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FJ154847.1 gg_id:312556 Jujube witches'-broom phytoplasma str. ZQ FJ1548
U16758.1 gg_id:15696 Mycoplasma feliminutum str. ATCC 25749 U16758
EU006252.1 gg_id:257027 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU456203.1 gg_id:314291 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU456
FJ681157.1 gg_id:529539 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU794312.1 gg_id:354444 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L44 EU7943
EF604794.1 gg_id:228310 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EU774401.1 gg_id:315971 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1! EU7744
M25050.1 gg_id:15703 Anaeroplasma abactoclasticum M2505
EF604918.1 gg_id:231986 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EU344682.1 gg_id:262497 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
EU794279.1 gg_id:305348 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_G18 EU7942
FJ683969.1 gg_id:528228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
GQ897174.1 gg_id:555555 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ797091.1 gg_id:185593 human fecal clone RL386_aao86h04 DQ797
DQ797049.1 gg_id:179979 human fecal clone RL386_aao86c09 DQ797
NR_028691.1 gg_id:591314 Entomoplasma freundtii str. BARC318; ATCC 51999 NR_028
GQ275106.1 gg_id:581987 gut symbionts are tightly linked herbivory ants extract single ant clone #130 GQ275
AE017263.1 gg_id:100309 Mesoplasma florum L1 str. L1; ATCC 33453 AE0172
AY187288.1 gg_id:79099 Mesoplasma tabanidae str. BARC 857; ATCC 49584 AY1872
AF042194.1 gg_id:15792 Mycoplasma monodon str. Australiain AF0421
AY168929.2 gg_id:75831 Mesoplasma corruscae str. ATCC 49579 AY1689
AY166704.1 gg_id:76006 Mesoplasma chauliocola str. ATCC 49578 AY1667
DQ157864.1 gg_id:139255 Mycoplasma capricolum str. 700 DQ157
U26055.1 gg_id:15786 Mycoplasma putrefaciens str. KS-1 U26055
AY155670.1 gg_id:75155 Entomoplasma luminosum str. ATCC 49195; PIMN-1 AY1556
GQ275109.1 gg_id:568610 gut symbionts are tightly linked herbivory ants extract single ant clone #133 GQ275
GQ275144.1 gg_id:555846 gut symbionts are tightly linked herbivory ants extract single ant clone #168 GQ275
AY538169.1 gg_id:104104 Acholeplasma multilocale str. PN525 AY5381
AF303132.1 gg_id:71794 Mesoplasma lactucae str. 831-C4; ATCC 49193 ATCC AF3031
DQ861915.1 gg_id:168652 Spiroplasma cantharicola str. Q-6 DQ861
X63781.1 gg_id:15803 Spiroplasma citri str. R8A2HP X63781
DQ112020.1 gg_id:130516 Spiroplasma citri str. Car6 DQ112
AJ006775.1 gg_id:41072 Spiroplasma sp AJ0067
NR_025706.1 gg_id:534716 Spiroplasma lampyridicola str. PUP-1; ATCC 43206 NR_025
AY189309.1 gg_id:99424 Spiroplasma syrphidicola str. ATCC 33826; EA-1 AY1893
AY189132.1 gg_id:101796 Spiroplasma helicoides str. ATCC 51746; TABS-2 AY1891
AY345990.1 gg_id:93470 Entomoplasma melaleucae str. M1 AY3459
AY189125.1 gg_id:106072 Spiroplasma alleghenense str. ATCC 51752; PLHS-1 AY1891
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AY189133.1 gg_id:101955 Spiroplasma insolitum str. ATCC 33502; M55 AY1891
DQ917756.1 gg_id:258655 Spiroplasma mirum DQ917
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AY772395.1 gg_id:108248 Spiroplasma phoeniceum str. P40 AY7723
AY189318.1 gg_id:104368 Spiroplasma sp. str. TIUS-1 AY1893
AY189129.1 gg_id:106700 Spiroplasma culicicola str. ATCC 35112; AES-1 AY1891
DQ860101.1 gg_id:166158 Spiroplasma platyhelix str. PALS-1 DQ860
AY189305.1 gg_id:107782 Spiroplasma leptinotarsae str. ATCC 43213; LD-1B AY1893
NR_025703.1 gg_id:544767 Spiroplasma floricola str. 23-6; ATCC 29989 NR_025
DQ319068.1 gg_id:148669 Spiroplasma kunkelii str. CR2-3x DQ319
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AY325304.1 gg_id:100058 Spiroplasma melliferum str. BC-3 AY3253
NR_025709.1 gg_id:565097 Spiroplasma montanense str. HYOS-1; ATCC 51745 NR_025
AY189310.1 gg_id:103192 Spiroplasma turonicum str. ATCC 700271; Tab-4c AY1893
NR_025713.1 gg_id:561932 Spiroplasma velocicrescens str. MQ-4; ATCC 35262 NR_025
GQ129114.1 gg_id:526608 Prevalence geographical canine hemotropic mycoplasma infections Mediterranean GQ129
EF424082.1 gg_id:209237 Mycoplasma sp. China-1 EF4240
AY831867.1 gg_id:133123 Mycoplasma sp. 'feline hemotropic Switzerland' AY8318
DQ825454.1 gg_id:222355 Worldwide occurrence feline hemoplasma infections wild felid species Tanzania DQ825
NC_009497.1 gg_id:233772 Mycoplasma agalactiae str. PG2 NC_009
AF332745.1 gg_id:73703 Mycoplasma agalactiae str. 396/12 AF3327
AF332751.1 gg_id:70015 Mycoplasma agalactiae str. 35 AF3327
AF060821.1 gg_id:15907 Mycoplasma agassizii str. K120 AF0608
NR_025985.1 gg_id:565268 Mycoplasma alvi str. Isley; NCTC 10157 NR_025
AY531656.1 gg_id:111859 Mycoplasma amphoriforme str. M5572 AY5316
FJ226575.1 gg_id:326725 Mycoplasma amphoriforme str. A39 FJ2265
NR_029180.1 gg_id:550692 Mycoplasma gateae str. ATCC 23392 NR_029
CP001047.1 gg_id:308649 Mycoplasma arthritidis str. 158L3-1 CP0010
AF340023.1 gg_id:74000 Mycoplasma canis str. PG14 AF3400
AF412973.1 gg_id:70402 Mycoplasma citelli str. RG-2C(T) AF4129
FJ226571.1 gg_id:310264 Mycoplasma conjunctivae str. Goat 655 FJ2265
GU227404.1 gg_id:579318 Mycoplasma flocculare str. USP9T GU227
L08896.4 gg_id:15854 Mycoplasma gallisepticum str. A5969 L08896
AF412980.1 gg_id:72545 Mycoplasma gallopavonis str. WR1(T) AF4129
AY466443.1 gg_id:107609 Mycoplasma genitalium str. M2288 AY4664
DQ825438.1 gg_id:217964 Mycoplasma haemofelis 111 DQ825
EU930823.1 gg_id:340543 Mycoplasma haemofelis Porto Alegre EU9308
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AY150973.1 gg_id:71517 Mycoplasma haemocanis Germany Munich no. 1 AY1509

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NR_025064.1 gg_id:562555 Mycoplasma iners str. PG30; ATCC 19705 NR_02
EF447273.1 gg_id:210500 Mycoplasma iowae str. HTL04-4846A EF4472
AF221116.1 gg_id:47885 Mycoplasma maculosum PG15(T) AF221
U22415.1 gg_id:15832 Mycoplasma microti str. IL-372 U22415
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AF538961.1 gg_id:71629 Mycoplasma opalescens str. MHS408 AF5389
U44771.1 gg_id:15870 Mycoplasma ovipneumoniae str. Y-98 U4477
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EU827597.1 gg_id:349932 Mycoplasma phocidae str. CSL 7498-2 EU8275
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NC_000912.1 gg_id:108728 Mycoplasma pneumoniae str. M129 NC_00
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FJ263944.1 gg_id:316748 Mycoplasma suis str. HN FJ2639
AE017245.1 gg_id:200524 Mycoplasma synoviae str. 53 AE0172
U19768.1 gg_id:202917 Mycoplasma str. H3110 U19768
EU367963.1 gg_id:258287 Mycoplasma wenyonii cattle no. 48 EU3679
DQ530428.1 gg_id:233952 Mycoplasma zalophi str. CSL 5195 DQ530
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GQ502581.1 gg_id:590759 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AB089055.1 gg_id:78062 termite gut homogenate clone Rs-G80 AB089
U09788.1 gg_id:15851 Mycoplasma str. ATCC 43263 U09788
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AB192228.1 gg_id:142809 termite gut homogenate clone RsTu1-65 AB192
AF125879.1 gg_id:15849 Mycoplasma cavipharyngis str. 117C(T) AF1258
AB089057.1 gg_id:77895 termite gut homogenate clone Rs-E42 AB089
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NR_024981.1 gg_id:573950 Mycoplasma subdolum str. TB; ATCC 29870 NR_02
AY121109.1 gg_id:72631 Mycoplasma bovigenitalium 398/87 AY1211
FJ226566.1 gg_id:349001 Mycoplasma sp. str. LR5794 FJ2265
FM165076.1 gg_id:325252 Mycoplasma sp. 2F1AT str. 2F1A FM165
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NR_025186.1 gg_id:543508 Mycoplasma moatsii str. MK405; ATCC 27625 NR_02
AF412974.1 gg_id:28253 Mycoplasma collis str. 58B(T) AF412
AY050170.1 gg_id:60547 Mycoplasma timone AY050
AF412989.1 gg_id:28733 Mycoplasma verecundum str. GIH(T) AF412
FM878042.1 gg_id:557236 Mycoplasma sp. str. 51CL FM878
EF510815.1 gg_id:219506 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5108
AF125591.1 gg_id:15897 Mycoplasma falconis str. H/T1(T) AF125
DQ340198.1 gg_id:146814 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
AF150495.1 gg_id:15925 Mycoplasma sp. str. 94630 AF150
AF412981.1 gg_id:70918 Mycoplasma glycophilum str. 486(T) AF412
NR_024982.1 gg_id:567316 Mycoplasma gypis str. B1/T1; ATCC 51370 NR_02
NR_025914.1 gg_id:557285 Mycoplasma meleagridis str. 17529; ATCC 25294 NR_02
EF510816.1 gg_id:227513 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5108
AF412971.1 gg_id:69777 Mycoplasma buteonis str. BbT2g(T) AF412
M24582.1 gg_id:15954 Mycoplasma californicum M2458
U15795.1 gg_id:15943 Mycoplasma felifaucium str. ATCC 43428 U1579
EF510786.1 gg_id:220695 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5107
FM196534.1 gg_id:331374 Mycoplasma sp. str. Zaradi2 FM196
U09787.1 gg_id:15917 Mycoplasma felis str. ATCC 23391 U0978
AM182893.1 gg_id:190324 Mycoplasma sp. str. 11CL2 AM182
U16760.1 gg_id:15944 Mycoplasma leopharyngis str. ATCC 49889 U1676
AF170102.1 gg_id:15921 Mycoplasma capricolum AF170
AF221115.1 gg_id:19295 Mycoplasma lipofaciens R171(T) AF221
NR_025182.1 gg_id:555208 Mycoplasma dispar str. 462/2; ATCC 27140 NR_02
AY492086.1 gg_id:136766 Mycoplasma suis str. Guangdong AY492
AF178676.1 gg_id:51934 Candidatus Mycoplasma haemodidelphidis Illinois AF178
AF306346.1 gg_id:136331 Candidatus Mycoplasma haemolamae str. Michigan AF306
EU165510.1 gg_id:339052 Mycoplasma ovis Mo-Hu-3-05.2007 EU165
AY171918.1 gg_id:87318 Mycoplasma coccoides AY171
EF221880.1 gg_id:206167 Mycoplasma wenyonii str. CGXD EF2218
U82963.1 gg_id:15860 Mycoplasma haemomuris str. Shizuoka U8296
EU134687.1 gg_id:255073 tallgrass prarie soil clone FFCH10627 EU134
GU293201.1 gg_id:568172 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EF516576.1 gg_id:219640 grassland soil clone FCPT702 EF5165
AY500249.1 gg_id:102371 Candidatus Hepatoplasma crinochetorum clone 48 AY500
EU646193.1 gg_id:285164 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor EU646
EU646198.1 gg_id:280566 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor EU646
AF001173.1 gg_id:15899 Candidatus Mycoplasma ravipulmonis AF001
U62937.2 gg_id:15831 Ureaplasma gallorale str. ATCC 43346 U6293
GU227393.1 gg_id:580923 Ureaplasma sp. str. USP S/N GU227

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U06097.1 gg_id:15816 Ureaplasma urealyticum str. 354 (serovar 5) U0609
EU844042.1 gg_id:310545 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU459553.1 gg_id:294314 capybara feces clone CAP_aah99g08 EU459
FJ172803.1 gg_id:348767 Qinghai Yak Ruminal and Fungi China rumen clone RB-3C9 FJ1728
EU382038.1 gg_id:268757 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
FJ366886.1 gg_id:370110 feces adult twins and mothers; TS28 clone TS28_a01a06 FJ3668
FJ671998.1 gg_id:521062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
AF371530.1 gg_id:21652 swine intestine clone p-1735-b3 AF371
DQ805924.1 gg_id:175271 human fecal clone RL306aal92g01 DQ805
GQ167173.1 gg_id:567437 Effects Hydraulic Retention Time on Anaerobic Hydrogenation Performance Microbi GQ167
GQ897787.1 gg_id:578177 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ448417.1 gg_id:576850 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
GU303669.1 gg_id:561959 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AM275414.2 gg_id:234959 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
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FJ681340.1 gg_id:519348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
AM275475.2 gg_id:233848 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
GQ896843.1 gg_id:569244 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
FJ673493.1 gg_id:515507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ684684.1 gg_id:529404 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
GQ897386.1 gg_id:585199 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU474506.1 gg_id:292635 bighorn sheep feces clone BHSD_aaa03h12.Contig2 EU474
GU303586.1 gg_id:566240 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU850597.1 gg_id:311889 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF427 EU850
AY985740.1 gg_id:117030 human stool clone C771 AY985
GQ451187.1 gg_id:513605 Fecal Yunnan snub-nosed monkey feces clone J19 GQ451
FJ673434.1 gg_id:518672 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF445272.1 gg_id:213966 dairy cow rumen clone NED4E12 EF4452
DQ057362.1 gg_id:131450 chicken ileum/cecum clone cc106 DQ057
EU773287.1 gg_id:306877 BigHorn sheep feces clone BH1_aao27e05 EU773
DQ326418.1 gg_id:148285 Metagenomic gut microbiome healthy human stool clone C469 DQ326
FJ673790.1 gg_id:515508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
EU844544.1 gg_id:325403 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ680415.1 gg_id:515855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ673176.1 gg_id:527857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU344185.1 gg_id:277047 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU475428.1 gg_id:297545 springbok feces clone SBSD_aaa04g12 EU475
EU850542.1 gg_id:342412 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF336 EU850

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FJ367190.1 gg_id:367962 feces adult twins and mothers; TS28 clone TS28_a04e12 FJ3671
FJ678613.1 gg_id:531345 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
AY916353.1 gg_id:114378 human stool clone D051 AY9163
EU381774.1 gg_id:265197 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ832322.1 gg_id:558715 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_19C03 FJ8323
EU463631.1 gg_id:303133 domesticated horse feces clone horsej_aai90a12 EU463
FJ440078.1 gg_id:567506 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
FJ682646.1 gg_id:513042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
EU844825.1 gg_id:327546 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU871410.1 gg_id:324570 Genetic Bovine (Bos taurus) Rumen Thailand clone CF378 EU8714
DQ456306.1 gg_id:158491 pre-adolescent turkey cecum clone CFT211G6 DQ456
EU381733.1 gg_id:265925 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
DQ353915.1 gg_id:146314 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z32 DQ353
EU843681.1 gg_id:325563 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU844239.1 gg_id:327857 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8442
AF001742.1 gg_id:15698 rumen clone RF9 AF0017
GQ451225.1 gg_id:545091 Fecal Yunnan snub-nosed monkey feces clone J128 GQ451
AM277561.2 gg_id:229533 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
GU303762.1 gg_id:580081 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU622737.1 gg_id:279179 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
AY916186.1 gg_id:114444 human ascending colon biopsy clone LW88 AY9161
EU344299.1 gg_id:271356 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
FJ833479.1 gg_id:591398 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_78F10 FJ8334
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EF406725.1 gg_id:211308 mouse colon clone infected_14days-B9 EF4067
EU842453.1 gg_id:316729 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
AY986020.1 gg_id:127092 human stool clone D332 AY9860
EU764308.1 gg_id:341905 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
FJ172880.1 gg_id:352691 Qinghai Yak Ruminal and Fungi China rumen clone RB-2D1 FJ1728
EU844758.1 gg_id:347587 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8447
GU476604.1 gg_id:522127 microbial biogas fermentation enrichment clone BBMC-4 GU476
GU208279.1 gg_id:537538 Study on Sediment Dongping Lake sediment clone 6F1-3 GU208
EU358689.1 gg_id:325820 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3586
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AB192099.1 gg_id:143019 termite gut homogenate clone M1NP1-24 AB1920
AB192110.1 gg_id:144845 termite gut homogenate clone M1PT4-30 AB1921
AB255930.1 gg_id:164433 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
EF454354.2 gg_id:220027 termite hindgut clone 290cost002-P3L-1996 EF4543
EF454970.2 gg_id:227321 termite hindgut clone 290cost002-P3L-828 EF4549
AB243293.1 gg_id:149384 acetone-preserved termite gut clone M2PB4a-088 AB2432
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GQ348358.1 gg_id:560472 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AY876379.1 gg_id:111757 Deinococcus deserti str. VCD117 AY8763
AJ585983.1 gg_id:97958 Deinococcus sp. str. AA752 AJ5859
AJ585981.1 gg_id:97107 Deinococcus sp. str. AA692 AJ5859
NZ_AAHE01000002.1 gg_id:131883 Deinococcus geothermalis str. DSM 11300 NZ_AA
AAHE01000005.1 gg_id:134272 Deinococcus geothermalis str. DSM 11300 AAHE0
AY743256.1 gg_id:138843 Deinococcus hohokamensis str. KR-40 AY7432
AY743275.1 gg_id:138931 Deinococcus maricopensis str. KR-1 AY7432
AB264133.1 gg_id:171820 Deinococcus sp. str. TDMA-21 AB2641
AY743280.1 gg_id:138834 Deinococcus papagonensis str. KR-241 AY7432
AE000513.1 gg_id:146329 Deinococcus radiodurans str. R1 AE0005
AY743284.1 gg_id:138790 Deinococcus sonorensis str. KR-90 AY7432
GQ043868.1 gg_id:461798 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EF141348.1 gg_id:247857 Deinococcus peraridilitoris str. KR-200 EF1413
AY743267.1 gg_id:139200 Deinococcus apachensis str. KR-32 AY7432
AM988777.1 gg_id:568744 Deinococcus sp. str. K4.1 AM988
AF385541.1 gg_id:136570 Prevalent species and phylotypes advanced noma lesions Deinococcus oral clone CB(AF3855
DQ532354.2 gg_id:168505 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
EU834252.1 gg_id:347125 Deinococcus aquaticus str. DS27 EU8342
DQ883809.1 gg_id:163551 Deinococcus cellulolytica str. 5516J-15 DQ883
NR_026403.1 gg_id:562641 Deinococcus radiopugnans str. ATCC 19172 NR_02
EU029127.1 gg_id:238409 Deinococcus sp. str. 2A2 EU0291
EF635408.1 gg_id:285250 Deinococcus alpinitundrae str. ME-04-04-52 EF6354
GQ357648.1 gg_id:546802 Deinococcus sp. str. YIM 75723 GQ357
GQ441240.1 gg_id:556010 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
EU029130.1 gg_id:250755 Deinococcus sp. str. 3A5 EU0291
AB374383.1 gg_id:271722 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
M21413.1 gg_id:1418 Deinococcus radiodurans M2141
EU626561.1 gg_id:282134 Deinococcus xinjiangensis str. X-82 EU6265
DQ022077.1 gg_id:136712 Truepera radiovictrix str. TU-8 DQ022
EU622978.1 gg_id:279041 Deinococcus sp. str. 5516T-9 EU6229
EU427464.1 gg_id:264010 Deinococcus sp. str. I-0 EU4274
GQ058151.1 gg_id:406491 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ058
AY743279.1 gg_id:138901 Deinococcus yavapaiensis str. KR-236 AY7432
EU362143.1 gg_id:332198 and Mesquite Flats Site Death Valley dune sand clone 14 EU3621
EF522236.1 gg_id:219134 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS01 EF5222
GQ058104.1 gg_id:395808 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ058
AM283039.1 gg_id:159842 Deinococcus sp. str. Han23 AM283
GQ072152.1 gg_id:389682 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw192g11 GQ072
AM292065.1 gg_id:249433 Deinococcus radiodurans zf-69-II AM292
GQ130053.1 gg_id:435637 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130

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DQ130032.1 gg_id:138316 microbial biota normal forearm human skin clone GL109 DQ130
DQ847439.1 gg_id:170011 human forearm skin clone GL2-41 DQ847
DQ366016.1 gg_id:152980 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 21 DQ366
EU622979.1 gg_id:279558 Deinococcus sp. str. 5516T-11 EU622
AB473897.1 gg_id:568788 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB473
DQ883808.1 gg_id:169628 Deinococcus aeria str. 5516J-6 DQ883
GQ130015.1 gg_id:405062 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130
FJ444684.1 gg_id:562787 Cotton Rhizosphere cotton rhizosphere clone 2y-56 FJ4446
FJ176238.1 gg_id:307654 Deinococcus sp. str. ZLM-202 FJ1762
GQ026439.1 gg_id:453803 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
EU029134.1 gg_id:250725 Deinococcus sp. str. 5A5 EU029
AM940971.1 gg_id:263628 Deinococcus aquatilis str. CCUG 53370 AM940
AJ585985.1 gg_id:95404 Deinococcus sp. str. AA69 AJ5859
GQ052823.1 gg_id:377731 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
DQ223543.2 gg_id:171337 Deinococcus sp. X2 DQ223
FM872722.1 gg_id:365101 occupant source house floor dust clone FB01A10 FM872
AY743278.1 gg_id:139150 Deinococcus pimensis str. KR-242 AY743
AY250871.1 gg_id:86556 lichen-dominated Antarctic cryptoendolithic community clone FBP266 bacterium AY250
GU214174.1 gg_id:593108 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
DQ366015.1 gg_id:153959 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3 DQ366
DQ130037.1 gg_id:137532 microbial biota normal forearm human skin clone GR66 DQ130
GQ023518.1 gg_id:486153 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319e11 GQ023
DQ683348.1 gg_id:172621 Deinococcus piscis str. 3ax DQ683
NR_026421.1 gg_id:555743 Meiothermus cerbereus str. GY-1 NR_02
DQ916146.1 gg_id:167558 Meiothermus rosaceus str. WQBGR2-3 DQ916
NR_027614.1 gg_id:543137 Meiothermus ruber 1279 str. DSM 1279; ATCC 35948 NR_02
AJ871173.1 gg_id:114851 Meiothermus ruber str. SPS-242 AJ8711
X84211.1 gg_id:1405 Meiothermus silvanus str. V1-R2 X84211
AF418002.1 gg_id:20802 Meiothermus taiwanensis str. WR-220 AF418
AF418001.1 gg_id:26209 Meiothermus taiwanensis str. WR-30 AF418
AJ871171.1 gg_id:114643 Meiothermus timidus str. RQ-12 AJ8711
DQ899883.1 gg_id:238702 structure receiving long-term augmentations chromium contaminated wastes landfi DQ899
NR_026244.1 gg_id:540285 Meiothermus chliarophilus str. ALT-8; ATCC 700543; BCRC 17113 NR_02
AJ871172.1 gg_id:114775 Meiothermus ruber str. SPS-241 AJ8711
L37521.1 gg_id:1398 Thermus sp str. ac-2 L37521
FN178497.1 gg_id:573829 Meiothermus sp. str. CAL-12 FN178
EU249978.1 gg_id:239060 Polyphasic description Pocillopora mucus secreted Pacillopora meandrina coral color EU249
AB107956.1 gg_id:85579 Oceanithermus desulfurans str. St55B AB107
Y18412.1 gg_id:35343 Thermus antranikianii str. HE-5 Y18412
NR_026501.1 gg_id:533728 Thermus igniterrae str. RF-4; DSM 12459 NR_02

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EU616794.1 gg_id:273039 Thermus thermophilus str. WG EU616
AY557603.1 gg_id:105041 Thermus yunnanensis AY557
NR_025901.1 gg_id:535809 Thermus filiformis str. Wai33; ATCC 43280 NR_02
Y18409.1 gg_id:30085 Thermus brockianus str. 15038T Y18409
Y18416.1 gg_id:45920 Thermus oshimai str. SPS-17T Y18416
AF018197.1 gg_id:1324 temperature clone env.OPS 15 AF018
L09663.1 gg_id:1345 Thermus aquaticus L09663
AF331969.1 gg_id:41572 Thermus rehai str. RH99-02 AF331
FJ638543.1 gg_id:511615 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
GU233838.1 gg_id:537430 effects temperature pH salinity and sinter growth rate on microbial Icelandic waters GU233
AY861866.1 gg_id:112463 Obsidian Pool prime community clone OPPB146 AY861
AF020205.1 gg_id:1335 Thermus scotoductus str. SA-01 AF020
EU701067.3 gg_id:290466 Thermus sp. str. K-39 EU701
Y18408.1 gg_id:47782 Thermus igniterrae str. GE-2 Y18408
EU924248.1 gg_id:326104 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C EU924
AB071811.1 gg_id:24092 Thermus kawarayuensis str. KW11 AB071
EU753248.1 gg_id:352672 Thermus sp. str. PRI-2268 EU753
AY028380.1 gg_id:67904 Thermus sp. str. C4 AY028
AF521188.1 gg_id:63588 Thermus sp. str. RH-1514 AF521
L77877.1 gg_id:106875 Thermothrix thiopara L77877
L37522.1 gg_id:1357 Thermus sp str. ac-7 L37522
AF255591.1 gg_id:17962 Thermus sp. str. SRI-248 AF255
Y18410.1 gg_id:26144 Thermus scotoductus str. ITI-252T Y18410
AJ507298.1 gg_id:60062 Vulcanithermus mediatlanticus str. TR AJ5072
DQ832056.1 gg_id:165232 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
DQ832059.1 gg_id:165655 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
NR_028639.1 gg_id:540517 Marinithermus hydrothermalis str. T1; JCM 11576 NR_02
DQ832060.1 gg_id:173448 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
DQ924664.1 gg_id:177658 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
DQ924670.1 gg_id:189281 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
EU435435.1 gg_id:273276 Thermodesulfatator sp. str. AT1325 EU435
AJ969460.1 gg_id:157635 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AY280428.1 gg_id:102075 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
AB282756.1 gg_id:230931 Thermosulfidobacterium lithotrophicum str. ABI70S6 (= JCM13301 = DSM 17441 AB282
EU635930.1 gg_id:279109 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EF077228.1 gg_id:253157 Anaerobic oxidation short-chain hydrocarbons marine sulphate-reducing Guaymas B EF0772
AM712345.1 gg_id:247140 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
NR_025146.1 gg_id:570497 Thermodesulfobacterium hydrogeniphilum str. SL6; DSM 14290 NR_02
FJ638609.1 gg_id:537018 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6386
AF419676.1 gg_id:25647 Guaymas Basin hydrothermal sediment clone a2b002 AF419

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CU924090.1 gg_id:565047 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
Z49117.1 gg_id:1227 Fervidobacterium gondwanense Z49117
EU851047.2 gg_id:325520 Fervidobacterium sp. str. 1445t EU851
AF509468.1 gg_id:66261 Geotoga aestuarianus str. T3B AF5094
EU245202.1 gg_id:245616 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-A11 EU245
DQ080153.1 gg_id:128210 sediment clone BFA-T46 DQ080
DQ080178.1 gg_id:128351 sediment clone A2 DQ080
DQ080154.1 gg_id:133990 sediment clone BFA-K27 DQ080
CP001634.1 gg_id:422862 Kosmotoga olearia str. TBF 19.5.1 CP001
CU918298.1 gg_id:557400 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU542473.1 gg_id:258468 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FJ901103.1 gg_id:540611 Polymorphism microbial reservoirs water cut stage oil field clone Z-49 FJ9011
AB530678.1 gg_id:539611 Kosmotoga sp. str. S304 AB530
AJ431250.1 gg_id:107334 Thermotogales str. Dex60-136 AJ4312
AJ250439.1 gg_id:1220 Marinitoga camini MV1075 AJ2504
FM253687.1 gg_id:341893 Marinitoga sp. str. MC3 FM253
AJ431249.1 gg_id:79381 Thermotogales str. Dex60-32 AJ4312
DQ834030.1 gg_id:167691 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ834
CP000879.1 gg_id:256420 Petrotoga mobilis str. SJ95 CP000
EU999020.1 gg_id:321922 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
GQ385331.1 gg_id:575997 Petrotoga sp. str. AR80 GQ385
NR_029058.1 gg_id:590603 Petrotoga mexicana str. Met-12; DSM 14811; CIP 107371 NR_02
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AAWB01000011.1 gg_id:187003 Thermotoga petrophila str. RKU-1 AAWB
EU924246.1 gg_id:303956 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU924
AJ401017.1 gg_id:72408 Thermotoga maritima str. SL7 AJ401
AY526506.1 gg_id:136778 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone H8 AY526
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AJ401016.1 gg_id:35101 Thermotoga neapolitana str. NES AJ401
AJ431248.1 gg_id:79590 Thermotogales str. BHI80-139 AJ431
FN429790.1 gg_id:588200 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN429
DQ676372.1 gg_id:226370 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
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AF268992.1 gg_id:32172 obtained sequencing batch reactor and sequenced Paul Burrell clone SBRH58 AF268
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EF530679.1 gg_id:225631 Extremely acidic pendulous biofilms Frasassi cave system Italy microbial biofilm clone EF5306
AF507714.1 gg_id:65675 forest soil clone S1198 AF507
AY261809.1 gg_id:82807 UASB reactor granular sludge clone PD-UASB-12 AY261
AJ387898.1 gg_id:50582 TCB-dechlorinating consortium? clone C1-3 AJ3878
AJ009448.1 gg_id:10538 chlorobenzene-degrading consortium clone SJA-4 AJ0094
U81641.2 gg_id:10536 anaerobic sludge clone vadinBA07 U8164
EU038004.1 gg_id:238619 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and c EU038
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GU208307.1 gg_id:586450 Study on Sediment Dongping Lake sediment clone Ftt4-19 GU208
DQ499213.1 gg_id:159549 acidic cave snottite biofilm clone DSJB30 DQ499
EU037998.1 gg_id:247518 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and c EU037
EF516771.1 gg_id:226009 grassland soil clone FCPN632 EF5167
EU135363.1 gg_id:242950 tallgrass prarie soil clone FFCH1293 EU135
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GQ402802.1 gg_id:576700 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU386052.1 gg_id:259809 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386

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AY945884.1 gg_id:148869 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal AY945
FJ466109.1 gg_id:571249 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ542881.1 gg_id:528972 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
GU172187.1 gg_id:555087 Microbial Eucalyptus plantation soil clone DSM-R15 GU172
DQ395404.1 gg_id:154700 deep-sea octacoral clone ctg_BRRAA28 DQ395
EU385703.1 gg_id:272615 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
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EU038006.1 gg_id:239453 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc EU038
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DQ070831.1 gg_id:146798 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
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DQ404638.1 gg_id:152373 contaminated sediment clone 654967 DQ404
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EU135398.1 gg_id:257656 tallgrass prarie soil clone FFCH4275 EU135
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AY571850.1 gg_id:107654 hydrocarbon-contaminated soil clone 342B AY5718
EU861950.1 gg_id:316001 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
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AF507688.1 gg_id:65695 forest soil clone C1105 AF5076
FJ542918.1 gg_id:515209 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
EU703288.1 gg_id:566066 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF688335.1 gg_id:238281 soil clone F1-127 EF6883
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DQ815839.1 gg_id:169901 mouse cecum clone aab23a06 DQ815
AF432141.1 gg_id:17020 oral clone FR058 AF4321
EU431764.1 gg_id:575675 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
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GQ057266.1 gg_id:377444 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
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AF015925.1 gg_id:13724 hot spring clone OctSpA1-106 AF015
AF419683.1 gg_id:112352 Guaymas Basin hydrothermal sediment clone CS_B017 AF419
EU385715.1 gg_id:267027 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
GQ502666.1 gg_id:576499 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9- GQ502
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EF520638.1 gg_id:230312 structure lakes: what controls ? acid-impacted lake clone ADK-SGe02-31 EF5206
NC_010794.1 gg_id:295454 Methylokorus infernorum str. V4 NC_01
EU419170.1 gg_id:260358 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
EU419167.1 gg_id:274373 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
EU419166.1 gg_id:266894 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
FJ638587.1 gg_id:511517 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AJ229235.1 gg_id:1561 Opitutus terrae str. PB90-1 AJ2292
X99391.1 gg_id:1558 Opitutus sp. str. VeCb1 X99391
X99392.1 gg_id:1559 Opitutus sp. str. VeSm13 X99392
AM162468.1 gg_id:153174 and situ identification acidic sphagnum peat bog clone B70 AM162
AY922067.1 gg_id:114313 farm soil clone AKYG804 AY922
FJ478682.1 gg_id:567922 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FM866301.1 gg_id:357272 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-182 FM866
AY661974.1 gg_id:136998 uranium-contaminated groundwater clone 300G-H06 AY661
AM162467.1 gg_id:156120 and situ identification acidic sphagnum peat bog clone B36 AM162
EU800822.1 gg_id:350772 It's all ranking aquatic Delaware Bay NJ clone 2C229041 EU800
EF516172.1 gg_id:231447 grassland soil clone FCPT606 EF5161
AY297806.1 gg_id:89313 archaeological wood clone? pACH90 AY297
FJ769447.1 gg_id:553713 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7694
AB240503.1 gg_id:144089 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
GQ339177.1 gg_id:526112 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
AB369167.1 gg_id:237121 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AJ575730.1 gg_id:96609 lake water clone SW59 AJ5757
GQ264061.1 gg_id:566392 Structure Simulated Level Waste Site simulated level waste site clone WC3_16 GQ264
AB369179.1 gg_id:245910 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
GQ502665.1 gg_id:542290 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9- GQ502
AY820718.1 gg_id:109053 drilling fluid clone CCSD_DF2030_B14 AY820
DQ833492.1 gg_id:167091 detected analyses depth sediment Guanting Reservoir clone 35-54 DQ833
AY587231.1 gg_id:106739 termite gut clone AY587

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AJ633978.1 gg_id:114788 host's accessory nidamental gland clone I1ANG45 AJ6339
EU015115.1 gg_id:253831 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
AB286360.1 gg_id:216828 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AB062814.1 gg_id:18774 termite gut homogenate clone BCf3-05 AB0628
EU135529.1 gg_id:246267 tallgrass prarie soil clone FFCH9358 EU135
AY622244.1 gg_id:107299 subsurface soil clone B-I12 AY622
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DQ539046.1 gg_id:161645 Puniceibacter vermicola str. IMCC1545 DQ539
AB299565.1 gg_id:241161 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
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EU803670.1 gg_id:338096 It's all ranking aquatic Lake Gatun clone 5C231275 EU803
DQ302114.1 gg_id:153206 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
FM242275.1 gg_id:341545 sequences sediment clone 13bis T0h-oil FM242
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U81738.2 gg_id:1556 anaerobic digestor clone vadinHA64 U81738
AY695840.1 gg_id:105129 Opitutus sp. str. SA-9 AY6958
FM242391.1 gg_id:310512 sequences sediment clone 89 T12d-oil FM242
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EU617885.1 gg_id:332206 Seasonal variation microbial Yel Sea sediment clone D13S-153 EU617
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AB198611.1 gg_id:135899 termite gut fluid and protists fraction clone RsC01-040 AB198
EU283474.1 gg_id:278788 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A210 EU2834
AB299566.1 gg_id:256775 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
AB073978.1 gg_id:41135 Fucophilus fucoidanolyticus str. SI-1234 AB073
EU328081.1 gg_id:278462 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU328
FJ745063.1 gg_id:545467 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7450
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AB192188.1 gg_id:143442 termite gut homogenate clone RsTz-69 AB192
FJ516822.1 gg_id:513750 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5168
AF075271.2 gg_id:9675 Alterococcus agarolyticus str. ADT3; CCRC17102 AF075
FJ717327.1 gg_id:535151 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
FJ717277.1 gg_id:511489 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717325.1 gg_id:510475 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
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AB189371.1 gg_id:114335 cold seep sediment clone JT75-134 AB189
AF449255.1 gg_id:61856 vent worm clone R76-B128 AF449

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EU287160.1 gg_id:240419 Pacific arctic surface sediment clone P13-67 EU287
FJ717273.1 gg_id:510216 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717296.1 gg_id:510340 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717311.1 gg_id:572386 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
FJ717270.1 gg_id:568860 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FM165269.1 gg_id:564018 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
FJ717291.1 gg_id:548455 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
EU804364.1 gg_id:341372 It's all ranking aquatic 250 miles Panama City clone 6C232274 EU804
DQ513023.1 gg_id:160321 Microbial life fluids ridge flank crustal fluid clone FS142-12B-02 DQ513
AY222315.1 gg_id:113883 host hindgut caecum clone Ver 1 AY222
EF520620.1 gg_id:232855 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-31 EF5206
AJ575731.1 gg_id:97376 lake water clone NE06 AJ5757
EU703279.1 gg_id:554393 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF520637.1 gg_id:231528 structure lakes: what controls ? acid-impacted lake clone ADK-HDh02-03 EF5206
AY752089.1 gg_id:99083 lake water clone P38.12 AY752
FJ543046.1 gg_id:519253 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
FJ543079.1 gg_id:527379 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AJ863245.1 gg_id:127649 poplar tree microcosm, bulk soil, flooded clone 21BSF50 AJ8632
EF516165.1 gg_id:221896 grassland soil clone FCPP479 EF5161
FJ612408.1 gg_id:535790 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.22 FJ6124
AY792308.1 gg_id:123679 Humic Lake clone CrystalBog1B6 AY7923
AB369162.1 gg_id:256945 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AY388649.1 gg_id:108024 Chthoniobacter flavus AY3886
DQ450786.1 gg_id:160871 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EF516096.1 gg_id:224503 grassland soil clone FCPT710 EF5160
EF515981.1 gg_id:220364 grassland soil clone FCPT465 EF5159
EF516968.1 gg_id:223379 grassland soil clone FCPS729 EF5169
FJ822655.1 gg_id:588551 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
AY960766.1 gg_id:115027 Detection and Cultivation Soil Verrucomicrobia Ellin503 AY9607
EU135441.1 gg_id:251499 tallgrass prarie soil clone FFCH5517 EU1354
AB486453.1 gg_id:588961 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB374368.1 gg_id:270180 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
GQ402701.1 gg_id:541789 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF516529.1 gg_id:221334 grassland soil clone FCPN729 EF5165
FJ822636.1 gg_id:535268 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
GQ397058.1 gg_id:538238 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
FM877557.1 gg_id:358664 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-321 FM877
AY960770.1 gg_id:114998 Detection and Cultivation Soil Verrucomicrobia Ellin507 AY9607

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EU131041.1 gg_id:236458 alkaline China coal mine soil clone SIP CM42 EU131
EU644180.1 gg_id:286072 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
EF018510.1 gg_id:214306 aspen rhizosphere clone Amb_16S_1148 EF0185
EF018524.1 gg_id:207125 aspen rhizosphere clone Amb_16S_784 EF0185
GQ264267.1 gg_id:511817 Structure Simulated Level Waste Site simulated level waste site clone WW1_b71 GQ264
FJ822653.1 gg_id:554650 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
DQ228393.1 gg_id:142335 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU135556.1 gg_id:249859 tallgrass prarie soil clone FFCH4930 EU135
AY212589.1 gg_id:104784 water 10 m downstream manure clone 139ds10 AY212
FM253596.1 gg_id:325609 Rock gold mine unusually microbial biofilm clone D07-1 FM253
AY960769.1 gg_id:115085 Detection and Cultivation Soil Verrucomicrobia Ellin506 AY960
EU881176.1 gg_id:354713 Karst region natural restoration land soil clone KNR200711-119 EU881
AY395330.1 gg_id:100320 pasture soil clone EB1011 AY395
AY326520.1 gg_id:136989 Amazon soil clone 28-1 AY326
AY218772.1 gg_id:82424 penguin droppings sediments clone KD6-84 AY218
AY395325.1 gg_id:104976 pasture soil clone EB1006 AY395
EF018259.1 gg_id:213922 aspen rhizosphere clone Amb_16S_615 EF0182
EF516966.1 gg_id:223148 grassland soil clone FCPS574 EF5169
EF494340.1 gg_id:222682 Nunnock River granitic landscape clone NR.1.035 EF4943
EF516048.1 gg_id:222701 grassland soil clone FCPS405 EF5160
FJ592654.1 gg_id:557191 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
Y07576.1 gg_id:1624 grassland soil clone DA101 Y07576
DQ298012.1 gg_id:143982 Microbial hydrocarbon contaminated soil clone UA4 DQ298
EU881274.1 gg_id:335630 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EF018412.1 gg_id:213519 aspen rhizosphere clone Amb_16S_1028 EF0184
EU861826.1 gg_id:320598 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
EU881282.1 gg_id:320201 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EF494343.1 gg_id:227202 Nunnock River granitic landscape clone NR.1.076 EF4943
DQ404689.1 gg_id:154629 contaminated sediment clone 655902 DQ404
FJ822650.1 gg_id:582528 and metagenomic Verrucomicrobia former agricultural grassland rhizosphere soil clor FJ8226
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EF516045.1 gg_id:217322 grassland soil clone FCPN578 EF5160
DQ395984.1 gg_id:155782 deep-sea octacoral clone ctg_CGOGA62 DQ395
EF019129.1 gg_id:212017 aspen rhizosphere clone Amb_16S_1762 EF0191
EF516305.1 gg_id:225899 grassland soil clone FCPN716 EF5163
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EF019121.1 gg_id:206632 aspen rhizosphere clone Amb_16S_1750 EF0191
FM877556.1 gg_id:359072 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-107 FM877
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EF019126.1 gg_id:209352 aspen rhizosphere clone Amb_16S_1757 EF0191
EF516261.1 gg_id:220494 grassland soil clone FCPO467 EF5162
EF019883.1 gg_id:211980 aspen rhizosphere clone Elev_16S_1248 EF0198
GQ356142.1 gg_id:594250 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
CU919143.1 gg_id:572340 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918228.1 gg_id:549254 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU920760.1 gg_id:571409 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EU773048.1 gg_id:331675 Banteng feces clone BG_aaa03d04.Contig1 EU773
EU471776.1 gg_id:294166 Asiatic elephant feces clone AE2_aaa01b10 EU471
EU771419.1 gg_id:339447 Asiatic elephant feces clone AE1_aaa02h11 EU771
EU463717.1 gg_id:297614 domesticated horse feces clone horsej_aai91e11 EU463
EU471538.1 gg_id:291474 Asiatic elephant feces clone AE1_aaa02e02 EU471
EU471740.1 gg_id:291133 Asiatic elephant feces clone AE2_aaa04d02 EU471
EU473570.1 gg_id:300038 Somali wild ass feces clone WA_aaa01g06 EU473
EU775815.1 gg_id:338441 Horse feces clone horsem_aai95h08 EU775
EU471942.1 gg_id:292730 Asiatic elephant feces clone AE3_aaa04e08 EU471
EU471839.1 gg_id:298259 Asiatic elephant feces clone AE2_aaa02c03 EU471
EU471710.1 gg_id:288899 Asiatic elephant feces clone AE2_aaa01a07 EU471
EU773126.1 gg_id:349774 Banteng feces clone BG_aaa02h07.Contig1 EU773
AB185519.1 gg_id:99547 rumen clone F23-B04 AB185
EU470381.1 gg_id:298808 Grevy's zebra feces clone GZ_aaa02b08 EU470
EU776446.1 gg_id:326916 Red Kangaroo feces clone KO2_aai18a10 EU776
EU864491.1 gg_id:327984 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU864
AB015546.1 gg_id:203309 deep-sea sediments depths clone BD2-18 AB015
AY114334.1 gg_id:63771 anoxic marine sediment clone LD1-PB20 AY114
CU920931.1 gg_id:556915 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
GQ259319.1 gg_id:534591 Microbial activities coastal marine sediments and water column Svalbard surface se GQ259
FN396736.1 gg_id:546665 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
AY114328.1 gg_id:70013 anoxic marine sediment clone LD1-PA50 AY114
AY963317.1 gg_id:151682 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
EU881223.1 gg_id:333383 Karst region natural restoration land soil clone KNR200711-042 EU881
EU135433.1 gg_id:257941 tallgrass prarie soil clone FFCH3955 EU135
AM162463.1 gg_id:154318 and situ identification acidic sphagnum peat bog clone B69 AM162
EU135525.1 gg_id:236593 tallgrass prarie soil clone FFCH8458 EU135
EU135455.1 gg_id:240895 tallgrass prarie soil clone FFCH1225 EU135
EF516767.1 gg_id:220193 grassland soil clone FCPT575 EF5167
EU135479.1 gg_id:251458 tallgrass prarie soil clone FFCH10633 EU135
AF465651.1 gg_id:50325 thermal soil clone YNPRH34A AF465
EU135506.1 gg_id:249781 tallgrass prarie soil clone FFCH14037 EU135

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EF019719.1 gg_id:215142 aspen rhizosphere clone Elev_16S_885 EF0197
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EF516676.1 gg_id:221568 grassland soil clone FCPO598 EF5166
DQ676318.1 gg_id:221692 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AY212643.1 gg_id:107428 water 20 m upstream manure clone 190up AY2126
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FM209351.1 gg_id:567812 Microbial Negev desert s sand soil clone 2031 FM209
AM162456.1 gg_id:155778 and situ identification acidic sphagnum peat bog clone B52 AM162
FJ625341.1 gg_id:551837 Influence lead contamination on boreal pine forest soil clone HF_NC_2 FJ6253
AM162459.1 gg_id:151165 and situ identification acidic sphagnum peat bog clone B129 AM162
FJ479471.1 gg_id:512910 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF516574.1 gg_id:221251 grassland soil clone FCPP665 EF5165
EU335294.1 gg_id:251275 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EU135503.1 gg_id:238929 tallgrass prarie soil clone FFCH13652 EU135
DQ676422.1 gg_id:220892 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
EU335227.1 gg_id:248808 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
FJ478628.1 gg_id:512539 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
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EF516222.1 gg_id:218456 grassland soil clone FCPT508 EF5162
AJ617869.1 gg_id:110756 oxic-anoxic interphase flooded paddy soil clone D142114 AJ6178
EF516552.1 gg_id:217929 grassland soil clone FCPU600 EF5165
DQ125505.1 gg_id:132722 uranium contaminated soil clone AKAU3464 DQ125
FJ479069.1 gg_id:590252 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
AJ863241.1 gg_id:126772 poplar tree microcosm bulk soil flooded clone 21BSF21 AJ8632
EF516075.1 gg_id:223550 grassland soil clone FCPT406 EF5160
DQ450782.1 gg_id:161263 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU937949.1 gg_id:321753 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EF515942.1 gg_id:225894 grassland soil clone FCPP485 EF5159
FJ468383.1 gg_id:585431 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes FJ4683
EU135478.1 gg_id:250253 tallgrass prarie soil clone FFCH10577 EU135
EU135518.1 gg_id:253183 tallgrass prarie soil clone FFCH17360 EU135
AF523995.1 gg_id:63232 coal effluent wetland clone FW4 AF523
EF612425.1 gg_id:248066 historic semiarid lead-zinc mine tailings site soil clone OS-C04 EF6124
EF019315.1 gg_id:206560 aspen rhizosphere clone Elev_16S_510 EF0193
AM162462.1 gg_id:155827 and situ identification acidic sphagnum peat bog clone B64 AM162
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AM162461.1 gg_id:151640 and situ identification acidic sphagnum peat bog clone B147 AM162
DQ521482.1 gg_id:186160 Antarctic lake ice cover clone ANTLV1_D01 DQ521
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FJ592707.1 gg_id:543327 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5927
EU335255.1 gg_id:241999 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EF516775.1 gg_id:218032 grassland soil clone FCPU668 EF5167
GQ348914.1 gg_id:560563 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ155059.1 gg_id:318309 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone CB FJ1550
GQ348513.1 gg_id:542753 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ348797.1 gg_id:535223 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
DQ302118.1 gg_id:156301 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
FJ628330.1 gg_id:513658 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6283
FJ615181.1 gg_id:544538 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 125m anoxi FJ6151
FJ615159.1 gg_id:557490 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 100m anoxi FJ6151
DQ071110.1 gg_id:131960 marine surface water clone SJC1.38 DQ071
AY028219.1 gg_id:32593 marine clone Arctic97B-4 AY0282
DQ071044.1 gg_id:130139 islts and fld smplng Glf Strm Rng chlrphll mxmm cln Chl1.3 DQ071
AM176893.1 gg_id:159970 Recovery mangrove sediment clone SZB49 AM176
GU061235.1 gg_id:574533 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
GU208329.1 gg_id:570490 Study on Sediment Dongping Lake sediment clone Se2-17 GU208
EU135454.1 gg_id:237237 tallgrass prarie soil clone FFCH12732 EU1354
DQ125868.1 gg_id:131444 uranium contaminated soil clone AKAU4117 DQ125
EU135432.1 gg_id:254690 tallgrass prarie soil clone FFCH13487 EU1354
FJ479563.1 gg_id:579528 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EU135494.1 gg_id:237927 tallgrass prarie soil clone FFCH12670 EU1354
EU937926.1 gg_id:337426 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9379
AJ853567.1 gg_id:110302 landfill leachate clone GZKB73 AJ8535
CU917597.1 gg_id:546967 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
AF027005.1 gg_id:1572 hot spring clone OPB35 AF0270
FM994912.1 gg_id:550907 springs Velingrad region Bulgaria hot spring Mizinka clone VS-21 FM994
EU104111.1 gg_id:310462 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ017913.1 gg_id:134130 upland stream clone S-Btb7_11 DQ017
DQ396294.1 gg_id:153452 deep-sea octacoral clone ctg_NISA252 DQ396
FJ905685.1 gg_id:535898 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
EF516930.1 gg_id:225632 grassland soil clone FCPN502 EF5169
EF516856.1 gg_id:224253 grassland soil clone FCPS671 EF5168
EF018903.1 gg_id:212324 aspen rhizosphere clone Amb_16S_1397 EF0189
AY395425.1 gg_id:102024 pasture soil clone EB1106 AY3954
FJ478519.1 gg_id:536090 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785

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EU135434.1 gg_id:238183 tallgrass prarie soil clone FFCH7408 EU135
GQ402552.1 gg_id:593900 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF019592.1 gg_id:212455 aspen rhizosphere clone Elev_16S_1113 EF0195
DQ404817.1 gg_id:151664 contaminated sediment clone 655945 DQ404
DQ451523.1 gg_id:156917 forest soil clone FAC84 DQ451
EU335323.1 gg_id:242989 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EF099597.1 gg_id:184418 mouse cecum clone SWPT4_aaa01f05 EF0995
EU459611.1 gg_id:291051 ring-tailed lemur feces clone RT_aai09c04 EU459
EF099110.1 gg_id:192171 mouse cecum clone SWPT2_aaa02d09 EF0991
CP001071.1 gg_id:278234 Akkermansia muciniphila str. ATCC BAA-835 CP001
DQ807825.1 gg_id:178569 human fecal clone RL180_aah37f08 DQ807
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EF099112.1 gg_id:174132 mouse cecum clone SWPT2_aaa02d11 EF0991
EF604904.1 gg_id:230139 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6049
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EU459638.1 gg_id:298839 ring-tailed lemur feces clone RT_aai09g05 EU459
EU763463.1 gg_id:345321 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7634
EF604517.1 gg_id:234298 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
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EU506706.1 gg_id:261175 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54h02 EU506
DQ807201.1 gg_id:185152 human fecal clone RL244_aaj47e04 DQ807
DQ805485.1 gg_id:174822 human fecal clone RL203_aai63c06 DQ805
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EU506506.1 gg_id:274986 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03b03 EU506
DQ805539.1 gg_id:185779 human fecal clone RL203_aai64a01 DQ805
FJ365265.1 gg_id:368894 feces adult twins and mothers; TS1 clone TS1_a04g10 FJ3652
AJ408970.1 gg_id:31006 human colonic clone HuCA18 AJ4089
EU507500.1 gg_id:258589 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b09 EU507
FJ364958.1 gg_id:359195 feces adult twins and mothers; TS1 clone TS1_a01c01 FJ3649
AY986145.1 gg_id:116910 human stool clone D491 AY986
EU006397.1 gg_id:255263 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
DQ805319.1 gg_id:195328 human fecal clone RL203_aai61b04 DQ805
EU763313.1 gg_id:334717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ365018.1 gg_id:365334 feces adult twins and mothers; TS1 clone TS1_a01h05 FJ3650
DQ803989.1 gg_id:181549 human fecal clone RL200_aai60g06 DQ803
DQ805473.1 gg_id:197876 human fecal clone RL203_aai63b03 DQ805

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DQ803720.1 gg_id:179163 human fecal clone RL200_aai57e09 DQ803
DQ803687.1 gg_id:177813 human fecal clone RL200_aai57b09 DQ803
EU763746.1 gg_id:346624 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EF099090.1 gg_id:180789 mouse cecum clone SWPT2_aaa02b02 EF099
EF099511.1 gg_id:185740 mouse cecum clone SWPT3_aaa04b11 EF099
DQ805333.1 gg_id:187220 human fecal clone RL203_aai61c08 DQ805
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FJ371231.1 gg_id:359222 feces adult twins and mothers; TS6 clone TS6_a02e02 FJ3712
FJ364037.1 gg_id:360894 feces adult twins and mothers; TS150 clone TS150_a02c03 FJ3640
FJ365015.1 gg_id:367987 feces adult twins and mothers; TS1 clone TS1_a01h02 FJ3650
EU768083.1 gg_id:340215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ364103.1 gg_id:366847 feces adult twins and mothers; TS150 clone TS150_a03a07 FJ3641
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FJ363943.1 gg_id:359085 feces adult twins and mothers; TS150 clone TS150_a01b10 FJ3639
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FJ369644.1 gg_id:366982 feces adult twins and mothers; TS51 clone TS51_a03b04 FJ3696
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FJ369652.1 gg_id:365331 feces adult twins and mothers; TS51 clone TS51_a03c03 FJ3696
EU768211.1 gg_id:349733 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ364059.1 gg_id:368699 feces adult twins and mothers; TS150 clone TS150_a02e04 FJ3640
DQ803799.1 gg_id:180056 human fecal clone RL200_aai58e09 DQ803
DQ806904.1 gg_id:187104 human fecal clone RL198_aaj75b08 DQ806
EU768169.1 gg_id:344643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ803992.1 gg_id:185431 human fecal clone RL200_aai60g09 DQ803
FJ371678.1 gg_id:366631 feces adult twins and mothers; TS8 clone TS8_a01a06 FJ3716
FJ365028.1 gg_id:359843 feces adult twins and mothers; TS1 clone TS1_a02a04 FJ3650
EU506426.1 gg_id:277079 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01e12 EU506
FJ371109.1 gg_id:358268 feces adult twins and mothers; TS6 clone TS6_a01a10 FJ3711
AY978065.1 gg_id:120670 human cecum mucosal biopsy clone LI24 AY978
DQ805371.1 gg_id:191984 human fecal clone RL203_aai61g09 DQ805
DQ805313.1 gg_id:185545 human fecal clone RL203_aai61a06 DQ805
FJ369694.1 gg_id:359376 feces adult twins and mothers; TS51 clone TS51_a03f11 FJ3696
FJ371129.1 gg_id:364544 feces adult twins and mothers; TS6 clone TS6_a01c08 FJ3711
EU509276.1 gg_id:263476 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47a09 EU509

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EU768293.1 gg_id:335652 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7682
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AY982465.1 gg_id:118488 human sigmoid colon mucosal biopsy clone MM09 AY9824
GQ491900.1 gg_id:546153 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU006398.1 gg_id:239988 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF605166.1 gg_id:230601 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6051
EF099268.1 gg_id:175690 mouse cecum clone SWPT2_aaa04g11 EF0992
GQ492728.1 gg_id:575407 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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DQ803798.1 gg_id:179022 human fecal clone RL200_aai58e08 DQ803
EF098506.1 gg_id:198546 mouse cecum clone SWPT15_aaa04e05 EF0985
EU458622.1 gg_id:299422 European rabbit feces clone RA_h03_1 EU458
DQ794836.1 gg_id:186705 human fecal clone RL240_aaj32h12 DQ794
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DQ806918.1 gg_id:181978 human fecal clone RL198_aaj75d07 DQ806
EU507531.1 gg_id:258255 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04f08 EU507
EU508159.1 gg_id:264121 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02a06 EU508
DQ793672.1 gg_id:184483 human fecal clone RL246_aai75d06 DQ793
EU459667.1 gg_id:288635 ring-tailed lemur feces clone RT_aai10e08 EU459
DQ797676.1 gg_id:190478 human fecal clone RL206_aaj14e06 DQ797
DQ803739.1 gg_id:174281 human fecal clone RL200_aai57g10 DQ803
EU506565.1 gg_id:277003 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04d05 EU506
GQ492737.1 gg_id:585879 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU506534.1 gg_id:260817 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03e12 EU506
DQ795501.1 gg_id:182004 human fecal clone RL178_aan65b11 DQ795
EU006176.1 gg_id:255048 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
DQ806760.1 gg_id:178399 human fecal clone RL186_aao48d05 DQ806
DQ803815.1 gg_id:197646 human fecal clone RL200_aai58g02 DQ803
EF098337.1 gg_id:191825 mouse cecum clone SWPT15_aaa01a11 EF0983
EF099264.1 gg_id:191956 mouse cecum clone SWPT2_aaa04g06 EF0992
EF099136.1 gg_id:191681 mouse cecum clone SWPT2_aaa02g09 EF0991
EF602830.1 gg_id:234575 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
DQ803955.1 gg_id:174718 human fecal clone RL200_aai60d02 DQ803
DQ793678.1 gg_id:173820 human fecal clone RL246_aai75e04 DQ793
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EU006177.1 gg_id:253234 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
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EU507388.1 gg_id:276012 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02e06 EU507
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DQ824465.1 gg_id:199450 human fecal clone RL304_aal76c12 DQ824
EU451703.1 gg_id:316576 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU451
EU006404.1 gg_id:254430 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF605151.1 gg_id:234253 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EF603854.1 gg_id:230720 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6038
DQ803856.1 gg_id:179974 human fecal clone RL200_aai59b12 DQ803

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GQ493707.1 gg_id:588996 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU474343.1 gg_id:297296 western lowland gorilla feces clone GORSD_aaa02d12 EU4743
DQ803801.1 gg_id:175615 human fecal clone RL200_aai58e11 DQ803
EU508365.1 gg_id:262989 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03h06 EU5083
FJ367694.1 gg_id:364483 feces adult twins and mothers; TS2 clone TS2_a02e02 FJ3676
DQ797786.1 gg_id:197591 human fecal clone RL206_aaj15g12 DQ797
DQ824257.1 gg_id:192313 human fecal clone RL304_aal73f01 DQ824
EF605153.1 gg_id:232422 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6051
EF603066.1 gg_id:230664 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF099628.1 gg_id:184620 mouse cecum clone SWPT4_aaa02b07 EF0996
EF099133.1 gg_id:198936 mouse cecum clone SWPT2_aaa02g06 EF0991
EU507293.1 gg_id:262054 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01c03 EU5072
GQ493815.1 gg_id:568909 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509193.1 gg_id:268293 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f10 EU5091
GQ448638.1 gg_id:544288 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU474260.1 gg_id:294287 western lowland gorilla feces clone GORSD_aaa03a03 EU4742
EF604906.1 gg_id:234335 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EF099038.1 gg_id:178077 mouse cecum clone SWPT2_aaa01d08 EF0990
EU459692.1 gg_id:300791 ring-tailed lemur feces clone RT_aai10h12 EU4596
EF603938.1 gg_id:227678 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
GQ493480.1 gg_id:540440 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ824314.1 gg_id:194496 human fecal clone RL304_aal74d01 DQ824
GQ491874.1 gg_id:550767 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU508387.1 gg_id:270147 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04g02 EU5083
EF604791.1 gg_id:232493 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
GQ492159.1 gg_id:561627 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU451506.1 gg_id:353432 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4515
EF604911.1 gg_id:227993 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
DQ807255.1 gg_id:187988 human fecal clone RL244_aaj48b11 DQ807
GQ493932.1 gg_id:570491 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY980944.1 gg_id:121335 human rectum mucosal biopsy clone LR95 AY9809
EU474294.1 gg_id:294378 western lowland gorilla feces clone GORSD_aaa03b05 EU4742
DQ824408.1 gg_id:199666 human fecal clone RL304_aal75f10 DQ824
EU506595.1 gg_id:269033 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53a03 EU5065
EF099070.1 gg_id:175442 mouse cecum clone SWPT2_aaa01g10 EF0990
EF099675.1 gg_id:187986 mouse cecum clone SWPT4_aaa02g06 EF0996
EF602794.1 gg_id:228401 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
EF099117.1 gg_id:180918 mouse cecum clone SWPT2_aaa02e08 EF0991
GQ492323.1 gg_id:588591 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ803906.1 gg_id:183355 human fecal clone RL200_aai59g07 DQ803

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GQ493776.1 gg_id:555563 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509172.1 gg_id:269922 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45d02 EU509
GQ491371.1 gg_id:546571 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF602896.1 gg_id:234636 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EF603614.1 gg_id:231947 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
EF602832.1 gg_id:227688 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EF605159.1 gg_id:232648 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EU507757.1 gg_id:262819 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04c08 EU507
EU453217.1 gg_id:340374 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
DQ793746.1 gg_id:183820 human fecal clone RL246_aai76f06 DQ793
GQ493424.1 gg_id:594106 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU506859.1 gg_id:275140 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07d09 EU506
DQ302110.1 gg_id:153007 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
AF513965.1 gg_id:62479 Verrucomicrobia clone LA1-B30N AF513
EF632724.1 gg_id:239291 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
AB252090.1 gg_id:155636 entrapped Puruogangri ice core clone PIC-D19 AB252
DQ015833.1 gg_id:140683 Antarctic lake water clone ELB19-212 DQ015
AJ318188.1 gg_id:46876 Waste-gas biofilter clone BItii14 AJ3181
GU208316.1 gg_id:546058 Study on Sediment Dongping Lake sediment clone Ser1-21 GU208
AB154319.1 gg_id:105709 freshwater clone S9JA-40 AB1543
FJ437947.1 gg_id:509859 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
DQ396121.1 gg_id:154817 deep-sea octacoral clone ctg_NISA122 DQ396
AY770729.1 gg_id:111348 Verrucomicrobia sea urchin Paracentrotus lividus clone PlS48 AY770
FJ715972.1 gg_id:558186 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7159
FJ437966.1 gg_id:511993 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
FJ825946.1 gg_id:556103 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea; FJ8259
GQ850550.1 gg_id:586112 surface water northern Bering Sea clone u82 GQ850
EU682496.1 gg_id:517793 Four Primer Sets Detecting Anammox s estuary sediment Mai Po Nature Reserve clo EU6824
GU061933.1 gg_id:570181 and function microbial mesoscale eddy perturbations South China Sea clone S-5m-9 GU061
NR_026024.1 gg_id:564314 Prosthecobacter fusiformis str. FC4; ATCC 25309 NR_02
U60012.1 gg_id:1588 Prosthecobacter dejongeii U6001
U60013.1 gg_id:1593 Prosthecobacter vanneervenii str. FC2 U6001
EU104166.1 gg_id:319751 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ612153.1 gg_id:585360 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.2.74 FJ6121
EU580493.1 gg_id:556878 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret EU5804
AY922120.1 gg_id:113378 farm soil clone AKYH1486 AY9221
AB305640.1 gg_id:248402 Prosthecobacter sp. str. HAQ-1 AB3056
EF516716.1 gg_id:225469 grassland soil clone FCPT546 EF5167
AB297805.1 gg_id:246659 Rubritalea spongiae str. YM21-132 AB2978

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AF454310.2 gg_id:63827 Mono lake clone ML316M-1 AF4543
AM040118.1 gg_id:149984 sandy sediments clone Sylt 22 AM040
AJ401121.1 gg_id:39097 Elbe river clone DEV055 AJ4011
EU491625.1 gg_id:258236 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
EU050932.1 gg_id:238891 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_56 EU0509
FJ437955.1 gg_id:549407 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
FJ543052.1 gg_id:523568 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
FJ437954.1 gg_id:565073 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
DQ300578.1 gg_id:146066 microbial ocean's interior amplicon single fosmid library pool 10m depth HOT statior DQ300
AY344427.1 gg_id:91270 Lake Kauhako 30 m clone K2-30-31 AY3444
EU236414.1 gg_id:290527 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F4 EU2364
DQ071119.1 gg_id:134657 marine surface water clone SJC3.21 DQ071
FJ205365.1 gg_id:549372 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
DQ395400.1 gg_id:155518 deep-sea octacoral clone ctg_BRRAA57 DQ395
GQ350683.1 gg_id:562414 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU491679.1 gg_id:269422 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
FJ542863.1 gg_id:522575 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
AM997555.1 gg_id:562351 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AJ441222.1 gg_id:55975 hydrothermal vent polychaete mucous clone P. palm C 85 AJ4412
DQ499289.1 gg_id:159582 acidic cave snottite biofilm clone CV35 DQ499
X90515.1 gg_id:1596 Verrucomicrobium spinosum X90515
FJ872374.1 gg_id:591617 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8723
AJ441243.1 gg_id:57441 hydrothermal vent polychaete mucous clone P. palm A 54 AJ4412
GQ167324.1 gg_id:585845 Microbial Life -13C Brine Ice-Sealed Antarctic ice-entrained brine 16.5 m Lake Vida c GQ167
FJ623333.1 gg_id:510359 Efficient polyhydroxyalkanoates production waste-activated submitted process seque FJ6233
FJ543001.1 gg_id:526403 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AB240273.1 gg_id:142471 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clor AB240
GQ259220.1 gg_id:552165 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
EU135492.1 gg_id:255112 tallgrass prarie soil clone FFCH1244 EU1354
FJ543027.1 gg_id:525506 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AF234714.1 gg_id:23971 sludge clone A38 AF2347
GQ452903.1 gg_id:544574 Biodiversity planktonic bottom water Northern Bering Sea clone b31 GQ452
EU050940.1 gg_id:240964 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_25 EU0509
EU236322.1 gg_id:293293 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a1A9 EU2363
GQ259291.1 gg_id:560235 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
AJ401116.1 gg_id:48886 Elbe river clone DEV035 AJ4011
EU245399.1 gg_id:253042 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-B1: EU2453
AM259830.1 gg_id:211686 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-2-28 AM259
DQ513026.1 gg_id:161217 Microbial life fluids ridge flank crustal fluid clone FS142-18B-02 DQ513

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AY114332.1 gg_id:63773 anoxic marine sediment clone LD1-PB19 AY1143
FJ716267.1 gg_id:563562 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
FJ712501.1 gg_id:526723 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
AM745159.1 gg_id:290797 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
DQ067003.1 gg_id:131050 Lake Washington sediment clone pLW-69 DQ067
GQ500696.1 gg_id:556217 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
EU528261.1 gg_id:281647 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AJ854267.1 gg_id:211083 Impact flooding on (Populus sp.) trees poplar tree microcosm bulk soil unflooded clor AJ8542
AJ582051.1 gg_id:94268 soil near uranium mill tailings clone JG36-GS-103 AJ5820
AJ390482.1 gg_id:22777 soil clone PRR-12 AJ3904
FJ479218.1 gg_id:570966 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU135569.1 gg_id:240877 tallgrass prarie soil clone FFCH3040 EU135
FJ479480.1 gg_id:540938 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF032778.1 gg_id:185827 cyanobacterial mat in lava cave clone HAVOmat06 EF0327
FJ478598.1 gg_id:553028 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AM991194.1 gg_id:277712 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
AJ863228.1 gg_id:125819 poplar tree microcosm bulk soil flooded clone 21BSF64 AJ8632
AJ390458.1 gg_id:28793 soil clone PBS-III-30 AJ3904
EU135567.1 gg_id:242108 tallgrass prarie soil clone FFCH1818 EU135
EU135572.1 gg_id:243244 tallgrass prarie soil clone FFCH12488 EU135
AY921903.1 gg_id:113334 farm soil clone AKYG868 AY921
FJ479290.1 gg_id:585878 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU135568.1 gg_id:254604 tallgrass prarie soil clone FFCH18316 EU135
AF280852.1 gg_id:45661 bioreactor clone mle1-16 AF280
FJ712468.1 gg_id:525404 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
FN396645.1 gg_id:541341 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_I FN396
FJ484438.1 gg_id:567353 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
EF999394.1 gg_id:247500 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn EF9993
EF602491.1 gg_id:228206 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
DQ521801.1 gg_id:161669 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
AY114325.1 gg_id:63782 anoxic marine sediment clone LD1-PA39 AY1143
FJ485054.1 gg_id:555839 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
EU491142.1 gg_id:260737 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ289929.2 gg_id:172911 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ485078.1 gg_id:562684 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
FJ902124.1 gg_id:552555 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9021
EF602497.1 gg_id:231901 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EU135574.1 gg_id:248536 tallgrass prarie soil clone FFCH4663 EU135
AF317770.1 gg_id:136806 Nullarbor cave clone wb1_H11 AF3177

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k__Bacteria	k__Bacteria	p__WS3	c__PRR-12
k__Bacteria	k__Bacteria	p__WS6	c__SC72
k__Bacteria	k__Bacteria	p__WS6	c__SC72
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g__sfA
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EU652628.1 gg_id:279399 Seasonal variation microbial Yel Sea sediment clone A8S-81	EU652
GU208350.1 gg_id:580844 Study on Sediment Dongping Lake sediment clone Td3-9	GU208
GQ347695.1 gg_id:534156 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ347
EU721779.1 gg_id:550488 microbial production water Alaskan mesothermic petroleum reservoir two methods	EU721
GU112185.1 gg_id:590013 library biogas slurry anaerobic fermentation pig manure clone 180	GU112
DQ329651.1 gg_id:200370 Guerrero Negro hypersaline microbial mat clone 062DZ75	DQ329
DQ329650.1 gg_id:201943 Guerrero Negro hypersaline microbial mat clone 062DZ40	DQ329
FJ719034.1 gg_id:529088 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_A0	FJ7190
EF516850.1 gg_id:218322 grassland soil clone FCPS649	EF5168
AY532578.1 gg_id:106562 uranium-contaminated aquifer clone 1013-28-CG38	AY5325
EF516449.1 gg_id:225148 grassland soil clone FCPT678	EF5164
AY850299.1 gg_id:135358 depending on what microbial treatment present soil clone c1	AY8502
AB089068.1 gg_id:78071 termite gut homogenate clone Rs-J96	AB089
EF454817.2 gg_id:218493 termite hindgut clone 290cost002-P3L-449	EF4548
EF454921.2 gg_id:225715 termite hindgut clone 290cost002-P3L-678	EF4549
AB192117.1 gg_id:141608 termite gut homogenate clone M2PT2-63	AB192
EF454187.2 gg_id:217932 termite hindgut clone 290cost002-P3L-1771	EF4541
AB188635.1 gg_id:113660 termite gut homogenate clone Pl-P1-21	AB188
GQ340261.1 gg_id:572828 Prokaryotic Marathonas Reservoir Greece water column clone A08-131-BAC	GQ340
DQ520188.1 gg_id:161631 shal China sequences hypertrophic freshwater lake clone ML-9-34.2	DQ520
DQ300591.1 gg_id:146168 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static	DQ300
GQ350069.1 gg_id:588419 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ350

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Community Analysis: Hybridization Intensities*

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k__Bacteria	k__Bacteria	p__ABY1_OD1	c__unclassified
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k__Bacteria	k__Bacteria	p__ABY1_OD1	c__unclassified
k__Bacteria	k__Bacteria	p__ABY1_OD1	c__unclassified
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	Taxo
genus	
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g__sfC	
g__sfD	
g__sfE	
g__sfF	
g__sfG	
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s__unclassified	74776
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representative gene
GQ354923.1 gg_id:540167 structure between two geochemically distinct springs Alum Rock Park spring clone M
DQ676460.1 gg_id:220280 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
EU644237.1 gg_id:284266 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T
DQ676456.1 gg_id:224443 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
GQ339139.1 gg_id:528049 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv
AB179495.1 gg_id:99699 sedimentary rock clone MIZ04
AB193900.1 gg_id:108824 deep-sea vent clone Mb-NB06
DQ676475.1 gg_id:223552 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M
GQ346852.1 gg_id:562467 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ348940.1 gg_id:577547 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU283579.1 gg_id:278529 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A285
FJ234919.1 gg_id:346434 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl
GU196235.1 gg_id:578115 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana
AJ543755.1 gg_id:96419 anoxic sediment Lake Cadagno clone 1
EF192905.1 gg_id:202214 sediments temperate artificial lake Rapel reservoir sediment clone Rap2_24C
AJ290978.1 gg_id:112449 anaerobic bioreactor clone SHA-114
AB186797.1 gg_id:105224 polychlorinated dioxin dechlorinating microcosm clone TSBZ04
AY297964.1 gg_id:88282 thermophilic anaerobic terephthalate-degrading sludge clone TTA_B4
EU385779.1 gg_id:267654 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
AM712334.1 gg_id:254942 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h
AY592377.1 gg_id:106589 deep-sea mud volcano clone Amsterdam-2B-17; BC20-2B-17
EU385806.1 gg_id:261876 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
EF492945.1 gg_id:241470 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AF245036.1 gg_id:44004 soil metagenomic library clone 17F9
FJ793158.1 gg_id:529323 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB13
EF516094.1 gg_id:226261 grassland soil clone FCPS413
FJ004718.1 gg_id:561968 Acidobacteria former agricultural soil rhizosphere clone 1Fe
EU132222.1 gg_id:246947 tallgrass prarie soil clone FFCH14447
EU925922.1 gg_id:347057 sediments sediment station DBS1 northern Bering Sea clone 160I37
Z95707.1 gg_id:1740 soil clone 11-14
EU881247.1 gg_id:352805 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
GU230433.1 gg_id:556512 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo
AY703459.1 gg_id:138920 Detection and ly acidobacterial analyses Altamira Cave clone ALT24
EF516178.1 gg_id:222997 grassland soil clone FCPT460
FJ004643.1 gg_id:533715 Acidobacteria former agricultural bulk soil clone 72L1B
AY922011.1 gg_id:113257 farm soil clone AKYG433
EF516869.1 gg_id:219766 grassland soil clone FCPU565

		Array Hybridization Intensity					
accession representative	gg_id representative	R5_S16	R5_S17	R5_S18	R5_S19	R5_S20	R5_S21
GQ354923.1	540167	5262.5	6277.3	10553.4	6189.8	7268.1	7159.8
DQ676460.1	220280	933.5	1029.9	4097.0	2155.5	798.3	484.4
EU644237.1	284266	7580.8	6059.7	8006.6	3622.2	2751.3	3926.2
DQ676456.1	224443	51.8	81.5	1090.2	132.3	60.9	30.2
GQ339139.1	528049	13553.8	10480.9	12314.3	12431.5	6797.2	9739.3
AB179495.1	99699	630.4	911.2	1575.1	707.4	150.3	200.3
AB193900.1	108824	335.2	339.6	5693.3	1524.1	63.0	111.1
DQ676475.1	223552	129.7	27.8	740.8	74.4	58.4	26.0
GQ346852.1	562467	4811.7	7908.6	15258.3	6327.9	7186.0	6535.0
GQ348940.1	577547	6681.0	6413.2	11110.4	6277.3	7808.9	5945.5
EU283579.1	278529	8143.0	9028.4	13961.0	8936.9	6951.0	7302.9
FJ234919.1	346434	7840.4	9021.4	15983.1	6058.6	4465.9	3519.8
GU196235.1	578115	3253.9	4845.5	4308.4	2934.7	7571.0	5324.6
AJ543755.1	96419	217.4	333.6	440.6	256.0	186.6	294.6
EF192905.1	202214	66.0	126.1	332.1	93.7	87.6	107.2
AJ290978.1	112449	75.8	156.9	196.4	43.6	53.9	56.9
AB186797.1	105224	1783.9	2005.3	1282.6	1950.4	530.6	1305.6
AY297964.1	88282	154.6	330.9	146.0	288.7	210.5	156.9
EU385779.1	267654	8710.6	10552.6	9198.2	6706.1	7901.0	7554.7
AM712334.1	254942	1607.1	3194.0	4293.3	1413.3	3136.3	3518.9
AY592377.1	106589	154.1	309.9	276.2	327.6	354.0	524.1
EU385806.1	261876	1349.3	1297.7	1702.1	779.8	852.6	885.8
EF492945.1	241470	2415.5	1136.5	2798.2	1809.9	1461.7	2162.8
AF245036.1	44004	4325.4	4715.5	4339.6	3713.6	3546.1	4667.2
FJ793158.1	529323	4067.6	2614.9	1684.0	4123.2	4160.8	4082.1
EF516094.1	226261	143.4	464.0	431.9	98.4	78.5	112.1
FJ004718.1	561968	699.0	1548.3	1906.5	691.5	948.6	1732.2
EU132222.1	246947	409.9	1065.5	1789.4	1758.7	1425.6	1198.3
EU925922.1	347057	842.8	2100.6	3583.7	1399.2	1008.3	3466.5
Z95707.1	1740	43.3	94.2	301.7	77.7	73.7	62.1
EU881247.1	352805	6198.0	5559.5	5572.6	3856.4	3131.8	5899.2
GU230433.1	556512	1731.0	2895.7	3644.5	3258.0	2629.0	4120.6
AY703459.1	138920	1367.4	1454.6	1553.1	1010.2	405.3	896.6
EF516178.1	222997	75.7	264.1	614.2	110.7	410.1	833.4
FJ004643.1	533715	2188.3	3995.9	7426.2	3590.2	3574.6	5521.1
AY922011.1	113257	3593.3	4514.3	4415.5	2563.7	2806.3	4508.4
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EU193029.1 gg_id:329690 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
DQ513087.1 gg_id:161093 Microbial life fluids ridge flank crustal fluid clone FS266-72B-03
EF516647.1 gg_id:222528 grassland soil clone FCPU544
DQ463182.1 gg_id:157927 Acid Drainage Tong Lushan Copper Mine China acid mine drainage clone tls1-4
D26171.1 gg_id:3704 Acidobacterium capsulatum
AJ292576.1 gg_id:38048 PCB-polluted soil clone WD217
NC_008009.1 gg_id:159436 Korebacter versatilis Ellin345
EF020028.1 gg_id:211355 aspen rhizosphere clone Elev_16S_1423
AM934736.1 gg_id:564102 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AB486931.1 gg_id:540833 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR
AB240248.1 gg_id:143307 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
GQ402790.1 gg_id:535450 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AY234523.1 gg_id:112314 soil isolate Ellin5106
EF018237.1 gg_id:206267 aspen rhizosphere clone Amb_16S_588
AB240373.1 gg_id:144577 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon
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AY963401.1 gg_id:156032 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU680441.1 gg_id:285726 unculturable forest Gaoligong Mountains Yunnan soil clone S5-14
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AY963484.1 gg_id:150977 structures and correlated ecological factors soils two evergreen broad-leaved forests
DQ528761.1 gg_id:160117 Edaphobacter modestum str. Wbg-1
AY963496.1 gg_id:155420 structures and correlated ecological factors soils two evergreen broad-leaved forests
AY326573.1 gg_id:136280 Amazon soil clone 81-2
FJ466338.1 gg_id:571120 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
DQ660894.1 gg_id:162763 Terriglobus roseus str. KBS 68
EF018694.1 gg_id:212239 aspen rhizosphere clone Amb_16S_988
DQ532229.1 gg_id:168599 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C
EU035939.2 gg_id:320478 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor
EF516123.1 gg_id:221631 grassland soil clone FCPN626
FJ466377.1 gg_id:509471 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF492914.1 gg_id:243138 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EF516926.1 gg_id:220395 grassland soil clone FCPP741
AY963394.1 gg_id:153608 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU132221.1 gg_id:239485 tallgrass prarie soil clone FFCH14327
FJ902583.1 gg_id:587792 phreatic limestone sinkholes northeastern Mexico biofilm 1m deep hydrothermal ver
EU440640.1 gg_id:540618 Soil are Changed Agricultural Practices agricultural soil clone Plot17-H09

DQ906800.1	240618	127.5	60.7	80.9	137.3	124.2	58.2
DQ984540.1	240646	1955.6	1889.5	1214.6	1104.0	1265.9	1023.1
EF018279.1	212863	36.8	37.2	75.0	45.7	55.2	56.8
EU193029.1	329690	4403.9	4488.5	3451.2	4529.2	2311.2	4765.2
DQ513087.1	161093	544.6	880.8	579.6	533.4	351.8	558.3
EF516647.1	222528	15440.8	16054.0	7593.5	6335.1	6468.0	7733.6
DQ463182.1	157927	293.6	1217.0	3167.4	741.2	669.5	1537.8
D26171.1	3704	29.7	32.2	111.7	53.5	75.7	113.0
AJ292576.1	38048	83.3	121.8	914.1	101.5	100.4	338.7
NC_008009.1	159436	36.5	60.7	99.4	83.2	84.5	31.0
EF020028.1	211355	32.8	53.2	282.4	73.4	76.8	80.6
AM934736.1	564102	6351.5	6180.3	8729.2	4828.1	6841.2	7863.2
AB486931.1	540833	116.8	175.7	396.4	119.3	421.9	219.3
AB240248.1	143307	497.6	728.8	2001.3	1195.9	944.7	519.6
GQ402790.1	535450	74.6	241.5	2212.8	162.9	342.1	903.7
AY234523.1	112314	48.6	94.2	228.1	118.8	385.6	1553.3
EF018237.1	206267	494.8	728.0	2107.0	484.5	1200.9	610.2
AB240373.1	144577	685.0	612.9	230.4	215.2	293.9	1191.1
EF516733.1	222434	1596.7	1002.1	1553.0	260.5	356.3	1252.7
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EU680441.1	285726	164.8	233.5	998.9	156.7	172.5	265.0
EU680442.1	284815	6561.3	8575.0	10954.2	4682.9	3942.4	5936.4
EF516334.1	223904	47.4	121.8	264.4	97.6	83.5	92.0
AB307653.1	267261	163.7	346.0	930.1	176.5	308.8	324.1
AY963484.1	150977	807.8	1020.0	2132.4	1020.1	459.5	954.4
DQ528761.1	160117	19.4	98.7	54.4	55.9	178.0	31.7
AY963496.1	155420	2434.3	2219.5	4617.9	2097.5	1182.3	1458.9
AY326573.1	136280	609.4	753.6	1576.4	164.6	53.5	314.0
FJ466338.1	571120	465.1	842.2	1791.2	340.1	1057.2	1515.0
DQ660894.1	162763	147.0	305.2	1490.2	178.2	124.7	328.6
EF018694.1	212239	1376.0	2657.0	3144.0	2099.8	3333.1	2838.9
DQ532229.1	168599	288.9	879.7	1773.3	326.2	216.8	550.4
EU035939.2	320478	3262.5	3927.0	4016.9	2835.5	2299.1	3122.8
EF516123.1	221631	100.6	549.4	2102.5	246.2	1255.0	830.9
FJ466377.1	509471	183.6	252.8	288.5	139.1	284.0	333.1
EF492914.1	243138	7850.6	10741.9	18236.8	8587.2	11597.8	12693.3
EF516926.1	220395	160.8	742.5	2560.4	284.8	262.7	477.1
AY963394.1	153608	2705.9	3435.2	3780.2	3230.4	3322.1	4221.8
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FJ902583.1	587792	16843.6	16913.6	15095.7	13522.6	18448.9	15346.5
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AF465659.1 gg_id:41797 Acidobacterium group clone YNPRH72A
FJ269341.1 gg_id:588263 Microbes marine sponges sponge tissue clone XC1E08
EF019289.1 gg_id:209203 aspen rhizosphere clone Elev_16S_476
EU491200.1 gg_id:262940 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
EU132218.1 gg_id:257702 tallgrass prarie soil clone FFCH13847
EF492905.1 gg_id:248553 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EF494349.1 gg_id:223415 Nunnock River granitic landscape clone NR.1.090
AY395361.1 gg_id:106724 pasture soil clone EB1042
AY913359.1 gg_id:114204 forest soil clone DUNssu152 (+7A) (OTU#097)
EU250262.1 gg_id:235484 acid mine drainage clone GXDC-48
EF612359.1 gg_id:245188 historic semiarid lead-zinc mine tailings site soil clone OS-C161
DQ451440.1 gg_id:156686 forest soil clone FAC1
AY922122.1 gg_id:113404 farm soil clone AKYH1493
AY212587.1 gg_id:104490 water 10 m downstream manure clone 137ds10
AM072423.1 gg_id:138534 Untersuchung Verschiebung der bakteriellen Populationen mit U(VI) inokulierten Bc
AF465656.1 gg_id:46677 Acidobacterium group clone YNPRH46A
AF200698.1 gg_id:16327 soil clone UA2
FJ536905.1 gg_id:535248 Linking performance microbiology biofilters treating dimethyl sulphide presence and
DQ906061.1 gg_id:223389 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1H5
DQ404598.1 gg_id:151613 contaminated sediment clone 656042
FJ479257.1 gg_id:577226 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY395347.1 gg_id:106465 pasture soil clone EB1028
AY587227.1 gg_id:102666 soil clone
AY326572.1 gg_id:136267 Amazon soil clone 1031-2
AJ292587.1 gg_id:39070 PCB-polluted soil clone WD277
AY234608.1 gg_id:112338 soil isolate Ellin5257
AB240272.1 gg_id:143367 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
GQ500876.1 gg_id:564241 Surveys Biofilms and Sediments Mammoth Karst Aquifers Bio-Sep beads containing
GQ264031.1 gg_id:592891 Structure Simulated Level Waste Site simulated level waste site clone WC3_122
FM873307.1 gg_id:362254 occupant source house floor dust clone FD01E01
GU359061.1 gg_id:518576 rhizosphere soil peanut clone 1S9
GU134916.1 gg_id:584087 Acid-tolerant microaerophilic oxdizing enhance Fe(III) accumulation Fe(II) oxidizing e
GQ487990.1 gg_id:556931 Microbial metal soil polluted heavy metals clone V20-30
DQ395032.1 gg_id:151522 harbor sediment clone VHS-B5-13
EU150215.1 gg_id:278437 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_26
EU132259.1 gg_id:244025 tallgrass prarie soil clone FFCH8685
FJ478546.1 gg_id:582523 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY289389.1 gg_id:88072 soil clone ABS-318
EU669640.1 gg_id:308898 soil clone S8-19
AY225650.1 gg_id:97371 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-57

GQ396810.1	559480	3628.7	5519.3	6240.6	3023.0	7945.1	8371.1
AF465659.1	41797	40.0	37.4	179.9	55.4	76.4	77.7
FJ269341.1	588263	4328.5	4469.9	4732.8	2579.6	3136.6	3575.2
EF019289.1	209203	23.9	59.9	199.7	63.4	66.2	72.3
EU491200.1	262940	8535.2	5854.5	7619.6	5442.4	5047.4	6952.0
EU132218.1	257702	1867.3	1368.3	3265.9	1588.3	452.8	1034.7
EF492905.1	248553	9563.5	10314.2	9470.8	12159.1	14986.9	12919.2
EF494349.1	223415	38.6	61.7	24.3	43.9	68.7	43.4
AY395361.1	106724	288.0	415.1	788.2	125.1	689.9	500.0
AY913359.1	114204	766.4	1058.8	3408.8	1182.0	1408.1	3694.0
EU250262.1	235484	9625.1	10037.3	4980.3	3655.1	5308.8	6341.8
EF612359.1	245188	881.7	1685.7	2665.9	312.7	1026.7	1117.9
DQ451440.1	156686	4780.5	4070.7	3058.2	4699.9	6664.7	7220.9
AY922122.1	113404	606.3	1921.8	5825.7	501.4	1368.9	1344.9
AY212587.1	104490	1996.4	2764.0	2620.0	2233.3	2704.4	2561.4
AM072423.1	138534	8612.1	9168.9	3293.9	6536.2	9974.6	9451.5
AF465656.1	46677	44.0	70.7	375.0	76.0	64.4	157.6
AF200698.1	16327	4580.4	5003.4	5146.5	5204.1	4573.3	5815.0
FJ536905.1	535248	3608.0	3130.8	4728.4	4296.9	4755.0	8546.2
DQ906061.1	223389	6134.3	8018.5	6704.4	6077.7	10430.3	12429.3
DQ404598.1	151613	212.9	176.5	410.3	428.3	132.3	221.0
FJ479257.1	577226	74.6	273.7	4194.6	218.1	222.5	764.1
AY395347.1	106465	707.8	1924.3	3841.1	1221.5	666.4	1498.5
AY587227.1	102666	6128.3	7460.6	8799.2	6195.5	7529.6	5815.1
AY326572.1	136267	2448.8	1922.6	2475.0	2580.2	1371.4	1959.6
AJ292587.1	39070	160.6	680.3	2762.3	404.2	2618.5	2063.8
AY234608.1	112338	30.7	28.2	43.8	47.8	58.8	55.3
AB240272.1	143367	1439.1	1873.0	5178.4	2037.0	2718.4	3631.6
GQ500876.1	564241	1013.9	1400.4	5626.9	488.6	4803.5	1673.5
GQ264031.1	592891	1835.5	6394.7	14152.8	2391.9	4272.1	6856.5
FM873307.1	362254	1923.5	2371.3	2536.4	1415.4	2022.3	2126.1
GU359061.1	518576	655.1	1151.3	2670.6	732.1	686.5	1854.3
GU134916.1	584087	799.6	1342.2	3037.2	666.2	392.3	1169.4
GQ487990.1	556931	174.7	297.7	1029.4	555.0	450.8	1048.0
DQ395032.1	151522	117.2	314.8	1172.8	297.5	2878.0	731.7
EU150215.1	278437	527.1	1136.1	1928.7	268.1	327.0	461.2
EU132259.1	244025	3537.7	4790.2	7556.4	5363.2	5118.4	6309.3
FJ478546.1	582523	12000.1	11405.2	10760.2	10700.6	11464.5	9736.6
AY289389.1	88072	47.0	57.2	38.5	77.6	57.3	66.9
EU669640.1	308898	439.1	2075.3	4425.9	772.7	779.6	2646.7
AY225650.1	97371	71.5	202.2	164.6	89.0	106.5	140.1

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AY922158.1 gg_id:113717 farm soil clone AKYH822
FJ466048.1 gg_id:511685 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF018405.1 gg_id:212293 aspen rhizosphere clone Amb_16S_1019
FJ810547.1 gg_id:405751 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
GQ487992.1 gg_id:546910 Microbial metal soil polluted heavy metals clone V8-11
FJ478777.1 gg_id:592157 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF018834.1 gg_id:211129 aspen rhizosphere clone Amb_16S_1315
EF019762.1 gg_id:216690 aspen rhizosphere clone Elev_16S_943
GQ500711.1 gg_id:557097 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa
GU363035.1 gg_id:543451 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
EU735013.1 gg_id:347978 assemblages sediment station DBSE Northern Bering Sea clone 109A50
DQ458047.1 gg_id:158731 acid mine drainage clone DX6
FM872925.1 gg_id:369871 occupant source house floor dust clone FB04F12
AY922132.1 gg_id:114129 farm soil clone AKYH511
FM872996.1 gg_id:359837 occupant source house floor dust clone FB02F09
AJ863211.1 gg_id:126401 poplar tree microcosm bulk soil unflooded clone 20BSU25
FM866297.1 gg_id:360249 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-173
EU276526.1 gg_id:358489 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
EU150201.1 gg_id:279537 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_12
AY493934.1 gg_id:136869 Fingerprinting aggregates soil clone 117
EF516417.1 gg_id:227524 grassland soil clone FCPN713
EU132307.1 gg_id:244850 tallgrass prarie soil clone FFCH7214
EU491340.1 gg_id:271398 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
AB252946.1 gg_id:162343 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 033
DQ395960.1 gg_id:155016 deep-sea octacoral clone ctg_CGOGA68
EU335199.1 gg_id:241341 Changes microbial metabolic and along hydrogeochemically variable profile saturate
FJ203529.1 gg_id:352218 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
AY326582.1 gg_id:136930 Amazon soil clone 31-1
EU665054.1 gg_id:541146 Soil are Changed Agricultural Practices agricultural soil clone Plot22-B06
FJ466242.1 gg_id:547399 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AF154085.1 gg_id:1813 hydrocarbon seep clone BPC015
AY963491.1 gg_id:153165 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF492949.1 gg_id:255562 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AM935750.1 gg_id:538422 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU881222.1 gg_id:336433 Karst region natural restoration land soil clone KNR200711-030
AB192240.1 gg_id:144515 termite gut homogenate clone RsTu1-92
EU250256.1 gg_id:257823 acid mine drainage clone GXDC-42
EU335409.1 gg_id:253648 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF018918.1 gg_id:213165 aspen rhizosphere clone Amb_16S_1420
FJ478490.1 gg_id:568935 species richness estimates obtained nearly and simulated pyrosequencing-generated

EF494335.1	221964	2027.5	3140.4	991.5	1911.3	984.3	1235.5
AY922158.1	113717	428.2	714.9	4030.6	338.9	831.5	901.6
FJ466048.1	511685	90.5	484.4	1813.9	143.3	148.4	496.0
EF018405.1	212293	1819.3	2137.2	2719.0	2206.0	3213.9	1638.6
FJ810547.1	405751	408.7	849.8	2340.9	279.2	1060.2	1463.5
GQ487992.1	546910	1045.6	1322.3	1999.2	1224.3	1255.2	1851.5
FJ478777.1	592157	8488.0	8472.0	6188.3	5973.0	7432.4	7039.7
EF018834.1	211129	61.0	121.0	384.9	82.3	611.9	698.9
EF019762.1	216690	43.7	76.8	642.2	103.5	76.6	222.6
GQ500711.1	557097	9245.8	11456.3	11762.2	7651.5	11923.9	9192.2
GU363035.1	543451	9363.8	9306.3	5515.7	6726.4	4316.7	5104.4
EU735013.1	347978	8531.9	10430.5	11638.8	9536.2	13376.2	9167.9
DQ458047.1	158731	3063.9	2892.5	4502.0	2312.0	2699.8	5008.7
FM872925.1	369871	5434.4	5226.2	6734.8	5095.6	3130.4	4056.1
AY922132.1	114129	1846.6	2903.3	3168.5	2049.5	2056.2	1521.6
FM872996.1	359837	11198.5	10153.9	7889.5	7481.3	10181.3	10815.8
AJ863211.1	126401	3080.6	4856.9	6030.5	2650.1	649.1	2026.9
FM866297.1	360249	99.4	563.1	1838.7	136.2	183.0	964.5
EU276526.1	358489	16163.6	11620.9	14250.0	10250.9	13647.9	11989.0
EU150201.1	279537	78.6	369.8	1388.8	196.4	210.0	827.6
AY493934.1	136869	2084.3	2449.8	3119.3	3654.0	3781.1	4944.7
EF516417.1	227524	101.9	130.0	338.0	121.4	74.2	91.6
EU132307.1	244850	4993.4	4267.5	5335.4	2512.8	4700.0	4516.9
EU491340.1	271398	4507.0	4819.1	3045.2	2548.2	3825.4	4286.6
AB252946.1	162343	63.6	245.0	771.8	143.6	145.8	405.5
DQ395960.1	155016	1760.1	2981.5	6577.0	2707.8	2015.1	2902.1
EU335199.1	241341	212.2	942.0	3089.0	266.8	537.8	1335.4
FJ203529.1	352218	1976.7	3250.1	1881.9	1798.9	3592.3	5584.8
AY326582.1	136930	16407.2	8708.6	9050.6	9116.0	5883.2	5213.7
EU665054.1	541146	1790.3	3475.8	7157.4	1997.3	4068.6	4635.3
FJ466242.1	547399	11873.5	10705.6	7058.0	8037.0	11496.0	8210.7
AF154085.1	1813	7400.4	9339.9	5334.4	5073.7	5990.6	6758.3
AY963491.1	153165	6128.2	5222.6	8298.3	5584.6	5677.6	3587.6
EF492949.1	255562	4327.1	4113.2	2866.1	3522.1	3662.7	3614.4
AM935750.1	538422	4726.2	4035.8	5960.4	3680.6	3675.4	3781.6
EU881222.1	336433	765.3	2068.7	4697.9	1135.9	6149.7	2764.5
AB192240.1	144515	86.6	173.1	222.6	220.5	131.3	174.0
EU250256.1	257823	5760.4	5940.8	7252.7	4943.0	6702.1	6650.3
EU335409.1	253648	15765.5	13837.2	8050.6	10489.7	13210.4	12857.7
EF018918.1	213165	1549.1	1690.0	5156.3	1961.9	1285.8	2623.8
FJ478490.1	568935	5129.0	4768.9	9245.3	6913.3	6240.9	4996.7

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EF018439.1 gg_id:212726 aspen rhizosphere clone Amb_16S_1060
AF013534.2 gg_id:1828 soil clone C112
DQ660878.1 gg_id:251359 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCK-I-1
GQ500739.1 gg_id:538176 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
AJ581628.1 gg_id:100705 soil near uranium mill tailings clone KCM-C-25
AY922137.1 gg_id:113301 farm soil clone AKYH551
FM872961.1 gg_id:361264 occupant source house floor dust clone FB02B12
AF234701.1 gg_id:28670 sludge clone A22
EU193040.1 gg_id:334337 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU700181.1 gg_id:297788 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU39
AY963351.1 gg_id:154229 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF597706.1 gg_id:238131 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian
EU050884.1 gg_id:250701 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_20
AY921956.1 gg_id:113944 farm soil clone AKYG1148
EU589288.1 gg_id:270648 China Ningxia rice paddy field soil clone 2_B10
EU132175.1 gg_id:256235 tallgrass prarie soil clone FFCH11537
DQ017915.1 gg_id:129839 upland stream clone S-Btb7_44
EF612353.1 gg_id:243634 historic semiarid lead-zinc site mine tailings clone K6-C86
EU449736.1 gg_id:551546 Soil are Changed Agricultural Practices agricultural soil clone Plot4-H05
EU449671.1 gg_id:545542 Soil are Changed Agricultural Practices agricultural soil clone Plot4-2E07
EU276508.1 gg_id:359433 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
DQ289915.1 gg_id:172055 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
EF019507.1 gg_id:216553 aspen rhizosphere clone Elev_16S_1009
AJ863210.1 gg_id:124071 poplar tree microcosm bulk soil unflooded clone 20BSU7
GU118680.1 gg_id:539508 Threatened Corals Provide Microbial Habitats clone Mfav_G07
EU881185.1 gg_id:310755 Karst region natural restoration land soil clone KNR200711-117
EU202779.1 gg_id:319420 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU440593.1 gg_id:553987 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2H08
EF061945.1 gg_id:180033 Xiamen China mangrove sediment clone XME61
DQ811916.1 gg_id:169706 mangrove soil clone MSB-3H10
AF280856.1 gg_id:71241 bioreactor clone mle1-25
AJ536875.1 gg_id:78582 uranium mining waste pile soil sample clone JG30a-KF-145 sp.
EF208702.1 gg_id:202031 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2
EF019194.1 gg_id:213048 aspen rhizosphere clone Amb_16S_1868
AY963461.1 gg_id:155408 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU449729.1 gg_id:571898 Soil are Changed Agricultural Practices agricultural soil clone Plot4-G06
AY963360.1 gg_id:154596 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF494338.1 gg_id:226552 Nunnock River granitic landscape clone NR.1.045
EF516272.1 gg_id:224515 grassland soil clone FCPN628
DQ833470.1 gg_id:162661 detected analyses depth sediment Guanting Reservoir clone 5-35
AY289378.1 gg_id:88876 soil clone DS-231

EF018439.1	212726	34.6	138.7	1171.5	97.2	110.3	266.8
AF013534.2	1828	7154.5	7474.9	5779.6	7539.8	4584.5	6605.5
DQ660878.1	251359	54.3	44.6	52.9	71.2	71.2	33.5
GQ500739.1	538176	62.8	217.1	1824.2	147.0	276.4	2079.4
AJ581628.1	100705	12346.9	14298.8	8889.8	10960.3	15874.2	11997.1
AY922137.1	113301	4847.7	6023.6	2325.4	1631.3	1832.5	2732.1
FM872961.1	361264	6719.1	6859.1	7948.8	5671.3	6487.8	8089.3
AF234701.1	28670	120.0	350.0	1439.2	161.8	154.1	302.4
EU193040.1	334337	9815.0	10708.2	11552.2	9118.6	12708.2	11868.6
EU700181.1	297788	2977.3	3962.0	6936.5	4957.9	4327.1	5572.8
AY963351.1	154229	1135.1	1315.0	1549.1	771.4	1168.0	1587.3
EF597706.1	238131	1515.3	2104.3	3368.7	1615.5	1168.4	3145.8
EU050884.1	250701	402.3	1189.9	4668.6	851.0	766.8	1544.3
AY921956.1	113944	4569.8	5832.0	6756.4	2535.2	6920.0	8009.5
EU589288.1	270648	10777.6	6303.3	9532.8	7313.4	6347.4	6874.4
EU132175.1	256235	3726.2	4329.9	5165.2	4395.2	6962.9	5049.4
DQ017915.1	129839	23.9	26.2	207.4	60.9	67.0	26.6
EF612353.1	243634	4693.0	3022.8	2130.8	327.5	430.4	1571.9
EU449736.1	551546	3837.8	4958.7	4651.6	4147.9	2945.3	4002.1
EU449671.1	545542	7888.5	8772.8	9614.2	5674.8	8740.3	7884.7
EU276508.1	359433	4431.5	2701.4	4777.1	4331.8	3363.0	5604.7
DQ289915.1	172055	455.7	1005.3	1284.2	346.6	1328.0	1721.5
EF019507.1	216553	131.0	178.9	1120.4	90.0	197.7	227.7
AJ863210.1	124071	94.4	134.7	312.9	94.3	75.3	66.2
GU118680.1	539508	7392.1	9058.0	8095.1	8459.8	6738.0	6249.6
EU881185.1	310755	149.7	542.4	2075.3	207.4	251.0	507.3
EU202779.1	319420	157.7	388.8	1739.0	211.6	381.7	466.6
EU440593.1	553987	11990.4	10389.3	7676.5	7650.2	10176.5	11548.8
EF061945.1	180033	49.5	242.9	317.6	76.2	77.9	70.2
DQ811916.1	169706	80.0	168.5	339.5	92.8	79.4	129.2
AF280856.1	71241	1230.3	3298.0	3877.8	1106.6	1397.1	2483.9
AJ536875.1	78582	23.4	32.2	56.0	60.1	58.3	33.4
EF208702.1	202031	20.6	35.6	20.2	45.4	59.3	20.0
EF019194.1	213048	29.8	54.7	335.0	65.8	64.6	49.3
AY963461.1	155408	96.1	78.8	55.2	63.5	52.0	56.9
EU449729.1	571898	7801.4	10044.8	11770.8	6963.6	9356.3	9987.6
AY963360.1	154596	3359.3	4752.3	2632.0	1177.9	679.3	1340.8
EF494338.1	226552	40.9	98.5	176.9	86.1	159.0	315.1
EF516272.1	224515	54.2	53.8	97.3	66.5	80.3	45.2
DQ833470.1	162661	46.2	118.2	122.8	90.6	98.1	177.2
AY289378.1	88876	678.3	2480.2	1354.3	1348.5	1153.7	1411.8

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EU335210.1 gg_id:256500 Changes microbial metabolic and along hydrogeochemically variable profile saturate
EF492967.1 gg_id:251273 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EU491617.1 gg_id:258921 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EF020018.1 gg_id:211775 aspen rhizosphere clone Elev_16S_1409
AJ519379.1 gg_id:75044 uranium mining waste pile clone JG37-AG-73 sp.
EU276472.1 gg_id:359394 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
EF018874.1 gg_id:212877 aspen rhizosphere clone Amb_16S_1358
DQ837260.1 gg_id:256297 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_67
EU202778.1 gg_id:316315 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AY913238.1 gg_id:112964 forest soil clone DUNssu017 (+1B) (OTU#052)
EU680459.1 gg_id:280233 unculturable forest Gaoligong Mountains Yunnan soil clone S13-37
DQ984553.1 gg_id:240236 Mt. Nan-Jen soil clone IFD_41
FJ466387.1 gg_id:553417 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF018503.1 gg_id:204592 aspen rhizosphere clone Amb_16S_1139
FJ466241.1 gg_id:512006 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
DQ202227.1 gg_id:140433 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo
EF042585.2 gg_id:232738 Microbial and geochemical dynamics extremely acidic metal-rich stream massive sulf
AY289385.1 gg_id:90452 soil clone DS-87
EF018868.1 gg_id:215513 aspen rhizosphere clone Amb_16S_1351
AY963368.1 gg_id:155297 structures and correlated ecological factors soils two evergreen broad-leaved forests
AJ581608.1 gg_id:93865 soil near uranium mill tailings clone KCM-B-77
EU050885.1 gg_id:256652 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_91
EF999370.1 gg_id:252534 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn
EU202826.1 gg_id:314799 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ465984.1 gg_id:553387 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF061943.1 gg_id:194730 Xiamen China mangrove sediment clone XME2
FJ466047.1 gg_id:559379 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AY922048.1 gg_id:112734 farm soil clone AKYG647
EF516699.1 gg_id:224638 grassland soil clone FCPN431
GQ402710.1 gg_id:566158 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ917891.1 gg_id:226056 Microbial profiles bleached and wild-type Muricea elongata Acidobacteria clone ME
EU881286.1 gg_id:331724 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
AF524859.1 gg_id:77390 sphagnum peat bog clone K-5b10
AY963390.1 gg_id:154565 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF600574.1 gg_id:302530 soil clone E5-34
EF018170.1 gg_id:211684 aspen rhizosphere clone Amb_16S_507
AY765992.1 gg_id:108645 Acidobacteriaceae KP3
DQ984543.1 gg_id:256036 Mt. Nan-Jen soil clone IFD_19
EF019556.1 gg_id:213076 aspen rhizosphere clone Elev_16S_1065
EF600563.1 gg_id:291339 soil clone E5-8

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EU335210.1	256500	1571.3	3491.5	6708.5	1323.0	2548.8	3317.4
EF492967.1	251273	334.3	466.7	1053.4	569.8	108.1	603.5
EU491617.1	258921	606.4	1396.4	2403.4	488.2	491.0	1221.5
EF020018.1	211775	81.5	97.3	1959.8	111.9	99.5	279.7
AJ519379.1	75044	33.3	90.3	385.6	72.8	214.4	302.6
EU276472.1	359394	887.4	590.5	3648.2	335.1	683.1	2101.0
EF018874.1	212877	1284.9	1822.5	3748.9	1862.6	1099.5	2825.2
DQ837260.1	256297	8211.4	9286.0	10847.8	5905.1	9892.8	9151.4
EU202778.1	316315	44.0	340.6	2419.2	128.8	130.0	552.9
AY913238.1	112964	104.1	119.3	186.8	73.5	76.0	83.6
EU680459.1	280233	24.8	52.8	675.0	72.9	68.1	185.1
DQ984553.1	240236	2957.7	4012.2	3564.6	2467.1	4210.3	6142.6
FJ466387.1	553417	4831.3	6783.0	6426.4	4915.3	6373.6	7355.6
EF018503.1	204592	45.2	59.7	140.3	71.7	83.7	59.3
FJ466241.1	512006	5067.2	5395.5	2625.5	4053.2	4497.3	4365.6
DQ202227.1	140433	4674.0	6447.8	3319.7	4595.7	3024.1	3965.0
EF042585.2	232738	34.1	88.4	177.5	56.7	100.0	121.5
AY289385.1	90452	105.7	138.3	178.7	86.6	86.0	103.7
EF018868.1	215513	1898.2	2439.8	2286.5	937.5	1861.4	1580.3
AY963368.1	155297	18.5	26.8	12.5	40.6	48.2	54.2
AJ581608.1	93865	187.0	937.6	2391.5	575.8	412.1	1187.9
EU050885.1	256652	1677.2	1997.8	6123.3	2166.0	1165.8	979.0
EF999370.1	252534	1005.3	2272.5	4168.7	664.4	1808.5	3186.4
EU202826.1	314799	560.2	1117.6	3595.2	738.7	362.9	1205.9
FJ465984.1	553387	2074.7	3143.4	3976.2	2009.9	2914.6	4341.9
EF061943.1	194730	4117.5	4155.4	4624.6	5241.5	2166.6	2701.2
FJ466047.1	559379	708.3	1394.1	2946.7	557.1	471.3	929.1
AY922048.1	112734	8754.8	10581.4	5772.0	6965.6	9383.9	11325.6
EF516699.1	224638	71.6	107.8	346.3	123.6	496.4	152.3
GQ402710.1	566158	431.8	822.1	1848.4	1038.8	920.5	1084.0
DQ917891.1	226056	29.1	129.1	175.5	77.5	90.1	198.4
EU881286.1	331724	3033.4	3797.1	4916.0	2861.8	3178.8	4749.6
AF524859.1	77390	3657.1	4163.3	2943.9	4249.7	2351.1	2512.9
AY963390.1	154565	4203.2	4972.9	3537.0	4641.8	6751.2	5043.2
EF600574.1	302530	6565.0	8259.0	6582.6	5607.5	5103.1	5392.1
EF018170.1	211684	1646.1	2520.8	3687.0	2275.2	4946.5	4089.8
AY765992.1	108645	313.8	658.7	2827.7	498.4	233.4	699.9
DQ984543.1	256036	381.0	1458.1	2466.7	1838.6	816.6	1696.5
EF019556.1	213076	48.8	82.9	117.8	160.0	72.1	86.4
EF600563.1	291339	3933.5	5328.2	5518.4	4362.8	8658.3	10008.1

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AY922151.1 gg_id:114240 farm soil clone AKYH715
DQ450715.1 gg_id:160091 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
DQ058684.1 gg_id:138816 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit
EF018355.1 gg_id:215113 aspen rhizosphere clone Amb_16S_728
AY963471.1 gg_id:154234 structures and correlated ecological factors soils two evergreen broad-leaved forests
AY234636.1 gg_id:111882 soil isolate Ellin5285
EF580946.1 gg_id:278766 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM6
EU150213.1 gg_id:278429 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_24
FJ478852.1 gg_id:545536 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU491650.1 gg_id:265935 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
FM877546.1 gg_id:357743 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-119
FJ466293.1 gg_id:541280 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU132210.1 gg_id:247003 tallgrass prarie soil clone FFCH13193
EF516049.1 gg_id:217420 grassland soil clone FCPS633
GQ120646.1 gg_id:375577 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on heavy
FJ479234.1 gg_id:582150 species richness estimates obtained nearly and simulated pyrosequencing-generated
AF234142.1 gg_id:28512 Sturt arid-zone soil clone #0319-7F19
FJ478926.1 gg_id:578528 species richness estimates obtained nearly and simulated pyrosequencing-generated
FM877548.1 gg_id:369088 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-130
AY289399.1 gg_id:90674 soil clone ABS-10
DQ906060.1 gg_id:220544 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1H3
FJ152605.1 gg_id:311752 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
EU335268.1 gg_id:257461 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU449702.1 gg_id:567134 Soil are Changed Agricultural Practices agricultural soil clone Plot4-C01
FJ205234.1 gg_id:570312 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
AY963500.1 gg_id:152510 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF597694.1 gg_id:248253 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian
FJ466210.1 gg_id:544431 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AJ292578.1 gg_id:45591 PCB-polluted soil clone WD228
DQ829645.1 gg_id:249932 Acidobacteria (Spain) Donana National Park clone DON6
GQ402674.1 gg_id:567036 Accessing microbial biodiversity and metabolic potential tropical -based approach p
FJ466400.1 gg_id:571342 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU202738.1 gg_id:327251 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ466332.1 gg_id:544403 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU370269.1 gg_id:363971 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e
EU202782.1 gg_id:309400 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
FJ466085.1 gg_id:548939 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AJ850100.1 gg_id:198267 Sponge Italy:Lingurian Sea clone SLIIK0
FJ466166.1 gg_id:552854 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ466014.1 gg_id:575126 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea

AY922010.1	113782	51.8	77.2	376.0	102.8	84.9	128.9
AY922151.1	114240	48.7	314.6	2747.9	141.6	147.4	603.7
DQ450715.1	160091	3044.9	7694.1	1758.4	1152.3	683.9	1083.7
DQ058684.1	138816	50.2	142.8	632.2	168.7	133.9	191.0
EF018355.1	215113	30.9	56.2	48.0	60.6	67.6	34.5
AY963471.1	154234	75.9	166.8	487.3	108.6	126.2	344.4
AY234636.1	111882	3185.6	3982.2	4571.5	4704.3	3914.7	4533.5
EF580946.1	278766	3022.9	2977.0	2739.9	2184.8	3117.1	2622.9
EU150213.1	278429	8379.8	11858.7	4044.7	6980.0	10428.7	7303.9
FJ478852.1	545536	900.7	1080.4	2556.0	646.2	2864.6	2984.5
EU491650.1	265935	2679.6	3397.5	4441.9	3043.2	7502.8	8758.0
FM877546.1	357743	514.2	621.3	3641.9	560.0	278.2	238.2
FJ466293.1	541280	95.4	295.2	598.7	161.8	88.0	291.6
EU132210.1	247003	5343.7	6862.6	6714.0	6089.6	6757.7	6127.0
EF516049.1	217420	1787.9	2899.9	2657.1	620.4	439.2	1256.0
GQ120646.1	375577	23.2	47.9	54.1	51.9	68.6	64.5
FJ479234.1	582150	8777.5	8917.8	4120.4	6550.2	9131.2	8934.8
AF234142.1	28512	108.8	339.2	358.5	113.7	97.7	135.8
FJ478926.1	578528	2609.9	4164.4	7864.3	3909.2	6661.4	5335.5
FM877548.1	369088	3921.7	5065.4	4094.2	3336.9	7418.0	8291.9
AY289399.1	90674	8203.4	10759.4	9210.4	8462.2	10009.5	11963.2
DQ906060.1	220544	832.2	1508.4	1655.4	1161.4	1218.0	1871.3
FJ152605.1	311752	2960.9	4918.2	5240.7	4427.4	6260.3	5287.1
EU335268.1	257461	95.4	207.2	271.9	126.9	119.3	325.0
EU449702.1	567134	6543.9	6868.5	4411.2	4736.4	6020.9	6338.9
FJ205234.1	570312	6618.0	7376.2	11071.8	8684.4	8298.3	9006.3
AY963500.1	152510	186.0	206.4	426.1	121.3	240.5	363.8
EF597694.1	248253	2679.0	3898.4	4975.1	2503.7	2664.7	3920.0
FJ466210.1	544431	822.6	608.6	381.3	624.5	203.4	474.9
AJ292578.1	45591	33.7	33.8	216.8	89.7	68.8	94.8
DQ829645.1	249932	4992.1	4543.7	4010.1	5195.5	2326.4	3419.4
GQ402674.1	567036	707.5	2036.9	1325.4	940.1	2749.0	2593.3
FJ466400.1	571342	4376.3	5151.3	4596.9	2238.2	4417.2	4139.9
EU202738.1	327251	112.1	407.3	4337.6	141.9	67.1	214.1
FJ466332.1	544403	3365.0	3760.6	4733.2	4816.8	5113.1	6392.0
EU370269.1	363971	3740.4	3471.0	4847.3	5104.9	7246.8	6029.8
EU202782.1	309400	810.2	1962.4	2815.4	741.3	1521.7	2261.0
FJ466085.1	548939	6219.8	7317.2	4310.1	5110.5	4114.3	6786.0
AJ850100.1	198267	141.8	440.3	999.7	222.9	191.4	345.1
FJ466166.1	552854	2129.9	3274.9	4312.8	2103.8	1762.1	2336.1
FJ466014.1	575126	7134.3	8689.7	10104.4	5459.1	11907.7	14187.7

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EF018357.1 gg_id:205244 aspen rhizosphere clone Amb_16S_732
DQ404735.1 gg_id:151798 contaminated sediment clone 655075
DQ906783.1 gg_id:241820 Oman subsurface soil clone 2B-4
EF516149.1 gg_id:223221 grassland soil clone FCPU726
AY922112.1 gg_id:114322 farm soil clone AKYH1441
EU276532.1 gg_id:370090 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
DQ451491.1 gg_id:156804 forest soil clone FAC52
EU335330.1 gg_id:254143 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
FJ529274.1 gg_id:554828 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze
EU491480.1 gg_id:260260 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
AY395324.1 gg_id:104834 pasture soil clone EB1005
FM873305.1 gg_id:363171 occupant source house floor dust clone FD01D10
DQ451496.1 gg_id:156857 forest soil clone FAC57
AM162414.1 gg_id:151114 and situ identification acidic sphagnum peat bog clone B59
EF999388.1 gg_id:252185 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn
EU150228.1 gg_id:279590 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_1
FJ466428.1 gg_id:563945 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU193005.1 gg_id:321058 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AJ292581.1 gg_id:25003 PCB-polluted soil clone WD247
GU208393.1 gg_id:582704 Study on Sediment Dongping Lake sediment clone Fh1-6
AY963503.1 gg_id:154268 structures and correlated ecological factors soils two evergreen broad-leaved forests
AM162415.1 gg_id:152327 and situ identification acidic sphagnum peat bog clone B62
EF688384.1 gg_id:241619 soil clone F6-100
EU373956.1 gg_id:261742 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU276529.1 gg_id:362467 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
Z95710.1 gg_id:22391 Holophaga/Acidobacterium phylum clone 32-10
EU117175.1 gg_id:238372 Scratching surface rare biosphere tag primers recent progress made toward microbi
AY493928.1 gg_id:136996 Fingerprinting aggregates soil clone 537
AY922148.1 gg_id:113191 farm soil clone AKYH694
FJ479477.1 gg_id:577222 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY289380.1 gg_id:89699 soil clone ABS-150
EF494364.1 gg_id:220562 Nunnock River granitic landscape clone NR.1.008
FJ478491.1 gg_id:553968 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU449733.1 gg_id:548647 Soil are Changed Agricultural Practices agricultural soil clone Plot4-G12
DQ829644.1 gg_id:236775 Acidobacteria (Spain) Donana National Park clone DON5
GU061236.1 gg_id:584106 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater
EF018559.1 gg_id:211201 aspen rhizosphere clone Amb_16S_822
AY289382.1 gg_id:89580 soil clone DS-130
FJ004671.1 gg_id:566891 Acidobacteria former agricultural soil rhizosphere clone 246
EU373917.1 gg_id:264000 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc

FJ466050.1	545180	6552.2	9151.9	8202.2	5031.6	7133.7	6848.2
EF018357.1	205244	5231.2	4864.5	5794.8	5086.8	3579.6	6719.0
DQ404735.1	151798	21.5	37.2	67.0	72.9	85.5	66.6
DQ906783.1	241820	8905.1	13534.0	5285.5	6160.9	9489.4	8770.4
EF516149.1	223221	31.4	65.2	141.8	67.3	55.2	23.8
AY922112.1	114322	201.5	901.0	4034.7	319.9	641.9	1322.9
EU276532.1	370090	43.8	198.3	357.8	79.0	173.3	238.3
DQ451491.1	156804	3635.4	4222.6	3786.4	533.4	2225.1	2996.3
EU335330.1	254143	828.2	1426.8	2595.8	628.6	1245.5	713.9
FJ529274.1	554828	4767.3	3910.1	8235.0	5770.6	4983.0	6085.3
EU491480.1	260260	7855.8	6512.2	5160.8	7894.4	4994.2	5704.9
AY395324.1	104834	15589.7	16452.6	12535.9	12401.2	15166.9	12336.8
FM873305.1	363171	2371.7	2704.0	2885.3	2017.3	610.2	2014.4
DQ451496.1	156857	426.2	2101.8	4221.1	967.4	3264.5	2067.8
AM162414.1	151114	2238.4	2527.0	2500.8	715.2	1674.6	1076.7
EF999388.1	252185	4654.9	5796.3	10510.5	5715.7	5113.3	7377.7
EU150228.1	279590	12064.5	9776.6	10388.0	7577.0	10860.2	9306.3
FJ466428.1	563945	10808.5	11331.1	7630.7	7342.8	8376.0	9558.5
EU193005.1	321058	4854.3	3188.8	5476.7	4588.8	3411.8	3704.3
AJ292581.1	25003	33.4	42.3	375.0	99.5	89.3	83.7
GU208393.1	582704	241.6	1888.1	2902.1	179.0	282.5	651.4
AY963503.1	154268	84.1	109.1	783.2	119.9	87.3	381.6
AM162415.1	152327	3726.2	3634.0	1227.8	2878.8	3747.8	3560.5
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EU373956.1	261742	11699.2	11274.4	9247.2	10594.6	12336.4	8120.2
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AY493928.1	136996	367.2	1025.7	3764.0	508.0	308.1	1250.1
AY922148.1	113191	545.4	1192.2	2333.9	439.9	1657.8	1646.2
FJ479477.1	577222	444.0	1509.2	5042.6	409.1	1183.8	1472.2
AY289380.1	89699	3551.2	3600.3	8372.6	2970.4	4923.1	4291.9
EF494364.1	220562	4980.6	4815.7	3665.6	4536.2	4921.7	5789.2
FJ478491.1	553968	2366.3	2106.9	3483.7	1887.3	1934.6	1953.1
EU449733.1	548647	878.6	2225.5	4964.6	1086.1	1786.0	3164.1
DQ829644.1	236775	4904.1	5060.7	4547.4	766.8	563.1	1455.5
GU061236.1	584106	3763.4	3408.6	4841.6	4861.7	2061.6	2883.2
EF018559.1	211201	13.3	25.7	26.1	54.2	66.8	26.0
AY289382.1	89580	1182.3	1479.6	1141.4	572.1	3312.4	2097.4
FJ004671.1	566891	663.7	1633.2	963.5	544.9	368.2	737.1
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FJ466328.1 gg_id:533475 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
DQ310740.1 gg_id:145786 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC(
AB240247.1 gg_id:144789 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
EF492906.1 gg_id:248716 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
DQ083303.1 gg_id:128109 Acidobacteria pasture soil clone EC1113
EF516913.1 gg_id:226506 grassland soil clone FCPT635
DQ837256.1 gg_id:242275 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_56
AY703470.1 gg_id:139008 Detection and ly acidobacterial analyses Altamira Cave clone ALT5
AY921764.1 gg_id:113851 farm soil clone AKYG1603
EU335387.1 gg_id:244133 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AJ532720.1 gg_id:75652 uranium mining waste pile clone JG34-KF-135
AJ519368.1 gg_id:75679 uranium mining waste pile clone JG37-AG-31 sp.
EU925917.1 gg_id:315699 sediments sediment station DBS1 northern Bering Sea clone 154H76
AB240301.1 gg_id:142005 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
FN396687.1 gg_id:543863 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V
EF999365.1 gg_id:254954 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn
DQ451492.1 gg_id:156776 forest soil clone FAC53
FM872485.1 gg_id:362116 occupant source house floor dust clone FA01A05
DQ648903.1 gg_id:183276 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate
EF019375.1 gg_id:213210 aspen rhizosphere clone Elev_16S_601
DQ811917.1 gg_id:161945 mangrove soil clone MSB-4dx5
AY913329.1 gg_id:114314 forest soil clone DUNssu124 (+1B) (OTU#092)
AY921985.1 gg_id:112801 farm soil clone AKYG1765
EF018706.1 gg_id:212676 aspen rhizosphere clone Amb_16S_1157
EF061944.1 gg_id:193841 Xiamen China mangrove sediment clone XME31
GQ264340.1 gg_id:539385 Structure Simulated Level Waste Site simulated level waste site clone WW2_174
GU205312.1 gg_id:531776 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
GQ402599.1 gg_id:508855 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AY963463.1 gg_id:150792 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ152824.1 gg_id:331686 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
AY703461.1 gg_id:139345 Detection and ly acidobacterial analyses Altamira Cave clone ALT21
AF317741.1 gg_id:136924 Nullarbor cave clone wb1_A08
AB486755.1 gg_id:565220 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(
EF492944.1 gg_id:245527 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
FJ004689.1 gg_id:560014 Acidobacteria former agricultural soil rhizosphere clone 6Fe
EU276463.1 gg_id:361472 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
AY493932.1 gg_id:136838 Fingerprinting aggregates soil clone 1283
FJ479104.1 gg_id:538113 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ500793.1 gg_id:540282 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta
X97098.1 gg_id:3730 peat bog clone TM2
EF597699.1 gg_id:240765 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian

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AB240247.1	144789	2679.3	3691.9	3058.3	1019.3	3600.7	3295.2
EF492906.1	248716	670.4	663.2	1426.3	437.2	212.1	483.7
DQ083303.1	128109	71.9	96.3	146.3	135.7	133.1	108.9
EF516913.1	226506	853.7	1847.7	4565.6	288.3	456.6	1136.9
DQ837256.1	242275	6694.4	7247.3	7622.5	6032.4	6853.2	8078.3
AY703470.1	139008	6379.6	8778.8	9023.6	3745.5	8733.4	7056.9
AY921764.1	113851	4256.7	4680.0	5822.2	6361.9	4474.4	3161.3
EU335387.1	244133	1642.9	1708.5	2209.8	2524.0	2049.0	2755.8
AJ532720.1	75652	840.0	457.0	350.5	1961.1	125.1	148.4
AJ519368.1	75679	3558.0	4974.3	7214.0	2691.8	4098.2	4610.1
EU925917.1	315699	12773.3	11580.1	10789.5	9764.6	11773.3	10067.2
AB240301.1	142005	65.8	247.3	452.9	110.9	106.4	86.3
FN396687.1	543863	7279.8	8011.9	10647.8	7613.4	6403.9	8230.7
EF999365.1	254954	7098.3	11142.2	23500.0	6727.7	13149.5	15737.6
DQ451492.1	156776	275.2	368.6	3044.8	217.5	210.0	489.1
FM872485.1	362116	2862.6	4061.4	6613.5	2958.0	1973.9	3988.6
DQ648903.1	183276	3693.0	5247.9	7394.5	4813.3	10185.8	6798.4
EF019375.1	213210	28.8	44.0	226.8	66.9	67.3	36.9
DQ811917.1	161945	19.4	24.2	18.3	43.1	56.5	23.5
AY913329.1	114314	3308.6	2983.6	1560.9	2307.1	1884.2	2547.1
AY921985.1	112801	48.1	141.0	332.2	139.8	219.1	563.8
EF018706.1	212676	4881.5	5210.4	3809.5	4982.7	3596.7	3432.7
EF061944.1	193841	2907.6	4681.6	4566.1	2097.3	844.6	1380.6
GQ264340.1	539385	8102.1	7460.5	3756.6	2184.5	2413.8	4492.4
GU205312.1	531776	314.6	326.1	689.7	279.7	276.7	435.2
GQ402599.1	508855	64.3	187.0	451.0	199.1	146.5	370.4
AY963463.1	150792	12127.0	13360.3	7957.2	10458.2	15465.6	14566.4
FJ152824.1	331686	4485.6	6500.5	10751.0	3894.7	2114.3	3942.1
AY703461.1	139345	4604.3	7659.4	11200.3	4311.7	6569.6	8218.4
AF317741.1	136924	7874.5	4840.1	6353.2	6399.1	5688.4	7987.6
AB486755.1	565220	209.4	1061.6	2372.4	323.2	263.2	679.1
EF492944.1	245527	1025.5	853.2	1847.8	1143.8	545.8	676.3
FJ004689.1	560014	20.1	66.0	90.8	85.1	77.2	54.4
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EF597699.1	240765	7937.7	9279.0	8461.3	5939.2	8451.1	6411.3

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EU250234.1 gg_id:247591 acid mine drainage clone GXDC-20
AB240252.1 gg_id:141140 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
EF018530.1 gg_id:209723 aspen rhizosphere clone Amb_16S_790
AY922154.1 gg_id:113332 farm soil clone AKYH735
EF125431.1 gg_id:195246 mangrove soil clone MSB-2D12
AY850302.1 gg_id:136684 depending on what microbial treatment present soil clone cw7
DQ906775.1 gg_id:236062 Oman subsurface soil clone 2A-3
EU676420.1 gg_id:302540 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
EF018157.1 gg_id:212760 aspen rhizosphere clone Amb_16S_492
EF173346.1 gg_id:182111 Options situ remediation contaminated mixture chlorinated hydrocarbons hydrocarb
GU172193.1 gg_id:582540 Microbial Eucalyptus plantation soil clone DSM-R21
DQ451525.1 gg_id:156611 forest soil clone FAC86
FJ465992.1 gg_id:546843 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF516950.1 gg_id:221187 grassland soil clone FCPP719
FJ152801.1 gg_id:346446 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EU132094.1 gg_id:253652 tallgrass prarie soil clone FFCH4380
EU734939.1 gg_id:322030 assemblages sediment station DBSE Northern Bering Sea clone 030C26
EF600570.1 gg_id:291945 soil clone E5-24
EF494374.1 gg_id:217344 Nunnock River granitic landscape clone NR.1.127
GQ402697.1 gg_id:538729 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AY963323.1 gg_id:155327 structures and correlated ecological factors soils two evergreen broad-leaved forests
AB262723.1 gg_id:243925 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-12
EU421852.1 gg_id:271460 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-27
FJ517001.1 gg_id:551640 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c
EF019493.1 gg_id:206727 aspen rhizosphere clone Elev_16S_761
AB300068.1 gg_id:220849 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone S
AB300075.1 gg_id:218783 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone S
GQ246334.1 gg_id:590912 Temporal and spatial China North Yel Sea sediments clone Sd1-53
AY225646.1 gg_id:97685 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-28
EU385737.1 gg_id:276636 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S
AB177178.1 gg_id:133702 seafloor methane hydrate clone ODP1230B23.02
EU925844.1 gg_id:347415 sediments sediment station DBS1 northern Bering Sea clone 035E60
GQ246376.1 gg_id:587607 Temporal and spatial China North Yel Sea sediments clone Cm1-39
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EU925841.1 gg_id:323947 sediments sediment station DBS1 northern Bering Sea clone 022E38
EU287157.1 gg_id:236701 Pacific arctic surface sediment clone P13-64
GQ246383.1 gg_id:558182 Temporal and spatial China North Yel Sea sediments clone Cm1-46
EU734964.1 gg_id:342871 assemblages sediment station DBSE Northern Bering Sea clone 058D16
AM176872.1 gg_id:160549 Recovery mangrove sediment clone SZB79
EU246285.1 gg_id:242979 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-C11

EF208619.1	200645	2015.1	3499.1	3226.1	1141.6	3359.1	3681.6
EU250234.1	247591	4731.1	3992.7	4036.2	4514.3	4349.5	4210.4
AB240252.1	141140	29.5	102.1	565.7	96.2	58.8	85.1
EF018530.1	209723	1207.0	1770.8	7633.0	1197.2	634.9	2059.5
AY922154.1	113332	1755.6	2042.6	5156.2	3108.2	2519.1	2564.7
EF125431.1	195246	153.1	419.9	618.8	114.1	92.3	93.3
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EF173346.1	182111	2352.3	2843.7	3244.1	2509.9	948.6	2384.8
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DQ451525.1	156611	3579.5	4882.8	7931.9	3810.3	3420.8	3945.3
FJ465992.1	546843	493.8	1242.6	2618.3	1019.1	1324.4	2271.7
EF516950.1	221187	14.8	46.5	331.6	53.4	67.5	95.2
FJ152801.1	346446	16350.3	17807.1	12241.3	13299.3	17503.8	15534.5
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AY963323.1	155327	46.3	102.5	357.0	87.8	95.4	93.1
AB262723.1	243925	2231.6	2625.6	6320.7	2049.5	2059.3	3128.3
EU421852.1	271460	289.8	711.3	1531.5	325.8	241.0	839.6
FJ517001.1	551640	2519.8	5587.5	9813.3	3276.1	5260.9	5058.7
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AB300068.1	220849	562.7	790.9	2576.4	462.0	720.9	908.9
AB300075.1	218783	27.1	46.7	45.3	50.6	54.1	28.6
GQ246334.1	590912	5181.5	5568.0	5724.4	4593.5	3935.0	3549.5
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EU385737.1	276636	793.0	894.2	1411.3	2035.8	603.6	544.7
AB177178.1	133702	122.8	322.2	445.6	125.4	181.2	87.2
EU925844.1	347415	2775.1	3607.3	6898.5	3515.1	5229.5	3115.3
GQ246376.1	587607	10633.9	11571.4	9110.2	6825.6	8100.9	7074.6
EU386023.1	267584	8440.1	8433.5	6477.3	5503.1	4213.1	7224.3
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EU491345.1 gg_id:270093 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
FJ205355.1 gg_id:555830 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
EU373945.1 gg_id:259584 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU328055.1 gg_id:279230 dynamics during bioremediation crude oil contaminated moderate saline soil clone B
FJ748804.1 gg_id:512374 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estuar
FJ269346.1 gg_id:587166 Microbes marine sponges sponge tissue clone XE1A06
DQ297966.1 gg_id:144752 Microbial hydrocarbon contaminated soil clone UD7
EF127615.1 gg_id:208380 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE014
EF492965.1 gg_id:256992 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AB240484.1 gg_id:141861 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei
EF516139.1 gg_id:221008 grassland soil clone FCPU691
AY250867.1 gg_id:86097 lichen-dominated Antarctic cryptoendolithic community clone FBP241
EU150230.1 gg_id:279384 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_4
FJ592765.1 gg_id:511315 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pur
AM116734.1 gg_id:142650 Interactions U(VI) added natural dependance on various incubation conditions soil u
EF584528.1 gg_id:234366 mixed granule anammox reactor clone KIST-JJY008
AF173822.1 gg_id:1768 Antarctic clone LB3-30
EU132395.1 gg_id:253431 tallgrass prarie soil clone FFCH1720
GU459003.1 gg_id:563320 microbiota human male female forehead forearm and influence make-up skin clone
EU223961.1 gg_id:247010 -RFLP microbes Qinghai-Tin rail soil clone 149
AY289362.1 gg_id:88737 soil clone DS-249
AY921973.1 gg_id:113400 farm soil clone AKYG1698
EF018286.1 gg_id:209520 aspen rhizosphere clone Amb_16S_647
AY289372.1 gg_id:112292 soil clone DS-13
EF516486.1 gg_id:221484 grassland soil clone FCPP426
EU669595.1 gg_id:351338 soil clone S11-2
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EF019956.1 gg_id:209832 aspen rhizosphere clone Elev_16S_1335
EU335391.1 gg_id:239226 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AF368181.1 gg_id:55946 non-EBPR sludge clone SBRT166
FJ478811.1 gg_id:578620 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF516663.1 gg_id:223948 grassland soil clone FCPU688
AY211077.1 gg_id:81698 anaerobic VC-degrading enrichment clone VC47 bacterium
AM777958.1 gg_id:246222 nonsaline . Influence pore-size filters determination structure alkaline groundwater
EF516301.1 gg_id:223489 grassland soil clone FCPN505
DQ648917.1 gg_id:185831 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate
EF127618.1 gg_id:204154 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE075
FJ479148.1 gg_id:509991 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ648922.1 gg_id:193986 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate
EU979109.1 gg_id:340198 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere be

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EU328055.1	279230	5155.0	5396.4	6218.6	5404.5	3732.9	5396.6
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DQ297966.1	144752	1674.6	1320.0	4494.6	1619.7	1534.7	2124.1
EF127615.1	208380	23.8	90.9	97.4	54.2	134.7	66.5
EF492965.1	256992	4730.6	4136.1	5540.2	2453.2	3730.0	2741.5
AB240484.1	141861	1264.2	4195.2	3281.3	1488.6	4674.5	6377.0
EF516139.1	221008	20.6	51.0	101.5	45.7	76.8	140.4
AY250867.1	86097	26.5	33.0	27.7	50.0	57.4	20.5
EU150230.1	279384	36.0	338.1	611.6	104.1	134.2	215.2
FJ592765.1	511315	5787.2	6607.4	4111.5	6416.5	3457.1	4268.4
AM116734.1	142650	34.7	45.5	71.2	71.5	66.4	65.0
EF584528.1	234366	31.2	142.2	119.4	61.8	105.6	49.8
AF173822.1	1768	2545.8	2842.8	3428.7	5053.2	1623.2	2579.2
EU132395.1	253431	165.8	1404.5	745.0	598.4	420.4	344.8
GU459003.1	563320	569.1	868.5	1217.6	852.8	1184.3	771.7
EU223961.1	247010	156.8	269.4	356.5	178.2	840.0	269.7
AY289362.1	88737	14720.7	17603.5	10983.7	15265.0	12266.3	13158.0
AY921973.1	113400	199.5	1650.1	2591.5	308.7	504.6	576.2
EF018286.1	209520	8721.9	6529.0	4340.4	6626.4	6944.2	7814.0
AY289372.1	112292	6063.6	5411.3	5498.0	5788.2	5627.2	5742.2
EF516486.1	221484	40.9	79.4	4692.2	79.4	67.6	35.7
EU669595.1	351338	926.0	1417.1	2605.7	907.6	793.1	1430.8
EU786139.1	564389	3549.7	3252.0	4881.1	4263.4	2121.4	3087.1
EF019956.1	209832	438.6	1116.0	520.3	192.4	480.5	507.3
EU335391.1	239226	376.1	2343.8	3651.7	437.1	1268.4	972.8
AF368181.1	55946	421.6	484.1	488.7	811.7	528.1	453.6
FJ478811.1	578620	29.7	48.8	191.3	71.0	60.5	33.9
EF516663.1	223948	6081.6	6694.1	5893.3	7061.9	6759.3	7460.1
AY211077.1	81698	316.1	719.4	907.1	88.8	127.6	147.8
AM777958.1	246222	772.5	1710.0	1509.8	1046.5	2009.7	1662.0
EF516301.1	223489	37.0	288.1	235.0	70.4	167.6	87.4
DQ648917.1	185831	13925.2	14412.7	13104.2	12749.9	13957.8	12305.1
EF127618.1	204154	478.8	1366.7	1138.7	925.4	588.4	726.2
FJ479148.1	509991	100.9	471.8	1016.6	230.0	218.6	219.9
DQ648922.1	193986	7002.4	6575.2	5257.8	5992.5	5492.1	6447.8
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EU669608.1 gg_id:322898 soil clone S11-33
DQ648925.1 gg_id:197697 biodiversity and rhizosphere polluted site TGGE screening libraries PCB contaminate
FJ004727.1 gg_id:573937 Acidobacteria former agricultural bulk soil clone 1L2B
AF097766.1 gg_id:1776 activated sludge clone 2951
FJ790561.1 gg_id:549105 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB43
AY493926.1 gg_id:136943 Fingerprinting aggregates soil clone 539
FJ479201.1 gg_id:513643 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF494321.1 gg_id:218151 Nunnock River granitic landscape clone NR.4.007
DQ450705.1 gg_id:161241 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EF516128.1 gg_id:224218 grassland soil clone FCPT565
FJ479029.1 gg_id:556814 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ264352.1 gg_id:567627 Structure Simulated Level Waste Site simulated level waste site clone WW2_25
DQ532357.2 gg_id:164562 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
FJ479240.1 gg_id:589151 species richness estimates obtained nearly and simulated pyrosequencing-generated
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DQ083266.1 gg_id:128164 Acidobacteria pasture soil clone EC1038
AF173824.1 gg_id:1767 Antarctic clone LB3-92
DQ532263.1 gg_id:171397 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce
EU150244.1 gg_id:277931 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_21
EU669596.1 gg_id:341165 soil clone S11-7
GQ029460.1 gg_id:401741 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw861f09
CU921698.1 gg_id:565019 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ275099.1 gg_id:586270 gut symbionts are tightly linked herbivory ants extract single ant clone #123
EU131955.1 gg_id:242792 tallgrass prarie soil clone FFCH15207
EF019535.1 gg_id:209516 aspen rhizosphere clone Elev_16S_1040
FJ479597.1 gg_id:588240 species richness estimates obtained nearly and simulated pyrosequencing-generated
EF018479.1 gg_id:216034 aspen rhizosphere clone Amb_16S_1107
EF019534.1 gg_id:206841 aspen rhizosphere clone Elev_16S_1038
EU276488.1 gg_id:367606 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
EF492911.1 gg_id:247203 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
FJ466180.1 gg_id:566535 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU132318.1 gg_id:257472 tallgrass prarie soil clone FFCH10172
FJ152715.1 gg_id:315631 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EU335388.1 gg_id:255794 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU335275.1 gg_id:250547 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AY509523.1 gg_id:136325 cyanobacterial blooms four Swedish lakes freshwater clone LiUU-11-191
EU202757.1 gg_id:340218 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU131979.1 gg_id:236098 tallgrass prarie soil clone FFCH2893

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EU669608.1	322898	3455.0	4960.5	3110.9	4727.9	5038.1	7785.7
DQ648925.1	197697	86.7	119.5	117.3	85.7	82.6	80.7
FJ004727.1	573937	820.2	1303.8	2000.0	389.3	222.1	491.8
AF097766.1	1776	1853.0	2982.7	997.4	2482.3	3308.2	2002.1
FJ790561.1	549105	2519.8	1779.3	4851.2	2321.0	1546.1	2620.7
AY493926.1	136943	659.0	778.0	1256.4	592.0	756.6	557.3
FJ479201.1	513643	3749.0	4856.2	3556.1	2633.7	4504.8	4638.2
EF494321.1	218151	2630.2	1078.2	4134.0	1863.1	2760.3	1925.6
DQ450705.1	161241	296.1	195.1	1182.0	94.6	446.2	120.0
EF516128.1	224218	20.5	220.1	89.9	45.6	111.2	19.7
FJ479029.1	556814	3855.4	3896.0	5342.2	3595.7	3441.3	3537.7
GQ264352.1	567627	301.4	1121.8	541.3	1107.4	444.7	530.1
DQ532357.2	164562	130.9	1310.5	1388.0	401.2	1373.5	443.1
FJ479240.1	589151	3375.6	4741.9	4806.6	2160.1	5218.1	4828.0
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EU979032.1	340207	2260.8	3656.8	4961.3	1616.3	5093.2	2022.1
DQ648920.1	191363	1860.0	3335.4	4176.5	2698.2	4732.6	7251.5
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EU150244.1	277931	39.5	55.5	1473.8	62.6	41.1	28.6
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GQ275099.1	586270	5287.4	5742.3	5309.8	4403.6	4334.0	4568.2
EU131955.1	242792	1503.5	1502.0	1421.4	972.3	1155.5	786.9
EF019535.1	209516	18.8	28.5	17.5	47.1	63.4	15.0
FJ479597.1	588240	1456.9	1509.0	2530.3	2364.5	1917.2	3364.1
EF018479.1	216034	6975.9	10101.0	7683.5	10722.4	12508.5	12741.4
EF019534.1	206841	6820.7	7319.5	5568.3	6837.4	6235.2	7202.7
EU276488.1	367606	1747.5	2398.4	1893.0	2482.8	2697.4	2678.9
EF492911.1	247203	223.8	290.3	107.6	701.4	966.4	495.4
FJ466180.1	566535	10823.2	9312.8	9215.2	6975.9	6137.1	9034.1
EU132318.1	257472	10962.4	12080.1	10178.5	12791.0	10113.4	12118.9
FJ152715.1	315631	167.8	165.6	353.1	102.6	108.0	76.0
EU335388.1	255794	4252.8	5672.4	7390.7	4114.3	4678.1	8411.2
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AY509523.1	136325	4655.0	6261.0	7474.2	5935.7	5465.8	7009.6
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FJ535093.1 gg_id:556648 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM88
EF612356.1 gg_id:238966 historic semiarid lead-zinc mine tailings site soil clone OS-C85
AM902631.1 gg_id:237774 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa
EU669607.1 gg_id:336301 soil clone S11-31
EU192989.1 gg_id:353698 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU131934.1 gg_id:249598 tallgrass prarie soil clone FFCH11145
FJ478812.1 gg_id:558300 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU881303.1 gg_id:307883 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
EU132097.1 gg_id:242038 tallgrass prarie soil clone FFCH1205
DQ532341.1 gg_id:166649 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C
FJ790570.1 gg_id:568934 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB74
EF205575.1 gg_id:210897 among geographically regions central Tibet geothermal spring mat clone TP32
EF205532.1 gg_id:208981 among geographically regions central Tibet geothermal spring mat clone DTB48
FJ478484.1 gg_id:543361 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU335287.1 gg_id:251244 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
FN396738.1 gg_id:575010 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II
AB303221.1 gg_id:289370 Acanthopleuribacter pedis str. NBRC 101209
U41563.1 gg_id:1736 "Geothrix fermentans"
DQ660831.1 gg_id:237050 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I-4
GQ390238.1 gg_id:562850 oxic-anoxic interface meromictic crater lake Lac Pavin clone eub62A6
DQ660849.1 gg_id:240444 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCN-I-2
AB240350.1 gg_id:144899 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
EU803304.1 gg_id:322696 It's all ranking aquatic Lake Gatun clone 5C230854
AB240249.1 gg_id:142414 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo
FJ810540.1 gg_id:373070 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
EU156148.1 gg_id:252532 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65
AM086131.1 gg_id:149184 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone
AB192122.1 gg_id:142455 termite gut homogenate clone M1PL1-36
FJ810545.1 gg_id:433880 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su
GQ472456.1 gg_id:542134 Microbial Dongping Lake lake sediment clone 5F1-11
AM180887.1 gg_id:149516 situ detection Acidobacteria mats chemoautotrophic cave (Lower Kane Cave WY US
EU169840.1 gg_id:361234 Bio-reduction Trichloroethene Hydrogen-Based Membrane Biofilm Reactor membra
X77215.1 gg_id:1732 Holophaga foetida
EU340170.1 gg_id:235707 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
AJ009478.1 gg_id:1733 anaerobic TCB-transforming consortium clone SJA-87
AB192121.1 gg_id:144303 termite gut homogenate clone M1NP1-62
DQ066997.1 gg_id:133176 Lake Washington sediment clone pLW-59
FN554392.1 gg_id:554680 Isolation members group 8 Acidobacteria subdivision 1 Verrucomicrobia and other h
GQ487951.1 gg_id:553643 Microbial metal soil polluted heavy metals clone T7-99
GU169059.1 gg_id:592179 Biofilms formed on substances: response f conditions and carbon concentrations sy

EU132025.1	240289	1166.0	1929.3	5809.8	1283.3	656.0	840.1
FJ535093.1	556648	2773.2	8093.5	2942.1	2506.8	3590.5	3342.7
EF612356.1	238966	14155.3	14965.2	11122.2	8601.6	9244.0	8793.5
AM902631.1	237774	8083.0	10061.0	10440.1	5929.1	4977.3	6612.0
EU669607.1	336301	6634.7	8711.6	7905.3	5081.5	2220.8	3693.6
EU192989.1	353698	12641.0	12474.2	8254.5	8046.5	6743.7	8271.4
EU131934.1	249598	12823.1	12595.6	14601.6	12253.3	17657.5	15515.1
FJ478812.1	558300	3976.2	5261.4	6269.8	4955.8	4119.3	4929.7
EU881303.1	307883	328.6	949.5	1246.3	756.1	1996.5	850.3
EU132097.1	242038	406.9	791.4	1581.4	1253.1	976.0	787.4
DQ532341.1	166649	136.9	419.8	511.6	260.4	162.6	221.5
FJ790570.1	568934	76.7	220.5	419.9	180.4	257.3	190.8
EF205575.1	210897	2396.0	2800.9	2847.6	1627.6	2818.9	2637.6
EF205532.1	208981	8902.1	7248.9	11106.9	7155.7	6834.4	8397.8
FJ478484.1	543361	7878.7	9106.7	6956.3	6374.9	8805.1	8897.4
EU335287.1	251244	642.2	1119.6	2308.3	1406.2	6081.9	3621.0
FN396738.1	575010	856.0	1363.8	828.5	1327.5	594.3	671.3
AB303221.1	289370	138.0	287.7	998.4	105.3	150.0	248.2
U41563.1	1736	416.7	1153.2	12252.4	634.0	355.0	670.4
DQ660831.1	237050	1040.0	1758.7	7876.9	1803.7	2522.4	2381.3
GQ390238.1	562850	638.5	1153.4	10390.3	1007.5	133.2	254.5
DQ660849.1	240444	6722.1	9011.1	13296.5	7428.4	9781.1	8371.4
AB240350.1	144899	535.9	791.2	4738.1	928.8	2283.1	300.0
EU803304.1	322696	9154.2	9592.8	13889.4	10265.4	13185.3	12315.4
AB240249.1	142414	604.3	1511.8	11968.5	1106.8	273.4	396.8
FJ810540.1	373070	6974.2	8607.6	10705.3	5831.9	9453.3	7916.3
EU156148.1	252532	999.6	1418.3	5461.3	1489.6	6275.8	884.0
AM086131.1	149184	4155.7	5581.3	5584.1	2705.9	4918.1	5568.4
AB192122.1	142455	476.4	777.8	2776.4	2523.6	725.2	1514.1
FJ810545.1	433880	10800.4	10588.3	9146.9	7156.2	11267.7	8205.4
GQ472456.1	542134	1116.6	1488.2	7168.3	1692.9	743.3	1013.7
AM180887.1	149516	77.5	245.6	1607.5	294.6	63.4	59.7
EU169840.1	361234	4618.8	5288.7	7256.6	5559.0	8005.5	6273.7
X77215.1	1732	102.9	57.6	139.7	77.7	126.0	32.0
EU340170.1	235707	11095.0	9427.9	14285.1	8298.0	11370.9	9356.8
AJ009478.1	1733	1241.5	1468.1	6307.8	1835.7	585.4	750.0
AB192121.1	144303	82.7	103.4	421.7	167.3	82.5	82.3
DQ066997.1	133176	114.8	376.0	2378.5	291.6	247.7	178.5
FN554392.1	554680	5023.4	5382.3	6441.3	2547.7	5574.4	3858.2
GQ487951.1	553643	1554.2	2770.1	11831.6	2008.5	740.3	1238.6
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AF529125.1 gg_id:55664 trichloroethene-contaminated site clone FTLM5 bacterium
EU360308.1 gg_id:274047 microbial fuel cell enriched sediment clone FWS 726
EF032758.1 gg_id:194029 cyanobacterial mat in lava cave clone HAVOmat71
EU404024.1 gg_id:311763 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
AY963514.1 gg_id:154909 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF494334.1 gg_id:225918 Nunnock River granitic landscape clone NR.1.031
AB240310.1 gg_id:144019 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
AB486063.1 gg_id:586133 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
EF516537.1 gg_id:218957 grassland soil clone FCPT436
EU132113.1 gg_id:251439 tallgrass prarie soil clone FFCH10391
Z95713.1 gg_id:1728 soil clone 32-20
AB486378.1 gg_id:588194 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
DQ906890.1 gg_id:251805 Oman subsurface soil clone 11B-20
AY395447.1 gg_id:103470 pasture soil clone EB1128
AB488104.1 gg_id:578435 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
EF516616.1 gg_id:224372 grassland soil clone FCPN715
DQ450820.1 gg_id:160986 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EF515929.1 gg_id:218370 grassland soil clone FCPS615
GQ397044.1 gg_id:586275 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
GQ302583.1 gg_id:542433 prokaryotic sediment Shawan methods cold spring clone sw-xj162
AY921868.1 gg_id:113021 farm soil clone AKYG1139
EF492961.1 gg_id:250693 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
Z95729.1 gg_id:1718 soil clone iii1-8
FJ545583.1 gg_id:565231 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-65
FJ479007.1 gg_id:509899 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ378223.1 gg_id:151990 oil-polluted soil clone M01_Pitesti
EF632944.1 gg_id:237284 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh
EF515913.1 gg_id:224501 grassland soil clone FCPP604
EU925899.1 gg_id:324084 sediments sediment station DBS1 northern Bering Sea clone 124H8
EF516669.1 gg_id:219348 grassland soil clone FCPN472
AB488081.1 gg_id:592475 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSURC
AY289394.1 gg_id:111806 soil clone DS-215
FN424397.1 gg_id:565655 structure sediments Bizerte (Tunisia) southern Mediterranean coastal anthropized la
FJ479328.1 gg_id:511937 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ228377.1 gg_id:143029 microbial compositions two subglacial possible role microbes chemical weathering p
FJ868852.1 gg_id:509795 Effects nitrogen form on excessive fertilization soil Earth-cumuli-orthic anthrosols clo
AY493935.1 gg_id:136569 Fingerprinting aggregates soil clone 869
DQ001620.1 gg_id:157110 Microbial seeps asphalt seep clone E91-12
GQ016556.1 gg_id:493114 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ302580.1 gg_id:563979 prokaryotic sediment Shawan methods cold spring clone sw-xj147
AB128876.1 gg_id:103558 deep marine sediments Nankai Trough Japan; ODP Leg 190 clone 1174-1091-17

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AY963514.1	154909	2803.2	2568.0	2119.3	1880.6	2695.7	3592.6
EF494334.1	225918	1031.7	1086.9	2471.3	2116.6	506.0	740.0
AB240310.1	144019	40.3	32.8	218.7	63.2	68.8	33.9
AB486063.1	586133	689.1	945.1	1183.4	836.9	676.4	1042.2
EF516537.1	218957	19.4	33.5	47.5	56.6	62.0	68.1
EU132113.1	251439	2321.2	6017.4	7273.8	4130.2	8871.5	7920.4
Z95713.1	1728	638.8	1213.8	1798.2	984.7	1725.5	2357.3
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DQ906890.1	251805	4526.0	5289.8	6710.6	2047.8	4041.8	3275.8
AY395447.1	103470	34.1	56.7	88.3	76.9	105.9	83.7
AB488104.1	578435	9538.0	11192.1	8432.5	8398.9	7876.4	8619.9
EF516616.1	224372	509.7	743.2	3007.1	1164.5	1654.0	3329.1
DQ450820.1	160986	10296.0	11304.9	11272.6	7972.7	13878.4	10845.1
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GQ302583.1	542433	697.0	1355.5	2468.1	825.3	2304.0	1704.9
AY921868.1	113021	28.6	54.0	212.1	65.3	59.0	43.1
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FJ479007.1	509899	162.2	465.2	951.4	245.0	287.0	734.1
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DQ228377.1	143029	339.1	308.0	85.0	57.4	58.3	41.6
FJ868852.1	509795	5016.4	6146.6	7270.3	6922.0	5171.2	6101.9
AY493935.1	136569	27.3	38.1	49.2	53.8	71.2	34.6
DQ001620.1	157110	747.0	1499.1	862.6	578.0	1399.9	1372.2
GQ016556.1	493114	12805.1	13256.8	11568.4	11668.8	12723.2	11639.9
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EF516758.1 gg_id:217242 grassland soil clone FCPN518
AB240376.1 gg_id:141305 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
DQ415770.1 gg_id:158462 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid
AB426221.1 gg_id:272259 -situ identification study benzene-degrading s under methanogenic condition anaerc
AB426190.1 gg_id:263608 -situ identification study benzene-degrading s under methanogenic condition anaerc
AY177760.1 gg_id:78424 subsurface soil beneath grassland clone
GQ402795.1 gg_id:584529 Accessing microbial biodiversity and metabolic potential tropical -based approach pe
AB240315.1 gg_id:142591 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
FJ825470.1 gg_id:532951 Microbial during start-up mesophilic biogas plant clone 150b_BE4_38
AM902640.1 gg_id:252937 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa
AB426230.1 gg_id:263257 -situ identification study benzene-degrading s under methanogenic condition anaerc
FJ478644.1 gg_id:543083 species richness estimates obtained nearly and simulated pyrosequencing-generated
AF523992.1 gg_id:63234 forested wetland clone FW32
EU132238.1 gg_id:237679 tallgrass prarie soil clone FFCH15579
AY222310.1 gg_id:113738 host hindgut caecum clone Aci 1
AB300113.1 gg_id:226421 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K
EF688201.1 gg_id:333448 Detection microbial sludge anaerobic wastewater treatment system clone 4F4_cons
DQ811915.1 gg_id:170193 mangrove soil clone MSB-3G5
GU208397.1 gg_id:583865 Study on Sediment Dongping Lake sediment clone Fh1-16
DQ676398.1 gg_id:222747 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
AJ240998.1 gg_id:1724 marine sediment clone Sva0450
EU617730.1 gg_id:310379 Seasonal variation microbial Yel Sea sediment clone C13S-4
FJ416122.1 gg_id:361045 sediments sediment station NEC5 Northern Bering Sea clone 111N77
EF125429.1 gg_id:178099 mangrove soil clone MSB-2C8
DQ154825.1 gg_id:138946 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl
GQ472454.1 gg_id:556802 Microbial Dongping Lake lake sediment clone 5F4-8
GQ249526.1 gg_id:556154 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor
EU925849.1 gg_id:333078 sediments sediment station DBS1 northern Bering Sea clone 041E69
AB525453.1 gg_id:541520 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed
FM242439.1 gg_id:318951 sequences sediment clone 20 T12d+oil
GQ259274.1 gg_id:576470 Microbial activities coastal marine sediments and water column Svalbard deep sedir
GU180169.1 gg_id:583825 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment
EU617731.1 gg_id:309253 Seasonal variation microbial Yel Sea sediment clone C13S-111
GQ356996.1 gg_id:584697 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeLive(
AB426217.1 gg_id:261015 -situ identification study benzene-degrading s under methanogenic condition anaerc
EF597692.1 gg_id:257405 Metagenomics deep mediterranean warm bathypelagic habitat 3010m depth Ionian
FJ902087.1 gg_id:555433 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca
EU132182.1 gg_id:236707 tallgrass prarie soil clone FFCH11809
FJ269274.1 gg_id:580045 Microbes marine sponges sponge tissue clone XA2D09F
FJ535081.1 gg_id:539336 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM22

EU132022.1	244993	3278.0	4408.9	6948.4	3991.1	4454.7	4911.2
EF516758.1	217242	1974.6	2447.8	2460.5	654.2	470.4	741.3
AB240376.1	141305	97.1	491.5	826.9	80.5	61.6	55.7
DQ415770.1	158462	164.6	373.7	775.3	106.9	237.5	109.7
AB426221.1	272259	2247.4	2404.6	3143.5	1532.1	1388.1	1028.1
AB426190.1	263608	164.6	269.8	1237.0	126.8	107.5	204.5
AY177760.1	78424	5651.1	4282.0	2446.6	2574.9	3083.0	4055.7
GQ402795.1	584529	34.9	157.4	1509.7	57.2	46.6	19.8
AB240315.1	142591	1194.1	1185.1	1900.0	1466.5	1379.1	1014.4
FJ825470.1	532951	504.7	737.9	2264.6	459.3	634.5	379.4
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EU132238.1	237679	11055.2	9740.0	6638.2	8856.6	8110.7	7379.1
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GQ249526.1	556154	12099.4	12668.9	11549.9	9734.6	12153.4	12271.9
EU925849.1	333078	2257.4	3014.5	4282.5	1737.1	1980.6	2430.6
AB525453.1	541520	404.0	689.3	327.9	348.5	599.8	579.8
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GQ356996.1	584697	3499.8	3391.0	3053.5	6218.1	5214.8	6032.1
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FJ902087.1	555433	5527.5	4249.6	3780.5	4696.5	3114.9	2419.8
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EU440553.1 gg_id:533735 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2B08
EU131970.1 gg_id:241576 tallgrass prarie soil clone FFCH4330
AM997364.1 gg_id:538317 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU734973.1 gg_id:316232 assemblages sediment station DBSE Northern Bering Sea clone 067C77
GU363017.1 gg_id:559646 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu
EU491320.1 gg_id:267857 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
AY225648.1 gg_id:96645 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-42
EU617725.1 gg_id:319376 Seasonal variation microbial Yel Sea sediment clone C13S-2
EU542527.1 gg_id:266442 Effects chemical structure concentration on pathways microbial during dechlorinatio
DQ017924.1 gg_id:130184 upland stream clone S-Rwb_44
EU542539.1 gg_id:272225 Effects chemical structure concentration on pathways microbial during dechlorinatio
EU617727.1 gg_id:303596 Seasonal variation microbial Yel Sea sediment clone C13S-122
AM997885.1 gg_id:567516 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
AJ241004.1 gg_id:1717 marine sediment clone Sva0515
EF687475.1 gg_id:283700 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s
GU208413.1 gg_id:587824 Study on Sediment Dongping Lake sediment clone Fh3-4
AY592346.1 gg_id:100195 deep-sea mud volcano clone Amsterdam-1B-45; BC20-1B-45
AY375053.1 gg_id:98520 deep sea sediment clone B141
AM040134.1 gg_id:145520 sandy sediments clone Sylt 38
EU373931.1 gg_id:267499 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
EU925891.1 gg_id:311833 sediments sediment station DBS1 northern Bering Sea clone 105G48
EU734954.1 gg_id:349855 assemblages sediment station DBSE Northern Bering Sea clone 046C55
FM242328.1 gg_id:315097 sequences sediment clone 88 T9d-oil
EF999391.1 gg_id:254631 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 22cn
EU491274.1 gg_id:263001 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
AM936860.1 gg_id:541468 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU734990.1 gg_id:318148 assemblages sediment station DBSE Northern Bering Sea clone 084B31
GQ850551.1 gg_id:591217 surface water northern Bering Sea clone u87
AM997505.1 gg_id:535394 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
EU491086.1 gg_id:269053 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU491807.1 gg_id:258891 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GQ472421.1 gg_id:572063 Microbial Dongping Lake lake sediment clone 4F2-8
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EU131992.1 gg_id:251390 tallgrass prarie soil clone FFCH458
DQ351815.1 gg_id:148861 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac
AM997605.1 gg_id:537795 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A
FJ205358.1 gg_id:508870 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se
EU287098.1 gg_id:247920 Pacific arctic surface sediment clone P13-5
EU652505.1 gg_id:277687 Seasonal variation microbial Yel Sea sediment clone D8S-107
EU043622.1 gg_id:240534 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c

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EF687475.1	283700	8734.5	7408.1	5051.4	6649.3	3159.9	5664.1
GU208413.1	587824	3529.0	4180.6	5438.0	5504.5	2383.8	3280.5
AY592346.1	100195	9490.3	9000.6	3342.9	4503.5	3361.5	4932.6
AY375053.1	98520	120.8	142.2	117.6	148.8	115.9	109.1
AM040134.1	145520	111.5	194.5	421.1	99.4	171.6	231.7
EU373931.1	267499	15523.2	15067.7	7231.0	9282.5	7511.9	10454.4
EU925891.1	311833	1331.9	1501.6	2612.5	924.0	987.8	1212.3
EU734954.1	349855	8607.8	10416.5	9716.4	8138.3	5812.1	7700.6
FM242328.1	315097	3210.2	4723.6	6754.3	3399.6	5385.4	5208.1
EF999391.1	254631	535.0	1871.6	3279.7	769.1	873.0	1729.3
EU491274.1	263001	1218.2	1100.6	1383.0	2132.6	615.4	1315.8
AM936860.1	541468	2321.1	2412.4	4753.5	4036.8	1345.5	1307.6
EU734990.1	318148	12588.5	13134.7	10650.9	9724.3	10191.1	10587.5
GQ850551.1	591217	1733.3	3470.2	5216.3	1307.3	4148.6	4239.8
AM997505.1	535394	9209.1	7415.5	9115.6	9449.9	6178.5	8381.3
EU491086.1	269053	4051.6	6259.2	5899.5	774.9	588.4	847.9
EU491807.1	258891	6167.0	7202.8	8581.4	7400.8	6063.6	6914.2
GQ472421.1	572063	1181.1	2010.5	3700.1	1158.8	1053.7	1824.9
AM072424.1	137899	587.8	878.9	1371.7	166.1	231.8	225.3
EU131992.1	251390	10968.4	11159.8	11878.1	11277.4	7486.8	7474.4
DQ351815.1	148861	49.1	92.1	83.4	125.7	85.6	76.4
AM997605.1	537795	6962.0	7014.4	8033.5	3164.3	2526.9	3820.0
FJ205358.1	508870	4555.1	7051.6	4593.0	2510.7	1161.0	2116.9
EU287098.1	247920	8273.4	8033.3	7099.7	5927.3	3357.3	4048.9
EU652505.1	277687	5013.6	7088.8	9271.2	4745.5	8790.8	7089.5
EU043622.1	240534	338.2	592.8	1740.8	283.6	1443.3	871.4

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EU132197.1 gg_id:252933 tallgrass prarie soil clone FFCH12594
AJ966601.1 gg_id:138615 and screening metagenomic library 5274m depth Pacific nodule province deep sea se
EU386096.1 gg_id:259105 Biogeographical and microbes sediments on subseafloor sediment South China Sea c
EU202817.1 gg_id:329074 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
EU287123.1 gg_id:256935 Pacific arctic surface sediment clone P13-30
AY225649.1 gg_id:95646 Mid-Atlantic Ridge hydrothermal sediment clone AT-s54
EF492943.1 gg_id:244081 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AM935858.1 gg_id:574623 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ484816.1 gg_id:513563 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator
GQ487923.1 gg_id:581733 Microbial metal soil polluted heavy metals clone T1-98
EU652507.1 gg_id:278012 Seasonal variation microbial Yel Sea sediment clone B8S-56
EU050878.1 gg_id:249658 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_05_33
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EU192982.1 gg_id:327098 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
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GQ402590.1 gg_id:537224 Accessing microbial biodiversity and metabolic potential tropical -based approach p
FJ516981.1 gg_id:567172 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s
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EF018429.1 gg_id:210152 aspen rhizosphere clone Amb_16S_1048
AB486803.1 gg_id:579143 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR
EF205576.1 gg_id:211735 among geographically regions central Tibet geothermal spring mat clone TP146
FJ466104.1 gg_id:557785 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
FJ004654.1 gg_id:540110 Acidobacteria former agricultural rhizosphere soil clone 6C2R
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EF589996.2 gg_id:233946 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni
FJ465983.1 gg_id:561042 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU373937.1 gg_id:268134 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl
DQ450709.1 gg_id:160412 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura
AB300108.1 gg_id:220379 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K
AJ292589.1 gg_id:31570 PCB-polluted soil clone WD292
GQ264513.1 gg_id:590045 Structure Simulated Level Waste Site simulated level waste site clone WW3_65
EU150240.1 gg_id:278511 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_17
AF186410.1 gg_id:3678 sponge symbiont clone PAUC26f
GU208471.1 gg_id:540593 Study on Sediment Dongping Lake sediment clone Shr2-7

EF019795.1	207151	259.5	317.4	340.2	124.3	232.7	63.9
EU132197.1	252933	7227.2	8704.9	9249.0	7304.4	9502.3	9159.9
AJ966601.1	138615	114.6	188.9	246.5	264.9	95.3	139.5
EU386096.1	259105	7169.1	7915.3	9089.7	7145.0	8600.8	10042.7
EU202817.1	329074	9364.2	9242.0	9625.9	9820.6	8917.6	11036.2
EU287123.1	256935	11849.9	12543.1	10534.4	8932.9	8689.9	7581.4
AY225649.1	95646	324.7	211.1	87.7	94.3	62.8	205.3
EF492943.1	244081	7059.9	8134.9	10468.3	8297.6	8323.0	8626.2
AM935858.1	574623	4536.0	5399.4	8357.2	6528.0	8994.3	8729.8
FJ484816.1	513563	6092.6	7795.0	9493.4	4043.7	4025.0	5929.5
GQ487923.1	581733	4871.9	6698.6	9839.3	7007.0	8543.5	8266.8
EU652507.1	278012	5737.6	3883.5	7729.1	4148.3	3396.4	2812.3
EU050878.1	249658	12287.9	15208.6	14340.1	9983.2	15251.4	14090.4
DQ431890.1	204817	50.0	74.4	138.8	88.3	181.8	91.2
EU617729.1	321065	3500.7	4805.9	6348.2	4597.4	5180.8	5598.0
EU335214.1	255335	1987.6	3361.3	6459.8	1288.3	3106.6	3199.7
CP000473.1	187098	1527.1	2234.9	3378.3	1763.8	2450.4	3009.5
AF407714.1	60585	38.8	91.2	424.5	50.1	58.1	65.7
FJ466444.1	547632	6354.8	6398.4	5321.9	6101.2	4199.3	5357.8
EU192982.1	327098	2942.3	4972.8	9564.1	5933.5	6236.7	6653.4
AY963381.1	154988	244.6	314.4	1443.3	423.5	449.0	808.9
GQ402590.1	537224	5454.7	5555.8	11035.4	6108.8	8448.6	9066.6
FJ516981.1	567172	2436.2	2951.3	6384.4	4485.1	4864.4	6355.8
GQ402745.1	582351	392.2	464.0	1797.8	423.7	2080.7	3654.1
EF018429.1	210152	13650.4	12558.3	16971.0	12142.6	8313.1	10654.8
AB486803.1	579143	1638.1	2956.8	6183.9	2119.6	3082.2	2791.7
EF205576.1	211735	2154.9	2838.2	7888.6	4027.1	3070.6	4034.9
FJ466104.1	557785	4643.2	3772.3	7416.0	5437.5	4768.8	6623.7
FJ004654.1	540110	153.9	694.1	4111.2	379.5	740.6	1613.2
GU208327.1	575999	1524.4	1773.5	5129.4	1794.1	1933.0	4034.9
AJ617852.1	110461	124.1	151.0	149.6	299.8	169.0	385.5
EF589996.2	233946	6146.6	4751.9	4135.3	6258.7	6250.9	6103.3
FJ465983.1	561042	306.1	748.7	1659.4	521.0	201.5	479.2
EU373937.1	268134	6721.9	7259.7	7713.0	3640.5	4465.9	4341.6
DQ450709.1	160412	123.3	292.2	1147.7	190.2	623.9	1075.7
AB300108.1	220379	25.7	69.5	115.0	53.1	84.0	260.3
AJ292589.1	31570	229.7	375.4	925.6	218.2	253.1	472.3
GQ264513.1	590045	4752.2	6631.9	8615.6	4636.0	7916.7	9236.5
EU150240.1	278511	5542.9	7775.1	16641.4	7336.3	10163.1	10902.6
AF186410.1	3678	96.3	187.7	455.9	327.3	160.4	175.0
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DQ404599.1 gg_id:154141 contaminated sediment clone 656043
GQ402596.1 gg_id:559586 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EU335355.1 gg_id:257039 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EF018600.1 gg_id:213933 aspen rhizosphere clone Amb_16S_874
AY963431.1 gg_id:154089 structures and correlated ecological factors soils two evergreen broad-leaved forests
AY963354.1 gg_id:154309 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF520625.1 gg_id:231211 structure lakes: what controls ? acid-impacted lake clone ADK-SGh02-62
AB262728.1 gg_id:245506 microorganisms shal subsurface Sarobetsu mire peat soil clone HSM050P-B-17
EF515945.1 gg_id:217695 grassland soil clone FCPN757
AB486891.1 gg_id:580183 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR
DQ451519.1 gg_id:156650 forest soil clone FAC80
EF019301.1 gg_id:203801 aspen rhizosphere clone Elev_16S_492
AY913513.1 gg_id:113638 forest soil clone DUNssu336 (+7B) (OTU#091)
EU399672.1 gg_id:272782 and localization microbial consortium full-scale granular activated carbon anaerobic
EU445204.1 gg_id:532631 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R17
AY395354.1 gg_id:102185 pasture soil clone EB1035
EF492952.1 gg_id:245898 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AY234723.1 gg_id:111405 soil isolate Ellin6071
FN594692.1 gg_id:581422 and arsenic mobilization rock biofilms ancient biofilom gold mine Zloty Stok clone a8
FJ461997.1 gg_id:581847 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AM162425.1 gg_id:156359 and situ identification acidic sphagnum peat bog clone B119
GQ340081.1 gg_id:588765 Prokaryotic Marathonas Reservoir Greece water column clone A07-42-BAC
GQ263798.1 gg_id:540293 Structure Simulated Level Waste Site simulated level waste site clone WC1_b37
EU861915.1 gg_id:332934 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
GQ402586.1 gg_id:556383 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF018723.1 gg_id:207760 aspen rhizosphere clone Amb_16S_1178
EU202741.1 gg_id:347427 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
AM749736.1 gg_id:256750 Isolation ing candidate division soils New Zealand steam-affected geothermal soil c
AM935398.1 gg_id:534931 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY963366.1 gg_id:154125 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF018819.1 gg_id:210872 aspen rhizosphere clone Amb_16S_1297
AY963393.1 gg_id:152086 structures and correlated ecological factors soils two evergreen broad-leaved forests
DQ451511.1 gg_id:156603 forest soil clone FAC72
GQ402695.1 gg_id:574269 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AJ536873.1 gg_id:79020 uranium mining waste pile soil sample clone JG30a-KF-40 sp.
GQ402805.1 gg_id:513782 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ066995.1 gg_id:131970 Lake Washington sediment clone pLW-63
AY963443.1 gg_id:152545 structures and correlated ecological factors soils two evergreen broad-leaved forests
AY963420.1 gg_id:156507 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF126260.1 gg_id:263285 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph
AY493924.1 gg_id:136281 Fingerprinting aggregates soil clone 355

DQ404599.1	154141	1413.2	2593.8	4264.4	1802.3	4029.4	4225.0
GQ402596.1	559586	1642.4	3679.5	3313.0	5698.2	2459.3	1954.5
EU335355.1	257039	3279.8	3801.7	3233.6	2161.5	4580.7	4131.1
EF018600.1	213933	903.3	1240.0	2054.1	1389.8	1072.2	1023.8
AY963431.1	154089	2790.6	3856.5	5018.6	2025.2	2526.4	4081.2
AY963354.1	154309	136.7	574.2	1456.4	224.7	269.6	830.3
EF520625.1	231211	37.5	82.4	215.5	82.6	56.4	60.0
AB262728.1	245506	242.0	403.8	2232.2	459.3	514.4	1098.2
EF515945.1	217695	61.2	27.0	554.5	87.5	261.9	81.2
AB486891.1	580183	1652.5	2798.6	6831.5	2254.3	2704.8	4577.5
DQ451519.1	156650	61.8	82.0	181.3	130.9	121.1	32.9
EF019301.1	203801	329.7	298.2	749.1	177.7	678.1	2256.0
AY913513.1	113638	58.9	190.4	282.7	90.4	158.1	72.5
EU399672.1	272782	2961.8	4497.2	4997.0	2187.3	7545.2	4137.2
EU445204.1	532631	25.3	100.1	470.7	87.2	79.0	84.0
AY395354.1	102185	2362.6	3596.3	3242.3	5791.9	9367.9	6422.4
EF492952.1	245898	40.0	57.5	323.1	76.2	41.2	25.3
AY234723.1	111405	221.3	636.8	1918.6	314.4	555.1	959.2
FN594692.1	581422	3081.1	2881.4	1251.7	1366.8	1817.0	1945.6
FJ461997.1	581847	2006.8	3526.6	3621.5	1385.9	2212.9	3776.0
AM162425.1	156359	67.4	146.9	115.9	128.7	114.1	97.2
GQ340081.1	588765	11367.2	9886.6	7913.8	9875.7	12312.7	11574.3
GQ263798.1	540293	2195.7	2875.7	5158.2	2205.9	2832.7	3368.5
EU861915.1	332934	2263.3	2073.6	1495.7	2233.7	2796.5	1530.3
GQ402586.1	556383	2723.7	1919.5	2492.0	1870.3	597.3	1187.2
EF018723.1	207760	6362.7	6625.3	2994.3	403.4	2154.6	605.2
EU202741.1	347427	287.2	925.2	2086.0	872.6	2683.2	3614.8
AM749736.1	256750	2017.3	2674.3	3792.6	2551.0	3758.0	4266.0
AM935398.1	534931	256.6	528.5	1735.0	229.5	500.6	635.1
AY963366.1	154125	18.4	34.6	22.6	33.9	58.9	36.8
EF018819.1	210872	503.7	1045.1	1747.4	501.0	1785.5	3083.4
AY963393.1	152086	4543.3	5228.4	5816.5	5210.0	4785.0	5892.7
DQ451511.1	156603	31.6	68.0	2472.4	110.7	89.3	79.6
GQ402695.1	574269	196.1	653.9	1143.6	247.0	1323.5	2620.4
AJ536873.1	79020	413.1	617.0	2947.6	408.7	1737.7	1936.7
GQ402805.1	513782	874.8	1696.1	3883.8	1128.1	1624.0	2316.1
DQ066995.1	131970	361.1	648.1	1616.4	332.6	956.0	1638.6
AY963443.1	152545	46.5	170.0	1190.7	102.2	213.3	284.4
AY963420.1	156507	1298.9	883.8	558.5	1371.5	5790.4	7232.4
EF126260.1	263285	266.8	644.3	1885.8	431.1	302.4	570.7
AY493924.1	136281	60.4	129.9	205.2	94.6	133.0	179.7

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FJ466389.1 gg_id:539027 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF600568.1 gg_id:297775 soil clone E5-18
FJ478620.1 gg_id:589802 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU676415.1 gg_id:287625 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
EU044116.1 gg_id:237652 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c
AB254784.1 gg_id:161597 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
FJ466097.1 gg_id:557180 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
GU205285.1 gg_id:525931 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
EU335301.1 gg_id:242467 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AY212581.1 gg_id:103580 water 10 m downstream manure clone 130ds10
AJ306764.1 gg_id:66935 DCP-dechlorinating consortium clone SHA-261
AM712324.1 gg_id:241307 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h
EF019821.1 gg_id:209523 aspen rhizosphere clone Elev_16S_1166
AM162421.1 gg_id:155041 and situ identification acidic sphagnum peat bog clone B18
AY963378.1 gg_id:155208 structures and correlated ecological factors soils two evergreen broad-leaved forests
FM877544.1 gg_id:369392 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-110
AY326548.1 gg_id:136292 Amazon soil clone 157-2
EU132409.1 gg_id:237818 tallgrass prarie soil clone FFCH2202
AJ536863.1 gg_id:78832 uranium mining waste pile soil sample clone JG30-KF-C5 sp.
AM162419.1 gg_id:152963 and situ identification acidic sphagnum peat bog clone B15
AY963364.1 gg_id:153346 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ479149.1 gg_id:572184 species richness estimates obtained nearly and simulated pyrosequencing-generated
AB179516.1 gg_id:101119 sedimentary rock clone MIZ25
FJ535085.1 gg_id:593912 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 3PJM113
FJ462107.1 gg_id:592473 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi
AY493921.1 gg_id:136304 Fingerprinting aggregates soil clone 351
AM935004.1 gg_id:545992 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ466071.1 gg_id:564195 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AB179509.1 gg_id:105453 sedimentary rock clone MIZ18
GQ263793.1 gg_id:566933 Structure Simulated Level Waste Site simulated level waste site clone WC1_b31
DQ906868.1 gg_id:256303 Oman subsurface soil clone 11A-3
EF018657.1 gg_id:204324 aspen rhizosphere clone Amb_16S_943
GQ402789.1 gg_id:582679 Accessing microbial biodiversity and metabolic potential tropical -based approach p
AB486182.1 gg_id:584693 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
FJ466148.1 gg_id:544575 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
AY963331.1 gg_id:154822 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ466083.1 gg_id:533572 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU676414.1 gg_id:299684 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals-
FJ466197.1 gg_id:513591 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EF018283.1 gg_id:210615 aspen rhizosphere clone Amb_16S_644
EU335379.1 gg_id:240295 Changes microbial metabolic and along hydrogeochemically variable profile unsatura

FJ466389.1	539027	48.2	95.6	952.5	177.4	162.6	210.9
EF600568.1	297775	2091.7	2616.4	6308.1	4082.5	3868.7	4408.0
FJ478620.1	589802	224.2	553.5	1331.6	380.4	827.6	1204.7
EU676415.1	287625	10302.0	11816.8	6036.1	9192.4	9694.7	10032.1
EU044116.1	237652	6290.2	4733.8	4194.1	6087.4	6806.3	10961.5
AB254784.1	161597	40.8	70.1	72.0	94.8	117.9	57.0
FJ466097.1	557180	880.8	1217.5	4182.5	1806.8	1682.5	2233.7
GU205285.1	525931	6950.1	7102.8	4419.5	6459.3	7006.7	7003.5
EU335301.1	242467	6394.3	4792.0	4936.2	4636.7	5353.3	5057.9
AY212581.1	103580	143.8	288.8	573.7	106.3	221.1	277.4
AJ306764.1	66935	53.3	287.9	826.4	105.4	164.0	179.4
AM712324.1	241307	483.7	1251.1	2769.1	566.9	631.2	1048.5
EF019821.1	209523	255.6	1098.5	2126.7	389.1	416.3	1281.7
AM162421.1	155041	3391.9	4141.0	3689.3	4109.3	3766.3	3968.9
AY963378.1	155208	179.3	543.4	3223.4	322.5	399.8	1738.9
FM877544.1	369392	3754.4	5047.5	3141.1	2967.3	5264.2	4652.8
AY326548.1	136292	1612.5	2830.0	1404.1	893.4	3423.4	3533.3
EU132409.1	237818	2816.7	3879.7	8255.5	3977.2	6177.8	6771.3
AJ536863.1	78832	44.5	92.8	175.6	89.7	113.8	172.3
AM162419.1	152963	65.0	256.5	1383.1	159.4	238.7	728.4
AY963364.1	153346	1807.7	3676.3	2527.0	2340.4	5881.6	6993.0
FJ479149.1	572184	2919.3	5050.2	4776.9	1390.8	1401.2	2677.8
AB179516.1	101119	55.8	243.1	923.1	109.4	416.7	1550.5
FJ535085.1	593912	1159.0	1910.1	2440.2	1607.8	1125.0	2377.2
FJ462107.1	592473	1396.3	3076.9	5814.2	1948.9	3516.8	5524.7
AY493921.1	136304	42.6	71.3	68.2	83.2	181.7	345.1
AM935004.1	545992	1230.4	1799.3	3618.3	858.7	3472.9	4324.5
FJ466071.1	564195	5409.9	6652.9	5774.4	2697.0	2458.8	3810.8
AB179509.1	105453	130.6	360.5	1710.6	156.9	262.2	806.1
GQ263793.1	566933	13236.5	14597.6	16171.6	12385.0	9713.4	13568.8
DQ906868.1	256303	9659.3	9721.2	9325.7	7989.4	8599.6	9196.4
EF018657.1	204324	119.0	160.4	437.8	223.8	230.4	382.0
GQ402789.1	582679	3123.4	3220.9	4106.9	2831.8	2951.9	3899.9
AB486182.1	584693	3518.4	4079.6	4732.5	4246.5	4260.4	5543.8
FJ466148.1	544575	1024.5	1473.1	2356.1	1322.5	863.5	1469.4
AY963331.1	154822	4011.2	4272.7	2341.1	2553.3	755.4	2531.7
FJ466083.1	533572	71.9	229.6	293.1	163.8	167.2	398.1
EU676414.1	299684	5966.6	6244.0	8016.8	5726.9	6650.7	7425.4
FJ466197.1	513591	394.7	792.8	1542.5	1088.9	547.7	1259.8
EF018283.1	210615	152.3	282.1	1989.6	214.5	534.7	924.0
EU335379.1	240295	83.7	96.8	764.9	94.4	81.7	144.8

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EU132045.1 gg_id:240983 tallgrass prarie soil clone FFCH9825
EF516126.1 gg_id:226281 grassland soil clone FCPT514
DQ129637.1 gg_id:138184 microarray level air two cities Texas urban aerosol clone AKIW659
EF019147.1 gg_id:208718 aspen rhizosphere clone Amb_16S_1790
GQ263218.1 gg_id:592008 Structure Simulated Level Waste Site simulated level waste site clone F3_25X
FJ152859.1 gg_id:350446 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_
EF018719.1 gg_id:210677 aspen rhizosphere clone Amb_16S_1170
GQ264287.1 gg_id:544353 Structure Simulated Level Waste Site simulated level waste site clone WW2_101
EU881125.1 gg_id:322588 Karst region primary forest soil clone KPF200711-143
EF018078.1 gg_id:204993 aspen rhizosphere clone Amb_16S_404
GQ402709.1 gg_id:587893 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EF020033.1 gg_id:215120 aspen rhizosphere clone Elev_16S_1428
EF516689.1 gg_id:226313 grassland soil clone FCPN758
EU150203.1 gg_id:278495 acidobacteria and soil Niwot Ridge LTER; spruce fir forest clone NiA_SF_14
FJ901511.1 gg_id:568755 phreatic limestone sinkholes northeastern Mexico biomat 80m deep cenote La Palita
DQ833485.1 gg_id:161914 detected analyses depth sediment Guanting Reservoir clone 35-19
FJ004679.1 gg_id:553090 Acidobacteria former agricultural soil rhizosphere clone 89
DQ404851.1 gg_id:153227 contaminated sediment clone 655981
EU044114.1 gg_id:249968 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c
GQ402578.1 gg_id:545323 Accessing microbial biodiversity and metabolic potential tropical -based approach p
EU132362.1 gg_id:242626 tallgrass prarie soil clone FFCH13873
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EF019667.1 gg_id:205391 aspen rhizosphere clone Elev_16S_822
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EF516304.1 gg_id:222573 grassland soil clone FCPT689
DQ017939.1 gg_id:134417 upland stream clone S-Jos_51
DQ001647.1 gg_id:158148 Microbial seeps asphalt seep clone E101-54
AM749754.1 gg_id:246440 Isolation ing candidate division soils New Zealand steam-affected geothermal soil c
AY963377.1 gg_id:150731 structures and correlated ecological factors soils two evergreen broad-leaved forests
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DQ984552.1 gg_id:241889 Mt. Nan-Jen soil clone IFD_30
EF516032.1 gg_id:219884 grassland soil clone FCPP523
AY963418.1 gg_id:154876 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU150229.1 gg_id:278164 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_2
FJ465995.1 gg_id:544523 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU331380.1 gg_id:250740 Influence Nitrate on Microbial Reduction Pertechnetate microcosm sediment contan
EF516947.1 gg_id:227230 grassland soil clone FCPS681
AJ009495.1 gg_id:3677 chlorobenzene-degrading consortium clone SJA-149
EF019981.1 gg_id:206392 aspen rhizosphere clone Elev_16S_1368
AM935451.1 gg_id:557468 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF494337.1 gg_id:222398 Nunnock River granitic landscape clone NR.1.044

EU132045.1	240983	3346.2	2987.2	2577.2	532.0	651.6	1294.5
EF516126.1	226281	67.5	131.1	623.0	81.2	114.6	100.9
DQ129637.1	138184	1207.6	1642.6	479.6	2025.2	311.8	717.8
EF019147.1	208718	7354.4	6475.7	3045.6	7424.4	8703.2	8510.2
GQ263218.1	592008	8426.3	9755.2	4291.8	11548.5	13855.3	13272.1
FJ152859.1	350446	479.7	1244.8	1727.2	1101.0	492.0	1142.1
EF018719.1	210677	692.9	985.8	1430.8	1368.3	820.7	1607.5
GQ264287.1	544353	2330.8	1633.4	4439.5	2636.5	4341.2	4728.2
EU881125.1	322588	4456.8	4176.8	5627.2	4861.7	1661.7	4014.8
EF018078.1	204993	63.8	93.6	284.9	134.2	107.0	89.9
GQ402709.1	587893	11528.3	13005.6	6208.1	6747.6	9398.4	8487.7
EF020033.1	215120	247.4	433.6	1087.8	263.8	144.6	592.9
EF516689.1	226313	1066.7	1740.2	6258.7	2499.2	1492.2	2457.5
EU150203.1	278495	207.6	559.3	1921.8	221.7	419.6	984.5
FJ901511.1	568755	212.5	431.2	693.5	219.8	335.3	291.8
DQ833485.1	161914	73.4	275.5	1276.2	274.8	825.2	1796.2
FJ004679.1	553090	597.5	1270.0	1001.4	518.3	364.7	489.1
DQ404851.1	153227	962.4	1179.7	1217.1	1398.2	1099.9	1774.0
EU044114.1	249968	10295.5	7048.7	8506.8	6066.3	6342.6	7149.6
GQ402578.1	545323	3126.1	3904.1	4839.1	3351.7	4867.7	5378.5
EU132362.1	242626	1383.4	2356.6	1431.5	559.0	1204.3	1787.7
EF516577.1	221845	642.5	1468.9	2841.3	929.1	1633.5	2594.6
EF019667.1	205391	70.6	88.1	936.0	125.6	110.1	87.5
FJ466067.1	575896	3696.9	4959.9	7357.4	4260.5	4226.9	5043.7
EF516304.1	222573	38.8	126.2	241.7	69.8	47.1	99.0
DQ017939.1	134417	5122.3	6062.9	7650.4	6238.4	8674.8	9481.9
DQ001647.1	158148	2887.3	3333.7	3603.7	3251.5	2305.5	4454.7
AM749754.1	246440	8590.9	10681.2	18562.8	8680.6	12590.1	14601.7
AY963377.1	150731	15130.4	13918.2	6553.7	13298.6	14963.0	13325.8
FJ004775.1	554827	78.8	141.3	565.8	213.0	194.8	182.0
DQ984552.1	241889	610.4	888.0	2995.3	1038.9	1155.9	1677.7
EF516032.1	219884	1242.1	1386.1	3869.9	1775.2	2686.4	3816.0
AY963418.1	154876	45.1	131.2	286.3	76.3	179.9	224.7
EU150229.1	278164	2041.3	2656.9	5342.2	3188.2	3022.1	5704.2
FJ465995.1	544523	72.0	211.9	375.8	104.5	128.8	282.0
EU331380.1	250740	118.5	229.2	1222.8	113.3	369.7	1029.7
EF516947.1	227230	709.3	930.1	2945.4	972.1	744.4	1072.9
AJ009495.1	3677	84.1	255.3	351.2	124.7	166.5	136.4
EF019981.1	206392	6528.7	6957.4	11325.3	6873.4	7700.8	8925.6
AM935451.1	557468	3297.1	4538.7	5346.3	3134.5	3484.1	3535.9
EF494337.1	222398	639.2	1878.0	3676.3	1220.4	2498.3	3027.1

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AY913265.1 gg_id:114356 forest soil clone DUNssu045 (-2B) (OTU#121)
FJ478535.1 gg_id:583760 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ205213.1 gg_id:549259 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
EF492968.1 gg_id:247708 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AY922037.1 gg_id:112776 farm soil clone AKYG600
AF465650.1 gg_id:17775 thermal soil clone YNPRH2B
GU172173.1 gg_id:536567 Microbial Eucalyptus plantation soil clone DSM-R1
EU445207.1 gg_id:541749 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R20
EF492956.1 gg_id:241718 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
EF515983.1 gg_id:226166 grassland soil clone FCPS403
FJ479535.1 gg_id:553939 species richness estimates obtained nearly and simulated pyrosequencing-generated
DQ450706.1 gg_id:161275 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
EU150248.1 gg_id:278253 acidobacteria and dry meadow soil Niwot Ridge LTER clone NiA_DM_26
FJ793181.1 gg_id:526228 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB66
AY963425.1 gg_id:151183 structures and correlated ecological factors soils two evergreen broad-leaved forests
FJ004745.1 gg_id:575745 Acidobacteria former agricultural bulk soil clone 26L2B
EF157254.1 gg_id:241324 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EF032754.1 gg_id:190912 cyanobacterial mat in lava cave clone HAVOmat42
FJ466195.1 gg_id:543818 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea
EU202739.1 gg_id:343210 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo
GU444079.1 gg_id:519245 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L
FJ624931.1 gg_id:566511 Influence lead contamination on boreal pine forest soil clone HF_C_58
FJ710779.1 gg_id:510168 Abundance and microbial long-term operated anammox biofilm reactors initiated ino
EF018396.1 gg_id:205033 aspen rhizosphere clone Amb_16S_1009
GQ264426.1 gg_id:589387 Structure Simulated Level Waste Site simulated level waste site clone WW3_116
FJ479270.1 gg_id:594169 species richness estimates obtained nearly and simulated pyrosequencing-generated
AB186882.1 gg_id:105319 polychlorinated dioxin dechlorinating microcosm clone TSBb06
EF019361.1 gg_id:216341 aspen rhizosphere clone Elev_16S_581
GU118588.1 gg_id:588882 Threatened Corals Provide Microbial Habitats clone Mfav_P18
AB240298.1 gg_id:141801 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone
FJ592762.1 gg_id:562807 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
AM935189.1 gg_id:558353 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AY703464.1 gg_id:139346 Detection and ly acidobacterial analyses Altamira Cave clone ALT40
GU187034.1 gg_id:578443 Isolation -yet Acidobacteria on solid dilute media surface soil clone IGE-015
EF018402.1 gg_id:210745 aspen rhizosphere clone Amb_16S_1015
EU132316.1 gg_id:240950 tallgrass prarie soil clone FFCH1016
EF516154.1 gg_id:221233 grassland soil clone FCPO684
EF494368.1 gg_id:225293 Nunnock River granitic landscape clone NR.1.042
EF018351.1 gg_id:209415 aspen rhizosphere clone Amb_16S_723
EF494344.1 gg_id:220327 Nunnock River granitic landscape clone NR.1.077
DQ066994.1 gg_id:136128 Lake Washington sediment clone pLW-64

AY913265.1	114356	49.8	108.7	594.9	104.0	202.8	490.7
FJ478535.1	583760	1745.5	2168.4	4082.8	2382.5	3969.6	5328.9
FJ205213.1	549259	1346.9	2386.2	2121.4	2177.6	1519.4	2116.9
EF492968.1	247708	8297.2	9939.9	11445.6	9560.3	12229.6	10567.4
AY922037.1	112776	40.3	96.2	93.9	70.2	287.9	111.5
AF465650.1	17775	9736.4	9862.1	5874.7	8252.3	1171.6	2221.5
GU172173.1	536567	6588.8	6497.8	7791.6	5717.3	5324.3	6148.7
EU445207.1	541749	725.5	1572.9	1023.1	276.4	1214.5	596.3
EF492956.1	241718	1764.6	1445.2	689.8	707.7	1248.9	1574.9
EF515983.1	226166	179.0	490.4	2729.5	571.3	492.7	687.5
FJ479535.1	553939	2934.3	3126.5	3367.4	1938.3	4266.0	3708.5
DQ450706.1	161275	345.9	950.0	4691.9	267.1	897.3	1721.8
EU150248.1	278253	1487.7	1739.0	2505.3	2259.6	2718.5	3588.9
FJ793181.1	526228	299.5	668.5	2469.3	298.9	240.5	582.5
AY963425.1	151183	3535.6	1847.0	1872.2	1346.1	276.7	818.8
FJ004745.1	575745	196.4	263.1	716.2	145.8	660.3	442.9
EF157254.1	241324	1393.6	2631.3	4450.9	3405.5	1691.9	4105.1
EF032754.1	190912	44.0	50.4	109.5	82.9	79.7	33.6
FJ466195.1	543818	185.1	305.4	1179.8	431.4	398.0	1131.4
EU202739.1	343210	1477.1	2550.6	4856.3	2322.5	3296.2	5141.5
GU444079.1	519245	1139.1	1562.9	2467.0	1679.9	1939.4	4046.7
FJ624931.1	566511	55.0	81.1	336.4	97.9	86.2	81.4
FJ710779.1	510168	783.9	1431.0	3566.4	1392.2	1581.7	2906.5
EF018396.1	205033	1768.9	3373.2	2777.5	1745.9	2098.5	2424.4
GQ264426.1	589387	9159.4	10500.8	8241.0	8557.7	9965.4	6255.1
FJ479270.1	594169	4969.2	4563.4	6921.4	4594.0	4617.5	6043.8
AB186882.1	105319	30.7	85.7	133.8	80.2	92.7	33.9
EF019361.1	216341	152.7	297.6	1311.9	212.6	125.2	606.2
GU118588.1	588882	1212.0	2055.4	1695.3	2088.8	1712.9	1880.8
AB240298.1	141801	1788.8	2427.6	4677.7	1723.2	2619.3	2230.9
FJ592762.1	562807	51.1	119.4	1560.3	154.9	497.7	2045.1
AM935189.1	558353	3564.0	4663.5	6641.2	4625.6	5570.3	7296.0
AY703464.1	139346	305.2	502.7	1063.8	644.7	397.8	500.5
GU187034.1	578443	282.6	536.4	1044.7	507.2	1329.3	2345.4
EF018402.1	210745	83.8	222.6	496.3	128.5	128.4	175.4
EU132316.1	240950	152.5	298.9	569.7	209.7	376.9	1491.4
EF516154.1	221233	387.8	619.5	2139.9	421.4	1175.2	756.4
EF494368.1	225293	5848.7	5991.0	7841.7	7305.7	4738.9	6349.3
EF018351.1	209415	204.1	247.5	701.5	496.3	256.8	559.1
EF494344.1	220327	2486.8	2526.2	3786.2	3367.7	2403.3	3695.3
DQ066994.1	136128	300.2	1226.2	4108.7	299.8	1477.5	1191.2

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FJ592751.1 gg_id:569539 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
AY963419.1 gg_id:156406 structures and correlated ecological factors soils two evergreen broad-leaved forests
AY963359.1 gg_id:151094 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU491161.1 gg_id:272414 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
GQ263191.1 gg_id:577141 Structure Simulated Level Waste Site simulated level waste site clone F3_152X
EF018769.1 gg_id:211221 aspen rhizosphere clone Amb_16S_1230
AY913237.1 gg_id:113212 forest soil clone DUNssu016 (+1B) (OTU#120)
EU665077.1 gg_id:545745 Soil are Changed Agricultural Practices agricultural soil clone Plot22-H02
EU132291.1 gg_id:254271 tallgrass prarie soil clone FFCH4169
EF020317.1 gg_id:204462 aspen rhizosphere clone Elev_16S_1890
EF688388.1 gg_id:245809 soil clone F6-128
AY963374.1 gg_id:151872 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU335292.1 gg_id:250451 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU881304.1 gg_id:305083 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
AY913231.1 gg_id:113763 forest soil clone DUNssu010 (+1B) (OTU#116)
EF492904.1 gg_id:254383 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule
AY118153.1 gg_id:60816 anaerobic benzene-degrading clone Cart-N4
EF516655.1 gg_id:221341 grassland soil clone FCPU664
AM162427.1 gg_id:151955 and situ identification acidic sphagnum peat bog clone B22
AB234235.1 gg_id:145554 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm
AB426196.1 gg_id:274878 -situ identification study benzene-degrading s under methanogenic condition anaerc
EU132276.1 gg_id:253770 tallgrass prarie soil clone FFCH2719
AY963303.1 gg_id:153327 structures and correlated ecological factors soils two evergreen broad-leaved forests
EU881313.1 gg_id:339795 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM
AY555784.1 gg_id:101141 Bor Khlueng hot spring clone PK34
AJ519364.1 gg_id:75894 uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-5
AJ617858.1 gg_id:110291 oxic-anoxic interphase flooded paddy soil clone D282110
EU404033.1 gg_id:313796 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (
FJ197547.1 gg_id:310970 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN29a_4C_ FL
DQ676411.1 gg_id:220290 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M
EF018300.1 gg_id:212449 aspen rhizosphere clone Amb_16S_662
DQ328617.1 gg_id:145959 microorganisms populating site extreme acid mine drainage sediment clone H5
AY963324.1 gg_id:156453 structures and correlated ecological factors soils two evergreen broad-leaved forests
EF516650.1 gg_id:222943 grassland soil clone FCPP504
AB369160.1 gg_id:241567 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De
FJ625319.1 gg_id:570620 Influence lead contamination on boreal pine forest soil clone HF_M_16
DQ129640.1 gg_id:137789 microarray level air two cities Texas urban aerosol clone AKIW863
EU780449.1 gg_id:316355 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite
EF494361.1 gg_id:223616 Nunnock River granitic landscape clone NR.1.005
GU183624.1 gg_id:557366 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a
AM997648.1 gg_id:542627 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A

FJ592751.1	569539	8627.9	12001.0	8764.6	9905.7	11093.7	11347.7
AY963419.1	156406	4165.3	6919.4	5801.1	2999.5	4581.4	4650.9
AY963359.1	151094	535.2	1448.2	3248.4	981.5	2009.8	2995.7
EU491161.1	272414	5147.4	6369.4	10193.4	5892.5	8415.1	7902.7
GQ263191.1	577141	7447.8	9241.0	7281.4	10755.4	10938.6	12481.6
EF018769.1	211221	1588.2	2078.7	2984.4	1913.6	1386.9	2662.4
AY913237.1	113212	80.2	397.9	480.3	73.5	281.9	613.0
EU665077.1	545745	895.9	2204.2	3497.7	784.2	1975.7	3561.6
EU132291.1	254271	36.0	114.7	702.1	100.2	115.3	217.9
EF020317.1	204462	13.0	27.7	21.1	54.4	102.1	102.4
EF688388.1	245809	1878.6	3869.1	4232.1	2425.8	3895.4	5320.8
AY963374.1	151872	1955.6	781.8	3775.4	2423.2	1140.6	2560.2
EU335292.1	250451	48.5	217.8	1358.3	129.1	168.6	515.6
EU881304.1	305083	2510.5	2694.5	3927.7	2314.0	921.6	4108.8
AY913231.1	113763	6186.7	2376.2	7741.4	4982.5	3194.5	3739.7
EF492904.1	254383	965.3	1493.4	488.4	1492.9	1123.4	1616.0
AY118153.1	60816	43.0	60.5	112.5	66.6	169.9	174.7
EF516655.1	221341	74.3	302.7	174.4	130.0	69.1	123.9
AM162427.1	151955	15.5	18.6	13.3	33.9	62.4	19.2
AB234235.1	145554	217.7	456.7	488.2	675.3	333.4	444.0
AB426196.1	274878	435.1	790.6	683.4	571.8	363.5	749.1
EU132276.1	253770	749.7	1390.6	2239.5	809.8	472.8	1047.9
AY963303.1	153327	4897.7	4586.3	3592.7	5069.4	4031.4	3837.1
EU881313.1	339795	1213.0	2001.3	4301.3	2605.2	3687.7	4921.6
AY555784.1	101141	96.1	305.8	1360.5	153.9	221.8	305.8
AJ519364.1	75894	97.0	110.6	1079.9	160.6	1883.3	3489.5
AJ617858.1	110291	5266.6	5925.5	7598.8	5415.0	4408.1	5118.5
EU404033.1	313796	893.9	1852.7	1911.3	1794.4	1968.1	3458.3
FJ197547.1	310970	8298.2	7963.8	8019.7	9621.0	12554.7	11341.1
DQ676411.1	220290	112.2	466.6	1193.8	160.4	551.3	1225.8
EF018300.1	212449	235.6	439.0	1351.2	1465.5	708.0	1038.9
DQ328617.1	145959	44.7	104.7	132.1	67.5	204.0	752.1
AY963324.1	156453	4521.6	3855.8	2420.4	5128.6	3404.5	4708.2
EF516650.1	222943	3450.3	3980.3	4877.2	4691.3	6213.8	4454.4
AB369160.1	241567	2057.1	2149.1	4208.8	1614.7	1876.4	1437.3
FJ625319.1	570620	1621.1	1631.8	4470.4	4445.4	1463.0	2474.0
DQ129640.1	137789	273.4	400.0	582.8	291.4	466.4	878.5
EU780449.1	316355	1452.4	3138.4	3498.8	1868.7	852.1	1832.0
EF494361.1	223616	438.7	1344.0	1392.9	486.7	1841.2	1546.6
GU183624.1	557366	2771.5	3600.6	3130.9	1774.5	3218.0	2971.7
AM997648.1	542627	6118.4	6192.2	7576.4	4322.8	4990.8	4755.0

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EF125450.1 gg_id:186035 mangrove soil clone MSB-2F3
AY225643.1 gg_id:96804 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-37
AM040133.1 gg_id:149857 sandy sediments clone Sylt 37
DQ070820.1 gg_id:149756 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
GQ246348.1 gg_id:535475 Temporal and spatial China North Yel Sea sediments clone Cm1-11
EU734999.1 gg_id:311554 assemblages sediment station DBSE Northern Bering Sea clone 093B48
EU491394.1 gg_id:259756 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone
EU652606.1 gg_id:279002 Seasonal variation microbial Yel Sea sediment clone D8S-76
FJ205208.1 gg_id:574895 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se
FJ358923.1 gg_id:550228 and redox-stratified sediments marine reef sandy sediment clone SO13
EF125465.1 gg_id:187788 mangrove soil clone MSB-2Y4
AJ241003.1 gg_id:1702 Norway:(Svalbard)Hornsund clone Sva0725
EU287099.1 gg_id:251889 Pacific arctic surface sediment clone P13-6
GQ984352.1 gg_id:590289 surface water Northern Bering Sea clone DBS1g27
GU369908.1 gg_id:532228 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
EU734944.1 gg_id:320242 assemblages sediment station DBSE Northern Bering Sea clone 036C37
EU132194.1 gg_id:255963 tallgrass prarie soil clone FFCH12382
EU881271.1 gg_id:313254 (long-term grazing and burned annual) Karst region serious disturbance field soil clor
AY703465.1 gg_id:139386 Detection and ly acidobacterial analyses Altamira Cave clone ALT41
EF516971.1 gg_id:223577 grassland soil clone FCPU401
FJ444736.1 gg_id:588064 Cotton Rhizosphere cotton rhizosphere clone 4h-60
EF516941.1 gg_id:223804 grassland soil clone FCPP416
AY921811.1 gg_id:113092 farm soil clone AKYG1685
EF516929.1 gg_id:224421 grassland soil clone FCPO720
FJ269289.1 gg_id:568362 Microbes marine sponges sponge tissue clone XA3A05F
FJ269325.1 gg_id:572216 Microbes marine sponges sponge tissue clone XB3A06F
FJ269329.1 gg_id:585767 Microbes marine sponges sponge tissue clone XB3C09F
AJ347029.1 gg_id:60180 sponge clone TK29
FJ269250.1 gg_id:543969 Microbes marine sponges sponge tissue clone XA1C09F
FJ269318.1 gg_id:512056 Microbes marine sponges sponge tissue clone XB2F01F
FJ269338.1 gg_id:576211 Microbes marine sponges sponge tissue clone XB3A12F
DQ070804.1 gg_id:147802 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
EU491423.1 gg_id:259892 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone
EU735006.1 gg_id:354311 assemblages sediment station DBSE Northern Bering Sea clone 100B74
EU617739.1 gg_id:337079 Seasonal variation microbial Yel Sea sediment clone D13S-60
EU287096.1 gg_id:257517 Pacific arctic surface sediment clone P13-3
DQ521823.1 gg_id:161000 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexicc
DQ521809.1 gg_id:161180 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexicc
GQ246332.1 gg_id:568581 Temporal and spatial China North Yel Sea sediments clone Sd1-51
AB294958.1 gg_id:219459 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma

EU617735.1	326888	5639.2	5615.5	6013.7	6310.3	5155.9	4695.0
EF125450.1	186035	31.6	88.2	66.1	94.4	102.3	78.4
AY225643.1	96804	7738.9	5156.7	3246.1	5496.1	7177.0	6577.3
AM040133.1	149857	214.9	439.9	119.5	237.1	159.7	144.7
DQ070820.1	149756	48.6	64.9	36.9	74.3	67.1	36.9
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EU734944.1	320242	4097.5	5247.9	7556.6	4362.2	3270.5	4299.3
EU132194.1	255963	165.5	605.9	1100.8	315.9	724.7	924.3
EU881271.1	313254	334.2	769.4	904.0	490.9	452.6	857.5
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FJ269325.1	572216	15076.7	17599.1	11064.9	13158.9	15011.5	14710.3
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FJ269250.1	543969	13726.3	16383.8	11963.1	12312.4	13851.8	12928.4
FJ269318.1	512056	6318.0	7175.6	7376.2	6978.2	5818.3	7058.2
FJ269338.1	576211	8677.8	11497.5	8160.7	8314.0	11262.2	11426.9
DQ070804.1	147802	16.2	30.6	25.3	57.5	69.1	30.5
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EU734969.1 gg_id:314393 assemblages sediment station DBSE Northern Bering Sea clone 063D30
AY225642.1 gg_id:98176 Mid-Atlantic Ridge hydrothermal sediment clone AT-s3-59
FJ202186.1 gg_id:347056 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
EU491665.1 gg_id:259485 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
EU735010.1 gg_id:328268 assemblages sediment station DBSE Northern Bering Sea clone 106A42
EF125415.1 gg_id:185747 soil naked tidal flat sediment near mangrove clone MSB-1F2
GU454881.1 gg_id:522212 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir
FJ437927.1 gg_id:543301 Benthic okenone production Fayetteville New York Green Lake surface sediments 16.
EU755076.1 gg_id:351025 and Dioxygenase Genes Coal Tar Contaminated Soils coal tar-contaminated soil clone
EF020070.1 gg_id:213078 aspen rhizosphere clone Elev_16S_1477
EU491064.1 gg_id:269664 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X
EU132115.1 gg_id:241435 tallgrass prarie soil clone FFCH1005
EF092234.1 gg_id:264224 Persistent Axinella corrugata Geobacter clone B2706_E4
FJ425650.1 gg_id:363109 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata g
DQ289910.1 gg_id:168493 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
FJ358922.1 gg_id:594049 and redox-stratified sediments marine reef sandy sediment clone AO15
EU735636.1 gg_id:326715 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone
AM259858.1 gg_id:204709 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-23
AF385537.1 gg_id:73910 swab advanced noma lesion clone CA002
DQ833472.1 gg_id:169792 detected analyses depth sediment Guanting Reservoir clone 5-38
EU528207.1 gg_id:286946 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
DQ129284.1 gg_id:137747 microarray level air two cities Texas urban aerosol clone AKIW896
EU133029.1 gg_id:249727 tallgrass prarie soil clone FFCH18764
FJ478643.1 gg_id:581307 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ479273.1 gg_id:591093 species richness estimates obtained nearly and simulated pyrosequencing-generated
GQ263231.1 gg_id:574576 Structure Simulated Level Waste Site simulated level waste site clone F3_41X
EU132594.1 gg_id:253941 tallgrass prarie soil clone FFCH10110
EU133117.1 gg_id:237496 tallgrass prarie soil clone FFCH5344
EU132829.1 gg_id:253573 tallgrass prarie soil clone FFCH13720
AY093463.1 gg_id:55589 deep marine sediment clone MB-A2-108
EF018262.1 gg_id:215928 aspen rhizosphere clone Amb_16S_619
EF516773.1 gg_id:224718 grassland soil clone FCPT593
AJ863190.1 gg_id:121375 poplar tree microcosm bulk soil unflooded clone 20BSU18
AB486164.1 gg_id:532857 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC
DQ067014.1 gg_id:128299 Lake Washington sediment clone pLW-76
FJ479558.1 gg_id:577549 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU133207.1 gg_id:236133 tallgrass prarie soil clone FFCH8340
FJ479097.1 gg_id:545487 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ478871.1 gg_id:513347 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU132575.1 gg_id:238110 tallgrass prarie soil clone FFCH10523
GQ263065.1 gg_id:547749 Structure Simulated Level Waste Site simulated level waste site clone F2_188X

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FJ202186.1	347056	3669.8	3839.2	2996.3	1639.2	4310.6	3325.8
EU491665.1	259485	2203.8	2756.1	7945.8	2921.9	1977.1	2446.8
EU735010.1	328268	46.6	127.0	106.2	283.4	414.7	206.3
EF125415.1	185747	42.8	88.6	156.1	137.2	81.1	63.3
GU454881.1	522212	300.8	758.1	2731.6	302.4	792.9	809.7
FJ437927.1	543301	18976.0	17011.1	8093.3	11358.6	10516.4	10422.0
EU755076.1	351025	15489.9	15712.0	14651.8	14363.2	15663.9	14440.1
EF020070.1	213078	41.4	80.1	107.4	431.2	559.3	143.6
EU491064.1	269664	11242.0	12541.4	9929.3	8899.2	8072.5	7635.2
EU132115.1	241435	2548.0	2558.3	1913.1	2463.4	2128.1	1724.0
EF092234.1	264224	3254.4	4012.0	6615.6	5285.3	2156.5	3796.7
FJ425650.1	363109	3686.3	4127.8	8210.5	3061.9	2143.7	4278.3
DQ289910.1	168493	7787.7	7292.2	5321.5	3710.6	9674.2	5953.5
FJ358922.1	594049	6793.7	7102.2	5374.7	6127.1	9051.8	6395.7
EU735636.1	326715	2026.6	2886.4	2938.4	3952.1	3036.9	4435.0
AM259858.1	204709	10808.8	9587.6	6906.9	6619.5	10744.0	8666.6
AF385537.1	73910	22.2	33.5	29.1	44.6	58.8	19.7
DQ833472.1	169792	3855.3	5344.1	9993.9	4453.3	1896.5	3510.3
EU528207.1	286946	12454.2	12435.6	8270.9	10446.5	9746.4	10340.5
DQ129284.1	137747	11903.2	9304.6	10126.6	7950.2	7226.5	6611.0
EU133029.1	249727	8375.3	6973.8	6458.5	5992.3	1415.3	3591.5
FJ478643.1	581307	8368.4	9084.3	5079.4	5873.0	3329.8	3757.2
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EU132594.1	253941	3332.8	3329.5	3700.1	2256.8	2074.5	2157.2
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EF516773.1	224718	124.8	158.5	168.3	225.8	111.6	118.9
AJ863190.1	121375	6684.2	6600.7	4535.4	3067.8	887.3	2507.5
AB486164.1	532857	4287.4	4382.8	3789.4	4906.6	2990.7	2379.2
DQ067014.1	128299	1658.7	856.1	1131.1	379.5	476.7	966.5
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EU133207.1	236133	1764.8	1922.2	722.4	1832.9	322.5	792.5
FJ479097.1	545487	6312.0	7283.3	4920.7	4932.9	2285.5	2662.0
FJ478871.1	513347	5645.3	6202.3	4015.0	6180.2	3850.4	4888.5
EU132575.1	238110	14265.1	14954.8	15531.0	12127.1	15755.3	12115.9
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FJ444654.1 gg_id:577683 Cotton Rhizosphere cotton rhizosphere clone 2h-26
EU132482.1 gg_id:248375 tallgrass prarie soil clone FFCH5992
U75647.1 gg_id:11419 Acidimicrobium ferrooxidans
EF621760.1 gg_id:240050 Acidimicrobium ferrooxidans str. TH3
AF251436.2 gg_id:37993 Ferrimicrobium acidiphilum str. T23
GQ402621.1 gg_id:540625 Accessing microbial biodiversity and metabolic potential tropical -based approach p
GQ402557.1 gg_id:582560 Accessing microbial biodiversity and metabolic potential tropical -based approach p
X92698.1 gg_id:11631 peat bog clone TM112
X92710.1 gg_id:11426 peat bog clone TM262
AJ290022.1 gg_id:39131 Germany: Lake Fuchskuhle south basin clone FukuS5 FukuS5
AB254795.1 gg_id:160047 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
X92702.1 gg_id:11632 peat bog clone TM187
EU370318.1 gg_id:360360 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e
X92701.1 gg_id:13505 peat bog clone TM177
AY792236.1 gg_id:128358 Temporal Variation and Humic Lake clone CrystalBog2A8
X92700.1 gg_id:11536 peat bog clone TM167
EU372631.1 gg_id:548811 Evaluation Leptospirillum spp. Rio Tinto basin model interest biohydrometallurgy se
EU370302.1 gg_id:357619 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e
AM936856.1 gg_id:573254 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
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X92703.1 gg_id:11394 peat bog clone TM208
EF019399.1 gg_id:207124 aspen rhizosphere clone Elev_16S_634
GQ060701.1 gg_id:434040 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d05
AJ347027.1 gg_id:56660 sponge clone TK14
AY093455.1 gg_id:63126 marine sediment clone MB-A2-100
FJ674692.1 gg_id:509223 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface
DQ906064.1 gg_id:225385 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-B9
DQ450881.1 gg_id:156584 acidophile waste ore deposits acid mine drainage site clone S5
GQ487905.1 gg_id:582749 Microbial metal soil polluted heavy metals clone T1-39
EU050926.1 gg_id:254366 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_15
AF454307.1 gg_id:56545 actinobacterium clone ML817J-10
DQ458034.1 gg_id:157830 acid mine drainage clone DX65
EF516779.1 gg_id:225319 grassland soil clone FCPP721
GU168002.1 gg_id:578668 Iron Oxidizing Various Sulfidic Mine Waste Dumps heap soil
X92708.1 gg_id:11397 peat bog clone TM226
EU370274.1 gg_id:364140 structure photosynthetic complex biofilm acidophilic streams Rio Tinto (SW Spain) e
AM749756.1 gg_id:249582 Isolation ing candidate division soils New Zealand steam-affected geothermal soil c
EU340182.1 gg_id:251247 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
FJ152940.1 gg_id:328654 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C
FJ466121.1 gg_id:557394 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea

DQ906794.1	235305	6586.6	6869.1	5706.1	7818.5	4426.3	5958.3
FJ444654.1	577683	13977.9	13896.0	11949.7	13169.6	13327.7	10920.3
EU132482.1	248375	14606.0	13141.9	6623.7	6416.7	5470.6	5660.8
U75647.1	11419	18479.5	19646.2	14178.1	15700.5	17478.9	16960.7
EF621760.1	240050	6062.6	5486.7	5125.0	2537.0	670.0	1183.1
AF251436.2	37993	108.1	213.3	66.1	91.3	59.3	33.1
GQ402621.1	540625	13807.5	14637.9	13891.9	11017.7	6802.3	7831.5
GQ402557.1	582560	10889.7	10929.6	7037.6	6226.9	6416.6	5979.1
X92698.1	11631	2869.6	2148.2	1852.1	3210.7	948.8	1163.1
X92710.1	11426	3422.6	3303.5	4890.9	5828.4	2766.4	2959.7
AJ290022.1	39131	4030.8	3465.2	3684.6	1997.4	228.9	658.0
AB254795.1	160047	1719.5	2250.5	1616.6	915.2	493.7	729.0
X92702.1	11632	102.6	174.3	202.9	95.9	107.7	79.1
EU370318.1	360360	2299.0	2058.9	3318.0	1071.7	460.2	1318.5
X92701.1	13505	8462.7	8828.2	5675.3	6299.9	6975.8	6040.9
AY792236.1	128358	12302.2	14771.2	12192.3	9777.6	10395.6	10794.2
X92700.1	11536	5062.2	3617.1	3968.5	4393.1	1473.8	2538.9
EU372631.1	548811	68.3	128.2	457.4	75.3	201.0	351.0
EU370302.1	357619	452.7	875.2	432.3	130.5	221.8	267.7
AM936856.1	573254	3735.9	3402.8	3739.4	2672.7	663.7	1941.9
AY913578.1	113656	1315.3	2207.9	1489.9	2490.8	359.9	954.3
X92703.1	11394	15263.2	14528.3	13928.8	12536.7	15098.6	13555.4
EF019399.1	207124	377.4	314.7	2138.6	165.9	181.9	677.6
GQ060701.1	434040	3758.1	3779.8	4188.4	3746.6	3155.1	3041.9
AJ347027.1	56660	2964.6	3379.4	4150.9	3449.6	2522.0	3413.9
AY093455.1	63126	266.8	387.0	379.2	90.0	171.0	357.6
FJ674692.1	509223	6570.4	6741.7	2677.4	3014.5	736.6	2163.1
DQ906064.1	225385	252.2	297.1	200.6	104.7	187.2	347.2
DQ450881.1	156584	4649.6	4535.4	4411.8	6963.0	4142.2	7723.5
GQ487905.1	582749	11721.5	12801.4	11372.1	10053.1	7817.6	8350.8
EU050926.1	254366	6224.1	5816.9	4270.5	7526.4	3234.8	2350.1
AF454307.1	56545	15021.4	14274.4	8262.6	10185.1	4734.8	4810.6
DQ458034.1	157830	2468.2	3092.0	3074.9	2714.7	3011.6	3106.6
EF516779.1	225319	183.4	326.9	642.8	273.4	345.9	325.6
GU168002.1	578668	15502.1	13741.2	13323.9	9712.9	11486.1	12451.0
X92708.1	11397	60.4	94.8	138.3	64.2	59.7	61.9
EU370274.1	364140	6041.3	6684.7	4834.8	4786.7	4223.1	4340.9
AM749756.1	249582	493.6	435.5	658.1	330.1	286.1	485.4
EU340182.1	251247	2669.8	2474.5	2370.0	1373.4	1477.1	1404.3
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FJ466121.1	557394	11257.1	11261.8	11029.7	10400.1	6790.5	7695.1

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AM749759.1 gg_id:245321 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl
X92706.1 gg_id:12861 peat bog clone TM214
GQ225722.1 gg_id:573091 Acidophilic acidic coal spoil clone BC10
AB254796.1 gg_id:159923 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
EF613015.1 gg_id:235014 acid mine drainage clone YSK16S-52
DQ906055.1 gg_id:217588 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1C5
AM749739.1 gg_id:236029 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl
EU287048.1 gg_id:237721 Pacific arctic surface sediment clone B78-84
AM889149.1 gg_id:532624 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an
EU491799.1 gg_id:266217 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
X92705.1 gg_id:11396 peat bog clone TM213
FJ592827.1 gg_id:559669 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
AM749755.1 gg_id:253790 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl
GQ263011.1 gg_id:590427 Structure Simulated Level Waste Site simulated level waste site clone F2_135X
DQ906070.1 gg_id:221609 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-D12
GU167995.1 gg_id:562452 Iron Oxidizing Various Sulfidic Mine Waste Dumps heap soil
EF127609.1 gg_id:209725 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE037
DQ906083.1 gg_id:222011 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-H10
EF464627.1 gg_id:215003 Identification sulfate reducing methylmercury contaminated SSU genes gold mine tai
DQ451514.1 gg_id:156655 forest soil clone FAC75
GQ402597.1 gg_id:569556 Accessing microbial biodiversity and metabolic potential tropical -based approach p
DQ316372.2 gg_id:151098 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EU236409.1 gg_id:289344 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E9
EU117171.1 gg_id:250067 Scratching surface rare biosphere tag primers recent progress made toward microbi
AM936079.1 gg_id:562332 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM935566.1 gg_id:536920 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EF516519.1 gg_id:223441 grassland soil clone FCPS579
EF409867.1 gg_id:211564 acid mine drainage clone YSK21-06
AF047642.1 gg_id:11393 acid mine drainage clone TRA2-10
EU133154.1 gg_id:256166 tallgrass prarie soil clone FFCH677
FJ478790.1 gg_id:539421 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY395429.1 gg_id:102636 pasture soil clone EB1110
EU491711.1 gg_id:265696 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
GQ402759.1 gg_id:590637 Accessing microbial biodiversity and metabolic potential tropical -based approach p
GQ225721.1 gg_id:582989 Acidithiomicrobium sp. str. P2
AF523913.1 gg_id:63307 forested wetland clone RCP2-105
FJ479261.1 gg_id:556910 species richness estimates obtained nearly and simulated pyrosequencing-generated
AJ347031.1 gg_id:60177 sponge clone TK39
AJ581605.1 gg_id:94227 soil near uranium mill tailings clone KCM-B-10
DQ458030.1 gg_id:157129 acid mine drainage clone DX38
EU286995.1 gg_id:251178 Pacific arctic surface sediment clone B78-31

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X92706.1	12861	5504.0	4391.4	9381.5	7947.0	3449.0	5675.5
GQ225722.1	573091	5244.6	1667.2	7362.5	4735.4	2017.5	2350.8
AB254796.1	159923	117.4	362.7	737.8	107.9	129.3	377.3
EF613015.1	235014	72.1	156.3	182.6	79.7	70.2	212.0
DQ906055.1	217588	5104.5	4365.8	3562.2	3997.9	2967.5	3585.1
AM749739.1	236029	7149.1	8058.1	9612.9	6327.3	5967.3	6329.7
EU287048.1	237721	7029.1	6960.7	4486.9	7615.7	6615.6	3844.8
AM889149.1	532624	8189.3	7279.7	7579.8	6782.7	6955.2	7184.8
EU491799.1	266217	7596.1	6900.6	2852.2	7737.6	2398.1	3044.8
X92705.1	11396	3392.8	4131.3	3157.8	5187.2	3844.0	4987.4
FJ592827.1	559669	9945.6	10632.0	4656.9	7950.9	4052.1	5228.1
AM749755.1	253790	3270.3	2270.8	2048.9	3342.8	1921.0	1958.9
GQ263011.1	590427	42.4	64.3	88.0	54.6	41.1	22.9
DQ906070.1	221609	6586.5	5846.1	7281.7	4781.1	2970.1	4592.1
GU167995.1	562452	5540.7	3779.7	3058.6	996.3	910.4	1213.0
EF127609.1	209725	3200.7	2455.6	963.2	6698.6	1400.0	1220.5
DQ906083.1	222011	2726.1	3474.8	4366.8	2327.8	2453.7	2581.3
EF464627.1	215003	173.1	224.7	169.4	85.2	61.4	50.7
DQ451514.1	156655	2152.2	2323.5	3044.5	2723.1	765.7	1823.1
GQ402597.1	569556	1731.5	1217.8	1264.9	292.5	336.1	260.6
DQ316372.2	151098	1866.9	1345.5	521.2	363.9	62.9	214.7
EU236409.1	289344	2585.9	3092.4	3175.2	2769.3	1194.2	1383.0
EU117171.1	250067	2725.8	3510.2	2418.5	2786.7	3664.1	2006.6
AM936079.1	562332	1718.7	2579.4	1617.7	1464.1	1316.8	1276.8
AM935566.1	536920	1553.3	1908.8	997.4	1146.0	607.1	1641.1
EF516519.1	223441	101.1	128.4	438.2	101.2	100.1	114.5
EF409867.1	211564	5401.5	4337.9	4214.3	3961.6	1001.1	2148.5
AF047642.1	11393	7101.0	8715.7	5301.6	2757.9	4155.4	5129.5
EU133154.1	256166	3290.6	3834.8	2943.5	3576.6	3542.3	2987.8
FJ478790.1	539421	7956.8	7076.3	6539.8	8327.9	1964.6	3421.3
AY395429.1	102636	277.6	267.1	423.7	109.4	98.3	209.4
EU491711.1	265696	5561.1	5560.5	4227.3	2997.7	772.2	1047.0
GQ402759.1	590637	8455.6	9237.2	8522.9	9223.2	6398.7	6812.2
GQ225721.1	582989	4448.9	5550.5	5554.7	4287.6	3723.3	4236.1
AF523913.1	63307	44.7	34.1	61.4	50.5	41.5	47.3
FJ479261.1	556910	2347.9	2363.4	1050.0	921.8	947.1	776.5
AJ347031.1	60177	3989.6	4310.7	3544.9	4660.0	3752.5	5293.5
AJ581605.1	94227	524.5	623.4	354.2	125.3	247.5	221.4
DQ458030.1	157129	12810.2	13364.6	10604.9	9914.1	9017.9	8942.0
EU286995.1	251178	3870.7	3560.2	3191.1	4530.8	994.1	1089.1

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EU132486.1 gg_id:254897 tallgrass prarie soil clone FFCH10951
AJ241005.1 gg_id:11418 marine sediment clone Sva0996
DQ521532.1 gg_id:174445 Antarctic lake ice cover clone ANTLV2_H11
AM259924.1 gg_id:245061 Chondrilla nucula-specific sponge mesohyl clone CN81
GQ094396.1 gg_id:410072 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
FJ478712.1 gg_id:548077 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU491192.1 gg_id:260851 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
FJ592832.1 gg_id:562817 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu
GU167997.1 gg_id:575724 Iron Oxidizing Various Sulfidic Mine Waste Dumps heap soil
DQ906077.1 gg_id:221218 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-F5
AB254776.1 gg_id:160500 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi
EF516392.1 gg_id:225849 grassland soil clone FCPT402
EU440648.1 gg_id:564553 Soil are Changed Agricultural Practices agricultural soil clone Plot17-A07
EU419132.1 gg_id:269564 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi
EU440646.1 gg_id:538728 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2B10
X92695.1 gg_id:11399 peat bog clone TM56
DQ814564.1 gg_id:167937 zebrafish digestive tract clone aaa31f03
FJ477629.1 gg_id:512880 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 98I
AY882848.2 gg_id:111607 hot spring clone SK299
DQ451513.1 gg_id:156849 forest soil clone FAC74
AJ581606.1 gg_id:94128 soil near uranium mill tailings clone KCM-B-37
GQ246415.1 gg_id:592877 Temporal and spatial China North Yel Sea sediments clone Ld1-20
FJ543054.1 gg_id:518645 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B
EF157185.1 gg_id:238707 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU369127.1 gg_id:315138 libraries oyster shell clone MBIOS-11
AM936704.1 gg_id:573814 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
DQ129383.1 gg_id:138117 microarray level air two cities Texas urban aerosol clone AKIW874
AM936076.1 gg_id:535146 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
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AM936649.1 gg_id:542020 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd

AM259895.1	215181	2033.9	1620.8	1225.7	1624.1	685.4	1861.7
EU132486.1	254897	6806.6	6397.7	6557.9	5734.1	2744.1	4394.1
AJ241005.1	11418	962.3	1369.0	281.5	136.1	470.2	267.6
DQ521532.1	174445	160.9	336.6	240.9	181.1	856.6	530.2
AM259924.1	245061	2739.1	3820.3	2455.0	2811.9	547.9	1083.8
GQ094396.1	410072	5237.8	4530.4	2907.1	7159.7	3601.3	4168.0
FJ478712.1	548077	3681.6	3983.0	4117.6	3450.9	642.6	1597.9
EU491192.1	260851	4524.4	3473.3	3518.7	9702.4	637.6	1455.6
FJ592832.1	562817	6138.1	5922.4	4411.4	5941.2	2188.5	3282.5
GU167997.1	575724	9856.0	8877.0	7943.0	8668.5	3781.0	6376.0
DQ906077.1	221218	283.8	620.7	206.7	160.3	106.4	184.7
AB254776.1	160500	1882.6	2625.1	2684.2	2699.0	594.8	1496.8
EF516392.1	225849	128.3	163.2	107.3	73.8	79.5	142.1
EU440648.1	564553	1427.3	1208.1	1737.1	946.3	482.3	1184.4
EU419132.1	269564	9707.4	10348.4	5237.6	3863.9	4529.3	4567.3
EU440646.1	538728	3389.7	4638.0	1783.5	5431.1	417.0	1128.2
X92695.1	11399	5597.6	5049.1	4901.3	5162.7	1862.0	3752.5
DQ814564.1	167937	1510.4	1843.3	1345.1	520.1	1767.9	1281.0
FJ477629.1	512880	9853.8	11090.1	5852.3	10485.4	6713.0	8764.6
AY882848.2	111607	59.2	72.9	71.1	105.7	71.1	38.8
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DQ129383.1	138117	4088.6	2617.1	2690.1	4558.2	1015.9	1234.9
AM936076.1	535146	1075.2	1636.2	2053.4	1306.7	1217.1	2386.9
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FJ479385.1	534888	4096.8	3721.1	3586.2	3643.5	1680.2	1982.3
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EU133198.1	252462	814.4	782.5	1088.0	857.9	792.9	1356.1
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AM936831.1 gg_id:565029 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
AM935924.1 gg_id:568855 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ670881.1 gg_id:525442 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ479142.1 gg_id:574692 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU132696.1 gg_id:254130 tallgrass prarie soil clone FFCH11231
GQ093936.1 gg_id:424457 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
DQ521525.1 gg_id:197548 Antarctic lake ice cover clone ANTLV2_G03
FN582327.1 gg_id:583303 situ detection (Hippocampus guttulatus) intestinal content and mucus farmed seaho
EU803985.1 gg_id:310703 It's all ranking aquatic Lake Gatun clone 5C231663
DQ316378.2 gg_id:153262 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
GQ340246.1 gg_id:534170 Prokaryotic Marathonas Reservoir Greece water column clone VE07-96-BAC
AY921917.1 gg_id:113190 farm soil clone AKYH901
EU236418.1 gg_id:298250 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92G4
GQ850547.1 gg_id:563246 surface water northern Bering Sea clone u72
AJ863196.1 gg_id:125157 poplar tree microcosm bulk soil unflooded clone 20BSU6
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GU118194.1 gg_id:590548 Threatened Corals Provide Microbial Habitats clone Dstr_N17
GQ396937.1 gg_id:575662 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s
FJ827859.1 gg_id:548521 Seasonal nutrient additions eutrophic integrated lake epilimnion clone ME002B4
DQ316381.2 gg_id:150770 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EU132614.1 gg_id:244549 tallgrass prarie soil clone FFCH10283
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AF418962.1 gg_id:39516 USA: Colorado Fort collins Horsetooth Reservoir clone HTG5
EU234292.1 gg_id:253600 penicillin G production wastewater receiving river and un techniques upstream Wan
EU801921.1 gg_id:324132 It's all ranking aquatic Chesapeake Bay MD clone 3C003302
EU592386.1 gg_id:592515 Seasonal changes Salton Sea hypersaline water clone SSW178N
EU234258.1 gg_id:237217 river and un techniques downstream Wang Yang River receiving penicillin G producti
EU803621.1 gg_id:346911 It's all ranking aquatic Lake Gatun clone 5C231220
EU703218.1 gg_id:392975 lakes on Eastern Tin Plateau oligosaline lake altitude 4718 masl clone XZNMC66
AB491851.1 gg_id:554927 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac
EU528238.1 gg_id:282746 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime
AY921723.1 gg_id:113149 farm soil clone AKYG1901
FJ152677.1 gg_id:354357 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
EF019264.1 gg_id:211255 aspen rhizosphere clone Elev_16S_446
GQ021461.1 gg_id:488207 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27
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DQ520183.1 gg_id:161639 shal China sequences hypertrophic freshwater lake clone ML-7-116.2

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AM935924.1	568855	5293.6	4570.2	5812.3	4766.1	1926.9	3496.6
FJ670881.1	525442	16305.1	16351.3	13443.8	11345.6	12558.1	11464.6
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GQ093936.1	424457	5932.7	5761.4	5730.5	3831.5	3660.8	1652.6
DQ521525.1	197548	10811.7	10334.2	6386.5	6353.3	3977.6	7999.2
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EU803621.1	346911	14673.8	14013.7	13389.3	12538.2	7452.2	8462.3
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AB491851.1	554927	6838.1	6326.3	4585.3	5387.1	2934.9	3332.1
EU528238.1	282746	5014.7	5399.7	4347.5	4627.6	3227.6	3756.0
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GQ021461.1	488207	10433.7	11798.1	6014.0	7849.5	8077.4	5961.7
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GQ016492.1	493175	6230.8	5615.2	8191.2	7878.5	2608.4	2517.1
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EU803967.1 gg_id:355005 It's all ranking aquatic Lake Gatun clone 5C231638
GQ340213.1 gg_id:584272 Prokaryotic Marathonas Reservoir Greece water column clone VE07-28-BAC
EU132590.1 gg_id:255512 tallgrass prarie soil clone FFCH1008
EU132666.1 gg_id:257176 tallgrass prarie soil clone FFCH1091
EU340186.1 gg_id:256498 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY
EF516030.1 gg_id:222035 grassland soil clone FCPT456
AM935299.1 gg_id:542933 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU132977.1 gg_id:255449 tallgrass prarie soil clone FFCH17424
EF019232.1 gg_id:207912 aspen rhizosphere clone Elev_16S_404
EU925881.1 gg_id:350536 sediments sediment station DBS1 northern Bering Sea clone 087F85
AM935740.1 gg_id:559985 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ478803.1 gg_id:584385 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU132782.1 gg_id:235653 tallgrass prarie soil clone FFCH12764
AY221045.1 gg_id:84258 Mammoth cave clone CCM13a
EF516604.1 gg_id:218712 grassland soil clone FCPO472
DQ316376.2 gg_id:155271 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EF516535.1 gg_id:219570 grassland soil clone FCPS488
AY395413.1 gg_id:105527 pasture soil clone EB1094
EF019813.1 gg_id:213344 aspen rhizosphere clone Elev_16S_1157
DQ128808.2 gg_id:180978 no tillage soil clone HSB NT53_D06
FJ478634.1 gg_id:562659 species richness estimates obtained nearly and simulated pyrosequencing-generated
EU335429.1 gg_id:251886 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
EU335147.1 gg_id:243610 Changes microbial metabolic and along hydrogeochemically variable profile saturate
AB487439.1 gg_id:559205 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0
DQ395955.1 gg_id:152101 deep-sea octacoral clone ctg_CGOGA19
EF157223.1 gg_id:257150 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
AM935802.1 gg_id:543152 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
EU440650.1 gg_id:537124 Soil are Changed Agricultural Practices agricultural soil clone Plot17-H03
AJ581630.1 gg_id:93175 soil near uranium mill tailings clone KCM-C-53
FM209069.1 gg_id:533501 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr
AB360448.1 gg_id:265034 Iamibacter majanohamensis str. NBRC 102561
GQ500878.1 gg_id:593462 Surveys Biofilms and Sediments Mammoth Karst Aquifers Bio-Sep beads containing
CU466698.1 gg_id:342630 Evry wastewater treatment plant anoxic basin clone
EU133138.1 gg_id:244545 tallgrass prarie soil clone FFCH604
AY102341.1 gg_id:65445 heavy metal-contaminated soil clone a13156
AM935499.1 gg_id:548072 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd
FJ478585.1 gg_id:512041 species richness estimates obtained nearly and simulated pyrosequencing-generated
AY921951.1 gg_id:113885 farm soil clone AKYG1106
EF020060.1 gg_id:217034 aspen rhizosphere clone Elev_16S_1467
AY234598.1 gg_id:112160 soil isolate Ellin5247
EU669633.1 gg_id:333608 soil clone S1-9

EU803967.1	355005	15468.2	15578.9	6738.6	11427.8	11755.3	10787.2
GQ340213.1	584272	10339.7	10963.8	11855.1	9667.0	10817.4	10911.1
EU132590.1	255512	1443.7	1700.3	3458.5	607.5	336.9	590.5
EU132666.1	257176	3067.2	2889.4	4292.4	3324.9	4955.1	3749.7
EU340186.1	256498	7650.6	7338.9	6924.3	9543.6	3292.4	3729.0
EF516030.1	222035	28.3	58.8	582.1	83.8	56.3	38.0
AM935299.1	542933	59.5	126.1	1282.6	96.7	121.1	88.7
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EF019232.1	207912	42.4	126.2	172.1	61.9	88.9	124.5
EU925881.1	350536	3299.8	3339.6	2087.9	1120.0	1295.3	1874.1
AM935740.1	559985	1377.3	1726.6	2070.8	313.9	1022.3	583.8
FJ478803.1	584385	7203.0	6627.2	9406.4	5974.4	1592.6	2774.4
EU132782.1	235653	2458.2	3120.2	3715.9	2356.1	2194.0	3187.5
AY221045.1	84258	2190.1	1672.9	674.8	693.1	1186.1	578.0
EF516604.1	218712	566.4	479.4	1827.0	1027.0	171.8	493.2
DQ316376.2	155271	49.2	74.2	99.8	60.3	74.2	46.0
EF516535.1	219570	78.6	135.3	1382.1	124.7	132.9	295.3
AY395413.1	105527	8441.7	8018.3	4244.8	5117.6	7838.6	7536.6
EF019813.1	213344	6789.8	8161.8	4630.4	6140.3	4477.9	4336.8
DQ128808.2	180978	1591.9	2822.8	2686.9	2186.3	4987.5	4059.4
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EU335429.1	251886	17639.9	18577.6	12017.7	16426.4	18171.5	16327.9
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EU440650.1	537124	6003.8	5479.5	2110.8	2307.9	492.5	1982.6
AJ581630.1	93175	426.4	534.1	211.5	69.9	60.7	2741.6
FM209069.1	533501	4358.1	5258.4	3678.5	2344.7	2278.5	4104.3
AB360448.1	265034	5811.6	6210.4	7004.0	4270.8	3006.7	3687.3
GQ500878.1	593462	2533.4	3163.5	2279.3	2344.5	681.2	2581.6
CU466698.1	342630	1461.2	1987.2	2135.0	866.6	254.9	569.9
EU133138.1	244545	552.1	409.6	237.9	155.6	69.8	132.1
AY102341.1	65445	199.4	399.8	60.1	891.8	415.7	151.8
AM935499.1	548072	2798.9	2984.8	2290.6	858.3	870.8	1680.0
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EF020060.1	217034	326.9	364.8	124.8	107.6	67.1	80.8
AY234598.1	112160	22273.1	22969.4	13702.4	15526.6	19388.7	22610.8
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AY234624.1 gg_id:112066 soil isolate Ellin5273
CU466701.1 gg_id:320666 Evry wastewater treatment plant anoxic basin clone
CT573827.1 gg_id:156127 Evry municipal wastewater treatment plant clone 013H08_B_SD_P15
AY921962.1 gg_id:113586 farm soil clone AKYG1583
EF516937.1 gg_id:221634 grassland soil clone FCPU395
FJ999602.1 gg_id:389275 sponge Haliclona simulans South China Sea clone B55
FJ202465.1 gg_id:335185 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k
AM911370.1 gg_id:369680 Phenotype-specific (Scleractinia) their implications coral's nutrition health and cold-
DQ070822.1 gg_id:146815 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal
AB476265.1 gg_id:574727 Compositional and functional transition epibiotic microbial hydrothermal vent galath
FN424398.1 gg_id:576054 structure sediments Bizerte (Tunisia) southern Mediterranean coastal anthropized la
GU118878.1 gg_id:542569 Threatened Corals Provide Microbial Habitats clone Past_I10
DQ270650.1 gg_id:142032 hydrothermal carbonate chimney clone LC1228B-35
EU491619.1 gg_id:264768 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39
CU917839.1 gg_id:546297 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
AB286641.1 gg_id:210507 Reducing production and domination comamonadaceae reducing oxygen supply was
CU466705.1 gg_id:331084 Evry wastewater treatment plant anoxic basin clone
DQ316384.1 gg_id:151097 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EU488068.1 gg_id:540668 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and
DQ450797.1 gg_id:160075 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat
GQ340284.1 gg_id:591444 Prokaryotic Marathonas Reservoir Greece water column clone B08-103-BAC
AM176889.1 gg_id:160187 Recovery mangrove sediment clone SZB6
EF019788.1 gg_id:215846 aspen rhizosphere clone Elev_16S_974
FJ356666.1 gg_id:556595 Intra- Microheterogeneity Multiple Displacement Single-cells Marine Cyanobacteria L
DQ289932.1 gg_id:172264 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh
GU061197.1 gg_id:575752 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se
FJ615171.1 gg_id:578870 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic
FJ529346.1 gg_id:573369 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze
FJ229956.1 gg_id:566439 Microbes marine sponges Indonesia: Manado clone XC1C08
FJ229949.1 gg_id:575087 Microbes marine sponges USA: Key Largo Florida clone XB3E12F
AJ347026.1 gg_id:60183 sponge clone TK06
AF317769.1 gg_id:136346 Nullarbor cave clone wb1_P06
FJ203303.1 gg_id:331758 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
EU491133.1 gg_id:276243 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak
DQ070807.1 gg_id:148554 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl
FJ203322.1 gg_id:344834 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c
GU369911.1 gg_id:521448 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v
FJ203655.1 gg_id:315494 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h
EU374087.1 gg_id:272708 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc
GQ350187.1 gg_id:550067 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF382122.1 gg_id:79134 bacterioplankton clone ZA3409c

AY234624.1	112066	5165.7	5354.2	5717.3	4452.0	1519.7	3031.9
CU466701.1	320666	14057.7	11757.8	8775.2	10466.3	9324.0	8076.6
CT573827.1	156127	9715.3	7435.2	5775.6	7610.4	6400.4	7726.8
AY921962.1	113586	5670.7	4908.2	2166.4	5794.1	1307.1	2125.9
EF516937.1	221634	1165.0	1260.0	638.7	396.2	135.7	395.8
FJ999602.1	389275	1762.4	1196.7	1506.5	2437.6	971.0	963.1
FJ202465.1	335185	94.9	275.2	1097.2	166.0	305.7	242.3
AM911370.1	369680	4531.2	3119.0	2505.1	7498.9	1114.5	1437.0
DQ070822.1	146815	1842.8	2315.3	1155.8	1955.2	341.5	951.8
AB476265.1	574727	1456.2	951.1	731.4	1076.9	171.7	199.6
FN424398.1	576054	3623.0	3241.1	2070.6	2843.6	377.8	868.2
GU118878.1	542569	598.7	675.6	804.7	401.1	192.1	176.9
DQ270650.1	142032	7591.5	6868.4	7407.0	7396.1	6275.8	8847.6
EU491619.1	264768	2689.2	3535.4	1232.2	2918.7	2373.7	1658.2
CU917839.1	546297	136.5	202.4	137.2	82.0	98.1	51.5
AB286641.1	210507	2993.2	3874.6	636.1	390.1	90.0	165.7
CU466705.1	331084	5485.7	3339.4	2588.4	2080.4	432.4	1459.4
DQ316384.1	151097	435.4	646.0	896.4	1017.6	215.7	583.1
EU488068.1	540668	11474.9	10896.5	7949.5	10433.9	10137.8	8139.6
DQ450797.1	160075	8007.9	7717.4	5149.7	4632.2	1045.8	1906.3
GQ340284.1	591444	4827.7	4758.2	4608.6	4317.4	1362.5	2600.4
AM176889.1	160187	987.3	1622.9	2483.8	2258.0	883.9	1134.2
EF019788.1	215846	8006.7	6643.5	3426.7	4511.7	4780.9	5325.7
FJ356666.1	556595	1120.5	1575.8	1691.2	1472.2	159.6	347.6
DQ289932.1	172264	58.2	70.8	49.9	123.4	79.2	77.5
GU061197.1	575752	4337.0	6178.1	909.8	1399.9	443.3	964.1
FJ615171.1	578870	15053.6	15345.1	9479.8	11462.8	12604.5	10306.8
FJ529346.1	573369	2882.9	1992.0	2691.8	409.0	1522.9	1216.9
FJ229956.1	566439	5014.4	5093.4	2779.2	2168.8	492.5	1143.4
FJ229949.1	575087	10761.6	11094.8	5097.4	6879.6	4133.6	5012.4
AJ347026.1	60183	3359.4	4696.7	3601.1	2111.9	5377.4	3220.2
AF317769.1	136346	812.2	662.0	507.3	892.7	132.2	295.4
FJ203303.1	331758	3518.3	2258.6	2075.3	4775.6	456.9	718.2
EU491133.1	276243	4366.9	3950.1	2177.6	7059.7	502.2	1522.8
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FJ203655.1	315494	5353.8	5261.1	5923.8	4379.5	7819.5	5210.9
EU374087.1	272708	9057.5	8250.1	7548.5	10597.2	4121.0	5997.7
GQ350187.1	550067	5309.8	5119.0	3090.3	4295.5	6438.7	6984.7
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GQ350443.1 gg_id:557337 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
FJ615149.1 gg_id:582610 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 100m anoxi
GQ348064.1 gg_id:556769 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
DQ009431.1 gg_id:119667 bacterioplankton clone SPOTSFEB02_70m35
GQ351092.1 gg_id:548197 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347207.1 gg_id:563738 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350426.1 gg_id:542333 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ347157.1 gg_id:538949 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350379.1 gg_id:543378 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ346944.1 gg_id:577150 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
GQ350844.1 gg_id:535697 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
EU265955.1 gg_id:588313 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni
GQ348458.1 gg_id:534913 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AF382139.1 gg_id:100695 bacterioplankton clone ZA3635c
GU061498.1 gg_id:589639 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC
GQ350624.1 gg_id:581082 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich
AJ575534.1 gg_id:97218 freshwater clone NM1
GQ340205.1 gg_id:588079 Prokaryotic Marathonas Reservoir Greece water column clone VE07-10-BAC
GQ340275.1 gg_id:585868 Prokaryotic Marathonas Reservoir Greece water column clone A08-156-BAC
GQ340192.1 gg_id:548098 Prokaryotic Marathonas Reservoir Greece water column clone K07-91-BAC
EU117943.1 gg_id:239240 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TR1C3
DQ316345.1 gg_id:153606 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
AY792229.1 gg_id:123628 Humic Lake clone CrystalBog022E4
AJ575546.1 gg_id:97083 freshwater clone SW1
EU803672.1 gg_id:323127 It's all ranking aquatic Lake Gatun clone 5C231277
EU117813.1 gg_id:241892 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LT1A9
EU117787.1 gg_id:236761 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1C12
EU117629.1 gg_id:251849 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CH1H9
EU117950.1 gg_id:256871 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TR1D12
DQ316353.1 gg_id:152280 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EU117596.1 gg_id:255636 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CL1D7
EU117759.1 gg_id:243730 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone JB3H7
EU117929.1 gg_id:244953 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone SA1H8
EU117792.1 gg_id:247597 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1D10
AY466487.1 gg_id:101690 actinobacterium clone SL29
GQ390230.1 gg_id:551438 oxic-anoxic interface meromictic crater lake Lac Pavin clone Eub62C1211
EU117590.1 gg_id:251197 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CL1B5
EU117638.1 gg_id:242429 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CB7G1
AY863101.1 gg_id:111721 wastewater treatment pool clone SXAU070
EU117607.1 gg_id:255862 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CH1B9
GU305764.1 gg_id:555795 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res

GQ350443.1	557337	4382.4	4250.7	4406.0	6091.6	3862.2	3665.5
FJ615149.1	582610	9223.1	8040.2	8480.9	10854.9	5242.0	4835.5
GQ348064.1	556769	5982.9	3439.4	1707.2	8694.0	3153.4	4028.2
DQ009431.1	119667	376.9	473.7	226.5	108.0	70.3	32.2
GQ351092.1	548197	9368.2	9020.2	4073.7	7018.2	3313.7	5106.2
GQ347207.1	563738	3723.7	2934.2	3602.2	3827.8	2387.5	3475.8
GQ350426.1	542333	6308.4	4998.1	3027.1	5790.7	5476.6	6315.7
GQ347157.1	538949	10191.3	9061.0	6369.7	11991.6	11855.2	8857.8
GQ350379.1	543378	4146.7	3555.1	4881.5	3809.3	1261.5	1583.6
GQ346944.1	577150	11350.6	11567.8	9694.7	9450.4	10239.2	9341.6
GQ350844.1	535697	13255.7	13083.3	8993.4	13392.3	15111.1	13211.3
EU265955.1	588313	398.3	472.1	3859.3	758.0	155.6	291.6
GQ348458.1	534913	3022.3	2322.0	3418.1	2882.3	1440.7	1531.5
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GQ350624.1	581082	5974.0	6861.9	2033.4	3624.9	1379.1	1493.1
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GQ340205.1	588079	8749.2	4221.9	5407.8	9381.9	495.9	852.8
GQ340275.1	585868	5989.7	2660.3	1841.7	6042.7	1123.1	1164.0
GQ340192.1	548098	15097.7	13165.7	9696.5	15535.5	6389.1	7550.1
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AY792229.1	123628	7193.1	7400.3	10847.1	7103.9	4215.9	4626.0
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EU800635.1 gg_id:322266 It's all ranking aquatic Delaware Bay NJ clone 2C228795
EU117835.1 gg_id:255319 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LT1E10
GQ020257.1 gg_id:489410 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu266d07
EU117736.1 gg_id:235280 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone IW1D3
EU804007.1 gg_id:349848 It's all ranking aquatic Lake Gatun clone 5C231689
EU117793.1 gg_id:242895 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1D3
EU117597.1 gg_id:243443 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CL1D8
EU117981.1 gg_id:254057 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TW1D9
AJ575555.1 gg_id:97386 freshwater clone NO1
AY792226.1 gg_id:120109 Humic Lake clone CrystalBog1D1
EU803598.1 gg_id:347586 It's all ranking aquatic Lake Gatun clone 5C231197
EU735737.1 gg_id:352333 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_M47
EU117766.1 gg_id:239774 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone ME7C12
AJ575513.1 gg_id:96722 freshwater clone S12
EU117908.1 gg_id:238827 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone SA1B5
DQ316343.2 gg_id:153128 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EU117975.1 gg_id:236670 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TW1B9
EU117634.1 gg_id:251604 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone CB7E2
EU801039.1 gg_id:331093 It's all ranking aquatic Delaware Bay NJ clone 2C229336
EU117886.1 gg_id:235511 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone RC1A7
EU117746.1 gg_id:247629 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone IW1G7
AF418967.1 gg_id:30680 USA: Colorado Fort collins Horsetooth Reservoir clone HT2E3
EU117775.1 gg_id:239896 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone ME7F6
DQ316346.1 gg_id:151307 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EU117689.1 gg_id:244911 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone GR1A4
GU305811.1 gg_id:557202 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res
EU117655.1 gg_id:257661 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone FF1A7
EU117873.1 gg_id:255402 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone MI1E8
EU117795.1 gg_id:246865 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1E10
EU117757.1 gg_id:241264 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone JB3G11
EU117806.1 gg_id:252598 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone LA1H10
EU801147.1 gg_id:324019 It's all ranking aquatic Delaware Bay NJ clone 2C229494
EU703381.1 gg_id:431445 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH87
EU117698.1 gg_id:256870 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone GR1C5
AY792223.1 gg_id:122328 Humic Lake clone CrystalBog5G8
EU117557.1 gg_id:249857 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone BR1A5
EU117988.1 gg_id:254459 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone TW1H4
EU117652.1 gg_id:242933 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone FF1A1
EU117776.1 gg_id:249545 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone ME7G10
EU234301.1 gg_id:248946 penicillin G production wastewater receiving river and un techniques upstream Wan

GQ340321.1	570543	4446.5	3180.7	4003.8	8756.0	3762.2	5031.2
EU800635.1	322266	10600.5	9815.1	8309.3	12550.4	4528.3	4629.3
EU117835.1	255319	16189.6	13770.5	9052.9	16078.0	9864.0	9294.7
GQ020257.1	489410	130.9	53.3	53.8	876.2	59.3	12.0
EU117736.1	235280	5733.3	2969.5	1668.7	11806.6	176.7	265.4
EU804007.1	349848	1326.9	459.8	628.7	2179.1	99.8	72.6
EU117793.1	242895	5977.2	3274.8	3579.1	7409.0	686.2	1083.0
EU117597.1	243443	7492.3	4449.0	5796.9	10006.5	3884.5	4173.8
EU117981.1	254057	8436.2	5332.0	9054.9	11400.5	557.9	1555.7
AJ575555.1	97386	9325.7	5753.3	2427.2	13924.1	1212.3	741.2
AY792226.1	120109	6523.8	5148.1	3345.3	6974.9	782.3	1495.7
EU803598.1	347586	9293.5	7745.3	14898.5	12882.6	6062.5	6121.8
EU735737.1	352333	8847.5	5736.3	7826.4	9027.8	608.7	1360.8
EU117766.1	239774	10255.2	6873.4	9682.7	12104.8	2967.5	5062.6
AJ575513.1	96722	11295.6	11696.8	9420.9	16291.7	4021.8	6959.4
EU117908.1	238827	14673.2	12162.7	11258.9	17808.1	9843.7	2990.2
DQ316343.2	153128	14254.9	12087.6	11856.9	14974.2	4759.6	5465.9
EU117975.1	236670	6589.8	3680.3	5201.0	9780.4	1638.6	1554.1
EU117634.1	251604	172.6	122.7	194.0	278.6	86.3	41.7
EU801039.1	331093	11531.9	7703.0	9094.1	14229.7	2546.2	3592.5
EU117886.1	235511	5275.6	3276.3	7387.6	7198.5	424.6	1194.3
EU117746.1	247629	8768.4	5705.9	2700.0	11559.2	1028.9	1916.0
AF418967.1	30680	8083.9	4614.1	6509.1	11725.8	2102.1	1610.5
EU117775.1	239896	12381.5	7098.7	5187.6	13472.4	2152.0	2107.8
DQ316346.1	151307	14138.0	11591.7	6714.3	17167.8	9106.9	8722.9
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GU305811.1	557202	4774.1	3081.9	3374.6	6300.9	648.8	1265.5
EU117655.1	257661	11537.3	6708.3	3179.8	15709.6	326.9	472.9
EU117873.1	255402	10450.7	7215.1	6462.4	13377.2	2685.1	2770.6
EU117795.1	246865	14883.9	11872.1	13967.1	15789.8	6841.5	6835.4
EU117757.1	241264	12887.6	13546.4	6833.8	14446.5	5471.2	7040.0
EU117806.1	252598	10796.2	8394.0	8940.1	13922.7	3678.6	6134.1
EU801147.1	324019	8020.4	4842.6	6096.6	15657.2	1537.9	2525.7
EU703381.1	431445	5910.4	3548.9	3767.7	8074.5	490.0	607.1
EU117698.1	256870	3458.1	1626.2	169.4	3765.5	281.1	336.6
AY792223.1	122328	5426.1	3618.6	2616.7	7133.6	1454.7	1671.5
EU117557.1	249857	7317.1	4973.5	7169.7	11412.5	2470.8	4094.3
EU117988.1	254459	7630.3	5897.1	7150.8	11272.6	2313.2	3867.0
EU117652.1	242933	16920.3	14737.3	10365.0	17111.6	10284.6	10315.8
EU117776.1	249545	7391.2	7386.6	14036.3	10658.6	2459.1	5097.1
EU234301.1	248946	13599.3	10434.0	3971.5	14960.6	7967.7	7540.6

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EU117880.1 gg_id:247754 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone MI1G3
EU800363.1 gg_id:307023 It's all ranking aquatic Delaware Bay NJ clone 2C228427
EU803878.1 gg_id:324989 It's all ranking aquatic Lake Gatun clone 5C231522
EU117741.1 gg_id:253508 Ecology Freshwater Actinobacteria acI Lineage lake epilimnion clone IW1F2
FJ711191.1 gg_id:541769 Actinobaculum massiliense str. NML 070284
FJ711180.1 gg_id:574249 Actinobaculum schaalii str. NML 99A018
NR_028978.1 gg_id:582466 Actinobaculum urinale str. R9242; CCUG 46093
AJ276805.1 gg_id:47874 Actinomyces catuli str. CCUG 41709
NR_026181.1 gg_id:547861 Actinomyces denticolens str. NCTC 11490
Y08828.1 gg_id:12562 Actinomyces europaeus str. CCUG 32789A
AF489584.1 gg_id:94067 Actinomyces hyovaginalis str. D3
AJ276405.1 gg_id:33765 Actinomyces marimammalium str. CCUG 41710
AY244766.1 gg_id:104354 Actinomyces sp. str. 2002-2301122
X78721.1 gg_id:12574 Actinomyces turicensis str. APL11
X82451.1 gg_id:12571 Actinomyces meyeri str. C.I.P. 103148T
AJ234040.1 gg_id:52899 Actinomyces odontolyticus str. CCUG 20536T
GQ048196.1 gg_id:439901 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ074395.1 gg_id:448385 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c
AJ234049.1 gg_id:23267 Actinomyces sp. str. CCUG 33931
X82453.1 gg_id:12545 Actinomyces viscosus str. NCTC 10951
GQ421314.1 gg_id:542967 Actinomyces oris str. A19A1
AF543282.1 gg_id:58296 Actinomyces naeslundii str. ChDC B204
FJ823139.1 gg_id:556324 Actinomyces viscosus str. TeTC
GQ067994.1 gg_id:397505 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw145
X81062.1 gg_id:12551 Actinomyces naeslundii str. NCTC 10301
GQ063069.1 gg_id:458238 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
NZ_ACUY02000007.1 gg_id:484320 Actinomyces sp. oral taxon 848 str. F0332
AJ243791.1 gg_id:40580 Actinomyces urogenitalis
AJ427451.1 gg_id:82476 Actinomyces vaccimaxillae str. R10176T
GQ014220.1 gg_id:495445 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760c
AJ271894.1 gg_id:44463 Actinomyces lingnae str. CCUG 32865
NR_028905.1 gg_id:588670 Actinomyces coleocanis str. M343/98/2; CCUG 41708
AJ277385.1 gg_id:67513 Actinomyces suimastitidis str. CCUG 39276
FJ393117.1 gg_id:357502 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel
AY221601.1 gg_id:90040 metal and hydrocarbon contaminated soil clone HN1-52
NR_028960.1 gg_id:541935 Actinomyces funkei str. CCUG 42773
X78720.1 gg_id:12567 Actinomyces sp str. APL10
GQ091902.1 gg_id:389728 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
AJ421779.1 gg_id:60136 Actinomyces cardiffensis str. CCUG 44997
AJ243892.1 gg_id:44425 Actinomyces canis
AB490162.1 gg_id:560661 Actinomyces sp. str. GTC3949

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EU800363.1	307023	8491.4	5887.2	3279.8	8992.8	585.0	623.3
EU803878.1	324989	3368.7	3555.8	6603.4	5689.5	2793.5	3717.8
EU117741.1	253508	8401.8	4870.1	4452.4	10810.1	2483.6	2145.2
FJ711191.1	541769	30.1	33.1	35.0	60.5	70.5	39.7
FJ711180.1	574249	34.0	46.8	44.4	63.1	73.8	50.8
NR_028978.1	582466	49.9	60.5	35.5	79.9	101.7	52.3
AJ276805.1	47874	4277.5	5153.8	3887.3	4355.9	2702.5	2730.1
NR_026181.1	547861	3366.9	2937.2	1867.4	1081.1	1221.8	912.7
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AF489584.1	94067	2059.7	2144.1	4477.8	1904.2	1809.7	1769.2
AJ276405.1	33765	17.7	21.7	27.8	49.2	58.9	16.4
AY244766.1	104354	50.8	64.0	60.0	141.6	73.2	53.9
X78721.1	12574	2699.2	2355.4	1685.2	5054.1	1662.8	1793.0
X82451.1	12571	3256.8	3045.5	1317.7	5131.8	2007.2	2025.2
AJ234040.1	52899	3730.1	3051.0	1307.9	5128.4	1867.0	1435.2
GQ048196.1	439901	5920.2	6280.3	5820.8	9353.6	6629.0	5536.2
GQ074395.1	448385	2490.0	3185.7	4458.0	2950.7	935.2	1231.0
AJ234049.1	23267	1993.3	1430.3	3924.1	2969.8	883.6	979.2
X82453.1	12545	2846.5	3276.1	2305.8	2196.7	1040.1	1726.4
GQ421314.1	542967	3825.0	4168.3	2795.4	4273.2	3084.8	3540.6
AF543282.1	58296	3180.6	4584.6	2715.0	2141.0	1104.3	1793.3
FJ823139.1	556324	1085.1	1229.0	1313.5	1254.6	464.5	1026.0
GQ067994.1	397505	3833.1	3064.2	6902.1	4908.3	2684.0	4098.8
X81062.1	12551	10718.4	12535.9	5120.8	10278.5	9264.9	10028.4
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NZ_ACUY02000007.1	484320	874.6	802.9	1748.1	3037.4	416.9	436.9
AJ243791.1	40580	5044.7	4799.5	3970.3	3890.1	2319.9	2657.0
AJ427451.1	82476	107.1	90.1	81.0	108.3	156.1	119.6
GQ014220.1	495445	1920.9	2433.7	5666.0	3650.8	638.1	1191.5
AJ271894.1	44463	4522.6	3396.2	2537.6	5451.0	2144.1	1372.1
NR_028905.1	588670	1654.4	2109.4	2308.4	5473.2	1289.2	2176.6
AJ277385.1	67513	748.3	477.3	1733.3	2411.0	253.5	829.3
FJ393117.1	357502	4534.9	3018.6	5873.4	8480.3	2292.7	2235.1
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NR_028960.1	541935	2203.0	1937.5	2213.0	1786.1	429.5	559.0
X78720.1	12567	3284.8	2536.0	1290.8	8325.5	373.5	719.1
GQ091902.1	389728	5648.1	4927.8	4112.8	5223.4	7203.5	7007.0
AJ421779.1	60136	3135.2	3329.9	3008.1	2799.3	3681.0	3463.6
AJ243892.1	44425	2614.5	1931.2	1480.9	5322.2	459.4	1138.6
AB490162.1	560661	1079.2	1405.1	2214.7	1926.4	447.1	1434.9

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DQ378185.1 gg_id:151007 oil-polluted soil clone F21_Pitesti
DQ278863.1 gg_id:152869 Actinomyces sp. 152R-3
GQ004952.1 gg_id:504710 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65b0
GQ091872.1 gg_id:437735 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FJ542912.1 gg_id:522040 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
FJ542871.1 gg_id:527314 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
NR_026182.1 gg_id:561441 Actinomyces georgiae str. DSM 6843
DQ378174.1 gg_id:153783 oil-polluted soil clone F09_Pitesti
AF287750.1 gg_id:29001 Actinomyces sp. oral strain str. B27SC
AF433168.1 gg_id:19270 Actinomyces hongkongensis str. HKU8
AY207066.1 gg_id:83011 Actinobaculum sp. P1 str. P2P_19
FJ234422.1 gg_id:545415 Actinomyces naturae sp. nov. able grow presence concentrations chlorinated solvent
AJ507295.1 gg_id:58541 Actinomyces oricola str. CCUG 46090
FM873627.1 gg_id:368710 occupant source house mattress dust clone MA01G06
AJ697609.1 gg_id:109929 Actinomyces dentalis str. R18165
EF558367.1 gg_id:278919 Actinomyces massiliensis str. 4401292
GQ010287.1 gg_id:499378 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GU227166.1 gg_id:551431 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier
GQ421317.1 gg_id:593883 Actinomyces oris str. CCUG 33920
GU227175.1 gg_id:571103 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier
AB545933.1 gg_id:541516 Actinomyces johnsonii str. JCM 16129
AJ234056.1 gg_id:27124 Actinomyces viscosus str. CCUG 35332
AJ243792.1 gg_id:16513 Actinomyces cf. urogenitalis M560/98/1
AJ540309.1 gg_id:79234 Actinomyces graevenitzii str. CCUG 27294
X81061.1 gg_id:12548 Actinomyces bovis str. NCTC 11535
AJ251986.1 gg_id:26223 Actinomyces radicidentis str. CCUG 36733T
GQ073149.1 gg_id:441099 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205f08c1
GQ099503.1 gg_id:450107 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51
AJ234066.1 gg_id:40753 Actinomyces slackii str. CCUG 32792
X80414.1 gg_id:12560 Actinomyces gerencseriae str. DSM 6844
AJ234039.1 gg_id:24150 Actinomyces bowdenii str. M1956/95/1
FM873536.1 gg_id:366843 occupant source house mattress dust clone MA01H12
AJ234048.1 gg_id:30901 Actinomyces naeslundii str. CCUG 33914
AJ635359.1 gg_id:106166 Actinomyces naeslundii
FM873274.1 gg_id:358736 occupant source house floor dust clone FC04H05
EU484334.1 gg_id:539951 Actinomyces sp. str. 7400942
X80411.1 gg_id:12558 Actinomyces howellii str. NCTC 11636
AM696983.1 gg_id:223408 sequencing libraries indoor dust clone BF0001B009
GQ077230.1 gg_id:416528 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw115E
AF543286.1 gg_id:58292 Actinomyces viscosus str. ChDC OS34
GQ017278.1 gg_id:492389 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu116

DQ378185.1	151007	1234.6	2700.8	2986.9	3242.4	2549.6	1777.7
DQ278863.1	152869	196.7	155.3	341.2	408.0	193.6	202.4
GQ004952.1	504710	6878.8	5837.0	11821.2	10358.9	2961.0	3455.1
GQ091872.1	437735	2401.3	1693.8	1987.4	2343.0	1859.1	1750.7
FJ542912.1	522040	5155.3	4055.1	6737.6	8722.7	4209.2	4138.1
FJ542871.1	527314	5163.4	3194.3	5347.9	10956.4	3651.4	3325.4
NR_026182.1	561441	180.7	291.0	392.9	199.5	155.6	235.8
DQ378174.1	153783	1134.2	973.7	1732.5	2242.0	242.5	610.9
AF287750.1	29001	1265.1	1143.4	2406.2	1863.9	695.8	964.3
AF433168.1	19270	3859.3	3696.4	1499.6	3921.2	1017.0	1131.3
AY207066.1	83011	572.7	382.0	277.0	177.1	401.8	179.7
FJ234422.1	545415	3661.3	4717.6	3501.5	3831.7	3429.1	3260.7
AJ507295.1	58541	32.5	31.7	28.7	54.9	74.0	36.4
FM873627.1	368710	2957.8	2164.0	2819.1	6546.9	1017.1	1490.4
AJ697609.1	109929	38.4	41.7	33.9	49.1	87.5	41.2
EF558367.1	278919	662.1	549.7	362.9	293.7	600.8	345.5
GQ010287.1	499378	3734.0	2610.8	3306.9	7461.1	316.1	762.3
GU227166.1	551431	260.5	359.9	1336.3	2152.9	552.2	904.9
GQ421317.1	593883	4433.3	4560.2	4039.5	3523.2	2359.8	2328.8
GU227175.1	571103	7101.0	7374.0	6111.9	6545.4	2888.2	3918.0
AB545933.1	541516	3927.2	5388.9	2745.9	2263.5	1408.8	1288.0
AJ234056.1	27124	2408.6	1632.0	4391.6	3660.1	644.0	1024.5
AJ243792.1	16513	1461.5	1850.6	951.1	780.5	161.2	515.0
AJ540309.1	79234	133.1	111.5	119.7	74.6	60.0	64.7
X81061.1	12548	1257.4	872.5	631.3	1292.0	139.4	393.9
AJ251986.1	26223	1509.3	3067.6	2482.1	682.0	851.0	1140.6
GQ073149.1	441099	3456.6	4455.8	2102.6	2862.7	912.2	1660.2
GQ099503.1	450107	1546.3	1215.0	740.7	2355.2	244.0	495.2
AJ234066.1	40753	76.0	237.5	759.8	465.9	281.5	320.6
X80414.1	12560	1838.0	735.3	1244.6	3469.3	611.8	1640.9
AJ234039.1	24150	3011.8	2974.8	5626.5	4469.7	1203.4	1776.2
FM873536.1	366843	8986.0	6979.2	8754.7	7273.4	4568.8	4618.8
AJ234048.1	30901	909.8	1039.5	1378.3	1124.6	507.7	847.1
AJ635359.1	106166	1920.2	2157.5	2127.2	1849.7	574.5	906.9
FM873274.1	358736	7507.2	7111.4	3421.8	5992.8	4468.7	3929.0
EU484334.1	539951	3748.6	2826.9	4733.5	2759.4	1105.8	1591.6
X80411.1	12558	1357.3	725.1	1843.5	2464.2	1068.8	1064.7
AM696983.1	223408	4594.6	3477.1	7060.4	5251.2	1254.8	1541.7
GQ077230.1	416528	8372.7	6148.4	6296.9	8082.6	9791.2	8786.4
AF543286.1	58292	3094.0	3017.7	3962.5	3002.0	1183.0	1521.1
GQ017278.1	492389	4788.2	4329.7	5286.5	5266.8	1362.2	2727.8

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o__Actinomycetales	f__Actinomycetaceae
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AY349363.1 gg_id:92262 human oral cavity clone IO076
EU409526.1 gg_id:275066 Arcanobacterium haemolyticum str. 3801
EU915469.1 gg_id:309072 Arcanobacterium pluranimalium str. 1128
X79224.1 gg_id:12595 Arcanobacterium bernardiae str. LCDC 89/0504 = DSM 9152
EU267795.1 gg_id:253789 Arcanobacterium pyogenes RY 11-3
EU268191.1 gg_id:247375 Arcanobacterium pyogenes HC-H 13-2
EU268193.1 gg_id:257909 Arcanobacterium pyogenes HC-H 10
EF061225.1 gg_id:192142 Arcanobacterium sp. str. NML 06501
EU289136.1 gg_id:239780 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
AJ243794.1 gg_id:25077 Arcanobacterium sp. CCUG 41705
AJ879697.1 gg_id:112481 Arcanobacterium sp. 106-04
AJ576076.1 gg_id:94295 Mobiluncus mulieris str. CCUG 22331
EU289072.1 gg_id:258140 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e
FJ672024.1 gg_id:516662 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
CU914909.1 gg_id:384164 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se
FJ671401.1 gg_id:517932 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF419390.1 gg_id:215248 Substantial alterations cutaneous biota psoriatic lesions human skin clone 4P2-49
FJ672120.1 gg_id:516856 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ671584.1 gg_id:509470 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ675566.1 gg_id:524033 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ671451.1 gg_id:514203 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EU535629.1 gg_id:285786 profile human microbiota antecubital fossa (inner elbow) skin clone nbt28d02
EF063623.1 gg_id:181971 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo
AB062818.1 gg_id:33488 termite gut homogenate clone BCf3-22
NR_026225.1 gg_id:533806 Actinomyces hordeovulneris str. CIP 103149
EF688243.1 gg_id:303554 Detection microbial sludge anaerobic wastewater treatment system clone 6B10_con
AJ508455.1 gg_id:58582 Actinomyces nasicola str. CCUG 46092
AY959048.1 gg_id:131712 Microbes on human vaginal epithelium clone rRNA275
FJ169868.1 gg_id:327484 Varibaculum cambriense str. M398
FJ169869.1 gg_id:328472 Varibaculum cambriense str. M380
DQ923134.1 gg_id:181134 Actinopolyspora xinjiangensis str. YIM 90829
GQ263862.1 gg_id:574018 Structure Simulated Level Waste Site simulated level waste site clone WC2_107
FJ152655.1 gg_id:343126 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_
AY234439.1 gg_id:111971 soil isolate Ellin5022
AB048864.1 gg_id:47825 Actinokineospora sp. str. YU 923-201
AF114799.1 gg_id:12995 Actinokineospora inagensis str. NRRL B-24050T
EU570742.1 gg_id:259282 Actinokineospora terrae str. 173846
GQ166953.1 gg_id:552367 Amycolatopsis fastidiosa str. LCB1001
X84447.1 gg_id:12969 Actinosynnema mirum str. DSM 43827
D85475.1 gg_id:12986 Actinosynnema mirum str. IFO14064
AJ512464.1 gg_id:57769 Kibdelosporangium philippinense str. DSM 44226

AY349363.1	92262	299.8	488.1	567.7	326.1	386.2	365.3
EU409526.1	275066	2818.7	1903.6	2123.5	6255.4	1117.5	1225.6
EU915469.1	309072	1106.4	954.0	3081.7	5234.1	371.7	875.3
X79224.1	12595	54.7	26.7	22.0	236.3	79.5	50.7
EU267795.1	253789	2954.5	3233.5	3591.6	5412.6	5309.3	3468.4
EU268191.1	247375	7199.0	7213.5	6352.1	7425.5	6008.8	6296.8
EU268193.1	257909	1043.7	752.6	1013.7	2119.2	560.4	846.8
EF061225.1	192142	3851.3	3029.1	4575.3	5108.1	3316.7	2729.0
EU289136.1	239780	1688.7	1578.3	4876.1	5807.4	4773.1	3290.0
AJ243794.1	25077	1643.1	1109.0	1054.8	1268.2	1733.8	998.2
AJ879697.1	112481	422.0	291.8	298.5	268.1	294.0	294.3
AJ576076.1	94295	265.9	291.2	268.3	129.1	150.5	168.4
EU289072.1	258140	4677.0	4115.4	8616.5	8267.2	3651.0	6298.9
FJ672024.1	516662	2278.9	41.9	2936.8	1872.7	1063.3	1384.2
CU914909.1	384164	4026.3	3137.4	6117.9	6485.8	1384.2	1691.7
FJ671401.1	517932	9631.7	8851.1	3538.0	6479.6	8678.5	8808.4
EF419390.1	215248	884.0	807.2	502.5	373.2	408.8	222.8
FJ672120.1	516856	6947.7	7292.4	4081.0	5685.3	6461.7	7729.5
FJ671584.1	509470	10589.7	10577.3	7616.2	12955.5	8044.3	7395.2
FJ675566.1	524033	10201.6	7681.8	9323.1	9446.8	7005.2	7957.7
FJ671451.1	514203	8780.7	7575.2	5380.7	8418.1	4811.1	5924.1
EU535629.1	285786	3772.6	3345.6	4820.7	7097.0	1421.7	1345.6
EF063623.1	181971	3333.1	2352.7	2307.8	4648.9	758.0	1168.9
AB062818.1	33488	43.8	39.9	43.7	105.7	65.4	28.8
NR_026225.1	533806	1347.3	1653.3	385.1	808.6	61.4	1994.9
EF688243.1	303554	417.6	489.1	396.1	384.5	172.9	265.2
AJ508455.1	58582	28.5	48.0	52.6	569.5	389.8	51.6
AY959048.1	131712	129.6	144.2	105.5	229.7	93.7	121.2
FJ169868.1	327484	93.3	84.6	64.6	201.3	78.3	87.6
FJ169869.1	328472	178.7	214.9	145.7	298.8	119.0	171.1
DQ923134.1	181134	6149.3	5541.9	6654.6	7545.9	1977.4	3516.7
GQ263862.1	574018	1037.2	1201.1	2373.2	1519.4	1425.1	1142.9
FJ152655.1	343126	4170.4	4049.3	2505.5	6568.9	2603.6	2812.8
AY234439.1	111971	6336.6	4217.9	6010.1	8502.1	1346.6	1322.7
AB048864.1	47825	4459.3	3899.5	4488.2	4174.7	1265.8	1861.7
AF114799.1	12995	5380.8	5542.8	3767.6	7414.6	2974.5	1993.4
EU570742.1	259282	3633.7	2921.8	5092.1	6605.5	2083.5	2931.7
GQ166953.1	552367	4073.9	3046.4	3485.2	3349.9	883.9	2570.8
X84447.1	12969	368.2	636.8	126.4	183.1	634.4	655.8
D85475.1	12986	11654.2	12621.6	8115.3	9855.5	11241.2	10258.6
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AF114801.1 gg_id:12989 Kutzneria kofuensis str. NRRL B-24061T
NR_028760.1 gg_id:578419 Lentzea californiensis str. NRRL B-16137
Y09158.1 gg_id:12966 IMSNU 50711T)
AJ242633.1 gg_id:46572 Lentzea violacea str. LM 036T (=IMSNU 50388T)
X84321.1 gg_id:12965 Lentzea albidocapillata str. IMMIB D-958
AJ242634.1 gg_id:30376 Lentzea violacea str. LM 044
AF183957.4 gg_id:12967 Lentzea flaviverrucosa str. AS4.0578
AF183958.1 gg_id:12968 Lentzea flavoverrucoides
AF114813.1 gg_id:12972 Lentzea waywayandensis str. NRRL B-16159T
EU593719.1 gg_id:267698 Lentzea violacea str. 174493
EU570340.1 gg_id:271073 Lentzea sp. str. 173316
AB020029.1 gg_id:12982 Lentzea waywayandensis str. JCM 9114
AB006176.1 gg_id:12981 Lentzea albida str. IFO16102
AF114815.1 gg_id:12970 Saccharothrix texasensis str. NRRL B-16107T
FJ486317.1 gg_id:567831 Saccharothrix xinjiangensis str. HBUM173796
EU570355.1 gg_id:276163 Saccharothrix texasensis str. 173789
EU593595.1 gg_id:277548 Saccharothrix xinjiangensis str. 173800
AF114803.1 gg_id:12960 Saccharothrix australiensis str. NRRL 11239T
AF114812.1 gg_id:12973 Saccharothrix syringae str. NRRL B-16468T
X53193.1 gg_id:136685 Saccharothrix australiensis
AB284261.2 gg_id:206788 Actinosynnema violaceoruber str. NBRC 102064
GQ917213.1 gg_id:582929 Dactylosporangium variesporum
AY135693.3 gg_id:60437 Saccharothrix xinjiangensis str. AS 4.1731
AF114805.1 gg_id:12963 Saccharothrix coeruleofusca str. NRRL B-16115T
FJ486394.1 gg_id:560514 Saccharothrix espanaensis str. HBUM174894
AF114807.1 gg_id:12959 Saccharothrix espanaensis str. NRRL 15764T
EU841603.1 gg_id:306457 Saccharothrix longispora str. HBUM174878
AF114809.1 gg_id:12975 Saccharothrix longispora str. NRRL B-116116T
EU570357.1 gg_id:265885 Saccharothrix longispora str. 173645
AB297962.1 gg_id:248764 Streptomyces tenebrarius str. NBRC 16177
AF114800.1 gg_id:12978 Actinosynnema subsp. pretiosum str. NRRL B-16060T subsp.
EU841595.1 gg_id:329490 Lechevalieria aerocolonigenes str. HBUM174553
NR_028738.1 gg_id:548297 Lechevalieria aerocolonigenes str. NRRL B-3298
EU593584.1 gg_id:272843 Lechevalieria aerocolonigenes str. 173443
AJ512462.1 gg_id:57772 Kibdelosporangium albatum str. DSM 44149
EU570361.1 gg_id:259817 Lentzea waywayandensis str. 173621
AB020031.1 gg_id:12984 Saccharothrix tangerinus str. MK27-91F2
DQ898283.2 gg_id:161869 Lechevalieria xinjiangensis str. R24
EU570744.1 gg_id:261512 Lentzea albidocapillata str. 173856
AF114808.1 gg_id:12976 Lechevalieria flava str. NRRL B-16131T

DQ298331.1	155487	2480.8	2113.2	4390.4	4093.1	1817.4	2124.6
AF114801.1	12989	1050.8	885.4	735.7	560.8	394.7	829.9
NR_028760.1	578419	16130.1	14541.9	11410.7	14436.8	12039.0	13402.4
Y09158.1	12966	105.6	85.1	133.5	114.8	86.3	64.8
AJ242633.1	46572	354.9	235.3	486.9	383.6	91.4	106.1
X84321.1	12965	357.4	248.5	489.1	371.0	99.8	87.5
AJ242634.1	30376	1755.1	1199.1	931.7	710.9	842.2	408.7
AF183957.4	12967	2153.7	1983.0	3605.3	2613.1	656.6	1057.3
AF183958.1	12968	5062.6	5066.3	4242.4	5857.0	3134.2	3184.7
AF114813.1	12972	5461.6	3959.0	5369.2	2967.0	1392.6	1328.1
EU593719.1	267698	3280.0	2555.1	4150.5	4439.2	990.5	2280.9
EU570340.1	271073	2452.3	1941.8	1802.6	861.9	259.4	330.8
AB020029.1	12982	2756.1	2031.8	2435.8	1497.3	456.6	692.0
AB006176.1	12981	698.9	392.7	515.9	841.5	127.4	331.6
AF114815.1	12970	942.7	950.1	1452.4	619.9	1431.3	1227.2
FJ486317.1	567831	1731.6	1913.4	1764.8	1084.5	384.0	858.7
EU570355.1	276163	1484.1	1121.8	1039.5	1667.0	279.2	506.5
EU593595.1	277548	1859.9	1812.7	2037.4	3314.7	531.2	961.5
AF114803.1	12960	1967.1	1549.7	2668.5	2208.9	832.3	1478.3
AF114812.1	12973	9917.5	8015.4	6566.0	7284.3	9557.6	10283.3
X53193.1	136685	6725.9	3869.5	4818.0	7318.7	706.5	558.6
AB284261.2	206788	1949.2	1660.8	1563.1	2613.5	349.4	605.9
GQ917213.1	582929	363.1	587.7	340.8	278.9	413.8	924.6
AY135693.3	60437	2190.3	2242.1	1992.2	1658.9	1069.6	1225.5
AF114805.1	12963	1667.2	1865.8	1956.4	718.2	973.9	1604.5
FJ486394.1	560514	872.6	925.1	988.1	658.4	601.8	1061.3
AF114807.1	12959	6148.6	4836.5	7578.2	5665.3	2607.5	3538.9
EU841603.1	306457	3039.8	3055.0	3902.7	4938.7	2525.1	2349.5
AF114809.1	12975	2308.8	2058.7	1634.6	2975.7	843.4	763.9
EU570357.1	265885	3923.6	2228.3	2205.6	4414.4	534.9	584.1
AB297962.1	248764	1231.0	1200.2	1251.1	855.9	778.2	854.0
AF114800.1	12978	1844.1	1533.1	1708.9	1655.1	1649.6	1387.8
EU841595.1	329490	1379.9	1050.6	678.4	381.9	197.6	198.3
NR_028738.1	548297	18.3	37.6	36.2	59.6	151.4	87.8
EU593584.1	272843	3590.3	3032.7	3968.7	6641.1	648.7	1948.3
AJ512462.1	57772	5088.8	3758.0	5887.5	6799.3	1890.3	2294.2
EU570361.1	259817	2091.7	1975.3	3419.8	3248.0	779.4	1265.0
AB020031.1	12984	985.9	491.4	512.5	2036.4	182.5	203.2
DQ898283.2	161869	576.3	417.5	977.5	837.9	94.2	202.0
EU570744.1	261512	3529.6	2721.9	4152.8	4164.3	962.4	2253.7
AF114808.1	12976	11496.9	11239.6	3506.5	5789.1	9764.0	7232.5

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s__Brevibacterium casei	40691
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s__Brevibacterium luteolum	40460
s__Brevibacterium otitidis	40327
s__Brevibacterium otitidis	40954
s__Brevibacterium paucivorans	40983
s__Brevibacterium sanguinis	40820
s__Brevibacterium sanguinis	41003
s__unclassified	40146
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s__unclassified	40677

AF183956.1 gg_id:12980 Saccharothrixopsis albidus str. AS4.0423
AF328679.1 gg_id:109082 Actinosynnema mirum str. IMSNU 20048T (IFO 14064T)
DQ291145.1 gg_id:144510 Lentzea kentuckyensis str. NRRL B-24416
AB303365.1 gg_id:225758 Actinosynnema subsp. pretiosum str. NBRC 15621
DQ298327.1 gg_id:151750 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
DQ298350.1 gg_id:152567 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos
EU221376.1 gg_id:244196 Salana multivorans str. Y2S8
NR_027613.1 gg_id:542896 Beutenbergia cavernae str. HKI 0122; DSM 12333
NR_025495.1 gg_id:568991 Salana multivorans str. Se-3111; DSM 13521; NRRL B-24118
EU863843.1 gg_id:338853 Georgenia sp. E9
X94155.2 gg_id:73976 Georgenia muralis str. 1A-C
EU095256.1 gg_id:241541 Georgenia ferrireducens str. F64
AY880044.1 gg_id:111575 Georgenia sp. T04-04
FJ671468.1 gg_id:521907 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ203185.1 gg_id:139651 Ruania flava str. YIM 004
EF601725.1 gg_id:232214 Georgenia deserti str. YIM 80691
FJ671531.1 gg_id:511138 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ670794.1 gg_id:515169 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
FJ672173.1 gg_id:509013 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
Y09911.1 gg_id:12542 Bogoriella caseolytica str. HKI0088T
AB211980.2 gg_id:148397 Brevibacterium linens
AY243343.1 gg_id:107500 Brevibacterium permense str. VKM Ac-2280
AM937247.2 gg_id:276481 oligotrophic riverine carrying -cassette capturing genetic devices their genome river
X83813.1 gg_id:12522 Brevibacterium iodinum str. DSM 2062T
GU143785.1 gg_id:573804 Brevibacterium casei str. SV2
EU086802.1 gg_id:236962 Brevibacterium casei str. 60
GQ221248.1 gg_id:541292 Brevibacterium casei str. SRKP2
AJ488509.2 gg_id:73538 Brevibacterium luteolum str. CF87
AB210987.2 gg_id:145220 Brevibacterium luteolum str. SSCS1-2
D88212.1 gg_id:12518 Brevibacterium sp
EU086822.1 gg_id:251743 Brevibacterium otitidis str. G696
NR_025375.1 gg_id:554922 Brevibacterium paucivorans str. CF 62; DSM 13657
AY468365.1 gg_id:99934 Brevibacterium casei str. FM1A
AB288106.1 gg_id:178942 Brevibacterium sanguinis I-16
FJ672800.1 gg_id:522372 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
DQ344485.1 gg_id:172245 Brevibacterium samyangensis str. SST-8
FJ675524.1 gg_id:529096 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF459545.1 gg_id:204447 Brevibacterium antiquum KFC-74
EF035139.1 gg_id:176058 Brevibacterium sp. str. MT5-11
DQ223419.1 gg_id:140760 Brevibacterium sp. LB12
GQ040457.1 gg_id:430434 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw954g

AF183956.1	12980	110.6	160.5	339.8	1032.6	75.7	157.7
AF328679.1	109082	550.0	543.9	529.9	547.1	241.6	260.4
DQ291145.1	144510	376.4	534.5	713.3	256.2	316.9	225.6
AB303365.1	225758	1117.1	1057.9	648.9	318.9	813.3	931.0
DQ298327.1	151750	101.7	138.6	177.5	299.9	96.9	71.7
DQ298350.1	152567	146.4	144.1	82.2	422.3	135.4	133.9
EU221376.1	244196	27.8	30.4	28.3	46.0	72.2	16.7
NR_027613.1	542896	5595.4	4886.0	6437.7	8381.4	1703.0	2111.2
NR_025495.1	568991	4468.5	3490.6	4822.5	6588.9	942.7	1211.5
EU863843.1	338853	1429.4	984.5	1621.4	1200.9	524.2	770.1
X94155.2	73976	1173.0	1302.0	2440.9	2007.0	1170.2	1957.5
EU095256.1	241541	549.3	332.1	986.4	1123.4	228.1	565.0
AY880044.1	111575	106.1	270.8	275.1	168.1	166.5	287.6
FJ671468.1	521907	1249.9	1309.3	1013.1	2711.2	266.9	337.0
DQ203185.1	139651	126.7	74.0	192.1	831.5	90.1	67.5
EF601725.1	232214	3701.2	3065.4	6044.9	7790.8	690.6	2222.9
FJ671531.1	511138	2465.1	3754.0	2674.9	5145.2	1705.1	2598.4
FJ670794.1	515169	641.9	773.9	1166.0	2216.7	764.3	808.5
FJ672173.1	509013	5307.4	4191.8	4372.0	6403.3	2296.6	3914.7
Y09911.1	12542	172.8	116.3	113.9	810.2	71.5	83.3
AB211980.2	148397	5242.0	3411.0	3071.8	4245.6	2176.3	1392.9
AY243343.1	107500	11791.1	10097.2	11110.1	13405.5	11255.0	10126.6
AM937247.2	276481	4794.4	3400.8	2799.4	5650.7	3663.3	2546.9
X83813.1	12522	2742.5	1543.7	1978.7	4189.6	227.8	585.2
GU143785.1	573804	7100.7	6100.8	3589.6	9105.2	1582.8	2138.8
EU086802.1	236962	10070.3	8010.9	8305.9	13266.8	5894.3	7595.2
GQ221248.1	541292	2612.7	1620.1	2138.7	7315.5	1136.2	1357.1
AJ488509.2	73538	401.2	274.9	304.8	530.1	133.6	351.3
AB210987.2	145220	12346.6	14772.0	10073.4	10366.4	13176.4	10673.9
D88212.1	12518	1540.0	1052.6	5776.2	6114.9	806.3	683.7
EU086822.1	251743	3496.2	3734.9	3180.2	3565.3	738.3	1171.0
NR_025375.1	554922	2666.9	923.3	226.8	3444.1	144.7	246.3
AY468365.1	99934	14541.2	11418.3	8806.8	14772.0	2858.6	2903.3
AB288106.1	178942	7278.8	4997.4	6494.0	11952.3	3164.4	4789.1
FJ672800.1	522372	5300.6	3242.2	4357.4	7633.5	756.7	1793.8
DQ344485.1	172245	1176.6	951.6	913.2	2847.3	246.5	1019.6
FJ675524.1	529096	7515.4	7071.1	5204.2	7340.0	6903.4	6046.2
EF459545.1	204447	9620.8	7579.4	7848.8	14681.0	3535.0	4927.0
EF035139.1	176058	4020.3	3274.5	2502.6	6801.4	1486.8	1429.6
DQ223419.1	140760	8130.7	7941.2	4659.5	10903.5	4666.3	6507.6
GQ040457.1	430434	2800.8	3389.8	1955.6	3569.1	166.5	818.3

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o__Actinomycetales	f__Brevibacteriaceae
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s__Tropheryma whipplei	38988
s__Tropheryma whipplei	39490

EU099382.1 gg_id:258101 Brevibacterium sp. str. SC9
X76567.1 gg_id:12520 Brevibacterium iodinum str. NCDO 613
FJ670694.1 gg_id:516893 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
X77451.1 gg_id:12521 Brevibacterium linens str. DSM 20425
FJ674759.1 gg_id:529325 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
EF419416.1 gg_id:206826 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6PN34
AM421807.1 gg_id:216329 Brevibacterium mariniaquaticum str. HFW-26
DQ361016.1 gg_id:146469 Brevibacterium linens str. 1MF
EU868814.1 gg_id:592745 Brevibacterium sp. str. 5401308
AB327249.1 gg_id:254761 Catenulispora subtropica str. TT 01-19 (= NBRC 103396)
EF451662.1 gg_id:217192 Cellulomonas sp. str. KAR32
EF063610.1 gg_id:177558 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo
AJ229245.1 gg_id:12346 Actinobacteria str. VeCb6
X79458.1 gg_id:12343 Cellulomonas fermentans str. DSM 3133
AJ863164.1 gg_id:159316 Cellulomonas bogoriensis str. 69B4
AY554419.1 gg_id:104027 Cellulomonas sp. 9A1
AY655726.1 gg_id:105859 Cellulomonas denverensis str. W6124
FJ200381.1 gg_id:315369 Cellulomonas hominis str. 3089BRRJ
EU373531.1 gg_id:564028 Cellulomonas hominis str. FR1_148_P
AY655731.1 gg_id:101233 Cellulomonas parahominis str. W7336
AB259960.1 gg_id:159820 Cellulomonas uda
NR_029095.1 gg_id:556569 Cellulomonas xylanilytica str. XIL11; LMG 21723
X79463.1 gg_id:12315 Cellulomonas flavigena str. NCIMB 8073
EU834248.1 gg_id:350859 Cellulomonas denverensis str. DS21
AB268586.1 gg_id:173567 Cellulomonas chitinilytica str. X.bu-b
AF064702.1 gg_id:12319 Cellulomonas iranensis str. O
X79462.1 gg_id:12331 Cellulomonas biazotea str. DSM 20112
NR_024913.1 gg_id:535428 Cellulomonas persica str. I; ATCC 700642
AF282627.1 gg_id:47463 Cellulomonas gelida
AJ245568.1 gg_id:12332 Cellulomonas sp. str. GM13
AJ292035.1 gg_id:61987 Cellulomonas sp. str. d6
X83799.1 gg_id:12323 Cellulomonas flavigena str. DSM 20109T
EF688360.1 gg_id:235695 soil clone F4-169
AM902253.3 gg_id:326434 Cellulomonas sp. str. KB23
AB166884.1 gg_id:104614 Cellulomonas gelida str. T5-10
EU050924.1 gg_id:252063 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_15
EU697083.1 gg_id:289962 Cellulomonas sp. str. F11
AB471560.1 gg_id:534681 Demequina sp. str. KV-811
AJ314849.1 gg_id:54867 Oerskovia jenensis str. DSM 46001
AF251035.1 gg_id:39437 Tropheryma whipplei Twist str. twist
AF190688.1 gg_id:25685 Tropheryma whipplei

EU099382.1	258101	3940.0	3503.8	2413.8	4449.4	1644.1	1775.0
X76567.1	12520	3939.4	3406.4	3841.6	6444.3	1951.9	2559.4
FJ670694.1	516893	3567.4	2571.2	1748.2	5017.0	414.2	388.6
X77451.1	12521	8116.2	8690.0	8451.5	9818.8	7554.3	7561.5
FJ674759.1	529325	9874.1	7765.3	5376.0	8374.7	3305.9	3436.5
EF419416.1	206826	9660.7	7106.0	9608.4	9844.3	3702.9	6748.7
AM421807.1	216329	2723.3	2904.0	2899.5	4350.3	1669.3	2867.9
DQ361016.1	146469	10637.0	7976.0	8599.3	15871.6	2982.0	4632.2
EU868814.1	592745	8245.4	6401.3	9138.4	11386.3	5189.5	6307.7
AB327249.1	254761	17.4	27.4	19.6	50.9	53.9	17.4
EF451662.1	217192	502.3	450.1	411.2	1907.6	122.5	141.2
EF063610.1	177558	2561.0	2010.0	6374.3	5516.2	1146.0	1501.9
AJ229245.1	12346	1631.0	1405.1	1313.9	2315.2	270.7	480.7
X79458.1	12343	4001.8	3107.4	8001.4	9371.9	281.7	406.6
AJ863164.1	159316	1183.9	928.9	4492.5	2965.0	480.3	360.1
AY554419.1	104027	849.9	743.7	1214.1	1964.1	220.6	266.0
AY655726.1	105859	1232.8	1105.8	2655.0	5725.9	384.9	641.9
FJ200381.1	315369	2658.3	1898.7	4709.6	5997.3	456.1	512.8
EU373531.1	564028	2720.8	1880.7	5004.0	5963.1	458.5	412.3
AY655731.1	101233	1564.1	967.4	3646.4	6831.8	258.3	297.6
AB259960.1	159820	3784.7	3328.2	4793.2	6562.3	1976.3	2162.6
NR_029095.1	556569	2566.4	3712.4	3286.0	1942.8	2591.8	2148.2
X79463.1	12315	2798.2	2726.3	3326.6	3201.5	624.3	1065.0
EU834248.1	350859	2259.8	1615.9	3637.5	3397.8	443.9	357.4
AB268586.1	173567	2044.5	709.7	1274.2	8896.6	169.6	176.8
AF064702.1	12319	1869.5	1164.4	4199.3	5388.2	494.4	543.5
X79462.1	12331	270.9	416.9	1110.9	310.3	224.9	249.4
NR_024913.1	535428	603.5	367.4	954.2	2803.9	139.1	143.0
AF282627.1	47463	812.2	610.7	2576.3	4570.0	178.3	434.2
AJ245568.1	12332	250.1	262.3	849.5	356.1	75.5	210.3
AJ292035.1	61987	1678.8	1338.2	4384.8	3870.9	660.7	585.5
X83799.1	12323	6086.2	6406.7	3789.6	7330.1	6989.6	7527.9
EF688360.1	235695	4597.4	3843.9	4716.3	9493.3	2367.2	2769.9
AM902253.3	326434	1157.0	995.4	1938.7	3180.8	749.3	1186.2
AB166884.1	104614	9779.5	8170.0	12980.1	11711.1	4885.1	4394.5
EU050924.1	252063	2352.4	2538.5	875.5	3261.6	419.5	695.8
EU697083.1	289962	11610.6	8240.7	11280.6	15692.3	2598.2	2714.5
AB471560.1	534681	28.2	40.8	135.7	56.7	69.2	32.6
AJ314849.1	54867	1738.0	1144.0	1895.5	2850.4	325.8	522.7
AF251035.1	39437	4673.9	3524.5	6816.3	7151.4	3082.9	3962.4
AF190688.1	25685	1802.4	1083.3	4217.4	7228.8	670.4	539.5

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AY250865.1 gg_id:83082 lichen-dominated Antarctic cryptoendolithic community clone FBP218
GU205277.1 gg_id:525009 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
GQ502471.1 gg_id:571864 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf1-
DQ366005.1 gg_id:151679 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone
EU132492.1 gg_id:246070 tallgrass prarie soil clone FFCH14477
EU276542.1 gg_id:366196 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c
AY250882.1 gg_id:86523 lichen-dominated Antarctic cryptoendolithic community clone FBP406
CU920319.1 gg_id:575392 Towards definition core microorganisms involved digestion mesophilic anaerobic dig
GQ088433.1 gg_id:373239 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw:
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AB491284.1 gg_id:514224 Tomitella biformata str. AHU 1820
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AM697139.1 gg_id:218761 sequencing libraries indoor dust clone BF0002B089
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EF157260.1 gg_id:247211 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
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EU289493.1 gg_id:253651 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched
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AY534743.1 gg_id:99194 Millisia brevis str. J82
AY250883.1 gg_id:83514 lichen-dominated Antarctic cryptoendolithic community clone FBP417
EF127613.1 gg_id:213535 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE090
AB288888.1 gg_id:201506 termite gut homogenate clone BOf2-16
DQ125551.1 gg_id:130787 uranium contaminated soil clone AKAU3527
EU104204.1 gg_id:331234 Evidence Comamonadaceae determinants settling performance activated sludge clo
EF471701.1 gg_id:267662 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
AJ867924.1 gg_id:142681 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone D3
EU803916.1 gg_id:346841 It's all ranking aquatic Lake Gatun clone 5C231574

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EU132492.1	246070	1988.1	958.4	2293.2	4717.8	250.5	403.3
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CU920319.1	575392	10284.6	10718.3	5039.5	10420.8	6329.3	7279.0
GQ088433.1	373239	4266.3	3610.7	5936.1	8473.5	619.9	856.1
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GQ088228.1	390260	661.3	8586.5	6942.0	7791.1	563.0	6335.0
AB234237.1	148806	15.6	17.9	30.2	45.7	62.7	25.5
AY534743.1	99194	3297.4	2377.2	1836.2	5419.4	1279.5	2302.1
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CR933228.1 gg_id:110305 Evry municipal wastewater treatment plant clone 054C09_B_DI_P58
FJ769434.1 gg_id:568643 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana
GQ017242.1 gg_id:492424 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu116
DQ015810.1 gg_id:139725 Antarctic lake water clone ELB16-113
GQ340357.1 gg_id:553793 Prokaryotic Marathonas Reservoir Greece water column clone VE08-149-BAC
GQ111879.1 gg_id:451456 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
DQ347943.1 gg_id:200646 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi
AF227165.1 gg_id:111731 Propioniferax innocua str. ATCC49929
AY566575.1 gg_id:108722 sp. str. PG-02
FJ916097.1 gg_id:586357 Evidence structuring organic carbon source temperate lakes integrated lake epilimnic
AM980985.1 gg_id:311573 Ponticoccus gilvus str. MSW-19
GQ340189.1 gg_id:548357 Prokaryotic Marathonas Reservoir Greece water column clone K07-85-BAC
DQ520173.1 gg_id:160626 shal China sequences hypertrophic freshwater lake clone ML-7-10.2
DQ316366.2 gg_id:156400 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater
EF125420.1 gg_id:193229 soil naked tidal flat sediment near mangrove clone MSB-1F9
EU812989.1 gg_id:305551 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M
EU801210.1 gg_id:318920 It's all ranking aquatic Chesapeake Bay MD clone 3C002457
FJ479550.1 gg_id:550173 species richness estimates obtained nearly and simulated pyrosequencing-generated
FJ937869.1 gg_id:467626 Marine Sponge Gelliodes carnosa coastal waters Lingshui Bay Hainan Island South Ch
GQ357647.1 gg_id:575785 Streptomyces sp. str. YIM 75704
GU227180.1 gg_id:592605 Microbiological immunological Adolescent Moroccan Aggressive Periodontitis Patier
AB198453.1 gg_id:135406 termite gut wall fraction clone RsW01-014
AJ576385.1 gg_id:104294 midgut homogenate Pachnoda ephippiata larva clone PeM15
GQ850574.1 gg_id:557602 bottom water northern Bering Sea clone d118
AY948059.1 gg_id:142745 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl
EU907900.1 gg_id:323949 Identification hexahydro-135-trinitro-135-triazine (RDX)-degrading microorganisms v
FJ542902.1 gg_id:525816 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A
EF520362.1 gg_id:234186 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-65
FM874965.1 gg_id:359343 occupant source house dust skin surface swab clone SB01D12
AY566577.1 gg_id:108724 Eubacterium sp. str. PG-04
EF471698.1 gg_id:277468 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay
GU305824.1 gg_id:556516 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res
AF513101.1 gg_id:65420 activated sludge foam clone 7
GQ340111.1 gg_id:586558 Prokaryotic Marathonas Reservoir Greece water column clone B07-05-BAC
EU930868.1 gg_id:315328 Jannaschia sp. str. psc3
DQ062659.1 gg_id:133829 Kribbia dieselivorans str. R33
EU467938.1 gg_id:296510 cheetah feces clone CE2_e12
EF157137.1 gg_id:254649 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon
EU179735.1 gg_id:263649 Cellulosimicrobium sp. str. HY-12
X83804.1 gg_id:12330 Cellulomonas cellasea str. DSM 20118T
EF451632.1 gg_id:208675 Cellulomonas sp. str. KAR2

CR933228.1	110305	6150.9	5399.6	5213.5	7150.3	2876.4	4024.4
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GQ017242.1	492424	1497.3	1719.4	887.0	759.4	727.5	459.2
DQ015810.1	139725	9743.9	8259.3	6361.8	9256.5	972.2	2346.9
GQ340357.1	553793	8727.2	7712.9	6626.6	8138.4	4582.5	6129.7
GQ111879.1	451456	1864.9	1454.2	3921.0	3439.5	544.9	1126.3
DQ347943.1	200646	29.0	46.1	64.6	52.4	54.1	37.1
AF227165.1	111731	3380.0	2363.1	2518.6	3337.2	1589.6	1583.8
AY566575.1	108722	724.9	464.2	840.5	4155.6	226.2	231.4
FJ916097.1	586357	13319.3	10442.7	7023.4	10511.8	4584.9	4544.7
AM980985.1	311573	661.4	543.9	234.6	146.4	104.7	116.5
GQ340189.1	548357	4586.4	3304.3	3028.8	4125.3	1192.9	1660.6
DQ520173.1	160626	134.3	102.3	44.6	109.5	95.0	47.3
DQ316366.2	156400	2576.2	1874.9	4150.6	7072.8	931.5	2461.7
EF125420.1	193229	2042.7	1280.1	748.8	1227.1	106.3	117.6
EU812989.1	305551	3473.3	2667.0	2505.3	4911.1	534.1	1080.2
EU801210.1	318920	2927.4	2426.1	1946.1	3406.0	1380.7	1948.7
FJ479550.1	550173	3104.7	2429.5	3543.9	4610.9	722.6	943.3
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GQ357647.1	575785	9431.9	7451.0	4661.7	13179.1	5704.7	5350.1
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FJ542902.1	525816	2248.1	1604.5	1142.9	1632.3	192.0	236.5
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GU305824.1	556516	6451.8	5517.3	2636.8	8382.7	2693.9	3623.0
AF513101.1	65420	7156.0	6413.4	4023.3	6073.8	1461.7	1698.8
GQ340111.1	586558	6235.9	5620.8	6274.6	6359.6	2569.4	3139.2
EU930868.1	315328	219.0	117.9	1250.2	1335.5	85.0	46.7
DQ062659.1	133829	4297.1	2198.3	9192.7	11979.3	514.1	628.5
EU467938.1	296510	557.4	348.7	646.2	2780.6	122.8	216.3
EF157137.1	254649	5140.1	3729.9	3471.8	8413.2	345.0	1188.8
EU179735.1	263649	521.9	449.0	1899.6	2908.8	163.2	239.6
X83804.1	12330	1928.9	1288.6	2271.6	6978.4	517.6	775.4
EF451632.1	208675	59.4	71.0	47.8	538.5	82.5	43.5

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s__Corynebacterium diphtheriae	37211

FM955877.1 gg_id:593259 Cellulomonas sp. str. Asd M7A1
FJ971722.1 gg_id:429838 microbial autrotrophic denitrification granular sludge clone E-B7
EF688154.1 gg_id:326817 Detection microbial sludge anaerobic wastewater treatment system clone 1F4_cons
DQ223670.1 gg_id:161011 Cellulomonas sp. zf-IIRht4
FN397670.1 gg_id:386689 Arsenicicoccus sp. str. AMV4
FJ230840.1 gg_id:338568 Oerskovia sp. str. SB3
EU560979.1 gg_id:259886 Cellulomonas sp. str. 5420S-23
EU644102.1 gg_id:280631 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_
FJ005066.1 gg_id:344364 Cellulomonas sp. str. RCML-44
NR_028904.1 gg_id:575780 Dermatophilus chelonae str. W16; DSM 44178
DQ521505.1 gg_id:193536 Antarctic lake ice cover clone ANTLV2_A07
GQ094386.1 gg_id:381291 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
AF527583.1 gg_id:62967 EBPR sludge lab scale clone LPB21
EF451634.1 gg_id:215481 Cellulomonas sp. str. KAR4
DQ303278.1 gg_id:141216 Microbial ecology macroscopic filaments extreme Tinto River acidic river clone fc3
AB193570.1 gg_id:108280 Actinomadura sp. str. Shinshu-MS-03
EF019023.1 gg_id:203722 aspen rhizosphere clone Amb_16S_1562
DQ985164.1 gg_id:194841 Actinomadura alba str. YIM 45681
EU133137.1 gg_id:250813 tallgrass prarie soil clone FFCH598
EU335334.1 gg_id:246169 Changes microbial metabolic and along hydrogeochemically variable profile unsatura
AY234546.1 gg_id:111386 soil isolate Ellin5129
EU861937.1 gg_id:334140 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin
GQ263304.1 gg_id:511050 Structure Simulated Level Waste Site simulated level waste site clone FW1_a52
AF498716.1 gg_id:72811 soil isolate Ellin334
Y07606.2 gg_id:12061 Drentse grassland soil clone DA016
EU038018.1 gg_id:251707 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc
GU205304.1 gg_id:525863 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal
GQ001448.1 gg_id:508215 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173b04
GQ014722.1 gg_id:494944 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw763c
GQ002396.1 gg_id:507265 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176h09
AY230773.1 gg_id:83313 Corynebacterium sp. 'Smarlab BioMol-2301292' str. Smarlab BioMol 2301292 'Smarlal
AF537589.1 gg_id:69384 Corynebacterium argentoratense National Microbiology Laboratory Special identifier
X83955.1 gg_id:13418 Corynebacterium argentoratense str. CIP 104296
AM990811.1 gg_id:278095 Corynebacterium sp. MOLA 35
Y13777.2 gg_id:13372 Corynebacterium auriscanis str. M135/96/2
AF311390.1 gg_id:37493 Corynebacterium bovis str. 33
AF311389.1 gg_id:23997 Corynebacterium bovis str. 32
AF311415.1 gg_id:33060 Corynebacterium bovis str. 115
Y15887.1 gg_id:13500 Corynebacterium confusum str. DMMZ 3259
X82058.1 gg_id:13421 Corynebacterium cystitidis str. CIP 103424T
AF145257.1 gg_id:13348 Corynebacterium xerosis str. 71376

FM955877.1	593259	3047.8	2649.8	4329.3	2626.5	534.5	653.3
FJ971722.1	429838	6833.1	5511.8	7013.8	8362.7	4399.0	4875.7
EF688154.1	326817	3963.1	2902.3	7152.2	6438.8	1199.6	1854.9
DQ223670.1	161011	2157.9	1707.6	1473.5	4446.8	890.0	1391.5
FN397670.1	386689	1883.2	1411.5	2295.3	3554.1	566.4	1189.3
FJ230840.1	338568	3342.1	2625.5	1672.1	3439.0	414.7	756.2
EU560979.1	259886	2541.0	1642.7	4788.2	4319.3	381.9	335.8
EU644102.1	280631	6962.9	4991.8	7580.8	14734.0	1702.7	3086.4
FJ005066.1	344364	5022.3	3655.2	3535.6	5674.7	263.0	301.9
NR_028904.1	575780	944.2	764.6	828.0	4101.2	728.1	913.2
DQ521505.1	193536	1034.1	933.5	1289.1	2125.3	170.8	197.8
GQ094386.1	381291	928.8	1013.8	1752.3	1121.2	1588.6	1091.3
AF527583.1	62967	6023.4	4955.8	2226.8	5917.8	389.5	1089.2
EF451634.1	215481	1377.0	525.8	1738.2	4152.8	473.3	135.7
DQ303278.1	141216	1081.3	501.8	1979.0	2518.7	140.2	203.8
AB193570.1	108280	1883.8	1131.1	2765.8	6165.1	397.1	790.1
EF019023.1	203722	1610.6	2107.1	1041.1	1519.2	686.3	1513.5
DQ985164.1	194841	2274.9	2224.7	3257.1	5357.3	729.4	1531.2
EU133137.1	250813	5379.4	4123.0	6566.4	4770.2	2158.6	1337.3
EU335334.1	246169	5094.9	5337.8	2990.5	7959.7	1311.1	2333.4
AY234546.1	111386	4251.0	2682.6	5086.7	7493.3	1021.1	1190.8
EU861937.1	334140	1452.8	1467.0	987.7	2524.9	314.9	269.0
GQ263304.1	511050	4664.1	5400.7	2065.2	6908.4	5455.9	5201.6
AF498716.1	72811	2449.9	2575.3	2562.1	1959.9	1724.2	1973.6
Y07606.2	12061	66.3	77.7	86.1	129.4	116.5	66.3
EU038018.1	251707	5717.0	5327.7	4247.7	6216.6	8296.7	9243.6
GU205304.1	525863	1923.8	1750.9	3680.1	2438.3	1472.6	1376.8
GQ001448.1	508215	2942.6	3423.2	612.4	5528.0	1057.7	1506.4
GQ014722.1	494944	3784.1	3131.6	3266.8	4024.3	2479.4	3621.2
GQ002396.1	507265	1911.6	1698.3	2685.2	3774.9	679.9	1322.6
AY230773.1	83313	3883.6	2255.9	1780.9	6066.4	823.9	1524.7
AF537589.1	69384	1504.5	697.3	1289.2	3190.0	161.8	534.7
X83955.1	13418	447.6	455.8	1945.2	1068.7	166.5	269.6
AM990811.1	278095	5004.4	3772.4	3039.3	4630.3	1752.0	2240.7
Y13777.2	13372	841.8	944.5	1853.3	3541.2	440.5	1042.8
AF311390.1	37493	1112.1	786.9	476.7	1645.3	1113.7	985.7
AF311389.1	23997	70.6	158.2	150.0	132.9	140.7	105.9
AF311415.1	33060	3685.2	2540.8	927.8	4603.0	4298.1	4193.2
Y15887.1	13500	292.0	345.1	87.9	596.5	1153.9	479.2
X82058.1	13421	41.8	61.7	34.4	90.5	78.3	43.6
AF145257.1	13348	2610.0	2121.0	5068.9	3685.9	462.1	2040.6

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s__Corynebacterium matruchotii	36965
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s__Corynebacterium pseudogenitalium	28928
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s__Corynebacterium urealyticum	37117

BX248360.1 gg_id:136033 Corynebacterium diphtheriae str. NCTC13129
AF543285.1 gg_id:58295 Corynebacterium durum str. ChDC OS33
BA000035.2 gg_id:107869 Corynebacterium efficiens str. YS-314
X84441.1 gg_id:13463 Corynebacterium flavescens str. NCDO 1320
AJ292762.1 gg_id:73485 Corynebacterium freneyi str. 20695110
FM213375.1 gg_id:335388 Corynebacterium xerosis str. St51377/1
AJ292763.1 gg_id:37739 Corynebacterium freneyi str. 20395347
FN179322.1 gg_id:565070 Corynebacterium xerosis str. St53244
FN179328.1 gg_id:536505 Corynebacterium xerosis str. St47126
EF462413.1 gg_id:250643 Corynebacterium freneyi 3526
X86688.1 gg_id:13425 Corynebacterium glucuronolyticum str. GF 838 (=DSM 44120)
CR931997.1 gg_id:137456 Corynebacterium jeikeium str. K411 = NCTC 11915
AY524774.1 gg_id:105080 Corynebacterium kroppenstedtii VA1719_2000
EU540561.1 gg_id:285399 profile human microbiota antecubital fossa (inner elbow) skin clone nbt119g01
NR_026370.1 gg_id:550368 Corynebacterium lipophiloflavum str. DMMZ 1944; CCUG 37336; DSM 44291
FM173121.1 gg_id:351541 Corynebacterium sp. str. KSS-10Se
FM173119.1 gg_id:304633 Corynebacterium sp. str. KSS-3Se
AB354691.1 gg_id:244209 Corynebacterium macginleyi str. EC009
AB359408.1 gg_id:255771 Corynebacterium mastitidis str. TBS-19
ACEB01000045.1 gg_id:548125 Corynebacterium matruchotii str. ATCC 33806
X84246.1 gg_id:13467 Corynebacterium pilosum str. NCTC 11862
GQ051353.1 gg_id:389984 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ026272.1 gg_id:414000 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ051205.1 gg_id:412681 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ047349.1 gg_id:377112 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu5(
X81911.1 gg_id:13397 Corynebacterium diphtheriae str. CCUG 2708
X84255.1 gg_id:13414 Corynebacterium pseudotuberculosis str. NCTC 3450
GQ118343.1 gg_id:445441 Corynebacterium ulcerans str. CD074; NCTC 12077
D37806.1 gg_id:70082 Corynebacterium renale str. HR59
GQ009105.1 gg_id:500560 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw827c0:
GQ030945.1 gg_id:417964 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ031548.1 gg_id:395038 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ030984.1 gg_id:449470 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ031648.1 gg_id:452484 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ028326.1 gg_id:378263 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ065486.1 gg_id:392448 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
FJ671806.1 gg_id:512806 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I
AJ438043.1 gg_id:85890 Corynebacterium tuberculostearicum str. CIP102622
GQ034989.1 gg_id:426313 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu330e11
GQ015980.1 gg_id:493683 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
NR_027597.1 gg_id:543063 Corynebacterium urealyticum 7109 str. DSM 7109; ATCC 43042

BX248360.1	136033	439.9	489.4	1276.4	516.3	245.6	578.6
AF543285.1	58295	84.0	87.8	80.3	191.7	92.5	78.2
BA000035.2	107869	482.0	399.8	714.4	570.4	529.5	361.0
X84441.1	13463	7746.7	5893.4	6839.7	9251.1	2486.1	3804.6
AJ292762.1	73485	1039.0	946.0	988.7	2119.4	530.0	1328.9
FM213375.1	335388	17016.9	17385.7	8476.2	12771.0	13665.3	11285.7
AJ292763.1	37739	552.9	980.2	1470.4	827.2	528.0	1317.5
FN179322.1	565070	22290.3	21086.5	12700.8	18217.7	20577.0	18090.1
FN179328.1	536505	3524.6	2418.5	3294.2	5449.4	670.2	1997.5
EF462413.1	250643	5217.0	3188.8	2291.0	6592.0	1549.5	4032.2
X86688.1	13425	961.3	723.7	837.5	1097.9	340.1	435.2
CR931997.1	137456	289.5	458.9	1051.5	1714.3	184.8	282.4
AY524774.1	105080	309.1	534.0	99.7	162.7	292.9	872.9
EU540561.1	285399	5450.5	5298.7	5670.0	5067.7	3441.4	3432.3
NR_026370.1	550368	1395.9	1259.3	911.7	2397.8	689.8	1431.2
FM173121.1	351541	3900.1	3483.5	3505.0	5760.2	3809.0	3033.6
FM173119.1	304633	3695.4	3314.2	3384.9	5484.2	3774.5	3038.6
AB354691.1	244209	1714.1	1956.5	2402.4	2669.9	2242.6	2154.6
AB359408.1	255771	534.1	874.2	986.6	1047.5	1158.3	1823.1
ACEB01000045.1	548125	169.3	177.0	406.7	306.4	250.5	94.4
X84246.1	13467	28.7	64.1	52.7	59.3	84.0	82.1
GQ051353.1	389984	2621.9	1687.6	5732.5	5784.2	637.3	2258.9
GQ026272.1	414000	23701.6	26489.4	13413.2	22425.1	25031.2	21136.8
GQ051205.1	412681	1954.1	2129.3	922.3	3190.2	946.4	832.0
GQ047349.1	377112	5660.4	4082.0	7361.8	13068.7	2691.9	3413.7
X81911.1	13397	181.6	136.1	90.0	503.3	139.3	116.6
X84255.1	13414	184.3	136.8	288.4	510.9	106.8	64.0
GQ118343.1	445441	190.1	135.7	91.9	524.7	118.9	68.4
D37806.1	70082	1082.7	1127.1	509.0	1723.8	662.9	1342.9
GQ009105.1	500560	192.3	220.9	195.8	254.4	207.2	347.1
GQ030945.1	417964	14543.0	13200.6	17923.6	14948.4	12632.5	12880.1
GQ031548.1	395038	5758.6	6072.3	3787.7	6967.8	4598.8	3954.5
GQ030984.1	449470	10929.6	13039.8	5618.7	8351.7	7736.4	7115.9
GQ031648.1	452484	465.2	457.6	2013.8	758.1	326.0	274.2
GQ028326.1	378263	988.1	738.3	1152.5	3540.7	739.5	654.7
GQ065486.1	392448	2083.4	1110.6	1504.1	3632.8	1386.8	1084.4
FJ671806.1	512806	4622.7	3109.7	3814.1	5082.5	1629.6	2658.4
AJ438043.1	85890	1012.2	1094.2	980.6	1473.2	607.9	1653.6
GQ034989.1	426313	1918.6	1619.2	1276.7	2600.6	711.7	1868.1
GQ015980.1	493683	1012.2	1094.2	980.6	1473.2	607.9	1653.6
NR_027597.1	543063	325.0	597.8	269.2	367.1	615.9	713.4

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AJ222816.1 gg_id:13387 Corynebacterium variabile str. DSM 20536
AY730711.1 gg_id:106078 Corynebacterium variabile str. 120804KB5
GQ070700.1 gg_id:420001 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ080454.1 gg_id:425988 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw113
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GQ110679.1 gg_id:429430 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ092505.1 gg_id:375996 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ029097.1 gg_id:441124 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
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GQ034944.1 gg_id:383236 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu329h08
GQ074780.1 gg_id:457016 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ062647.1 gg_id:462695 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ029018.1 gg_id:395610 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
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GQ112809.1 gg_id:386007 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588e05c1
GQ005142.1 gg_id:504520 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ005156.1 gg_id:504507 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ041775.1 gg_id:373458 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932d1
GQ097241.1 gg_id:407663 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ024276.1 gg_id:485394 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ031279.1 gg_id:455759 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
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GQ050842.1 gg_id:459757 Topographical and Temporal Human Skin Microbiome skin nare clone nbu439f11c1
GQ028533.1 gg_id:409185 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ016032.1 gg_id:493634 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ003777.1 gg_id:505883 Topographical and Temporal Human Skin Microbiome skin nare clone nbu57b10c1
GQ051358.1 gg_id:407108 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ028496.1 gg_id:416489 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ050873.1 gg_id:441175 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440c01c1
GQ066205.1 gg_id:404066 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ048273.1 gg_id:454240 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ096870.1 gg_id:381920 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw

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FM874948.1	358896	7904.0	8362.9	4680.8	8055.1	8308.4	9475.5
GQ110679.1	429430	15626.5	17556.1	12319.1	15284.6	11246.5	13006.0
GQ092505.1	375996	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ029097.1	441124	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ112689.1	374732	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ050235.1	411917	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ029974.1	407125	24016.5	22737.9	13775.6	12199.8	10732.5	17395.9
GQ032817.1	446381	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ036404.1	386016	2513.9	2569.0	418.6	2115.5	4582.7	4381.5
GQ034944.1	383236	12689.2	12885.4	5622.4	8517.2	5932.2	4971.9
GQ074780.1	457016	7542.6	7351.7	3415.3	9443.1	11331.7	17288.7
GQ062647.1	462695	8851.9	9038.8	3347.2	3618.3	287.5	558.3
GQ029018.1	395610	3223.1	2180.6	2221.8	7319.9	573.1	1347.1
GQ043639.1	422186	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ112809.1	386007	31517.9	32436.8	31197.0	25777.4	31765.6	27214.6
GQ005142.1	504520	4487.1	7163.4	8483.8	6846.3	5365.1	7239.6
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GQ097241.1	407663	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
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GQ050873.1	441175	5876.8	4818.4	2410.4	10705.6	789.5	1306.1
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GQ066381.1 gg_id:465291 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ050910.1 gg_id:452547 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440g09c1
GQ051181.1 gg_id:417376 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ051224.1 gg_id:373300 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ026668.1 gg_id:463122 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ031968.1 gg_id:381810 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ030372.1 gg_id:378294 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw877c02c
GQ018064.1 gg_id:491604 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ031122.1 gg_id:440896 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ058985.1 gg_id:456381 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu58
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GQ028460.1 gg_id:422202 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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FM873604.1 gg_id:357969 occupant source house mattress dust clone MA01C10
GQ052453.1 gg_id:466125 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu536d02
GQ036445.1 gg_id:435496 Topographical and Temporal Human Skin Microbiome skin palm clone nbu364f02c1
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GQ028139.1 gg_id:386868 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ017865.1 gg_id:491805 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ047866.1 gg_id:418352 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
FM875252.1 gg_id:364849 occupant source house dust skin surface swab clone SB04F12
GQ009903.1 gg_id:499762 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

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GQ066381.1	465291	7254.1	6314.5	6367.5	10782.4	5866.2	7026.5
GQ050910.1	452547	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ051181.1	417376	4656.6	3681.6	6452.2	8412.5	2301.7	4135.1
GQ051224.1	373300	5414.4	4497.5	6893.6	8903.1	3163.5	4896.0
GQ026668.1	463122	25743.2	25042.9	9247.1	22436.6	27104.8	22128.2
GQ031968.1	381810	9486.7	14221.6	5605.5	10877.3	3006.2	2982.2
GQ030372.1	378294	1349.5	1898.4	2313.5	939.3	4728.2	5513.6
GQ018064.1	491604	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ031122.1	440896	5912.4	4536.7	6448.2	4119.3	4330.5	12691.3
GQ058985.1	456381	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ036556.1	426266	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ028460.1	422202	3521.4	4184.4	5924.9	3394.7	5821.8	5549.5
GQ094998.1	396373	28434.6	27715.6	16101.1	22968.2	27633.9	24393.9
GQ062520.1	433801	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ034360.1	407242	1021.8	1702.3	1029.7	1831.6	1165.9	510.5
GQ028278.1	441424	12305.3	10003.2	4544.0	11296.5	13291.8	11912.6
GQ017772.1	491895	11339.0	7063.4	17080.9	16192.4	7012.9	7877.9
GQ028572.1	452964	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ066383.1	373044	23770.4	21733.0	24148.8	21992.3	18749.4	18916.8
GQ000175.1	468740	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ041976.1	371862	3829.0	3342.5	6865.6	14194.4	2002.1	4202.9
GQ058975.1	393022	253.3	460.6	1005.5	555.4	461.0	497.7
GQ054074.1	374853	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ010157.1	499508	15935.5	17479.6	4945.3	14981.1	9488.5	9027.4
GQ058199.1	426101	2303.5	1770.1	1233.4	3001.5	532.6	925.3
GQ065423.1	394303	23215.7	24570.1	17739.9	18583.9	19704.2	17595.9
GQ100248.1	442841	18693.4	19305.4	7927.3	12442.2	9982.6	7661.6
GQ032709.1	422683	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ110859.1	466299	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ034447.1	421250	12400.9	10740.7	6650.5	10859.1	1852.9	3130.6
GQ092352.1	399738	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
FM873604.1	357969	578.2	611.4	752.4	835.3	436.6	1066.2
GQ052453.1	466125	18992.5	20999.6	8841.0	17027.9	16550.5	8890.4
GQ036445.1	435496	26252.5	26377.8	18121.8	23009.5	25358.6	22662.1
GQ054303.1	426934	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ028139.1	386868	23245.9	23063.3	15871.1	18898.9	18327.7	18896.7
GQ017865.1	491805	1685.2	1152.7	488.2	738.1	813.8	722.8
GQ047866.1	418352	8871.8	8806.2	7911.7	13909.8	14061.4	15036.9
FM875252.1	364849	578.2	611.4	752.4	835.3	436.6	1066.2
GQ009903.1	499762	9767.0	10753.3	5657.3	13837.2	9623.9	10966.3

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GQ062877.1 gg_id:408403 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw37
GQ048825.1 gg_id:427150 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5
GQ036564.1 gg_id:393296 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ025318.1 gg_id:382338 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ030502.1 gg_id:402175 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw879b08c
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GQ111246.1 gg_id:453125 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ041028.1 gg_id:454279 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ077342.1 gg_id:371064 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ046232.1 gg_id:382502 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ037791.1	400005	669.4	442.7	1607.2	580.0	460.4	328.6
GQ008864.1	500801	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ010123.1	499541	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ035291.1	462754	977.8	733.8	1458.8	623.2	608.2	595.7
GQ074177.1	410677	14614.5	11665.0	16420.4	15401.6	10314.1	12691.3
GQ075724.1	445323	113.4	132.1	173.5	118.0	496.3	167.1
GQ062877.1	408403	22588.9	23658.1	17959.3	17306.6	23436.6	19744.3
GQ048825.1	427150	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ036564.1	393296	326.0	511.0	193.0	610.6	652.1	1530.8
GQ025318.1	382338	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ030502.1	402175	11035.4	8216.6	2445.7	16325.4	13099.5	12188.3
GQ049115.1	416900	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ017746.1	491921	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ111246.1	453125	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ028523.1	444182	431.5	614.6	69.1	263.6	905.9	2290.4
GQ043616.1	439877	1530.0	1268.0	836.1	5219.5	917.7	2020.0
GQ051191.1	386387	21958.2	19969.2	24709.9	20073.5	18708.2	18462.6
GQ035069.1	456310	9798.3	8027.6	4157.1	9938.0	12381.5	11924.2
GQ041028.1	454279	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ077342.1	371064	10900.9	10928.0	4745.3	11668.4	8033.8	7428.9
GQ064790.1	384307	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ111586.1	426885	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ044138.1	381684	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
GQ046964.1	434196	24704.2	26626.3	14173.5	20669.7	22091.7	19926.1
GQ009880.1	499786	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ034704.1	381737	15673.6	13558.2	13876.6	17885.1	13776.9	14478.1
GQ037060.1	392398	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ061964.1	405989	16191.0	15299.5	7481.3	16312.4	7551.3	10271.3
GQ028542.1	385209	17492.3	17419.6	7325.2	17389.3	11401.5	10656.3
GQ028475.1	415765	21339.5	22006.5	8416.8	12492.2	10346.0	7754.1
GQ049393.1	383373	4101.2	2628.4	1131.7	7382.7	6134.4	7352.3
GQ022157.1	487511	11103.4	11272.4	7176.3	10639.7	11120.6	8151.1
GQ041848.1	396472	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ019977.1	489689	18075.8	17955.9	10058.3	17198.8	11958.6	13181.1
GQ046232.1	382502	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ050539.1	378947	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ100082.1	402004	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ053410.1	386136	18847.9	19654.8	5354.7	12970.7	8122.8	6901.1
GQ016635.1	493032	15009.2	17899.5	9162.7	13562.2	8166.0	7917.0
GQ051849.1	380776	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2

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GQ028628.1 gg_id:418550 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ059739.1 gg_id:391563 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw4C
GQ054998.1 gg_id:423058 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ036749.1 gg_id:435900 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ048122.1 gg_id:412895 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu45
GQ053725.1 gg_id:383823 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ010132.1 gg_id:499533 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ028569.1 gg_id:380375 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ002452.1 gg_id:507210 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ034554.1 gg_id:453571 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ005214.1 gg_id:504449 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ048846.1 gg_id:439849 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5
GQ062726.1 gg_id:400298 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ036679.1 gg_id:393363 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ044833.1 gg_id:438571 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ009165.1 gg_id:500500 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ031602.1 gg_id:383077 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ005086.1 gg_id:504576 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ112645.1 gg_id:451012 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586a05c1
GQ062029.1 gg_id:467668 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw27b1
GQ062823.1 gg_id:413115 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ032821.1 gg_id:387359 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw918f05
GQ010098.1 gg_id:499567 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ041297.1 gg_id:442835 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ055961.1 gg_id:391023 Topographical and Temporal Human Skin Microbiome skin nare clone nbw1041e08c
GQ036609.1 gg_id:380834 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ041178.1 gg_id:423065 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ028433.1 gg_id:415985 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ010929.1 gg_id:498737 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ005029.1 gg_id:504633 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ111159.1 gg_id:396566 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ064342.1 gg_id:375206 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ027623.1 gg_id:402796 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ061318.1 gg_id:431018 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ049294.1 gg_id:420621 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ047490.1 gg_id:406747 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ078731.1 gg_id:385297 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ041299.1 gg_id:465471 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

GQ022930.1	486739	585.8	1002.2	673.0	956.6	1147.9	2176.0
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GQ028628.1	418550	17342.1	10928.1	7118.5	15591.9	11317.2	10824.8
GQ059739.1	391563	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ054998.1	423058	18108.7	18506.3	8693.7	17736.1	13812.0	12180.9
GQ036749.1	435900	8130.6	11406.4	10885.5	12068.4	12114.9	14392.0
GQ048122.1	412895	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
GQ053725.1	383823	22610.3	21667.9	6614.9	17468.7	21687.7	18138.5
GQ010132.1	499533	25697.3	26770.6	14149.7	22388.6	25219.0	22837.1
GQ028569.1	380375	10850.6	8729.6	9637.9	12636.1	5247.3	5806.2
GQ028631.1	419423	8357.2	7671.2	7034.2	8831.7	9682.8	9538.9
GQ002452.1	507210	9460.3	12962.8	7767.2	12881.6	19976.2	14573.0
GQ034554.1	453571	14669.3	16845.3	5165.0	14575.4	7731.3	9167.9
GQ005214.1	504449	4101.2	2628.4	1131.7	7382.7	6134.4	7352.3
GQ048846.1	439849	6021.6	5641.1	2972.3	6077.6	8364.8	8540.5
GQ062726.1	400298	25196.7	26651.2	13210.0	18968.1	21796.6	19964.5
GQ036679.1	393363	13694.0	17487.7	7551.6	12343.1	7013.2	6688.9
GQ044833.1	438571	15006.7	19005.7	7484.7	14376.8	14422.6	8981.1
GQ009165.1	500500	26512.6	27117.6	20870.7	21732.5	27113.8	25157.1
GQ031602.1	383077	15989.4	17463.5	15188.5	15449.4	18646.7	16545.4
GQ005086.1	504576	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ112645.1	451012	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
GQ062029.1	467668	1003.2	728.7	2437.0	1623.4	1108.2	1050.6
GQ062823.1	413115	10535.1	9234.4	8851.3	9215.0	10913.2	9561.7
GQ032821.1	387359	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ010098.1	499567	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ041297.1	442835	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ055961.1	391023	26488.4	27101.6	19048.7	21848.2	26480.6	23036.8
GQ036609.1	380834	18693.4	19305.4	7927.3	12442.2	9982.6	7661.6
GQ041178.1	423065	5718.3	6618.7	3771.2	4613.8	1662.5	1945.4
GQ028433.1	415985	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ010929.1	498737	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ005029.1	504633	12266.2	12980.5	6642.4	11258.2	10427.6	11181.2
GQ111159.1	396566	17695.4	17961.3	6889.9	13937.2	9478.1	8879.4
GQ064342.1	375206	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ027623.1	402796	13665.6	13144.6	7739.8	9392.4	9264.8	7880.0
GQ061318.1	431018	23583.5	23974.0	17902.6	18613.5	21921.4	21910.1
GQ049294.1	420621	3806.8	2974.5	596.0	4371.6	3060.0	8390.7
GQ047490.1	406747	12777.0	13585.0	10434.9	16203.5	17818.5	22690.2
GQ078731.1	385297	21958.2	19969.2	24709.9	20073.5	18708.2	18462.6
GQ041299.1	465471	24016.5	22737.9	13775.6	12199.8	20832.0	17395.9

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GQ036624.1 gg_id:374044 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ030727.1 gg_id:450573 Topographical and Temporal Human Skin Microbiome skin palm clone nbw882a07c1
GQ075690.1 gg_id:395779 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ036747.1 gg_id:411958 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ028151.1 gg_id:396295 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ040038.1 gg_id:408025 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw94
GQ112705.1 gg_id:435153 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586g09c1
GQ044146.1 gg_id:394509 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1019f0
GQ010183.1 gg_id:499482 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ087123.1 gg_id:419186 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ034410.1 gg_id:415703 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ034620.1 gg_id:433613 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ031281.1 gg_id:391594 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ036482.1 gg_id:421760 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ041871.1 gg_id:380357 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw933
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GQ034418.1 gg_id:436064 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ049896.1 gg_id:385699 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu431f11
AM696955.1 gg_id:222496 sequencing libraries indoor dust clone BF0002A140
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GQ052458.1 gg_id:458427 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu536d1
GQ030680.1 gg_id:464838 Topographical and Temporal Human Skin Microbiome skin palm clone nbw881d04c
GQ019211.1 gg_id:490457 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
FM875174.1 gg_id:368582 occupant source house dust skin surface swab clone SB03H01
GQ075679.1 gg_id:441004 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ038291.1 gg_id:449335 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ088006.1 gg_id:411579 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ036576.1 gg_id:375448 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ062523.1 gg_id:440428 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ046169.1 gg_id:394299 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ027569.1 gg_id:448735 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

GQ019378.1	490290	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ036624.1	374044	18520.0	24733.3	9197.7	17100.0	14041.7	12501.5
GQ030727.1	450573	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ075690.1	395779	10597.4	9939.4	11632.3	12684.9	11463.8	13111.6
GQ036747.1	411958	27270.5	26309.9	19082.5	20813.6	20404.0	18812.3
GQ028151.1	396295	19046.7	18395.0	9907.9	17593.8	12713.1	13891.3
GQ040038.1	408025	122.9	285.0	26.0	0.6	206.6	344.6
GQ112705.1	435153	15525.4	13742.1	12720.6	20876.8	10216.3	10312.5
GQ044146.1	394509	12517.6	17241.0	2215.1	8593.5	5803.3	4914.0
GQ010183.1	499482	4220.6	2684.8	5031.5	3265.6	234.0	908.6
GQ087123.1	419186	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ034410.1	415703	7004.4	11202.0	4068.3	10274.2	710.0	1449.8
GQ034620.1	433613	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031281.1	391594	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036482.1	421760	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ041871.1	380357	22558.2	24598.8	15208.8	15948.0	17338.8	13171.7
GQ043493.1	411016	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ031564.1	453600	19206.2	18635.0	8428.1	18241.7	13653.3	15363.7
GQ062608.1	436672	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ045687.1	433619	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ053479.1	422744	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ034418.1	436064	10463.1	5986.1	14943.6	13482.1	26281.9	9325.8
GQ049896.1	385699	11617.7	16329.0	13362.0	12422.6	14859.3	11147.3
AM696955.1	222496	578.2	611.4	752.4	835.3	436.6	1066.2
GQ004538.1	505125	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ052458.1	458427	1982.6	1493.9	1050.4	2968.2	457.6	875.4
GQ030680.1	464838	27913.4	25346.0	20319.6	23112.0	19623.2	15776.7
GQ019211.1	490457	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
FM875174.1	368582	578.2	611.4	752.4	835.3	436.6	1066.2
GQ075679.1	441004	14918.1	13197.6	11331.7	17234.6	9943.0	11521.8
GQ038291.1	449335	7545.1	8697.1	3640.3	7486.2	4067.6	4668.8
GQ088006.1	411579	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ036576.1	375448	28196.2	27930.7	21535.3	22830.0	28754.8	25047.9
GQ062523.1	440428	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ046169.1	394299	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ069593.1	412994	15259.2	12847.9	7415.9	18282.0	13356.1	18163.4
GQ071683.1	378896	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ017802.1	491866	21339.5	22006.5	8416.8	12492.2	10346.0	7754.1
GQ029980.1	396355	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
GQ029387.1	464508	121.5	308.8	308.3	138.5	100.7	269.5
GQ027569.1	448735	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8

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GQ048404.1	379822	9797.3	13653.2	6976.3	8113.3	9267.7	8395.0
GQ109679.1	450724	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ041655.1	384377	720.9	1369.7	421.8	326.2	974.2	3439.0
GQ050838.1	447382	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ027325.1	406207	2075.2	2052.7	456.3	1523.0	4696.2	3415.0
GQ028871.1	452656	12305.3	10003.2	4544.0	11296.5	13291.8	11912.6
GQ025564.1	454321	24796.7	23902.3	16649.9	21186.8	22036.3	20646.5
GQ052324.1	410846	14669.3	16845.3	5165.0	14575.4	7731.3	9167.9
GQ050896.1	402089	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ054165.1	422715	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ097117.1	398613	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ056769.1	463025	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ112719.1	420213	2498.5	2006.1	496.2	5422.0	699.5	1150.3
GQ029073.1	395010	790.7	929.8	779.2	1483.0	1113.1	1336.3
GQ059766.1	409251	10582.4	9129.6	9071.4	10009.3	5441.6	6153.0
GQ010101.1	499564	24156.7	24513.0	10521.8	19703.2	24015.9	20458.4
GQ040686.1	451841	13340.7	19766.8	4225.5	16816.1	6637.6	5814.8
GQ039605.1	409615	13823.9	13418.9	8727.8	9708.3	14562.6	10640.0
GQ016585.1	493082	4429.2	4450.5	2354.5	9923.9	4169.1	3426.7
GQ046268.1	374659	3323.2	3716.9	3200.4	6200.1	2851.8	5678.3
GQ075673.1	459131	14806.1	17722.8	3549.8	6540.8	6014.3	3896.8
GQ071749.1	458634	14620.1	15480.9	10263.2	12881.3	8665.8	8675.8
GQ051380.1	429869	5084.1	5275.1	7539.6	9091.8	5443.5	7517.8
GQ100219.1	373561	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ028629.1	435014	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ038792.1	395447	3601.3	5722.1	8483.8	4969.7	4637.5	5761.7
GQ097561.1	422678	18620.4	21411.6	6638.3	12556.4	7034.5	9090.7
GQ062678.1	427488	18757.3	16017.6	17625.0	18139.2	12698.4	13988.4
GQ034611.1	442870	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
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GQ100293.1	448691	9680.7	11237.2	9346.2	9205.4	5497.2	6041.6
GQ112496.1	385922	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
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GQ030086.1 gg_id:378064 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866h1
GQ041064.1 gg_id:452051 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ005284.1 gg_id:504379 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ075302.1 gg_id:434677 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ101436.1 gg_id:436745 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495a
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GQ027954.1 gg_id:461541 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

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GQ036471.1	423300	19443.9	18435.1	14963.4	18599.2	16662.3	18154.9
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GQ028506.1	402408	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ100171.1	416866	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ071644.1	391025	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ112826.1	378234	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
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GQ069970.1	422013	14299.2	9041.3	17312.3	18241.3	7991.0	9780.4
GQ080142.1	437414	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ062531.1	380515	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ028469.1	449920	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ057634.1	401281	15128.0	19933.9	7692.5	14270.0	16450.3	8788.8
GQ059708.1	464622	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ051246.1	405835	21135.1	16795.0	5242.1	15948.2	11828.4	10198.1
GQ010193.1	499473	26550.3	26439.8	23935.3	23430.1	25847.1	24100.1
GQ085887.1	433806	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031535.1	422540	3743.9	5405.7	9898.5	7810.7	11634.5	16134.6
GQ030086.1	378064	25998.7	27193.8	17897.2	21942.4	26164.4	24240.8
GQ041064.1	452051	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ005284.1	504379	12723.4	13270.8	12283.3	15723.7	14956.3	15730.2
GQ061587.1	418962	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ075302.1	434677	63.4	128.6	42.2	118.5	87.7	111.1
GQ101436.1	436745	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ056842.1	444232	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ032793.1	402786	8892.3	9505.0	8337.5	8798.2	9376.9	11307.6
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GQ017548.1	492119	9460.3	12962.8	7767.2	12881.6	19976.2	14573.0
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GQ026550.1 gg_id:443345 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ077393.1 gg_id:380762 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ062003.1 gg_id:390936 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw26h0
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GQ075279.1 gg_id:429666 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ057432.1 gg_id:415439 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc

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GQ026550.1	443345	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ077393.1	380762	1982.6	1493.9	1050.4	2968.2	457.6	875.4
GQ062003.1	390936	23693.7	21730.6	8617.4	15461.4	12802.2	11245.0
GQ050648.1	455263	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ031589.1	384057	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ075279.1	429666	12323.7	11572.9	9299.8	7465.3	10745.2	8893.5
GQ112170.1	418310	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ051371.1	426567	3071.2	1974.0	6190.8	6849.1	728.8	2644.9
GQ052454.1	425521	4943.1	4182.3	2308.9	7580.5	1329.7	1768.2
GQ041041.1	450593	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ043472.1	455156	26987.8	26014.6	26882.8	22684.8	26972.8	24902.0
GQ075732.1	430459	242.9	247.7	7558.6	420.7	124.5	94.8
GQ005080.1	504583	11758.3	11267.9	4611.3	10647.6	7345.7	9777.5
GQ100298.1	411718	187.0	160.3	124.3	224.3	263.9	215.0
GQ036765.1	406994	12852.9	10109.1	9705.2	17436.0	5266.1	9639.9
GQ071635.1	420821	4280.5	4358.5	1406.5	3902.3	6810.9	5984.5
GQ061358.1	402176	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ059833.1	393704	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ003899.1	505762	21013.5	21947.0	12751.7	16157.2	16507.3	14239.1
GQ069993.1	441966	12489.8	12731.5	8617.8	9802.2	10993.0	10232.0
GQ028978.1	414868	27114.6	29358.9	17409.3	21110.0	28532.3	24488.0
GQ028939.1	386641	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ026501.1	440350	1219.5	1259.1	1758.7	2569.6	505.5	967.2
GQ064734.1	428399	2543.4	1558.2	4825.5	3452.0	1375.7	2757.0
GQ112726.1	373392	26396.6	26561.8	15509.1	22013.0	28269.5	23229.2
GQ088727.1	459759	3705.0	2211.9	2045.3	5699.9	2535.1	8941.2
GQ005234.1	504429	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ062357.1	450784	6744.1	4849.0	5701.4	7102.3	4296.4	4323.9
GQ027211.1	442702	24015.6	23668.5	22703.9	19792.6	19280.4	18358.4
GQ047102.1	409651	18748.3	19295.6	13382.7	15114.1	17210.8	12443.3
GQ072324.1	399169	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ031835.1	417337	30841.2	29648.7	21659.3	23016.3	29765.3	26158.2
GQ028499.1	465434	19971.7	19075.4	10410.3	19438.3	11779.8	10897.5
GQ053387.1	428011	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ028754.1	447719	4236.6	3227.7	576.5	6548.1	4970.9	3450.7
GQ048745.1	409748	1939.0	1827.4	1778.4	3659.9	379.7	790.6
GQ094740.1	432317	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ031656.1	418110	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
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GQ030709.1 gg_id:389003 Topographical and Temporal Human Skin Microbiome skin palm clone nbw881g05c1
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GQ044015.1 gg_id:457912 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017h(
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GQ039762.1 gg_id:435146 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu428c06
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GQ028344.1 gg_id:375054 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ050866.1 gg_id:376977 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440b01c1
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GQ056353.1 gg_id:407051 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ013221.1 gg_id:496445 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw8
GQ061551.1 gg_id:453508 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw22
GQ059401.1 gg_id:439539 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw1
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GQ096846.1	392265	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ030709.1	389003	14614.5	11665.0	16420.4	15401.6	10314.1	12691.3
GQ051207.1	433103	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ005047.1	504615	5064.1	2997.6	1151.3	8774.6	6889.9	7031.5
GQ055491.1	416360	25991.9	25330.4	16491.7	21986.8	25899.1	21420.6
GQ047864.1	374286	2335.9	1379.0	1861.6	6610.9	1557.2	1316.0
GQ044015.1	457912	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ087706.1	410916	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ039762.1	435146	22103.6	11466.9	11679.5	21222.2	3417.5	12063.4
GQ017701.1	491963	3694.3	2591.2	3886.2	7679.8	238.3	761.6
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GQ043650.1	461789	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ010041.1	499624	6429.8	4708.5	5471.0	7102.3	3766.5	3806.7
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GQ065728.1	417620	1579.8	2555.9	329.4	468.4	1658.1	6897.3
GQ041140.1	422189	15259.2	12847.9	7415.9	18282.0	13356.1	18163.4
GQ073762.1	383590	15280.4	15564.5	13480.2	13072.4	11257.8	9776.3
GQ071814.1	454390	16399.4	20633.3	8625.3	16434.8	13113.7	13520.0
GQ039707.1	422671	5282.4	4362.5	6339.0	7995.3	762.8	2477.0
GQ057074.1	408191	23315.1	23394.5	11158.8	15470.1	11662.5	8586.5
GQ074132.1	383918	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ050866.1	376977	11903.8	11851.1	4660.3	10013.6	8526.7	7794.9
GQ064455.1	390603	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
GQ028427.1	447121	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ077406.1	467332	720.9	1369.7	421.8	326.2	974.2	3439.0
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GQ037107.1	390130	25194.2	25764.4	16897.1	22382.5	25355.3	23184.2
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GQ028554.1	375016	9256.7	11610.6	4206.2	9658.1	13933.1	9753.8
GQ031207.1	443238	298.7	636.4	304.7	1148.3	1777.6	6220.2
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o__Actinomycetales	f__Corynebacteriaceae
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o__Actinomycetales	f__Corynebacteriaceae

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GQ039616.1 gg_id:418086 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu425c01
GQ000323.1 gg_id:468888 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
GQ006451.1 gg_id:503213 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu8
GQ100307.1 gg_id:420995 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480d11c1
GQ031543.1 gg_id:380575 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ050870.1 gg_id:450986 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440b07c1
GQ028557.1 gg_id:442534 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ039767.1 gg_id:423332 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu428e01
GQ009909.1 gg_id:499757 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ062527.1 gg_id:384484 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ035113.1 gg_id:457730 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu332c08
GQ061844.1 gg_id:374201 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw25bC
FM875152.1 gg_id:358584 occupant source house dust skin surface swab clone SB03E11
GQ048744.1 gg_id:449288 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5
GQ010529.1 gg_id:499136 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ049382.1 gg_id:427387 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ071534.1 gg_id:446888 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ066073.1 gg_id:413854 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ022549.1 gg_id:487119 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ013866.1 gg_id:495800 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ064277.1 gg_id:448126 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6
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GQ053741.1 gg_id:408697 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ028950.1 gg_id:447458 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ025551.1 gg_id:389567 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ061025.1 gg_id:398556 Topographical and Temporal Human Skin Microbiome skin nare clone nbw09c10c1
GQ030874.1 gg_id:462922 Topographical and Temporal Human Skin Microbiome skin palm clone nbw884a11c1
GQ027232.1 gg_id:393977 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ036464.1 gg_id:441048 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ050872.1 gg_id:467816 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440b10c1
GQ078757.1 gg_id:428563 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

FM875273.1	368847	578.2	611.4	752.4	835.3	436.6	1066.2
GQ039616.1	418086	4755.4	6059.3	1952.6	4413.0	1599.6	2750.7
GQ000323.1	468888	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ006451.1	503213	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
GQ100307.1	420995	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031543.1	380575	20682.6	26198.5	16419.0	18081.6	10469.7	12355.4
GQ050870.1	450986	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ028557.1	442534	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ039767.1	423332	3075.5	1898.4	6768.8	6451.2	750.4	2654.6
GQ009909.1	499757	25196.7	26651.2	13210.0	18968.1	21796.6	19964.5
GQ028448.1	404059	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ062527.1	384484	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ035113.1	457730	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ061844.1	374201	10251.7	10297.7	8070.6	13179.9	13983.7	20732.9
FM875152.1	358584	1058.0	882.0	929.5	1346.6	432.2	1100.7
GQ048744.1	449288	10021.8	9130.7	2793.0	9281.4	10450.0	8470.3
GQ010529.1	499136	13747.3	11466.6	12720.6	15741.3	10277.0	10342.8
GQ049382.1	427387	12221.9	12078.1	7205.5	16235.4	9972.4	11433.9
GQ020196.1	489473	2619.1	3448.4	2368.2	4581.0	3338.8	2910.3
GQ080144.1	456563	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ071480.1	465295	13403.4	16620.1	6066.3	12087.6	6416.0	6211.1
GQ071534.1	446888	9585.1	10942.4	12971.9	11215.1	8849.1	9559.3
GQ033827.1	389165	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ071685.1	387970	1398.1	2571.7	1137.6	4063.2	861.3	481.4
GQ013883.1	495783	3560.5	2496.5	843.5	6201.8	4811.7	4871.9
GQ066073.1	413854	7437.7	6646.0	3839.6	6967.3	8920.2	8285.6
GQ022549.1	487119	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ013866.1	495800	64.6	93.5	49.8	55.9	115.9	414.2
GQ064277.1	448126	24580.9	26225.2	12583.2	21301.5	25022.8	21415.3
GQ075197.1	402172	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ048163.1	459928	30053.8	28692.0	15528.8	22565.2	30194.0	25507.8
GQ053741.1	408697	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ062641.1	445509	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ028950.1	447458	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ025551.1	389567	18058.0	20017.1	18189.0	19561.8	15366.0	18349.3
GQ061025.1	398556	11072.0	10952.9	9537.0	15140.7	14333.6	13753.8
GQ030874.1	462922	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ027232.1	393977	5632.6	14818.0	5166.9	6273.7	1528.3	2806.3
GQ036464.1	441048	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ050872.1	467816	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ078757.1	428563	8423.9	8819.7	1700.4	3237.3	3605.9	2125.6

k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
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o__Actinomycetales	f__Corynebacteriaceae
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GQ075167.1 gg_id:429577 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ030124.1 gg_id:384090 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw867e0
GQ016072.1 gg_id:493594 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ031715.1 gg_id:435327 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ026844.1 gg_id:435893 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ002404.1 gg_id:507257 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ022452.1 gg_id:487217 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ085996.1 gg_id:378560 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ036396.1 gg_id:386809 Topographical and Temporal Human Skin Microbiome skin palm clone nbu363h08c1
GQ036214.1 gg_id:399889 Topographical and Temporal Human Skin Microbiome skin palm clone nbu361e08c1
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GQ036607.1 gg_id:392193 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ069944.1 gg_id:429392 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw243f07
GQ054339.1 gg_id:458861 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108
GQ059851.1 gg_id:461676 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ011061.1 gg_id:498605 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ050908.1 gg_id:436452 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440g07c1
GQ036475.1 gg_id:402083 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ025586.1 gg_id:465626 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ000238.1 gg_id:468803 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
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GQ020232.1 gg_id:489436 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu265h1(
GQ054718.1 gg_id:408610 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1100e
GQ054143.1 gg_id:380986 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099b
GQ041133.1 gg_id:439272 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ030898.1 gg_id:446065 Topographical and Temporal Human Skin Microbiome skin palm clone nbw884d04c
GQ046892.1 gg_id:437523 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ002424.1 gg_id:507238 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ038348.1 gg_id:464993 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ094695.1 gg_id:403334 Topographical and Temporal Human Skin Microbiome skin nare clone nbw373f11c1
GQ115513.1 gg_id:415922 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686g03
GQ022104.1 gg_id:487564 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3
GQ055017.1 gg_id:407258 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ112690.1 gg_id:433574 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586f02c1

GQ036135.1	458614	17342.1	10928.1	7118.5	15591.9	11317.2	10824.8
GQ075167.1	429577	20716.0	20480.0	12166.3	18837.8	15926.0	14190.2
GQ030124.1	384090	2966.6	2348.0	4556.5	7496.6	2231.7	4115.4
GQ016072.1	493594	3150.5	3277.5	1410.8	1145.2	393.5	650.4
GQ031715.1	435327	157.0	181.6	154.2	113.9	70.0	188.6
GQ026844.1	435893	5027.4	4160.1	7378.5	11272.9	11908.9	10286.4
GQ002404.1	507257	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ022452.1	487217	6960.2	6296.6	5041.9	11700.3	4913.9	8689.9
GQ085996.1	378560	9509.9	10160.6	2721.2	8842.4	5537.0	7930.4
GQ036396.1	386809	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036214.1	399889	11370.8	11393.1	4391.9	4893.4	5907.6	4519.7
GQ028440.1	434869	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ021663.1	488005	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ036607.1	392193	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ069944.1	429392	13474.1	16110.1	12319.7	16023.3	10858.2	13824.3
GQ054339.1	458861	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ059851.1	461676	22609.1	23023.2	14195.7	19227.8	22943.8	20175.8
GQ011061.1	498605	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ050908.1	436452	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ036475.1	402083	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ028838.1	420777	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ025586.1	465626	13890.7	12494.9	16273.7	15455.7	10606.8	12301.6
GQ000238.1	468803	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ062714.1	397652	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ017754.1	491914	10283.7	11060.7	1814.1	14160.9	5186.2	4752.3
GQ080100.1	412378	2376.9	2216.9	4041.6	3198.6	1058.0	3230.2
GQ026676.1	439156	22424.3	22345.2	17662.4	20282.0	22886.6	22435.7
GQ029183.1	461337	4487.1	7163.4	8483.8	6846.3	5365.1	7239.6
GQ020232.1	489436	15987.7	16500.0	11097.2	16321.6	18242.0	21024.5
GQ054718.1	408610	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ054143.1	380986	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ041133.1	439272	17342.1	10928.1	7118.5	15591.9	11317.2	10824.8
GQ030898.1	446065	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
GQ046892.1	437523	8229.5	5153.6	8617.4	14733.0	2390.1	3954.9
GQ002424.1	507238	10866.3	9313.7	4011.9	11983.9	5249.9	4730.1
GQ038348.1	464993	9458.2	9726.2	15189.0	9692.6	14422.3	9984.3
GQ094695.1	403334	9125.4	8293.2	4400.3	13736.2	10841.8	13855.5
GQ115513.1	415922	15259.2	12847.9	7415.9	18282.0	13356.1	18163.4
GQ022104.1	487564	26633.3	29329.8	15060.5	22013.5	27071.1	22938.2
GQ055017.1	407258	12517.6	17241.0	2215.1	8593.5	5803.3	4914.0
GQ112690.1	433574	26373.7	27484.3	22182.3	21917.9	26287.4	24253.2

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GQ090666.1 gg_id:450429 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ036468.1 gg_id:427056 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ054337.1 gg_id:407900 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108
GQ116037.1 gg_id:439170 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6
GQ092491.1 gg_id:462275 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ004455.1 gg_id:505207 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ002405.1 gg_id:507258 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ020369.1 gg_id:489299 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu268c09
GQ049285.1 gg_id:433658 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu472h07
GQ100336.1 gg_id:427655 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480g11c1
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GQ031381.1 gg_id:450481 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873a
GQ022457.1 gg_id:487212 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ009952.1 gg_id:499713 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ031702.1 gg_id:453228 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
FM875163.1 gg_id:367677 occupant source house dust skin surface swab clone SB03F10
GQ032133.1 gg_id:422396 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ010176.1 gg_id:499489 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ062794.1 gg_id:432266 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ046161.1 gg_id:410787 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ061859.1 gg_id:452750 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw25c1
GQ036306.1 gg_id:389322 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362f02c1
GQ026874.1 gg_id:432435 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ028220.1 gg_id:449461 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ098572.1 gg_id:421180 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw703g
GQ028696.1 gg_id:408691 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw919a0
GQ030671.1 gg_id:423965 Topographical and Temporal Human Skin Microbiome skin palm clone nbw881c06c1
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GQ100148.1 gg_id:413846 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478e03c1
GQ001634.1 gg_id:508027 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu175d11
GQ071785.1 gg_id:446281 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
FM872783.1 gg_id:356906 occupant source house floor dust clone FB01H08
GQ048653.1 gg_id:404258 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ044783.1 gg_id:446123 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ028621.1 gg_id:429563 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ036611.1 gg_id:407731 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ056107.1 gg_id:454308 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ044018.1 gg_id:406432 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017h(
GQ036703.1 gg_id:442425 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ005228.1 gg_id:504435 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu

GQ046487.1	382036	5588.3	6907.7	9854.3	6198.4	3784.7	3445.0
GQ090666.1	450429	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ036468.1	427056	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ054337.1	407900	3874.6	4740.5	1700.3	6739.1	2671.4	3288.1
GQ116037.1	439170	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ092491.1	462275	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ004455.1	505207	3631.6	2769.1	2578.6	7369.5	482.6	854.3
GQ002405.1	507258	6647.6	5591.1	3622.4	5903.7	2565.6	4407.1
GQ020369.1	489299	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ049285.1	433658	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ100336.1	427655	24337.2	21311.7	22622.9	22172.3	19914.0	18030.3
GQ033705.1	387108	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ031381.1	450481	11916.8	8603.8	9487.3	19457.8	6620.3	10359.3
GQ022457.1	487212	5805.8	6650.5	4009.5	9692.5	7410.5	6998.6
GQ009952.1	499713	15259.2	12847.9	7415.9	18282.0	13356.1	18163.4
GQ031702.1	453228	12308.6	12101.0	9945.9	12715.8	10071.4	9168.3
FM875163.1	367677	6102.6	5885.7	3962.4	5915.7	4268.5	4448.4
GQ032133.1	422396	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ010176.1	499489	21518.6	20617.8	17443.1	21504.1	11464.6	11695.4
GQ062794.1	432266	8916.2	9487.7	1721.5	12343.4	3491.5	2575.7
GQ046161.1	410787	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ061859.1	452750	9798.3	8027.6	4157.1	9938.0	12381.5	11924.2
GQ036306.1	389322	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ026874.1	432435	5221.6	9324.0	1481.3	1936.2	607.6	1319.7
GQ028220.1	449461	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ098572.1	421180	24016.5	22737.9	13775.6	12199.8	20832.0	17395.9
GQ028696.1	408691	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ030671.1	423965	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ034624.1	435424	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ100148.1	413846	9798.3	8027.6	4157.1	9938.0	12381.5	11924.2
GQ001634.1	508027	4323.4	2330.1	7695.8	9825.0	258.1	1145.6
GQ071785.1	446281	28084.4	27338.2	35137.3	24104.5	25410.8	25415.2
FM872783.1	356906	6107.0	6197.6	3229.8	5454.3	3728.1	4435.9
GQ048653.1	404258	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
GQ044783.1	446123	16399.4	20633.3	5410.6	16434.8	4701.5	6305.2
GQ028621.1	429563	12248.4	11629.6	10752.5	15624.4	13995.8	14981.9
GQ036611.1	407731	3767.1	2786.6	8073.6	8101.3	802.7	1702.3
GQ056107.1	454308	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ044018.1	406432	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ036703.1	442425	14458.4	13262.8	18338.5	15127.1	12333.9	11709.2
GQ005228.1	504435	101.5	102.9	145.0	154.0	111.2	109.1

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GQ035519.1 gg_id:413263 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
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GQ022432.1 gg_id:487238 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ029176.1 gg_id:375548 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw86
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FM872839.1 gg_id:363696 occupant source house floor dust clone FB03F01
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GQ074096.1	443543	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031262.1	454129	25539.5	25240.7	17534.2	20715.6	24340.0	21794.1
GQ035519.1	413263	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ037676.1	407836	7162.6	5323.7	5144.1	12381.0	2634.8	3144.4
GQ026564.1	464960	6238.1	5075.5	7168.9	13268.0	5710.3	5570.4
GQ050724.1	417722	18595.4	18201.3	18830.8	22354.1	17753.7	16922.1
GQ025539.1	452856	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ000170.1	468735	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
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GQ100105.1	467859	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ072248.1	458261	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ074667.1	401761	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
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GQ052297.1	440831	26151.6	27008.1	18333.4	21796.3	26746.2	24151.5
GQ090557.1	448971	31517.9	32436.8	31197.0	25777.4	31765.6	27214.6
GQ075296.1	372713	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
GQ028500.1	452858	19198.9	18350.6	10545.2	18414.5	10927.9	11313.1
GQ005260.1	504403	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ046905.1	457051	13431.5	6932.9	1687.2	2296.4	796.2	3742.4
GQ022432.1	487238	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ029176.1	375548	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ031652.1	406961	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
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GQ002148.1	507514	14628.1	10607.1	14970.4	18920.2	11978.3	12113.5
GQ036772.1	392614	16281.0	14490.3	13691.1	18920.2	16463.0	17924.8
GQ038309.1	454859	669.4	442.7	1607.2	580.0	460.4	328.6
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GQ087176.1 gg_id:445019 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ069257.1 gg_id:430692 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw241c09
GQ062304.1 gg_id:414065 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ036535.1 gg_id:440527 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ002409.1 gg_id:507254 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ030042.1 gg_id:401527 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866d0
GQ071750.1 gg_id:409776 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ110548.1 gg_id:420481 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ020534.1 gg_id:489134 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ049171.1 gg_id:424244 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu470b01
GQ005053.1 gg_id:504609 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ075730.1 gg_id:430659 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ035730.1 gg_id:432727 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ042005.1 gg_id:457256 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw935
GQ040001.1 gg_id:411614 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw94
GQ028442.1 gg_id:425297 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ031988.1 gg_id:390961 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ043989.1 gg_id:381277 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ029398.1 gg_id:452300 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw925e1
GQ112781.1 gg_id:388217 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588b07c1
GQ027220.1 gg_id:374347 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ062662.1 gg_id:371934 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ112782.1 gg_id:442041 Topographical and Temporal Human Skin Microbiome skin nare clone nbw588b08c1
GQ115532.1 gg_id:376959 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw687b02
GQ036608.1 gg_id:442231 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu

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GQ010154.1	499511	4000.9	2798.1	4066.1	8014.0	324.5	779.1
GQ030526.1	446470	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ038382.1	434502	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ059582.1	371537	122.9	285.0	75.0	603.4	206.6	344.6
GQ054954.1	403286	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ030102.1	396680	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ050529.1	393348	8532.7	7091.1	4610.4	12860.2	3819.1	4418.4
GQ077686.1	440262	6423.2	7365.3	4345.3	7317.2	10216.4	10194.6
GQ112649.1	440291	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ066228.1	402413	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031510.1	389706	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036578.1	414800	3223.1	2180.6	2221.8	7319.9	573.1	1347.1
GQ092358.1	388018	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ056195.1	432161	12305.3	10003.2	4544.0	11296.5	13291.8	11912.6
GQ044540.1	406713	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ087176.1	445019	14669.3	16845.3	5165.0	14575.4	7731.3	9167.9
GQ069257.1	430692	1485.4	911.9	2283.8	2287.9	766.3	827.5
GQ062304.1	414065	17578.9	17610.2	9086.0	15942.6	7355.4	8977.9
GQ036535.1	440527	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ002409.1	507254	19512.5	21790.7	8493.2	12814.5	10258.2	8428.4
GQ030042.1	401527	7580.4	6304.5	4422.4	9140.9	6642.3	6407.4
GQ071750.1	409776	6423.2	7365.3	4345.3	7317.2	10216.4	10194.6
GQ110548.1	420481	25631.2	25418.8	20109.3	21605.3	23986.2	21892.0
GQ020534.1	489134	15259.2	12847.9	7415.9	18282.0	13356.1	18163.4
GQ049171.1	424244	2022.1	1812.8	501.6	5115.0	398.3	707.1
GQ005053.1	504609	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ075730.1	430659	8731.6	10968.1	3407.5	6891.2	4427.6	4170.7
GQ035730.1	432727	6572.7	6555.3	3673.3	11134.2	7110.4	7165.1
GQ042005.1	457256	7413.2	6647.9	2215.8	3213.1	6466.4	6115.9
GQ040001.1	411614	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ028442.1	425297	8586.9	6025.6	6127.5	15622.7	3577.7	5186.3
GQ031988.1	390961	12291.3	13150.5	4165.5	12879.7	13785.1	11013.2
GQ043989.1	381277	17342.1	10928.1	7118.5	15591.9	11317.2	10824.8
GQ029398.1	452300	3024.3	1949.7	5028.2	6443.9	646.5	2417.3
GQ112781.1	388217	1534.2	840.2	688.1	834.4	539.1	1167.5
GQ027220.1	374347	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ062662.1	371934	19479.5	17904.1	11337.6	13194.0	10222.1	7955.4
GQ112782.1	442041	26419.2	23960.0	25927.1	23161.5	23799.1	22085.1
GQ115532.1	376959	31517.9	32436.8	31197.0	25777.4	31765.6	27214.6
GQ036608.1	442231	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4

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GQ028600.1 gg_id:410411 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ033601.1 gg_id:436572 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu336
GQ075322.1 gg_id:371021 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ060707.1 gg_id:376521 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04e01
GQ038766.1 gg_id:373026 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu522g11
GQ022610.1 gg_id:487059 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ047011.1 gg_id:393489 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ051178.1 gg_id:456610 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ005149.1 gg_id:504513 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ100282.1 gg_id:375797 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480b03c1
GQ017781.1 gg_id:491887 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ038203.1 gg_id:411449 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ054713.1 gg_id:419374 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1100d
GQ054118.1 gg_id:432811 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1098g
GQ051237.1 gg_id:424755 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ065396.1 gg_id:381229 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ093611.1 gg_id:457393 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw367a0
GQ031316.1 gg_id:400951 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ021884.1 gg_id:487784 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ010447.1 gg_id:499217 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ075234.1 gg_id:453874 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ038276.1 gg_id:444936 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ110857.1 gg_id:441023 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ032727.1 gg_id:431703 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw917d0
GQ028477.1 gg_id:414988 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ090593.1 gg_id:380677 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ031525.1 gg_id:377071 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ020662.1 gg_id:489006 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ017669.1 gg_id:491998 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ060559.1 gg_id:438949 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03c08
GQ048807.1 gg_id:445120 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu5
GQ054957.1 gg_id:423098 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ056847.1 gg_id:381784 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl

GQ048365.1	403597	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ028600.1	410411	9982.3	8479.3	8320.0	13047.3	6392.3	6850.1
GQ033601.1	436572	7448.4	5836.9	3093.4	10549.8	10645.0	10392.2
GQ075322.1	371021	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ060707.1	376521	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ038766.1	373026	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ022610.1	487059	17413.9	18241.7	8077.5	12195.9	11151.5	7942.5
GQ047011.1	393489	6423.2	7365.3	4345.3	7317.2	10216.4	10194.6
GQ051178.1	456610	2612.9	1716.2	5253.6	5792.3	629.6	2278.1
GQ005149.1	504513	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ100282.1	375797	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ017781.1	491887	23503.6	23629.4	17009.5	18957.8	22326.6	21418.3
GQ038203.1	411449	7545.1	8697.1	3640.3	7486.2	4067.6	4668.8
GQ054713.1	419374	26987.8	26014.6	26882.8	22684.8	26972.8	24902.0
GQ054118.1	432811	11831.3	13328.8	8351.7	12135.1	7916.7	7371.1
GQ051237.1	424755	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ065396.1	381229	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ093611.1	457393	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ031316.1	400951	24240.3	20558.4	18856.4	20136.2	18014.0	16560.7
GQ021884.1	487784	472.8	468.8	798.0	2602.2	799.0	811.2
GQ010447.1	499217	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ075234.1	453874	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ038276.1	444936	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ110857.1	441023	24539.1	24707.5	8695.6	20091.0	23530.3	19895.3
GQ032727.1	431703	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ028477.1	414988	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ061998.1	400457	21339.5	22006.5	8416.8	12492.2	10346.0	7754.1
GQ090593.1	380677	26104.3	27056.8	18103.3	21388.0	28533.0	23568.3
GQ031525.1	377071	20729.1	19423.9	23627.3	19673.7	18957.8	17239.3
GQ020662.1	489006	4509.7	2649.4	2632.0	5259.3	3528.4	1426.5
GQ017669.1	491998	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ000901.1	469466	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ066185.1	455647	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ000370.1	468936	0.7	0.7	1.1	0.6	0.6	0.6
GQ030161.1	456999	15128.0	19933.9	7692.5	14270.0	16450.3	8788.8
GQ039672.1	437374	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ067407.1	399123	380.5	188.5	1916.4	280.7	219.5	112.0
GQ060559.1	438949	12018.1	9508.7	2997.0	15125.8	16312.8	14901.2
GQ048807.1	445120	14822.7	11858.2	8647.9	13524.0	9043.7	8001.7
GQ054957.1	423098	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ056847.1	381784	14055.5	12672.9	8009.9	12814.3	13654.6	12045.4

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GQ043446.1 gg_id:406222 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97
GQ036229.1 gg_id:391845 Topographical and Temporal Human Skin Microbiome skin palm clone nbu361g03c1
GQ072050.1 gg_id:421406 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw191e09
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GQ048568.1 gg_id:445118 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
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GQ111821.1 gg_id:405257 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
X84247.1 gg_id:13488 Corynebacterium tuberculostearicum str. ATCC 35692
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GQ033995.1 gg_id:418630 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ032127.1 gg_id:406165 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ005938.1 gg_id:503725 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ058244.1 gg_id:459547 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ056150.1 gg_id:427985 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ054162.1 gg_id:405858 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099d

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GQ050580.1	400753	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ038540.1	406055	5739.6	4426.3	6275.9	9095.6	4103.4	5303.6
GQ062512.1	453266	6422.4	9160.0	2595.6	4867.9	2854.4	3341.2
GQ054990.1	376163	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ029481.1	459690	8580.4	8054.0	12688.7	9365.8	6510.0	7207.3
GQ074776.1	412650	9247.2	11927.8	5808.7	9692.5	2042.6	3730.5
GQ010066.1	499599	18693.4	19305.4	7927.3	12442.2	9982.6	7661.6
GQ043446.1	406222	13262.0	15177.3	4264.8	13182.4	4282.0	6071.5
GQ036229.1	391845	15038.3	13359.7	13760.5	15765.9	12605.0	11545.4
GQ072050.1	421406	16081.2	14096.0	19389.1	18515.1	13151.7	13265.2
GQ034307.1	457681	4124.7	2504.8	4397.0	9127.4	300.6	904.1
GQ048568.1	445118	8959.8	8990.9	1890.6	12556.2	2892.2	3284.1
GQ051309.1	439991	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ049331.1	403474	9180.9	7932.4	5813.3	9466.3	2688.2	2430.9
GQ111821.1	405257	22440.0	25028.7	8190.7	15447.6	15106.8	11749.6
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GQ033995.1	418630	4167.0	2307.4	2224.6	9997.4	515.7	1248.5
GQ032127.1	406165	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ049378.1	389618	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ005938.1	503725	27270.5	26309.9	19082.5	20813.6	20404.0	18812.3
GQ037016.1	372359	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ080155.1	463719	22978.0	21861.7	23838.8	20220.9	19817.9	19961.4
GQ045105.1	414080	22752.1	24068.6	16097.2	18569.3	22108.1	19241.3
GQ110646.1	376355	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031834.1	396853	4505.1	3355.2	18856.4	803.9	4155.9	5018.8
GQ052471.1	448800	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ036637.1	401991	21421.8	22494.9	15380.7	16208.8	12007.3	10735.3
GQ092634.1	436339	13643.5	14381.8	13792.8	10809.6	16812.8	12592.5
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GQ100117.1	381647	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ038389.1	465466	32539.6	31785.1	25590.9	24737.8	31822.6	25563.3
GQ049073.1	420096	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
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GQ058244.1	459547	26716.9	25598.1	18270.0	19222.7	26930.5	21864.9
GQ028592.1	451347	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ056150.1	427985	16150.8	20769.2	19345.9	15308.6	26371.3	21544.6
GQ054162.1	405858	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8

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GQ051198.1 gg_id:424370 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ005251.1 gg_id:504412 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ036923.1 gg_id:371396 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu385h07
GQ017788.1 gg_id:491880 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ057416.1 gg_id:416937 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ027505.1 gg_id:465912 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw84
GQ062419.1 gg_id:454458 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ006419.1 gg_id:503245 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu8
GQ050891.1 gg_id:468088 Topographical and Temporal Human Skin Microbiome skin nare clone nbu440e03c1
GQ000202.1 gg_id:468767 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
GQ064651.1 gg_id:388656 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ051293.1 gg_id:396160 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ005091.1 gg_id:504571 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ030352.1 gg_id:405038 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw876h
GQ036634.1 gg_id:428516 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ000389.1 gg_id:468954 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
GQ075208.1 gg_id:410008 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ031554.1 gg_id:376509 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ029060.1 gg_id:403912 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ005161.1 gg_id:504501 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ051164.1 gg_id:455425 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ020064.1 gg_id:489604 Topographical and Temporal Human Skin Microbiome skin nare clone nbu202e02c1
GQ022469.1 gg_id:487198 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ005116.1 gg_id:504546 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ048407.1 gg_id:400889 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
FM875141.1 gg_id:362739 occupant source house dust skin surface swab clone SB03D10
GQ026859.1 gg_id:387715 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ060363.1 gg_id:408505 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ058967.1 gg_id:371427 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu58
GQ046219.1 gg_id:378599 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ051249.1 gg_id:401718 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ112707.1 gg_id:385956 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586g11c1
GQ112766.1 gg_id:393164 Topographical and Temporal Human Skin Microbiome skin nare clone nbw587h07c1
GQ074688.1 gg_id:439300 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ036584.1 gg_id:410821 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ077662.1 gg_id:463136 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ075282.1 gg_id:434605 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ031008.1 gg_id:430471 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

GQ077546.1	435301	6744.1	4849.0	5701.4	7102.3	4296.4	4323.9
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GQ046689.1	454043	2109.6	2002.7	3617.6	6546.0	1391.1	2959.5
GQ051198.1	424370	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ005251.1	504412	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ036923.1	371396	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ017788.1	491880	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ057416.1	416937	18077.2	20270.6	6013.6	9728.7	6897.9	4901.1
GQ027505.1	465912	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ062419.1	454458	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ006419.1	503245	18503.3	19646.3	10955.9	18185.3	15056.2	16675.9
GQ050891.1	468088	25417.1	25266.9	17552.0	20245.6	22586.2	21179.2
GQ000202.1	468767	4487.1	7163.4	8483.8	6846.3	5365.1	7239.6
GQ064651.1	388656	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ051293.1	396160	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ005091.1	504571	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ030352.1	405038	24016.5	22737.9	13775.6	17982.1	20832.0	17395.9
GQ036634.1	428516	13497.4	10936.1	6641.1	16149.4	12075.5	15353.2
GQ000389.1	468954	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ075208.1	410008	185.1	145.3	173.5	238.6	182.6	104.1
GQ031554.1	376509	15032.4	17177.6	8208.5	11634.4	15135.9	14776.0
GQ029060.1	403912	23233.6	23034.6	18551.1	20876.8	21047.4	18601.4
GQ005161.1	504501	7360.8	5387.4	11389.8	12112.5	1725.6	3014.3
GQ051164.1	455425	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ020064.1	489604	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ022469.1	487198	19663.7	19943.0	8396.3	11233.1	9526.1	7530.5
GQ005116.1	504546	18160.0	14809.7	7348.3	16656.5	6698.9	10689.2
GQ048407.1	400889	6423.2	7365.3	4345.3	7317.2	10216.4	10194.6
FM875141.1	362739	578.2	611.4	752.4	835.3	436.6	1066.2
GQ026859.1	387715	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ060363.1	408505	22019.4	20649.8	15257.3	18975.8	17020.1	18174.6
GQ058967.1	371427	1158.7	618.5	3080.5	8607.1	331.8	455.6
GQ046219.1	378599	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ051249.1	401718	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ112707.1	385956	18595.4	18201.3	18830.8	22354.1	17753.7	16922.1
GQ112766.1	393164	28099.4	27860.0	16288.4	22707.0	27322.0	24728.1
GQ074688.1	439300	23093.2	23685.7	16088.3	18099.3	24176.4	20939.6
GQ036584.1	410821	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ077662.1	463136	2532.6	3238.7	904.0	2524.3	6773.5	5236.4
GQ075282.1	434605	242.1	321.7	990.0	321.4	229.3	424.9
GQ031008.1	430471	10446.5	5565.0	4585.1	3261.7	8545.7	7947.4

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GQ064473.1 gg_id:422062 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
GQ044000.1 gg_id:443578 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017f0
GQ044361.1 gg_id:400720 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ029224.1 gg_id:453393 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ075311.1 gg_id:401457 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ033484.1 gg_id:416729 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbu334
GQ036650.1 gg_id:429594 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ036356.1 gg_id:467693 Topographical and Temporal Human Skin Microbiome skin palm clone nbu363c12c1
GQ024103.1 gg_id:485566 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ027213.1 gg_id:423959 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ017627.1 gg_id:492040 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ032081.1 gg_id:405787 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ044220.1 gg_id:382116 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1020g(
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GQ020642.1 gg_id:489026 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ028118.1 gg_id:390923 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ028573.1 gg_id:445580 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ032427.1 gg_id:407841 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542g10
GQ031047.1 gg_id:422903 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ036554.1 gg_id:462597 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ060703.1 gg_id:437541 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw04d08
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GQ033935.1 gg_id:443118 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ033396.1 gg_id:398099 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
FM873884.1 gg_id:367423 occupant source house mattress dust clone MB02E03
GQ009248.1 gg_id:500417 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ016166.1 gg_id:493501 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw

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GQ064473.1	422062	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ044000.1	443578	4187.1	5170.6	6087.2	5234.5	7231.6	5189.3
GQ044361.1	400720	13089.5	12450.9	13057.1	12354.8	6435.3	7613.3
GQ029224.1	453393	11069.5	14800.8	5300.8	9423.3	6916.6	7378.9
GQ075311.1	401457	12281.1	11565.8	6988.4	7421.4	10744.6	8911.4
GQ033484.1	416729	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ036650.1	429594	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036356.1	467693	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ024103.1	485566	1464.6	1056.8	2595.4	4029.9	617.9	765.1
GQ027213.1	423959	18160.0	14809.7	7348.3	16656.5	6698.9	10689.2
GQ017627.1	492040	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ032081.1	405787	1434.6	1055.6	1746.0	1654.3	1282.2	1092.9
GQ048778.1	397137	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ054760.1	401422	8916.2	9487.7	1721.5	12343.4	3491.5	2575.7
GQ071508.1	467591	27270.5	26309.9	19082.5	20813.6	20404.0	18812.3
GQ044220.1	382116	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ028222.1	447554	4547.6	5351.0	1249.2	5881.7	5655.7	10150.4
GQ020642.1	489026	27825.5	28026.4	18819.1	22779.0	28280.1	25061.4
GQ028118.1	390923	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ051346.1	460750	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ030076.1	467395	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ062482.1	374182	19663.7	19943.0	8396.3	11233.1	9526.1	7530.5
GQ062813.1	427808	10561.8	10379.7	6963.4	11968.6	7328.6	5708.7
GQ028573.1	445580	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ044044.1	403693	6808.4	11040.3	4160.4	9887.1	651.6	1237.2
GQ032427.1	407841	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ031047.1	422903	28084.4	27338.2	35137.3	24104.5	25410.8	25415.2
GQ055502.1	464083	19142.5	20679.0	8922.3	17945.3	31081.0	9325.8
GQ097059.1	384860	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ036554.1	462597	22824.6	23461.4	16911.4	19076.1	22488.5	20375.9
GQ060703.1	437541	24016.5	22737.9	13775.6	12199.8	20832.0	17395.9
GQ112198.1	449284	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ111216.1	411334	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ010081.1	499584	19227.4	19838.0	13659.3	15637.9	16996.3	16776.7
GQ054924.1	458884	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ033935.1	443118	585.8	1002.2	673.0	956.6	1147.9	2176.0
GQ033396.1	398099	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
FM873884.1	367423	578.2	611.4	752.4	835.3	436.6	1066.2
GQ009248.1	500417	19889.4	20230.0	11587.4	19482.8	15082.6	16675.9
GQ016166.1	493501	10285.3	10104.4	4070.5	13214.0	14866.2	15995.2

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GQ005282.1 gg_id:504381 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ059621.1 gg_id:377295 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw38
GQ038259.1 gg_id:376179 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ051282.1 gg_id:383060 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ072365.1 gg_id:374775 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw195d03
GQ041954.1 gg_id:419471 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw934
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FM875228.1 gg_id:357159 occupant source house dust skin surface swab clone SB04D09
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GQ031017.1 gg_id:450491 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ027228.1 gg_id:422836 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ041786.1 gg_id:423664 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw932e1
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GQ112746.1 gg_id:462567 Topographical and Temporal Human Skin Microbiome skin nare clone nbw587e08c1
GQ075702.1 gg_id:425846 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw

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GQ092565.1	437130	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ031056.1	383955	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ041009.1	432246	19663.7	19943.0	8396.3	11233.1	9526.1	7530.5
GQ005282.1	504381	19944.6	17376.9	15670.3	17955.0	17658.3	32752.7
GQ046079.1	377843	12305.3	10003.2	4544.0	11296.5	13291.8	11912.6
GQ059621.1	377295	24240.3	20558.4	18856.4	20136.2	18014.0	16560.7
GQ038259.1	376179	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ051282.1	383060	3200.8	2149.4	6190.8	6278.7	1297.3	3040.6
GQ072365.1	374775	37691.4	33672.5	18687.1	35371.3	23530.2	23932.3
GQ041954.1	419471	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ062762.1	374808	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ036540.1	410237	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ044013.1	449456	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ112696.1	459910	26576.0	25112.3	27310.1	23614.6	22051.4	21275.6
GQ021126.1	488542	29701.3	29263.3	24205.9	24497.8	30332.8	26429.1
GQ056407.1	430789	5846.3	8278.1	3157.7	7133.6	3783.6	3504.8
FM875228.1	357159	865.2	927.8	828.0	1367.0	481.2	1425.3
GQ062843.1	392507	9509.7	11604.5	10231.0	9514.3	13468.2	14129.6
GQ051196.1	466924	1203.0	2041.2	3457.8	829.4	1052.9	3487.1
GQ015870.1	493795	9591.5	8514.2	8016.9	14179.3	5311.9	6026.6
GQ048370.1	445406	7540.1	6641.7	8426.2	9935.3	5241.0	5941.0
GQ028578.1	400928	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ066206.1	422160	21958.2	19969.2	24709.9	20073.5	18708.2	18462.6
GQ054686.1	375728	6345.7	4724.3	4188.9	10544.9	541.8	1359.7
GQ031617.1	405730	6111.8	4360.1	4942.6	11902.0	664.7	1597.4
GQ033648.1	412373	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ069980.1	443520	18780.0	18619.0	11000.2	14660.3	18706.0	16851.2
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GQ013197.1	496469	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ003839.1	505824	19925.9	20596.8	14842.4	17780.6	11788.6	18307.8
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GQ005262.1	504402	18693.4	19305.4	7927.3	12442.2	9982.6	7661.6
GQ037233.1	415256	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ031017.1	450491	3268.5	4105.0	5080.2	6034.7	3085.5	4189.2
GQ027228.1	422836	26421.7	27466.0	16762.0	21570.5	28581.2	23918.3
GQ041786.1	423664	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ061557.1	448953	19601.8	17040.7	12482.4	19135.1	9246.3	12485.2
GQ112746.1	462567	3223.1	2180.6	2221.8	7319.9	573.1	1347.1
GQ075702.1	425846	23597.8	23011.5	30847.3	21435.9	21468.1	21665.7

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GQ048133.1 gg_id:401917 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu45(
GQ071529.1 gg_id:376963 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ000924.1 gg_id:508738 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu10
GQ020482.1 gg_id:489186 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ031178.1 gg_id:420098 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ051222.1 gg_id:432784 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ031201.1 gg_id:409184 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ035289.1 gg_id:435610 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35(
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GQ066215.1 gg_id:409656 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ036474.1 gg_id:450581 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ033899.1 gg_id:391597 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ050614.1 gg_id:409775 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488b
GQ069880.1 gg_id:400254 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw242g0
GQ097252.1 gg_id:389528 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ016005.1 gg_id:493661 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ036678.1 gg_id:386753 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ028466.1 gg_id:433531 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ050388.1 gg_id:424784 Topographical and Temporal Human Skin Microbiome skin nare clone nbu437b05c1
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GQ025621.1 gg_id:417762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ075227.1 gg_id:391143 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ015010.1 gg_id:494656 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8

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GQ029538.1	397033	7435.7	6113.8	9742.3	12485.9	7899.4	8111.6
GQ048133.1	401917	716.1	1169.5	1515.8	1278.3	1247.1	1451.7
GQ071529.1	376963	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ100277.1	440048	17827.1	17251.3	12608.8	15259.8	13474.7	12627.9
GQ000924.1	508738	20333.8	21051.6	22144.5	20866.3	13137.4	12748.5
GQ020482.1	489186	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ031178.1	420098	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ051222.1	432784	18009.6	16544.4	8740.0	15096.7	13741.9	12143.8
GQ031201.1	409184	2596.4	2188.6	4842.2	3683.3	2999.2	7563.7
GQ035289.1	435610	14927.5	11096.5	17291.8	17353.8	8676.3	11338.5
GQ100266.1	395558	24357.3	23993.5	12860.2	21220.6	23393.6	21117.9
GQ066215.1	409656	7224.5	6564.8	1721.5	12343.4	3491.5	2575.7
GQ036474.1	450581	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ032744.1	377043	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ020449.1	489219	5978.6	8088.2	3850.1	8591.0	3554.3	5544.0
GQ033899.1	391597	10533.7	12098.7	5994.4	9273.3	7434.3	7963.5
GQ050614.1	409775	22458.0	22611.8	14383.1	18793.8	19883.8	19188.5
GQ069880.1	400254	4189.8	4189.6	3823.5	8363.9	2785.8	5876.1
GQ097252.1	389528	7004.4	11202.0	4068.3	10274.2	710.0	1449.8
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GQ036678.1	386753	4106.0	2788.3	3535.8	8390.6	1695.1	3619.1
GQ028466.1	433531	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ050388.1	424784	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ072367.1	422966	25071.2	23053.6	25691.0	22699.7	22338.9	20503.6
GQ092413.1	464439	14571.7	14989.3	7618.9	11654.0	8454.2	6941.0
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GQ052333.1	396092	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
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FM875156.1	358619	578.2	611.4	752.4	835.3	436.6	1066.2
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GQ112825.1	468130	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ022039.1	487630	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ024642.1	485030	21090.7	24176.8	6290.3	13131.2	17155.6	10105.0
GQ050551.1	386879	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
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GQ015010.1	494656	14669.3	16845.3	5165.0	14575.4	7731.3	9167.9

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GQ075313.1 gg_id:419278 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ071610.1 gg_id:462196 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ027608.1 gg_id:386119 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ112671.1 gg_id:407474 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586d04c1
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GQ009996.1 gg_id:499669 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ062683.1 gg_id:444234 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ051928.1 gg_id:402356 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu5
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GQ028699.1 gg_id:454440 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw919a0
GQ059688.1 gg_id:391469 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw39
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GQ048301.1 gg_id:403229 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ056446.1 gg_id:415179 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor

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GQ071610.1	462196	1982.6	1493.9	1050.4	2968.2	457.6	875.4
GQ027608.1	386119	19773.1	36763.5	27469.7	34908.4	12888.4	27935.9
GQ112671.1	407474	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ059698.1	372620	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ009996.1	499669	26965.6	25962.0	23270.1	22721.8	25676.5	23724.9
GQ062683.1	444234	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ051928.1	402356	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ032824.1	432593	3693.0	3528.5	7000.9	5112.4	1770.3	3048.4
GQ051266.1	451027	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ010187.1	499477	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ039731.1	373804	2523.9	2979.1	6782.7	4950.1	2065.3	2089.4
GQ028998.1	457548	6334.2	4856.4	13789.5	9736.9	13669.9	12349.1
GQ112167.1	424564	5091.1	3859.7	3277.8	9441.8	2688.7	3375.6
GQ034453.1	395550	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ014954.1	494712	16780.4	17488.0	6692.3	12187.6	5954.9	6283.1
GQ048158.1	417224	19227.4	19838.0	13659.3	15637.9	16996.3	16776.7
GQ036534.1	373443	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ034782.1	391535	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
FM875058.1	368622	578.2	611.4	752.4	835.3	436.6	1066.2
GQ043646.1	409039	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
FM872914.1	361152	578.2	611.4	752.4	835.3	436.6	1066.2
GQ037077.1	393146	433.5	749.2	2070.4	1192.4	1106.3	940.0
GQ054897.1	386637	17342.1	10928.1	7118.5	15591.9	11317.2	10824.8
GQ040649.1	463501	12808.5	16645.7	11955.0	20075.4	20025.9	17042.8
GQ046100.1	451203	15907.0	13828.1	10880.4	16766.8	13387.6	13062.0
GQ028453.1	446032	16895.1	18348.4	11238.4	13370.8	12359.7	10383.6
GQ111871.1	460439	15259.2	12847.9	7415.9	18282.0	13356.1	18163.4
GQ075610.1	452408	6156.1	5980.8	3967.2	5741.4	5524.7	4641.8
GQ095000.1	401279	3370.3	3385.2	3719.7	3347.5	903.5	1677.8
GQ039612.1	399787	1494.2	1559.8	2435.3	6655.0	254.3	505.6
GQ038244.1	437953	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ049077.1	408149	9096.4	10415.8	4943.4	9634.3	9456.5	10389.6
GQ028699.1	454440	4187.1	5170.6	6087.2	5234.5	7231.6	5189.3
GQ059688.1	391469	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ061881.1	441649	26512.6	27117.6	20870.7	21732.5	27113.8	25157.1
GQ033719.1	446332	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ088750.1	389875	12305.3	10003.2	4544.0	11296.5	13291.8	11912.6
GQ048301.1	403229	12431.3	12294.8	7205.5	16258.6	10402.6	11620.2
GQ056446.1	415179	3694.3	2591.2	3886.2	7679.8	238.3	761.6

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GQ059332.1 gg_id:392768 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ009961.1 gg_id:499704 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ052270.1 gg_id:456423 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu533e04
GQ071736.1 gg_id:415847 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ022481.1 gg_id:487184 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
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GQ031041.1 gg_id:439167 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ054365.1 gg_id:446347 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108
GQ015228.1 gg_id:494437 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765h11c
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GQ054011.1 gg_id:373237 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1097e
GQ031830.1 gg_id:431464 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ028514.1 gg_id:393839 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ005166.1 gg_id:504496 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ092439.1 gg_id:456776 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ031627.1 gg_id:406850 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ055012.1 gg_id:466845 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ038269.1 gg_id:375171 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ065579.1 gg_id:460532 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw90d02
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GQ028983.1 gg_id:467587 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ013382.1 gg_id:496284 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8

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GQ050590.1	445715	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ059332.1	392768	18971.4	18738.8	16277.9	19587.3	24002.5	19550.1
GQ009961.1	499704	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ052270.1	456423	22492.4	27242.2	25123.0	20981.1	21444.3	10710.5
GQ071736.1	415847	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ022481.1	487184	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ092455.1	428401	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031041.1	439167	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ054365.1	446347	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ015228.1	494437	23412.5	21919.7	9671.3	20497.0	19356.7	18458.6
GQ030711.1	416493	2355.8	2022.4	2501.7	3515.6	1203.9	1511.0
GQ054011.1	373237	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031830.1	431464	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ028514.1	393839	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ028240.1	439977	7004.4	11202.0	4068.3	10274.2	710.0	1449.8
GQ044442.1	380893	222.2	264.7	180.5	273.1	204.7	111.1
GQ028108.1	418281	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ089087.1	432225	23358.7	19672.8	18603.4	15537.6	10520.5	13998.3
GQ005166.1	504496	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
GQ075255.1	456431	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ033547.1	446962	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ092439.1	456776	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031627.1	406850	6450.8	5813.4	5821.8	12538.3	12085.1	14073.7
GQ054146.1	395531	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ062452.1	409995	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ055012.1	466845	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ112732.1	449347	23445.8	23736.7	15922.1	18216.0	21471.4	20961.5
GQ038269.1	375171	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ028593.1	398726	924.0	2279.7	1234.8	775.3	1348.0	1307.9
GQ042143.1	409906	25012.4	25583.4	16876.9	22597.5	24990.7	23299.5
GQ036680.1	411410	10866.3	9313.7	4011.9	11983.9	5249.9	4730.1
GQ004412.1	505250	10003.4	8486.0	7969.2	12359.5	10742.9	9559.4
GQ065579.1	460532	144.3	128.6	5897.4	195.6	167.6	2884.4
GQ046212.1	401163	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ016879.1	492788	20615.9	21506.8	6030.8	12289.4	10222.1	7492.1
GQ050384.1	409090	10050.4	7245.9	905.6	11793.5	12418.5	11042.0
GQ028763.1	379605	8902.8	8451.3	10045.9	14789.7	14021.6	17768.2
GQ075651.1	397172	18693.4	19305.4	7927.3	12442.2	9982.6	7661.6
GQ028983.1	467587	5297.8	8453.2	11255.1	7441.8	5765.3	6068.3
GQ013382.1	496284	17342.1	10928.1	7118.5	15591.9	11317.2	10824.8

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GQ100147.1 gg_id:465199 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478e02c1
GQ062656.1 gg_id:405610 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ044062.1 gg_id:413554 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1018d(
GQ038237.1 gg_id:420541 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ025515.1 gg_id:373428 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ036505.1 gg_id:465597 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ044092.1 gg_id:441589 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1018g(
GQ049405.1 gg_id:383087 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ005261.1 gg_id:504401 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ031306.1 gg_id:424955 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ010732.1 gg_id:498933 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw738b0
GQ015209.1 gg_id:494451 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765g02c1
GQ009929.1 gg_id:499736 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ026815.1 gg_id:458180 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ004231.1 gg_id:505431 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ064859.1 gg_id:401442 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ022483.1 gg_id:487185 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31
GQ048187.1 gg_id:398830 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ038220.1 gg_id:390423 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ017853.1 gg_id:491817 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ075629.1 gg_id:391008 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ112207.1 gg_id:464650 Topographical and Temporal Human Skin Microbiome skin nare clone nbw585h05c1
GQ017859.1 gg_id:491809 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ036617.1 gg_id:396098 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ026655.1 gg_id:396789 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ029068.1 gg_id:437542 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ030415.1 gg_id:420828 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw877h04c
GQ071645.1 gg_id:390583 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ028623.1 gg_id:399203 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ104235.1 gg_id:452913 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
FM874993.1 gg_id:369408 occupant source house dust skin surface swab clone SB01G05
GQ048212.1 gg_id:409925 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ080646.1 gg_id:392142 Topographical and Temporal Human Skin Microbiome skin nare clone nbw1139d07c
GQ094796.1 gg_id:425920 Topographical and Temporal Human Skin Microbiome skin nare clone nbw374h04c1
GQ088651.1 gg_id:375711 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

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GQ033205.1	384636	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ100147.1	465199	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ062656.1	405610	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ044062.1	413554	1797.6	1061.5	1793.5	3296.5	712.5	871.4
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GQ036505.1	465597	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ044092.1	441589	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
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GQ005261.1	504401	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ031306.1	424955	17637.8	19460.5	11266.3	16543.5	14686.6	11082.6
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GQ009929.1	499736	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ026815.1	458180	16442.7	19614.0	6768.3	12601.7	15866.4	15319.6
GQ036504.1	399802	8725.7	7191.1	7757.0	11229.7	4058.4	4405.7
GQ004231.1	505431	24253.4	42548.9	24365.8	21504.2	30321.1	8024.3
GQ064859.1	401442	3665.7	2790.8	4661.1	6483.0	558.6	1128.5
GQ022483.1	487185	21138.5	20520.1	13839.4	18987.5	15042.3	13596.7
GQ048187.1	398830	10173.6	11085.3	6597.7	8589.8	6445.8	5962.4
GQ038220.1	390423	10472.0	8955.0	9071.4	9998.9	5304.0	5706.5
GQ017853.1	491817	11916.8	8603.8	9487.3	19457.8	6620.3	10359.3
GQ075629.1	391008	21958.2	19969.2	24709.9	20073.5	18708.2	18462.6
GQ112207.1	464650	5064.1	2997.6	1151.3	8774.6	6889.9	7031.5
GQ017859.1	491809	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ062842.1	387581	22092.6	19611.7	24526.1	20430.4	19521.5	18768.8
GQ033865.1	431699	21339.5	22006.5	8416.8	12492.2	10346.0	7754.1
GQ016230.1	493437	19475.6	20845.9	19118.0	17863.1	30855.4	22837.8
GQ036617.1	396098	23073.2	23840.8	13895.2	20366.0	23610.9	21391.1
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GQ028623.1	399203	25743.1	25999.2	12377.5	21083.9	25196.3	21936.1
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GQ080646.1	392142	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ094796.1	425920	19663.7	19943.0	8396.3	11233.1	9526.1	7530.5
GQ088651.1	375711	10272.2	9129.4	8225.6	15272.6	6707.4	6933.2

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GQ034194.1 gg_id:440626 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ050602.1 gg_id:411456 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu487h
GQ078737.1 gg_id:436048 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ050494.1 gg_id:484604 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu486e
GQ025562.1 gg_id:394805 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ034713.1 gg_id:421023 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ062617.1 gg_id:393730 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ112646.1 gg_id:411809 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586a06c1
GQ036716.1 gg_id:424153 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ059659.1 gg_id:389011 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw38
GQ031423.1 gg_id:399273 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw873g
GQ014242.1 gg_id:495424 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw760f
GQ034421.1 gg_id:418010 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ062511.1 gg_id:389879 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ036672.1 gg_id:457933 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ058227.1 gg_id:464245 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ065415.1 gg_id:413928 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ070124.1 gg_id:420489 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
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GQ034158.1 gg_id:422999 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
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GQ050602.1	411456	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ078737.1	436048	144.3	128.6	173.5	195.6	124.5	94.8
GQ050494.1	484604	466.4	974.6	619.6	743.0	767.0	1914.1
GQ025562.1	394805	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ034713.1	421023	12599.1	11402.2	13867.5	15936.7	15413.5	14517.7
GQ062617.1	393730	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ112646.1	411809	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036716.1	424153	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ059659.1	389011	5982.5	6056.0	1020.8	2827.8	1224.2	2337.4
GQ031423.1	399273	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ014242.1	495424	5876.8	4818.4	2410.4	10705.6	789.5	1306.1
GQ034421.1	418010	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ062511.1	389879	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ066327.1	404299	3112.5	1980.0	5394.8	4367.9	2528.1	3289.1
GQ078661.1	406559	10888.3	11541.9	3939.4	10854.3	7595.9	6740.3
GQ050532.1	456575	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ053471.1	425101	26581.3	25257.2	27720.0	23311.0	22820.0	22466.4
GQ033358.1	456580	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ066417.1	459531	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ044246.1	439372	470.6	841.5	377.7	430.3	601.9	1592.8
GQ024216.1	485455	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ038217.1	397992	10472.0	8955.0	9071.4	9998.9	5304.0	5706.5
GQ041310.1	442759	9792.9	7886.4	5054.5	5994.4	11874.1	5397.9
GQ036958.1	411423	7606.6	8276.3	919.7	9374.2	4758.0	3303.8
GQ053468.1	384465	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ059745.1	465334	18048.2	18085.9	10660.5	14289.1	10111.3	9027.1
GQ032059.1	459401	6423.2	7365.3	4345.3	7317.2	10216.4	10194.6
GQ036672.1	457933	3829.0	3342.5	6865.6	14194.4	2002.1	4202.9
GQ018919.1	490747	4220.6	2684.8	5031.5	3265.6	234.0	908.6
GQ066339.1	416631	17413.0	15246.9	14856.8	21318.2	12955.9	14895.7
GQ058227.1	464245	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ065415.1	413928	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ070124.1	420489	15525.4	20370.2	10534.6	10619.4	7671.9	7757.9
GQ038265.1	386722	10472.0	8955.0	9071.4	9998.9	5304.0	5706.5
GQ036787.1	468554	585.8	1002.2	673.0	956.6	1147.9	2176.0
GQ051247.1	450448	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ034158.1	422999	26521.0	26174.4	20990.1	21959.2	25942.2	21885.2
GQ075337.1	402406	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ000940.1	508722	21214.3	21274.9	9016.2	19105.1	18493.4	19974.4

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GQ036409.1 gg_id:389166 Topographical and Temporal Human Skin Microbiome skin palm clone nbu364b05c1
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GQ071731.1 gg_id:386054 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ034778.1 gg_id:414265 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ100165.1 gg_id:372371 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478f10c1
GQ011516.1 gg_id:498150 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw792h07
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GQ045651.1 gg_id:383982 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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GQ056992.1	434910	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ051197.1	444172	5820.2	5013.1	6076.3	13363.3	11073.8	10968.3
GQ036409.1	389166	3023.7	2989.0	2117.2	3296.7	3718.7	3770.6
GQ044822.1	410513	26086.0	26147.1	28995.9	23255.5	22759.3	22349.9
GQ040808.1	401172	144.3	128.6	148.7	344.4	124.5	94.8
GQ036465.1	382332	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ042060.1	405635	20698.2	22315.3	11587.8	15159.7	17981.0	18568.9
GQ036497.1	373797	13939.0	14209.8	7477.6	13558.3	1449.2	2977.5
GQ036704.1	407982	19786.2	20458.8	9425.5	12420.0	12941.9	12239.5
GQ005098.1	504564	14669.3	16845.3	5165.0	14575.4	7731.3	9167.9
GQ071731.1	386054	19681.7	20089.7	9243.2	14067.7	11397.3	9528.9
GQ048554.1	426643	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ009313.1	500351	16003.7	15804.7	7733.3	16712.8	9509.3	7014.5
GQ041728.1	400735	23889.0	23401.0	8764.6	19296.3	23938.2	19906.0
GQ005081.1	504581	7684.4	9738.1	6614.7	4307.9	4388.2	6667.2
GQ059677.1	441464	16430.9	17324.4	8079.7	11654.0	8454.2	6941.0
GQ041693.1	373878	17308.3	14235.3	17450.3	19379.6	7007.8	11366.9
GQ044086.1	410764	19228.0	19275.0	11952.5	16813.5	10067.3	11184.2
GQ011680.1	497987	30309.6	30778.8	24743.8	25312.6	29866.5	25774.5
GQ048382.1	418318	945.6	2522.3	1833.3	1917.3	738.0	1619.0
GQ048703.1	392254	6757.5	8862.3	8060.1	13903.6	12323.4	22783.5
GQ100087.1	438205	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ028975.1	424438	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ046495.1	484614	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ004401.1	505261	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ018067.1	491601	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ035288.1	412430	6626.6	6331.2	5621.3	8404.8	5313.4	5957.1
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GQ028888.1	424234	26097.9	26171.0	12563.3	20195.3	26386.5	21971.5
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GQ062619.1	419990	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ034778.1	414265	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ100165.1	372371	9802.1	10858.1	5875.2	5873.1	5280.0	4187.4
GQ011516.1	498150	3693.0	3528.5	7000.9	5112.4	1770.3	3048.4
GQ021344.1	488324	22108.1	21809.7	17369.9	19366.2	16994.7	31495.4
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GQ029973.1 gg_id:459023 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw865d1
GQ057409.1 gg_id:376725 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ010142.1 gg_id:499523 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ109195.1 gg_id:458647 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ065597.1 gg_id:386752 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw90f02c
GQ043996.1 gg_id:390604 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1017f0
GQ052007.1 gg_id:447017 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu5
GQ028439.1 gg_id:396670 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ032090.1 gg_id:388746 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ016090.1 gg_id:493577 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ054917.1 gg_id:439029 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ053503.1 gg_id:422665 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ005177.1 gg_id:504485 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ010162.1 gg_id:499503 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ038398.1 gg_id:441225 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ112183.1 gg_id:447763 Topographical and Temporal Human Skin Microbiome skin nare clone nbw585e11c1
GQ070040.1 gg_id:375697 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw244h0
GQ061732.1 gg_id:431631 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw23
GQ026823.1 gg_id:395667 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ017770.1 gg_id:491900 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ034896.1 gg_id:449212 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu329c09
GQ049270.1 gg_id:439350 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu472c06
GQ038325.1 gg_id:411998 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ029171.1 gg_id:427397 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw86
GQ020504.1 gg_id:489163 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ059456.1 gg_id:371093 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ031490.1 gg_id:445386 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw874f
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GQ028109.1 gg_id:429511 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ056147.1 gg_id:438147 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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GQ028390.1	437773	17237.7	17005.3	9263.3	14418.7	15049.2	15269.1
GQ028434.1	408118	4101.2	2628.4	1131.7	7382.7	6134.4	7352.3
GQ029973.1	459023	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ057409.1	376725	7776.9	6755.2	3519.3	7752.1	10136.4	9692.4
GQ010142.1	499523	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ109195.1	458647	3621.8	2200.2	6054.0	8107.6	469.0	1227.4
GQ065597.1	386752	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ043996.1	390604	3621.8	2200.2	6054.0	8107.6	469.0	1227.4
GQ052007.1	447017	11096.7	11927.8	5808.7	9692.5	5386.1	7083.0
GQ028439.1	396670	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ069966.1	424224	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ032090.1	388746	10866.3	9313.7	4011.9	11983.9	5249.9	4730.1
GQ016090.1	493577	14726.1	13073.9	13297.2	16615.1	15352.3	14496.0
GQ054917.1	439029	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ031655.1	421612	8883.5	9026.7	8981.1	12103.8	7076.5	7942.6
GQ036577.1	402793	27270.5	26309.9	19082.5	20813.6	20404.0	18812.3
GQ053503.1	422665	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ005177.1	504485	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ010162.1	499503	18722.7	18402.3	13865.4	16272.2	17226.9	15696.2
GQ038398.1	441225	14653.4	15260.1	8452.6	13520.6	12028.2	9948.1
GQ112183.1	447763	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ070040.1	375697	9957.3	8154.0	10472.4	15020.7	5789.6	6381.7
GQ061732.1	431631	1656.9	1427.3	2509.9	3420.4	804.7	846.0
GQ026823.1	395667	24016.5	22737.9	13775.6	12199.8	20832.0	17395.9
GQ017770.1	491900	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ037072.1	442918	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ034896.1	449212	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ049270.1	439350	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ038325.1	411998	7140.2	9539.7	7225.7	9538.1	15210.6	10656.3
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GQ028109.1	429511	13431.5	6932.9	1687.2	2296.4	796.2	3742.4
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FM875202.1 gg_id:362532 occupant source house dust skin surface swab clone SB04B06
GQ058016.1 gg_id:458911 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ028527.1 gg_id:439418 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ026894.1 gg_id:447601 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ035272.1 gg_id:455287 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35
GQ005215.1 gg_id:504447 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ051216.1 gg_id:422008 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ054301.1 gg_id:376727 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1107
GQ064699.1 gg_id:446730 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ030360.1 gg_id:451950 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw877a07c
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GQ038293.1 gg_id:466028 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ065581.1 gg_id:448725 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw90d05c

GQ039769.1	377465	3941.3	2326.2	6900.4	8292.9	579.7	2102.7
FM875202.1	362532	578.2	611.4	752.4	835.3	436.6	1066.2
GQ058016.1	458911	15006.7	19005.7	7484.7	14376.8	14422.6	8981.1
GQ028527.1	439418	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ026894.1	447601	24016.5	22737.9	13775.6	17982.1	20832.0	17395.9
GQ035272.1	455287	2913.2	3798.3	6854.6	5201.4	6240.2	11341.4
GQ005215.1	504447	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ051216.1	422008	19773.1	36763.5	27469.7	34908.4	12888.4	27935.9
GQ054301.1	376727	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ064699.1	446730	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ062709.1	408993	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ029560.1	433266	23856.7	23369.9	12413.1	19859.6	24533.0	21368.3
GQ085879.1	460598	19663.7	19943.0	8396.3	11233.1	9526.1	7530.5
GQ009051.1	500614	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ112714.1	435821	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ025558.1	447958	16913.0	18368.5	9398.5	15056.7	18449.0	15642.4
GQ032707.1	457705	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ030101.1	420041	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ061963.1	380326	14826.8	13071.0	12374.5	16097.2	9787.3	10711.6
GQ040101.1	386652	1246.4	986.7	2662.7	2662.3	4059.9	2423.3
GQ044538.1	417844	22552.2	23158.3	30196.2	17182.0	23602.9	27214.6
GQ071800.1	462079	5305.4	6265.5	4342.7	5501.2	2415.2	3470.0
GQ112140.1	415601	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ051254.1	433888	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ033754.1	435704	14778.3	16587.9	5482.5	9870.4	8252.5	6678.2
GQ004450.1	505214	172.8	128.6	173.5	227.0	124.5	94.8
GQ036498.1	407992	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ057997.1	460961	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ031273.1	431820	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ011113.1	498554	13469.8	12444.7	13905.0	15918.2	11850.7	15764.0
GQ037333.1	446589	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036511.1	377483	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ064498.1	430818	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ113693.1	416561	21818.2	20667.1	19215.0	20868.9	19104.1	18249.1
GQ020245.1	489423	16235.0	15466.8	13269.4	14917.2	12084.6	10491.7
GQ018953.1	490714	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ030360.1	451950	25196.7	26651.2	13210.0	18968.1	21796.6	19964.5
GQ032804.1	418698	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ075670.1	439819	21339.5	22006.5	8416.8	12492.2	10346.0	7754.1
GQ038293.1	466028	13711.6	13670.8	4555.6	13135.3	10046.2	11133.6
GQ065581.1	448725	3094.6	2682.6	497.8	1812.0	280.9	341.2

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GQ050845.1 gg_id:441242 Topographical and Temporal Human Skin Microbiome skin nare clone nbu439g06c1
GQ073643.1 gg_id:459104 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ043068.1 gg_id:455493 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012h
GQ030477.1 gg_id:423412 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw878g09c
GQ029043.1 gg_id:409235 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ031717.1 gg_id:427344 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ024152.1 gg_id:485518 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ010042.1 gg_id:499623 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ049872.1 gg_id:384350 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu431c12
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GQ092703.1 gg_id:399319 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ034225.1 gg_id:383108 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
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GQ050845.1	441242	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ073643.1	459104	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ059741.1	437671	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ016878.1	492789	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ078523.1	433396	11283.8	10974.9	8482.3	10348.8	8878.9	8614.3
GQ043068.1	455493	18968.8	18158.0	10231.3	12651.9	11224.1	10563.2
GQ030477.1	423412	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ029043.1	409235	18892.7	14315.6	6029.3	10828.8	7299.8	6564.5
GQ031717.1	427344	6506.2	4394.6	4958.8	13090.9	8289.1	9762.3
GQ024152.1	485518	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ010042.1	499623	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ080128.1	387560	16399.4	20075.8	7828.7	16434.8	11264.7	12637.2
GQ027571.1	427181	607.6	988.7	665.0	783.9	923.9	2391.3
GQ036605.1	406616	18517.3	20234.4	3924.3	11008.4	9563.9	7964.6
GQ093734.1	376577	8046.6	7953.3	3620.9	15525.6	3470.3	4309.4
GQ031618.1	407508	9659.4	9249.7	5795.4	8784.4	10110.4	9473.1
GQ007487.1	502178	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ034310.1	453537	13399.0	13803.8	13490.0	14102.7	7792.6	7789.5
GQ077307.1	413924	16493.1	16820.4	12183.6	13892.5	10377.2	14189.1
GQ046915.1	378527	26266.3	25830.3	22614.4	23950.0	22831.5	22686.7
GQ043592.1	423632	12262.5	12598.3	7487.1	13876.1	8925.9	10497.7
GQ075299.1	374656	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ094772.1	415142	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ071687.1	384463	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ028663.1	421143	19344.4	20229.5	17067.8	19201.3	21913.7	22848.3
GQ065512.1	426800	25417.1	25266.9	17552.0	20245.6	22586.2	21179.2
GQ049872.1	384350	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
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GQ092703.1	399319	10849.3	10561.1	6113.5	8962.1	11363.8	10578.2
GQ034225.1	383108	13658.9	12637.6	10109.1	11232.5	7903.2	8284.7
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GQ059667.1	406764	1819.7	1027.2	2452.9	803.9	621.4	849.5
GQ051180.1	468211	19802.1	18721.1	8138.4	12689.2	7800.9	6419.0
GQ045368.1	422206	12018.1	9508.7	2412.0	15125.8	16312.8	14901.2
GQ100836.1	379994	9798.3	8027.6	4157.1	9938.0	12381.5	11924.2
GQ061785.1	431772	23420.5	22265.2	13071.5	20305.6	19474.1	19133.2
GQ032030.1	465843	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ026334.1	373103	18388.4	18292.4	6708.9	17593.7	15579.2	13096.0

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o__Actinomycetales	f__Corynebacteriaceae
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o__Actinomycetales	f__Corynebacteriaceae

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GQ071523.1 gg_id:442670 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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FM875263.1 gg_id:367615 occupant source house dust skin surface swab clone SB04G11
GQ028575.1 gg_id:420562 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ057285.1 gg_id:444039 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ038215.1 gg_id:399846 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ031576.1 gg_id:457170 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ029132.1 gg_id:421830 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw86
GQ029006.1 gg_id:415003 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
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GQ027924.1 gg_id:424581 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ108649.1 gg_id:394751 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6
GQ038299.1 gg_id:466471 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ029984.1 gg_id:438920 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw865e1
GQ053999.1 gg_id:437650 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1097c
GQ055972.1 gg_id:414112 Topographical and Temporal Human Skin Microbiome skin nare clone nbw1042d03c
GQ065296.1 gg_id:407094 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw

GQ048901.1	408176	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ075300.1	431003	16473.1	17278.4	9197.4	15684.4	17330.9	13260.7
GQ050676.1	460857	5953.8	4989.4	1128.3	5900.4	1788.2	1690.5
GQ028970.1	438314	3705.0	2211.9	2045.3	5699.9	2535.1	8941.2
GQ075332.1	459959	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ043578.1	435145	19614.9	19449.9	12236.0	19014.3	17137.8	14576.4
GQ050791.1	398385	19071.5	17425.1	23801.3	18969.7	16939.1	16085.6
GQ104591.1	454472	16252.0	17932.7	8083.3	13364.2	12661.2	10060.5
GQ031534.1	406640	4366.6	20197.9	23214.6	17465.0	1279.3	941.9
GQ061863.1	415079	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ041172.1	408970	585.8	1002.2	673.0	956.6	1147.9	2176.0
GQ071523.1	442670	1419.5	2209.2	2194.5	4094.9	1349.7	1238.5
GQ048656.1	374565	4487.1	7163.4	8483.8	6846.3	5365.1	7239.6
GQ051365.1	429094	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
GQ048790.1	418492	13184.4	10054.4	3823.4	13247.2	9181.1	8235.5
GQ012634.1	497032	9678.1	7242.1	10601.5	13245.0	4006.5	4683.6
GQ044960.1	448013	24077.5	25025.1	15996.9	22597.5	24741.7	22750.6
GQ028736.1	429020	790.7	929.8	779.2	1483.0	1113.1	1044.6
FM875263.1	367615	578.2	611.4	752.4	835.3	436.6	1066.2
GQ028575.1	420562	20064.2	19360.5	12045.7	18682.1	11649.6	11911.4
GQ057285.1	444039	8265.7	7483.7	3394.5	10994.2	1721.3	1947.5
GQ038215.1	399846	10472.0	8955.0	9071.4	9998.9	5304.0	5706.5
GQ032055.1	432342	16780.4	17488.0	6692.3	12187.6	8126.6	6283.1
GQ054114.1	374410	29421.9	27316.4	23241.6	24094.0	27015.0	25689.5
GQ031576.1	457170	27114.6	29358.9	21546.0	21110.0	28532.3	24488.0
GQ029132.1	421830	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ029006.1	415003	4487.1	7163.4	8483.8	6846.3	5365.1	7239.6
GQ053691.1	433211	24420.3	24416.5	19635.1	20636.8	23562.5	20931.1
GQ030491.1	422389	7828.9	8629.7	5052.7	6919.3	2371.0	2853.0
GQ038363.1	439689	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ000310.1	468875	16798.1	13409.5	17788.9	14305.9	29185.9	25233.3
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GQ057907.1	459804	19663.7	19943.0	8396.3	11233.1	9526.1	7530.5
GQ027924.1	424581	28084.4	27338.2	35137.3	24104.5	25410.8	25415.2
GQ108649.1	394751	17536.2	17336.8	18173.0	18156.8	22993.1	17469.7
GQ038299.1	466471	6626.6	6331.2	5621.3	8404.8	5313.4	5957.1
GQ029984.1	438920	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ053999.1	437650	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ055972.1	414112	14549.4	16809.2	9223.5	13984.6	12887.0	14917.6
GQ065296.1	407094	18789.1	13914.4	23121.0	21050.1	14765.6	14669.6

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GQ071807.1 gg_id:440061 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ038355.1 gg_id:402307 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ097976.1 gg_id:436081 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw399h05
GQ028636.1 gg_id:431080 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ044818.1 gg_id:434365 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ002471.1 gg_id:507191 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu
GQ015214.1 gg_id:494453 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765g07c1
GQ034925.1 gg_id:403055 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu329f09
GQ088721.1 gg_id:465511 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ041339.1 gg_id:419478 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ087768.1 gg_id:381008 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ035631.1 gg_id:424766 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
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GQ112648.1 gg_id:410054 Topographical and Temporal Human Skin Microbiome skin nare clone nbw586a08c1
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GQ036586.1 gg_id:454799 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
FM874927.1 gg_id:357938 occupant source house dust skin surface swab clone SB01A08
AJ438041.1 gg_id:83125 Corynebacterium tuberculostearicum str. CIP102857
GQ053693.1 gg_id:437259 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
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GQ026469.1 gg_id:418754 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ097047.1 gg_id:439117 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ028952.1 gg_id:374807 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ070311.1 gg_id:404644 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ100316.1 gg_id:428546 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480e08c1
GQ030099.1 gg_id:385681 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw867b0
GQ083938.1 gg_id:411225 Topographical and Temporal Human Skin Microbiome skin nare clone nbw255h07c1
GQ013418.1 gg_id:496247 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ014380.1 gg_id:495286 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ068443.1 gg_id:398396 Topographical and Temporal Human Skin Microbiome skin nare clone nbw150f07c1
GQ062565.1 gg_id:405059 Topographical and Temporal Human Skin Microbiome skin nare clone nbw12d03c1
GQ062014.1 gg_id:416027 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw27a0
GQ013312.1 gg_id:496354 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ015073.1 gg_id:494596 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ058952.1 gg_id:376937 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu58
GQ046167.1 gg_id:440673 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ042203.1 gg_id:404023 Topographical and Temporal Human Skin Microbiome skin nare clone nbw937e03c1
GQ070145.1 gg_id:454856 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1

GQ086722.1	412897	8422.8	12945.8	2586.0	7608.7	8266.5	5794.6
GQ071807.1	440061	607.6	988.7	665.0	783.9	923.9	2391.3
GQ038355.1	402307	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ097976.1	436081	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ028636.1	431080	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ044818.1	434365	19810.5	18690.7	20470.3	19645.3	15952.8	16995.8
GQ002471.1	507191	1612.1	1981.6	303.7	918.4	3897.2	3878.4
GQ015214.1	494453	986.8	913.8	661.1	2902.6	1089.0	1489.8
GQ034925.1	403055	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ088721.1	465511	26040.5	28660.9	20657.5	21995.7	28903.3	24469.5
GQ044941.1	398200	4922.2	3661.4	12619.7	14447.9	2637.7	5223.2
GQ041339.1	419478	648.9	1219.2	1075.0	2889.1	394.8	671.0
GQ087768.1	381008	21160.7	21594.8	12010.8	21480.2	17867.0	15545.9
GQ035631.1	424766	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ025396.1	466132	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ106280.1	400790	10336.5	9717.4	10428.5	9257.8	7673.9	9310.7
GQ112648.1	410054	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ038336.1	413292	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ036586.1	454799	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
FM874927.1	357938	14148.4	12860.5	15152.2	12913.1	12193.3	11556.0
AJ438041.1	83125	1012.2	1094.2	980.6	1473.2	607.9	1653.6
GQ053693.1	437259	19227.4	19838.0	13659.3	15637.9	16996.3	16776.7
GQ064627.1	431697	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ026469.1	418754	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ097047.1	439117	17605.9	17369.1	10080.8	14963.5	16457.9	15608.1
GQ028952.1	374807	4220.6	2684.8	5031.5	3265.6	234.0	908.6
GQ070311.1	404644	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ100316.1	428546	4156.9	2678.5	2320.7	8942.7	659.5	1578.7
GQ030099.1	385681	9604.9	9490.2	7127.4	10704.4	8205.1	9316.7
GQ083938.1	411225	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ013418.1	496247	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ014380.1	495286	5064.1	2997.6	1151.3	8774.6	6889.9	7031.5
GQ068443.1	398396	3796.7	4006.1	2302.3	5970.0	4578.1	4050.1
GQ062565.1	405059	489.9	741.3	333.0	2222.4	1013.1	3437.3
GQ062014.1	416027	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ013312.1	496354	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ015073.1	494596	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ058952.1	376937	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ046167.1	440673	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ042203.1	404023	2973.6	930.0	766.6	1867.7	595.6	703.2
GQ070145.1	454856	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4

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GQ077335.1 gg_id:390917 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ047640.1 gg_id:378669 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137b09c
GQ003826.1 gg_id:505834 Topographical and Temporal Human Skin Microbiome skin nare clone nbu57g08c1
GQ030160.1 gg_id:397078 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw868a0
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GQ027203.1 gg_id:389781 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ015902.1 gg_id:493764 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ083771.1 gg_id:391115 Topographical and Temporal Human Skin Microbiome skin nare clone nbw253e08c1
FJ557981.1 gg_id:520309 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat

GQ014449.1	495219	3101.7	8200.5	731.8	667.0	3027.9	1708.0
GQ077335.1	390917	8902.8	8451.3	10045.9	14789.7	14021.6	17768.2
GQ047640.1	378669	6435.9	12202.6	4487.1	5067.7	4498.6	3774.1
GQ003826.1	505834	1237.1	846.2	3515.7	3296.5	284.1	3275.5
GQ030160.1	397078	4622.4	5017.8	6097.1	5099.3	4674.1	6604.2
GQ046197.1	384329	11734.8	13390.8	7812.6	7681.3	6032.5	4572.6
GQ029319.1	439230	1033.0	1707.0	461.2	4343.7	4592.6	11990.3
GQ003853.1	505809	4652.5	6943.7	2349.6	3776.6	2132.1	2821.1
GQ065408.1	424202	14871.5	15414.4	10250.2	16986.6	11650.6	10991.4
GQ027203.1	389781	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ014532.1	495134	9402.2	12921.1	11397.6	9614.5	14405.9	9969.8
GQ100167.1	400807	9800.0	10216.2	7754.6	12920.0	14842.8	20334.0
GQ044899.1	389498	25681.1	27520.2	22436.7	18841.0	21401.7	18257.1
GQ091836.1	375809	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ030745.1	391319	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ030818.1	371896	122.9	141.5	99.8	195.6	167.6	111.1
GQ060773.1	384910	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ015902.1	493764	995.8	1343.9	1529.8	3781.0	191.0	367.0
GQ004493.1	505168	13431.5	6932.9	1687.2	2296.4	796.2	3742.4
GQ036327.1	397262	886.1	1155.4	1884.9	477.8	3006.2	1099.8
GQ046861.1	458743	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ013983.1	495683	12680.1	24691.7	15815.7	9682.1	12317.1	11947.8
GQ042214.1	375077	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ003779.1	505885	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ070212.1	412957	12.1	24.5	2960.3	22.0	102.1	2855.5
GQ062359.1	446965	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ017765.1	491903	4101.2	2628.4	1131.7	7382.7	6134.4	7352.3
GQ065357.1	398786	24074.4	24004.4	12635.8	20596.3	13123.9	12279.8
GQ099682.1	415910	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ013317.1	496349	14625.4	17419.9	7398.9	13481.6	12020.0	9940.9
GQ013823.1	495843	8923.3	17694.9	704.0	2859.7	3522.6	2522.6
GQ011905.1	497761	7933.9	7803.8	2273.8	4398.7	3241.4	3484.9
GQ100143.1	375781	8187.2	7172.0	6621.8	8176.4	5216.8	5404.7
GQ015007.1	494667	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ070221.1	405353	20742.1	24118.0	8559.3	16580.0	20696.0	17461.8
GQ087884.1	447809	607.6	988.7	665.0	783.9	923.9	2391.3
GQ003864.1	505798	506.4	503.1	1305.5	1337.9	268.1	445.9
GQ013880.1	495785	12743.7	14774.0	6632.4	11782.5	8549.7	9313.8
GQ037399.1	380463	669.4	442.7	1607.2	580.0	460.4	328.6
GQ083771.1	391115	14569.0	14248.5	8224.8	12737.8	10216.8	10186.0
FJ557981.1	520309	358.9	596.5	201.9	1650.9	152.3	234.3

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X80500.1 gg_id:13484 Corynebacterium accolens str. CCUG 28779T=ATCC 4972T
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GQ052379.1 gg_id:422190 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu535c08
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GQ041167.1 gg_id:446115 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ100225.1 gg_id:396739 Topographical and Temporal Human Skin Microbiome skin nare clone nbw479e02c1

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GQ028473.1	431448	10831.4	13372.8	7827.7	12634.5	4366.7	4914.3
GQ027357.1	413750	4450.6	3236.5	1983.9	8248.9	1138.6	1590.9
GQ061057.1	385796	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ014492.1	495173	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ042868.1	411961	677.2	540.9	2455.2	3181.8	160.9	194.9
GQ012286.1	497379	1312.3	1093.4	4422.1	3296.5	668.5	1598.5
GQ017271.1	492396	6572.8	5792.5	3740.1	7783.9	6760.9	7102.0
GQ004611.1	505051	10836.0	10870.5	2616.1	6076.3	4703.4	3631.2
GQ015012.1	494655	3748.5	3229.1	5216.7	9010.6	1835.6	2301.5
GQ112477.1	420122	23352.8	23079.9	12467.8	20476.2	20607.5	17908.0
GQ053697.1	373319	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ034574.1	413386	14669.3	16845.3	5165.0	14575.4	7731.3	9167.9
GQ014206.1	495460	5475.9	6417.3	2457.1	9603.1	2355.4	2627.9
GQ013848.1	495818	16279.2	17351.4	14482.6	13796.6	11136.2	11012.3
GQ100119.1	407179	17884.7	18369.4	11759.3	16134.9	18172.5	16360.3
GQ055955.1	409373	1797.6	1061.5	1793.5	3296.5	712.5	871.4
X84437.1	13487	1124.6	970.2	869.0	2384.8	465.7	1261.7
X80500.1	13484	1124.6	970.2	869.0	2384.8	465.7	1261.7
GQ015743.1	493925	22.0	110.2	36.2	39.4	97.1	44.3
GQ036643.1	426710	25327.0	25047.6	15595.3	22143.3	22978.4	20217.9
GQ052379.1	422190	18517.3	20234.4	3924.3	11008.4	9563.9	7964.6
GQ004499.1	505162	15174.4	13390.0	10078.9	15909.5	11249.6	12159.8
GQ100272.1	453700	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ042179.1	446159	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ042164.1	465460	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ016001.1	493665	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ061140.1	444725	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ028954.1	435562	7065.1	8222.9	8339.4	6323.4	10804.0	8674.9
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GQ061694.1	463421	1230.5	6258.6	6189.1	6773.7	1434.6	8212.5
GQ047542.1	406001	2590.3	3383.5	5382.4	3122.9	5002.9	3751.9
GQ019568.1	490098	3979.9	4648.2	1287.2	3296.5	3118.9	2128.0
GQ086044.1	408250	5649.8	11271.8	522.0	2651.0	916.3	1415.5
GQ043251.1	400614	3478.6	4698.5	1273.9	6447.2	1959.1	2141.5
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GQ041167.1	446115	6334.2	4856.4	13789.5	9736.9	13669.9	12349.1
GQ100225.1	396739	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9

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GQ064884.1 gg_id:465046 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ035613.1 gg_id:380947 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ061602.1 gg_id:371106 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw22
GQ075841.1 gg_id:422743 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ087084.1 gg_id:387281 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ086038.1 gg_id:408271 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ069454.1 gg_id:430402 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
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GQ042488.1 gg_id:379997 Topographical and Temporal Human Skin Microbiome skin nare clone nbw940h03c1
GQ039855.1 gg_id:440316 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
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GQ041876.1 gg_id:421902 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw933
GQ037939.1 gg_id:390622 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ034366.1 gg_id:434484 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35
GQ079422.1 gg_id:407308 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ032033.1 gg_id:387839 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ033665.1 gg_id:449784 Topographical and Temporal Human Skin Microbiome skin nare clone nbu337c09c1
GQ004481.1 gg_id:505182 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59a08c1
GQ088702.1 gg_id:427350 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

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GQ042477.1	392537	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ015697.1	493970	3150.5	3277.5	1410.8	1145.2	393.5	650.4
GQ033745.1	384374	22157.3	22167.1	11568.6	17525.3	22412.9	18549.6
GQ011568.1	498098	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ022567.1	487102	8902.8	8451.3	10045.9	14789.7	14021.6	17768.2
GQ032818.1	444410	3220.6	3706.1	3940.6	2684.7	5832.0	1270.3
GQ098394.1	446600	13977.8	14984.6	3186.3	5709.4	5043.3	4285.3
GQ042493.1	382855	1189.1	1076.6	2145.2	2012.1	1529.5	1299.3
GQ013354.1	496312	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ062669.1	462709	8655.5	17752.1	4291.3	8062.0	6708.7	6059.1
GQ033804.1	431565	132.9	137.4	302.3	463.9	67.2	88.7
GQ014972.1	494694	12243.1	10998.6	6420.7	7532.7	4835.7	7332.9
GQ054201.1	395525	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ036674.1	376460	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ071777.1	425596	20420.4	21556.7	11942.5	17213.0	19459.3	17261.0
GQ004549.1	505113	8299.8	7808.5	6836.1	12237.1	11365.8	10827.6
GQ011709.1	497957	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ070753.1	392309	22670.1	22699.5	13510.1	18162.2	15094.7	13517.5
GQ064884.1	465046	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ035613.1	380947	23.3	33.1	28.0	62.1	64.2	34.0
GQ061602.1	371106	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ075841.1	422743	11507.5	13930.8	6965.2	11441.8	7677.7	6852.5
GQ087084.1	387281	16777.2	16714.1	12933.2	14518.7	13056.7	9991.3
GQ086038.1	408271	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ069454.1	430402	14472.6	19829.3	9075.1	11479.3	14844.7	13332.8
GQ003849.1	505816	7114.0	8049.4	3407.0	4568.7	6572.9	5625.5
GQ042488.1	379997	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ039855.1	440316	3442.1	2964.8	4109.7	4767.4	2424.7	2671.1
GQ068413.1	454550	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ013453.1	496214	10469.4	10856.0	9260.3	11947.0	9217.0	9665.4
GQ061126.1	409476	591.5	489.8	390.5	2263.9	335.1	654.3
GQ061062.1	452892	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ041876.1	421902	10142.4	9742.9	10157.0	11905.4	8607.8	10230.1
GQ037939.1	390622	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ034366.1	434484	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ079422.1	407308	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ032033.1	387839	2059.7	1529.1	1401.3	4498.2	1405.0	4809.5
GQ033665.1	449784	7018.8	10070.7	6119.6	9896.2	16270.8	11477.0
GQ004481.1	505182	13344.9	12609.9	11069.9	13238.3	6454.8	7743.6
GQ088702.1	427350	17320.3	19620.4	12313.3	12991.4	13365.7	11907.2

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GQ011727.1 gg_id:497938 Topographical and Temporal Human Skin Microbiome skin nare clone nbw744d01c1
GQ034294.1 gg_id:437121 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35
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GQ073492.1 gg_id:381356 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl
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GQ034294.1	437121	647.7	1193.6	1476.9	2175.8	561.6	781.9
GQ049249.1	381419	21238.0	19368.1	23686.6	19398.7	17521.5	17529.3
GQ013784.1	495882	17348.4	20817.2	8978.3	15682.9	14023.9	12577.5
GQ073492.1	381356	470.8	369.0	380.6	1807.0	185.0	263.3
GQ083737.1	419982	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ083793.1	459821	555.4	620.3	1133.7	2664.3	243.3	654.3
GQ050746.1	377945	4936.7	3617.6	3202.3	10409.0	744.6	1377.3
GQ068538.1	411889	3171.7	4397.0	2445.7	3003.3	3045.9	2680.8
GQ046960.1	412036	24925.0	24039.8	17546.9	20521.7	23905.8	21495.0
GQ014516.1	495150	60.9	47.1	5824.3	70.8	2903.9	7923.9
GQ061108.1	388604	9798.3	8027.6	4157.1	9938.0	12381.5	11924.2
GQ058705.1	415077	12583.8	12219.8	7628.4	16235.4	10166.3	11585.7
GQ014026.1	495640	12622.4	12064.7	10401.0	14130.0	6649.1	9952.2
GQ011745.1	497920	6106.8	6749.1	2783.3	8006.3	4162.6	4563.0
GQ100186.1	443480	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ016691.1	492975	343.5	306.8	3148.9	690.3	8517.6	3978.8
GQ033844.1	423868	8851.9	9038.8	3347.2	3618.3	287.5	558.3
GQ014934.1	494730	17624.6	21320.1	9864.6	14320.9	18479.7	16050.5
GQ014752.1	494914	5295.0	5239.6	5381.8	6460.6	3570.0	3844.9
GQ046055.1	440128	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ014945.1	494721	7509.1	16381.3	6506.8	3953.3	15046.8	10009.5
GQ088660.1	389892	13209.4	14999.8	7139.6	12383.6	7606.8	7709.7
GQ035645.1	434430	5062.0	3066.2	2818.9	7962.1	2711.2	2774.4
GQ057396.1	396558	8922.3	10815.3	10508.8	8709.3	7559.3	6883.5
GQ100156.1	454517	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ100183.1	442997	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ014291.1	495375	875.0	932.2	1645.1	2202.3	372.8	477.6
GQ077413.1	398707	13694.9	12035.2	14848.1	15501.0	11737.8	9405.5
GQ102996.1	426836	1629.8	2217.7	353.0	1409.6	1088.5	3182.5
GQ015014.1	494652	8018.4	9970.3	8477.2	8822.0	7450.4	5123.0
GQ026279.1	400102	5450.1	3605.7	7521.0	6057.5	2669.4	2988.0
GQ061666.1	436332	4287.7	4661.5	3529.5	4884.1	5880.1	5940.5
GQ014298.1	495368	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ100222.1	449016	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ098656.1	463547	18006.4	16347.5	17922.7	18935.1	14595.8	16290.1
GQ040276.1	456047	3575.6	2484.7	1747.6	4679.8	555.3	1294.4
GQ006403.1	503262	14269.6	13038.1	9051.9	17282.4	16366.4	13013.5
GQ013350.1	496316	10650.2	9833.3	6542.5	12421.7	5815.1	8473.1
GQ062587.1	407917	489.9	741.3	333.0	2222.4	1013.1	3437.3

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GQ044804.1 gg_id:377879 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ004514.1 gg_id:505147 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59d07c1
GQ013423.1 gg_id:496243 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
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GQ013781.1 gg_id:495885 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ009522.1 gg_id:500146 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77
GQ011450.1 gg_id:498216 Topographical and Temporal Human Skin Microbiome skin nare clone nbw744a03c1
GQ054159.1 gg_id:417868 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099c
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GQ030175.1 gg_id:412765 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw868c1
GQ034274.1 gg_id:422839 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35
GQ043614.1 gg_id:408511 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1016d
GQ034551.1 gg_id:444463 Topographical and Temporal Human Skin Microbiome skin external auditory canal c
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GQ029352.1 gg_id:456451 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ045911.1 gg_id:453577 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ055959.1 gg_id:421461 Topographical and Temporal Human Skin Microbiome skin nare clone nbw1041e03c
GQ013879.1 gg_id:495787 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
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GQ058204.1 gg_id:389936 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ032118.1 gg_id:458114 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ035751.1 gg_id:451473 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu
GQ015801.1 gg_id:493866 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ015945.1 gg_id:493723 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ003896.1 gg_id:505765 Topographical and Temporal Human Skin Microbiome skin nare clone nbu58f11c1
GQ020696.1 gg_id:488972 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ006536.1 gg_id:503128 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu

GQ054056.1	457769	9148.4	8524.9	8097.5	14436.8	15215.5	13569.0
GQ017755.1	491913	12765.3	27667.7	13237.3	9164.0	16721.8	12172.5
GQ044804.1	377879	5666.2	5826.3	5002.5	10897.6	3977.3	8416.5
GQ004514.1	505147	3968.3	2477.3	1360.8	5704.7	2480.7	2828.5
GQ013423.1	496243	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ070193.1	409175	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ086043.1	452883	13203.8	12805.3	9237.5	12342.4	9577.4	9356.9
GQ013781.1	495885	4357.3	5118.3	3056.5	8180.7	3190.6	5300.2
GQ009522.1	500146	30841.2	29648.7	21659.3	23016.3	29765.3	26158.2
GQ011450.1	498216	385.6	354.8	217.4	1697.2	183.8	298.9
GQ054159.1	417868	13744.0	12926.8	11122.4	14805.6	13207.1	17059.5
GQ000880.1	469445	555.4	620.3	1133.7	2664.3	243.3	654.3
GQ030175.1	412765	7423.5	7729.7	4762.1	7467.6	7046.2	8132.2
GQ034274.1	422839	144.3	128.6	173.5	195.6	81.4	94.8
GQ043614.1	408511	8711.4	11881.9	5713.9	8140.0	6725.0	6073.6
GQ034551.1	444463	13269.6	13772.4	9796.6	12592.4	6703.2	7276.5
GQ044181.1	461329	16550.3	16721.1	5954.2	16734.4	10504.8	12357.4
GQ029352.1	456451	1237.7	3655.2	1168.4	783.1	4695.4	5484.6
GQ045911.1	453577	1033.0	1707.0	461.2	4343.7	4592.6	11990.3
GQ069895.1	411806	10416.1	11892.8	6809.3	9920.8	5287.6	5692.0
GQ014964.1	494702	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ055959.1	421461	6251.4	4947.6	1117.4	6807.2	1377.2	1495.4
GQ013879.1	495787	2481.9	1787.4	1260.3	6424.8	336.5	725.0
GQ071752.1	408006	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ058204.1	389936	4483.8	7077.2	1331.7	10064.6	1323.5	1773.9
GQ032118.1	458114	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ099990.1	377538	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ013387.1	496278	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ035603.1	378276	20617.3	20675.5	11668.2	15894.8	15994.9	14193.5
GQ013409.1	496257	15552.1	16114.4	14671.5	11582.0	8632.0	9831.2
GQ013334.1	496332	2043.1	2135.9	838.2	4848.1	655.6	763.2
GQ100149.1	380329	3260.8	3542.6	1224.6	3239.3	6567.1	5138.6
GQ042622.1	380445	949.5	874.5	2003.3	1870.9	517.0	635.4
GQ019602.1	490066	7637.5	7456.7	5511.5	4877.5	8992.5	9576.0
GQ036130.1	414314	10627.8	9152.8	11224.9	11882.8	10014.0	9622.7
GQ035751.1	451473	24896.0	23967.4	18008.1	22363.3	18496.6	17143.7
GQ015801.1	493866	2953.4	6212.1	5619.6	9358.6	1064.2	4200.6
GQ015945.1	493723	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ003896.1	505765	2790.6	1863.5	1132.7	5468.8	3909.6	4029.1
GQ020696.1	488972	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ006536.1	503128	2946.7	5081.5	23.2	1980.5	525.9	306.7

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GQ003887.1 gg_id:505774 Topographical and Temporal Human Skin Microbiome skin nare clone nbu58e09c1
GQ034945.1 gg_id:372934 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu329h1(
GQ338419.1 gg_id:524798 Corynebacterium accolens str. CHL-B21438
GQ040823.1 gg_id:467023 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw959a09c
GQ075668.1 gg_id:447972 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ067209.1 gg_id:374275 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ054197.1 gg_id:439216 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099g
GQ043488.1 gg_id:421827 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1014f0
GQ035263.1 gg_id:392274 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35
GQ026387.1 gg_id:416416 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ034129.1 gg_id:405040 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ060200.1 gg_id:467944 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ030035.1 gg_id:435017 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866c0
GQ025486.1 gg_id:456315 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
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GQ098633.1 gg_id:412340 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw704f
GQ016823.1 gg_id:492844 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825h0
GQ035638.1 gg_id:397245 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ028641.1 gg_id:381517 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
GQ090588.1 gg_id:423861 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
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GQ016167.1 gg_id:493500 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ069500.1 gg_id:467497 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
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GQ033863.1 gg_id:465590 Topographical and Temporal Human Skin Microbiome skin nare clone nbu340e11c1
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GQ100320.1 gg_id:463360 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480f01c1
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GQ083980.1 gg_id:446214 Topographical and Temporal Human Skin Microbiome skin nare clone nbw256e07c1
GQ076864.1 gg_id:467377 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154
GQ062839.1 gg_id:406990 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ088723.1 gg_id:387942 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

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GQ034945.1	372934	1410.9	1929.3	5618.0	3565.4	1744.2	1699.2
GQ338419.1	524798	1124.6	970.2	869.0	2384.8	465.7	1261.7
GQ040823.1	467023	12343.3	13504.6	6130.7	14928.2	8688.9	12705.6
GQ075668.1	447972	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ067209.1	374275	12191.8	11689.6	10794.4	14732.3	14767.4	13122.4
GQ054197.1	439216	2384.3	3316.3	948.9	4359.6	1450.3	1609.8
GQ043488.1	421827	8978.2	8146.9	14004.0	8787.3	7575.6	6898.0
GQ035263.1	392274	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ026387.1	416416	18928.5	17736.6	21330.2	16859.3	15961.1	15248.0
GQ034129.1	405040	6447.9	7953.6	3135.0	6737.9	3893.8	2875.9
GQ060200.1	467944	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ030035.1	435017	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ025486.1	456315	19573.0	20307.2	6422.5	13154.3	9058.3	7542.0
GQ053365.1	402462	13694.9	12035.2	14848.1	15501.0	11737.8	9405.5
GQ098633.1	412340	29219.2	29700.4	27665.5	24718.6	29300.0	27026.8
GQ016823.1	492844	12765.3	27667.7	13237.3	9164.0	16721.8	12172.5
GQ035638.1	397245	1024.1	1484.7	2226.2	2883.6	774.0	1045.2
GQ028641.1	381517	21379.7	21449.9	12096.3	17135.5	19145.6	16650.9
GQ090588.1	423861	24240.3	20558.4	18856.4	20136.2	18014.0	16560.7
GQ011783.1	497882	13643.5	14381.8	13792.8	10809.6	16812.8	12592.5
GQ042261.1	443248	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ017815.1	491851	1243.9	1956.8	1386.2	705.3	1156.5	630.7
GQ091856.1	427223	23924.9	22238.3	25402.0	22031.1	19630.5	20180.5
GQ114375.1	454226	4805.2	4128.2	4039.9	11188.4	5660.9	6525.8
GQ016167.1	493500	24357.3	23993.5	12860.2	21220.6	23393.6	21117.9
GQ069500.1	467497	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ062598.1	400426	13391.4	13574.5	8301.2	8776.1	14804.8	12342.1
GQ016082.1	493588	10839.0	13004.2	5294.8	10675.6	18593.2	16503.7
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GQ100203.1	395441	9804.2	11010.1	9648.0	6404.0	5872.3	5173.3
GQ004568.1	505093	3979.9	4648.2	1287.2	3296.5	3118.9	2128.0
GQ052973.1	460304	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ100320.1	463360	9246.3	7859.8	7444.2	11360.6	4295.5	4860.3
GQ061671.1	423828	13427.0	10771.7	13051.4	15640.1	5114.9	8352.2
GQ083980.1	446214	12481.3	10882.1	9206.9	13083.5	8320.5	9522.2
GQ076864.1	467377	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ062839.1	406990	1907.5	2024.9	59.3	125.0	2048.6	1522.5
GQ088723.1	387942	155.6	108.5	79.4	102.6	104.3	67.7

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GQ076577.1 gg_id:391130 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
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GQ042254.1 gg_id:434943 Topographical and Temporal Human Skin Microbiome skin nare clone nbw938b02c1
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GQ087347.1 gg_id:452012 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ056289.1 gg_id:466671 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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GQ014924.1 gg_id:494742 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8

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GQ042254.1	434943	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ088565.1	380845	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
FJ557823.1	529269	144.3	128.6	173.5	198.6	124.5	94.8
GQ042218.1	441987	9486.9	10671.9	6841.1	10466.2	6705.8	6242.7
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GQ041209.1	422390	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ015836.1	493830	12.1	24.5	19.0	22.0	96.3	40.0
GQ060464.1	384476	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ091516.1	434792	1002.2	2013.1	463.0	2156.1	416.9	468.9
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GQ100184.1	387255	14873.3	15385.8	7554.0	14251.8	12042.8	10069.8
GQ004536.1	505127	2440.2	1592.6	1328.0	5561.7	347.9	704.2
GQ068354.1	447905	698.7	596.5	380.6	3269.6	242.8	415.4
GQ077351.1	388793	6345.7	4724.3	4188.9	10544.9	541.8	1359.7
GQ061029.1	461605	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ033776.1	414380	14480.7	15449.6	5286.3	8066.3	6170.9	5042.9
GQ022856.1	486813	15928.8	15307.8	11298.4	15064.9	11169.6	11320.1
GQ042264.1	411337	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ087347.1	452012	4187.1	5170.6	6087.2	5234.5	7231.6	5189.3
GQ056289.1	466671	18052.3	16150.4	8054.4	18082.0	3496.1	5202.7
GQ001481.1	508182	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ030786.1	398219	185.1	145.3	173.5	238.6	182.6	104.1
GQ046223.1	398655	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ015066.1	494600	6759.3	13817.6	4956.0	3231.9	8901.5	9156.0
GQ046430.1	382057	8595.3	9106.9	3093.4	8408.8	2429.3	3244.1
FJ557842.1	526375	4895.6	3546.4	5267.1	7149.3	3423.5	3234.9
GQ042391.1	420764	1237.1	846.2	757.3	3296.5	308.3	654.3
GQ042165.1	455874	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ042249.1	460200	6978.6	8821.0	4023.1	3638.1	4014.0	4574.9
GQ054108.1	377082	26781.1	27222.2	16690.5	21837.0	27177.9	24108.6
GQ026247.1	468129	14809.1	13997.2	18168.1	11505.5	12700.6	11855.0
GQ082199.1	466739	14707.5	14502.4	10942.7	18109.9	15724.6	14869.7
GQ035538.1	380100	23753.6	22462.7	14371.2	19395.0	14854.0	12447.9
GQ042547.1	442082	3222.9	2510.1	10072.7	10401.5	1727.3	3635.8
GQ088598.1	443582	9637.3	11745.8	11229.2	9145.3	8305.5	7988.2
GQ108618.1	411315	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ014973.1	494693	9957.8	20645.1	2060.6	4430.7	4612.4	3211.2
GQ014924.1	494742	919.4	1027.2	1238.1	418.0	621.5	451.4

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GQ031037.1 gg_id:463170 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ035777.1 gg_id:398686 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu
GQ112472.1 gg_id:413986 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ077396.1 gg_id:425309 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ028476.1 gg_id:430410 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ034564.1 gg_id:375232 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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GQ040777.1 gg_id:450367 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958e09c
GQ077388.1 gg_id:422095 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ110888.1 gg_id:428903 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw

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GQ016628.1	493039	3705.0	2211.9	2045.3	5699.9	2535.1	8941.2
FJ557987.1	516668	9998.0	8905.0	6995.9	11004.2	3643.9	4670.7
GQ031037.1	463170	20494.3	20050.2	27010.0	18768.1	19601.0	17726.7
GQ069436.1	484566	448.8	959.0	426.8	517.7	619.0	1580.4
GQ088657.1	454452	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
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GQ042363.1	412935	6744.1	4849.0	5701.4	7102.3	4296.4	4323.9
GQ035777.1	398686	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ112472.1	413986	161.5	437.6	118.0	586.1	967.6	3155.2
GQ077396.1	425309	2075.2	2052.7	456.3	1523.0	4696.2	3415.0
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GQ075752.1	461448	5232.8	11005.0	4561.5	3161.5	8534.1	7866.0
GQ014904.1	494762	19620.5	21207.4	7571.0	16635.6	16453.8	15681.5
GQ013960.1	495706	22545.0	30836.1	22652.9	17160.3	23597.5	19811.6
GQ016625.1	493042	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ042406.1	411543	3047.5	1717.8	766.9	4451.1	254.1	523.2
GQ026881.1	376587	12682.7	11113.4	12927.4	12931.4	14299.5	12072.0
GQ012054.1	497612	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ069344.1	468065	1201.6	7421.3	355.7	657.5	176.7	245.6
GQ014831.1	494835	10505.9	10872.7	2640.2	9112.3	5753.1	5672.7
GQ003852.1	505810	7933.9	7803.8	2273.8	4398.7	3241.4	3484.9
GQ065612.1	441432	19339.2	19181.9	12519.8	18545.4	23540.2	20084.6
GQ100268.1	394402	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ080545.1	414377	2163.0	1850.4	1360.8	3680.4	1303.3	1524.1
GQ071477.1	448389	470.8	369.0	380.6	1807.0	185.0	263.3
GQ015099.1	494567	18197.3	19231.2	17199.1	17303.7	15658.2	16290.2
GQ011778.1	497888	14480.7	15449.6	5286.3	8066.3	6170.9	5042.9
GQ068975.1	433896	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ083334.1	462578	22204.8	21437.8	25548.5	20165.8	19286.5	18995.4
GQ011976.1	497688	20698.2	22315.3	11587.8	15159.7	17981.0	18568.9
GQ033726.1	416244	7124.6	6511.5	4834.5	6182.3	6079.1	4581.9
GQ042279.1	446251	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ028476.1	430410	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ034564.1	375232	144.3	128.6	5897.4	195.6	167.6	2884.4
GQ019996.1	489673	9675.4	7155.6	7137.4	10050.1	6028.1	7750.2
GQ040777.1	450367	405.3	620.3	1004.3	1319.0	190.1	558.2
GQ077388.1	422095	11617.1	9956.4	4585.8	15434.2	12427.2	11113.4
GQ100161.1	403875	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ042312.1	412679	385.6	354.8	217.4	1697.2	183.8	298.9
GQ110888.1	428903	919.4	1027.2	1238.1	418.0	621.5	451.4

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GQ077379.1 gg_id:452475 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ053958.1 gg_id:380440 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ003858.1 gg_id:505803 Topographical and Temporal Human Skin Microbiome skin nare clone nbu58c01c1
GQ013411.1 gg_id:496256 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ052463.1 gg_id:433865 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu536e08
GQ014325.1 gg_id:495341 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ015772.1 gg_id:493895 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ049388.1 gg_id:394683 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ112159.1 gg_id:424269 Topographical and Temporal Human Skin Microbiome skin nare clone nbw585c08c1
GQ008566.1 gg_id:501099 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ100115.1 gg_id:387409 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478b03c1
GQ035530.1 gg_id:400115 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
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GQ069334.1 gg_id:382647 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ046266.1 gg_id:386199 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ100250.1 gg_id:466143 Topographical and Temporal Human Skin Microbiome skin nare clone nbw479g06c1
GQ088664.1 gg_id:465382 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ042344.1 gg_id:457434 Topographical and Temporal Human Skin Microbiome skin nare clone nbw939b11c1
GQ010572.1 gg_id:499093 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ070330.1 gg_id:453541 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ100080.1 gg_id:406095 Topographical and Temporal Human Skin Microbiome skin nare clone nbw477f12c1
GQ101009.1 gg_id:399870 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw48
GQ015773.1 gg_id:493894 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ042265.1 gg_id:436871 Topographical and Temporal Human Skin Microbiome skin nare clone nbw938c02c1
GQ015687.1 gg_id:493980 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ081984.1 gg_id:391716 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11
GQ013872.1 gg_id:495794 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ005012.1 gg_id:504651 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65h0
GQ035545.1 gg_id:400397 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ016811.1 gg_id:492856 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw825g0
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GQ087693.1 gg_id:415281 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n

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GQ053958.1	380440	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ003858.1	505803	8457.5	7751.7	8754.9	9644.8	7495.9	5402.9
GQ013411.1	496256	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ052463.1	433865	5218.3	3096.4	14711.6	5491.5	4449.5	3703.4
GQ014325.1	495341	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ015772.1	493895	13117.2	18442.6	4736.0	10145.9	11421.6	11323.7
GQ014979.1	494686	9267.3	11790.8	3447.4	4626.9	3687.2	3129.8
GQ035764.1	431876	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ049388.1	394683	16399.4	20633.3	5410.6	16434.8	6895.2	8737.8
GQ112159.1	424269	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ008566.1	501099	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ100115.1	387409	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ035530.1	400115	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ003782.1	505881	1784.4	981.3	1427.6	3296.5	243.3	813.3
GQ069334.1	382647	6246.4	11927.1	4279.1	4536.7	5988.1	4161.9
GQ046266.1	386199	10265.3	9807.3	3220.0	12700.0	14833.6	18309.4
GQ100250.1	466143	2731.4	3480.1	1128.9	5397.0	1470.1	1728.3
GQ088664.1	465382	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ042344.1	457434	397.8	577.5	493.8	1031.4	172.0	461.9
GQ010572.1	499093	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ070330.1	453541	2732.1	2347.1	2861.1	5426.3	197.3	579.0
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GQ101009.1	399870	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ015773.1	493894	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ042265.1	436871	7179.7	9366.6	7657.0	10811.9	12503.5	14342.7
GQ015687.1	493980	13388.2	12553.3	18120.6	14295.3	11595.9	11087.2
GQ081984.1	391716	26987.8	26014.6	26882.8	22684.8	26972.8	24902.0
GQ013872.1	495794	559.4	844.4	97.9	1196.1	102.1	144.1
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GQ016811.1	492856	22264.0	24537.4	12950.0	21068.8	23773.2	21114.4
GQ077653.1	420840	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ046330.1	447266	13388.2	12553.3	15389.6	14295.3	10569.8	11797.0
GQ060289.1	406343	470.8	369.0	380.6	1807.0	185.0	263.3
GQ069448.1	462091	22752.5	26257.7	11867.4	17872.7	22574.5	20417.2
GQ006390.1	503274	11749.1	9370.5	7093.2	12099.3	6001.8	6453.2
GQ062148.1	457092	12.1	24.5	2960.3	22.0	102.1	2855.5
GQ087693.1	415281	37691.4	33672.5	18687.1	35371.3	23530.2	23932.3

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GQ083993.1 gg_id:457969 Topographical and Temporal Human Skin Microbiome skin nare clone nbw256f11c1
GQ032116.1 gg_id:419273 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ014407.1 gg_id:495259 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ014956.1 gg_id:494710 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ011935.1 gg_id:497731 Topographical and Temporal Human Skin Microbiome skin nare clone nbw747a01c1
GQ034361.1 gg_id:410168 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35
GQ100112.1 gg_id:436395 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478a12c1
GQ042262.1 gg_id:457616 Topographical and Temporal Human Skin Microbiome skin nare clone nbw938b11c1
GQ015863.1 gg_id:493804 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ062820.1 gg_id:466079 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ085950.1 gg_id:375063 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ054976.1 gg_id:419460 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ028616.1 gg_id:451908 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ077302.1 gg_id:454638 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ103520.1 gg_id:436524 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ033642.1 gg_id:427560 Topographical and Temporal Human Skin Microbiome skin nare clone nbu337a04c1

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GQ083993.1	457969	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ032116.1	419273	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ014407.1	495259	1497.1	1997.3	2969.3	2708.2	688.1	1140.8
GQ014956.1	494710	22305.7	23281.9	15127.7	16787.9	20562.1	19872.8
GQ011935.1	497731	14815.6	15440.9	12445.0	13565.6	17527.4	16808.5
GQ034361.1	410168	3953.1	2898.5	13721.3	5265.3	167.6	2751.3
GQ100112.1	436395	1933.4	1748.9	975.2	2201.9	293.4	653.0
GQ042262.1	457616	6848.5	6689.6	5143.3	6813.3	5826.1	5513.4
GQ015863.1	493804	4320.8	4372.7	7326.9	10247.4	3333.5	9248.2
GQ062820.1	466079	7328.9	5875.0	7439.1	10389.0	2275.0	2966.6
GQ085950.1	375063	14972.3	16008.1	5595.6	9440.1	6560.1	5394.9
GQ054976.1	419460	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ001553.1	508109	15555.9	18179.8	5075.4	12750.2	5051.9	11388.3
GQ036415.1	459334	15733.5	21760.6	20865.6	22848.7	14295.3	20709.3
GQ004477.1	505186	28428.1	27036.1	23120.8	24407.0	25801.7	25420.4
GQ042422.1	394066	14299.2	9041.3	17312.3	18241.3	7991.0	9780.4
GQ003794.1	505871	1629.8	2217.7	353.0	1409.6	1088.5	3182.5
GQ109403.1	418610	7357.0	21754.4	3323.0	4258.9	3802.4	4382.0
GQ040886.1	432759	470.8	369.0	380.6	1807.0	185.0	263.3
GQ003893.1	505769	7179.7	9366.6	7657.0	10811.9	12503.5	14342.7
GQ014955.1	494711	228.9	18563.5	9308.5	11735.4	259.1	9482.7
GQ090589.1	410569	1906.0	1050.1	3550.4	4616.2	894.5	1732.6
GQ020397.1	489271	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ054051.1	443956	21917.2	22176.8	23107.9	18777.8	19155.2	17448.5
GQ003342.1	506319	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ003807.1	505855	6779.8	5031.2	6996.6	5725.9	4422.1	4488.4
GQ057207.1	373540	9957.8	20645.1	2060.6	4430.7	4612.4	3211.2
GQ068604.1	441584	2566.4	2700.1	1104.0	2543.3	667.4	884.3
GQ070089.1	378300	12.1	24.5	19.0	22.0	97.1	40.0
GQ006272.1	503392	14560.8	17290.2	8983.6	13508.2	16575.0	14657.3
GQ032086.1	441861	9653.6	6134.8	16739.5	13692.5	6239.3	6847.2
GQ100068.1	415624	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ100126.1	461080	9849.1	11138.6	5486.6	6207.8	12562.7	9942.6
GQ020200.1	489468	13431.5	6932.9	1687.2	2296.4	796.2	3742.4
GQ100199.1	425701	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ013351.1	496315	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ028616.1	451908	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ077302.1	454638	9764.0	9031.7	5305.5	7429.1	5833.8	6411.5
GQ103520.1	436524	14628.2	13768.1	11338.4	14760.1	11997.8	11365.7
GQ033642.1	427560	6251.4	4947.6	1117.4	6807.2	1377.2	1495.4

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GQ033725.1	443966	11238.1	12261.1	1240.6	13716.2	4233.6	4294.2
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GQ062812.1	437212	73.2	149.1	59.3	82.5	149.8	75.2
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GQ042397.1	425704	3971.8	2819.5	3159.3	6920.7	392.5	1029.7
GQ068521.1	392386	961.9	1123.3	246.3	1455.0	2604.1	3246.5
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GQ035769.1	438004	13822.3	12954.1	6275.0	10661.4	8073.1	7493.1
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GQ070047.1	384185	19316.8	17314.7	18661.4	18847.8	14689.0	16190.7
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GQ030869.1	381961	185.1	145.3	173.5	238.6	182.6	104.1
GQ039749.1	463141	2126.7	1309.4	1338.8	4738.1	686.4	803.6
GQ081105.1	396176	1201.6	7421.3	355.7	657.5	176.7	245.6
GQ015061.1	494606	6100.3	16546.2	3467.7	1992.5	3923.0	4154.9
GQ062572.1	443378	489.9	741.3	333.0	2222.4	1013.1	3437.3
GQ102908.1	413351	14911.7	15146.0	9352.8	12302.1	14890.2	13542.8
GQ102222.1	438588	14911.7	15146.0	9352.8	12302.1	14890.2	13542.8
GQ022260.1	487408	7870.8	9535.4	3272.0	10462.4	8018.9	7234.2
GQ100021.1	398477	5457.4	4019.1	2110.1	8374.9	7528.5	7567.7
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GQ006249.1	503415	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ035543.1	377246	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4

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GQ055000.1 gg_id:397106 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ042182.1 gg_id:434537 Topographical and Temporal Human Skin Microbiome skin nare clone nbw937c05c1
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GQ035319.1 gg_id:393410 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu35(
GQ001078.1 gg_id:508584 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu1(
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GQ088548.1 gg_id:380314 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ042721.1 gg_id:396177 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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GQ091713.1 gg_id:411096 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
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GQ076803.1 gg_id:419480 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1153
GQ061143.1 gg_id:463102 Topographical and Temporal Human Skin Microbiome skin nare clone nbw10g09c1
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GQ075638.1 gg_id:394444 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
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GQ048369.1 gg_id:438728 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
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GQ035753.1 gg_id:442358 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ031962.1 gg_id:461743 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ005295.1 gg_id:504368 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ035668.1 gg_id:391472 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3

GQ062533.1	419864	3335.5	1823.9	3529.8	8959.3	221.6	744.4
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GQ043146.1	405537	8711.4	11881.9	5713.9	8140.0	6725.0	6073.6
GQ015083.1	494583	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ055000.1	397106	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ042182.1	434537	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ026109.1	378693	3185.8	2452.4	636.8	5464.3	3514.3	2547.1
GQ014341.1	495325	18865.3	18075.6	10539.9	17550.6	9031.6	10773.1
GQ068599.1	434615	10242.4	9919.5	9844.8	12942.0	6518.2	8886.1
GQ035319.1	393410	669.4	442.7	1607.2	580.0	460.4	328.6
GQ001078.1	508584	14472.6	19829.3	9075.1	11479.3	14844.7	13332.8
GQ046420.1	404754	8833.7	8434.9	3388.8	8625.1	14556.6	11789.7
GQ088548.1	380314	10416.1	11892.8	6809.3	9920.8	5287.6	5692.0
GQ042721.1	396177	222.2	264.7	180.5	273.1	204.7	111.1
GQ033680.1	401419	6111.0	6050.5	5116.9	4807.1	8625.1	8286.0
GQ091713.1	411096	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ062504.1	417143	73.2	149.1	59.3	82.5	149.8	75.2
GQ060774.1	418671	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ076803.1	419480	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ061143.1	463102	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ061670.1	443515	9509.7	11604.5	10231.0	9514.3	13468.2	14129.6
GQ100025.1	421676	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ083917.1	419464	25991.9	25330.4	16491.7	21986.8	25505.1	21420.6
GQ015051.1	494615	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ042392.1	454053	16150.3	16067.3	8997.3	12063.5	8406.8	7786.0
GQ075638.1	394444	4187.1	5170.6	6087.2	5234.5	7231.6	5189.3
GQ013367.1	496298	7717.0	17117.9	2538.0	6763.2	2338.3	2824.1
GQ013416.1	496250	21936.9	24967.8	15778.3	18544.1	21117.8	18854.1
GQ086045.1	468277	8999.3	9667.5	7291.2	9019.8	8582.9	6164.8
GQ035516.1	421789	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ042401.1	466909	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ014413.1	495254	26335.2	26187.0	15272.4	20975.7	27640.5	21687.8
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GQ062394.1	424808	15488.1	17891.4	11902.2	13572.8	10254.1	13920.5
GQ003843.1	505818	1775.5	1095.9	1134.1	3323.4	284.1	893.2
GQ035753.1	442358	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ031962.1	461743	20357.6	17068.4	11050.6	10334.0	17146.2	14468.1
GQ005295.1	504368	22538.1	21096.5	22331.7	21455.3	20198.7	20147.9
GQ035668.1	391472	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4

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GQ000288.1 gg_id:468854 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu11
GQ064912.1 gg_id:414178 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ060565.1 gg_id:463519 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03d02
GQ047103.1 gg_id:397983 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ014489.1 gg_id:495177 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ042672.1 gg_id:433401 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ077676.1 gg_id:455549 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ080656.1 gg_id:409585 Topographical and Temporal Human Skin Microbiome skin nare clone nbw1139e12c
GQ068426.1 gg_id:421743 Topographical and Temporal Human Skin Microbiome skin nare clone nbw150d11c1
GQ004876.1 gg_id:504787 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ100303.1 gg_id:395078 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480d05c1
GQ014998.1 gg_id:494668 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
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GQ060870.1 gg_id:430674 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw06f
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GQ083929.1 gg_id:439717 Topographical and Temporal Human Skin Microbiome skin nare clone nbw255g02c1
GQ069264.1 gg_id:394668 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw241d0
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GQ100322.1 gg_id:390018 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480f05c1
GQ015064.1 gg_id:494602 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
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GQ042298.1 gg_id:391138 Topographical and Temporal Human Skin Microbiome skin nare clone nbw938f04c1

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GQ000288.1	468854	21224.1	20654.5	14386.7	18073.1	14809.7	16907.4
GQ064912.1	414178	6345.7	4724.3	4188.9	10544.9	541.8	1359.7
GQ060565.1	463519	3090.1	3858.7	805.4	4059.1	2389.7	2408.5
GQ047103.1	397983	3225.8	2151.8	18387.5	12104.9	105.7	242.5
GQ014489.1	495177	3637.8	5119.7	2542.7	4530.8	4767.3	3948.6
GQ042672.1	433401	3378.0	3899.2	631.9	3350.5	5033.4	4426.3
GQ077676.1	455549	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ080656.1	409585	6203.5	9012.0	10126.0	8820.6	6535.5	8170.2
GQ068426.1	421743	10573.5	9991.6	14040.5	8046.6	7979.9	7533.7
GQ004876.1	504787	1119.7	1429.6	557.9	2726.3	330.1	561.6
GQ100303.1	395078	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ014998.1	494668	12765.3	27667.7	13237.3	9164.0	16721.8	12172.5
GQ083931.1	393040	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ035651.1	440287	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ038243.1	382704	18598.9	18628.6	15911.5	16725.3	12453.5	12737.4
GQ049893.1	397708	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ045373.1	468558	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ012281.1	497385	1652.4	1632.6	1509.5	3296.5	3064.4	1490.8
GQ102263.1	381990	691.6	718.4	380.6	1827.8	322.2	654.3
GQ013786.1	495879	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ042215.1	385765	1023.9	1647.1	1156.4	3317.6	706.6	838.6
GQ013820.1	495846	2821.7	4358.2	946.9	2311.8	6521.6	4928.6
GQ034380.1	417866	594.7	1144.7	418.0	1211.5	285.1	318.8
GQ100050.1	459321	15020.6	11843.1	22812.9	20956.9	14224.0	15781.5
GQ011891.1	497775	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ110856.1	430560	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ061677.1	395661	1680.3	1048.9	732.5	4211.5	417.2	759.9
GQ060670.1	455735	16125.2	17129.5	4880.2	16096.6	12446.2	9999.6
GQ012252.1	497414	1147.6	1060.3	1498.4	3296.5	4883.4	2123.2
GQ062585.1	389578	1515.9	2176.4	3430.5	1159.5	1049.4	3613.3
GQ015943.1	493724	19025.5	20239.8	7540.4	12816.3	9128.6	7376.2
GQ060870.1	430674	14809.1	13997.2	18168.1	11505.5	12700.6	11855.0
GQ004639.1	505021	8884.9	7045.2	4300.9	7695.0	6629.5	6185.3
GQ083929.1	439717	1443.5	1018.1	1794.6	4671.3	243.3	509.4
GQ069264.1	394668	3290.9	3209.7	3538.1	3307.1	4405.0	4274.6
GQ015019.1	494647	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ100322.1	390018	26104.3	27056.8	18103.3	21388.0	27624.0	23375.8
GQ015064.1	494602	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ077280.1	391844	26633.3	29329.8	15060.5	22013.5	27071.1	22938.2
GQ042298.1	391138	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9

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GQ061020.1 gg_id:456801 Topographical and Temporal Human Skin Microbiome skin nare clone nbw09c03c1
AJ439344.1 gg_id:83943 Corynebacterium segmentosum str. CIP107068 (CCUG37878)
GQ083894.1 gg_id:435564 Topographical and Temporal Human Skin Microbiome skin nare clone nbw255c07c1
GQ035785.1 gg_id:376230 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ014975.1 gg_id:494690 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ015029.1 gg_id:494637 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ083897.1 gg_id:458201 Topographical and Temporal Human Skin Microbiome skin nare clone nbw255c10c1
GQ036372.1 gg_id:456438 Topographical and Temporal Human Skin Microbiome skin palm clone nbu363e08c1
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GQ015028.1 gg_id:494638 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
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GQ033223.1 gg_id:425061 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ019339.1 gg_id:490328 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ055035.1 gg_id:421573 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ085979.1 gg_id:448706 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ076430.1 gg_id:429248 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7
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GQ011896.1	497769	716.1	1169.5	1515.8	1278.3	1247.1	1451.7
GQ104602.1	466522	691.6	718.4	380.6	1827.8	322.2	654.3
GQ083940.1	384268	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ061020.1	456801	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
AJ439344.1	83943	1124.6	970.2	869.0	2384.8	465.7	1261.7
GQ083894.1	435564	3187.6	2753.0	4640.3	3985.6	4809.3	3770.3
GQ035785.1	376230	4366.6	20197.9	23214.6	17465.0	1279.3	941.9
GQ014975.1	494690	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ015029.1	494637	11648.8	13742.1	10583.7	10593.2	7853.7	10434.4
GQ083897.1	458201	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ036372.1	456438	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ065939.1	374572	12556.4	12228.0	6476.1	9383.3	6187.5	4728.9
GQ015057.1	494609	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ013365.1	496302	10416.1	11892.8	6809.3	9920.8	5287.6	5692.0
GQ071821.1	422392	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ015078.1	494588	2748.1	2451.1	5968.1	6493.5	598.4	1219.3
GQ026812.1	393313	25431.4	24511.1	27431.4	23155.0	23668.6	22576.4
GQ015028.1	494638	14592.5	15796.2	13859.6	14375.0	15156.2	12608.7
GQ015042.1	494624	3113.4	4359.7	829.5	2081.7	6422.7	4513.0
GQ058079.1	418846	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ042330.1	428439	6779.8	5031.2	6996.6	5725.9	4422.1	4488.4
GQ042089.1	454579	24589.2	24607.8	20445.4	19070.0	23004.6	21939.7
GQ033223.1	425061	9491.6	7512.0	10155.7	12217.6	6009.7	7525.7
GQ019339.1	490328	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ055035.1	421573	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ085979.1	448706	3090.1	3858.7	805.4	4059.1	2389.7	2408.5
GQ016246.1	493421	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ033309.1	451166	8418.8	8310.0	7891.0	8665.4	6032.8	5469.0
GQ050762.1	451796	18693.4	19305.4	7927.3	12442.2	9982.6	7661.6
GQ100075.1	400585	3606.0	2748.7	7838.1	11146.2	1756.5	3831.4
GQ016149.1	493518	684.3	1091.9	1040.5	1549.8	1081.0	1317.2
GQ054100.1	375692	7322.2	7055.7	8368.9	7444.9	6601.7	6813.2
GQ043768.1	462114	3094.6	2682.6	497.8	1812.0	280.9	341.2
GQ076430.1	429248	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ033807.1	449100	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ035741.1	435411	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ083742.1	390515	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ015055.1	494607	14633.8	14937.9	8763.6	13524.5	8166.8	9858.1
GQ100163.1	424002	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9

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GQ053005.1 gg_id:401018 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbu
GQ013857.1 gg_id:495808 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ070289.1 gg_id:373494 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
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GQ014345.1 gg_id:495320 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ028153.1 gg_id:425067 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
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GQ046049.1	392627	15332.9	13604.9	8395.1	17423.7	17668.6	18547.2
GQ042414.1	431868	9644.8	9202.2	4702.7	9243.2	905.8	1931.7
GQ100045.1	459447	12759.0	15201.2	6385.4	12498.8	9530.3	8555.8
GQ092347.1	412129	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ042348.1	436418	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ064462.1	455253	8692.4	9495.4	6345.1	14280.3	13299.8	14200.6
GQ090622.1	387190	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ014542.1	495124	1605.1	2930.9	298.0	399.5	1799.8	6872.0
GQ014854.1	494812	12.1	24.5	19.0	22.0	97.1	40.0
GQ028547.1	452670	13881.7	11892.8	9071.4	19135.1	7016.1	7571.6
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GQ028307.1	398929	12.1	24.5	19.0	22.0	97.1	40.0
GQ003877.1	505784	25194.2	25764.4	16897.1	22382.5	25355.3	23184.2
GQ016264.1	493403	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ053005.1	401018	16683.5	16881.4	4008.4	16868.3	11473.6	15504.1
GQ013857.1	495808	3422.7	2349.5	1587.6	4235.9	2697.6	3330.3
GQ070289.1	373494	926.2	2808.9	1450.2	327.9	7373.1	2752.5
GQ043914.1	450610	1349.5	1898.4	2313.5	939.3	4728.2	5513.6
GQ014345.1	495320	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ028153.1	425067	10391.8	8400.6	2336.0	13942.6	13194.4	12724.0
GQ082497.1	373232	32.4	115.8	23.2	39.4	97.1	65.8
GQ017771.1	491897	322.0	614.5	450.6	352.1	102.1	53.2
GQ069563.1	428703	11515.9	26500.4	9387.1	9090.6	14016.4	12144.0
GQ014866.1	494800	10127.8	10936.1	4166.2	12120.1	8084.4	11528.2
GQ011969.1	497697	1629.8	2217.7	353.0	1409.6	1088.5	3182.5
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GQ061657.1	438885	4278.7	7348.8	1493.6	4765.1	1561.6	1421.0
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GQ080489.1 gg_id:440915 Topographical and Temporal Human Skin Microbiome skin nare clone nbw1137d06c
GQ009280.1 gg_id:500385 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ083753.1 gg_id:444522 Topographical and Temporal Human Skin Microbiome skin nare clone nbw253c07c1
GQ100127.1 gg_id:417088 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478c03c1
GQ100054.1 gg_id:389627 Topographical and Temporal Human Skin Microbiome skin nare clone nbw477d08c1
GQ100174.1 gg_id:376422 Topographical and Temporal Human Skin Microbiome skin nare clone nbw478g07c1
GQ087984.1 gg_id:416182 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ028182.1 gg_id:455261 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ033655.1 gg_id:447472 Topographical and Temporal Human Skin Microbiome skin nare clone nbu337b07c1

GQ077714.1	401471	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ014951.1	494715	9414.3	12258.1	9477.1	10261.0	13205.4	14298.5
GQ014850.1	494816	7717.0	17117.9	2538.0	6763.2	2338.3	2824.1
GQ083777.1	458088	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ022456.1	487213	1464.6	1056.8	2595.4	4029.9	617.9	765.1
GQ083020.1	380557	13431.5	6932.9	1687.2	2296.4	796.2	3742.4
GQ085881.1	432848	4790.0	8228.9	3589.6	7708.9	3038.1	5125.0
GQ083782.1	419377	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ013758.1	495908	4643.7	5747.2	4213.3	5301.8	4834.5	3000.1
GQ083949.1	412579	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ014887.1	494779	208.8	322.4	578.2	305.6	104.3	103.6
GQ031608.1	466594	22851.9	21973.4	13582.2	20286.8	17343.8	15962.9
GQ013339.1	496327	1201.6	7421.3	355.7	657.5	176.7	245.6
GQ077357.1	434623	607.6	988.7	665.0	783.9	923.9	2391.3
GQ048364.1	385362	635.5	682.1	1598.2	1437.3	482.5	681.8
GQ014402.1	495263	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ087651.1	438029	986.8	913.8	661.1	2902.6	1089.0	1489.8
GQ083975.1	406094	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ058437.1	452214	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ077661.1	419357	23395.6	23013.1	13923.6	19771.8	22858.9	20904.8
GQ016702.1	492965	24454.5	24956.4	12374.4	19134.6	26718.4	20188.3
GQ006546.1	503117	14234.1	15345.7	6507.2	14934.2	13832.7	14643.0
GQ004513.1	505149	15269.3	13398.0	6278.0	11712.2	8273.6	7541.6
GQ061689.1	417843	8352.8	11927.8	5808.7	9692.5	7410.5	10726.5
GQ080525.1	417162	12853.1	14248.4	8845.8	13117.6	9833.9	10009.4
GQ090511.1	394938	30536.1	32425.2	27005.4	26694.8	31408.8	28253.3
GQ070213.1	417795	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ083872.1	386244	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ085940.1	374003	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ099229.1	371515	17140.0	19582.5	12945.3	17023.5	12804.3	11397.4
GQ011724.1	497941	14882.4	16270.9	6115.4	9431.8	7679.6	5922.7
GQ014987.1	494680	9643.4	14011.1	7792.4	9153.3	5486.3	6031.9
GQ080489.1	440915	3128.7	1832.3	6001.1	4528.1	182.3	640.6
GQ009280.1	500385	26876.8	25632.1	25122.5	23234.2	24121.0	21164.3
GQ083753.1	444522	4575.6	3961.0	4011.9	3930.5	1975.6	4153.6
GQ100127.1	417088	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ100054.1	389627	1078.6	1206.4	792.3	1401.6	715.7	1799.8
GQ100174.1	376422	4119.5	3801.8	1144.1	6916.2	4970.2	5995.9
GQ087984.1	416182	18625.3	20454.5	13396.2	16321.6	23790.4	22427.4
GQ028182.1	455261	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ033655.1	447472	585.8	1002.2	673.0	956.6	1147.9	2176.0

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GQ012859.1 gg_id:496806 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ014936.1 gg_id:494731 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ059841.1 gg_id:421087 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ046271.1 gg_id:459784 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
GQ015097.1 gg_id:494571 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ015777.1 gg_id:493890 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ071017.1 gg_id:443748 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ054727.1 gg_id:443605 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1100e
GQ077087.1 gg_id:460716 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1206g
GQ100227.1 gg_id:430757 Topographical and Temporal Human Skin Microbiome skin nare clone nbw479e04c1
GQ054176.1 gg_id:415876 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1099e
GQ009213.1 gg_id:500452 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ075263.1 gg_id:439536 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ042282.1 gg_id:435603 Topographical and Temporal Human Skin Microbiome skin nare clone nbw938d11c1
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GQ013792.1 gg_id:495874 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
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GQ026982.1 gg_id:379572 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ017373.1 gg_id:492294 Topographical and Temporal Human Skin Microbiome skin nare clone nbu120a06c1
GQ011752.1 gg_id:497915 Topographical and Temporal Human Skin Microbiome skin nare clone nbw744f04c1
GQ039972.1 gg_id:457967 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ050440.1 gg_id:449609 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu485g
GQ011807.1 gg_id:497859 Topographical and Temporal Human Skin Microbiome skin nare clone nbw745c06c1
GQ070206.1 gg_id:446715 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ066920.1 gg_id:391106 Topographical and Temporal Human Skin Microbiome skin back clone nbw730e08c1
GQ044157.1 gg_id:412225 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1019g
GQ077298.1 gg_id:456457 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
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GQ071825.1 gg_id:460259 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ108612.1 gg_id:411835 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6
GQ035592.1 gg_id:427704 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
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GQ077766.1 gg_id:442224 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ015096.1 gg_id:494570 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8

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GQ012859.1	496806	7124.6	6511.5	4834.5	6182.3	6079.1	4581.9
GQ014936.1	494731	13083.2	15070.0	9989.8	11490.2	8103.5	7381.3
GQ059841.1	421087	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ046271.1	459784	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0
GQ015097.1	494571	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ015777.1	493890	15003.4	11651.6	9298.6	15468.6	12241.1	12074.1
GQ071017.1	443748	3478.6	4698.5	1273.9	6447.2	1959.1	2141.5
GQ054727.1	443605	1002.2	2013.1	463.0	2156.1	416.9	468.9
GQ077087.1	460716	9894.2	12247.2	10704.5	15304.6	17430.6	19318.2
GQ100227.1	430757	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ054176.1	415876	5479.3	5806.8	5597.8	8525.2	5911.6	7593.0
GQ009213.1	500452	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ075263.1	439536	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ042282.1	435603	9936.2	11450.2	7977.5	10149.0	5516.6	6180.1
GQ106306.1	436522	7564.0	7345.6	4417.8	9820.7	6444.4	5298.5
GQ100096.1	466181	11728.4	9051.0	4415.7	14168.4	9034.1	12692.6
GQ068422.1	427514	15073.9	14389.0	15283.3	15076.1	13343.2	13333.8
GQ061136.1	418688	22108.7	22296.1	20361.2	19150.2	19169.8	17546.2
GQ013792.1	495874	20073.4	26261.2	11561.1	15201.9	20345.9	18382.6
GQ043007.1	398567	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ026982.1	379572	4298.1	2566.9	1936.1	8988.1	532.1	1243.5
GQ017373.1	492294	2079.8	1095.9	911.1	3296.5	267.7	665.6
GQ011752.1	497915	1237.1	846.2	757.3	3296.5	243.3	654.3
GQ039972.1	457967	7514.8	7259.0	9768.5	8769.7	8827.6	9644.0
GQ050440.1	449609	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ011807.1	497859	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ070206.1	446715	3383.6	4717.2	1718.9	2513.3	7318.8	5767.7
GQ066920.1	391106	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ044157.1	412225	3882.3	3491.7	1644.1	7152.1	2060.1	1949.6
GQ077298.1	456457	27175.4	26365.2	15376.4	22036.1	25048.4	24167.0
GQ101293.1	400411	18207.5	16930.6	16136.8	17420.8	11408.5	11615.7
GQ071825.1	460259	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ100325.1	396839	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ061082.1	379886	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ108612.1	411835	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ035592.1	427704	13431.5	6932.9	1687.2	2296.4	796.2	3742.4
GQ011826.1	497839	591.5	489.8	390.5	2263.9	335.1	654.3
GQ042485.1	377773	16545.4	17296.7	6522.3	9242.6	6185.8	4649.0
GQ077766.1	442224	3090.1	3858.7	805.4	4059.1	2389.7	2408.5
GQ015096.1	494570	8922.3	10815.3	10508.8	8709.3	7559.3	6883.5

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GQ016644.1 gg_id:493023 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw

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FM874479.1	367054	699.4	1223.6	99.5	231.3	548.6	3095.8
GQ061691.1	415327	874.1	929.8	779.2	2887.1	543.5	823.0
GQ042444.1	425905	6978.6	8821.0	4023.1	3638.1	4014.0	4574.9
GQ069846.1	383474	11534.3	17752.1	8377.3	8081.7	6704.0	11874.0
GQ014548.1	495118	12765.3	27667.7	13237.3	9164.0	16721.8	12172.5
GQ004574.1	505088	6251.4	4947.6	1117.4	6807.2	1377.2	1495.4
GQ043157.1	399563	187.0	160.3	124.3	224.3	263.9	215.0
GQ014906.1	494760	21889.2	25324.7	20222.3	18738.8	19147.0	17441.2
GQ100323.1	455989	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
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GQ013407.1	496259	10845.7	12620.1	7419.0	8776.6	6498.5	6833.5
GQ071758.1	442391	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ036024.1	387472	7688.9	9272.0	5134.2	9012.5	2750.3	2543.4
GQ083956.1	432572	7467.3	6368.5	5745.8	7771.7	3735.1	4320.1
GQ010784.1	498882	16063.4	18091.0	6823.7	13052.6	5568.8	7385.3
GQ042271.1	454593	7124.6	6511.5	4834.5	6182.3	6079.1	4581.9
GQ020085.1	489583	2115.9	2375.6	1723.8	3296.5	4786.4	5904.6
GQ111873.1	429095	5629.2	4657.2	10563.3	13979.2	1822.5	2955.5
GQ080874.1	405215	2455.4	2305.4	2153.0	2301.0	1819.4	1450.4
GQ083798.1	446682	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ011819.1	497847	3997.3	3518.2	4408.7	8600.1	6283.4	8030.7
GQ000929.1	508733	4373.0	5210.8	1458.8	3182.1	10635.3	8284.6
GQ004630.1	505032	6528.0	6183.8	1077.4	4296.6	1007.3	1835.5
GQ069401.1	466425	2424.0	4231.3	4042.6	3034.5	4849.0	3291.0
GQ013812.1	495854	130.2	501.8	506.6	165.2	196.5	395.9
GQ075844.1	462984	19.1	2355.1	23.2	32.2	102.1	53.2
GQ044799.1	399484	23685.7	24113.3	11803.2	15236.9	15931.3	12714.3
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GQ004601.1	505057	9349.8	9497.6	952.3	5477.7	3950.1	4550.3
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GQ068306.1	448168	785.5	846.2	450.2	3296.5	243.3	654.3
GQ083746.1	438231	14068.0	13792.2	6637.7	11859.2	7319.8	7019.8
GQ029993.1	389219	7381.7	8814.2	2885.5	6889.3	8903.9	8271.2
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GQ042827.1	452400	15449.3	17239.9	7647.5	14583.7	8986.4	8706.1
GQ069689.1	442959	9117.9	12200.1	4569.0	9611.1	6754.2	6269.1
GQ100237.1	414877	10097.1	9348.1	6497.6	11439.1	8687.0	7980.5
GQ016644.1	493023	5774.3	4730.8	7551.4	12905.7	12219.4	10367.3

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GQ010018.1 gg_id:499647 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw
GQ098349.1 gg_id:410236 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw558c
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GQ047598.1 gg_id:444876 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu5
GQ088676.1 gg_id:389478 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ065773.1 gg_id:372683 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw92g06c
GQ083973.1 gg_id:392550 Topographical and Temporal Human Skin Microbiome skin nare clone nbw256d10c1
GQ069258.1 gg_id:381319 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw241d0
GQ014370.1 gg_id:495295 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ003903.1 gg_id:505759 Topographical and Temporal Human Skin Microbiome skin nare clone nbu58g09c1
GQ042169.1 gg_id:423558 Topographical and Temporal Human Skin Microbiome skin nare clone nbw937b01c1
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GQ112212.1 gg_id:381887 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ031477.1 gg_id:382923 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw874e
GQ062119.1 gg_id:384128 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw28b1
GQ042260.1 gg_id:393180 Topographical and Temporal Human Skin Microbiome skin nare clone nbw938b09c1
GQ027956.1 gg_id:381122 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ050760.1 gg_id:407176 Topographical and Temporal Human Skin Microbiome skin nare clone nbu438d10c1
GQ052071.1 gg_id:432989 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu5
GQ083954.1 gg_id:454971 Topographical and Temporal Human Skin Microbiome skin nare clone nbw256b10c1
GQ079485.1 gg_id:439234 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n
GQ075840.1 gg_id:404386 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ003902.1 gg_id:505760 Topographical and Temporal Human Skin Microbiome skin nare clone nbu58g08c1
GQ004488.1 gg_id:505174 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59b05c1
GQ049183.1 gg_id:400287 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu470d01
GQ062324.1 gg_id:392523 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv

GQ062576.1	451476	1437.6	970.1	757.3	3296.5	202.5	571.5
GQ013391.1	496274	75.1	179.1	23.2	68.2	231.2	186.0
GQ100152.1	384127	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ100333.1	465883	9605.6	9104.5	8010.7	12858.6	4547.0	4924.8
GQ010018.1	499647	16880.6	17084.5	18364.5	17938.7	22719.9	17394.5
GQ098349.1	410236	5781.0	4123.0	7842.5	13068.7	2742.9	3450.2
GQ075221.1	402185	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ013745.1	495921	9125.4	8293.2	4400.3	13736.2	10841.8	13855.5
GQ083822.1	425852	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ015093.1	494574	15886.4	20938.4	16046.9	13004.8	17168.7	13747.2
GQ013817.1	495849	10127.8	10936.1	4166.2	12120.1	8084.4	11528.2
GQ003850.1	505812	19717.3	19219.7	9147.3	15764.3	19245.2	17210.0
GQ108664.1	456163	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ091712.1	449247	17852.7	17930.5	15997.6	15326.5	13814.8	13712.8
GQ003870.1	505791	14249.6	15566.1	14379.8	9419.2	9138.4	6965.1
GQ006423.1	503241	11100.1	12623.1	9649.3	10854.4	10447.5	8079.3
GQ061015.1	402995	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ076450.1	386744	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ047598.1	444876	1031.3	584.3	2452.9	574.2	654.3	480.3
GQ088676.1	389478	12.1	24.5	19.0	22.0	97.1	40.0
GQ065773.1	372683	11721.3	24349.2	8836.8	7469.1	12995.8	10654.4
GQ083973.1	392550	25896.0	25228.0	19831.3	21032.5	16913.6	16593.4
GQ069258.1	381319	470.8	369.0	380.6	1807.0	185.0	263.3
GQ014370.1	495295	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ003903.1	505759	22420.2	21497.5	24809.3	19164.3	19950.4	19723.2
GQ042169.1	423558	1275.8	846.2	818.4	3296.5	383.8	654.3
GQ004558.1	505103	385.6	354.8	217.4	1697.2	183.8	298.9
GQ112212.1	381887	18823.5	16490.6	21251.5	19440.9	15253.2	15654.4
GQ031477.1	382923	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ062119.1	384128	12050.7	16610.0	8340.0	8979.4	10947.5	10022.0
GQ042260.1	393180	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ027956.1	381122	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ050760.1	407176	7871.0	5177.7	1151.8	7434.1	2791.1	893.2
GQ052071.1	432989	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ083954.1	454971	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ079485.1	439234	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ075840.1	404386	11730.4	16620.1	5310.9	9837.9	5626.8	5441.4
GQ003902.1	505760	4529.1	7387.0	1113.3	5465.7	1557.4	2169.2
GQ004488.1	505174	28196.2	27930.7	21535.3	22830.0	28754.8	25047.9
GQ049183.1	400287	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
GQ062324.1	392523	5725.6	6169.8	1374.0	7939.6	2584.7	1828.9

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GQ083740.1 gg_id:387168 Topographical and Temporal Human Skin Microbiome skin nare clone nbw253a10c1
GQ042217.1 gg_id:376193 Topographical and Temporal Human Skin Microbiome skin nare clone nbw937f05c1
GQ100339.1 gg_id:399228 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480h02c1
GQ028172.1 gg_id:404812 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc
GQ100332.1 gg_id:449049 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480g06c1
GQ061005.1 gg_id:413449 Topographical and Temporal Human Skin Microbiome skin nare clone nbw09a10c1
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GQ042583.1 gg_id:396772 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ034455.1 gg_id:442713 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
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GQ061962.1 gg_id:437149 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw26d1
GQ003830.1 gg_id:505832 Topographical and Temporal Human Skin Microbiome skin nare clone nbu57g12c1
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GQ032342.1 gg_id:413046 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu541c06
GQ028940.1 gg_id:374738 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw85
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GQ101525.1 gg_id:443183 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw496b
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GQ009169.1 gg_id:500496 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw

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GQ083740.1	387168	1062.0	1501.6	916.5	1498.2	2564.8	3638.8
GQ042217.1	376193	22402.9	20587.4	22634.6	20044.0	19475.7	18769.8
GQ100339.1	399228	1804.4	1952.4	2005.7	3296.5	7464.1	3172.5
GQ028172.1	404812	3094.6	2682.6	497.8	1812.0	280.9	341.2
GQ100332.1	449049	7317.7	7478.6	5152.0	6483.1	7763.0	6748.9
GQ061005.1	413449	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ013380.1	496285	4187.1	5170.6	6087.2	5234.5	7231.6	5189.3
GQ042208.1	431350	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ082599.1	442444	32.4	115.8	23.2	39.4	97.1	65.8
GQ011858.1	497808	9331.7	8875.8	9035.8	13926.8	8903.9	10406.2
GQ046177.1	378516	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ042583.1	396772	21964.9	21864.5	18029.0	18583.1	21125.9	18861.3
GQ034455.1	442713	14856.9	14168.9	13408.0	13567.5	12406.3	12033.8
GQ083841.1	424391	1775.5	1095.9	1134.1	3323.4	284.1	893.2
GQ077326.1	429642	298.7	636.4	304.7	1148.3	1777.6	6220.2
GQ013456.1	496210	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ061962.1	437149	12.1	24.5	2960.3	22.0	102.1	2855.5
GQ003830.1	505832	11432.5	12457.7	6412.0	11861.2	11670.5	12090.9
GQ042468.1	372107	6111.0	6050.5	5116.9	4807.1	8625.1	8286.0
GQ004631.1	505031	9841.3	9964.8	11675.3	10617.6	14451.4	10179.8
GQ032342.1	413046	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5
GQ028940.1	374738	14069.6	11965.9	13463.5	14974.1	10652.6	11469.9
GQ069956.1	464499	19601.8	17040.7	12306.2	19135.1	9610.6	10872.8
GQ101525.1	443183	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ041270.1	399224	5370.0	3841.1	7439.9	12892.6	2519.1	3281.3
GQ100313.1	397249	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ060295.1	370716	7967.5	9393.7	8746.8	9910.6	8198.4	9440.3
GQ082165.1	421570	2973.6	1555.5	1443.4	2796.7	416.9	1303.2
GQ032535.1	448764	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ011919.1	497747	13410.0	15551.5	4921.1	10694.4	11451.9	11463.7
GQ101398.1	448817	13921.1	13578.1	6888.1	13330.1	1616.2	3730.5
GQ004376.1	505286	822.9	929.8	1453.5	1154.5	127.1	317.5
GQ015089.1	494572	11638.9	12683.0	10150.0	10297.2	10017.7	8906.7
GQ015023.1	494642	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ109352.1	443400	24337.2	21311.7	22622.9	22172.3	19914.0	18030.3
GQ042349.1	423446	15728.2	15807.7	12041.1	14342.8	10280.1	14025.5
GQ004569.1	505094	14567.9	14066.5	9420.9	10033.4	15697.4	12556.1
GQ069553.1	383989	1943.3	2156.8	4562.0	6523.6	1164.9	2233.4
GQ070226.1	383224	3841.2	5655.5	6872.2	5109.1	102.1	2722.3
GQ009169.1	500496	15752.0	15394.0	24304.9	13473.6	14974.8	14458.8

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GQ035534.1 gg_id:418032 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu
GQ034434.1 gg_id:421120 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ062229.1 gg_id:382463 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ070323.1 gg_id:462180 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
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GQ017343.1 gg_id:492324 Topographical and Temporal Human Skin Microbiome skin nare clone nbu119f11c1
GQ036355.1 gg_id:425354 Topographical and Temporal Human Skin Microbiome skin palm clone nbu363c11c1
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GQ046859.1 gg_id:406969 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ071715.1 gg_id:419483 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
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GQ038404.1 gg_id:422808 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu385a05
GQ046113.1 gg_id:383522 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw
GQ048422.1 gg_id:427771 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu

GQ015966.1	493700	2344.3	2245.5	3909.9	7009.4	1450.6	1337.0
GQ004492.1	505171	4220.6	2684.8	5031.5	3265.6	234.0	908.6
GQ083971.1	379766	10855.2	9193.6	7087.0	11215.8	5333.1	5902.0
GQ068530.1	436576	453.6	342.5	408.2	940.6	109.3	139.0
GQ003869.1	505792	2669.2	1737.3	944.5	5339.6	3252.7	4003.3
GQ061636.1	386340	3260.8	3542.6	1224.6	3239.3	6567.1	5138.6
GQ019992.1	489675	5363.7	3889.6	1222.3	2796.5	519.8	1683.7
GQ075758.1	400511	20974.6	21502.3	9007.8	17511.4	12577.5	13704.1
GQ111661.1	425117	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ035534.1	418032	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ034434.1	421120	10416.1	11892.8	6809.3	9920.8	5287.6	5692.0
GQ062229.1	382463	555.4	620.3	1133.7	2664.3	243.3	654.3
GQ070323.1	462180	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ004629.1	505033	1775.5	1095.9	1134.1	3323.4	284.1	893.2
GQ036463.1	389990	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ006320.1	503344	2699.6	2540.6	9232.3	6884.9	2358.1	1753.1
GQ014491.1	495175	774.2	2169.2	954.1	321.7	2973.4	1070.9
GQ083733.1	380795	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ088663.1	414505	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ015033.1	494634	8613.7	8868.5	7972.7	8212.8	5583.7	6084.1
GQ017343.1	492324	6528.0	6183.8	1077.4	4296.6	1007.3	1835.5
GQ036355.1	425354	11704.8	10341.9	12720.6	10671.2	7704.1	7762.1
GQ009100.1	500565	5833.2	4616.4	3574.5	10126.6	6217.5	10104.0
GQ058223.1	406519	21410.9	20316.3	6687.8	17227.8	20219.7	14651.9
GQ015719.1	493948	2720.2	2769.0	8230.6	4844.9	1256.8	2176.9
GQ047299.1	436570	12583.8	12219.8	7628.4	16235.4	10166.3	11585.7
GQ033660.1	437314	1435.7	919.9	1370.6	3296.5	518.7	719.6
GQ103030.1	457825	14911.7	15146.0	9352.8	12302.1	14890.2	13542.8
GQ090535.1	385967	3694.3	2591.2	3886.2	7679.8	238.3	761.6
GQ011938.1	497728	6450.8	5813.4	5821.8	12538.3	12085.1	14073.7
GQ046859.1	406969	4813.9	2764.7	7841.6	10349.5	262.6	1185.1
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GQ017361.1	492307	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ046425.1	446209	14809.1	13997.2	18168.1	11505.5	12700.6	11855.0
GQ070252.1	395495	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ071715.1	419483	12808.5	16645.7	11955.0	20075.4	20025.9	17042.8
GQ098393.1	484514	16021.9	14235.6	6464.8	11951.2	17175.2	15340.2
GQ003846.1	505814	18400.6	18057.2	12447.0	16371.3	16859.6	15293.4
GQ038404.1	422808	9413.2	8360.3	10033.1	10751.9	6953.7	6917.5
GQ046113.1	383522	22900.1	20370.2	18829.5	20876.8	15082.6	15285.4
GQ048422.1	427771	16998.7	34793.9	8377.3	15925.7	13000.8	11874.0

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GQ046934.1 gg_id:425170 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ061698.1 gg_id:465991 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw23
GQ006538.1 gg_id:503125 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu8
GQ035672.1 gg_id:446360 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbu3
GQ015717.1 gg_id:493950 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ016291.1 gg_id:493376 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv
GQ100071.1 gg_id:438105 Topographical and Temporal Human Skin Microbiome skin nare clone nbw477f03c1
GQ034464.1 gg_id:378697 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ087131.1 gg_id:406291 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ003772.1 gg_id:505890 Topographical and Temporal Human Skin Microbiome skin nare clone nbu57b03c1
GQ038578.1 gg_id:423337 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4
GQ004575.1 gg_id:505085 Topographical and Temporal Human Skin Microbiome skin nare clone nbu60b01c1
GQ100213.1 gg_id:462893 Topographical and Temporal Human Skin Microbiome skin nare clone nbw479d02c1
GQ040776.1 gg_id:398963 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958e08c
GQ061846.1 gg_id:429339 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw25b0
GQ028202.1 gg_id:433092 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw
GQ019932.1 gg_id:489736 Topographical and Temporal Human Skin Microbiome skin nare clone nbu201a09c1
GQ069374.1 gg_id:455299 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1
GQ042598.1 gg_id:381897 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl
GQ054682.1 gg_id:387263 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1100a
GQ042198.1 gg_id:420583 Topographical and Temporal Human Skin Microbiome skin nare clone nbw937d09c1
GQ058201.1 gg_id:432668 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbu
GQ013412.1 gg_id:496254 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ069076.1 gg_id:393597 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw
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GQ039909.1 gg_id:405679 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor
GQ011883.1 gg_id:497783 Topographical and Temporal Human Skin Microbiome skin nare clone nbw746d02c1
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GQ013292.1 gg_id:496374 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ014017.1 gg_id:495649 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw8
GQ100308.1 gg_id:378176 Topographical and Temporal Human Skin Microbiome skin nare clone nbw480d12c1
GQ019984.1 gg_id:489686 Topographical and Temporal Human Skin Microbiome skin nare clone nbu201f04c1
GQ050554.1 gg_id:376429 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu487c

GQ075614.1	380799	21620.5	21406.8	9733.3	17004.8	11500.3	9255.1
GQ046934.1	425170	4597.3	3530.8	1182.6	1253.2	460.4	1310.6
GQ061698.1	465991	2874.3	2634.4	4558.1	4507.1	1261.3	2250.3
GQ006538.1	503125	11486.8	13581.8	5958.4	8171.3	6836.2	6821.7
GQ035672.1	446360	20322.4	21385.0	13206.3	15628.3	10183.3	9264.5
GQ015717.1	493950	15174.6	14283.3	13382.6	15059.6	15659.3	12237.6
GQ016291.1	493376	110.3	388.0	101.9	117.0	172.0	53.2
GQ100071.1	438105	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ034464.1	378697	10472.0	8955.0	9071.4	9998.9	5304.0	5706.5
GQ087131.1	406291	20915.3	24061.5	14180.8	13915.4	11029.5	9271.4
GQ003772.1	505890	1804.4	1952.4	2005.7	3296.5	7464.1	3172.5
GQ038578.1	423337	144.3	128.6	173.5	195.6	124.5	94.8
GQ004575.1	505085	1237.1	846.2	757.3	3296.5	263.0	893.2
GQ100213.1	462893	1275.8	846.2	6738.6	3296.5	3095.1	8231.1
GQ040776.1	398963	24016.5	22737.9	13775.6	12199.8	20832.0	17395.9
GQ061846.1	429339	7179.5	4144.1	1369.2	12098.9	9121.2	7841.4
GQ028202.1	433092	7509.1	16381.3	6506.8	3953.3	15046.8	10009.5
GQ019932.1	489736	11587.8	10493.0	4082.5	13193.6	6434.2	5743.7
GQ069374.1	455299	8922.3	10815.3	10508.8	8709.3	7559.3	6883.5
GQ042598.1	381897	320.7	141.5	1133.3	461.7	137.0	132.6
GQ054682.1	387263	20357.6	17068.4	11050.6	10334.0	17146.2	14468.1
GQ042198.1	420583	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ058201.1	432668	16491.0	19946.7	4042.3	13244.1	6074.5	7639.5
GQ013412.1	496254	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ069076.1	393597	7742.8	11329.8	2517.7	5944.2	2220.8	2631.1
GQ060836.1	463312	4868.9	3761.5	3974.1	8188.6	809.4	1457.7
GQ039909.1	405679	2339.3	1699.4	2244.6	4198.2	342.2	585.5
GQ011883.1	497783	18160.0	14809.7	7348.3	16656.5	6698.9	10689.2
GQ014421.1	495245	3239.0	3859.4	1952.3	5768.1	3511.8	7014.8
GQ069445.1	446611	5518.1	7747.6	3106.5	5659.4	4596.2	6068.2
GQ112822.1	401591	16464.4	16223.4	11014.9	16428.0	7428.3	9995.3
GQ017441.1	492226	8387.3	8738.6	7062.2	5598.9	15137.8	10429.4
GQ061712.1	451710	919.4	1027.2	1238.1	418.0	621.5	451.4
GQ055963.1	463074	1797.6	1061.5	1793.5	3296.5	712.5	871.4
GQ061966.1	403237	73.2	149.1	59.3	82.5	149.8	75.2
GQ013885.1	495784	2821.7	4358.2	946.9	2311.8	6521.6	4928.6
GQ013292.1	496374	11648.8	13742.1	9546.3	10593.2	7687.7	7747.7
GQ014017.1	495649	12.1	24.5	2960.3	22.0	102.1	2855.5
GQ100308.1	378176	12087.9	10608.2	9824.0	12086.6	7733.2	7969.9
GQ019984.1	489686	11534.7	11536.3	2924.7	12344.4	7788.9	9572.7
GQ050554.1	376429	16280.1	9049.0	1477.5	10317.9	2463.4	2336.5