369823.1	364058	1239.6	965.8	1408.0	1587.6	925.8	2673.0
FJ684742.1	520441	61.2	62.8	194.4	88.3	40.2	21.9
FJ370273.1	362326	247.2	393.5	872.8	236.3	227.8	344.7
EU765118.1	309167	34.4	60.7	54.9	73.5	76.9	35.8
FJ362692.1	366820	398.2	489.5	1286.7	309.8	336.6	525.4
FJ367260.1	369708	12438.5	11985.4	10822.0	12869.3	11151.9	12066.5
FJ363053.1	370232	310.3	108.8	230.7	157.2	356.7	1247.1
FJ371283.1	360702	2386.2	1885.0	3192.8	4177.9	2869.8	3190.5
FJ365677.1	367205	254.8	269.4	254.4	149.2	573.6	243.4
DQ799510.1	186884	792.5	1036.3	676.2	318.1	221.1	229.3
GQ175373.1	584966	73.5	81.8	192.1	112.1	93.2	46.3
EF402512.1	203664	7567.1	7987.9	9236.2	8914.2	5218.2	7580.8
FJ673240.1	516744	128.4	207.5	265.7	101.9	325.3	205.1
FJ371180.1	365540	2714.1	2887.9	5381.9	3507.4	2337.3	4267.3
FJ683865.1	523118	1267.1	1229.3	1462.2	2078.7	2190.5	1389.0
EF401959.1	212271	314.7	376.8	647.6	205.8	246.0	341.4
FJ673944.1	523733	32.3	29.8	34.8	52.2	67.4	20.6
FJ364604.1	365932	938.4	1345.3	752.2	1562.7	428.9	671.3
AY983235.1	122065	2226.1	2179.1	596.0	3101.1	940.5	828.9
DQ804507.1	186014	508.8	655.2	1561.9	399.4	349.3	1080.8
DQ808734.1	199447	381.2	433.6	498.3	61.9	96.2	77.4
FJ680784.1	530524	104.9	107.6	236.9	139.9	165.2	239.7
FJ679029.1	513799	2674.2	4033.0	4541.4	3934.1	6058.1	5587.3
DQ808691.1	190119	677.7	414.4	1295.3	377.4	396.2	341.4
FJ367381.1	365214	26.4	24.5	165.5	108.7	492.7	882.8
EF402416.1	206779	2472.4	2863.3	4143.7	2294.9	1466.3	2727.1
FJ371107.1	364493	3850.4	3768.8	5343.5	7281.3	6785.7	8640.5
DQ802576.1	188600	6869.7	7207.6	2928.1	6779.3	10303.5	8646.2
FJ679591.1	522278	1743.1	1888.4	2476.2	3074.3	2289.4	3021.9
FJ679377.1	516690	357.4	405.8	910.5	244.2	208.4	352.8
DQ825338.1	192202	907.1	232.1	838.7	241.8	58.8	270.8
EF400945.1	208336	100.2	166.5	420.8	124.3	133.2	169.0

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FJ675969.1 gg_id:530963 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF404511.1 gg_id:207963 human fecal clone SJTU_C_11_29
FJ673301.1 gg_id:525513 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795114.1 gg_id:177532 human fecal clone RL310_aam40d06
DQ798521.1 gg_id:192503 human fecal clone RL181_aan97g05
GQ897282.1 gg_id:558123 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
EF402700.1 gg_id:214090 human fecal clone SJTU_B_11_34
DQ825176.1 gg_id:178234 human fecal clone RL185_aan86c10
DQ801178.1 gg_id:188051 human fecal clone RL116_aaf00a03
FJ370149.1 gg_id:360416 feces adult twins and mothers; TS56 clone TS56_a01a04
FJ367847.1 gg_id:364381 feces adult twins and mothers; TS2 clone TS2_a04c07
DQ469229.1 gg_id:158909 Microbial and ecology water Zhong Tiaoshan mine Shanxi province China AMD clone
FJ683359.1 gg_id:523960 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF403721.1 gg_id:212755 human fecal clone SJTU_A2_05_86
DQ797650.1 gg_id:192042 human fecal clone RL206_aaj14c03
DQ798554.1 gg_id:194392 human fecal clone RL181_aan98b11
FJ367121.1 gg_id:360386 feces adult twins and mothers; TS28 clone TS28_a03g04
EU766034.1 gg_id:352547 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
EU778232.1 gg_id:308969 feces clone RL388_aao95a03
FJ365927.1 gg_id:366110 feces adult twins and mothers; TS21 clone TS21_a04g04
DQ796459.1 gg_id:188277 human fecal clone RL179_aah28f11
FJ362745.1 gg_id:369094 feces adult twins and mothers; TS13 clone TS13_a02f05
FJ371672.1 gg_id:358662 feces adult twins and mothers; TS7 clone TS7_a04h10
FJ675980.1 gg_id:511246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766901.1 gg_id:306887 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ823998.1 gg_id:184400 human fecal clone RL204_aaj57h10
FJ370290.1 gg_id:362757 feces adult twins and mothers; TS56 clone TS56_a03a01
FJ681145.1 gg_id:530484 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF400967.1 gg_id:204553 human fecal clone SJTU_D_04_90
EU764451.1 gg_id:323792 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ675800.1 gg_id:531629 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682966.1 gg_id:522398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ369910.1 gg_id:359256 feces adult twins and mothers; TS55 clone TS55_a02b11
DQ905116.1 gg_id:161788 human fecal clone 002C-b5
DQ793377.1 gg_id:197159 human fecal clone RL199_aaj43a01
EU766025.1 gg_id:304228 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
FJ673225.1 gg_id:521732 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682288.1 gg_id:519606 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673158.1 gg_id:522957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682107.1 gg_id:516615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370322.1 gg_id:367382 feces adult twins and mothers; TS56 clone TS56_a03e02

FJ675969.1	530963	16212.9	17465.1	10249.9	11452.6	17039.6	16133.3
EF404511.1	207963	212.1	608.6	415.0	153.0	580.5	224.8
FJ673301.1	525513	8367.4	7887.6	5880.7	6462.3	8567.9	9211.1
DQ795114.1	177532	3455.7	3653.2	2418.8	3937.4	3050.0	3034.9
DQ798521.1	192503	1582.6	1463.0	2458.2	2516.1	1547.2	2089.4
GQ897282.1	558123	2368.5	2584.4	3649.1	3196.0	2501.2	3914.4
EF402700.1	214090	2145.4	1763.5	2099.2	2361.9	1391.1	2079.7
DQ825176.1	178234	322.2	231.9	214.6	180.8	459.1	174.4
DQ801178.1	188051	38.1	56.3	60.6	93.5	76.6	31.8
FJ370149.1	360416	7395.7	7330.4	4663.5	6496.5	6409.2	5940.1
FJ367847.1	364381	241.7	169.7	208.0	126.8	192.9	965.4
DQ469229.1	158909	1701.1	2698.8	2461.2	2144.5	2753.1	2832.8
FJ683359.1	523960	277.0	408.5	740.2	951.0	1070.4	711.2
EF403721.1	212755	3307.2	3746.0	4885.2	3578.3	4196.1	6759.6
DQ797650.1	192042	6121.0	6629.2	4737.7	4365.4	7062.3	8836.5
DQ798554.1	194392	6184.2	4028.1	4294.1	5558.6	4356.9	4169.9
FJ367121.1	360386	27.1	42.3	39.0	67.9	67.8	30.0
EU766034.1	352547	891.2	1649.6	520.3	214.9	356.1	480.4
EU778232.1	308969	457.7	530.6	2393.9	2253.9	1814.3	1745.5
FJ365927.1	366110	1855.7	134.2	545.8	3075.8	1230.8	1341.1
DQ796459.1	188277	14644.6	12130.7	11797.1	11234.2	10955.4	9345.5
FJ362745.1	369094	1266.2	1521.5	3032.5	1160.3	1797.2	1877.0
FJ371672.1	358662	5828.9	6363.6	3657.1	3106.9	2312.4	2589.2
FJ675980.1	511246	2332.8	1743.9	1493.5	2997.4	5523.8	4989.4
EU766901.1	306887	12.8	19.2	12.1	39.8	45.8	12.4
DQ823998.1	184400	4380.4	3780.1	2984.8	5608.9	9509.1	7613.2
FJ370290.1	362757	2232.1	2376.9	1113.2	512.1	1454.4	2059.8
FJ681145.1	530484	7392.5	5246.4	2673.8	7481.5	6978.3	6223.9
EF400967.1	204553	1759.9	1942.9	3279.6	2236.2	1607.1	2959.6
EU764451.1	323792	29.7	39.3	37.6	66.6	55.8	37.1
FJ675800.1	531629	6773.8	3523.2	2622.5	7153.0	7074.7	7395.5
FJ682966.1	522398	2804.6	3175.9	1598.9	1466.3	4716.6	3248.8
FJ369910.1	359256	35.8	59.1	87.8	65.5	67.6	99.1
DQ905116.1	161788	387.8	553.8	1348.0	265.1	290.4	510.9
DQ793377.1	197159	46.8	54.4	72.0	69.7	72.0	26.7
EU766025.1	304228	106.7	164.6	399.0	138.0	146.1	168.5
FJ673225.1	521732	63.1	70.8	326.9	1290.9	337.0	385.3
FJ682288.1	519606	2035.6	2770.8	2383.2	2995.8	3049.0	3150.2
FJ673158.1	522957	8338.8	7737.1	1588.9	5006.0	3780.9	3203.7
FJ682107.1	516615	36.4	46.8	25.3	58.2	61.8	30.4
FJ370322.1	367382	458.5	788.6	1654.3	417.5	901.2	1623.9

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FJ371385.1 gg_id:362570 feces adult twins and mothers; TS6 clone TS6_a04c10
FJ682406.1 gg_id:531662 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798507.1 gg_id:183096 human fecal clone RL181_aan97e12
FJ677575.1 gg_id:515083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY983422.1 gg_id:123823 human descending colon mucosal biopsy clone NK14
FJ683598.1 gg_id:522106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798678.1 gg_id:198469 human fecal clone RL181_aao00a04
EF402454.1 gg_id:203687 human fecal clone SJTU_B_08_14
FJ683257.1 gg_id:528148 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY981461.1 gg_id:118731 human sigmoid colon mucosal biopsy clone L558
EU767939.1 gg_id:341514 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
FJ362628.1 gg_id:367786 feces adult twins and mothers; TS13 clone TS13_a01c05
FJ673672.1 gg_id:524310 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767080.1 gg_id:340311 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ368434.1 gg_id:359625 feces adult twins and mothers; TS3 clone TS3_a04c09
FJ364880.1 gg_id:365919 feces adult twins and mothers; TS19 clone TS19_a04c05
FJ367215.1 gg_id:366962 feces adult twins and mothers; TS28 clone TS28_a04h05
FJ678145.1 gg_id:518849 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799361.1 gg_id:186348 human fecal clone RL305aal85d03
FJ683668.1 gg_id:520472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364280.1 gg_id:364565 feces adult twins and mothers; TS15 clone TS15_a01a12
FJ366929.1 gg_id:361813 feces adult twins and mothers; TS28 clone TS28_a01e02
FJ363897.1 gg_id:366974 feces adult twins and mothers; TS14 clone TS14_a04f07
FJ367152.1 gg_id:364498 feces adult twins and mothers; TS28 clone TS28_a04b04
GQ492964.1 gg_id:591625 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ797761.1 gg_id:184060 human fecal clone RL206_aaj15e10
FJ679711.1 gg_id:530337 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676397.1 gg_id:526989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673113.1 gg_id:512268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801294.1 gg_id:176684 human fecal clone RL388_aao93e09
EF399852.1 gg_id:206460 human fecal clone SJTU_E_04_61
FJ371178.1 gg_id:362345 feces adult twins and mothers; TS6 clone TS6_a01h01
GQ448356.1 gg_id:580587 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr
FJ676463.1 gg_id:521552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677694.1 gg_id:513781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681996.1 gg_id:516655 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368879.1 gg_id:366263 feces adult twins and mothers; TS4 clone TS4_a01f06
EF401378.1 gg_id:210066 human fecal clone SJTU_D_09_55
DQ805727.1 gg_id:184345 human fecal clone RL306aal90c11
DQ796525.1 gg_id:197708 human fecal clone RL179aan74b04
DQ809575.1 gg_id:194381 human fecal clone RL184_aan81a10

FJ371385.1	362570	1482.0	1825.2	3425.9	1845.8	1670.8	2522.3
FJ682406.1	531662	3060.8	4612.1	6504.5	2572.9	4449.9	5789.9
DQ798507.1	183096	2068.4	2328.0	1083.9	4769.0	4750.0	3961.1
FJ677575.1	515083	1317.7	2172.7	5250.2	2613.6	1324.0	2187.9
AY983422.1	123823	3216.6	4556.6	4146.7	4113.3	2865.0	3422.0
FJ683598.1	522106	50.7	67.5	182.7	1106.1	291.8	286.0
DQ798678.1	198469	10890.5	13642.4	5008.4	9660.5	6903.0	6833.4
EF402454.1	203687	1684.8	1545.4	2753.0	2356.0	1467.6	2045.9
FJ683257.1	528148	38.5	36.5	31.8	55.9	55.1	20.9
AY981461.1	118731	2392.2	2139.8	838.4	689.6	453.6	832.5
EU767939.1	341514	14253.8	13717.3	11200.1	13491.8	12024.0	13857.0
FJ362628.1	367786	23.6	76.9	26.3	53.2	72.6	26.1
FJ673672.1	524310	47.5	83.3	126.9	91.5	108.4	119.8
EU767080.1	340311	1561.1	1730.3	363.4	1568.7	696.5	819.3
FJ368434.1	359625	302.5	524.9	946.1	278.5	252.8	354.0
FJ364880.1	365919	13426.9	14511.8	5212.8	13291.5	11007.2	10994.9
FJ367215.1	366962	2274.0	2564.8	2838.3	3988.0	3009.4	4917.2
FJ678145.1	518849	1580.6	2342.6	1448.0	1096.8	3094.1	2636.0
DQ799361.1	186348	25.9	31.7	37.4	76.4	60.1	29.1
FJ683668.1	520472	690.4	825.6	2213.3	3098.4	2448.1	2184.9
FJ364280.1	364565	2015.7	1486.6	3078.8	1552.6	2368.5	2081.0
FJ366929.1	361813	4186.1	4805.8	3206.9	4134.1	4026.7	5683.7
FJ363897.1	366974	992.3	770.9	1274.3	1917.8	183.0	386.4
FJ367152.1	364498	5447.4	7126.6	5995.1	8071.2	6576.9	6441.4
GQ492964.1	591625	40.6	36.0	183.6	79.6	75.9	66.9
DQ797761.1	184060	4576.3	2757.3	2643.8	5077.9	2582.4	3853.5
FJ679711.1	530337	1577.4	1647.5	2087.5	4797.2	6544.2	5529.4
FJ676397.1	526989	131.6	198.8	337.2	136.6	212.0	220.0
FJ673113.1	512268	1534.7	1514.9	377.0	1012.4	615.0	1025.6
DQ801294.1	176684	13853.5	13895.1	10325.2	11360.2	14239.2	14469.6
EF399852.1	206460	137.4	194.1	813.1	139.9	206.5	304.8
FJ371178.1	362345	1486.3	1313.0	2225.5	3624.0	1883.0	1473.9
GQ448356.1	580587	2109.9	3763.4	2026.7	1756.9	4811.1	4045.8
FJ676463.1	521552	7375.9	8833.5	6448.4	4282.6	11655.5	11589.5
FJ677694.1	513781	2272.8	2515.2	5118.8	1870.0	3578.5	3015.4
FJ681996.1	516655	81.1	123.1	351.8	100.5	805.8	314.7
FJ368879.1	366263	17.7	27.0	37.9	50.1	74.3	14.8
EF401378.1	210066	6047.2	5894.4	4661.0	6067.5	6238.8	4720.9
DQ805727.1	184345	63.2	112.3	117.1	213.8	282.6	125.5
DQ796525.1	197708	333.5	496.8	995.5	431.0	415.1	635.3
DQ809575.1	194381	521.2	600.2	217.2	2889.0	324.5	267.7

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DQ796982.1 gg_id:176800 human fecal clone RL386_aao85c12
FJ367002.1 gg_id:367845 feces adult twins and mothers; TS28 clone TS28_a02c09
AY983882.1 gg_id:121178 human descending colon mucosal biopsy clone MA45
DQ797931.1 gg_id:190417 human fecal clone RL302_aal93e09
DQ797343.1 gg_id:183574 human fecal clone RL248_aai98b05
FJ364420.1 gg_id:361296 feces adult twins and mothers; TS15 clone TS15_a02g03
FJ371744.1 gg_id:370012 feces adult twins and mothers; TS8 clone TS8_a01g01
GQ898023.1 gg_id:593129 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ798241.1 gg_id:187941 human fecal clone RL181_aah39d04
DQ824074.1 gg_id:193147 human fecal clone RL204_aaj59a06
FJ677745.1 gg_id:519105 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767143.1 gg_id:354400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EF399615.1 gg_id:204783 human fecal clone SJTU_E_01_19
DQ797984.1 gg_id:173930 human fecal clone RL302_aal94b07
FJ367273.1 gg_id:367414 feces adult twins and mothers; TS29 clone TS29_a01e11
DQ801207.1 gg_id:176772 human fecal clone RL116_aaf01b03
FJ680161.1 gg_id:509641 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU467468.1 gg_id:292663 Sumatran orangutan feces clone orang1_b07_1
EF404759.1 gg_id:207172 human fecal clone SJTU_C_16_02
AY978993.1 gg_id:117865 human transverse colon mucosal biopsy clone NI25
FJ371951.1 gg_id:365814 feces adult twins and mothers; TS8 clone TS8_a04a11
EU765841.1 gg_id:311856 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
AY984598.1 gg_id:117840 human stool clone B538
DQ823889.1 gg_id:197321 human fecal clone RL250_aaj80e04
DQ805135.1 gg_id:176841 human fecal clone RL249_aaj81g07
EF402826.1 gg_id:213151 human fecal clone SJTU_B_13_04
DQ794060.1 gg_id:181139 human fecal clone RL176_aan57d12
FJ363917.1 gg_id:361782 feces adult twins and mothers; TS14 clone TS14_a04h05
EU764825.1 gg_id:304968 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
FJ674170.1 gg_id:517053 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681616.1 gg_id:514621 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ806320.1 gg_id:175470 human fecal clone RL186_aan90e10
FJ672977.1 gg_id:514264 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ806282.1 gg_id:192267 human fecal clone RL186_aan89g11
EU766845.1 gg_id:308323 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
GQ897146.1 gg_id:579284 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ677737.1 gg_id:514226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ365873.1 gg_id:365362 feces adult twins and mothers; TS21 clone TS21_a04a11
DQ905134.1 gg_id:166310 human fecal clone 002C-d11
DQ824337.1 gg_id:198459 human fecal clone RL304_aal74f10

FJ370091.1	366409	1591.8	768.9	989.7	2386.9	178.6	586.0
DQ796982.1	176800	30.5	42.2	33.4	56.6	58.2	28.5
FJ367002.1	367845	552.1	422.7	724.0	2816.0	341.3	538.8
AY983882.1	121178	2293.1	3345.4	3544.7	2553.8	3081.3	3438.6
DQ797931.1	190417	2798.6	5746.8	1778.3	1702.7	590.0	1161.6
DQ797343.1	183574	1651.6	1914.0	2291.5	2238.5	1983.9	2635.7
FJ364420.1	361296	190.5	181.7	274.3	117.5	1029.8	239.7
FJ371744.1	370012	3322.0	3184.9	1987.2	1629.5	2000.1	3027.8
GQ898023.1	593129	630.4	922.6	609.0	911.5	452.6	626.3
DQ798241.1	187941	2518.9	3374.6	4667.9	4064.7	3506.5	4375.9
DQ824074.1	193147	1061.3	1678.6	5740.8	1854.1	1235.7	2118.5
FJ677745.1	519105	3920.8	4053.1	2916.3	1627.3	3931.0	4224.3
EU767143.1	354400	2722.6	2558.9	2850.6	3148.0	7379.2	4481.2
EF399615.1	204783	1420.1	2256.0	1028.0	1051.4	2768.4	2693.0
DQ797984.1	173930	5972.6	6949.4	6827.8	5878.5	4275.8	8491.8
FJ367273.1	367414	3227.6	3261.0	3316.0	3593.5	3331.7	3174.9
DQ801207.1	176772	77.1	89.1	143.8	114.5	119.5	82.0
FJ680161.1	509641	5408.3	5552.1	5414.6	5728.3	4150.1	4692.4
EU467468.1	292663	4265.2	3208.2	3257.3	5026.9	4589.7	3998.8
EF404759.1	207172	4197.9	4234.7	4076.5	3113.7	3821.5	3710.2
AY978993.1	117865	7775.1	7441.0	1728.3	4169.1	8145.4	7477.4
FJ371951.1	365814	157.1	195.4	222.6	84.0	303.7	194.5
EU765841.1	311856	45.3	41.3	30.6	56.9	53.0	21.9
AY984598.1	117840	9571.8	8569.1	10262.7	8208.7	10265.9	9506.9
DQ823889.1	197321	4837.7	7709.0	2101.8	2043.4	1259.0	1774.3
DQ805135.1	176841	13672.6	14294.1	9742.0	8777.0	10598.0	9740.8
EF402826.1	213151	132.2	235.6	786.4	226.7	190.7	201.8
DQ794060.1	181139	6219.3	5249.1	5356.7	4908.6	5654.6	5568.0
FJ363917.1	361782	172.7	102.6	147.3	90.1	216.5	91.0
EU764825.1	304968	35.0	40.9	45.5	73.6	63.0	32.2
FJ674170.1	517053	36.9	90.0	84.1	84.9	69.1	55.5
FJ681616.1	514621	494.1	947.4	1327.5	294.0	306.4	581.6
DQ806320.1	175470	1425.6	1499.6	2174.1	2471.4	1490.8	2185.2
FJ672977.1	514264	3161.2	2420.2	2838.2	5829.2	3525.6	3695.0
DQ806282.1	192267	461.1	540.6	1245.4	275.7	372.8	551.2
EU766845.1	308323	3201.5	1729.4	1400.2	2172.1	1268.1	1750.0
GQ897146.1	579284	37.7	92.8	70.1	62.9	67.6	37.8
FJ677737.1	514226	589.7	616.9	705.7	1208.3	1536.5	1512.1
FJ365873.1	365362	4202.6	3993.2	4042.2	3807.9	7870.3	4786.3
DQ905134.1	166310	310.6	454.5	914.8	235.8	200.0	343.6
DQ824337.1	198459	973.0	999.6	1173.6	1319.0	501.0	1007.8

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DQ797471.1 gg_id:197681 human fecal clone RL248_aai99g06
EU764009.1 gg_id:353680 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
DQ805302.1 gg_id:181045 human fecal clone RL249_aaj84g09
EU765096.1 gg_id:329822 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
FJ371751.1 gg_id:356933 feces adult twins and mothers; TS8 clone TS8_a01g08
FJ371913.1 gg_id:365185 feces adult twins and mothers; TS8 clone TS8_a03f06
FJ673425.1 gg_id:531791 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673914.1 gg_id:522500 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ365029.1 gg_id:364449 feces adult twins and mothers; TS1 clone TS1_a02a05
FJ365142.1 gg_id:358772 feces adult twins and mothers; TS1 clone TS1_a03d05
FJ362744.1 gg_id:365960 feces adult twins and mothers; TS13 clone TS13_a02f04
FJ683387.1 gg_id:517313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU764113.1 gg_id:341093 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
DQ797772.1 gg_id:187746 human fecal clone RL206_aaj15f09
DQ797534.1 gg_id:183136 human fecal clone RL248_aaj00f10
EU764195.1 gg_id:348580 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
FJ673014.1 gg_id:511426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU761607.1 gg_id:348796 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ677915.1 gg_id:529462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF405259.1 gg_id:208204 human fecal clone SJTU_G_03_12
FJ676446.1 gg_id:530143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796680.1 gg_id:196638 human fecal clone RL179_aao53b02
DQ801683.1 gg_id:178701 human fecal clone RL201_aai45d10
DQ806770.1 gg_id:181056 human fecal clone RL186_aao48e04
DQ808834.1 gg_id:192290 human fecal clone RL243_aai85h09
AY976679.1 gg_id:116489 human cecum mucosal biopsy clone K250
GQ175391.1 gg_id:558789 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
FJ674228.1 gg_id:516246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801519.1 gg_id:199423 human fecal clone RL388_aao96e10
DQ809610.1 gg_id:180497 human fecal clone RL184_aan81e09
DQ801990.1 gg_id:193716 human fecal clone RL241_aaj01e07
FJ366675.1 gg_id:367013 feces adult twins and mothers; TS27 clone TS27_a02e04
FJ372098.1 gg_id:363190 feces adult twins and mothers; TS9 clone TS9_a01g03
FJ369985.1 gg_id:363252 feces adult twins and mothers; TS55 clone TS55_a03b04
EU766632.1 gg_id:355409 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ798390.1 gg_id:179266 human fecal clone RL181_aah41h08
FJ367658.1 gg_id:361552 feces adult twins and mothers; TS2 clone TS2_a02a10
FJ682429.1 gg_id:519971 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797383.1 gg_id:198948 human fecal clone RL248_aai98f08
EU765795.1 gg_id:347325 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
DQ801446.1 gg_id:197808 human fecal clone RL388_aao95f06

DQ797471.1	197681	545.7	798.0	1931.8	470.2	763.0	876.7
EU764009.1	353680	439.2	306.5	1850.1	299.5	684.7	979.7
DQ805302.1	181045	60.2	61.6	63.9	112.6	64.1	34.6
EU765096.1	329822	26.0	22.7	25.2	56.9	59.0	23.2
FJ371751.1	356933	6326.8	5407.9	3094.7	8743.1	867.8	1905.6
FJ371913.1	365185	250.4	219.8	678.2	312.0	70.6	52.1
FJ673425.1	531791	31.9	65.8	70.5	86.5	64.5	39.2
FJ673914.1	522500	2213.6	1580.6	1888.3	5461.6	4645.8	4436.3
FJ365029.1	364449	4601.2	2734.6	5247.3	3951.2	3456.0	4538.2
FJ365142.1	358772	2903.2	3576.4	3794.4	2798.3	4752.5	7386.9
FJ362744.1	365960	10509.5	10765.7	21467.0	9770.1	9627.0	9520.7
FJ683387.1	517313	1046.6	1330.2	1193.6	711.0	1462.1	979.5
EU764113.1	341093	1768.0	2515.5	3098.2	2096.6	2131.7	2994.0
DQ797772.1	187746	733.9	914.4	1570.0	461.1	481.9	801.2
DQ797534.1	183136	49.6	66.0	33.5	71.7	113.1	46.4
EU764195.1	348580	1380.0	1283.2	1039.7	606.4	1400.5	1154.4
FJ673014.1	511426	108.7	218.4	250.0	82.1	319.2	179.7
EU761607.1	348796	337.4	268.1	137.3	366.1	604.6	417.8
FJ677915.1	529462	4613.8	3513.4	4008.7	8770.6	2624.0	2416.2
EF405259.1	208204	78.7	128.4	70.6	170.5	90.0	60.8
FJ676446.1	530143	27.5	39.1	35.2	51.5	68.5	33.7
DQ796680.1	196638	1318.9	2261.7	2768.1	1214.4	2981.2	3120.0
DQ801683.1	178701	4496.6	4570.0	1224.1	1476.2	1903.6	1752.4
DQ806770.1	181056	907.3	1030.2	896.8	2470.6	848.9	970.5
DQ808834.1	192290	1848.3	2405.7	3560.0	2213.6	2054.4	3094.7
AY976679.1	116489	10866.4	12097.9	4520.3	7406.0	13326.9	8446.2
GQ175391.1	558789	10351.2	9405.1	2507.6	3292.4	726.7	1453.5
FJ674228.1	516246	34.4	62.1	104.0	76.0	90.5	103.8
DQ801519.1	199423	366.5	496.9	1278.1	303.7	323.5	483.8
DQ809610.1	180497	2470.0	3118.8	3187.1	1041.1	1943.3	3139.1
DQ801990.1	193716	1985.0	1544.3	1201.2	2157.2	1908.9	3705.3
FJ366675.1	367013	3790.8	3129.4	2814.2	1668.1	3180.0	3552.5
FJ372098.1	363190	197.9	152.4	434.9	177.3	303.1	219.0
FJ369985.1	363252	379.8	224.3	377.2	372.5	81.1	46.9
EU766632.1	355409	1599.4	115.3	441.0	2875.1	1038.5	1211.3
DQ798390.1	179266	1204.7	1567.3	566.4	1060.5	392.4	826.6
FJ367658.1	361552	2383.2	2611.3	2059.4	2969.7	2729.8	4236.9
FJ682429.1	519971	4480.6	3513.6	1813.8	3256.1	4792.6	4343.5
DQ797383.1	198948	1331.1	2259.7	1665.6	388.4	951.2	1567.7
EU765795.1	347325	1503.9	1359.7	1761.9	2106.7	3633.7	4709.6
DQ801446.1	197808	414.3	479.1	981.5	311.4	798.3	805.8

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AY984022.1 gg_id:126113 human descending colon mucosal biopsy clone MD70
GQ896716.1 gg_id:542108 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s
FJ678508.1 gg_id:520211 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676564.1 gg_id:528965 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ794660.1 gg_id:192639 human fecal clone RL240_aaj30g09
DQ796603.1 gg_id:180806 human fecal clone RL179aan75f08
GQ898587.1 gg_id:581146 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ367324.1 gg_id:367882 feces adult twins and mothers; TS29 clone TS29_a02b08
EU530324.1 gg_id:266565 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
DQ797997.1 gg_id:183690 human fecal clone RL302_aal94c12
FJ365543.1 gg_id:357034 feces adult twins and mothers; TS20 clone TS20_a04b04
FJ682343.1 gg_id:532151 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ369100.1 gg_id:368378 feces adult twins and mothers; TS4 clone TS4_a04c02
DQ800205.1 gg_id:193761 human fecal clone RL303_aal69f05
EF404910.1 gg_id:212246 human fecal clone SJTU_G_08_82
DQ823816.1 gg_id:183130 human fecal clone RL250_aaj79e01
DQ825130.1 gg_id:179990 human fecal clone RL185_aan85g01
FJ673886.1 gg_id:529617 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798665.1 gg_id:199278 human fecal clone RL181_aan99g06
FJ371302.1 gg_id:361142 feces adult twins and mothers; TS6 clone TS6_a03d05
EU762609.1 gg_id:331713 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
AY981634.1 gg_id:120836 human sigmoid colon mucosal biopsy clone L882
FJ685245.1 gg_id:520987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796422.1 gg_id:199691 human fecal clone RL179_aah28b03
EU762758.1 gg_id:309246 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ683417.1 gg_id:522721 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677548.1 gg_id:512140 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677427.1 gg_id:522865 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798435.1 gg_id:177901 human fecal clone RL181_aah42f03
DQ808929.1 gg_id:194039 human fecal clone RL243_aai87b03
FJ370405.1 gg_id:366787 feces adult twins and mothers; TS56 clone TS56_a04f03
FJ674086.1 gg_id:518723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY980789.1 gg_id:115448 human rectum mucosal biopsy clone LN96
DQ905151.1 gg_id:165073 human fecal clone 002C-e4
FJ363345.1 gg_id:362865 feces adult twins and mothers; TS149 clone TS149_a02b06
DQ793304.1 gg_id:189470 human fecal clone RL199_aaj42a04
DQ798518.1 gg_id:182532 human fecal clone RL181_aan97g01
FJ371667.1 gg_id:364017 feces adult twins and mothers; TS7 clone TS7_a04h05
DQ805129.1 gg_id:198350 human fecal clone RL249_aaj81f06
DQ799479.1 gg_id:178024 human fecal clone RL305aal86g06
DQ801480.1 gg_id:194565 human fecal clone RL388_aao96b02

AY984022.1	126113	880.8	1308.9	731.5	541.3	1930.4	1350.8
GQ896716.1	542108	2543.8	1958.3	2914.6	3096.2	3115.8	3067.5
FJ678508.1	520211	4169.5	1932.5	550.2	270.6	879.9	233.7
FJ676564.1	528965	1879.8	3102.3	2260.6	532.5	2302.5	2177.8
DQ794660.1	192639	18226.2	19664.9	20375.2	14116.9	16251.9	15085.9
DQ796603.1	180806	5401.4	5956.2	1517.0	1398.2	2157.8	2361.8
GQ898587.1	581146	1419.5	1729.3	3091.7	2190.9	1974.6	2793.2
FJ367324.1	367882	4010.8	5765.5	6208.3	6095.2	6652.2	8956.2
EU530324.1	266565	2543.3	2561.9	3939.0	4131.4	3012.6	4529.7
DQ797997.1	183690	2570.4	2814.6	1503.5	3655.3	5968.4	6538.4
FJ365543.1	357034	30.3	82.7	39.0	72.9	73.8	41.4
FJ682343.1	532151	624.1	833.6	857.7	193.9	1531.3	868.4
FJ369100.1	368378	3155.5	3380.6	2626.8	3667.7	1421.1	2036.8
DQ800205.1	193761	2650.2	3423.8	3024.3	2831.5	4228.1	5017.2
EF404910.1	212246	106.8	141.0	235.1	113.0	102.3	92.8
DQ823816.1	183130	1955.4	2718.9	3939.3	3916.8	3652.4	4375.7
DQ825130.1	179990	1144.0	629.4	860.7	1906.3	121.7	271.0
FJ673886.1	529617	831.5	626.4	1054.8	1514.3	885.1	1949.6
DQ798665.1	199278	6802.5	4433.3	5052.8	8908.7	6490.0	8773.3
FJ371302.1	361142	2139.8	2059.8	1501.9	3953.3	3279.0	3668.6
EU762609.1	331713	70.6	83.5	302.6	148.2	103.3	109.4
AY981634.1	120836	13006.3	12949.8	5597.5	14268.0	16868.6	12673.3
FJ685245.1	520987	58.0	71.2	283.3	1202.4	325.7	354.1
DQ796422.1	199691	540.5	647.1	1473.0	1272.5	655.0	1247.5
EU762758.1	309246	1718.2	3277.7	4114.2	3258.4	6072.0	5917.5
FJ683417.1	522721	2237.9	3111.7	1510.5	1726.1	4306.6	3362.6
FJ677548.1	512140	35.8	58.1	57.2	64.3	82.0	42.4
FJ677427.1	522865	4471.9	3517.2	1684.6	2821.3	5273.0	4133.2
DQ798435.1	177901	2167.5	2501.9	7429.7	5545.7	3163.6	2853.7
DQ808929.1	194039	8824.0	7171.5	7770.9	9210.9	9617.4	8695.4
FJ370405.1	366787	14418.7	12691.3	6774.5	16910.9	21896.6	17779.3
FJ674086.1	518723	9581.1	9531.1	6734.4	9388.7	9502.0	8239.0
AY980789.1	115448	1258.1	1123.2	1089.7	1628.6	940.9	1923.3
DQ905151.1	165073	309.7	852.1	2026.4	758.2	682.0	1248.7
FJ363345.1	362865	2147.2	2447.4	4951.2	5255.3	3221.3	4439.2
DQ793304.1	189470	3010.8	3279.3	2535.4	3621.2	3415.1	2814.7
DQ798518.1	182532	29.7	34.4	26.8	44.1	58.4	21.7
FJ371667.1	364017	1259.9	1130.6	1024.4	1151.8	257.6	410.5
DQ805129.1	198350	3041.8	2498.2	2625.5	4303.2	4674.1	4221.9
DQ799479.1	178024	7496.4	7550.9	3821.4	7625.4	9834.2	9364.2
DQ801480.1	194565	1086.8	1000.5	3432.9	597.9	1702.2	1170.6

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GQ896629.1 gg_id:586659 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s
DQ809292.1 gg_id:183138 human fecal clone RL308_aal84g06
FJ681165.1 gg_id:522292 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364574.1 gg_id:368806 feces adult twins and mothers; TS15 clone TS15_a04e10
FJ371121.1 gg_id:361332 feces adult twins and mothers; TS6 clone TS6_a01b10
FJ366966.1 gg_id:367186 feces adult twins and mothers; TS28 clone TS28_a01h04
FJ365772.1 gg_id:364220 feces adult twins and mothers; TS21 clone TS21_a02g10
FJ371239.1 gg_id:360105 feces adult twins and mothers; TS6 clone TS6_a02f01
EF401978.1 gg_id:213059 human fecal clone SJTU_B_02_07
FJ370385.1 gg_id:361908 feces adult twins and mothers; TS56 clone TS56_a04c07
FJ371972.1 gg_id:359377 feces adult twins and mothers; TS8 clone TS8_a04c09
FJ682937.1 gg_id:524620 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ804722.1 gg_id:177290 human fecal clone RL187_aao71h01
FJ674211.1 gg_id:521267 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674262.1 gg_id:509902 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366994.1 gg_id:365372 feces adult twins and mothers; TS28 clone TS28_a02c01
DQ797057.1 gg_id:199702 human fecal clone RL386_aao86d06
EF401918.1 gg_id:211569 human fecal clone SJTU_B_01_36
FJ677730.1 gg_id:529525 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682261.1 gg_id:515263 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676043.1 gg_id:523341 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684204.1 gg_id:528631 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372174.1 gg_id:364920 feces adult twins and mothers; TS9 clone TS9_a02f01
EU763635.1 gg_id:346744 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
FJ678787.1 gg_id:518372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370357.1 gg_id:369735 feces adult twins and mothers; TS56 clone TS56_a03h06
DQ801136.1 gg_id:176406 human fecal clone RL387_aao92g07
EF403779.1 gg_id:211449 human fecal clone SJTU_A2_01_87
FJ684659.1 gg_id:522195 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673761.1 gg_id:523868 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673351.1 gg_id:528895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677040.1 gg_id:524573 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ326036.1 gg_id:145325 Metagenomic gut microbiome healthy human stool clone B995
EU763234.1 gg_id:308821 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ823731.1 gg_id:186747 human fecal clone RL250_aaj78c08
FJ673135.1 gg_id:524901 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY984095.1 gg_id:125128 human descending colon mucosal biopsy clone MF44
FJ681597.1 gg_id:524607 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673131.1 gg_id:524709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ175392.1 gg_id:513594 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
FJ677929.1 gg_id:514388 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

GQ896629.1	586659	517.6	762.0	1393.2	413.4	403.2	560.4
DQ809292.1	183138	15.6	35.3	156.4	108.8	129.0	61.9
FJ681165.1	522292	2648.0	3332.0	2554.1	4846.6	4969.8	5371.7
FJ364574.1	368806	1759.4	2148.1	3233.7	2039.6	2062.1	2933.4
FJ371121.1	361332	531.9	716.4	564.9	428.0	792.9	569.7
FJ366966.1	367186	2591.2	2921.6	2877.6	5302.3	6118.7	6504.6
FJ365772.1	364220	75.8	94.9	186.1	99.6	47.3	36.3
FJ371239.1	360105	7787.3	7740.6	4031.4	7419.3	7756.1	6643.9
EF401978.1	213059	11867.6	12954.3	6890.3	9432.5	12133.4	10332.1
FJ370385.1	361908	905.0	915.0	1742.3	1433.9	501.9	621.2
FJ371972.1	359377	5998.5	4745.3	3087.8	6639.3	3767.1	6091.3
FJ682937.1	524620	1299.5	1144.5	1620.5	2381.2	1271.4	1589.6
DQ804722.1	177290	1205.4	1707.0	1357.7	1682.2	2010.7	3918.9
FJ674211.1	521267	12832.2	10995.2	9336.3	10084.5	16636.9	11670.5
FJ674262.1	509902	9307.7	7097.0	3248.7	7276.0	9189.6	9237.1
FJ366994.1	365372	1282.8	991.9	1241.2	1630.0	1096.8	2716.0
DQ797057.1	199702	44.6	86.9	157.5	66.5	77.3	51.6
EF401918.1	211569	783.5	1440.6	529.0	618.8	561.8	376.1
FJ677730.1	529525	25.5	79.2	35.9	60.7	68.3	34.7
FJ682261.1	515263	6250.1	5498.1	5348.3	6856.0	6467.8	5036.4
FJ676043.1	523341	49.2	52.0	61.0	70.0	62.6	37.3
FJ684204.1	528631	20.7	51.1	33.4	49.7	68.1	39.4
FJ372174.1	364920	526.9	391.6	476.3	1090.5	89.6	129.4
EU763635.1	346744	39.6	31.6	169.2	80.5	67.4	69.7
FJ678787.1	518372	4142.1	5503.7	4224.2	6331.4	4517.7	4402.7
FJ370357.1	369735	6334.7	6120.7	5224.4	6026.9	6477.7	6318.1
DQ801136.1	176406	2285.5	3011.6	1939.9	1742.5	431.4	640.9
EF403779.1	211449	455.3	1095.2	619.4	212.2	1079.3	391.0
FJ684659.1	522195	1281.7	1066.2	1178.4	1363.9	1185.7	1576.4
FJ673761.1	523868	352.2	517.8	1380.7	298.1	346.9	571.2
FJ673351.1	528895	3248.1	2038.9	606.7	4064.1	3422.8	3121.2
FJ677040.1	524573	94.2	102.2	269.2	75.4	67.4	24.6
DQ326036.1	145325	1969.0	2372.4	2422.0	3527.0	2632.4	3094.9
EU763234.1	308821	1896.6	2123.7	2449.6	2208.2	2959.5	3145.3
DQ823731.1	186747	2651.1	2924.9	5054.0	2739.0	1022.2	1384.7
FJ673135.1	524901	5641.5	3637.4	3575.6	5841.4	10023.9	7799.1
AY984095.1	125128	4378.4	5034.1	941.8	3410.0	3948.5	2544.4
FJ681597.1	524607	45.5	42.3	66.4	61.5	71.7	26.5
FJ673131.1	524709	2740.6	3026.9	1927.9	5134.8	6929.0	7616.3
GQ175392.1	513594	2692.6	2838.0	1873.7	1218.7	2424.7	1042.8
FJ677929.1	514388	3515.9	3255.1	1870.0	3837.8	4977.7	4790.5

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FJ673842.1 gg_id:527733 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767009.1 gg_id:338144 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EU763835.1 gg_id:336251 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
DQ808548.1 gg_id:182564 human fecal clone RL239_aaj10a05
FJ673880.1 gg_id:509345 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372054.1 gg_id:367381 feces adult twins and mothers; TS9 clone TS9_a01c04
EF403391.1 gg_id:205407 human fecal clone SJTU_A1_7_63
EU762875.1 gg_id:339857 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ823947.1 gg_id:188746 human fecal clone RL204_aaj57c11
FJ676061.1 gg_id:514351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF399739.1 gg_id:206680 human fecal clone SJTU_E_02_77
FJ683906.1 gg_id:531564 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FM872976.1 gg_id:368070 occupant source house floor dust clone FB02D07
AY977987.1 gg_id:124878 human cecum mucosal biopsy clone LH20
DQ809400.1 gg_id:195007 human fecal clone RL184_aah20d03
FJ673167.1 gg_id:526881 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681199.1 gg_id:530877 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673280.1 gg_id:530737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371430.1 gg_id:362768 feces adult twins and mothers; TS6 clone TS6_a04h04
FJ363908.1 gg_id:367938 feces adult twins and mothers; TS14 clone TS14_a04g06
FJ364309.1 gg_id:364689 feces adult twins and mothers; TS15 clone TS15_a01d10
FJ364475.1 gg_id:357928 feces adult twins and mothers; TS15 clone TS15_a03d07
FJ368050.1 gg_id:363378 feces adult twins and mothers; TS30 clone TS30_a03d03
FJ364919.1 gg_id:356959 feces adult twins and mothers; TS19 clone TS19_a04g04
DQ797025.1 gg_id:189637 human fecal clone RL386_aao85h11
DQ797572.1 gg_id:193525 human fecal clone RL206_aaj13b11
EF404830.1 gg_id:208589 human fecal clone SJTU_G_09_03
DQ798824.1 gg_id:191107 human fecal clone RL242_aaj97g11
EU767214.1 gg_id:346411 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
DQ801929.1 gg_id:189446 human fecal clone RL201_aai48f03
FJ364480.1 gg_id:363456 feces adult twins and mothers; TS15 clone TS15_a03e01
DQ797715.1 gg_id:192366 human fecal clone RL206_aaj15a03
FJ364561.1 gg_id:367331 feces adult twins and mothers; TS15 clone TS15_a04d07
FJ363596.1 gg_id:363155 feces adult twins and mothers; TS14 clone TS14_a01b08
FJ678584.1 gg_id:517247 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364312.1 gg_id:367840 feces adult twins and mothers; TS15 clone TS15_a01e02
AY980741.1 gg_id:127355 human rectum mucosal biopsy clone LN11
DQ825253.1 gg_id:181977 human fecal clone RL185_aan87d01
DQ904946.1 gg_id:168940 human fecal clone 002-c5
EU767293.1 gg_id:318264 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
DQ795812.1 gg_id:185120 human fecal clone RL245_aai82g07

FJ673842.1	527733	9263.8	11428.3	9402.3	7270.6	11559.1	11580.2
EU767009.1	338144	175.0	65.1	101.0	1030.2	175.7	125.8
EU763835.1	336251	20.4	27.2	47.8	53.2	56.5	24.3
DQ808548.1	182564	246.2	473.3	2384.9	2948.3	4202.0	3842.4
FJ673880.1	509345	3002.4	2980.8	1206.4	4091.2	5185.0	4411.1
FJ372054.1	367381	693.5	791.0	676.6	261.2	1859.3	2142.9
EF403391.1	205407	7609.0	8351.4	7185.6	8144.6	11223.7	11548.2
EU762875.1	339857	2614.4	1469.1	2567.1	2830.1	3427.8	3437.5
DQ823947.1	188746	95.5	103.6	381.9	2026.3	492.4	571.1
FJ676061.1	514351	833.3	1097.7	1576.7	2322.2	1375.0	1742.4
EF399739.1	206680	184.1	223.7	773.5	1174.4	371.9	492.0
FJ683906.1	531564	23.5	50.8	19.8	50.7	53.4	16.1
FM872976.1	368070	72.9	91.0	301.9	82.6	141.9	121.6
AY977987.1	124878	2807.5	3606.8	151.1	1805.7	441.2	242.2
DQ809400.1	195007	518.3	460.9	1918.4	2001.3	111.9	181.3
FJ673167.1	526881	1348.9	1465.3	794.4	1496.3	973.4	1173.7
FJ681199.1	530877	10497.2	11289.0	8518.6	7829.4	10287.4	10360.1
FJ673280.1	530737	9125.1	5103.4	1934.0	7630.8	5769.7	7057.2
FJ371430.1	362768	1641.7	2311.2	3027.5	2059.4	2094.5	2954.6
FJ363908.1	367938	37.2	25.2	111.6	73.1	65.8	64.0
FJ364309.1	364689	581.7	714.2	1482.0	890.2	664.9	389.3
FJ364475.1	357928	336.6	254.1	437.5	265.1	67.8	131.1
FJ368050.1	363378	3769.4	4013.3	4766.1	6194.1	1816.8	2971.9
FJ364919.1	356959	2158.6	3088.9	2817.6	2479.8	3321.1	4354.5
DQ797025.1	189637	1609.8	468.3	1508.5	3400.1	1631.2	2546.8
DQ797572.1	193525	7375.7	5237.8	8051.1	5572.6	5241.6	6242.3
EF404830.1	208589	2304.4	2624.7	4844.1	2863.8	3081.6	3336.0
DQ798824.1	191107	4376.3	2076.5	859.4	4154.0	3947.3	3902.7
EU767214.1	346411	41.7	71.1	154.2	92.8	73.7	85.8
DQ801929.1	189446	10490.8	8891.4	4802.4	9582.8	10816.1	9369.6
FJ364480.1	363456	370.6	464.5	579.4	634.4	217.4	375.4
DQ797715.1	192366	5334.6	5348.7	4818.1	7925.8	6800.5	5908.5
FJ364561.1	367331	2518.5	1497.2	2087.4	4532.5	801.4	448.2
FJ363596.1	363155	828.2	805.9	898.1	988.0	195.7	306.8
FJ678584.1	517247	3837.1	4327.2	752.9	6404.7	4536.2	5242.4
FJ364312.1	367840	2044.2	1658.5	895.4	1616.4	813.4	1029.0
AY980741.1	127355	4851.8	2576.8	2376.1	4984.1	2136.8	3231.3
DQ825253.1	181977	2098.7	1247.0	4049.9	1390.2	575.6	982.3
DQ904946.1	168940	1495.9	1095.9	733.5	1765.5	1312.3	1318.0
EU767293.1	318264	1113.9	1241.8	1912.6	1265.4	1279.2	1907.7
DQ795812.1	185120	4489.2	3636.7	1988.2	593.5	1561.1	818.2

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FJ673126.1 gg_id:528614 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678678.1 gg_id:530711 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372080.1 gg_id:367167 feces adult twins and mothers; TS9 clone TS9_a01e07
EF404020.1 gg_id:210297 human fecal clone SJTU_C_03_63
EU763991.1 gg_id:347489 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
EF403746.1 gg_id:208266 human fecal clone SJTU_A2_06_74
DQ794455.1 gg_id:198064 human fecal clone RL197_aah88b02
FJ363555.1 gg_id:368277 feces adult twins and mothers; TS149 clone TS149_a04f03
FJ368449.1 gg_id:366410 feces adult twins and mothers; TS3 clone TS3_a04e04
FJ676057.1 gg_id:522987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368948.1 gg_id:358414 feces adult twins and mothers; TS4 clone TS4_a02d11
DQ904681.1 gg_id:167675 human fecal clone 001-d7
FJ367435.1 gg_id:369311 feces adult twins and mothers; TS29 clone TS29_a03e05
DQ802632.1 gg_id:189025 human fecal clone RL188_aan94d04
DQ806704.1 gg_id:174221 human fecal clone RL186_aao47g05
FJ683437.1 gg_id:522024 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ362735.1 gg_id:364591 feces adult twins and mothers; TS13 clone TS13_a02e05
FJ371863.1 gg_id:364576 feces adult twins and mothers; TS8 clone TS8_a03b01
DQ794141.1 gg_id:184017 human fecal clone RL176_aan58f01
DQ797385.1 gg_id:177118 human fecal clone RL248_aai98f10
GQ042945.1 gg_id:462301 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011c(
DQ905305.1 gg_id:173589 human fecal clone 013B-C3
FJ363175.1 gg_id:359393 feces adult twins and mothers; TS148 clone TS148_a04a07
AY977661.1 gg_id:115899 human cecum mucosal biopsy clone LD13
EU766645.1 gg_id:324915 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EU768539.1 gg_id:312962 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
FJ678292.1 gg_id:525849 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679695.1 gg_id:520078 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766096.1 gg_id:334683 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
FJ677406.1 gg_id:520572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682009.1 gg_id:523936 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF403983.1 gg_id:210503 human fecal clone SJTU_C_03_19
FJ372162.1 gg_id:364809 feces adult twins and mothers; TS9 clone TS9_a02d10
FJ370175.1 gg_id:360481 feces adult twins and mothers; TS56 clone TS56_a01d01
FJ673279.1 gg_id:509946 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673248.1 gg_id:515026 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY976695.1 gg_id:117685 human cecum mucosal biopsy clone K270
FJ368153.1 gg_id:360870 feces adult twins and mothers; TS30 clone TS30_a04h03
FJ683367.1 gg_id:521272 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370921.1 gg_id:357718 feces adult twins and mothers; TS5 clone TS5_a02g11
FJ673101.1 gg_id:522788 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

FJ673126.1	528614	1350.1	823.0	424.1	2831.1	1176.3	1275.6
FJ678678.1	530711	7211.6	10424.7	1598.3	4902.0	4426.0	5134.3
FJ372080.1	367167	5328.8	5189.4	3492.5	4675.5	1863.8	3333.8
EF404020.1	210297	123.6	125.6	499.7	122.4	218.1	217.2
EU763991.1	347489	194.6	552.8	2134.6	527.1	1953.8	1696.5
EF403746.1	208266	66.8	171.5	422.6	117.6	284.3	225.3
DQ794455.1	198064	442.5	519.8	1358.6	816.8	435.7	570.1
FJ363555.1	368277	4138.3	3916.2	3105.9	3956.1	4911.6	5972.7
FJ368449.1	366410	6063.5	5507.8	2744.6	6619.2	6537.1	6765.2
FJ676057.1	522987	24.4	75.6	87.9	83.3	89.9	110.3
FJ368948.1	358414	32.8	38.1	93.1	63.4	91.2	28.5
DQ904681.1	167675	3596.0	3905.3	2979.5	2383.2	1797.7	2260.7
FJ367435.1	369311	4266.8	5492.7	5671.4	3703.6	6306.7	5850.6
DQ802632.1	189025	2286.8	2150.6	1092.0	2267.3	2301.8	1704.2
DQ806704.1	174221	47.4	85.4	46.0	65.1	90.1	43.5
FJ683437.1	522024	3245.5	3600.1	2748.3	3659.7	2306.0	1513.5
FJ362735.1	364591	9506.6	8172.2	5101.3	9820.6	3266.6	6189.1
FJ371863.1	364576	8233.9	8121.8	5944.6	7072.6	8311.3	7300.3
DQ794141.1	184017	884.2	567.1	116.0	706.3	451.2	216.3
DQ797385.1	177118	260.5	394.9	371.2	272.0	809.6	1739.7
GQ042945.1	462301	59.5	262.9	386.2	93.0	129.1	610.7
DQ905305.1	173589	14784.8	15516.8	14461.6	13100.5	17008.2	14175.1
FJ363175.1	359393	1562.2	1933.4	2869.5	1984.5	592.7	986.3
AY977661.1	115899	9487.8	8866.7	5078.7	4342.8	7795.6	6532.7
EU766645.1	324915	876.2	358.4	551.1	1819.2	90.7	152.6
EU768539.1	312962	59.0	92.1	59.9	90.0	68.6	46.6
FJ678292.1	525849	3829.3	3408.0	2046.5	2635.6	2818.2	1971.2
FJ679695.1	520078	6564.7	9212.2	5291.4	5823.7	9207.5	6896.7
EU766096.1	334683	4769.1	7573.5	5598.5	7598.2	5336.4	6250.4
FJ677406.1	520572	28.0	58.3	118.2	77.9	90.4	111.3
FJ682009.1	523936	12588.8	11884.3	12176.5	12257.1	11217.1	10516.6
EF403983.1	210503	2922.5	2899.0	196.9	1347.4	207.9	210.9
FJ372162.1	364809	2784.9	2486.8	1528.2	3556.7	5381.7	6189.4
FJ370175.1	360481	507.6	392.8	671.2	586.0	138.2	252.6
FJ673279.1	509946	7043.3	6795.4	5580.4	4853.4	7192.1	6099.4
FJ673248.1	515026	1951.1	3001.1	1808.4	1591.5	4238.0	3887.1
AY976695.1	117685	589.0	621.4	1537.3	1209.1	673.1	995.3
FJ368153.1	360870	625.2	779.4	517.1	412.8	926.3	611.7
FJ683367.1	521272	140.9	132.5	2957.9	1309.1	191.9	125.6
FJ370921.1	357718	2550.3	2575.4	3015.7	1665.2	3162.7	4217.7
FJ673101.1	522788	38.4	39.3	24.3	56.2	51.7	17.1

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o__Clostridiales	f__Ruminococcaceae
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FJ674104.1 gg_id:517574 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676185.1 gg_id:514313 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368033.1 gg_id:365896 feces adult twins and mothers; TS30 clone TS30_a03a05
DQ801157.1 gg_id:183243 human fecal clone RL116_aae99c08
FJ679875.1 gg_id:523155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673177.1 gg_id:532034 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU768423.1 gg_id:312477 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
DQ326327.1 gg_id:149193 Metagenomic gut microbiome healthy human stool clone C315
EU764558.1 gg_id:355240 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ370347.1 gg_id:358643 feces adult twins and mothers; TS56 clone TS56_a03g05
EU778247.1 gg_id:349382 feces clone RL387_aao92c08
FJ682228.1 gg_id:522028 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679783.1 gg_id:514644 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ363269.1 gg_id:361887 feces adult twins and mothers; TS149 clone TS149_a01c06
DQ801692.1 gg_id:177072 human fecal clone RL201_aai45e11
EF402548.1 gg_id:208161 human fecal clone SJTU_B_09_39
DQ798083.1 gg_id:178796 human fecal clone RL302_aal95c11
FJ680412.1 gg_id:520169 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU530340.1 gg_id:268093 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
EF404586.1 gg_id:212232 human fecal clone SJTU_C_13_14
DQ796742.1 gg_id:181648 human fecal clone RL179_aao53h05
FJ674232.1 gg_id:518469 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ672979.1 gg_id:510804 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ408966.1 gg_id:35563 human colonic clone HuCA11
FJ679091.1 gg_id:523363 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677986.1 gg_id:528075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674197.1 gg_id:519966 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682603.1 gg_id:517546 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU530466.1 gg_id:264386 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M7
FJ683111.1 gg_id:530863 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF404843.1 gg_id:214451 human fecal clone SJTU_G_09_17
AY979427.1 gg_id:121148 human transverse colon mucosal biopsy clone M032
AY976159.1 gg_id:115926 human ascending colon mucosal biopsy clone LV59
EU762974.1 gg_id:334009 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ672910.1 gg_id:525713 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ682002.1 gg_id:530882 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU530352.1 gg_id:262491 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
FJ683338.1 gg_id:512733 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683940.1 gg_id:516959 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801314.1 gg_id:178935 human fecal clone RL388_aao93g12
DQ797655.1 gg_id:189836 human fecal clone RL206_aaj14c08

FJ674104.1	517574	9984.1	6369.3	4828.8	7472.6	5505.7	8465.5
FJ676185.1	514313	5470.0	6005.0	4212.6	5098.1	6465.8	5648.8
FJ368033.1	365896	329.9	944.3	368.6	990.8	1122.3	2360.1
DQ801157.1	183243	391.3	502.9	1253.9	274.6	297.9	458.6
FJ679875.1	523155	1851.9	1568.1	700.1	1818.0	1882.2	1648.1
FJ673177.1	532034	5902.2	5489.2	4648.1	5709.0	8801.9	7115.3
EU768423.1	312477	10015.7	10478.8	3907.4	7631.4	11365.7	11077.8
DQ326327.1	149193	2536.7	4430.9	3933.4	2342.1	4628.0	3603.2
EU764558.1	355240	160.6	1802.2	2920.9	151.4	3560.2	3747.0
FJ370347.1	358643	1239.2	873.3	1682.0	2027.9	359.4	607.1
EU778247.1	349382	16.2	27.4	17.2	37.3	57.0	8.5
FJ682228.1	522028	4188.8	3886.4	1788.1	6056.1	2161.5	1950.0
FJ679783.1	514644	958.5	1397.9	1517.4	720.1	1775.6	1553.5
FJ363269.1	361887	2943.1	5478.6	3693.8	2438.3	4115.2	4176.7
DQ801692.1	177072	41.4	49.2	53.7	88.0	67.0	32.3
EF402548.1	208161	1859.9	1534.6	3049.5	2137.1	752.6	1163.2
DQ798083.1	178796	1900.4	2317.4	4405.1	2342.5	2235.8	3999.1
FJ680412.1	520169	5044.1	4246.9	3672.2	5672.6	6363.8	5264.1
EU530340.1	268093	4117.9	4763.0	4222.9	4026.3	5401.8	5186.5
EF404586.1	212232	196.3	280.8	773.4	170.0	252.9	330.9
DQ796742.1	181648	460.5	541.7	1186.0	266.8	360.1	551.0
FJ674232.1	518469	12001.6	10354.0	6464.1	7238.6	11560.0	12283.8
FJ672979.1	510804	7510.6	5679.7	1278.8	7899.2	11177.8	8851.0
AJ408966.1	35563	582.3	635.3	484.2	275.1	1404.1	478.3
FJ679091.1	523363	4755.9	5485.2	1228.8	2897.6	1612.0	2002.6
FJ677986.1	528075	6065.8	5356.4	9151.8	7890.1	8890.3	9437.1
FJ674197.1	519966	2640.5	1148.8	1941.8	502.5	2710.3	1160.2
FJ682603.1	517546	1696.3	1711.2	1509.4	1824.7	283.6	523.1
EU530466.1	264386	1625.4	2207.9	2877.8	2232.3	1603.2	2401.1
FJ683111.1	530863	4151.2	4666.6	3225.9	6137.7	4715.0	3642.5
EF404843.1	214451	446.8	580.7	489.4	798.9	964.0	552.2
AY979427.1	121148	219.2	158.9	234.0	117.4	255.1	105.4
AY976159.1	115926	2298.3	1676.4	640.3	997.1	1813.3	1424.0
EU762974.1	334009	1697.5	2516.1	4250.3	4185.6	3201.7	4381.5
FJ672910.1	525713	869.9	1287.1	937.1	1012.6	1778.5	1598.4
FJ682002.1	530882	2269.6	2668.4	3142.8	1267.1	5024.0	3663.0
EU530352.1	262491	10314.2	11107.6	6459.8	12505.9	14964.6	16251.6
FJ683338.1	512733	717.2	959.2	764.3	528.8	1184.4	1281.9
FJ683940.1	516959	9545.0	10732.5	9957.4	6988.6	9153.1	8094.2
DQ801314.1	178935	3567.4	4146.6	4264.1	3610.3	4841.1	9534.8
DQ797655.1	189836	227.2	204.7	315.2	1992.1	100.7	577.9

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Ruminococcaceae
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DQ801315.1 gg_id:183047 human fecal clone RL388_aao93h01
EF402117.1 gg_id:204987 human fecal clone SJTU_B_03_84
DQ801254.1 gg_id:191186 human fecal clone RL388_aao93a06
EU767170.1 gg_id:344490 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ366465.1 gg_id:367462 feces adult twins and mothers; TS26 clone TS26_a03f04
AY977950.1 gg_id:118536 human cecum mucosal biopsy clone LG70
FJ673387.1 gg_id:524753 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371184.1 gg_id:369649 feces adult twins and mothers; TS6 clone TS6_a01h07
FJ370915.1 gg_id:366041 feces adult twins and mothers; TS5 clone TS5_a02g05
AY979470.1 gg_id:122222 human transverse colon mucosal biopsy clone M092
FJ679979.1 gg_id:515455 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ047267.1 gg_id:403182 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010g
FJ674186.1 gg_id:521986 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799695.1 gg_id:174015 human fecal clone RL182_aah31f02
GQ106316.1 gg_id:380987 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
FJ368141.1 gg_id:357932 feces adult twins and mothers; TS30 clone TS30_a04f07
EF071238.1 gg_id:183485 library survey and quantitative measurement major mucosa- IBD human colonic muc
GQ175442.1 gg_id:582425 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
FJ676411.1 gg_id:527284 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366075.1 gg_id:365371 feces adult twins and mothers; TS25 clone TS25_a02d08
FJ364308.1 gg_id:362640 feces adult twins and mothers; TS15 clone TS15_a01d09
DQ904672.1 gg_id:168550 human fecal clone 001-d10
FJ367413.1 gg_id:368212 feces adult twins and mothers; TS29 clone TS29_a03c03
FJ682295.1 gg_id:529230 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY984418.1 gg_id:125596 human stool clone B328
FJ677882.1 gg_id:522565 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU768686.1 gg_id:325407 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
FJ672989.1 gg_id:530262 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU768184.1 gg_id:336459 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
AY985258.1 gg_id:123149 human stool clone C139
DQ802049.1 gg_id:175347 human fecal clone RL241_aaj02d07
DQ824866.1 gg_id:182546 human fecal clone RL185_aao70c04
FJ372036.1 gg_id:366709 feces adult twins and mothers; TS9 clone TS9_a01a10
FJ362604.1 gg_id:359991 feces adult twins and mothers; TS13 clone TS13_a01a04
DQ824923.1 gg_id:187440 human fecal clone RL185_aao71a08
DQ798715.1 gg_id:188471 human fecal clone RL181_aao00e01
DQ806296.1 gg_id:191926 human fecal clone RL186_aan90a08
FJ682262.1 gg_id:519476 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679434.1 gg_id:520774 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ793517.1 gg_id:194086 human fecal clone RL199_aaj44g11
DQ798741.1 gg_id:174949 human fecal clone RL181_aao00g06

DQ801315.1	183047	738.9	1136.7	858.3	1401.5	1595.7	1555.0
EF402117.1	204987	1789.4	1029.0	2089.1	3585.4	1883.9	2425.2
DQ801254.1	191186	390.0	521.0	1355.6	280.7	313.0	467.2
EU767170.1	344490	91.4	77.5	290.5	90.3	81.8	43.3
FJ366465.1	367462	556.9	771.0	1586.8	487.0	717.3	960.4
AY977950.1	118536	525.4	589.7	1195.7	1134.6	675.0	1128.9
FJ673387.1	524753	2881.8	2388.4	5485.3	5168.4	7087.4	6565.5
FJ371184.1	369649	2029.3	2635.4	2861.4	2168.5	2412.1	5241.7
FJ370915.1	366041	361.1	194.8	922.6	185.1	83.1	141.2
AY979470.1	122222	566.4	503.4	329.0	135.6	770.0	106.7
FJ679979.1	515455	1528.0	2362.9	1968.5	2466.4	4532.2	3502.3
GQ047267.1	403182	556.4	1129.4	159.0	165.0	1049.5	305.4
FJ674186.1	521986	264.8	173.2	744.8	2825.9	1736.5	1317.7
DQ799695.1	174015	704.8	332.8	1990.4	369.7	188.2	267.2
GQ106316.1	380987	1374.5	847.9	477.9	3065.2	1199.1	1509.7
FJ368141.1	357932	6939.6	8211.5	5381.0	5424.4	5996.0	5091.6
EF071238.1	183485	13.2	19.3	21.5	34.2	49.9	8.9
GQ175442.1	582425	2385.4	2325.8	1410.5	1531.1	1489.7	1265.0
FJ676411.1	527284	7969.4	5652.2	2267.5	3981.4	4562.2	3023.0
FJ366075.1	365371	659.8	916.9	1672.9	503.8	435.4	794.7
FJ364308.1	362640	2998.1	2436.9	3849.3	1589.4	896.3	1616.1
DQ904672.1	168550	154.6	212.2	872.1	265.3	194.8	175.5
FJ367413.1	368212	445.2	847.6	1809.3	1246.3	3211.0	2524.0
FJ682295.1	529230	10076.4	8948.9	5360.6	5196.5	7371.3	6696.2
AY984418.1	125596	1562.2	208.2	918.8	2190.6	1048.9	1215.5
FJ677882.1	522565	3331.3	3481.4	2547.8	3125.3	3686.5	3104.1
EU768686.1	325407	15381.6	13776.0	4479.4	12007.9	14062.1	11653.5
FJ672989.1	530262	10638.5	12483.9	5720.6	10142.6	13075.8	10899.4
EU768184.1	336459	23420.5	22265.2	13071.5	20305.6	19474.1	19133.2
AY985258.1	123149	189.2	115.8	146.5	107.0	252.4	154.9
DQ802049.1	175347	487.6	227.3	473.0	724.4	114.8	112.0
DQ824866.1	182546	39.2	58.1	53.3	61.4	70.4	26.7
FJ372036.1	366709	2583.4	2110.2	2390.6	5596.1	1883.3	1957.4
FJ362604.1	359991	1271.1	1525.2	3041.4	1178.4	1810.3	1999.4
DQ824923.1	187440	194.6	176.1	275.0	1151.7	596.8	433.7
DQ798715.1	188471	38.9	92.1	43.0	60.4	73.7	33.9
DQ806296.1	191926	3069.8	3564.2	1780.8	5492.4	6443.7	5212.0
FJ682262.1	519476	1185.9	874.8	1405.8	1960.9	325.7	260.8
FJ679434.1	520774	7657.9	7111.2	3684.0	4608.1	4060.1	4827.4
DQ793517.1	194086	3211.4	3943.8	4963.6	4174.8	3396.4	3827.3
DQ798741.1	174949	26.1	34.4	40.5	65.9	82.9	29.4

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FJ683692.1 gg_id:527764 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU776790.1 gg_id:354485 Mongoose lemur feces clone ML_aaj26g10
FJ371876.1 gg_id:364037 feces adult twins and mothers; TS8 clone TS8_a03c03
AY984825.1 gg_id:117416 human stool clone B788
FJ683631.1 gg_id:522895 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802096.1 gg_id:184026 human fecal clone RL241_aaj03a08
AY978106.1 gg_id:116676 human cecum mucosal biopsy clone LI74
DQ905841.2 gg_id:168587 human fecal clone 29E-e9
EU778267.1 gg_id:311473 feces clone RL387_aao91b03
DQ798294.1 gg_id:175197 human fecal clone RL181_aah40c08
FJ680530.1 gg_id:523892 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371264.1 gg_id:362859 feces adult twins and mothers; TS6 clone TS6_a02h08
FJ364511.1 gg_id:363309 feces adult twins and mothers; TS15 clone TS15_a03g10
DQ823719.1 gg_id:177631 human fecal clone RL250_aaj78b05
FJ363893.1 gg_id:365586 feces adult twins and mothers; TS14 clone TS14_a04f03
FJ363292.1 gg_id:358118 feces adult twins and mothers; TS149 clone TS149_a01e07
DQ797073.1 gg_id:199280 human fecal clone RL386_aao86f06
DQ825260.1 gg_id:194237 human fecal clone RL185_aan87d08
FJ368417.1 gg_id:363241 feces adult twins and mothers; TS3 clone TS3_a04b03
DQ798527.1 gg_id:189625 human fecal clone RL181_aan97g11
DQ793443.1 gg_id:180165 human fecal clone RL199_aaj43g08
FJ674179.1 gg_id:523438 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798705.1 gg_id:190561 human fecal clone RL181_aao00d02
FJ363606.1 gg_id:370127 feces adult twins and mothers; TS14 clone TS14_a01c06
EU763100.1 gg_id:340083 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ673868.1 gg_id:516798 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797952.1 gg_id:187550 human fecal clone RL302_aal93g09
AY976628.1 gg_id:115592 human cecum mucosal biopsy clone K185
DQ796725.1 gg_id:175411 human fecal clone RL179_aao53f10
FJ682306.1 gg_id:521483 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683390.1 gg_id:525600 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF404495.1 gg_id:208261 human fecal clone SJTU_C_10_93
AY979567.1 gg_id:120401 human transverse colon mucosal biopsy clone M232
FJ371786.1 gg_id:370259 feces adult twins and mothers; TS8 clone TS8_a02b10
FJ364386.1 gg_id:367288 feces adult twins and mothers; TS15 clone TS15_a02c09
AY984573.1 gg_id:117999 human stool clone B512
FJ365469.1 gg_id:362327 feces adult twins and mothers; TS20 clone TS20_a03c06
FJ371852.1 gg_id:362302 feces adult twins and mothers; TS8 clone TS8_a03a01
DQ801186.1 gg_id:189437 human fecal clone RL116_aaf00b11
FJ677356.1 gg_id:512856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800972.1 gg_id:183872 human fecal clone RL387_aao90b04

FJ683692.1	527764	2256.6	3821.0	794.2	290.3	364.1	535.2
EU776790.1	354485	11386.9	10729.6	8491.1	7029.0	8862.0	8908.3
FJ371876.1	364037	247.5	134.3	327.2	176.3	56.5	32.1
AY984825.1	117416	427.1	689.9	258.1	126.7	208.4	238.5
FJ683631.1	522895	2798.5	3132.0	110.0	1536.5	368.0	242.8
DQ802096.1	184026	30.8	31.0	140.6	76.8	81.2	28.7
AY978106.1	116676	32.7	59.0	57.0	51.0	69.2	14.8
DQ905841.2	168587	77.0	77.3	134.2	126.3	102.3	52.9
EU778267.1	311473	28.4	36.9	52.6	43.1	61.5	14.8
DQ798294.1	175197	289.6	288.7	1106.6	259.3	214.4	466.3
FJ680530.1	523892	28.9	44.1	43.9	63.6	64.2	33.1
FJ371264.1	362859	8682.6	8887.3	4088.3	6708.2	6569.3	8277.7
FJ364511.1	363309	1213.0	1888.5	2071.4	2397.6	4383.6	3740.7
DQ823719.1	177631	334.4	529.3	339.7	875.9	1900.3	1721.6
FJ363893.1	365586	391.5	492.9	1758.5	502.1	426.7	709.5
FJ363292.1	358118	336.2	462.2	857.5	261.1	223.2	330.7
DQ797073.1	199280	2097.7	1875.5	713.4	2189.3	2989.3	2660.2
DQ825260.1	194237	29.7	36.0	45.4	66.8	83.8	21.8
FJ368417.1	363241	1243.6	1274.1	1070.1	1601.5	1066.1	1918.4
DQ798527.1	189625	1087.7	1330.2	1685.5	1779.3	4632.5	3809.1
DQ793443.1	180165	5665.4	6406.9	6462.5	5335.5	2218.2	4026.9
FJ674179.1	523438	129.0	196.7	273.9	99.5	328.9	204.4
DQ798705.1	190561	2394.3	1918.5	3327.4	2348.9	2761.9	2867.7
FJ363606.1	370127	1649.0	2968.4	3111.6	1395.7	2493.2	3123.4
EU763100.1	340083	129.6	137.7	438.8	161.0	74.8	57.2
FJ673868.1	516798	7326.6	6132.4	2729.4	6429.7	3948.3	4381.2
DQ797952.1	187550	6624.1	6808.0	8514.9	7925.5	7415.3	6595.6
AY976628.1	115592	62.7	68.6	73.2	71.4	79.8	48.5
DQ796725.1	175411	1776.2	1560.7	2358.7	2220.9	960.5	2060.6
FJ682306.1	521483	1594.2	1227.5	1685.5	2372.3	1466.8	1824.7
FJ683390.1	525600	16.7	23.1	23.1	51.1	49.1	12.0
EF404495.1	208261	170.4	219.4	838.6	185.6	727.0	326.1
AY979567.1	120401	39.4	50.3	54.4	73.6	77.5	21.6
FJ371786.1	370259	5068.1	2664.9	3976.7	6165.0	2317.4	4432.4
FJ364386.1	367288	3038.4	2546.0	2562.8	3146.0	3575.9	5140.5
AY984573.1	117999	513.5	665.4	257.3	1978.0	796.2	449.8
FJ365469.1	362327	1536.5	2004.4	1713.3	1866.5	1433.4	2852.5
FJ371852.1	362302	3113.5	2295.8	478.8	1251.9	834.4	986.5
DQ801186.1	189437	6883.7	6657.9	2356.6	3918.7	2183.0	2894.9
FJ677356.1	512856	1127.7	1239.6	1901.0	1245.7	1246.4	1714.9
DQ800972.1	183872	741.0	2737.4	2351.6	3178.7	2874.8	2559.7

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FJ367138.1 gg_id:369996 feces adult twins and mothers; TS28 clone TS28_a03h12
FJ674111.1 gg_id:531152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ493258.1 gg_id:554436 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ362958.1 gg_id:358162 feces adult twins and mothers; TS148 clone TS148_a01c05
DQ797687.1 gg_id:184688 human fecal clone RL206_aaj14f06
FJ364362.1 gg_id:364691 feces adult twins and mothers; TS15 clone TS15_a02a09
FJ364484.1 gg_id:367460 feces adult twins and mothers; TS15 clone TS15_a03e05
FJ363807.1 gg_id:367928 feces adult twins and mothers; TS14 clone TS14_a03e10
FJ679348.1 gg_id:519744 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371375.1 gg_id:358117 feces adult twins and mothers; TS6 clone TS6_a04b12
FJ367066.1 gg_id:366315 feces adult twins and mothers; TS28 clone TS28_a03b05
FJ676310.1 gg_id:515950 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678060.1 gg_id:517235 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ362986.1 gg_id:368011 feces adult twins and mothers; TS148 clone TS148_a01e10
FJ364439.1 gg_id:366516 feces adult twins and mothers; TS15 clone TS15_a03a02
EU766804.1 gg_id:328877 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ674266.1 gg_id:512154 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364737.1 gg_id:364401 feces adult twins and mothers; TS19 clone TS19_a02d10
EF402524.1 gg_id:212770 human fecal clone SJTU_B_09_09
DQ801272.1 gg_id:185246 human fecal clone RL388_aao93c07
EU778265.1 gg_id:323557 feces clone RL388_aao94d09
DQ798404.1 gg_id:182641 human fecal clone RL181_aah42b01
EU768521.1 gg_id:322716 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
FJ681399.1 gg_id:530749 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU764987.1 gg_id:352648 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
FJ371734.1 gg_id:358134 feces adult twins and mothers; TS8 clone TS8_a01f03
EU765813.1 gg_id:307235 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
FJ674074.1 gg_id:528122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU778234.1 gg_id:349081 feces clone RL116_aaf02b06
FJ684453.1 gg_id:530787 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767130.1 gg_id:354618 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ797991.1 gg_id:178056 human fecal clone RL302_aal94c03
FJ370413.1 gg_id:360290 feces adult twins and mothers; TS56 clone TS56_a04g08
FJ673187.1 gg_id:524511 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372110.1 gg_id:364108 feces adult twins and mothers; TS9 clone TS9_a01h03
FJ684625.1 gg_id:518196 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU768164.1 gg_id:353312 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
DQ905685.1 gg_id:165926 human fecal clone 014C-G2
FJ368148.1 gg_id:368219 feces adult twins and mothers; TS30 clone TS30_a04g06
FJ368038.1 gg_id:359551 feces adult twins and mothers; TS30 clone TS30_a03b03

FJ369071.1	360935	4123.5	5378.8	5495.0	3665.4	3795.6	6671.0
FJ367138.1	369996	4200.2	3538.9	2677.7	6632.8	6169.2	7478.4
FJ674111.1	531152	3849.9	5520.3	7080.5	5767.4	6561.5	7913.3
GQ493258.1	554436	2331.5	3082.6	1948.0	4141.0	4837.0	2635.3
FJ362958.1	358162	3920.9	2890.8	2819.7	6281.5	6500.7	5670.8
DQ797687.1	184688	2777.3	2480.8	3602.3	5145.4	2017.9	2940.3
FJ364362.1	364691	143.9	122.0	206.9	108.0	58.5	98.1
FJ364484.1	367460	1548.1	1553.1	3236.4	3082.5	804.9	1433.8
FJ363807.1	367928	166.2	168.3	91.0	131.7	77.4	45.9
FJ679348.1	519744	2088.6	2825.2	1594.9	1504.0	3967.0	3379.6
FJ371375.1	358117	460.7	608.7	533.9	354.5	930.4	2208.5
FJ367066.1	366315	1444.3	1708.0	837.1	255.3	1174.2	2166.0
FJ676310.1	515950	4806.3	3195.5	2152.3	2784.7	3679.2	4029.8
FJ678060.1	517235	1470.5	2333.6	1419.9	1093.8	3077.2	2628.1
FJ362986.1	368011	7082.5	6395.4	1726.5	3092.8	2584.5	3414.0
FJ364439.1	366516	1524.3	1649.7	666.0	3975.8	593.5	533.8
EU766804.1	328877	22.5	42.6	40.9	63.0	64.7	24.9
FJ674266.1	512154	8881.1	12137.4	7246.3	10174.6	10564.4	8274.7
FJ364737.1	364401	756.3	1361.4	993.0	584.0	1711.4	1298.9
EF402524.1	212770	125.5	180.3	902.3	207.6	310.1	356.7
DQ801272.1	185246	659.5	543.8	495.2	584.4	882.7	305.4
EU778265.1	323557	1651.0	1300.7	2602.6	2192.0	2191.9	1234.7
DQ798404.1	182641	42.4	70.8	44.0	57.5	70.2	55.2
EU768521.1	322716	638.2	742.1	1683.1	482.3	696.4	986.5
FJ681399.1	530749	3263.8	4202.0	2794.4	2391.8	5926.5	6206.0
EU764987.1	352648	576.7	545.1	907.3	331.1	1854.8	1356.2
FJ371734.1	358134	7412.0	7681.0	4420.3	4109.1	6032.5	6224.8
EU765813.1	307235	333.4	481.6	2189.6	2230.7	1718.7	1503.5
FJ674074.1	528122	158.7	45.3	102.1	1067.5	144.9	114.6
EU778234.1	349081	25.8	30.2	53.0	58.8	63.5	22.3
FJ684453.1	530787	334.7	490.1	228.7	86.9	80.1	94.0
EU767130.1	354618	41.5	52.4	82.6	89.4	76.8	28.6
DQ797991.1	178056	4932.9	4280.7	3934.8	4276.1	3186.1	3801.5
FJ370413.1	360290	3349.5	2440.1	2843.8	4762.7	2570.5	5154.8
FJ673187.1	524511	2349.2	2539.2	2582.3	4842.5	3869.0	3204.8
FJ372110.1	364108	2344.9	1925.4	1107.3	2649.3	413.5	1243.0
FJ684625.1	518196	11892.4	12321.6	6650.6	8953.6	11125.4	8826.8
EU768164.1	353312	176.5	233.4	625.4	211.4	239.4	383.5
DQ905685.1	165926	99.8	183.7	379.4	198.2	99.5	104.3
FJ368148.1	368219	333.1	472.7	390.9	176.7	893.7	1578.2
FJ368038.1	359551	1295.3	1050.9	954.3	1121.7	2359.0	1128.0

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FJ678955.1 gg_id:520398 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680925.1 gg_id:514232 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676032.1 gg_id:521684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682075.1 gg_id:513892 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683291.1 gg_id:516284 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674196.1 gg_id:519723 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678852.1 gg_id:520763 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366549.1 gg_id:368072 feces adult twins and mothers; TS27 clone TS27_a01a10
FJ677213.1 gg_id:514787 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ456476.1 gg_id:157645 pre-adolescent turkey cecum clone CFT214A6
DQ800946.1 gg_id:186241 human fecal clone RL387_aao89g04
DQ793487.1 gg_id:191141 human fecal clone RL199_aaj44d08
FJ672951.1 gg_id:520500 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371153.1 gg_id:366167 feces adult twins and mothers; TS6 clone TS6_a01e10
EF400140.1 gg_id:214439 human fecal clone SJTU_E_09_36
EU776883.1 gg_id:331861 Mongoose lemur feces clone ML_aaj27h08
DQ905706.1 gg_id:173135 human fecal clone 29A-a5
FJ371246.1 gg_id:363885 feces adult twins and mothers; TS6 clone TS6_a02f10
DQ798093.1 gg_id:186928 human fecal clone RL302_aal95d09
DQ801240.1 gg_id:174910 human fecal clone RL116_aaf02d04
DQ805697.1 gg_id:193638 human fecal clone RL306aal89h10
FJ363638.1 gg_id:358653 feces adult twins and mothers; TS14 clone TS14_a01f03
AY983802.1 gg_id:127508 human descending colon mucosal biopsy clone M857
FJ678737.1 gg_id:527250 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795930.1 gg_id:178865 human fecal clone RL202_aai49b02
FJ370104.1 gg_id:370287 feces adult twins and mothers; TS55 clone TS55_a04d12
FJ676047.1 gg_id:528616 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ798655.1 gg_id:179391 human fecal clone RL181_aan99f04
DQ808591.1 gg_id:176396 human fecal clone RL239_aaj10e10
FJ371097.1 gg_id:361306 feces adult twins and mothers; TS5 clone TS5_a04h06
DQ806591.1 gg_id:183000 human fecal clone RL186_aao46e01
EF403860.1 gg_id:214234 human fecal clone SJTU_C_01_49
DQ905186.1 gg_id:169306 human fecal clone 002C-h7
FJ676092.1 gg_id:524421 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767030.1 gg_id:315946 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ806427.1 gg_id:175791 human fecal clone RL186_aan92c04
DQ798416.1 gg_id:179829 human fecal clone RL181_aah42c09
DQ798223.1 gg_id:176932 human fecal clone RL181_aah39a12
FJ677305.1 gg_id:530886 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ796705.1 gg_id:188452 human fecal clone RL179_aao53d09

FJ679857.1	530876	4173.6	2823.0	1099.2	3279.2	1535.6	861.0
FJ678955.1	520398	11674.7	9195.8	5794.7	8086.6	9725.1	10216.4
FJ680925.1	514232	4757.8	5363.1	4528.6	3893.2	4760.5	4101.9
FJ676032.1	521684	2103.8	2207.3	561.4	380.5	622.7	1070.5
FJ682075.1	513892	4716.4	3943.8	3302.6	2318.2	5739.5	4656.2
FJ683291.1	516284	5811.0	6196.4	2382.7	3778.3	4290.3	4738.7
FJ674196.1	519723	13291.4	17910.2	10445.4	10955.1	12919.0	11987.9
FJ678852.1	520763	2282.1	2138.4	1009.3	2113.3	2142.7	1458.2
FJ366549.1	368072	3017.3	3249.6	3133.4	2433.5	2294.5	5664.7
FJ677213.1	514787	1427.9	1943.7	998.2	1082.2	2434.4	2246.4
DQ456476.1	157645	138.0	175.4	181.5	139.3	157.6	91.8
DQ800946.1	186241	15585.9	15759.4	17897.0	13725.1	15603.9	15040.9
DQ793487.1	191141	15431.8	16569.2	14829.4	15823.0	17393.3	15357.9
FJ672951.1	520500	6611.5	5347.4	2220.8	9946.1	10843.9	8389.6
FJ371153.1	366167	148.5	204.4	609.9	197.7	70.8	56.8
EF400140.1	214439	438.9	389.6	310.5	850.1	224.3	487.2
EU776883.1	331861	152.9	215.0	278.1	206.1	73.4	34.2
DQ905706.1	173135	20.9	39.1	30.1	51.6	71.5	21.1
FJ371246.1	363885	10776.7	6632.5	4576.9	10866.9	5513.0	8976.6
DQ798093.1	186928	24.7	30.8	34.6	46.4	69.9	18.4
DQ801240.1	174910	21.8	29.8	42.0	43.0	55.7	15.9
DQ805697.1	193638	6372.6	6173.2	2608.8	8265.7	8070.7	6877.2
FJ363638.1	358653	3530.5	6602.5	3871.5	1026.0	3182.1	2320.2
AY983802.1	127508	8299.9	6431.6	4518.2	8002.4	11494.0	10132.7
FJ678737.1	527250	1371.0	2327.7	1420.5	1162.2	3085.4	2627.1
DQ795930.1	178865	5847.1	4731.1	5330.6	6097.5	4293.5	6913.2
FJ370104.1	370287	1187.6	700.9	903.0	446.5	115.5	179.5
FJ676047.1	528616	6006.2	7209.7	5341.4	6309.0	7314.0	6543.9
DQ798655.1	179391	20.3	34.8	51.4	45.5	65.0	19.9
DQ808591.1	176396	33.3	39.2	30.6	56.3	76.4	31.4
FJ371097.1	361306	4988.9	6022.4	5983.7	3902.9	4826.6	6315.9
DQ806591.1	183000	399.0	474.8	1175.1	274.2	350.5	449.6
EF403860.1	214234	44.3	75.5	143.7	106.3	105.5	53.6
DQ905186.1	169306	1740.9	1844.0	2921.0	3378.7	2078.7	3071.8
FJ676092.1	524421	218.1	592.4	1097.9	239.4	176.6	207.0
EU767030.1	315946	1774.6	1715.3	1656.6	2846.2	214.1	418.5
DQ806427.1	175791	1260.6	1312.6	1387.6	1118.0	1245.7	1344.5
DQ798416.1	179829	119.7	181.0	84.1	826.9	207.6	161.8
DQ798223.1	176932	5237.1	4310.1	3356.2	2576.6	2773.8	2842.8
FJ677305.1	530886	41.6	41.8	44.2	47.2	56.9	16.9
DQ796705.1	188452	800.5	321.2	507.9	487.7	264.6	522.2

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FJ365506.1 gg_id:369035 feces adult twins and mothers; TS20 clone TS20_a03f08
DQ796847.1 gg_id:184231 human fecal clone RL179_aao55d05
FJ370960.1 gg_id:366197 feces adult twins and mothers; TS5 clone TS5_a03c07
EU763792.1 gg_id:342779 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
FJ673785.1 gg_id:529284 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371147.1 gg_id:365835 feces adult twins and mothers; TS6 clone TS6_a01e04
GQ448258.1 gg_id:577127 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr
FJ370249.1 gg_id:369759 feces adult twins and mothers; TS56 clone TS56_a02d04
FJ365152.1 gg_id:362683 feces adult twins and mothers; TS1 clone TS1_a03e03
DQ798369.1 gg_id:179321 human fecal clone RL181_aah41f06
FJ371336.1 gg_id:367543 feces adult twins and mothers; TS6 clone TS6_a03g04
EF402817.1 gg_id:209333 human fecal clone SJTU_B_12_88
EF403128.1 gg_id:207179 human fecal clone SJTU_A1_1_31
DQ804660.1 gg_id:182605 human fecal clone RL187_aao71a06
FJ371675.1 gg_id:359679 feces adult twins and mothers; TS8 clone TS8_a01a03
DQ805298.1 gg_id:191990 human fecal clone RL249_aaj84g02
DQ825317.1 gg_id:188494 human fecal clone RL185_aan88d07
FJ681707.1 gg_id:527647 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY983857.1 gg_id:121748 human descending colon mucosal biopsy clone M976
DQ801459.1 gg_id:195653 human fecal clone RL388_aao95g10
FJ369135.1 gg_id:368234 feces adult twins and mothers; TS4 clone TS4_a04f08
EU765784.1 gg_id:305773 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
EU773399.1 gg_id:338066 Black lemur feces clone BKLE_h03_1
FJ676620.1 gg_id:511300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU778112.1 gg_id:305800 feces clone RL387_aao91d06
DQ806446.1 gg_id:187439 human fecal clone RL186_aan92e11
FJ678558.1 gg_id:518265 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797469.1 gg_id:176953 human fecal clone RL248_aai99g02
EU766774.1 gg_id:306661 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EU778110.1 gg_id:325310 feces clone RL388_aao96c05
EF405102.1 gg_id:205664 human fecal clone SJTU_G_07_93
DQ794050.1 gg_id:183259 human fecal clone RL176_aan57c08
EU774236.1 gg_id:327585 Chimpanzee feces clone CHIMP1_aaj37c05
FJ363566.1 gg_id:364894 feces adult twins and mothers; TS149 clone TS149_a04g05
FJ368436.1 gg_id:369275 feces adult twins and mothers; TS3 clone TS3_a04c11
DQ797452.1 gg_id:190572 human fecal clone RL248_aai99e06
FJ365840.1 gg_id:368102 feces adult twins and mothers; TS21 clone TS21_a03f09
FJ363037.1 gg_id:359542 feces adult twins and mothers; TS148 clone TS148_a02c01
DQ801524.1 gg_id:185679 human fecal clone RL388_aao96f03
FJ367888.1 gg_id:357299 feces adult twins and mothers; TS2 clone TS2_a04g04
AY978232.1 gg_id:120586 human transverse colon mucosal biopsy clone F043

FJ365506.1	369035	2827.8	3401.5	2482.1	3056.3	1653.1	3297.3
DQ796847.1	184231	1468.4	1488.7	4474.9	1251.8	1420.7	2077.3
FJ370960.1	366197	2631.9	2247.8	1823.7	1537.7	3457.7	2342.4
EU763792.1	342779	37.4	37.6	44.1	67.4	66.3	23.7
FJ673785.1	529284	3591.1	4152.8	4817.6	4227.1	7417.4	6337.3
FJ371147.1	365835	666.1	909.8	504.9	416.0	838.9	545.3
GQ448258.1	577127	2716.0	3450.5	1985.5	2726.8	4955.6	5525.2
FJ370249.1	369759	5435.3	5939.1	4260.2	4305.5	6538.8	6405.6
FJ365152.1	362683	743.9	633.0	1836.1	536.4	606.5	1040.4
DQ798369.1	179321	201.7	113.6	83.8	201.5	132.0	30.3
FJ371336.1	367543	234.6	393.4	453.2	149.6	772.4	441.9
EF402817.1	209333	91.2	156.5	231.4	99.8	153.4	148.1
EF403128.1	207179	2715.5	2362.4	2882.7	2317.8	2935.9	2530.8
DQ804660.1	182605	745.4	884.5	2154.5	532.3	460.2	750.4
FJ371675.1	359679	3014.1	3160.5	1985.8	2845.9	2141.8	2762.9
DQ805298.1	191990	108.2	114.8	169.6	112.4	731.5	374.1
DQ825317.1	188494	1655.1	2617.1	3556.2	2309.8	2269.1	3203.7
FJ681707.1	527647	32.4	45.0	60.1	92.6	81.6	30.2
AY983857.1	121748	432.6	730.8	432.2	562.0	2122.5	2369.0
DQ801459.1	195653	104.1	104.4	62.6	120.0	68.4	73.0
FJ369135.1	368234	119.9	150.1	231.0	332.8	337.9	288.0
EU765784.1	305773	48.6	47.4	33.5	59.2	56.7	21.1
EU773399.1	338066	27.8	112.1	33.7	893.1	84.6	48.1
FJ676620.1	511300	2003.8	2082.7	6318.4	4233.5	2823.2	1992.7
EU778112.1	305800	349.4	325.4	225.8	82.7	84.5	103.9
DQ806446.1	187439	89.6	61.6	320.4	91.0	71.7	11.5
FJ678558.1	518265	1858.4	1512.4	803.2	2880.7	1775.0	1958.0
DQ797469.1	176953	5306.9	11151.8	5396.7	6246.9	10160.3	10965.0
EU766774.1	306661	37.4	28.3	119.8	66.7	62.0	59.8
EU778110.1	325310	57.7	108.8	46.0	102.2	305.0	236.9
EF405102.1	205664	399.5	136.3	587.6	1970.0	355.3	532.2
DQ794050.1	183259	1059.3	1667.4	2604.6	1393.6	1442.7	2157.2
EU774236.1	327585	35.2	54.5	70.1	81.1	65.1	27.0
FJ363566.1	364894	1783.8	2616.3	4582.0	4219.3	3288.1	4243.9
FJ368436.1	369275	9647.4	9107.6	6290.3	9884.4	11464.3	11107.7
DQ797452.1	190572	3696.0	3745.2	970.4	2287.4	1882.6	3040.9
FJ365840.1	368102	3218.3	2872.1	3261.9	2904.5	3152.7	4836.6
FJ363037.1	359542	1227.0	1816.0	999.1	707.6	1453.8	1092.8
DQ801524.1	185679	22.7	36.1	44.5	61.6	88.7	29.3
FJ367888.1	357299	889.4	671.5	670.9	863.7	2237.5	1157.0
AY978232.1	120586	142.5	118.9	215.1	110.4	59.9	144.0

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EU761610.1 gg_id:327933 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ679163.1 gg_id:527463 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF403098.1 gg_id:216037 human fecal clone SJTU_B_10_61
EF404629.1 gg_id:206291 human fecal clone SJTU_C_13_72
FJ362929.1 gg_id:365179 feces adult twins and mothers; TS13 clone TS13_a04h05
EF403882.1 gg_id:210159 human fecal clone SJTU_C_01_81
EU762976.1 gg_id:353328 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ799125.1 gg_id:189425 human fecal clone RL205_aaj17h11
EU765069.1 gg_id:318023 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
FJ371388.1 gg_id:365191 feces adult twins and mothers; TS6 clone TS6_a04d02
FJ368195.1 gg_id:357057 feces adult twins and mothers; TS3 clone TS3_a01d02
EU766953.1 gg_id:342269 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EU763850.1 gg_id:308850 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
EU764022.1 gg_id:333428 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
EU764359.1 gg_id:327190 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ675734.1 gg_id:529354 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681114.1 gg_id:528002 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ363265.1 gg_id:367426 feces adult twins and mothers; TS149 clone TS149_a01c02
DQ325575.1 gg_id:148122 Metagenomic gut microbiome healthy human stool clone B071
DQ802390.1 gg_id:174026 human fecal clone RL188_aah17b01
DQ808569.1 gg_id:183333 human fecal clone RL239_aaj10c06
FJ372331.1 gg_id:359063 feces adult twins and mothers; TS9 clone TS9_a04d03
FJ365338.1 gg_id:359646 feces adult twins and mothers; TS20 clone TS20_a01f11
FJ362983.1 gg_id:369741 feces adult twins and mothers; TS148 clone TS148_a01e07
FJ681527.1 gg_id:511454 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681525.1 gg_id:519470 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ371371.1 gg_id:365514 feces adult twins and mothers; TS6 clone TS6_a04b08
EF404214.1 gg_id:208301 human fecal clone SJTU_C_06_52
DQ797735.1 gg_id:176811 human fecal clone RL206_aaj15c06
DQ802387.1 gg_id:193218 human fecal clone RL188_aah17a10
DQ801698.1 gg_id:183272 human fecal clone RL201_aai45f07
FJ683934.1 gg_id:520449 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ367378.1 gg_id:357380 feces adult twins and mothers; TS29 clone TS29_a02g06
DQ795994.1 gg_id:185878 human fecal clone RL202_aai50a04
DQ800176.1 gg_id:188379 human fecal clone RL303_aal69c01
FJ365498.1 gg_id:361816 feces adult twins and mothers; TS20 clone TS20_a03e12
GQ898100.1 gg_id:549326 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ905073.1 gg_id:168039 human fecal clone 2-002-f8
FJ674188.1 gg_id:525812 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ808596.1 gg_id:194672 human fecal clone RL239_aaj10f03
FJ682161.1 gg_id:522847 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

EU761610.1	327933	7880.4	6372.7	2838.0	4358.8	4637.7	3427.0
FJ679163.1	527463	31.7	37.5	29.4	47.0	76.5	21.8
EF403098.1	216037	2285.2	1713.9	2448.4	2704.4	5974.7	4298.6
EF404629.1	206291	130.8	208.4	496.9	224.0	128.6	146.2
FJ362929.1	365179	195.1	99.4	154.7	131.9	184.1	955.7
EF403882.1	210159	638.4	200.0	759.0	2272.6	1252.3	1306.7
EU762976.1	353328	26.4	24.6	113.2	61.2	71.7	25.7
DQ799125.1	189425	1540.4	133.9	449.4	1989.4	1180.3	1136.6
EU765069.1	318023	13226.2	13519.7	6848.2	10415.3	3406.6	4346.2
FJ371388.1	365191	2913.3	3894.5	3428.4	5495.1	7302.6	6470.0
FJ368195.1	357057	572.1	570.1	1205.1	1420.7	1533.9	1815.2
EU766953.1	342269	40.9	49.0	179.9	86.8	70.4	80.1
EU763850.1	308850	60.4	96.1	291.0	93.0	91.5	96.6
EU764022.1	333428	237.6	74.4	209.3	745.6	219.9	242.7
EU764359.1	327190	19.6	46.2	23.4	44.8	63.4	20.2
FJ675734.1	529354	1668.7	2842.0	1917.9	2311.6	2335.8	3589.7
FJ681114.1	528002	93.0	123.3	194.7	865.5	71.6	176.7
FJ363265.1	367426	4798.3	7240.3	6128.4	4468.1	5913.8	7427.2
DQ325575.1	148122	25.6	51.2	44.6	55.1	94.6	39.0
DQ802390.1	174026	16245.0	7606.0	2985.3	8750.9	5579.7	2790.8
DQ808569.1	183333	3637.8	2070.8	4341.1	2863.7	3498.6	4029.8
FJ372331.1	359063	1140.6	882.0	1030.5	970.2	1455.7	2223.5
FJ365338.1	359646	1156.3	1863.6	1979.6	3844.5	3876.9	2889.1
FJ362983.1	369741	2108.8	2549.5	3607.4	1936.9	3180.9	2818.4
FJ681527.1	511454	30.9	51.8	41.3	56.2	74.5	34.3
FJ681525.1	519470	567.7	976.7	472.4	338.4	551.7	333.2
FJ371371.1	365514	1589.6	2614.9	3234.3	1576.4	3636.4	4565.5
EF404214.1	208301	580.8	645.3	1152.2	1191.9	673.9	1666.8
DQ797735.1	176811	246.9	445.7	162.3	451.5	90.0	58.5
DQ802387.1	193218	249.6	479.7	451.6	223.0	139.0	266.6
DQ801698.1	183272	4213.6	2591.2	677.1	2070.4	848.5	1106.5
FJ683934.1	520449	566.1	555.9	166.2	246.1	1040.5	658.4
FJ367378.1	357380	146.1	158.5	632.8	145.5	212.4	122.0
DQ795994.1	185878	8.9	19.1	20.7	48.2	37.3	10.6
DQ800176.1	188379	3707.7	3789.8	360.3	2760.7	3823.8	3248.7
FJ365498.1	361816	1713.1	2550.5	3441.5	2868.9	2964.3	2519.0
GQ898100.1	549326	2678.9	1651.6	3531.1	1584.8	1407.5	1358.9
DQ905073.1	168039	3708.2	2962.2	5133.1	3651.4	3401.2	3470.4
FJ674188.1	525812	1068.8	815.2	691.4	3218.2	1589.9	1573.0
DQ808596.1	194672	367.6	501.6	545.0	336.9	2230.3	2333.7
FJ682161.1	522847	224.5	412.0	493.3	116.8	631.6	386.4

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DQ801458.1 gg_id:175743 human fecal clone RL388_aao95g09
AY983994.1 gg_id:120170 human descending colon mucosal biopsy clone MD11
DQ824062.1 gg_id:196818 human fecal clone RL204_aaj58h03
FJ685187.1 gg_id:530922 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FM873865.1 gg_id:370037 occupant source house mattress dust clone MB02A07
FJ678640.1 gg_id:520383 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802202.1 gg_id:189156 human fecal clone RL241_aaj04d07
DQ798729.1 gg_id:188748 human fecal clone RL181_aao00f06
FJ680125.1 gg_id:525032 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ825062.1 gg_id:190667 human fecal clone RL185_aao72h05
AY976163.1 gg_id:116614 human ascending colon mucosal biopsy clone LV63
EU763182.1 gg_id:304534 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
AY981860.1 gg_id:118738 human sigmoid colon mucosal biopsy clone NW64
FJ682340.1 gg_id:512027 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ675866.1 gg_id:516407 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370371.1 gg_id:369756 feces adult twins and mothers; TS56 clone TS56_a04b01
FJ367318.1 gg_id:370209 feces adult twins and mothers; TS29 clone TS29_a02b02
FJ370292.1 gg_id:362950 feces adult twins and mothers; TS56 clone TS56_a03a03
FJ680864.1 gg_id:522506 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797569.1 gg_id:195296 human fecal clone RL206_aaj13b08
EU762970.1 gg_id:344903 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EU764795.1 gg_id:341292 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B
DQ823827.1 gg_id:194156 human fecal clone RL250_aaj79f05
DQ904651.1 gg_id:163289 human fecal clone 001-b12
FJ674264.1 gg_id:522817 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU768309.1 gg_id:321223 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C
FJ368096.1 gg_id:357577 feces adult twins and mothers; TS30 clone TS30_a03h12
FJ683802.1 gg_id:528836 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ363799.1 gg_id:363481 feces adult twins and mothers; TS14 clone TS14_a03e01
GQ016078.1 gg_id:493589 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
DQ824126.1 gg_id:176546 human fecal clone RL204_aaj59f10
FJ682360.1 gg_id:524527 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ364311.1 gg_id:360764 feces adult twins and mothers; TS15 clone TS15_a01d12
EU475256.1 gg_id:296250 bonobo feces clone BNO_aaa01d04
GQ079614.1 gg_id:462293 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231h
FJ366185.1 gg_id:357470 feces adult twins and mothers; TS25 clone TS25_a03f10
FJ370813.1 gg_id:361408 feces adult twins and mothers; TS5 clone TS5_a01e11
DQ801695.1 gg_id:185663 human fecal clone RL201_aai45f02
DQ798344.1 gg_id:190278 human fecal clone RL181_aah41c04
FJ673805.1 gg_id:530252 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801134.1 gg_id:187888 human fecal clone RL387_aao92g05

DQ801458.1	175743	23.1	18.3	32.5	71.8	47.2	18.0
AY983994.1	120170	704.2	715.6	1531.9	2339.3	922.5	1092.0
DQ824062.1	196818	616.0	625.1	1303.8	933.9	1255.6	1826.8
FJ685187.1	530922	4597.4	3924.2	4472.3	2468.6	4541.0	4856.3
FM873865.1	370037	750.7	1412.0	2063.2	438.5	1116.7	1206.5
FJ678640.1	520383	511.7	846.0	1836.3	483.0	703.7	885.7
DQ802202.1	189156	50.9	44.5	796.5	101.2	103.6	69.2
DQ798729.1	188748	4619.2	4202.7	4165.1	5109.7	4127.9	6426.9
FJ680125.1	525032	1702.2	2107.2	1237.1	1096.3	3008.5	3256.3
DQ825062.1	190667	42.6	89.6	166.9	1098.7	342.0	347.3
AY976163.1	116614	2031.5	2428.1	6775.9	4524.1	2615.3	2249.3
EU763182.1	304534	806.4	589.2	927.5	588.2	1385.6	1425.8
AY981860.1	118738	370.0	482.1	240.6	1302.1	391.3	148.8
FJ682340.1	512027	9356.7	7641.1	3534.6	8558.7	7270.7	7196.0
FJ675866.1	516407	5421.0	5871.3	3340.7	6690.2	5170.3	4656.2
FJ370371.1	369756	466.9	509.6	1284.0	283.1	359.8	490.1
FJ367318.1	370209	618.2	1462.6	2147.0	903.6	3876.9	3902.2
FJ370292.1	362950	918.7	1235.2	801.9	568.4	1523.2	1228.9
FJ680864.1	522506	421.7	296.1	318.1	486.1	278.2	187.5
DQ797569.1	195296	676.1	783.4	1792.3	435.4	751.2	914.5
EU762970.1	344903	1850.1	3269.4	4098.1	3242.4	6982.1	6327.7
EU764795.1	341292	707.9	1146.5	508.8	141.4	370.7	460.5
DQ823827.1	194156	5960.5	7869.2	3616.4	3005.6	1079.7	2180.4
DQ904651.1	163289	9504.0	8551.6	6174.6	6483.6	10509.5	6227.8
FJ674264.1	522817	50.2	83.2	182.3	1053.1	317.3	275.4
EU768309.1	321223	459.7	890.1	3309.3	878.6	2253.9	2304.6
FJ368096.1	357577	3535.7	2975.4	2444.6	2691.4	3463.1	2758.2
FJ683802.1	528836	113.4	240.7	308.2	112.0	341.4	211.6
FJ363799.1	363481	42.7	36.8	170.4	83.5	69.1	69.9
GQ016078.1	493589	1492.4	1157.7	2587.9	1208.4	1130.1	1033.0
DQ824126.1	176546	33.1	60.0	43.8	55.3	77.6	36.5
FJ682360.1	524527	31.7	48.2	50.0	47.4	46.8	21.7
FJ364311.1	360764	6400.5	8700.1	8502.0	7342.7	13140.0	13489.7
EU475256.1	296250	10306.9	11338.7	1417.9	5366.0	6444.6	6371.3
GQ079614.1	462293	28.1	47.9	19.8	42.6	79.7	40.9
FJ366185.1	357470	34.2	34.5	38.2	66.2	58.0	96.1
FJ370813.1	361408	1189.1	1024.3	1268.0	3314.2	1304.0	2777.9
DQ801695.1	185663	1006.4	1740.9	4208.9	1094.2	800.5	1631.5
DQ798344.1	190278	12454.1	12731.0	9708.0	13604.4	13318.3	12827.7
FJ673805.1	530252	2574.7	2994.5	2067.4	2760.7	4408.1	3882.2
DQ801134.1	187888	336.0	153.2	217.8	137.9	79.5	75.6

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EF403606.1 gg_id:216458 human fecal clone SJTU_A2_04_26
FJ673295.1 gg_id:515518 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684079.1 gg_id:523830 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370286.1 gg_id:365598 feces adult twins and mothers; TS56 clone TS56_a02h06
FJ685011.1 gg_id:524400 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ802801.1 gg_id:193378 human fecal clone RL188_aan96g03
FJ676677.1 gg_id:510685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682588.1 gg_id:524482 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU778627.1 gg_id:340204 Ring-tailed lemur feces clone RT_aai09d01
DQ904690.1 gg_id:168007 human fecal clone 001-e4
DQ797233.1 gg_id:178267 human fecal clone RL386_aao88f12
EU766846.1 gg_id:315226 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ366972.1 gg_id:362118 feces adult twins and mothers; TS28 clone TS28_a02a03
FJ364419.1 gg_id:360543 feces adult twins and mothers; TS15 clone TS15_a02g02
EF402383.1 gg_id:212008 human fecal clone SJTU_B_07_15
EF403845.1 gg_id:207336 human fecal clone SJTU_C_01_32
DQ797376.1 gg_id:179644 human fecal clone RL248_aai98e11
DQ904873.1 gg_id:169773 human fecal clone 001C-e12
DQ823885.1 gg_id:180532 human fecal clone RL250_aaj80d09
AF371723.1 gg_id:39948 swine intestine clone p-366-a3
FJ681951.1 gg_id:510322 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682732.1 gg_id:513225 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372292.1 gg_id:365149 feces adult twins and mothers; TS9 clone TS9_a03h10
DQ805429.1 gg_id:189660 human fecal clone RL203_aai62e03
FJ679931.1 gg_id:527631 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU778303.1 gg_id:331363 feces clone RL388_aao93a11
GQ898754.1 gg_id:585524 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ798053.1 gg_id:197507 human fecal clone RL302_aal95a03
DQ801515.1 gg_id:182931 human fecal clone RL388_aao96e06
FJ682430.1 gg_id:530685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680211.1 gg_id:526612 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679369.1 gg_id:519122 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ370312.1 gg_id:367326 feces adult twins and mothers; TS56 clone TS56_a03c09
DQ809064.1 gg_id:195742 human fecal clone RL243_aai88h06
FJ364975.1 gg_id:362407 feces adult twins and mothers; TS1 clone TS1_a01d06
DQ797365.1 gg_id:175570 human fecal clone RL248_aai98d09
EU466841.1 gg_id:292490 African elephant feces clone AFEL2_aao30c02
FJ674077.1 gg_id:525715 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ898171.1 gg_id:549196 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ678426.1 gg_id:522074 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ799443.1 gg_id:195250 human fecal clone RL305aal86d01

EF403606.1	216458	26.9	45.6	89.9	55.7	83.5	63.3
FJ673295.1	515518	5608.9	6591.2	3473.5	4247.1	8336.2	6602.5
FJ684079.1	523830	2542.9	2755.3	1337.1	1031.5	645.7	878.2
FJ370286.1	365598	2867.7	3599.1	2797.9	3281.5	4393.1	6082.9
FJ685011.1	524400	1748.0	1308.1	993.0	2221.6	1690.7	1740.5
DQ802801.1	193378	373.7	493.7	1151.6	299.1	319.4	440.0
FJ676677.1	510685	990.1	1097.7	516.7	216.0	315.4	337.0
FJ682588.1	524482	3956.4	3535.4	753.3	6176.0	6959.5	7034.7
EU778627.1	340204	14.6	57.9	22.5	51.4	64.3	18.3
DQ904690.1	168007	10839.5	10302.8	16146.8	10392.1	9044.7	8114.8
DQ797233.1	178267	1161.8	131.5	643.1	2671.3	1026.0	1151.9
EU766846.1	315226	101.7	305.0	452.0	117.0	163.5	118.5
FJ366972.1	362118	49.9	80.3	174.3	1184.4	347.2	329.7
FJ364419.1	360543	1883.3	1778.7	943.7	2216.1	1951.8	1869.5
EF402383.1	212008	2399.5	2392.8	3352.7	3293.4	1644.3	3607.2
EF403845.1	207336	2779.3	2005.5	1765.0	2413.7	1140.4	2130.5
DQ797376.1	179644	472.4	428.5	758.8	324.9	1982.2	1864.6
DQ904873.1	169773	644.1	625.0	1276.5	810.2	262.0	534.8
DQ823885.1	180532	582.4	1136.4	976.2	582.8	1026.5	1130.4
AF371723.1	39948	69.6	174.7	544.2	107.5	1019.4	421.2
FJ681951.1	510322	1594.8	1154.3	1681.6	2373.1	1478.3	1843.6
FJ682732.1	513225	2777.2	2918.6	929.1	6979.4	4389.8	4214.3
FJ372292.1	365149	36.8	46.1	179.4	74.8	99.5	59.7
DQ805429.1	189660	3391.6	4033.8	1431.4	2577.5	496.5	1064.1
FJ679931.1	527631	51.1	71.8	169.5	1090.8	332.7	286.1
EU778303.1	331363	3616.3	4792.7	1897.3	2183.2	3710.7	3019.8
GQ898754.1	585524	54.7	93.6	148.8	131.5	73.1	96.5
DQ798053.1	197507	7185.1	8022.2	5991.9	8124.0	8743.1	9595.0
DQ801515.1	182931	839.1	1531.7	2730.8	2468.2	3972.5	4910.8
FJ682430.1	530685	42.3	61.8	171.6	1085.4	314.1	303.6
FJ680211.1	526612	813.7	888.9	3412.4	2601.9	2367.0	2371.8
FJ679369.1	519122	1918.9	1903.3	293.9	794.4	677.1	162.2
FJ370312.1	367326	28.9	44.5	68.3	65.4	101.3	46.5
DQ809064.1	195742	1087.9	3074.8	2286.0	582.6	979.5	1094.9
FJ364975.1	362407	3096.9	3764.5	3512.9	2436.7	3791.0	4056.8
DQ797365.1	175570	138.1	107.8	153.0	86.4	73.0	42.5
EU466841.1	292490	13.5	28.0	24.8	44.3	50.1	25.5
FJ674077.1	525715	15764.6	16929.1	7223.3	15188.0	17032.4	15594.1
GQ898171.1	549196	1842.2	1950.8	2840.5	2917.2	2627.0	3767.0
FJ678426.1	522074	43.9	42.6	40.9	55.0	62.7	26.0
DQ799443.1	195250	218.4	304.1	413.1	268.7	172.1	161.8

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EU778236.1 gg_id:316304 feces clone RL388_aao94b11
FJ678870.1 gg_id:512472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF400999.1 gg_id:203591 human fecal clone SJTU_D_04_49
FJ680972.1 gg_id:519973 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ806688.1 gg_id:183513 human fecal clone RL186_aao47e12
EU766495.1 gg_id:305290 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
FJ362752.1 gg_id:367710 feces adult twins and mothers; TS13 clone TS13_a02g01
FJ372208.1 gg_id:359289 feces adult twins and mothers; TS9 clone TS9_a03a03
FJ367380.1 gg_id:365407 feces adult twins and mothers; TS29 clone TS29_a02g08
FJ363839.1 gg_id:360232 feces adult twins and mothers; TS14 clone TS14_a04a01
FJ678151.1 gg_id:528937 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680786.1 gg_id:526274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU762845.1 gg_id:304517 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ677432.1 gg_id:528151 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ368415.1 gg_id:358955 feces adult twins and mothers; TS3 clone TS3_a04b01
EF402952.1 gg_id:213907 human fecal clone SJTU_B_14_69
FJ683751.1 gg_id:530843 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ905111.1 gg_id:163491 human fecal clone 002C-b12
FJ364490.1 gg_id:362754 feces adult twins and mothers; TS15 clone TS15_a03e11
FJ685392.1 gg_id:530094 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673343.1 gg_id:517507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ825000.1 gg_id:174877 human fecal clone RL185_aao72b01
EU768621.1 gg_id:318450 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
FJ678887.1 gg_id:521067 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ365105.1 gg_id:359049 feces adult twins and mothers; TS1 clone TS1_a02h06
FJ364590.1 gg_id:362559 feces adult twins and mothers; TS15 clone TS15_a04g06
FJ365386.1 gg_id:359852 feces adult twins and mothers; TS20 clone TS20_a02c08
FJ367541.1 gg_id:370253 feces adult twins and mothers; TS29 clone TS29_a04g06
FJ680223.1 gg_id:520109 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU763241.1 gg_id:307220 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ681568.1 gg_id:527811 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676504.1 gg_id:522876 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ362885.1 gg_id:359008 feces adult twins and mothers; TS13 clone TS13_a04d04
FJ678804.1 gg_id:516818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673487.1 gg_id:527547 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801384.1 gg_id:178047 human fecal clone RL388_aao94g07
AY984170.1 gg_id:118701 human stool clone B054
AY979049.1 gg_id:126578 human transverse colon mucosal biopsy clone NJ45
FJ673097.1 gg_id:520459 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ674043.1 gg_id:523328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673534.1 gg_id:523016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

EU778236.1	316304	14.5	21.2	39.2	60.0	66.6	20.5
FJ678870.1	512472	11175.1	10442.3	6770.4	9732.5	11817.7	10233.2
EF400999.1	203591	16955.9	13792.1	15890.5	10725.9	14238.0	16761.4
FJ680972.1	519973	971.8	1463.2	346.7	2139.9	2276.7	2007.7
DQ806688.1	183513	24.6	41.6	68.3	64.3	75.3	22.1
EU766495.1	305290	3218.2	3829.6	3310.7	3590.0	3566.8	3388.0
FJ362752.1	367710	5810.4	7325.2	2578.3	6049.9	4896.8	5635.3
FJ372208.1	359289	506.2	584.4	1200.9	1121.4	684.4	1061.9
FJ367380.1	365407	32.0	35.3	30.1	45.2	59.5	13.4
FJ363839.1	360232	25.6	18.4	58.3	65.1	70.8	32.7
FJ678151.1	528937	25.3	27.9	28.8	57.4	53.6	30.0
FJ680786.1	526274	35.1	47.0	176.7	71.0	57.6	34.4
EU762845.1	304517	2259.8	2058.1	3796.3	3544.6	4985.0	4322.0
FJ677432.1	528151	5214.7	4577.5	1347.8	2562.4	1001.0	1084.3
FJ368415.1	358955	1080.3	1509.1	656.1	383.7	1969.1	1040.8
EF402952.1	213907	5527.8	8239.7	3422.2	4010.9	9247.2	7620.1
FJ683751.1	530843	31.0	42.8	48.6	60.7	86.9	38.0
DQ905111.1	163491	1733.3	1600.4	2929.9	3271.8	2659.4	3039.2
FJ364490.1	362754	991.7	2644.8	2969.8	2612.0	5897.9	6255.9
FJ685392.1	530094	9875.4	7132.6	2833.2	2077.9	3024.3	3112.5
FJ673343.1	517507	378.7	575.9	479.1	641.1	481.0	661.3
DQ825000.1	174877	18.3	26.9	39.7	50.6	56.7	16.9
EU768621.1	318450	507.4	354.2	1046.5	2169.9	604.1	849.6
FJ678887.1	521067	1536.2	1532.9	1634.4	1549.9	1580.7	1510.9
FJ365105.1	359049	2589.6	2853.9	2351.7	2132.2	2296.8	4045.4
FJ364590.1	362559	3016.2	3232.7	2361.5	2144.5	2300.8	4050.4
FJ365386.1	359852	191.0	223.4	183.2	238.8	93.6	43.6
FJ367541.1	370253	3594.6	3411.7	2085.4	4894.0	9952.5	7643.7
FJ680223.1	520109	3020.9	2146.8	717.5	5385.2	3827.1	4017.5
EU763241.1	307220	80.0	129.5	375.0	89.7	507.1	251.2
FJ681568.1	527811	1054.5	1106.7	1638.0	1002.5	2247.3	1228.6
FJ676504.1	522876	3689.9	3765.1	2626.4	3774.4	4477.3	5077.6
FJ362885.1	359008	6836.2	6386.0	1161.7	6861.9	10613.3	8067.4
FJ678804.1	516818	11006.4	12147.3	5866.0	9922.8	14446.1	11857.3
FJ673487.1	527547	2681.4	1622.3	274.9	3514.6	3236.1	3142.3
DQ801384.1	178047	2370.1	1984.6	2928.4	4308.4	2520.2	3441.8
AY984170.1	118701	412.6	737.3	125.5	138.4	567.9	265.1
AY979049.1	126578	1737.6	2432.6	1660.0	1471.9	1660.8	2881.6
FJ673097.1	520459	484.8	716.2	612.5	414.8	826.3	564.4
FJ674043.1	523328	2236.9	3227.4	1749.3	2583.9	4765.2	3646.7
FJ673534.1	523016	150.3	162.5	122.6	208.3	60.7	68.3

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GQ898476.1 gg_id:585428 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ326372.1 gg_id:149213 Metagenomic gut microbiome healthy human stool clone C386
DQ796992.1 gg_id:195038 human fecal clone RL386_aao85e04
DQ823803.1 gg_id:191333 human fecal clone RL250_aaj79c08
FJ678240.1 gg_id:525494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683918.1 gg_id:520517 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677025.1 gg_id:519119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801244.1 gg_id:187010 human fecal clone RL116_aaf02f02
GQ448921.1 gg_id:548379 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr
FJ365385.1 gg_id:361941 feces adult twins and mothers; TS20 clone TS20_a02c07
FJ678517.1 gg_id:516135 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ043044.1 gg_id:460138 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012e
FJ682899.1 gg_id:525479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ362810.1 gg_id:363538 feces adult twins and mothers; TS13 clone TS13_a03e01
EU778238.1 gg_id:325784 feces clone RL388_aao96a06
AB185655.1 gg_id:107235 rumen clone F24-H11
DQ455829.1 gg_id:158222 pre-adolescent turkey cecum clone CFT19A8
EU775925.1 gg_id:326785 Horse feces clone horsem_aai93f12
FJ362828.1 gg_id:366573 feces adult twins and mothers; TS13 clone TS13_a03f08
DQ815311.1 gg_id:167509 mouse cecum clone aab45c07
EU504766.1 gg_id:259535 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g09
EU503968.1 gg_id:273637 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d07
EU474488.1 gg_id:301032 bighorn sheep feces clone BHSD_aaa02f09
EF401657.1 gg_id:205604 human fecal clone SJTU_D_14_93
FJ367640.1 gg_id:368423 feces adult twins and mothers; TS2 clone TS2_a01h01
EF436308.2 gg_id:209712 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC22
EU137434.1 gg_id:267999 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
AY985959.1 gg_id:118285 human stool clone D258
DQ794276.1 gg_id:187564 human fecal clone RL176_aan60e05
FJ823863.1 gg_id:526665 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial
GQ491174.1 gg_id:544996 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
DQ394655.1 gg_id:155341 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
EU844238.1 gg_id:309451 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU776785.1 gg_id:313471 Mongoose lemur feces clone ML_aaj26e11
EF602811.1 gg_id:230941 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
AB234463.1 gg_id:149007 termite gut homogenate clone MgMjD-058
DQ798394.1 gg_id:194661 human fecal clone RL181_aah41h12
EU458004.1 gg_id:304013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75
AY916303.1 gg_id:114021 human sigmoid colon biopsy clone MM71
EU763882.1 gg_id:331742 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
FJ372305.1 gg_id:369053 feces adult twins and mothers; TS9 clone TS9_a04a11

GQ898476.1	585428	2488.4	2128.8	2489.0	4248.5	2396.5	3158.1
DQ326372.1	149213	58.5	75.4	198.4	1098.8	340.5	293.7
DQ796992.1	195038	7033.1	6672.9	4616.3	5131.2	6078.2	5236.6
DQ823803.1	191333	36.5	32.5	22.5	38.6	66.3	21.1
FJ678240.1	525494	2283.3	2147.8	939.5	2115.4	2151.4	1478.1
FJ683918.1	520517	33.2	49.9	135.2	1020.8	321.4	258.0
FJ677025.1	519119	1301.5	2724.3	2843.1	1719.3	2712.7	2385.8
DQ801244.1	187010	25.5	45.0	79.9	77.2	64.7	22.5
GQ448921.1	548379	24.0	23.0	36.7	46.7	44.7	15.2
FJ365385.1	361941	486.5	319.2	479.1	2514.1	404.7	463.7
FJ678517.1	516135	2960.2	2557.1	1629.5	2129.1	1306.1	1013.5
GQ043044.1	460138	3593.2	2664.2	5532.7	4769.5	2814.1	2979.1
FJ682899.1	525479	4723.4	4631.6	2149.2	3868.5	4030.0	4958.8
FJ362810.1	363538	495.3	564.4	1328.1	343.4	302.9	553.7
EU778238.1	325784	28.1	36.8	67.4	48.9	71.2	27.0
AB185655.1	107235	2390.2	2401.5	1032.7	624.4	368.6	627.1
DQ455829.1	158222	186.9	443.1	764.2	657.3	160.2	448.9
EU775925.1	326785	6859.7	4536.0	7584.8	8604.8	3104.4	6120.5
FJ362828.1	366573	5691.5	6001.7	6640.8	5211.0	6630.2	7234.3
DQ815311.1	167509	63.8	59.1	205.8	64.6	53.2	35.7
EU504766.1	259535	5814.9	6506.8	4463.3	5785.6	7114.5	6085.2
EU503968.1	273637	1401.9	997.1	788.4	4693.1	432.3	759.0
EU474488.1	301032	4397.1	6200.3	4724.3	6796.2	7579.2	8969.6
EF401657.1	205604	758.0	654.6	1707.8	486.3	142.4	264.3
FJ367640.1	368423	7379.9	9467.7	4622.5	5018.1	5993.2	6214.5
EF436308.2	209712	23.5	56.7	106.2	59.5	63.7	28.8
EU137434.1	267999	1905.8	1485.7	1152.8	1405.2	175.6	406.1
AY985959.1	118285	4421.7	5494.5	3895.2	3183.6	2386.9	3039.7
DQ794276.1	187564	4788.3	5662.0	4519.1	2867.8	5120.1	4884.6
FJ823863.1	526665	2151.0	1749.7	3221.3	1263.3	1256.0	1204.9
GQ491174.1	544996	2019.7	1639.4	1391.2	1010.9	2439.4	3078.2
DQ394655.1	155341	387.9	280.6	869.1	211.9	204.2	481.4
EU844238.1	309451	4743.5	5357.9	4597.2	7334.0	2926.3	4002.0
EU776785.1	313471	323.4	238.6	626.8	165.4	110.7	173.5
EF602811.1	230941	2643.4	2843.7	4098.1	2057.4	2585.5	2281.7
AB234463.1	149007	50.0	76.9	63.6	68.0	90.9	59.9
DQ798394.1	194661	4631.8	2702.9	2492.6	5625.9	3328.4	3252.2
EU458004.1	304013	2288.8	3710.7	1480.2	2643.0	6441.4	5192.7
AY916303.1	114021	577.2	1287.6	235.0	370.6	411.9	825.5
EU763882.1	331742	4543.5	5517.3	5425.5	4413.9	4355.4	4686.7
FJ372305.1	369053	134.2	237.5	542.4	223.3	351.4	533.3

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FJ366580.1 gg_id:362243 feces adult twins and mothers; TS27 clone TS27_a01d05
FJ366573.1 gg_id:363823 feces adult twins and mothers; TS27 clone TS27_a01c10
DQ456220.1 gg_id:158722 pre-adolescent turkey cecum clone CFT29G9
DQ014822.1 gg_id:134301 mouse cecum clone M1_b06_3
EU461564.1 gg_id:288270 black rhinoceros feces clone RH_aaj92e10
EU461544.1 gg_id:298072 black rhinoceros feces clone RH_aaj92b07
AB218336.1 gg_id:147024 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-135
EU504992.1 gg_id:271491 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01c11
GU302582.1 gg_id:585073 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
DQ801356.1 gg_id:195943 human fecal clone RL388_aao94d10
FJ366352.1 gg_id:365719 feces adult twins and mothers; TS26 clone TS26_a01g07
DQ804825.1 gg_id:175497 human fecal clone RL385_aao81b11.Contig2
EF604816.1 gg_id:229824 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
EU452624.1 gg_id:328445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75
EU456254.1 gg_id:338796 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80
GQ896697.1 gg_id:532748 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ362655.1 gg_id:362777 feces adult twins and mothers; TS13 clone TS13_a01e10
GQ449217.1 gg_id:549950 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g
FJ363502.1 gg_id:363316 feces adult twins and mothers; TS149 clone TS149_a04a04
EF025275.1 gg_id:191239 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N6
DQ805440.1 gg_id:183410 human fecal clone RL203_aai62f07
EU761793.1 gg_id:311033 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
EU843460.1 gg_id:321337 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU530368.1 gg_id:263665 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
EF400373.1 gg_id:206513 human fecal clone SJTU_E_12_37
EF098593.1 gg_id:185752 mouse cecum clone SWPT16_aaa01h04
FJ681249.1 gg_id:522699 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797153.1 gg_id:203545 human fecal clone RL386_aao87f05
DQ824395.1 gg_id:195397 human fecal clone RL304_aal75e08
GU304189.1 gg_id:548161 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
FJ365085.1 gg_id:366486 feces adult twins and mothers; TS1 clone TS1_a02f07
DQ799134.1 gg_id:191902 human fecal clone RL205_aaj18a10
EU453686.1 gg_id:316428 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77
AB238598.1 gg_id:249174 Oscillibacter valericigenes str. Sjm18-20 (= NBRC 101213)
FJ369766.1 gg_id:362078 feces adult twins and mothers; TS51 clone TS51_a04e10
DQ673487.1 gg_id:168795 rumen fluid clone GRC22
DQ904783.1 gg_id:171303 human fecal clone 001B-e1
EU462532.1 gg_id:297465 Sumatran orangutan feces clone orang1_aai56e09
EU509002.1 gg_id:274686 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41f02
EU505557.1 gg_id:276535 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02f07
EF401625.1 gg_id:213633 human fecal clone SJTU_D_13_45

FJ366580.1	362243	7508.1	7304.6	3970.4	8687.8	10616.2	9280.0
FJ366573.1	363823	470.3	574.6	767.1	305.2	1163.0	1774.4
DQ456220.1	158722	185.8	352.3	857.8	211.0	230.8	477.3
DQ014822.1	134301	1508.9	1967.0	1478.9	4734.1	3983.8	5310.7
EU461564.1	288270	6034.3	7223.0	5940.5	5686.2	9446.2	8189.2
EU461544.1	298072	937.3	2022.0	2572.7	1158.5	1686.0	1141.2
AB218336.1	147024	29.1	33.0	37.3	58.2	65.2	25.6
EU504992.1	271491	483.0	454.4	654.9	244.4	336.3	175.3
GU302582.1	585073	11573.9	11947.6	6447.5	9045.3	11946.9	11006.8
DQ801356.1	195943	231.1	551.7	572.4	202.7	241.4	165.2
FJ366352.1	365719	2949.9	3825.0	2061.0	2174.4	1552.5	2061.4
DQ804825.1	175497	6318.4	4040.5	4863.6	5360.4	5725.6	6404.3
EF604816.1	229824	739.9	436.8	731.8	837.5	1207.6	492.0
EU452624.1	328445	4157.2	3568.7	1890.4	3827.3	1479.5	2284.5
EU456254.1	338796	62.5	152.9	352.9	180.0	171.5	232.9
GQ896697.1	532748	1497.7	1793.0	3965.7	1381.9	1397.4	1449.8
FJ362655.1	362777	79.6	184.3	109.1	200.9	95.8	140.2
GQ449217.1	549950	734.8	1095.3	2205.1	515.8	1215.5	839.2
FJ363502.1	363316	357.2	619.3	1490.2	695.9	731.6	830.7
EF025275.1	191239	3944.7	5177.4	4630.9	3751.7	6867.8	6819.2
DQ805440.1	183410	26.5	34.7	86.4	55.4	70.1	31.5
EU761793.1	311033	923.0	1699.1	2197.8	742.8	1651.1	1828.8
EU843460.1	321337	1524.4	1280.0	2767.8	948.3	1768.0	1904.3
EU530368.1	263665	3122.2	1870.1	3126.3	2532.5	811.8	856.3
EF400373.1	206513	968.5	862.1	1254.7	578.3	715.3	983.9
EF098593.1	185752	21.3	28.7	22.7	55.5	57.0	29.6
FJ681249.1	522699	589.4	490.6	308.3	167.8	411.1	160.9
DQ797153.1	203545	269.3	204.0	661.4	404.9	185.7	305.8
DQ824395.1	195397	5991.5	5206.6	3209.4	8255.3	6586.3	6326.6
GU304189.1	548161	882.4	874.9	1484.5	898.2	178.3	158.0
FJ365085.1	366486	8535.4	8552.7	5570.5	6827.0	9954.8	6930.9
DQ799134.1	191902	9266.7	9211.3	10686.2	9651.2	8622.6	10653.4
EU453686.1	316428	1257.2	2895.7	2975.2	2304.3	7243.4	6669.1
AB238598.1	249174	630.1	612.4	615.9	544.2	280.7	509.8
FJ369766.1	362078	2398.9	3665.7	1315.4	1170.7	893.4	1153.2
DQ673487.1	168795	2249.0	2039.1	3401.6	2398.5	1167.5	1233.7
DQ904783.1	171303	460.6	1131.4	1013.0	499.0	1457.2	1165.8
EU462532.1	297465	23.6	33.1	39.0	63.4	72.6	25.6
EU509002.1	274686	5579.6	4821.5	6747.8	5658.5	2776.8	3481.8
EU505557.1	276535	2263.1	1448.8	688.0	2981.4	2380.8	2140.0
EF401625.1	213633	15970.7	20947.6	11286.9	13979.6	14248.7	13007.1

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EU764883.1 gg_id:347184 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
EU774621.1 gg_id:320768 Angola Colobus feces clone EAC_2_aaa02f02
EU452440.1 gg_id:303454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU463672.1 gg_id:298918 domesticated horse feces clone horsej_aai90g11
EU771312.1 gg_id:356187 Asiatic elephant feces clone AE1_aaa03d05
EF096980.1 gg_id:192115 mouse cecum clone SWPT13_aaa03f07
EU772150.1 gg_id:354379 Argali sheep feces clone AS1_aao40g10.Contig1
DQ809326.1 gg_id:189943 human fecal clone RL184_aah19c02
FJ366181.1 gg_id:361863 feces adult twins and mothers; TS25 clone TS25_a03f06
DQ793427.1 gg_id:192058 human fecal clone RL199_aaj43f01
EU457751.1 gg_id:327701 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU455083.1 gg_id:322211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
DQ808890.1 gg_id:195102 human fecal clone RL243_aai86f05
EU475806.1 gg_id:296144 white-faced saki feces clone Saki_aaj61g02
EF096534.1 gg_id:193435 mouse cecum clone obob2_aaa04e06
EF602930.1 gg_id:235072 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AY992715.1 gg_id:130454 mouse cecum clone C23_p23
DQ905136.1 gg_id:165954 human fecal clone 002C-d1
GQ897639.1 gg_id:536897 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ365979.1 gg_id:360331 feces adult twins and mothers; TS25 clone TS25_a01d02
EU452820.1 gg_id:336127 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EF096624.1 gg_id:198635 mouse cecum clone SWPT11_aaa02b09
FJ681029.1 gg_id:520720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ815674.1 gg_id:164465 mouse cecum clone aab44f06
DQ326565.1 gg_id:146558 Metagenomic gut microbiome healthy human stool clone C747
EU775865.1 gg_id:336216 Horse feces clone horsem_aai95a08
DQ808842.1 gg_id:181304 human fecal clone RL243_aai86a08
DQ015246.1 gg_id:134096 mouse cecum clone M2_g12_3
EU774932.1 gg_id:327337 Flying Fox feces clone FF_f03_1
EF602809.1 gg_id:228426 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ809986.1 gg_id:199055 human fecal clone RL184_aao66f12
EU771406.1 gg_id:323903 Asiatic elephant feces clone AE2_aaa03h12
DQ014634.1 gg_id:135369 mouse cecum clone M1_h06
FJ879271.1 gg_id:427738 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
AY985603.1 gg_id:121620 human stool clone C593
DQ796558.1 gg_id:190220 human fecal clone RL179aan74f10
EU509249.1 gg_id:273592 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46f03
EU461246.1 gg_id:295371 hamadryas baboon feces clone BAZ_aah91d08
FJ362625.1 gg_id:365734 feces adult twins and mothers; TS13 clone TS13_a01c02
EU775024.1 gg_id:314582 Francois Langur feces clone FL_1aaa01h10
DQ796802.1 gg_id:180980 human fecal clone RL179_aao54g01

EU764883.1	347184	6918.0	8843.0	3065.4	6113.2	6781.5	6938.4
EU774621.1	320768	4505.0	6070.5	4971.3	4741.7	3165.6	3906.2
EU452440.1	303454	1492.0	2069.0	1320.8	761.0	1652.3	1518.4
EU463672.1	298918	1591.1	1304.8	3730.1	1064.9	1783.7	1807.4
EU771312.1	356187	158.8	321.9	353.3	132.4	335.3	276.1
EF096980.1	192115	4037.3	5311.1	1249.6	3682.2	1731.3	3400.3
EU772150.1	354379	2568.3	4552.0	4203.0	3375.9	7466.8	7313.8
DQ809326.1	189943	6140.1	6204.2	2700.2	6724.8	9240.9	8589.4
FJ366181.1	361863	8335.0	9695.0	5777.3	6948.4	5730.2	5824.3
DQ793427.1	192058	5566.1	4000.5	1062.2	7489.3	2990.6	3176.4
EU457751.1	327701	1056.1	1597.8	1098.2	815.9	1643.6	1240.1
EU455083.1	322211	13732.8	13325.8	10535.7	9670.9	15754.3	13821.1
DQ808890.1	195102	361.5	359.5	357.0	123.9	115.0	95.1
EU475806.1	296144	4201.8	5216.3	3094.1	1682.6	3921.3	2723.5
EF096534.1	193435	12403.6	12088.2	5430.4	10810.5	8091.8	8363.1
EF602930.1	235072	6647.0	7004.2	3193.0	5264.2	6390.5	5272.1
AY992715.1	130454	6228.4	5580.9	5295.1	5147.0	8556.4	7233.5
DQ905136.1	165954	15.0	18.7	24.0	47.0	99.2	26.4
GQ897639.1	536897	4765.3	8047.7	2273.2	3797.8	4863.1	5198.2
FJ365979.1	360331	304.3	685.4	391.5	187.4	195.4	646.0
EU452820.1	336127	4634.8	5541.8	1366.8	3648.3	4480.7	3526.4
EF096624.1	198635	14.5	41.7	101.5	64.2	63.8	75.0
FJ681029.1	520720	175.0	240.4	237.9	206.5	622.4	192.6
DQ815674.1	164465	33.9	52.6	98.4	74.5	62.5	31.4
DQ326565.1	146558	2020.9	2218.6	2308.4	1622.4	1794.9	1739.1
EU775865.1	336216	6937.8	9029.4	5630.5	7407.4	4921.3	4793.3
DQ808842.1	181304	1334.0	1145.3	2423.3	1480.9	956.5	939.4
DQ015246.1	134096	465.9	423.8	1407.8	354.2	1776.7	1621.0
EU774932.1	327337	2302.0	2171.9	4515.7	3693.4	1162.4	2584.4
EF602809.1	228426	2466.0	3906.7	3579.2	3216.1	4089.7	3358.0
DQ809986.1	199055	1061.9	1183.5	2227.3	617.5	330.5	476.1
EU771406.1	323903	5889.7	6562.9	4182.4	3642.5	6334.2	4918.7
DQ014634.1	135369	6049.9	5573.3	867.4	5065.6	3515.7	2296.9
FJ879271.1	427738	1069.8	1420.0	1891.9	876.4	4049.4	294.6
AY985603.1	121620	1236.4	3239.0	2340.4	1399.0	1126.6	2072.2
DQ796558.1	190220	356.1	694.4	161.3	786.1	2177.7	913.7
EU509249.1	273592	2417.5	3865.5	1351.9	1200.3	5342.3	2794.3
EU461246.1	295371	6610.1	7398.1	5950.9	3691.6	1493.1	3111.0
FJ362625.1	365734	3433.9	2714.7	904.0	1992.9	188.5	407.4
EU775024.1	314582	1440.6	885.4	2636.3	1195.6	218.8	562.6
DQ796802.1	180980	42.1	68.9	153.1	84.4	77.2	42.1

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o__Clostridiales	f__Ruminococcaceae
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s__Ruminococcus bromii	26928

DQ798301.1 gg_id:192986 human fecal clone RL181_aah40d04
EU764810.1 gg_id:330949 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
EU843610.1 gg_id:333248 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ809094.1 gg_id:189555 human fecal clone RL308_aal81d05
EU765801.1 gg_id:325064 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
FJ363434.1 gg_id:361450 feces adult twins and mothers; TS149 clone TS149_a03c01
EU469102.1 gg_id:293060 Speke's gazelle feces clone SP3_e04
FJ671876.1 gg_id:526225 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU463455.1 gg_id:287790 domesticated horse feces clone horsem_aai94c07
EU775161.1 gg_id:320483 Francois Langur feces clone FL_1aaa04a09
EU771243.1 gg_id:306711 Asiatic elephant feces clone AE3_aaa01e02
EU469097.1 gg_id:299222 Speke's gazelle feces clone SP3_d08
DQ795965.1 gg_id:193632 human fecal clone RL202_aai49e08
AY684396.2 gg_id:110998 mucosal biopsies human intestine clone HuDI51
EU765035.1 gg_id:306745 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
EU504706.1 gg_id:276511 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04g08
EF098196.1 gg_id:197863 mouse cecum clone SWPT14_aaa02h07
EU466225.1 gg_id:298036 bighorn sheep feces clone BH1_aao28d06
AY985428.1 gg_id:121349 human stool clone C372
EU766503.1 gg_id:335417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU511173.1 gg_id:262677 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h03
EU765204.1 gg_id:356417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
DQ815864.1 gg_id:171239 mouse cecum clone aab23e01
EU842347.1 gg_id:315851 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
DQ815490.1 gg_id:164810 mouse cecum clone aab41e05
EU472398.1 gg_id:299755 Angola colobus feces clone EAC_1aaa01c10
EU508250.1 gg_id:276985 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04e02
EU506574.1 gg_id:260741 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04e08
AY983978.1 gg_id:117068 human descending colon mucosal biopsy clone MC71
FJ681514.1 gg_id:529688 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU463554.1 gg_id:292439 domesticated horse feces clone horsem_aai96a07
EU463726.1 gg_id:293353 domesticated horse feces clone horsej_aai91g05
EU463427.1 gg_id:298457 domesticated horse feces clone horsem_aai93g03
AB301912.1 gg_id:240231 Ruminococcus albus
FJ372107.1 gg_id:360830 feces adult twins and mothers; TS9 clone TS9_a01g12
FJ365585.1 gg_id:357253 feces adult twins and mothers; TS20 clone TS20_a04f02
FJ366914.1 gg_id:363146 feces adult twins and mothers; TS28 clone TS28_a01c11
FJ371844.1 gg_id:366240 feces adult twins and mothers; TS8 clone TS8_a02h01
FJ363657.1 gg_id:368173 feces adult twins and mothers; TS14 clone TS14_a01g10
FJ371275.1 gg_id:365709 feces adult twins and mothers; TS6 clone TS6_a03a09
GQ898568.1 gg_id:594381 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons

DQ798301.1	192986	2473.4	2176.9	2342.5	2724.9	4241.4	8744.9
EU764810.1	330949	5800.0	6196.7	1510.5	5069.7	4735.0	5377.2
EU843610.1	333248	11764.0	10820.8	7104.9	7195.5	9667.3	9287.6
DQ809094.1	189555	1256.0	1131.3	499.7	2992.8	1250.4	1239.5
EU765801.1	325064	1229.6	2655.4	676.0	569.9	1714.5	1581.3
FJ363434.1	361450	38.6	76.4	30.9	38.7	73.4	29.8
EU469102.1	293060	3071.4	4401.9	2218.6	1916.5	836.0	1642.4
FJ671876.1	526225	3719.5	4656.0	2521.8	3935.4	6033.9	7042.8
EU463455.1	287790	9916.0	12536.1	5743.1	7518.1	10390.8	8181.8
EU775161.1	320483	2173.3	2322.8	3199.6	2286.4	923.9	737.5
EU771243.1	306711	365.1	212.4	788.4	223.3	190.0	193.9
EU469097.1	299222	145.6	72.1	742.2	126.5	107.1	187.8
DQ795965.1	193632	2008.6	1997.4	1577.6	1169.1	1461.6	863.1
AY684396.2	110998	209.6	153.0	434.5	268.7	85.1	81.7
EU765035.1	306745	6642.7	8050.6	5345.3	5350.7	5505.0	5999.6
EU504706.1	276511	919.1	460.9	204.5	167.5	190.3	218.6
EF098196.1	197863	5060.0	5632.8	3932.6	4564.1	8260.6	6621.8
EU466225.1	298036	3582.7	2060.1	5505.4	2300.4	2389.5	2870.5
AY985428.1	121349	743.5	384.4	1453.5	488.8	137.8	357.0
EU766503.1	335417	3692.2	5833.1	2656.7	2362.9	6508.6	5652.3
EU511173.1	262677	6577.0	8475.5	14495.4	7675.8	9482.4	10899.0
EU765204.1	356417	3004.0	3649.3	4079.1	3390.6	6084.2	5170.9
DQ815864.1	171239	5202.2	4139.3	2770.8	6003.8	6418.8	5101.8
EU842347.1	315851	8111.0	8632.6	6137.4	8870.1	12433.3	9973.2
DQ815490.1	164810	2304.8	2309.6	2289.6	4644.3	3343.6	4964.3
EU472398.1	299755	274.8	294.6	1492.8	282.8	157.4	231.5
EU508250.1	276985	4381.5	6211.2	2479.3	2951.6	1774.3	4284.8
EU506574.1	260741	392.9	617.8	1387.0	925.1	657.8	748.2
AY983978.1	117068	2920.3	2924.1	2389.7	813.0	1762.0	1576.3
FJ681514.1	529688	6666.9	7073.4	2775.6	4061.8	7424.5	5396.7
EU463554.1	292439	3122.5	3475.4	6567.0	8062.3	3293.2	2746.2
EU463726.1	293353	399.1	1164.5	1247.1	321.1	1196.2	922.8
EU463427.1	298457	12548.7	11467.4	12933.6	12327.6	11115.6	11160.6
AB301912.1	240231	1980.7	2653.1	2725.5	3159.9	1713.2	1182.5
FJ372107.1	360830	5496.3	4131.3	4485.5	6548.5	4057.2	5942.1
FJ365585.1	357253	3717.3	3218.7	1848.1	2641.4	4230.2	2826.3
FJ366914.1	363146	5121.7	4085.5	6040.9	4407.0	4342.8	4593.1
FJ371844.1	366240	2043.7	3700.5	2560.8	2439.9	7890.5	4972.8
FJ363657.1	368173	9482.4	9830.9	6288.3	9022.3	12723.6	10584.1
FJ371275.1	365709	3870.3	5441.5	4622.7	3099.3	4520.7	4512.0
GQ898568.1	594381	9841.6	10669.7	7509.4	8648.0	7871.4	7437.8

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EF399806.1 gg_id:209727 human fecal clone SJTU_E_03_58
EU763249.1 gg_id:337339 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
FJ368454.1 gg_id:362323 feces adult twins and mothers; TS3 clone TS3_a04e09
FJ366609.1 gg_id:361468 feces adult twins and mothers; TS27 clone TS27_a01f12
FJ363691.1 gg_id:358965 feces adult twins and mothers; TS14 clone TS14_a02b08
DQ905192.1 gg_id:173445 human fecal clone 013-a1
EU768452.1 gg_id:320547 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
FJ365601.1 gg_id:363923 feces adult twins and mothers; TS20 clone TS20_a04g09
EU762103.1 gg_id:322081 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
DQ807613.1 gg_id:182342 human fecal clone RL307_aam08h07
FJ366911.1 gg_id:365471 feces adult twins and mothers; TS28 clone TS28_a01c08
DQ798028.1 gg_id:182455 human fecal clone RL302_aal94f12
AY976187.1 gg_id:121324 human ascending colon mucosal biopsy clone LV95
EU761738.1 gg_id:352927 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
AF104841.1 gg_id:16066 Ruminococcus flavefaciens str. AR72
EU777840.1 gg_id:323801 European rabbit feces clone RA_c04_1
EU469685.1 gg_id:294797 flying fox feces clone FF_a06_1
EU468685.1 gg_id:291859 okapi feces clone OK2_e08_1
EF445196.1 gg_id:205179 rabbit cecum clone NED3F5
EU779250.1 gg_id:324482 Trancaspian Urial feces clone TU1_aaa04c10
AF104846.1 gg_id:16065 Ruminococcus flavefaciens str. Y1
FJ879092.1 gg_id:459944 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU468531.1 gg_id:290894 okapi feces clone OK1_b08_1
EU774461.1 gg_id:320332 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14
FJ880174.1 gg_id:418064 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
GU303548.1 gg_id:539847 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
AF104835.1 gg_id:16041 Ruminococcus flavefaciens str. LP-R1-Adx
EU460043.1 gg_id:296857 mammals their gut microbes eastern black and white colobus feces clone COL_aai13
EF602945.1 gg_id:233404 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ879630.1 gg_id:438358 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU465615.1 gg_id:288191 argali sheep feces clone AS1_aao39g11.Contig1
FJ880749.1 gg_id:460253 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
AF104837.1 gg_id:16040 Ruminococcus flavefaciens str. AR46
FJ832845.1 gg_id:563574 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_33A05
EU774973.1 gg_id:317714 Flying Fox feces clone FF_-aag84b01
FJ879772.1 gg_id:386333 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
AB034020.1 gg_id:45766 rumen clone 4C0d-7
FJ366125.1 gg_id:362036 feces adult twins and mothers; TS25 clone TS25_a03a05
EU469261.1 gg_id:298912 Speke's gazelle feces clone SP3_a07_1
FJ879853.1 gg_id:383102 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ879578.1 gg_id:433149 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr

EF399806.1	209727	10645.5	9912.9	1356.8	5843.9	7915.7	6127.3
EU763249.1	337339	2707.1	3441.5	2940.7	3114.7	5084.8	2976.7
FJ368454.1	362323	5788.6	6058.9	850.0	4699.5	5855.1	4687.6
FJ366609.1	361468	14183.7	15292.7	8316.8	9312.4	12786.3	10410.5
FJ363691.1	358965	480.6	649.7	843.8	656.1	201.7	311.8
DQ905192.1	173445	6996.7	5852.6	5135.2	6300.4	7317.8	8617.8
EU768452.1	320547	4070.0	4127.0	1811.1	1311.2	1082.6	792.1
FJ365601.1	363923	832.8	1016.3	3238.7	1012.8	2125.2	1484.1
EU762103.1	322081	369.2	319.8	835.6	256.1	229.4	221.8
DQ807613.1	182342	4250.1	4250.4	4126.0	4509.6	6535.9	6727.3
FJ366911.1	365471	141.9	86.9	611.4	1067.8	115.6	50.5
DQ798028.1	182455	8512.6	10572.4	3728.1	5443.8	7229.9	5235.1
AY976187.1	121324	225.6	370.6	372.5	451.6	162.9	200.3
EU761738.1	352927	3036.8	2273.5	1732.3	2885.0	4179.8	4795.8
AF104841.1	16066	4047.2	4796.7	4594.3	4701.0	4648.5	5036.6
EU777840.1	323801	3407.6	2085.0	5704.0	1236.0	1421.4	1520.2
EU469685.1	294797	3705.0	5229.2	2794.3	3823.2	1035.4	2490.0
EU468685.1	291859	1546.0	1451.8	1729.6	2038.9	804.5	916.6
EF445196.1	205179	4053.5	5950.4	3314.7	685.2	6991.3	4332.7
EU779250.1	324482	914.2	1693.1	1898.1	2599.8	967.5	1544.9
AF104846.1	16065	6472.2	3137.2	995.3	5426.8	5982.5	6208.8
FJ879092.1	459944	1746.0	1774.2	1762.2	2610.7	2481.6	1640.6
EU468531.1	290894	5405.6	4120.3	3803.8	3316.1	2009.2	2793.4
EU774461.1	320332	1946.5	594.8	605.0	412.0	327.3	145.1
FJ880174.1	418064	6588.1	7090.4	2936.2	5508.9	5381.8	3051.7
GU303548.1	539847	10081.2	7616.5	5426.8	3424.1	1505.3	3171.2
AF104835.1	16041	1794.9	1382.2	503.1	1835.8	923.4	1067.7
EU460043.1	296857	1718.3	578.1	1395.6	512.2	131.6	139.5
EF602945.1	233404	1627.4	1537.1	1747.4	1676.9	2148.1	1736.2
FJ879630.1	438358	24367.1	21310.4	13127.1	12591.6	19985.6	16499.4
EU465615.1	288191	4953.5	5714.0	2968.1	3757.1	3307.0	4325.4
FJ880749.1	460253	11136.9	10146.8	6390.5	4819.4	10313.4	9991.6
AF104837.1	16040	10119.2	9044.8	3245.6	12024.9	6980.8	6472.6
FJ832845.1	563574	1808.9	1854.7	1052.7	1523.0	244.3	661.9
EU774973.1	317714	1590.1	546.6	1250.1	342.9	191.8	512.5
FJ879772.1	386333	6484.8	6025.0	4965.9	5933.2	7080.3	7855.1
AB034020.1	45766	2647.9	2002.1	1653.3	1953.5	176.1	1776.4
FJ366125.1	362036	5322.8	5010.8	6244.9	3386.7	1104.0	1786.9
EU469261.1	298912	1705.8	2548.2	5920.1	3392.6	2139.0	3791.6
FJ879853.1	383102	990.5	902.0	2247.5	406.4	1314.4	975.8
FJ879578.1	433149	10822.9	9523.4	5802.1	7531.2	11066.9	10094.8

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DQ394631.1 gg_id:153029 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o
FJ880209.1 gg_id:407405 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU469949.1 gg_id:296346 trancaspain urial feces clone TU1_aaa01f10
EU779402.1 gg_id:343313 Grevy's Zebra feces clone GZ_aaa04c09
EU381701.1 gg_id:260559 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU475092.1 gg_id:301195 visayam warty pig feces clone VWP_aaa03c01
EU775809.1 gg_id:315666 Horse feces clone horsem_e12
FJ673061.1 gg_id:512575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU774487.1 gg_id:356167 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1
FJ682773.1 gg_id:522772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ882650.1 gg_id:172296 Ruminococcus sp. str. YE281
EF401397.1 gg_id:207190 human fecal clone SJTU_D_09_78
FJ673313.1 gg_id:514709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU774954.1 gg_id:347335 Flying Fox feces clone FF_-aag84b12
FJ682475.1 gg_id:510095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB034071.1 gg_id:29057 rumen clone 6C3d-10
FJ879569.1 gg_id:461354 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
DQ807559.1 gg_id:174923 human fecal clone RL307_aam08b12
FJ881003.1 gg_id:385017 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
GU303205.1 gg_id:560753 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
FJ681243.1 gg_id:528589 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683277.1 gg_id:509351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682760.1 gg_id:511748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AF132277.1 gg_id:72970 adult human fecal matter clone adhufec58
EU453081.1 gg_id:312665 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83
FJ880489.1 gg_id:415638 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
AJ515913.1 gg_id:102671 Ruminococcus sp. str. 18P13
FJ678989.1 gg_id:528232 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ079248.1 gg_id:409845 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d
FJ366993.1 gg_id:358351 feces adult twins and mothers; TS28 clone TS28_a02b12
DQ905838.2 gg_id:163243 human fecal clone 29E-e5
FJ363583.1 gg_id:365147 feces adult twins and mothers; TS14 clone TS14_a01a05
DQ800995.1 gg_id:191448 human fecal clone RL387_aao90f01
EF088328.1 gg_id:199654 Clostridium islandicum str. AK1
EU761602.1 gg_id:334170 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ366126.1 gg_id:368142 feces adult twins and mothers; TS25 clone TS25_a03a06
EU453704.1 gg_id:309828 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83
EU773178.1 gg_id:349431 BigHorn sheep feces clone BHSD_aaa03h06
GQ042993.1 gg_id:431222 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011h
FJ672106.1 gg_id:529789 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
EU470140.1 gg_id:291360 trancaspain urial feces clone TU2_aaa03c09

DQ394631.1	153029	9108.3	11582.2	4979.2	7547.4	5409.5	6251.1
FJ880209.1	407405	9528.2	8549.8	5738.4	7783.0	9570.2	7663.1
EU469949.1	296346	2109.6	2286.4	3842.2	521.6	3534.8	5673.0
EU779402.1	343313	868.2	1125.6	1421.8	1045.0	1063.8	1484.3
EU381701.1	260559	1834.2	3490.9	4738.6	3884.4	3632.6	2967.0
EU475092.1	301195	954.5	1013.0	1792.7	575.7	498.8	540.1
EU775809.1	315666	1154.1	1429.1	2378.9	786.8	245.8	417.6
FJ673061.1	512575	1862.1	1238.1	1083.6	456.3	157.8	139.8
EU774487.1	356167	685.3	1043.2	2344.0	603.7	472.5	1055.4
FJ682773.1	522772	1928.4	1500.9	970.5	1857.0	2376.3	3057.2
DQ882650.1	172296	2913.0	2143.6	1342.8	1991.5	745.7	867.7
EF401397.1	207190	767.5	909.7	2148.8	787.1	1069.6	598.2
FJ673313.1	514709	6409.8	7871.7	1170.7	7680.1	7803.2	7833.8
EU774954.1	347335	525.3	779.4	2276.3	494.2	1935.1	2106.1
FJ682475.1	510095	4918.1	7855.1	5508.8	3695.5	5192.1	7173.9
AB034071.1	29057	9964.4	12378.1	4941.1	5902.1	7265.5	6621.9
FJ879569.1	461354	15114.9	15077.3	13720.7	11376.3	14306.7	12352.0
DQ807559.1	174923	7860.0	5813.0	2984.3	8544.5	8340.6	8043.8
FJ881003.1	385017	1072.6	863.5	1644.2	863.9	209.4	209.8
GU303205.1	560753	3419.7	3006.9	1786.2	3341.8	3561.1	2936.3
FJ681243.1	528589	2248.9	2873.9	3068.8	1075.7	2277.9	2158.1
FJ683277.1	509351	3501.7	2501.6	1430.5	3087.3	1673.4	3309.8
FJ682760.1	511748	5279.2	5372.7	3772.6	7325.3	8626.1	8076.6
AF132277.1	72970	457.4	573.4	905.7	308.5	243.7	261.5
EU453081.1	312665	499.0	1312.0	640.8	468.5	608.4	1206.0
FJ880489.1	415638	4461.8	4415.5	1016.7	5850.2	4790.6	4392.2
AJ515913.1	102671	1961.0	2532.7	1379.3	2710.2	198.6	904.0
FJ678989.1	528232	187.2	121.9	641.0	158.1	103.7	110.5
GQ079248.1	409845	3335.8	3356.2	1898.5	1872.1	2855.1	2927.6
FJ366993.1	358351	539.5	440.7	999.4	183.4	538.0	495.6
DQ905838.2	163243	11112.3	11031.9	2578.8	4555.6	5947.2	5577.3
FJ363583.1	365147	7786.7	7741.1	3991.8	6491.4	7769.2	7581.8
DQ800995.1	191448	3778.6	4646.4	1913.6	2288.4	2807.0	2799.7
EF088328.1	199654	600.7	1056.7	320.2	216.7	294.6	187.3
EU761602.1	334170	7226.5	7060.3	4502.3	4221.1	3415.2	5582.1
FJ366126.1	368142	2291.9	3462.7	909.0	1864.8	1974.8	3540.4
EU453704.1	309828	5151.8	4864.4	3004.4	3343.5	663.3	887.3
EU773178.1	349431	1178.1	793.6	2490.6	1263.1	1607.0	1666.2
GQ042993.1	431222	529.8	716.9	661.1	391.3	272.0	654.9
FJ672106.1	529789	2523.9	1465.2	2233.1	3407.1	1244.6	2192.2
EU470140.1	291360	76.8	200.7	242.4	113.3	113.0	140.4

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AB494864.1 gg_id:535519 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N
FJ881268.1 gg_id:381511 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
DQ807388.1 gg_id:195966 human fecal clone RL307_aam05h08
EU762145.1 gg_id:350180 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ680003.1 gg_id:520618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ515914.1 gg_id:94504 Ruminococcus sp. str. 7L75
AY986181.1 gg_id:117716 human stool clone D538
GQ502527.1 gg_id:593965 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
EF686574.1 gg_id:241489 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6
FJ673393.1 gg_id:520904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ079249.1 gg_id:408551 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d(
FJ367031.1 gg_id:364206 feces adult twins and mothers; TS28 clone TS28_a02f09
EF400797.1 gg_id:212533 human fecal clone SJTU_D_01_64
GQ079235.1 gg_id:381044 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230b(
FJ683473.1 gg_id:516504 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683719.1 gg_id:529159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ793927.1 gg_id:196776 human fecal clone RL176_aah45d05
FJ881336.1 gg_id:383369 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU381483.1 gg_id:259252 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
FJ682645.1 gg_id:528548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683228.1 gg_id:527236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801085.1 gg_id:183189 human fecal clone RL387_aao91h09
FJ682883.1 gg_id:514296 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801034.1 gg_id:182668 human fecal clone RL387_aao91c01
EU475067.1 gg_id:303213 visayam warty pig feces clone VWP_aaa03h09
FJ880441.1 gg_id:463901 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU201675.1 gg_id:240642 species intestinal microbiota between fiber- and liquid phase human fecal clone sd68
FJ880300.1 gg_id:460027 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ683326.1 gg_id:530604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ014676.1 gg_id:130775 mouse cecum clone M1_d06_1
EF401179.1 gg_id:216596 human fecal clone SJTU_D_06_75
FJ682715.1 gg_id:520680 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU767484.1 gg_id:311384 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
FJ677927.1 gg_id:527685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801328.1 gg_id:181220 human fecal clone RL388_aao94a10
EU462655.1 gg_id:290967 Sumatran orangutan feces clone orang2_aai66g11
EU381835.1 gg_id:271639 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
EU777137.1 gg_id:347585 Okapi feces clone OK1_a08
FJ683874.1 gg_id:513947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676801.1 gg_id:528312 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY858410.2 gg_id:112362 gastrointestinal tract Grant's gazelle clone GRANT74

AB494864.1	535519	4320.5	4711.9	3823.5	4436.7	4199.9	3475.3
FJ881268.1	381511	558.8	362.8	404.9	248.3	117.2	160.2
DQ807388.1	195966	2189.4	2842.2	2834.6	3474.7	5475.9	6427.9
EU762145.1	350180	1894.2	1785.6	3761.5	2162.1	3288.5	4354.0
FJ680003.1	520618	690.4	765.6	698.2	690.8	248.6	498.1
AJ515914.1	94504	7578.1	8819.5	4156.7	9373.0	9375.0	7326.1
AY986181.1	117716	584.8	1179.8	362.3	1937.8	1937.1	1219.7
GQ502527.1	593965	2428.4	2668.9	2988.0	2076.6	3768.3	1718.1
EF686574.1	241489	80.4	92.0	81.3	123.7	69.3	42.4
FJ673393.1	520904	6459.1	11799.8	3344.7	5293.0	9499.2	8018.3
GQ079249.1	408551	94.2	130.9	248.6	122.7	250.2	243.1
FJ367031.1	364206	4958.0	4256.7	5668.6	5194.7	4390.1	3924.5
EF400797.1	212533	3898.8	4098.5	2568.7	2485.0	2696.3	3079.7
GQ079235.1	381044	3580.5	3191.5	3092.3	2613.4	527.3	930.5
FJ683473.1	516504	4976.7	7219.9	1804.4	3392.9	6112.5	4995.9
FJ683719.1	529159	4421.1	6273.0	5141.1	4496.1	9138.8	10369.3
DQ793927.1	196776	104.8	93.0	114.2	99.0	113.4	96.6
FJ881336.1	383369	159.6	131.8	602.9	187.6	75.1	93.1
EU381483.1	259252	352.7	230.7	489.2	281.2	112.4	145.2
FJ682645.1	528548	3331.7	3619.7	1450.2	5581.4	5494.5	7508.8
FJ683228.1	527236	6211.7	8075.1	3152.8	5048.6	8834.6	7530.2
DQ801085.1	183189	4609.3	5698.5	1955.8	4343.4	5262.2	4494.9
FJ682883.1	514296	1870.6	3333.4	1087.2	1201.6	4932.5	2470.9
DQ801034.1	182668	1995.9	1815.2	1917.8	2367.1	2279.8	1832.0
EU475067.1	303213	785.2	1136.0	683.1	419.3	180.7	264.8
FJ880441.1	463901	130.9	88.8	223.1	149.0	66.1	34.3
EU201675.1	240642	3931.4	3101.8	3649.8	2333.1	1184.7	1904.0
FJ880300.1	460027	1644.1	2346.7	727.9	722.8	2037.5	1101.9
FJ683326.1	530604	1450.3	2126.6	2182.5	1541.6	1663.5	1515.0
DQ014676.1	130775	32.0	39.7	199.5	63.5	42.4	27.3
EF401179.1	216596	3808.3	3443.3	2446.8	2920.0	1332.5	2655.9
FJ682715.1	520680	450.7	563.1	624.4	1206.7	465.8	980.3
EU767484.1	311384	1989.3	1253.6	952.2	2760.2	991.7	1328.7
FJ677927.1	527685	5170.8	5486.7	5849.5	4755.5	11159.9	8440.3
DQ801328.1	181220	504.7	794.2	771.5	353.8	1325.0	953.7
EU462655.1	290967	2898.4	3248.0	2811.0	636.9	326.1	893.9
EU381835.1	271639	3725.8	3863.4	4853.5	3894.6	4006.0	3705.7
EU777137.1	347585	2306.9	2968.9	4001.6	970.2	3834.6	2861.4
FJ683874.1	513947	2063.4	2241.9	2857.5	1387.1	887.6	2076.3
FJ676801.1	528312	5849.6	5765.8	1296.4	7706.2	9325.7	9767.9
AY858410.2	112362	482.0	784.4	1717.9	366.0	356.4	824.0

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FJ678795.1 gg_id:525082 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366709.1 gg_id:369797 feces adult twins and mothers; TS27 clone TS27_a02h07
EU777134.1 gg_id:308293 Okapi feces clone OK1_f06
FJ673663.1 gg_id:521226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB034039.1 gg_id:33321 rumen clone 5C0d-6
EU767319.1 gg_id:341274 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
EU748314.1 gg_id:311120 neotropical folivorous flying bird adult hoatzin crop clone hoa46_84D11
FJ683336.1 gg_id:517337 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ175496.1 gg_id:548621 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
DQ801337.1 gg_id:173810 human fecal clone RL388_aao94b09
GQ079200.1 gg_id:440181 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229f1
DQ808310.1 gg_id:195868 human fecal clone RL180_aao75b04
EU762806.1 gg_id:305114 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
EU845601.1 gg_id:327387 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ671379.1 gg_id:528679 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ808451.1 gg_id:186429 human fecal clone RL180_aao76g01
EU777639.1 gg_id:348060 Sumatran orangutan feces clone orang2_aai66f03
FJ683503.1 gg_id:532036 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683645.1 gg_id:530800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB185796.1 gg_id:106698 rumen clone U29-F08
FJ367012.1 gg_id:367055 feces adult twins and mothers; TS28 clone TS28_a02d10
FJ673216.1 gg_id:515428 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF098027.1 gg_id:199742 mouse cecum clone SWPT12_aaa04c08
FJ880780.1 gg_id:385933 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EF401603.1 gg_id:217078 human fecal clone SJTU_D_12_80
FJ673489.1 gg_id:525315 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ808084.1 gg_id:193314 human fecal clone RL180_aan72b07
GQ898105.1 gg_id:556976 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
AF018544.1 gg_id:16077 rumen fluid clone JW3
EU472362.1 gg_id:295892 Angola colobus feces clone EAC_1aaa02g07
EU842465.1 gg_id:341817 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU381723.1 gg_id:270733 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
GQ448900.1 gg_id:557051 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_10wks_gr
DQ793356.1 gg_id:181961 human fecal clone RL199_aaj42f09
DQ673540.1 gg_id:163800 rumen fluid clone GRC75
FJ679803.1 gg_id:522426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ800439.1 gg_id:188212 human fecal clone RL183_aah24d07
FJ682636.1 gg_id:514231 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ879544.1 gg_id:445343 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU344189.1 gg_id:268936 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ682735.1 gg_id:525180 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

FJ678795.1	525082	6173.4	4552.4	1788.6	7070.5	7797.3	6568.6
FJ366709.1	369797	488.8	805.3	244.1	718.2	1432.0	755.9
EU777134.1	308293	1087.0	765.3	2610.6	1197.5	610.7	1115.5
FJ673663.1	521226	2452.7	4118.6	1207.7	2329.5	1632.9	999.4
AB034039.1	33321	1050.5	1380.4	944.4	731.4	941.9	461.2
EU767319.1	341274	667.3	263.2	959.7	602.1	217.3	212.3
EU748314.1	311120	2257.2	974.7	1828.9	615.9	1003.3	2036.3
FJ683336.1	517337	2279.8	2729.7	2412.2	3520.6	3351.0	2522.4
GQ175496.1	548621	767.8	776.9	606.2	1111.0	647.5	490.6
DQ801337.1	173810	583.5	543.8	511.8	282.8	799.8	136.1
GQ079200.1	440181	7723.1	9775.8	6112.4	6640.4	8749.9	8410.3
DQ808310.1	195868	30.5	47.8	55.5	56.0	100.2	41.5
EU762806.1	305114	1485.8	5255.9	705.1	1333.9	2110.4	1757.7
EU845601.1	327387	1270.8	1792.2	1426.2	1479.1	726.8	701.6
FJ671379.1	528679	3467.4	3428.3	6214.4	4758.2	3748.9	3623.1
DQ808451.1	186429	1554.2	1316.7	534.1	645.9	255.8	707.8
EU777639.1	348060	5894.9	6794.4	7402.5	6568.6	6017.1	6857.2
FJ683503.1	532036	87.6	97.7	277.9	103.3	74.3	88.9
FJ683645.1	530800	2891.2	2742.1	1031.6	2948.9	985.1	2006.2
AB185796.1	106698	2555.4	3073.3	791.9	3071.0	3221.5	2049.3
FJ367012.1	367055	7969.3	7171.8	6446.9	5640.2	7409.9	7191.0
FJ673216.1	515428	4307.2	5973.2	3453.5	3314.2	3775.8	4091.1
EF098027.1	199742	4316.6	3470.4	3220.6	3724.3	594.2	1176.2
FJ880780.1	385933	596.4	678.6	546.9	306.7	204.5	209.9
EF401603.1	217078	1404.5	933.9	2438.8	2850.1	312.1	1046.9
FJ673489.1	525315	1303.0	2124.1	2549.2	3014.3	2288.7	2243.9
DQ808084.1	193314	479.6	422.9	106.0	132.5	93.4	68.2
GQ898105.1	556976	567.1	1706.8	814.4	1085.5	780.3	801.6
AF018544.1	16077	216.1	473.5	287.2	118.1	173.9	180.0
EU472362.1	295892	48.5	33.2	49.1	111.6	66.0	25.8
EU842465.1	341817	3304.5	2446.7	2339.3	2916.3	1481.1	1620.5
EU381723.1	270733	1640.2	1651.2	1257.1	1638.1	349.9	410.4
GQ448900.1	557051	395.7	267.6	669.7	147.0	855.3	263.6
DQ793356.1	181961	5393.7	5357.8	7055.0	5432.7	2811.1	3354.8
DQ673540.1	163800	106.4	154.0	537.8	155.9	114.4	121.2
FJ679803.1	522426	6563.0	7173.4	4556.4	4140.9	5720.5	6059.8
DQ800439.1	188212	150.1	178.8	133.3	79.8	71.5	79.6
FJ682636.1	514231	3137.8	7387.8	2704.8	1371.1	2737.1	4170.6
FJ879544.1	445343	742.0	662.0	1534.9	1543.6	1693.3	703.3
EU344189.1	268936	788.1	844.7	921.2	678.2	1001.7	646.1
FJ682735.1	525180	11123.8	13247.8	9912.9	8525.7	10039.7	8330.1

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EU381595.1 gg_id:273843 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
FJ682919.1 gg_id:516302 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ676403.1 gg_id:530207 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU466401.1 gg_id:293178 bighorn sheep feces clone BH2_aao23b06
EU381726.1 gg_id:268964 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EF400818.1 gg_id:217014 human fecal clone SJTU_D_01_96
EF515535.1 gg_id:223059 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
EU469287.1 gg_id:294007 Speke's gazelle feces clone SP3_d08_3
EU462675.1 gg_id:302094 Sumatran orangutan feces clone orang2_aai67b01
AJ515916.1 gg_id:94758 Ruminococcus sp. str. 25F6
FJ365090.1 gg_id:365676 feces adult twins and mothers; TS1 clone TS1_a02g01
EF436370.1 gg_id:205159 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC84
FJ372101.1 gg_id:368749 feces adult twins and mothers; TS9 clone TS9_a01g06
FJ683482.1 gg_id:520858 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ683285.1 gg_id:530742 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU472479.1 gg_id:297065 Angola colobus feces clone EAC_2_aaa02f09
GU304502.1 gg_id:562441 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
DQ795096.1 gg_id:175713 human fecal clone RL310_aam40b09
FJ367666.1 gg_id:368428 feces adult twins and mothers; TS2 clone TS2_a02b06
EU467336.1 gg_id:297875 chimpanzee feces clone CHIMP1_c02
EF402085.1 gg_id:207480 human fecal clone SJTU_B_03_46
FJ673679.1 gg_id:523326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682787.1 gg_id:530594 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ882649.1 gg_id:162660 Ruminococcus bromii str. YE282
FJ673846.1 gg_id:530234 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473649.1 gg_id:293409 banteng feces clone BG_aaa04a03.Contig1
FJ682570.1 gg_id:511998 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU511872.1 gg_id:269378 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10b09
EU728796.1 gg_id:319681 Ruminococcus sp. str. DJF_VR87
FJ683078.1 gg_id:509155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ880361.1 gg_id:458950 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU764268.1 gg_id:304940 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
AB270050.1 gg_id:172453 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos
EU762132.1 gg_id:349408 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
FJ680579.1 gg_id:514059 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU766698.1 gg_id:336413 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EU777557.1 gg_id:304044 Sumatran orangutan feces clone orang1_aai55b05
FJ363111.1 gg_id:364931 feces adult twins and mothers; TS148 clone TS148_a03b10
DQ777945.1 gg_id:169698 rat feces clone R-1141(5)
GQ339149.1 gg_id:517495 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv

FJ674239.1	511048	2345.6	2946.2	805.9	3584.4	3267.1	3220.4
EU381595.1	273843	203.0	453.7	1307.0	919.5	190.2	217.6
FJ682919.1	516302	4305.5	4456.8	2062.2	5133.5	6067.3	7277.3
FJ676403.1	530207	7832.1	10133.5	5665.8	9256.3	12415.2	9616.0
EU466401.1	293178	8048.6	8044.1	8422.6	7192.8	8956.4	7029.8
EU381726.1	268964	1279.7	1090.3	1521.2	1282.5	468.7	973.1
EF400818.1	217014	3642.7	3576.6	3715.9	4981.9	2345.2	4982.7
EF515535.1	223059	2435.0	2821.9	4146.3	3604.6	4629.9	4579.7
EU469287.1	294007	4271.9	3843.2	4827.8	4187.5	4363.3	4305.8
EU462675.1	302094	2157.7	1804.6	2838.2	4018.4	1056.1	830.7
AJ515916.1	94758	6058.6	6215.1	3884.5	7083.0	5182.0	4063.0
FJ365090.1	365676	7835.5	10685.5	5131.7	6043.3	8683.7	5586.3
EF436370.1	205159	128.2	377.9	37.5	39.3	63.1	18.8
FJ372101.1	368749	26.9	38.9	109.4	63.0	58.2	30.4
FJ683482.1	520858	610.3	1171.6	1855.3	762.8	326.6	852.3
FJ683285.1	530742	7884.3	10268.0	6238.0	5106.0	5957.0	6677.6
EU472479.1	297065	893.3	784.7	797.0	236.0	147.2	70.4
GU304502.1	562441	8024.4	6911.9	3683.6	4897.5	3618.6	5478.5
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FJ367666.1	368428	2435.6	2741.9	1990.8	3184.4	2990.4	1723.2
EU467336.1	297875	718.3	470.7	663.1	391.6	123.4	223.1
EF402085.1	207480	4896.5	3921.1	4255.1	2969.9	4121.6	3683.2
FJ673679.1	523326	5450.9	6636.2	2590.1	3956.8	5888.7	5139.9
FJ682787.1	530594	12297.2	11575.2	6340.4	11456.6	13250.8	11033.3
DQ882649.1	162660	131.5	198.0	314.1	259.8	130.9	195.6
FJ673846.1	530234	1153.2	904.2	610.5	786.4	265.9	178.7
EU473649.1	293409	3390.6	2934.5	2368.6	997.2	576.2	955.2
FJ682570.1	511998	9994.7	9414.5	13081.8	10441.1	8995.2	12987.8
EU511872.1	269378	6297.2	6350.0	7581.8	8485.7	6416.9	6004.3
EU728796.1	319681	530.8	645.0	1091.2	578.7	3281.4	1580.5
FJ683078.1	509155	676.1	1606.4	1272.9	880.3	3250.8	1592.1
FJ880361.1	458950	371.8	442.0	1406.3	748.1	229.3	281.5
EU764268.1	304940	485.7	554.4	526.3	444.5	478.7	293.2
AB270050.1	172453	1276.5	1379.4	839.1	1265.1	2971.7	2512.5
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EU777557.1	304044	78.7	233.0	313.2	141.3	95.9	300.0
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DQ777945.1	169698	203.0	125.9	311.0	119.4	214.5	63.3
GQ339149.1	517495	5258.5	6869.5	8624.2	4073.4	3443.9	4261.6

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FJ683946.1 gg_id:514035 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ879137.1 gg_id:450782 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
FJ682062.1 gg_id:511125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ680636.1 gg_id:516987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ905927.2 gg_id:166276 human fecal clone 29c-h4
EU530308.1 gg_id:259951 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4
AJ515915.1 gg_id:94902 Ruminococcus sp. str. 25F8
EU469049.1 gg_id:298925 Speke's gazelle feces clone SP2_e03_1
DQ823690.1 gg_id:198813 human fecal clone RL250_aaj77f11
EF686591.1 gg_id:242020 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8(
FJ363110.1 gg_id:367447 feces adult twins and mothers; TS148 clone TS148_a03b09
DQ394694.1 gg_id:156441 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
EF402563.1 gg_id:208165 human fecal clone SJTU_B_09_56
EF406472.1 gg_id:217186 mouse colon clone control_14days-C5
EU472052.1 gg_id:294107 francois langur feces clone FL_1aaa01f10
AY916385.1 gg_id:114000 human stool clone D739
EU767209.1 gg_id:331645 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
DQ394690.1 gg_id:155809 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
FJ675754.1 gg_id:527270 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
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FJ674069.1 gg_id:515630 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
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FJ682410.1 gg_id:527856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
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EU475424.1 gg_id:295802 springbok feces clone SBSD_aaa04c06
EU843667.1 gg_id:322552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ685421.1 gg_id:527958 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU381538.1 gg_id:269531 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
AM404501.2 gg_id:563164 percent G+C fraction libraries number Actinobacteria human faecal clone AP08K.26
EU748111.1 gg_id:311383 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42a10
GQ491920.1 gg_id:539328 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ371896.1 gg_id:365465 feces adult twins and mothers; TS8 clone TS8_a03d11
GQ493718.1 gg_id:581908 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ366766.1 gg_id:362381 feces adult twins and mothers; TS27 clone TS27_a03f03
DQ798110.1 gg_id:181710 human fecal clone RL302_aal95f05
EF402950.1 gg_id:207652 human fecal clone SJTU_B_14_66
EU460195.1 gg_id:300508 mammals their gut microbes eastern black and white colobus feces clone COL_aai16
EU460164.1 gg_id:290723 mammals their gut microbes eastern black and white colobus feces clone COL_aai15
EU774396.1 gg_id:323229 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1(
DQ673538.1 gg_id:172967 rumen fluid clone GRC73

AB185787.1	101849	96.6	108.3	564.0	100.5	100.8	74.5
FJ683946.1	514035	974.2	1244.8	1652.4	1098.3	362.7	652.7
FJ879137.1	450782	6589.4	4655.9	1776.7	7489.6	5417.9	5476.6
FJ682062.1	511125	346.5	698.7	1423.2	630.3	1207.8	1109.2
FJ680636.1	516987	549.7	1282.9	840.9	342.7	697.1	1161.7
DQ905927.2	166276	6780.6	4009.3	2444.7	5532.5	2938.5	3799.5
EU530308.1	259951	1484.7	1573.6	1628.3	2936.8	1250.1	2016.4
AJ515915.1	94902	4255.9	4270.0	3095.4	5708.6	2761.1	2736.2
EU469049.1	298925	1211.0	1253.6	2819.8	1401.0	634.1	1294.1
DQ823690.1	198813	1404.9	2514.8	633.1	754.1	587.6	1570.6
EF686591.1	242020	682.7	1188.8	1750.1	748.5	1195.3	1156.7
FJ363110.1	367447	7496.8	10703.1	7823.0	6156.9	6093.2	6359.0
DQ394694.1	156441	9579.1	8527.3	4731.3	8580.0	10505.0	8033.5
EF402563.1	208165	8436.8	8019.6	7249.2	8693.2	11125.9	14539.9
EF406472.1	217186	5517.4	4539.7	2699.1	6964.0	1931.0	1669.2
EU472052.1	294107	81.9	75.0	155.6	75.0	65.1	56.1
AY916385.1	114000	28.3	54.1	99.7	63.7	77.6	71.3
EU767209.1	331645	5418.6	4597.5	1647.8	7141.7	9771.7	7021.9
DQ394690.1	155809	3923.4	3784.3	2892.2	2453.0	5167.2	4486.2
FJ675754.1	527270	63.7	119.0	869.1	82.1	112.6	118.9
DQ807190.1	189116	12425.1	12806.8	6512.8	8056.3	15251.3	10352.3
FJ674069.1	515630	11071.2	10383.3	15315.8	10243.3	10756.6	11257.1
EU469135.1	302167	146.8	691.8	388.7	114.5	118.5	125.1
FJ682410.1	527856	7240.8	6489.0	4699.9	6271.2	7002.5	6932.8
EU774116.1	318581	1270.9	1298.9	1957.8	998.4	906.0	2917.6
EU475424.1	295802	2662.2	2536.2	2953.5	3249.4	2261.1	1695.7
EU843667.1	322552	1139.1	1286.4	1145.0	1790.0	1038.2	554.9
FJ685421.1	527958	655.4	735.0	2314.2	533.2	444.8	762.5
EU381538.1	269531	264.8	332.6	992.4	345.0	212.3	227.8
AM404501.2	563164	17.1	16.7	15.3	43.0	47.8	12.1
EU748111.1	311383	6340.3	6954.0	3318.4	3190.2	4394.2	4815.9
GQ491920.1	539328	7561.1	4487.9	5843.2	5552.4	5336.3	5667.3
FJ371896.1	365465	4800.4	4942.8	1499.4	3645.5	2420.7	2594.6
GQ493718.1	581908	14173.2	15156.0	14507.9	12630.9	12078.9	11411.7
FJ366766.1	362381	7259.8	9137.6	2786.5	5031.7	5600.8	5386.8
DQ798110.1	181710	2895.6	3176.7	1154.9	2153.5	2653.3	3197.8
EF402950.1	207652	4445.3	3186.8	3933.7	3732.7	1934.6	2780.2
EU460195.1	300508	2903.5	3893.5	1693.4	300.8	2189.0	2932.4
EU460164.1	290723	766.6	557.4	1558.3	703.8	200.1	267.8
EU774396.1	323229	904.9	947.8	2291.7	1198.0	637.0	778.5
DQ673538.1	172967	52.9	119.2	130.8	74.5	165.9	86.2

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GQ491705.1 gg_id:560898 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ364282.1 gg_id:361072 feces adult twins and mothers; TS15 clone TS15_a01b03
GQ896914.1 gg_id:562943 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
EU774563.1 gg_id:341482 Douc langur feces clone DL_2aaa04b11
DQ798279.1 gg_id:191890 human fecal clone RL181_aah40a10
FJ366403.1 gg_id:356858 feces adult twins and mothers; TS26 clone TS26_a02f09
FJ363910.1 gg_id:369703 feces adult twins and mothers; TS14 clone TS14_a04g08
DQ794459.1 gg_id:186667 human fecal clone RL197_aah88b08
AB185770.1 gg_id:104606 rumen clone U29-C11
FJ363821.1 gg_id:362970 feces adult twins and mothers; TS14 clone TS14_a03g05
FJ365359.1 gg_id:367180 feces adult twins and mothers; TS20 clone TS20_a02a02
FJ364504.1 gg_id:360766 feces adult twins and mothers; TS15 clone TS15_a03g02
FM873540.1 gg_id:367036 occupant source house mattress dust clone MA02D04
GQ043070.1 gg_id:381331 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012h
FJ832323.1 gg_id:590062 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_23G03
FJ365570.1 gg_id:357204 feces adult twins and mothers; TS20 clone TS20_a04d09
GQ493584.1 gg_id:541439 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ372016.1 gg_id:357258 feces adult twins and mothers; TS8 clone TS8_a04g10
EU344162.1 gg_id:272649 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU460201.1 gg_id:299680 mammals their gut microbes eastern black and white colobus feces clone COL_aai16
DQ804617.1 gg_id:195090 human fecal clone RL187_aao70d11
FJ365420.1 gg_id:368081 feces adult twins and mothers; TS20 clone TS20_a02f09
EU381440.1 gg_id:262572 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
FJ365555.1 gg_id:367799 feces adult twins and mothers; TS20 clone TS20_a04c05
FJ363045.1 gg_id:363989 feces adult twins and mothers; TS148 clone TS148_a02c09
AB034019.1 gg_id:33345 rumen clone 4C0d-6
AB034029.1 gg_id:19747 rumen clone 4C0d-16
DQ798127.1 gg_id:190960 human fecal clone RL302_aal95g12
FJ366384.1 gg_id:366039 feces adult twins and mothers; TS26 clone TS26_a02d05
FJ367406.1 gg_id:364014 feces adult twins and mothers; TS29 clone TS29_a03b05
FJ833984.1 gg_id:512314 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_78F10
EU381844.1 gg_id:262632 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
EU344365.1 gg_id:265090 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU530508.1 gg_id:270438 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader
FJ374224.1 gg_id:367864 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg
EU474848.1 gg_id:290278 takin feces clone TAK_aaa04h07
FJ881036.1 gg_id:380392 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EF614895.1 gg_id:232257 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU475330.1 gg_id:292243 rock hyrax feces clone RHSD_aaa03a07
EU777851.1 gg_id:345556 European rabbit feces clone RA_b02_1
DQ815323.1 gg_id:168054 mouse cecum clone aab45e04

GQ491705.1	560898	7245.7	7535.7	7656.4	8635.4	11606.7	10920.2
FJ364282.1	361072	6775.8	8318.4	6257.7	4749.6	5764.1	5488.6
GQ896914.1	562943	5747.1	4361.4	3383.8	7187.2	6247.4	6580.2
EU774563.1	341482	10954.1	11713.8	12531.5	7117.2	3624.7	4826.7
DQ798279.1	191890	4530.5	4092.6	2364.9	3189.4	4443.9	4811.5
FJ366403.1	356858	15218.6	15013.5	15627.0	11976.3	15713.8	14945.7
FJ363910.1	369703	61.3	65.8	177.7	103.4	61.0	33.9
DQ794459.1	186667	2249.1	2815.3	2621.4	2863.6	5308.2	6938.5
AB185770.1	104606	480.5	218.5	304.9	128.7	63.8	58.5
FJ363821.1	362970	6851.4	5973.1	6209.3	7362.3	12675.1	10977.4
FJ365359.1	367180	2654.9	3553.7	1128.0	2929.1	1474.8	2206.8
FJ364504.1	360766	5814.2	6703.4	2914.5	4570.0	4476.3	4592.6
FM873540.1	367036	7732.8	7296.4	4703.6	8580.5	7807.4	7787.8
GQ043070.1	381331	6082.2	6175.1	6320.0	5321.0	7387.3	7646.9
FJ832323.1	590062	14679.4	15437.8	4291.6	12216.2	11695.9	13112.1
FJ365570.1	357204	8093.9	10561.2	3987.1	7095.6	10105.8	9627.4
GQ493584.1	541439	5048.4	3041.7	5785.2	6209.4	3609.3	3822.1
FJ372016.1	357258	982.1	508.4	696.3	892.2	657.9	814.5
EU344162.1	272649	5172.7	5237.0	10145.0	8649.4	9464.8	7963.9
EU460201.1	299680	4931.2	5414.2	6674.4	7076.4	6079.6	8814.0
DQ804617.1	195090	276.0	201.9	936.6	169.3	136.9	204.1
FJ365420.1	368081	2507.4	3162.8	5248.5	2957.6	7662.8	9247.6
EU381440.1	262572	5714.6	3556.1	4348.7	6497.8	2805.4	5640.8
FJ365555.1	367799	563.5	1240.6	1490.9	341.3	2343.4	1675.4
FJ363045.1	363989	96.2	432.9	685.5	305.3	651.6	580.6
AB034019.1	33345	3772.8	3463.6	2944.3	5842.1	1131.9	3167.5
AB034029.1	19747	160.4	345.8	215.3	330.2	93.9	39.7
DQ798127.1	190960	2608.3	3464.8	779.1	1823.7	495.6	817.3
FJ366384.1	366039	3293.8	3725.3	1700.9	2830.6	4378.4	4655.5
FJ367406.1	364014	3921.3	4243.4	3126.6	1696.8	2702.7	2602.9
FJ833984.1	512314	793.1	841.0	2485.6	1917.0	2232.4	1292.2
EU381844.1	262632	5999.5	5411.5	5603.0	5365.5	3663.0	4168.3
EU344365.1	265090	8273.3	8922.6	13380.5	7579.4	7828.2	7961.2
EU530508.1	270438	1199.8	1008.4	1036.9	1289.3	886.8	992.9
FJ374224.1	367864	2209.8	3132.7	2033.3	1832.7	2111.8	2290.4
EU474848.1	290278	647.9	413.9	297.0	2260.0	56.0	66.4
FJ881036.1	380392	1434.9	1843.0	1306.5	3098.0	1541.1	2466.4
EF614895.1	232257	68.5	401.0	118.5	282.7	321.5	532.6
EU475330.1	292243	1167.4	1455.3	2455.8	417.0	263.2	820.4
EU777851.1	345556	4486.1	7730.7	4992.7	3088.1	10997.6	6194.2
DQ815323.1	168054	10959.3	9223.7	10480.2	9789.2	6677.0	7258.0

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o__Clostridiales	f__Ruminococcaceae
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EU843714.1 gg_id:348260 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
GQ449203.1 gg_id:581463 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g
EU459351.1 gg_id:299233 cheetah feces clone CE3_aai05b03
EU009811.1 gg_id:253896 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_F48
AY791247.1 gg_id:109481 insect associated clone PBg1-130
DQ815450.1 gg_id:165952 mouse cecum clone aab48f03
FJ365258.1 gg_id:369294 feces adult twins and mothers; TS1 clone TS1_a04g01
EU472325.1 gg_id:294908 Angola colobus feces clone EAC_1aaa01g09
FJ365014.1 gg_id:360002 feces adult twins and mothers; TS1 clone TS1_a01h01
EU507046.1 gg_id:270303 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10d04
FJ366853.1 gg_id:359339 feces adult twins and mothers; TS27 clone TS27_a04f04
X81125.1 gg_id:16072 Clostridium viride str. T2-7 (DSM 6836)
EF614670.1 gg_id:234137 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU470243.1 gg_id:295095 trancaspain urial feces clone TU2_aaa01f08
FJ680615.1 gg_id:519246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ809155.1 gg_id:198744 human fecal clone RL308_aal82e06
DQ326189.1 gg_id:147297 Metagenomic gut microbiome healthy human stool clone C101
EU509226.1 gg_id:275461 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b06
FJ172853.1 gg_id:303627 Qinghai Yak Ruminal and Fungi China rumen clone RB-3F5
AB185764.1 gg_id:100135 rumen clone U29-C04
EU465598.1 gg_id:302257 argali sheep feces clone AS1_aao39a10.Contig1
DQ394300.1 gg_id:152583 Effect probiotics on gastrointestinal broilers intestine clone BY12
EU844875.1 gg_id:342940 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU471673.1 gg_id:298819 Asiatic elephant feces clone AE1_aaa02c06
EU464154.1 gg_id:300628 reticulated giraffe feces clone gir_aah95a09
DQ057394.1 gg_id:130048 chicken ileum/cecum clone cc345
EU511908.1 gg_id:260762 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11a08
EU452998.1 gg_id:332814 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU843264.1 gg_id:339035 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ815824.1 gg_id:168145 mouse cecum clone aab22g08
EF098064.1 gg_id:194182 mouse cecum clone SWPT14_aaa01a06
EU464416.1 gg_id:297278 hamadryas baboon feces clone AFBAB_aai04g02
FJ367833.1 gg_id:362395 feces adult twins and mothers; TS2 clone TS2_a04b03
AB234457.1 gg_id:149078 termite gut homogenate clone MgMjD-041
FJ681152.1 gg_id:530945 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU382058.1 gg_id:272613 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
EU506544.1 gg_id:270066 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03g02
EU509962.1 gg_id:270866 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24d08
AJ488075.1 gg_id:66188 chlorobenzene-degrading consortium clone IA-24
EU451755.1 gg_id:339667 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
FJ365202.1 gg_id:365220 feces adult twins and mothers; TS1 clone TS1_a04a12

EU843714.1	348260	8003.8	8254.5	5320.5	7127.8	10165.5	7737.0
GQ449203.1	581463	115.2	135.4	1111.2	349.6	227.6	390.3
EU459351.1	299233	992.6	923.5	2550.0	1555.4	1095.9	1244.0
EU009811.1	253896	1628.1	1119.9	1869.7	783.3	409.5	354.1
AY791247.1	109481	24.0	19.7	62.9	54.6	49.7	18.1
DQ815450.1	165952	7387.6	9324.2	3075.9	8453.5	10391.4	8912.2
FJ365258.1	369294	8634.1	5496.0	5896.7	4927.9	6828.1	6358.5
EU472325.1	294908	3732.2	2932.0	7219.3	3380.6	2834.6	2469.0
FJ365014.1	360002	5657.4	5123.1	8083.3	5807.9	7395.4	5937.2
EU507046.1	270303	11468.6	13862.7	5920.5	8798.0	7926.5	7884.8
FJ366853.1	359339	1251.2	848.9	2599.3	642.7	153.9	528.1
X81125.1	16072	25.7	55.4	113.0	52.3	134.7	29.3
EF614670.1	234137	27.5	33.1	607.7	90.5	68.8	24.8
EU470243.1	295095	990.4	599.9	1021.8	826.3	166.2	226.7
FJ680615.1	519246	14086.9	14158.5	4973.3	11617.1	12815.7	11274.8
DQ809155.1	198744	29.3	25.9	47.6	69.0	61.5	26.0
DQ326189.1	147297	340.5	394.1	1641.8	578.5	388.4	441.0
EU509226.1	275461	9238.3	9656.9	11483.1	9562.2	9119.3	10626.5
FJ172853.1	303627	560.3	626.5	1303.2	670.2	276.9	246.0
AB185764.1	100135	7978.4	8635.0	8838.5	7667.1	8434.0	4654.6
EU465598.1	302257	201.3	318.8	1609.1	326.2	158.1	538.5
DQ394300.1	152583	817.5	1582.2	1344.5	2084.9	716.6	402.2
EU844875.1	342940	737.6	868.3	1770.6	2193.6	750.4	678.9
EU471673.1	298819	2294.0	1441.2	1551.7	2425.2	1515.1	2201.7
EU464154.1	300628	5343.6	5791.9	6402.7	5498.1	6321.6	6586.9
DQ057394.1	130048	111.1	131.2	594.8	133.3	161.5	79.9
EU511908.1	260762	2937.3	2593.2	797.6	3678.7	4234.5	4033.2
EU452998.1	332814	5371.2	5485.5	4525.6	5850.7	6302.1	3624.7
EU843264.1	339035	181.2	95.3	266.1	117.3	633.3	1005.9
DQ815824.1	168145	2120.7	733.9	3579.1	1289.0	2377.0	1300.6
EF098064.1	194182	67.5	52.9	123.0	56.9	78.5	37.5
EU464416.1	297278	6891.2	8923.5	8578.1	5047.8	13226.0	15342.9
FJ367833.1	362395	2341.5	2698.4	1089.7	1734.1	2812.5	2285.9
AB234457.1	149078	329.9	454.8	333.1	339.7	1000.1	727.9
FJ681152.1	530945	2547.2	3382.4	2296.2	4092.7	5743.5	3046.1
EU382058.1	272613	7850.7	6977.9	4871.1	5961.2	6155.6	5218.0
EU506544.1	270066	12922.5	11430.0	3409.9	8679.0	9371.7	10162.2
EU509962.1	270866	3550.7	3990.0	4483.3	2411.2	2884.3	2673.2
AJ488075.1	66188	1215.0	1250.5	3037.0	1292.3	1435.0	1467.8
EU451755.1	339667	118.8	300.1	564.3	120.1	138.4	77.5
FJ365202.1	365220	2495.9	1459.8	2889.5	5305.7	392.2	1080.2

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
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o__Clostridiales	f__Ruminococcaceae
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GU304299.1 gg_id:579244 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU452722.1 gg_id:344329 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU776814.1 gg_id:339944 Mongoose lemur feces clone ML_aaj26e09
EU465532.1 gg_id:295223 argali sheep feces clone AS1_aao37a11.Contig1
EU458546.1 gg_id:301573 spotted hyena feces clone HY2_h08_2
FJ680266.1 gg_id:519941 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY992951.1 gg_id:130016 mouse cecum clone C22_k16
EU511675.1 gg_id:262671 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08g07
DQ815617.1 gg_id:167514 mouse cecum clone aab43f04
EU844732.1 gg_id:340116 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ805512.1 gg_id:181769 human fecal clone RL203_aai63f02
EU468922.1 gg_id:289860 Speke's gazelle feces clone SP2_c09_1
FJ542840.1 gg_id:525763 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
EU850604.1 gg_id:326444 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF436
EU774081.1 gg_id:352918 Chimpanzee feces clone CHIMP12_b04_1
NR_025025.1 gg_id:539939 Papillibacter cinnamivorans str. CIN1; DSM12816
FJ374227.1 gg_id:369389 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
EF604698.1 gg_id:228902 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ680261.1 gg_id:521792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF096916.1 gg_id:175377 mouse cecum clone SWPT13_aaa02f07
EU463678.1 gg_id:289426 domesticated horse feces clone horsej_aai90h08
EU506333.1 gg_id:270498 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d10
DQ796729.1 gg_id:179422 human fecal clone RL179_aao53g02
FJ684521.1 gg_id:532424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ880481.1 gg_id:373181 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
GQ047255.1 gg_id:375644 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010e
EF403010.1 gg_id:204126 human fecal clone SJTU_B_15_54
EU465687.1 gg_id:302641 argali sheep feces clone AS2_aao33e07
AB198539.1 gg_id:135453 termite gut wall fraction clone RsW02-066
EU766175.1 gg_id:349740 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
FJ681934.1 gg_id:524439 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU470345.1 gg_id:292656 Grevy's zebra feces clone GZ_aaa01b08
AB192279.1 gg_id:143711 termite gut homogenate clone RPK-59
EU504413.1 gg_id:275288 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03h04
EU470328.1 gg_id:297796 Grevy's zebra feces clone GZ_aaa04g03
DQ796579.1 gg_id:196210 human fecal clone RL179aan75b11
DQ125557.1 gg_id:134357 uranium contaminated soil clone AKAU3538
EU468690.1 gg_id:302712 okapi feces clone OK2_f06_1
EU871383.1 gg_id:351055 Genetic Bovine (Bos taurus) Rumen Thailand clone CF225
DQ815605.1 gg_id:169578 mouse cecum clone aab43e04
EU505544.1 gg_id:258903 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02d10

GU304299.1	579244	2930.9	3247.8	3997.0	2045.6	3214.2	2853.0
EU452722.1	344329	1307.9	614.5	2468.4	798.1	941.6	869.1
EU776814.1	339944	72.3	68.9	148.7	87.9	102.6	86.6
EU465532.1	295223	2782.7	2581.4	3141.9	1982.7	1447.6	1594.2
EU458546.1	301573	6241.5	7899.8	3797.4	4260.3	7288.8	4133.0
FJ680266.1	519941	8265.1	9172.8	6659.9	8371.0	11189.7	9974.0
AY992951.1	130016	6013.9	9372.2	6847.3	5143.8	11114.5	9793.1
EU511675.1	262671	1095.6	1219.1	3157.4	642.4	1929.5	2261.8
DQ815617.1	167514	1558.0	2234.4	1651.3	3161.0	1221.9	2183.1
EU844732.1	340116	1490.4	2175.2	1840.2	996.2	2905.4	2432.4
DQ805512.1	181769	450.3	311.9	506.9	528.4	378.0	350.3
EU468922.1	289860	23839.5	23337.1	9250.8	15610.9	18480.6	19178.4
FJ542840.1	525763	1669.1	1283.3	1873.0	1895.7	988.1	2280.4
EU850604.1	326444	4956.9	3812.7	1614.5	3227.0	3466.4	3508.3
EU774081.1	352918	815.7	428.3	1439.6	288.5	1711.0	1859.4
NR_025025.1	539939	68.4	68.1	151.3	75.8	69.4	36.8
FJ374227.1	369389	6320.0	5955.2	6733.0	5774.4	6687.1	7096.4
EF604698.1	228902	6173.9	3686.1	2448.0	5178.3	2665.7	5422.5
FJ680261.1	521792	4569.4	6576.0	3389.9	3038.7	2691.9	2490.8
EF096916.1	175377	1269.3	1867.3	1000.4	930.6	690.0	979.9
EU463678.1	289426	1859.8	2943.6	1458.8	1604.9	1631.1	2024.3
EU506333.1	270498	854.7	1048.5	1255.2	660.2	390.5	271.2
DQ796729.1	179422	2602.1	2039.5	2376.0	5402.0	1421.0	1610.1
FJ684521.1	532424	6780.9	6743.7	5462.6	4336.9	5402.9	3241.9
FJ880481.1	373181	8967.5	11854.9	4801.3	6726.4	3888.8	5962.0
GQ047255.1	375644	610.3	584.6	1006.7	157.2	142.1	310.0
EF403010.1	204126	1343.1	1132.1	1620.9	464.9	901.4	471.6
EU465687.1	302641	31.5	55.6	180.3	51.3	62.2	13.5
AB198539.1	135453	367.3	418.6	441.5	169.9	115.0	63.3
EU766175.1	349740	371.3	242.0	882.3	212.8	133.3	184.6
FJ681934.1	524439	796.3	1248.3	1585.9	1015.2	1968.0	2265.3
EU470345.1	292656	172.0	190.8	384.9	182.1	938.7	2308.2
AB192279.1	143711	299.7	267.1	1071.8	176.1	146.7	252.3
EU504413.1	275288	2470.8	3249.3	1545.2	1497.3	2033.3	5406.9
EU470328.1	297796	1574.4	2397.1	2398.6	937.0	509.2	743.8
DQ796579.1	196210	473.2	297.2	511.7	890.6	1222.9	927.8
DQ125557.1	134357	160.9	181.7	1236.2	169.5	103.1	136.1
EU468690.1	302712	1673.5	1399.2	652.2	1444.8	3329.8	4847.4
EU871383.1	351055	1365.9	1379.9	1320.3	514.6	307.0	590.9
DQ815605.1	169578	4382.1	5534.7	3419.1	4970.1	5934.8	5183.7
EU505544.1	258903	8279.0	9348.2	4068.5	6132.9	8466.0	8847.5

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EU763617.1 gg_id:321571 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
EU508708.1 gg_id:270059 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g03
EU765286.1 gg_id:344815 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
EU775069.1 gg_id:327573 Francois Langur feces clone FL_1aaa03e06
EF605057.1 gg_id:233530 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ815489.1 gg_id:173329 mouse cecum clone aab41e04
EU764061.1 gg_id:305588 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
EU454514.1 gg_id:322836 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
AF371803.1 gg_id:43950 swine intestine clone p-1316-a5
EU472220.1 gg_id:288423 francois langur feces clone FL_2aaa01e02
EU766049.1 gg_id:324024 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4
EU777228.1 gg_id:305121 Okapi feces clone OK1_d05
EU507866.1 gg_id:273781 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02d03
EU779203.1 gg_id:319642 Trancaspian Urial feces clone TU2_aaa03h10
EU504299.1 gg_id:268671 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01h12
EU512008.1 gg_id:273519 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12f05
EF434364.1 gg_id:215468 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont
AF001761.1 gg_id:16027 rumen clone RF29
EU885041.1 gg_id:347991 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2H7
FJ365158.1 gg_id:357678 feces adult twins and mothers; TS1 clone TS1_a03e11
EU779132.1 gg_id:356550 Trancaspian Urial feces clone TU2_aaa04c08
EU473497.1 gg_id:293727 Somali wild ass feces clone WA_aaa01h08
AY992778.1 gg_id:133495 mouse cecum clone C22_a17
EF401851.1 gg_id:216263 human fecal clone SJTU_D_05_87
DQ795112.1 gg_id:178288 human fecal clone RL310_aam40d04
AY980920.1 gg_id:116165 human rectum mucosal biopsy clone LR29
EF603654.1 gg_id:231593 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ815430.1 gg_id:163633 mouse cecum clone aab48c09
EU460978.1 gg_id:292639 red kangaroo feces clone KO1_aai41e04
EF445154.1 gg_id:210292 rabbit cecum clone NED2F7
EU382039.1 gg_id:260436 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
EU779391.1 gg_id:345353 Somali Wild Ass feces clone WA_aaa01c12
EU777115.1 gg_id:311308 Okapi feces clone OK3_f10
EU508202.1 gg_id:274847 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03b05
GU302819.1 gg_id:551289 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EU455639.1 gg_id:349725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
FJ366757.1 gg_id:367176 feces adult twins and mothers; TS27 clone TS27_a03e06
EU777102.1 gg_id:342600 Okapi feces clone OK1_f06_1
EF096437.1 gg_id:199046 mouse cecum clone obob2_aaa02g08
EU773165.1 gg_id:352908 BigHorn sheep feces clone BHSD_aaa01b04
GQ175508.1 gg_id:589507 Chicken intestinal microbiota modulations various feed supplementations DGGE anc

EU763617.1	321571	3108.8	3880.3	4327.5	3040.1	4439.4	3417.4
EU508708.1	270059	8423.5	11480.3	5085.4	7051.1	8877.4	15047.6
EU765286.1	344815	1009.6	1640.7	3167.4	1752.6	2764.0	3036.7
EU775069.1	327573	7586.2	8379.1	3469.4	6005.4	8730.5	7467.2
EF605057.1	233530	12844.5	13531.9	11283.4	13145.5	13133.2	10346.6
DQ815489.1	173329	11249.9	14959.6	5673.4	9581.1	10685.1	9731.3
EU764061.1	305588	78.1	120.0	329.1	133.6	115.4	160.9
EU454514.1	322836	122.9	117.1	276.6	107.0	81.4	65.1
AF371803.1	43950	84.2	109.0	231.2	158.9	631.5	215.9
EU472220.1	288423	5205.5	4556.7	3913.9	4230.9	5596.0	7554.9
EU766049.1	324024	5988.9	6442.6	7378.5	6553.8	6369.6	7348.8
EU777228.1	305121	1078.7	1753.0	2644.7	1390.1	1452.4	1687.3
EU507866.1	273781	6174.4	7462.4	1762.2	4323.8	4428.1	6003.9
EU779203.1	319642	2033.3	1517.0	2686.1	1047.0	1705.8	725.2
EU504299.1	268671	667.1	571.7	1073.7	325.5	230.5	299.2
EU512008.1	273519	9466.1	10947.4	6871.2	7836.1	7908.1	11559.7
EF434364.1	215468	271.4	345.6	700.6	363.3	629.6	414.3
AF001761.1	16027	27.9	26.2	28.5	66.2	66.7	27.3
EU885041.1	347991	2855.5	3043.8	3537.4	1943.7	700.9	1818.5
FJ365158.1	357678	3964.5	3648.5	3834.7	5029.3	4155.4	6110.5
EU779132.1	356550	6438.1	6974.3	4515.3	5056.5	6113.5	6055.9
EU473497.1	293727	1631.8	1361.0	4381.6	1082.0	860.7	1065.1
AY992778.1	133495	13.5	16.7	18.2	30.0	56.1	20.1
EF401851.1	216263	191.8	236.9	590.7	431.4	400.1	460.4
DQ795112.1	178288	3537.4	2828.0	1176.1	1361.1	1593.9	1982.3
AY980920.1	116165	1951.2	2491.0	968.0	2679.2	659.6	831.2
EF603654.1	231593	2689.9	2042.8	141.6	3291.7	3838.1	3284.2
DQ815430.1	163633	1473.4	697.5	1562.0	601.5	785.7	224.6
EU460978.1	292639	3056.9	2666.9	4491.3	2575.2	2892.4	5505.0
EF445154.1	210292	50.2	39.8	46.6	55.5	67.1	49.5
EU382039.1	260436	903.5	937.9	1433.2	481.4	657.6	400.5
EU779391.1	345353	2730.3	2428.3	3607.5	3191.2	2726.5	2540.2
EU777115.1	311308	1645.3	4578.8	1913.3	3428.5	2820.2	3511.4
EU508202.1	274847	6487.1	5843.8	3873.2	5633.0	4474.8	4243.1
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FJ366757.1	367176	7069.1	6048.9	3078.7	2705.2	4927.2	7079.2
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EF096437.1	199046	1423.6	395.9	2487.4	537.4	620.8	608.0
EU773165.1	352908	1933.3	1692.5	2069.1	1556.3	353.6	476.0
GQ175508.1	589507	1675.1	2087.7	3708.9	2010.6	4340.9	5152.8

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AF371937.1 gg_id:34823 swine intestine clone p-5152-2Wb3
EU473725.1 gg_id:294467 douc langur feces clone DL_2aaa01g03
FJ880941.1 gg_id:410327 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU469833.1 gg_id:293546 western lowland gorilla feces clone GOR_aag72a09
EU772173.1 gg_id:312152 Argali sheep feces clone AS1_aao37d04.Contig1
AB185773.1 gg_id:105047 rumen clone U29-D02
EU850524.1 gg_id:331952 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF310
EU470209.1 gg_id:298302 trancaspain urial feces clone TU2_aaa02h10
EU472107.1 gg_id:290859 francois langur feces clone FL_1aaa01e09
EU463636.1 gg_id:292001 domesticated horse feces clone horsej_aai90b08
EU773172.1 gg_id:320029 BigHorn sheep feces clone BH2_aao23c10
GU303920.1 gg_id:561716 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EU458079.1 gg_id:308523 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
DQ014986.1 gg_id:131359 mouse cecum clone M1_1b09_1
FJ881217.1 gg_id:371870 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU009770.1 gg_id:247551 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AF39
FJ680773.1 gg_id:515004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU454896.1 gg_id:327567 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU772027.1 gg_id:354741 Argali sheep feces clone AS1_aao37a07.Contig1
EF071402.1 gg_id:187846 library survey and quantitative measurement major mucosa- IBD human colonic muc
EU844698.1 gg_id:306375 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU773275.1 gg_id:319693 BigHorn sheep feces clone BH1_aao25d09
AY858503.2 gg_id:110968 gastrointestinal tract eland clone ELAND_41
FJ680312.1 gg_id:532384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ793455.1 gg_id:186654 human fecal clone RL199_aaj43h12
FJ879227.1 gg_id:445626 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU506351.1 gg_id:271290 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64a01
EU776815.1 gg_id:333249 Mongoose lemur feces clone ML_aae88a09
EU779144.1 gg_id:321963 Trancaspian Urial feces clone TU2_aaa03b05
EU506252.1 gg_id:276388 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61d11
FJ680395.1 gg_id:515362 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU474545.1 gg_id:297237 bighorn sheep feces clone BHSD_aaa04e05
DQ809638.1 gg_id:195252 human fecal clone RL184_aan81h11
FJ880264.1 gg_id:431899 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ880708.1 gg_id:372146 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
GQ897911.1 gg_id:589989 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ088761.1 gg_id:132303 0.7 1.4 kmbls sctn cntnntl crst cln BE325FW032701CTS_hl1-41
EU776496.1 gg_id:330252 Red Kangaroo feces clone KO1_aai41c09
DQ815620.1 gg_id:166466 mouse cecum clone aab43f08
CU927388.1 gg_id:557458 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EF401251.1 gg_id:207166 human fecal clone SJTU_D_07_85

AF371937.1	34823	47.4	45.4	255.4	86.8	93.6	193.0
EU473725.1	294467	2530.7	1952.7	2436.5	2263.7	889.9	2136.0
FJ880941.1	410327	1894.1	2914.5	4290.0	2801.4	4288.0	4455.6
EU469833.1	293546	1629.1	1875.1	991.4	437.9	1512.6	2160.0
EU772173.1	312152	7283.7	6432.1	8664.2	7393.8	2781.1	3717.2
AB185773.1	105047	5915.8	7054.6	8866.5	5331.9	7426.7	7144.7
EU850524.1	331952	7767.5	7986.5	4496.7	5200.2	8103.9	11990.9
EU470209.1	298302	232.2	82.5	556.9	120.0	72.4	112.3
EU472107.1	290859	102.4	75.1	329.8	149.7	70.0	85.2
EU463636.1	292001	6504.5	9310.6	9473.6	5419.0	4934.2	5289.9
EU773172.1	320029	4761.3	4643.8	4099.5	3437.8	1440.9	2621.0
GU303920.1	561716	4015.6	2849.9	4284.1	2922.2	1517.8	3342.3
EU458079.1	308523	1932.9	2449.9	2477.2	3861.2	1699.3	1186.9
DQ014986.1	131359	9543.2	7863.7	9703.8	10774.6	8917.6	8766.1
FJ881217.1	371870	303.7	476.6	590.7	724.3	443.5	861.5
EU009770.1	247551	2956.5	3026.5	1639.4	2911.0	1354.9	1183.4
FJ680773.1	515004	6860.2	6827.1	8110.9	7110.1	5415.2	6455.9
EU454896.1	327567	7906.6	9518.6	2880.5	5470.3	8059.3	13499.8
EU772027.1	354741	2389.2	2726.9	3241.8	1770.8	1392.7	1086.2
EF071402.1	187846	125.4	621.5	51.7	181.8	61.1	37.7
EU844698.1	306375	7284.3	11138.6	4758.7	7966.5	9564.3	10088.3
EU773275.1	319693	14186.1	16442.5	6722.4	12504.5	13787.1	11787.0
AY858503.2	110968	2901.7	2786.4	3905.8	2306.0	2511.9	2907.6
FJ680312.1	532384	1980.8	2775.7	3063.5	2285.0	2131.8	2463.0
DQ793455.1	186654	39.2	143.7	183.5	142.3	98.1	48.5
FJ879227.1	445626	12719.7	16695.6	10016.2	10127.5	8226.4	9191.9
EU506351.1	271290	6195.3	5483.9	3992.0	4438.7	6729.4	5090.7
EU776815.1	333249	1583.3	1305.7	2303.9	2029.5	813.8	1590.8
EU779144.1	321963	1403.5	2296.2	3783.2	1886.2	1540.0	2581.4
EU506252.1	276388	78.5	56.5	277.3	70.0	51.9	17.5
FJ680395.1	515362	3486.4	3526.4	4582.5	3784.9	4708.8	4124.5
EU474545.1	297237	2737.4	2695.1	3727.1	3836.3	3902.7	3261.9
DQ809638.1	195252	1781.0	2251.3	366.0	583.1	352.2	148.7
FJ880264.1	431899	2617.1	1667.1	2943.6	1052.1	931.4	1021.2
FJ880708.1	372146	90.8	123.8	239.9	146.2	73.7	72.3
GQ897911.1	589989	1223.1	2132.6	2938.0	640.6	390.7	441.3
DQ088761.1	132303	77.9	46.9	85.4	85.4	384.9	52.4
EU776496.1	330252	1610.5	2352.5	6437.9	1776.7	659.7	1322.8
DQ815620.1	166466	3765.1	3987.3	2394.3	2596.9	1751.0	1239.6
CU927388.1	557458	2342.0	1720.6	4401.6	2378.4	3086.7	3173.6
EF401251.1	207166	1743.0	1634.2	2416.4	2932.4	714.1	964.8

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EU466076.1 gg_id:290337 bighorn sheep feces clone BH1_aao25d04
EF097979.1 gg_id:192930 mouse cecum clone SWPT12_aaa03c10
EU505220.1 gg_id:261998 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04f10
DQ801156.1 gg_id:198841 human fecal clone RL116_aae99c04
EU504194.1 gg_id:274083 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03g11
EU777204.1 gg_id:347980 Okapi feces clone OK3_d02_3
FJ880790.1 gg_id:463116 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
FJ673102.1 gg_id:517347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU468528.1 gg_id:293630 okapi feces clone OK1_a08_1
EU507527.1 gg_id:277388 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e12
EF098062.1 gg_id:190396 mouse cecum clone SWPT14_aaa01a03
FJ371773.1 gg_id:365161 feces adult twins and mothers; TS8 clone TS8_a02a09
AY854298.1 gg_id:110901 herbivore gastrointestinal tract clone Thompsons100
EF097074.1 gg_id:196191 mouse cecum clone SWPT18_aaa01a07
EU464390.1 gg_id:303345 hamadryas baboon feces clone AFBAB_aai04b12
CU926151.1 gg_id:562681 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU468950.1 gg_id:294437 Speke's gazelle feces clone SP2_g12
EU474858.1 gg_id:287505 takin feces clone TAK_aaa01h06
EU470234.1 gg_id:294545 trancaspain urial feces clone TU2_aaa02e05
EF096746.1 gg_id:193198 mouse cecum clone SWPT11_aaa04a09
DQ799903.1 gg_id:199317 human fecal clone RL247_aaj21f02
FJ680818.1 gg_id:532083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU470155.1 gg_id:295979 trancaspain urial feces clone TU2_aaa04h08
DQ800334.1 gg_id:184208 human fecal clone RL303_aal71g01
EU771790.1 gg_id:333206 African elephant feces clone AFEL3_aao14d01
EU464228.1 gg_id:292382 reticulated giraffe feces clone gir_aah96f04
EU458586.1 gg_id:292513 European rabbit feces clone RA_d11
EU794151.1 gg_id:307643 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H9
EU471983.1 gg_id:293667 francois langur feces clone FL_1aaa01h03
DQ808904.1 gg_id:175511 human fecal clone RL243_aai86g11
FJ366541.1 gg_id:363783 feces adult twins and mothers; TS27 clone TS27_a01a02
GU174111.1 gg_id:563490 Microbial Bactrian camel estimated rumen clone XJC5
EU456560.1 gg_id:321019 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU452476.1 gg_id:313021 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU506190.1 gg_id:273910 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03a05
EU469336.1 gg_id:287585 springbok feces clone SBK_f11
EU766271.1 gg_id:340006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU475523.1 gg_id:289882 springbok feces clone SBSD_aaa01f06
EU509854.1 gg_id:264775 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e06
EU776270.1 gg_id:344111 Red Kangaroo feces clone KO2_aai18g10

EU466130.1	301743	2035.4	1723.2	2387.3	3562.1	2997.4	3231.3
EU466076.1	290337	5242.4	6048.7	1732.8	2999.7	4784.1	7380.9
EF097979.1	192930	1613.9	1671.6	2244.6	1740.0	2114.5	1360.1
EU505220.1	261998	2989.6	3591.1	2203.6	1685.4	1161.2	1196.1
DQ801156.1	198841	97.1	176.8	370.0	134.8	55.9	108.3
EU504194.1	274083	9457.3	11625.1	4435.1	7928.8	9371.3	14629.9
EU777204.1	347980	6456.0	6591.6	2654.4	4573.6	3805.4	4487.8
FJ880790.1	463116	145.6	438.9	921.5	125.3	664.0	285.1
FJ673102.1	517347	3419.7	2964.8	3801.4	4548.6	2057.5	4759.9
EU468528.1	293630	3129.5	3396.2	6753.0	2859.9	6744.5	6623.7
EU507527.1	277388	14483.5	15231.5	9960.3	10362.9	13058.8	11738.6
EF098062.1	190396	2950.0	2362.5	1796.8	1591.1	2403.3	2117.0
FJ371773.1	365161	7872.2	8886.4	5815.4	6087.7	4471.9	4896.9
AY854298.1	110901	2622.2	3592.2	1465.6	1929.9	925.6	1994.2
EF097074.1	196191	21.6	32.9	20.0	48.2	64.9	25.7
EU464390.1	303345	2332.3	1984.5	5012.4	812.2	1516.0	1253.5
CU926151.1	562681	3096.2	3395.7	1442.4	2745.8	275.5	435.0
EU468950.1	294437	2504.6	3427.6	2630.0	3691.7	3396.8	2793.7
EU474858.1	287505	894.8	1793.4	2698.6	709.1	1549.7	1841.8
EU470234.1	294545	3620.3	5009.6	6409.5	3516.3	8269.8	5504.6
EF096746.1	193198	3654.5	4008.0	2348.4	2600.0	3104.4	2826.7
DQ799903.1	199317	4187.9	2317.2	3344.7	5080.3	1828.2	2185.5
FJ680818.1	532083	13675.0	13011.2	11036.2	13511.2	16027.4	13579.4
EU470155.1	295979	3550.4	2881.5	1797.8	3801.8	6797.1	5204.9
DQ800334.1	184208	10271.4	9461.3	3886.7	9985.5	14950.6	10457.5
EU771790.1	333206	4915.8	6480.6	4182.6	4529.2	7950.0	8055.8
EU464228.1	292382	1067.4	1959.5	2934.8	807.3	181.7	709.9
EU458586.1	292513	1132.7	2177.0	5836.6	2058.9	3869.7	4129.2
EU794151.1	307643	2886.0	1696.9	3590.0	2827.8	368.9	1447.3
EU471983.1	293667	5009.6	6353.6	1583.9	4659.9	5971.3	7394.9
DQ808904.1	175511	6448.0	5648.5	5001.6	6585.0	9525.1	9724.8
FJ366541.1	363783	6145.2	5017.7	1691.5	7873.5	7348.5	6420.2
GU174111.1	563490	1076.9	717.0	1415.6	839.5	1362.6	821.2
EU456560.1	321019	12454.2	14004.5	6869.0	10718.6	13091.4	9465.3
EU452476.1	313021	5402.6	6095.8	8594.1	4726.4	7254.2	7080.8
EU506190.1	273910	6860.2	7181.2	6791.0	5909.6	4503.4	5753.9
EU469336.1	287585	4096.1	3973.8	1978.9	3297.4	1982.9	2515.3
EU766271.1	340006	476.8	548.6	1230.3	244.1	171.4	224.2
EU475523.1	289882	3914.0	5040.1	3784.6	3170.5	4748.3	2071.5
EU509854.1	264775	8482.0	8589.9	7284.6	5677.9	1998.5	3147.9
EU776270.1	344111	2476.9	4975.8	5869.1	3948.3	6879.3	6298.4

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DQ794239.1 gg_id:180468 human fecal clone RL176_aan60a04
EF099665.1 gg_id:196556 mouse cecum clone SWPT4_aaa02f04
EU622645.1 gg_id:281242 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
EF097943.1 gg_id:194809 mouse cecum clone SWPT12_aaa02e11
EU504880.1 gg_id:266512 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03f12
EU465571.1 gg_id:292962 argali sheep feces clone AS1_aao38b02.Contig1
FJ879507.1 gg_id:400748 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU506869.1 gg_id:266845 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07e08
EU472333.1 gg_id:297020 Angola colobus feces clone EAC_1aaa02f01
FJ681547.1 gg_id:527760 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF096100.1 gg_id:192849 mouse cecum clone lean2_aaa04b06
AM405156.2 gg_id:564320 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.15
EU506930.1 gg_id:264668 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08e06
EU773138.1 gg_id:329808 BigHorn sheep feces clone BH1_aao27h11
EU470403.1 gg_id:290531 Grevy's zebra feces clone GZ_aaa01c07
EF098922.1 gg_id:199445 mouse cecum clone SWPT1_aaa03c09
AF371795.1 gg_id:48325 swine intestine clone p-2027-s959-5
FJ880774.1 gg_id:377756 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
DQ825126.1 gg_id:186321 human fecal clone RL185_aan85f09
GU302815.1 gg_id:593396 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
DQ815699.1 gg_id:162151 mouse cecum clone aab21b05
EU779200.1 gg_id:348872 Trancaspian Urial feces clone TU2_aaa03a08
EU463773.1 gg_id:299331 domesticated horse feces clone horsej_aai92f01
EF434333.1 gg_id:205309 gastrointestinal tract microbiota microarray reference pool created pooling products
EU506958.1 gg_id:269532 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08h10
EU843115.1 gg_id:353088 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ833519.1 gg_id:557177 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q301_40H05
DQ014588.1 gg_id:131678 mouse cecum clone M1_d04
AF129864.1 gg_id:16031 microbial anaerobic digestor determined clone BC09
DQ326172.1 gg_id:146132 Metagenomic gut microbiome healthy human stool clone C071
EU511693.1 gg_id:263255 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07a12
AY244908.1 gg_id:85153 cow rumen clone BF30
EU532006.1 gg_id:268937 Predominant role host genetics controlling gut microbiota FMF remission stool clone
FJ371294.1 gg_id:357511 feces adult twins and mothers; TS6 clone TS6_a03c05
FJ674035.1 gg_id:529236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB264082.1 gg_id:194322 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-185
EU773210.1 gg_id:306212 BigHorn sheep feces clone BH1_aao27f06
EU772832.1 gg_id:308307 Bush dog feces clone bdog1_aai77b11
EU458006.1 gg_id:327808 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU451213.1 gg_id:327675 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EF454073.2 gg_id:224826 termite hindgut clone 290cost002-P3L-1599

DQ794239.1	180468	81.5	121.2	117.9	94.2	79.3	30.5
EF099665.1	196556	1881.4	982.4	336.4	293.4	1700.4	1053.2
EU622645.1	281242	29.5	29.9	27.2	56.2	55.2	26.5
EF097943.1	194809	9011.5	9111.9	3981.1	4656.4	1728.7	2242.2
EU504880.1	266512	2261.3	3274.4	3874.6	2594.4	2311.8	3302.1
EU465571.1	292962	519.4	548.0	1942.9	588.0	801.2	840.4
FJ879507.1	400748	293.7	367.5	1331.2	314.7	162.5	314.3
EU506869.1	266845	3027.2	3965.9	3425.5	4828.6	6452.2	5085.5
EU472333.1	297020	365.1	202.9	524.4	422.0	129.3	255.0
FJ681547.1	527760	1580.1	1523.2	1491.2	1688.7	1885.5	1842.2
EF096100.1	192849	680.2	468.6	1686.2	630.5	133.8	295.1
AM405156.2	564320	828.8	1392.2	1142.4	947.5	573.5	413.0
EU506930.1	264668	5824.5	7408.9	3648.0	5512.1	8642.7	7486.5
EU773138.1	329808	2548.4	2704.7	2607.1	1724.7	3869.4	5405.9
EU470403.1	290531	1540.8	1123.9	1883.7	1561.7	1547.7	1524.6
EF098922.1	199445	29.0	30.9	38.1	66.1	57.3	24.1
AF371795.1	48325	295.1	242.3	355.8	110.2	126.6	75.7
FJ880774.1	377756	2146.1	2459.6	2766.3	2092.1	2577.0	2493.3
DQ825126.1	186321	23.8	51.3	23.6	56.4	49.3	16.9
GU302815.1	593396	2391.1	2664.2	4370.7	2825.4	4120.1	3840.2
DQ815699.1	162151	1908.0	3190.7	1376.4	1450.2	938.9	1926.9
EU779200.1	348872	3019.7	2937.9	2123.0	3538.0	4963.3	2801.2
EU463773.1	299331	686.8	744.7	1796.5	1646.5	467.3	1095.7
EF434333.1	205309	880.4	1153.8	1365.0	378.1	1081.0	1972.5
EU506958.1	269532	3682.1	3014.6	2142.3	3208.4	2010.5	2885.7
EU843115.1	353088	390.3	243.8	540.0	163.2	128.0	176.3
FJ833519.1	557177	5117.8	4748.9	8136.4	4177.9	3597.3	4356.4
DQ014588.1	131678	8368.5	9624.1	5012.8	6878.0	6985.3	4331.9
AF129864.1	16031	1626.8	1913.8	1174.9	2196.0	3227.2	3719.0
DQ326172.1	146132	4765.5	5234.3	3380.5	5232.3	499.6	1659.9
EU511693.1	263255	55.5	150.6	224.6	98.8	133.0	69.1
AY244908.1	85153	257.5	652.6	188.9	206.6	81.9	124.6
EU532006.1	268937	2504.4	2998.2	3744.8	2983.8	4615.3	3118.4
FJ371294.1	357511	8890.0	10729.3	5513.7	6029.6	8313.7	6690.0
FJ674035.1	529236	4292.1	4977.9	2161.2	5153.9	6353.8	5682.0
AB264082.1	194322	14566.9	11052.7	9040.9	8215.8	11126.1	8979.4
EU773210.1	306212	1191.8	1286.3	5261.5	1362.5	2518.2	1402.2
EU772832.1	308307	4390.1	4629.7	1543.9	5258.4	4856.1	5799.1
EU458006.1	327808	3945.8	6127.2	3384.2	3574.5	6980.4	4439.4
EU451213.1	327675	4322.0	5436.7	1556.7	5301.9	2510.3	2508.9
EF454073.2	224826	27.2	34.8	55.2	54.9	80.4	30.7

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FJ678688.1 gg_id:509467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU468277.1 gg_id:294117 domesticated horse feces clone horsej_c02
EU509543.1 gg_id:272048 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60e08
EU622710.1 gg_id:278359 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
EF602807.1 gg_id:230994 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
EU468306.1 gg_id:289975 domesticated horse feces clone horsem_e06_1
GQ451226.1 gg_id:592773 Fecal Yunnan snub-nosed monkey feces clone J132
EU458596.1 gg_id:292888 European rabbit feces clone RA_a12_1
EU510699.1 gg_id:277228 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39e11
EU344213.1 gg_id:258933 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU344226.1 gg_id:268753 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
DQ327493.1 gg_id:147815 Metagenomic gut microbiome healthy human stool clone EA65
EU844171.1 gg_id:330603 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU381463.1 gg_id:261686 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid
EU474449.1 gg_id:299201 bighorn sheep feces clone BHSD_aaa02c08
DQ815474.1 gg_id:164242 mouse cecum clone aab41c04
FJ880592.1 gg_id:433422 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU469205.1 gg_id:301405 Speke's gazelle feces clone SP3_a12_1
DQ673520.1 gg_id:172035 rumen fluid clone GRC55
EF099878.1 gg_id:194478 mouse cecum clone SWPT5_aaa01f08
EU509449.1 gg_id:273706 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e09
EF097158.1 gg_id:173971 mouse cecum clone SWPT18_aaa02c05
GU174120.1 gg_id:543168 Microbial Bactrian camel estimated rumen clone XJC50
EU509440.1 gg_id:270062 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58d07
FJ880832.1 gg_id:455786 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EF099659.1 gg_id:184823 mouse cecum clone SWPT4_aaa02e08
EF025238.1 gg_id:182479 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_B31
EU779173.1 gg_id:305394 Trancaspian Urial feces clone TU2_aaa04c09
AY916365.1 gg_id:113336 human stool clone D330
FJ681328.1 gg_id:511240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU470398.1 gg_id:300619 Grevy's zebra feces clone GZ_aaa03g04
AF129861.1 gg_id:16034 anaerobic digestor clone BA18
EU457607.1 gg_id:349783 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78
EU472116.1 gg_id:295144 francois langur feces clone FL_1aaa01h04
EU469146.1 gg_id:299718 Speke's gazelle feces clone SP3_c02_1
EU506974.1 gg_id:275040 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09c01
AB189696.1 gg_id:113007 termite gut homogenate clone Tc-64
EU844447.1 gg_id:310518 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AF371933.1 gg_id:41628 swine intestine clone p-5013-2Wa5
EF099118.1 gg_id:179933 mouse cecum clone SWPT2_aaa02e09
AB486052.1 gg_id:579562 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC

FJ678688.1	509467	12820.4	9657.7	10644.7	11016.1	7540.1	7864.0
EU468277.1	294117	916.9	868.5	613.1	461.6	1656.5	267.2
EU509543.1	272048	3664.3	3374.1	3931.8	2822.3	4683.7	4417.4
EU622710.1	278359	815.8	717.1	1333.9	688.2	470.3	1168.4
EF602807.1	230994	1466.9	1719.3	1359.3	851.7	473.7	982.0
EU468306.1	289975	6147.6	6526.6	3632.4	5902.9	5821.7	6198.0
GQ451226.1	592773	12017.1	9405.7	6614.9	7669.6	7623.9	7453.3
EU458596.1	292888	1556.0	1474.0	1008.7	1466.1	743.8	1154.6
EU510699.1	277228	1298.8	2832.1	782.0	587.9	3824.7	2375.8
EU344213.1	258933	10180.0	9288.9	11871.5	10182.5	10013.0	8895.8
EU344226.1	268753	2312.8	3203.9	6177.8	2379.1	5246.6	4156.4
DQ327493.1	147815	2184.7	2364.2	1574.6	1258.4	1232.4	1053.2
EU844171.1	330603	1495.2	2486.7	1653.8	1184.7	4341.5	3507.3
EU381463.1	261686	403.0	179.3	535.4	179.1	1089.6	2538.4
EU474449.1	299201	1146.0	2579.8	2173.5	1814.9	1688.7	2947.0
DQ815474.1	164242	7302.7	7438.4	4450.6	5637.9	7365.2	7507.5
FJ880592.1	433422	3848.8	3555.7	1629.2	4463.1	5281.4	4412.7
EU469205.1	301405	6750.1	7457.9	8109.3	6993.0	1845.3	4713.4
DQ673520.1	172035	295.4	355.8	445.6	288.7	690.5	1306.6
EF099878.1	194478	6747.9	8788.8	1016.0	3031.2	1500.3	2102.3
EU509449.1	273706	5937.2	6933.2	7371.9	3274.3	3605.8	5505.3
EF097158.1	173971	47.5	50.5	109.5	60.8	60.1	27.6
GU174120.1	543168	4710.9	4431.9	3893.3	5467.2	4458.3	4494.9
EU509440.1	270062	2964.6	2350.2	996.3	1264.4	1122.5	1124.3
FJ880832.1	455786	1348.5	1657.6	1721.4	1153.8	1861.8	1220.2
EF099659.1	184823	1194.4	1806.1	1071.3	800.8	1995.9	1204.2
EF025238.1	182479	2153.7	1972.8	1825.0	1023.7	1487.6	1334.2
EU779173.1	305394	1219.3	1006.3	1206.7	1959.6	417.3	609.9
AY916365.1	113336	1658.6	2104.1	1863.6	1164.8	3615.9	6788.5
FJ681328.1	511240	14380.5	11923.9	7481.3	10130.8	10080.4	11555.7
EU470398.1	300619	1324.3	1620.1	2349.7	721.5	164.2	592.8
AF129861.1	16034	29.2	34.1	28.7	50.0	56.5	30.9
EU457607.1	349783	10482.0	10791.0	8956.3	10971.2	10528.9	9092.7
EU472116.1	295144	2381.2	3509.1	983.3	1336.2	859.0	2185.9
EU469146.1	299718	2394.7	3189.4	2339.2	2044.9	2506.1	2503.2
EU506974.1	275040	1541.6	1267.8	1356.0	1649.7	1130.9	1393.4
AB189696.1	113007	8598.8	8764.1	7803.8	8244.0	9158.6	10513.9
EU844447.1	310518	274.8	106.2	724.9	123.5	61.0	97.3
AF371933.1	41628	138.3	310.3	979.2	364.6	275.5	450.3
EF099118.1	179933	3401.4	4158.1	1083.1	1079.5	778.5	463.1
AB486052.1	579562	1461.2	2564.6	1218.1	1036.0	1955.2	1945.8

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EU452720.1 gg_id:344906 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU509869.1 gg_id:264539 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h01
EU509336.1 gg_id:259091 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48c05
EU471605.1 gg_id:301418 Asiatic elephant feces clone AE1_aaa03h12
DQ532267.1 gg_id:170620 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
EU465548.1 gg_id:298616 argali sheep feces clone AS1_aao37d10.Contig1
DQ014996.1 gg_id:133446 mouse cecum clone M1_1d03_1
EF603680.1 gg_id:234600 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU461342.1 gg_id:291171 red kangaroo feces clone KO2_aai18a02
EU358720.1 gg_id:326879 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EU463535.1 gg_id:298695 domesticated horse feces clone horsem_aai95f08
EU458633.1 gg_id:291920 European rabbit feces clone RA_c10_1
EU509225.1 gg_id:262672 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b05
FJ684123.1 gg_id:521615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB185802.1 gg_id:102301 rumen clone U29-G04
FJ680288.1 gg_id:525143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU776832.1 gg_id:336032 Mongoose lemur feces clone ML_aae88b01
EU779365.1 gg_id:329869 Somali Wild Ass feces clone WA_aaa03g09
AB486861.1 gg_id:578216 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
DQ794759.1 gg_id:186541 human fecal clone RL240_aaj32a06
AB185813.1 gg_id:107450 rumen clone U29-H08
EU506784.1 gg_id:271281 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56c02
FJ880114.1 gg_id:433722 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU844375.1 gg_id:340263 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ880118.1 gg_id:418903 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ365102.1 gg_id:364621 feces adult twins and mothers; TS1 clone TS1_a02h02
EF402847.1 gg_id:215231 human fecal clone SJTU_B_13_26
EU773239.1 gg_id:312805 BigHorn sheep feces clone BH1_aao26d11
DQ809188.1 gg_id:186037 human fecal clone RL308_aal83a11
EU511248.1 gg_id:258340 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak17a12
EF602935.1 gg_id:234474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ905668.1 gg_id:165979 human fecal clone 014C-E4
FJ881201.1 gg_id:379762 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU451818.1 gg_id:313324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
FJ679087.1 gg_id:512339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB192035.1 gg_id:143918 termite gut homogenate clone M2PB4-66
EU453946.1 gg_id:328060 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU462528.1 gg_id:300388 Sumatran orangutan feces clone orang1_aai56d11
FJ978658.1 gg_id:434584 feces clone CL_F_333
FJ681272.1 gg_id:525681 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ502526.1 gg_id:571808 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-

EU452720.1	344906	7046.7	5519.6	4160.4	3502.7	5914.8	8480.0
EU509869.1	264539	1568.5	1554.1	2040.0	1490.1	291.6	587.5
EU509336.1	259091	2169.5	1345.4	3751.2	1750.7	2651.5	5803.1
EU471605.1	301418	815.1	1453.7	2434.2	1126.9	1073.3	718.4
DQ532267.1	170620	212.3	336.3	562.0	144.5	100.3	239.7
EU465548.1	298616	2315.5	3010.0	3293.3	1058.6	768.1	1098.2
DQ014996.1	133446	29.4	28.0	74.7	59.8	40.7	21.0
EF603680.1	234600	3666.6	3513.1	3215.6	3910.4	2322.8	3440.6
EU461342.1	291171	2483.8	2851.9	2229.7	3536.0	8403.8	7005.0
EU358720.1	326879	802.4	2737.0	2416.0	342.2	104.5	88.4
EU463535.1	298695	2221.4	2295.0	2463.0	1645.1	1620.3	2457.0
EU458633.1	291920	525.9	651.0	647.0	892.7	2307.9	1749.3
EU509225.1	262672	974.3	1161.4	1788.1	609.8	890.7	2572.1
FJ684123.1	521615	3073.4	2600.1	3149.1	2235.9	1679.6	1944.8
AB185802.1	102301	4407.6	2893.4	2684.8	5274.8	5222.9	4320.2
FJ680288.1	525143	15010.4	15733.9	8976.5	13518.2	16057.9	13772.2
EU776832.1	336032	4772.8	5313.1	2007.1	3405.0	4862.0	3482.3
EU779365.1	329869	84.4	97.2	752.5	142.1	71.8	59.7
AB486861.1	578216	1909.0	1624.3	3322.9	1461.5	1758.8	2801.6
DQ794759.1	186541	3284.4	3693.3	1268.2	3043.6	2248.0	1743.5
AB185813.1	107450	8553.2	11307.4	8302.2	9159.2	13511.2	11698.6
EU506784.1	271281	6630.0	8732.6	6225.6	4895.5	9286.4	7942.3
FJ880114.1	433722	3556.5	3205.8	8992.3	3840.3	2246.5	2445.1
EU844375.1	340263	4105.7	4311.5	3646.2	3502.9	3879.3	6782.5
FJ880118.1	418903	208.4	250.5	700.1	157.1	85.2	143.2
FJ365102.1	364621	9702.3	9773.8	7152.5	9481.4	15793.4	12206.9
EF402847.1	215231	27.9	37.9	52.5	71.3	73.3	28.0
EU773239.1	312805	11935.4	12913.1	5108.7	8131.1	7914.8	9066.0
DQ809188.1	186037	76.2	116.6	182.3	131.7	104.7	86.6
EU511248.1	258340	1916.6	3284.1	6459.3	1974.7	3264.5	7156.4
EF602935.1	234474	414.9	464.3	495.8	606.5	521.9	184.5
DQ905668.1	165979	15.6	22.6	13.2	42.0	47.6	8.8
FJ881201.1	379762	1713.6	2008.9	858.9	862.2	3319.5	1997.8
EU451818.1	313324	621.2	1318.2	423.2	400.6	174.1	206.2
FJ679087.1	512339	4851.7	6787.4	3115.6	3940.3	5884.1	8065.0
AB192035.1	143918	404.9	692.2	782.3	796.4	592.3	1725.3
EU453946.1	328060	8257.4	9856.7	4539.2	5664.5	5522.5	8462.1
EU462528.1	300388	3146.4	2780.2	3019.7	3258.9	3222.7	4351.0
FJ978658.1	434584	7431.0	10549.6	6892.8	7784.1	11805.1	13703.7
FJ681272.1	525681	2498.5	4823.5	6862.5	5440.4	5498.3	7790.6
GQ502526.1	571808	1361.5	1129.2	1581.2	1451.4	278.6	456.8

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DQ805638.1 gg_id:180108 human fecal clone RL306aal89c06
EU463410.1 gg_id:296065 domesticated horse feces clone horsem_aai93d03
EU775729.1 gg_id:326022 Horse feces clone horsem_aai93b08
GQ491853.1 gg_id:577408 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
AF376229.1 gg_id:46657 ckncm325-B3-50 clone
AY992419.1 gg_id:133769 mouse cecum clone C23_c21
EF097039.1 gg_id:197925 mouse cecum clone SWPT13_aaa04e08
AF371792.1 gg_id:25957 swine intestine clone p-2479-18B5
EU773132.1 gg_id:340732 BigHorn sheep feces clone BH1_aao27g09
EU506308.1 gg_id:261877 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63a07
EF098273.1 gg_id:195904 mouse cecum clone SWPT14_aaa04a05
EU885034.1 gg_id:339994 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2C1
EU462489.1 gg_id:289958 Sumatran orangutan feces clone orang1_aai55f11
FJ880091.1 gg_id:407216 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
AB307642.1 gg_id:272210 clay wall used Japanese traditional buildings clone R70
DQ799877.1 gg_id:193310 human fecal clone RL247_aaj21c06
EU507770.1 gg_id:268725 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04e05
DQ057415.1 gg_id:131039 chicken ileum/cecum clone oc30
EU453106.1 gg_id:304019 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
AB192010.1 gg_id:144056 termite gut homogenate clone M2PT2-13
GQ448400.1 gg_id:571165 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr
FJ368251.1 gg_id:358150 feces adult twins and mothers; TS3 clone TS3_a02a08
AM176887.1 gg_id:161109 Recovery mangrove sediment clone SZB63
EU885033.1 gg_id:315891 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2B3
EU775785.1 gg_id:348949 Horse feces clone horsem_aai93g06
GQ451286.1 gg_id:594119 Fecal Yunnan snub-nosed monkey feces clone J287
EU507013.1 gg_id:273022 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09g09
EU779486.1 gg_id:338681 Grevy's Zebra feces clone GZ_aaa04a02
GQ448458.1 gg_id:565308 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g
EU508142.1 gg_id:271619 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01d04
GU304152.1 gg_id:580305 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
AF371785.1 gg_id:38344 swine intestine clone p-397-o3
DQ805454.1 gg_id:178841 human fecal clone RL203_aai62h05
DQ793317.1 gg_id:193865 human fecal clone RL199_aaj42b08
EU465624.1 gg_id:293285 argali sheep feces clone AS1_aao40a12.Contig1
EF098326.1 gg_id:195497 mouse cecum clone SWPT14_aaa04g10
EU509792.1 gg_id:266715 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b03
EU842787.1 gg_id:308413 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU871413.1 gg_id:321628 Genetic Bovine (Bos taurus) Rumen Thailand clone CF386
FJ880997.1 gg_id:373909 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EF434371.1 gg_id:209327 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont

DQ805638.1	180108	21.4	28.3	16.6	43.9	62.1	18.8
EU463410.1	296065	1260.5	1336.4	1114.3	349.9	491.1	275.2
EU775729.1	326022	639.4	1110.1	1244.1	1681.1	1371.6	1803.0
GQ491853.1	577408	379.6	632.2	532.7	416.9	114.2	312.7
AF376229.1	46657	1743.0	1607.8	2847.9	1750.2	1227.8	1098.5
AY992419.1	133769	6065.5	7028.5	5153.8	5969.2	3748.2	4681.5
EF097039.1	197925	2268.2	3016.0	830.0	4552.8	2417.1	4308.4
AF371792.1	25957	36.3	68.9	147.1	49.8	273.5	195.0
EU773132.1	340732	2577.6	1705.0	3495.3	1988.4	3474.1	5398.5
EU506308.1	261877	519.8	1079.6	3556.9	873.0	731.8	2066.6
EF098273.1	195904	1810.4	1080.1	3738.5	1187.1	2221.6	5803.1
EU885034.1	339994	971.8	1173.6	1463.6	275.4	1494.9	469.4
EU462489.1	289958	5772.2	5877.2	3981.1	4992.6	3497.7	5522.8
FJ880091.1	407216	4237.3	3790.4	3544.8	2199.8	514.6	2152.6
AB307642.1	272210	1921.0	1214.3	4709.5	1024.8	2794.4	3520.0
DQ799877.1	193310	713.0	614.8	654.0	565.7	302.6	428.1
EU507770.1	268725	5726.7	8233.6	4649.0	7514.2	10092.9	9162.8
DQ057415.1	131039	33.6	30.6	47.2	163.6	101.3	136.5
EU453106.1	304019	1263.8	2272.1	7581.4	2187.3	3110.6	3859.6
AB192010.1	144056	125.9	193.0	1057.9	296.7	933.1	933.7
GQ448400.1	571165	5222.1	4208.0	5001.0	3196.8	2569.7	4002.4
FJ368251.1	358150	4964.3	4601.2	2241.9	3581.7	2492.6	2958.9
AM176887.1	161109	19.2	18.9	26.8	49.0	46.5	26.7
EU885033.1	315891	604.3	1020.9	1846.9	243.7	351.2	270.5
EU775785.1	348949	4154.1	6893.3	7523.9	5843.7	5997.5	4632.3
GQ451286.1	594119	481.8	807.4	1463.6	251.2	127.5	196.5
EU507013.1	273022	6572.3	6775.6	5021.1	4193.6	2908.1	2701.5
EU779486.1	338681	2098.1	3964.1	1228.6	1746.4	1406.7	762.8
GQ448458.1	565308	159.9	180.3	427.6	201.0	131.3	162.2
EU508142.1	271619	1851.8	2351.6	589.1	3594.7	5272.8	3259.1
GU304152.1	580305	2780.5	3029.0	1475.4	2108.4	2839.3	3609.4
AF371785.1	38344	4626.3	5616.2	4440.2	3690.8	5638.9	6921.3
DQ805454.1	178841	562.3	347.2	1401.3	483.6	97.6	244.4
DQ793317.1	193865	1002.0	1395.9	259.9	1696.6	637.2	511.5
EU465624.1	293285	646.0	1140.1	1159.2	1246.0	522.8	194.5
EF098326.1	195497	480.3	340.8	315.9	368.6	112.4	87.5
EU509792.1	266715	388.4	340.6	698.1	649.4	114.1	160.6
EU842787.1	308413	1194.9	1020.0	1066.1	172.2	173.7	323.7
EU871413.1	321628	3035.8	4905.4	5757.6	3143.6	7407.2	9017.0
FJ880997.1	373909	190.8	242.2	850.7	151.3	849.4	1904.7
EF434371.1	209327	87.4	83.8	246.5	89.0	93.0	85.8

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FJ881346.1 gg_id:454021 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU461799.1 gg_id:287883 white-faced saki feces clone Saki_aaj61c06
EU457236.1 gg_id:326950 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
FJ366005.1 gg_id:369544 feces adult twins and mothers; TS25 clone TS25_a01f04
GQ502525.1 gg_id:578230 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
EU771554.1 gg_id:350467 Hamadryas Baboon feces clone AFBAB_aai02d07
EU506866.1 gg_id:276749 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07e05
EF603969.1 gg_id:231028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU777238.1 gg_id:317218 Okapi feces clone OK3_b10
EU771370.1 gg_id:345938 Asiatic elephant feces clone AE2_aaa01h05
EU509664.1 gg_id:276522 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak46g10
EU842226.1 gg_id:335384 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
DQ327001.1 gg_id:148379 Metagenomic gut microbiome healthy human stool clone E502
EU794177.1 gg_id:313908 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A02
EU466381.1 gg_id:302069 bighorn sheep feces clone BH2_aao22g11
EU464525.1 gg_id:301028 African elephant feces clone AFEL_aai30e12
FJ393118.1 gg_id:358001 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel
EF604700.1 gg_id:234202 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU764407.1 gg_id:322133 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
EU469147.1 gg_id:292438 Speke's gazelle feces clone SP3_c03_1
EU509134.1 gg_id:276902 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44e04
FJ880490.1 gg_id:436835 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ681177.1 gg_id:516395 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ815618.1 gg_id:170926 mouse cecum clone aab43f05
AB234447.1 gg_id:148791 termite gut homogenate clone MgMjD-018
AY212772.1 gg_id:101572 equine manure clone wet70
EU843894.1 gg_id:331387 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EF445187.1 gg_id:216140 rabbit cecum clone NED3D6
AY976153.1 gg_id:117430 human ascending colon mucosal biopsy clone LV48
FJ365228.1 gg_id:367866 feces adult twins and mothers; TS1 clone TS1_a04d04
EU777385.1 gg_id:348651 Sumatran orangutan feces clone orang1_aai53h04
AY916184.1 gg_id:113111 human ascending colon biopsy clone LV67
EU458679.1 gg_id:295715 European rabbit feces clone RA_h01_3
EU842293.1 gg_id:309123 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU467441.1 gg_id:295906 Sumatran orangutan feces clone orang1_c01
EU470041.1 gg_id:294340 trancaspain urial feces clone TU1_aaa02a08
FJ879644.1 gg_id:422337 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
DQ326566.1 gg_id:148532 Metagenomic gut microbiome healthy human stool clone C748
EU506557.1 gg_id:265758 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04b04
EU842386.1 gg_id:321135 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
FJ678622.1 gg_id:528111 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

FJ881346.1	454021	68.3	72.9	264.9	88.9	97.3	58.2
EU461799.1	287883	1081.8	779.7	882.3	418.8	868.1	409.4
EU457236.1	326950	7816.0	8418.8	4359.5	6554.8	4602.3	3667.3
FJ366005.1	369544	401.5	500.7	1344.9	393.7	235.2	593.5
GQ502525.1	578230	2784.6	3145.2	4308.8	5044.1	3905.9	8296.3
EU771554.1	350467	4935.1	4283.3	4427.2	4030.5	1879.6	3545.0
EU506866.1	276749	12313.0	9633.2	5560.5	8464.9	7636.9	8105.4
EF603969.1	231028	2397.9	2938.6	1101.3	1552.4	580.8	488.1
EU777238.1	317218	487.8	1375.3	2236.2	851.4	336.0	687.0
EU771370.1	345938	93.3	508.0	331.7	119.3	178.5	242.3
EU509664.1	276522	3620.8	4566.1	2106.1	3535.8	5630.9	4586.1
EU842226.1	335384	30.9	32.6	196.0	100.4	76.4	41.4
DQ327001.1	148379	5494.0	4449.0	2719.8	4181.1	5481.1	5442.2
EU794177.1	313908	1101.3	763.2	2396.9	661.7	293.5	438.1
EU466381.1	302069	1130.4	1399.5	1177.4	1043.0	667.8	458.5
EU464525.1	301028	962.4	1002.5	745.6	904.0	769.4	1312.8
FJ393118.1	358001	1737.8	2121.5	2859.1	1472.5	2636.8	3174.5
EF604700.1	234202	10749.6	9283.9	6935.1	7974.8	10296.7	7783.1
EU764407.1	322133	5375.9	6755.9	835.9	1866.5	3233.5	2318.5
EU469147.1	292438	2842.7	3266.0	3054.9	1586.4	2145.4	1499.7
EU509134.1	276902	2875.3	3436.6	1454.4	2038.4	923.9	982.3
FJ880490.1	436835	2309.5	2330.1	1105.9	3262.6	2528.7	2582.2
FJ681177.1	516395	28.3	31.5	74.6	57.5	89.2	44.6
DQ815618.1	170926	1259.5	1016.6	2421.6	739.1	679.2	781.6
AB234447.1	148791	4636.9	4587.3	5064.8	3846.5	5128.8	4471.1
AY212772.1	101572	2703.0	2953.7	1833.3	3126.9	3734.4	2089.3
EU843894.1	331387	1069.1	855.1	2546.1	440.0	828.6	791.4
EF445187.1	216140	36.0	47.2	48.1	63.6	73.6	34.0
AY976153.1	117430	16.7	19.4	13.8	42.5	43.2	20.8
FJ365228.1	367866	6658.2	8164.2	4049.6	8745.1	10402.8	7948.6
EU777385.1	348651	982.5	1146.4	3143.7	1408.4	2027.1	1351.7
AY916184.1	113111	55.9	58.8	214.6	582.3	86.7	54.9
EU458679.1	295715	507.5	681.9	337.2	662.5	829.0	1096.9
EU842293.1	309123	1292.6	900.5	4187.9	1215.4	825.3	1048.9
EU467441.1	295906	860.2	1225.9	2083.6	950.5	2223.2	1917.1
EU470041.1	294340	7583.1	8968.5	7630.5	5576.1	11990.4	12680.9
FJ879644.1	422337	2629.4	5873.2	1874.9	1778.2	4042.9	2960.8
DQ326566.1	148532	24.0	72.6	410.8	250.0	59.3	45.5
EU506557.1	265758	5902.4	3894.5	8978.9	6737.4	5178.8	6366.7
EU842386.1	321135	3747.7	3758.5	4122.1	3548.4	4870.4	2717.6
FJ678622.1	528111	7747.3	6907.9	1715.9	5460.9	3099.8	3344.0

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FJ680717.1 gg_id:529561 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473436.1 gg_id:294626 Somali wild ass feces clone WA_aaa01c10
AY975617.1 gg_id:115444 human ascending colon mucosal biopsy clone NB69
GU304498.1 gg_id:543553 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EF399731.1 gg_id:209830 human fecal clone SJTU_E_02_68
EU505664.1 gg_id:276996 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04d06
DQ801199.1 gg_id:178252 human fecal clone RL116_aaf00g02
FJ880144.1 gg_id:424613 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU777857.1 gg_id:355155 European rabbit feces clone RA_b07
FJ880076.1 gg_id:422278 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EF097727.1 gg_id:190646 mouse cecum clone SWPT20_aaa02g10
EU473597.1 gg_id:288349 Somali wild ass feces clone WA_aaa02g11
EU774656.1 gg_id:351422 Angola Colobus feces clone EAC_2_aaa04h09
FJ879462.1 gg_id:382733 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU458617.1 gg_id:293735 European rabbit feces clone RA_f11
EU506600.1 gg_id:270508 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53b03
DQ793945.1 gg_id:186640 human fecal clone RL176_aah45f04
EF097537.1 gg_id:198821 mouse cecum clone SWPT19_aaa04a09
EU778171.1 gg_id:353173 feces clone RL388_aao93e04
AB198472.1 gg_id:135737 termite gut wall fraction clone RsW01-038
DQ815459.1 gg_id:171864 mouse cecum clone aab48g10
EU506211.1 gg_id:260799 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03h12
EU509851.1 gg_id:275622 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e03
FJ366802.1 gg_id:369416 feces adult twins and mothers; TS27 clone TS27_a04a08
EU773296.1 gg_id:338000 BigHorn sheep feces clone BHSD_aaa03c07
EU463669.1 gg_id:287931 domesticated horse feces clone horsej_aai90g05
EU773231.1 gg_id:314186 BigHorn sheep feces clone BH1_aao25h07
EU475075.1 gg_id:287835 visayam warty pig feces clone VWP_aaa03h03
FJ367779.1 gg_id:363229 feces adult twins and mothers; TS2 clone TS2_a03e05
EU471638.1 gg_id:300851 Asiatic elephant feces clone AE1_aaa02g01
GQ079310.1 gg_id:386396 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c(
EU507314.1 gg_id:258637 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01e06
EU474530.1 gg_id:291888 bighorn sheep feces clone BHSD_aaa02b07
EU506880.1 gg_id:274508 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07g01
EU777156.1 gg_id:326925 Okapi feces clone OK2_f08_3
AB034042.1 gg_id:17907 rumen clone 5C0d-9
AF371791.1 gg_id:16559 swine intestine clone p-1617-c5
EF096046.1 gg_id:178180 mouse cecum clone lean2_aaa02g07
EU457632.1 gg_id:334251 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
EU009861.1 gg_id:240271 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Z48
FJ365000.1 gg_id:358904 feces adult twins and mothers; TS1 clone TS1_a01f08

FJ680717.1	529561	9868.0	10210.3	8043.2	8524.2	10777.9	9151.2
EU473436.1	294626	11137.0	9759.6	3609.3	7216.1	8670.9	8687.9
AY975617.1	115444	24.0	46.5	18.1	45.6	50.0	12.0
GU304498.1	543553	114.0	45.6	514.6	233.9	271.0	182.4
EF399731.1	209830	6364.5	6393.6	1751.0	8243.3	9660.9	8786.2
EU505664.1	276996	237.8	194.1	616.4	205.8	119.0	91.7
DQ801199.1	178252	1502.9	987.4	1333.9	1318.5	2498.4	1008.2
FJ880144.1	424613	2980.9	4406.8	2217.0	3603.5	3682.0	4113.8
EU777857.1	355155	5697.7	8193.5	5267.7	4524.5	9580.9	6897.2
FJ880076.1	422278	1551.6	1001.0	1029.6	1109.6	397.0	590.9
EF097727.1	190646	9768.5	11195.5	4330.6	9837.2	8713.6	9373.9
EU473597.1	288349	1293.8	1667.6	2558.2	821.5	671.3	1001.1
EU774656.1	351422	1612.6	2039.2	2650.9	1714.7	846.4	1202.6
FJ879462.1	382733	187.1	452.7	335.2	126.1	135.4	79.1
EU458617.1	293735	6656.8	5730.3	5698.6	6377.3	5832.8	6620.9
EU506600.1	270508	3846.0	2266.9	2212.5	4642.4	1840.8	2420.1
DQ793945.1	186640	3079.9	2529.5	2416.8	2991.1	2191.2	1882.2
EF097537.1	198821	3651.2	4694.8	3581.9	5156.2	9038.5	7188.9
EU778171.1	353173	112.3	72.5	200.0	155.4	115.3	184.7
AB198472.1	135737	34.0	47.2	40.4	63.0	59.9	30.1
DQ815459.1	171864	5679.7	8640.3	3100.3	5033.2	6617.4	4314.3
EU506211.1	260799	60.3	104.6	330.2	203.5	120.5	38.7
EU509851.1	275622	33.1	63.3	151.9	52.2	103.0	38.9
FJ366802.1	369416	1588.4	1853.5	1312.8	2102.1	1937.8	3067.1
EU773296.1	338000	3308.4	4917.6	6765.1	3166.5	1997.9	3828.0
EU463669.1	287931	5098.9	5794.5	3426.1	3214.5	393.6	1155.3
EU773231.1	314186	3649.1	2076.4	3452.5	4962.7	1657.1	3168.5
EU475075.1	287835	5340.7	6255.4	7911.5	6288.4	8345.5	6076.7
FJ367779.1	363229	2285.6	2223.7	2455.4	1363.2	2043.9	1502.9
EU471638.1	300851	1810.2	1774.7	2245.5	2487.9	479.3	1112.2
GQ079310.1	386396	8381.5	9330.3	9725.0	6527.7	8814.0	8341.1
EU507314.1	258637	4573.0	4137.7	2758.6	2953.5	3597.6	3031.1
EU474530.1	291888	9354.5	8294.9	9947.3	9762.8	7939.2	9119.1
EU506880.1	274508	5675.2	6626.7	6493.7	7098.1	7742.9	8321.6
EU777156.1	326925	189.5	478.2	1699.6	210.4	134.3	300.4
AB034042.1	17907	2649.9	3843.4	1601.6	1711.0	2493.3	2694.0
AF371791.1	16559	1831.2	1306.0	948.0	2596.9	259.9	382.8
EF096046.1	178180	13323.6	15853.6	4159.9	9738.7	10591.4	9768.4
EU457632.1	334251	5796.7	4822.9	3213.4	4201.1	2196.5	4156.6
EU009861.1	240271	114.5	211.7	452.5	157.6	196.2	322.1
FJ365000.1	358904	1376.1	982.3	748.2	561.1	181.8	348.9

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DQ824307.1 gg_id:174984 human fecal clone RL304_aal74c04
EU468603.1 gg_id:290441 okapi feces clone OK1_h02_2
EU474862.1 gg_id:299736 takin feces clone TAK_aaa03a09
EU774668.1 gg_id:351100 Angola Colobus feces clone EAC_2_aaa03g09
EF603972.1 gg_id:232943 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
EU506398.1 gg_id:270870 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01b10
FJ879124.1 gg_id:378376 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU465599.1 gg_id:295748 argali sheep feces clone AS1_aao39a12.Contig1
FJ681681.1 gg_id:531339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU777625.1 gg_id:329861 Sumatran orangutan feces clone orang1_aai56c01
FJ677944.1 gg_id:520833 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU622764.1 gg_id:278667 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
EF404912.1 gg_id:208751 human fecal clone SJTU_G_08_79
EU458619.1 gg_id:291348 European rabbit feces clone RA_g05_1
EU775085.1 gg_id:353620 Francois Langur feces clone FL_1aaa01f09
EU774718.1 gg_id:324219 Angola Colobus feces clone EAC_2_aaa04f11
EU777117.1 gg_id:338991 Okapi feces clone OK1_b05_2
DQ800867.1 gg_id:178242 human fecal clone RL183_aao04e06
FJ366788.1 gg_id:362813 feces adult twins and mothers; TS27 clone TS27_a03h03
EU777072.1 gg_id:336005 Okapi feces clone OK3_g10_1
EU779162.1 gg_id:315683 Trancaspian Urial feces clone TU2_aaa01f06
FJ880155.1 gg_id:400545 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EF614841.1 gg_id:234630 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o
EU459641.1 gg_id:293767 ring-tailed lemur feces clone RT_aai09g11
FJ879015.1 gg_id:427159 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU463652.1 gg_id:296591 domesticated horse feces clone horsej_aai90d12
EU763460.1 gg_id:327692 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4
DQ777916.1 gg_id:171499 rat feces clone R-1268
FJ833370.1 gg_id:578399 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q301_90B12
EU458608.1 gg_id:295662 European rabbit feces clone RA_d09
EU344276.1 gg_id:277185 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
EU470451.1 gg_id:302165 Grevy's zebra feces clone GZ_aaa02d10
EU468576.1 gg_id:302061 okapi feces clone OK1_c08_3
EU509562.1 gg_id:275576 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60h04
EU466209.1 gg_id:300969 bighorn sheep feces clone BH1_aao28a09
FJ880004.1 gg_id:412229 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU457289.1 gg_id:342402 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N
GQ448399.1 gg_id:511180 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr
EU622765.1 gg_id:278758 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
EU531935.1 gg_id:265234 Predominant role host genetics controlling gut microbiota FMF remission stool clone
EU465629.1 gg_id:288944 argali sheep feces clone AS1_aao40b11.Contig1

DQ824307.1	174984	203.0	146.6	1038.7	173.1	119.9	153.9
EU468603.1	290441	13740.5	15711.5	10998.6	9744.0	13496.7	14398.4
EU474862.1	299736	6357.9	6339.6	4697.2	4724.3	3018.5	3168.4
EU774668.1	351100	656.3	680.4	2326.9	502.9	326.3	542.8
EF603972.1	232943	247.1	201.5	559.1	210.0	123.7	246.7
EU506398.1	270870	13949.9	11483.3	11123.3	11038.7	8616.9	9820.7
FJ879124.1	378376	1673.0	1130.9	3025.5	1296.2	897.7	938.9
EU465599.1	295748	1186.1	766.9	2545.8	432.1	307.9	631.7
FJ681681.1	531339	923.0	1740.3	3454.0	515.7	1195.0	1786.0
EU777625.1	329861	718.7	816.2	322.3	552.3	1166.5	1068.7
FJ677944.1	520833	3768.9	2480.9	2504.2	3413.8	1760.9	2341.8
EU622764.1	278667	4549.1	5790.0	2457.4	1663.0	957.9	1428.5
EF404912.1	208751	5138.8	5746.3	6826.4	4902.3	9462.0	8463.6
EU458619.1	291348	2949.7	3583.7	2248.0	2353.6	2118.7	2375.4
EU775085.1	353620	1220.8	1139.0	1963.1	582.9	700.3	476.7
EU774718.1	324219	137.2	96.1	641.6	168.0	162.7	261.3
EU777117.1	338991	576.8	697.0	3363.4	363.6	305.3	1196.1
DQ800867.1	178242	16871.3	15545.2	9103.2	11568.2	14949.9	13983.5
FJ366788.1	362813	956.5	1951.4	1351.1	1272.3	498.0	868.1
EU777072.1	336005	775.0	1033.3	1037.7	1667.6	281.7	348.6
EU779162.1	315683	4486.5	5648.6	4253.9	3937.4	4021.3	4512.4
FJ880155.1	400545	1769.6	2636.8	5336.0	1968.0	2562.0	2818.2
EF614841.1	234630	11076.9	12170.9	8323.1	8422.7	8535.3	8261.1
EU459641.1	293767	1258.4	1090.0	2301.0	609.7	2309.5	3741.0
FJ879015.1	427159	4250.7	4985.9	3346.7	3660.5	5958.6	6621.8
EU463652.1	296591	4512.1	4571.5	1778.2	1760.4	1406.2	1924.3
EU763460.1	327692	3761.3	6257.9	1657.9	2564.2	998.4	1882.5
DQ777916.1	171499	83.2	143.0	602.9	96.4	73.4	25.2
FJ833370.1	578399	6338.1	3948.4	5016.6	4740.6	1883.1	2476.8
EU458608.1	295662	382.3	632.2	733.3	353.5	164.6	404.4
EU344276.1	277185	4609.7	5046.8	2930.3	2970.3	1494.7	2673.0
EU470451.1	302165	3688.8	3751.7	2707.9	4967.3	5715.4	6260.7
EU468576.1	302061	309.7	373.6	1132.7	1685.8	432.9	314.3
EU509562.1	275576	5793.0	7630.0	6723.2	5502.5	5619.5	6138.3
EU466209.1	300969	4803.0	4423.7	2490.4	571.7	2115.6	3263.5
FJ880004.1	412229	2080.7	3111.0	5762.1	2753.3	3901.1	4439.7
EU457289.1	342402	145.9	131.1	54.5	552.4	51.8	43.0
GQ448399.1	511180	8655.5	6352.5	5262.5	7057.0	6534.9	8106.1
EU622765.1	278758	4640.3	4231.3	1673.6	1408.2	2200.4	1313.6
EU531935.1	265234	1527.3	1802.4	2198.3	795.9	1537.3	1693.4
EU465629.1	288944	2103.4	4137.6	1947.2	1248.3	3387.4	2351.0

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FJ879588.1 gg_id:414089 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU843150.1 gg_id:310031 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
DQ815858.1 gg_id:166226 mouse cecum clone aab23c10
EU844883.1 gg_id:317405 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU772004.1 gg_id:323702 Argali sheep feces clone AS2_aao36g03
DQ243771.1 gg_id:143396 Archaeal and Geochemically Hot Springs Yellowstone National Park USA Obsidian Pc
EU469210.1 gg_id:292548 Speke's gazelle feces clone SP3_b05_2
EU458577.1 gg_id:297073 European rabbit feces clone RA_b02
AB299543.1 gg_id:255350 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G
FJ880460.1 gg_id:466851 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU777400.1 gg_id:332376 Sumatran orangutan feces clone orang1_aai53d06
EU470077.1 gg_id:294748 trancaspain urial feces clone TU1_aaa02a09
EU779460.1 gg_id:322194 Grevy's Zebra feces clone GZ_aaa04c04
DQ795724.1 gg_id:183479 human fecal clone RL245_aai81c09
EU511442.1 gg_id:269418 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20d04
EF096031.1 gg_id:183985 mouse cecum clone lean2_aaa02d05
EU771896.1 gg_id:317870 Southern three-banded armadillo feces clone arma_a03
GQ867355.1 gg_id:591284 and prevalence blaTEM genes Arctic seals colon content clone WSp112
EF096279.1 gg_id:185967 mouse cecum clone obob1_aaa04a07
EU471906.1 gg_id:300186 Asiatic elephant feces clone AE3_aaa02c07
EU471573.1 gg_id:298751 Asiatic elephant feces clone AE1_aaa03b09
EU747962.1 gg_id:303763 neotropical folivorous flying bird adult hoatzin crop clone hoa11_26B04
EU504516.1 gg_id:260720 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01f12
EU511746.1 gg_id:265963 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf08d08
FJ833392.1 gg_id:580128 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_40H05
FJ679065.1 gg_id:520809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AF371805.1 gg_id:51722 swine intestine clone p-1877-s962-3
EU774701.1 gg_id:347085 Angola Colobus feces clone EAC_2_aaa02e10
DQ394593.1 gg_id:155059 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o
EF400162.1 gg_id:216310 human fecal clone SJTU_E_09_66
DQ015070.1 gg_id:132441 mouse cecum clone M2_f11
AY991978.1 gg_id:132424 mouse cecum clone C20_n22
EU776363.1 gg_id:335362 Red Kangaroo feces clone KO1_aai43b06
EF605058.1 gg_id:231459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
EU505144.1 gg_id:273462 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03e05
FJ881001.1 gg_id:468255 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
FJ680493.1 gg_id:531808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU473598.1 gg_id:290698 Somali wild ass feces clone WA_aaa02h04
EF454508.2 gg_id:224436 termite hindgut clone 290cost002-P3L-2244
GU174135.1 gg_id:539506 Microbial Bactrian camel estimated rumen clone XJC128
EU747942.1 gg_id:328823 neotropical folivorous flying bird adult hoatzin crop clone hoa13_91C12

FJ879588.1	414089	1173.3	646.2	1269.4	1946.1	154.3	341.9
EU843150.1	310031	3985.3	2779.0	1814.0	982.0	688.7	1246.7
DQ815858.1	166226	450.3	389.3	94.2	268.8	84.8	50.7
EU844883.1	317405	160.8	201.7	743.1	209.7	378.6	292.1
EU772004.1	323702	3349.6	5814.0	2492.5	5117.9	5685.6	6143.2
DQ243771.1	143396	39.9	57.1	117.3	59.5	53.2	39.6
EU469210.1	292548	189.6	385.6	1810.3	548.7	326.5	1204.8
EU458577.1	297073	5758.9	5986.2	1922.1	4440.8	2488.2	5329.7
AB299543.1	255350	329.0	728.5	1364.5	740.1	96.5	178.5
FJ880460.1	466851	44.0	39.3	82.7	61.1	112.7	27.8
EU777400.1	332376	3907.6	4937.1	1725.3	2423.9	1306.4	2009.2
EU470077.1	294748	1685.1	1434.3	2870.0	1486.3	1123.2	1875.7
EU779460.1	322194	4031.7	3971.7	3924.5	5822.4	4381.6	4340.7
DQ795724.1	183479	252.4	297.0	432.2	102.6	86.3	126.9
EU511442.1	269418	1207.8	856.1	1300.5	785.7	92.6	369.5
EF096031.1	183985	82.4	182.2	125.5	114.4	107.2	110.4
EU771896.1	317870	3446.7	4159.1	1167.8	1986.8	1671.2	1487.6
GQ867355.1	591284	2325.0	1821.2	4773.0	1730.8	2079.1	4089.1
EF096279.1	185967	4620.1	5078.4	2470.3	4148.5	6231.3	5387.2
EU471906.1	300186	7637.5	8075.2	4354.0	7301.3	7375.1	6778.8
EU471573.1	298751	6001.1	6617.0	4155.4	4541.5	5574.1	6638.7
EU747962.1	303763	724.9	759.4	1870.1	645.0	2927.2	5051.5
EU504516.1	260720	1510.5	1444.3	1876.1	2354.3	392.7	814.5
EU511746.1	265963	5009.0	3623.4	2560.8	2446.5	1351.1	2105.3
FJ833392.1	580128	1049.3	1279.3	3117.4	710.8	472.1	761.5
FJ679065.1	520809	4871.2	4672.7	3026.9	4228.5	3575.5	4575.3
AF371805.1	51722	394.4	376.0	660.8	360.3	716.5	647.6
EU774701.1	347085	2700.3	1930.0	2588.3	1847.3	1026.9	1782.5
DQ394593.1	155059	839.4	738.8	559.0	1046.9	267.7	318.3
EF400162.1	216310	1772.3	771.9	1207.9	1309.1	239.3	451.8
DQ015070.1	132441	236.9	290.8	1085.9	275.9	240.1	367.5
AY991978.1	132424	171.2	444.1	819.2	653.9	817.3	1187.2
EU776363.1	335362	3071.5	3188.2	1566.8	2945.6	6073.9	5896.6
EF605058.1	231459	1558.3	1928.4	3546.6	1283.6	2884.3	1758.6
EU505144.1	273462	3039.2	3260.7	1902.4	2982.4	2542.3	4094.9
FJ881001.1	468255	858.5	649.9	2298.4	672.4	142.9	294.6
FJ680493.1	531808	8208.2	8846.3	5357.4	8825.9	12908.2	10675.3
EU473598.1	290698	572.0	1584.6	1773.8	1012.7	649.3	1267.3
EF454508.2	224436	25.0	31.3	31.9	28.1	75.1	30.2
GU174135.1	539506	197.9	54.2	53.7	75.3	79.3	87.3
EU747942.1	328823	387.6	153.5	610.7	149.1	124.3	331.5

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EU465621.1 gg_id:301410 argali sheep feces clone AS1_aao40a08.Contig1
EU622694.1 gg_id:278901 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
EU506877.1 gg_id:276273 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07f08
AB270051.1 gg_id:166168 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos
FJ879323.1 gg_id:408513 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EF096450.1 gg_id:189527 mouse cecum clone obob2_aaa03a07
EU779309.1 gg_id:309070 Visayam Warty Pig feces clone VWP_aaa02g07
EU775150.1 gg_id:314421 Francois Langur feces clone FL_1aaa02a01
EF603178.1 gg_id:228975 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU772202.1 gg_id:329529 Argali sheep feces clone AS1_aao39g01.Contig1
EF644508.1 gg_id:253716 Structure and performance microbial involved reductive dechlorination 1122-tetrach
DQ805484.1 gg_id:181448 human fecal clone RL203_aai63c05
GU120121.1 gg_id:538805 Real time ruminal microbial sheep fed hay or corn:hay mix adherent fraction rumen
EU460085.1 gg_id:296424 mammals their gut microbes eastern black and white colobus feces clone COL_aai14
EU454100.1 gg_id:309302 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
FJ881171.1 gg_id:413391 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU453959.1 gg_id:341713 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S
EU843243.1 gg_id:336486 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ369537.1 gg_id:358078 feces adult twins and mothers; TS51 clone TS51_a01g04
DQ815409.1 gg_id:170399 mouse cecum clone aab47f08
EU507544.1 gg_id:270027 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04g11
EU451074.1 gg_id:355178 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N
EU470093.1 gg_id:292704 trancaspain urial feces clone TU1_aaa03h12
DQ014710.1 gg_id:135420 mouse cecum clone M1_g07_1
EU777884.1 gg_id:341092 European rabbit feces clone RA_g01
FJ368283.1 gg_id:366143 feces adult twins and mothers; TS3 clone TS3_a02d09
GQ011731.1 gg_id:497935 Topographical and Temporal Human Skin Microbiome skin nare clone nbw744d05c1
EU358724.1 gg_id:334839 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EU773998.1 gg_id:331659 Cheetah feces clone CE3_aai07f02
DQ801008.1 gg_id:194735 human fecal clone RL387_aao90g09
EU842331.1 gg_id:332860 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EF098919.1 gg_id:177578 mouse cecum clone SWPT1_aaa03c05
EU775419.1 gg_id:351927 Western lowland gorilla feces clone GOR_aag73e08
FJ880305.1 gg_id:398138 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
FJ680934.1 gg_id:508925 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU506923.1 gg_id:273345 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08d09
AB192011.1 gg_id:144692 termite gut homogenate clone M1NP1-81
EU503919.1 gg_id:273549 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02f03
FJ881052.1 gg_id:397444 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU771330.1 gg_id:336513 Asiatic elephant feces clone AE2_aaa02f07
EU468977.1 gg_id:292793 Speke's gazelle feces clone SP2_c06

EU465621.1	301410	827.0	1227.8	517.1	474.3	245.2	269.7
EU622694.1	278901	951.4	1294.2	1683.1	1703.7	1430.3	2877.1
EU506877.1	276273	31.7	70.4	61.8	60.5	71.0	29.4
AB270051.1	166168	1686.6	2199.6	6428.9	2958.1	2320.1	2828.5
FJ879323.1	408513	6400.5	5527.8	4420.9	4941.4	4351.4	4582.7
EF096450.1	189527	681.1	667.1	1048.7	837.8	961.5	720.3
EU779309.1	309070	639.1	372.8	955.1	362.3	931.3	232.9
EU775150.1	314421	2642.0	3255.1	2273.9	722.7	2331.2	1781.8
EF603178.1	228975	12034.9	11148.3	6198.9	9441.5	10261.9	9101.9
EU772202.1	329529	782.5	1262.1	938.7	795.0	116.7	411.0
EF644508.1	253716	2237.6	2490.6	1991.7	2299.6	1992.0	2128.0
DQ805484.1	181448	102.1	141.9	655.3	163.7	677.7	1240.6
GU120121.1	538805	102.9	191.6	591.1	139.8	97.8	279.0
EU460085.1	296424	622.3	1022.5	3533.2	309.4	265.0	352.6
EU454100.1	309302	28.8	26.6	35.8	74.5	54.7	53.5
FJ881171.1	413391	1503.0	985.2	2055.9	1231.8	427.5	677.3
EU453959.1	341713	6292.2	6682.8	5052.7	3959.1	2179.5	2051.9
EU843243.1	336486	5293.8	4551.0	6345.4	3439.4	3487.5	3894.4
FJ369537.1	358078	5529.6	4450.4	3351.1	5203.7	1964.2	4639.8
DQ815409.1	170399	1575.5	1439.2	1119.7	852.4	2221.2	2003.8
EU507544.1	270027	1875.2	2171.3	1371.9	759.3	1301.9	1395.1
EU451074.1	355178	1886.7	2409.5	1839.8	3129.9	7216.0	5134.6
EU470093.1	292704	1002.5	1699.2	2530.0	1302.7	383.9	573.8
DQ014710.1	135420	1521.5	2715.6	1824.6	894.5	1943.0	2478.4
EU777884.1	341092	4219.6	2096.1	2998.7	3911.5	2549.3	4400.1
FJ368283.1	366143	1664.9	2166.1	3026.3	2059.9	2119.6	2357.5
GQ011731.1	497935	8826.8	9782.9	5259.4	6370.6	9842.8	8815.1
EU358724.1	334839	156.0	108.1	296.6	112.7	150.8	114.3
EU773998.1	331659	259.4	304.7	1573.5	651.6	149.2	299.0
DQ801008.1	194735	181.8	454.0	859.0	313.0	2490.1	1478.6
EU842331.1	332860	790.3	837.9	1166.3	2265.3	679.2	993.1
EF098919.1	177578	28.8	33.7	53.7	41.0	62.9	31.2
EU775419.1	351927	2886.2	2367.9	3037.2	1017.3	1221.8	2408.0
FJ880305.1	398138	1021.6	1203.8	2646.1	1168.1	190.9	412.6
FJ680934.1	508925	4315.7	5163.9	3632.3	7889.1	5566.9	7713.1
EU506923.1	273345	2404.7	3394.5	2246.8	1418.6	1623.0	1364.4
AB192011.1	144692	281.0	543.7	1436.0	1153.4	582.6	1098.0
EU503919.1	273549	5097.2	2056.7	2711.7	4916.1	733.2	367.7
FJ881052.1	397444	3133.6	2609.2	2816.9	3957.4	1242.2	1923.8
EU771330.1	336513	245.9	316.6	975.1	286.4	413.1	940.7
EU468977.1	292793	1181.0	1694.7	2585.3	1390.2	3751.3	3009.4

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EF608542.1 gg_id:230370 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges
EF097622.1 gg_id:180235 mouse cecum clone SWPT20_aaa01d09
DQ806289.1 gg_id:180565 human fecal clone RL186_aan89h10
GQ491367.1 gg_id:549281 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU458674.1 gg_id:288936 European rabbit feces clone RA_f11_2
DQ455867.1 gg_id:158230 pre-adolescent turkey cecum clone CFT19E6
EU850450.1 gg_id:333245 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF12
AF001758.1 gg_id:16019 rumen clone RF26
FJ683056.1 gg_id:523244 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681401.1 gg_id:531867 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF406825.1 gg_id:205987 mouse colon clone infected_28days-D10
EU511801.1 gg_id:260417 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_09d04.Contig2
DQ799972.1 gg_id:190124 human fecal clone RL247_aaj22e08
EU776838.1 gg_id:310416 Mongoose lemur feces clone ML_aae89e01
DQ795909.1 gg_id:183187 human fecal clone RL245_aai84f06
DQ327133.1 gg_id:145883 Metagenomic gut microbiome healthy human stool clone E652
EU773365.1 gg_id:332481 BigHorn sheep feces clone BH1_aao26a07
EU774411.1 gg_id:326991 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1
EU888005.1 gg_id:315439 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
EU465646.1 gg_id:293696 argali sheep feces clone AS1_aao40f11.Contig1
EF406869.1 gg_id:206744 mouse colon clone infected_28days-G8
FJ172851.1 gg_id:336231 Qinghai Yak Ruminal and Fungi China rumen clone RB-3E10
EU459663.1 gg_id:297045 ring-tailed lemur feces clone RT_aai10d08
FJ880548.1 gg_id:439880 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet;
EU344680.1 gg_id:264114 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
AB234482.1 gg_id:146578 termite gut homogenate clone MgMjR-021
DQ796871.1 gg_id:197125 human fecal clone RL179_aao55g01
EU468696.1 gg_id:290392 okapi feces clone OK2_g05_1
EU467108.1 gg_id:288100 mongoose lemur feces clone ML_aae88d09
FJ367531.1 gg_id:365767 feces adult twins and mothers; TS29 clone TS29_a04f07
DQ326345.1 gg_id:145888 Metagenomic gut microbiome healthy human stool clone C336
FJ367522.1 gg_id:357913 feces adult twins and mothers; TS29 clone TS29_a04e09
EF402491.1 gg_id:212641 human fecal clone SJTU_B_08_60
EU462180.1 gg_id:291266 black-handed spider monkey feces clone SPIM_aaj36f07
DQ904856.1 gg_id:173724 human fecal clone 001C-c7
FJ365644.1 gg_id:365410 feces adult twins and mothers; TS21 clone TS21_a01c11
FJ367519.1 gg_id:364229 feces adult twins and mothers; TS29 clone TS29_a04e06
DQ825169.1 gg_id:178670 human fecal clone RL185_aan86c02
DQ794729.1 gg_id:186912 human fecal clone RL240_aaj31f06
FJ362635.1 gg_id:361266 feces adult twins and mothers; TS13 clone TS13_a01c12
FJ367119.1 gg_id:368394 feces adult twins and mothers; TS28 clone TS28_a03g02

EF608542.1	230370	720.1	969.7	677.9	178.9	130.2	102.3
EF097622.1	180235	571.0	1234.1	178.2	94.4	131.6	64.1
DQ806289.1	180565	791.7	1532.6	2006.9	1200.3	1840.2	2121.9
GQ491367.1	549281	1243.5	1543.5	3289.9	953.6	658.6	2261.2
EU458674.1	288936	5950.5	7005.4	1914.1	3532.2	3335.4	2311.1
DQ455867.1	158230	13080.7	13139.6	7741.1	11079.8	10207.0	11853.7
EU850450.1	333245	3072.8	2288.8	4500.4	2759.2	1416.4	1471.0
AF001758.1	16019	247.5	359.6	668.5	210.1	655.2	1417.1
FJ683056.1	523244	2975.9	2367.0	2526.5	2582.0	3694.2	2758.8
FJ681401.1	531867	5622.7	5090.0	6234.2	7210.6	8259.4	8098.2
EF406825.1	205987	291.6	203.4	1322.2	304.4	77.4	169.3
EU511801.1	260417	2853.2	2693.7	341.9	2943.9	950.0	1661.2
DQ799972.1	190124	36.8	33.8	147.0	55.6	67.4	43.5
EU776838.1	310416	166.8	203.1	639.9	151.5	622.6	342.2
DQ795909.1	183187	32.8	28.1	29.5	52.3	68.9	23.2
DQ327133.1	145883	16.6	27.1	20.2	32.4	61.9	18.6
EU773365.1	332481	7919.5	8463.3	5010.3	5203.6	7407.4	7680.9
EU774411.1	326991	8204.0	7160.8	4347.4	4132.9	1337.5	2128.3
EU888005.1	315439	4488.3	4893.7	2911.5	3105.3	4338.2	3813.0
EU465646.1	293696	3328.7	4189.9	2270.8	3128.9	6093.4	4451.4
EF406869.1	206744	140.6	118.7	308.5	136.3	77.6	40.4
FJ172851.1	336231	779.5	1420.1	1130.9	358.1	453.8	381.4
EU459663.1	297045	761.0	638.7	1558.6	616.3	301.7	423.4
FJ880548.1	439880	5195.3	6469.7	3060.6	3030.2	3755.4	4230.7
EU344680.1	264114	1698.3	2407.5	3926.1	1361.7	3749.3	3012.5
AB234482.1	146578	24.6	30.4	19.1	44.1	48.5	19.3
DQ796871.1	197125	794.5	468.7	779.3	186.7	113.7	254.1
EU468696.1	290392	6551.8	6678.1	6672.2	5388.5	4578.4	7853.5
EU467108.1	288100	1348.2	863.5	1383.4	2022.8	174.4	798.5
FJ367531.1	365767	4217.2	3547.9	759.5	1617.2	4794.3	1956.6
DQ326345.1	145888	12.3	18.9	17.5	42.5	38.7	18.4
FJ367522.1	357913	2643.3	3602.8	4023.0	2649.6	5087.6	5820.6
EF402491.1	212641	9486.5	9990.6	5563.9	8090.4	11518.1	9786.9
EU462180.1	291266	5245.7	5590.9	2443.2	1981.1	1997.1	1154.3
DQ904856.1	173724	5188.2	5064.4	1871.5	1807.6	224.1	1373.7
FJ365644.1	365410	3797.6	4106.6	2350.8	3459.9	3578.3	3709.5
FJ367519.1	364229	2219.3	1943.3	630.1	1148.6	1834.8	1436.8
DQ825169.1	178670	9387.6	6666.4	2409.3	2735.7	2585.8	1815.2
DQ794729.1	186912	117.1	741.8	131.0	223.1	491.1	445.8
FJ362635.1	361266	2884.1	2911.7	1068.5	1951.8	2245.6	2306.0
FJ367119.1	368394	9742.5	8676.0	6595.5	7445.9	8549.0	6824.6

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EF403080.1 gg_id:211100 human fecal clone SJTU_B_03_40
FJ372373.1 gg_id:357365 feces adult twins and mothers; TS9 clone TS9_a04h03
DQ793621.1 gg_id:198214 human fecal clone RL246_aai74e10
DQ800988.1 gg_id:199182 human fecal clone RL387_aao90d10
FJ367903.1 gg_id:358152 feces adult twins and mothers; TS2 clone TS2_a04h08
DQ805771.1 gg_id:182051 human fecal clone RL306aal90g11
DQ801641.1 gg_id:186456 human fecal clone RL117_aae93c11
FJ365197.1 gg_id:361811 feces adult twins and mothers; TS1 clone TS1_a04a07
EU771688.1 gg_id:349437 African elephant feces clone AFYEL_aaj67g07
AF376218.1 gg_id:73575 ckncm314-B7-17 clone
FJ683715.1 gg_id:524587 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366945.1 gg_id:359422 feces adult twins and mothers; TS28 clone TS28_a01f06
DQ797744.1 gg_id:174636 human fecal clone RL206_aaj15d05
EU767217.1 gg_id:325765 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
DQ801018.1 gg_id:187632 human fecal clone RL387_aao91a03
EU765302.1 gg_id:319980 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
EU778932.1 gg_id:336217 Black-handed Spider Monkey feces clone SPIM_g09
EU773495.1 gg_id:311824 Bonobo feces clone BNO_aaa01e06
EF434341.1 gg_id:214444 human infant gastrointestinal tract microbiota stool mother baby 3 day delivery clon
DQ794628.1 gg_id:196233 human fecal clone RL240_aaj30d10
EU766126.1 gg_id:344856 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
DQ802754.1 gg_id:177495 human fecal clone RL188_aan96b07
DQ793301.1 gg_id:181290 human fecal clone RL199_aaj41h12
DQ798600.1 gg_id:199246 human fecal clone RL181_aan98g09
DQ797494.1 gg_id:182059 human fecal clone RL248_aaj00a11
EU768767.1 gg_id:330678 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
DQ905339.1 gg_id:170592 human fecal clone 013B-F1
DQ456222.1 gg_id:157966 pre-adolescent turkey cecum clone CFT29G11
DQ793929.1 gg_id:198885 human fecal clone RL176_aah45d07
FJ363399.1 gg_id:368137 feces adult twins and mothers; TS149 clone TS149_a02g05
DQ810085.1 gg_id:194784 human fecal clone RL184_aao67h08
DQ905150.1 gg_id:170385 human fecal clone 002C-e3
DQ808308.1 gg_id:199463 human fecal clone RL180_aao75b02
FJ367475.1 gg_id:364674 feces adult twins and mothers; TS29 clone TS29_a04a04
DQ794501.1 gg_id:198907 human fecal clone RL197_aah88g05
DQ798340.1 gg_id:194552 human fecal clone RL181_aah41b08
AF376220.1 gg_id:72147 ckncm316-B4-5 clone
DQ325549.1 gg_id:150385 Metagenomic gut microbiome healthy human stool clone B006
DQ905891.1 gg_id:162492 human fecal clone 29c-c1
GQ043004.1 gg_id:371426 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012a
EF403280.1 gg_id:212619 human fecal clone SJTU_A1_3_61

EF403080.1	211100	1310.8	2056.5	653.3	692.0	929.8	837.3
FJ372373.1	357365	17.5	25.0	39.8	63.3	49.8	23.4
DQ793621.1	198214	2981.8	3317.2	2873.6	4872.1	7690.9	4886.1
DQ800988.1	199182	41.8	96.4	98.1	127.5	76.3	28.6
FJ367903.1	358152	4116.9	4192.9	585.9	1530.1	1151.2	2128.1
DQ805771.1	182051	2172.8	2310.0	823.4	1157.3	2104.8	2067.8
DQ801641.1	186456	8367.2	8839.6	4525.3	6317.2	10288.5	6981.0
FJ365197.1	361811	6023.2	5671.6	2638.9	4048.6	3217.3	3649.7
EU771688.1	349437	440.8	343.0	425.7	108.0	82.4	155.2
AF376218.1	73575	93.6	77.6	175.9	93.0	196.3	423.9
FJ683715.1	524587	2203.4	2363.2	2907.8	2739.8	4746.1	3951.4
FJ366945.1	359422	1360.9	2142.3	421.8	718.3	2326.9	1184.3
DQ797744.1	174636	6397.5	5242.4	2495.2	5826.6	6458.8	6926.2
EU767217.1	325765	4279.7	3429.8	3812.0	4658.8	4478.7	5630.1
DQ801018.1	187632	1760.6	2091.2	2217.3	1925.9	5986.8	4151.0
EU765302.1	319980	3020.8	3121.7	2287.4	2159.9	6357.2	5332.8
EU778932.1	336217	460.0	725.3	876.4	162.3	457.9	487.3
EU773495.1	311824	700.2	1250.4	3500.5	1335.0	1407.7	1790.1
EF434341.1	214444	1416.4	1398.3	2747.5	1744.1	301.3	719.6
DQ794628.1	196233	209.1	183.0	103.4	352.2	156.7	239.6
EU766126.1	344856	2840.0	2481.6	2380.3	2304.8	3551.0	3545.2
DQ802754.1	177495	3613.6	6105.7	4898.1	3312.3	1271.4	3860.7
DQ793301.1	181290	9694.6	9249.9	6447.4	4663.5	7934.1	6795.2
DQ798600.1	199246	236.9	345.4	63.5	49.1	60.1	46.1
DQ797494.1	182059	233.0	338.2	1693.7	194.6	135.4	345.0
EU768767.1	330678	28.2	41.6	31.0	58.2	51.4	29.0
DQ905339.1	170592	2716.1	2081.5	3568.5	1792.4	1772.0	1933.5
DQ456222.1	157966	52.1	54.3	86.9	61.4	53.9	38.1
DQ793929.1	198885	411.3	880.3	2685.8	1006.3	815.6	223.5
FJ363399.1	368137	1873.1	2629.4	1003.4	2549.5	1589.3	739.3
DQ810085.1	194784	2777.6	2798.4	5153.5	2041.1	1961.5	1974.6
DQ905150.1	170385	373.8	561.4	528.9	961.1	1630.5	1159.5
DQ808308.1	199463	116.9	105.3	250.0	632.4	126.2	131.7
FJ367475.1	364674	189.1	142.5	234.7	203.3	82.6	56.2
DQ794501.1	198907	16841.4	15034.2	12678.4	12501.2	14019.9	13677.0
DQ798340.1	194552	32.0	36.3	71.3	67.0	58.1	18.3
AF376220.1	72147	4545.6	4662.8	4011.3	5482.7	6222.0	4326.3
DQ325549.1	150385	5485.9	5088.6	3433.2	2275.9	655.1	1177.1
DQ905891.1	162492	8984.8	5416.3	2399.6	1706.9	307.1	644.1
GQ043004.1	371426	3321.5	3420.0	3588.0	1605.9	3263.4	3368.9
EF403280.1	212619	444.6	408.3	811.6	283.0	358.1	745.0

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GQ175477.1 gg_id:579000 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
DQ798321.1 gg_id:184093 human fecal clone RL181_aah40f11
DQ794285.1 gg_id:196796 human fecal clone RL176_aan60f03
DQ797648.1 gg_id:175443 human fecal clone RL206_aaj14b12
FJ366956.1 gg_id:357225 feces adult twins and mothers; TS28 clone TS28_a01g05
DQ798361.1 gg_id:189047 human fecal clone RL181_aah41e05
FJ367394.1 gg_id:357231 feces adult twins and mothers; TS29 clone TS29_a03a04
EU461656.1 gg_id:300092 mongoose lemur feces clone ML_aaj26d06
DQ057414.1 gg_id:136271 chicken ileum/cecum clone oc23
AF371716.1 gg_id:46691 swine intestine clone p-2814-24E5
DQ794019.1 gg_id:189800 human fecal clone RL176_aah46f11
FJ368985.1 gg_id:357740 feces adult twins and mothers; TS4 clone TS4_a02h07
FJ679137.1 gg_id:518735 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801472.1 gg_id:190467 human fecal clone RL388_aao96a02
EU767122.1 gg_id:342124 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ363687.1 gg_id:359284 feces adult twins and mothers; TS14 clone TS14_a02b04
FJ363795.1 gg_id:367084 feces adult twins and mothers; TS14 clone TS14_a03d09
DQ455909.1 gg_id:158360 pre-adolescent turkey cecum clone CFT111A10
EU728786.1 gg_id:334557 Subdoligranulum sp. str. DJF_VR33k2
GQ175440.1 gg_id:594206 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
AB264065.1 gg_id:187741 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-25
DQ793941.1 gg_id:193786 human fecal clone RL176_aah45e09
DQ798183.1 gg_id:186702 human fecal clone RL302_aal96e09
EU461689.1 gg_id:301750 mongoose lemur feces clone ML_aaj27b12
EU768362.1 gg_id:335270 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
EU766446.1 gg_id:339125 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU768798.1 gg_id:319831 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
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DQ797996.1 gg_id:178744 human fecal clone RL302_aal94c11
FJ682973.1 gg_id:514399 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ810168.1 gg_id:184292 human fecal clone RL184_aao68g11
DQ905437.1 gg_id:168776 human fecal clone 013C-F11
FJ372141.1 gg_id:367989 feces adult twins and mothers; TS9 clone TS9_a02b11
FJ365745.1 gg_id:367703 feces adult twins and mothers; TS21 clone TS21_a02e04
DQ807932.1 gg_id:176619 human fecal clone RL180_aan69d03
DQ809649.1 gg_id:178390 human fecal clone RL184_aan82b04
DQ795975.1 gg_id:188631 human fecal clone RL202_aai49f12
FJ363732.1 gg_id:361579 feces adult twins and mothers; TS14 clone TS14_a02f05
FJ368274.1 gg_id:360904 feces adult twins and mothers; TS3 clone TS3_a02c10
DQ799468.1 gg_id:193053 human fecal clone RL305aal86f07

DQ057466.1	129761	819.1	683.1	227.9	128.4	67.5	160.1
GQ175477.1	579000	807.2	660.6	538.7	620.7	247.1	160.1
DQ798321.1	184093	8566.1	6767.5	5277.6	8576.2	6491.4	5631.5
DQ794285.1	196796	34.1	43.0	85.9	65.0	79.5	65.7
DQ797648.1	175443	274.3	446.5	242.5	209.5	724.6	527.5
FJ366956.1	357225	2570.6	2193.6	991.3	2228.7	4833.8	4473.0
DQ798361.1	189047	1406.3	941.6	86.9	414.7	481.0	104.9
FJ367394.1	357231	5940.3	3835.0	4138.1	4681.2	2328.2	3874.9
EU461656.1	300092	1501.1	1533.3	2338.0	725.9	410.8	983.1
DQ057414.1	136271	611.2	575.0	212.2	342.3	355.4	362.8
AF371716.1	46691	54.0	84.6	234.4	366.6	53.7	18.9
DQ794019.1	189800	1250.6	1111.8	1803.7	2584.4	809.2	1076.1
FJ368985.1	357740	7333.9	7112.8	4173.0	2906.1	5591.9	4547.3
FJ679137.1	518735	74.6	239.1	992.9	652.1	116.1	82.3
DQ801472.1	190467	125.0	146.7	215.1	108.0	230.7	193.7
EU767122.1	342124	59.3	165.5	214.3	124.0	139.4	340.8
FJ363687.1	359284	3320.1	2930.9	2405.8	3627.5	2771.4	3184.6
FJ363795.1	367084	309.3	454.9	79.1	117.8	138.7	74.7
DQ455909.1	158360	342.4	230.2	448.5	459.1	255.4	292.9
EU728786.1	334557	4573.7	4612.7	5108.8	4742.7	10437.7	7417.8
GQ175440.1	594206	128.0	157.7	194.6	106.1	85.7	77.9
AB264065.1	187741	81.0	55.4	88.3	67.4	70.5	35.0
DQ793941.1	193786	362.7	297.5	154.1	132.2	135.5	71.2
DQ798183.1	186702	32.9	47.0	84.6	98.4	71.7	60.3
EU461689.1	301750	36.3	94.3	45.2	2110.9	101.3	81.2
EU768362.1	335270	30.8	39.3	57.2	70.7	74.7	64.8
EU766446.1	339125	938.0	835.6	198.9	388.2	274.3	256.3
EU768798.1	319831	3630.6	3328.8	2608.6	2441.7	574.9	1646.6
DQ794902.1	181213	25.7	45.5	37.0	54.8	62.3	32.0
DQ797996.1	178744	7161.1	6786.9	7503.7	4769.6	13842.4	11299.4
FJ682973.1	514399	2409.2	2476.0	2125.7	4578.7	5499.7	3472.1
DQ810168.1	184292	73.5	73.5	97.8	77.8	57.5	40.0
DQ905437.1	168776	1257.6	1978.1	402.6	380.8	322.8	247.4
FJ372141.1	367989	542.0	462.5	548.0	843.5	190.8	335.0
FJ365745.1	367703	1258.7	1919.5	2663.6	1950.0	2496.2	2722.9
DQ807932.1	176619	339.8	415.0	150.9	654.8	876.9	757.3
DQ809649.1	178390	101.5	140.4	315.7	559.6	365.7	131.8
DQ795975.1	188631	1877.5	1478.7	965.7	1077.0	883.1	1386.9
FJ363732.1	361579	93.6	109.9	76.5	101.9	105.0	58.4
FJ368274.1	360904	8499.7	5266.7	2740.9	8271.0	6809.5	8462.1
DQ799468.1	193053	1905.2	2287.5	2184.4	1053.3	4323.2	3322.8

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DQ809892.1 gg_id:187969 human fecal clone RL184_aao65f02
DQ810127.1 gg_id:193572 human fecal clone RL184_aao68d03
DQ797593.1 gg_id:190126 human fecal clone RL206_aaj13d10
EF445171.1 gg_id:205155 rabbit cecum clone NED1B8
DQ801703.1 gg_id:185329 human fecal clone RL201_aai45g05
DQ823743.1 gg_id:188160 human fecal clone RL250_aaj78d11
FJ367539.1 gg_id:368178 feces adult twins and mothers; TS29 clone TS29_a04g04
DQ793937.1 gg_id:197542 human fecal clone RL176_aah45e04
DQ905796.2 gg_id:163561 human fecal clone 29E-a8
FJ367386.1 gg_id:357496 feces adult twins and mothers; TS29 clone TS29_a02h03
DQ809792.1 gg_id:178470 human fecal clone RL184_aan84c07
DQ801603.1 gg_id:195608 human fecal clone RL117_aae92d11
EU764665.1 gg_id:322947 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ369707.1 gg_id:369903 feces adult twins and mothers; TS51 clone TS51_a03h01
DQ808067.1 gg_id:174837 human fecal clone RL180_aan71g05
DQ456024.1 gg_id:157417 pre-adolescent turkey cecum clone CFT112D5
DQ794206.1 gg_id:194933 human fecal clone RL176_aan59d12
FJ371854.1 gg_id:368906 feces adult twins and mothers; TS8 clone TS8_a03a03
DQ801585.1 gg_id:190660 human fecal clone RL117_aae92a08
FJ367477.1 gg_id:366886 feces adult twins and mothers; TS29 clone TS29_a04a06
GQ491881.1 gg_id:586525 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU765568.1 gg_id:306962 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3
FJ366821.1 gg_id:362432 feces adult twins and mothers; TS27 clone TS27_a04c06
FJ683678.1 gg_id:509821 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ797710.1 gg_id:176442 human fecal clone RL206_aaj14h09
FJ365885.1 gg_id:369922 feces adult twins and mothers; TS21 clone TS21_a04b11
DQ825076.1 gg_id:196616 human fecal clone RL185_aan85a12
GQ898028.1 gg_id:572956 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
FJ365932.1 gg_id:364083 feces adult twins and mothers; TS21 clone TS21_a04g10
FJ677101.1 gg_id:529556 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ456177.1 gg_id:158252 pre-adolescent turkey cecum clone CFT29C8
FJ366691.1 gg_id:361827 feces adult twins and mothers; TS27 clone TS27_a02f11
FJ372109.1 gg_id:358744 feces adult twins and mothers; TS9 clone TS9_a01h02
EU766189.1 gg_id:354737 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
DQ904685.1 gg_id:167251 human fecal clone 001-e11
EU764575.1 gg_id:348449 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
FJ366231.1 gg_id:367348 feces adult twins and mothers; TS25 clone TS25_a04c05
DQ905880.2 gg_id:164867 human fecal clone 29c-a4
DQ905769.2 gg_id:167863 human fecal clone 29A-f12
FJ365793.1 gg_id:361283 feces adult twins and mothers; TS21 clone TS21_a03b03
DQ905791.2 gg_id:165346 human fecal clone 29E-a3

DQ809892.1	187969	1103.3	1057.6	1387.4	1647.1	665.5	739.7
DQ810127.1	193572	412.2	502.0	65.3	317.0	490.8	227.4
DQ797593.1	190126	12537.5	12068.3	7932.1	8453.2	11403.1	9229.6
EF445171.1	205155	43.6	79.6	295.9	90.3	88.3	147.7
DQ801703.1	185329	1144.6	57.8	835.6	2025.0	1006.4	1140.8
DQ823743.1	188160	473.4	717.8	167.0	1033.6	1368.7	2061.2
FJ367539.1	368178	2517.7	1218.4	1437.8	3758.0	235.5	314.9
DQ793937.1	197542	139.3	267.8	232.0	247.0	88.5	47.0
DQ905796.2	163561	1576.1	1170.9	1962.5	2882.5	872.7	1337.4
FJ367386.1	357496	62.2	821.1	649.4	313.4	109.8	65.9
DQ809792.1	178470	140.5	84.4	193.5	103.6	63.5	45.1
DQ801603.1	195608	317.1	662.7	584.5	466.7	364.3	328.6
EU764665.1	322947	2590.3	4045.5	648.3	1776.5	2779.2	2264.9
FJ369707.1	369903	209.2	125.3	112.8	232.7	64.3	343.9
DQ808067.1	174837	144.1	797.8	261.3	146.5	299.7	178.3
DQ456024.1	157417	75.1	173.2	144.7	114.9	165.4	133.2
DQ794206.1	194933	76.5	86.1	198.8	149.1	78.2	72.6
FJ371854.1	368906	3117.4	2289.6	1180.9	4487.4	3118.8	3009.7
DQ801585.1	190660	4062.2	2884.8	3159.1	7629.0	641.7	1959.9
FJ367477.1	366886	2474.9	1984.0	2143.1	327.2	2434.2	2419.2
GQ491881.1	586525	1854.2	4224.5	1837.5	1100.1	4524.8	2603.7
EU765568.1	306962	47.2	77.7	44.7	54.5	154.2	89.0
FJ366821.1	362432	4923.1	4871.0	5077.1	6224.8	4981.2	5024.7
FJ683678.1	509821	4548.6	4273.8	6161.2	2210.2	5043.3	4000.6
DQ797710.1	176442	249.7	667.8	333.9	500.6	126.3	522.0
FJ365885.1	369922	9.3	22.2	39.1	59.6	49.9	15.7
DQ825076.1	196616	2792.8	1632.9	488.7	1650.7	856.5	1119.5
GQ898028.1	572956	5539.6	5273.4	2276.1	6175.6	8687.0	8617.0
FJ365932.1	364083	2602.5	1412.3	1329.3	2541.3	242.1	490.5
FJ677101.1	529556	3939.2	4902.0	2172.7	4804.1	5816.3	5059.2
DQ456177.1	158252	53.6	102.6	141.3	76.9	50.0	29.6
FJ366691.1	361827	1868.9	1674.3	2154.4	2953.2	1212.0	1297.3
FJ372109.1	358744	11679.2	11719.9	7050.7	7168.7	4900.9	5736.9
EU766189.1	354737	2849.5	1877.9	1742.0	3958.5	1027.4	1566.7
DQ904685.1	167251	8221.7	4906.8	3635.2	7098.7	3034.1	4316.2
EU764575.1	348449	21.5	51.5	16.8	61.0	75.0	27.5
FJ366231.1	367348	2850.1	3764.5	1386.7	1836.2	4675.6	2550.7
DQ905880.2	164867	2285.1	2257.1	1408.9	2176.3	3032.0	2573.5
DQ905769.2	167863	1223.7	836.8	1333.8	918.1	2935.9	3366.0
FJ365793.1	361283	1643.1	2402.6	1912.2	3559.0	2459.1	2981.2
DQ905791.2	165346	307.2	1177.0	433.0	3036.8	1130.1	1417.7

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EF401318.1 gg_id:206073 human fecal clone SJTU_D_08_72
EU768535.1 gg_id:342263 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5
DQ794362.1 gg_id:193007 human fecal clone RL197_aah86d10
FJ366400.1 gg_id:363257 feces adult twins and mothers; TS26 clone TS26_a02f05
DQ794224.1 gg_id:197701 human fecal clone RL176_aan59g02
FJ372259.1 gg_id:361667 feces adult twins and mothers; TS9 clone TS9_a03e08
FJ368378.1 gg_id:366286 feces adult twins and mothers; TS3 clone TS3_a03f07
FJ372007.1 gg_id:367712 feces adult twins and mothers; TS8 clone TS8_a04f10
FJ367415.1 gg_id:360771 feces adult twins and mothers; TS29 clone TS29_a03c05
EU459904.1 gg_id:293874 Prevost's squirrel feces clone SQ_aah81a02
FJ375910.1 gg_id:323534 and prevalence blaTEM genes polar bear feces clone PBM_a2
DQ801353.1 gg_id:181976 human fecal clone RL388_aao94d07
DQ798168.1 gg_id:198554 human fecal clone RL302_aal96d01
DQ794297.1 gg_id:185762 human fecal clone RL176_aan60g10
GQ175410.1 gg_id:565952 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
EF400910.1 gg_id:212549 human fecal clone SJTU_D_03_29
FJ363972.1 gg_id:361798 feces adult twins and mothers; TS150 clone TS150_a01e06
EU767998.1 gg_id:347967 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
DQ796772.1 gg_id:199502 human fecal clone RL179_aao54c08
DQ808683.1 gg_id:199269 human fecal clone RL239_aaj11g11
FJ363956.1 gg_id:361122 feces adult twins and mothers; TS150 clone TS150_a01c12
EU509787.1 gg_id:271488 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21a08
FJ683794.1 gg_id:531444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795560.1 gg_id:195561 human fecal clone RL178_aan66c03
EU766373.1 gg_id:332702 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EF404114.1 gg_id:211295 human fecal clone SJTU_C_04_87
AY169430.1 gg_id:81198 Faecalibacterium prausnitzii
DQ057482.2 gg_id:134174 str. ic1395
DQ905832.2 gg_id:170094 human fecal clone 29E-d11
FJ676304.1 gg_id:523814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU009761.1 gg_id:237211 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AB8
FJ362743.1 gg_id:366267 feces adult twins and mothers; TS13 clone TS13_a02f03
DQ810028.1 gg_id:193622 human fecal clone RL184_aao67c03
DQ798283.1 gg_id:183674 human fecal clone RL181_aah40b05
FJ367251.1 gg_id:362328 feces adult twins and mothers; TS29 clone TS29_a01c11
DQ808060.1 gg_id:191541 human fecal clone RL180_aan71f03
GQ896642.1 gg_id:568845 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
DQ806793.1 gg_id:178419 human fecal clone RL186_aao48g07
GQ897259.1 gg_id:584951 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
AY916158.1 gg_id:113956 human transverse colon biopsy clone M479
EU778922.1 gg_id:306633 Black-handed Spider Monkey feces clone SPIM_aaj36g11

EF401318.1	206073	3900.3	2464.6	817.5	4538.7	4655.0	4627.6
EU768535.1	342263	3879.2	3673.9	1189.9	2549.2	2611.6	1640.8
DQ794362.1	193007	8536.3	7755.0	5919.1	10173.8	8910.0	7890.3
FJ366400.1	363257	16664.6	14145.9	15713.3	9894.3	17618.3	15175.0
DQ794224.1	197701	7151.9	6625.1	2190.5	2961.0	3235.4	4069.6
FJ372259.1	361667	1360.0	926.1	1108.5	1242.2	611.1	559.3
FJ368378.1	366286	1707.3	1527.8	921.7	2734.2	2301.9	1772.9
FJ372007.1	367712	641.3	1121.9	335.0	609.4	146.8	144.8
FJ367415.1	360771	1681.9	2217.2	583.9	737.9	1192.6	1063.1
EU459904.1	293874	491.1	512.4	315.2	129.1	189.0	150.6
FJ375910.1	323534	1864.6	1864.6	2377.1	838.5	2216.8	1478.7
DQ801353.1	181976	95.2	75.3	253.1	67.7	57.3	43.3
DQ798168.1	198554	6429.8	5040.6	1327.1	6356.5	7829.5	6446.9
DQ794297.1	185762	1484.4	1611.8	1630.7	1319.6	2627.7	2214.9
GQ175410.1	565952	1597.2	1194.8	655.0	340.2	496.0	317.1
EF400910.1	212549	416.2	405.2	1136.8	1057.1	262.1	907.6
FJ363972.1	361798	1379.1	693.6	170.8	92.9	249.9	67.7
EU767998.1	347967	500.1	548.0	397.2	429.0	2072.5	2027.2
DQ796772.1	199502	19.0	15.7	6.9	46.4	58.5	25.5
DQ808683.1	199269	12604.6	9323.5	7181.5	11938.4	10853.7	10040.9
FJ363956.1	361122	4851.2	4841.3	1712.1	4936.7	5940.9	5084.3
EU509787.1	271488	405.0	852.5	752.7	343.2	345.0	498.6
FJ683794.1	531444	2120.5	1955.3	2843.0	1483.4	1354.6	2041.0
DQ795560.1	195561	1060.9	1644.0	392.4	690.4	2730.6	1425.8
EU766373.1	332702	5321.8	4596.1	592.1	270.2	3548.0	310.6
EF404114.1	211295	1354.1	1685.0	2023.6	1455.3	1488.1	1215.3
AY169430.1	81198	6447.7	6362.4	6844.9	7365.2	5321.1	5463.2
DQ057482.2	134174	80.1	59.6	49.3	98.3	87.6	44.7
DQ905832.2	170094	6778.2	9317.7	6211.3	6573.5	11414.0	9558.4
FJ676304.1	523814	791.6	902.4	453.7	490.8	1067.0	1278.0
EU009761.1	237211	127.6	64.3	172.8	92.2	62.6	78.3
FJ362743.1	366267	327.1	1038.1	865.1	469.8	244.0	219.4
DQ810028.1	193622	26.4	31.5	18.5	44.6	60.9	18.5
DQ798283.1	183674	6996.2	6981.3	5386.1	6909.6	9682.9	8551.1
FJ367251.1	362328	4463.1	4800.9	3241.4	5277.0	10675.5	8093.2
DQ808060.1	191541	1168.1	1314.5	2062.1	1298.2	1109.2	1556.2
GQ896642.1	568845	772.7	640.1	866.2	1977.6	287.0	305.3
DQ806793.1	178419	169.8	344.7	298.9	153.5	1049.0	795.5
GQ897259.1	584951	1330.1	1416.9	1608.0	2735.8	395.9	1205.0
AY916158.1	113956	2290.1	3148.3	4346.2	3002.3	3022.9	3524.8
EU778922.1	306633	41.1	76.9	104.5	84.1	73.2	66.0

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FJ367523.1 gg_id:360297 feces adult twins and mothers; TS29 clone TS29_a04e10
FJ367399.1 gg_id:357525 feces adult twins and mothers; TS29 clone TS29_a03a09
DQ905064.1 gg_id:170262 human fecal clone 2-002-f10
EU461598.1 gg_id:295083 mongoose lemur feces clone ML_aaj25c08
EF071254.1 gg_id:178512 library survey and quantitative measurement major mucosa- IBD human colonic muc
GQ897730.1 gg_id:593300 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
DQ825124.1 gg_id:196499 human fecal clone RL185_aan85f07
GQ175380.1 gg_id:511009 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
DQ455878.1 gg_id:157455 pre-adolescent turkey cecum clone CFT19F7
EU763901.1 gg_id:345683 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5
EU462171.1 gg_id:297013 black-handed spider monkey feces clone SPIM_aaj36d03
DQ801092.1 gg_id:176861 human fecal clone RL387_aao92a10
EU778057.1 gg_id:307224 Rock hyrax feces clone RHSD_aaa03e07_1
DQ809793.1 gg_id:190067 human fecal clone RL184_aan84c10
DQ793432.1 gg_id:174458 human fecal clone RL199_aaj43f06
EU766782.1 gg_id:336071 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
FJ833044.1 gg_id:546069 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_14F02
DQ794181.1 gg_id:194219 human fecal clone RL176_aan59b08
DQ797283.1 gg_id:178578 human fecal clone RL248_aai97c11
DQ806652.1 gg_id:195391 human fecal clone RL186_aao47b11
FJ904264.1 gg_id:552251 Further evidence absence horsehair worms (Nematomorpha: Gordiidae) Gordius robu
DQ327429.1 gg_id:145346 Metagenomic gut microbiome healthy human stool clone E988
EF603324.1 gg_id:229642 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU506238.1 gg_id:276137 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c04
EU509367.1 gg_id:259581 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48f12
EF603651.1 gg_id:230125 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ805523.1 gg_id:177311 human fecal clone RL203_aai63g02
EU778221.1 gg_id:306021 feces clone RL387_aao90e02
EU462031.1 gg_id:290645 black-handed spider monkey feces clone SPIM_aaj33f07
AM278254.2 gg_id:234724 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
EF604546.1 gg_id:228893 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF445283.1 gg_id:216004 dairy cow rumen clone NED4G8
AY858434.2 gg_id:111671 gastrointestinal tract Grant's gazelle clone GRANT15
EU469998.1 gg_id:296456 trancaspain urial feces clone TU1_aaa03e06
EU381467.1 gg_id:275170 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p
EU468548.1 gg_id:291584 okapi feces clone OK1_e02_1
EU459548.1 gg_id:293827 capybara feces clone CAP_aah99f08
EU885025.1 gg_id:304728 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3D10
AY985261.1 gg_id:119310 human stool clone C142
EU778974.1 gg_id:353817 Prevost's squirrel feces clone SQ_aah81b08
AB089046.1 gg_id:78294 termite gut homogenate clone Rs-C61 bacterium

FJ367523.1	360297	4534.3	7906.5	3551.1	3064.5	4776.5	4911.4
FJ367399.1	357525	13378.7	12036.5	7899.5	9473.5	10984.1	9754.8
DQ905064.1	170262	29.3	37.2	116.1	72.4	60.5	24.0
EU461598.1	295083	433.5	849.8	708.3	968.5	280.3	526.0
EF071254.1	178512	54.6	61.6	63.3	105.8	62.6	55.5
GQ897730.1	593300	133.4	58.7	192.8	153.0	111.1	40.0
DQ825124.1	196499	5485.9	5004.5	2600.8	3259.4	7094.7	5421.0
GQ175380.1	511009	362.9	193.3	405.3	290.3	131.0	148.1
DQ455878.1	157455	55.5	123.5	339.3	75.7	81.5	44.4
EU763901.1	345683	2076.0	3023.3	656.1	361.9	1527.9	1775.6
EU462171.1	297013	8017.4	8418.4	6481.5	5832.1	8824.0	8619.4
DQ801092.1	176861	1855.5	1305.6	924.9	1234.8	995.9	926.2
EU778057.1	307224	349.3	304.4	402.8	168.3	244.9	287.1
DQ809793.1	190067	4493.3	3555.5	3671.6	3698.8	1955.8	3014.6
DQ793432.1	174458	1254.4	1758.4	399.9	423.2	661.6	1300.8
EU766782.1	336071	18.4	29.0	25.0	61.6	61.7	16.0
FJ833044.1	546069	3541.1	4390.2	3214.0	1750.3	4315.8	2987.1
DQ794181.1	194219	272.8	233.1	563.6	228.4	376.4	332.4
DQ797283.1	178578	459.6	582.5	1757.8	600.0	4038.4	4069.0
DQ806652.1	195391	771.3	206.2	1740.0	2174.2	59.3	80.9
FJ904264.1	552251	768.3	1350.3	1498.9	358.1	355.9	582.3
DQ327429.1	145346	412.6	533.8	1110.6	639.5	1464.9	1291.9
EF603324.1	229642	13373.8	15137.9	7141.9	9276.3	5957.2	6848.3
EU506238.1	276137	144.4	324.4	233.6	105.0	157.8	204.8
EU509367.1	259581	224.8	887.8	1022.3	142.3	229.6	470.6
EF603651.1	230125	1294.8	1148.0	1032.3	2743.6	556.0	1191.3
DQ805523.1	177311	2418.9	2617.1	2544.2	4363.7	461.5	1664.7
EU778221.1	306021	871.8	626.8	487.4	559.1	245.2	191.8
EU462031.1	290645	622.6	2038.2	4210.0	1830.0	4983.2	2082.6
AM278254.2	234724	5304.7	6636.7	3130.7	4972.8	5014.5	4862.3
EF604546.1	228893	4073.1	4430.2	1834.1	1236.6	3169.4	3752.3
EF445283.1	216004	85.3	84.3	76.4	93.6	65.8	11.8
AY858434.2	111671	2612.3	6945.5	7411.8	7883.2	1438.1	7479.2
EU469998.1	296456	3626.8	3042.5	1097.7	4263.9	2892.0	4620.0
EU381467.1	275170	2480.8	2544.4	3890.7	2689.5	2581.0	2627.8
EU468548.1	291584	12261.2	13251.3	9241.8	11529.4	12450.5	10733.8
EU459548.1	293827	10839.2	10657.6	9333.3	10210.0	12619.1	10872.5
EU885025.1	304728	4612.9	5586.3	5529.4	3153.9	5863.5	4353.2
AY985261.1	119310	203.1	572.4	1720.2	551.9	205.3	921.4
EU778974.1	353817	599.1	379.8	612.4	360.4	115.9	166.6
AB089046.1	78294	43.6	66.5	164.2	89.5	161.3	44.7

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o__Clostridiales	f__Ruminococcaceae
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FJ374219.1 gg_id:363511 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
EU777853.1 gg_id:342571 European rabbit feces clone RA_g09
DQ808989.1 gg_id:189844 human fecal clone RL243_aai87h07
EU466083.1 gg_id:303148 bighorn sheep feces clone BH1_aao25e08
DQ804796.1 gg_id:183299 human fecal clone RL187_aao72g10
EU470212.1 gg_id:291405 trancaspain urial feces clone TU2_aaa01d03
AM697026.1 gg_id:223318 sequencing libraries indoor dust clone BF0001B052
AY916375.1 gg_id:113620 human stool clone D577
GQ079311.1 gg_id:435792 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c(
EU844792.1 gg_id:355063 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU468771.1 gg_id:295107 okapi feces clone OK3_d08
EU507525.1 gg_id:265635 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e09
DQ794266.1 gg_id:196637 human fecal clone RL176_aan60d03
EU462535.1 gg_id:298204 Sumatran orangutan feces clone orang1_aai56e12
DQ798661.1 gg_id:192677 human fecal clone RL181_aan99f11
AB288904.1 gg_id:201203 termite gut homogenate clone BOf5-23
EU774126.1 gg_id:352182 Chimpanzee feces clone CHIMP1_aaj39f05
DQ905206.1 gg_id:165257 human fecal clone 013-b3
DQ799538.1 gg_id:194197 human fecal clone RL305aal87d11
DQ793626.1 gg_id:180995 human fecal clone RL246_aai74f03
GQ493785.1 gg_id:591839 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU622690.1 gg_id:279659 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
AB088959.1 gg_id:77706 termite gut homogenate clone Rs-B44
EU842424.1 gg_id:349962 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
DQ168656.1 gg_id:158569 sediment-free PCB-dechlorinating enrichment culture clone JN18_V41_S
AY991981.1 gg_id:135396 mouse cecum clone C20_o04
EU468795.1 gg_id:299019 okapi feces clone OK3_c07_1
FJ677881.1 gg_id:530146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU451989.1 gg_id:320505 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
EU463774.1 gg_id:300041 domesticated horse feces clone horsej_aai92f03
EU842712.1 gg_id:346029 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU506915.1 gg_id:265625 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08c05
DQ824345.1 gg_id:187264 human fecal clone RL304_aal74g08
DQ015569.1 gg_id:130945 mouse cecum clone M3_f07_1
FJ364993.1 gg_id:360916 feces adult twins and mothers; TS1 clone TS1_a01f01
AY980462.1 gg_id:123025 human rectum mucosal biopsy clone X044
EU504886.1 gg_id:275779 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03g09
EU468744.1 gg_id:292147 okapi feces clone OK3_e09
CU927061.1 gg_id:568110 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY916261.1 gg_id:114087 human rectum biopsy clone LL87
EF434358.1 gg_id:207991 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont

FJ374219.1	363511	2526.4	2431.6	4404.2	3498.4	1482.3	3105.2
EU777853.1	342571	2236.1	2176.1	1878.4	3773.3	1207.2	1928.2
DQ808989.1	189844	1219.5	1049.2	1004.1	1564.4	857.1	832.7
EU466083.1	303148	4527.0	5238.8	5168.4	2907.6	1346.7	1927.3
DQ804796.1	183299	187.6	117.6	225.2	185.2	606.2	425.1
EU470212.1	291405	1820.4	2230.0	1840.7	1697.7	2108.7	2857.1
AM697026.1	223318	6626.5	5568.4	2963.4	2886.4	2099.7	1883.8
AY916375.1	113620	5346.3	4411.1	4475.0	4364.0	4603.5	3192.7
GQ079311.1	435792	941.3	1231.7	2126.8	532.7	980.5	1944.8
EU844792.1	355063	1204.8	1428.5	3101.1	1020.7	2293.3	1984.5
EU468771.1	295107	1213.2	1780.1	1195.6	1196.2	1060.2	1514.0
EU507525.1	265635	4696.4	4858.7	4088.9	4653.5	4024.6	4627.5
DQ794266.1	196637	1703.9	1944.6	1442.1	1558.4	250.7	520.5
EU462535.1	298204	7849.1	7292.5	3080.4	8292.0	7499.3	7298.4
DQ798661.1	192677	665.9	968.6	3389.9	929.8	4156.7	4721.5
AB288904.1	201203	65.2	100.8	72.8	79.4	97.9	62.1
EU774126.1	352182	2692.5	2780.7	4529.6	3246.3	8191.7	7795.9
DQ905206.1	165257	15.8	31.4	27.5	46.2	41.3	18.8
DQ799538.1	194197	20.1	20.0	31.3	52.2	49.9	25.6
DQ793626.1	180995	437.3	276.8	542.1	1612.7	89.4	289.6
GQ493785.1	591839	1747.3	1032.0	2823.4	3211.0	161.4	487.7
EU622690.1	279659	859.9	1183.5	4043.0	807.7	912.0	1100.5
AB088959.1	77706	4317.5	2946.3	1438.2	4170.0	3031.0	2326.5
EU842424.1	349962	1275.4	1821.2	2446.7	2394.1	961.4	1439.6
DQ168656.1	158569	463.3	638.4	939.5	1207.7	611.3	844.7
AY991981.1	135396	777.2	498.7	1624.8	749.7	625.5	1122.5
EU468795.1	299019	177.2	1690.3	640.6	557.1	1246.0	879.6
FJ677881.1	530146	5835.1	6559.4	5306.1	5733.9	4484.0	4014.5
EU451989.1	320505	1171.9	1589.8	1393.3	466.0	2425.6	1956.6
EU463774.1	300041	704.6	582.4	1211.7	738.1	187.9	369.6
EU842712.1	346029	2760.8	3116.8	4420.1	3187.2	5336.3	5266.9
EU506915.1	265625	2555.3	2930.9	3328.8	5102.7	3395.0	3904.2
DQ824345.1	187264	38.5	23.9	28.2	41.2	66.2	28.6
DQ015569.1	130945	2374.1	1648.3	3688.1	2406.6	2237.5	1986.6
FJ364993.1	360916	5656.8	5944.6	1880.0	6112.5	8271.8	7747.3
AY980462.1	123025	1657.4	1621.1	494.1	1150.6	2158.7	1388.8
EU504886.1	275779	30.8	153.0	584.1	112.2	54.3	38.1
EU468744.1	292147	840.9	960.3	2026.0	732.5	1066.9	936.3
CU927061.1	568110	1156.4	992.2	960.9	359.2	385.7	1104.4
AY916261.1	114087	186.4	236.3	614.5	114.4	528.1	406.1
EF434358.1	207991	1789.6	1499.6	918.2	940.8	511.5	751.4

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o__Clostridiales	f__Ruminococcaceae
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DQ071530.1 gg_id:233711 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw7
EU470080.1 gg_id:289802 trancaspain urial feces clone TU1_aaa03f09
AM697405.1 gg_id:221429 sequencing libraries indoor dust clone BF0001D020
AY916159.1 gg_id:113797 human transverse colon biopsy clone M490
AB089039.1 gg_id:77833 termite gut homogenate clone Rs-K92 bacterium
FJ371922.1 gg_id:366885 feces adult twins and mothers; TS8 clone TS8_a03g03
DQ797006.1 gg_id:187006 human fecal clone RL386_aao85f09
EU622658.1 gg_id:278098 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a
EU766883.1 gg_id:347024 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
DQ803678.1 gg_id:198988 human fecal clone RL200_aai57a11
EU887971.1 gg_id:323501 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
EU506802.1 gg_id:260776 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56f01
EF603362.1 gg_id:232918 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU452114.1 gg_id:332037 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N
DQ815954.1 gg_id:167276 mouse cecum clone aab24g06
EF603499.1 gg_id:232260 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ679323.1 gg_id:517248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU471941.1 gg_id:296850 Asiatic elephant feces clone AE3_aaa04e06
DQ793811.1 gg_id:178684 human fecal clone RL176_aah43f06
EU469735.1 gg_id:291917 flying fox feces clone FF_h04_1
DQ795793.1 gg_id:194778 human fecal clone RL245_aai82e04
GQ897459.1 gg_id:540055 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
FJ368429.1 gg_id:366722 feces adult twins and mothers; TS3 clone TS3_a04c03
EU509946.1 gg_id:262944 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b08
DQ905341.1 gg_id:173282 human fecal clone 013B-F5
FJ879345.1 gg_id:394512 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU452674.1 gg_id:332282 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
AY916207.1 gg_id:112958 human cecum biopsy clone LF02
EU455446.1 gg_id:355041 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N
AJ488078.1 gg_id:66186 chlorobenzene-degrading consortium clone IB-18
FJ879403.1 gg_id:392407 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU451140.1 gg_id:329458 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
AY570589.1 gg_id:108465 -temperature biodegraded Canadian oil reservoir clone PL-38B12
AY487928.1 gg_id:100412 Acetanaerobacterium elongatum str. Z7
EF402779.1 gg_id:207624 human fecal clone SJTU_B_12_36
EU845152.1 gg_id:347819 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU775744.1 gg_id:339121 Horse feces clone horsem_aai94d08
FJ269107.1 gg_id:338187 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil
FJ367099.1 gg_id:358674 feces adult twins and mothers; TS28 clone TS28_a03e06
EF604611.1 gg_id:231168 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ502524.1 gg_id:590995 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-

DQ071530.1	233711	232.0	246.7	52.7	113.2	76.9	55.4
EU470080.1	289802	6953.6	5905.6	5964.8	10737.2	5361.9	5883.1
AM697405.1	221429	114.3	112.1	214.1	108.1	97.1	53.6
AY916159.1	113797	1458.8	1344.4	1361.2	1108.1	2802.4	1594.7
AB089039.1	77833	7058.6	6465.2	3749.2	5965.3	6977.4	6000.1
FJ371922.1	366885	5531.2	4946.3	2985.8	5589.6	8210.6	6760.7
DQ797006.1	187006	2595.5	4638.1	2548.9	2025.7	2600.9	2319.6
EU622658.1	278098	41.7	38.5	111.0	99.5	81.6	43.9
EU766883.1	347024	25.0	28.5	47.7	36.9	55.3	23.1
DQ803678.1	198988	1876.5	1324.0	1998.9	1872.1	2818.7	1925.3
EU887971.1	323501	4286.8	4198.6	5170.0	3130.6	2142.6	2201.6
EU506802.1	260776	1820.0	2110.0	1773.1	2413.2	1717.2	1291.8
EF603362.1	232918	5147.4	7634.2	4577.9	6913.8	8304.0	6902.5
EU452114.1	332037	1000.3	1771.2	2816.5	2256.9	588.0	1497.9
DQ815954.1	167276	982.6	627.1	1343.0	790.1	244.4	529.9
EF603499.1	232260	11257.2	10357.5	9062.8	9729.2	7998.9	9836.9
FJ679323.1	517248	2013.5	3520.7	5276.3	2889.7	5205.1	3816.3
EU471941.1	296850	6180.5	6811.9	5972.2	6626.5	5348.7	5751.4
DQ793811.1	178684	3562.3	2781.4	2219.0	4152.5	1724.6	2279.3
EU469735.1	291917	11490.7	11002.8	4545.6	9240.5	9712.7	9333.5
DQ795793.1	194778	15136.3	16307.9	7233.6	9006.3	10177.9	10441.0
GQ897459.1	540055	4198.0	3644.3	7199.5	3402.5	2796.1	2276.7
FJ368429.1	366722	1325.5	1728.4	2775.8	2179.3	2662.3	2745.6
EU509946.1	262944	172.8	119.3	536.7	167.2	190.6	135.9
DQ905341.1	173282	2303.4	4499.2	4152.8	5699.0	2252.6	1850.9
FJ879345.1	394512	6625.5	7156.6	4721.8	4338.4	1844.1	4644.6
EU452674.1	332282	7424.0	6247.3	1962.3	6355.8	6230.9	5226.1
AY916207.1	112958	734.3	1397.4	3395.6	528.4	549.1	1218.6
EU455446.1	355041	3213.7	2626.7	1967.9	3192.9	2800.3	4364.5
AJ488078.1	66186	63.1	84.6	157.1	87.7	74.5	33.9
FJ879403.1	392407	62.6	113.6	90.2	75.7	111.8	44.0
EU451140.1	329458	9402.7	9455.9	6157.2	4027.6	3887.0	4776.1
AY570589.1	108465	68.9	118.7	188.5	489.7	206.5	85.5
AY487928.1	100412	95.7	79.3	81.9	86.3	60.5	55.7
EF402779.1	207624	24.8	29.7	24.8	32.2	48.8	19.2
EU845152.1	347819	934.2	1387.7	1729.6	826.2	2883.3	2727.3
EU775744.1	339121	503.7	673.2	1121.6	274.7	733.5	667.5
FJ269107.1	338187	11716.9	8166.4	6698.9	6648.0	10045.6	7626.3
FJ367099.1	358674	462.9	697.9	1682.2	743.7	1872.1	2522.1
EF604611.1	231168	4936.4	3644.0	1402.4	6932.0	6088.3	7061.3
GQ502524.1	590995	3069.0	2952.8	6145.1	3604.9	4496.4	3359.4

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EU462611.1 gg_id:294242 Sumatran orangutan feces clone orang2_aai66a12
EU506329.1 gg_id:260859 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d05
EU506188.1 gg_id:268806 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02g02
DQ805002.1 gg_id:187524 human fecal clone RL385_aao83h09
DQ796382.1 gg_id:189994 human fecal clone RL179_aah26e06
EU463788.1 gg_id:291111 domesticated horse feces clone horsej_aai92h01
DQ904661.1 gg_id:168845 human fecal clone 001-c11
AY622268.1 gg_id:100124 subsurface soil clone S-F26
EU452362.1 gg_id:312979 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N
DQ905623.1 gg_id:170271 human fecal clone 014B-H9
DQ807121.1 gg_id:179301 human fecal clone RL244_aaj46e08
EU469245.1 gg_id:289125 Speke's gazelle feces clone SP3_g02_1
FJ825458.1 gg_id:550485 Microbial during start-up mesophilic biogas plant clone 135_BE5_6
AB270141.1 gg_id:172165 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos
AY984523.1 gg_id:123415 human stool clone B450
EU506576.1 gg_id:272283 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04f01
EU765144.1 gg_id:314884 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
GQ867487.1 gg_id:579293 and prevalence blaTEM genes Arctic seals colon content clone CSG58
EU531982.1 gg_id:276231 Predominant role host genetics controlling gut microbiota FMF remission stool clone
DQ800460.1 gg_id:174827 human fecal clone RL183_aah24h03
EU472119.1 gg_id:296626 francois langur feces clone FL_1aaa02g05
EU456056.1 gg_id:315580 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EF071169.1 gg_id:195415 library survey and quantitative measurement major mucosa- IBD human colonic muc
EU462752.1 gg_id:302382 Sumatran orangutan feces clone orang2_aai68e04
AB234479.1 gg_id:148075 termite gut homogenate clone MgMjR-012
GU303965.1 gg_id:538145 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
DQ015351.1 gg_id:131324 mouse cecum clone M3_a07
EU461068.1 gg_id:289969 red kangaroo feces clone KO1_aai43e06
GQ448715.1 gg_id:532859 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g
DQ817325.1 gg_id:173276 mouse cecum clone aaa73d09
AJ576369.1 gg_id:103744 hindgut homogenate Pachnoda ephippiata larva clone PeH56
EU771106.1 gg_id:333205 Asiatic elephant feces clone AE3_aaa02b02
EU506196.1 gg_id:261365 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03c05
GQ047291.1 gg_id:423254 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011a
EF603339.1 gg_id:234992 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ800226.1 gg_id:181527 human fecal clone RL303_aal69h06
EU506587.1 gg_id:263968 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04g10
EU794136.1 gg_id:307564 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE37
FJ368767.1 gg_id:362041 feces adult twins and mothers; TS49 clone TS49_a04c07
EU455609.1 gg_id:345861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80N
EU454483.1 gg_id:310557 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S

EU462611.1	294242	7515.1	8334.8	5933.1	7228.3	12465.0	12119.1
EU506329.1	260859	1020.7	1664.7	2618.9	2314.3	2599.8	1789.7
EU506188.1	268806	1864.6	1292.1	2492.7	1350.3	748.8	944.4
DQ805002.1	187524	3756.8	5155.0	5505.2	4024.9	6754.5	4909.0
DQ796382.1	189994	6806.2	6498.2	4835.3	7853.6	7568.7	8561.5
EU463788.1	291111	1037.6	1863.0	1999.0	2072.0	1601.8	3307.7
DQ904661.1	168845	4098.9	4118.6	5846.4	8954.6	7082.1	7133.5
AY622268.1	100124	288.6	106.6	401.3	111.0	96.4	100.0
EU452362.1	312979	636.2	515.5	563.5	1314.6	163.4	207.4
DQ905623.1	170271	5407.1	4417.9	4003.2	5859.8	3256.3	3704.1
DQ807121.1	179301	1698.2	2819.4	1549.0	863.0	1572.2	3137.0
EU469245.1	289125	1169.4	593.4	1503.4	686.2	159.7	156.3
FJ825458.1	550485	1595.4	1066.8	3045.0	2103.1	391.2	1361.7
AB270141.1	172165	716.0	940.7	1868.9	444.1	1771.9	2543.5
AY984523.1	123415	3174.5	3230.8	4464.1	6591.8	1158.7	2362.9
EU506576.1	272283	739.7	1276.0	262.8	944.1	1596.3	1197.2
EU765144.1	314884	147.9	147.8	251.3	218.2	72.9	151.5
GQ867487.1	579293	13059.0	11700.0	9254.8	9796.9	11598.3	15001.9
EU531982.1	276231	6832.4	8309.9	6928.9	5513.4	7529.6	5663.3
DQ800460.1	174827	1281.3	1189.0	858.0	1138.5	1103.3	1754.6
EU472119.1	296626	1016.3	1259.4	1525.8	594.4	2278.7	1918.1
EU456056.1	315580	129.7	30.2	416.9	142.7	85.7	49.4
EF071169.1	195415	31.4	41.1	24.8	50.0	65.7	27.0
EU462752.1	302382	4038.3	4304.1	2995.4	4775.7	2769.7	2855.4
AB234479.1	148075	25.3	30.0	21.9	47.2	38.7	36.5
GU303965.1	538145	1089.4	1012.8	989.4	1425.0	247.8	822.5
DQ015351.1	131324	1642.1	3269.2	2134.7	740.0	2160.7	970.4
EU461068.1	289969	427.9	466.6	329.1	1607.3	254.0	386.8
GQ448715.1	532859	1729.1	2129.7	997.5	2962.7	2490.4	796.8
DQ817325.1	173276	356.2	199.3	52.6	515.3	1646.7	553.9
AJ576369.1	103744	127.2	404.3	629.5	333.1	294.2	353.2
EU771106.1	333205	2251.6	2041.5	2001.1	4525.5	4092.8	2985.0
EU506196.1	261365	1957.3	1001.5	1858.5	1439.7	559.3	1236.0
GQ047291.1	423254	30.9	48.9	55.7	78.9	71.8	43.9
EF603339.1	234992	8427.3	9753.5	4115.8	5316.8	4895.3	3578.2
DQ800226.1	181527	20.6	26.3	21.6	48.8	66.7	16.4
EU506587.1	263968	571.7	1229.4	1367.3	1630.9	2310.4	1214.2
EU794136.1	307564	3191.8	4338.4	6016.8	3316.8	3003.7	2877.2
FJ368767.1	362041	1444.9	1647.0	985.3	1713.0	1493.1	1079.2
EU455609.1	345861	1126.1	1792.6	2945.8	3969.7	1960.8	1673.5
EU454483.1	310557	7536.0	7068.3	5103.5	8151.2	10919.7	10269.5

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FJ879335.1 gg_id:420816 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr
EU467284.1 gg_id:291196 hamadryas baboon feces clone BAZ_a12
EU453205.1 gg_id:350575 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N
FJ368179.1 gg_id:365529 feces adult twins and mothers; TS3 clone TS3_a01b08
EU767264.1 gg_id:335138 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2
DQ455846.1 gg_id:157888 pre-adolescent turkey cecum clone CFT19C4
EF603241.1 gg_id:232048 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
AY854324.1 gg_id:109841 herbivore gastrointestinal tract clone Thompsons37
EU472376.1 gg_id:297774 Angola colobus feces clone EAC_1aaa04b03
EU766492.1 gg_id:328236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
EU772256.1 gg_id:333948 Argali sheep feces clone AS2_aao34b08
FJ368800.1 gg_id:362922 feces adult twins and mothers; TS49 clone TS49_a04g02
EF604823.1 gg_id:228391 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EF603352.1 gg_id:232042 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ809978.1 gg_id:189758 human fecal clone RL184_aao66f03
EU871402.1 gg_id:305146 Genetic Bovine (Bos taurus) Rumen Thailand clone CF342
GQ175456.1 gg_id:535444 Chicken intestinal microbiota modulations various feed supplementations DGGE and
EU510091.1 gg_id:261325 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01c01
EU506686.1 gg_id:258926 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54e03
EU505553.1 gg_id:272277 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02e12
GQ451212.1 gg_id:575559 Fecal Yunnan snub-nosed monkey feces clone J66
DQ015035.1 gg_id:131182 mouse cecum clone M2_c06
GQ491889.1 gg_id:560663 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU451586.1 gg_id:349538 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU507209.1 gg_id:271754 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03e10
DQ815929.1 gg_id:167166 mouse cecum clone aab24d05
EU509948.1 gg_id:264695 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b10
AF371759.1 gg_id:30067 swine intestine clone p-2506-18B5
EU509855.1 gg_id:258260 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e08
EU773500.1 gg_id:325524 Bonobo feces clone BNO_aaa04e04
EU778735.1 gg_id:322931 Springbok feces clone SBSD_aaa04b06_1
EU767072.1 gg_id:307566 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1
EU259422.1 gg_id:253559 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC46
FJ672969.1 gg_id:530829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU358715.1 gg_id:351451 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EU468521.1 gg_id:287988 okapi feces clone OK1_h03_1
DQ796435.1 gg_id:198029 human fecal clone RL179_aah28d02
EU764739.1 gg_id:347893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
EU474451.1 gg_id:291314 bighorn sheep feces clone BHSD_aaa02b12
FJ364955.1 gg_id:360031 feces adult twins and mothers; TS1 clone TS1_a01b10
EU461035.1 gg_id:291117 red kangaroo feces clone KO1_aai42g02

FJ879335.1	420816	837.4	773.2	811.7	526.5	1053.5	887.5
EU467284.1	291196	472.6	785.9	1378.1	579.3	992.7	848.1
EU453205.1	350575	7409.0	6847.0	2884.1	5729.8	7096.0	6036.3
FJ368179.1	365529	1538.5	1864.8	2026.7	1511.5	2731.1	2582.3
EU767264.1	335138	3092.4	2548.3	3219.9	2383.1	7058.3	6506.6
DQ455846.1	157888	27.7	39.5	95.0	65.3	63.9	40.2
EF603241.1	232048	15336.3	15748.5	9707.1	10291.7	13971.3	11316.8
AY854324.1	109841	93.3	47.2	139.5	197.5	66.7	21.0
EU472376.1	297774	5301.6	4657.6	1579.8	5091.2	5358.5	6037.0
EU766492.1	328236	212.2	129.0	1503.6	277.0	77.6	252.0
EU772256.1	333948	6745.4	5594.7	4827.2	6923.0	5958.5	8954.2
FJ368800.1	362922	1988.1	2405.6	3212.1	2337.6	5107.7	5389.4
EF604823.1	228391	15191.1	14956.0	9833.2	14209.4	12111.4	13911.6
EF603352.1	232042	2992.4	3769.5	581.0	6312.8	4221.7	5274.1
DQ809978.1	189758	6101.2	4301.3	2447.6	5483.8	4267.3	4688.0
EU871402.1	305146	1131.0	1438.7	3543.6	1405.9	2225.5	2384.4
GQ175456.1	535444	190.0	170.5	582.8	286.3	76.6	46.9
EU510091.1	261325	2308.2	2088.1	3011.8	3790.5	2510.5	2433.6
EU506686.1	258926	800.5	1734.1	2306.6	3370.8	1710.0	1855.1
EU505553.1	272277	3384.4	3371.6	4488.4	3039.9	4936.6	4745.3
GQ451212.1	575559	298.3	651.3	499.2	544.8	2406.0	1191.4
DQ015035.1	131182	58.7	110.4	53.2	79.1	93.5	79.6
GQ491889.1	560663	139.8	388.2	166.9	154.7	214.1	451.8
EU451586.1	349538	1902.5	2114.8	2852.3	1454.2	2324.4	1729.3
EU507209.1	271754	7305.9	8348.2	5766.8	6545.0	8837.5	9725.5
DQ815929.1	167166	9931.0	10960.0	4752.9	6889.5	9178.4	7800.8
EU509948.1	264695	3825.7	5701.2	4520.8	2534.5	4163.7	4051.2
AF371759.1	30067	383.7	391.8	336.4	327.5	340.1	318.0
EU509855.1	258260	1542.2	1578.0	2893.8	654.5	3023.7	2554.8
EU773500.1	325524	237.8	234.8	599.7	132.3	127.9	60.5
EU778735.1	322931	564.6	551.4	738.2	1925.7	211.8	580.9
EU767072.1	307566	6045.7	8819.7	3667.4	3856.1	5179.9	5198.0
EU259422.1	253559	5414.1	5083.2	5296.6	6279.7	6710.6	8267.4
FJ672969.1	530829	7099.4	7755.9	8445.0	8639.4	11028.0	9353.9
EU358715.1	351451	6770.3	6714.9	6251.4	3941.6	2857.0	3844.4
EU468521.1	287988	5571.1	6470.1	6434.7	6519.7	2407.9	4509.5
DQ796435.1	198029	538.2	921.5	157.7	286.3	393.1	411.6
EU764739.1	347893	4084.8	2840.2	2703.8	3537.3	2429.3	3954.0
EU474451.1	291314	5593.4	5659.8	4812.0	5972.6	7644.7	7891.3
FJ364955.1	360031	3366.3	4681.9	1236.7	1787.8	3950.9	2966.9
EU461035.1	291117	1195.1	1629.3	3807.6	2471.2	1309.6	1464.8

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EF603271.1 gg_id:229291 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ502529.1 gg_id:589530 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
EU768072.1 gg_id:314565 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
EU850470.1 gg_id:304165 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF49
EU510224.1 gg_id:270297 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03b09
EF603286.1 gg_id:234373 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU763025.1 gg_id:304725 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
AY976193.1 gg_id:125597 human ascending colon mucosal biopsy clone LW10
DQ327508.1 gg_id:145878 Metagenomic gut microbiome healthy human stool clone EA83
DQ325649.1 gg_id:146048 Metagenomic gut microbiome healthy human stool clone B215
EF603298.1 gg_id:232031 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ365192.1 gg_id:368412 feces adult twins and mothers; TS1 clone TS1_a04a02
EF099963.1 gg_id:195689 mouse cecum clone SWPT5_aaa02h03
DQ800544.1 gg_id:195667 human fecal clone RL183_aah29d10
EU455299.1 gg_id:333969 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
EU506732.1 gg_id:276761 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55c08
GQ896776.1 gg_id:590125 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do
EU768021.1 gg_id:328363 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4
AF371766.1 gg_id:107272 swine intestine clone p-4546-4Wb3
EU774361.1 gg_id:353322 Chimpanzee feces clone CHIMP1_aaj37f02
DQ793759.1 gg_id:177903 human fecal clone RL246_aai76h04
EF559116.1 gg_id:220174 mesophilic anaerobic digester clone C35_D7_H_B_C05
DQ116011.1 gg_id:130793 bovine teat canal clone D-74
FJ366095.1 gg_id:367681 feces adult twins and mothers; TS25 clone TS25_a02f06
EU772286.1 gg_id:340066 Argali sheep feces clone AS2_aao36e12
GQ448532.1 gg_id:510233 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr
EU158190.1 gg_id:235474 Clostridium sp. str. SW512
AM277638.2 gg_id:233253 fecal microbiota irritable bowel syndrome patients significantly that healthy subject
EF603366.1 gg_id:229110 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU778786.1 gg_id:349884 Springbok feces clone SBSD_aaa02e08_1
DQ800873.1 gg_id:185826 human fecal clone RL183_aao04f02
FJ363634.1 gg_id:363716 feces adult twins and mothers; TS14 clone TS14_a01e11
DQ794088.1 gg_id:187393 human fecal clone RL176_aan57h02
EF603784.1 gg_id:244484 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal m
EU454869.1 gg_id:311725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S
FJ366738.1 gg_id:361920 feces adult twins and mothers; TS27 clone TS27_a03c09
FJ440066.1 gg_id:546958 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou
FJ680947.1 gg_id:531238 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ366104.1 gg_id:361201 feces adult twins and mothers; TS25 clone TS25_a02g04
EU779323.1 gg_id:342446 Visayam Warty Pig feces clone VWP_aaa02g01
EU511636.1 gg_id:271303 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08a08

EF603271.1	229291	968.6	2012.6	2901.9	909.6	820.4	1349.5
GQ502529.1	589530	1281.2	2437.4	1998.1	1517.4	1692.5	2094.7
EU768072.1	314565	853.3	634.5	267.3	480.4	259.2	333.1
EU850470.1	304165	8775.8	8096.4	7776.4	7012.9	6675.9	6632.8
EU510224.1	270297	73.1	80.5	247.4	62.7	56.3	45.7
EF603286.1	234373	4686.3	5787.3	1622.3	3065.8	4197.8	3849.6
EU763025.1	304725	6170.6	5785.1	4143.9	4789.2	5682.9	5933.2
AY976193.1	125597	155.4	164.0	1204.9	194.2	2646.7	2436.1
DQ327508.1	145878	3033.6	3248.3	1740.1	1643.1	2509.3	2000.3
DQ325649.1	146048	57.5	60.8	39.6	71.7	86.8	28.9
EF603298.1	232031	6631.2	6267.4	3132.2	3913.1	5522.9	4617.9
FJ365192.1	368412	378.1	318.9	1464.4	218.0	535.2	537.5
EF099963.1	195689	3348.6	3196.3	2669.9	3065.7	5857.4	5665.0
DQ800544.1	195667	3645.2	2857.6	4025.0	4202.4	1747.4	4365.7
EU455299.1	333969	10177.0	10012.9	5529.1	10539.6	11996.6	11394.0
EU506732.1	276761	1477.7	1625.0	1391.0	797.0	1072.7	2029.2
GQ896776.1	590125	4107.6	3359.4	3420.7	4638.9	3804.2	3413.7
EU768021.1	328363	333.9	410.9	596.4	775.3	65.8	141.6
AF371766.1	107272	86.5	173.3	73.4	52.0	135.7	120.2
EU774361.1	353322	561.4	471.6	1717.9	255.0	247.2	288.1
DQ793759.1	177903	966.4	1082.0	564.0	2346.6	3290.4	6569.4
EF559116.1	220174	39.3	67.1	87.8	88.3	82.2	55.4
DQ116011.1	130793	1333.7	1057.7	916.3	2015.9	265.1	445.8
FJ366095.1	367681	5503.2	5648.0	3592.1	5259.0	4437.2	6329.3
EU772286.1	340066	6374.0	7367.8	6469.5	7151.9	10330.4	10774.7
GQ448532.1	510233	576.0	474.6	212.4	137.6	162.4	201.9
EU158190.1	235474	467.4	306.4	1290.4	193.3	390.6	420.2
AM277638.2	233253	18.8	17.7	17.6	49.1	55.6	23.6
EF603366.1	229110	256.2	150.9	309.0	240.1	69.8	58.8
EU778786.1	349884	8789.1	8064.6	9021.9	11041.3	14735.3	12163.8
DQ800873.1	185826	1348.0	1625.9	1491.1	2791.5	4988.7	3790.7
FJ363634.1	363716	563.6	749.8	1103.2	1286.7	154.3	353.6
DQ794088.1	187393	219.2	294.4	425.0	377.3	738.7	218.5
EF603784.1	244484	4228.9	4355.8	4124.3	6459.5	5260.1	5803.1
EU454869.1	311725	4380.3	3094.4	5208.3	4896.6	1177.0	4527.0
FJ366738.1	361920	1436.2	1514.6	1618.5	2803.3	419.3	1319.6
FJ440066.1	546958	4939.8	4518.5	3625.0	3098.9	648.4	1123.1
FJ680947.1	531238	4130.6	4113.3	6225.5	4108.7	1672.2	3538.2
FJ366104.1	361201	628.2	411.7	895.2	503.3	233.9	451.4
EU779323.1	342446	77.9	54.7	70.2	54.9	85.8	32.4
EU511636.1	271303	1702.8	2564.4	3317.8	1317.3	1403.4	1586.3

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EU509971.1 gg_id:273737 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24f03
GQ491419.1 gg_id:558068 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ491157.1 gg_id:581278 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU842952.1 gg_id:303785 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU748046.1 gg_id:355404 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43g04
EU465638.1 gg_id:301382 argali sheep feces clone AS1_aao40e01.Contig1
EU844075.1 gg_id:328379 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ374214.1 gg_id:369525 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
FN436123.1 gg_id:539296 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
FJ363880.1 gg_id:361066 feces adult twins and mothers; TS14 clone TS14_a04d11
EU506986.1 gg_id:274921 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09d08
EF603494.1 gg_id:234342 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
FJ881322.1 gg_id:459119 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU006198.1 gg_id:256016 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
AJ608244.1 gg_id:149660 human biopsies ulcerative colitis biopsy clone UC7-69
DQ802767.1 gg_id:199696 human fecal clone RL188_aan96c12
EU764801.1 gg_id:331168 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2
GQ451266.1 gg_id:565404 Fecal Yunnan snub-nosed monkey feces clone J245
FJ368624.1 gg_id:361341 feces adult twins and mothers; TS49 clone TS49_a02e05
EU474535.1 gg_id:289015 bighorn sheep feces clone BHSD_aaa04h11
DQ456247.1 gg_id:158456 pre-adolescent turkey cecum clone CFT211A12
EF686627.1 gg_id:257352 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1:
EF445160.1 gg_id:215193 rabbit cecum clone NED3A12
FJ365131.1 gg_id:370011 feces adult twins and mothers; TS1 clone TS1_a03c05
EF603330.1 gg_id:230238 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
EU453550.1 gg_id:341015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU507924.1 gg_id:268722 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e09
DQ904669.1 gg_id:164541 human fecal clone 001-c7
AB288879.1 gg_id:200879 termite gut homogenate clone BOf1-09
EU507998.1 gg_id:276229 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01e10
AY916333.1 gg_id:114325 human stool clone C342
GQ451236.1 gg_id:578147 Fecal Yunnan snub-nosed monkey feces clone J158
FJ371419.1 gg_id:358780 feces adult twins and mothers; TS6 clone TS6_a04g03
EU508713.1 gg_id:269238 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g09
DQ796608.1 gg_id:192022 human fecal clone RL179aan75g07
DQ325941.1 gg_id:147410 Metagenomic gut microbiome healthy human stool clone B814
FJ363232.1 gg_id:362622 feces adult twins and mothers; TS148 clone TS148_a04g08
DQ793709.1 gg_id:176372 human fecal clone RL246_aai76a06
EU772408.1 gg_id:315393 Hamadryas Baboon feces clone BAZ_aah91d12
DQ815688.1 gg_id:173264 mouse cecum clone aab21a03
EF603333.1 gg_id:228320 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse

EU509971.1	273737	4626.8	6010.9	4288.9	2354.7	1465.2	2091.7
GQ491419.1	558068	41.6	44.7	56.7	82.0	74.7	26.9
GQ491157.1	581278	2872.0	1753.0	2169.8	1836.0	4031.7	2301.2
EU842952.1	303785	853.6	1977.6	2052.9	1787.7	2960.5	3392.5
EU748046.1	355404	5876.3	6067.1	8956.2	8036.8	6664.6	6168.0
EU465638.1	301382	2696.6	6134.7	3737.7	3742.6	1754.5	3048.6
EU844075.1	328379	423.4	263.9	304.2	166.5	96.1	88.9
FJ374214.1	369525	321.4	543.9	1171.6	512.4	1174.3	809.2
FN436123.1	539296	2487.8	2338.4	1290.5	3844.5	819.6	2137.3
FJ363880.1	361066	5594.8	5298.5	5378.7	7907.7	7509.5	8301.3
EU506986.1	274921	19.1	28.0	21.2	56.7	54.5	22.5
EF603494.1	234342	706.8	1832.4	2950.0	667.5	2056.3	1208.0
FJ881322.1	459119	1601.4	1581.7	1522.1	3660.7	3616.2	3389.6
EU006198.1	256016	2887.3	4135.7	1997.0	2140.7	1549.0	1931.0
AJ608244.1	149660	839.3	704.3	646.8	276.3	216.4	278.7
DQ802767.1	199696	298.2	279.8	655.8	305.7	1556.6	2140.0
EU764801.1	331168	5402.9	4739.3	4685.1	2945.3	2377.5	2480.6
GQ451266.1	565404	1459.1	1783.2	3924.5	2157.4	3247.2	2488.5
FJ368624.1	361341	8389.2	9820.5	5754.5	5822.1	7055.3	8261.1
EU474535.1	289015	486.4	618.6	1783.0	338.2	193.2	350.9
DQ456247.1	158456	69.1	98.2	162.4	58.6	156.1	45.0
EF686627.1	257352	1888.6	1558.7	6004.3	1769.5	3303.9	2882.5
EF445160.1	215193	25.2	28.2	42.2	53.5	56.6	24.6
FJ365131.1	370011	2252.7	3056.5	889.5	1058.0	1563.8	1773.5
EF603330.1	230238	14054.9	13845.5	7656.2	8463.8	7073.2	8067.4
EU453550.1	341015	3635.9	3814.8	1328.8	4358.8	5699.7	6173.9
EU507924.1	268722	4631.6	4888.5	1881.3	5453.5	7151.7	6262.8
DQ904669.1	164541	9973.0	7873.7	5117.7	11049.8	11163.9	10210.2
AB288879.1	200879	53.3	105.8	44.7	61.5	105.3	58.5
EU507998.1	276229	3162.7	3296.8	1612.8	2000.3	2202.5	2029.1
AY916333.1	114325	6911.5	6618.9	6169.5	6379.0	5030.2	6054.3
GQ451236.1	578147	2172.7	2924.0	2004.8	1917.5	4455.3	3958.2
FJ371419.1	358780	385.4	481.7	756.8	1006.9	120.4	256.5
EU508713.1	269238	1751.2	1272.7	1273.7	987.8	2309.0	1925.2
DQ796608.1	192022	1092.3	1150.5	1222.2	3415.9	247.3	561.7
DQ325941.1	147410	27.9	67.5	130.7	54.8	71.4	59.8
FJ363232.1	362622	2249.5	2607.0	3721.3	5152.8	2942.3	4070.7
DQ793709.1	176372	829.7	563.8	1347.2	886.9	125.2	341.9
EU772408.1	315393	6942.4	7047.2	7433.5	4537.3	5368.4	5738.4
DQ815688.1	173264	6522.6	5460.8	4174.2	5710.5	3772.5	3431.6
EF603333.1	228320	3259.2	4523.9	3643.6	4723.3	7344.7	7140.3

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EF686600.1 gg_id:247858 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8
EU469255.1 gg_id:297622 Speke's gazelle feces clone SP3_h06_1
EU453520.1 gg_id:343276 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83
EU170433.1 gg_id:240700 Clostridium sp. str. W72
FJ365004.1 gg_id:366702 feces adult twins and mothers; TS1 clone TS1_a01g01
DQ793719.1 gg_id:185168 human fecal clone RL246_aai76b08
EU463106.1 gg_id:294065 naked mole-rat feces clone molerat_aai70a01
AB307643.1 gg_id:268556 clay wall used Japanese traditional buildings clone B42
DQ800879.1 gg_id:198184 human fecal clone RL183_aao04f08
EU457334.1 gg_id:331013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80
EF400652.1 gg_id:210777 human fecal clone SJTU_E_16_56
DQ015580.1 gg_id:131378 mouse cecum clone M3_g06_2
DQ394651.1 gg_id:155932 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee
DQ808780.1 gg_id:190703 human fecal clone RL243_aai85b07
FJ366863.1 gg_id:357503 feces adult twins and mothers; TS27 clone TS27_a04g03
EU843786.1 gg_id:343476 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU509268.1 gg_id:263766 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46h08
AM693109.2 gg_id:525997 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar
EF404038.1 gg_id:213124 human fecal clone SJTU_C_03_83
EF603287.1 gg_id:231021 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous
GQ449055.1 gg_id:561879 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g
EF409954.1 gg_id:211472 Isolation equol-producing fecal clone QE4
EU470456.1 gg_id:297964 Grevy's zebra feces clone GZ_aaa02h03
AY916351.1 gg_id:113822 human stool clone D036
FJ364575.1 gg_id:361644 feces adult twins and mothers; TS15 clone TS15_a04e11
AF376224.1 gg_id:50072 ckncm320-B3-25 clone
EU775897.1 gg_id:330061 Horse feces clone horsem_aai93d07
DQ800561.1 gg_id:178571 human fecal clone RL183_aah29g05
DQ905474.1 gg_id:170185 human fecal clone 014-b10
DQ803929.1 gg_id:189820 human fecal clone RL200_aai60a09
EU764469.1 gg_id:311864 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
EU469193.1 gg_id:291668 Speke's gazelle feces clone SP3_h03_1
EU468601.1 gg_id:302588 okapi feces clone OK1_g10_1
FJ673780.1 gg_id:527976 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ175446.1 gg_id:566899 Chicken intestinal microbiota modulations various feed supplementations DGGE anc
AY854329.1 gg_id:110824 herbivore gastrointestinal tract clone Thompsons41
EU461148.1 gg_id:294246 hamadryas baboon feces clone BAZ_aah89b06
EU508360.1 gg_id:271519 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03g03
DQ237939.1 gg_id:143881 influence fumarate disodium on ruminal metabolism goats goat rumen clone M2
FJ368475.1 gg_id:362854 feces adult twins and mothers; TS3 clone TS3_a04g11
EU761698.1 gg_id:338035 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1

EF686600.1	247858	1040.1	1460.4	1084.9	791.0	220.7	408.2
EU469255.1	297622	8494.0	7743.7	4464.2	5795.7	8307.3	6344.5
EU453520.1	343276	1778.0	2852.2	1160.0	887.8	908.3	987.8
EU170433.1	240700	15261.5	16412.1	12912.1	12952.8	12557.3	13211.5
FJ365004.1	366702	6018.8	7526.6	4148.6	4284.4	5033.1	5527.5
DQ793719.1	185168	107.7	107.2	216.3	275.4	161.5	149.6
EU463106.1	294065	2355.8	3753.1	3620.4	3499.2	6035.1	4995.9
AB307643.1	268556	487.9	756.7	1304.8	501.5	998.6	746.8
DQ800879.1	198184	78.8	156.8	215.2	215.2	135.0	65.3
EU457334.1	331013	1304.0	1144.8	1148.1	2955.4	224.6	428.0
EF400652.1	210777	941.9	541.9	1076.0	701.7	448.5	60.3
DQ015580.1	131378	5319.5	6638.9	4030.3	5191.0	8279.7	6391.9
DQ394651.1	155932	75.6	202.6	310.8	94.5	177.2	213.7
DQ808780.1	190703	3935.9	3723.1	2424.8	1705.8	195.2	780.5
FJ366863.1	357503	1842.0	1588.7	309.7	1678.0	319.5	199.8
EU843786.1	343476	483.4	492.0	686.2	254.1	211.3	648.6
EU509268.1	263766	2952.8	3267.9	2271.6	1951.7	5811.7	4726.6
AM693109.2	525997	95.2	102.6	259.0	62.4	68.0	46.3
EF404038.1	213124	25.2	34.2	26.0	42.6	53.9	21.9
EF603287.1	231021	4347.5	5083.9	4299.7	3242.2	4470.2	5542.3
GQ449055.1	561879	6527.1	6875.1	3878.1	4075.8	4005.7	5185.3
EF409954.1	211472	43.8	81.5	56.1	94.1	116.0	49.9
EU470456.1	297964	151.6	454.5	633.4	501.3	405.1	677.7
AY916351.1	113822	6765.9	8421.8	7077.4	6048.4	7945.3	7119.6
FJ364575.1	361644	1363.0	1049.5	2622.1	848.0	2497.6	5273.1
AF376224.1	50072	34.6	47.3	20.2	46.9	65.7	29.7
EU775897.1	330061	4436.2	4597.4	1720.3	3876.0	2864.7	3204.9
DQ800561.1	178571	289.7	403.2	236.6	305.3	286.5	702.9
DQ905474.1	170185	1244.9	1102.7	1170.1	2814.2	884.0	1042.2
DQ803929.1	189820	46.5	31.6	32.4	55.9	40.2	25.7
EU764469.1	311864	2963.1	4828.9	4176.9	3502.3	4636.2	3022.4
EU469193.1	291668	13711.0	10819.7	3762.8	6271.6	6262.1	6324.4
EU468601.1	302588	1464.6	1664.3	3144.5	3661.5	3346.8	3391.1
FJ673780.1	527976	6003.7	7556.2	9056.1	5481.3	11095.2	9088.2
GQ175446.1	566899	482.1	477.2	58.6	138.3	94.8	34.2
AY854329.1	110824	33.3	44.5	24.7	58.1	94.2	23.0
EU461148.1	294246	2752.1	2791.6	1789.6	1592.5	2629.0	2743.0
EU508360.1	271519	10107.0	10042.9	10328.7	8746.2	9893.4	9259.5
DQ237939.1	143881	104.0	145.7	164.0	110.3	97.0	207.9
FJ368475.1	362854	3117.0	3323.6	2153.8	3401.3	5366.6	3861.2
EU761698.1	338035	3336.8	3476.1	6578.2	4567.5	6536.4	2651.5

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DQ800732.1 gg_id:176290 human fecal clone RL183_aao02g01
EF434360.1 gg_id:208911 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont
AB234454.1 gg_id:146455 termite gut homogenate clone MgMjD-029
DQ673514.1 gg_id:161997 rumen fluid clone GRC49
EU842855.1 gg_id:352007 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU381669.1 gg_id:263881 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p
AY980635.1 gg_id:122955 human rectum mucosal biopsy clone LL09
DQ809631.1 gg_id:196782 human fecal clone RL184_aan81g10
EU472112.1 gg_id:287351 francois langur feces clone FL_1aaa04a01
EF402506.1 gg_id:210552 human fecal clone SJTU_B_08_85
FJ366734.1 gg_id:367775 feces adult twins and mothers; TS27 clone TS27_a03c04
GU304571.1 gg_id:548654 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU468515.1 gg_id:292708 okapi feces clone OK1_f10
EF603304.1 gg_id:230751 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
GQ502533.1 gg_id:574604 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
EU506537.1 gg_id:266214 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03f04
EU794307.1 gg_id:346705 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L25
EU794105.1 gg_id:345871 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_W46
DQ014883.1 gg_id:130110 mouse cecum clone M1_h02_3
GU174108.1 gg_id:592004 Microbial Bactrian camel estimated rumen clone XJC79
EU842993.1 gg_id:308786 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB234478.1 gg_id:146871 termite gut homogenate clone MgMjW-23
FJ366107.1 gg_id:364527 feces adult twins and mothers; TS25 clone TS25_a02g07
DQ815960.1 gg_id:169219 mouse cecum clone aab24h04
EU504849.1 gg_id:270413 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03c03
EU511174.1 gg_id:270030 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h04
DQ793285.1 gg_id:189122 human fecal clone RL199_aaj41g04
EU887972.1 gg_id:323591 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
DQ804871.1 gg_id:187847 human fecal clone RL385_aao81h01
FJ371344.1 gg_id:370052 feces adult twins and mothers; TS6 clone TS6_a03h02
EU006164.1 gg_id:236225 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r
DQ798670.1 gg_id:199475 human fecal clone RL181_aan99g11
EF603268.1 gg_id:232658 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse
DQ809981.1 gg_id:175170 human fecal clone RL184_aao66f07
DQ795049.1 gg_id:178859 human fecal clone RL310_aam39e10
FJ367663.1 gg_id:369320 feces adult twins and mothers; TS2 clone TS2_a02b03
EU453675.1 gg_id:313431 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N
AY986321.1 gg_id:121129 human stool clone D715
GQ897679.1 gg_id:559659 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
EU774417.1 gg_id:309482 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14
EU463401.1 gg_id:299759 domesticated horse feces clone horsem_aai93c02

DQ800732.1	176290	2884.8	2697.0	2534.8	1816.5	2409.4	3172.3
EF434360.1	208911	31.3	44.5	58.4	41.0	103.3	38.2
AB234454.1	146455	534.8	421.1	2272.6	300.4	148.5	384.4
DQ673514.1	161997	60.4	53.2	84.8	71.3	104.9	57.5
EU842855.1	352007	255.4	211.0	600.7	1773.7	131.1	149.0
EU381669.1	263881	3941.3	3621.0	1585.5	2310.3	2386.7	1795.1
AY980635.1	122955	101.9	231.8	106.0	77.1	771.4	31.4
DQ809631.1	196782	2635.1	2752.9	1876.6	669.1	349.6	601.8
EU472112.1	287351	416.1	897.3	707.3	295.1	879.9	1128.6
EF402506.1	210552	4125.7	4280.5	2139.6	1916.2	239.1	473.1
FJ366734.1	367775	9823.3	11483.7	5392.7	7494.1	8973.5	8885.0
GU304571.1	548654	531.6	255.1	489.2	468.6	164.4	209.8
EU468515.1	292708	11209.8	11392.6	12359.8	8819.1	10243.0	10030.7
EF603304.1	230751	12213.6	9029.0	11733.0	9092.2	9663.6	9143.1
GQ502533.1	574604	5749.0	4195.7	7300.1	5941.8	3235.0	4294.3
EU506537.1	266214	174.4	177.4	98.6	402.9	63.0	55.2
EU794307.1	346705	3768.7	4711.9	5644.7	3249.5	1857.2	1962.4
EU794105.1	345871	6783.6	5781.9	2747.3	3193.5	2540.1	2212.1
DQ014883.1	130110	7852.2	8603.0	1602.7	7682.4	7440.0	3655.7
GU174108.1	592004	779.9	975.9	1020.9	414.8	1536.6	952.5
EU842993.1	308786	408.8	1022.7	1826.7	1008.8	1910.3	1065.0
AB234478.1	146871	81.9	97.3	376.2	72.5	54.6	53.7
FJ366107.1	364527	1406.7	2244.6	3733.9	2114.3	419.6	957.9
DQ815960.1	169219	5288.4	5342.3	2565.4	4950.9	6990.5	7454.3
EU504849.1	270413	10371.0	8957.5	7047.3	8713.3	12402.4	10217.6
EU511174.1	270030	645.7	1034.6	1888.5	847.7	314.5	404.0
DQ793285.1	189122	5814.7	3717.8	3302.6	6787.4	2373.6	3902.5
EU887972.1	323591	941.0	1043.0	1749.7	1420.7	292.7	730.4
DQ804871.1	187847	1465.0	1597.2	969.4	589.0	1516.0	2220.1
FJ371344.1	370052	2920.0	3011.0	2130.8	2773.8	2659.0	3865.1
EU006164.1	236225	9878.5	8692.8	5562.6	10174.4	11586.0	10101.3
DQ798670.1	199475	2181.5	1735.9	1037.2	1397.5	680.5	1073.5
EF603268.1	232658	2639.5	2384.6	868.0	3513.6	4321.6	4674.7
DQ809981.1	175170	244.4	116.4	303.3	142.5	244.9	466.9
DQ795049.1	178859	1325.4	1888.6	2337.5	1336.0	2281.6	1941.1
FJ367663.1	369320	2342.8	2035.3	5208.6	1357.9	2033.5	2442.8
EU453675.1	313431	6568.4	8196.2	5862.5	8414.3	4100.3	4611.1
AY986321.1	121129	4232.8	4323.0	3389.5	3416.0	744.9	1879.2
GQ897679.1	559659	47.3	67.4	87.5	92.7	74.2	55.3
EU774417.1	309482	11118.0	10758.2	4582.3	5342.5	8585.9	6699.8
EU463401.1	299759	1902.2	2213.3	508.8	335.3	138.6	201.4

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EU773222.1 gg_id:349444 BigHorn sheep feces clone BH1_aao25h06
DQ796716.1 gg_id:184287 human fecal clone RL179_aao53e11
EF445157.1 gg_id:216557 rabbit cecum clone NED1A10
GU304029.1 gg_id:590712 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
DQ673580.1 gg_id:171848 rumen fluid clone GRC115
EU465584.1 gg_id:296437 argali sheep feces clone AS1_aao38f10.Contig1
FJ880813.1 gg_id:437273 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
EU461017.1 gg_id:302744 red kangaroo feces clone KO1_aai42d09
EU470386.1 gg_id:293477 Grevy's zebra feces clone GZ_aaa02e11
EU382005.1 gg_id:272899 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
GU303495.1 gg_id:582952 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU470037.1 gg_id:303164 trancaspain urial feces clone TU1_aaa03b09
DQ801064.1 gg_id:193895 human fecal clone RL387_aao91f04
EU250958.1 gg_id:363509 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose
DQ793756.1 gg_id:188225 human fecal clone RL246_aai76g11
AB185540.1 gg_id:104439 rumen clone F23-D09
EU464078.1 gg_id:303244 reticulated giraffe feces clone gir_aah93b06
EU469077.1 gg_id:296415 Speke's gazelle feces clone SP3_a12
EU462596.1 gg_id:295615 Sumatran orangutan feces clone orang2_aai65h01
EU506620.1 gg_id:258946 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53e02
EF096988.1 gg_id:198512 mouse cecum clone SWPT13_aaa03g08
EU842961.1 gg_id:315150 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU466444.1 gg_id:287377 bighorn sheep feces clone BH2_aao23g10
FJ681223.1 gg_id:528725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU842439.1 gg_id:340770 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
EU794257.1 gg_id:344025 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J17
AB198524.1 gg_id:135518 termite gut wall fraction clone RsW02-034
EF454875.2 gg_id:221978 termite hindgut clone 290cost002-P3L-568
EU465567.1 gg_id:299012 argali sheep feces clone AS1_aao37h07.Contig1
AY858483.2 gg_id:109604 gastrointestinal tract eland clone ELAND_3
EU794310.1 gg_id:307291 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P3
AB185579.1 gg_id:103145 rumen clone F24-A06
EU794264.1 gg_id:354632 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L34
AF050582.1 gg_id:16073 contaminated aquifer clone WCHB1-54
EU794192.1 gg_id:323910 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E02
AM183003.1 gg_id:251289 and its spatial composts compost clone SMA17
EU844610.1 gg_id:311446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AB009176.1 gg_id:16063 rumen clone RFN17 bacterium
EU775199.1 gg_id:329360 Reticulated giraffe feces clone gir_aah94d12
DQ801076.1 gg_id:176718 human fecal clone RL387_aao91g09
EU794129.1 gg_id:356245 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE6

EU773222.1	349444	3835.4	4826.1	2771.0	2660.2	4032.3	4290.5
DQ796716.1	184287	1197.7	867.9	109.8	167.4	1025.8	106.2
EF445157.1	216557	81.2	132.0	84.5	203.3	86.7	104.4
GU304029.1	590712	4752.5	5193.4	3702.9	5898.4	7323.6	6958.7
DQ673580.1	171848	744.8	1177.9	1159.1	835.4	1092.3	1060.3
EU465584.1	296437	6143.7	8322.1	10089.7	5425.6	12263.0	12249.3
FJ880813.1	437273	2914.3	3033.8	3167.4	3800.2	2798.9	2951.6
EU461017.1	302744	15514.2	16785.7	9715.8	9364.5	9829.9	9578.0
EU470386.1	293477	1492.4	2547.5	1544.4	1068.1	1590.7	1668.6
EU382005.1	272899	3659.0	4330.2	2794.9	2905.1	2387.3	2746.6
GU303495.1	582952	8293.5	8091.7	3637.4	8651.4	5694.0	6961.4
EU470037.1	303164	2364.4	2506.6	2588.8	2717.8	3223.2	2656.9
DQ801064.1	193895	30.5	45.0	90.9	46.4	76.2	29.6
EU250958.1	363509	476.3	460.7	1020.9	625.8	128.9	904.2
DQ793756.1	188225	17.3	28.8	20.8	35.3	40.7	15.5
AB185540.1	104439	82.8	105.2	207.2	91.4	108.2	91.3
EU464078.1	303244	9010.4	11281.2	11089.8	8340.0	11575.1	11373.2
EU469077.1	296415	668.7	723.4	1890.2	422.4	200.5	642.6
EU462596.1	295615	3552.3	3522.2	5222.9	2938.9	592.3	3034.1
EU506620.1	258946	3444.8	5602.0	2549.2	3257.3	6446.0	5375.0
EF096988.1	198512	368.7	1230.8	1702.0	384.3	2537.2	3085.9
EU842961.1	315150	2359.0	2056.0	1408.8	1258.8	206.5	510.1
EU466444.1	287377	1922.2	1948.0	3813.1	1494.3	382.1	794.9
FJ681223.1	528725	3800.3	5338.2	3498.8	1760.4	2096.1	2504.1
EU842439.1	340770	2562.5	3170.8	2940.2	2612.1	2898.5	2577.8
EU794257.1	344025	73.0	88.6	510.6	108.4	64.6	139.4
AB198524.1	135518	59.0	34.0	77.2	326.7	55.2	39.8
EF454875.2	221978	930.2	795.9	531.3	515.1	100.3	164.6
EU465567.1	299012	41.5	42.5	109.6	68.6	59.5	47.2
AY858483.2	109604	69.0	343.5	475.9	153.3	142.1	179.2
EU794310.1	307291	5782.0	7412.2	8150.4	4750.1	7934.8	6244.2
AB185579.1	103145	42.3	78.9	84.4	85.0	50.6	40.5
EU794264.1	354632	2857.3	2764.3	4925.5	3176.9	3029.5	3952.7
AF050582.1	16073	4570.1	5816.6	4428.4	8844.8	5370.7	4257.0
EU794192.1	323910	425.8	497.7	1496.0	1099.7	223.6	785.8
AM183003.1	251289	3534.7	3604.0	3282.2	3511.0	1616.7	2064.8
EU844610.1	311446	9701.7	9640.5	5932.2	6697.4	4955.4	6106.9
AB009176.1	16063	1570.9	572.6	1391.2	1533.4	143.5	366.0
EU775199.1	329360	505.4	519.6	899.1	287.7	521.9	401.4
DQ801076.1	176718	6605.5	7411.4	8381.3	6064.7	3324.4	5645.0
EU794129.1	356245	2435.7	2148.9	999.9	283.0	973.1	205.8

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GQ402104.1 gg_id:512146 alpacas and sheep forestomach clone ALP8
EU474824.1 gg_id:300854 takin feces clone TAK_aaa02g06
EU774438.1 gg_id:342510 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1!
EU844076.1 gg_id:354499 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU794087.1 gg_id:312992 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_U43
EU773732.1 gg_id:346413 Cheetah feces clone CE3_aai05h11
DQ394632.1 gg_id:151144 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o
DQ394634.1 gg_id:151267 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o
EU794085.1 gg_id:314757 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_Z35
EU471995.1 gg_id:298553 francois langur feces clone FL_1aaa03c03
AB233996.1 gg_id:156549 anaerobic reactor clone B-3
GQ451308.1 gg_id:592857 Fecal Yunnan snub-nosed monkey feces clone J325
EU453210.1 gg_id:349798 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S
EU844645.1 gg_id:339252 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU794156.1 gg_id:349201 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L42
AB198484.1 gg_id:135720 termite gut wall fraction clone RsW01-056
EU466282.1 gg_id:289200 bighorn sheep feces clone BH2_aao21c11
GU454868.1 gg_id:518493 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
EU461091.1 gg_id:301917 red kangaroo feces clone KO1_aai44a02
EU468985.1 gg_id:301716 Speke's gazelle feces clone SP2_d07_1
GU174133.1 gg_id:551562 Microbial Bactrian camel estimated rumen clone XJC124
EU844169.1 gg_id:326767 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU461512.1 gg_id:303394 black rhinoceros feces clone RH_aaj91c12
EU462243.1 gg_id:299441 chimpanzee feces clone CHIMP1_aaj38c11
AB185776.1 gg_id:105514 rumen clone U29-D05
EU762139.1 gg_id:307647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1
EU468725.1 gg_id:290201 okapi feces clone OK2_g04_1
EU794278.1 gg_id:325883 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H46
EU509875.1 gg_id:270519 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h11
DQ797051.1 gg_id:199149 human fecal clone RL386_aao86c11
EU850568.1 gg_id:303584 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF379
EU381809.1 gg_id:273552 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
FJ681730.1 gg_id:522625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ681667.1 gg_id:517931 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU773299.1 gg_id:329112 BigHorn sheep feces clone BHSD_aaa04e12
EU464400.1 gg_id:295056 hamadryas baboon feces clone AFBAB_aai04d05
DQ808758.1 gg_id:177437 human fecal clone RL239_aaj12h05
EU469314.1 gg_id:293987 Speke's gazelle feces clone SP3_h03_3
FJ681337.1 gg_id:518060 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ456148.1 gg_id:157036 pre-adolescent turkey cecum clone CFT29A2
EU776470.1 gg_id:340210 Red Kangaroo feces clone KO2_aai17e12

GQ402104.1	512146	674.5	1621.4	2315.0	1160.4	1070.9	2573.3
EU474824.1	300854	4362.1	5791.7	6054.8	4824.4	7539.7	8777.7
EU774438.1	342510	2743.2	2649.7	564.9	1619.2	1691.8	1713.9
EU844076.1	354499	2920.9	4582.3	2536.9	2193.2	1221.3	2102.3
EU794087.1	312992	1194.4	1156.5	1682.9	1012.2	1109.0	893.7
EU773732.1	346413	2692.1	5191.9	4654.3	5706.3	5224.9	4529.5
DQ394632.1	151144	78.3	116.3	86.4	101.3	147.6	82.8
DQ394634.1	151267	2432.6	2655.8	1799.1	3558.7	2467.9	3400.8
EU794085.1	314757	3028.3	2484.1	1353.5	1796.1	535.4	1260.3
EU471995.1	298553	4066.6	4460.8	3018.8	5122.3	6586.5	5293.2
AB233996.1	156549	878.1	1619.7	4515.7	1707.8	2558.4	2008.0
GQ451308.1	592857	371.6	346.7	481.7	304.5	183.9	316.8
EU453210.1	349798	2837.6	3676.5	1439.0	2602.7	1486.9	2589.7
EU844645.1	339252	2439.2	2828.0	3278.4	3454.2	2102.4	2654.8
EU794156.1	349201	399.1	664.1	1368.5	532.8	204.0	371.7
AB198484.1	135720	41.0	41.1	94.3	53.8	56.2	25.9
EU466282.1	289200	5123.5	5075.7	7414.7	2415.2	2272.6	2633.6
GU454868.1	518493	5420.3	5211.3	4788.2	8469.7	4468.5	4108.2
EU461091.1	301917	5324.8	4909.8	5809.9	5901.6	2902.1	5905.3
EU468985.1	301716	690.1	1382.9	2192.6	801.7	446.0	408.6
GU174133.1	551562	438.7	364.8	1055.9	436.9	126.7	254.2
EU844169.1	326767	10823.1	12446.3	11830.3	10107.0	13536.9	14500.9
EU461512.1	303394	2546.0	2254.2	3930.8	1648.3	1767.2	2070.3
EU462243.1	299441	5589.8	7348.4	6421.6	3885.7	7311.9	6784.8
AB185776.1	105514	15.3	26.9	21.4	45.7	75.5	19.1
EU762139.1	307647	7955.8	10303.8	5103.8	6107.0	12583.9	11572.5
EU468725.1	290201	2428.9	2583.6	2334.8	893.5	1977.4	2177.9
EU794278.1	325883	218.1	414.6	847.0	234.6	393.7	313.9
EU509875.1	270519	1737.8	1833.2	2568.1	1142.9	1223.8	1686.1
DQ797051.1	199149	759.5	1287.2	442.9	464.3	1060.1	1138.6
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EU381809.1	273552	4532.1	4471.9	1176.9	1758.4	233.9	216.3
FJ681730.1	522625	5636.0	6072.7	1179.2	3942.6	6104.3	5428.0
FJ681667.1	517931	1532.4	1308.2	671.9	647.1	204.5	205.4
EU773299.1	329112	4349.4	4577.8	2443.7	3766.9	1676.3	1050.1
EU464400.1	295056	844.5	804.4	2018.2	738.2	254.7	442.7
DQ808758.1	177437	67.5	76.5	62.6	72.5	97.0	108.1
EU469314.1	293987	1229.0	2129.4	1548.6	829.7	395.2	852.8
FJ681337.1	518060	12289.7	11196.0	9390.2	10448.5	14612.0	11781.3
DQ456148.1	157036	3028.2	3766.0	4225.3	4350.6	6131.4	4812.7
EU776470.1	340210	1131.2	1592.5	820.0	679.6	653.1	1260.5

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EU775007.1 gg_id:318972 Francois Langur feces clone FL_1aaa04e03
FJ366012.1 gg_id:366309 feces adult twins and mothers; TS25 clone TS25_a01f12
GQ449144.1 gg_id:511242 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr
EU773276.1 gg_id:349695 BigHorn sheep feces clone BH2_aao22h09
EU771349.1 gg_id:321127 Asiatic elephant feces clone AE2_aaa02h02
EU776451.1 gg_id:354054 Red Kangaroo feces clone KO2_aai17g04
EU844199.1 gg_id:304015 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU472419.1 gg_id:293879 Angola colobus feces clone EAC_1aaa03d10
DQ801138.1 gg_id:181671 human fecal clone RL387_aao92g09
EU776342.1 gg_id:320831 Red Kangaroo feces clone KO1_aai42g11
EF686635.1 gg_id:237134 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1:
EU465539.1 gg_id:289774 argali sheep feces clone AS1_aao37c02.Contig1
EU464112.1 gg_id:296798 reticulated giraffe feces clone gir_aah93h11
AF050581.1 gg_id:16062 contaminated aquifer clone WCHB1-49
EU470437.1 gg_id:289438 Grevy's zebra feces clone GZ_aaa03g08
EU843153.1 gg_id:353179 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
EU463648.1 gg_id:288212 domesticated horse feces clone horsej_aai90d05
EU773265.1 gg_id:333820 BigHorn sheep feces clone BHSD_aaa03a03
EU470173.1 gg_id:292016 trancaspain urial feces clone TU2_aaa03h02
EU794179.1 gg_id:331046 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A15
EU470148.1 gg_id:300089 trancaspain urial feces clone TU2_aaa02b09
EU470366.1 gg_id:287724 Grevy's zebra feces clone GZ_aaa01d12
GQ502523.1 gg_id:583328 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
DQ805504.1 gg_id:187508 human fecal clone RL203_aai63e04
EU458486.1 gg_id:291270 spotted hyena feces clone HY2_h02
EU772024.1 gg_id:335757 Argali sheep feces clone AS2_aao36e09
GQ451202.1 gg_id:578310 Fecal Yunnan snub-nosed monkey feces clone J52
GQ448531.1 gg_id:594107 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr
EU779127.1 gg_id:328671 Trancaspian Urial feces clone TU2_aaa02e08
DQ801040.1 gg_id:196502 human fecal clone RL387_aao91c07
AB192042.1 gg_id:142583 termite gut homogenate clone M1NP1-42
AB198499.1 gg_id:135452 termite gut wall fraction clone RsW01-073
EF686609.1 gg_id:239644 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9:
EU468734.1 gg_id:297952 okapi feces clone OK3_b09
FJ366638.1 gg_id:362693 feces adult twins and mothers; TS27 clone TS27_a02a10
GQ448437.1 gg_id:547348 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g
FJ684375.1 gg_id:528722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU772128.1 gg_id:337202 Argali sheep feces clone AS2_aao36f02
EU779349.1 gg_id:344615 Somali Wild Ass feces clone WA_aaa04g06
FJ680570.1 gg_id:522248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU844036.1 gg_id:344137 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi

EU775007.1	318972	2119.5	2126.6	2286.1	1785.0	159.1	324.2
FJ366012.1	366309	1631.4	1902.0	2295.8	2148.2	511.3	1083.8
GQ449144.1	511242	2532.6	2600.4	1233.0	1522.1	1698.8	882.9
EU773276.1	349695	803.9	4881.4	3511.9	2758.3	575.4	1914.2
EU771349.1	321127	7765.3	7172.7	4425.5	7616.2	3608.2	5105.6
EU776451.1	354054	234.1	331.4	1059.4	294.7	252.9	342.9
EU844199.1	304015	3821.3	3260.3	1593.4	4046.2	4186.7	3190.8
EU472419.1	293879	284.6	822.4	1493.8	319.9	881.2	671.2
DQ801138.1	181671	2880.7	2101.2	2762.2	3414.3	1991.6	1507.5
EU776342.1	320831	5144.9	6000.8	5996.5	4309.3	7306.4	6337.9
EF686635.1	237134	4644.4	7504.7	8892.5	4336.4	7706.2	6652.1
EU465539.1	289774	3156.1	3434.7	6309.6	3475.9	1515.7	1586.1
EU464112.1	296798	2968.7	4161.4	4219.6	3518.7	2334.4	3296.6
AF050581.1	16062	320.0	485.8	155.3	884.0	284.0	126.3
EU470437.1	289438	2590.0	3163.7	3986.2	3479.8	2604.3	2976.2
EU843153.1	353179	2704.2	2643.3	4466.3	3300.4	1521.2	2331.1
EU463648.1	288212	6244.2	5116.6	8064.7	6247.8	5044.8	5779.0
EU773265.1	333820	1335.1	4403.1	4213.1	1222.8	2890.2	2274.8
EU470173.1	292016	9894.4	10352.5	9946.1	9345.5	12718.4	10582.6
EU794179.1	331046	8485.3	8618.0	5803.1	7166.7	5968.1	8033.8
EU470148.1	300089	5276.4	4550.4	6679.1	6423.5	5793.2	4172.8
EU470366.1	287724	10377.6	8935.1	6873.4	9355.5	5545.4	7159.9
GQ502523.1	583328	2493.0	4185.5	5563.2	2968.0	1514.7	3078.2
DQ805504.1	187508	3950.0	2758.2	2889.3	3786.1	2241.1	3663.2
EU458486.1	291270	68.9	152.0	410.8	87.8	90.8	90.4
EU772024.1	335757	4925.0	7973.0	4483.4	5072.1	5665.6	5631.7
GQ451202.1	578310	2519.4	3019.4	4317.6	1120.0	2961.5	3264.2
GQ448531.1	594107	5199.7	7951.0	3208.0	4832.3	3687.2	3473.4
EU779127.1	328671	1380.3	1874.9	1596.7	1002.2	621.0	873.3
DQ801040.1	196502	2634.0	2845.3	3113.1	3421.8	1373.0	1565.9
AB192042.1	142583	2077.9	2692.8	2495.1	1366.8	6518.5	2234.0
AB198499.1	135452	1931.2	2359.9	4371.3	2673.5	3192.2	1940.8
EF686609.1	239644	2709.1	2523.4	2742.6	3578.4	4081.3	4968.8
EU468734.1	297952	8937.6	7544.6	10721.6	9129.2	5471.0	5561.2
FJ366638.1	362693	3663.0	4274.3	1554.6	4329.8	1816.0	2843.5
GQ448437.1	547348	4268.1	4622.5	3886.6	4972.1	1700.6	4078.7
FJ684375.1	528722	1761.5	2924.0	2635.6	879.8	2266.6	2449.6
EU772128.1	337202	2959.6	2689.2	3882.4	2528.9	2660.7	3084.1
EU779349.1	344615	6634.5	7349.5	4424.6	3834.6	3317.6	4309.7
FJ680570.1	522248	6010.2	7266.4	4893.4	4346.4	6690.5	6721.7
EU844036.1	344137	4196.3	5118.7	6161.5	7856.9	3954.8	6421.5

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FJ680572.1 gg_id:528121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU794263.1 gg_id:326926 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J18
EU794233.1 gg_id:346556 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AF12
EU509795.1 gg_id:264941 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b06
GQ898040.1 gg_id:552448 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons
EU466218.1 gg_id:290974 bighorn sheep feces clone BH1_aao28c02
EU466103.1 gg_id:296496 bighorn sheep feces clone BH1_aao25h04
EU470320.1 gg_id:297021 Grevy's zebra feces clone GZ_aaa04h11
EU468812.1 gg_id:291161 okapi feces clone OK3_g06_2
EF088287.1 gg_id:190918 Sulfobacillus acidophilus str. 1
AY007665.2 gg_id:33263 Sulfobacillus yellowstonensis str. YTF-1
EU495236.1 gg_id:275497 Sulfobacillus benefaciens str. MT606
EU499919.1 gg_id:279555 Sulfobacillus thermosulfidooxidans str. N19-50-01
U75648.1 gg_id:14342 Sulfobacillus thermosulfidooxidans str. BC1
EF612374.1 gg_id:236874 historic semiarid lead-zinc site mine tailings clone K6-C04
EU419196.1 gg_id:264046 Sulfobacillus acidophilus str. DK-I15/45
AY079150.1 gg_id:60544 Sulfobacillus sibiricus str. N1
EU419151.1 gg_id:270741 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
DQ464142.1 gg_id:157528 acid mine drainage clone D3-5
EF612378.1 gg_id:244429 historic semiarid lead-zinc site mine tailings clone K6-C81
DQ834229.1 gg_id:164112 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National
AM749742.1 gg_id:246891 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl
EF612379.1 gg_id:250416 historic semiarid lead-zinc site mine tailings clone K6-C107
EU419149.1 gg_id:273033 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
EU419137.1 gg_id:275460 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
DQ464143.1 gg_id:157541 acid mine drainage clone D3-28
AY805540.1 gg_id:108883 thermophilic bioleaching clone JTC05
EU419152.1 gg_id:266474 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
NR_028814.1 gg_id:583050 Thermaerobacter subterraneus str. C21; ATCC BAA-137
AB061441.1 gg_id:50462 Thermaerobacter nagasakiensis str. JCM 11223
AB454087.1 gg_id:323069 Thermaerobacter sp. str. Ni80
EU214629.1 gg_id:331773 Thermaerobacter subterraneus ir-12
AY936496.1 gg_id:114490 Thermaerobacter riparius str. KW1
AB011495.1 gg_id:13721 Thermaerobacter marianensis
AB254790.1 gg_id:160816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
DQ234653.1 gg_id:143589 subsurface water clone DR546BH1103001SAD85
AF465653.1 gg_id:25424 G+C Gram-positive clone YNPRH70A
EF612375.1 gg_id:255886 historic semiarid lead-zinc site mine tailings clone K6-C05
AF391988.1 gg_id:27433 thermal soil clone YNPFFP9
EU419144.1 gg_id:275922 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
AM749765.1 gg_id:240376 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl

FJ680572.1	528121	4065.4	4451.2	2276.6	5712.6	6954.3	8994.6
EU794263.1	326926	3853.8	4879.3	4396.3	3830.6	1875.6	3009.1
EU794233.1	346556	4265.3	4915.0	5476.5	4717.2	7260.1	6077.2
EU509795.1	264941	3930.4	5749.8	2424.5	3369.8	5740.0	4883.0
GQ898040.1	552448	3723.8	3807.9	3604.0	5881.9	4940.3	4897.5
EU466218.1	290974	7736.2	8011.6	3929.0	6355.4	8549.9	7028.1
EU466103.1	296496	305.9	298.6	668.9	261.8	98.5	164.4
EU470320.1	297021	7418.7	7447.7	1152.1	2499.1	519.1	354.3
EU468812.1	291161	8788.7	7730.6	7185.3	5727.5	6886.5	6753.1
EF088287.1	190918	2068.3	2506.7	530.7	318.9	910.1	902.2
AY007665.2	33263	626.7	1101.4	92.6	101.2	371.2	332.3
EU495236.1	275497	2577.8	3942.9	2657.0	2816.9	3141.0	2853.1
EU499919.1	279555	4565.8	7080.7	3932.9	2502.3	1284.9	1833.1
U75648.1	14342	9111.2	10049.7	5617.2	5310.1	7003.5	6058.3
EF612374.1	236874	11619.3	16658.5	12021.8	7595.6	9198.7	7600.0
EU419196.1	264046	1927.6	2544.0	823.6	313.0	599.6	904.7
AY079150.1	60544	7404.8	6644.2	4669.0	1695.9	673.1	1466.7
EU419151.1	270741	1028.6	1286.6	876.4	460.9	357.0	596.9
DQ464142.1	157528	45.3	56.0	58.5	63.1	102.9	107.7
EF612378.1	244429	6989.3	8357.5	4991.9	4614.8	5635.3	5842.3
DQ834229.1	164112	236.8	963.8	338.0	477.3	763.5	887.5
AM749742.1	246891	1453.1	3463.9	5040.1	1837.1	1605.4	1391.7
EF612379.1	250416	3841.6	5157.8	3261.0	3667.4	2495.6	2607.0
EU419149.1	273033	7703.5	8957.1	5117.2	6743.6	7846.9	10767.5
EU419137.1	275460	6181.9	7536.1	4803.7	4452.9	7734.8	6063.7
DQ464143.1	157541	40.9	56.2	80.9	84.2	83.8	25.7
AY805540.1	108883	84.8	235.1	43.7	59.2	75.0	35.3
EU419152.1	266474	59.6	63.5	178.2	117.9	101.4	63.2
NR_028814.1	583050	2555.2	3270.3	2746.1	2193.7	1721.2	2698.2
AB061441.1	50462	3191.6	4371.0	4087.8	2208.2	2013.1	2792.0
AB454087.1	323069	5793.0	7888.6	4020.3	4775.2	6368.5	6794.0
EU214629.1	331773	3091.1	3951.9	3199.4	2767.2	6178.2	3320.9
AY936496.1	114490	1769.7	2249.3	2645.6	2205.6	1155.8	2127.8
AB011495.1	13721	3542.4	5231.2	3833.1	2775.0	3913.7	4392.0
AB254790.1	160816	697.0	287.3	461.8	986.2	182.7	280.0
DQ234653.1	143589	8520.1	9058.0	6544.4	9484.5	7500.0	6842.3
AF465653.1	25424	3293.4	4091.2	4377.6	4580.3	2480.6	4104.7
EF612375.1	255886	769.4	3695.5	7544.1	3340.7	2658.8	4674.3
AF391988.1	27433	8454.3	9664.9	6670.3	10577.5	6041.5	6789.0
EU419144.1	275922	499.1	1359.4	1174.3	350.8	955.9	458.1
AM749765.1	240376	2118.4	2353.4	4662.2	3081.3	1274.7	2303.2

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g__Syntrophomonas
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g__Syntrophomonas
g__Syntrophomonas
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g__unclassified
g__unclassified
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g__Thermoanaerobacterium
g__Thermoanaerobacterium

s__Symbiobacterium thermophilum	49734
s__unclassified	49267
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s__unclassified	49310
s__Syntrophomonas erecta	49077
s__Syntrophomonas wolfei	48459
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s__unclassified	48631
s__unclassified	48915
s__Thermoanaerobacterium saccharolyticum	48260
s__Thermoanaerobacterium saccharolyticum	48816
s__Thermoanaerobacterium saccharolyticum	49101
s__Thermoanaerobacterium saccharolyticum	49412
s__Thermoanaerobacterium saccharolyticum	49460
s__Thermoanaerobacterium saccharolyticum	49703
s__Thermoanaerobacterium saccharolyticum	49843
s__unclassified	48403
s__unclassified	49269
s__unclassified	49618

AP006840.1 gg_id:129187 Symbiobacterium thermophilum IAM 14863 str. IAM14863
AB361629.1 gg_id:243859 Symbiobacterium sp. str. KY38
AB455238.1 gg_id:322976 Symbiobacterium sp. str. KY46
AB455239.1 gg_id:344098 Symbiobacterium sp. str. KA13
DQ112187.1 gg_id:132753 Syntrophomonas sporosyntrophas str. Y4-1
FJ799130.1 gg_id:559105 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr
AF050586.1 gg_id:13690 contaminated aquifer clone WCHB1-82
AF482445.1 gg_id:77471 granular sludge clone R5p27
DQ984666.1 gg_id:257916 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) preser
AY290767.1 gg_id:87293 Syntrophomonas curvata str. GB8-1
AB252683.1 gg_id:172658 and activities propionate-oxidizing that affected propionate concentration anaerobic
AB186861.1 gg_id:103994 polychlorinated dioxin dechlorinating microcosm clone TSBW01
AB248633.1 gg_id:146259 mesophilic anaerobic butyrate-degrading reactor clone BHB04
EF559161.1 gg_id:217350 mesophilic anaerobic digester clone G35_D8_L_B_A02
AM947547.1 gg_id:259682 Minor changes detected microbial structure and after three week thermophilic dige
CR933176.1 gg_id:110152 Evry municipal wastewater treatment plant clone 008H01_B_SD_P15
AB248623.1 gg_id:149149 mesophilic anaerobic butyrate-degrading reactor clone BLB01
FJ799160.1 gg_id:511304 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr
AB234271.1 gg_id:150183 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
X99980.1 gg_id:13689 Thermosyntropha lipolytica str. JW265
DQ339710.1 gg_id:208155 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni
DQ080135.1 gg_id:137138 reductive dechlorination 2345-tetrachlorobiphenyl three s: evidence involvement D
AB192059.1 gg_id:141089 termite gut homogenate clone M1PL1-18
AB248632.1 gg_id:145683 mesophilic anaerobic butyrate-degrading reactor clone BHB03
AB234008.1 gg_id:154827 anaerobic reactor clone B-15
NR_028910.1 gg_id:552212 Pelospora glutarica str. WoGl3; DSM 6652
EF515712.1 gg_id:222308 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
FJ799131.1 gg_id:510041 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr
AB274497.1 gg_id:203894 packed-bed reactor clone CFB-8
AB021305.1 gg_id:13691 Syntrophothermus lipocalidus str. TGB-C1
AB539943.1 gg_id:567072 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t
X76743.1 gg_id:13762 Clostridium thermoamylolyticum str. DSM2335
AY350594.2 gg_id:221143 Thermoanaerobacterium aciditolerans str. 761-119
EU999016.1 gg_id:322435 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field For
FJ268955.1 gg_id:356922 Thermoanaerobacterium saccharolyticum str. B6A
EU563363.1 gg_id:272616 Thermoanaerobacterium saccharolyticum str. D22
FM999998.1 gg_id:532726 Thermoanaerobacterium sp. PO-2009
L09172.1 gg_id:13755 Thermoanaerobacterium xylanolyticum str. LXIIT
AY140670.1 gg_id:59208 Thermoanaerobacterium bryantii str. mel9
AY331143.1 gg_id:106330 Mahella australiensis str. 50-1-BON
AF247003.1 gg_id:27592 Thermoanaerobacterium thermosaccharolyticum str. D120-70

AP006840.1	129187	59.0	99.6	138.7	81.4	74.0	49.9
AB361629.1	243859	3081.0	4509.1	6265.8	3232.2	4570.5	4844.0
AB455238.1	322976	3117.5	3808.4	4568.5	4716.2	2833.2	2950.3
AB455239.1	344098	4339.1	4485.6	1588.1	2588.6	1633.9	1979.4
DQ112187.1	132753	227.7	343.4	215.3	347.3	90.5	215.1
FJ799130.1	559105	147.9	160.7	304.8	174.6	76.1	72.2
AF050586.1	13690	12217.1	14119.3	7033.8	6374.4	8584.7	12200.4
AF482445.1	77471	119.7	163.4	433.7	178.1	153.0	188.1
DQ984666.1	257916	22.7	29.9	19.7	54.1	53.0	21.3
AY290767.1	87293	42.1	136.6	490.0	70.7	57.8	63.6
AB252683.1	172658	3761.3	4911.7	4974.9	3197.8	6435.3	5386.6
AB186861.1	103994	9859.4	11979.2	7618.9	8076.6	8651.7	10742.7
AB248633.1	146259	1197.0	2851.1	875.1	1756.3	840.1	1816.0
EF559161.1	217350	70.1	129.8	97.4	101.3	85.3	43.6
AM947547.1	259682	4565.3	5117.7	2738.4	3775.6	1605.1	3515.6
CR933176.1	110152	50.4	41.5	94.7	65.7	48.5	15.9
AB248623.1	149149	501.8	1897.4	2320.0	423.1	69.3	31.1
FJ799160.1	511304	305.0	435.7	415.8	474.6	349.6	632.1
AB234271.1	150183	19.7	19.8	44.3	36.3	44.7	19.9
X99980.1	13689	2209.6	4728.5	2301.1	1470.6	1155.9	1189.9
DQ339710.1	208155	57.1	50.8	141.0	47.9	51.2	87.9
DQ080135.1	137138	4876.5	4772.2	2695.2	3381.6	3235.9	2904.9
AB192059.1	141089	10.1	25.7	20.1	60.5	58.1	25.3
AB248632.1	145683	132.0	119.1	983.4	51.7	61.9	106.8
AB234008.1	154827	4317.8	5597.5	7395.8	4963.4	9768.0	5881.6
NR_028910.1	552212	1394.3	2173.5	1118.5	1748.1	3159.7	1454.4
EF515712.1	222308	3836.6	4279.9	4139.0	2523.3	2759.7	2220.0
FJ799131.1	510041	9232.1	10430.9	6377.7	9223.7	9111.5	8643.7
AB274497.1	203894	7348.3	10453.0	12962.5	6131.9	8650.7	5764.1
AB021305.1	13691	14.7	24.4	26.9	38.9	51.2	14.7
AB539943.1	567072	4677.5	5760.1	8424.5	4360.1	4428.2	4090.8
X76743.1	13762	204.1	449.3	1182.3	292.1	257.3	588.8
AY350594.2	221143	628.9	925.6	4126.6	1541.2	804.2	1219.0
EU999016.1	322435	11112.9	10656.0	11700.8	10527.8	10485.5	10937.5
FJ268955.1	356922	475.7	856.4	4202.8	1105.0	789.6	1187.9
EU563363.1	272616	464.9	818.2	3296.8	550.3	512.0	558.2
FM999998.1	532726	1833.2	2921.7	4585.4	1029.7	3359.4	2700.9
L09172.1	13755	1457.4	1403.7	3319.6	2203.3	707.5	1105.0
AY140670.1	59208	6264.0	7207.2	2987.5	4308.0	3556.7	2866.2
AY331143.1	106330	225.4	248.8	687.9	262.6	142.9	254.2
AF247003.1	27592	163.7	356.7	1248.7	268.7	233.9	567.7

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

o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Veillonellaceae
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o__Clostridiales	f__Veillonellaceae

g__Thermoanaerobacterium
g__Acidaminococcus
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g__Anaeroglobus
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s__unclassified	49893
s__Acidaminococcus fermentans	50245
s__Acidaminococcus fermentans	50272
s__Acidaminococcus fermentans	50535
s__Acidaminococcus intestini	50571
s__unclassified	50834
s__unclassified	50482
s__Anaerospora hongkongensis	50927
s__unclassified	50142
s__unclassified	50647
s__Desulfosporomusa polytropa	50530
s__unclassified	50137
s__unclassified	50211
s__unclassified	50394
s__unclassified	50486
s__unclassified	50672
s__unclassified	50673
s__unclassified	50712
s__Dialister invisus	50107
s__Dialister invisus	50213
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s__Dialister invisus	50828
s__Dialister invisus	50958
s__Dialister micraerophilus	50124
s__Dialister pneumosintes	50428
s__unclassified	49995
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s__unclassified	50224
s__unclassified	50258
s__unclassified	50275

EF507903.1 gg_id:239939 Caldanaerobium fijiensis str. JW/YJL-F3
EF060090.1 gg_id:199473 Acidaminococcus fermentans str. ADV 6092.03
EF060091.1 gg_id:176163 Acidaminococcus fermentans str. ADV 1338.05
EU728758.1 gg_id:337187 Acidaminococcus sp. str. DJF_RP55
EF028685.1 gg_id:199297 Acidaminococcus intestinalis str. LBN 321
EU773566.1 gg_id:307454 Goeldi's Marmoset feces clone CAL_b10_1
NR_028812.1 gg_id:539819 Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 4477
AY372050.1 gg_id:94360 Anaerospora hongkongensis str. HKU15
AY728067.1 gg_id:104334 decayed velvetleaf seed clone S1-6-CL2
DQ816346.1 gg_id:172987 mouse cecum clone aaa80f06
EU981222.1 gg_id:340874 sulfate reducing living bench scale aquifer packed bed clone A7_FB
AB288880.1 gg_id:201846 termite gut homogenate clone BOf1-11
EF454547.2 gg_id:224315 termite hindgut clone 290cost002-P3L-2304
FJ542917.1 gg_id:510013 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
AM158322.1 gg_id:156235 Sporomusa rhizae str. RS
AJ279799.1 gg_id:21147 Sporomusa malonica str. DSM 5090 Type
AJ279801.1 gg_id:25868 Sporomusa sphaeroides str. DSM 2875 Type
NR_025415.1 gg_id:541895 Sporomusa acidovorans str. DSM 3132
GQ047238.1 gg_id:466398 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010d
FJ372052.1 gg_id:364054 feces adult twins and mothers; TS9 clone TS9_a01c02
DQ794346.1 gg_id:187487 human fecal clone RL197_aah86a07
EU762181.1 gg_id:340520 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A
DQ803760.1 gg_id:180927 human fecal clone RL200_aai58a11
NZ_ACIM02000001.1 gg_id:470239 Dialister invisus str. DSM 15470
FJ370202.1 gg_id:369002 feces adult twins and mothers; TS56 clone TS56_a01g01
FJ363905.1 gg_id:358364 feces adult twins and mothers; TS14 clone TS14_a04g03
AF473837.2 gg_id:136415 Dialister micraerophilus str. ADV 04.01
U13040.1 gg_id:13826 Dialister pneumosintes str. SC3D
FM872697.1 gg_id:365104 occupant source house floor dust clone FA02F02
EU461194.1 gg_id:290748 hamadryas baboon feces clone BAZ_aah90c07
DQ071524.1 gg_id:229365 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc32
FJ364585.1 gg_id:363398 feces adult twins and mothers; TS15 clone TS15_a04g01
FJ833261.1 gg_id:512439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_40H05
FJ832358.1 gg_id:593767 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_87G11
DQ326331.1 gg_id:145728 Metagenomic gut microbiome healthy human stool clone C320
EU464320.1 gg_id:293799 hamadryas baboon feces clone AFBAB_aai02f07
FJ834270.1 gg_id:564560 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_63G08
AY850119.1 gg_id:109904 Dialister sp. str. ADV 1053.03
EU773545.1 gg_id:349811 Goeldi's Marmoset feces clone CAL_e11
EU764686.1 gg_id:325573 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1
DQ353930.1 gg_id:145968 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z83

EF507903.1	239939	121.9	105.0	152.1	65.7	69.8	72.0
EF060090.1	199473	3319.8	3824.1	2254.4	2869.8	1617.7	4306.0
EF060091.1	176163	2093.9	3124.8	3975.7	4455.1	1927.7	4300.5
EU728758.1	337187	3039.0	3466.7	3452.2	3079.5	2587.5	3461.4
EF028685.1	199297	54.2	50.5	273.3	107.0	62.7	37.8
EU773566.1	307454	3086.3	3356.6	3586.5	3562.7	2602.7	3377.1
NR_028812.1	539819	37.6	45.1	34.7	57.3	65.6	26.1
AY372050.1	94360	4038.2	4451.7	6708.7	5650.6	4210.7	5020.7
AY728067.1	104334	835.5	644.0	2118.4	1000.8	1172.1	1337.9
DQ816346.1	172987	6414.5	6645.6	7299.2	8263.9	9138.7	10230.9
EU981222.1	340874	7467.8	7471.6	5955.3	7073.5	7160.2	7660.9
AB288880.1	201846	5980.3	7203.0	12175.8	5684.1	4887.6	6056.4
EF454547.2	224315	8888.5	7756.7	7877.7	6566.2	6252.3	5436.1
FJ542917.1	510013	3956.4	5335.2	2195.8	1357.4	426.7	1099.9
AM158322.1	156235	57.7	59.8	305.4	79.9	139.0	71.3
AJ279799.1	21147	3870.3	4804.5	3076.6	1627.7	1411.8	2237.1
AJ279801.1	25868	1982.9	2577.0	464.9	2071.0	806.8	759.9
NR_025415.1	541895	4172.0	4598.5	2141.2	2104.1	1032.6	920.1
GQ047238.1	466398	4514.3	3712.7	1849.0	4289.8	3128.2	3526.0
FJ372052.1	364054	6398.6	6171.9	2204.8	4272.1	3741.3	3982.9
DQ794346.1	187487	1067.2	1020.7	361.4	2017.0	911.1	261.4
EU762181.1	340520	4098.5	4617.4	3229.4	2421.3	1518.1	3601.1
DQ803760.1	180927	152.7	298.9	260.0	147.7	182.7	82.0
NZ_ACIM02000001.1	470239	1856.9	3594.3	1981.6	1524.2	336.5	1429.9
FJ370202.1	369002	7602.1	7923.3	7292.1	7911.9	9173.8	8308.4
FJ363905.1	358364	15401.8	13930.3	9100.5	8581.7	7079.6	6589.9
AF473837.2	136415	23.9	30.0	32.6	58.7	66.5	19.2
U13040.1	13826	27.0	37.5	33.9	64.4	60.2	28.7
FM872697.1	365104	9214.8	6125.2	5328.3	8760.2	7239.0	7127.8
EU461194.1	290748	7677.3	7972.8	9938.8	6897.0	6962.4	7044.2
DQ071524.1	229365	60.0	83.5	77.7	96.7	87.6	60.6
FJ364585.1	363398	1038.6	1198.8	1288.1	670.8	3192.0	2717.3
FJ833261.1	512439	3163.4	4079.8	2646.6	5582.3	3033.5	3933.3
FJ832358.1	593767	6330.8	6703.8	5419.7	6201.8	3536.6	4981.6
DQ326331.1	145728	4849.4	4754.9	3946.7	4101.5	1998.3	2720.1
EU464320.1	293799	5510.6	7037.9	3624.2	2833.8	2473.3	3364.6
FJ834270.1	564560	4786.9	6598.5	6766.3	6683.7	8754.2	7980.6
AY850119.1	109904	377.9	401.5	909.5	491.5	764.7	249.4
EU773545.1	349811	395.2	541.0	199.2	1321.1	445.2	272.4
EU764686.1	325573	4392.3	4698.7	2275.6	4071.0	3317.9	3071.4
DQ353930.1	145968	71.3	73.3	133.8	60.9	126.7	137.2

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DQ796597.1 gg_id:184999 human fecal clone RL179aan75f02
EU009830.1 gg_id:240947 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_M8
EU464269.1 gg_id:287863 hamadryas baboon feces clone AFBAB_aai01d11
DQ325965.1 gg_id:148937 Metagenomic gut microbiome healthy human stool clone B855
AY958942.1 gg_id:128228 Microbes on human vaginal epithelium clone rRNA169
DQ809210.1 gg_id:196169 human fecal clone RL308_aal83d11
GQ014629.1 gg_id:495037 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw762b
GQ156497.1 gg_id:590051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti
DQ353912.1 gg_id:146557 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z25
FJ833651.1 gg_id:563580 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_64H08
DQ325967.1 gg_id:146807 Metagenomic gut microbiome healthy human stool clone B859
GQ082178.1 gg_id:382947 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
DQ325932.1 gg_id:150078 Metagenomic gut microbiome healthy human stool clone B792
NR_028862.1 gg_id:585826 Allisonella histaminiformans str. MR2; DSM 15230
EU009856.1 gg_id:255834 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_X48
FJ832445.1 gg_id:582014 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_25A04
EU475193.1 gg_id:295381 bonobo feces clone BNO_aaa01c01
AY959160.1 gg_id:130495 Microbes on human vaginal epithelium clone rRNA387
FJ832730.1 gg_id:562702 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q101_38F05
EU775402.1 gg_id:342839 Western lowland gorilla feces clone GOR_aag73e12
DQ071435.1 gg_id:228821 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw4
FJ489245.1 gg_id:513909 Megamonas hypermegale str. ABXD_AE27
DQ071446.1 gg_id:228113 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw1
NR_025514.1 gg_id:552592 Megamonas hypermegale str. DSM 1672
EU465518.1 gg_id:287786 lion feces clone LI3_aah78g03
EU939429.1 gg_id:343257 Fecal wild pygmy loris feces clone WF16S_275
U95029.1 gg_id:53032 Megasphaera elsdenii str. S3
AY038996.1 gg_id:24370 Megasphaera elsdenii str. YJ-4
DQ905695.1 gg_id:170226 human fecal clone 014C-G12
DQ904992.1 gg_id:170296 human fecal clone 002-g5
DQ278866.1 gg_id:151623 Megasphaera sp. TrE9262
DQ904832.1 gg_id:168912 human fecal clone 001C-a6
DQ904811.1 gg_id:173152 human fecal clone 001B-g7
ABWK02000005.1 gg_id:579171 Mitsuokella multacida str. DSM 20544
NZ_ABWK02000010.1 gg_id:470692 Mitsuokella multacida str. DSM 20544
AY985193.1 gg_id:119553 human stool clone C039
DQ325931.1 gg_id:148483 Metagenomic gut microbiome healthy human stool clone B785
AY982411.1 gg_id:117325 human sigmoid colon mucosal biopsy clone MK92
AY977807.1 gg_id:123930 human cecum mucosal biopsy clone LE93
NR_028840.1 gg_id:590732 Mitsuokella jalaludinii str. M9; DSM 13811
DQ223731.1 gg_id:140868 Pectinatus haikarae str. VTT E-88329; DSM 16980

DQ796597.1	184999	6407.5	6649.7	5233.0	6550.1	6540.9	6816.1
EU009830.1	240947	1093.2	1273.5	566.2	1085.6	303.0	522.2
EU464269.1	287863	10458.6	12440.5	7825.9	7919.5	11133.0	10124.2
DQ325965.1	148937	5611.4	5336.9	3512.5	4996.7	3982.8	4129.4
AY958942.1	128228	4522.0	4642.3	4501.7	5767.9	3032.3	4292.1
DQ809210.1	196169	17.9	69.7	313.4	66.7	90.2	53.8
GQ014629.1	495037	8673.7	8227.0	8820.5	7418.6	9485.6	9993.2
GQ156497.1	590051	9044.4	12308.7	12140.1	13562.9	9118.0	11091.4
DQ353912.1	146557	28.5	33.1	40.2	50.0	47.6	22.4
FJ833651.1	563580	3383.8	2340.0	3395.4	4642.8	873.9	1835.7
DQ325967.1	146807	11628.2	11932.1	5345.4	7919.5	6120.4	6003.8
GQ082178.1	382947	2290.7	3703.9	3664.0	1739.4	1391.2	1833.9
DQ325932.1	150078	365.7	257.9	290.1	366.2	80.4	114.4
NR_028862.1	585826	40.5	67.8	107.6	73.6	66.9	34.3
EU009856.1	255834	4722.0	4040.8	4537.6	5253.3	648.7	2235.1
FJ832445.1	582014	5463.5	5181.8	3236.5	4453.0	1197.0	3655.1
EU475193.1	295381	2526.1	2132.7	284.9	4020.9	4188.9	4648.7
AY959160.1	130495	10269.1	11725.7	7953.6	8819.9	9661.5	8616.7
FJ832730.1	562702	4618.4	6263.4	4198.2	5731.7	5612.9	6955.8
EU775402.1	342839	210.1	173.8	792.3	151.4	205.1	198.0
DQ071435.1	228821	10387.2	8823.4	8645.6	5748.2	12453.6	7991.4
FJ489245.1	513909	746.5	759.2	982.2	491.5	215.3	334.4
DQ071446.1	228113	1599.7	1659.3	3117.4	577.1	5587.1	1442.3
NR_025514.1	552592	24.4	25.5	27.1	45.8	53.3	24.8
EU465518.1	287786	2200.3	2379.2	2476.0	2034.7	1980.6	3048.9
EU939429.1	343257	2393.5	3701.5	3357.5	1265.8	2714.6	2477.5
U95029.1	53032	496.7	288.5	749.5	244.8	143.1	625.6
AY038996.1	24370	1701.8	1697.2	1954.6	2315.7	1500.8	2226.9
DQ905695.1	170226	1487.6	1784.1	2250.2	1345.3	158.6	991.4
DQ904992.1	170296	6366.4	6557.3	5419.9	5657.9	7337.8	7627.6
DQ278866.1	151623	58.8	64.2	37.7	85.6	60.6	43.0
DQ904832.1	168912	4288.6	3690.4	3615.8	1819.9	601.7	1271.9
DQ904811.1	173152	3341.2	2902.3	2568.8	932.0	421.5	855.3
ABWK02000005.1	579171	2605.2	4011.7	2800.1	3178.3	1990.4	4291.7
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AY985193.1	119553	501.3	774.7	782.0	1845.6	356.4	672.6
DQ325931.1	148483	1506.6	1392.6	1829.1	4017.4	597.2	1479.9
AY982411.1	117325	7701.3	6236.1	6836.6	7848.1	8772.1	7531.2
AY977807.1	123930	1534.0	1693.3	1165.7	771.3	307.0	753.8
NR_028840.1	590732	44.1	71.1	521.7	88.8	62.0	28.3
DQ223731.1	140868	32.5	35.4	67.0	60.9	50.4	55.7

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GQ492364.1 gg_id:556835 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
GQ491916.1 gg_id:591490 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ366265.1 gg_id:370318 feces adult twins and mothers; TS25 clone TS25_a04f05
EF404155.1 gg_id:206419 human fecal clone SJTU_C_05_48
GQ493381.1 gg_id:587536 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ368136.1 gg_id:357831 feces adult twins and mothers; TS30 clone TS30_a04f02
DQ805306.1 gg_id:183098 human fecal clone RL249_aaj84h07
GQ492054.1 gg_id:594375 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
FJ362702.1 gg_id:367004 feces adult twins and mothers; TS13 clone TS13_a02b03
EU009791.1 gg_id:255530 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_A48
EF400225.1 gg_id:212456 human fecal clone SJTU_E_10_50
X72867.1 gg_id:13860 Phascolarctobacterium faecium
GQ492591.1 gg_id:575113 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice
EU009762.1 gg_id:239970 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AC19
NR_025418.1 gg_id:559721 Propionispora vibrioides str. FKBS1; DSM 13305
AY878646.1 gg_id:112413 Selenomonas noxia str. AIP 45-92
AY947498.2 gg_id:114498 subgingival plaque clone OH4A
AY878645.1 gg_id:111934 Selenomonas noxia str. AIP 518-78
AF161581.1 gg_id:13799 Selenomonas ruminantium str. K2
EU381812.1 gg_id:276744 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
AY685145.1 gg_id:99746 Selenomonas ruminantium L6
EU327399.1 gg_id:237808 Selenomonas ruminantium str. LongL1
AB198429.1 gg_id:257094 Selenomonas ruminantium str. S36
DQ673518.1 gg_id:165042 rumen fluid clone GRC53
EF112197.1 gg_id:178224 Selenomonas ruminantium str. 65
AB003379.1 gg_id:13812 Selenomonas ruminantium str.JCM6582
AF001774.1 gg_id:13813 rumen clone RFP7
ACKP02000033.1 gg_id:589013 Selenomonas sputigena str. ATCC 35185
AF373023.1 gg_id:17310 Selenomonas sputigena str. ATCC35185
EF195237.1 gg_id:180877 Selenomonas sp. str. MCB2
AY685142.1 gg_id:99281 Selenomonas ruminantium M40
AY207052.1 gg_id:83279 human mouth clone P2PA_80
AF287790.1 gg_id:23591 human subgingival plaque clone DM071
NR_028796.1 gg_id:550364 Selenomonas noxia str. ATCC 43541
EU669564.1 gg_id:292356 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O(
AY349403.1 gg_id:93019 human oral cavity clone FT050
DQ673510.1 gg_id:168649 rumen fluid clone GRC45
AM419977.1 gg_id:252996 Noma subgingival plaque clone 101H05(oral)
AF538861.1 gg_id:59529 Selenomonas sp. oral clone P4PA_36 P2
AY878647.1 gg_id:112215 Selenomonas sp. str. AIP 308-97
FM873718.1 gg_id:368850 occupant source house mattress dust clone MA03E01

GQ492364.1	556835	5621.7	2922.4	5974.8	3846.8	9194.5	7608.3
GQ491916.1	591490	8464.1	6812.4	5105.7	5309.0	2460.4	3668.4
FJ366265.1	370318	7541.1	8950.9	8315.5	5001.4	10763.7	13843.1
EF404155.1	206419	3559.7	2812.6	2416.1	3760.2	2183.2	3615.7
GQ493381.1	587536	252.3	270.4	411.2	233.5	89.9	76.4
FJ368136.1	357831	12853.0	13079.4	7864.8	6215.1	3578.4	4988.5
DQ805306.1	183098	7268.2	6644.1	6125.6	4909.4	4056.2	5324.3
GQ492054.1	594375	9100.0	8494.2	5247.2	6960.0	7193.8	4605.3
FJ362702.1	367004	7597.8	7690.1	3724.1	1356.6	7814.4	5790.0
EU009791.1	255530	3194.0	2679.0	3499.7	3273.8	2600.5	2965.5
EF400225.1	212456	5171.7	5403.1	1936.7	5062.3	3182.7	3599.4
X72867.1	13860	6633.1	4516.3	4570.9	4279.0	2275.9	3829.0
GQ492591.1	575113	7096.7	5484.0	1816.8	2269.5	1184.9	1951.7
EU009762.1	239970	85.1	192.2	88.8	110.5	53.9	516.1
NR_025418.1	559721	32.6	40.7	46.7	66.5	67.6	18.6
AY878646.1	112413	5192.2	5155.2	12948.4	4818.2	6270.5	6498.5
AY947498.2	114498	9587.6	9345.5	4848.7	9208.0	8668.8	8914.3
AY878645.1	111934	209.9	347.3	393.3	99.5	82.4	70.7
AF161581.1	13799	23.0	26.7	17.6	37.4	53.9	21.3
EU381812.1	276744	6624.0	9803.4	7887.4	5624.0	9276.7	1896.1
AY685145.1	99746	6132.7	6568.8	3225.9	4793.2	5118.8	4769.8
EU327399.1	237808	5583.5	5681.9	2767.6	7080.6	5281.4	3061.4
AB198429.1	257094	200.2	523.3	838.2	178.4	117.8	243.1
DQ673518.1	165042	585.4	967.7	2146.9	1003.8	391.0	756.3
EF112197.1	178224	81.9	110.2	554.8	147.4	95.4	221.6
AB003379.1	13812	2741.2	2489.0	3594.8	3336.8	7296.9	10310.8
AF001774.1	13813	2426.8	3518.7	4052.4	2710.0	1918.1	1569.0
ACKP02000033.1	589013	1724.8	2742.5	2578.5	1601.5	3192.9	3566.8
AF373023.1	17310	5161.0	4110.1	2894.8	2334.3	3911.3	3133.1
EF195237.1	180877	5514.2	6129.7	5491.8	9060.0	3395.1	4480.1
AY685142.1	99281	516.6	649.2	588.4	462.0	159.0	329.7
AY207052.1	83279	2161.9	2489.0	3461.7	2111.9	2457.1	2416.9
AF287790.1	23591	4496.7	6526.9	5280.9	3596.5	5861.7	5580.8
NR_028796.1	550364	2382.5	3007.0	5891.2	3094.6	2553.1	4190.7
EU669564.1	292356	1613.7	3191.5	4687.3	1536.6	1513.6	2567.7
AY349403.1	93019	1946.7	3100.6	1544.6	830.0	3070.7	2332.2
DQ673510.1	168649	177.3	306.0	540.8	158.9	93.5	109.1
AM419977.1	252996	27.4	21.6	35.9	46.9	58.6	25.3
AF538861.1	59529	351.7	780.0	1484.0	434.7	334.0	620.9
AY878647.1	112215	123.0	124.1	1107.3	269.4	337.4	687.2
FM873718.1	368850	2700.7	3786.7	2121.6	2241.2	4207.9	4354.5

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DQ003636.1 gg_id:120969 human mouth clone MB3_C41
AY349409.1 gg_id:92349 human oral cavity clone JI021
AM420026.1 gg_id:254272 Noma subgingival plaque clone 201F02(oral)
GU302661.1 gg_id:586155 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
EU850496.1 gg_id:329400 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF265
AY278627.1 gg_id:86707 Selenomonas genomosp. C1
AM420028.1 gg_id:252936 Noma subgingival plaque clone 201F04(oral)
AY341820.1 gg_id:92263 Selenomonas genomosp. P5
AM419959.1 gg_id:241050 Noma subgingival plaque clone 101C02(oral)
GQ006802.1 gg_id:502861 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87h08c
GQ006643.1 gg_id:503020 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86a02c
AM420074.1 gg_id:238385 Noma subgingival plaque clone 301F12(oral)
EU669566.1 gg_id:295019 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O(
AM420113.1 gg_id:240321 Noma subgingival plaque clone 303G10(oral)
DQ394645.1 gg_id:155308 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o
DQ145536.1 gg_id:141405 Geosinus fermentans str. R7
NZ_AAWL01000001.1 gg_id:192281 Thermosinus carboxydivorans str. Nor1
AJ009486.1 gg_id:13842 TCB-transforming consortium clone SJA-112
DQ125719.1 gg_id:134207 uranium contaminated soil clone AKAU3815
AF275913.1 gg_id:72075 anaerobic digestor clone AA01
AB195907.1 gg_id:109195 Anaerobic sludge clone N39
AB486682.1 gg_id:559077 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(
EU864464.1 gg_id:310615 structures under selection pressure levels antibiotics Xiao River receiving treated ox
AB240309.1 gg_id:141751 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon
AB487569.1 gg_id:571451 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
FJ673072.1 gg_id:516219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB486151.1 gg_id:586628 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
FJ683262.1 gg_id:512213 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU843176.1 gg_id:304446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
AJ006980.1 gg_id:13862 Succinispira mobilis str. 19gly1
EU344280.1 gg_id:273405 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ683898.1 gg_id:521321 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AF407698.1 gg_id:60600 Great Artesian Basin clone G07
FJ880994.1 gg_id:405629 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet;
NR_025298.1 gg_id:575973 Anaeroarcus burkinensis str. DSM 6283
FJ676048.1 gg_id:530548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ038559.1 gg_id:383518 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
AY244964.1 gg_id:84451 cow rumen clone BS10
FJ799146.1 gg_id:583522 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr
FJ672960.1 gg_id:519106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ801441.1 gg_id:198328 human fecal clone RL388_aao95e11

DQ003636.1	120969	6894.8	8281.9	2042.5	4319.6	5212.9	4272.6
AY349409.1	92349	826.5	437.2	3061.8	462.7	116.0	1325.6
AM420026.1	254272	1463.4	3229.9	641.1	1721.8	1864.2	2258.0
GU302661.1	586155	35.2	61.3	31.3	54.9	99.3	40.6
EU850496.1	329400	675.8	414.1	2208.7	1812.3	285.4	859.5
AY278627.1	86707	73.9	110.1	106.6	151.2	97.4	105.3
AM420028.1	252936	944.0	1460.0	2854.2	633.3	568.4	1272.7
AY341820.1	92263	4429.5	6794.2	5456.3	3738.3	3679.7	4743.8
AM419959.1	241050	1297.1	1601.2	2325.2	1673.9	1026.2	1542.7
GQ006802.1	502861	55.3	63.1	98.3	71.0	84.3	141.5
GQ006643.1	503020	7093.5	8046.4	7569.8	6156.4	8445.4	7156.1
AM420074.1	238385	2895.6	2685.7	2710.7	2486.5	1874.4	2490.9
EU669566.1	295019	25.0	449.0	26.9	52.6	77.2	65.9
AM420113.1	240321	10180.4	11537.4	8416.8	6804.8	15263.4	9613.3
DQ394645.1	155308	27.4	56.0	216.0	42.0	88.6	153.3
DQ145536.1	141405	3903.8	3895.8	7920.7	5339.9	859.3	1386.4
NZ_AAWL01000001.1	192281	73.7	55.8	111.1	65.3	46.4	32.3
AJ009486.1	13842	1547.7	1190.0	1422.4	1210.9	603.6	594.9
DQ125719.1	134207	3961.7	5083.7	1618.7	3282.0	1666.4	2592.8
AF275913.1	72075	1216.3	1509.8	3900.6	2352.3	1793.5	2891.5
AB195907.1	109195	917.3	1309.6	3425.0	1083.1	200.1	1031.0
AB486682.1	559077	725.3	487.9	2505.5	789.0	133.1	857.6
EU864464.1	310615	579.9	197.7	1646.5	801.8	132.0	213.4
AB240309.1	141751	2915.0	2589.1	4596.7	2005.3	977.3	1043.4
AB487569.1	571451	2240.9	2123.8	6244.8	1987.6	422.0	909.5
FJ673072.1	516219	2235.5	2682.5	2661.7	2303.0	2847.5	2730.9
AB486151.1	586628	413.4	520.4	1028.6	295.8	96.3	426.4
FJ683262.1	512213	3100.2	3755.6	3880.0	2744.6	7417.5	5737.2
EU843176.1	304446	1759.4	2213.2	1387.3	284.3	830.5	883.9
AJ006980.1	13862	158.3	248.0	183.1	149.2	133.5	97.2
EU344280.1	273405	1991.8	2975.5	2156.2	1589.1	2113.7	1998.3
FJ683898.1	521321	26.5	102.1	77.0	60.0	99.8	216.2
AF407698.1	60600	5142.1	5052.1	11306.2	5404.2	5440.7	8084.7
FJ880994.1	405629	7924.4	8529.6	5023.7	5493.2	2706.3	3840.2
NR_025298.1	575973	4280.9	3343.7	5429.2	2301.7	944.8	1080.9
FJ676048.1	530548	1064.5	840.5	3068.1	422.6	140.8	1299.4
GQ038559.1	383518	69.0	125.2	279.3	99.7	85.2	72.8
AY244964.1	84451	1069.0	1461.6	1099.4	490.5	421.6	843.5
FJ799146.1	583522	4122.9	4083.0	7791.6	2434.2	2342.4	3427.6
FJ672960.1	519106	9609.3	12243.5	5474.0	6066.2	5601.1	7773.2
DQ801441.1	198328	9390.7	11453.9	8298.3	4869.7	622.7	1043.5

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FJ678610.1 gg_id:522237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ832386.1 gg_id:533799 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_22F03
EU775040.1 gg_id:351818 Francois Langur feces clone FL_2aaa04b12
AB487852.1 gg_id:548067 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
FJ681608.1 gg_id:517653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ386549.1 gg_id:364845 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar
FJ834254.1 gg_id:575321 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_14F02
EU773455.1 gg_id:328240 Black lemur feces clone BKLE_g09_1
DQ833299.1 gg_id:170560 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed
FJ684672.1 gg_id:532119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678209.1 gg_id:528615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY684401.2 gg_id:110815 mucosal biopsies human intestine clone HuAC20
AB486629.1 gg_id:577345 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(
EU531895.1 gg_id:263067 Predominant role host genetics controlling gut microbiota FMF remission stool clone
AF071415.1 gg_id:13851 Anaeromusa acidaminophila str. DSM 3853
EU469036.1 gg_id:303124 Speke's gazelle feces clone SP2_c09_3
DQ824735.1 gg_id:179447 human fecal clone RL185_aaj72d08
FJ683901.1 gg_id:521470 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GU304004.1 gg_id:549795 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
FJ673979.1 gg_id:516340 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ833301.1 gg_id:164274 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed
FJ682035.1 gg_id:525023 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU307091.1 gg_id:251142 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AB034135.1 gg_id:48795 rumen clone 4C28d-2
DQ904885.1 gg_id:163607 human fecal clone 001C-f2
GQ005015.1 gg_id:504647 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65h1
FJ676618.1 gg_id:532032 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678334.1 gg_id:527813 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB486685.1 gg_id:572648 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(
FJ678463.1 gg_id:527603 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU845665.1 gg_id:336552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ682745.1 gg_id:527983 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ684630.1 gg_id:514989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU774198.1 gg_id:346793 Chimpanzee feces clone CHIMP1_aaj39c11
EU307090.1 gg_id:243204 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU775009.1 gg_id:316336 Francois Langur feces clone FL_2aaa02b05
EU747937.1 gg_id:337267 neotropical folivorous flying bird adult hoatzin crop clone hoa13_77E10
DQ310746.1 gg_id:199797 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC(
AY995255.1 gg_id:123766 human vagina clone FX8B2-5
AY667269.1 gg_id:103280 TCE-dechlorinating groundwater clone TANB127
FJ674118.1 gg_id:518615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee

FJ678610.1	522237	2714.6	3119.1	1145.0	997.4	1045.5	1215.7
FJ832386.1	533799	8910.6	7279.1	6581.5	7158.0	6426.5	6507.7
EU775040.1	351818	11135.3	12221.3	8027.6	6738.0	7689.2	6760.9
AB487852.1	548067	3845.3	3129.7	7433.0	4513.5	1727.0	3195.1
FJ681608.1	517653	4010.7	5150.1	4498.1	3302.9	4582.7	4463.1
FJ386549.1	364845	7649.8	8277.1	4797.0	6375.7	3946.0	4916.0
FJ834254.1	575321	1725.7	1358.5	1312.3	3146.5	1176.2	3157.0
EU773455.1	328240	7811.3	8500.0	5917.0	6246.1	7738.2	7728.2
DQ833299.1	170560	2433.5	1788.8	3029.0	4415.8	1678.5	2331.2
FJ684672.1	532119	2545.0	2070.0	4046.0	2403.5	2079.5	1965.1
FJ678209.1	528615	8308.1	5576.5	7043.6	3061.6	2952.0	4311.3
AY684401.2	110815	331.3	245.1	375.0	520.0	63.2	63.2
AB486629.1	577345	15179.8	12324.8	8276.8	6883.7	4325.9	6446.3
EU531895.1	263067	4114.6	3560.4	4829.0	5773.3	2457.3	5568.1
AF071415.1	13851	5937.5	4684.8	6173.4	7353.4	1618.5	4464.8
EU469036.1	303124	8790.7	11117.1	3483.7	9676.7	6576.4	8197.3
DQ824735.1	179447	491.5	289.6	390.8	171.4	224.6	363.0
FJ683901.1	521470	5882.7	5317.7	3706.1	3987.3	6133.9	7142.7
GU304004.1	549795	5404.9	6084.4	6819.4	5153.6	3727.3	5954.5
FJ673979.1	516340	3789.3	4409.3	3579.9	2966.9	4309.0	4262.2
DQ833301.1	164274	9591.2	8516.6	9319.9	3569.5	1266.8	4413.6
FJ682035.1	525023	1441.9	1197.3	5381.5	2288.2	325.0	1465.8
EU307091.1	251142	7500.8	6783.2	6910.7	4426.7	4417.2	4021.6
AB034135.1	48795	25.5	34.2	46.1	55.9	60.7	28.7
DQ904885.1	163607	2810.0	3337.7	3486.2	2121.9	2371.6	2379.4
GQ005015.1	504647	3763.9	3103.3	3573.3	5856.2	4702.8	8747.9
FJ676618.1	532032	4787.3	4656.2	3987.3	6642.4	8024.6	8324.6
FJ678334.1	527813	566.5	702.5	2292.0	895.4	2442.9	2382.9
AB486685.1	572648	15898.4	17998.8	12416.0	8777.3	5064.3	8468.5
FJ678463.1	527603	3973.8	5274.1	4898.3	2875.9	1432.8	2582.4
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FJ682745.1	527983	1503.0	1963.7	4344.3	1855.3	725.5	1651.0
FJ684630.1	514989	8510.6	7319.5	6461.6	8050.9	4109.8	5686.4
EU774198.1	346793	4558.6	6674.5	6280.3	5502.0	7094.9	6204.0
EU307090.1	243204	883.8	744.5	1750.8	811.3	139.8	635.0
EU775009.1	316336	14281.6	14302.4	13556.1	10785.2	12266.7	13771.0
EU747937.1	337267	10101.8	9304.6	6519.0	6030.0	9002.9	8357.8
DQ310746.1	199797	4019.0	5134.8	7552.0	4496.4	2194.7	1813.6
AY995255.1	123766	114.0	116.4	201.3	91.7	63.0	54.9
AY667269.1	103280	6470.8	6253.1	7577.9	7452.6	4377.9	5221.9
FJ674118.1	518615	3717.1	4329.9	3630.0	2345.2	6685.7	5774.2

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GQ179679.1 gg_id:455949 Heterogeneity vaginal microbial within individuals vagina clone VE44F01
FJ678138.1 gg_id:521053 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678575.1 gg_id:531578 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682764.1 gg_id:518322 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AY672080.2 gg_id:149234 Microbial on patients stomatitis and healthy biofilm denture wearers clone DWE10
DQ217599.1 gg_id:139963 Zymophilus raffinosivorans str. VTT E-90406; DSM 20765; ATCC 496
FJ673355.1 gg_id:525608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ679306.1 gg_id:520520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372095.1 gg_id:363046 feces adult twins and mothers; TS9 clone TS9_a01f12
AB034141.1 gg_id:28188 rumen clone 3C28d-10
AY985859.1 gg_id:117810 human stool clone D133
DQ113674.1 gg_id:132784 dog colon clone C2-26
AB185750.1 gg_id:103463 rumen clone U29-B01
GU303125.1 gg_id:570205 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium
EU842705.1 gg_id:318812 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi
FJ674045.1 gg_id:521328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB034079.1 gg_id:51519 rumen clone 3C3d-10
FJ680777.1 gg_id:510572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EU747918.1 gg_id:346208 neotropical folivorous flying bird adult hoatzin crop clone hoa12_26B04
FJ673180.1 gg_id:514372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB486409.1 gg_id:546268 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AF371705.1 gg_id:45688 swine intestine clone p-286-a3
AB486202.1 gg_id:575498 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
FJ684083.1 gg_id:520119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AJ009494.1 gg_id:13843 anaerobic TCB-transforming consortium clone SJA-143
GQ060518.1 gg_id:462753 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02g03
GQ451274.1 gg_id:514095 Fecal Yunnan snub-nosed monkey feces clone J269
AF357557.1 gg_id:72198 mpn-isolate group 9
AF371701.1 gg_id:34987 swine intestine clone p-2365-55G5
AB198438.1 gg_id:237356 Selenomonas ruminantium str. S206
AF473834.1 gg_id:38606 Megasphaera micronuciformis str. AIP 412.00; CIP 107280
EU382011.1 gg_id:268506 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase
EU794209.1 gg_id:334383 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O30
EU475011.1 gg_id:296159 red river hog feces clone RRH_aaa03c07
FJ674071.1 gg_id:521929 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ372342.1 gg_id:368157 feces adult twins and mothers; TS9 clone TS9_a04e03
EF063619.1 gg_id:193173 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo
DQ223729.1 gg_id:140753 Megasphaera sueciensis str. VTT E-97791
EU779137.1 gg_id:354926 Trancaspian Urial feces clone TU1_aaa03b10
FN563256.1 gg_id:554464 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
EU747978.1 gg_id:349584 neotropical folivorous flying bird adult hoatzin crop clone hoa13_48H06

GQ179679.1	455949	10188.2	7057.2	8952.4	12161.6	1701.8	3823.3
FJ678138.1	521053	2942.6	2686.0	1975.3	1177.5	393.3	1344.0
FJ678575.1	531578	2462.9	2532.4	3618.9	1244.5	2558.4	3170.5
FJ682764.1	518322	1131.3	974.7	3676.7	1332.6	312.6	1047.9
AY672080.2	149234	35.5	67.2	30.9	65.6	57.1	48.0
DQ217599.1	139963	4322.2	4402.3	7531.7	3385.5	3049.0	3391.7
FJ673355.1	525608	7611.6	6976.2	5176.0	9306.4	10473.9	10328.8
FJ679306.1	520520	4884.5	5153.1	4743.5	4487.9	2738.9	2370.1
FJ372095.1	363046	2346.8	4414.7	3631.3	2212.3	1272.4	3068.1
AB034141.1	28188	198.8	216.6	236.5	95.8	88.4	56.5
AY985859.1	117810	103.4	167.6	215.7	108.3	175.6	36.4
DQ113674.1	132784	543.0	498.9	1179.6	417.6	182.2	443.2
AB185750.1	103463	11860.2	13150.4	13403.4	8483.4	11191.7	12293.1
GU303125.1	570205	1067.0	1680.4	888.8	226.7	613.1	957.8
EU842705.1	318812	4074.6	5509.3	4661.7	2653.6	2141.4	3675.6
FJ674045.1	521328	5130.1	5705.2	5318.5	5749.8	10664.8	10840.2
AB034079.1	51519	5055.4	4604.4	3112.4	5096.6	3698.6	3521.4
FJ680777.1	510572	1959.6	1537.3	3468.0	1387.4	343.9	857.2
EU747918.1	346208	1748.9	1937.8	2246.5	1791.0	2554.3	2823.8
FJ673180.1	514372	7575.0	9512.8	4738.4	5626.0	4768.1	5355.5
AB486409.1	546268	574.8	453.0	4524.0	1135.4	230.1	839.5
AF371705.1	45688	9758.6	12719.4	9094.1	6864.1	10841.9	3820.6
AB486202.1	575498	3884.5	5073.8	8483.1	4358.7	2227.8	1620.4
FJ684083.1	520119	3099.8	5221.7	3668.5	1882.6	331.4	2282.7
AJ009494.1	13843	290.1	274.8	450.3	264.6	137.3	124.1
GQ060518.1	462753	2402.0	3518.9	1893.1	985.8	4323.4	3282.7
GQ451274.1	514095	16228.9	15629.6	12408.8	8738.0	2726.2	4102.1
AF357557.1	72198	135.5	140.6	395.2	187.9	139.0	130.3
AF371701.1	34987	4524.4	5429.7	3262.4	1833.7	1403.6	623.4
AB198438.1	237356	4169.6	7079.6	1568.5	1082.3	1888.9	1300.4
AF473834.1	38606	124.7	178.7	294.5	186.9	278.9	154.0
EU382011.1	268506	5700.6	8083.4	7663.8	5818.7	4361.4	6221.7
EU794209.1	334383	10031.6	8381.9	7288.9	7282.3	5574.1	7562.4
EU475011.1	296159	10807.4	10822.1	11331.7	9656.6	13243.3	14881.9
FJ674071.1	521929	11058.7	12180.6	8935.3	8810.9	6979.3	9734.5
FJ372342.1	368157	3949.8	5792.9	5384.3	3021.3	1164.4	2046.8
EF063619.1	193173	15443.2	15142.0	10245.8	11418.1	15529.7	13017.8
DQ223729.1	140753	22.3	21.1	45.7	57.3	67.3	23.4
EU779137.1	354926	6336.8	7799.6	2028.1	1496.5	2301.9	4021.9
FN563256.1	554464	11112.0	11020.4	8348.5	6649.9	9456.1	8764.5
EU747978.1	349584	8674.9	9927.9	8684.2	6236.4	11140.7	13063.2

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CU920189.1 gg_id:572427 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB486952.1 gg_id:541359 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
AY959093.1 gg_id:131417 Microbes on human vaginal epithelium clone rRNA320
FJ675815.1 gg_id:531229 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ678660.1 gg_id:519991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673588.1 gg_id:526829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ673153.1 gg_id:529494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB198425.1 gg_id:246110 Selenomonas ruminantium str. S2
EU850607.1 gg_id:334117 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF440
AB034134.1 gg_id:42912 rumen clone 4C28d-6
AB218316.1 gg_id:148501 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-66
AY958931.1 gg_id:153751 Microbes on human vaginal epithelium clone rRNA158
GQ004077.1 gg_id:505586 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu68d0
AB486076.1 gg_id:569899 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
AB487430.1 gg_id:540748 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
FJ682840.1 gg_id:520575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ393127.1 gg_id:362899 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel
U81750.2 gg_id:13861 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHB04
FJ833201.1 gg_id:594131 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_39G05
FJ673713.1 gg_id:524216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
GQ006579.1 gg_id:503085 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85b11c
FJ386554.1 gg_id:369923 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar
FJ673625.1 gg_id:530256 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
EF399619.1 gg_id:206942 human fecal clone SJTU_E_01_29
EU009839.1 gg_id:254812 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Q48
EU234118.1 gg_id:252011 receiving river and un techniques anaerobic process WWTP treating penicillin G prod
AB198432.1 gg_id:242601 Selenomonas ruminantium str. S109
DQ295866.1 gg_id:191985 Pelosinus fermentans str. UFO1
FJ172883.1 gg_id:352391 Qinghai Yak Ruminal and Fungi China rumen clone RB-2F2
FJ680477.1 gg_id:523055 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ682404.1 gg_id:513552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
AB486876.1 gg_id:578241 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
EU259482.1 gg_id:241086 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC106
AY981016.1 gg_id:116502 human rectum mucosal biopsy clone V190
FJ680012.1 gg_id:515217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
FJ677302.1 gg_id:528220 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
DQ795993.1 gg_id:188086 human fecal clone RL202_aai50a03
GU214167.1 gg_id:593991 and biota slimes Canadian paper mills slime mill taken wet section around papermal
DQ777892.2 gg_id:166356 rat feces clone R-1170
AB034191.1 gg_id:38984 Anaerovibrio lipolyticus str. ATCC 33276
EU748414.1 gg_id:328699 neotropical folivorous flying bird adult hoatzin crop clone hoa5_08h08

CU920189.1	572427	1637.6	2190.6	1436.5	2543.3	1563.3	1529.7
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AY959093.1	131417	10650.5	8373.0	5072.6	6115.4	9989.5	11106.7
FJ675815.1	531229	4847.6	3896.2	1317.9	6789.2	5402.7	5969.8
FJ678660.1	519991	453.2	492.1	2251.1	203.5	124.5	309.4
FJ673588.1	526829	9314.0	12821.7	5368.7	4880.2	6235.1	7683.0
FJ673153.1	529494	3056.1	4715.3	3246.3	1833.7	305.6	452.9
AB198425.1	246110	1880.6	2715.8	3521.7	880.6	5515.4	3978.0
EU850607.1	334117	7817.5	9914.4	3804.8	2607.3	3018.0	4934.5
AB034134.1	42912	327.7	537.2	696.6	246.3	464.4	677.3
AB218316.1	148501	26.6	24.8	49.5	82.7	64.0	29.7
AY958931.1	153751	1383.7	1330.6	888.2	379.5	452.8	561.3
GQ004077.1	505586	4419.1	4357.7	5769.2	3892.7	3633.5	4866.7
AB486076.1	569899	729.5	409.4	1500.9	438.8	67.9	282.2
AB487430.1	540748	4799.3	3922.9	9829.9	7141.7	655.8	1267.9
FJ682840.1	520575	2345.5	2235.0	3388.1	1713.7	546.8	2447.5
FJ393127.1	362899	4884.1	4065.0	6263.5	4815.1	2263.8	3414.4
U81750.2	13861	5194.4	6835.7	4982.3	3961.1	2788.3	4216.5
FJ833201.1	594131	4306.9	5484.5	5117.6	4393.6	3404.3	4571.4
FJ673713.1	524216	9609.1	9888.0	5693.5	10575.3	13550.2	12959.3
GQ006579.1	503085	6052.1	5843.3	4758.4	5804.8	7492.9	9960.5
FJ386554.1	369923	6300.6	8120.0	2271.8	1025.7	896.3	411.9
FJ673625.1	530256	10129.1	10833.1	7924.1	6620.8	7323.2	7783.5
EF399619.1	206942	113.1	100.7	971.1	130.6	66.9	87.5
EU009839.1	254812	3634.5	3794.8	3464.7	1881.5	1716.6	2088.3
EU234118.1	252011	367.4	843.2	710.2	298.7	687.7	667.3
AB198432.1	242601	9957.9	9666.1	2584.8	6690.9	4819.6	3707.4
DQ295866.1	191985	2683.0	2847.5	7031.7	4165.2	397.2	1130.7
FJ172883.1	352391	6877.1	7939.7	8139.5	3520.0	4754.2	6936.5
FJ680477.1	523055	11141.2	11769.0	10685.7	10041.4	7844.3	8109.8
FJ682404.1	513552	6855.5	8459.2	6603.3	4260.2	4406.1	6867.9
AB486876.1	578241	1548.3	1862.8	3525.2	1483.3	1848.9	2035.8
EU259482.1	241086	268.8	82.1	386.9	66.2	56.5	64.5
AY981016.1	116502	8045.5	8655.6	2237.5	5606.2	1390.2	1825.8
FJ680012.1	515217	6993.3	7986.8	1941.1	1928.7	4886.7	3878.8
FJ677302.1	528220	15108.5	17470.6	13226.8	12242.2	14403.1	18221.1
DQ795993.1	188086	8621.4	9061.4	6982.7	6225.6	5910.6	5902.5
GU214167.1	593991	7971.4	7675.4	7879.8	7498.1	5808.4	6553.5
DQ777892.2	166356	32.6	35.8	34.1	61.9	59.2	25.5
AB034191.1	38984	23.3	33.5	29.1	44.9	56.0	24.8
EU748414.1	328699	659.1	860.9	582.2	338.0	210.8	349.0

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AJ229233.1 gg_id:16834 anoxic bulk soil flooded rice microcosm clone BSV90 clone
AY244972.1 gg_id:83021 cow rumen clone BS18
FJ683141.1 gg_id:528857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee
NR_029357.1 gg_id:547456 Propionispira arboris str. 12B4; DSM 2179
GQ004964.1 gg_id:504698 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65d0
EU344158.1 gg_id:260291 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad
FJ825568.1 gg_id:559706 Microbial during start-up mesophilic biogas plant clone 21_BS5_39
AB198435.1 gg_id:236008 Selenomonas ruminantium str. S150
AB486785.1 gg_id:541916 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(
EU461059.1 gg_id:288601 red kangaroo feces clone KO1_aai43d02
DQ168841.1 gg_id:154690 Fermentative biohydrogen production heated anaerobic sludge clone J25
EU468247.1 gg_id:290103 domesticated horse feces clone horsej_h07
EU463594.1 gg_id:302001 domesticated horse feces clone horsej_aai89d11
GQ102701.1 gg_id:458599 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
EU096495.1 gg_id:253506 Veillonella sp. 18
GQ073513.1 gg_id:403167 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ006562.1 gg_id:503102 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85a06c
AY514996.1 gg_id:99976 Veillonella rodentium str. ATCC 17743
GQ073646.1 gg_id:458617 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ086352.1 gg_id:443529 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ074436.1 gg_id:406819 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162h
GQ010293.1 gg_id:499375 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ114701.1 gg_id:381455 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
FJ558085.1 gg_id:528199 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
EF434331.1 gg_id:210713 gastrointestinal tract microbiota microarray reference pool created pooling products
GQ091818.1 gg_id:411006 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
EF515580.1 gg_id:218801 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery
GQ338722.1 gg_id:573384 and function human intestinal microbiota ileostomy effluent healthy patient clone A
EU460862.1 gg_id:301827 short-beaked echidna feces clone ECH_aai39e05
GQ101329.1 gg_id:453095 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493g
GQ006752.1 gg_id:502912 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87c06c
GQ022064.1 gg_id:487605 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
FJ374768.1 gg_id:585419 Veillonella sp. str. S101
GQ109121.1 gg_id:448078 Topographical and Temporal Human Skin Microbiome skin palm clone nbw608f12c1
GQ031217.1 gg_id:422979 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ055579.1 gg_id:381881 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1117e1
GQ011614.1 gg_id:498054 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794c08
GQ113791.1 gg_id:414090 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
GQ030037.1 gg_id:437122 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866c08
AY995768.1 gg_id:119118 Veillonella atypica str. ATCC 17744
GQ030108.1 gg_id:459734 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw867c0(

AJ229233.1	16834	168.6	95.6	364.2	91.5	77.7	61.4
AY244972.1	83021	1724.2	2921.1	2581.6	557.5	637.9	2005.6
FJ683141.1	528857	696.9	1087.5	718.3	853.0	175.3	431.2
NR_029357.1	547456	1286.1	1262.1	2746.0	1246.5	1460.9	1948.5
GQ004964.1	504698	10074.2	11430.8	4245.5	6462.2	3052.1	4925.4
EU344158.1	260291	8520.1	7354.9	6354.7	7536.9	7261.3	6859.0
FJ825568.1	559706	14141.7	13704.2	5730.4	12174.2	12850.9	16404.6
AB198435.1	236008	7445.2	6309.0	2479.2	7001.0	4452.0	4295.9
AB486785.1	541916	2414.1	2629.5	9135.3	4216.2	2352.0	2980.6
EU461059.1	288601	2977.1	3707.7	3425.8	1081.9	1838.9	2030.2
DQ168841.1	154690	5962.8	7062.1	2950.4	3825.0	1292.4	2632.1
EU468247.1	290103	5269.7	6419.6	7258.1	2427.5	4375.9	3813.4
EU463594.1	302001	6329.4	5582.2	7750.6	7665.2	3996.8	5986.5
GQ102701.1	458599	8036.5	6324.9	10582.2	7362.9	5660.4	7282.3
EU096495.1	253506	2062.4	3333.6	4823.1	2014.2	2983.0	3127.2
GQ073513.1	403167	8927.6	9872.0	6864.0	7839.7	5300.1	6472.2
GQ006562.1	503102	366.6	377.7	254.7	445.6	64.9	57.2
AY514996.1	99976	1635.1	689.2	1976.4	2621.8	219.4	572.7
GQ073646.1	458617	2129.9	2118.5	1755.1	1214.1	1280.1	2689.4
GQ086352.1	443529	183.1	270.0	267.6	66.9	49.1	42.7
GQ074436.1	406819	1407.2	1753.2	1251.6	580.5	341.6	994.2
GQ010293.1	499375	1955.2	3781.2	400.7	1573.2	1888.1	2841.7
GQ114701.1	381455	673.6	1213.3	654.2	211.1	583.3	465.5
FJ558085.1	528199	295.5	1112.2	522.4	86.9	70.3	52.7
EF434331.1	210713	6327.5	5416.9	5376.1	6111.5	3489.6	3452.6
GQ091818.1	411006	6609.9	5485.3	9630.0	6527.8	5203.7	6454.4
EF515580.1	218801	347.0	322.3	624.0	143.8	56.8	169.3
GQ338722.1	573384	83.0	174.6	101.7	67.3	1457.6	365.5
EU460862.1	301827	6168.6	6755.1	5321.9	5277.6	6358.4	6130.3
GQ101329.1	453095	3011.3	3624.4	1656.8	2570.7	5048.8	6111.8
GQ006752.1	502912	800.7	565.0	429.1	855.1	89.7	148.5
GQ022064.1	487605	831.0	1389.4	786.6	599.7	3485.1	1565.9
FJ374768.1	585419	243.0	243.3	544.3	224.5	90.6	156.4
GQ109121.1	448078	348.8	559.3	553.1	1315.9	81.5	155.2
GQ031217.1	422979	9087.3	7499.7	5299.2	7852.5	5012.8	4546.0
GQ055579.1	381881	8837.8	8126.5	6000.6	6659.0	6334.7	6481.9
GQ011614.1	498054	13468.7	13856.9	8498.4	10499.4	13563.7	11932.0
GQ113791.1	414090	2338.1	2750.0	2613.7	1462.2	1973.3	2229.2
GQ030037.1	437122	1326.2	582.5	2407.6	4405.3	170.9	908.7
AY995768.1	119118	81.0	98.0	150.4	71.2	57.7	120.6
GQ030108.1	459734	641.4	1023.1	818.3	536.2	362.8	766.8

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AY244769.1 gg_id:85594 Veillonella montpellierensis str. 2001-112662
GQ005879.1 gg_id:503784 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu97g
GQ006870.1 gg_id:502794 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g07c
GQ113854.1 gg_id:375581 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AM697482.1 gg_id:219084 sequencing libraries indoor dust clone BF0001D097
GQ016366.1 gg_id:493301 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
DQ346420.2 gg_id:145149 individual-specific oral microflora during initial colonization enamel human mouth; ir
GQ073330.1 gg_id:427426 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207g06c1
AY995769.1 gg_id:127371 Veillonella parvula str. ATCC 17745
GQ022740.1 gg_id:486930 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
AF186072.1 gg_id:13824 Veillonella criceti str. ATCC17747
GQ113989.1 gg_id:468332 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ088982.1 gg_id:465651 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ114846.1 gg_id:374291 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ075584.1 gg_id:437044 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ073254.1 gg_id:420928 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206h05c
X84007.1 gg_id:13822 Veillonella atypica str. DSM 20739
GQ019382.1 gg_id:490287 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189d
GQ030048.1 gg_id:430534 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866d0
EU774885.1 gg_id:329844 Short-beaked Echidna feces clone ECH_aai40g10
GQ101667.1 gg_id:404939 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497g11c
GQ071993.1 gg_id:459656 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190h04
GQ005607.1 gg_id:504056 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
EU774889.1 gg_id:324786 Short-beaked Echidna feces clone ECH_aai38d06
GQ006690.1 gg_id:502974 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86e02c
GQ114743.1 gg_id:381926 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ113658.1 gg_id:405229 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EF185167.1 gg_id:192322 Veillonella dentocariosa str. RBV106
AY355140.1 gg_id:95347 Veillonella caviae str. DSM 20738
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GQ114136.1 gg_id:439586 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ031800.1 gg_id:464887 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ000861.1 gg_id:469425 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ101676.1 gg_id:458976 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497h10c
GQ019421.1 gg_id:490247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189g
FJ558100.1 gg_id:517047 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
GQ027279.1 gg_id:416279 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ073269.1 gg_id:467872 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207a10c1

GQ048471.1	389670	7465.6	7287.9	7264.2	5705.1	7814.4	7235.5
AY244769.1	85594	60.1	76.7	104.0	66.0	62.6	79.6
GQ005879.1	503784	592.5	368.6	232.1	745.9	70.6	110.6
GQ006870.1	502794	3474.8	4146.3	3267.2	2512.8	3639.1	4200.7
GQ113854.1	375581	7432.7	6549.5	6443.5	6084.6	4981.6	5271.7
AM697482.1	219084	480.2	399.9	1446.5	263.9	124.3	583.4
GQ016366.1	493301	245.8	613.8	432.3	79.8	49.1	55.6
DQ346420.2	145149	990.7	1310.3	1242.1	329.5	4545.1	1292.1
GQ073330.1	427426	169.3	101.9	216.3	84.4	60.5	65.7
AY995769.1	127371	315.5	1269.3	630.1	126.0	62.8	85.2
GQ022740.1	486930	1577.2	571.9	340.1	768.7	162.5	222.7
AF186072.1	13824	992.1	1811.7	4844.3	1743.0	683.5	2285.1
GQ113989.1	468332	71.6	268.5	146.4	74.6	56.1	45.3
GQ088982.1	465651	8247.1	8892.2	5939.5	5183.8	2096.4	3768.3
GQ114846.1	374291	2142.9	2172.0	2498.8	1481.2	1965.7	2392.2
GQ075584.1	437044	5947.7	5739.0	5736.0	5362.2	3866.9	5179.6
GQ073254.1	420928	253.9	274.6	270.1	90.8	69.6	86.3
X84007.1	13822	2051.7	2118.7	1907.2	1944.3	1293.3	1035.8
GQ019382.1	490287	2434.1	2443.3	2690.6	1572.3	1973.6	2826.3
GQ030048.1	430534	10002.1	6984.8	5839.9	2363.7	3895.0	1702.4
EU774885.1	329844	1540.9	1144.5	4547.6	663.7	903.9	1485.7
GQ101667.1	404939	518.3	996.1	590.1	425.6	80.9	139.4
GQ071993.1	459656	4980.9	6165.2	5060.2	2987.9	8790.2	9330.0
GQ005607.1	504056	6514.7	6589.4	6450.7	6081.7	4983.8	5271.3
EU774889.1	324786	14270.0	15501.2	11700.4	12552.7	12982.0	12846.0
GQ006690.1	502974	175.7	241.2	277.5	71.5	43.4	41.9
GQ114743.1	381926	1874.7	2926.0	2503.7	1886.4	3508.3	5926.2
GQ113658.1	405229	2405.9	2782.3	2776.8	1520.2	1974.7	2274.0
EF185167.1	192322	888.1	1023.8	2090.9	877.7	1162.7	1513.0
AY355140.1	95347	1810.9	2290.9	1729.8	1973.6	1690.7	1463.8
GQ006838.1	502826	690.3	757.8	586.0	742.6	211.3	204.3
GQ114136.1	439586	3843.8	4376.1	3450.8	2432.3	4007.2	4610.8
GQ101225.1	420790	7050.6	7221.3	4670.1	6889.3	4637.7	5603.3
GQ048453.1	429982	177.5	364.8	176.4	394.6	66.3	40.3
GQ031800.1	464887	100.0	72.3	109.5	58.4	62.2	65.0
GQ000861.1	469425	4219.9	4524.8	1322.6	4191.7	1953.7	2840.8
GQ101676.1	458976	4793.6	5950.6	4607.1	2460.2	2813.0	2927.5
GQ019421.1	490247	2345.1	2320.0	2656.4	1432.8	1970.1	2639.6
FJ558100.1	517047	3357.2	3652.9	1321.3	2539.7	2810.3	3825.9
GQ027279.1	416279	1967.6	1533.5	1783.8	1837.6	3134.7	2092.7
GQ073269.1	467872	264.9	177.4	429.9	166.1	63.8	136.2

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GQ081299.1 gg_id:452838 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ027242.1 gg_id:430526 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9
GQ054340.1 gg_id:386212 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108
GQ113978.1 gg_id:387664 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ026752.1 gg_id:424674 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ012701.1 gg_id:496965 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8
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AF473836.1 gg_id:26894 Veillonella montpellierensis str. ADV 281.99
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GQ087817.1 gg_id:375551 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359b0
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GQ086284.1 gg_id:422736 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc

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GQ113978.1	387664	1491.5	1906.9	1516.0	723.2	989.6	1279.7
GQ026752.1	424674	1070.2	1259.1	626.6	686.8	1217.5	953.4
GQ012701.1	496965	8806.4	7347.4	1216.0	926.8	928.6	578.6
GQ012679.1	496988	4591.2	4269.8	2703.5	4607.0	2991.3	2049.4
GQ073407.1	468068	1005.5	1305.6	515.9	632.5	1203.9	911.1
GQ032582.1	375502	446.1	156.2	220.2	573.9	78.2	113.2
GQ073344.1	393528	1257.0	1448.1	478.9	660.6	1389.5	1006.9
GQ076880.1	400365	1016.8	1311.2	590.2	668.3	1136.5	936.6
GQ032461.1	463442	521.7	203.7	364.7	631.9	82.2	137.5
GQ073357.1	459514	1016.2	1299.5	580.0	638.9	1211.3	920.3
GQ057614.1	372040	463.8	308.9	428.8	500.3	246.4	277.5
GQ073343.1	395352	9625.8	9667.8	7121.2	7386.4	9367.3	8197.8
GQ114938.1	377847	4393.1	4661.5	3604.6	4031.8	3644.3	3579.8
GQ054349.1	409913	11406.4	12854.9	5953.8	8505.2	13699.3	10515.6
GQ073109.1	378037	453.7	168.1	188.5	977.7	92.1	137.5
GQ032236.1	433236	2288.8	2436.1	1496.6	2551.8	2529.0	2627.9
GQ073722.1	412083	161.2	126.2	196.9	78.0	76.3	78.8
GQ012772.1	496894	1096.4	977.7	776.3	859.2	798.4	1196.8
GQ076847.1	408841	5913.2	6008.9	5955.8	5582.1	3595.4	5771.3
GQ033104.1	434692	119.0	101.2	134.4	73.1	69.2	57.8
GQ027285.1	428376	7771.9	7594.3	2227.3	5211.2	3647.5	4018.1
GQ032864.1	466022	1159.5	1497.0	667.8	727.8	1297.3	1060.3
GQ032144.1	465685	1156.5	1487.8	651.7	719.4	1403.5	1054.3
GQ032547.1	383330	6973.1	5930.9	6376.4	6702.6	6859.7	5521.1
GQ032561.1	379283	459.3	146.5	248.5	589.4	86.4	130.3
GQ032526.1	443459	826.3	270.3	579.8	1046.0	122.6	242.5
GQ027702.1	462502	3839.9	3961.6	727.3	2864.6	906.4	973.1
GQ009508.1	500157	522.6	194.8	347.6	639.0	87.0	149.4
GQ054356.1	383423	4529.6	4347.3	3679.9	4018.5	3635.8	3754.5
GQ016840.1	492829	1037.9	380.0	874.5	1141.9	240.5	336.5
GQ076950.1	377262	3490.1	4805.9	5645.2	7361.7	11904.2	9566.1
AF439639.1	25275	1002.6	1495.3	1648.5	1049.2	1491.0	1569.1
X84006.1	13820	1043.7	946.5	569.8	627.8	314.0	359.8
AF473836.1	26894	28.3	33.8	29.0	52.8	64.7	25.1
GQ006633.1	503031	2986.4	3297.9	5671.1	5023.8	3493.6	3441.7
GQ087817.1	375551	11159.8	11204.8	6527.4	11643.7	8874.2	9122.4
GQ073137.1	388944	1504.2	1074.1	2137.1	3904.5	1060.9	1897.8
GQ086284.1	422736	495.4	145.2	141.6	943.6	82.5	91.6

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EU766448.1 gg_id:328607 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5
GQ047868.1 gg_id:451862 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
AM179906.1 gg_id:148234 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G3-1
GQ006791.1 gg_id:502872 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87g04c
AY947495.2 gg_id:114821 subgingival plaque clone OH1A
AF439641.1 gg_id:35224 Veillonella atypica str. ATCC 17744
GQ027353.1 gg_id:421354 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
EF510493.1 gg_id:217660 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
GQ032280.1 gg_id:370470 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ074330.1 gg_id:430796 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161f
GQ084875.1 gg_id:431117 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26
GQ086120.1 gg_id:463770 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ114042.1 gg_id:373803 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ086092.1 gg_id:404253 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ114025.1 gg_id:385911 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
AF439640.1 gg_id:30716 Veillonella parvula str. CIP 60.1
EF510428.1 gg_id:218682 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug
GQ027272.1 gg_id:457673 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ006604.1 gg_id:503059 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85e02c
GQ072552.1 gg_id:374904 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19
FJ557333.1 gg_id:518743 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat
FJ369852.1 gg_id:361643 feces adult twins and mothers; TS55 clone TS55_a01e08
FJ369825.1 gg_id:357386 feces adult twins and mothers; TS55 clone TS55_a01c04
FJ370053.1 gg_id:358239 feces adult twins and mothers; TS55 clone TS55_a03h07
AB478008.1 gg_id:576201 Microbial aquifer subsurface accretionary prism Japan geothermal groundwater clon
AY538171.1 gg_id:98963 Desulfitobacter alkalitolerans str. Sk.kt5
FJ638550.1 gg_id:570010 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
DQ230961.1 gg_id:142730 subsurface water clone DR938CH110701SACH36
EU639075.1 gg_id:306415 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
DQ413080.1 gg_id:153409 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
GQ502520.1 gg_id:542395 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4-
DQ988278.1 gg_id:192181 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with
EU638492.1 gg_id:319720 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AB118592.1 gg_id:93438 Endosymbiont 'TC1' Trimyema compressum clone TC1
FJ712502.1 gg_id:526485 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AB439298.1 gg_id:541578 and microbial oils produced Asia petroleum crude oil (Daqing) imported China clone
EU981271.1 gg_id:353812 sulfate reducing living bench scale aquifer column water clone E9_SW
U32594.1 gg_id:14315 Halanaerobium acetethylicum str. EIGI; DSM 3532
L22016.1 gg_id:14309 Halothermothrix orenii
X89072.1 gg_id:14311 Halocella cellulolsilytica str. DSM 7362
L22890.1 gg_id:14313 Halanaerobium salsuginis str. VS-752

EU766448.1	328607	5177.6	4809.6	4490.6	6523.2	2119.3	3834.4
GQ047868.1	451862	1658.7	1151.9	2129.4	1072.9	996.6	1291.1
AM179906.1	148234	1631.7	1131.1	917.2	588.8	330.5	315.8
GQ006791.1	502872	2458.6	3610.2	1261.9	1556.3	1167.1	2578.1
AY947495.2	114821	53.6	102.1	147.1	128.0	111.4	79.4
AF439641.1	35224	1305.1	991.6	709.2	623.9	146.2	237.3
GQ027353.1	421354	248.4	402.5	514.2	369.7	85.0	106.2
EF510493.1	217660	7341.9	5890.2	5664.8	5418.1	3686.3	4744.0
GQ032280.1	370470	4505.1	4114.6	2386.0	5625.2	4836.1	4176.8
GQ074330.1	430796	3047.8	1325.2	1564.8	3297.8	1594.5	3469.8
GQ084875.1	431117	386.5	120.7	146.4	644.4	82.5	66.1
GQ086120.1	463770	1745.8	758.3	436.0	1793.9	291.0	476.2
GQ114042.1	373803	7660.4	6812.0	3520.4	3384.9	3442.4	5035.8
GQ086092.1	404253	376.4	274.1	478.2	1263.5	78.0	168.8
GQ114025.1	385911	2938.1	1453.5	2478.7	3440.1	993.4	3056.0
AF439640.1	30716	1910.2	1582.9	669.9	1102.9	525.4	390.5
EF510428.1	218682	3206.5	2327.9	4145.0	1687.2	1900.6	2421.4
GQ027272.1	457673	1074.9	459.6	1118.6	3126.6	206.6	614.2
GQ006604.1	503059	1657.7	1309.6	2112.7	1288.5	999.9	1347.6
GQ072552.1	374904	893.4	616.6	835.8	1810.2	283.9	452.3
FJ557333.1	518743	3794.9	2635.7	2824.3	4903.6	1516.1	2154.6
FJ369852.1	361643	481.6	430.6	1029.3	218.3	68.0	194.6
FJ369825.1	357386	818.5	771.5	3282.6	444.0	394.8	974.7
FJ370053.1	358239	7617.5	10071.8	4994.6	8038.3	9033.6	11116.5
AB478008.1	576201	8465.1	9235.8	12042.4	9267.5	7681.2	8178.3
AY538171.1	98963	1608.2	1193.8	1950.4	250.2	206.9	372.0
FJ638550.1	570010	6152.0	6078.6	4635.4	5079.1	1582.4	3671.2
DQ230961.1	142730	50.8	174.8	138.3	118.3	89.4	105.8
EU639075.1	306415	46.5	129.5	86.4	67.2	75.6	29.1
DQ413080.1	153409	6194.9	7228.1	7467.5	6749.0	8816.9	9527.2
GQ502520.1	542395	6495.1	8115.4	5563.7	5449.5	8641.0	7082.4
DQ988278.1	192181	6530.0	6130.8	8735.8	5208.6	7286.4	7332.0
EU638492.1	319720	3705.7	3216.3	2943.9	1500.6	2237.7	2175.9
AB118592.1	93438	13818.2	13399.1	7603.8	8860.4	12893.2	10450.8
FJ712502.1	526485	4453.9	6820.4	8712.9	8837.7	7727.9	8429.4
AB439298.1	541578	2270.8	2457.5	2744.5	2079.0	2708.2	3133.4
EU981271.1	353812	1775.7	2316.4	2007.2	2062.8	943.6	1887.1
U32594.1	14315	112.9	490.5	64.6	91.2	75.9	33.1
L22016.1	14309	4335.6	5155.7	4535.4	5641.3	1484.4	2832.9
X89072.1	14311	3084.1	3157.0	2381.2	2406.6	2851.1	2209.2
L22890.1	14313	4712.5	5921.5	3244.9	2769.0	2544.5	5020.4

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EF585982.1 gg_id:247996 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_A
EF558989.1 gg_id:244525 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EU869420.1 gg_id:316746 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARD
EU245629.1 gg_id:249184 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-H0
EF559026.1 gg_id:238840 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EF106374.1 gg_id:201587 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2
EU245738.1 gg_id:255254 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M5-F07
EF106367.1 gg_id:202585 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2
FJ202891.1 gg_id:320426 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AM947558.1 gg_id:264238 Minor changes detected microbial structure and after three week thermophilic dige
X89077.1 gg_id:14308 Acetohalobium arabaticum
NR_028804.1 gg_id:581342 Selenihalanaerobacter shriftii str. DSSE-1; ATCC BAA-73
EF459724.1 gg_id:219578 Prokaryotic Hypersaline Inland Turkey Tuz Lake (hypersaline) clone 4-62B
EU327343.1 gg_id:288770 Halobacteroides sp. str. 6SANG
X89074.1 gg_id:14301 Halobacteroides halobius str. DSM 5150
GU452712.1 gg_id:525021 Natroniella sp. str. AHT18
X89073.1 gg_id:14302 Orenia marismortui str. DSM 5156
Y18485.1 gg_id:69790 Orenia salinaria str. SG3902
EU245188.1 gg_id:242318 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-G09
EF559012.1 gg_id:250397 Microbial functional groups solid waste digestor stable isotope probing thermophilic
AM947554.1 gg_id:270282 Minor changes detected microbial structure and after three week thermophilic dige
EF586067.1 gg_id:246373 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_
EF558957.1 gg_id:238729 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EF586053.1 gg_id:257232 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_
EU878323.1 gg_id:567033 Investigation factors influencing production large-scale municipal biogas plant therm
EU639242.1 gg_id:313846 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
FN436027.1 gg_id:539789 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t
AM947555.1 gg_id:266221 Minor changes detected microbial structure and after three week thermophilic dige
EF559059.1 gg_id:243394 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EF586029.1 gg_id:252533 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_
EF559123.1 gg_id:226234 mesophilic anaerobic digester clone C35_D63_H_B_F12
EF559004.1 gg_id:248896 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EF586046.1 gg_id:241887 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_
GU455299.1 gg_id:522555 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
EU358734.1 gg_id:312486 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas
EF422412.2 gg_id:224884 Dethiobacter alkaliphilus str. AHT1
AF507887.1 gg_id:62675 Mono Lake at depth 35m station 6 July 2000 clone ML635J-4
AJ295640.1 gg_id:31598 uranium mill tailing clone KF-Gitt2-16
AJ582199.1 gg_id:93440 soil near uranium mill tailings clone Gitt-GS-113
DQ432150.1 gg_id:156668 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Fazda sediment clone
AF507888.1 gg_id:55772 Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C

EF585982.1	247996	7374.2	6667.5	2994.9	3266.4	2046.1	2399.2
EF558989.1	244525	8061.2	10420.4	5019.1	5711.4	9505.9	5224.8
EU869420.1	316746	3803.1	5020.4	3568.6	4083.1	3816.5	4746.5
EU245629.1	249184	5366.4	5190.3	3765.7	4535.8	2020.4	3102.5
EF559026.1	238840	11690.2	12275.9	8891.9	10057.8	4242.3	6827.3
EF106374.1	201587	25.4	34.5	35.0	55.3	61.0	27.7
EU245738.1	255254	7761.3	7626.1	4830.6	5733.1	7019.2	5303.7
EF106367.1	202585	1232.7	908.1	1615.1	1582.3	1504.4	1482.4
FJ202891.1	320426	51.7	45.0	104.0	67.6	63.7	34.3
AM947558.1	264238	9431.4	11566.3	5088.5	7147.8	6029.0	5862.0
X89077.1	14308	320.4	249.2	324.2	294.4	142.8	147.0
NR_028804.1	581342	54.5	76.8	82.0	85.8	74.9	50.8
EF459724.1	219578	61.5	58.4	145.4	102.1	62.6	67.2
EU327343.1	288770	7926.0	5052.3	10035.6	6437.7	3745.2	3012.0
X89074.1	14301	2746.4	6611.4	2087.1	2639.7	1941.2	2277.1
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X89073.1	14302	306.3	277.0	631.6	283.6	589.0	576.1
Y18485.1	69790	3964.6	4977.6	6857.1	6050.8	3196.4	4557.1
EU245188.1	242318	2150.5	2691.6	4000.2	4349.8	2531.6	2957.5
EF559012.1	250397	5020.1	3832.0	4448.8	1847.6	673.4	1496.5
AM947554.1	270282	7218.3	6408.5	6455.6	6009.1	4013.9	4782.5
EF586067.1	246373	13275.2	11135.9	7763.9	8997.7	9353.5	10483.6
EF558957.1	238729	153.2	264.5	471.0	349.4	242.8	545.9
EF586053.1	257232	647.8	515.0	963.9	335.7	301.9	297.7
EU878323.1	567033	7263.3	6157.3	6281.4	5286.6	5959.1	6255.9
EU639242.1	313846	11707.7	12822.4	11676.4	9635.9	11307.1	10999.8
FN436027.1	539789	1972.5	2008.8	2068.0	793.2	2437.5	1323.0
AM947555.1	266221	1692.5	1793.4	1375.9	1923.8	1063.4	1431.2
EF559059.1	243394	3330.7	3427.0	2440.1	1571.1	1951.1	2005.8
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EF559123.1	226234	1636.0	1901.4	3996.6	1637.8	1101.2	1254.2
EF559004.1	248896	1303.4	2168.2	3840.1	1414.0	2184.1	2591.7
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EU358734.1	312486	1861.7	1951.2	1409.9	1014.7	159.2	249.2
EF422412.2	224884	5637.1	4795.2	4939.3	5039.6	2239.2	3259.4
AF507887.1	62675	3332.0	4029.7	731.8	1332.7	602.2	464.3
AJ295640.1	31598	41.3	52.1	44.2	88.6	115.4	39.2
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DQ432150.1	156668	844.2	672.9	553.7	304.5	200.1	365.3
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AJ853529.1 gg_id:110524 landfill leachate clone GZKB35
GQ848216.1 gg_id:544950 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac
EU878335.1 gg_id:554328 Investigation factors influencing production large-scale municipal biogas plant therm
DQ206412.1 gg_id:139538 microbial mediates arsenate reduction soda lake water clone ML-AsS-10
DQ837275.1 gg_id:244602 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_61
FJ203016.1 gg_id:351673 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
GQ848219.1 gg_id:541684 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac
EU812988.1 gg_id:341763 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-N
EU592468.1 gg_id:573525 Seasonal changes Salton Sea hypersaline sediment clone SSS47A
GU083673.1 gg_id:542800 Microorganism Xiarinur soda lake sediment clone x269
GQ848204.1 gg_id:588856 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac
AF454298.1 gg_id:63836 Bacillus sp. clone ML1228J-1
NZ_ABKR01000005.1 gg_id:261070 Natranaerobius thermophilus str. JW/NM-WN-LF
AJ271451.1 gg_id:73970 Natronoanaerobium halophilum G-M14CH-4
AJ271450.1 gg_id:23520 Natronoanaerobium salstagnum O-M12SP-2
AJ271452.1 gg_id:72206 Natronoanaerobium aggerbacterium G-M16NWC-4
DQ354747.1 gg_id:155876 subsurface water clone MS149BH1062003_30
AB539949.1 gg_id:571087 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t
DQ088759.1 gg_id:132063 0.7 1.4 kmbls sctn cntnntl crst cln BE325FW032701CTS_hl1-69
EU250948.1 gg_id:358480 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose
AY330127.1 gg_id:95976 methanogenic landfill leachate bioreactor clone AC039
DQ125604.1 gg_id:134479 uranium contaminated soil clone AKAU3609
GQ402678.1 gg_id:512997 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ125579.1 gg_id:132342 uranium contaminated soil clone AKAU3574
DQ125547.1 gg_id:129508 uranium contaminated soil clone AKAU3523
DQ887916.1 gg_id:168335 thermophilic anaerobic solid waste bioreactor clone GHB3B06
DQ125708.1 gg_id:133296 uranium contaminated soil clone AKAU3802
FJ381977.1 gg_id:583118 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT
EF585978.1 gg_id:246509 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_A
AY330129.1 gg_id:95835 methanogenic landfill leachate bioreactor clone AC007
DQ887936.1 gg_id:169354 thermophilic anaerobic solid waste bioreactor clone GMB4H09
AB274500.1 gg_id:215152 packed-bed reactor clone CFB-11
DQ125736.1 gg_id:134788 uranium contaminated soil clone AKAU3845
EU887985.1 gg_id:339192 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach
AM947551.1 gg_id:260695 Minor changes detected microbial structure and after three week thermophilic dige
FJ985789.1 gg_id:451463 depths Colombia South America soil 0-10 m depth former landfill clone -1
FJ985786.1 gg_id:402134 depths Colombia South America soil 5 m depth former landfill clone C5-11
CU919747.1 gg_id:567508 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU919791.1 gg_id:534056 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY684074.1 gg_id:133964 methanogenic enrichment 'MRE50' clone MRE50b10
CU919182.1 gg_id:566892 Towards definition core microorganisms involved digestion mesophilic anaerobic dig

AJ853529.1	110524	72.7	87.9	183.7	120.0	101.7	59.1
GQ848216.1	544950	9817.7	6288.4	4497.5	3574.0	2742.7	4626.1
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DQ206412.1	139538	31.7	23.5	44.4	49.4	46.2	31.2
DQ837275.1	244602	5097.8	4753.3	3703.5	3843.2	2166.0	2254.3
FJ203016.1	351673	7563.7	8150.7	9118.1	6931.8	8168.2	7352.3
GQ848219.1	541684	8751.9	9353.8	8656.8	7385.1	12034.3	9344.5
EU812988.1	341763	8297.8	10750.7	10620.4	4833.0	6902.7	6314.8
EU592468.1	573525	4810.8	5286.0	3646.5	1835.3	3955.2	1801.3
GU083673.1	542800	10460.9	10057.1	8466.5	8074.3	7945.1	5457.2
GQ848204.1	588856	152.1	385.5	1100.3	207.6	642.8	308.8
AF454298.1	63836	51.9	82.8	58.3	103.7	219.3	557.8
NZ_ABKR01000005.1	261070	2066.0	2748.5	1595.2	2149.8	2047.8	1875.2
AJ271451.1	73970	635.9	508.5	314.5	170.2	281.3	182.1
AJ271450.1	23520	215.0	226.1	245.4	144.5	77.5	146.2
AJ271452.1	72206	2042.5	2209.2	1436.1	1273.2	430.2	534.8
DQ354747.1	155876	5091.5	5717.3	3330.6	802.9	805.6	1802.6
AB539949.1	571087	6003.2	8243.1	8866.4	5665.3	5365.0	5526.0
DQ088759.1	132063	35.7	48.1	30.0	53.9	69.7	79.1
EU250948.1	358480	901.9	754.7	2317.0	567.6	752.7	932.7
AY330127.1	95976	1304.2	1831.3	1738.9	1205.9	1757.7	1291.7
DQ125604.1	134479	158.9	250.5	597.2	145.4	277.3	764.3
GQ402678.1	512997	4880.4	5777.4	6898.2	6981.9	15911.6	13911.4
DQ125579.1	132342	4756.5	3984.8	2564.3	4883.8	2422.5	4369.0
DQ125547.1	129508	566.5	518.5	1911.2	646.7	230.0	772.4
DQ887916.1	168335	2892.1	2863.7	1607.7	1364.1	273.3	1663.8
DQ125708.1	133296	3360.3	3668.3	2047.5	3037.9	2225.4	1861.8
FJ381977.1	583118	639.5	1551.2	2507.3	1608.9	3440.1	5205.7
EF585978.1	246509	3919.1	4465.7	2686.9	3753.2	1033.8	1959.2
AY330129.1	95835	5962.5	6963.6	4465.7	6819.4	5625.2	5498.3
DQ887936.1	169354	1677.2	1606.2	2954.9	921.8	694.2	2002.3
AB274500.1	215152	28.8	39.9	59.9	96.3	77.9	79.4
DQ125736.1	134788	3385.3	4665.6	2516.2	1587.4	1121.9	1664.5
EU887985.1	339192	5435.3	6488.7	5305.5	4523.9	2520.8	4729.8
AM947551.1	260695	125.9	223.3	488.7	131.0	426.0	391.1
FJ985789.1	451463	7451.2	7838.4	3122.0	6665.5	3614.6	4059.1
FJ985786.1	402134	1965.5	1727.7	3626.2	2598.3	1407.6	1872.2
CU919747.1	567508	9648.6	13132.9	6488.7	10445.3	15198.4	11347.8
CU919791.1	534056	8079.9	6850.7	7030.4	8580.1	6763.9	7169.3
AY684074.1	133964	10845.9	11568.7	9117.9	7599.6	10435.2	9337.6
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CU927811.1 gg_id:560195 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY684100.1 gg_id:131930 methanogenic enrichment 'MRE50' clone MRE50b22
AY684090.1 gg_id:130626 methanogenic enrichment 'MRE50' clone MRE50b08
CT573824.1 gg_id:150758 Evry municipal wastewater treatment plant clone 013H11_B_SD_P15
AY526502.1 gg_id:136583 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone D3
CU919826.1 gg_id:551199 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
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EU638947.1 gg_id:342798 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EF559227.1 gg_id:222005 mesophilic anaerobic digester clone A35_D28_H_B_B01
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EU878344.1 gg_id:593716 Investigation factors influencing production large-scale municipal biogas plant therm
EF198048.1 gg_id:185617 Microbial structures mesophilic and methanogenic consortia anaerobic thermophilic
EU639113.1 gg_id:306099 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AB374111.1 gg_id:246025 Effect temperature on microbial glucose-degrading methanogenic consortium under
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CU918937.1 gg_id:549084 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU921330.1 gg_id:570394 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ899892.1 gg_id:257323 structure receiving long-term augmentations chromium contaminated wastes landfi
DQ018807.1 gg_id:132376 anaerobic swine lagoon clone C-131
AB234270.1 gg_id:145732 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
DQ018815.1 gg_id:132872 Unq Mcrbl Anrbc Swn Lgns anrbc swn lgn cln C-146
EF586045.1 gg_id:245235 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_
EF586061.1 gg_id:243276 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_
EF559043.1 gg_id:238463 Microbial functional groups solid waste digestor stable isotope probing thermophilic
AB234000.1 gg_id:152360 anaerobic reactor clone B-7
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CP000679.1 gg_id:224527 Caldicellulosiruptor saccharolyticus str. DSM 8903
EF100909.1 gg_id:193269 Caldicellulosiruptor kronotskiensis str. 2002
U80596.1 gg_id:16088 Caldicellulosiruptor owensensis str. OL
L35151.1 gg_id:16089 Caldicellulosiruptor sp. str. Rt8B.4
EF100907.1 gg_id:181163 Caldicellulosiruptor kristjanssonii str. 117
AJ004811.1 gg_id:16095 Caldicellulosiruptor kristjanssonii str. I77R1B
L09183.1 gg_id:16093 Thermoanaerobacter cellulolyticus str. NA 10B
FJ189575.1 gg_id:351375 digester anaerobic sludge clone EUB_54

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CU927811.1	560195	1530.5	1564.5	2649.6	2142.6	3678.2	1939.3
AY684100.1	131930	6328.2	7013.8	7242.6	3071.6	3717.5	5566.8
AY684090.1	130626	1093.8	1413.9	4278.2	345.9	1249.2	930.6
CT573824.1	150758	6694.6	6392.2	4847.3	3692.9	1997.0	4769.6
AY526502.1	136583	416.2	911.9	1424.7	1199.7	1150.1	801.2
CU919826.1	551199	1738.4	2238.4	5033.2	3531.3	1702.8	1365.4
CU919394.1	554083	5744.2	6695.0	5772.8	5961.7	7088.8	5413.9
EU639084.1	320495	7716.0	8422.2	7017.3	10619.7	14002.1	10314.5
EU638947.1	342798	68.6	95.6	75.8	103.3	83.1	165.4
EF559227.1	222005	2363.4	2313.2	4860.5	4303.1	1271.0	3526.4
CU919273.1	572645	1543.7	2092.1	3169.5	2084.7	5461.4	3240.2
CU918907.1	539546	1344.1	1504.7	2344.3	785.5	2809.1	974.4
AB434894.1	277048	11240.0	10078.3	8697.4	7677.7	4604.1	4185.6
EU878344.1	593716	2768.6	2627.4	5353.3	1803.6	2081.1	2001.7
EF198048.1	185617	6918.4	7481.7	8856.8	4250.5	7930.8	7720.8
EU639113.1	306099	10894.0	12421.6	5342.6	7477.0	8881.4	8288.7
AB374111.1	246025	56.0	67.7	56.1	86.3	76.2	83.4
CR933199.1	110387	5871.1	4160.2	2570.2	7339.3	6056.0	5621.0
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CU921330.1	570394	4346.9	4515.6	3241.7	2987.6	1595.6	2245.6
DQ899892.1	257323	3408.1	4265.6	8264.3	2557.4	1447.6	4434.5
DQ018807.1	132376	5400.8	5270.3	3727.2	4657.0	2542.8	2617.1
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DQ018815.1	132872	2156.1	2394.5	2498.5	753.4	855.6	787.3
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EF554597.1 gg_id:233108 Fervidomicrobium thiophilum str. SR
NC_003869.1 gg_id:471376 Thermoanaerobacter tengcongensis MB4 str. MB4T
AF174484.1 gg_id:39044 Carboxydibrachium pacificum str. JM
EU109461.1 gg_id:237130 Thermoanaerobacter subterraneus str. S2302
AF212925.1 gg_id:26976 Thermoanaerobacter yonseiensis str. KB1
EF554599.1 gg_id:234626 Thermoanaerobacter subterraneus str. 2707
EF195126.1 gg_id:175440 Caldanaerobacter hydrothermalis str. K67
FJ189534.1 gg_id:349650 digester anaerobic sludge clone EUB_13
EF554598.1 gg_id:232884 Thermoanaerobacter subterraneus str. SP47
AY278483.1 gg_id:87364 Thermoanaerobacter keratinophilus str. 2KXI
DQ115806.1 gg_id:134076 Thermoanaerobacter tengcongensis str. 185y2
CP000141.1 gg_id:140847 Carboxydothermus hydrogenoformans str. Z-2901
U76363.1 gg_id:13728 Thermoterrabacterium ferrireducens
U76364.1 gg_id:13730 Thermoterrabacterium ferrireducens
EF542810.1 gg_id:218099 Carboxydothermus siderophilus str. 1315
AF487538.1 gg_id:82633 Moorella mulderi str. TMS
EU638616.1 gg_id:334086 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AY684084.1 gg_id:153109 first genome data rice I methanogens combination cultivation and techniques metha
FJ189582.1 gg_id:324196 digester anaerobic sludge clone EUB_61
EU638454.1 gg_id:309145 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
AB222053.1 gg_id:137796 Clostridium sp. str. EBR-02E-0600
AB020336.1 gg_id:13717 Thermacetogenium phaeum str. PB
EF559057.1 gg_id:243312 Microbial functional groups solid waste digestor stable isotope probing thermophilic
DQ647145.1 gg_id:257640 Microbial structure -temperature oil-field produced water Troll formations North Se
EF558950.1 gg_id:246613 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EU386162.1 gg_id:265020 Thermacetogenium sp. str. Sp3
AB332113.1 gg_id:246435 Continuous cultivation and structure thermophilc propionate-degrading microbial co
DQ097678.2 gg_id:134576 oil field clone B11_otu13
DQ887938.1 gg_id:165206 thermophilic anaerobic solid waste bioreactor clone GMB4F03
AF542519.1 gg_id:59095 Thermoanaerobacter ethanolicus str. X521
AF542521.1 gg_id:59098 Thermoanaerobacter ethanolicus str. X524
DQ128182.1 gg_id:138446 Thermoanaerobacter ethanolicus 3
AY701757.1 gg_id:106184 Thermoanaerobacter sp. str. AIP 504.99
NC_010321.1 gg_id:259585 Thermoanaerobacter pseudethanolicus 33223 str. ATCC 33223; 39E
EU262599.1 gg_id:240738 Thermoanaerobacter inferii str. AK15
L09167.1 gg_id:13780 Thermoanaerobacter thermocopriae str. JT-3T
DQ128177.1 gg_id:137851 Thermoanaerobacter ethanolicus 6
DQ128183.1 gg_id:202453 Thermoanaerobacter ethanolicus 2

EF100908.1	185074	265.1	401.7	735.5	272.5	510.8	663.1
DQ152922.1	139369	1587.9	2038.7	2333.3	1245.8	2446.6	2679.4
CP001785.1	521670	4929.4	5787.7	5563.9	2388.2	2627.4	3380.9
EF554597.1	233108	389.3	425.7	969.9	362.3	228.5	570.2
NC_003869.1	471376	8654.2	7053.5	6991.7	6011.1	3590.2	5781.4
AF174484.1	39044	2286.8	2195.6	2312.7	1845.0	2449.7	2848.5
EU109461.1	237130	227.5	322.0	368.8	162.4	174.9	318.4
AF212925.1	26976	4702.7	4430.2	3609.0	4800.8	4209.7	4841.4
EF554599.1	234626	2617.0	2443.4	3375.1	2267.8	2882.6	2648.2
EF195126.1	175440	446.1	1164.0	758.8	302.6	1186.1	862.3
FJ189534.1	349650	493.9	483.9	744.8	278.9	864.2	565.8
EF554598.1	232884	1676.9	1109.0	1017.9	790.5	397.4	912.3
AY278483.1	87364	197.4	136.1	195.8	139.2	142.5	246.2
DQ115806.1	134076	9462.4	11716.3	7757.3	9110.1	13187.2	10620.4
CP000141.1	140847	2050.7	2161.6	1945.0	1249.4	1170.2	2828.8
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EF542810.1	218099	2137.9	3740.5	3981.1	3989.1	8890.1	7393.2
AF487538.1	82633	7640.2	9777.0	4593.5	8210.4	10145.1	10173.0
EU638616.1	334086	2247.7	3890.9	2981.7	4086.2	3627.1	3808.6
AY684084.1	153109	10027.3	11891.3	9942.4	9335.7	9062.3	6047.5
FJ189582.1	324196	13455.9	14907.3	10293.0	12337.7	13912.7	12114.6
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AB222053.1	137796	607.1	932.4	1453.6	1272.9	1779.2	1543.3
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EF559057.1	243312	4515.7	4549.2	5410.7	2313.7	2782.8	3037.0
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EF558950.1	246613	6462.2	6903.7	7592.6	5595.2	4414.1	5319.8
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DQ097678.2	134576	691.8	626.7	241.2	176.3	136.5	151.8
DQ887938.1	165206	627.2	607.3	240.3	433.4	79.0	282.0
AF542519.1	59095	44.8	69.6	101.7	66.6	73.9	42.9
AF542521.1	59098	3503.0	3781.3	5861.4	2321.1	2973.2	2922.8
DQ128182.1	138446	3321.5	1917.1	5593.0	3915.3	2644.6	3085.5
AY701757.1	106184	75.8	152.4	148.9	83.2	91.2	92.6
NC_010321.1	259585	158.0	236.1	364.1	102.5	84.3	107.4
EU262599.1	240738	867.4	1884.1	4264.1	1476.1	1327.1	1733.9
L09167.1	13780	50.1	131.1	171.5	74.5	91.1	154.5
DQ128177.1	137851	3421.5	1769.0	4593.6	3757.8	2258.4	3468.6
DQ128183.1	202453	6871.7	3668.3	10820.8	7641.1	4767.4	6234.2

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DQ128178.1 gg_id:137799 Thermoanaerobacter ethanolicus 1
NR_029301.1 gg_id:574119 Thermoanaerobacter wiegelii str. Rt8.B1; DSM 10319
DQ128181.1 gg_id:137863 Thermoanaerobacter ethanolicus 4
L09160.1 gg_id:13765 Thermoanaerobacter kivui
DQ681066.1 gg_id:163311 Thermoanaerobacter wiegelii str. B5
AF234164.1 gg_id:29733 Thermoanaerobacter sulfurigignens str. JW/SL826T
L09164.1 gg_id:13789 Thermoanaerobacter ethanolicus ATCC 33223 str. 39E
EU731003.1 gg_id:338174 single-species ecosystem deep within Earth fracture water borehole MP104 level 10
FJ712408.1 gg_id:523660 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EU730994.1 gg_id:353154 single-species ecosystem deep within Earth fracture water borehole MP104 level 10
EU419136.1 gg_id:267107 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
FJ748761.1 gg_id:545194 Thermoanaerobacter sp. str. RH0804
AB062280.1 gg_id:20457 Thermanaeromonas toyohensis str. ToBE
DQ887945.1 gg_id:168959 thermophilic anaerobic solid waste bioreactor clone GMB4H08
AY216596.1 gg_id:85134 Thermoanaerobacter subterraneus str. OCA1
AB374119.1 gg_id:250276 Effect temperature on microbial glucose-degrading methanogenic consortium under
EU638335.1 gg_id:348663 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
FJ638536.1 gg_id:572985 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
AB374120.1 gg_id:243918 Effect temperature on microbial glucose-degrading methanogenic consortium under
AB434897.1 gg_id:271632 Effect temperature on microbial glucose-degrading methanogenic consortium under
AE013109.1 gg_id:66678 Thermoanaerobacter tengcongensis str. MB4
AB374132.1 gg_id:243488 Effect temperature on microbial glucose-degrading methanogenic consortium under
AB374117.1 gg_id:238691 Effect temperature on microbial glucose-degrading methanogenic consortium under
AB374134.1 gg_id:256314 Effect temperature on microbial glucose-degrading methanogenic consortium under
DQ097675.2 gg_id:134191 oil field clone B5_otu10
AY703479.1 gg_id:138789 Thermosediminibacter litoriperuensis str. JW/YJL-1230-2
EU638920.1 gg_id:316096 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EU639339.1 gg_id:323523 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
EF174273.1 gg_id:190840 direct activated sludge compost maturation stage clone H42-814
CU920710.1 gg_id:539239 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ079649.1 gg_id:137457 deep terrestrial subsurface fluid-filled fracture clone EV818FW062101BH4MD9
AB260059.1 gg_id:179484 Microbial black exposed hot ridge flank crustal fluids Black rust formation on boreho
AB300079.1 gg_id:220063 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A
AM777947.1 gg_id:237589 nonsaline . Influence pore-size filters determination structure alkaline groundwater
DQ088764.1 gg_id:133580 subsurface clone BE325FW032701CTS_hole1-27
DQ088772.1 gg_id:131486 subsurface clone BE325FW032701CTS_hole1-1
AB426224.1 gg_id:275227 -situ identification study benzene-degrading s under methanogenic condition anaerc
EF632928.1 gg_id:246403 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
FJ203601.1 gg_id:339359 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AB539950.1 gg_id:517375 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t
DQ256302.1 gg_id:142791 subsurface water clone EV818BHEB6102702SAFF42

DQ128178.1	137799	10224.5	10109.6	6449.7	9638.7	16029.9	14216.1
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DQ128181.1	137863	8169.5	9294.0	6262.4	6914.1	9608.2	8222.1
L09160.1	13765	5171.7	5647.4	5394.2	5220.6	8802.3	5854.3
DQ681066.1	163311	2953.1	4268.1	3356.2	3595.2	2668.6	3062.0
AF234164.1	29733	108.5	367.1	338.5	122.4	103.1	47.4
L09164.1	13789	9095.5	8818.1	9639.1	7637.8	8038.1	8116.6
EU731003.1	338174	589.5	1191.2	1568.6	355.0	524.6	755.7
FJ712408.1	523660	44.4	107.3	307.2	96.2	59.8	60.5
EU730994.1	353154	123.2	177.9	62.5	61.9	179.1	49.8
EU419136.1	267107	19759.2	19527.9	12744.5	10746.7	9655.1	10855.4
FJ748761.1	545194	2373.8	2081.9	334.0	2061.5	2639.7	2171.1
AB062280.1	20457	21.5	35.8	53.1	40.4	321.2	176.7
DQ887945.1	168959	7819.3	8035.8	9184.0	6949.4	4436.1	4292.4
AY216596.1	85134	848.2	1264.4	2696.8	1580.6	1403.4	1169.8
AB374119.1	250276	11809.3	11048.3	7746.5	6493.2	6473.0	7565.8
EU638335.1	348663	31.5	36.8	27.4	61.3	82.5	38.4
FJ638536.1	572985	369.6	500.4	719.8	856.7	155.7	188.1
AB374120.1	243918	2837.8	3682.7	5092.1	3512.6	2985.8	2922.9
AB434897.1	271632	1280.4	2261.7	2935.5	1123.0	1815.7	1683.9
AE013109.1	66678	9.9	24.6	17.5	38.8	60.4	18.6
AB374132.1	243488	748.3	1164.8	1988.6	644.3	1420.2	825.5
AB374117.1	238691	2748.6	2761.8	2828.6	1949.8	2908.6	2617.7
AB374134.1	256314	497.8	931.7	491.2	261.8	528.3	317.7
DQ097675.2	134191	9298.0	10389.7	8268.2	6757.8	9677.4	8286.6
AY703479.1	138789	7625.0	8776.1	6024.0	4410.5	4253.8	4379.7
EU638920.1	316096	3346.8	3457.7	3863.7	3547.4	5657.4	3937.6
EU639339.1	323523	5099.9	4388.3	5217.4	4757.6	4782.7	5277.8
EF174273.1	190840	1140.9	2055.1	1383.7	535.4	232.6	1158.7
CU920710.1	539239	742.2	1374.3	2109.3	672.6	394.2	1403.6
DQ079649.1	137457	20.3	47.8	29.1	50.4	66.5	32.4
AB260059.1	179484	837.0	876.0	437.0	186.3	1130.1	573.3
AB300079.1	220063	306.1	234.6	424.3	250.1	193.9	222.9
AM777947.1	237589	7862.8	8056.7	8542.5	5349.1	2981.6	5415.7
DQ088764.1	133580	29.4	47.8	26.9	55.3	64.8	29.4
DQ088772.1	131486	35.1	74.7	254.7	64.6	70.6	80.9
AB426224.1	275227	2338.7	3013.6	5722.3	3249.8	4104.9	5968.1
EF632928.1	246403	149.7	184.0	325.9	252.4	106.5	120.4
FJ203601.1	339359	7001.7	7851.8	4089.9	3732.9	4759.0	4242.8
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AJ431236.1 gg_id:79101 Cytophaga sp. str. BHI60-57B
EF585979.1 gg_id:257911 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_A
EF559068.1 gg_id:252254 Microbial functional groups solid waste digestor stable isotope probing thermophilic
AM947532.1 gg_id:265589 Minor changes detected microbial structure and after three week thermophilic dige
AF282252.1 gg_id:17524 Ferribacter thermoautotrophicus str. JW/JH-Fiji-2
DQ815026.1 gg_id:169250 zebrafish digestive tract clone aab49a06
DQ815290.1 gg_id:171837 zebrafish digestive tract clone aab52g10
DQ815286.1 gg_id:171805 zebrafish digestive tract clone aab52g04
DQ815110.1 gg_id:173268 zebrafish digestive tract clone aab50b10
DQ815013.1 gg_id:161980 zebrafish digestive tract clone aab56g09
AM179923.1 gg_id:145422 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G15-2
DQ815269.1 gg_id:172292 zebrafish digestive tract clone aab52e06
DQ815170.1 gg_id:168343 zebrafish digestive tract clone aab51a08
DQ815292.1 gg_id:170458 zebrafish digestive tract clone aab52h02
EU460633.1 gg_id:297393 polar bear feces clone PB2_aai23f09
EU460497.1 gg_id:293496 polar bear feces clone PB2_aai21g01
DQ815229.1 gg_id:164983 zebrafish digestive tract clone aab51h04
EU460618.1 gg_id:287660 polar bear feces clone PB2_aai23e02
EU460666.1 gg_id:296915 polar bear feces clone PB2_aai24b06
X78419.1 gg_id:11302 Cetobacterium ceti
EU460449.1 gg_id:296950 polar bear feces clone PB2_aai21a07
EU460631.1 gg_id:298501 polar bear feces clone PB2_aai23f07
EU460679.1 gg_id:297037 polar bear feces clone PB2_aai24c12
EU460629.1 gg_id:293351 polar bear feces clone PB2_aai23f05
GU293194.1 gg_id:562985 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content
EU460532.1 gg_id:297473 polar bear feces clone PB2_aai22c03
EU460361.1 gg_id:297672 polar bear feces clone PB1_aai27c07
EU460550.1 gg_id:291093 polar bear feces clone PB2_aai22e07
EU460627.1 gg_id:291261 polar bear feces clone PB2_aai23f02
EU460489.1 gg_id:294813 polar bear feces clone PB2_aai21f01
EU460637.1 gg_id:298087 polar bear feces clone PB2_aai23g02
NR_025679.1 gg_id:554906 Fusobacterium canifelinum str. RMA 12708; CCUG 49735 Q11
AJ295750.1 gg_id:34266 Fusobacterium equinum str. horse VPB 4027
X74408.1 gg_id:11309 Fusobacterium necrophorum str. B FnS-40
X74407.1 gg_id:11305 Fusobacterium necrophorum str. AB FnS-1
FJ471661.1 gg_id:524898 Fusobacterium nucleatum str. ChDC F319
GQ004485.1 gg_id:505177 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59b02c1
EU772809.1 gg_id:306442 Bush dog feces clone bdog1_aai77h07
AF543300.1 gg_id:58280 Fusobacterium nucleatum str. ChDC OS50
GQ448468.1 gg_id:511044 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_2wks_gr
AF481217.1 gg_id:68347 Fusobacterium nucleatum str. E9_12

AJ431236.1	79101	1037.2	1786.5	2001.8	949.0	1334.8	2262.3
EF585979.1	257911	71.9	101.4	833.6	104.2	55.4	85.3
EF559068.1	252254	847.5	983.4	3481.4	833.8	1813.2	437.4
AM947532.1	265589	8005.1	10002.2	6579.2	5250.2	4597.8	4889.3
AF282252.1	17524	54.7	113.5	193.9	68.3	157.6	327.8
DQ815026.1	169250	134.4	135.3	77.4	107.9	180.0	83.2
DQ815290.1	171837	4989.3	5232.8	7028.9	6289.1	5658.3	4959.1
DQ815286.1	171805	985.1	1685.7	3346.8	1097.2	2120.8	1196.9
DQ815110.1	173268	3386.9	2973.3	7076.6	3796.6	3084.4	3925.8
DQ815013.1	161980	2992.4	3196.7	7269.8	3104.0	4327.6	4342.3
AM179923.1	145422	53.5	95.6	33.3	55.0	63.7	30.3
DQ815269.1	172292	4417.1	4503.2	11312.4	6220.2	5720.6	5556.4
DQ815170.1	168343	357.2	652.4	5789.8	1235.1	188.0	178.5
DQ815292.1	170458	67.4	83.7	113.7	83.7	60.1	38.4
EU460633.1	297393	7217.9	7246.9	11568.2	7786.4	5661.5	7346.4
EU460497.1	293496	4246.4	4003.6	5568.7	5111.9	3347.7	6765.6
DQ815229.1	164983	518.8	994.7	2987.2	779.0	1366.8	631.3
EU460618.1	287660	1868.2	1811.0	5674.5	2178.9	2604.5	3249.7
EU460666.1	296915	6951.7	6836.7	9486.3	7773.4	5718.8	7753.1
X78419.1	11302	52.7	72.6	281.9	186.0	73.8	28.2
EU460449.1	296950	2046.7	2349.9	6724.4	3339.9	2652.1	3477.8
EU460631.1	298501	908.2	1135.6	4066.4	1484.3	1385.2	2345.6
EU460679.1	297037	1116.3	1870.8	4970.7	1590.0	1582.1	2853.9
EU460629.1	293351	4772.1	6835.1	6850.4	5810.3	8820.1	10222.5
GU293194.1	562985	5937.7	7761.9	6031.6	4543.3	7386.4	7409.7
EU460532.1	297473	3213.4	5339.1	6623.0	3950.1	7192.4	9483.4
EU460361.1	297672	3247.4	3954.6	5211.4	4316.8	5529.4	4545.5
EU460550.1	291093	17319.1	19745.5	9835.8	13732.1	17811.2	16189.4
EU460627.1	291261	4700.2	4565.6	5930.9	6393.5	4383.4	6357.3
EU460489.1	294813	5626.3	5186.4	10244.3	6196.6	3307.5	4470.4
EU460637.1	298087	4309.2	3615.7	7523.2	4462.0	1948.7	4451.0
NR_025679.1	554906	2806.8	2188.9	4405.3	2084.5	1572.2	2014.3
AJ295750.1	34266	3515.9	4037.5	7072.4	4787.9	2649.7	1738.9
X74408.1	11309	345.3	304.5	1909.0	659.4	409.9	201.1
X74407.1	11305	2007.6	1826.8	3883.0	607.2	1423.3	612.8
FJ471661.1	524898	4547.7	4576.9	7961.7	5762.8	3906.6	4224.5
GQ004485.1	505177	5065.7	4600.9	10541.1	4812.5	4028.8	3113.6
EU772809.1	306442	1084.8	1506.5	5169.9	2754.5	430.2	117.9
AF543300.1	58280	1224.9	1485.9	6134.0	2224.0	2176.2	1595.9
GQ448468.1	511044	2312.2	3686.3	3000.4	2356.4	6014.0	3196.9
AF481217.1	68347	2832.6	2066.8	5124.2	2795.8	1578.1	2019.6

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FJ959515.1 gg_id:550936 bottlenose dolphin upper respiratory tract blowhole clone D896_106
NZ_ACET01000043.1 gg_id:470433 Fusobacterium gonidiaformans str. ATCC 25563
FJ471649.1 gg_id:529903 Fusobacterium nucleatum str. ChDC F290
GQ091870.1 gg_id:449592 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ113263.1 gg_id:375228 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
FJ978721.1 gg_id:408384 feces clone CL_F_417
EU774026.1 gg_id:308389 Cheetah feces clone CE3_aai08d02
EF089177.1 gg_id:185041 Fusobacterium nucleatum str. Ulm 14
FJ978724.1 gg_id:381867 feces clone CL_F_422
FJ978541.1 gg_id:427042 feces clone CL_F_080
FJ471639.2 gg_id:514347 Fusobacterium nucleatum str. ChDC F113
GQ088072.1 gg_id:459200 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ471673.1 gg_id:520375 Fusobacterium periodonticum str. ChDC F334
DQ440563.1 gg_id:156573 Fusobacterium nucleatum str. Ulm
GQ087757.1 gg_id:395408 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ014795.1 gg_id:494871 Topographical and Temporal Human Skin Microbiome skin palm clone nbw764c09c1
FJ978525.1 gg_id:468118 feces clone CL_F_056
CP001685.1 gg_id:529857 Leptotrichia buccalis C-1013-b str. DSM 1135
FJ577251.2 gg_id:568972 Leptotrichia hofstadii str. F0254
AF206305.1 gg_id:71541 Leptotrichia trevisanii
AY134896.1 gg_id:59574 oral periodontitis clone EX103
AM420035.1 gg_id:241454 Noma subgingival plaque clone 201G10(oral)
CP001685.1 gg_id:529859 Leptotrichia buccalis C-1013-b str. DSM 1135
GQ129984.1 gg_id:399980 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
AY207053.1 gg_id:83573 human mouth clone P2PB_51
AF432138.1 gg_id:31235 tongue dorsum scrapings clone FP036
GQ000682.1 gg_id:469247 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ000882.1 gg_id:469447 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
AY349385.1 gg_id:92131 human oral cavity clone GT020
FJ976353.1 gg_id:578509 Interindividual healthy human oral microbiota mouth clone 12BB57
AM420193.1 gg_id:258023 Noma subgingival plaque clone 502D06(oral)
GQ016176.1 gg_id:493491 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
FJ577259.2 gg_id:566658 Leptotrichia goodfellowii str. F0264
AY029803.1 gg_id:70629 Leptotrichia hofstadii str. LB23
AF287814.1 gg_id:38061 human subgingival plaque clone F138
GQ032449.1 gg_id:403062 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
AF385571.1 gg_id:70038 crevicular epithelial cells clone EI013
GQ016227.1 gg_id:493440 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
EU137409.1 gg_id:267538 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C
NZ_ACVB02000014.1 gg_id:484462 Leptotrichia hofstadii str. F0254
AM420110.1 gg_id:256867 Noma subgingival plaque clone 303F08(oral)

FJ959515.1	550936	511.6	434.4	5507.9	1070.9	847.8	553.5
NZ_ACET01000043.1	470433	230.2	243.7	5471.3	643.5	87.8	108.1
FJ471649.1	529903	4968.2	4731.3	5479.3	4096.3	7875.7	2500.7
GQ091870.1	449592	2687.0	3919.5	6850.3	4902.7	3354.7	1454.7
GQ113263.1	375228	420.6	489.3	5072.3	1784.6	341.5	120.4
FJ978721.1	408384	9342.0	10473.4	7809.2	9182.7	10590.1	9474.4
EU774026.1	308389	520.8	676.4	1089.8	1643.9	482.6	1134.7
EF089177.1	185041	2123.0	2163.4	4234.0	2789.7	2508.7	2482.8
FJ978724.1	381867	1493.6	1575.5	4555.1	2048.8	2057.8	1552.9
FJ978541.1	427042	310.7	458.6	2650.7	434.6	1424.9	113.5
FJ471639.2	514347	3963.1	3560.8	5869.0	5483.4	2150.2	2754.7
GQ088072.1	459200	2940.0	3675.3	5162.1	3934.3	4038.6	2976.2
FJ471673.1	520375	3041.2	2532.5	3935.3	6079.1	2239.7	3411.8
DQ440563.1	156573	3698.4	3017.5	5342.6	3959.0	3340.6	2929.8
GQ087757.1	395408	1611.1	3075.9	4199.1	2800.0	3508.0	2268.5
GQ014795.1	494871	5134.9	4146.1	3086.1	6711.9	8586.5	5739.3
FJ978525.1	468118	26.5	37.8	37.9	71.6	77.0	32.9
CP001685.1	529857	4330.9	5554.9	3948.0	6493.3	6388.5	5574.2
FJ577251.2	568972	3120.9	3172.3	5159.2	3481.5	2103.4	3198.9
AF206305.1	71541	3761.6	3995.4	6571.9	4720.7	2494.2	3199.6
AY134896.1	59574	441.5	794.4	2234.5	288.6	508.1	399.5
AM420035.1	241454	5515.7	6167.6	4306.4	7717.2	4191.6	4169.5
CP001685.1	529859	2491.1	4772.6	5845.0	3019.7	1920.9	1673.0
GQ129984.1	399980	9826.9	10385.9	10996.8	9376.1	14502.6	12609.6
AY207053.1	83573	4479.0	5477.4	4681.9	5352.8	1788.0	4898.8
AF432138.1	31235	9170.2	5947.3	5410.6	6886.1	6248.2	7064.8
GQ000682.1	469247	4475.3	5617.3	8242.7	6022.4	4412.3	6052.3
GQ000882.1	469447	1916.6	2357.3	4144.3	2657.3	3041.3	3038.3
AY349385.1	92131	497.4	1601.4	2869.5	600.5	338.6	926.2
FJ976353.1	578509	4179.4	3810.1	6667.4	3923.0	1363.1	2402.0
AM420193.1	258023	3070.0	3414.5	6761.6	3173.0	2461.7	4367.0
GQ016176.1	493491	1510.0	2024.1	1629.1	1347.0	364.4	1867.3
FJ577259.2	566658	347.6	518.7	955.9	272.4	1459.5	276.3
AY029803.1	70629	3130.3	3423.6	4826.6	3549.8	1969.2	3494.2
AF287814.1	38061	8010.2	8117.4	6678.4	6033.0	8271.1	8320.9
GQ032449.1	403062	3551.3	3780.9	4576.0	3243.1	2964.9	3520.9
AF385571.1	70038	10914.5	7698.0	9529.3	6513.7	9222.2	7620.2
GQ016227.1	493440	9440.3	7198.7	9103.7	6141.7	4921.0	7425.1
EU137409.1	267538	6824.6	8075.6	7592.3	6027.7	8441.8	8660.5
NZ_ACVB02000014.1	484462	3124.7	3140.7	4999.3	3511.0	1968.5	3206.1
AM420110.1	256867	2094.3	2275.3	3312.6	2427.4	2228.2	2916.3

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GQ111263.1 gg_id:375876 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ032233.1 gg_id:381314 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ422731.1 gg_id:555711 Leptotrichia sp. oral taxon 225 str. FEA2
GQ000663.1 gg_id:469228 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
GU086183.1 gg_id:593385 Leptotrichia shahii str. PW1036
NR_026243.1 gg_id:557791 Propionigenium maris str. 10succ1; DSM 9537
EU236316.1 gg_id:296908 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bD2
X54275.1 gg_id:11301 Propionigenium modestum
AJ877255.1 gg_id:112138 Ilyobacter psychrophilus str. FQ50
AJ307980.1 gg_id:52873 Ilyobacter insuetus str. DSM 6831 T
Y16799.1 gg_id:42042 Propionigenium maris str. DSL-1
FJ264772.1 gg_id:324952 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
FJ717186.1 gg_id:510621 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
FJ717188.1 gg_id:558150 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King
EU052253.1 gg_id:240997 degradation kinetics and current efficiency cells supplied anode microbial fuel cell f
AY770718.1 gg_id:110394 Fusobacteria sea urchin Paracentrotus lividus clone PlS49
CP001739.1 gg_id:518403 Sebaldella termitidis str. ATCC 33386
EF608534.1 gg_id:228694 predatory Poecilus chalcites their response lab rearing and antibiotic treatment dige
EF218611.1 gg_id:212738 Leptotrichia amnionii str. CCUG 51847
AY078425.1 gg_id:29566 Leptotrichia amnionii str. AMN-1
AJ344093.1 gg_id:58542 Sneathia sanguinegens str. CCUG 41628T
AB330759.1 gg_id:236558 Streptobacillus moniliformis str. KWG2
GQ072215.1 gg_id:447942 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193e1
GQ850557.1 gg_id:591820 surface water northern Bering Sea clone u114
FJ456795.1 gg_id:545014 microbiota two Antarctic notothenioid fish species intestinal flora clone A007_NCI
DQ206413.1 gg_id:139839 microbial mediates arsenate reduction soda lake water clone ML-AsS-15
EU044321.1 gg_id:256629 uences structure fosters richness subtropical Altamaha Ohopee River Valley inland d
EF019213.1 gg_id:213629 aspen rhizosphere clone Amb_16S_1909
DQ490008.1 gg_id:158907 Microbial Great Boiling Spring sediment hot spring; temperature 80 C clone GBS_L1_
EU134698.1 gg_id:255244 tallgrass prarie soil clone FFCH14117
FM873495.1 gg_id:363705 occupant source house floor dust clone FD04E09
EF018217.1 gg_id:216704 aspen rhizosphere clone Amb_16S_564
EF540422.1 gg_id:220442 oil-shale semi-coke solid waste clone MK51
GQ113134.1 gg_id:433730 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw675f0
EU283562.1 gg_id:278836 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1853
FJ444672.1 gg_id:591271 Cotton Rhizosphere cotton rhizosphere clone 2y-23
AB240260.1 gg_id:142399 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
DQ640655.1 gg_id:234041 full-scale EBPR sludge clone Skagenf3
GQ090575.1 gg_id:440096 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
AB234279.1 gg_id:146305 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm

GQ070510.1	399174	3354.5	3470.5	2598.1	3864.7	3808.2	3912.7
GQ111263.1	375876	435.2	1227.3	2509.8	913.5	811.7	558.1
GQ032233.1	381314	2824.2	3770.2	4159.0	4184.1	1907.5	2764.0
GQ422731.1	555711	4887.6	5263.5	9208.5	5052.9	2232.4	3386.6
GQ000663.1	469228	6064.0	7076.3	7689.9	6306.4	10440.7	10423.6
GU086183.1	593385	3540.3	3765.2	3892.4	3175.3	2951.4	3261.6
NR_026243.1	557791	2202.4	3021.4	7107.9	4096.9	4014.8	4130.1
EU236316.1	296908	2393.3	2019.0	9107.5	4196.4	4232.7	3923.0
X54275.1	11301	1988.0	1640.0	5380.8	1596.7	2025.2	1567.6
AJ877255.1	112138	2628.6	1879.7	2357.8	2733.0	463.1	1095.8
AJ307980.1	52873	2247.2	1779.7	5056.1	1489.8	2737.8	1885.1
Y16799.1	42042	2874.5	2531.4	5178.5	4741.1	4461.7	3705.5
FJ264772.1	324952	2141.3	1703.4	4800.7	3222.4	1076.8	576.9
FJ717186.1	510621	3652.9	4622.7	7519.0	5461.0	5939.6	5524.2
FJ717188.1	558150	3417.1	3411.6	10029.3	7306.6	4214.7	3962.4
EU052253.1	240997	1162.8	1343.7	3848.2	2622.4	2139.3	2522.4
AY770718.1	110394	4014.0	2945.1	8569.9	6197.6	4250.7	3898.7
CP001739.1	518403	575.8	578.6	1567.8	459.2	931.5	729.0
EF608534.1	228694	70.0	69.5	58.3	63.1	106.7	25.4
EF218611.1	212738	982.5	944.9	1229.1	1478.1	482.8	368.8
AY078425.1	29566	2206.8	1589.7	2697.8	2986.0	915.3	734.9
AJ344093.1	58542	24.3	31.7	21.6	41.3	52.3	17.0
AB330759.1	236558	54.4	101.2	2120.2	209.6	76.3	35.0
GQ072215.1	447942	6777.0	6710.8	5623.9	5424.6	5196.9	5718.1
GQ850557.1	591820	878.6	1102.7	4847.3	1264.7	791.2	1350.9
FJ456795.1	545014	7856.5	7914.4	9212.1	6280.8	9890.2	10625.1
DQ206413.1	139839	353.5	495.7	4269.2	641.0	195.3	275.5
EU044321.1	256629	14194.3	12911.0	8104.5	8901.6	5252.6	6100.3
EF019213.1	213629	1996.6	2433.4	873.8	2433.5	1905.4	3268.6
DQ490008.1	158907	12576.9	11237.4	5025.8	7574.2	5992.1	5488.3
EU134698.1	255244	13532.6	15833.6	10905.6	8631.6	8396.7	8362.4
FM873495.1	363705	881.6	1378.8	784.3	526.1	1211.4	2168.0
EF018217.1	216704	5312.8	7491.3	5112.2	5173.8	7693.8	6832.8
EF540422.1	220442	41.3	80.1	107.9	68.4	67.7	45.2
GQ113134.1	433730	10026.6	11106.8	8474.4	8620.4	10677.9	9796.1
EU283562.1	278836	949.8	2715.9	1979.2	795.5	719.9	1235.0
FJ444672.1	591271	23.9	35.9	35.2	57.5	75.6	31.3
AB240260.1	142399	1261.6	960.5	619.3	381.5	2193.7	1626.6
DQ640655.1	234041	393.2	907.9	1470.9	573.5	823.2	1066.7
GQ090575.1	440096	1339.1	1970.1	3876.3	929.9	2248.0	1666.3
AB234279.1	146305	77.6	194.2	224.2	97.0	96.8	137.2

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AF432648.1 gg_id:104785 lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Pro
EF157193.1 gg_id:243247 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EF018812.1 gg_id:214676 aspen rhizosphere clone Amb_16S_1283
FJ478758.1 gg_id:512313 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF203205.1 gg_id:207957 phylotypes sediments Lake Kastoria Greece sediment clone Kas174B
AF432635.1 gg_id:99232 lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Prod
DQ067025.1 gg_id:133200 Lake Washington sediment clone pLW-82
FJ536876.1 gg_id:587747 Linking performance microbiology biofilters treating dimethyl sulphide presence and
DQ520169.1 gg_id:160270 shal China sequences hypertrophic freshwater lake clone ML-5-110.2
EF018312.1 gg_id:207648 aspen rhizosphere clone Amb_16S_675
AF545649.1 gg_id:72899 shortgrass steppe soil (Stunner series fine loamy over sandy Ustic Calciargid) under Bc
AY218696.1 gg_id:81623 penguin droppings sediments clone KD8-87
AB426207.1 gg_id:264973 -situ identification study benzene-degrading s under methanogenic condition anaerc
EU979110.1 gg_id:336425 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
DQ906809.1 gg_id:239203 Oman subsurface soil clone 5B-5
EF516323.1 gg_id:225306 grassland soil clone FCPT668
EF019647.1 gg_id:215970 aspen rhizosphere clone Elev_16S_798
DQ067020.1 gg_id:129424 Lake Washington sediment clone pLW-79
FJ479207.1 gg_id:588566 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF019081.1 gg_id:204271 aspen rhizosphere clone Amb_16S_1670
FJ152750.1 gg_id:339480 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EU044086.1 gg_id:237353 fluences structure fosters richness subtropical Altamaha Ohopee River Valley inland
EU193066.1 gg_id:360943 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AM934748.1 gg_id:549433 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY921939.1 gg_id:114406 farm soil clone AKYG583
EU881263.1 gg_id:329628 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
AY922055.1 gg_id:114310 farm soil clone AKYG703
AY921712.1 gg_id:112987 farm soil clone AKYG963
AY921894.1 gg_id:114101 farm soil clone AKYG1555
EF612383.1 gg_id:237047 historic semiarid lead-zinc mine tailings site soil clone OS-C17
AY395378.1 gg_id:103904 pasture soil clone EB1059
AY192277.1 gg_id:79951 Rocky Mountain alpine soil clone W2a-1F
GU359099.1 gg_id:518957 rhizosphere soil peanut clone 2G11
DQ906907.1 gg_id:253096 Oman subsurface soil clone 12B-7
EU801865.1 gg_id:314599 It's all ranking aquatic Chesapeake Bay MD clone 3C003242
FJ746162.1 gg_id:512463 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EF020040.1 gg_id:211950 aspen rhizosphere clone Elev_16S_1437
FJ230809.1 gg_id:325203 Microclimate and limits photosynthesis cyanobacteria Northern Australia hypolithic s
AB257644.1 gg_id:259192 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo
AY921918.1 gg_id:113407 farm soil clone AKYG1585
EU283563.1 gg_id:279650 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1336

AF432648.1	104785	1816.3	1372.4	3035.8	2666.3	2729.3	3000.0
EF157193.1	243247	629.7	1568.8	1902.4	1054.8	138.0	768.2
EF018812.1	214676	51.2	107.3	68.2	73.3	75.2	67.6
FJ478758.1	512313	3016.5	4444.1	7479.1	5293.1	9453.2	7657.6
EF203205.1	207957	2769.2	3250.9	3423.7	3828.3	2761.5	3556.2
AF432635.1	99232	2429.8	2481.4	2563.0	2110.3	3115.2	2989.3
DQ067025.1	133200	431.3	1799.4	3655.3	374.9	1471.6	718.1
FJ536876.1	587747	38.2	53.0	111.9	70.8	60.8	83.7
DQ520169.1	160270	45.3	66.7	261.7	76.5	73.3	111.6
EF018312.1	207648	7204.3	7211.5	3931.2	6476.9	8058.9	9554.5
AF545649.1	72899	28.3	41.3	44.1	60.2	69.4	31.4
AY218696.1	81623	65.8	81.6	522.6	103.2	74.2	87.1
AB426207.1	264973	2343.2	4202.6	5983.9	1501.7	1791.5	2993.6
EU979110.1	336425	75.6	373.0	2492.0	141.7	671.5	468.1
DQ906809.1	239203	3283.7	3626.6	2376.2	4396.4	6152.9	4706.4
EF516323.1	225306	436.3	474.5	1393.2	783.5	402.5	744.0
EF019647.1	215970	6577.9	9107.1	8359.9	7813.8	10954.7	9918.8
DQ067020.1	129424	161.0	261.8	4120.1	569.7	82.6	63.6
FJ479207.1	588566	1864.4	1925.2	3993.6	1165.8	1617.8	2785.5
EF019081.1	204271	512.6	464.9	958.1	1501.8	1424.3	1655.0
FJ152750.1	339480	4635.3	3899.1	777.8	938.1	1530.7	1158.8
EU044086.1	237353	4774.1	5997.8	6228.3	4308.3	6797.2	8897.1
EU193066.1	360943	3080.7	3347.6	4192.2	4318.5	5027.4	4107.2
AM934748.1	549433	10012.8	10755.5	11426.5	9703.5	8958.2	9991.5
AY921939.1	114406	96.1	123.8	257.0	100.8	168.3	176.5
EU881263.1	329628	381.9	684.4	2269.3	278.7	347.0	329.8
AY922055.1	114310	2660.9	3995.6	4944.1	2628.0	2697.8	3884.9
AY921712.1	112987	3823.0	3437.2	5450.9	2878.2	5850.2	4422.4
AY921894.1	114101	24.3	39.9	68.9	51.6	77.7	49.3
EF612383.1	237047	8044.5	8180.2	9033.7	5896.6	8815.7	7943.7
AY395378.1	103904	9537.7	8920.8	7597.2	4725.3	9021.1	7635.3
AY192277.1	79951	4376.7	4237.8	4905.1	4709.0	2608.3	3568.1
GU359099.1	518957	5311.8	4562.3	5338.2	7498.9	3250.4	4330.0
DQ906907.1	253096	4669.5	4480.3	4499.6	3985.2	669.7	2115.8
EU801865.1	314599	91.2	221.7	705.4	62.3	301.7	90.5
FJ746162.1	512463	2221.4	2901.3	3795.8	1239.7	3014.7	1946.5
EF020040.1	211950	1005.5	649.8	2047.5	1057.9	383.6	598.2
FJ230809.1	325203	1322.6	2131.6	4180.7	1391.9	3220.1	2471.6
AB257644.1	259192	1440.3	2529.6	4830.2	1354.4	3358.8	3271.6
AY921918.1	113407	447.4	502.5	1002.6	376.7	154.7	474.1
EU283563.1	279650	6274.1	4827.0	7932.9	3452.1	1913.7	3330.2

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EU134840.1 gg_id:249299 tallgrass prarie soil clone FFCH11609
AY913252.1 gg_id:112876 forest soil clone DUNssu032 (+2C) (OTU#201)
AB257643.1 gg_id:265561 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo\
EU652636.1 gg_id:277713 Seasonal variation microbial Yel Sea sediment clone D8S-116
EU048610.1 gg_id:254529 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B3
AY922130.1 gg_id:114403 farm soil clone AKYH466
AY673312.1 gg_id:110882 Gemmatimonadetes Ellin7146
FJ479068.1 gg_id:560811 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY922123.1 gg_id:113603 farm soil clone AKYH1517
EF020045.1 gg_id:207989 aspen rhizosphere clone Elev_16S_1446
AY921994.1 gg_id:112986 farm soil clone AKYG1838
GQ396903.1 gg_id:557467 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
AY921912.1 gg_id:114146 farm soil clone AKYG1614
EU676443.1 gg_id:289924 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
EF018145.1 gg_id:208048 aspen rhizosphere clone Amb_16S_479
GU205280.1 gg_id:516178 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
FJ152768.1 gg_id:335807 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
AY289480.1 gg_id:90194 soil clone ABS-650
GQ113661.1 gg_id:384470 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(
EF516935.1 gg_id:219517 grassland soil clone FCPN548
EU193059.1 gg_id:360637 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
DQ532275.1 gg_id:168856 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
EF688378.1 gg_id:250371 soil clone F6-84
AY921776.1 gg_id:113308 farm soil clone AKYG961
EU234231.1 gg_id:242383 river and un techniques downstream Wang Yang River receiving penicillin G producti
EU881123.1 gg_id:308062 Karst region primary forest soil clone KPF200711-086
DQ067019.1 gg_id:128235 Lake Washington sediment clone pLW-78
EU134880.1 gg_id:249280 tallgrass prarie soil clone FFCH2651
DQ833499.1 gg_id:166488 detected analyses depth sediment Guanting Reservoir clone 69-18
AY921771.1 gg_id:113042 farm soil clone AKYG666
EF492900.1 gg_id:246196 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EU134828.1 gg_id:249948 tallgrass prarie soil clone FFCH6230
EU861901.1 gg_id:325238 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
FJ755752.1 gg_id:565312 vertical archaeal water and Lake Taihu sediment clone LT-SB-B6
AY218678.1 gg_id:82251 penguin droppings sediments clone KD8-105
AY921899.1 gg_id:114389 farm soil clone AKYG781
DQ906808.1 gg_id:243477 Oman subsurface soil clone 5B-4
GQ263232.1 gg_id:590444 Structure Simulated Level Waste Site simulated level waste site clone F3_42X
FJ444711.1 gg_id:511297 Cotton Rhizosphere cotton rhizosphere clone 3y-46
GQ263030.1 gg_id:576743 Structure Simulated Level Waste Site simulated level waste site clone F2_153X
EF174264.1 gg_id:197816 direct activated 4th maturation stage sludge clone F37-814

EU134840.1	249299	118.4	336.1	1129.1	341.3	798.9	1273.4
AY913252.1	112876	96.7	174.9	105.1	103.2	108.6	92.1
AB257643.1	265561	6331.5	6881.1	7200.2	7516.2	7429.6	7844.4
EU652636.1	277713	4384.0	6515.3	9184.7	5770.2	7158.1	7692.3
EU048610.1	254529	3774.6	3963.1	4255.3	5684.2	6554.0	6003.4
AY922130.1	114403	8784.7	10371.9	9787.7	8941.3	15766.0	14318.3
AY673312.1	110882	47.4	78.6	106.3	73.7	60.3	53.7
FJ479068.1	560811	7573.8	7999.0	5787.3	6265.0	8068.1	7135.4
AY922123.1	113603	882.1	1609.4	1710.8	2226.0	373.7	1300.7
EF020045.1	207989	141.5	562.5	978.8	125.1	197.1	494.6
AY921994.1	112986	116.5	172.6	429.2	118.3	112.5	199.7
GQ396903.1	557467	458.8	693.6	2230.0	225.5	1266.8	637.8
AY921912.1	114146	96.4	183.3	358.3	269.7	100.4	150.4
EU676443.1	289924	4602.5	4487.7	1689.6	457.2	1166.9	1314.0
EF018145.1	208048	1208.4	1615.7	743.0	1382.6	1435.8	1054.3
GU205280.1	516178	3357.6	4257.2	4735.6	3360.8	2865.4	2961.6
FJ152768.1	335807	446.6	483.7	2415.5	301.0	1994.7	1717.4
AY289480.1	90194	1697.1	1466.3	2254.3	1914.9	2166.4	2843.4
GQ113661.1	384470	6793.6	8074.8	9265.0	7959.4	12132.7	10930.5
EF516935.1	219517	41.1	73.9	125.8	63.3	78.4	66.1
EU193059.1	360637	2873.3	3388.7	3427.7	3932.5	3663.4	4137.2
DQ532275.1	168856	6306.4	6696.5	8200.0	6723.1	8504.4	9083.8
EF688378.1	250371	3217.2	4220.2	7133.5	4858.7	7172.5	6410.8
AY921776.1	113308	4774.2	4546.0	4909.5	6118.6	4765.9	5912.7
EU234231.1	242383	10571.3	10087.8	11945.9	6315.5	6086.1	6470.0
EU881123.1	308062	4618.7	5822.9	4820.7	3362.7	2627.5	3069.0
DQ067019.1	128235	32.9	43.7	52.7	50.8	77.6	38.6
EU134880.1	249280	4654.9	5258.3	6713.2	4557.6	4949.3	5319.0
DQ833499.1	166488	175.0	210.4	254.8	215.9	357.2	324.2
AY921771.1	113042	2135.1	2170.7	1953.5	2096.0	1763.2	1829.9
EF492900.1	246196	7080.2	6706.5	6124.8	3302.2	4742.3	5546.1
EU134828.1	249948	4063.1	5693.0	9472.8	5572.5	7851.1	7903.3
EU861901.1	325238	5094.9	6194.9	6178.7	6604.7	5933.6	6773.8
FJ755752.1	565312	32.8	106.6	133.1	89.5	73.4	86.9
AY218678.1	82251	2213.1	3892.9	2454.6	1434.8	1406.3	1911.9
AY921899.1	114389	600.9	610.8	952.0	783.6	100.4	317.9
DQ906808.1	243477	966.3	2848.3	2197.7	1905.2	3272.3	1975.6
GQ263232.1	590444	17548.3	18858.5	16923.5	14682.1	19846.4	16708.6
FJ444711.1	511297	8651.6	9616.2	11053.1	6980.4	8799.9	7597.7
GQ263030.1	576743	5844.7	7103.2	7820.4	6350.1	8299.3	7080.4
EF174264.1	197816	4638.5	3849.6	3550.0	2407.4	4030.3	4594.7

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EU037358.2 gg_id:277360 structure landfill sediments receiving long-term augmentations wastes chromium co
GQ263154.1 gg_id:579054 Structure Simulated Level Waste Site simulated level waste site clone F3_100X
GQ397033.1 gg_id:586289 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
GQ262951.1 gg_id:563031 Structure Simulated Level Waste Site simulated level waste site clone F1_87X2
EU979063.1 gg_id:344838 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
EF157266.1 gg_id:248780 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
FJ152642.1 gg_id:312327 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
GQ263158.1 gg_id:553767 Structure Simulated Level Waste Site simulated level waste site clone F3_106X
AM935432.1 gg_id:550147 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
GQ262827.1 gg_id:584041 Structure Simulated Level Waste Site simulated level waste site clone F1_15X2
GQ263089.1 gg_id:593457 Structure Simulated Level Waste Site simulated level waste site clone F2_39X
GQ263091.1 gg_id:561233 Structure Simulated Level Waste Site simulated level waste site clone F2_41X
GQ262961.1 gg_id:538070 Structure Simulated Level Waste Site simulated level waste site clone F1_92X
FJ425592.1 gg_id:363208 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl
DQ300602.1 gg_id:147735 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static
GQ346931.1 gg_id:591890 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ295242.1 gg_id:148154 Fragments Six Marine Planktonic Antarctic sea water clone Ant4D5
AJ567595.1 gg_id:89477 deep-sea sediment clone MBAE42
EU287180.1 gg_id:251953 Pacific arctic surface sediment clone P13-87
EU374078.1 gg_id:276624 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
AM997489.1 gg_id:548429 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
FJ205357.1 gg_id:512804 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
AM935228.1 gg_id:574770 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU652634.1 gg_id:277772 Seasonal variation microbial Yel Sea sediment clone A8S-129
FJ746291.1 gg_id:572935 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
AY592149.1 gg_id:106730 marine ANAMMOX sediment clone AY592149
EU287420.1 gg_id:244505 Pacific arctic surface sediment clone S26-120
AF186415.1 gg_id:11593 sponge symbiont clone PAUC43f
FJ024313.1 gg_id:359471 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I
AB294923.1 gg_id:226129 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
AF286033.1 gg_id:37339 saltmarsh clone LCP-68
EU979085.1 gg_id:308997 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
FJ444650.1 gg_id:560438 Cotton Rhizosphere cotton rhizosphere clone 2h-20
EF540395.1 gg_id:225607 oil-shale semi-coke solid waste clone 1_11MK
EU134894.1 gg_id:248455 tallgrass prarie soil clone FFCH6442
EU134893.1 gg_id:239710 tallgrass prarie soil clone FFCH12021
EU193063.1 gg_id:369973 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AY921663.1 gg_id:113478 farm soil clone AKYH1024
AY493976.1 gg_id:136870 Fingerprinting aggregates soil clone 5
DQ431899.1 gg_id:208663 microorganisms catalyzing nitrogen removal and organic matter metabolism perme
EU491861.1 gg_id:270789 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39

EU037358.2	277360	679.4	1022.3	792.5	351.2	979.3	732.9
GQ263154.1	579054	11131.4	12630.9	7670.9	9312.9	13499.7	10996.4
GQ397033.1	586289	4702.6	7400.5	5997.7	7130.2	6988.2	5391.7
GQ262951.1	563031	17013.9	17993.2	14304.9	11819.7	16279.9	12457.4
EU979063.1	344838	17196.0	17496.0	16568.0	13638.6	20578.2	16287.1
EF157266.1	248780	2426.6	4192.4	2607.2	719.2	2250.2	1637.1
FJ152642.1	312327	5224.3	6884.0	8008.2	3839.0	3556.5	3355.6
GQ263158.1	553767	13330.6	14107.6	11564.3	12194.7	16207.6	12073.0
AM935432.1	550147	7614.8	15725.1	8765.7	6327.6	7317.1	6974.4
GQ262827.1	584041	8185.2	9962.1	8532.4	4465.1	8641.4	6295.8
GQ263089.1	593457	6667.8	9228.9	3743.4	5701.7	7772.4	6144.1
GQ263091.1	561233	14755.3	16423.4	12739.5	9547.4	15105.6	10594.6
GQ262961.1	538070	7764.7	8066.2	6170.5	6604.9	7369.4	5692.4
FJ425592.1	363208	12448.7	13714.1	15092.8	9553.1	12176.4	10532.1
DQ300602.1	147735	6856.6	7798.7	4231.9	3986.2	2861.6	3867.1
GQ346931.1	591890	5056.8	6138.0	6690.0	5789.9	8269.1	7192.6
DQ295242.1	148154	6086.7	7521.1	4618.8	5628.1	3554.0	3633.2
AJ567595.1	89477	5405.7	6261.1	8218.5	5442.1	4062.4	6947.4
EU287180.1	251953	4642.0	5179.3	3824.1	4646.7	3333.0	4108.5
EU374078.1	276624	7515.1	8100.3	7141.9	7343.8	8809.7	8308.0
AM997489.1	548429	1899.9	2048.5	2261.4	2587.2	3088.4	2741.9
FJ205357.1	512804	6670.4	4711.2	5897.4	6930.2	7949.3	6788.9
AM935228.1	574770	3627.3	5714.2	7231.7	5412.7	7843.5	7378.7
EU652634.1	277772	11741.5	14557.6	12068.1	7896.8	12382.6	8640.6
FJ746291.1	572935	4757.6	5985.9	6390.8	4339.3	9682.4	6328.6
AY592149.1	106730	3460.0	3709.0	4283.1	4895.9	633.1	1084.0
EU287420.1	244505	8963.3	9226.8	9150.4	6345.6	8629.0	8590.4
AF186415.1	11593	250.7	498.4	584.7	146.6	564.9	260.2
FJ024313.1	359471	6650.4	7460.2	8913.8	7415.5	4504.5	5186.4
AB294923.1	226129	192.6	472.0	582.2	453.7	410.3	269.8
AF286033.1	37339	2746.5	4863.8	2486.7	3236.1	7754.0	4640.7
EU979085.1	308997	8537.0	8707.7	5877.1	6847.5	9343.1	8559.0
FJ444650.1	560438	7960.3	8330.9	12336.6	7936.0	6457.2	7316.2
EF540395.1	225607	73.1	82.4	121.9	88.9	159.8	67.6
EU134894.1	248455	3089.4	2840.5	5183.3	4560.4	1605.9	2032.3
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EU193063.1	369973	5784.9	4974.3	3862.0	7083.9	7976.1	7839.8
AY921663.1	113478	3550.8	3651.1	3168.1	3063.0	2497.6	1209.2
AY493976.1	136870	4084.9	6054.3	4865.1	7391.9	9018.4	6256.2
DQ431899.1	208663	1365.4	2748.1	3470.4	2099.6	623.1	1481.2
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EU134886.1 gg_id:254415 tallgrass prarie soil clone FFCH1365
EU134854.1 gg_id:240326 tallgrass prarie soil clone FFCH14573
AY921936.1 gg_id:113023 farm soil clone AKYG548
AJ347028.1 gg_id:60181 sponge symbiont clone TK19
GU118643.1 gg_id:557462 Threatened Corals Provide Microbial Habitats clone Mfav_E13
GU118605.1 gg_id:565653 Threatened Corals Provide Microbial Habitats clone Mfav_L08
GU118693.1 gg_id:544625 Threatened Corals Provide Microbial Habitats clone Mfav_D05
GU118648.1 gg_id:586196 Threatened Corals Provide Microbial Habitats clone Mfav_H20
GQ095375.1 gg_id:443417 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4
EF516463.1 gg_id:218620 grassland soil clone FCPU694
EF516718.1 gg_id:217803 grassland soil clone FCPU461
EU289488.1 gg_id:254895 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
AY921785.1 gg_id:113624 farm soil clone AKYH1201
FJ152619.1 gg_id:356469 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
FJ152871.1 gg_id:322098 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
FJ152673.1 gg_id:342606 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
GU083675.1 gg_id:585141 Microorganism Xiarinur soda lake sediment clone x271
EU374077.1 gg_id:267176 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
GQ143755.1 gg_id:373545 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes
AF317745.1 gg_id:136926 Nullarbor cave clone wb1_A18
AM943577.1 gg_id:269262 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hyper
AY592110.1 gg_id:99079 marine ANAMMOX sediment clone AY592110
GQ262856.1 gg_id:554991 Structure Simulated Level Waste Site simulated level waste site clone F1_32X2
DQ906881.1 gg_id:241659 Oman subsurface soil clone 11B-8
EU682493.1 gg_id:530814 Four Primer Sets Detecting Anammox s estuary sediment Mai Po Nature Reserve clo
EU652631.1 gg_id:277923 Seasonal variation microbial Yel Sea sediment clone C8S-21
EU245438.1 gg_id:237565 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-F03
EU369136.1 gg_id:304950 libraries oyster shell clone MBIOS-20
EU219931.1 gg_id:247892 study prokaryotic approach landfill soil 5.5 ft. depth clone C6B
EU369154.1 gg_id:317743 libraries oyster shell clone MBHOS-05
EF125397.1 gg_id:182109 soil naked tidal flat sediment near mangrove clone MSB-1C5
AB491850.1 gg_id:542631 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac
EU134887.1 gg_id:252091 tallgrass prarie soil clone FFCH15678
EU134863.1 gg_id:255390 tallgrass prarie soil clone FFCH17465
GU056071.1 gg_id:579069 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Being
FJ152883.1 gg_id:351400 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CE
AB250557.1 gg_id:160916 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #2-2
EU283598.1 gg_id:279155 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A406
FJ205371.1 gg_id:510313 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
EU700157.1 gg_id:288295 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU15

FJ152644.1	322198	2760.7	4692.4	7174.8	4365.5	9678.5	7698.0
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EU134854.1	240326	5560.0	5947.5	5757.8	4826.1	5758.3	4398.9
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EU652631.1	277923	2842.7	4138.4	3292.6	3094.1	1538.9	2214.5
EU245438.1	237565	2289.8	2738.7	4150.0	2710.1	2181.9	2747.8
EU369136.1	304950	6986.1	8296.7	4507.4	5263.5	5803.4	6057.7
EU219931.1	247892	15998.9	16706.7	18649.1	18096.5	20766.5	17358.0
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AB491850.1	542631	5988.1	6155.8	5657.6	4168.9	4983.2	5690.1
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AB250557.1	160916	2913.5	2706.4	3369.9	2927.9	6185.8	3676.3
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AF507713.1 gg_id:65673 forest soil clone S166
EU491859.1 gg_id:264825 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GQ347441.1 gg_id:581615 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ234160.2 gg_id:144617 determined library mangrove clone DS076
DQ329577.1 gg_id:159133 Guerrero Negro hypersaline microbial mat clone 05D2Z07
DQ397339.1 gg_id:159241 Guerrero Negro hypersaline microbial mat clone 02D2Z08
AB192119.1 gg_id:142691 termite gut homogenate clone M2PT2-27
FJ791860.1 gg_id:571248 Unexpectedly archaeal species shift between rare and dominant over thousand year
AY197400.1 gg_id:86409 Guaymas Basin hydrothermal vent sediments clone B02R018
FJ959985.1 gg_id:579816 bottlenose dolphin upper respiratory tract blowhole clone D940_045
AB232534.1 gg_id:154098 Prokaryotic gills deep-sea hydrothermal vent shrimp gill Alvinocaris longirostris clone
EU052256.1 gg_id:256207 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe
AF367482.1 gg_id:17620 deep-sea hydrothermal vent clone VC1.2-cl02
GQ349327.1 gg_id:562277 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU265935.1 gg_id:537633 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni
EU101198.1 gg_id:237363 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa
GU061180.1 gg_id:585963 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se
EU245804.1 gg_id:257757 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-F03
DQ330597.1 gg_id:159245 Guerrero Negro hypersaline microbial mat clone 09D2Z91
FJ712458.1 gg_id:523166 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EU385807.1 gg_id:258358 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU245526.1 gg_id:256848 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-F08
FJ810558.1 gg_id:405181 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
FJ416124.1 gg_id:357229 sediments sediment station NEC5 Northern Bering Sea clone 115O3
EU542519.1 gg_id:273867 Effects chemical structure concentration on pathways microbial during dechlorinatio
DQ811954.1 gg_id:162191 mangrove soil clone MSB-5A5
EU487916.1 gg_id:564815 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EF203188.1 gg_id:204759 phylotypes sediments Lake Kastoria Greece sediment clone Kas139B
EU048677.1 gg_id:254199 and archaeal surface marine sediment Slope South China Sea clone MD2896-B18
EU487964.1 gg_id:573020 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
EU245855.1 gg_id:256405 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M7-C07
DQ329580.1 gg_id:159470 Guerrero Negro hypersaline microbial mat clone 062DZ43
DQ154831.1 gg_id:138844 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl
GQ246356.1 gg_id:548387 Temporal and spatial China North Yel Sea sediments clone Cm1-19
FJ264777.1 gg_id:340190 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
FM165273.1 gg_id:566144 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone
FJ264598.1 gg_id:317416 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime
EU246145.1 gg_id:257436 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-C07
EU245601.1 gg_id:257385 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-E09
DQ329606.1 gg_id:159400 Guerrero Negro hypersaline microbial mat clone 04D2Z65
DQ329608.1 gg_id:159092 Guerrero Negro hypersaline microbial mat clone 05D2Z01

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DQ234160.2	144617	34.9	54.5	132.7	64.0	54.8	26.6
DQ329577.1	159133	93.6	102.6	363.6	108.5	69.9	25.2
DQ397339.1	159241	1353.9	1795.1	906.6	2670.6	517.6	1268.8
AB192119.1	142691	34.5	63.6	87.9	80.7	62.0	28.5
FJ791860.1	571248	104.6	94.6	204.0	90.0	506.1	36.6
AY197400.1	86409	18.7	57.1	90.4	68.1	55.2	18.5
FJ959985.1	579816	1991.2	2286.9	3955.7	1930.8	913.8	1206.0
AB232534.1	154098	31.5	22.2	348.9	47.0	71.0	50.9
EU052256.1	256207	5966.8	5785.6	7389.1	3778.5	4207.9	3527.6
AF367482.1	17620	955.1	1122.1	2393.2	1162.3	1194.3	508.7
GQ349327.1	562277	67.2	133.0	1328.1	142.6	94.3	51.0
EU265935.1	537633	4528.4	3404.1	1617.4	1886.1	2134.0	1290.6
EU101198.1	237363	1679.1	2589.8	3360.3	2132.2	659.0	816.0
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EU245804.1	257757	5617.4	5349.0	3592.1	2137.8	3341.0	2330.7
DQ330597.1	159245	2566.6	3496.4	3133.3	3573.3	3144.9	2385.8
FJ712458.1	523166	4801.6	5019.2	8983.1	4343.8	4273.3	4712.9
EU385807.1	258358	2545.0	3857.7	8529.6	2636.5	4560.1	5361.0
EU245526.1	256848	60.8	82.1	168.4	80.7	85.9	121.5
FJ810558.1	405181	2148.1	2648.7	4361.3	2261.1	5100.9	4387.6
FJ416124.1	357229	222.7	404.8	2033.9	657.9	1554.9	842.3
EU542519.1	273867	4858.0	4912.2	2522.8	1876.5	1121.8	1676.4
DQ811954.1	162191	20473.9	21093.8	20101.3	20408.6	19284.3	16211.3
EU487916.1	564815	13509.8	12573.3	10732.9	12291.1	10976.9	11677.7
EF203188.1	204759	209.4	337.7	546.2	856.3	123.9	87.5
EU048677.1	254199	4302.3	3954.0	5624.2	6990.2	1645.3	4010.4
EU487964.1	573020	7974.4	9933.8	8119.2	8374.4	7724.1	6150.8
EU245855.1	256405	42.9	81.9	116.1	71.9	94.8	84.7
DQ329580.1	159470	55.5	80.5	41.9	110.4	252.1	118.6
DQ154831.1	138844	30.0	43.9	28.5	78.2	67.8	28.8
GQ246356.1	548387	1697.3	3623.2	3494.0	1525.0	4014.6	5079.8
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FM165273.1	566144	8224.2	9413.9	11814.6	5763.7	6219.1	7160.4
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EU246145.1	257436	20.9	44.8	41.6	57.7	55.7	12.7
EU245601.1	257385	498.7	233.2	61.7	223.3	184.1	104.6
DQ329606.1	159400	531.6	715.0	1056.2	1814.8	855.9	1409.7
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EU134901.1 gg_id:255924 tallgrass prarie soil clone FFCH3687
AB300086.1 gg_id:225464 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A
EU134900.1 gg_id:248928 tallgrass prarie soil clone FFCH18260
FJ901586.1 gg_id:567970 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita
AB240362.1 gg_id:143463 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
EU134904.1 gg_id:249081 tallgrass prarie soil clone FFCH18804
AY050577.1 gg_id:106690 MCB-contaminated groundwater-treating reactor clone GOUTA4
AJ543759.1 gg_id:95866 anoxic sediment Lake Cadagno clone 49
FJ746261.1 gg_id:567096 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
AB237732.1 gg_id:139838 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW
EU386097.1 gg_id:261462 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EF688196.1 gg_id:351571 Detection microbial sludge anaerobic wastewater treatment system clone 4E1_cons
FJ645694.1 gg_id:550022 Microbial dynamics during -temperature biotreatment PCP-contaminated wastestrea
EU622292.1 gg_id:298479 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv
DQ415793.1 gg_id:158359 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
EF602489.1 gg_id:233633 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone
EF687508.1 gg_id:283688 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
GQ249498.1 gg_id:562766 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor
DQ329567.1 gg_id:159197 Guerrero Negro hypersaline microbial mat clone 08D2Z50
DQ329541.1 gg_id:159505 Guerrero Negro hypersaline microbial mat clone 05D2Z11
EU246164.1 gg_id:237663 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E12
DQ329542.1 gg_id:159334 Guerrero Negro hypersaline microbial mat clone 05D2Z93
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FJ484771.1 gg_id:566342 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
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DQ811937.1 gg_id:162879 mangrove soil clone MSB-5B5
EU617724.1 gg_id:346244 Seasonal variation microbial Yel Sea sediment clone C13S-9
AM086123.1 gg_id:149924 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
FJ712479.1 gg_id:532343 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
EU386122.1 gg_id:261859 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AF286032.1 gg_id:26077 saltmarsh clone LCP-89
FJ716412.1 gg_id:562251 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water
EU048684.1 gg_id:246605 and archaeal surface marine sediment Slope South China Sea clone MD2896-B27
FJ716279.1 gg_id:551134 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept
GU363012.1 gg_id:532990 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
AY114321.1 gg_id:63785 anoxic marine sediment clone LD1-PA32
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EU622292.1	298479	90.8	190.9	90.0	84.2	44.6	41.2
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EU050936.1 gg_id:237639 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_46
EU617881.1 gg_id:308950 Seasonal variation microbial Yel Sea sediment clone C13S-64
EU373977.1 gg_id:275456 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
DQ903989.1 gg_id:243625 Cytophaga sp. PRPR22
AB189358.1 gg_id:113979 cold seep sediment clone JT75-104
AJ431234.1 gg_id:79161 Cytophaga sp. str. Dex80-43
CU918294.1 gg_id:575335 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU236367.1 gg_id:299835 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91E2
GU302469.1 gg_id:552105 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
FJ172855.1 gg_id:349140 Qinghai Yak Ruminal and Fungi China rumen clone RB-3G5
DQ067008.1 gg_id:131533 Lake Washington sediment clone pLW-89
FJ172836.1 gg_id:306087 Qinghai Yak Ruminal and Fungi China rumen clone RB-4D9
AB062771.1 gg_id:32071 termite gut homogenate clone BCf1-10
EU885059.1 gg_id:323370 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2F3
EU491122.1 gg_id:266959 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
U81755.2 gg_id:1542 anaerobic digestor clone vadinHB65
AB009200.1 gg_id:14576 rumen clone RFN44
EU491130.1 gg_id:265874 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU850520.1 gg_id:342488 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF297
EF092196.1 gg_id:274447 Persistent Axinella corrugata Lentisphaerae clone Ax29_B12
NZ_ABDE01000031.1 gg_id:235858 Victivallis vadensis str. ATCC BAA-548
FJ833297.1 gg_id:551530 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q401_04D01
EU462436.1 gg_id:290815 Sumatran orangutan feces clone orang1_aai54e09
DQ353908.1 gg_id:148459 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z20
EU465080.1 gg_id:288148 African elephant feces clone AFYEL_aaj67g06
CU920558.1 gg_id:551462 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
CU924053.1 gg_id:571561 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU459524.1 gg_id:287575 capybara feces clone CAP_aah99b07
AJ536842.1 gg_id:97002 chemocline clone 362
FJ755755.1 gg_id:563388 vertical archaeal water and Lake Taihu sediment clone LT-SB-B11
EU050937.1 gg_id:255593 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_35
GU196208.1 gg_id:584283 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
EF602493.1 gg_id:233246 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone
AJ431235.1 gg_id:79502 Cytophaga sp. str. Dex80-64
AY553939.1 gg_id:113934 Baltimore Harbor sediment clone FA6
EU048683.1 gg_id:251056 and archaeal surface marine sediment Slope South China Sea clone MD2896-B26
GQ246316.1 gg_id:511355 Temporal and spatial China North Yel Sea sediments clone Sd1-35
GU180194.1 gg_id:547075 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
EU385673.1 gg_id:265544 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
DQ521806.1 gg_id:160216 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic

NR_027571.1	568139	288.9	282.6	1694.7	1591.3	372.9	362.4
EU050936.1	237639	1076.9	886.9	1349.8	1082.6	842.2	1697.6
EU617881.1	308950	1052.7	810.8	772.6	1982.0	162.6	190.5
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DQ903989.1	243625	7020.0	10109.7	8332.9	7108.4	4434.6	4264.4
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FJ172836.1	306087	4973.8	5731.9	4858.6	7859.8	10718.6	8196.1
AB062771.1	32071	261.3	87.3	136.1	146.6	149.1	100.5
EU885059.1	323370	6632.0	7356.5	8365.8	9458.6	13174.4	11179.3
EU491122.1	266959	2245.2	2245.3	2180.2	3377.7	2223.8	2624.9
U81755.2	1542	118.3	452.3	475.0	192.3	174.0	153.4
AB009200.1	14576	71.1	104.6	368.4	114.5	154.9	93.8
EU491130.1	265874	5655.0	7505.2	9146.6	6395.4	7547.2	7611.9
EU850520.1	342488	21.6	52.9	49.5	70.3	73.3	27.4
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EU459524.1	287575	5722.6	9507.4	11902.1	7662.6	10265.6	9206.7
AJ536842.1	97002	86.5	109.3	201.1	110.5	85.7	64.6
FJ755755.1	563388	1753.3	2005.3	3154.5	645.8	324.8	979.1
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EU385673.1	265544	12714.3	13603.4	11017.7	10191.5	11837.6	10560.2
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EU542528.1 gg_id:269354 Effects chemical structure concentration on pathways microbial during dechlorinatio
EU181498.1 gg_id:251185 Prokaryotic enhanced organic matter remineralization continental margin marine se
DQ521805.1 gg_id:160462 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic
EF106489.1 gg_id:202958 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2
AJ133617.1 gg_id:1688 brine sediment clone KTK 32
EU246019.1 gg_id:246314 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-F02
FN393496.1 gg_id:552766 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1H1
GU390826.1 gg_id:526942 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre
AJ536840.1 gg_id:95720 chemocline clone 331
AB539947.1 gg_id:569847 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t
CU921965.1 gg_id:554874 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AY570581.1 gg_id:108459 -temperature biodegraded Canadian oil reservoir clone PL-11B10
GU476613.1 gg_id:515032 microbial biogas fermentation enrichment clone BBMC-13
FJ462041.1 gg_id:580192 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
DQ354746.1 gg_id:152989 subsurface water clone MS149BH1062003_13
GU196193.1 gg_id:591769 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
EU844484.1 gg_id:335853 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ748807.1 gg_id:578422 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estua
AJ519650.1 gg_id:75874 uranium mill tailings soil sample clone Sh765B-TzT-35
AB426199.1 gg_id:274653 -situ identification study benzene-degrading s under methanogenic condition anaerc
AB486305.1 gg_id:538794 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EF492972.1 gg_id:257902 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AF351214.1 gg_id:71271 coal tar-contaminated groundwater clone 12-24
FJ621558.1 gg_id:561816 Enrichment and detection denitrifying methanotrophic NC10 phylum eutrophic fresh
DQ837250.1 gg_id:239257 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_43
FJ907182.1 gg_id:573993 Enrichment anoxic methane utilizing denitrification (AnMUD) microorganisms mixed i
DQ369742.1 gg_id:156874 microbial consortium couples oxidation denitrification anaerobic methane oxidation
AB179508.1 gg_id:105296 sedimentary rock clone MIZ17
DQ906849.1 gg_id:250973 Oman subsurface soil clone 10A-11
DQ906843.1 gg_id:244437 Oman subsurface soil clone 7C-23
FJ205220.1 gg_id:556077 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
AM991185.1 gg_id:278069 Microbial groundwater and their potential use biomonitoring karst spring water clo
EU491416.1 gg_id:260370 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EU491462.1 gg_id:269959 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
AY177763.1 gg_id:79044 vadose clone 5G01
AF317743.1 gg_id:136988 Nullarbor cave clone wb1_A12
EU373968.1 gg_id:273635 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl
EU335184.1 gg_id:242324 Changes microbial metabolic and along hydrogeochemically variable profile saturate
AF351231.1 gg_id:42281 upgradient coal tar waste-contaminated groundwater clone 4-29 sp.
GU208486.1 gg_id:589700 Study on Sediment Dongping Lake sediment clone Shs2-20
DQ138963.1 gg_id:138815 rice straw paddy soil clone JG118

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EU181498.1	251185	7926.4	8931.8	5685.1	7510.1	12779.0	11220.2
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EF106489.1	202958	247.0	305.6	235.4	205.5	105.8	62.2
AJ133617.1	1688	33.5	68.1	44.0	67.9	63.6	36.3
EU246019.1	246314	33.1	55.3	28.2	61.6	76.9	25.8
FN393496.1	552766	1272.8	1478.0	2431.1	2471.0	4912.9	2470.6
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AJ536840.1	95720	3989.7	3600.7	587.6	5281.1	6129.7	5071.6
AB539947.1	569847	7269.4	6945.8	11475.8	7787.2	11465.4	10171.4
CU921965.1	554874	11872.9	12806.8	8169.4	7707.1	6424.4	6654.1
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GU476613.1	515032	6193.7	7252.2	10938.2	5394.0	11929.2	11087.6
FJ462041.1	580192	9338.0	9724.2	5149.5	7774.1	4672.1	5620.1
DQ354746.1	152989	7237.8	8380.7	7090.1	5892.4	4770.5	5609.3
GU196193.1	591769	1421.2	2228.4	4084.7	1954.4	723.7	1578.1
EU844484.1	335853	4691.5	6147.6	9366.9	7407.2	7751.1	8031.9
FJ748807.1	578422	1968.0	3285.2	3978.4	1617.3	2327.9	4346.5
AJ519650.1	75874	238.0	481.7	970.1	345.1	351.5	497.0
AB426199.1	274653	1677.9	2094.6	6548.7	3275.4	1917.0	3354.7
AB486305.1	538794	11803.7	13460.9	12886.6	6765.6	6778.5	7022.4
EF492972.1	257902	2705.2	1561.5	5388.0	2469.4	3531.6	2452.7
AF351214.1	71271	249.1	690.5	3424.2	209.0	432.1	685.3
FJ621558.1	561816	9952.3	7647.6	6158.3	7466.1	5433.9	4027.9
DQ837250.1	239257	11088.8	11703.2	14969.0	7762.7	9491.1	9923.8
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AB179508.1	105296	5744.8	7501.1	6040.2	3520.0	9187.7	9517.9
DQ906849.1	250973	6887.3	8072.6	5379.1	3733.8	5926.3	5480.4
DQ906843.1	244437	20016.6	21288.3	13079.3	8767.7	9610.8	8624.9
FJ205220.1	556077	14984.0	18694.7	13633.2	10539.1	12052.7	13009.0
AM991185.1	278069	1054.2	2402.7	4321.8	2044.2	1056.6	1767.2
EU491416.1	260370	1868.5	2372.9	2338.0	1182.0	1701.9	1765.2
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AY177763.1	79044	9830.6	10563.8	11114.8	8788.5	10335.3	9648.8
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DQ138964.1 gg_id:138554 rice straw paddy soil clone JG325
AF356831.1 gg_id:50647 Leptospirillum ferriphilum str. Warwick
EU733647.1 gg_id:319964 Leptospirillum ferriphilum str. YTW315
GU168010.1 gg_id:584037 Leptospirillum ferriphilum
DQ451017.1 gg_id:156803 Leptospirillum ferriphilum str. GX
DQ464149.1 gg_id:157346 acid mine drainage clone D1-90
AF544226.1 gg_id:58150 acid mine drainage clone ASL9
AB254780.1 gg_id:159816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
EU372645.1 gg_id:564896 Evaluation Leptospirillum spp. Rio Tinto basin model interest biohydrometallurgy wa
DQ328622.1 gg_id:149323 microorganisms populating site extreme acid mine drainage sediment clone H50
FJ228338.1 gg_id:347059 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur
DQ464151.1 gg_id:158060 acid mine drainage clone D1-95
EF409845.1 gg_id:211316 acid mine drainage clone FKBZ-53-06
AF543509.1 gg_id:56204 acid mine drainage clone BA33
FJ228276.1 gg_id:344157 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur
FJ228310.1 gg_id:311765 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur
AF356835.1 gg_id:24590 Leptospirillum ferrooxidans str. Chil-Lf2
AF356833.1 gg_id:41859 Leptospirillum ferrooxidans str. BCT2
X86776.1 gg_id:1509 Leptospirillum ferrooxidans str. L15 DSM 2705
GU168016.1 gg_id:565828 Leptospirillum ferrooxidans
AF356839.1 gg_id:39980 Leptospirillum ferrooxidans str. Sy
AY952274.1 gg_id:153665 Leptospirillum ferrooxidans
EF025338.1 gg_id:191142 Leptospirillum ferriphilum str. ZTS
DQ659194.1 gg_id:221094 acid mine drainage clone DBS-Clone19
GU168013.1 gg_id:571763 Leptospirillum ferriphilum
DQ223208.1 gg_id:143919 subsurface water clone EV221H2111601SAH4
EF018100.1 gg_id:203943 aspen rhizosphere clone Amb_16S_432
AF155154.1 gg_id:1493 Nitrospira cf. moscoviensis str. SBR2016
AJ617918.1 gg_id:110103 oxic-anoxic interphase flooded paddy soil clone D023010
AY555798.1 gg_id:106808 Bor Khlueng hot spring clone PK287
EU287071.1 gg_id:237590 Pacific arctic surface sediment clone B78-107
AM997652.1 gg_id:542056 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU803576.1 gg_id:332256 It's all ranking aquatic Lake Gatun clone 5C231165
GQ249372.1 gg_id:583840 Research on biodiversity sludge bioflim Biological Aeration Filter clone B14
DQ814725.1 gg_id:173004 zebrafish digestive tract clone aaa35h01
AJ617920.1 gg_id:109789 oxic-anoxic interphase flooded paddy soil clone D023011
AY921743.1 gg_id:114282 farm soil clone AKYG586
EU491464.1 gg_id:276859 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
DQ128338.2 gg_id:183441 conventional tillage soil clone HSB CT52_D06

AY050579.1	28363	1624.3	2280.7	3847.1	2011.2	3221.8	2686.7
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DQ138964.1	138554	1890.1	2845.6	2478.9	2717.5	1033.7	1757.6
AF356831.1	50647	124.7	284.8	796.8	204.2	288.0	972.3
EU733647.1	319964	1859.7	2024.9	2394.1	1928.4	1012.3	2187.5
GU168010.1	584037	1336.5	1259.7	1777.0	1763.1	938.4	2296.6
DQ451017.1	156803	15350.4	15090.2	13397.6	11164.7	15617.6	16088.6
DQ464149.1	157346	1131.5	977.1	2306.1	1154.4	1248.6	1506.7
AF544226.1	58150	5055.6	4775.6	3867.3	3659.3	4042.8	4593.6
AB254780.1	159816	645.1	915.8	2102.1	1012.1	1031.5	454.4
EU372645.1	564896	6677.9	5707.4	6431.5	5349.5	4817.3	5638.5
DQ328622.1	149323	21.0	31.8	51.0	61.2	66.5	48.0
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DQ464151.1	158060	2200.6	3398.9	10247.7	3612.9	1405.5	2578.9
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FJ228310.1	311765	12505.9	11890.0	11100.1	8658.6	11179.1	10857.4
AF356835.1	24590	3137.1	2235.0	7577.9	4428.7	1945.9	2542.4
AF356833.1	41859	9639.2	8451.2	3302.3	10387.2	12272.8	12904.8
X86776.1	1509	5413.3	3994.2	1293.7	4814.8	6259.8	7008.7
GU168016.1	565828	1054.6	1236.4	1744.3	951.0	1152.5	1616.6
AF356839.1	39980	81.5	229.4	331.2	134.3	212.4	226.8
AY952274.1	153665	2927.6	3335.4	2338.6	2772.6	3023.7	3978.5
EF025338.1	191142	4309.5	4139.8	4353.4	6221.8	485.5	1178.7
DQ659194.1	221094	565.4	399.5	1175.4	744.0	357.7	451.4
GU168013.1	571763	49.0	90.4	120.4	75.9	82.1	98.9
DQ223208.1	143919	274.6	425.9	644.1	930.5	96.8	203.0
EF018100.1	203943	382.0	937.9	1617.3	324.9	240.3	435.8
AF155154.1	1493	271.4	646.8	828.1	206.4	2419.5	1946.7
AJ617918.1	110103	58.2	138.4	97.9	108.3	276.0	215.4
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AM997652.1	542056	19.6	34.6	21.8	47.3	50.0	12.7
EU803576.1	332256	2673.9	2707.9	4579.4	3145.0	3423.4	5775.8
GQ249372.1	583840	6469.6	6606.2	6937.6	8037.9	8828.9	9256.7
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AY921743.1	114282	12000.2	10682.5	12238.4	10502.8	15814.1	18230.3
EU491464.1	276859	11860.6	10870.2	12315.6	10114.0	9134.1	12049.3
DQ128338.2	183441	20.8	39.5	37.3	58.7	53.2	49.8

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FJ535097.1 gg_id:511523 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM17
EU035954.2 gg_id:316621 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor
GU118642.1 gg_id:549595 Threatened Corals Provide Microbial Habitats clone Mfav_D14
EF492939.1 gg_id:257467 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
GQ848453.1 gg_id:588843 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal
GQ500804.1 gg_id:586905 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
EF594048.1 gg_id:234702 mixed granule anammox reactor clone KIST-JJY015
AY921494.2 gg_id:153641 Changes soils rice field soil clone AP19
AY493911.1 gg_id:136740 Fingerprinting aggregates soil clone 1183
NR_029287.1 gg_id:554350 Nitrospira moscoviensis str. NSP M-1; DSM 10035
DQ451477.1 gg_id:156598 forest soil clone FAC38
EU287156.1 gg_id:246040 Pacific arctic surface sediment clone P13-63
AJ863251.1 gg_id:120977 poplar tree microcosm bulk soil flooded clone 21BSF62
AJ617917.1 gg_id:111105 oxic-anoxic interphase flooded paddy soil clone D02307
GQ214107.1 gg_id:536771 China loess clone P859
AB176700.1 gg_id:102911 subsurface geothermal water clone HAuD-LB/2-23
CU466688.1 gg_id:309217 Evry wastewater treatment plant anoxic basin clone
AY921873.1 gg_id:113562 farm soil clone AKYG388
AJ617919.1 gg_id:110431 oxic-anoxic interphase flooded paddy soil clone D14423
AY328715.1 gg_id:88698 drinking water system simulator clone DSSD16
EF612393.1 gg_id:246188 historic semiarid lead-zinc mine tailings site soil clone OS-C76
FJ529312.1 gg_id:570363 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze
EF092255.1 gg_id:260626 Persistent Axinella corrugata Nitrospira clone MAx27_C6
EU652665.1 gg_id:279215 Seasonal variation microbial Yel Sea sediment clone D8S-37
DQ058679.1 gg_id:139106 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit
AF317764.1 gg_id:136664 Nullarbor cave clone wb1_F07
EU491363.1 gg_id:274991 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
GQ472347.1 gg_id:545624 Microbial Dongping Lake lake sediment clone 3C2-9
EF562103.1 gg_id:243273 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum
AJ863252.1 gg_id:123055 poplar tree microcosm bulk soil flooded clone 21BSF5
EF019030.1 gg_id:210132 aspen rhizosphere clone Amb_16S_1574
AB015536.1 gg_id:150698 deep-sea sediments depths clone BD2-6
FJ416081.1 gg_id:368981 sediments sediment station NEC5 Northern Bering Sea clone 009K2
GQ357017.1 gg_id:582662 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_
EU491391.1 gg_id:269847 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
EU734917.1 gg_id:307509 assemblages sediment station DBSE Northern Bering Sea clone 008A10
EU925847.1 gg_id:329091 sediments sediment station DBS1 northern Bering Sea clone 038E63
EU780676.1 gg_id:304501 magnetic-enriched magnetotactic Miyun reservoir Beijing China fresh water sedimer
DQ478745.1 gg_id:157587 UASB reactor treating brewery wastewater clone CLONG59
AB179690.1 gg_id:101911 groundwater 0.2 m-captured fraction clone KNA6-EB14

DQ811892.1	166567	5144.1	4986.8	5838.1	5801.1	11608.8	12843.0
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GQ848453.1	588843	5538.8	5295.8	8173.9	5949.6	5617.8	9753.8
GQ500804.1	586905	2346.0	2644.0	3165.6	1705.9	4301.7	4605.6
EF594048.1	234702	134.2	413.2	784.7	155.8	1518.0	1329.0
AY921494.2	153641	130.9	552.5	1448.2	176.9	3628.3	4538.8
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AB176700.1	102911	328.7	484.5	1635.2	392.2	2063.3	2047.1
CU466688.1	309217	1829.6	3542.9	4010.0	2534.8	4489.1	6677.1
AY921873.1	113562	668.1	1094.7	3164.5	1177.4	4346.0	5731.0
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EU652665.1	279215	4085.1	4569.0	7177.1	3906.3	7746.3	6988.6
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GU208344.1 gg_id:555144 Study on Sediment Dongping Lake sediment clone Tds3-9
AB240285.1 gg_id:142177 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
GQ402751.1 gg_id:513871 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
FJ755775.1 gg_id:581592 vertical archaeal water and Lake Taihu sediment clone LT-SB-B104
GQ402791.1 gg_id:572073 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
DQ450806.1 gg_id:160776 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
DQ395024.1 gg_id:151318 harbor sediment clone VHS-B5-55
DQ138962.1 gg_id:138089 rice straw paddy soil clone JG131
EU617719.1 gg_id:331634 Seasonal variation microbial Yel Sea sediment clone A13S-27
GU208367.1 gg_id:565006 Study on Sediment Dongping Lake sediment clone Td1-7
EF648166.1 gg_id:238866 dynamics during produced water treatment aerobic activated sludge clone XJ134
DQ354748.1 gg_id:155453 subsurface water clone MS149BH1062003_38
FJ484454.1 gg_id:540847 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
AF286037.1 gg_id:51852 mercury and PCB contaminated saltmarsh sediment clone LCP-6 LCP-6
DQ811894.1 gg_id:171789 mangrove soil clone MSB-3B5
DQ833491.1 gg_id:167800 detected analyses depth sediment Guanting Reservoir clone 35-52
FJ902311.1 gg_id:558620 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal
EU592458.1 gg_id:594158 Seasonal changes Salton Sea hypersaline sediment clone SSS22N
DQ811893.1 gg_id:167447 mangrove soil clone MSB-4D12
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CP001147.1 gg_id:336962 Thermodesulfovibrio yellowstonii str. DSM 11347
AB231858.1 gg_id:138300 Thermodesulfovibrio yellowstonii str. YP87
EF081294.1 gg_id:188164 Thermodesulfovibrio sp. str. Hbr5
GQ844371.1 gg_id:584184 Microbial anoxic tank full-scale water treatment plant influent produced wastewate
FJ638591.1 gg_id:511823 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
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X96726.1 gg_id:1523 Thermodesulfovibrio islandicus str. R1ha3
EF205565.1 gg_id:208106 among geographically regions central Tibet geothermal spring mat clone TP17
AB183860.1 gg_id:99703 deep aquifer Great Artesian Basin clone GAB-B04
AF255602.1 gg_id:27466 Nitrospira sp. str. SRI-237
AB021302.1 gg_id:1530 Thermodesulfovibrio sp. str. TGE-P1
AY947906.1 gg_id:143270 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c
GU289667.1 gg_id:526213 Moderately thermophilic magnetotactic Nevada USA hot springs clone HSMV-1
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FJ497655.1 gg_id:590984 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
DQ640738.1 gg_id:232235 full-scale EBPR sludge clone Skagen116
FM213079.1 gg_id:568248 Biodiversity and shifts assessment biology tools Biotrickling treating loads biotricklin
FJ497309.1 gg_id:540736 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ516826.1 gg_id:552017 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower se
EF520619.1 gg_id:235051 structure lakes: what controls ? acid-impacted lake clone ACK-BTH02-32

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GQ402751.1	513871	2621.7	3273.7	3983.9	3844.9	2153.7	3815.4
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AF286037.1	51852	47.2	58.2	101.6	71.6	63.3	32.9
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AB231858.1	138300	4735.9	6321.8	5120.6	4889.3	5562.7	4639.6
EF081294.1	188164	76.9	117.4	182.2	88.5	81.6	53.6
GQ844371.1	584184	701.8	960.9	1903.9	433.4	205.6	251.6
FJ638591.1	511823	678.6	1024.5	2804.6	600.5	478.9	640.0
AB231857.1	200798	31.5	58.6	77.9	72.0	77.8	33.1
X96726.1	1523	670.2	720.8	2382.1	306.0	470.1	812.4
EF205565.1	208106	93.2	118.8	204.7	149.8	120.4	99.4
AB183860.1	99703	1574.7	1358.5	2835.0	1338.2	835.6	1009.4
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DQ395545.1 gg_id:154578 deep-sea octacoral clone ctg_CGOCA85
GU302451.1 gg_id:546200 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h
FJ497634.1 gg_id:570634 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
FJ497567.1 gg_id:539167 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun
GQ246342.1 gg_id:566822 Temporal and spatial China North Yel Sea sediments clone Cm1-5
EU617857.1 gg_id:306314 Seasonal variation microbial Yel Sea sediment clone C13S-3
FJ769506.1 gg_id:514019 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana
EU245141.1 gg_id:238328 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-H0E
GQ848462.1 gg_id:591704 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal
EU491069.1 gg_id:263387 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU385825.1 gg_id:269047 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU591656.1 gg_id:275968 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic
AJ306780.1 gg_id:66921 DCP degrading consortium clone SHA-100
DQ067040.1 gg_id:132726 Lake Washington sediment clone pLW-99
GU118009.1 gg_id:554824 Threatened Corals Provide Microbial Habitats clone Apal_G06
AY193179.1 gg_id:80983 thermal spring mat clone O1aA90
EU635936.1 gg_id:278503 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp
EU635935.1 gg_id:278911 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp
EU924242.1 gg_id:310156 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C
DQ404838.1 gg_id:202174 contaminated sediment clone 655967
FJ189542.1 gg_id:340415 digester anaerobic sludge clone EUB_21
AY218580.1 gg_id:82092 penguin droppings sediments clone KD2-26
AY218586.1 gg_id:82149 penguin droppings sediments clone KD2-5
AY188303.1 gg_id:80684 marine? clone KD3-145
EU542445.1 gg_id:264265 Effects chemical structure concentration on pathways microbial during dechlorinatio
AY188301.1 gg_id:99822 marine? clone KD2-44
AF050600.1 gg_id:10566 contaminated aquifer clone WCHB1-07
EF019888.1 gg_id:210172 aspen rhizosphere clone Elev_16S_1253
EU386078.1 gg_id:269947 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EF019157.1 gg_id:206209 aspen rhizosphere clone Amb_16S_1804
EU134976.1 gg_id:255464 tallgrass prarie soil clone FFCH9932
FJ479589.1 gg_id:509215 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ298014.1 gg_id:142268 Microbial hydrocarbon contaminated soil clone UB12
AF422676.1 gg_id:42849 TCE-sediment clone d153
CU924193.1 gg_id:534077 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ710771.1 gg_id:593853 Abundance and microbial long-term operated anammox biofilm reactors initiated ino
GQ356089.1 gg_id:556282 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
EU050864.1 gg_id:253554 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_10
EU386076.1 gg_id:274390 Biogeographical and microbes sediments on subseafloor sediment South China Sea c

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EU385825.1	269047	2370.4	874.6	2458.8	2669.7	267.1	1211.6
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AY218580.1	82092	118.4	44.8	352.9	94.2	60.8	26.7
AY218586.1	82149	66.5	38.2	168.5	61.3	63.1	35.7
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EU386078.1	269947	7107.8	7604.8	11651.3	8394.4	5527.8	6370.8
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EU386007.1 gg_id:266385 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
AB015559.1 gg_id:1665 deep-sea sediment clone BD4-9
EU385777.1 gg_id:271294 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
FJ746242.1 gg_id:511521 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EU386085.1 gg_id:258248 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
GQ356152.1 gg_id:575286 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
EU385765.1 gg_id:266542 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU385956.1 gg_id:271229 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU800499.1 gg_id:331078 It's all ranking aquatic Delaware Bay NJ clone 2C228620
AM997403.1 gg_id:534821 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AM991275.1 gg_id:279473 Microbial groundwater and their potential use biomonitoring karst spring water clo
DQ676354.1 gg_id:226121 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
AM997371.1 gg_id:538271 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AF507707.1 gg_id:65679 forest soil clone S042
AY661975.1 gg_id:137070 uranium-contaminated groundwater clone 300E2-C09
EU491175.1 gg_id:264161 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
AM997579.1 gg_id:552101 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
GU208411.1 gg_id:592150 Study on Sediment Dongping Lake sediment clone Fh2-22
AY667264.1 gg_id:102531 TCE-dechlorinating groundwater clone TANB84
DQ837261.1 gg_id:238430 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_70
AB232806.1 gg_id:138097 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con
EF019262.1 gg_id:204198 aspen rhizosphere clone Elev_16S_444
AB294344.1 gg_id:211556 Microbial structure deep coal seem groundwater stream clone SWB33
EU881347.1 gg_id:317758 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
EU491266.1 gg_id:274405 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU373974.1 gg_id:272286 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
FJ901639.1 gg_id:509494 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita
FJ901656.1 gg_id:593533 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita
EU385757.1 gg_id:266325 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
DQ676379.1 gg_id:225089 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
GQ356163.1 gg_id:534717 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
EF032777.1 gg_id:176040 cyanobacterial mat in lava cave clone HAVOmat111
FJ719059.1 gg_id:517884 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_G0
AB294345.1 gg_id:204818 Microbial structure deep coal seem groundwater stream clone SWB34
AY850293.1 gg_id:137151 depending on what microbial treatment present soil clone w3
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EU048680.1 gg_id:252470 and archaeal surface marine sediment Slope South China Sea clone MD2896-B22
EU385872.1 gg_id:263088 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
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GQ143758.1 gg_id:395003 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes

EU386072.1	264190	2336.8	2098.5	1504.8	2030.6	4169.5	3537.4
EU386007.1	266385	1654.6	2680.1	4838.9	2164.3	5616.3	3864.1
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EU385777.1	271294	5442.3	4768.7	7102.9	4858.6	3202.6	8441.3
FJ746242.1	511521	5011.5	7057.9	3725.5	6428.6	4762.1	6892.1
EU386085.1	258248	4443.0	4448.5	5023.1	3196.9	3806.5	3633.0
GQ356152.1	575286	717.1	999.9	5482.5	1283.6	1481.2	1163.7
EU385765.1	266542	1560.3	2587.5	5869.3	4424.4	4532.0	5657.7
EU385956.1	271229	2013.2	4076.9	9114.3	3457.3	5996.9	4376.5
EU800499.1	331078	8201.5	7066.8	8847.7	3738.9	7945.0	7815.5
AM997403.1	534821	8689.4	9717.6	7341.7	10678.3	5681.7	6517.6
AM991275.1	279473	2297.7	2990.1	4858.8	3205.6	2219.5	2973.4
DQ676354.1	226121	696.5	165.9	2401.8	469.1	286.4	156.8
AM997371.1	538271	7509.1	8881.2	8909.5	10590.6	8581.3	8150.3
AF507707.1	65679	1752.6	2536.3	6411.5	3916.1	525.9	2022.7
AY661975.1	137070	25.9	38.0	2642.6	183.2	74.8	33.1
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AM997579.1	552101	2086.3	3168.9	4299.6	4664.4	3967.4	3422.3
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DQ837261.1	238430	15.8	37.5	2632.3	226.8	69.8	31.1
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AJ704718.1	109302	30.8	55.7	29.0	56.7	62.1	34.3
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EU385676.1 gg_id:260694 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EU181480.1 gg_id:249848 Prokaryotic enhanced organic matter remineralization continental margin marine se
EU245272.1 gg_id:252038 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B04
AB177161.1 gg_id:133316 seafloor methane hydrate clone ODP1230B18.23
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FJ746322.1 gg_id:551173 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
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DQ811949.1 gg_id:169350 mangrove soil clone MSB-3A8
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AB189340.1 gg_id:113184 cold seep sediment clone JT58-14
FJ712453.1 gg_id:530784 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
AF419682.1 gg_id:72683 Guaymas Basin hydrothermal sediment clone CS_B013

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EU386091.1 gg_id:273192 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU290732.1 gg_id:242377 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling
AF154105.1 gg_id:13713 hydrocarbon seep sediment clone GCA018
EU639265.1 gg_id:335164 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
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CU919427.1 gg_id:541379 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
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EF559042.1 gg_id:249738 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EF558973.1 gg_id:248313 Microbial functional groups solid waste digestor stable isotope probing thermophilic
EU635950.1 gg_id:278345 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp
AF027082.1 gg_id:1654 hot spring clone OPB47
AJ306782.1 gg_id:66918 DCP-dechlorinating consortium clone SHA-1
AB195912.1 gg_id:109200 Anaerobic sludge clone N10
CU925213.1 gg_id:561559 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB195913.1 gg_id:109201 Anaerobic sludge clone N16
GU118564.1 gg_id:592392 Threatened Corals Provide Microbial Habitats clone Mfav_F21
AY485295.1 gg_id:106114 marine sponge clone 232
AY627378.1 gg_id:103111 marine clone AY627378
GQ349157.1 gg_id:575293 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ746128.1 gg_id:539443 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EF076099.1 gg_id:238478 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San
EU617889.1 gg_id:327521 Seasonal variation microbial Yel Sea sediment clone D13S-68
FJ208807.1 gg_id:307010 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
FJ208813.1 gg_id:305954 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
GQ348002.1 gg_id:540414 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ208832.1 gg_id:332638 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
DQ058681.1 gg_id:139290 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit
BX294710.2 gg_id:84726 aerobic basin clone CY0ARA025G12
EF575301.1 gg_id:227921 site S25 near Coco's Island marine clone S25_1645
FJ485411.1 gg_id:509346 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
EU236408.1 gg_id:290327 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E7
EF208657.1 gg_id:201142 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2
GQ246374.1 gg_id:577122 Temporal and spatial China North Yel Sea sediments clone Cm1-37
AM997498.1 gg_id:560658 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
FJ208809.1 gg_id:352790 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
L10943.1 gg_id:2910 Marine sp. (aggregate agg27) generated fragment
EU478627.1 gg_id:339005 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
AY907752.1 gg_id:137332 identification picoplankton contrasting waters Arabian Sea water clone A314014
AM997936.1 gg_id:548511 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A

AY592418.1	100189	9084.2	8154.5	8599.2	7250.5	4736.0	4548.7
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CU919953.1	542554	4595.9	6377.9	7710.9	6360.5	5368.7	5510.6
CU919427.1	541379	4939.0	4638.7	4649.8	3702.5	5151.1	3566.6
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EF558973.1	248313	2986.2	4314.4	2362.8	3479.5	6036.2	4354.7
EU635950.1	278345	433.5	346.9	1019.2	131.1	381.5	272.2
AF027082.1	1654	1420.7	1225.3	1008.5	2288.2	3075.9	2278.3
AJ306782.1	66918	21380.8	21863.4	13931.3	14640.8	17579.1	16350.9
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CU925213.1	561559	10576.5	8694.8	5809.0	3827.8	3278.7	5067.6
AB195913.1	109201	11645.8	10975.0	6949.6	8548.6	9895.5	8809.8
GU118564.1	592392	12039.2	14368.3	12378.3	10950.4	12058.5	12191.8
AY485295.1	106114	1610.7	2411.7	1940.7	4163.1	2319.8	3995.9
AY627378.1	103111	1635.3	1827.5	1954.9	393.6	341.2	898.3
GQ349157.1	575293	4256.2	4408.9	5420.4	5209.5	3630.4	2891.6
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FJ208807.1	307010	1129.5	1835.0	3037.2	1585.3	541.7	1140.5
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GQ348002.1	540414	4723.2	7209.5	11571.0	4558.5	2786.1	3743.6
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DQ058681.1	139290	41.9	66.3	131.7	74.5	108.6	32.3
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GQ246374.1	577122	1040.2	1870.9	2360.7	2491.8	2207.3	2949.7
AM997498.1	560658	2439.0	4580.1	6698.3	4030.4	6468.0	4424.1
FJ208809.1	352790	15076.3	17503.6	16924.1	12752.8	14867.4	15021.7
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DQ513072.1 gg_id:160383 Microbial life fluids ridge flank crustal fluid clone FS266-6B-03
EF092217.1 gg_id:270621 Persistent Axinella corrugata clone B255_19a
FJ208822.1 gg_id:333159 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
FJ208814.1 gg_id:336106 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
FJ208815.1 gg_id:318107 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
EF516837.1 gg_id:223894 grassland soil clone FCPS655
GQ349982.1 gg_id:579975 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ513105.1 gg_id:161200 Microbial life fluids ridge flank crustal fluid clone FS275-24B-03
EU373996.1 gg_id:270915 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU491188.1 gg_id:266276 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU478635.1 gg_id:332383 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
EF645945.1 gg_id:242961 Potential interactions particle- anammox and archaeal partners namibian Namibian u
GU118095.1 gg_id:584707 Threatened Corals Provide Microbial Habitats clone Apal_E05
EU050872.1 gg_id:237785 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_05
DQ070801.1 gg_id:147446 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
CU917688.1 gg_id:569653 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AM056027.1 gg_id:137533 anammox wastewater treatment plant
AM490671.1 gg_id:550928 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir
AY266450.1 gg_id:85294 Baltimore Harbor sediment clone B4
EU478641.1 gg_id:338211 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
FN396716.1 gg_id:565403 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II
EU135126.1 gg_id:257290 tallgrass prarie soil clone FFCH12905
FJ444691.1 gg_id:565666 Cotton Rhizosphere cotton rhizosphere clone 3h-166
FJ905739.1 gg_id:535979 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F106b
GQ339140.1 gg_id:527968 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
EU617888.1 gg_id:353402 Seasonal variation microbial Yel Sea sediment clone D13S-58
EU638793.1 gg_id:340317 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n
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EU478694.1 gg_id:312765 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
FJ710640.1 gg_id:513938 Abundance and microbial long-term operated anammox reactors initiated inocula upf
FJ710627.1 gg_id:534693 Abundance and microbial long-term operated anammox reactors initiated inocula upf
GQ356125.1 gg_id:576581 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
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GQ175284.1 gg_id:578161 nitrogen removal reactors lab scale SBR inorganic medium and glucose influence org
AY254883.1 gg_id:102606 rotating biological contactor clone EN 8
AY257181.1 gg_id:92388 Candidatus Scalindua sorokinii
DQ386151.1 gg_id:206446 Anaerobic Ammonium Oxidizing Marine Widespread Occurrence but sea water Gulli
EF602038.1 gg_id:296196 Anammox marine sediments: cell numbers potential anammox activity and pore nutr

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DQ513072.1	160383	1862.9	3568.2	3611.7	2831.4	1436.3	3311.9
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EF516837.1	223894	53.5	82.6	221.8	77.9	52.1	40.4
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DQ513105.1	161200	376.2	615.9	744.7	237.5	100.4	228.4
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EU491188.1	266276	7075.9	8109.1	9455.0	5739.2	5043.9	6635.3
EU478635.1	332383	135.3	791.5	1387.5	162.8	109.2	140.7
EF645945.1	242961	5453.2	7548.8	8246.1	7694.2	6413.7	4826.2
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DQ070801.1	147446	39.8	42.4	55.5	65.2	81.7	45.7
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AY266450.1	85294	19.7	26.8	22.6	53.3	66.1	29.1
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FJ444691.1	565666	1332.2	2094.0	4491.8	1566.3	927.1	2445.0
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GQ339140.1	527968	8865.4	11520.9	10864.5	7971.7	12442.0	10994.4
EU617888.1	353402	4199.7	5826.0	5799.4	2526.7	2143.9	3041.3
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GQ347619.1	580887	5264.7	7428.1	9075.9	2802.9	4590.1	2229.4
AF314425.1	39505	5801.8	6615.1	9304.8	6594.9	5589.9	6229.6
EU478694.1	312765	166.1	202.1	575.1	385.5	97.7	92.9
FJ710640.1	513938	8121.8	7542.9	9493.0	4539.2	7604.1	6210.0
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GQ356125.1	576581	1394.2	1367.5	646.3	945.7	358.4	358.3
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GQ175284.1	578161	53.4	44.9	182.7	86.6	55.9	20.5
AY254883.1	102606	8576.6	10522.5	9804.4	5998.3	7948.2	6952.9
AY257181.1	92388	10035.2	10615.7	13811.7	6033.7	9061.8	8865.4
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EU142947.1 gg_id:324638 Enrichment and two marine anammox involved nitrogen gas production anaerobic a
AB300486.1 gg_id:219357 Detection Activity and Anammox Genes Coastal Marine Sediments Japan intertidal s
AB281489.1 gg_id:194829 anaerobic ammonium-oxidizing planctomycete JMK-2
EU478593.1 gg_id:324123 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
EU039861.1 gg_id:316215 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper
EU478626.1 gg_id:345186 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
EU478620.1 gg_id:307226 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
EU478663.1 gg_id:308582 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
GQ350985.1 gg_id:588411 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU039851.1 gg_id:334236 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper
EU478595.1 gg_id:335981 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
DQ869384.1 gg_id:173040 evidence broad anaerobic ammonium-oxidizing freshwater and marine sediments B
EU039841.1 gg_id:338086 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper
EU478687.1 gg_id:306841 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
EU039858.1 gg_id:318377 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper
EU039856.1 gg_id:305926 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper
GQ143786.1 gg_id:381880 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes
EU478661.1 gg_id:328021 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
EU039855.1 gg_id:347502 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper
EU478664.1 gg_id:307650 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
DQ534739.1 gg_id:229398 Anaerobic ammonium oxidation contributes significantly nitrogen loss Peruvian oxyg
EU385873.1 gg_id:258876 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU385800.1 gg_id:262268 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
AB177204.1 gg_id:131205 seafloor methane hydrate clone ODP1230B31.20
EU050874.1 gg_id:239076 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_21
AB474364.1 gg_id:554768 Phycisphaera mikrensis str. NBRC 102668
FJ516779.1 gg_id:569736 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm
EU236426.1 gg_id:302876 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92H6
FJ202723.1 gg_id:356606 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU491354.1 gg_id:261113 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
AF445715.1 gg_id:44762 Planctomycetales clone SM2B12
DQ811901.1 gg_id:173711 mangrove soil clone MSB-4A3
EF632950.1 gg_id:252359 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
AY344414.1 gg_id:91792 Lake Kauhako surface clone K2-S-7
FJ205228.1 gg_id:533393 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
EU135058.1 gg_id:239668 tallgrass prarie soil clone FFCH1059
FJ205225.1 gg_id:568694 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
EU801770.1 gg_id:341049 It's all ranking aquatic Chesapeake Bay MD clone 3C003141
FJ626886.1 gg_id:510050 Identification Phytodetritus Degrading Microbial Sublittoral Gulf Mexico Sands ocean
EU135079.1 gg_id:247437 tallgrass prarie soil clone FFCH3889
AB430337.1 gg_id:276470 Removal Nitrogen Compounds Coupling Anoxic Ammonium Oxidation and Nitrate Re

EU142947.1	324638	1746.2	2171.3	3943.8	1675.8	1985.8	2414.3
AB300486.1	219357	222.6	846.1	3132.5	591.8	613.7	498.6
AB281489.1	194829	2992.8	3630.1	9932.5	2558.8	2401.3	3300.2
EU478593.1	324123	976.8	1103.9	1262.3	416.2	598.3	713.1
EU039861.1	316215	7041.4	4512.2	3729.6	4537.5	3507.3	4643.6
EU478626.1	345186	6731.5	8331.5	6911.6	7387.1	6792.5	6839.8
EU478620.1	307226	10920.0	9021.9	5627.8	8094.0	8469.3	9600.2
EU478663.1	308582	1905.7	3386.2	6775.6	1691.7	1910.5	3453.7
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EU039851.1	334236	2890.2	2472.2	2051.1	1931.1	1954.4	2059.2
EU478595.1	335981	12936.2	18768.8	12050.7	10214.0	14721.5	14955.2
DQ869384.1	173040	5572.4	6818.4	8518.9	4725.6	3291.9	4405.5
EU039841.1	338086	4147.5	6144.5	6561.3	5748.6	7948.3	7693.9
EU478687.1	306841	4693.9	6036.1	3389.3	4698.6	7982.3	6850.3
EU039858.1	318377	11833.1	8498.9	6907.8	9593.0	6392.6	8553.5
EU039856.1	305926	5493.5	4786.6	4047.4	6144.8	5308.8	6690.7
GQ143786.1	381880	9433.6	10101.2	11023.8	8355.7	11283.0	10688.3
EU478661.1	328021	6879.1	8163.4	11082.0	5031.6	7223.2	7428.5
EU039855.1	347502	7073.6	5638.4	6953.1	4901.4	8731.1	7764.0
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DQ534739.1	229398	5290.0	2956.2	6939.8	6256.8	8933.2	7830.6
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AB177204.1	131205	15908.8	15261.7	14200.0	11995.1	11464.7	13815.9
EU050874.1	239076	9446.9	9651.4	7659.4	8374.1	10217.1	8940.8
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FJ202723.1	356606	24.3	46.0	36.6	60.2	62.8	16.8
EU491354.1	261113	1068.8	2371.8	5554.7	1904.6	1188.0	1350.1
AF445715.1	44762	53.3	122.3	106.5	108.6	64.6	67.7
DQ811901.1	173711	29.8	105.9	132.7	49.8	86.0	40.6
EF632950.1	252359	409.2	816.3	1335.1	384.0	1023.7	543.9
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EU135058.1	239668	105.0	377.5	629.1	173.8	94.8	94.5
FJ205225.1	568694	30.3	47.0	36.2	35.1	51.7	15.9
EU801770.1	341049	24.4	47.9	50.4	52.4	100.9	79.5
FJ626886.1	510050	1369.4	1390.1	917.0	296.3	373.0	398.0
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AB430337.1	276470	33.6	59.0	83.1	51.7	62.9	26.3

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AB434262.1 gg_id:340702 Effect concentration on treatment non-woven biomass carrier sludge taken anammc
DQ351812.1 gg_id:146588 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
EU236371.1 gg_id:294838 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9F4
AM086132.1 gg_id:145659 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone (
FJ612210.1 gg_id:561975 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.3.10
DQ396220.1 gg_id:151370 deep-sea octacoral clone ctg_NISA377
DQ513014.1 gg_id:160569 Microbial life fluids ridge flank crustal fluid clone FS140-16B-02
AY162125.1 gg_id:135863 Cultivating Sargasso Sea clone GMD15D02
EF574227.1 gg_id:231309 site S25 near Coco's Island marine clone S25_571
EF632831.1 gg_id:237452 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir
AY957928.1 gg_id:115016 drinking water biofilm clone B3NR69D13
EU135121.1 gg_id:248077 tallgrass prarie soil clone FFCH5834
DQ450805.1 gg_id:200837 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EU662552.1 gg_id:553506 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb
EF515938.1 gg_id:218719 grassland soil clone FCPP573
FJ901683.1 gg_id:591480 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita (
GU359065.1 gg_id:531410 rhizosphere soil peanut clone 1S21
AF407717.1 gg_id:201735 microbial Australia's Great Artesian Basin 52 deg. C brown filament clone B16
GQ356133.1 gg_id:566719 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
EU881297.1 gg_id:304737 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
AF312220.1 gg_id:199817 -based BTX-catabolizing microbial African sandy soil South Africa: KwaZulu-Natal Prov
EF580964.1 gg_id:277693 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1(
AF121889.1 gg_id:200587 analyses sulfidogenic and phenol-degrading microbial consortia 2-bromophenol-deha
DQ521520.1 gg_id:202207 Antarctic lake ice cover clone ANTLV2_E09
AJ616270.1 gg_id:202670 and seasonal changes planctomycetales biofilms river biofilm clone DEL26
AB240380.1 gg_id:201941 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
EF516039.1 gg_id:225108 grassland soil clone FCPN712
EF125955.1 gg_id:581157 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose
FJ232661.1 gg_id:308368 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
AB486233.1 gg_id:540991 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EU135254.1 gg_id:255557 tallgrass prarie soil clone FFCH8636
FJ479411.1 gg_id:572242 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU135178.1 gg_id:237749 tallgrass prarie soil clone FFCH7061
FJ232680.1 gg_id:333924 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
AY963421.1 gg_id:203044 analyses structures soils evergreen broad-leaved forests south-west China soil clone
FJ479427.1 gg_id:586523 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF580956.1 gg_id:279355 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM9!
DQ413078.1 gg_id:201687 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge
EU881243.1 gg_id:312527 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
EU135175.1 gg_id:248027 tallgrass prarie soil clone FFCH6996
EU044117.1 gg_id:239077 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c

AB434262.1	340702	3121.1	1459.8	3703.8	2470.7	1249.5	1963.9
DQ351812.1	146588	26.8	101.0	157.8	66.6	119.2	135.8
EU236371.1	294838	7341.4	8415.8	3707.2	1298.9	3251.6	2029.5
AM086132.1	145659	4626.1	5949.0	3997.0	3755.7	6854.9	4508.5
FJ612210.1	561975	2707.3	2861.0	3748.7	3986.1	1341.6	3196.8
DQ396220.1	151370	116.6	94.7	152.1	435.9	69.4	30.8
DQ513014.1	160569	314.6	555.2	527.8	1030.1	1083.1	849.1
AY162125.1	135863	37.0	52.8	48.9	52.1	56.7	27.5
EF574227.1	231309	23.8	81.1	36.1	66.3	67.4	39.7
EF632831.1	237452	31.6	58.4	40.7	53.2	62.6	25.7
AY957928.1	115016	186.0	499.0	812.9	133.8	272.9	1111.7
EU135121.1	248077	2422.8	3509.9	5640.8	1127.0	1329.1	1992.8
DQ450805.1	200837	69.0	140.6	125.4	87.3	231.5	179.6
EU662552.1	553506	198.2	1060.9	1753.1	167.9	262.0	510.6
EF515938.1	218719	2750.5	3846.1	6111.3	826.7	3403.3	3266.2
FJ901683.1	591480	12721.0	14614.7	13805.6	9136.8	15010.0	12469.6
GU359065.1	531410	614.5	2115.2	3647.2	312.0	394.3	873.9
AF407717.1	201735	101.4	132.8	57.5	106.6	61.2	64.8
GQ356133.1	566719	6672.1	10040.4	10290.5	4392.2	4906.7	5092.6
EU881297.1	304737	6001.7	8591.2	9544.5	4153.9	3840.0	4934.2
AF312220.1	199817	64.4	158.9	409.6	167.9	152.5	157.6
EF580964.1	277693	1693.4	7218.4	9665.2	1716.7	3630.5	4435.7
AF121889.1	200587	13095.1	11238.2	10026.4	8351.1	12264.3	12624.9
DQ521520.1	202207	371.7	1886.6	4027.5	320.7	1104.0	1340.6
AJ616270.1	202670	2359.4	3056.9	1992.2	2842.8	2413.3	2658.4
AB240380.1	201941	10410.6	14959.3	15674.1	7928.5	10679.8	10318.1
EF516039.1	225108	79.4	279.3	186.4	87.3	101.2	69.5
EF125955.1	581157	3755.9	10313.8	4778.8	3709.3	1305.1	2475.0
FJ232661.1	308368	2370.5	2759.7	4846.4	2403.9	760.1	1949.5
AB486233.1	540991	2129.4	4046.5	2493.6	1753.2	2997.6	2778.8
EU135254.1	255557	51.6	138.8	293.3	96.1	83.8	151.6
FJ479411.1	572242	462.3	833.8	1308.9	509.6	626.8	1037.1
EU135178.1	237749	97.5	410.8	1493.6	303.3	158.7	210.2
FJ232680.1	333924	1642.7	2356.2	1890.5	532.2	607.9	1066.2
AY963421.1	203044	234.2	197.0	69.4	192.1	392.7	75.3
FJ479427.1	586523	10705.8	11041.5	11804.3	5963.8	8944.8	6744.1
EF580956.1	279355	1100.0	3194.1	6811.6	765.5	1560.4	1775.2
DQ413078.1	201687	45.5	107.9	60.3	75.7	71.4	43.1
EU881243.1	312527	440.9	978.2	1579.3	349.1	1657.7	2075.5
EU135175.1	248027	7696.5	12684.2	13597.2	6336.7	9573.5	9159.0
EU044117.1	239077	5190.2	7438.2	8858.4	4120.8	6151.3	6822.7

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CU921500.1 gg_id:549231 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU135265.1 gg_id:236310 tallgrass prarie soil clone FFCH18216
EU135274.1 gg_id:242459 tallgrass prarie soil clone FFCH18590
EU881267.1 gg_id:321885 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
FJ612288.1 gg_id:576167 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.14
FJ466217.1 gg_id:563036 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ536899.1 gg_id:590906 Linking performance microbiology biofilters treating dimethyl sulphide presence and
FJ203423.1 gg_id:331911 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU135107.1 gg_id:249175 tallgrass prarie soil clone FFCH2726
FJ232673.1 gg_id:325828 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
EF516153.1 gg_id:220916 grassland soil clone FCPN669
GQ093878.1 gg_id:397840 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
FJ652504.1 gg_id:593106 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-38
EF019897.1 gg_id:205038 aspen rhizosphere clone Elev_16S_1264
EU881193.1 gg_id:326719 Karst region natural restoration land soil clone KNR200711-121
EU135245.1 gg_id:250454 tallgrass prarie soil clone FFCH17044
AJ231195.1 gg_id:2884 Isosphaera pallida
DQ814661.1 gg_id:201392 Reciprocal Gut Microbiota Transplants Zebrafish and Mice Germ-free Recipients Hos
DQ814734.1 gg_id:200402 Reciprocal Gut Microbiota Transplants Zebrafish and Mice Germ-free Recipients Hos
AM902526.1 gg_id:250059 Singulisphaera acidiphila str. PO2
AY234528.1 gg_id:112330 soil isolate Ellin5111
GQ402671.1 gg_id:552820 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
AB238776.1 gg_id:146076 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-013
GQ264465.1 gg_id:545566 Structure Simulated Level Waste Site simulated level waste site clone WW3_167
DQ986200.1 gg_id:186517 planctomycete member Isosphaera genus freshwater aquarium Isosphaera-like str.
EU669616.1 gg_id:340209 soil clone S22-2
EU289510.1 gg_id:246083 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s
AJ252623.1 gg_id:20352 agricultural soil clone SC-I-20
EF515969.1 gg_id:220676 grassland soil clone FCPP710
AB254788.1 gg_id:160585 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
AJ867920.1 gg_id:202171 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone C8
EU861926.1 gg_id:345379 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
EF019037.1 gg_id:215283 aspen rhizosphere clone Amb_16S_1586
X81959.1 gg_id:2877 Isophaera sp. str. 640
DQ532192.1 gg_id:170729 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
AJ292683.1 gg_id:27191 PCB-polluted soil clone 2112
X81958.1 gg_id:2879 Isophaera sp. str. 666
EF492942.1 gg_id:249037 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AF465649.1 gg_id:35108 planctomycete clone YNPRH1A
EF516492.1 gg_id:222936 grassland soil clone FCPS404
EU335237.1 gg_id:241588 Changes microbial metabolic and along hydrogeochemically variable profile unsatura

CU921500.1	549231	12630.8	18372.8	18939.0	9079.8	13983.3	13483.5
EU135265.1	236310	4213.8	6895.5	7961.5	2259.6	2072.8	3791.8
EU135274.1	242459	120.9	637.3	248.0	89.4	456.2	385.9
EU881267.1	321885	3775.7	5651.1	4767.6	3780.3	5916.9	5619.9
FJ612288.1	576167	11482.0	13067.2	9334.1	6594.8	4651.4	4604.8
FJ466217.1	563036	3955.5	8387.4	7162.9	3537.0	3837.4	4998.2
FJ536899.1	590906	27.0	67.6	224.0	51.3	68.3	51.8
FJ203423.1	331911	74.1	654.9	1332.6	369.3	473.2	573.0
EU135107.1	249175	7701.9	9232.0	9487.7	8831.9	5760.3	7117.9
FJ232673.1	325828	5171.6	5292.1	8772.4	3033.4	1181.4	2907.1
EF516153.1	220916	14.9	20.0	42.9	46.7	78.9	22.1
GQ093878.1	397840	2477.5	7773.3	10937.6	2779.9	3953.2	6056.6
FJ652504.1	593106	12763.9	16793.8	20398.3	10804.2	11572.7	11662.3
EF019897.1	205038	3779.2	5612.7	3258.9	2397.4	4225.5	3849.3
EU881193.1	326719	508.7	954.2	519.4	303.4	497.8	923.8
EU135245.1	250454	252.5	593.5	1334.1	373.8	259.2	370.6
AJ231195.1	2884	62.8	124.8	146.6	119.2	150.3	164.8
DQ814661.1	201392	1336.0	5142.8	822.8	1020.9	124.4	132.0
DQ814734.1	200402	3062.6	5422.9	6718.0	3150.4	5450.1	4526.3
AM902526.1	250059	3460.8	4889.4	3791.4	1243.2	3334.4	2586.2
AY234528.1	112330	186.5	891.6	91.2	199.5	60.4	54.0
GQ402671.1	552820	1445.2	3604.3	4974.1	1546.1	2254.8	2599.1
AB238776.1	146076	50.9	79.8	150.4	71.9	53.5	47.0
GQ264465.1	545566	1982.8	3063.8	4380.7	1330.3	2501.5	1966.7
DQ986200.1	186517	110.3	367.4	234.2	145.8	151.5	237.7
EU669616.1	340209	1153.7	3682.7	5647.9	1502.4	3299.1	2545.9
EU289510.1	246083	3891.8	3745.8	1063.4	888.3	1334.7	1615.8
AJ252623.1	20352	4074.6	3676.6	1114.4	1970.6	1111.9	1719.5
EF515969.1	220676	98.5	202.1	166.3	90.1	114.9	187.8
AB254788.1	160585	992.4	2832.3	4299.0	759.7	1708.6	2135.9
AJ867920.1	202171	2917.6	4330.5	2169.2	953.7	1769.9	1273.8
EU861926.1	345379	1820.5	3057.9	2868.4	758.0	1951.2	1417.9
EF019037.1	215283	44.3	188.1	103.5	72.9	146.7	88.8
X81959.1	2877	184.0	613.7	1892.9	251.9	333.1	544.6
DQ532192.1	170729	104.2	130.0	214.5	208.3	135.5	116.1
AJ292683.1	27191	854.3	2582.6	3848.0	1132.5	2592.3	1721.2
X81958.1	2879	2357.9	3795.0	3232.3	1803.7	3142.3	2770.6
EF492942.1	249037	4839.0	6672.1	8590.6	4327.1	5929.3	6270.4
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EF516492.1	222936	1351.0	2003.5	1013.4	376.7	645.0	546.1
EU335237.1	241588	2978.0	3064.8	5264.6	3608.0	2841.9	3078.3

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o__Planctomycetales	f__Planctomycetaceae
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EU135036.1 gg_id:241400 tallgrass prarie soil clone FFCH5359
EU135064.1 gg_id:252536 tallgrass prarie soil clone FFCH11875
FJ478520.1 gg_id:513639 species richness estimates obtained nearly and simulated pyrosequencing-generated
AF234700.1 gg_id:35556 sludge clone A25
GQ356088.1 gg_id:542965 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
EF516829.1 gg_id:219667 grassland soil clone FCPN696
EU135135.1 gg_id:235394 tallgrass prarie soil clone FFCH1662
EU589315.1 gg_id:273690 China Ningxia rice paddy field soil clone 2_H12
AF234760.1 gg_id:33376 sludge clone A17
FJ232659.1 gg_id:322102 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
FJ543069.1 gg_id:531452 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
X86391.1 gg_id:2815 Pirellula sp. str. AGA/M12
GQ264007.1 gg_id:509308 Structure Simulated Level Waste Site simulated level waste site clone WC3_03
M34126.1 gg_id:2826 Pirellula staleyi
AM902592.1 gg_id:245810 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa
AJ616292.1 gg_id:107831 river biofilm clone DEL77
EU135081.1 gg_id:257073 tallgrass prarie soil clone FFCH2281
AJ252628.1 gg_id:28765 agricultural soil clone SC-I-28
AF513967.1 gg_id:62476 planctomycete clone LA4-B40N
X62911.1 gg_id:2845 Planctomyces limnophilus
GQ850548.1 gg_id:568227 surface water northern Bering Sea clone u78
AJ231186.1 gg_id:2859 Planctomyces sp. str. 248
EF019893.1 gg_id:207109 aspen rhizosphere clone Elev_16S_1259
AJ616272.1 gg_id:106693 river biofilm clone DEL30
EU236333.1 gg_id:288195 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A6
AB286452.1 gg_id:205500 Reducing production and domination comamonadaceae reducing oxygen supply was
EU703485.1 gg_id:385507 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH76
GQ264049.1 gg_id:532634 Structure Simulated Level Waste Site simulated level waste site clone WC3_146
EU135201.1 gg_id:246619 tallgrass prarie soil clone FFCH11725
EU135291.1 gg_id:243965 tallgrass prarie soil clone FFCH3333
FJ232636.1 gg_id:318175 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
GU118118.1 gg_id:577627 Threatened Corals Provide Microbial Habitats clone Apal_L16
GQ093884.1 gg_id:415267 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
DQ256391.1 gg_id:143227 Cloning and microorganism genes alkaline soil clone pGXAR2
EF580936.1 gg_id:278198 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4
GQ202636.1 gg_id:576162 RFLP two library insect-resistant trans-genic and its control soil conventional cotton
FJ232624.1 gg_id:325188 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
FJ236055.1 gg_id:356355 three Parisian treatment plants approaches drinking water clone Joinville4
AJ576406.1 gg_id:105661 midgut homogenate Pachnoda ephippiata larva clone PeM40
GQ264445.1 gg_id:591299 Structure Simulated Level Waste Site simulated level waste site clone WW3_146
AJ231185.1 gg_id:2863 Planctomyces sp. str. 423

EU135036.1	241400	1001.8	2608.0	3110.4	1117.5	3459.6	3243.0
EU135064.1	252536	4965.7	6639.9	8153.4	3992.4	5215.8	5135.7
FJ478520.1	513639	5389.2	6231.2	10739.4	4102.6	3740.7	5236.2
AF234700.1	35556	275.2	791.6	2830.5	253.9	1217.8	1566.6
GQ356088.1	542965	72.7	508.8	381.7	159.1	474.2	245.8
EF516829.1	219667	199.4	913.4	878.1	130.0	276.6	215.8
EU135135.1	235394	3478.4	3582.7	4539.2	1993.3	2931.6	2617.3
EU589315.1	273690	3811.4	4843.0	6940.9	3102.1	3260.7	3863.8
AF234760.1	33376	6098.3	6643.8	10425.5	4069.6	3952.9	5458.1
FJ232659.1	322102	663.8	1330.4	4997.5	316.9	2133.3	2215.4
FJ543069.1	531452	2873.9	3403.1	1370.1	1783.5	1428.4	1420.1
X86391.1	2815	42.3	105.7	118.1	63.7	134.7	105.5
GQ264007.1	509308	5621.9	5186.5	2971.9	584.8	1186.1	2152.9
M34126.1	2826	57.4	327.8	664.7	128.2	357.5	290.1
AM902592.1	245810	2091.6	2581.7	4783.5	2167.9	751.0	1897.1
AJ616292.1	107831	492.2	1187.0	2372.4	512.7	1063.7	774.5
EU135081.1	257073	984.9	2174.2	4482.0	1337.7	648.3	972.1
AJ252628.1	28765	113.5	649.1	1193.3	99.3	223.8	265.1
AF513967.1	62476	25.1	86.9	180.4	93.5	81.0	332.4
X62911.1	2845	144.0	349.2	200.4	87.3	211.7	111.9
GQ850548.1	568227	31.7	51.9	34.8	54.7	75.1	43.5
AJ231186.1	2859	4353.3	5287.4	2289.2	3357.2	3519.0	3262.9
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AJ616272.1	106693	516.4	909.7	576.6	292.0	463.9	657.3
EU236333.1	288195	661.7	1350.9	1547.5	1948.3	113.1	69.3
AB286452.1	205500	2403.3	2807.7	1278.5	1140.3	2512.7	2184.4
EU703485.1	385507	3372.7	5045.5	1932.4	3234.4	1579.7	2172.7
GQ264049.1	532634	1440.6	2214.6	5179.5	1004.9	4529.1	1879.2
EU135201.1	246619	1410.2	1931.2	1634.3	1027.5	605.5	829.1
EU135291.1	243965	1201.7	5130.7	7874.2	1161.7	1644.6	2213.8
FJ232636.1	318175	153.9	736.4	985.5	92.4	216.0	93.7
GU118118.1	577627	30.8	143.8	156.9	82.2	95.3	102.9
GQ093884.1	415267	2403.1	5372.4	6881.6	3751.5	5651.2	4973.9
DQ256391.1	143227	722.3	522.4	634.1	1129.9	780.0	935.8
EF580936.1	278198	83.2	694.5	1174.6	214.0	160.9	217.6
GQ202636.1	576162	5372.9	8038.7	6897.1	4059.7	5719.4	5721.8
FJ232624.1	325188	6491.1	9471.3	6363.7	4303.0	4159.4	5106.7
FJ236055.1	356355	2456.8	3548.3	3411.2	2818.8	1966.0	2653.3
AJ576406.1	105661	6683.8	9109.3	11288.1	6130.7	7098.8	6164.9
GQ264445.1	591299	318.5	748.5	1560.9	340.5	1875.3	745.2
AJ231185.1	2863	558.6	1211.0	424.2	446.8	633.3	864.9

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EU332801.1 gg_id:368930 FACS assist identification TFO present aerobic enhanced biological phosphorus remo
FJ232625.1 gg_id:337721 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
X81954.1 gg_id:2868 Planctomyces sp. str. 658
GQ487909.1 gg_id:585391 Microbial metal soil polluted heavy metals clone T1-58
DQ228417.1 gg_id:199905 microbial compositions two subglacial possible role microbes chemical weathering p
EU979049.1 gg_id:308618 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b
AJ252614.1 gg_id:46917 agricultural soil clone SC-I-11
EF157243.1 gg_id:255306 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
GQ488002.1 gg_id:533542 Microbial metal soil polluted heavy metals clone V8-4
FJ624888.1 gg_id:509799 Influence lead contamination on boreal pine forest soil clone HF_C_15
GQ994843.1 gg_id:588567 planctomycete bloom eutrophic and simulated blooms algal microcosms lake sedim
FJ542938.1 gg_id:517269 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EU491846.1 gg_id:270163 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GQ487907.1 gg_id:589189 Microbial metal soil polluted heavy metals clone T1-42
FJ437980.1 gg_id:545573 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
EU617893.1 gg_id:314251 Seasonal variation microbial Yel Sea sediment clone D13S-21
DQ815011.1 gg_id:162552 zebrafish digestive tract clone aab56g07
FJ542891.1 gg_id:521367 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
GQ263999.1 gg_id:558118 Structure Simulated Level Waste Site simulated level waste site clone WC2_93
GU183590.1 gg_id:556104 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a
GQ009454.1 gg_id:500211 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
AJ616260.1 gg_id:101336 river biofilm clone DEL04
BX294907.2 gg_id:84917 anaerobic digester clone CY0ARA056H03
AY532587.1 gg_id:102577 uranium-contaminated aquifer clone 1013-28-CG52
AY328798.1 gg_id:88168 drinking water system simulator clone DSSD101
FJ230918.1 gg_id:339412 under Level Antibiotic Selection Pressures river water clone F45
DQ395915.1 gg_id:152923 deep-sea octacoral clone ctg_CGOF043
GQ402618.1 gg_id:512701 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF589344.1 gg_id:231022 Rhodopirellula baltica str. OJF17
EF421452.1 gg_id:211974 Rhodopirellula baltica str. OJF14
EF421451.1 gg_id:215170 Rhodopirellula baltica str. OJF13
EF589343.1 gg_id:227672 Rhodopirellula baltica str. OJF16
EF012748.1 gg_id:192974 Rhodopirellula baltica str. OJF4
EF012749.1 gg_id:180732 Rhodopirellula baltica str. OJF5
EU236437.1 gg_id:297164 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg63H3
AM259894.1 gg_id:212998 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-09
EU236342.1 gg_id:295035 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2H2
FJ624356.1 gg_id:440418 Rhodopirellula sp. str. SM50
DQ640663.1 gg_id:233756 full-scale EBPR sludge clone Skagenf17
FJ624322.1 gg_id:448778 Rhodopirellula sp. str. CS14

AF029079.1	2853	65.6	142.7	185.1	157.7	131.6	150.2
EU332801.1	368930	261.8	824.3	246.3	104.9	94.9	32.9
FJ232625.1	337721	13171.9	15047.3	17188.0	12170.7	8564.7	10124.8
X81954.1	2868	245.8	563.5	1281.0	225.2	301.6	237.8
GQ487909.1	585391	115.1	588.2	725.8	156.0	680.8	870.2
DQ228417.1	199905	93.8	586.8	1025.7	126.2	548.0	598.0
EU979049.1	308618	1977.7	6397.8	5839.0	3827.5	4898.2	4377.0
AJ252614.1	46917	20.5	65.4	138.2	61.8	83.1	69.8
EF157243.1	255306	12284.9	11348.6	9476.7	11212.7	11287.9	10658.9
GQ488002.1	533542	5323.9	5320.2	6540.4	4366.8	5702.9	5968.9
FJ624888.1	509799	124.4	622.4	2182.8	472.5	870.4	890.8
GQ994843.1	588567	66.5	89.7	81.5	99.5	167.7	264.5
FJ542938.1	517269	13939.1	17602.4	14757.8	9745.3	12932.1	12211.1
EU491846.1	270163	4240.9	6181.4	8962.3	3222.5	2273.2	4529.7
GQ487907.1	589189	3183.9	3562.0	2990.9	829.6	3072.1	1719.9
FJ437980.1	545573	1957.9	5749.0	1574.6	432.0	295.6	271.2
EU617893.1	314251	78.5	127.2	28.4	54.1	59.5	16.9
DQ815011.1	162552	190.9	550.6	596.9	125.2	339.4	314.4
FJ542891.1	521367	11316.4	11806.1	11942.9	10748.8	14676.9	14637.8
GQ263999.1	558118	5909.0	7801.1	10835.1	9117.7	13841.0	13281.0
GU183590.1	556104	4916.4	6070.7	3390.8	3484.5	4341.5	4354.5
GQ009454.1	500211	66.9	206.8	178.3	75.3	58.4	15.8
AJ616260.1	101336	18.7	24.9	27.4	53.2	56.3	16.6
BX294907.2	84917	5954.3	6673.8	6740.8	5198.4	4645.9	4788.5
AY532587.1	102577	20.2	46.3	156.5	55.1	73.9	1882.6
AY328798.1	88168	210.6	459.6	624.1	160.7	346.5	221.5
FJ230918.1	339412	1244.8	4455.9	2490.9	1095.4	1611.8	1791.0
DQ395915.1	152923	11071.1	11842.0	9139.7	10996.5	11300.8	13950.6
GQ402618.1	512701	1231.3	1520.7	1469.8	179.5	951.1	818.1
EF589344.1	231022	4858.6	5594.0	4785.8	2107.5	2466.3	2487.7
EF421452.1	211974	14406.3	14386.2	9838.7	3013.9	1933.6	3225.0
EF421451.1	215170	4484.4	5136.3	5173.7	2732.5	2936.8	3404.4
EF589343.1	227672	54.0	298.3	113.0	62.6	72.5	36.2
EF012748.1	192974	6457.1	6958.0	6519.5	3962.4	4061.5	5340.8
EF012749.1	180732	3306.9	3918.7	3044.3	1071.8	1528.1	1255.4
EU236437.1	297164	3867.5	3616.4	2739.9	2655.4	3907.2	3037.4
AM259894.1	212998	287.9	802.3	352.1	167.5	414.9	457.1
EU236342.1	295035	122.5	209.9	1164.8	91.8	91.4	81.3
FJ624356.1	440418	336.6	1030.1	832.8	264.2	650.5	576.5
DQ640663.1	233756	793.7	2081.0	1957.7	559.3	640.3	460.1
FJ624322.1	448778	2097.9	2422.3	1499.0	537.1	436.9	773.6

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GU305724.1 gg_id:558514 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res
X81942.1 gg_id:2801 Pirellula sp. str. 302
EU249951.1 gg_id:245163 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co
EF157256.1 gg_id:245908 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
FJ624353.1 gg_id:418512 Rhodopirellula sp. str. SM44
DQ986201.1 gg_id:190032 Pirellula sp. OJF3
EF012750.1 gg_id:184921 Rhodopirellula baltica str. OJF6
X81939.1 gg_id:2767 Pirellula sp. str. 140
EU812984.1 gg_id:323488 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-N
DQ499312.1 gg_id:159626 acidic cave snottite biofilm clone CV73
GQ246290.1 gg_id:512628 Temporal and spatial China North Yel Sea sediments clone Sd1-9
EU246802.1 gg_id:240923 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon
AJ616261.1 gg_id:101508 river biofilm clone DEL05
AY907796.1 gg_id:136912 identification picoplankton contrasting waters Arabian Sea water clone A714001
AB294955.1 gg_id:222378 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma
GU061671.1 gg_id:549851 and function microbial mesoscale eddy perturbations South China Sea clone CE2-DC
DQ903990.1 gg_id:235788 Microbes Hawaiian Marine Sponge Suberites zeteki USA: Oahu Hawaii clone PRPR39
X81940.1 gg_id:2783 Pirellula sp. str. 516
FJ624355.1 gg_id:399640 Rhodopirellula sp. str. SM49
EF574895.1 gg_id:233369 site S25 near Coco's Island marine clone S25_1239
FJ623363.1 gg_id:583343 Efficient polyhydroxyalkanoates production waste-activated submitted process seque
FJ624354.1 gg_id:395015 Rhodopirellula sp. str. SM48
GU061406.1 gg_id:569946 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m
EU037330.2 gg_id:269075 structure landfill sediments receiving long-term augmentations wastes chromium co
X81943.1 gg_id:2800 Pirellula sp. str. 382
X81941.1 gg_id:2787 Pirellula sp. str. 158
X81945.1 gg_id:2793 Pirellula sp. str. 139
FJ624364.1 gg_id:421926 Rhodopirellula sp. str. SM23
GQ302560.1 gg_id:542353 prokaryotic sediment Shawan methods cold spring clone sw-xj213
EU703306.1 gg_id:435220 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH106
AJ431347.1 gg_id:40268 Greenland:Ikka Fjord clone
AF468237.1 gg_id:80863 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKCH2Br2-9
EU491585.1 gg_id:271404 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
FJ624347.1 gg_id:400480 Rhodopirellula baltica str. SH155 IFAM 1436
FJ205295.1 gg_id:557224 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
EU050866.1 gg_id:237562 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_87
FJ485080.1 gg_id:560755 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114
FJ197610.1 gg_id:338655 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN29a_5E_FL
GQ143793.1 gg_id:403814 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes
GQ339128.1 gg_id:517627 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
AB177200.1 gg_id:137395 seafloor methane hydrate clone ODP1230B30.13

GU305724.1	558514	4317.9	6928.4	6118.6	1693.9	1961.2	2168.8
X81942.1	2801	156.4	341.1	214.7	142.9	173.4	219.4
EU249951.1	245163	24.7	66.2	98.6	72.0	59.0	20.2
EF157256.1	245908	624.1	1831.1	1940.3	566.1	542.0	1178.8
FJ624353.1	418512	2783.1	3977.6	5000.0	2675.2	3628.9	5007.0
DQ986201.1	190032	12403.9	9119.7	3677.1	3311.3	3639.8	2705.7
EF012750.1	184921	6042.3	7249.3	6677.4	3998.9	4345.1	5383.3
X81939.1	2767	1819.9	2625.2	2192.7	778.4	752.0	1513.6
EU812984.1	323488	1183.6	2653.7	2387.1	1550.5	290.3	705.9
DQ499312.1	159626	34.9	179.6	199.9	105.2	468.9	225.4
GQ246290.1	512628	106.9	828.5	239.1	134.1	141.6	116.6
EU246802.1	240923	499.3	2577.3	1858.7	424.6	779.9	781.3
AJ616261.1	101508	140.0	267.9	1087.0	308.5	151.4	419.4
AY907796.1	136912	33.3	71.4	50.1	80.6	86.3	49.8
AB294955.1	222378	2086.1	2142.5	3944.1	1689.0	1463.6	2388.9
GU061671.1	549851	48.1	83.2	284.0	96.6	93.5	59.3
DQ903990.1	235788	4811.0	4534.8	4077.1	2174.4	2618.2	2921.1
X81940.1	2783	225.6	752.7	551.2	370.1	151.8	418.4
FJ624355.1	399640	2227.1	3616.4	5039.4	977.9	1972.4	2342.2
EF574895.1	233369	695.1	1642.7	3907.0	809.5	838.3	982.8
FJ623363.1	583343	2912.7	3898.6	4235.4	1891.5	3260.0	2660.4
FJ624354.1	395015	3800.8	7066.4	10896.0	5446.9	4138.9	6737.6
GU061406.1	569946	37.3	67.4	50.4	80.7	84.4	29.3
EU037330.2	269075	4606.8	4420.3	5269.2	3614.1	844.9	1934.8
X81943.1	2800	88.4	504.7	564.4	134.4	192.7	130.9
X81941.1	2787	32.8	136.3	26.4	52.2	54.5	32.5
X81945.1	2793	35.3	142.2	39.5	79.6	63.3	35.8
FJ624364.1	421926	8049.5	8312.9	8421.4	6387.7	7879.7	10174.7
GQ302560.1	542353	1099.2	1605.1	2846.4	1029.4	310.5	565.5
EU703306.1	435220	2104.2	3206.2	3477.1	2480.3	1607.2	3443.6
AJ431347.1	40268	290.6	426.0	985.8	154.2	496.7	1111.4
AF468237.1	80863	10805.0	10066.9	7398.2	6811.3	6506.2	8109.6
EU491585.1	271404	34.5	230.6	135.0	64.9	118.1	96.3
FJ624347.1	400480	1589.1	4425.7	3869.0	1438.9	1667.0	2794.7
FJ205295.1	557224	4018.5	4256.9	4763.2	3855.4	3479.0	2818.2
EU050866.1	237562	2650.7	5302.2	6971.4	3615.4	3525.3	5411.4
FJ485080.1	560755	1042.6	2394.0	2029.4	1912.4	1518.3	2594.8
FJ197610.1	338655	9652.5	9742.4	8196.3	5469.4	6902.3	6998.0
GQ143793.1	403814	7695.8	8264.5	7571.0	5185.3	10368.5	9428.4
GQ339128.1	517627	10976.8	12188.5	8066.5	7150.5	7462.6	6818.1
AB177200.1	137395	9106.0	8824.5	12718.8	8656.1	10783.2	10883.7

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DQ676328.1 gg_id:219735 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AY921874.1 gg_id:114298 farm soil clone AKYG1711
GU444061.1 gg_id:523807 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
DQ206406.1 gg_id:139615 microbial mediates arsenate reduction soda lake water clone ML--10
AM997881.1 gg_id:576223 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EF516155.1 gg_id:227320 grassland soil clone FCPT723
AB530247.1 gg_id:544394 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B
AF507705.1 gg_id:65683 forest soil clone S165
DQ450803.1 gg_id:161593 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura
FJ746253.1 gg_id:510156 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m
EU048670.1 gg_id:257221 and archaeal surface marine sediment Slope South China Sea clone MD2896-B10
FJ873309.1 gg_id:562253 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo
EF688380.1 gg_id:237185 soil clone F6-89
EU245970.1 gg_id:250462 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-H0
GU322886.1 gg_id:548781 Metaproteomics -temperature anaerobic granular sludge cultivated temperatures c
GQ246434.1 gg_id:594302 Temporal and spatial China North Yel Sea sediments clone Ld1-39
AY493903.1 gg_id:136324 Fingerprinting aggregates soil clone 1430
FJ264747.1 gg_id:311487 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
CU923200.1 gg_id:550970 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ246448.1 gg_id:576923 Temporal and spatial China North Yel Sea sediments clone Ld1-53
AF507704.1 gg_id:55354 forest soil clone C167
AY963300.1 gg_id:156060 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU386080.1 gg_id:262812 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
FJ479214.1 gg_id:543366 species richness estimates obtained nearly and simulated pyrosequencing-generated
U81656.2 gg_id:2794 anaerobic digestor clone vadinBA30
EF019225.1 gg_id:210216 aspen rhizosphere clone Elev_16S_394
FJ712480.1 gg_id:518323 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
FJ638603.1 gg_id:576295 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc
EU622299.1 gg_id:296920 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv
EF019958.1 gg_id:215591 aspen rhizosphere clone Elev_16S_1337
EU245568.1 gg_id:248646 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B0
EU135296.1 gg_id:244874 tallgrass prarie soil clone FFCH4400
EU135033.1 gg_id:235601 tallgrass prarie soil clone FFCH5199
EF516309.1 gg_id:223655 grassland soil clone FCPT556
EU245782.1 gg_id:251795 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-C0
FJ264744.1 gg_id:327743 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim
EU385736.1 gg_id:271883 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
AF423302.1 gg_id:35667 soil clone 96-2
EU245905.1 gg_id:258094 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-A0
DQ329791.1 gg_id:159475 Guerrero Negro hypersaline microbial mat clone 05D2Z14
EF612394.1 gg_id:255351 historic semiarid lead-zinc mine tailings site soil clone OS-C18

DQ676328.1	219735	8883.0	7470.3	7425.7	5548.8	7702.4	5366.2
AY921874.1	114298	1304.0	1400.4	1537.5	2246.5	1778.6	2329.2
GU444061.1	523807	139.0	70.4	104.0	104.8	122.0	63.8
DQ206406.1	139615	62.6	88.8	31.7	101.8	111.8	50.3
AM997881.1	576223	60.8	114.9	98.9	78.8	157.4	126.1
EF516155.1	227320	30.0	48.8	66.3	56.8	66.3	28.8
AB530247.1	544394	115.0	175.7	316.7	119.2	104.1	128.7
AF507705.1	65683	48.2	121.4	56.9	48.5	55.9	40.4
DQ450803.1	161593	31.0	42.2	32.5	57.0	62.5	84.5
FJ746253.1	510156	81.2	63.6	94.9	117.8	212.1	35.3
EU048670.1	257221	1396.8	2576.6	4230.3	1061.6	2265.2	2598.7
FJ873309.1	562253	7979.9	8348.8	9883.1	7679.1	11044.7	8379.4
EF688380.1	237185	12020.2	10922.2	9738.4	8870.1	13930.5	10972.2
EU245970.1	250462	5968.9	4950.5	8666.6	5877.7	6776.1	7259.2
GU322886.1	548781	3821.4	8139.9	8112.4	2929.0	5967.7	6785.7
GQ246434.1	594302	8669.1	8352.4	6707.3	5675.9	7719.9	7267.2
AY493903.1	136324	78.4	146.3	273.4	95.4	261.4	237.6
FJ264747.1	311487	892.4	1216.3	2686.9	1585.2	862.8	1882.1
CU923200.1	550970	13530.1	14872.5	16736.9	11259.1	13912.0	13337.1
GQ246448.1	576923	193.3	268.7	499.6	300.0	159.5	135.7
AF507704.1	55354	217.2	511.8	461.8	224.4	889.2	838.5
AY963300.1	156060	1763.6	1824.4	1246.4	318.3	764.9	488.3
EU386080.1	262812	3624.9	4282.5	4643.7	3179.2	3203.6	4425.6
FJ479214.1	543366	3007.8	751.8	2344.3	4469.7	5116.7	4717.6
U81656.2	2794	17742.8	20925.8	15473.8	13828.4	19322.2	17315.2
EF019225.1	210216	49.2	154.4	73.2	62.3	93.8	65.5
FJ712480.1	518323	5348.8	4957.2	5563.6	4679.6	2032.7	2306.4
FJ638603.1	576295	2744.5	6088.2	7338.2	2156.3	8803.8	6953.6
EU622299.1	296920	7147.7	5850.6	8353.1	4256.8	1411.7	2646.1
EF019958.1	215591	881.1	660.2	484.8	809.6	679.8	713.2
EU245568.1	248646	2397.1	1390.1	1560.8	1360.8	502.5	1107.1
EU135296.1	244874	118.9	280.6	820.3	198.1	124.8	503.9
EU135033.1	235601	557.6	610.8	522.2	227.5	203.8	125.1
EF516309.1	223655	150.7	640.8	904.3	161.6	196.1	182.3
EU245782.1	251795	5633.3	5233.6	15165.3	7772.4	9416.0	7692.2
FJ264744.1	327743	201.8	753.9	1834.7	354.3	353.4	928.9
EU385736.1	271883	5215.8	5395.8	3141.9	4830.3	3148.2	2282.3
AF423302.1	35667	429.8	975.3	727.1	1788.9	1208.1	1300.8
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EF612394.1	255351	3907.8	5511.3	3537.3	2653.7	3566.4	3668.2

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EU386028.1 gg_id:265434 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU385723.1 gg_id:262361 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
CU919054.1 gg_id:548383 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EU786130.1 gg_id:556144 cotton rhizosphere soil clone 3H-211
EF018222.1 gg_id:203959 aspen rhizosphere clone Amb_16S_572
EU385921.1 gg_id:264090 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S
EU385781.1 gg_id:268863 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
FJ485338.1 gg_id:571346 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
EF540419.1 gg_id:220924 oil-shale semi-coke solid waste clone MK11
EF032768.1 gg_id:181593 cyanobacterial mat in lava cave clone HAVOmat68
EU245501.1 gg_id:245089 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-D0
AB177155.1 gg_id:136191 seafloor methane hydrate clone ODP1230B16.23
GQ844339.1 gg_id:543377 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B5
GQ472311.1 gg_id:573896 Microbial Dongping Lake lake sediment clone 2B3-12
FJ748808.1 gg_id:585249 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estua
GQ143768.1 gg_id:454105 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes
EU386008.1 gg_id:273669 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
DQ811900.1 gg_id:163946 mangrove soil clone MSB-5C12
FJ545451.1 gg_id:508778 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-19
EU245488.1 gg_id:235811 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-B0
EF208700.1 gg_id:200413 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2
EF516637.1 gg_id:225058 grassland soil clone FCPS673
AJ292685.1 gg_id:44216 PCB-polluted soil clone WD283
FJ444683.1 gg_id:588682 Cotton Rhizosphere cotton rhizosphere clone 2y-55
GU056117.1 gg_id:554003 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein
FN563400.1 gg_id:556620 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic
EF018678.1 gg_id:211992 aspen rhizosphere clone Amb_16S_968
EF515994.1 gg_id:219383 grassland soil clone FCPT539
EU181513.1 gg_id:237389 Prokaryotic enhanced organic matter remineralization continental margin marine se
EF019563.1 gg_id:214259 aspen rhizosphere clone Elev_16S_1077
EU491712.1 gg_id:272697 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ232638.1 gg_id:347560 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
FJ712491.1 gg_id:510851 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
GQ356165.1 gg_id:573216 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
FJ478514.1 gg_id:544225 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ232658.1 gg_id:353016 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg
EU491293.1 gg_id:271990 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU135104.1 gg_id:243304 tallgrass prarie soil clone FFCH17847
EU374014.1 gg_id:271620 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
AY592336.1 gg_id:104089 deep-sea mud volcano clone Amsterdam-1B-32; BC20-1B-32
FJ203528.1 gg_id:337295 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h

EU386028.1	265434	8365.4	8247.7	10994.3	6496.8	5993.3	6315.1
EU385723.1	262361	3492.7	4418.4	5272.4	2792.1	3937.4	5110.4
CU919054.1	548383	4671.1	6816.9	6907.5	4516.4	8505.4	5983.4
EU786130.1	556144	458.3	850.2	2612.6	448.7	1663.4	995.2
EF018222.1	203959	32.1	81.0	107.7	62.4	65.9	35.3
EU385921.1	264090	36.8	37.0	41.7	73.4	95.5	33.8
EU385781.1	268863	847.6	2621.7	3166.9	1122.8	2059.7	1445.2
FJ485338.1	571346	2181.0	2335.9	5887.0	3716.7	3874.5	4337.8
EF540419.1	220924	31.4	44.1	30.9	58.4	63.6	28.4
EF032768.1	181593	14.6	31.2	52.1	45.3	59.3	26.8
EU245501.1	245089	3071.4	5150.4	5201.9	4405.7	4786.3	6062.8
AB177155.1	136191	21.3	24.4	37.8	58.0	60.9	20.3
GQ844339.1	543377	1818.8	2781.7	3407.9	1486.7	2496.3	2827.3
GQ472311.1	573896	1556.3	2420.9	3082.8	1724.2	1670.5	2981.7
FJ748808.1	585249	2550.6	2587.6	1252.6	519.0	2575.8	1539.0
GQ143768.1	454105	3508.9	3116.5	3147.2	1804.5	597.5	1647.0
EU386008.1	273669	96.6	321.7	121.9	73.1	70.5	23.2
DQ811900.1	163946	31.3	43.4	72.4	53.5	55.2	22.4
FJ545451.1	508778	7157.3	10817.8	14546.6	9141.4	10019.3	9593.8
EU245488.1	235811	5324.6	4664.5	10931.4	6677.5	4886.3	4991.5
EF208700.1	200413	73.2	109.3	183.1	143.2	93.2	60.0
EF516637.1	225058	215.5	115.6	114.4	180.0	142.4	92.3
AJ292685.1	44216	25.6	47.7	59.4	47.1	69.4	31.2
FJ444683.1	588682	6541.8	7452.6	9823.7	8204.1	7884.2	8989.7
GU056117.1	554003	1056.3	1465.7	1960.4	1808.1	2039.1	3236.1
FN563400.1	556620	678.2	2765.0	5812.0	1683.8	1346.4	1982.4
EF018678.1	211992	86.6	99.9	75.0	66.4	84.5	42.8
EF515994.1	219383	9674.5	9404.4	5024.5	6326.2	8004.7	7260.1
EU181513.1	237389	5004.3	6204.1	7326.3	5487.8	6130.6	5121.8
EF019563.1	214259	34.3	60.2	239.1	61.2	62.8	39.2
EU491712.1	272697	4144.8	5228.1	4208.4	3694.0	4364.8	5247.3
FJ232638.1	347560	2779.9	2359.0	4707.8	1858.7	2399.1	2975.7
FJ712491.1	510851	1589.7	2688.6	6557.2	1989.8	1525.4	1995.9
GQ356165.1	573216	6058.2	7541.5	8198.4	5636.4	4401.5	5114.8
FJ478514.1	544225	2295.6	7416.7	6119.6	1401.1	2024.2	2645.4
FJ232658.1	353016	2085.5	3000.0	6370.4	2813.1	1626.6	3179.8
EU491293.1	271990	3258.0	3844.3	3607.6	2384.7	7089.6	5480.6
EU135104.1	243304	942.1	2622.5	3787.3	215.3	804.5	1249.0
EU374014.1	271620	4308.7	7899.1	10869.7	4793.8	4358.7	5698.3
AY592336.1	104089	7936.0	10096.1	6990.1	2788.4	1227.5	1983.8
FJ203528.1	337295	832.1	1501.7	2105.0	424.5	1036.9	1570.5

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GU118069.1 gg_id:568055 Threatened Corals Provide Microbial Habitats clone Apal_G07
FJ712558.1 gg_id:516943 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K
GU118019.1 gg_id:592923 Threatened Corals Provide Microbial Habitats clone Apal_F10
AY913229.1 gg_id:113272 forest soil clone DUNssu001 (+1B) (OTU#209)
GU118132.1 gg_id:588256 Threatened Corals Provide Microbial Habitats clone Apal_N24
DQ289921.1 gg_id:165216 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
FJ873317.1 gg_id:512846 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo
GQ356148.1 gg_id:571807 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
FJ516887.1 gg_id:535958 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
EU843071.1 gg_id:348461 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi
FJ652501.1 gg_id:582419 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-33
AY114326.1 gg_id:71342 anoxic marine sediment clone LD1-PA40
EU491864.1 gg_id:259028 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FJ203614.1 gg_id:306565 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
FJ203304.1 gg_id:323269 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
FJ232644.1 gg_id:337297 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
DQ396219.1 gg_id:152458 deep-sea octacoral clone ctg_NISA190
EF573103.1 gg_id:229876 Coco's Island site 23 marine clone S23_1202
GQ487912.1 gg_id:578134 Microbial metal soil polluted heavy metals clone T1-103
FJ205299.1 gg_id:548823 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi
FJ203110.1 gg_id:337594 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
EU734992.1 gg_id:341990 assemblages sediment station DBSE Northern Bering Sea clone 086B35
FJ203078.1 gg_id:355875 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
GQ356114.1 gg_id:512540 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox)
AB486712.1 gg_id:589011 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC
EF123574.1 gg_id:249219 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea
EF125439.1 gg_id:179213 mangrove soil clone MSB-2E1
GQ340148.1 gg_id:586939 Prokaryotic Marathonas Reservoir Greece water column clone B07-89-BAC
AM774187.1 gg_id:278832 lineages Planctomycetes densely colonize alkaline gut soil-feeding termites (Cubiter
AB192132.1 gg_id:202625 termite gut homogenate clone M1NP1-64
AM086149.1 gg_id:149208 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone c
GU369884.1 gg_id:518971 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent
AF234735.1 gg_id:50882 sludge clone A8
EF020031.1 gg_id:216224 aspen rhizosphere clone Elev_16S_1426
CU926663.1 gg_id:535989 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
EF125452.1 gg_id:190111 mangrove soil clone MSB-2F5
GU118783.1 gg_id:558104 Threatened Corals Provide Microbial Habitats clone Mfra_K07
GQ340267.1 gg_id:579129 Prokaryotic Marathonas Reservoir Greece water column clone A08-139-BAC
AJ306767.1 gg_id:66932 DCP-dechlorinating consortium clone SHA-87
FJ203428.1 gg_id:327231 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EF516721.1 gg_id:218584 grassland soil clone FCPU585

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FJ712558.1	516943	425.2	771.6	945.2	182.2	1263.0	1060.7
GU118019.1	592923	1546.8	3148.5	2423.0	1929.5	2217.3	2073.0
AY913229.1	113272	38.3	185.0	1078.7	67.3	102.1	65.8
GU118132.1	588256	33.7	107.5	96.0	47.8	153.7	95.0
DQ289921.1	165216	3068.7	2623.1	3724.9	1675.3	1943.5	1245.0
FJ873317.1	512846	2231.9	3596.5	8786.8	1981.9	954.2	2079.5
GQ356148.1	571807	4824.4	4244.6	4512.9	7040.2	4218.4	6208.8
FJ516887.1	535958	2903.3	4645.3	4885.7	1719.4	2852.7	3659.0
EU843071.1	348461	1599.2	2986.7	7765.2	2451.8	1503.3	2749.4
FJ652501.1	582419	1751.1	3196.4	4742.1	512.7	1247.3	3873.7
AY114326.1	71342	67.6	259.6	348.3	126.4	157.8	512.4
EU491864.1	259028	1253.7	1972.1	2272.0	1475.4	549.4	1521.0
FJ203614.1	306565	74.9	108.5	159.8	87.4	148.7	1004.5
FJ203304.1	323269	2305.0	4279.6	5807.0	1236.4	2592.3	2196.4
FJ232644.1	337297	1730.1	3526.1	6315.4	2765.7	3464.4	5114.5
DQ396219.1	152458	137.1	482.3	204.5	172.6	388.3	366.1
EF573103.1	229876	443.8	1388.4	417.1	154.0	285.5	345.7
GQ487912.1	578134	1176.2	3809.4	6630.9	1775.7	3381.3	3695.4
FJ205299.1	548823	422.8	1151.6	835.3	97.1	281.5	551.9
FJ203110.1	337594	41.8	74.8	44.3	60.6	82.2	33.0
EU734992.1	341990	374.2	1061.1	2424.0	290.3	473.7	474.3
FJ203078.1	355875	8357.9	7009.3	7045.3	4318.2	3503.9	4317.7
GQ356114.1	512540	280.8	1252.3	2010.0	408.1	471.1	852.2
AB486712.1	589011	901.8	2477.7	7277.2	726.9	1959.2	3252.7
EF123574.1	249219	4140.6	6755.9	10680.2	3095.6	2501.0	4560.6
EF125439.1	179213	53.7	188.4	101.7	126.1	96.1	70.8
GQ340148.1	586939	8621.7	9266.6	10560.7	10625.5	5578.8	9995.6
AM774187.1	278832	11384.7	16168.3	17333.9	7813.0	12377.2	11454.6
AB192132.1	202625	4377.4	6789.1	9399.4	3961.6	2610.4	4070.5
AM086149.1	149208	90.3	376.7	333.3	81.1	117.4	214.4
GU369884.1	518971	8771.0	12899.9	14444.6	5977.8	8094.3	7985.9
AF234735.1	50882	287.0	734.1	614.5	156.9	434.6	213.8
EF020031.1	216224	26.5	48.4	35.6	45.0	65.5	22.1
CU926663.1	535989	3353.9	3691.9	5350.0	2700.5	836.5	1600.3
EF125452.1	190111	232.5	763.4	1158.2	141.6	658.8	745.8
GU118783.1	558104	3073.4	3435.7	4031.6	1581.5	3477.5	4378.0
GQ340267.1	579129	5563.0	11171.9	12948.7	3607.2	5184.8	5676.0
AJ306767.1	66932	50.6	113.8	260.5	72.1	200.5	311.7
FJ203428.1	327231	33.8	37.7	63.0	66.9	100.2	92.7
EF516721.1	218584	111.6	340.0	1373.1	57.3	168.6	119.4

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EU245214.1 gg_id:237911 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-B12
DQ329768.1 gg_id:201435 Guerrero Negro hypersaline microbial mat clone 02D2Z12
EU386107.1 gg_id:265536 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
DQ070794.1 gg_id:147997 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
FJ203440.1 gg_id:321503 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AB486437.1 gg_id:552968 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
GU302676.1 gg_id:533316 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c
FJ232648.1 gg_id:323064 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
EU135213.1 gg_id:244630 tallgrass prarie soil clone FFCH13721
GQ214098.1 gg_id:562881 China loess clone P818
EF540354.1 gg_id:225493 oil-shale semi-coke solid waste clone 24B_MJK
AY704401.1 gg_id:112006 oceanic crust clone FS142-21B-02
FJ232639.1 gg_id:332829 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
GU118848.1 gg_id:532921 Threatened Corals Provide Microbial Habitats clone Mfra_N03
AJ390475.1 gg_id:200304 lineages (sub)division level detected signature nucleotide-targeted recovery genes bu
DQ404806.1 gg_id:155344 contaminated sediment clone 661261
EF205581.1 gg_id:214356 among geographically regions central Tibet geothermal spring mat clone TP5
GU118276.1 gg_id:548121 Threatened Corals Provide Microbial Habitats clone Dstr_C07
FJ232651.1 gg_id:351648 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
DQ404633.1 gg_id:152343 contaminated sediment clone 656078
EF125406.1 gg_id:178940 soil naked tidal flat sediment near mangrove clone MSB-1E4
FJ203554.1 gg_id:342344 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EF208715.1 gg_id:200049 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2
DQ289931.1 gg_id:170286 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
EF208689.1 gg_id:200911 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.FC
AB240225.1 gg_id:142901 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AB270056.1 gg_id:170512 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos
AJ290182.1 gg_id:200064 and seasonal changes planctomycetales biofilms extracted river biofilm s clone DSP2!
EU381635.1 gg_id:264273 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p
EF419414.1 gg_id:204219 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6P2-75
FJ516944.1 gg_id:509690 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
FJ542842.1 gg_id:525666 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
X81948.1 gg_id:2823 Pirellula str. 670
GQ246406.1 gg_id:536385 Temporal and spatial China North Yel Sea sediments clone Ld1-11
DQ289943.1 gg_id:168811 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
EU488313.1 gg_id:555142 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
FJ232657.1 gg_id:342256 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
AY225652.1 gg_id:96259 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-38
FJ437939.1 gg_id:544528 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
DQ070834.1 gg_id:150611 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal

AF027058.1	2799	298.5	787.0	578.6	193.9	279.3	337.1
EU245214.1	237911	3842.5	5611.0	4488.5	3203.8	5222.9	5718.5
DQ329768.1	201435	1768.1	3643.3	6314.0	1395.3	2105.1	3595.9
EU386107.1	265536	623.2	1769.1	2812.7	304.8	851.2	1301.4
DQ070794.1	147997	37.8	44.4	28.1	54.1	60.5	38.6
FJ203440.1	321503	1440.5	2141.1	2296.6	650.7	930.2	2324.9
AB486437.1	552968	14342.3	12688.2	12724.3	10233.3	11020.5	11335.5
GU302676.1	533316	15531.4	18559.6	18839.6	12253.7	15833.4	14361.6
FJ232648.1	323064	3485.4	4366.9	2281.3	396.7	1424.9	1419.1
EU135213.1	244630	5781.8	6398.4	7512.5	3723.5	2816.5	3528.7
GQ214098.1	562881	12162.4	16131.9	16760.6	8266.3	10960.5	11196.5
EF540354.1	225493	328.9	1234.2	2441.3	344.8	1051.0	1191.9
AY704401.1	112006	38.4	106.7	208.8	69.7	131.1	165.0
FJ232639.1	332829	672.8	2581.2	3345.5	440.2	1522.1	1497.4
GU118848.1	532921	367.5	1296.0	1381.0	288.3	783.0	798.6
AJ390475.1	200304	97.3	243.8	1509.2	114.2	147.1	153.6
DQ404806.1	155344	970.9	1518.0	2681.6	603.9	2084.0	2189.5
EF205581.1	214356	29.8	73.4	108.6	57.1	67.3	50.3
GU118276.1	548121	3599.8	4564.8	4017.2	2522.5	2489.5	2734.5
FJ232651.1	351648	4934.4	8083.5	5909.2	4255.9	4074.8	5768.5
DQ404633.1	152343	75.3	311.6	720.9	108.1	102.0	201.4
EF125406.1	178940	872.0	1750.0	1768.0	1201.6	380.0	1406.7
FJ203554.1	342344	206.7	641.2	1514.9	148.6	404.7	494.2
EF208715.1	200049	82.1	223.0	118.6	69.6	129.6	139.1
DQ289931.1	170286	40.6	123.2	77.2	64.3	120.8	73.3
EF208689.1	200911	164.8	538.0	777.0	138.5	225.5	385.6
AB240225.1	142901	79.3	221.9	2676.9	169.0	205.4	130.4
AB270056.1	170512	31.5	74.9	60.9	53.4	57.9	48.6
AJ290182.1	200064	5387.8	10905.5	11350.9	2799.7	4673.7	5903.3
EU381635.1	264273	4742.6	4183.4	3522.6	4246.4	2680.1	3718.2
EF419414.1	204219	6112.1	6434.7	4145.2	3635.4	1014.1	3086.9
FJ516944.1	509690	3498.5	6038.1	8053.1	3709.9	3585.0	4730.6
FJ542842.1	525666	4076.6	7310.8	3902.2	3433.7	3685.8	3226.7
X81948.1	2823	1767.7	3219.8	4605.4	833.8	1972.3	1792.2
GQ246406.1	536385	2272.6	2655.3	6636.1	1651.2	993.3	1484.1
DQ289943.1	168811	31.1	68.9	110.0	45.4	87.9	31.6
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FJ232657.1	342256	4336.3	6989.7	14720.0	4690.2	3801.4	4285.1
AY225652.1	96259	391.8	953.9	372.0	659.8	362.4	433.8
FJ437939.1	544528	3719.5	5703.2	5751.9	3501.1	2777.8	3551.0
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FJ542996.1 gg_id:514874 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EU734986.1 gg_id:353483 assemblages sediment station DBSE Northern Bering Sea clone 080B24
EU491549.1 gg_id:269000 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C
FJ172792.1 gg_id:344848 Qinghai Yak Ruminal and Fungi China rumen clone RB-2C12
FJ203088.1 gg_id:312705 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
EF494313.1 gg_id:224266 Nunnock River granitic landscape clone NR.4.006
DQ984569.1 gg_id:245832 Mt. Nan-Jen soil clone IFD_124
AB355065.1 gg_id:252268 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma
EF515912.1 gg_id:217349 grassland soil clone FCPO648
AB487699.1 gg_id:588740 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0
FJ208839.1 gg_id:351437 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
GQ402727.1 gg_id:545813 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
FJ905699.1 gg_id:513469 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F13b
FJ652511.1 gg_id:586795 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-24
FJ208828.1 gg_id:315617 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge
EU621897.1 gg_id:274014 and kinetic research ammonia mixed anaerobic ammonium oxidation reactor seedec
CU920107.1 gg_id:537364 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
FJ374260.1 gg_id:359089 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu
AB234544.1 gg_id:145313 termite gut homogenate clone MgMjD-104
AB234542.1 gg_id:149255 termite gut homogenate clone MgMjR-038
EF032767.1 gg_id:178484 cyanobacterial mat in lava cave clone HAVOmat22
AB252879.1 gg_id:171614 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 018
EU881130.1 gg_id:329424 Karst region primary forest soil clone KPF200711-199
EU135304.1 gg_id:244428 tallgrass prarie soil clone FFCH773
GU119349.1 gg_id:579236 Threatened Corals Provide Microbial Habitats reef water clone Reef_L13
GQ348014.1 gg_id:555348 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EF032766.1 gg_id:189073 cyanobacterial mat in lava cave clone HAVOmat101
EU617890.1 gg_id:309328 Seasonal variation microbial Yel Sea sediment clone D13S-65
EU135137.1 gg_id:242995 tallgrass prarie soil clone FFCH15608
EU478637.1 gg_id:324136 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir
AY947993.1 gg_id:143867 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl
AJ247193.1 gg_id:25580 Asticcacaulis biprosthecium str. DSM 4723(T)
AB016610.1 gg_id:5563 Asticcacaulis excentricus str. ATCC15261
AF296688.1 gg_id:23972 Brevundimonas alba str. H12C5
FJ950569.1 gg_id:436320 Brevundimonas diminuta str. c82
EU536433.1 gg_id:281870 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213g08
FJ658350.1 gg_id:568324 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
DQ335215.1 gg_id:145289 Brevundimonas terrae str. KSL-145
EU465068.1 gg_id:294281 African elephant feces clone AFYEL_aaj67e11
FJ950592.1 gg_id:424138 Brevundimonas diminuta str. c94

CT574224.1	154335	1878.2	3463.6	5095.8	914.6	2652.0	2667.2
FJ542996.1	514874	809.6	3314.2	3502.9	463.4	666.4	953.4
EU734986.1	353483	464.4	1750.8	5160.3	620.2	2723.6	2772.8
EU491549.1	269000	1273.0	1746.4	4941.9	761.5	1237.9	3127.1
FJ172792.1	344848	3834.5	5317.2	7738.8	3898.2	5675.7	5327.2
FJ203088.1	312705	107.7	633.3	221.8	112.7	138.5	102.9
EF494313.1	224266	115.8	553.5	1238.5	138.6	359.3	727.9
DQ984569.1	245832	984.9	2353.5	4759.7	1105.5	1770.3	1564.5
AB355065.1	252268	1180.7	2937.4	3098.9	834.2	1239.1	2228.6
EF515912.1	217349	10037.1	6170.6	8342.6	7726.2	10846.7	9334.4
AB487699.1	588740	12359.3	14637.4	14120.2	8753.9	12968.6	12807.9
FJ208839.1	351437	3427.8	7594.0	7130.9	3459.9	8536.5	7070.2
GQ402727.1	545813	6397.7	8037.0	9183.7	5189.2	10080.6	8957.3
FJ905699.1	513469	1975.4	4576.6	3605.9	1618.3	1702.8	1801.7
FJ652511.1	586795	4307.1	6266.6	6303.3	7189.5	2772.6	4667.8
FJ208828.1	315617	3788.1	4618.6	5665.4	1997.8	2457.7	4394.9
EU621897.1	274014	10492.7	15098.8	8798.8	7786.3	11147.4	10034.6
CU920107.1	537364	12166.2	14443.2	13995.5	8478.9	9638.5	8031.2
FJ374260.1	359089	7300.1	7002.3	9596.7	4028.4	4088.6	4539.6
AB234544.1	145313	4758.5	5916.2	4035.8	4531.5	4697.1	5919.3
AB234542.1	149255	4117.3	4356.8	3585.0	4609.4	4041.6	3423.8
EF032767.1	178484	22.9	26.1	465.8	58.1	71.0	59.8
AB252879.1	171614	58.6	67.6	127.4	86.8	93.2	98.8
EU881130.1	329424	954.9	2018.1	2570.0	1675.8	559.8	1173.4
EU135304.1	244428	1420.1	3884.7	6034.1	1782.7	1131.4	2514.9
GU119349.1	579236	5494.8	6361.7	4096.1	3636.9	1681.9	3121.5
GQ348014.1	555348	6187.5	6978.7	4050.6	7803.8	5394.5	6014.9
EF032766.1	189073	7139.4	9584.3	7231.5	5240.2	8458.5	7534.4
EU617890.1	309328	1232.7	3052.5	1842.3	851.9	1000.8	905.0
EU135137.1	242995	2031.6	3133.9	4746.4	1693.9	3385.4	2014.9
EU478637.1	324136	10708.0	12784.4	7019.2	10492.7	14773.9	11873.2
AY947993.1	143867	1149.4	1796.1	2472.8	484.8	2180.6	3407.2
AJ247193.1	25580	7104.7	8880.8	4597.0	5341.8	17665.5	8513.2
AB016610.1	5563	2319.4	5102.4	4362.0	1228.8	11664.6	6786.0
AF296688.1	23972	5132.2	7034.4	6099.6	5434.4	11878.1	10835.3
FJ950569.1	436320	4090.7	5114.1	2884.0	4556.0	6626.2	7191.3
EU536433.1	281870	15030.8	14741.8	15445.4	13477.6	18886.6	17932.1
FJ658350.1	568324	9407.2	10833.5	9031.8	9299.0	15271.8	13641.4
DQ335215.1	145289	2485.1	4761.7	6697.1	4310.1	7366.3	10408.6
EU465068.1	294281	2889.9	4247.8	3804.4	2952.3	11134.0	8455.2
FJ950592.1	424138	1601.1	3959.8	3469.6	1548.6	7769.6	8306.9

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EU434547.1 gg_id:262017 Brevundimonas diminuta str. b76
EU465065.1 gg_id:301063 African elephant feces clone AFYEL_aaj67e08
EU434576.1 gg_id:262199 Brevundimonas diminuta str. b108
EU464720.1 gg_id:297700 Hartmann's mountain zebra feces clone AFZEB_aaj69f09
FJ658310.1 gg_id:535144 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
FJ658395.1 gg_id:540941 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
EU434570.1 gg_id:265057 Brevundimonas diminuta str. b77
EU464980.1 gg_id:290745 African elephant feces clone AFYEL_aaj66b08
DQ824709.1 gg_id:183605 human fecal clone RL185_aaj72b02
FJ657857.1 gg_id:537717 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_
EU535556.1 gg_id:284254 profile human microbiota antecubital fossa (inner elbow) skin clone nbt27b12
GQ280032.1 gg_id:588010 Brevundimonas sp. str. BJ-22
FJ658136.1 gg_id:543663 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte
EU434575.1 gg_id:258759 Brevundimonas diminuta str. b124
AB021415.1 gg_id:5595 Brevundimonas diminuta str. IAM 12691T
EU465159.1 gg_id:296763 African elephant feces clone AFYEL_aaj68h07
FN433035.1 gg_id:559314 Brevundimonas terrae CCM24B
EU434509.1 gg_id:268353 Brevundimonas diminuta str. b215
EU464952.1 gg_id:291623 African elephant feces clone AFYEL_aaj65f11
AJ244706.1 gg_id:109577 Brevundimonas mediterranea str. V4.BO.18 LMG 22801 = MM_2367
AJ244707.1 gg_id:109696 Brevundimonas mediterranea str. V4.BE.56 LMG 22802 = MM_3001
AM402981.1 gg_id:162149 Brevundimonas sp. str. JO26
AY971369.1 gg_id:115361 Brevundimonas kwangchunensis str. KSL-110
EU834791.1 gg_id:585677 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se
EF363713.1 gg_id:204302 Brevundimonas lenta str. DS-18
GU321351.1 gg_id:547657 Brevundimonas sp. str. NMC11
AM412000.1 gg_id:198378 Brevundimonas nasdae Z66zhy
AY328801.1 gg_id:90161 drinking water OR9
EF157195.1 gg_id:241110 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AY169433.1 gg_id:82124 Brevundimonas vesicularis
AJ227782.1 gg_id:5579 Brevundimonas bacteroides str. CB7
AJ227797.1 gg_id:5583 Brevundimonas sp. str. FWC40
AJ227781.1 gg_id:5611 Brevundimonas vesicularis str. LMG 11141
AY293404.1 gg_id:87601 travertine terrace Yellowstone Hot Springs clone SM2A11
EF546433.1 gg_id:219465 Brevundimonas nasdae str. P1
EU182863.1 gg_id:247068 Brachybacterium sp. str. MH35
DQ825663.1 gg_id:162728 Brevundimonas sp. str. 5420S-28
AY328842.1 gg_id:89703 drinking water MB11
AJ227786.1 gg_id:53033 Brevundimonas intermedia str. ATCC 15262(T)
EU636022.1 gg_id:278329 Antarctic str. N97
EU182890.1 gg_id:250309 Brevundimonas sp. str. MH62

EU434547.1	262017	3994.3	5453.7	5120.5	2641.4	10658.3	8810.4
EU465065.1	301063	1879.6	3583.2	3573.9	2947.4	9804.9	7657.6
EU434576.1	262199	7796.4	9649.5	8977.7	5684.0	16309.3	13091.8
EU464720.1	297700	6822.8	6836.3	5962.2	5753.1	10532.2	11915.3
FJ658310.1	535144	5739.0	6278.3	5266.8	3659.0	14014.6	10761.3
FJ658395.1	540941	6853.4	6796.7	5602.9	5109.1	13092.5	10339.0
EU434570.1	265057	9623.8	11121.5	6653.6	6785.9	15603.5	14734.1
EU464980.1	290745	5154.7	7646.0	5548.6	8493.7	11723.8	10210.5
DQ824709.1	183605	10465.5	10334.6	6969.3	11114.3	18046.7	14354.5
FJ657857.1	537717	3959.3	5587.7	5917.7	2685.8	14759.8	10046.8
EU535556.1	284254	11259.0	10356.6	5820.2	7076.4	12414.5	11519.2
GQ280032.1	588010	1666.6	4360.4	3540.7	1304.8	9869.3	7503.6
FJ658136.1	543663	7284.3	7664.5	6491.9	7246.0	11338.6	11421.2
EU434575.1	258759	3583.2	6460.4	5334.8	3577.4	9064.3	8029.7
AB021415.1	5595	8898.3	8980.1	7902.4	10193.5	14472.6	18061.4
EU465159.1	296763	7343.1	7992.7	6450.2	5649.4	14458.5	10458.1
FN433035.1	559314	846.5	2226.8	2913.5	1449.8	8083.8	6208.7
EU434509.1	268353	10310.8	12296.6	7407.0	7507.0	14374.7	12580.6
EU464952.1	291623	1475.1	2923.7	2571.7	2643.7	8157.5	6277.5
AJ244706.1	109577	517.6	1599.4	1780.0	409.3	7761.2	4610.6
AJ244707.1	109696	271.3	1328.5	1671.6	370.5	2935.9	2859.1
AM402981.1	162149	356.3	590.2	565.3	515.6	2460.2	2004.9
AY971369.1	115361	5166.4	6874.6	5873.9	6987.3	11909.9	10542.7
EU834791.1	585677	5975.1	5284.3	6907.8	5363.3	14619.1	10869.3
EF363713.1	204302	2569.9	3181.8	2990.5	2412.9	8611.7	10822.2
GU321351.1	547657	4600.4	7077.8	4290.5	3367.5	6782.5	8312.4
AM412000.1	198378	1667.3	3164.9	1497.1	2142.7	9943.2	8540.1
AY328801.1	90161	15312.6	14456.9	9810.2	10427.7	19518.6	14866.7
EF157195.1	241110	2930.5	4120.7	3686.8	3291.5	10735.2	8256.1
AY169433.1	82124	7063.8	10032.1	8514.2	7478.3	18399.7	12494.1
AJ227782.1	5579	7031.0	8276.0	6038.6	5398.2	13619.1	9035.5
AJ227797.1	5583	2326.1	3533.7	2623.4	572.6	9996.0	7250.0
AJ227781.1	5611	717.4	2442.9	2502.1	694.2	10194.5	6854.4
AY293404.1	87601	1837.0	2363.5	2761.3	881.1	7103.7	7147.8
EF546433.1	219465	5722.0	5788.2	3365.4	3783.5	9515.3	7428.0
EU182863.1	247068	2430.5	2660.8	3337.7	1761.2	6552.2	6968.1
DQ825663.1	162728	1228.5	2556.8	1544.6	465.6	8281.3	5303.3
AY328842.1	89703	845.4	2132.7	1235.2	430.6	8774.8	5505.4
AJ227786.1	53033	561.5	1890.1	1267.4	414.9	8262.6	5498.7
EU636022.1	278329	2375.1	3471.9	4472.0	1957.4	10422.6	9576.2
EU182890.1	250309	969.3	2830.6	1342.9	514.7	8495.2	5642.1

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EU143355.1 gg_id:238339 Brevundimonas sp. str. J22
EU580513.1 gg_id:543062 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret
AJ007808.1 gg_id:5626 Brevundimonas variabilis str. ACM 5107 (T)
AB426562.1 gg_id:270554 Brevundimonas sp. str. HINF004
DQ372984.1 gg_id:152214 Brevundimonas sp. str. EMB102
AY328835.1 gg_id:89630 drinking water MA26
EU379308.1 gg_id:274963 Brevundimonas intermedia str. 6R-J-7d
AJ007802.1 gg_id:5568 Brevundimonas intermedia str. ACM 2608 (T)
AJ227784.1 gg_id:5617 Brevundimonas subvibrioides str. CB81
AJ495803.1 gg_id:63466 Brevundimonas sp. p22P
AJ227783.1 gg_id:43186 Brevundimonas variabilis str. ATCC 15255 (T)
EU434579.1 gg_id:266190 Brevundimonas aurantiaca str. e12
AM183353.1 gg_id:167639 Brevundimonas sp. 1228-1II
AB447548.1 gg_id:316703 Brevundimonas sp. str. SUWAF011
DQ981459.1 gg_id:203778 Brevundimonas sp. SB4
DQ442520.1 gg_id:191932 Streptomyces longisporoflavus str. NRRL ISP-5165T
FN397631.1 gg_id:452397 Brevundimonas sp. str. CM 272
DQ413152.1 gg_id:152156 Brevundimonas sp. str. EMB 68
AJ007803.1 gg_id:5518 Caulobacter fusiformis str. ACM 5108 (T)
AB008533.1 gg_id:5557 Caulobacter fusiformis str. ATCC15257
AJ007805.1 gg_id:5560 Caulobacter henricii str. ACM 5105 (T)
AE005673.1 gg_id:209341 Caulobacter crescentus str. CB15
AM921622.1 gg_id:248395 Caulobacter henricii PhyCEm-80
EF515958.1 gg_id:221595 grassland soil clone FCPT664
DQ124680.1 gg_id:154386 Caulobacter tundrae str. Z-0024
AF523036.1 gg_id:89365 natural mineral water clone D-1
EU730905.1 gg_id:352383 Caulobacter vibrioides str. 156
DQ532299.1 gg_id:164042 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
AY512823.1 gg_id:106146 Caulobacter vibrioides str. S13
AB271055.1 gg_id:165771 Caulobacter ginsengisoli str. Gsoil 317
AM940947.1 gg_id:278226 Caulobacter sp. ECN-2008
DQ404656.1 gg_id:151101 contaminated sediment clone 654987
GQ396801.1 gg_id:538121 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
FN556568.1 gg_id:518192 Brevundimonas sp. str. JW23.4a
EU434505.1 gg_id:263790 Brevundimonas bullata str. b350
DQ501309.1 gg_id:199553 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw
AY234477.1 gg_id:112129 soil isolate Ellin5060
FJ197848.1 gg_id:313604 Brevundimonas sp. 39(2008) str. 39
AJ717391.1 gg_id:111099 Phenylobacterium falsum str. AC49
AJ582031.1 gg_id:93768 soil near uranium mill tailings clone JG36-GS-63
AY921824.1 gg_id:114202 farm soil clone AKYG696

EU143355.1	238339	1611.7	2745.1	3589.3	1244.5	14665.0	10488.1
EU580513.1	543062	5515.0	6102.0	5103.6	3931.7	16599.1	10443.1
AJ007808.1	5626	4214.9	3891.0	4863.8	4088.8	7078.9	6674.2
AB426562.1	270554	1886.7	3519.5	3922.3	1880.7	7148.0	7531.0
DQ372984.1	152214	757.3	2529.9	2374.0	584.7	7576.7	4526.7
AY328835.1	89630	2900.4	4082.7	4042.2	1443.9	13577.0	7023.2
EU379308.1	274963	548.2	2011.2	1232.4	446.2	10590.6	6066.7
AJ007802.1	5568	4902.9	4928.4	2328.5	5331.9	11747.4	10473.2
AJ227784.1	5617	802.5	1582.6	2358.6	456.5	9173.2	5772.9
AJ495803.1	63466	11194.4	11521.8	10407.9	9472.6	18134.7	14418.2
AJ227783.1	43186	872.1	1674.8	1755.7	865.3	6880.4	4677.9
EU434579.1	266190	1348.9	2986.4	2858.4	1479.3	13114.9	8500.1
AM183353.1	167639	7008.4	7671.3	5237.8	7600.4	18257.2	12951.4
AB447548.1	316703	3548.1	5796.3	7411.3	3695.3	10717.0	11288.5
DQ981459.1	203778	763.5	2064.8	4510.9	865.7	20001.3	11411.2
DQ442520.1	191932	1548.5	3228.0	4585.8	2065.8	16930.6	9866.6
FN397631.1	452397	3958.8	6527.4	2254.8	1164.0	5934.1	5455.3
DQ413152.1	152156	2789.1	3703.6	4651.3	2980.1	12743.0	9973.1
AJ007803.1	5518	8177.9	9529.8	6305.5	7506.4	17681.4	11617.2
AB008533.1	5557	4871.2	6974.2	10515.6	3310.1	19539.6	12497.0
AJ007805.1	5560	4159.4	4570.8	4807.3	3732.0	16463.7	9170.3
AE005673.1	209341	1470.6	2132.7	2741.5	789.2	24971.3	4126.2
AM921622.1	248395	3005.8	5396.5	3103.3	2868.8	20220.8	7957.0
EF515958.1	221595	1372.1	2779.8	5010.0	1798.8	18259.6	10468.4
DQ124680.1	154386	643.6	1655.0	2251.9	549.5	22589.7	3436.6
AF523036.1	89365	6382.4	7644.0	11760.4	5241.0	16129.8	12770.2
EU730905.1	352383	761.6	1458.1	1835.7	691.9	22588.1	2997.8
DQ532299.1	164042	762.6	1904.2	3492.8	787.2	11119.0	3548.9
AY512823.1	106146	5898.6	7158.4	4474.6	5370.9	21685.9	7933.6
AB271055.1	165771	6373.5	6388.1	8629.4	5194.0	14484.5	9779.4
AM940947.1	278226	7084.3	7699.8	9823.1	6917.5	16641.8	12257.2
DQ404656.1	151101	893.2	622.4	688.2	1183.4	4583.7	1724.6
GQ396801.1	538121	2277.6	3835.3	4149.3	2484.0	13169.6	7947.3
FN556568.1	518192	1529.6	2134.1	2788.5	2417.6	5818.1	6431.0
EU434505.1	263790	753.5	2296.1	2785.7	746.6	7967.9	5053.3
DQ501309.1	199553	1934.8	3236.6	4078.4	2266.2	16792.2	9166.7
AY234477.1	112129	4532.1	5327.7	3326.3	5052.3	9353.8	6347.8
FJ197848.1	313604	7888.7	9807.2	13398.4	7116.0	25053.0	16437.7
AJ717391.1	111099	498.2	876.4	986.3	1188.7	2218.5	3078.3
AJ582031.1	93768	7068.8	8315.7	8227.4	5817.9	9312.5	9537.4
AY921824.1	114202	5087.8	6060.5	6561.4	5901.8	14271.2	7860.2

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GQ002488.1 gg_id:507172 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
AJ292592.1 gg_id:49162 PCB-polluted soil clone WD225
DQ202243.1 gg_id:140164 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo
GQ402724.1 gg_id:551851 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AB473899.1 gg_id:554330 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim
D49422.1 gg_id:5594 Brevundimonas diminuta str. IFO 3140
DQ984595.1 gg_id:240075 Mt. Nan-Jen litterfall clone IYF98
GQ402558.1 gg_id:592079 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ177484.1 gg_id:139814 Brevundimonas sp. str. Tibet-IK73
EF516954.1 gg_id:226283 grassland soil clone FCPT726
AJ292595.1 gg_id:30983 PCB-polluted soil clone WD233
AF289151.1 gg_id:70005 freshwater clone PRD01a003B
EU730914.1 gg_id:335822 Brevundimonas diminuta str. 207
EU445215.1 gg_id:565413 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R36
GU118509.1 gg_id:573233 Threatened Corals Provide Microbial Habitats clone Gven_K20
DQ532251.1 gg_id:168212 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C
GU169058.1 gg_id:570254 Biofilms formed on substances: response f conditions and carbon concentrations sy
FJ979845.1 gg_id:402409 Caulobacter sp. str. tsz12
AM697237.1 gg_id:227434 sequencing libraries indoor dust clone BF0001C078
AY922007.1 gg_id:113237 farm soil clone AKYG412
GU118288.1 gg_id:568445 Threatened Corals Provide Microbial Habitats clone Dstr_G22
GQ402816.1 gg_id:589382 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EU202832.1 gg_id:317304 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU434454.1 gg_id:264269 Brevundimonas diminuta str. a229
DQ177483.1 gg_id:140010 Brevundimonas sp. str. Tibet-IK53
GU118656.1 gg_id:575957 Threatened Corals Provide Microbial Habitats clone Mfav_J15
DQ532201.1 gg_id:171288 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C
EU881329.1 gg_id:324088 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone K
EF520395.1 gg_id:235185 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-51
EU784736.1 gg_id:336351 Brevundimonas sp. str. E8
AY569007.1 gg_id:103285 Nitrobacteria hamadaniensis str. 104
AB167225.1 gg_id:107935 Brevundimonas diminuta str. c66
EF520409.1 gg_id:231965 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-54
GQ402771.1 gg_id:587634 Accessing microbial biodiversity and metabolic potential tropical -based approach p
GU118170.1 gg_id:560087 Threatened Corals Provide Microbial Habitats clone Dstr_P10
AB473919.1 gg_id:573162 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim
EU665093.1 gg_id:547599 Soil are Changed Agricultural Practices agricultural soil clone Plot22-C12
AB374373.1 gg_id:272478 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss
AB167229.1 gg_id:107937 Brevundimonas diminuta str. c79
AY734246.1 gg_id:133283 spring water of alpine karst aquifer clone SDKAS1_2
DQ167245.1 gg_id:138986 Kopriimonas byunsanensis str. KOPRI 13522

GQ002488.1	507172	8341.5	7356.2	3844.2	6207.5	12954.0	10223.1
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DQ202243.1	140164	1379.0	1545.2	3575.7	1604.0	15794.0	8547.2
GQ402724.1	551851	1472.6	2598.5	2864.1	2046.1	12228.2	11428.4
AB473899.1	554330	458.0	1215.3	2716.7	483.8	7999.3	3170.3
D49422.1	5594	2997.8	4724.1	3769.0	3360.8	7881.5	8617.0
DQ984595.1	240075	659.5	1281.0	1679.0	1763.8	5271.8	3524.0
GQ402558.1	592079	4123.8	4752.2	5268.2	4270.6	13997.2	9525.6
DQ177484.1	139814	4391.8	6274.1	3480.9	4370.3	11212.3	8683.1
EF516954.1	226283	226.5	862.5	614.6	226.4	3093.9	1858.8
AJ292595.1	30983	37.6	112.7	133.8	102.0	491.8	803.7
AF289151.1	70005	118.9	225.7	1622.6	161.5	314.0	519.5
EU730914.1	335822	4418.5	4256.1	3958.6	3147.8	6756.1	5995.7
EU445215.1	565413	3812.2	5084.7	5048.8	5757.7	19504.6	7835.3
GU118509.1	573233	5053.8	8243.4	4615.1	4281.8	15790.4	12963.0
DQ532251.1	168212	1166.7	1155.8	4984.5	2251.8	6397.9	12508.4
GU169058.1	570254	7413.0	8859.2	6126.5	6785.8	17808.8	12522.4
FJ979845.1	402409	5408.8	5342.8	4207.5	3642.8	16445.8	9788.1
AM697237.1	227434	613.3	1169.6	3302.5	1088.6	8151.6	10295.1
AY922007.1	113237	2887.3	4221.4	7497.7	4017.2	13258.0	14640.6
GU118288.1	568445	15869.7	15973.2	12542.4	15067.1	27775.0	21414.4
GQ402816.1	589382	1778.9	2981.4	3372.5	1816.9	9684.6	8757.9
EU202832.1	317304	2263.1	3841.0	3162.7	2107.7	16553.2	3302.5
EU434454.1	264269	1022.1	1995.2	1235.2	782.2	11615.4	7561.0
DQ177483.1	140010	5465.0	6202.5	6917.0	4243.5	10341.7	9250.9
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DQ532201.1	171288	97.0	175.8	548.5	137.0	606.1	929.6
EU881329.1	324088	5432.6	5749.2	4030.1	5183.0	13675.0	10718.0
EF520395.1	235185	2600.5	4085.1	5028.6	2998.4	15119.1	12560.3
EU784736.1	336351	2836.1	5680.1	4825.5	1535.3	14037.7	7224.4
AY569007.1	103285	1750.2	2524.7	4129.0	3117.0	10278.5	9830.8
AB167225.1	107935	1500.1	3556.2	1447.2	895.4	5057.1	4139.1
EF520409.1	231965	7555.8	8212.2	9766.6	7714.3	13549.8	11315.6
GQ402771.1	587634	1079.7	2177.1	2862.0	1009.0	11503.9	6342.2
GU118170.1	560087	8280.8	9104.5	8774.0	7799.4	20456.6	17238.0
AB473919.1	573162	845.2	1508.9	3932.6	777.5	6845.2	5022.0
EU665093.1	547599	147.4	210.4	137.4	66.0	1108.9	179.5
AB374373.1	272478	8973.7	9356.1	9910.0	7810.1	15002.7	12252.4
AB167229.1	107937	1291.0	3252.8	2975.6	1690.8	2688.5	3940.4
AY734246.1	133283	611.7	1149.9	1104.9	396.6	4127.9	3630.0
DQ167245.1	138986	23.2	39.0	31.7	80.8	176.4	303.5

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FJ210804.1 gg_id:346096 Thalassospira sp. str. QDHT-08
AB373113.1 gg_id:277271 Thalassospira sp. str. N5EA13-1A
AB373114.1 gg_id:265832 Thalassospira sp. str. G12-1
AF358664.1 gg_id:35557 Thalassospira lucentensis
FJ202650.1 gg_id:316411 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AB006768.1 gg_id:4594 Terasakiella pusilla str. IFO13613
AY922191.1 gg_id:112927 whalefall clone 131616
EF092208.1 gg_id:260078 Persistent Axinella corrugata clone Ax36_F7
AJ633974.1 gg_id:114828 host's accessory nidamental gland clone 6ANG531
EF629835.1 gg_id:258350 Changes marine Mycale laxissima on transfer aqua sponge tissue
AY922227.1 gg_id:113991 whalefall clone 131732
GQ169074.1 gg_id:592716 Thalassospira lucentensis str. TVGB18
AY162078.1 gg_id:135758 Cultivating Sargasso Sea clone GMD37B4
EU880514.1 gg_id:352101 Thalassospira lucentensis str. P44
FJ952806.1 gg_id:399348 Thalassospira sp. str. 2ta2
AF143826.1 gg_id:25696 hydrocarbon-degrading consortium clone 4-Org1-58
GU118853.1 gg_id:541338 Threatened Corals Provide Microbial Habitats clone Mfra_C21
EU268103.1 gg_id:254391 summer Dalian and Liaodong bay determined sea water clone L0603
AY682384.1 gg_id:100730 Parvulomonas gwangyangensis str. GW14-5
DQ917818.1 gg_id:221237 Microbial profiles bleached and wild-type Muricea elongata Kordiimonas clone BME
GU119022.1 gg_id:554110 Threatened Corals Provide Microbial Habitats clone Past_K19
EU287361.1 gg_id:252140 Pacific arctic surface sediment clone S26-61
AB537162.1 gg_id:517870 Preparation single species magnetotactic multiple-displacement sediment water we
X81185.1 gg_id:11274 magnetic coccus MP17 str. TB24
X61607.1 gg_id:11262 magnetic coccus MP17
AAAN03000028.1 gg_id:130031 Magnetococcus sp. str. MC-1
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EF371486.1 gg_id:214607 magnetotactic China Jiaozhou Bay clone M-40
EF379386.1 gg_id:211078 magnetotactic China Jiaozhou Bay clone XSE-4
AJ863157.1 gg_id:111324 marine microcosm clone CF24
GQ468519.1 gg_id:540513 Temporal variation magnetotactic two freshwater microcosms fresh water sedimen
Y13213.1 gg_id:11268 magnetic coccus MP17 str. pa19
AJ863155.1 gg_id:109702 freshwater microcosm clone CF22
Y13210.1 gg_id:11281 Magnetic strain clone rj517
X81184.1 gg_id:11271 magnetic coccus MP17 str. CS981
X81182.1 gg_id:11270 magnetic coccus MP17 str. CS92
EU570899.1 gg_id:543851 transition and zone within near-shore anoxic basin: Nitinat Lake depth 13 m clone Ni
EF370485.1 gg_id:205086 Morphology and wild type magnetotactic Miyun reservoir near Beijing China fresh w
EF371485.1 gg_id:212269 magnetotactic China Jiaozhou Bay clone M-52

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EF437150.1	208597	6056.9	5445.1	6292.2	7041.4	5483.8	7070.6
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AB373113.1	277271	5828.5	7212.4	7596.3	9251.6	10316.9	13101.0
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AF358664.1	35557	10465.3	13171.8	10373.7	8400.4	11383.9	10690.6
FJ202650.1	316411	609.1	856.8	882.5	1187.3	7301.6	2097.1
AB006768.1	4594	62.3	123.0	183.2	64.9	770.9	472.5
AY922191.1	112927	781.8	721.5	897.8	1516.1	1436.7	822.6
EF092208.1	260078	4605.8	4223.6	4824.1	7168.1	5611.2	5201.8
AJ633974.1	114828	1458.6	1238.1	1170.1	6066.0	2435.7	6076.9
EF629835.1	258350	2904.3	2108.4	1778.8	2252.4	9072.0	4938.8
AY922227.1	113991	49.9	71.7	73.3	103.5	119.5	102.0
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AY162078.1	135758	4281.2	4220.9	4665.9	4657.2	6283.5	4650.6
EU880514.1	352101	1102.9	1101.6	1208.9	1529.6	2561.5	3499.2
FJ952806.1	399348	2958.5	3801.4	2858.2	3310.6	9237.5	3876.1
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EU268103.1	254391	1622.6	2422.9	2520.6	1297.5	3710.4	4488.6
AY682384.1	100730	99.6	160.4	93.5	239.1	148.5	87.3
DQ917818.1	221237	216.1	526.9	2438.3	807.2	3468.4	1565.4
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AB537162.1	517870	572.2	1233.8	2466.5	1118.9	2325.8	1898.4
X81185.1	11274	2327.3	1242.4	1484.5	2610.7	1045.5	1233.1
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EF371486.1	214607	698.7	509.5	2852.1	1469.5	3271.0	2319.3
EF379386.1	211078	1055.3	1722.7	5224.1	1055.0	4670.2	4253.4
AJ863157.1	111324	144.8	202.4	361.4	190.0	251.5	182.7
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Y13213.1	11268	1263.2	969.0	535.3	298.7	832.1	673.6
AJ863155.1	109702	51.8	85.5	72.9	104.4	83.2	33.7
Y13210.1	11281	1320.7	1832.1	4381.0	3697.2	2923.9	4461.4
X81184.1	11271	9229.0	10619.4	9195.5	9427.9	10894.6	8863.4
X81182.1	11270	81.8	222.2	120.3	120.8	250.1	213.4
EU570899.1	543851	7277.6	7934.9	4521.9	6927.8	7636.4	5026.5
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Y13212.1 gg_id:11267 magnetic coccus MP17 str. pa11
GQ468507.1 gg_id:593515 Temporal variation magnetotactic two freshwater microcosms fresh water sedimen
AY328711.1 gg_id:88630 drinking water system simulator clone DSSD12
GQ500720.1 gg_id:561524 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa
AF544015.1 gg_id:111917 Parvularcula bermudensis str. HTCC2503
AY625140.1 gg_id:104892 perchloroethylene-contaminated ground water clone I-6
AM934846.1 gg_id:544221 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FM242322.1 gg_id:318593 sequences sediment clone 63 T9d-oil
EF530680.1 gg_id:226147 Extremely acidic pendulous biofilms Frasassi cave system Italy microbial biofilm clone
AY193164.1 gg_id:80157 marine tidal mat clone BTM11
GU370118.1 gg_id:530853 Rhodovulum sulfidophilum str. P721(3)
EF173322.1 gg_id:185425 Sinorhizobium sp. MKI8
EU544515.1 gg_id:272510 Aurantimonas altamirensis str. IFP14.1
EU442518.1 gg_id:275257 Aurantimonas altamirensis str. NML 070722 LSPQ no. ID089387
EF512716.1 gg_id:218585 Aurantimonas coralicida str. JL661
AY178863.1 gg_id:77748 Fulvimarina litoralis str. HTCC2156
AJ508755.1 gg_id:110301 marine str. V4.MO.18
AJ508754.1 gg_id:110412 marine str. V4.MO.17
EF423363.1 gg_id:206636 Aurantimonas sp. str. N1
EF373540.1 gg_id:206133 Aurantimonas kwangyangensis str. CW5
AY178861.1 gg_id:77696 Fulvimarina pelagi str. HTCC2615
GQ009485.1 gg_id:500180 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
AM746691.1 gg_id:241968 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A13
FJ357425.1 gg_id:363192 Aurantimonas sp. str. YIM J01
FM872739.1 gg_id:365130 occupant source house floor dust clone FB01C04
EF489025.1 gg_id:221997 Bacillus sp. str. HB01085
FM872541.1 gg_id:368575 occupant source house floor dust clone FA01H06
FN421693.1 gg_id:536202 proteogenomics physiology phyllosphere soybean clone 3_E11
GQ115503.1 gg_id:421082 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686f02
AB257635.1 gg_id:262792 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov
GQ009554.1 gg_id:500111 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
DQ883810.1 gg_id:164020 Aerobacter ureolyica str. 5715S-12
Z70003.1 gg_id:5472 Bartonella bacilliformis str. LA6.3
X89208.1 gg_id:5476 Bartonella sp str. ATCC 51734
AB246808.1 gg_id:149483 Bartonella elizabethae str. Q-4
AB246801.2 gg_id:147120 Bartonella elizabethae str. R-5
AB440632.1 gg_id:338719 Bartonella sp. str. Fuji 18-1
AB242293.1 gg_id:141840 Bartonella sp. str. Fuji 12-1

X81183.1	11265	66.9	131.4	147.2	198.6	243.7	159.1
EF371491.1	209788	4531.0	5010.6	4305.9	6478.1	5655.2	4440.3
Y13208.1	11266	1333.8	2109.0	619.6	194.1	1331.1	1978.1
Y13212.1	11267	10023.5	10001.5	6876.3	8453.3	7267.5	8293.1
GQ468507.1	593515	7697.9	8570.1	4944.0	6382.9	6510.8	7776.1
AY328711.1	88630	223.7	418.3	774.8	416.0	234.8	671.9
GQ500720.1	561524	1861.5	3069.0	3732.9	991.1	4301.4	3768.9
AF544015.1	111917	3825.8	6415.2	8357.4	6210.4	6943.8	6505.4
AY625140.1	104892	5333.2	3746.0	4443.6	5171.1	5191.2	5769.9
AM934846.1	544221	1786.1	2284.7	2390.9	2295.4	6327.9	4889.6
FM242322.1	318593	1335.0	2321.7	668.5	1494.3	4279.3	2259.5
EF530680.1	226147	707.3	1380.1	8039.8	909.2	6126.0	7453.8
AY193164.1	80157	224.5	731.9	1473.5	582.0	3272.5	3070.0
GU370118.1	530853	5064.5	3766.6	5753.3	4780.7	3464.7	4692.6
EF173322.1	185425	191.7	628.9	1355.0	302.2	512.2	1079.3
EU544515.1	272510	5438.4	8847.6	8988.3	6395.3	10148.4	12728.7
EU442518.1	275257	3328.3	5259.7	4034.5	4034.0	5817.2	6432.1
EF512716.1	218585	416.9	986.8	1005.6	362.7	1604.1	2885.8
AY178863.1	77748	1362.1	2601.7	3412.5	1119.7	2667.0	4249.4
AJ508755.1	110301	1344.8	1856.4	3130.5	2216.9	4248.4	5536.6
AJ508754.1	110412	5280.4	5917.2	4074.8	8588.9	11164.7	12402.5
EF423363.1	206636	4499.1	4859.8	2368.1	3054.2	11009.2	8612.5
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AY178861.1	77696	1951.3	2991.2	5680.1	3986.5	7880.8	7135.7
GQ009485.1	500180	2668.7	3807.4	3816.9	1363.4	3557.8	2460.3
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EF489025.1	221997	2227.1	3519.9	3868.9	2497.7	8420.5	3930.3
FM872541.1	368575	466.3	725.8	2360.1	459.0	5549.8	2187.3
FN421693.1	536202	2296.1	3897.2	3409.9	1611.0	8845.0	5445.3
GQ115503.1	421082	423.3	971.6	1137.6	346.8	1427.9	2411.7
AB257635.1	262792	5539.1	8331.2	7503.4	4793.2	15265.6	12244.3
GQ009554.1	500111	3332.6	4712.2	3867.5	2237.8	7121.9	4815.5
DQ883810.1	164020	629.1	1801.2	1264.2	331.3	2757.9	3673.7
Z70003.1	5472	2755.3	3555.7	4133.2	1646.7	9772.4	4698.3
X89208.1	5476	1129.1	1879.4	2587.2	1306.6	6488.1	5692.3
AB246808.1	149483	21129.7	24081.3	16614.3	17566.1	20442.4	19750.3
AB246801.2	147120	1854.9	4377.0	5719.0	2859.5	9993.6	9061.8
AB440632.1	338719	2921.7	6780.0	4900.8	2869.0	9419.0	6393.5
AB242293.1	141840	1380.0	2674.9	3629.4	2411.6	5743.7	4963.7

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AB426635.1 gg_id:259103 Bartonella grahamii str. Cg4263alb
AB426630.1 gg_id:276614 Bartonella grahamii str. Hokkaido 48-1
AB529507.1 gg_id:594215 Bartonella grahamii str. cg147up
AB529498.1 gg_id:578474 Bartonella grahamii str. Korea 4-1
AY513504.1 gg_id:103693 Bartonella henselae str. 882_ANT5
U87831.1 gg_id:5492 aortic heart valve patient with endocarditis clone v9
Z11684.1 gg_id:5473 Bartonella henselae str. BA-TF
EU111755.1 gg_id:273803 Bartonella queenslandensis str. AUST/NH5
EU111749.1 gg_id:270242 Bartonella rattiaustraliensis str. AUST/NH4
EU111754.1 gg_id:263406 Bartonella queenslandensis str. AUST/NH12
NC_005955.1 gg_id:129029 Bartonella quintana str. Toulouse
AJ278187.1 gg_id:25998 Bartonella schoenbuchensis str. R1
AB519061.1 gg_id:550137 Bartonella washoensis str. DR1-1
AB519065.1 gg_id:548080 Bartonella washoensis str. SR25-1
AB519062.1 gg_id:548956 Bartonella washoensis str. DR3-1
EF682085.1 gg_id:331242 'Candidatus rudakovii' detected voles Western Siberia Candidatus Bartonella rudakov
AF293389.1 gg_id:49049 Bartonella capreoli str. IBS 193
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EU294521.1 gg_id:244723 Bartonella volans str. FSq-1
Z70001.1 gg_id:5501 Bartonella sp str. R-phy2
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AB292597.1 gg_id:211030 Bartonella washoensis str. Sb944nv
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EU111759.1 gg_id:268319 Bartonella coopersplainensis str. AUST/NH20
AF204274.1 gg_id:46747 Bartonella birtlesii str. 325
X89110.1 gg_id:5486 Wolbachia melophagi str. MO6
Z70004.1 gg_id:5484 Bartonella sp str. C7rat
DQ645425.1 gg_id:161188 Bartonella henselae str. M7SHD
AY370186.1 gg_id:103856 ground up bee tissues clone pAJ208
Z70006.1 gg_id:5498 Bartonella sp str. C1phy
EU111752.1 gg_id:260102 Bartonella rattiaustraliensis str. AUST/NH14
AY515119.1 gg_id:100507 Bartonella phoceensis str. 16120
NR_029368.1 gg_id:541643 Bartonella doshiae str. R18; NCTC 12862
AY254309.1 gg_id:104973 Bartonella chomelii
L01260.1 gg_id:5502 Bartonella elizabethae
DQ538394.1 gg_id:227943 Bartonella australis str. Aust/NH1
AY515118.1 gg_id:100352 Bartonella rattimassiliensis str. 16115
AJ002139.1 gg_id:5462 Bartonella alsatica str. 382
NR_029366.1 gg_id:571234 Bartonella grahamii str. V2; NCTC 12860

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AB426630.1	276614	593.6	1575.5	1787.6	685.3	3130.5	3679.4
AB529507.1	594215	498.5	1194.9	1433.4	402.6	2196.0	2664.0
AB529498.1	578474	438.1	1029.3	1151.7	413.2	1876.4	2388.6
AY513504.1	103693	4188.1	5956.0	6672.1	3787.3	11773.3	9205.5
U87831.1	5492	2152.2	2073.7	555.3	2258.8	1910.4	2318.7
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AB519061.1	550137	1631.0	2734.7	3640.9	1848.8	6278.4	6623.9
AB519065.1	548080	991.0	1817.0	1406.6	877.4	4473.2	5416.6
AB519062.1	548956	4118.6	4451.7	3672.4	4349.1	9012.8	10461.9
EF682085.1	331242	1856.4	3876.9	3108.5	1682.8	9764.5	8379.0
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FJ177634.1	353598	3145.0	4123.4	4989.5	2969.0	9474.0	7805.2
EU294521.1	244723	1463.4	3512.5	5247.0	1523.5	8110.1	9647.0
Z70001.1	5501	1540.9	2835.0	3172.4	2088.7	8833.7	7266.4
EF616480.1	249397	2140.0	3988.9	4720.7	3560.5	12009.7	10217.2
AB292597.1	211030	338.2	1367.9	1635.2	491.6	3139.2	7192.4
Z70005.1	5475	1155.3	2173.3	2787.6	1607.3	5405.8	4993.4
Z70008.1	5483	2347.9	4664.4	7423.6	3240.4	11993.2	8233.7
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AF204274.1	46747	1050.3	2983.0	3008.6	1421.4	5789.9	5737.3
X89110.1	5486	1530.7	1710.8	1914.4	787.7	2809.4	2836.1
Z70004.1	5484	2633.2	3983.2	6402.9	3402.1	10170.2	7495.4
DQ645425.1	161188	2720.7	2537.4	3629.8	2285.8	4410.3	4225.7
AY370186.1	103856	5358.1	4335.4	2015.8	4286.6	8509.0	4956.3
Z70006.1	5498	906.8	1759.5	2114.6	1166.4	5040.3	3634.8
EU111752.1	260102	3990.1	5486.4	9770.2	6108.1	13968.1	11537.6
AY515119.1	100507	5041.6	5608.0	8057.5	6115.3	9897.5	9578.6
NR_029368.1	541643	1351.8	2521.1	2814.6	938.4	3806.1	4826.9
AY254309.1	104973	3062.6	2955.6	2809.3	3286.0	6261.8	5970.4
L01260.1	5502	2309.4	4273.8	5102.9	3739.1	12941.7	11194.2
DQ538394.1	227943	5237.5	5527.8	4380.0	3139.8	6618.6	6285.9
AY515118.1	100352	2432.2	4556.9	7618.9	3616.7	12174.7	10272.5
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NR_029366.1	571234	750.1	1470.5	2008.8	795.1	3058.1	2912.6

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AB119197.1 gg_id:106044 Beijerinckia indica str. ATCC 9036
AB119199.1 gg_id:106358 Beijerinckia indica str. ATCC 19361
AJ563932.1 gg_id:100451 Beijerinckia mobilis str. DSM 2326
AB119210.1 gg_id:106197 Beijerinckia sp. str. TB16
AB119203.1 gg_id:101664 Beijerinckia sp. str. TB9
EF584507.1 gg_id:232942 Chelatococcus daeguensis str. K106
AM162441.1 gg_id:155035 and situ identification acidic sphagnum peat bog clone B56
AJ563926.1 gg_id:104947 Methylocella palustris str. Ch3
CP001280.1 gg_id:527956 Methylocella silvestris str. BL2
AJ555244.1 gg_id:83530 Methylocella tundrae str. T4
DQ450165.1 gg_id:155167 (Uruguay) Atlantic coastal lagoon clone R7C54
EU131038.1 gg_id:252176 alkaline China coal mine soil clone SIP CM24
GQ402592.1 gg_id:584864 Accessing microbial biodiversity and metabolic potential tropical -based approach p
FJ719048.1 gg_id:530044 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_D0
EF064161.1 gg_id:225511 Microbial sediment bottom AMD pool acid mine drainage clone Sed3
X97076.1 gg_id:4762 peat bog clone TM9
EU133271.1 gg_id:246401 tallgrass prarie soil clone FFCH2375
AF407384.1 gg_id:27469 MCB-contaminated groundwater-treating reactor clone RB7C5
FM253682.1 gg_id:348953 Rock gold mine unusually microbial biofilm clone H09-2
AF200697.1 gg_id:32333 13C- extracted 13C-methanol exposed soil clone UP3 proteobacterium
AB119198.1 gg_id:106192 Beijerinckia derxii str. ATCC 49361
FM253655.1 gg_id:349812 Rock gold mine unusually microbial biofilm clone E02-2
FN433469.1 gg_id:562500 Methylocapsa sp. str. KYG
CU926994.1 gg_id:551719 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ837242.1 gg_id:252587 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_23
GU205295.1 gg_id:524604 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
AY913393.1 gg_id:112985 forest soil clone DUNssu187 (-7A) (OTU#034)
DQ451456.1 gg_id:156677 forest soil clone FAC17
U87759.1 gg_id:4967 Afipia broomeae str. F186
AY513503.1 gg_id:103555 Afipia felis str. 2002033830
U87764.1 gg_id:4964 Afipia genosp. 2 str. G8965
EU499727.1 gg_id:276997 Field-based laboratory stable isotope probing surveys identities both aerobic and an
GQ032540.1 gg_id:375131 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
DQ222224.1 gg_id:140520 Bradyrhizobium sp. str. CCBAU 71283012
AY568510.1 gg_id:102699 Afipia massiliensis str. NW-12
AY029562.1 gg_id:58038 Afipia massiliensis str. 34633; CIP 107022; CCUG 45153
AY547290.1 gg_id:99065 Bradyrhizobium sp. str. CCBAU 7128301
AF288304.1 gg_id:41002 Afipia birgiae str. 34632
AB099659.1 gg_id:77914 Oligotropha carboxidovorans str. S23
FJ193001.1 gg_id:304744 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ165544.1 gg_id:559211 Microbially-enhanced Dissolution Karst Carbonates microbial biofilm Sonterra #8 well

AB119197.1	106044	4264.6	5345.8	3571.7	4702.7	7699.2	6677.4
AB119199.1	106358	3794.2	5066.5	6529.6	4588.0	12247.6	9923.9
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AB119210.1	106197	3144.4	3954.5	3019.8	3817.6	8761.3	8630.6
AB119203.1	101664	1238.9	2853.9	2205.4	2326.3	3899.5	4898.6
EF584507.1	232942	3217.7	4613.9	5710.2	2753.5	10058.9	9018.0
AM162441.1	155035	2164.5	4261.6	3494.6	2630.7	4373.6	6034.0
AJ563926.1	104947	2695.4	5725.7	4741.1	4295.7	8181.0	9357.1
CP001280.1	527956	591.0	1069.0	1130.2	1430.7	3071.9	7656.2
AJ555244.1	83530	1700.7	3837.9	4509.4	3001.8	8163.1	9379.0
DQ450165.1	155167	1932.4	3669.7	2574.3	2331.4	5502.4	6249.5
EU131038.1	252176	5561.5	7775.9	9008.7	6451.9	10509.4	7896.2
GQ402592.1	584864	2133.9	4193.6	7385.0	3027.7	7591.5	9402.8
FJ719048.1	530044	762.3	1861.3	6171.8	1577.4	2063.6	3157.9
EF064161.1	225511	5979.5	6972.1	6483.1	5529.6	7361.3	7125.7
X97076.1	4762	9258.2	7705.0	7180.8	4938.8	9031.1	6934.7
EU133271.1	246401	3584.8	4920.0	4519.8	3627.4	5069.9	5659.3
AF407384.1	27469	2273.8	3183.2	4530.2	3943.2	4901.6	6118.7
FM253682.1	348953	6513.2	6635.4	5321.0	7171.7	12218.5	11037.5
AF200697.1	32333	3187.9	4513.6	4688.5	3404.1	6509.4	8843.0
AB119198.1	106192	630.4	1388.4	757.0	1494.9	871.4	1519.4
FM253655.1	349812	2776.0	4763.9	6961.3	2700.2	7787.8	7594.2
FN433469.1	562500	3269.8	5282.1	9138.6	4992.3	10217.7	11897.3
CU926994.1	551719	1246.2	1651.7	1453.7	1017.8	3505.6	1056.1
DQ837242.1	252587	3502.7	3716.1	5862.6	3706.6	11497.3	10164.6
GU205295.1	524604	2667.8	3283.0	4270.5	2121.6	3565.5	5230.8
AY913393.1	112985	870.9	1184.6	740.9	1072.9	357.3	421.3
DQ451456.1	156677	614.0	1909.7	2013.8	1591.4	6640.8	9379.3
U87759.1	4967	5526.4	7000.6	14576.8	6494.6	20225.0	18875.4
AY513503.1	103555	389.2	710.1	1503.0	1788.3	5603.1	10776.9
U87764.1	4964	1684.5	2773.5	6949.2	2937.2	8840.2	16090.6
EU499727.1	276997	6076.7	7710.9	10172.7	7935.8	18272.5	19744.5
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DQ222224.1	140520	891.4	1751.4	6390.9	4859.5	14469.7	19538.8
AY568510.1	102699	3038.8	4048.2	10790.9	3995.3	12311.8	13572.1
AY029562.1	58038	1711.7	3521.6	9840.3	2628.4	12836.1	15621.8
AY547290.1	99065	6698.5	8080.7	7403.9	7591.5	16024.0	15186.0
AF288304.1	41002	1153.2	2412.8	6618.8	3984.3	16147.0	17468.0
AB099659.1	77914	1011.1	2757.6	6236.7	3391.4	17822.4	14637.1
FJ193001.1	304744	743.2	1303.4	9303.7	1659.6	8930.2	11676.5
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AY238503.1 gg_id:92573 Bradyrhizobium sp. str. 1
AJ295483.1 gg_id:40221 rape rhizosphere clone wr0024
U87761.1 gg_id:4971 Afipia broomeae str. G5958
AY568503.2 gg_id:106979 Afipia broomeae str. C-12
EF203409.1 gg_id:261125 Bradyrhizobium sp. str. URBM1
EF520400.1 gg_id:231834 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-40
EU308573.1 gg_id:243951 Deinococcus sp. str. 4A4
DQ838529.1 gg_id:161809 Methylobacterium sp. str. WSM3686
AJ871433.1 gg_id:111252 Chelatococcus asaccharovorans CP141b
DQ298340.1 gg_id:151224 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
FM160634.1 gg_id:292268 Microvirga sp. PCA19 PCA 19
AB098515.2 gg_id:78887 Balneimonas flocculans str. TFB
GQ103792.1 gg_id:446977 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AY776209.1 gg_id:108377 Methylobacterium sp. str. AC72a
AF338176.1 gg_id:68816 Blastobacter denitrificans str. IFAM 1005; LMG 8443
X66025.1 gg_id:5058 Blastobacter denitrificans str. LMG 8443
AF288306.1 gg_id:24179 Bosea vestrisii str. 34635
GU377117.1 gg_id:526769 Afipia sp. str. sptzw29
EU325943.1 gg_id:255748 Bosea sp. str. fei-4-9
DQ377760.1 gg_id:153195 Bosea sp. PD 19
AJ968692.1 gg_id:165499 Bosea sp. str. STM 358
AJ250796.1 gg_id:4822 Bosea thiooxidans str. DSM 9653
DQ104985.1 gg_id:136035 Bosea thiooxidans str. JS 11
EU730912.1 gg_id:324973 Bosea thiooxidans str. 187
AJ250797.1 gg_id:4823 Bosea thiooxidans str. RpPI5-VS
DQ303323.1 gg_id:149709 Bosea sp. TM19_7
EF114681.1 gg_id:194437 Bosea sp. str. SJH07
AF288307.1 gg_id:27298 Bosea massiliensis str. 34649
EU130951.1 gg_id:243491 Afipia sp. BAC312
AF288309.1 gg_id:47211 Bosea massiliensis str. 63287
EU584530.1 gg_id:263418 Afipia sp. str. Everest-gws-91
NR_028787.1 gg_id:583653 Bosea minatitlanensis str. AMX51; DSM 13099
EU561082.1 gg_id:273777 Bradyrhizobium sp. str. CTFI54
FJ390904.1 gg_id:589546 Bradyrhizobium canariense str. SEMIA 928
GQ899183.1 gg_id:569090 Bradyrhizobium canariense str. L-2
EU561083.1 gg_id:273925 Bradyrhizobium sp. str. CTFI410
EU420082.1 gg_id:569322 Bradyrhizobium canariense str. Cy-1
AY649429.1 gg_id:99495 Bradyrhizobium elkanii str. BR2001
EU170546.1 gg_id:251540 Bradyrhizobium elkanii str. CCBAA 05065
FJ192710.1 gg_id:319167 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AY904753.1 gg_id:111860 Bradyrhizobium elkanii str. SEMIA 6148

AY238503.1	92573	414.0	854.7	3785.8	2314.4	8884.3	13146.2
AJ295483.1	40221	905.2	1797.1	5220.7	2890.8	13385.9	13890.2
U87761.1	4971	5008.7	7533.8	10720.4	7252.3	22539.1	17843.6
AY568503.2	106979	2127.7	3982.0	12407.8	3776.7	17509.8	19980.7
EF203409.1	261125	776.7	1623.1	1957.1	1762.6	7917.8	8422.6
EF520400.1	231834	1141.4	2684.1	5025.6	1644.4	9309.7	12324.2
EU308573.1	243951	2592.4	2907.3	1491.5	3152.7	3723.0	4328.4
DQ838529.1	161809	370.0	387.7	2108.2	360.0	2382.0	2230.8
AJ871433.1	111252	6173.1	8419.5	4769.5	5093.2	6429.3	6200.6
DQ298340.1	151224	3637.7	3879.8	3584.8	4579.7	9257.1	5162.7
FM160634.1	292268	1338.3	1682.9	2435.0	1746.1	5063.8	3877.3
AB098515.2	78887	808.8	1293.3	710.3	1183.0	2054.4	1044.7
GQ103792.1	446977	3847.1	4446.8	3357.4	1965.9	3228.2	3470.2
AY776209.1	108377	723.0	1366.0	1534.7	566.1	1583.7	2720.9
AF338176.1	68816	324.5	546.5	3776.4	2114.3	13020.0	17479.5
X66025.1	5058	1121.1	1742.1	7379.9	4844.3	16879.0	20707.7
AF288306.1	24179	6325.0	7511.9	6028.5	7592.4	10628.5	8391.8
GU377117.1	526769	4521.8	6889.6	7086.4	4531.3	11231.6	8815.6
EU325943.1	255748	2541.7	4340.1	4298.9	3023.6	6178.4	5436.5
DQ377760.1	153195	2675.9	4269.1	3620.2	3007.8	6363.7	4900.2
AJ968692.1	165499	7245.8	9160.6	6160.7	7307.3	10299.6	8692.1
AJ250796.1	4822	2162.7	3447.2	4249.9	2176.3	5906.5	4904.7
DQ104985.1	136035	1433.4	3082.6	5748.6	2269.2	6392.3	7786.7
EU730912.1	324973	6471.2	7763.9	6167.6	7594.8	10480.0	8663.8
AJ250797.1	4823	2381.5	3951.6	3455.9	4844.2	8942.9	7967.7
DQ303323.1	149709	2167.0	3812.1	4408.9	1279.3	4288.5	4951.0
EF114681.1	194437	5986.7	6818.6	5373.7	6904.4	9491.7	7744.2
AF288307.1	27298	19113.1	20277.9	12183.1	13974.1	20008.4	18220.3
EU130951.1	243491	287.1	605.2	411.4	189.0	1020.7	1232.2
AF288309.1	47211	7099.7	8908.6	6022.6	7305.0	10448.1	8420.1
EU584530.1	263418	12407.5	13169.3	10197.0	9824.7	14429.2	13738.3
NR_028787.1	583653	3094.4	4135.7	3680.4	3572.9	7060.1	4729.6
EU561082.1	273777	12718.8	14441.3	11169.5	12305.7	23726.8	21708.5
FJ390904.1	589546	756.6	1609.3	6795.9	3042.2	15872.2	16181.6
GQ899183.1	569090	385.9	920.4	5748.7	2828.3	15301.6	15040.1
EU561083.1	273925	949.7	1780.5	8604.5	2538.5	16026.6	14611.7
EU420082.1	569322	987.8	1738.8	6804.2	5267.3	17032.2	20716.5
AY649429.1	99495	2520.1	3721.7	12622.5	4801.2	16273.8	17374.8
EU170546.1	251540	2365.4	4107.9	13646.2	3146.7	12668.7	14026.7
FJ192710.1	319167	3200.8	4366.3	14220.4	5693.2	18503.0	18412.8
AY904753.1	111860	13973.2	15632.7	19421.1	13824.8	24210.5	23820.5

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U35000.3 gg_id:4946 Bradyrhizobium elkanii str. USDA 76
AY904788.1 gg_id:112273 Bradyrhizobium elkanii str. SEMIA 6425
AY904762.1 gg_id:111745 Bradyrhizobium elkanii str. SEMIA 6160
AF417554.1 gg_id:21176 Bradyrhizobium elkanii str. DASA37005
AF208516.1 gg_id:55735 Bradyrhizobium elkanii str. USDA 46
FJ193395.1 gg_id:328559 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
DQ786801.1 gg_id:169640 Bradyrhizobium elkanii str. HaE4
FJ193017.1 gg_id:353693 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AF417553.1 gg_id:49609 Bradyrhizobium elkanii str. DASA38001
AY904736.1 gg_id:112163 Bradyrhizobium elkanii str. SEMIA 696
AY904748.1 gg_id:112153 Bradyrhizobium elkanii str. SEMIA 6100
FJ193380.1 gg_id:324669 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
AF417556.1 gg_id:44293 Bradyrhizobium elkanii str. DASA35013
GQ129847.1 gg_id:465190 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
EU399711.1 gg_id:271806 Bradyrhizobium elkanii str. CCBAU 05041
AY039016.1 gg_id:64297 Bradyrhizobium sp. ORS3260 str. ORS 3260
AF417555.1 gg_id:21431 Bradyrhizobium elkanii str. DASA35011
AY904744.1 gg_id:111950 Bradyrhizobium elkanii str. SEMIA 6028
EU170551.1 gg_id:242313 Bradyrhizobium elkanii str. CCBAU 23109
AY649433.1 gg_id:103679 Bradyrhizobium elkanii str. BR3279
AY904789.1 gg_id:112254 Bradyrhizobium elkanii str. SEMIA 6440
FJ192573.1 gg_id:321198 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior
FJ540914.1 gg_id:586787 Bradyrhizobium yuanmingense str. DTB8
FJ540920.1 gg_id:578473 Bradyrhizobium yuanmingense str. DTC5
AF417549.1 gg_id:20737 Bradyrhizobium japonicum str. DASA24015
AY904774.1 gg_id:111573 Bradyrhizobium japonicum str. SEMIA 6319
AF193818.1 gg_id:49866 Bradyrhizobium yuanmingense str. B071
FJ540960.1 gg_id:585297 Bradyrhizobium yuanmingense str. TSC9
AF417548.1 gg_id:45495 Bradyrhizobium japonicum str. DASA03183
EF070133.1 gg_id:196710 Bradyrhizobium yuanmingense str. CCBAU 43022
EF061098.1 gg_id:183640 Bradyrhizobium yuanmingense str. CCBAU 45079
AY649439.1 gg_id:104594 Bradyrhizobium japonicum str. BR3267
AY162036.1 gg_id:135634 Cultivating soil clone PI_GH1.1.B1
AF417543.1 gg_id:71773 Bradyrhizobium japonicum str. DASA12006
DQ303328.1 gg_id:146763 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
DQ133341.1 gg_id:137967 Bradyrhizobium liaoningense str. GXD1
DQ786798.1 gg_id:168591 Bradyrhizobium liaoningense str. DdE3
AB240363.1 gg_id:144998 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AF239843.2 gg_id:32699 Bradyrhizobium japonicum str. PRY40
EF221623.1 gg_id:207870 Bradyrhizobium sp. str. JR008

FJ418920.1	362396	2920.8	4409.0	15008.9	3365.9	13050.4	14566.8
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AY904762.1	111745	2129.8	3186.0	9740.0	5322.6	16273.7	17746.4
AF417554.1	21176	1619.2	2819.4	7268.7	2040.4	10357.7	12218.8
AF208516.1	55735	3069.3	4933.7	11660.1	4616.3	15548.9	16783.1
FJ193395.1	328559	4213.8	5932.9	11538.4	7222.0	13550.6	14448.6
DQ786801.1	169640	2544.1	3016.7	9816.5	5165.5	16108.4	16041.9
FJ193017.1	353693	2067.8	2858.5	10693.8	3368.5	11029.2	11896.9
AF417553.1	49609	5787.8	7994.1	10308.7	6856.5	17542.8	17942.4
AY904736.1	112163	1704.6	2458.7	9455.9	5348.1	10452.3	9604.5
AY904748.1	112153	9928.6	11446.9	10601.4	12475.2	19259.2	19181.3
FJ193380.1	324669	9426.2	9190.3	10510.4	9858.3	17362.4	17144.2
AF417556.1	44293	6084.0	9951.6	11420.3	6106.1	18215.7	19262.1
GQ129847.1	465190	5269.9	4833.1	5194.4	6229.9	12681.2	11334.8
EU399711.1	271806	2149.1	3097.8	11545.5	4453.9	16889.2	17621.1
AY039016.1	64297	2885.1	4316.9	12706.2	5188.6	16895.7	17073.4
AF417555.1	21431	3352.2	4385.0	13705.8	5977.2	18545.9	18667.8
AY904744.1	111950	7445.9	6135.9	10455.5	9954.9	14935.7	13811.1
EU170551.1	242313	3108.5	4376.3	12032.8	6143.5	18202.1	18611.2
AY649433.1	103679	2884.7	4095.4	13232.8	5909.8	17184.1	18337.5
AY904789.1	112254	3105.7	4217.6	12416.3	5674.2	16563.6	17100.9
FJ192573.1	321198	2584.4	3626.3	11860.8	4519.1	15785.6	16176.2
FJ540914.1	586787	2357.4	4396.1	12138.1	3713.5	18091.1	17043.6
FJ540920.1	578473	4102.3	5995.5	9606.3	5495.8	17894.4	15265.1
AF417549.1	20737	4266.8	4658.1	6823.8	5811.9	15424.6	15040.2
AY904774.1	111573	1065.0	2336.1	6598.1	2050.8	17455.7	14033.6
AF193818.1	49866	7737.0	10488.7	10940.5	6426.3	20775.5	16314.0
FJ540960.1	585297	3703.9	4758.3	5216.7	4909.4	16926.4	13664.1
AF417548.1	45495	6657.9	8652.3	2767.7	5033.4	7406.6	6836.8
EF070133.1	196710	10375.5	15574.8	9016.5	10467.2	21358.0	17417.9
EF061098.1	183640	1556.5	2743.6	3156.1	2433.0	8410.8	9641.6
AY649439.1	104594	3629.8	5607.5	14188.1	5204.7	19384.1	17694.5
AY162036.1	135634	6026.3	7320.1	17322.1	8311.1	16564.4	21429.3
AF417543.1	71773	809.8	1354.6	2744.8	2103.7	12081.9	9387.1
DQ303328.1	146763	3125.3	4123.2	10156.6	3135.9	13942.3	13991.9
DQ133341.1	137967	4241.8	5100.1	7490.3	5024.1	13711.7	11426.0
DQ786798.1	168591	603.3	1096.5	6760.3	1937.3	14735.8	12420.9
AB240363.1	144998	5428.5	5489.7	14271.2	5463.6	13674.3	12203.3
AF239843.2	32699	1841.3	3878.3	9412.6	4833.2	20532.3	18126.2
EF221623.1	207870	1408.3	2439.4	5639.7	3361.6	14074.3	12612.1

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DQ303349.1 gg_id:149227 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
U69636.1 gg_id:4932 Bradyrhizobium lupini str. FN 13 (USDA 3505)
AY904778.1 gg_id:112228 Bradyrhizobium elkanii str. SEMIA 6387
AY904757.1 gg_id:112271 Bradyrhizobium japonicum str. SEMIA 6155
DQ303324.1 gg_id:147536 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
EU145989.1 gg_id:236262 Bradyrhizobium liaoningense str. CCBAU 83684
EU170561.1 gg_id:245983 Bradyrhizobium elkanii str. CCBAU 41236
EU399713.1 gg_id:258733 Bradyrhizobium japonicum str. CCBAU 43170
AF417544.1 gg_id:32002 Bradyrhizobium japonicum str. DASA12007
GQ181045.1 gg_id:563588 Bradyrhizobium elkanii str. LN5
DQ303376.1 gg_id:145414 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
AF417542.1 gg_id:23765 Bradyrhizobium japonicum str. DASA02010
EU561080.1 gg_id:266287 Bradyrhizobium sp. str. CTFI47
FJ025097.1 gg_id:348667 Bradyrhizobium japonicum str. SEMIA 6153
EF394156.1 gg_id:210105 Bradyrhizobium japonicum str. CCBAU 65068
FJ390914.1 gg_id:591406 Bradyrhizobium japonicum str. SEMIA 512
AB195987.1 gg_id:132401 Bradyrhizobium elkanii str. MF834
X70403.1 gg_id:4945 Bradyrhizobium sp str. LMG 9566
AB179515.1 gg_id:100954 sedimentary rock clone MIZ24
AF363138.1 gg_id:24680 Bradyrhizobium japonicum str. MSDJ G94
EF394146.1 gg_id:214964 Bradyrhizobium japonicum str. CCBAU 53135
FJ418696.1 gg_id:364095 Bradyrhizobium japonicum str. CCBAU 33175
AY904746.1 gg_id:111411 Bradyrhizobium elkanii str. SEMIA 6069
DQ517956.1 gg_id:159686 Bradyrhizobium japonicum str. HHL-01
GQ181034.1 gg_id:510301 Bradyrhizobium elkanii str. LNW14
EU133476.1 gg_id:237433 tallgrass prarie soil clone FFCH17074
EF070138.1 gg_id:195443 Bradyrhizobium liaoningense str. CCBAU 33158
DQ303346.1 gg_id:145143 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
AY904756.1 gg_id:112304 Bradyrhizobium japonicum str. SEMIA 6152
DQ303348.1 gg_id:147522 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
AF239844.2 gg_id:51967 Bradyrhizobium japonicum str. PRY42
AY568513.2 gg_id:103141 Bradyrhizobium elkanii str. NW-6
DQ303379.1 gg_id:146676 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
EU335263.1 gg_id:257149 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
DQ303343.1 gg_id:148707 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
DQ303364.1 gg_id:148890 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
EF512281.1 gg_id:223867 Bradyrhizobium japonicum str. CCBAU 45002
AF363135.1 gg_id:18027 Bradyrhizobium japonicum str. MSDJ 5697
EF394151.1 gg_id:211052 Bradyrhizobium japonicum str. CCBAU 65619
DQ786799.1 gg_id:170123 Bradyrhizobium liaoningense str. BqE4

DQ303347.1	147207	4239.4	6379.7	18065.0	5358.4	18593.7	17591.8
DQ303349.1	149227	3708.7	6246.6	13674.3	4813.7	16050.1	16730.1
U69636.1	4932	7909.0	10553.1	12488.6	9385.2	21126.8	19695.9
AY904778.1	112228	8591.1	10636.7	14900.8	9600.0	16603.0	16168.6
AY904757.1	112271	2934.6	4575.3	9662.1	5328.9	20571.8	17471.1
DQ303324.1	147536	187.5	266.8	569.1	329.7	1246.0	1819.4
EU145989.1	236262	1300.5	1568.9	7319.3	2562.4	17096.7	13806.3
EU170561.1	245983	2488.1	3930.2	13496.8	4754.4	18025.4	17347.2
EU399713.1	258733	4180.8	4992.5	9514.8	4401.5	18016.8	14845.6
AF417544.1	32002	110.5	123.1	253.3	451.2	1690.6	3028.3
GQ181045.1	563588	4571.4	5896.0	12091.9	4479.3	14069.1	13450.6
DQ303376.1	145414	2424.6	3140.3	844.3	1945.8	4687.0	4870.3
AF417542.1	23765	266.8	778.6	1391.0	873.9	8580.2	8711.6
EU561080.1	266287	507.4	841.9	6842.1	1522.8	15330.4	11775.1
FJ025097.1	348667	2806.4	3927.0	11669.0	4474.8	17654.7	16318.7
EF394156.1	210105	484.2	1024.8	6201.6	2851.3	16892.5	15436.3
FJ390914.1	591406	762.7	1723.5	7984.1	3406.9	17790.5	17264.9
AB195987.1	132401	2417.6	3920.9	13113.2	4534.4	16460.0	16501.5
X70403.1	4945	2424.1	3802.1	14519.5	3665.4	16749.0	15794.8
AB179515.1	100954	1079.7	2265.7	8135.4	1955.3	6602.8	6971.6
AF363138.1	24680	3141.2	3957.4	10433.8	4029.5	18243.3	16555.8
EF394146.1	214964	872.9	1606.0	8958.7	3246.4	18713.8	16609.2
FJ418696.1	364095	548.3	1180.6	6753.4	3195.7	16878.9	15900.7
AY904746.1	111411	4709.8	6194.2	10490.2	2618.5	13182.4	9245.0
DQ517956.1	159686	1047.0	1959.8	6718.1	3557.4	16175.2	16237.1
GQ181034.1	510301	2414.3	3797.5	13340.7	4619.4	16912.3	16143.6
EU133476.1	237433	2546.3	3203.6	3636.5	2926.1	5659.3	7472.2
EF070138.1	195443	1396.1	1566.5	7140.8	2578.5	17149.3	13867.9
DQ303346.1	145143	2511.8	4436.0	6441.6	2777.7	11525.7	14872.9
AY904756.1	112304	4901.4	6114.9	12973.4	5599.5	18755.8	17751.1
DQ303348.1	147522	5245.6	7646.3	9416.3	6215.4	15578.0	15935.8
AF239844.2	51967	795.9	1873.3	8387.5	3531.8	18239.4	16812.3
AY568513.2	103141	2094.9	3032.3	12504.8	3674.9	17132.6	15889.8
DQ303379.1	146676	1113.2	2512.7	6529.5	2335.9	12602.8	16455.2
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DQ303343.1	148707	1351.1	3400.3	12869.4	2030.0	10686.2	12268.6
DQ303364.1	148890	127.2	252.8	513.5	244.8	859.8	1963.3
EF512281.1	223867	157.1	272.9	4242.4	2329.4	17349.2	14060.1
AF363135.1	18027	41.3	285.4	2559.9	617.6	8679.9	6494.0
EF394151.1	211052	878.4	1290.1	7065.0	2434.0	14036.7	12929.3
DQ786799.1	170123	2093.0	2366.4	9003.6	3713.3	17643.4	15099.7

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DQ303374.1 gg_id:146501 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
EU074195.1 gg_id:250401 Bradyrhizobium liaoningense str. CCBAU 03282
DQ303326.1 gg_id:149079 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
AF417541.1 gg_id:54256 Bradyrhizobium japonicum str. DASA02007
AF363133.1 gg_id:37117 Bradyrhizobium japonicum str. MSDJ 5718
AY599677.1 gg_id:104113 fungal ascocarp clone Cl-19-TB8-II
AF417545.1 gg_id:49277 Bradyrhizobium japonicum str. THA7
EU333380.1 gg_id:268064 Bradyrhizobium japonicum RLA09
EU083497.1 gg_id:240912 Evidence Carboxylation During Degradation Hexadecane Denitrifying Consortium he
DQ303335.1 gg_id:148648 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
AY904773.1 gg_id:111438 Bradyrhizobium elkanii str. SEMIA 6208
EF018750.1 gg_id:211106 aspen rhizosphere clone Amb_16S_1209
DQ517958.1 gg_id:160432 Bradyrhizobium sp. str. HMS-O1
EF019158.1 gg_id:204406 aspen rhizosphere clone Amb_16S_1805
U69637.1 gg_id:4921 Bradyrhizobium lupini str. KM50 90 (USDA 3514)
NC_010725.1 gg_id:289367 Methylobacterium populi str. BJ001
AF069958.1 gg_id:111772 Nitrobacter alkalicus str. AN4
AF069957.1 gg_id:73775 Nitrobacter alkalicus str. AN2
NC_007964.1 gg_id:156705 Nitrobacter hamburgensis str. X14
AM292301.1 gg_id:254106 Nitrobacter vulgaris str. BB3
AY055796.1 gg_id:17737 Nitrobacter winogradskyi str. ATCC 14123
AM286382.1 gg_id:220346 Nitrobacter vulgaris str. K55
AY055798.1 gg_id:56503 Nitrobacter sp. str. KB212
EU528247.1 gg_id:284778 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
L11661.1 gg_id:4840 Nitrobacter winogradskyi str. W
AM286390.1 gg_id:223530 Nitrobacter vulgaris str. 329
L11662.1 gg_id:4842 Nitrobacter sp str. LL
AF529115.1 gg_id:62406 trichloroethene-contaminated site clone FTLM116 proteobacterium
AB241411.1 gg_id:223626 Rhodopseudomonas lichen O5
AB196356.1 gg_id:109667 Rhodopseudomonas palustris str. LW-RE
AF487428.1 gg_id:68786 Rhodopseudomonas palustris str. Wai1S1
U09829.1 gg_id:4878 marine sediment clone JAP850 Rochelle
X87279.1 gg_id:4854 Rhodopseudomonas palustris str. DSM 126
EU018457.1 gg_id:252635 Rhodobacter sphaeroides PSB07-19
CP000463.1 gg_id:183860 Rhodopseudomonas palustris str. BisA53
AB167545.1 gg_id:100949 Rhodopseudomonas palustris str. KP0014 FERMP-19432
AJ968691.1 gg_id:166553 Rhodopseudomonas sp. 1416ri str. ORS 1416
CP000301.1 gg_id:153177 Rhodopseudomonas palustris str. BisB18
EF515308.1 gg_id:224099 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22f08
AB167544.1 gg_id:100793 Rhodopseudomonas palustris str. KP0003 FERMP-19430

FJ390900.1	545943	1634.4	3106.4	11137.7	3245.8	17023.3	15885.6
DQ303374.1	146501	4349.1	6715.8	15998.6	5675.3	16420.8	16682.8
EU074195.1	250401	1052.6	1972.1	9401.2	3372.0	17548.7	16498.8
DQ303326.1	149079	2946.9	5367.8	15427.3	4633.3	16769.6	17950.7
AF417541.1	54256	1832.4	2396.8	4944.0	2698.7	16434.5	12889.4
AF363133.1	37117	1152.5	1950.1	7559.4	3714.0	16417.6	16464.6
AY599677.1	104113	1880.8	2203.7	4773.9	1560.4	6016.3	7554.0
AF417545.1	49277	691.7	1260.9	8734.4	2106.3	17149.1	12415.6
EU333380.1	268064	752.8	1167.6	7755.2	2032.5	13962.3	12495.5
EU083497.1	240912	2716.5	3633.1	4747.3	5816.8	15245.5	16655.5
DQ303335.1	148648	7073.2	7482.9	15665.1	8352.8	20081.1	17673.7
AY904773.1	111438	2435.8	3821.9	13352.7	4471.0	16512.1	16170.4
EF018750.1	211106	3464.0	4949.9	10319.2	4160.3	13111.1	13431.0
DQ517958.1	160432	7646.2	6552.3	4926.0	8626.4	16904.1	14726.3
EF019158.1	204406	4250.2	6258.3	13305.5	5622.0	13242.4	17787.3
U69637.1	4921	4740.3	3530.2	5053.4	5516.9	14345.4	11932.4
NC_010725.1	289367	8624.9	11379.8	20234.3	10113.0	24958.2	24741.5
AF069958.1	111772	990.7	1652.9	6528.1	2083.5	11710.0	11080.4
AF069957.1	73775	2195.7	2840.2	8085.9	3110.6	13250.1	13669.1
NC_007964.1	156705	408.7	760.9	2164.6	2891.6	11448.1	11231.8
AM292301.1	254106	1225.8	1470.4	3494.3	1951.6	10625.8	9574.0
AY055796.1	17737	7427.7	6880.5	1005.5	4862.5	8360.7	8580.9
AM286382.1	220346	1448.6	1500.7	4289.6	1514.8	11246.9	9234.4
AY055798.1	56503	925.5	1716.1	1660.6	1236.7	4374.8	6292.8
EU528247.1	284778	6947.0	6380.1	5404.8	5788.0	10390.9	10506.5
L11661.1	4840	587.2	892.6	1900.5	611.3	4566.7	4408.1
AM286390.1	223530	3255.8	2998.2	8460.1	4456.2	10458.9	9734.4
L11662.1	4842	191.5	297.5	1349.6	741.0	3814.4	4570.8
AF529115.1	62406	1260.8	2506.2	8064.0	2111.8	4908.5	5273.7
AB241411.1	223626	1333.1	2948.5	8281.1	3550.8	17296.1	15200.7
AB196356.1	109667	1723.9	2457.4	7040.0	2514.7	13636.7	11346.1
AF487428.1	68786	588.5	1092.4	3893.4	3001.0	10398.0	9622.2
U09829.1	4878	409.8	1454.0	3042.0	806.1	7775.3	10932.1
X87279.1	4854	120.3	264.0	1471.1	812.5	7679.2	10431.0
EU018457.1	252635	4351.6	6976.8	8885.7	4953.0	18017.9	14783.8
CP000463.1	183860	1911.1	4822.1	5235.9	3503.9	13135.8	15389.2
AB167545.1	100949	1709.5	2720.0	5758.9	6226.2	14574.7	15070.4
AJ968691.1	166553	1080.9	1788.6	3836.6	1262.7	7232.2	10140.4
CP000301.1	153177	1552.0	3427.0	6197.0	5102.4	14962.8	16300.6
EF515308.1	224099	1032.3	1839.1	3720.7	1350.7	9620.6	12020.9
AB167544.1	100793	375.6	600.9	701.8	1023.9	3961.0	1808.6

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EU221585.1 gg_id:253925 Rhodopseudomonas palustris str. DX-1
AF509907.1 gg_id:111553 Bradyrhizobium sp. str. CMI23
AB079634.1 gg_id:62340 Rhodopseudomonas palustris VA2-2
L11664.1 gg_id:4866 Rhodopseudomonas palustris
DQ126338.1 gg_id:138381 Rhodopseudomonas sp. str. PSB-O
EU531568.1 gg_id:514717 Rhodopseudomonas palustris str. J
EU018458.1 gg_id:248384 Rhodopseudomonas palustris PSB07-21
GQ036328.1 gg_id:384524 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362h08c1
DQ984578.1 gg_id:245601 Mt. Nan-Jen litterfall clone IYF09
DQ497243.1 gg_id:157613 Chelatococcus sp
GQ421849.1 gg_id:550491 Microvirga sp. str. 5420S-16
FJ025099.1 gg_id:308491 Bradyrhizobium japonicum str. SEMIA 6396
AY904750.1 gg_id:112390 Bradyrhizobium japonicum str. SEMIA 6144
AJ009451.1 gg_id:4819 anaerobic TCB-transforming consortium clone SJA-9
EF121353.1 gg_id:216650 microbiota uninfected and Rickettsia-infected colonized cat fleas Ctenocephalides fel
EU861833.1 gg_id:309753 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog
FJ478995.1 gg_id:579612 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ025100.1 gg_id:309477 Bradyrhizobium japonicum str. SEMIA 6154
GU455366.1 gg_id:523224 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
AM412118.1 gg_id:247879 Chelatococcus sp. str. P-117
EU256461.1 gg_id:256534 Bradyrhizobium sp. str. CCBAU 85044
AM990457.1 gg_id:279499 Chelatococcus sp. str. I-21
DQ303342.1 gg_id:150032 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM
EF394148.1 gg_id:205693 Bradyrhizobium japonicum str. CCBAU 43277
X87272.1 gg_id:4980 Bradyrhizobium japonicum str. DSM 30131 T
AF530465.1 gg_id:61023 Bradyrhizobium japonicum JZ1
DQ129309.1 gg_id:138424 microarray level air two cities Texas urban aerosol clone AKIW763
EU276558.1 gg_id:362293 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
AF417550.1 gg_id:48037 Bradyrhizobium japonicum str. DASA01059
EF018822.1 gg_id:204655 aspen rhizosphere clone Amb_16S_1300
FJ716001.1 gg_id:579890 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina
AY345540.1 gg_id:91124 Lake Wai'ele'ele water clone LWSR-28
GQ129955.1 gg_id:434250 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc
AF417547.2 gg_id:33185 Bradyrhizobium japonicum str. DASA38025
GQ389009.1 gg_id:587997 quality deterioration drinking system during serious red water outbreak clone J57
DQ432334.1 gg_id:156941 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W
EF394142.1 gg_id:204550 Bradyrhizobium japonicum str. CCBAU 41267
AY649440.1 gg_id:99283 Bradyrhizobium japonicum str. BR3288
AB187010.1 gg_id:101203 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-N
AB195991.1 gg_id:130287 Bradyrhizobium japonicum str. MH615
AJ867909.1 gg_id:143411 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone B6

EU221585.1	253925	2645.1	4546.7	12976.3	4996.4	16810.2	16663.4
AF509907.1	111553	1465.0	2823.0	4212.6	3604.1	10927.9	13367.4
AB079634.1	62340	1688.9	2356.4	7691.7	2377.0	13651.9	11295.3
L11664.1	4866	929.0	2686.0	4393.3	886.2	9332.0	5913.6
DQ126338.1	138381	7885.0	10463.8	17465.0	8907.6	17517.3	15753.9
EU531568.1	514717	6230.4	6575.4	9670.3	7664.2	14892.1	14983.2
EU018458.1	248384	1145.7	1822.8	5546.5	1874.7	11776.5	10359.0
GQ036328.1	384524	6265.9	8036.8	3826.6	7724.8	14775.0	16411.8
DQ984578.1	245601	3976.0	3628.9	5062.5	2927.6	10665.0	12355.1
DQ497243.1	157613	5385.6	6529.8	4400.4	4248.2	9324.4	8428.2
GQ421849.1	550491	1172.5	1157.1	1471.9	601.9	2759.9	1224.8
FJ025099.1	308491	902.4	1654.1	6906.0	2068.0	13695.0	12975.7
AY904750.1	112390	2068.7	3465.1	9923.9	4567.5	21044.9	19615.0
AJ009451.1	4819	83.3	212.8	124.0	100.6	517.1	233.5
EF121353.1	216650	141.3	280.8	170.6	113.5	90.1	102.9
EU861833.1	309753	844.0	2263.1	6133.6	3553.1	11997.5	13735.5
FJ478995.1	579612	3783.3	5378.0	13719.4	5121.4	14905.8	17106.2
FJ025100.1	309477	5449.7	6516.9	12157.0	5361.3	18135.3	16591.8
GU455366.1	523224	653.0	1345.9	4764.6	2710.4	7936.7	8972.2
AM412118.1	247879	1251.5	2053.5	4631.6	1545.4	7458.0	7340.3
EU256461.1	256534	7061.9	6613.2	6720.6	6887.4	14228.4	10239.2
AM990457.1	279499	7372.8	8952.5	7398.1	7424.4	10890.9	9396.9
DQ303342.1	150032	1443.0	2419.6	12269.1	2581.3	13266.7	13976.8
EF394148.1	205693	1111.5	2036.4	8391.5	3350.7	18157.5	17332.6
X87272.1	4980	1113.0	1801.3	8649.8	3602.5	16639.5	16639.2
AF530465.1	61023	2049.2	1903.5	7456.8	3146.7	17089.1	13537.6
DQ129309.1	138424	239.5	691.5	427.5	328.8	1318.7	474.3
EU276558.1	362293	1921.3	2350.4	2933.0	1170.6	4614.2	5324.0
AF417550.1	48037	1874.0	2828.1	6074.2	4017.8	16942.1	17269.3
EF018822.1	204655	2929.1	3348.9	11503.2	5238.2	17142.0	19796.7
FJ716001.1	579890	1802.8	3647.8	11096.9	2576.1	11908.5	12787.9
AY345540.1	91124	581.7	1381.3	2974.9	1133.5	6376.4	5010.1
GQ129955.1	434250	684.1	1449.5	1902.1	788.3	3417.3	3951.3
AF417547.2	33185	1535.2	1562.8	1896.0	1796.2	8550.0	7190.5
GQ389009.1	587997	2287.8	2814.4	6849.2	1151.9	2320.2	2239.8
DQ432334.1	156941	209.1	405.3	1392.6	550.7	3719.9	2210.5
EF394142.1	204550	1111.4	1788.6	8703.9	3574.0	16855.7	17079.0
AY649440.1	99283	1404.8	1915.5	8081.0	2844.5	17562.3	14930.0
AB187010.1	101203	1236.5	2578.5	4093.0	1018.2	8382.5	6972.7
AB195991.1	130287	9366.4	16075.7	14766.6	8989.0	18483.0	18542.8
AJ867909.1	143411	666.6	1647.5	2625.6	1465.3	4506.9	7240.8

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AJ968693.1 gg_id:167720 Bosea sp. str. ORS 1414
EU878006.2 gg_id:576097 Salinarimonas rosea str. YIM YD3
GQ103050.1 gg_id:397383 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
FJ479132.1 gg_id:512302 species richness estimates obtained nearly and simulated pyrosequencing-generated
AM292299.1 gg_id:242856 Nitrobacter hamburgensis str. Y
AB195986.1 gg_id:128373 Bradyrhizobium canariense str. MH547
EU029133.1 gg_id:244029 Deinococcus sp. str. 5A4
AM411919.1 gg_id:253138 Bradyrhizobium sp. str. P-44
AB300992.1 gg_id:223242 Bradyrhizobium iriomotense str. EK05 (= NBRC 102520)
EF394144.1 gg_id:214300 Bradyrhizobium japonicum str. CCBAU 53152
AY963315.1 gg_id:154614 structures and correlated ecological factors soils two evergreen broad-leaved forests
AB426223.1 gg_id:263163 -situ identification study benzene-degrading s under methanogenic condition anaerc
AJ785294.1 gg_id:211869 Rhizobiales genosp. AL ARRI 185
CU927551.1 gg_id:545730 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
DQ351924.1 gg_id:173105 manganese oxidation soil clone JH-GY18
AF417552.1 gg_id:27428 Bradyrhizobium japonicum str. DASA37011
AY372184.1 gg_id:94343 Bradyrhizobium betae str. PL7HG1
EF516928.1 gg_id:222831 grassland soil clone FCPN762
AF208509.1 gg_id:56515 Bradyrhizobium japonicum str. USDA 129
AY904764.1 gg_id:112297 Bradyrhizobium japonicum str. SEMIA 6163
FJ382130.1 gg_id:582075 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
AF417551.1 gg_id:45827 Bradyrhizobium japonicum str. DASA37026
AY904758.1 gg_id:112060 Bradyrhizobium japonicum str. SEMIA 6156
FJ528273.1 gg_id:573764 Bradyrhizobium sp. str. Mf253
AF234889.2 gg_id:77279 Bradyrhizobium japonicum str. SEMIA 5080
AY904765.1 gg_id:112064 Bradyrhizobium japonicum str. SEMIA 6164
FJ382683.1 gg_id:510366 Potentially pathogenic and air stem cell transplant summer hospital shower water BM
AY904743.1 gg_id:111821 Bradyrhizobium japonicum str. SEMIA 6002
AF502220.1 gg_id:55851 EBPR sludge lab scale clone HP1B78
EF032655.1 gg_id:198655 structure riverine biofilms river biofilm clone SepB-6
FJ380996.1 gg_id:549917 Bradyrhizobium sp. str. BQN4T-01d
AY178079.1 gg_id:100322 Bradyrhizobium sp. Cmey1 Cmey 1
AY904732.1 gg_id:111515 Bradyrhizobium japonicum str. SEMIA 656
AF409021.1 gg_id:98929 Bradyrhizobium sp. str. Ellin179
D13430.1 gg_id:4937 Bradyrhizobium japonicum str. USDA 110
AB220164.1 gg_id:153145 Bradyrhizobium sp. QC1
AF508112.1 gg_id:66234 Bosea thiooxidans TJ1
GU377100.1 gg_id:514335 Balneimonas sp. str. sptzw09
AY169423.1 gg_id:81409 Bradyrhizobium japonicum
D78366.1 gg_id:5055 Agromonas oligotrophica str. JCM1494
GQ389186.1 gg_id:582505 quality deterioration drinking system during serious red water outbreak clone D59

AJ968693.1	167720	383.2	652.0	1039.2	610.3	713.0	408.4
EU878006.2	576097	4419.8	270.9	4613.0	2159.9	5469.6	5318.5
GQ103050.1	397383	3929.7	5498.3	8530.1	4131.4	11121.0	13387.0
FJ479132.1	512302	4886.3	4617.6	2476.2	6712.5	11971.5	11529.9
AM292299.1	242856	1108.6	2183.4	6788.3	2777.6	12337.4	13420.5
AB195986.1	128373	139.6	276.9	2388.9	428.9	9370.7	4354.5
EU029133.1	244029	1979.0	2579.8	2369.9	687.6	3097.2	4545.9
AM411919.1	253138	1160.8	2146.1	6145.3	1665.1	7647.0	9400.3
AB300992.1	223242	1102.8	2220.3	4397.1	4759.3	15195.9	16225.7
EF394144.1	214300	1700.1	2601.4	5738.2	5208.5	15289.3	17524.0
AY963315.1	154614	5155.2	6084.7	11027.0	5243.1	15603.3	11455.2
AB426223.1	263163	378.6	1164.5	988.0	470.5	5905.2	2127.4
AJ785294.1	211869	3318.4	5003.8	5328.0	3289.5	3851.4	4595.7
CU927551.1	545730	391.7	748.5	907.7	215.0	353.6	1402.3
DQ351924.1	173105	350.6	697.4	1774.4	552.8	1969.3	2058.4
AF417552.1	27428	3070.1	4512.5	6881.3	4350.6	10266.0	12364.5
AY372184.1	94343	858.4	1660.6	5925.9	2808.3	12242.7	12409.3
EF516928.1	222831	1985.5	4373.9	8773.9	3051.4	11522.9	15591.7
AF208509.1	56515	7488.4	7279.0	6251.0	11293.8	17969.5	17180.9
AY904764.1	112297	944.6	2193.4	6957.9	3761.6	14812.1	16725.8
FJ382130.1	582075	2151.2	3170.9	2514.1	2659.7	5632.3	7379.5
AF417551.1	45827	119.4	275.4	406.7	199.1	2267.6	2359.8
AY904758.1	112060	1853.8	3037.9	7476.0	3821.3	16929.1	12393.2
FJ528273.1	573764	1071.3	1002.0	4335.9	2300.5	13006.9	14030.6
AF234889.2	77279	724.0	1138.9	7216.7	2904.6	14640.0	14610.8
AY904765.1	112064	2454.7	3815.0	10268.4	4059.8	20630.9	19609.0
FJ382683.1	510366	1176.3	2174.9	2317.7	1235.4	4576.1	5450.6
AY904743.1	111821	1908.8	3334.1	11856.0	4176.5	20933.0	20597.3
AF502220.1	55851	394.8	982.3	2614.0	112.7	108.8	207.4
EF032655.1	198655	541.6	1353.3	784.1	738.6	1695.4	2032.5
FJ380996.1	549917	2725.8	4442.5	3576.9	2260.3	8884.0	4910.8
AY178079.1	100322	907.3	1886.9	6941.1	2320.2	14288.4	16130.9
AY904732.1	111515	675.1	1352.1	6951.3	1939.3	16269.8	15168.1
AF409021.1	98929	7789.7	8980.2	6113.2	7690.5	16802.4	16833.6
D13430.1	4937	8354.1	8447.3	14163.9	7395.5	15454.7	13894.0
AB220164.1	153145	1954.3	2078.2	8273.2	3385.0	17709.6	14697.0
AF508112.1	66234	1280.4	2351.7	4364.0	1342.0	4375.3	5752.6
GU377100.1	514335	23.3	24.8	28.0	55.1	57.6	26.9
AY169423.1	81409	1379.1	1677.1	7556.2	2393.3	17365.9	13541.2
D78366.1	5055	178.3	334.1	2848.8	1190.3	10674.5	12346.9
GQ389186.1	582505	6325.5	7105.8	6273.1	6796.5	13946.9	11458.6

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