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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium

s__unclassified	26525
s__unclassified	26527
s__unclassified	26531
s__unclassified	26532
s__unclassified	26534
s__unclassified	26537
s__unclassified	26542
s__unclassified	26544
s__unclassified	26545
s__unclassified	26546
s__unclassified	26547
s__unclassified	26548
s__unclassified	26549
s__unclassified	26550
s__unclassified	26552
s__unclassified	26553
s__unclassified	26555
s__unclassified	26556
s__unclassified	26558
s__unclassified	26562
s__unclassified	26564
s__unclassified	26567
s__unclassified	26569
s__unclassified	26570
s__unclassified	26573
s__unclassified	26574
s__unclassified	26575
s__unclassified	26576
s__unclassified	26578
s__unclassified	26579
s__unclassified	26580
s__unclassified	26581
s__unclassified	26582
s__unclassified	26585
s__unclassified	26586
s__unclassified	26587
s__unclassified	26588
s__unclassified	26590
s__unclassified	26592
s__unclassified	26594
s__unclassified	26595

EU778236.1 gg_id:316304 feces clone RL388_aao94b11 EU778
FJ678870.1 gg_id:512472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
EF400999.1 gg_id:203591 human fecal clone SJTU_D_04_49 EF4009
FJ680972.1 gg_id:519973 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ806688.1 gg_id:183513 human fecal clone RL186_aao47e12 DQ806
EU766495.1 gg_id:305290 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ362752.1 gg_id:367710 feces adult twins and mothers; TS13 clone TS13_a02g01 FJ3627
FJ372208.1 gg_id:359289 feces adult twins and mothers; TS9 clone TS9_a03a03 FJ3722
FJ367380.1 gg_id:365407 feces adult twins and mothers; TS29 clone TS29_a02g08 FJ3673
FJ363839.1 gg_id:360232 feces adult twins and mothers; TS14 clone TS14_a04a01 FJ3638
FJ678151.1 gg_id:528937 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
FJ680786.1 gg_id:526274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU762845.1 gg_id:304517 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
FJ677432.1 gg_id:528151 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ368415.1 gg_id:358955 feces adult twins and mothers; TS3 clone TS3_a04b01 FJ3684
EF402952.1 gg_id:213907 human fecal clone SJTU_B_14_69 EF4029
FJ683751.1 gg_id:530843 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ905111.1 gg_id:163491 human fecal clone 002C-b12 DQ905
FJ364490.1 gg_id:362754 feces adult twins and mothers; TS15 clone TS15_a03e11 FJ3644
FJ685392.1 gg_id:530094 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
FJ673343.1 gg_id:517507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ825000.1 gg_id:174877 human fecal clone RL185_aao72b01 DQ825
EU768621.1 gg_id:318450 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ678887.1 gg_id:521067 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ365105.1 gg_id:359049 feces adult twins and mothers; TS1 clone TS1_a02h06 FJ3651
FJ364590.1 gg_id:362559 feces adult twins and mothers; TS15 clone TS15_a04g06 FJ3645
FJ365386.1 gg_id:359852 feces adult twins and mothers; TS20 clone TS20_a02c08 FJ3653
FJ367541.1 gg_id:370253 feces adult twins and mothers; TS29 clone TS29_a04g06 FJ3675
FJ680223.1 gg_id:520109 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EU763241.1 gg_id:307220 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU763
FJ681568.1 gg_id:527811 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ676504.1 gg_id:522876 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
FJ362885.1 gg_id:359008 feces adult twins and mothers; TS13 clone TS13_a04d04 FJ3628
FJ678804.1 gg_id:516818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ673487.1 gg_id:527547 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
DQ801384.1 gg_id:178047 human fecal clone RL388_aao94g07 DQ801
AY984170.1 gg_id:118701 human stool clone B054 AY984
AY979049.1 gg_id:126578 human transverse colon mucosal biopsy clone NJ45 AY979
FJ673097.1 gg_id:520459 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ674043.1 gg_id:523328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ673534.1 gg_id:523016 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Faecalibacterium
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira

s__unclassified	26597
s__unclassified	26598
s__unclassified	26599
s__unclassified	26600
s__unclassified	26601
s__unclassified	26602
s__unclassified	26603
s__unclassified	26604
s__unclassified	26605
s__unclassified	26608
s__unclassified	26609
s__unclassified	26611
s__unclassified	26612
s__unclassified	26617
s__unclassified	27349
s__Oscillospira guilliermondii	22209
s__unclassified	21830
s__unclassified	21831
s__unclassified	21844
s__unclassified	21845
s__unclassified	21852
s__unclassified	21858
s__unclassified	21859
s__unclassified	21863
s__unclassified	21878
s__unclassified	21898
s__unclassified	21912
s__unclassified	21916
s__unclassified	21925
s__unclassified	21930
s__unclassified	21931
s__unclassified	21936
s__unclassified	21953
s__unclassified	21959
s__unclassified	21961
s__unclassified	21963
s__unclassified	21988
s__unclassified	21990
s__unclassified	21999
s__unclassified	22001
s__unclassified	22009

GQ898476.1 gg_id:585428 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ326372.1 gg_id:149213 Metagenomic gut microbiome healthy human stool clone C386 DQ326
DQ796992.1 gg_id:195038 human fecal clone RL386_aao85e04 DQ796
DQ823803.1 gg_id:191333 human fecal clone RL250_aaj79c08 DQ823
FJ678240.1 gg_id:525494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ683918.1 gg_id:520517 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FJ677025.1 gg_id:519119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ801244.1 gg_id:187010 human fecal clone RL116_aaf02f02 DQ801
GQ448921.1 gg_id:548379 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ365385.1 gg_id:361941 feces adult twins and mothers; TS20 clone TS20_a02c07 FJ3653
FJ678517.1 gg_id:516135 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GQ043044.1 gg_id:460138 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012e GQ043
FJ682899.1 gg_id:525479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ362810.1 gg_id:363538 feces adult twins and mothers; TS13 clone TS13_a03e01 FJ3628
EU778238.1 gg_id:325784 feces clone RL388_aao96a06 EU778
AB185655.1 gg_id:107235 rumen clone F24-H11 AB185
DQ455829.1 gg_id:158222 pre-adolescent turkey cecum clone CFT19A8 DQ455
EU775925.1 gg_id:326785 Horse feces clone horsem_aai93f12 EU775
FJ362828.1 gg_id:366573 feces adult twins and mothers; TS13 clone TS13_a03f08 FJ3628
DQ815311.1 gg_id:167509 mouse cecum clone aab45c07 DQ815
EU504766.1 gg_id:259535 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g09 EU504
EU503968.1 gg_id:273637 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa03d07 EU503
EU474488.1 gg_id:301032 bighorn sheep feces clone BHSD_aaa02f09 EU474
EF401657.1 gg_id:205604 human fecal clone SJTU_D_14_93 EF4016
FJ367640.1 gg_id:368423 feces adult twins and mothers; TS2 clone TS2_a01h01 FJ3676
EF436308.2 gg_id:209712 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC22 EF4363
EU137434.1 gg_id:267999 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU1374
AY985959.1 gg_id:118285 human stool clone D258 AY985
DQ794276.1 gg_id:187564 human fecal clone RL176_aan60e05 DQ794
FJ823863.1 gg_id:526665 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8238
GQ491174.1 gg_id:544996 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ394655.1 gg_id:155341 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EU844238.1 gg_id:309451 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU776785.1 gg_id:313471 Mongoose lemur feces clone ML_aaj26e11 EU776
EF602811.1 gg_id:230941 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
AB234463.1 gg_id:149007 termite gut homogenate clone MgMjD-058 AB2344
DQ798394.1 gg_id:194661 human fecal clone RL181_aah41h12 DQ798
EU458004.1 gg_id:304013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4580
AY916303.1 gg_id:114021 human sigmoid colon biopsy clone MM71 AY9163
EU763882.1 gg_id:331742 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU7638
FJ372305.1 gg_id:369053 feces adult twins and mothers; TS9 clone TS9_a04a11 FJ3723

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira

s__unclassified	22012
s__unclassified	22018
s__unclassified	22021
s__unclassified	22022
s__unclassified	22024
s__unclassified	22027
s__unclassified	22034
s__unclassified	22037
s__unclassified	22039
s__unclassified	22040
s__unclassified	22045
s__unclassified	22046
s__unclassified	22049
s__unclassified	22050
s__unclassified	22052
s__unclassified	22063
s__unclassified	22066
s__unclassified	22068
s__unclassified	22072
s__unclassified	22075
s__unclassified	22082
s__unclassified	22089
s__unclassified	22091
s__unclassified	22093
s__unclassified	22111
s__unclassified	22115
s__unclassified	22118
s__unclassified	22119
s__unclassified	22123
s__unclassified	22133
s__unclassified	22144
s__unclassified	22149
s__unclassified	22152
s__unclassified	22153
s__unclassified	22160
s__unclassified	22161
s__unclassified	22169
s__unclassified	22172
s__unclassified	22173
s__unclassified	22174
s__unclassified	22176

FJ366580.1 gg_id:362243 feces adult twins and mothers; TS27 clone TS27_a01d05 FJ3665
FJ366573.1 gg_id:363823 feces adult twins and mothers; TS27 clone TS27_a01c10 FJ3665
DQ456220.1 gg_id:158722 pre-adolescent turkey cecum clone CFT29G9 DQ456
DQ014822.1 gg_id:134301 mouse cecum clone M1_b06_3 DQ014
EU461564.1 gg_id:288270 black rhinoceros feces clone RH_aaj92e10 EU461
EU461544.1 gg_id:298072 black rhinoceros feces clone RH_aaj92b07 EU461
AB218336.1 gg_id:147024 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgC-135 AB218
EU504992.1 gg_id:271491 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01c11 EU504
GU302582.1 gg_id:585073 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ801356.1 gg_id:195943 human fecal clone RL388_aao94d10 DQ801
FJ366352.1 gg_id:365719 feces adult twins and mothers; TS26 clone TS26_a01g07 FJ3663
DQ804825.1 gg_id:175497 human fecal clone RL385_aao81b11.Contig2 DQ804
EF604816.1 gg_id:229824 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EU452624.1 gg_id:328445 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
EU456254.1 gg_id:338796 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
GQ896697.1 gg_id:532748 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
FJ362655.1 gg_id:362777 feces adult twins and mothers; TS13 clone TS13_a01e10 FJ3626
GQ449217.1 gg_id:549950 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ449
FJ363502.1 gg_id:363316 feces adult twins and mothers; TS149 clone TS149_a04a04 FJ3635
EF025275.1 gg_id:191239 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_N6 EF0252
DQ805440.1 gg_id:183410 human fecal clone RL203_aai62f07 DQ805
EU761793.1 gg_id:311033 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU843460.1 gg_id:321337 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
EU530368.1 gg_id:263665 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
EF400373.1 gg_id:206513 human fecal clone SJTU_E_12_37 EF4003
EF098593.1 gg_id:185752 mouse cecum clone SWPT16_aaa01h04 EF0985
FJ681249.1 gg_id:522699 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
DQ797153.1 gg_id:203545 human fecal clone RL386_aao87f05 DQ797
DQ824395.1 gg_id:195397 human fecal clone RL304_aal75e08 DQ824
GU304189.1 gg_id:548161 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
FJ365085.1 gg_id:366486 feces adult twins and mothers; TS1 clone TS1_a02f07 FJ3650
DQ799134.1 gg_id:191902 human fecal clone RL205_aaj18a10 DQ799
EU453686.1 gg_id:316428 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU4536
AB238598.1 gg_id:249174 Oscillibacter valericigenes str. Sjm18-20 (= NBRC 101213) AB2385
FJ369766.1 gg_id:362078 feces adult twins and mothers; TS51 clone TS51_a04e10 FJ3697
DQ673487.1 gg_id:168795 rumen fluid clone GRC22 DQ673
DQ904783.1 gg_id:171303 human fecal clone 001B-e1 DQ904
EU462532.1 gg_id:297465 Sumatran orangutan feces clone orang1_aai56e09 EU4625
EU509002.1 gg_id:274686 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap41f02 EU5090
EU505557.1 gg_id:276535 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02f07 EU5055
EF401625.1 gg_id:213633 human fecal clone SJTU_D_13_45 EF4016

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	0	1	0	0	1	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira

s__unclassified	22177
s__unclassified	22180
s__unclassified	22186
s__unclassified	22197
s__unclassified	22200
s__unclassified	22210
s__unclassified	22212
s__unclassified	22230
s__unclassified	22231
s__unclassified	22232
s__unclassified	22235
s__unclassified	22237
s__unclassified	22249
s__unclassified	22251
s__unclassified	22263
s__unclassified	22264
s__unclassified	22267
s__unclassified	22268
s__unclassified	22272
s__unclassified	22277
s__unclassified	22280
s__unclassified	22281
s__unclassified	22287
s__unclassified	22299
s__unclassified	22301
s__unclassified	22304
s__unclassified	22306
s__unclassified	22307
s__unclassified	22313
s__unclassified	22321
s__unclassified	22325
s__unclassified	22333
s__unclassified	22354
s__unclassified	22357
s__unclassified	22363
s__unclassified	22365
s__unclassified	22369
s__unclassified	22380
s__unclassified	22396
s__unclassified	22406
s__unclassified	22411

EU764883.1 gg_id:347184 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
EU774621.1 gg_id:320768 Angola Colobus feces clone EAC_2_aaa02f02 EU7746
EU452440.1 gg_id:303454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4524
EU463672.1 gg_id:298918 domesticated horse feces clone horsej_aai90g11 EU4636
EU771312.1 gg_id:356187 Asiatic elephant feces clone AE1_aaa03d05 EU7713
EF096980.1 gg_id:192115 mouse cecum clone SWPT13_aaa03f07 EF0969
EU772150.1 gg_id:354379 Argali sheep feces clone AS1_aao40g10.Contig1 EU7721
DQ809326.1 gg_id:189943 human fecal clone RL184_aah19c02 DQ809
FJ366181.1 gg_id:361863 feces adult twins and mothers; TS25 clone TS25_a03f06 FJ3661
DQ793427.1 gg_id:192058 human fecal clone RL199_aaj43f01 DQ793
EU457751.1 gg_id:327701 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4577
EU455083.1 gg_id:322211 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75M EU4550
DQ808890.1 gg_id:195102 human fecal clone RL243_aai86f05 DQ808
EU475806.1 gg_id:296144 white-faced saki feces clone Saki_aaj61g02 EU4758
EF096534.1 gg_id:193435 mouse cecum clone obob2_aaa04e06 EF0965
EF602930.1 gg_id:235072 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
AY992715.1 gg_id:130454 mouse cecum clone C23_p23 AY9927
DQ905136.1 gg_id:165954 human fecal clone 002C-d1 DQ905
GQ897639.1 gg_id:536897 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
FJ365979.1 gg_id:360331 feces adult twins and mothers; TS25 clone TS25_a01d02 FJ3659
EU452820.1 gg_id:336127 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83M EU4528
EF096624.1 gg_id:198635 mouse cecum clone SWPT11_aaa02b09 EF0966
FJ681029.1 gg_id:520720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
DQ815674.1 gg_id:164465 mouse cecum clone aab44f06 DQ815
DQ326565.1 gg_id:146558 Metagenomic gut microbiome healthy human stool clone C747 DQ326
EU775865.1 gg_id:336216 Horse feces clone horsem_aai95a08 EU7758
DQ808842.1 gg_id:181304 human fecal clone RL243_aai86a08 DQ808
DQ015246.1 gg_id:134096 mouse cecum clone M2_g12_3 DQ015
EU774932.1 gg_id:327337 Flying Fox feces clone FF_f03_1 EU7749
EF602809.1 gg_id:228426 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
DQ809986.1 gg_id:199055 human fecal clone RL184_aao66f12 DQ809
EU771406.1 gg_id:323903 Asiatic elephant feces clone AE2_aaa03h12 EU7714
DQ014634.1 gg_id:135369 mouse cecum clone M1_h06 DQ014
FJ879271.1 gg_id:427738 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
AY985603.1 gg_id:121620 human stool clone C593 AY9856
DQ796558.1 gg_id:190220 human fecal clone RL179aan74f10 DQ796
EU509249.1 gg_id:273592 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46f03 EU5092
EU461246.1 gg_id:295371 hamadryas baboon feces clone BAZ_aah91d08 EU4612
FJ362625.1 gg_id:365734 feces adult twins and mothers; TS13 clone TS13_a01c02 FJ3626
EU775024.1 gg_id:314582 Francois Langur feces clone FL_1aaa01h10 EU7750
DQ796802.1 gg_id:180980 human fecal clone RL179_aao54g01 DQ796

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Oscillospira
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__unclassified	22415
s__unclassified	22417
s__unclassified	22421
s__unclassified	22425
s__unclassified	22438
s__unclassified	22440
s__unclassified	22447
s__unclassified	22449
s__unclassified	22457
s__unclassified	22467
s__unclassified	22472
s__unclassified	22476
s__unclassified	22477
s__unclassified	22483
s__unclassified	22493
s__unclassified	22517
s__unclassified	22534
s__unclassified	22537
s__unclassified	22538
s__unclassified	22540
s__unclassified	22542
s__unclassified	22551
s__unclassified	22560
s__unclassified	22561
s__unclassified	22567
s__unclassified	22569
s__unclassified	22579
s__unclassified	22580
s__unclassified	22602
s__unclassified	22603
s__unclassified	27522
s__unclassified	27817
s__unclassified	28161
s__Ruminococcus albus	27318
s__Ruminococcus bromii	26632
s__Ruminococcus bromii	26675
s__Ruminococcus bromii	26746
s__Ruminococcus bromii	26874
s__Ruminococcus bromii	26888
s__Ruminococcus bromii	26910
s__Ruminococcus bromii	26928

DQ798301.1 gg_id:192986 human fecal clone RL181_aah40d04 DQ798
EU764810.1 gg_id:330949 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7648
EU843610.1 gg_id:333248 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8436
DQ809094.1 gg_id:189555 human fecal clone RL308_aal81d05 DQ809
EU765801.1 gg_id:325064 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU7658
FJ363434.1 gg_id:361450 feces adult twins and mothers; TS149 clone TS149_a03c01 FJ3634
EU469102.1 gg_id:293060 Speke's gazelle feces clone SP3_e04 EU4691
FJ671876.1 gg_id:526225 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
EU463455.1 gg_id:287790 domesticated horse feces clone horsem_aai94c07 EU4634
EU775161.1 gg_id:320483 Francois Langur feces clone FL_1aaa04a09 EU7751
EU771243.1 gg_id:306711 Asiatic elephant feces clone AE3_aaa01e02 EU7712
EU469097.1 gg_id:299222 Speke's gazelle feces clone SP3_d08 EU4690
DQ795965.1 gg_id:193632 human fecal clone RL202_aai49e08 DQ795
AY684396.2 gg_id:110998 mucosal biopsies human intestine clone HuDI51 AY6843
EU765035.1 gg_id:306745 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7650
EU504706.1 gg_id:276511 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04g08 EU5047
EF098196.1 gg_id:197863 mouse cecum clone SWPT14_aaa02h07 EF0981
EU466225.1 gg_id:298036 bighorn sheep feces clone BH1_aao28d06 EU4662
AY985428.1 gg_id:121349 human stool clone C372 AY9854
EU766503.1 gg_id:335417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
EU511173.1 gg_id:262677 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h03 EU5111
EU765204.1 gg_id:356417 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU7652
DQ815864.1 gg_id:171239 mouse cecum clone aab23e01 DQ815
EU842347.1 gg_id:315851 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
DQ815490.1 gg_id:164810 mouse cecum clone aab41e05 DQ815
EU472398.1 gg_id:299755 Angola colobus feces clone EAC_1aaa01c10 EU4723
EU508250.1 gg_id:276985 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa04e02 EU5082
EU506574.1 gg_id:260741 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04e08 EU5065
AY983978.1 gg_id:117068 human descending colon mucosal biopsy clone MC71 AY9839
FJ681514.1 gg_id:529688 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
EU463554.1 gg_id:292439 domesticated horse feces clone horsem_aai96a07 EU4635
EU463726.1 gg_id:293353 domesticated horse feces clone horsej_aai91g05 EU4637
EU463427.1 gg_id:298457 domesticated horse feces clone horsem_aai93g03 EU4634
AB301912.1 gg_id:240231 Ruminococcus albus AB3019
FJ372107.1 gg_id:360830 feces adult twins and mothers; TS9 clone TS9_a01g12 FJ3721
FJ365585.1 gg_id:357253 feces adult twins and mothers; TS20 clone TS20_a04f02 FJ3655
FJ366914.1 gg_id:363146 feces adult twins and mothers; TS28 clone TS28_a01c11 FJ3669
FJ371844.1 gg_id:366240 feces adult twins and mothers; TS8 clone TS8_a02h01 FJ3718
FJ363657.1 gg_id:368173 feces adult twins and mothers; TS14 clone TS14_a01g10 FJ3636
FJ371275.1 gg_id:365709 feces adult twins and mothers; TS6 clone TS6_a03a09 FJ3712
GQ898568.1 gg_id:594381 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
1	0	1	1	0	1	1	1	0	0	0	0	1
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__Ruminococcus bromii	26993
s__Ruminococcus bromii	27004
s__Ruminococcus bromii	27083
s__Ruminococcus bromii	27091
s__Ruminococcus bromii	27093
s__Ruminococcus bromii	27133
s__Ruminococcus bromii	27138
s__Ruminococcus bromii	27206
s__Ruminococcus callidus	26822
s__Ruminococcus callidus	26961
s__Ruminococcus callidus	27070
s__Ruminococcus callidus	27113
s__Ruminococcus callidus	27207
s__Ruminococcus callidus	27208
s__Ruminococcus flavefaciens	26640
s__Ruminococcus flavefaciens	26673
s__Ruminococcus flavefaciens	26674
s__Ruminococcus flavefaciens	26736
s__Ruminococcus flavefaciens	26739
s__Ruminococcus flavefaciens	26752
s__Ruminococcus flavefaciens	26753
s__Ruminococcus flavefaciens	26764
s__Ruminococcus flavefaciens	26777
s__Ruminococcus flavefaciens	26794
s__Ruminococcus flavefaciens	26814
s__Ruminococcus flavefaciens	26884
s__Ruminococcus flavefaciens	26906
s__Ruminococcus flavefaciens	26912
s__Ruminococcus flavefaciens	26935
s__Ruminococcus flavefaciens	26942
s__Ruminococcus flavefaciens	26965
s__Ruminococcus flavefaciens	27042
s__Ruminococcus flavefaciens	27046
s__Ruminococcus flavefaciens	27088
s__Ruminococcus flavefaciens	27103
s__Ruminococcus flavefaciens	27137
s__Ruminococcus flavefaciens	27146
s__Ruminococcus flavefaciens	27162
s__Ruminococcus flavefaciens	27168
s__Ruminococcus flavefaciens	27189
s__Ruminococcus flavefaciens	27209

EF399806.1 gg_id:209727 human fecal clone SJTU_E_03_58 EF3998
EU763249.1 gg_id:337339 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ368454.1 gg_id:362323 feces adult twins and mothers; TS3 clone TS3_a04e09 FJ3684
FJ366609.1 gg_id:361468 feces adult twins and mothers; TS27 clone TS27_a01f12 FJ3666
FJ363691.1 gg_id:358965 feces adult twins and mothers; TS14 clone TS14_a02b08 FJ3636
DQ905192.1 gg_id:173445 human fecal clone 013-a1 DQ905
EU768452.1 gg_id:320547 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ365601.1 gg_id:363923 feces adult twins and mothers; TS20 clone TS20_a04g09 FJ3656
EU762103.1 gg_id:322081 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
DQ807613.1 gg_id:182342 human fecal clone RL307_aam08h07 DQ807
FJ366911.1 gg_id:365471 feces adult twins and mothers; TS28 clone TS28_a01c08 FJ3669
DQ798028.1 gg_id:182455 human fecal clone RL302_aal94f12 DQ798
AY976187.1 gg_id:121324 human ascending colon mucosal biopsy clone LV95 AY976
EU761738.1 gg_id:352927 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
AF104841.1 gg_id:16066 Ruminococcus flavefaciens str. AR72 AF1048
EU777840.1 gg_id:323801 European rabbit feces clone RA_c04_1 EU777
EU469685.1 gg_id:294797 flying fox feces clone FF_a06_1 EU469
EU468685.1 gg_id:291859 okapi feces clone OK2_e08_1 EU468
EF445196.1 gg_id:205179 rabbit cecum clone NED3F5 EF4451
EU779250.1 gg_id:324482 Trancaspian Urial feces clone TU1_aaa04c10 EU779
AF104846.1 gg_id:16065 Ruminococcus flavefaciens str. Y1 AF1048
FJ879092.1 gg_id:459944 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
EU468531.1 gg_id:290894 okapi feces clone OK1_b08_1 EU468
EU774461.1 gg_id:320332 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14 EU774
FJ880174.1 gg_id:418064 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
GU303548.1 gg_id:539847 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AF104835.1 gg_id:16041 Ruminococcus flavefaciens str. LP-R1-Adx AF1048
EU460043.1 gg_id:296857 mammals their gut microbes eastern black and white colobus feces clone COL_aai13 EU460
EF602945.1 gg_id:233404 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
FJ879630.1 gg_id:438358 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
EU465615.1 gg_id:288191 argali sheep feces clone AS1_aao39g11.Contig1 EU465
FJ880749.1 gg_id:460253 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
AF104837.1 gg_id:16040 Ruminococcus flavefaciens str. AR46 AF1048
FJ832845.1 gg_id:563574 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_33A05 FJ8328
EU774973.1 gg_id:317714 Flying Fox feces clone FF_-aag84b01 EU774
FJ879772.1 gg_id:386333 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8797
AB034020.1 gg_id:45766 rumen clone 4C0d-7 AB034
FJ366125.1 gg_id:362036 feces adult twins and mothers; TS25 clone TS25_a03a05 FJ3661
EU469261.1 gg_id:298912 Speke's gazelle feces clone SP3_a07_1 EU469
FJ879853.1 gg_id:383102 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
FJ879578.1 gg_id:433149 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	1	0	0
0	0	0	0	1	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__Ruminococcus flavefaciens	27219
s__Ruminococcus flavefaciens	27222
s__Ruminococcus flavefaciens	27249
s__unclassified	22364
s__unclassified	26619
s__unclassified	26621
s__unclassified	26627
s__unclassified	26633
s__unclassified	26634
s__unclassified	26643
s__unclassified	26655
s__unclassified	26660
s__unclassified	26662
s__unclassified	26664
s__unclassified	26670
s__unclassified	26671
s__unclassified	26677
s__unclassified	26678
s__unclassified	26680
s__unclassified	26681
s__unclassified	26682
s__unclassified	26687
s__unclassified	26698
s__unclassified	26700
s__unclassified	26702
s__unclassified	26704
s__unclassified	26707
s__unclassified	26708
s__unclassified	26712
s__unclassified	26715
s__unclassified	26719
s__unclassified	26721
s__unclassified	26723
s__unclassified	26725
s__unclassified	26726
s__unclassified	26729
s__unclassified	26732
s__unclassified	26733
s__unclassified	26734
s__unclassified	26735
s__unclassified	26737

DQ394631.1 gg_id:153029 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
FJ880209.1 gg_id:407405 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EU469949.1 gg_id:296346 trancaspain urial feces clone TU1_aaa01f10 EU469
EU779402.1 gg_id:343313 Grevy's Zebra feces clone GZ_aaa04c09 EU779
EU381701.1 gg_id:260559 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU475092.1 gg_id:301195 visayam warty pig feces clone VWP_aaa03c01 EU475
EU775809.1 gg_id:315666 Horse feces clone horsem_e12 EU775
FJ673061.1 gg_id:512575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
EU774487.1 gg_id:356167 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
FJ682773.1 gg_id:522772 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ882650.1 gg_id:172296 Ruminococcus sp. str. YE281 DQ882
EF401397.1 gg_id:207190 human fecal clone SJTU_D_09_78 EF4013
FJ673313.1 gg_id:514709 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU774954.1 gg_id:347335 Flying Fox feces clone FF_-aag84b12 EU774
FJ682475.1 gg_id:510095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AB034071.1 gg_id:29057 rumen clone 6C3d-10 AB034
FJ879569.1 gg_id:461354 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
DQ807559.1 gg_id:174923 human fecal clone RL307_aam08b12 DQ807
FJ881003.1 gg_id:385017 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
GU303205.1 gg_id:560753 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
FJ681243.1 gg_id:528589 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ683277.1 gg_id:509351 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ682760.1 gg_id:511748 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
AF132277.1 gg_id:72970 adult human fecal matter clone adhufec58 AF132
EU453081.1 gg_id:312665 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
FJ880489.1 gg_id:415638 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
AJ515913.1 gg_id:102671 Ruminococcus sp. str. 18P13 AJ5159
FJ678989.1 gg_id:528232 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
GQ079248.1 gg_id:409845 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d GQ079
FJ366993.1 gg_id:358351 feces adult twins and mothers; TS28 clone TS28_a02b12 FJ3669
DQ905838.2 gg_id:163243 human fecal clone 29E-e5 DQ905
FJ363583.1 gg_id:365147 feces adult twins and mothers; TS14 clone TS14_a01a05 FJ3635
DQ800995.1 gg_id:191448 human fecal clone RL387_aao90f01 DQ800
EF088328.1 gg_id:199654 Clostridium islandicum str. AK1 EF0883
EU761602.1 gg_id:334170 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU761
FJ366126.1 gg_id:368142 feces adult twins and mothers; TS25 clone TS25_a03a06 FJ3661
EU453704.1 gg_id:309828 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
EU773178.1 gg_id:349431 BigHorn sheep feces clone BHSD_aaa03h06 EU773
GQ042993.1 gg_id:431222 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011h GQ042
FJ672106.1 gg_id:529789 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6721
EU470140.1 gg_id:291360 trancaspain urial feces clone TU2_aaa03c09 EU470

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__unclassified	26757
s__unclassified	26758
s__unclassified	26760
s__unclassified	26761
s__unclassified	26765
s__unclassified	26768
s__unclassified	26769
s__unclassified	26771
s__unclassified	26772
s__unclassified	26775
s__unclassified	26782
s__unclassified	26786
s__unclassified	26787
s__unclassified	26788
s__unclassified	26789
s__unclassified	26790
s__unclassified	26795
s__unclassified	26805
s__unclassified	26808
s__unclassified	26819
s__unclassified	26820
s__unclassified	26821
s__unclassified	26826
s__unclassified	26831
s__unclassified	26834
s__unclassified	26836
s__unclassified	26837
s__unclassified	26839
s__unclassified	26842
s__unclassified	26847
s__unclassified	26849
s__unclassified	26852
s__unclassified	26855
s__unclassified	26857
s__unclassified	26859
s__unclassified	26861
s__unclassified	26865
s__unclassified	26873
s__unclassified	26875
s__unclassified	26876
s__unclassified	26878

AB494864.1 gg_id:535519 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
FJ881268.1 gg_id:381511 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
DQ807388.1 gg_id:195966 human fecal clone RL307_aam05h08 DQ807
EU762145.1 gg_id:350180 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU762
FJ680003.1 gg_id:520618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
AJ515914.1 gg_id:94504 Ruminococcus sp. str. 7L75 AJ5159
AY986181.1 gg_id:117716 human stool clone D538 AY986
GQ502527.1 gg_id:593965 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EF686574.1 gg_id:241489 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC6 EF6865
FJ673393.1 gg_id:520904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
GQ079249.1 gg_id:408551 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230d GQ079
FJ367031.1 gg_id:364206 feces adult twins and mothers; TS28 clone TS28_a02f09 FJ3670
EF400797.1 gg_id:212533 human fecal clone SJTU_D_01_64 EF4007
GQ079235.1 gg_id:381044 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230b GQ079
FJ683473.1 gg_id:516504 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ683719.1 gg_id:529159 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ793927.1 gg_id:196776 human fecal clone RL176_aah45d05 DQ793
FJ881336.1 gg_id:383369 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU381483.1 gg_id:259252 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ682645.1 gg_id:528548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
FJ683228.1 gg_id:527236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
DQ801085.1 gg_id:183189 human fecal clone RL387_aao91h09 DQ801
FJ682883.1 gg_id:514296 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
DQ801034.1 gg_id:182668 human fecal clone RL387_aao91c01 DQ801
EU475067.1 gg_id:303213 visayam warty pig feces clone VWP_aaa03h09 EU475
FJ880441.1 gg_id:463901 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
EU201675.1 gg_id:240642 species intestinal microbiota between fiber- and liquid phase human fecal clone sd6 EU201
FJ880300.1 gg_id:460027 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
FJ683326.1 gg_id:530604 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
DQ014676.1 gg_id:130775 mouse cecum clone M1_d06_1 DQ014
EF401179.1 gg_id:216596 human fecal clone SJTU_D_06_75 EF4011
FJ682715.1 gg_id:520680 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
EU767484.1 gg_id:311384 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ677927.1 gg_id:527685 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
DQ801328.1 gg_id:181220 human fecal clone RL388_aao94a10 DQ801
EU462655.1 gg_id:290967 Sumatran orangutan feces clone orang2_aai66g11 EU462
EU381835.1 gg_id:271639 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU777137.1 gg_id:347585 Okapi feces clone OK1_a08 EU777
FJ683874.1 gg_id:513947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
FJ676801.1 gg_id:528312 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
AY858410.2 gg_id:112362 gastrointestinal tract Grant's gazelle clone GRANT74 AY858

0	0	0	0	1	0	1	0	0	0	0	0	1
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__unclassified	26879
s__unclassified	26880
s__unclassified	26885
s__unclassified	26890
s__unclassified	26894
s__unclassified	26899
s__unclassified	26902
s__unclassified	26903
s__unclassified	26904
s__unclassified	26907
s__unclassified	26911
s__unclassified	26915
s__unclassified	26916
s__unclassified	26926
s__unclassified	26933
s__unclassified	26938
s__unclassified	26946
s__unclassified	26953
s__unclassified	26954
s__unclassified	26962
s__unclassified	26964
s__unclassified	26966
s__unclassified	26967
s__unclassified	26968
s__unclassified	26972
s__unclassified	26975
s__unclassified	26977
s__unclassified	26979
s__unclassified	26985
s__unclassified	26989
s__unclassified	26991
s__unclassified	26992
s__unclassified	26994
s__unclassified	26996
s__unclassified	26997
s__unclassified	27003
s__unclassified	27007
s__unclassified	27011
s__unclassified	27016
s__unclassified	27024
s__unclassified	27025

FJ678795.1 gg_id:525082 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ366709.1 gg_id:369797 feces adult twins and mothers; TS27 clone TS27_a02h07 FJ3667
EU777134.1 gg_id:308293 Okapi feces clone OK1_f06 EU777
FJ673663.1 gg_id:521226 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
AB034039.1 gg_id:33321 rumen clone 5C0d-6 AB034
EU767319.1 gg_id:341274 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU748314.1 gg_id:311120 neotropical folivorous flying bird adult hoatzin crop clone hoa46_84D11 EU748
FJ683336.1 gg_id:517337 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
GQ175496.1 gg_id:548621 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ801337.1 gg_id:173810 human fecal clone RL388_aao94b09 DQ801
GQ079200.1 gg_id:440181 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229f1 GQ079
DQ808310.1 gg_id:195868 human fecal clone RL180_aao75b04 DQ808
EU762806.1 gg_id:305114 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
EU845601.1 gg_id:327387 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ671379.1 gg_id:528679 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
DQ808451.1 gg_id:186429 human fecal clone RL180_aao76g01 DQ808
EU777639.1 gg_id:348060 Sumatran orangutan feces clone orang2_aai66f03 EU777
FJ683503.1 gg_id:532036 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
FJ683645.1 gg_id:530800 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
AB185796.1 gg_id:106698 rumen clone U29-F08 AB185
FJ367012.1 gg_id:367055 feces adult twins and mothers; TS28 clone TS28_a02d10 FJ3670
FJ673216.1 gg_id:515428 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EF098027.1 gg_id:199742 mouse cecum clone SWPT12_aaa04c08 EF098
FJ880780.1 gg_id:385933 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EF401603.1 gg_id:217078 human fecal clone SJTU_D_12_80 EF401
FJ673489.1 gg_id:525315 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
DQ808084.1 gg_id:193314 human fecal clone RL180_aan72b07 DQ808
GQ898105.1 gg_id:556976 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do : GQ898
AF018544.1 gg_id:16077 rumen fluid clone JW3 AF018
EU472362.1 gg_id:295892 Angola colobus feces clone EAC_1aaa02g07 EU472
EU842465.1 gg_id:341817 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU381723.1 gg_id:270733 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid ; EU381
GQ448900.1 gg_id:557051 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_10wks_gr GQ448
DQ793356.1 gg_id:181961 human fecal clone RL199_aaj42f09 DQ793
DQ673540.1 gg_id:163800 rumen fluid clone GRC75 DQ673
FJ679803.1 gg_id:522426 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6798
DQ800439.1 gg_id:188212 human fecal clone RL183_aah24d07 DQ800
FJ682636.1 gg_id:514231 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
FJ879544.1 gg_id:445343 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU344189.1 gg_id:268936 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ682735.1 gg_id:525180 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	1	1	1	1	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__unclassified	27033
s__unclassified	27035
s__unclassified	27037
s__unclassified	27054
s__unclassified	27055
s__unclassified	27057
s__unclassified	27058
s__unclassified	27061
s__unclassified	27065
s__unclassified	27066
s__unclassified	27068
s__unclassified	27069
s__unclassified	27071
s__unclassified	27074
s__unclassified	27077
s__unclassified	27078
s__unclassified	27079
s__unclassified	27081
s__unclassified	27082
s__unclassified	27084
s__unclassified	27086
s__unclassified	27089
s__unclassified	27094
s__unclassified	27095
s__unclassified	27098
s__unclassified	27101
s__unclassified	27108
s__unclassified	27111
s__unclassified	27114
s__unclassified	27115
s__unclassified	27116
s__unclassified	27117
s__unclassified	27129
s__unclassified	27132
s__unclassified	27136
s__unclassified	27140
s__unclassified	27142
s__unclassified	27143
s__unclassified	27145
s__unclassified	27155
s__unclassified	27156

FJ674239.1 gg_id:511048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
EU381595.1 gg_id:273843 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ682919.1 gg_id:516302 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ676403.1 gg_id:530207 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
EU466401.1 gg_id:293178 bighorn sheep feces clone BH2_aao23b06 EU466
EU381726.1 gg_id:268964 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EF400818.1 gg_id:217014 human fecal clone SJTU_D_01_96 EF4008
EF515535.1 gg_id:223059 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EU469287.1 gg_id:294007 Speke's gazelle feces clone SP3_d08_3 EU469
EU462675.1 gg_id:302094 Sumatran orangutan feces clone orang2_aai67b01 EU462
AJ515916.1 gg_id:94758 Ruminococcus sp. str. 25F6 AJ5159
FJ365090.1 gg_id:365676 feces adult twins and mothers; TS1 clone TS1_a02g01 FJ3650
EF436370.1 gg_id:205159 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC84 EF4363
FJ372101.1 gg_id:368749 feces adult twins and mothers; TS9 clone TS9_a01g06 FJ3721
FJ683482.1 gg_id:520858 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ683285.1 gg_id:530742 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU472479.1 gg_id:297065 Angola colobus feces clone EAC_2_aaa02f09 EU472
GU304502.1 gg_id:562441 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
DQ795096.1 gg_id:175713 human fecal clone RL310_aam40b09 DQ795
FJ367666.1 gg_id:368428 feces adult twins and mothers; TS2 clone TS2_a02b06 FJ3676
EU467336.1 gg_id:297875 chimpanzee feces clone CHIMP1_c02 EU467
EF402085.1 gg_id:207480 human fecal clone SJTU_B_03_46 EF4020
FJ673679.1 gg_id:523326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ682787.1 gg_id:530594 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
DQ882649.1 gg_id:162660 Ruminococcus bromii str. YE282 DQ882
FJ673846.1 gg_id:530234 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
EU473649.1 gg_id:293409 banteng feces clone BG_aaa04a03.Contig1 EU473
FJ682570.1 gg_id:511998 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
EU511872.1 gg_id:269378 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10b09 EU511
EU728796.1 gg_id:319681 Ruminococcus sp. str. DJF_VR87 EU728
FJ683078.1 gg_id:509155 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ880361.1 gg_id:458950 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
EU764268.1 gg_id:304940 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU764
AB270050.1 gg_id:172453 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU762132.1 gg_id:349408 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ680579.1 gg_id:514059 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU766698.1 gg_id:336413 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU766
EU777557.1 gg_id:304044 Sumatran orangutan feces clone orang1_aai55b05 EU777
FJ363111.1 gg_id:364931 feces adult twins and mothers; TS148 clone TS148_a03b10 FJ3631
DQ777945.1 gg_id:169698 rat feces clone R-1141(5) DQ777
GQ339149.1 gg_id:517495 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus

s__unclassified	27158
s__unclassified	27159
s__unclassified	27165
s__unclassified	27167
s__unclassified	27177
s__unclassified	27179
s__unclassified	27183
s__unclassified	27187
s__unclassified	27188
s__unclassified	27190
s__unclassified	27193
s__unclassified	27198
s__unclassified	27200
s__unclassified	27203
s__unclassified	27204
s__unclassified	27205
s__unclassified	27210
s__unclassified	27211
s__unclassified	27213
s__unclassified	27218
s__unclassified	27221
s__unclassified	27223
s__unclassified	27237
s__unclassified	27238
s__unclassified	27239
s__unclassified	27246
s__unclassified	27251
s__unclassified	27257
s__unclassified	27259
s__unclassified	27267
s__unclassified	27269
s__unclassified	27277
s__unclassified	27290
s__unclassified	27295
s__unclassified	27323
s__unclassified	27332
s__unclassified	27392
s__unclassified	27425
s__unclassified	27457
s__unclassified	27461
s__unclassified	27480

AB185787.1 gg_id:101849 rumen clone U29-E09 AB185
FJ683946.1 gg_id:514035 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
FJ879137.1 gg_id:450782 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
FJ682062.1 gg_id:511125 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
FJ680636.1 gg_id:516987 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
DQ905927.2 gg_id:166276 human fecal clone 29c-h4 DQ905
EU530308.1 gg_id:259951 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU5303
AJ515915.1 gg_id:94902 Ruminococcus sp. str. 25F8 AJ5159
EU469049.1 gg_id:298925 Speke's gazelle feces clone SP2_e03_1 EU469
DQ823690.1 gg_id:198813 human fecal clone RL250_aaj77f11 DQ823
EF686591.1 gg_id:242020 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6865
FJ363110.1 gg_id:367447 feces adult twins and mothers; TS148 clone TS148_a03b09 FJ3631
DQ394694.1 gg_id:156441 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
EF402563.1 gg_id:208165 human fecal clone SJTU_B_09_56 EF4025
EF406472.1 gg_id:217186 mouse colon clone control_14days-C5 EF4064
EU472052.1 gg_id:294107 francois langur feces clone FL_1aaa01f10 EU472
AY916385.1 gg_id:114000 human stool clone D739 AY9163
EU767209.1 gg_id:331645 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ394690.1 gg_id:155809 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
FJ675754.1 gg_id:527270 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
DQ807190.1 gg_id:189116 human fecal clone RL244_aaj47d03 DQ807
FJ674069.1 gg_id:515630 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU469135.1 gg_id:302167 Speke's gazelle feces clone SP3_a09_1 EU469
FJ682410.1 gg_id:527856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
EU774116.1 gg_id:318581 Chimpanzee feces clone CHIMP1_aaj39e09 EU774
EU475424.1 gg_id:295802 springbok feces clone SBSD_aaa04c06 EU475
EU843667.1 gg_id:322552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ685421.1 gg_id:527958 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
EU381538.1 gg_id:269531 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
AM404501.2 gg_id:563164 percent G+C fraction libraries number Actinobacteria human faecal clone AP08K.26 AM404
EU748111.1 gg_id:311383 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42a10 EU748
GQ491920.1 gg_id:539328 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ371896.1 gg_id:365465 feces adult twins and mothers; TS8 clone TS8_a03d11 FJ3718
GQ493718.1 gg_id:581908 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ366766.1 gg_id:362381 feces adult twins and mothers; TS27 clone TS27_a03f03 FJ3667
DQ798110.1 gg_id:181710 human fecal clone RL302_aal95f05 DQ798
EF402950.1 gg_id:207652 human fecal clone SJTU_B_14_66 EF4029
EU460195.1 gg_id:300508 mammals their gut microbes eastern black and white colobus feces clone COL_aai16 EU460
EU460164.1 gg_id:290723 mammals their gut microbes eastern black and white colobus feces clone COL_aai15 EU460
EU774396.1 gg_id:323229 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
DQ673538.1 gg_id:172967 rumen fluid clone GRC73 DQ673

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Ruminococcus
g__Subdoligranulum
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	27536
s__unclassified	27556
s__unclassified	27566
s__unclassified	27572
s__unclassified	27575
s__unclassified	27585
s__unclassified	27589
s__unclassified	27613
s__unclassified	27625
s__unclassified	27627
s__unclassified	27656
s__unclassified	27714
s__unclassified	27728
s__unclassified	27756
s__unclassified	27786
s__unclassified	27811
s__unclassified	27813
s__unclassified	27814
s__unclassified	27836
s__unclassified	27841
s__unclassified	27872
s__unclassified	27878
s__unclassified	27891
s__unclassified	28008
s__unclassified	28016
s__unclassified	28020
s__unclassified	28069
s__unclassified	28079
s__unclassified	28087
s__unclassified	28126
s__unclassified	28148
s__unclassified	28159
s__unclassified	28202
s__unclassified	24510
s__unclassified	21829
s__unclassified	21832
s__unclassified	21833
s__unclassified	21834
s__unclassified	21835
s__unclassified	21836
s__unclassified	21837

GQ491705.1 gg_id:560898 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ364282.1 gg_id:361072 feces adult twins and mothers; TS15 clone TS15_a01b03 FJ3642
GQ896914.1 gg_id:562943 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU774563.1 gg_id:341482 Douc langur feces clone DL_2aaa04b11 EU774
DQ798279.1 gg_id:191890 human fecal clone RL181_aah40a10 DQ798
FJ366403.1 gg_id:356858 feces adult twins and mothers; TS26 clone TS26_a02f09 FJ3664
FJ363910.1 gg_id:369703 feces adult twins and mothers; TS14 clone TS14_a04g08 FJ3639
DQ794459.1 gg_id:186667 human fecal clone RL197_aah88b08 DQ794
AB185770.1 gg_id:104606 rumen clone U29-C11 AB185
FJ363821.1 gg_id:362970 feces adult twins and mothers; TS14 clone TS14_a03g05 FJ3638
FJ365359.1 gg_id:367180 feces adult twins and mothers; TS20 clone TS20_a02a02 FJ3653
FJ364504.1 gg_id:360766 feces adult twins and mothers; TS15 clone TS15_a03g02 FJ3645
FM873540.1 gg_id:367036 occupant source house mattress dust clone MA02D04 FM873
GQ043070.1 gg_id:381331 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012h GQ043
FJ832323.1 gg_id:590062 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_23G03 FJ8323
FJ365570.1 gg_id:357204 feces adult twins and mothers; TS20 clone TS20_a04d09 FJ3655
GQ493584.1 gg_id:541439 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ372016.1 gg_id:357258 feces adult twins and mothers; TS8 clone TS8_a04g10 FJ3720
EU344162.1 gg_id:272649 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU460201.1 gg_id:299680 mammals their gut microbes eastern black and white colobus feces clone COL_aai16 EU460
DQ804617.1 gg_id:195090 human fecal clone RL187_aao70d11 DQ804
FJ365420.1 gg_id:368081 feces adult twins and mothers; TS20 clone TS20_a02f09 FJ3654
EU381440.1 gg_id:262572 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
FJ365555.1 gg_id:367799 feces adult twins and mothers; TS20 clone TS20_a04c05 FJ3655
FJ363045.1 gg_id:363989 feces adult twins and mothers; TS148 clone TS148_a02c09 FJ3630
AB034019.1 gg_id:33345 rumen clone 4C0d-6 AB034
AB034029.1 gg_id:19747 rumen clone 4C0d-16 AB034
DQ798127.1 gg_id:190960 human fecal clone RL302_aal95g12 DQ798
FJ366384.1 gg_id:366039 feces adult twins and mothers; TS26 clone TS26_a02d05 FJ3663
FJ367406.1 gg_id:364014 feces adult twins and mothers; TS29 clone TS29_a03b05 FJ3674
FJ833984.1 gg_id:512314 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_78F10 FJ8339
EU381844.1 gg_id:262632 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU344365.1 gg_id:265090 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU530508.1 gg_id:270438 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
FJ374224.1 gg_id:367864 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg FJ3742
EU474848.1 gg_id:290278 takin feces clone TAK_aaa04h07 EU474
FJ881036.1 gg_id:380392 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
EF614895.1 gg_id:232257 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU475330.1 gg_id:292243 rock hyrax feces clone RHSD_aaa03a07 EU475
EU777851.1 gg_id:345556 European rabbit feces clone RA_b02_1 EU777
DQ815323.1 gg_id:168054 mouse cecum clone aab45e04 DQ815

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
1	0	1	1	1	1	1	1	1	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	21838
s__unclassified	21839
s__unclassified	21840
s__unclassified	21841
s__unclassified	21842
s__unclassified	21843
s__unclassified	21847
s__unclassified	21848
s__unclassified	21849
s__unclassified	21850
s__unclassified	21851
s__unclassified	21853
s__unclassified	21854
s__unclassified	21855
s__unclassified	21856
s__unclassified	21857
s__unclassified	21860
s__unclassified	21861
s__unclassified	21862
s__unclassified	21864
s__unclassified	21865
s__unclassified	21866
s__unclassified	21867
s__unclassified	21868
s__unclassified	21869
s__unclassified	21870
s__unclassified	21871
s__unclassified	21872
s__unclassified	21873
s__unclassified	21874
s__unclassified	21875
s__unclassified	21877
s__unclassified	21879
s__unclassified	21880
s__unclassified	21881
s__unclassified	21882
s__unclassified	21883
s__unclassified	21884
s__unclassified	21885
s__unclassified	21886
s__unclassified	21887

EU843714.1 gg_id:348260 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ449203.1 gg_id:581463 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ449
EU459351.1 gg_id:299233 cheetah feces clone CE3_aai05b03 EU459
EU009811.1 gg_id:253896 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_F48 EU009
AY791247.1 gg_id:109481 insect associated clone PBg1-130 AY791
DQ815450.1 gg_id:165952 mouse cecum clone aab48f03 DQ815
FJ365258.1 gg_id:369294 feces adult twins and mothers; TS1 clone TS1_a04g01 FJ3652
EU472325.1 gg_id:294908 Angola colobus feces clone EAC_1aaa01g09 EU472
FJ365014.1 gg_id:360002 feces adult twins and mothers; TS1 clone TS1_a01h01 FJ3650
EU507046.1 gg_id:270303 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar10d04 EU507
FJ366853.1 gg_id:359339 feces adult twins and mothers; TS27 clone TS27_a04f04 FJ3668
X81125.1 gg_id:16072 Clostridium viride str. T2-7 (DSM 6836) X81125
EF614670.1 gg_id:234137 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6146
EU470243.1 gg_id:295095 trancaspain urial feces clone TU2_aaa01f08 EU470
FJ680615.1 gg_id:519246 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
DQ809155.1 gg_id:198744 human fecal clone RL308_aal82e06 DQ809
DQ326189.1 gg_id:147297 Metagenomic gut microbiome healthy human stool clone C101 DQ326
EU509226.1 gg_id:275461 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b06 EU509
FJ172853.1 gg_id:303627 Qinghai Yak Ruminal and Fungi China rumen clone RB-3F5 FJ1728
AB185764.1 gg_id:100135 rumen clone U29-C04 AB185
EU465598.1 gg_id:302257 argali sheep feces clone AS1_aao39a10.Contig1 EU465
DQ394300.1 gg_id:152583 Effect probiotics on gastrointestinal broilers intestine clone BY12 DQ394
EU844875.1 gg_id:342940 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU471673.1 gg_id:298819 Asiatic elephant feces clone AE1_aaa02c06 EU471
EU464154.1 gg_id:300628 reticulated giraffe feces clone gir_aah95a09 EU464
DQ057394.1 gg_id:130048 chicken ileum/cecum clone cc345 DQ057
EU511908.1 gg_id:260762 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11a08 EU511
EU452998.1 gg_id:332814 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
EU843264.1 gg_id:339035 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
DQ815824.1 gg_id:168145 mouse cecum clone aab22g08 DQ815
EF098064.1 gg_id:194182 mouse cecum clone SWPT14_aaa01a06 EF098
EU464416.1 gg_id:297278 hamadryas baboon feces clone AFBAB_aai04g02 EU464
FJ367833.1 gg_id:362395 feces adult twins and mothers; TS2 clone TS2_a04b03 FJ3678
AB234457.1 gg_id:149078 termite gut homogenate clone MgMjD-041 AB234
FJ681152.1 gg_id:530945 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU382058.1 gg_id:272613 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU506544.1 gg_id:270066 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03g02 EU506
EU509962.1 gg_id:270866 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24d08 EU509
AJ488075.1 gg_id:66188 chlorobenzene-degrading consortium clone IA-24 AJ488
EU451755.1 gg_id:339667 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU451
FJ365202.1 gg_id:365220 feces adult twins and mothers; TS1 clone TS1_a04a12 FJ3652

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	0	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	21888
s__unclassified	21889
s__unclassified	21890
s__unclassified	21891
s__unclassified	21892
s__unclassified	21893
s__unclassified	21894
s__unclassified	21895
s__unclassified	21896
s__unclassified	21897
s__unclassified	21899
s__unclassified	21900
s__unclassified	21901
s__unclassified	21902
s__unclassified	21903
s__unclassified	21905
s__unclassified	21907
s__unclassified	21908
s__unclassified	21909
s__unclassified	21910
s__unclassified	21911
s__unclassified	21913
s__unclassified	21914
s__unclassified	21915
s__unclassified	21917
s__unclassified	21918
s__unclassified	21919
s__unclassified	21920
s__unclassified	21921
s__unclassified	21922
s__unclassified	21923
s__unclassified	21924
s__unclassified	21926
s__unclassified	21927
s__unclassified	21928
s__unclassified	21929
s__unclassified	21932
s__unclassified	21933
s__unclassified	21934
s__unclassified	21935
s__unclassified	21937

GU304299.1 gg_id:579244 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU452722.1 gg_id:344329 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
EU776814.1 gg_id:339944 Mongoose lemur feces clone ML_aaj26e09 EU776
EU465532.1 gg_id:295223 argali sheep feces clone AS1_aao37a11.Contig1 EU465
EU458546.1 gg_id:301573 spotted hyena feces clone HY2_h08_2 EU458
FJ680266.1 gg_id:519941 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
AY992951.1 gg_id:130016 mouse cecum clone C22_k16 AY992
EU511675.1 gg_id:262671 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08g07 EU511
DQ815617.1 gg_id:167514 mouse cecum clone aab43f04 DQ815
EU844732.1 gg_id:340116 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
DQ805512.1 gg_id:181769 human fecal clone RL203_aai63f02 DQ805
EU468922.1 gg_id:289860 Speke's gazelle feces clone SP2_c09_1 EU468
FJ542840.1 gg_id:525763 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
EU850604.1 gg_id:326444 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF436 EU850
EU774081.1 gg_id:352918 Chimpanzee feces clone CHIMP12_b04_1 EU774
NR_025025.1 gg_id:539939 Papillibacter cinnamivorans str. CIN1; DSM12816 NR_02
FJ374227.1 gg_id:369389 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
EF604698.1 gg_id:228902 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
FJ680261.1 gg_id:521792 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EF096916.1 gg_id:175377 mouse cecum clone SWPT13_aaa02f07 EF0969
EU463678.1 gg_id:289426 domesticated horse feces clone horsej_aai90h08 EU463
EU506333.1 gg_id:270498 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d10 EU506
DQ796729.1 gg_id:179422 human fecal clone RL179_aao53g02 DQ796
FJ684521.1 gg_id:532424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ880481.1 gg_id:373181 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
GQ047255.1 gg_id:375644 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010e GQ047
EF403010.1 gg_id:204126 human fecal clone SJTU_B_15_54 EF403
EU465687.1 gg_id:302641 argali sheep feces clone AS2_aao33e07 EU465
AB198539.1 gg_id:135453 termite gut wall fraction clone RsW02-066 AB198
EU766175.1 gg_id:349740 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
FJ681934.1 gg_id:524439 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
EU470345.1 gg_id:292656 Grevy's zebra feces clone GZ_aaa01b08 EU470
AB192279.1 gg_id:143711 termite gut homogenate clone RPK-59 AB192
EU504413.1 gg_id:275288 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03h04 EU504
EU470328.1 gg_id:297796 Grevy's zebra feces clone GZ_aaa04g03 EU470
DQ796579.1 gg_id:196210 human fecal clone RL179aan75b11 DQ796
DQ125557.1 gg_id:134357 uranium contaminated soil clone AKAU3538 DQ125
EU468690.1 gg_id:302712 okapi feces clone OK2_f06_1 EU468
EU871383.1 gg_id:351055 Genetic Bovine (Bos taurus) Rumen Thailand clone CF225 EU871
DQ815605.1 gg_id:169578 mouse cecum clone aab43e04 DQ815
EU505544.1 gg_id:258903 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02d10 EU505

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	1	0	1	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	21938
s__unclassified	21939
s__unclassified	21940
s__unclassified	21941
s__unclassified	21942
s__unclassified	21943
s__unclassified	21945
s__unclassified	21946
s__unclassified	21947
s__unclassified	21948
s__unclassified	21949
s__unclassified	21950
s__unclassified	21951
s__unclassified	21952
s__unclassified	21954
s__unclassified	21955
s__unclassified	21956
s__unclassified	21957
s__unclassified	21958
s__unclassified	21960
s__unclassified	21962
s__unclassified	21964
s__unclassified	21965
s__unclassified	21966
s__unclassified	21967
s__unclassified	21968
s__unclassified	21969
s__unclassified	21971
s__unclassified	21972
s__unclassified	21973
s__unclassified	21974
s__unclassified	21975
s__unclassified	21976
s__unclassified	21977
s__unclassified	21978
s__unclassified	21979
s__unclassified	21980
s__unclassified	21981
s__unclassified	21982
s__unclassified	21983
s__unclassified	21984

EU763617.1 gg_id:321571 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
EU508708.1 gg_id:270059 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g03 EU508
EU765286.1 gg_id:344815 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU775069.1 gg_id:327573 Francois Langur feces clone FL_1aaa03e06 EU775
EF605057.1 gg_id:233530 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF605
DQ815489.1 gg_id:173329 mouse cecum clone aab41e04 DQ815
EU764061.1 gg_id:305588 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
EU454514.1 gg_id:322836 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU454
AF371803.1 gg_id:43950 swine intestine clone p-1316-a5 AF371
EU472220.1 gg_id:288423 francois langur feces clone FL_2aaa01e02 EU472
EU766049.1 gg_id:324024 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
EU777228.1 gg_id:305121 Okapi feces clone OK1_d05 EU777
EU507866.1 gg_id:273781 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02d03 EU507
EU779203.1 gg_id:319642 Trancaspian Urial feces clone TU2_aaa03h10 EU779
EU504299.1 gg_id:268671 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa01h12 EU504
EU512008.1 gg_id:273519 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak12f05 EU512
EF434364.1 gg_id:215468 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
AF001761.1 gg_id:16027 rumen clone RF29 AF001
EU885041.1 gg_id:347991 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2H7 EU885
FJ365158.1 gg_id:357678 feces adult twins and mothers; TS1 clone TS1_a03e11 FJ3651
EU779132.1 gg_id:356550 Trancaspian Urial feces clone TU2_aaa04c08 EU779
EU473497.1 gg_id:293727 Somali wild ass feces clone WA_aaa01h08 EU473
AY992778.1 gg_id:133495 mouse cecum clone C22_a17 AY992
EF401851.1 gg_id:216263 human fecal clone SJTU_D_05_87 EF4018
DQ795112.1 gg_id:178288 human fecal clone RL310_aam40d04 DQ795
AY980920.1 gg_id:116165 human rectum mucosal biopsy clone LR29 AY980
EF603654.1 gg_id:231593 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
DQ815430.1 gg_id:163633 mouse cecum clone aab48c09 DQ815
EU460978.1 gg_id:292639 red kangaroo feces clone KO1_aai41e04 EU460
EF445154.1 gg_id:210292 rabbit cecum clone NED2F7 EF4451
EU382039.1 gg_id:260436 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU779391.1 gg_id:345353 Somali Wild Ass feces clone WA_aaa01c12 EU779
EU777115.1 gg_id:311308 Okapi feces clone OK3_f10 EU777
EU508202.1 gg_id:274847 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa03b05 EU508
GU302819.1 gg_id:551289 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU455639.1 gg_id:349725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU455
FJ366757.1 gg_id:367176 feces adult twins and mothers; TS27 clone TS27_a03e06 FJ3667
EU777102.1 gg_id:342600 Okapi feces clone OK1_f06_1 EU777
EF096437.1 gg_id:199046 mouse cecum clone obob2_aaa02g08 EF0964
EU773165.1 gg_id:352908 BigHorn sheep feces clone BHSD_aaa01b04 EU773
GQ175508.1 gg_id:589507 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	21985
s__unclassified	21986
s__unclassified	21987
s__unclassified	21989
s__unclassified	21992
s__unclassified	21994
s__unclassified	21995
s__unclassified	21996
s__unclassified	21997
s__unclassified	21998
s__unclassified	22000
s__unclassified	22002
s__unclassified	22003
s__unclassified	22004
s__unclassified	22006
s__unclassified	22007
s__unclassified	22008
s__unclassified	22010
s__unclassified	22011
s__unclassified	22013
s__unclassified	22015
s__unclassified	22016
s__unclassified	22017
s__unclassified	22019
s__unclassified	22023
s__unclassified	22025
s__unclassified	22026
s__unclassified	22028
s__unclassified	22029
s__unclassified	22030
s__unclassified	22031
s__unclassified	22032
s__unclassified	22033
s__unclassified	22035
s__unclassified	22036
s__unclassified	22038
s__unclassified	22041
s__unclassified	22042
s__unclassified	22043
s__unclassified	22044
s__unclassified	22047

AF371937.1 gg_id:34823 swine intestine clone p-5152-2Wb3 AF371
EU473725.1 gg_id:294467 douc langur feces clone DL_2aaa01g03 EU473
FJ880941.1 gg_id:410327 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EU469833.1 gg_id:293546 western lowland gorilla feces clone GOR_aag72a09 EU469
EU772173.1 gg_id:312152 Argali sheep feces clone AS1_aao37d04.Contig1 EU772
AB185773.1 gg_id:105047 rumen clone U29-D02 AB185
EU850524.1 gg_id:331952 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF310 EU850
EU470209.1 gg_id:298302 trancaspain urial feces clone TU2_aaa02h10 EU470
EU472107.1 gg_id:290859 francois langur feces clone FL_1aaa01e09 EU472
EU463636.1 gg_id:292001 domesticated horse feces clone horsej_aai90b08 EU463
EU773172.1 gg_id:320029 BigHorn sheep feces clone BH2_aao23c10 EU773
GU303920.1 gg_id:561716 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU458079.1 gg_id:308523 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU458
DQ014986.1 gg_id:131359 mouse cecum clone M1_1b09_1 DQ014
FJ881217.1 gg_id:371870 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EU009770.1 gg_id:247551 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AF39 EU009
FJ680773.1 gg_id:515004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU454896.1 gg_id:327567 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU454
EU772027.1 gg_id:354741 Argali sheep feces clone AS1_aao37a07.Contig1 EU772
EF071402.1 gg_id:187846 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0714
EU844698.1 gg_id:306375 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU773275.1 gg_id:319693 BigHorn sheep feces clone BH1_aao25d09 EU773
AY858503.2 gg_id:110968 gastrointestinal tract eland clone ELAND_41 AY858
FJ680312.1 gg_id:532384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
DQ793455.1 gg_id:186654 human fecal clone RL199_aaj43h12 DQ793
FJ879227.1 gg_id:445626 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU506351.1 gg_id:271290 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap64a01 EU506
EU776815.1 gg_id:333249 Mongoose lemur feces clone ML_aae88a09 EU776
EU779144.1 gg_id:321963 Trancaspian Urial feces clone TU2_aaa03b05 EU779
EU506252.1 gg_id:276388 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61d11 EU506
FJ680395.1 gg_id:515362 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU474545.1 gg_id:297237 bighorn sheep feces clone BHSD_aaa04e05 EU474
DQ809638.1 gg_id:195252 human fecal clone RL184_aan81h11 DQ809
FJ880264.1 gg_id:431899 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ880708.1 gg_id:372146 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
GQ897911.1 gg_id:589989 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ088761.1 gg_id:132303 0.7 1.4 kmbls sctn cntnntl crst cln BE325FW032701CTS_hl1-41 DQ088
EU776496.1 gg_id:330252 Red Kangaroo feces clone KO1_aai41c09 EU776
DQ815620.1 gg_id:166466 mouse cecum clone aab43f08 DQ815
CU927388.1 gg_id:557458 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
EF401251.1 gg_id:207166 human fecal clone SJTU_D_07_85 EF4012

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22048
s__unclassified	22051
s__unclassified	22053
s__unclassified	22054
s__unclassified	22055
s__unclassified	22056
s__unclassified	22057
s__unclassified	22058
s__unclassified	22060
s__unclassified	22062
s__unclassified	22065
s__unclassified	22067
s__unclassified	22069
s__unclassified	22070
s__unclassified	22071
s__unclassified	22073
s__unclassified	22074
s__unclassified	22076
s__unclassified	22077
s__unclassified	22078
s__unclassified	22079
s__unclassified	22080
s__unclassified	22081
s__unclassified	22083
s__unclassified	22084
s__unclassified	22085
s__unclassified	22086
s__unclassified	22087
s__unclassified	22088
s__unclassified	22090
s__unclassified	22092
s__unclassified	22094
s__unclassified	22095
s__unclassified	22096
s__unclassified	22097
s__unclassified	22098
s__unclassified	22099
s__unclassified	22100
s__unclassified	22101
s__unclassified	22102
s__unclassified	22103

EU466130.1 gg_id:301743 bighorn sheep feces clone BH1_aao26e12 EU466
EU466076.1 gg_id:290337 bighorn sheep feces clone BH1_aao25d04 EU466
EF097979.1 gg_id:192930 mouse cecum clone SWPT12_aaa03c10 EF0979
EU505220.1 gg_id:261998 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa04f10 EU505
DQ801156.1 gg_id:198841 human fecal clone RL116_aae99c04 DQ801
EU504194.1 gg_id:274083 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa03g11 EU504
EU777204.1 gg_id:347980 Okapi feces clone OK3_d02_3 EU777
FJ880790.1 gg_id:463116 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
FJ673102.1 gg_id:517347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU468528.1 gg_id:293630 okapi feces clone OK1_a08_1 EU468
EU507527.1 gg_id:277388 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e12 EU507
EF098062.1 gg_id:190396 mouse cecum clone SWPT14_aaa01a03 EF098
FJ371773.1 gg_id:365161 feces adult twins and mothers; TS8 clone TS8_a02a09 FJ3717
AY854298.1 gg_id:110901 herbivore gastrointestinal tract clone Thompsons100 AY854
EF097074.1 gg_id:196191 mouse cecum clone SWPT18_aaa01a07 EF097
EU464390.1 gg_id:303345 hamadryas baboon feces clone AFBAB_aai04b12 EU464
CU926151.1 gg_id:562681 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
EU468950.1 gg_id:294437 Speke's gazelle feces clone SP2_g12 EU468
EU474858.1 gg_id:287505 takin feces clone TAK_aaa01h06 EU474
EU470234.1 gg_id:294545 trancaspain urial feces clone TU2_aaa02e05 EU470
EF096746.1 gg_id:193198 mouse cecum clone SWPT11_aaa04a09 EF0967
DQ799903.1 gg_id:199317 human fecal clone RL247_aaj21f02 DQ799
FJ680818.1 gg_id:532083 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EU470155.1 gg_id:295979 trancaspain urial feces clone TU2_aaa04h08 EU470
DQ800334.1 gg_id:184208 human fecal clone RL303_aal71g01 DQ800
EU771790.1 gg_id:333206 African elephant feces clone AFEL3_aao14d01 EU771
EU464228.1 gg_id:292382 reticulated giraffe feces clone gir_aah96f04 EU464
EU458586.1 gg_id:292513 European rabbit feces clone RA_d11 EU458
EU794151.1 gg_id:307643 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H9 EU794
EU471983.1 gg_id:293667 francois langur feces clone FL_1aaa01h03 EU471
DQ808904.1 gg_id:175511 human fecal clone RL243_aai86g11 DQ808
FJ366541.1 gg_id:363783 feces adult twins and mothers; TS27 clone TS27_a01a02 FJ3665
GU174111.1 gg_id:563490 Microbial Bactrian camel estimated rumen clone XJC5 GU174
EU456560.1 gg_id:321019 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU456
EU452476.1 gg_id:313021 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
EU506190.1 gg_id:273910 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03a05 EU506
EU469336.1 gg_id:287585 springbok feces clone SBK_f11 EU469
EU766271.1 gg_id:340006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU766
EU475523.1 gg_id:289882 springbok feces clone SBSD_aaa01f06 EU475
EU509854.1 gg_id:264775 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e06 EU509
EU776270.1 gg_id:344111 Red Kangaroo feces clone KO2_aai18g10 EU776

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	0	1	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	1	0	0	0	1	1

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22104
s__unclassified	22105
s__unclassified	22106
s__unclassified	22107
s__unclassified	22108
s__unclassified	22109
s__unclassified	22110
s__unclassified	22113
s__unclassified	22114
s__unclassified	22116
s__unclassified	22117
s__unclassified	22120
s__unclassified	22121
s__unclassified	22122
s__unclassified	22124
s__unclassified	22125
s__unclassified	22126
s__unclassified	22127
s__unclassified	22129
s__unclassified	22130
s__unclassified	22134
s__unclassified	22135
s__unclassified	22136
s__unclassified	22137
s__unclassified	22138
s__unclassified	22139
s__unclassified	22140
s__unclassified	22141
s__unclassified	22142
s__unclassified	22143
s__unclassified	22145
s__unclassified	22146
s__unclassified	22147
s__unclassified	22148
s__unclassified	22150
s__unclassified	22151
s__unclassified	22154
s__unclassified	22155
s__unclassified	22156
s__unclassified	22157
s__unclassified	22158

DQ794239.1 gg_id:180468 human fecal clone RL176_aan60a04 DQ794
EF099665.1 gg_id:196556 mouse cecum clone SWPT4_aaa02f04 EF0996
EU622645.1 gg_id:281242 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF097943.1 gg_id:194809 mouse cecum clone SWPT12_aaa02e11 EF0979
EU504880.1 gg_id:266512 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03f12 EU5048
EU465571.1 gg_id:292962 argali sheep feces clone AS1_aao38b02.Contig1 EU465
FJ879507.1 gg_id:400748 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU506869.1 gg_id:266845 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07e08 EU5068
EU472333.1 gg_id:297020 Angola colobus feces clone EAC_1aaa02f01 EU4723
FJ681547.1 gg_id:527760 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
EF096100.1 gg_id:192849 mouse cecum clone lean2_aaa04b06 EF0961
AM405156.2 gg_id:564320 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.15 AM405
EU506930.1 gg_id:264668 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08e06 EU5069
EU773138.1 gg_id:329808 BigHorn sheep feces clone BH1_aao27h11 EU7731
EU470403.1 gg_id:290531 Grevy's zebra feces clone GZ_aaa01c07 EU4704
EF098922.1 gg_id:199445 mouse cecum clone SWPT1_aaa03c09 EF0989
AF371795.1 gg_id:48325 swine intestine clone p-2027-s959-5 AF3717
FJ880774.1 gg_id:377756 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
DQ825126.1 gg_id:186321 human fecal clone RL185_aan85f09 DQ825
GU302815.1 gg_id:593396 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ815699.1 gg_id:162151 mouse cecum clone aab21b05 DQ815
EU779200.1 gg_id:348872 Trancaspian Urial feces clone TU2_aaa03a08 EU7792
EU463773.1 gg_id:299331 domesticated horse feces clone horsej_aai92f01 EU4637
EF434333.1 gg_id:205309 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
EU506958.1 gg_id:269532 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08h10 EU5069
EU843115.1 gg_id:353088 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
FJ833519.1 gg_id:557177 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q301_40H05 FJ8335
DQ014588.1 gg_id:131678 mouse cecum clone M1_d04 DQ014
AF129864.1 gg_id:16031 microbial anaerobic digestor determined clone BC09 AF1298
DQ326172.1 gg_id:146132 Metagenomic gut microbiome healthy human stool clone C071 DQ326
EU511693.1 gg_id:263255 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf07a12 EU5116
AY244908.1 gg_id:85153 cow rumen clone BF30 AY2449
EU532006.1 gg_id:268937 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5320
FJ371294.1 gg_id:357511 feces adult twins and mothers; TS6 clone TS6_a03c05 FJ3712
FJ674035.1 gg_id:529236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
AB264082.1 gg_id:194322 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-185 AB2640
EU773210.1 gg_id:306212 BigHorn sheep feces clone BH1_aao27f06 EU7732
EU772832.1 gg_id:308307 Bush dog feces clone bdog1_aai77b11 EU7728
EU458006.1 gg_id:327808 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU4580
EU451213.1 gg_id:327675 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU4512
EF454073.2 gg_id:224826 termite hindgut clone 290cost002-P3L-1599 EF4540

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	1	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22159
s__unclassified	22162
s__unclassified	22163
s__unclassified	22164
s__unclassified	22165
s__unclassified	22166
s__unclassified	22167
s__unclassified	22168
s__unclassified	22170
s__unclassified	22171
s__unclassified	22175
s__unclassified	22178
s__unclassified	22179
s__unclassified	22181
s__unclassified	22182
s__unclassified	22183
s__unclassified	22184
s__unclassified	22187
s__unclassified	22188
s__unclassified	22189
s__unclassified	22190
s__unclassified	22191
s__unclassified	22192
s__unclassified	22193
s__unclassified	22194
s__unclassified	22195
s__unclassified	22196
s__unclassified	22198
s__unclassified	22199
s__unclassified	22201
s__unclassified	22202
s__unclassified	22203
s__unclassified	22204
s__unclassified	22205
s__unclassified	22206
s__unclassified	22207
s__unclassified	22208
s__unclassified	22211
s__unclassified	22213
s__unclassified	22214
s__unclassified	22215

FJ678688.1 gg_id:509467 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
EU468277.1 gg_id:294117 domesticated horse feces clone horsej_c02 EU468
EU509543.1 gg_id:272048 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60e08 EU509
EU622710.1 gg_id:278359 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF602807.1 gg_id:230994 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6028
EU468306.1 gg_id:289975 domesticated horse feces clone horsem_e06_1 EU468
GQ451226.1 gg_id:592773 Fecal Yunnan snub-nosed monkey feces clone J132 GQ451
EU458596.1 gg_id:292888 European rabbit feces clone RA_a12_1 EU458
EU510699.1 gg_id:277228 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39e11 EU510
EU344213.1 gg_id:258933 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU344226.1 gg_id:268753 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ327493.1 gg_id:147815 Metagenomic gut microbiome healthy human stool clone EA65 DQ327
EU844171.1 gg_id:330603 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU381463.1 gg_id:261686 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU474449.1 gg_id:299201 bighorn sheep feces clone BHSD_aaa02c08 EU474
DQ815474.1 gg_id:164242 mouse cecum clone aab41c04 DQ815
FJ880592.1 gg_id:433422 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EU469205.1 gg_id:301405 Speke's gazelle feces clone SP3_a12_1 EU469
DQ673520.1 gg_id:172035 rumen fluid clone GRC55 DQ673
EF099878.1 gg_id:194478 mouse cecum clone SWPT5_aaa01f08 EF0998
EU509449.1 gg_id:273706 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58e09 EU509
EF097158.1 gg_id:173971 mouse cecum clone SWPT18_aaa02c05 EF0971
GU174120.1 gg_id:543168 Microbial Bactrian camel estimated rumen clone XJC50 GU174
EU509440.1 gg_id:270062 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58d07 EU509
FJ880832.1 gg_id:455786 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EF099659.1 gg_id:184823 mouse cecum clone SWPT4_aaa02e08 EF0996
EF025238.1 gg_id:182479 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_B31 EF0252
EU779173.1 gg_id:305394 Trancaspian Urial feces clone TU2_aaa04c09 EU779
AY916365.1 gg_id:113336 human stool clone D330 AY9163
FJ681328.1 gg_id:511240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EU470398.1 gg_id:300619 Grevy's zebra feces clone GZ_aaa03g04 EU470
AF129861.1 gg_id:16034 anaerobic digestor clone BA18 AF1298
EU457607.1 gg_id:349783 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78 EU457
EU472116.1 gg_id:295144 francois langur feces clone FL_1aaa01h04 EU472
EU469146.1 gg_id:299718 Speke's gazelle feces clone SP3_c02_1 EU469
EU506974.1 gg_id:275040 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09c01 EU506
AB189696.1 gg_id:113007 termite gut homogenate clone Tc-64 AB189
EU844447.1 gg_id:310518 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
AF371933.1 gg_id:41628 swine intestine clone p-5013-2Wa5 AF371
EF099118.1 gg_id:179933 mouse cecum clone SWPT2_aaa02e09 EF0991
AB486052.1 gg_id:579562 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	1
0	1	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22216
s__unclassified	22217
s__unclassified	22218
s__unclassified	22219
s__unclassified	22220
s__unclassified	22221
s__unclassified	22222
s__unclassified	22223
s__unclassified	22224
s__unclassified	22225
s__unclassified	22226
s__unclassified	22227
s__unclassified	22228
s__unclassified	22229
s__unclassified	22233
s__unclassified	22234
s__unclassified	22238
s__unclassified	22239
s__unclassified	22240
s__unclassified	22241
s__unclassified	22242
s__unclassified	22243
s__unclassified	22244
s__unclassified	22245
s__unclassified	22246
s__unclassified	22247
s__unclassified	22248
s__unclassified	22250
s__unclassified	22252
s__unclassified	22254
s__unclassified	22255
s__unclassified	22256
s__unclassified	22257
s__unclassified	22258
s__unclassified	22259
s__unclassified	22260
s__unclassified	22261
s__unclassified	22262
s__unclassified	22265
s__unclassified	22266
s__unclassified	22269

EU452720.1 gg_id:344906 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
EU509869.1 gg_id:264539 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h01 EU5098
EU509336.1 gg_id:259091 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48c05 EU5093
EU471605.1 gg_id:301418 Asiatic elephant feces clone AE1_aaa03h12 EU4716
DQ532267.1 gg_id:170620 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
EU465548.1 gg_id:298616 argali sheep feces clone AS1_aao37d10.Contig1 EU4655
DQ014996.1 gg_id:133446 mouse cecum clone M1_1d03_1 DQ014
EF603680.1 gg_id:234600 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
EU461342.1 gg_id:291171 red kangaroo feces clone KO2_aai18a02 EU4613
EU358720.1 gg_id:326879 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU463535.1 gg_id:298695 domesticated horse feces clone horsem_aai95f08 EU4635
EU458633.1 gg_id:291920 European rabbit feces clone RA_c10_1 EU4586
EU509225.1 gg_id:262672 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b05 EU5092
FJ684123.1 gg_id:521615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
AB185802.1 gg_id:102301 rumen clone U29-G04 AB1858
FJ680288.1 gg_id:525143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
EU776832.1 gg_id:336032 Mongoose lemur feces clone ML_aae88b01 EU7768
EU779365.1 gg_id:329869 Somali Wild Ass feces clone WA_aaa03g09 EU7793
AB486861.1 gg_id:578216 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB4868
DQ794759.1 gg_id:186541 human fecal clone RL240_aaj32a06 DQ794
AB185813.1 gg_id:107450 rumen clone U29-H08 AB1858
EU506784.1 gg_id:271281 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56c02 EU5067
FJ880114.1 gg_id:433722 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU844375.1 gg_id:340263 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8443
FJ880118.1 gg_id:418903 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
FJ365102.1 gg_id:364621 feces adult twins and mothers; TS1 clone TS1_a02h02 FJ3651
EF402847.1 gg_id:215231 human fecal clone SJTU_B_13_26 EF4028
EU773239.1 gg_id:312805 BigHorn sheep feces clone BH1_aao26d11 EU7732
DQ809188.1 gg_id:186037 human fecal clone RL308_aal83a11 DQ809
EU511248.1 gg_id:258340 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak17a12 EU5112
EF602935.1 gg_id:234474 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6029
DQ905668.1 gg_id:165979 human fecal clone 014C-E4 DQ905
FJ881201.1 gg_id:379762 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
EU451818.1 gg_id:313324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4518
FJ679087.1 gg_id:512339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
AB192035.1 gg_id:143918 termite gut homogenate clone M2PB4-66 AB1920
EU453946.1 gg_id:328060 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4539
EU462528.1 gg_id:300388 Sumatran orangutan feces clone orang1_aai56d11 EU4625
FJ978658.1 gg_id:434584 feces clone CL_F_333 FJ9786
FJ681272.1 gg_id:525681 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
GQ502526.1 gg_id:571808 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502

0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	1	1	0
0	1	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22270
s__unclassified	22273
s__unclassified	22274
s__unclassified	22275
s__unclassified	22276
s__unclassified	22279
s__unclassified	22282
s__unclassified	22284
s__unclassified	22285
s__unclassified	22286
s__unclassified	22288
s__unclassified	22289
s__unclassified	22290
s__unclassified	22291
s__unclassified	22292
s__unclassified	22293
s__unclassified	22294
s__unclassified	22295
s__unclassified	22296
s__unclassified	22297
s__unclassified	22300
s__unclassified	22302
s__unclassified	22303
s__unclassified	22305
s__unclassified	22308
s__unclassified	22309
s__unclassified	22310
s__unclassified	22311
s__unclassified	22312
s__unclassified	22314
s__unclassified	22315
s__unclassified	22316
s__unclassified	22317
s__unclassified	22318
s__unclassified	22319
s__unclassified	22320
s__unclassified	22322
s__unclassified	22323
s__unclassified	22324
s__unclassified	22326
s__unclassified	22327

DQ805638.1 gg_id:180108 human fecal clone RL306aal89c06 DQ805
EU463410.1 gg_id:296065 domesticated horse feces clone horsem_aai93d03 EU463
EU775729.1 gg_id:326022 Horse feces clone horsem_aai93b08 EU775
GQ491853.1 gg_id:577408 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AF376229.1 gg_id:46657 ckncm325-B3-50 clone AF376
AY992419.1 gg_id:133769 mouse cecum clone C23_c21 AY992
EF097039.1 gg_id:197925 mouse cecum clone SWPT13_aaa04e08 EF097
AF371792.1 gg_id:25957 swine intestine clone p-2479-18B5 AF371
EU773132.1 gg_id:340732 BigHorn sheep feces clone BH1_aao27g09 EU773
EU506308.1 gg_id:261877 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63a07 EU506
EF098273.1 gg_id:195904 mouse cecum clone SWPT14_aaa04a05 EF098
EU885034.1 gg_id:339994 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2C1 EU885
EU462489.1 gg_id:289958 Sumatran orangutan feces clone orang1_aai55f11 EU462
FJ880091.1 gg_id:407216 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
AB307642.1 gg_id:272210 clay wall used Japanese traditional buildings clone R70 AB307
DQ799877.1 gg_id:193310 human fecal clone RL247_aaj21c06 DQ799
EU507770.1 gg_id:268725 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04e05 EU507
DQ057415.1 gg_id:131039 chicken ileum/cecum clone oc30 DQ057
EU453106.1 gg_id:304019 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
AB192010.1 gg_id:144056 termite gut homogenate clone M2PT2-13 AB192
GQ448400.1 gg_id:571165 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ448
FJ368251.1 gg_id:358150 feces adult twins and mothers; TS3 clone TS3_a02a08 FJ3682
AM176887.1 gg_id:161109 Recovery mangrove sediment clone SZB63 AM176
EU885033.1 gg_id:315891 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2B3 EU885
EU775785.1 gg_id:348949 Horse feces clone horsem_aai93g06 EU775
GQ451286.1 gg_id:594119 Fecal Yunnan snub-nosed monkey feces clone J287 GQ451
EU507013.1 gg_id:273022 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09g09 EU507
EU779486.1 gg_id:338681 Grevy's Zebra feces clone GZ_aaa04a02 EU779
GQ448458.1 gg_id:565308 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
EU508142.1 gg_id:271619 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa01d04 EU508
GU304152.1 gg_id:580305 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
AF371785.1 gg_id:38344 swine intestine clone p-397-o3 AF371
DQ805454.1 gg_id:178841 human fecal clone RL203_aai62h05 DQ805
DQ793317.1 gg_id:193865 human fecal clone RL199_aaj42b08 DQ793
EU465624.1 gg_id:293285 argali sheep feces clone AS1_aao40a12.Contig1 EU465
EF098326.1 gg_id:195497 mouse cecum clone SWPT14_aaa04g10 EF098
EU509792.1 gg_id:266715 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b03 EU509
EU842787.1 gg_id:308413 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU871413.1 gg_id:321628 Genetic Bovine (Bos taurus) Rumen Thailand clone CF386 EU871
FJ880997.1 gg_id:373909 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EF434371.1 gg_id:209327 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22328
s__unclassified	22329
s__unclassified	22330
s__unclassified	22331
s__unclassified	22332
s__unclassified	22334
s__unclassified	22335
s__unclassified	22336
s__unclassified	22337
s__unclassified	22338
s__unclassified	22339
s__unclassified	22340
s__unclassified	22341
s__unclassified	22342
s__unclassified	22343
s__unclassified	22344
s__unclassified	22345
s__unclassified	22346
s__unclassified	22347
s__unclassified	22348
s__unclassified	22349
s__unclassified	22350
s__unclassified	22351
s__unclassified	22353
s__unclassified	22355
s__unclassified	22356
s__unclassified	22358
s__unclassified	22359
s__unclassified	22360
s__unclassified	22361
s__unclassified	22362
s__unclassified	22366
s__unclassified	22367
s__unclassified	22368
s__unclassified	22370
s__unclassified	22371
s__unclassified	22372
s__unclassified	22373
s__unclassified	22374
s__unclassified	22375
s__unclassified	22376

FJ881346.1 gg_id:454021 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU461799.1 gg_id:287883 white-faced saki feces clone Saki_aaj61c06 EU461
EU457236.1 gg_id:326950 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU457
FJ366005.1 gg_id:369544 feces adult twins and mothers; TS25 clone TS25_a01f04 FJ3660
GQ502525.1 gg_id:578230 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU771554.1 gg_id:350467 Hamadryas Baboon feces clone AFBAB_aai02d07 EU771
EU506866.1 gg_id:276749 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07e05 EU5068
EF603969.1 gg_id:231028 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EU777238.1 gg_id:317218 Okapi feces clone OK3_b10 EU777
EU771370.1 gg_id:345938 Asiatic elephant feces clone AE2_aaa01h05 EU7713
EU509664.1 gg_id:276522 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak46g10 EU509
EU842226.1 gg_id:335384 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
DQ327001.1 gg_id:148379 Metagenomic gut microbiome healthy human stool clone E502 DQ327
EU794177.1 gg_id:313908 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A02 EU7941
EU466381.1 gg_id:302069 bighorn sheep feces clone BH2_aao22g11 EU4663
EU464525.1 gg_id:301028 African elephant feces clone AFEL_aai30e12 EU4645
FJ393118.1 gg_id:358001 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
EF604700.1 gg_id:234202 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EU764407.1 gg_id:322133 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7644
EU469147.1 gg_id:292438 Speke's gazelle feces clone SP3_c03_1 EU4691
EU509134.1 gg_id:276902 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44e04 EU5091
FJ880490.1 gg_id:436835 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
FJ681177.1 gg_id:516395 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
DQ815618.1 gg_id:170926 mouse cecum clone aab43f05 DQ815
AB234447.1 gg_id:148791 termite gut homogenate clone MgMjD-018 AB2344
AY212772.1 gg_id:101572 equine manure clone wet70 AY2127
EU843894.1 gg_id:331387 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8438
EF445187.1 gg_id:216140 rabbit cecum clone NED3D6 EF4451
AY976153.1 gg_id:117430 human ascending colon mucosal biopsy clone LV48 AY9761
FJ365228.1 gg_id:367866 feces adult twins and mothers; TS1 clone TS1_a04d04 FJ3652
EU777385.1 gg_id:348651 Sumatran orangutan feces clone orang1_aai53h04 EU7773
AY916184.1 gg_id:113111 human ascending colon biopsy clone LV67 AY9161
EU458679.1 gg_id:295715 European rabbit feces clone RA_h01_3 EU4586
EU842293.1 gg_id:309123 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8422
EU467441.1 gg_id:295906 Sumatran orangutan feces clone orang1_c01 EU4674
EU470041.1 gg_id:294340 trancaspain urial feces clone TU1_aaa02a08 EU4700
FJ879644.1 gg_id:422337 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
DQ326566.1 gg_id:148532 Metagenomic gut microbiome healthy human stool clone C748 DQ326
EU506557.1 gg_id:265758 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04b04 EU5065
EU842386.1 gg_id:321135 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8423
FJ678622.1 gg_id:528111 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786

0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22377
s__unclassified	22379
s__unclassified	22381
s__unclassified	22382
s__unclassified	22383
s__unclassified	22384
s__unclassified	22385
s__unclassified	22388
s__unclassified	22389
s__unclassified	22390
s__unclassified	22391
s__unclassified	22392
s__unclassified	22393
s__unclassified	22394
s__unclassified	22395
s__unclassified	22397
s__unclassified	22398
s__unclassified	22399
s__unclassified	22400
s__unclassified	22401
s__unclassified	22403
s__unclassified	22404
s__unclassified	22405
s__unclassified	22407
s__unclassified	22409
s__unclassified	22410
s__unclassified	22412
s__unclassified	22413
s__unclassified	22414
s__unclassified	22416
s__unclassified	22418
s__unclassified	22419
s__unclassified	22420
s__unclassified	22422
s__unclassified	22423
s__unclassified	22424
s__unclassified	22426
s__unclassified	22427
s__unclassified	22428
s__unclassified	22429
s__unclassified	22430

FJ680717.1 gg_id:529561 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU473436.1 gg_id:294626 Somali wild ass feces clone WA_aaa01c10 EU4734
AY975617.1 gg_id:115444 human ascending colon mucosal biopsy clone NB69 AY9756
GU304498.1 gg_id:543553 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EF399731.1 gg_id:209830 human fecal clone SJTU_E_02_68 EF3997
EU505664.1 gg_id:276996 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04d06 EU5056
DQ801199.1 gg_id:178252 human fecal clone RL116_aaf00g02 DQ801
FJ880144.1 gg_id:424613 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU777857.1 gg_id:355155 European rabbit feces clone RA_b07 EU7778
FJ880076.1 gg_id:422278 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EF097727.1 gg_id:190646 mouse cecum clone SWPT20_aaa02g10 EF0977
EU473597.1 gg_id:288349 Somali wild ass feces clone WA_aaa02g11 EU4735
EU774656.1 gg_id:351422 Angola Colobus feces clone EAC_2_aaa04h09 EU7746
FJ879462.1 gg_id:382733 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EU458617.1 gg_id:293735 European rabbit feces clone RA_f11 EU4586
EU506600.1 gg_id:270508 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53b03 EU5066
DQ793945.1 gg_id:186640 human fecal clone RL176_aah45f04 DQ793
EF097537.1 gg_id:198821 mouse cecum clone SWPT19_aaa04a09 EF0975
EU778171.1 gg_id:353173 feces clone RL388_aao93e04 EU7781
AB198472.1 gg_id:135737 termite gut wall fraction clone RsW01-038 AB1984
DQ815459.1 gg_id:171864 mouse cecum clone aab48g10 DQ815
EU506211.1 gg_id:260799 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03h12 EU5062
EU509851.1 gg_id:275622 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e03 EU5098
FJ366802.1 gg_id:369416 feces adult twins and mothers; TS27 clone TS27_a04a08 FJ3668
EU773296.1 gg_id:338000 BigHorn sheep feces clone BHSD_aaa03c07 EU7732
EU463669.1 gg_id:287931 domesticated horse feces clone horsej_aai90g05 EU4636
EU773231.1 gg_id:314186 BigHorn sheep feces clone BH1_aao25h07 EU7732
EU475075.1 gg_id:287835 visayam warty pig feces clone VWP_aaa03h03 EU4750
FJ367779.1 gg_id:363229 feces adult twins and mothers; TS2 clone TS2_a03e05 FJ3677
EU471638.1 gg_id:300851 Asiatic elephant feces clone AE1_aaa02g01 EU4716
GQ079310.1 gg_id:386396 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c0 GQ079
EU507314.1 gg_id:258637 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01e06 EU5073
EU474530.1 gg_id:291888 bighorn sheep feces clone BHSD_aaa02b07 EU4745
EU506880.1 gg_id:274508 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07g01 EU5068
EU777156.1 gg_id:326925 Okapi feces clone OK2_f08_3 EU7771
AB034042.1 gg_id:17907 rumen clone 5C0d-9 AB0340
AF371791.1 gg_id:16559 swine intestine clone p-1617-c5 AF3717
EF096046.1 gg_id:178180 mouse cecum clone lean2_aaa02g07 EF0960
EU457632.1 gg_id:334251 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU4576
EU009861.1 gg_id:240271 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Z48 EU0098
FJ365000.1 gg_id:358904 feces adult twins and mothers; TS1 clone TS1_a01f08 FJ3650

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	1	1	1	1	1	1	0	0	1	1	1	1
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22431
s__unclassified	22432
s__unclassified	22433
s__unclassified	22434
s__unclassified	22435
s__unclassified	22436
s__unclassified	22437
s__unclassified	22439
s__unclassified	22441
s__unclassified	22442
s__unclassified	22443
s__unclassified	22444
s__unclassified	22445
s__unclassified	22446
s__unclassified	22448
s__unclassified	22450
s__unclassified	22451
s__unclassified	22452
s__unclassified	22453
s__unclassified	22454
s__unclassified	22455
s__unclassified	22456
s__unclassified	22458
s__unclassified	22459
s__unclassified	22460
s__unclassified	22461
s__unclassified	22462
s__unclassified	22463
s__unclassified	22464
s__unclassified	22465
s__unclassified	22466
s__unclassified	22468
s__unclassified	22469
s__unclassified	22470
s__unclassified	22471
s__unclassified	22473
s__unclassified	22474
s__unclassified	22475
s__unclassified	22478
s__unclassified	22479
s__unclassified	22481

DQ824307.1 gg_id:174984 human fecal clone RL304_aal74c04 DQ824
EU468603.1 gg_id:290441 okapi feces clone OK1_h02_2 EU468
EU474862.1 gg_id:299736 takin feces clone TAK_aaa03a09 EU474
EU774668.1 gg_id:351100 Angola Colobus feces clone EAC_2_aaa03g09 EU774
EF603972.1 gg_id:232943 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6039
EU506398.1 gg_id:270870 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01b10 EU506
FJ879124.1 gg_id:378376 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EU465599.1 gg_id:295748 argali sheep feces clone AS1_aao39a12.Contig1 EU465
FJ681681.1 gg_id:531339 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU777625.1 gg_id:329861 Sumatran orangutan feces clone orang1_aai56c01 EU777
FJ677944.1 gg_id:520833 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6779
EU622764.1 gg_id:278667 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF404912.1 gg_id:208751 human fecal clone SJTU_G_08_79 EF4049
EU458619.1 gg_id:291348 European rabbit feces clone RA_g05_1 EU458
EU775085.1 gg_id:353620 Francois Langur feces clone FL_1aaa01f09 EU775
EU774718.1 gg_id:324219 Angola Colobus feces clone EAC_2_aaa04f11 EU774
EU777117.1 gg_id:338991 Okapi feces clone OK1_b05_2 EU777
DQ800867.1 gg_id:178242 human fecal clone RL183_aao04e06 DQ800
FJ366788.1 gg_id:362813 feces adult twins and mothers; TS27 clone TS27_a03h03 FJ3667
EU777072.1 gg_id:336005 Okapi feces clone OK3_g10_1 EU777
EU779162.1 gg_id:315683 Trancaspian Urial feces clone TU2_aaa01f06 EU779
FJ880155.1 gg_id:400545 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EF614841.1 gg_id:234630 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EU459641.1 gg_id:293767 ring-tailed lemur feces clone RT_aai09g11 EU459
FJ879015.1 gg_id:427159 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
EU463652.1 gg_id:296591 domesticated horse feces clone horsej_aai90d12 EU463
EU763460.1 gg_id:327692 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
DQ777916.1 gg_id:171499 rat feces clone R-1268 DQ777
FJ833370.1 gg_id:578399 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q301_90B12 FJ8333
EU458608.1 gg_id:295662 European rabbit feces clone RA_d09 EU458
EU344276.1 gg_id:277185 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU470451.1 gg_id:302165 Grevy's zebra feces clone GZ_aaa02d10 EU470
EU468576.1 gg_id:302061 okapi feces clone OK1_c08_3 EU468
EU509562.1 gg_id:275576 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap60h04 EU509
EU466209.1 gg_id:300969 bighorn sheep feces clone BH1_aao28a09 EU466
FJ880004.1 gg_id:412229 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
EU457289.1 gg_id:342402 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU457
GQ448399.1 gg_id:511180 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ448
EU622765.1 gg_id:278758 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU531935.1 gg_id:265234 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU465629.1 gg_id:288944 argali sheep feces clone AS1_aao40b11.Contig1 EU465

0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	0	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22482
s__unclassified	22484
s__unclassified	22485
s__unclassified	22486
s__unclassified	22487
s__unclassified	22488
s__unclassified	22489
s__unclassified	22491
s__unclassified	22492
s__unclassified	22494
s__unclassified	22495
s__unclassified	22496
s__unclassified	22498
s__unclassified	22499
s__unclassified	22500
s__unclassified	22501
s__unclassified	22502
s__unclassified	22503
s__unclassified	22504
s__unclassified	22505
s__unclassified	22506
s__unclassified	22507
s__unclassified	22508
s__unclassified	22509
s__unclassified	22510
s__unclassified	22511
s__unclassified	22512
s__unclassified	22513
s__unclassified	22514
s__unclassified	22515
s__unclassified	22518
s__unclassified	22519
s__unclassified	22520
s__unclassified	22521
s__unclassified	22522
s__unclassified	22523
s__unclassified	22524
s__unclassified	22525
s__unclassified	22526
s__unclassified	22527
s__unclassified	22529

FJ879588.1 gg_id:414089 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU843150.1 gg_id:310031 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
DQ815858.1 gg_id:166226 mouse cecum clone aab23c10 DQ815
EU844883.1 gg_id:317405 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU772004.1 gg_id:323702 Argali sheep feces clone AS2_aao36g03 EU7720
DQ243771.1 gg_id:143396 Archaeal and Geochemically Hot Springs Yellowstone National Park USA Obsidian Pc DQ243
EU469210.1 gg_id:292548 Speke's gazelle feces clone SP3_b05_2 EU4692
EU458577.1 gg_id:297073 European rabbit feces clone RA_b02 EU4585
AB299543.1 gg_id:255350 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
FJ880460.1 gg_id:466851 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
EU777400.1 gg_id:332376 Sumatran orangutan feces clone orang1_aai53d06 EU7774
EU470077.1 gg_id:294748 trancaspain urial feces clone TU1_aaa02a09 EU4700
EU779460.1 gg_id:322194 Grevy's Zebra feces clone GZ_aaa04c04 EU7794
DQ795724.1 gg_id:183479 human fecal clone RL245_aai81c09 DQ795
EU511442.1 gg_id:269418 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20d04 EU5114
EF096031.1 gg_id:183985 mouse cecum clone lean2_aaa02d05 EF0960
EU771896.1 gg_id:317870 Southern three-banded armadillo feces clone arma_a03 EU7718
GQ867355.1 gg_id:591284 and prevalence blaTEM genes Arctic seals colon content clone WSp112 GQ867
EF096279.1 gg_id:185967 mouse cecum clone obob1_aaa04a07 EF0962
EU471906.1 gg_id:300186 Asiatic elephant feces clone AE3_aaa02c07 EU4719
EU471573.1 gg_id:298751 Asiatic elephant feces clone AE1_aaa03b09 EU4715
EU747962.1 gg_id:303763 neotropical folivorous flying bird adult hoatzin crop clone hoa11_26B04 EU7479
EU504516.1 gg_id:260720 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01f12 EU5045
EU511746.1 gg_id:265963 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf08d08 EU5117
FJ833392.1 gg_id:580128 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_40H05 FJ8333
FJ679065.1 gg_id:520809 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
AF371805.1 gg_id:51722 swine intestine clone p-1877-s962-3 AF3718
EU774701.1 gg_id:347085 Angola Colobus feces clone EAC_2_aaa02e10 EU7747
DQ394593.1 gg_id:155059 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EF400162.1 gg_id:216310 human fecal clone SJTU_E_09_66 EF4001
DQ015070.1 gg_id:132441 mouse cecum clone M2_f11 DQ015
AY991978.1 gg_id:132424 mouse cecum clone C20_n22 AY9919
EU776363.1 gg_id:335362 Red Kangaroo feces clone KO1_aai43b06 EU7763
EF605058.1 gg_id:231459 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6050
EU505144.1 gg_id:273462 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03e05 EU5051
FJ881001.1 gg_id:468255 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
FJ680493.1 gg_id:531808 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
EU473598.1 gg_id:290698 Somali wild ass feces clone WA_aaa02h04 EU4735
EF454508.2 gg_id:224436 termite hindgut clone 290cost002-P3L-2244 EF4545
GU174135.1 gg_id:539506 Microbial Bactrian camel estimated rumen clone XJC128 GU174
EU747942.1 gg_id:328823 neotropical folivorous flying bird adult hoatzin crop clone hoa13_91C12 EU7479

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22530
s__unclassified	22531
s__unclassified	22532
s__unclassified	22533
s__unclassified	22535
s__unclassified	22536
s__unclassified	22539
s__unclassified	22541
s__unclassified	22543
s__unclassified	22544
s__unclassified	22545
s__unclassified	22546
s__unclassified	22547
s__unclassified	22548
s__unclassified	22549
s__unclassified	22550
s__unclassified	22552
s__unclassified	22554
s__unclassified	22555
s__unclassified	22556
s__unclassified	22557
s__unclassified	22558
s__unclassified	22559
s__unclassified	22562
s__unclassified	22563
s__unclassified	22564
s__unclassified	22565
s__unclassified	22566
s__unclassified	22568
s__unclassified	22570
s__unclassified	22571
s__unclassified	22572
s__unclassified	22573
s__unclassified	22574
s__unclassified	22575
s__unclassified	22576
s__unclassified	22577
s__unclassified	22578
s__unclassified	22581
s__unclassified	22582
s__unclassified	22583

EU465621.1 gg_id:301410 argali sheep feces clone AS1_aao40a08.Contig1 EU465
EU622694.1 gg_id:278901 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU506877.1 gg_id:276273 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07f08 EU506
AB270051.1 gg_id:166168 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ879323.1 gg_id:408513 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EF096450.1 gg_id:189527 mouse cecum clone obob2_aaa03a07 EF0964
EU779309.1 gg_id:309070 Visayam Warty Pig feces clone VWP_aaa02g07 EU779
EU775150.1 gg_id:314421 Francois Langur feces clone FL_1aaa02a01 EU775
EF603178.1 gg_id:228975 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
EU772202.1 gg_id:329529 Argali sheep feces clone AS1_aao39g01.Contig1 EU772
EF644508.1 gg_id:253716 Structure and performance microbial involved reductive dechlorination 1122-tetrach EF6445
DQ805484.1 gg_id:181448 human fecal clone RL203_aai63c05 DQ805
GU120121.1 gg_id:538805 Real time ruminal microbial sheep fed hay or corn:hay mix adherent fraction rumen GU120
EU460085.1 gg_id:296424 mammals their gut microbes eastern black and white colobus feces clone COL_aai14 EU460
EU454100.1 gg_id:309302 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU454
FJ881171.1 gg_id:413391 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
EU453959.1 gg_id:341713 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU453
EU843243.1 gg_id:336486 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ369537.1 gg_id:358078 feces adult twins and mothers; TS51 clone TS51_a01g04 FJ3695
DQ815409.1 gg_id:170399 mouse cecum clone aab47f08 DQ815
EU507544.1 gg_id:270027 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04g11 EU507
EU451074.1 gg_id:355178 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU451
EU470093.1 gg_id:292704 trancaspain urial feces clone TU1_aaa03h12 EU470
DQ014710.1 gg_id:135420 mouse cecum clone M1_g07_1 DQ014
EU777884.1 gg_id:341092 European rabbit feces clone RA_g01 EU777
FJ368283.1 gg_id:366143 feces adult twins and mothers; TS3 clone TS3_a02d09 FJ3682
GQ011731.1 gg_id:497935 Topographical and Temporal Human Skin Microbiome skin nare clone nbw744d05c1 GQ011
EU358724.1 gg_id:334839 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
EU773998.1 gg_id:331659 Cheetah feces clone CE3_aai07f02 EU773
DQ801008.1 gg_id:194735 human fecal clone RL387_aao90g09 DQ801
EU842331.1 gg_id:332860 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF098919.1 gg_id:177578 mouse cecum clone SWPT1_aaa03c05 EF0989
EU775419.1 gg_id:351927 Western lowland gorilla feces clone GOR_aag73e08 EU775
FJ880305.1 gg_id:398138 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
FJ680934.1 gg_id:508925 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
EU506923.1 gg_id:273345 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08d09 EU506
AB192011.1 gg_id:144692 termite gut homogenate clone M1NP1-81 AB192
EU503919.1 gg_id:273549 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa02f03 EU503
FJ881052.1 gg_id:397444 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
EU771330.1 gg_id:336513 Asiatic elephant feces clone AE2_aaa02f07 EU771
EU468977.1 gg_id:292793 Speke's gazelle feces clone SP2_c06 EU468

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	1	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	22584
s__unclassified	22585
s__unclassified	22586
s__unclassified	22587
s__unclassified	22588
s__unclassified	22589
s__unclassified	22590
s__unclassified	22591
s__unclassified	22592
s__unclassified	22593
s__unclassified	22595
s__unclassified	22596
s__unclassified	22597
s__unclassified	22598
s__unclassified	22599
s__unclassified	22600
s__unclassified	22601
s__unclassified	22604
s__unclassified	22605
s__unclassified	22606
s__unclassified	22607
s__unclassified	22608
s__unclassified	22609
s__unclassified	22610
s__unclassified	22611
s__unclassified	22612
s__unclassified	22613
s__unclassified	22614
s__unclassified	24397
s__unclassified	24418
s__unclassified	24424
s__unclassified	24426
s__unclassified	24459
s__unclassified	24473
s__unclassified	24494
s__unclassified	24500
s__unclassified	24504
s__unclassified	24507
s__unclassified	24511
s__unclassified	24518
s__unclassified	24522

EF608542.1 gg_id:230370 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
EF097622.1 gg_id:180235 mouse cecum clone SWPT20_aaa01d09 EF0976
DQ806289.1 gg_id:180565 human fecal clone RL186_aan89h10 DQ806
GQ491367.1 gg_id:549281 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU458674.1 gg_id:288936 European rabbit feces clone RA_f11_2 EU458
DQ455867.1 gg_id:158230 pre-adolescent turkey cecum clone CFT19E6 DQ455
EU850450.1 gg_id:333245 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF12 EU850
AF001758.1 gg_id:16019 rumen clone RF26 AF001
FJ683056.1 gg_id:523244 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ681401.1 gg_id:531867 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
EF406825.1 gg_id:205987 mouse colon clone infected_28days-D10 EF4068
EU511801.1 gg_id:260417 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_09d04.Contig2 EU5118
DQ799972.1 gg_id:190124 human fecal clone RL247_aaj22e08 DQ799
EU776838.1 gg_id:310416 Mongoose lemur feces clone ML_aae89e01 EU7768
DQ795909.1 gg_id:183187 human fecal clone RL245_aai84f06 DQ795
DQ327133.1 gg_id:145883 Metagenomic gut microbiome healthy human stool clone E652 DQ327
EU773365.1 gg_id:332481 BigHorn sheep feces clone BH1_aao26a07 EU7733
EU774411.1 gg_id:326991 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU7744
EU888005.1 gg_id:315439 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8880
EU465646.1 gg_id:293696 argali sheep feces clone AS1_aao40f11.Contig1 EU4656
EF406869.1 gg_id:206744 mouse colon clone infected_28days-G8 EF4068
FJ172851.1 gg_id:336231 Qinghai Yak Ruminal and Fungi China rumen clone RB-3E10 FJ1728
EU459663.1 gg_id:297045 ring-tailed lemur feces clone RT_aai10d08 EU4596
FJ880548.1 gg_id:439880 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
EU344680.1 gg_id:264114 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
AB234482.1 gg_id:146578 termite gut homogenate clone MgMjR-021 AB2344
DQ796871.1 gg_id:197125 human fecal clone RL179_aao55g01 DQ796
EU468696.1 gg_id:290392 okapi feces clone OK2_g05_1 EU4686
EU467108.1 gg_id:288100 mongoose lemur feces clone ML_aae88d09 EU4671
FJ367531.1 gg_id:365767 feces adult twins and mothers; TS29 clone TS29_a04f07 FJ3675
DQ326345.1 gg_id:145888 Metagenomic gut microbiome healthy human stool clone C336 DQ326
FJ367522.1 gg_id:357913 feces adult twins and mothers; TS29 clone TS29_a04e09 FJ3675
EF402491.1 gg_id:212641 human fecal clone SJTU_B_08_60 EF4024
EU462180.1 gg_id:291266 black-handed spider monkey feces clone SPIM_aaj36f07 EU4621
DQ904856.1 gg_id:173724 human fecal clone 001C-c7 DQ904
FJ365644.1 gg_id:365410 feces adult twins and mothers; TS21 clone TS21_a01c11 FJ3656
FJ367519.1 gg_id:364229 feces adult twins and mothers; TS29 clone TS29_a04e06 FJ3675
DQ825169.1 gg_id:178670 human fecal clone RL185_aan86c02 DQ825
DQ794729.1 gg_id:186912 human fecal clone RL240_aaj31f06 DQ794
FJ362635.1 gg_id:361266 feces adult twins and mothers; TS13 clone TS13_a01c12 FJ3626
FJ367119.1 gg_id:368394 feces adult twins and mothers; TS28 clone TS28_a03g02 FJ3671

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	24560
s__unclassified	24562
s__unclassified	24564
s__unclassified	24575
s__unclassified	24610
s__unclassified	24612
s__unclassified	24615
s__unclassified	24626
s__unclassified	24627
s__unclassified	24635
s__unclassified	24637
s__unclassified	24647
s__unclassified	24660
s__unclassified	24661
s__unclassified	24677
s__unclassified	24707
s__unclassified	24713
s__unclassified	24718
s__unclassified	24719
s__unclassified	24723
s__unclassified	24724
s__unclassified	24744
s__unclassified	24760
s__unclassified	24770
s__unclassified	24791
s__unclassified	24800
s__unclassified	24821
s__unclassified	24822
s__unclassified	24824
s__unclassified	24826
s__unclassified	24831
s__unclassified	24903
s__unclassified	24904
s__unclassified	24909
s__unclassified	24911
s__unclassified	24914
s__unclassified	24916
s__unclassified	24948
s__unclassified	24952
s__unclassified	24975
s__unclassified	24983

EF403080.1 gg_id:211100 human fecal clone SJTU_B_03_40 EF403
FJ372373.1 gg_id:357365 feces adult twins and mothers; TS9 clone TS9_a04h03 FJ3723
DQ793621.1 gg_id:198214 human fecal clone RL246_aai74e10 DQ793
DQ800988.1 gg_id:199182 human fecal clone RL387_aao90d10 DQ800
FJ367903.1 gg_id:358152 feces adult twins and mothers; TS2 clone TS2_a04h08 FJ3679
DQ805771.1 gg_id:182051 human fecal clone RL306aal90g11 DQ805
DQ801641.1 gg_id:186456 human fecal clone RL117_aae93c11 DQ801
FJ365197.1 gg_id:361811 feces adult twins and mothers; TS1 clone TS1_a04a07 FJ3651
EU771688.1 gg_id:349437 African elephant feces clone AFYEL_aaj67g07 EU771
AF376218.1 gg_id:73575 ckncm314-B7-17 clone AF3762
FJ683715.1 gg_id:524587 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
FJ366945.1 gg_id:359422 feces adult twins and mothers; TS28 clone TS28_a01f06 FJ3669
DQ797744.1 gg_id:174636 human fecal clone RL206_aaj15d05 DQ797
EU767217.1 gg_id:325765 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ801018.1 gg_id:187632 human fecal clone RL387_aao91a03 DQ801
EU765302.1 gg_id:319980 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU778932.1 gg_id:336217 Black-handed Spider Monkey feces clone SPIM_g09 EU778
EU773495.1 gg_id:311824 Bonobo feces clone BNO_aaa01e06 EU773
EF434341.1 gg_id:214444 human infant gastrointestinal tract microbiota stool mother baby 3 day delivery clon EF4343
DQ794628.1 gg_id:196233 human fecal clone RL240_aaj30d10 DQ794
EU766126.1 gg_id:344856 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ802754.1 gg_id:177495 human fecal clone RL188_aan96b07 DQ802
DQ793301.1 gg_id:181290 human fecal clone RL199_aaj41h12 DQ793
DQ798600.1 gg_id:199246 human fecal clone RL181_aan98g09 DQ798
DQ797494.1 gg_id:182059 human fecal clone RL248_aaj00a11 DQ797
EU768767.1 gg_id:330678 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ905339.1 gg_id:170592 human fecal clone 013B-F1 DQ905
DQ456222.1 gg_id:157966 pre-adolescent turkey cecum clone CFT29G11 DQ456
DQ793929.1 gg_id:198885 human fecal clone RL176_aah45d07 DQ793
FJ363399.1 gg_id:368137 feces adult twins and mothers; TS149 clone TS149_a02g05 FJ3633
DQ810085.1 gg_id:194784 human fecal clone RL184_aao67h08 DQ810
DQ905150.1 gg_id:170385 human fecal clone 002C-e3 DQ905
DQ808308.1 gg_id:199463 human fecal clone RL180_aao75b02 DQ808
FJ367475.1 gg_id:364674 feces adult twins and mothers; TS29 clone TS29_a04a04 FJ3674
DQ794501.1 gg_id:198907 human fecal clone RL197_aah88g05 DQ794
DQ798340.1 gg_id:194552 human fecal clone RL181_aah41b08 DQ798
AF376220.1 gg_id:72147 ckncm316-B4-5 clone AF3762
DQ325549.1 gg_id:150385 Metagenomic gut microbiome healthy human stool clone B006 DQ325
DQ905891.1 gg_id:162492 human fecal clone 29c-c1 DQ905
GQ043004.1 gg_id:371426 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012a GQ043
EF403280.1 gg_id:212619 human fecal clone SJTU_A1_3_61 EF4032

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	24991
s__unclassified	25021
s__unclassified	25029
s__unclassified	25040
s__unclassified	25042
s__unclassified	25048
s__unclassified	25053
s__unclassified	25058
s__unclassified	25068
s__unclassified	25084
s__unclassified	25087
s__unclassified	25108
s__unclassified	25111
s__unclassified	25117
s__unclassified	25194
s__unclassified	25214
s__unclassified	25223
s__unclassified	25233
s__unclassified	25238
s__unclassified	25246
s__unclassified	25274
s__unclassified	25296
s__unclassified	25301
s__unclassified	25323
s__unclassified	25364
s__unclassified	25372
s__unclassified	25387
s__unclassified	25393
s__unclassified	25403
s__unclassified	25416
s__unclassified	25426
s__unclassified	25437
s__unclassified	25463
s__unclassified	25474
s__unclassified	25513
s__unclassified	25528
s__unclassified	25548
s__unclassified	25554
s__unclassified	25570
s__unclassified	25572
s__unclassified	25586

DQ057466.1 gg_id:129761 str. ic1337 DQ057
GQ175477.1 gg_id:579000 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ798321.1 gg_id:184093 human fecal clone RL181_aah40f11 DQ798
DQ794285.1 gg_id:196796 human fecal clone RL176_aan60f03 DQ794
DQ797648.1 gg_id:175443 human fecal clone RL206_aaj14b12 DQ797
FJ366956.1 gg_id:357225 feces adult twins and mothers; TS28 clone TS28_a01g05 FJ3669
DQ798361.1 gg_id:189047 human fecal clone RL181_aah41e05 DQ798
FJ367394.1 gg_id:357231 feces adult twins and mothers; TS29 clone TS29_a03a04 FJ3673
EU461656.1 gg_id:300092 mongoose lemur feces clone ML_aaj26d06 EU461
DQ057414.1 gg_id:136271 chicken ileum/cecum clone oc23 DQ057
AF371716.1 gg_id:46691 swine intestine clone p-2814-24E5 AF3717
DQ794019.1 gg_id:189800 human fecal clone RL176_aah46f11 DQ794
FJ368985.1 gg_id:357740 feces adult twins and mothers; TS4 clone TS4_a02h07 FJ3689
FJ679137.1 gg_id:518735 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
DQ801472.1 gg_id:190467 human fecal clone RL388_aao96a02 DQ801
EU767122.1 gg_id:342124 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
FJ363687.1 gg_id:359284 feces adult twins and mothers; TS14 clone TS14_a02b04 FJ3636
FJ363795.1 gg_id:367084 feces adult twins and mothers; TS14 clone TS14_a03d09 FJ3637
DQ455909.1 gg_id:158360 pre-adolescent turkey cecum clone CFT111A10 DQ455
EU728786.1 gg_id:334557 Subdoligranulum sp. str. DJF_VR33k2 EU728
GQ175440.1 gg_id:594206 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AB264065.1 gg_id:187741 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-25 AB264
DQ793941.1 gg_id:193786 human fecal clone RL176_aah45e09 DQ793
DQ798183.1 gg_id:186702 human fecal clone RL302_aal96e09 DQ798
EU461689.1 gg_id:301750 mongoose lemur feces clone ML_aaj27b12 EU461
EU768362.1 gg_id:335270 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU766446.1 gg_id:339125 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU768798.1 gg_id:319831 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
DQ794902.1 gg_id:181213 human fecal clone RL310_aam37g03 DQ794
DQ797996.1 gg_id:178744 human fecal clone RL302_aal94c11 DQ797
FJ682973.1 gg_id:514399 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
DQ810168.1 gg_id:184292 human fecal clone RL184_aao68g11 DQ810
DQ905437.1 gg_id:168776 human fecal clone 013C-F11 DQ905
FJ372141.1 gg_id:367989 feces adult twins and mothers; TS9 clone TS9_a02b11 FJ3721
FJ365745.1 gg_id:367703 feces adult twins and mothers; TS21 clone TS21_a02e04 FJ3657
DQ807932.1 gg_id:176619 human fecal clone RL180_aan69d03 DQ807
DQ809649.1 gg_id:178390 human fecal clone RL184_aan82b04 DQ809
DQ795975.1 gg_id:188631 human fecal clone RL202_aai49f12 DQ795
FJ363732.1 gg_id:361579 feces adult twins and mothers; TS14 clone TS14_a02f05 FJ3637
FJ368274.1 gg_id:360904 feces adult twins and mothers; TS3 clone TS3_a02c10 FJ3682
DQ799468.1 gg_id:193053 human fecal clone RL305aal86f07 DQ799

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	25587
s__unclassified	25601
s__unclassified	25607
s__unclassified	25615
s__unclassified	25646
s__unclassified	25656
s__unclassified	25666
s__unclassified	25677
s__unclassified	25693
s__unclassified	25696
s__unclassified	25711
s__unclassified	25734
s__unclassified	25743
s__unclassified	25751
s__unclassified	25767
s__unclassified	25771
s__unclassified	25780
s__unclassified	25781
s__unclassified	25782
s__unclassified	25785
s__unclassified	25799
s__unclassified	25812
s__unclassified	25814
s__unclassified	25824
s__unclassified	25825
s__unclassified	25837
s__unclassified	25856
s__unclassified	25862
s__unclassified	25863
s__unclassified	25871
s__unclassified	25887
s__unclassified	25899
s__unclassified	25906
s__unclassified	25913
s__unclassified	25918
s__unclassified	25925
s__unclassified	25933
s__unclassified	25968
s__unclassified	25984
s__unclassified	26026
s__unclassified	26060

DQ809892.1 gg_id:187969 human fecal clone RL184_aao65f02 DQ809
DQ810127.1 gg_id:193572 human fecal clone RL184_aao68d03 DQ810
DQ797593.1 gg_id:190126 human fecal clone RL206_aaj13d10 DQ797
EF445171.1 gg_id:205155 rabbit cecum clone NED1B8 EF4451
DQ801703.1 gg_id:185329 human fecal clone RL201_aai45g05 DQ801
DQ823743.1 gg_id:188160 human fecal clone RL250_aaj78d11 DQ823
FJ367539.1 gg_id:368178 feces adult twins and mothers; TS29 clone TS29_a04g04 FJ3675
DQ793937.1 gg_id:197542 human fecal clone RL176_aah45e04 DQ793
DQ905796.2 gg_id:163561 human fecal clone 29E-a8 DQ905
FJ367386.1 gg_id:357496 feces adult twins and mothers; TS29 clone TS29_a02h03 FJ3673
DQ809792.1 gg_id:178470 human fecal clone RL184_aan84c07 DQ809
DQ801603.1 gg_id:195608 human fecal clone RL117_aae92d11 DQ801
EU764665.1 gg_id:322947 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ369707.1 gg_id:369903 feces adult twins and mothers; TS51 clone TS51_a03h01 FJ3697
DQ808067.1 gg_id:174837 human fecal clone RL180_aan71g05 DQ808
DQ456024.1 gg_id:157417 pre-adolescent turkey cecum clone CFT112D5 DQ456
DQ794206.1 gg_id:194933 human fecal clone RL176_aan59d12 DQ794
FJ371854.1 gg_id:368906 feces adult twins and mothers; TS8 clone TS8_a03a03 FJ3718
DQ801585.1 gg_id:190660 human fecal clone RL117_aae92a08 DQ801
FJ367477.1 gg_id:366886 feces adult twins and mothers; TS29 clone TS29_a04a06 FJ3674
GQ491881.1 gg_id:586525 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU765568.1 gg_id:306962 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
FJ366821.1 gg_id:362432 feces adult twins and mothers; TS27 clone TS27_a04c06 FJ3668
FJ683678.1 gg_id:509821 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
DQ797710.1 gg_id:176442 human fecal clone RL206_aaj14h09 DQ797
FJ365885.1 gg_id:369922 feces adult twins and mothers; TS21 clone TS21_a04b11 FJ3658
DQ825076.1 gg_id:196616 human fecal clone RL185_aan85a12 DQ825
GQ898028.1 gg_id:572956 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
FJ365932.1 gg_id:364083 feces adult twins and mothers; TS21 clone TS21_a04g10 FJ3659
FJ677101.1 gg_id:529556 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
DQ456177.1 gg_id:158252 pre-adolescent turkey cecum clone CFT29C8 DQ456
FJ366691.1 gg_id:361827 feces adult twins and mothers; TS27 clone TS27_a02f11 FJ3666
FJ372109.1 gg_id:358744 feces adult twins and mothers; TS9 clone TS9_a01h02 FJ3721
EU766189.1 gg_id:354737 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ904685.1 gg_id:167251 human fecal clone 001-e11 DQ904
EU764575.1 gg_id:348449 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
FJ366231.1 gg_id:367348 feces adult twins and mothers; TS25 clone TS25_a04c05 FJ3662
DQ905880.2 gg_id:164867 human fecal clone 29c-a4 DQ905
DQ905769.2 gg_id:167863 human fecal clone 29A-f12 DQ905
FJ365793.1 gg_id:361283 feces adult twins and mothers; TS21 clone TS21_a03b03 FJ3657
DQ905791.2 gg_id:165346 human fecal clone 29E-a3 DQ905

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26068
s__unclassified	26074
s__unclassified	26079
s__unclassified	26087
s__unclassified	26088
s__unclassified	26093
s__unclassified	26098
s__unclassified	26104
s__unclassified	26122
s__unclassified	26133
s__unclassified	26143
s__unclassified	26152
s__unclassified	26157
s__unclassified	26168
s__unclassified	26176
s__unclassified	26187
s__unclassified	26193
s__unclassified	26197
s__unclassified	26251
s__unclassified	26259
s__unclassified	26269
s__unclassified	26274
s__unclassified	26282
s__unclassified	26291
s__unclassified	26293
s__unclassified	26294
s__unclassified	26301
s__unclassified	26306
s__unclassified	26326
s__unclassified	26336
s__unclassified	26345
s__unclassified	26349
s__unclassified	26365
s__unclassified	26375
s__unclassified	26380
s__unclassified	26381
s__unclassified	26387
s__unclassified	26389
s__unclassified	26407
s__unclassified	26419
s__unclassified	26431

EF401318.1 gg_id:206073 human fecal clone SJTU_D_08_72 EF4013
EU768535.1 gg_id:342263 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7685
DQ794362.1 gg_id:193007 human fecal clone RL197_aah86d10 DQ794
FJ366400.1 gg_id:363257 feces adult twins and mothers; TS26 clone TS26_a02f05 FJ3664
DQ794224.1 gg_id:197701 human fecal clone RL176_aan59g02 DQ794
FJ372259.1 gg_id:361667 feces adult twins and mothers; TS9 clone TS9_a03e08 FJ3722
FJ368378.1 gg_id:366286 feces adult twins and mothers; TS3 clone TS3_a03f07 FJ3683
FJ372007.1 gg_id:367712 feces adult twins and mothers; TS8 clone TS8_a04f10 FJ3720
FJ367415.1 gg_id:360771 feces adult twins and mothers; TS29 clone TS29_a03c05 FJ3674
EU459904.1 gg_id:293874 Prevost's squirrel feces clone SQ_aah81a02 EU4599
FJ375910.1 gg_id:323534 and prevalence blaTEM genes polar bear feces clone PBM_a2 FJ3759
DQ801353.1 gg_id:181976 human fecal clone RL388_aao94d07 DQ801
DQ798168.1 gg_id:198554 human fecal clone RL302_aal96d01 DQ798
DQ794297.1 gg_id:185762 human fecal clone RL176_aan60g10 DQ794
GQ175410.1 gg_id:565952 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EF400910.1 gg_id:212549 human fecal clone SJTU_D_03_29 EF4009
FJ363972.1 gg_id:361798 feces adult twins and mothers; TS150 clone TS150_a01e06 FJ3639
EU767998.1 gg_id:347967 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7679
DQ796772.1 gg_id:199502 human fecal clone RL179_aao54c08 DQ796
DQ808683.1 gg_id:199269 human fecal clone RL239_aaj11g11 DQ808
FJ363956.1 gg_id:361122 feces adult twins and mothers; TS150 clone TS150_a01c12 FJ3639
EU509787.1 gg_id:271488 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21a08 EU5097
FJ683794.1 gg_id:531444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
DQ795560.1 gg_id:195561 human fecal clone RL178_aan66c03 DQ795
EU766373.1 gg_id:332702 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7663
EF404114.1 gg_id:211295 human fecal clone SJTU_C_04_87 EF4041
AY169430.1 gg_id:81198 Faecalibacterium prausnitzii AY1694
DQ057482.2 gg_id:134174 str. ic1395 DQ057
DQ905832.2 gg_id:170094 human fecal clone 29E-d11 DQ905
FJ676304.1 gg_id:523814 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6763
EU009761.1 gg_id:237211 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AB8 EU0097
FJ362743.1 gg_id:366267 feces adult twins and mothers; TS13 clone TS13_a02f03 FJ3627
DQ810028.1 gg_id:193622 human fecal clone RL184_aao67c03 DQ810
DQ798283.1 gg_id:183674 human fecal clone RL181_aah40b05 DQ798
FJ367251.1 gg_id:362328 feces adult twins and mothers; TS29 clone TS29_a01c11 FJ3672
DQ808060.1 gg_id:191541 human fecal clone RL180_aan71f03 DQ808
GQ896642.1 gg_id:568845 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
DQ806793.1 gg_id:178419 human fecal clone RL186_aao48g07 DQ806
GQ897259.1 gg_id:584951 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
AY916158.1 gg_id:113956 human transverse colon biopsy clone M479 AY9161
EU778922.1 gg_id:306633 Black-handed Spider Monkey feces clone SPIM_aaj36g11 EU7789

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26445
s__unclassified	26465
s__unclassified	26468
s__unclassified	26473
s__unclassified	26480
s__unclassified	26488
s__unclassified	26494
s__unclassified	26500
s__unclassified	26504
s__unclassified	26511
s__unclassified	26512
s__unclassified	26515
s__unclassified	26521
s__unclassified	26526
s__unclassified	26528
s__unclassified	26568
s__unclassified	26583
s__unclassified	26584
s__unclassified	26607
s__unclassified	26616
s__unclassified	26618
s__unclassified	26620
s__unclassified	26622
s__unclassified	26623
s__unclassified	26625
s__unclassified	26626
s__unclassified	26629
s__unclassified	26630
s__unclassified	26631
s__unclassified	26635
s__unclassified	26636
s__unclassified	26637
s__unclassified	26639
s__unclassified	26642
s__unclassified	26644
s__unclassified	26645
s__unclassified	26646
s__unclassified	26647
s__unclassified	26648
s__unclassified	26649
s__unclassified	26651

FJ367523.1 gg_id:360297 feces adult twins and mothers; TS29 clone TS29_a04e10 FJ3675
FJ367399.1 gg_id:357525 feces adult twins and mothers; TS29 clone TS29_a03a09 FJ3673
DQ905064.1 gg_id:170262 human fecal clone 2-002-f10 DQ905
EU461598.1 gg_id:295083 mongoose lemur feces clone ML_aaj25c08 EU461
EF071254.1 gg_id:178512 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0712
GQ897730.1 gg_id:593300 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ825124.1 gg_id:196499 human fecal clone RL185_aan85f07 DQ825
GQ175380.1 gg_id:511009 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
DQ455878.1 gg_id:157455 pre-adolescent turkey cecum clone CFT19F7 DQ455
EU763901.1 gg_id:345683 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
EU462171.1 gg_id:297013 black-handed spider monkey feces clone SPIM_aaj36d03 EU462
DQ801092.1 gg_id:176861 human fecal clone RL387_aao92a10 DQ801
EU778057.1 gg_id:307224 Rock hyrax feces clone RHSD_aaa03e07_1 EU778
DQ809793.1 gg_id:190067 human fecal clone RL184_aan84c10 DQ809
DQ793432.1 gg_id:174458 human fecal clone RL199_aaj43f06 DQ793
EU766782.1 gg_id:336071 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ833044.1 gg_id:546069 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q201_14F02 FJ8330
DQ794181.1 gg_id:194219 human fecal clone RL176_aan59b08 DQ794
DQ797283.1 gg_id:178578 human fecal clone RL248_aai97c11 DQ797
DQ806652.1 gg_id:195391 human fecal clone RL186_aao47b11 DQ806
FJ904264.1 gg_id:552251 Further evidence absence horsehair worms (Nematomorpha: Gordiidae) Gordius robı FJ9042
DQ327429.1 gg_id:145346 Metagenomic gut microbiome healthy human stool clone E988 DQ327
EF603324.1 gg_id:229642 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU506238.1 gg_id:276137 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap61c04 EU506
EU509367.1 gg_id:259581 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap48f12 EU509
EF603651.1 gg_id:230125 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
DQ805523.1 gg_id:177311 human fecal clone RL203_aai63g02 DQ805
EU778221.1 gg_id:306021 feces clone RL387_aao90e02 EU778
EU462031.1 gg_id:290645 black-handed spider monkey feces clone SPIM_aaj33f07 EU462
AM278254.2 gg_id:234724 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
EF604546.1 gg_id:228893 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EF445283.1 gg_id:216004 dairy cow rumen clone NED4G8 EF4452
AY858434.2 gg_id:111671 gastrointestinal tract Grant's gazelle clone GRANT15 AY8584
EU469998.1 gg_id:296456 trancaspain urial feces clone TU1_aaa03e06 EU469
EU381467.1 gg_id:275170 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid ı EU381
EU468548.1 gg_id:291584 okapi feces clone OK1_e02_1 EU468
EU459548.1 gg_id:293827 capybara feces clone CAP_aah99f08 EU459
EU885025.1 gg_id:304728 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A3D10 EU885
AY985261.1 gg_id:119310 human stool clone C142 AY985
EU778974.1 gg_id:353817 Prevost's squirrel feces clone SQ_aah81b08 EU778
AB089046.1 gg_id:78294 termite gut homogenate clone Rs-C61 bacterium AB089

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
1	1	1	0	1	1	1	0	0	1	0	1	1
1	1	1	1	1	1	1	1	0	1	1	1	1
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26652
s__unclassified	26653
s__unclassified	26654
s__unclassified	26656
s__unclassified	26657
s__unclassified	26659
s__unclassified	26661
s__unclassified	26663
s__unclassified	26665
s__unclassified	26667
s__unclassified	26672
s__unclassified	26676
s__unclassified	26679
s__unclassified	26683
s__unclassified	26684
s__unclassified	26685
s__unclassified	26686
s__unclassified	26689
s__unclassified	26690
s__unclassified	26691
s__unclassified	26692
s__unclassified	26695
s__unclassified	26696
s__unclassified	26697
s__unclassified	26699
s__unclassified	26701
s__unclassified	26703
s__unclassified	26705
s__unclassified	26706
s__unclassified	26710
s__unclassified	26711
s__unclassified	26713
s__unclassified	26716
s__unclassified	26717
s__unclassified	26718
s__unclassified	26720
s__unclassified	26722
s__unclassified	26724
s__unclassified	26727
s__unclassified	26730
s__unclassified	26738

FJ374219.1 gg_id:363511 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
EU777853.1 gg_id:342571 European rabbit feces clone RA_g09 EU777
DQ808989.1 gg_id:189844 human fecal clone RL243_aai87h07 DQ808
EU466083.1 gg_id:303148 bighorn sheep feces clone BH1_aao25e08 EU466
DQ804796.1 gg_id:183299 human fecal clone RL187_aao72g10 DQ804
EU470212.1 gg_id:291405 trancaspain urial feces clone TU2_aaa01d03 EU470
AM697026.1 gg_id:223318 sequencing libraries indoor dust clone BF0001B052 AM697
AY916375.1 gg_id:113620 human stool clone D577 AY916
GQ079311.1 gg_id:435792 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1231c GQ079
EU844792.1 gg_id:355063 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU468771.1 gg_id:295107 okapi feces clone OK3_d08 EU468
EU507525.1 gg_id:265635 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04e09 EU507
DQ794266.1 gg_id:196637 human fecal clone RL176_aan60d03 DQ794
EU462535.1 gg_id:298204 Sumatran orangutan feces clone orang1_aai56e12 EU462
DQ798661.1 gg_id:192677 human fecal clone RL181_aan99f11 DQ798
AB288904.1 gg_id:201203 termite gut homogenate clone BOf5-23 AB288
EU774126.1 gg_id:352182 Chimpanzee feces clone CHIMP1_aaj39f05 EU774
DQ905206.1 gg_id:165257 human fecal clone 013-b3 DQ905
DQ799538.1 gg_id:194197 human fecal clone RL305aal87d11 DQ799
DQ793626.1 gg_id:180995 human fecal clone RL246_aai74f03 DQ793
GQ493785.1 gg_id:591839 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU622690.1 gg_id:279659 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
AB088959.1 gg_id:77706 termite gut homogenate clone Rs-B44 AB088
EU842424.1 gg_id:349962 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
DQ168656.1 gg_id:158569 sediment-free PCB-dechlorinating enrichment culture clone JN18_V41_S DQ168
AY991981.1 gg_id:135396 mouse cecum clone C20_o04 AY991
EU468795.1 gg_id:299019 okapi feces clone OK3_c07_1 EU468
FJ677881.1 gg_id:530146 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6778
EU451989.1 gg_id:320505 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
EU463774.1 gg_id:300041 domesticated horse feces clone horsej_aai92f03 EU463
EU842712.1 gg_id:346029 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU506915.1 gg_id:265625 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar08c05 EU506
DQ824345.1 gg_id:187264 human fecal clone RL304_aal74g08 DQ824
DQ015569.1 gg_id:130945 mouse cecum clone M3_f07_1 DQ015
FJ364993.1 gg_id:360916 feces adult twins and mothers; TS1 clone TS1_a01f01 FJ3649
AY980462.1 gg_id:123025 human rectum mucosal biopsy clone X044 AY980
EU504886.1 gg_id:275779 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03g09 EU504
EU468744.1 gg_id:292147 okapi feces clone OK3_e09 EU468
CU927061.1 gg_id:568110 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
AY916261.1 gg_id:114087 human rectum biopsy clone LL87 AY916
EF434358.1 gg_id:207991 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343

0	1	1	0	1	1	1	0	0	0	0	1	1
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26740
s__unclassified	26741
s__unclassified	26742
s__unclassified	26743
s__unclassified	26744
s__unclassified	26747
s__unclassified	26748
s__unclassified	26749
s__unclassified	26751
s__unclassified	26754
s__unclassified	26759
s__unclassified	26762
s__unclassified	26763
s__unclassified	26766
s__unclassified	26767
s__unclassified	26770
s__unclassified	26773
s__unclassified	26774
s__unclassified	26776
s__unclassified	26778
s__unclassified	26779
s__unclassified	26783
s__unclassified	26784
s__unclassified	26785
s__unclassified	26791
s__unclassified	26792
s__unclassified	26793
s__unclassified	26796
s__unclassified	26797
s__unclassified	26798
s__unclassified	26799
s__unclassified	26801
s__unclassified	26802
s__unclassified	26803
s__unclassified	26804
s__unclassified	26806
s__unclassified	26807
s__unclassified	26810
s__unclassified	26811
s__unclassified	26812
s__unclassified	26813

DQ071530.1 gg_id:233711 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw7 DQ071
EU470080.1 gg_id:289802 trancaspain urial feces clone TU1_aaa03f09 EU470
AM697405.1 gg_id:221429 sequencing libraries indoor dust clone BF0001D020 AM697
AY916159.1 gg_id:113797 human transverse colon biopsy clone M490 AY916
AB089039.1 gg_id:77833 termite gut homogenate clone Rs-K92 bacterium AB089
FJ371922.1 gg_id:366885 feces adult twins and mothers; TS8 clone TS8_a03g03 FJ3719
DQ797006.1 gg_id:187006 human fecal clone RL386_aao85f09 DQ797
EU622658.1 gg_id:278098 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU766883.1 gg_id:347024 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ803678.1 gg_id:198988 human fecal clone RL200_aai57a11 DQ803
EU887971.1 gg_id:323501 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
EU506802.1 gg_id:260776 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56f01 EU506
EF603362.1 gg_id:232918 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU452114.1 gg_id:332037 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU452
DQ815954.1 gg_id:167276 mouse cecum clone aab24g06 DQ815
EF603499.1 gg_id:232260 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6034
FJ679323.1 gg_id:517248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
EU471941.1 gg_id:296850 Asiatic elephant feces clone AE3_aaa04e06 EU471
DQ793811.1 gg_id:178684 human fecal clone RL176_aah43f06 DQ793
EU469735.1 gg_id:291917 flying fox feces clone FF_h04_1 EU469
DQ795793.1 gg_id:194778 human fecal clone RL245_aai82e04 DQ795
GQ897459.1 gg_id:540055 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
FJ368429.1 gg_id:366722 feces adult twins and mothers; TS3 clone TS3_a04c03 FJ3684
EU509946.1 gg_id:262944 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b08 EU509
DQ905341.1 gg_id:173282 human fecal clone 013B-F5 DQ905
FJ879345.1 gg_id:394512 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EU452674.1 gg_id:332282 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
AY916207.1 gg_id:112958 human cecum biopsy clone LF02 AY916
EU455446.1 gg_id:355041 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU455
AJ488078.1 gg_id:66186 chlorobenzene-degrading consortium clone IB-18 AJ488
FJ879403.1 gg_id:392407 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EU451140.1 gg_id:329458 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU451
AY570589.1 gg_id:108465 -temperature biodegraded Canadian oil reservoir clone PL-38B12 AY570
AY487928.1 gg_id:100412 Acetanaerobacterium elongatum str. Z7 AY487
EF402779.1 gg_id:207624 human fecal clone SJTU_B_12_36 EF4027
EU845152.1 gg_id:347819 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
EU775744.1 gg_id:339121 Horse feces clone horsem_aai94d08 EU775
FJ269107.1 gg_id:338187 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2691
FJ367099.1 gg_id:358674 feces adult twins and mothers; TS28 clone TS28_a03e06 FJ3670
EF604611.1 gg_id:231168 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
GQ502524.1 gg_id:590995 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	1	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	0	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26816
s__unclassified	26817
s__unclassified	26823
s__unclassified	26824
s__unclassified	26825
s__unclassified	26827
s__unclassified	26828
s__unclassified	26829
s__unclassified	26830
s__unclassified	26832
s__unclassified	26833
s__unclassified	26835
s__unclassified	26838
s__unclassified	26840
s__unclassified	26841
s__unclassified	26844
s__unclassified	26845
s__unclassified	26846
s__unclassified	26848
s__unclassified	26850
s__unclassified	26851
s__unclassified	26853
s__unclassified	26854
s__unclassified	26856
s__unclassified	26858
s__unclassified	26860
s__unclassified	26862
s__unclassified	26863
s__unclassified	26864
s__unclassified	26866
s__unclassified	26867
s__unclassified	26868
s__unclassified	26870
s__unclassified	26871
s__unclassified	26877
s__unclassified	26882
s__unclassified	26883
s__unclassified	26886
s__unclassified	26887
s__unclassified	26889
s__unclassified	26891

EU462611.1 gg_id:294242 Sumatran orangutan feces clone orang2_aai66a12 EU462
EU506329.1 gg_id:260859 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aap63d05 EU506
EU506188.1 gg_id:268806 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa02g02 EU506
DQ805002.1 gg_id:187524 human fecal clone RL385_aao83h09 DQ805
DQ796382.1 gg_id:189994 human fecal clone RL179_aah26e06 DQ796
EU463788.1 gg_id:291111 domesticated horse feces clone horsej_aai92h01 EU463
DQ904661.1 gg_id:168845 human fecal clone 001-c11 DQ904
AY622268.1 gg_id:100124 subsurface soil clone S-F26 AY622
EU452362.1 gg_id:312979 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75 EU452
DQ905623.1 gg_id:170271 human fecal clone 014B-H9 DQ905
DQ807121.1 gg_id:179301 human fecal clone RL244_aaj46e08 DQ807
EU469245.1 gg_id:289125 Speke's gazelle feces clone SP3_g02_1 EU469
FJ825458.1 gg_id:550485 Microbial during start-up mesophilic biogas plant clone 135_BE5_6 FJ8254
AB270141.1 gg_id:172165 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
AY984523.1 gg_id:123415 human stool clone B450 AY984
EU506576.1 gg_id:272283 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04f01 EU506
EU765144.1 gg_id:314884 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU765
GQ867487.1 gg_id:579293 and prevalence blaTEM genes Arctic seals colon content clone CSG58 GQ867
EU531982.1 gg_id:276231 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
DQ800460.1 gg_id:174827 human fecal clone RL183_aah24h03 DQ800
EU472119.1 gg_id:296626 francois langur feces clone FL_1aaa02g05 EU472
EU456056.1 gg_id:315580 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU456
EF071169.1 gg_id:195415 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU462752.1 gg_id:302382 Sumatran orangutan feces clone orang2_aai68e04 EU462
AB234479.1 gg_id:148075 termite gut homogenate clone MgMjR-012 AB234
GU303965.1 gg_id:538145 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
DQ015351.1 gg_id:131324 mouse cecum clone M3_a07 DQ015
EU461068.1 gg_id:289969 red kangaroo feces clone KO1_aai43e06 EU461
GQ448715.1 gg_id:532859 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ448
DQ817325.1 gg_id:173276 mouse cecum clone aaa73d09 DQ817
AJ576369.1 gg_id:103744 hindgut homogenate Pachnoda ephippiata larva clone PeH56 AJ5763
EU771106.1 gg_id:333205 Asiatic elephant feces clone AE3_aaa02b02 EU771
EU506196.1 gg_id:261365 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa03c05 EU506
GQ047291.1 gg_id:423254 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1011a GQ047
EF603339.1 gg_id:234992 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6033
DQ800226.1 gg_id:181527 human fecal clone RL303_aal69h06 DQ800
EU506587.1 gg_id:263968 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04g10 EU506
EU794136.1 gg_id:307564 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE37 EU794
FJ368767.1 gg_id:362041 feces adult twins and mothers; TS49 clone TS49_a04c07 FJ3687
EU455609.1 gg_id:345861 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H80 EU455
EU454483.1 gg_id:310557 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU454

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26892
s__unclassified	26893
s__unclassified	26895
s__unclassified	26896
s__unclassified	26897
s__unclassified	26898
s__unclassified	26900
s__unclassified	26901
s__unclassified	26908
s__unclassified	26909
s__unclassified	26913
s__unclassified	26914
s__unclassified	26918
s__unclassified	26919
s__unclassified	26921
s__unclassified	26922
s__unclassified	26923
s__unclassified	26924
s__unclassified	26925
s__unclassified	26927
s__unclassified	26930
s__unclassified	26932
s__unclassified	26934
s__unclassified	26939
s__unclassified	26940
s__unclassified	26941
s__unclassified	26943
s__unclassified	26944
s__unclassified	26945
s__unclassified	26947
s__unclassified	26948
s__unclassified	26949
s__unclassified	26950
s__unclassified	26951
s__unclassified	26952
s__unclassified	26955
s__unclassified	26956
s__unclassified	26957
s__unclassified	26958
s__unclassified	26959
s__unclassified	26960

FJ879335.1 gg_id:420816 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8793
EU467284.1 gg_id:291196 hamadryas baboon feces clone BAZ_a12 EU467
EU453205.1 gg_id:350575 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
FJ368179.1 gg_id:365529 feces adult twins and mothers; TS3 clone TS3_a01b08 FJ3681
EU767264.1 gg_id:335138 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ455846.1 gg_id:157888 pre-adolescent turkey cecum clone CFT19C4 DQ455
EF603241.1 gg_id:232048 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
AY854324.1 gg_id:109841 herbivore gastrointestinal tract clone Thompsons37 AY8543
EU472376.1 gg_id:297774 Angola colobus feces clone EAC_1aaa04b03 EU4723
EU766492.1 gg_id:328236 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7664
EU772256.1 gg_id:333948 Argali sheep feces clone AS2_aao34b08 EU772
FJ368800.1 gg_id:362922 feces adult twins and mothers; TS49 clone TS49_a04g02 FJ3688
EF604823.1 gg_id:228391 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
EF603352.1 gg_id:232042 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
DQ809978.1 gg_id:189758 human fecal clone RL184_aao66f03 DQ809
EU871402.1 gg_id:305146 Genetic Bovine (Bos taurus) Rumen Thailand clone CF342 EU8714
GQ175456.1 gg_id:535444 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EU510091.1 gg_id:261325 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01c01 EU5100
EU506686.1 gg_id:258926 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54e03 EU5066
EU505553.1 gg_id:272277 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02e12 EU5055
GQ451212.1 gg_id:575559 Fecal Yunnan snub-nosed monkey feces clone J66 GQ451
DQ015035.1 gg_id:131182 mouse cecum clone M2_c06 DQ015
GQ491889.1 gg_id:560663 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU451586.1 gg_id:349538 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU4515
EU507209.1 gg_id:271754 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03e10 EU5072
DQ815929.1 gg_id:167166 mouse cecum clone aab24d05 DQ815
EU509948.1 gg_id:264695 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24b10 EU5099
AF371759.1 gg_id:30067 swine intestine clone p-2506-18B5 AF3717
EU509855.1 gg_id:258260 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22e08 EU5098
EU773500.1 gg_id:325524 Bonobo feces clone BNO_aaa04e04 EU7735
EU778735.1 gg_id:322931 Springbok feces clone SBSD_aaa04b06_1 EU7787
EU767072.1 gg_id:307566 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU7670
EU259422.1 gg_id:253559 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC46 EU2594
FJ672969.1 gg_id:530829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
EU358715.1 gg_id:351451 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EU468521.1 gg_id:287988 okapi feces clone OK1_h03_1 EU4685
DQ796435.1 gg_id:198029 human fecal clone RL179_aah28d02 DQ796
EU764739.1 gg_id:347893 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU7647
EU474451.1 gg_id:291314 bighorn sheep feces clone BHSD_aaa02b12 EU4744
FJ364955.1 gg_id:360031 feces adult twins and mothers; TS1 clone TS1_a01b10 FJ3649
EU461035.1 gg_id:291117 red kangaroo feces clone KO1_aai42g02 EU4610

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	1	1	0	0	0	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	1	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	1	1

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	26963
s__unclassified	26969
s__unclassified	26970
s__unclassified	26971
s__unclassified	26973
s__unclassified	26974
s__unclassified	26976
s__unclassified	26978
s__unclassified	26980
s__unclassified	26981
s__unclassified	26982
s__unclassified	26983
s__unclassified	26984
s__unclassified	26986
s__unclassified	26987
s__unclassified	26988
s__unclassified	26990
s__unclassified	26995
s__unclassified	26998
s__unclassified	26999
s__unclassified	27000
s__unclassified	27001
s__unclassified	27002
s__unclassified	27005
s__unclassified	27008
s__unclassified	27013
s__unclassified	27014
s__unclassified	27015
s__unclassified	27017
s__unclassified	27019
s__unclassified	27020
s__unclassified	27021
s__unclassified	27022
s__unclassified	27023
s__unclassified	27026
s__unclassified	27027
s__unclassified	27028
s__unclassified	27029
s__unclassified	27030
s__unclassified	27031
s__unclassified	27032

EF603271.1 gg_id:229291 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
GQ502529.1 gg_id:589530 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU768072.1 gg_id:314565 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU850470.1 gg_id:304165 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF49 EU850
EU510224.1 gg_id:270297 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03b09 EU510
EF603286.1 gg_id:234373 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
EU763025.1 gg_id:304725 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
AY976193.1 gg_id:125597 human ascending colon mucosal biopsy clone LW10 AY976
DQ327508.1 gg_id:145878 Metagenomic gut microbiome healthy human stool clone EA83 DQ327
DQ325649.1 gg_id:146048 Metagenomic gut microbiome healthy human stool clone B215 DQ325
EF603298.1 gg_id:232031 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
FJ365192.1 gg_id:368412 feces adult twins and mothers; TS1 clone TS1_a04a02 FJ3651
EF099963.1 gg_id:195689 mouse cecum clone SWPT5_aaa02h03 EF0999
DQ800544.1 gg_id:195667 human fecal clone RL183_aah29d10 DQ800
EU455299.1 gg_id:333969 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU455
EU506732.1 gg_id:276761 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55c08 EU506
GQ896776.1 gg_id:590125 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
EU768021.1 gg_id:328363 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AF371766.1 gg_id:107272 swine intestine clone p-4546-4Wb3 AF371
EU774361.1 gg_id:353322 Chimpanzee feces clone CHIMP1_aaj37f02 EU774
DQ793759.1 gg_id:177903 human fecal clone RL246_aai76h04 DQ793
EF559116.1 gg_id:220174 mesophilic anaerobic digester clone C35_D7_H_B_C05 EF5591
DQ116011.1 gg_id:130793 bovine teat canal clone D-74 DQ116
FJ366095.1 gg_id:367681 feces adult twins and mothers; TS25 clone TS25_a02f06 FJ3660
EU772286.1 gg_id:340066 Argali sheep feces clone AS2_aao36e12 EU772
GQ448532.1 gg_id:510233 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU158190.1 gg_id:235474 Clostridium sp. str. SW512 EU158
AM277638.2 gg_id:233253 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
EF603366.1 gg_id:229110 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU778786.1 gg_id:349884 Springbok feces clone SBSD_aaa02e08_1 EU778
DQ800873.1 gg_id:185826 human fecal clone RL183_aao04f02 DQ800
FJ363634.1 gg_id:363716 feces adult twins and mothers; TS14 clone TS14_a01e11 FJ3636
DQ794088.1 gg_id:187393 human fecal clone RL176_aan57h02 DQ794
EF603784.1 gg_id:244484 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal m EF6037
EU454869.1 gg_id:311725 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4548
FJ366738.1 gg_id:361920 feces adult twins and mothers; TS27 clone TS27_a03c09 FJ3667
FJ440066.1 gg_id:546958 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
FJ680947.1 gg_id:531238 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ366104.1 gg_id:361201 feces adult twins and mothers; TS25 clone TS25_a02g04 FJ3661
EU779323.1 gg_id:342446 Visayam Warty Pig feces clone VWP_aaa02g01 EU779
EU511636.1 gg_id:271303 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08a08 EU511

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	27036
s__unclassified	27038
s__unclassified	27040
s__unclassified	27041
s__unclassified	27043
s__unclassified	27044
s__unclassified	27045
s__unclassified	27048
s__unclassified	27050
s__unclassified	27051
s__unclassified	27052
s__unclassified	27053
s__unclassified	27056
s__unclassified	27059
s__unclassified	27060
s__unclassified	27063
s__unclassified	27064
s__unclassified	27067
s__unclassified	27072
s__unclassified	27073
s__unclassified	27075
s__unclassified	27076
s__unclassified	27080
s__unclassified	27087
s__unclassified	27090
s__unclassified	27096
s__unclassified	27097
s__unclassified	27099
s__unclassified	27100
s__unclassified	27102
s__unclassified	27104
s__unclassified	27105
s__unclassified	27106
s__unclassified	27107
s__unclassified	27110
s__unclassified	27112
s__unclassified	27118
s__unclassified	27119
s__unclassified	27121
s__unclassified	27124
s__unclassified	27125

EU509971.1 gg_id:273737 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak24f03 EU509
GQ491419.1 gg_id:558068 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ491157.1 gg_id:581278 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU842952.1 gg_id:303785 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU748046.1 gg_id:355404 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43g04 EU748
EU465638.1 gg_id:301382 argali sheep feces clone AS1_aao40e01.Contig1 EU465
EU844075.1 gg_id:328379 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ374214.1 gg_id:369525 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
FN436123.1 gg_id:539296 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
FJ363880.1 gg_id:361066 feces adult twins and mothers; TS14 clone TS14_a04d11 FJ3638
EU506986.1 gg_id:274921 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar09d08 EU506
EF603494.1 gg_id:234342 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6034
FJ881322.1 gg_id:459119 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8813
EU006198.1 gg_id:256016 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AJ608244.1 gg_id:149660 human biopsies ulcerative colitis biopsy clone UC7-69 AJ6082
DQ802767.1 gg_id:199696 human fecal clone RL188_aan96c12 DQ802
EU764801.1 gg_id:331168 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
GQ451266.1 gg_id:565404 Fecal Yunnan snub-nosed monkey feces clone J245 GQ451
FJ368624.1 gg_id:361341 feces adult twins and mothers; TS49 clone TS49_a02e05 FJ3686
EU474535.1 gg_id:289015 bighorn sheep feces clone BHSD_aaa04h11 EU474
DQ456247.1 gg_id:158456 pre-adolescent turkey cecum clone CFT211A12 DQ456
EF686627.1 gg_id:257352 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EF445160.1 gg_id:215193 rabbit cecum clone NED3A12 EF4451
FJ365131.1 gg_id:370011 feces adult twins and mothers; TS1 clone TS1_a03c05 FJ3651
EF603330.1 gg_id:230238 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
EU453550.1 gg_id:341015 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU507924.1 gg_id:268722 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e09 EU507
DQ904669.1 gg_id:164541 human fecal clone 001-c7 DQ904
AB288879.1 gg_id:200879 termite gut homogenate clone BOf1-09 AB288
EU507998.1 gg_id:276229 cecal contents Mus musculus strain C57BL/6J; MD25 clone MD25_aaa01e10 EU507
AY916333.1 gg_id:114325 human stool clone C342 AY916
GQ451236.1 gg_id:578147 Fecal Yunnan snub-nosed monkey feces clone J158 GQ451
FJ371419.1 gg_id:358780 feces adult twins and mothers; TS6 clone TS6_a04g03 FJ3714
EU508713.1 gg_id:269238 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49g09 EU508
DQ796608.1 gg_id:192022 human fecal clone RL179aan75g07 DQ796
DQ325941.1 gg_id:147410 Metagenomic gut microbiome healthy human stool clone B814 DQ325
FJ363232.1 gg_id:362622 feces adult twins and mothers; TS148 clone TS148_a04g08 FJ3632
DQ793709.1 gg_id:176372 human fecal clone RL246_aai76a06 DQ793
EU772408.1 gg_id:315393 Hamadryas Baboon feces clone BAZ_aah91d12 EU772
DQ815688.1 gg_id:173264 mouse cecum clone aab21a03 DQ815
EF603333.1 gg_id:228320 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	27126
s__unclassified	27127
s__unclassified	27128
s__unclassified	27131
s__unclassified	27134
s__unclassified	27135
s__unclassified	27139
s__unclassified	27141
s__unclassified	27144
s__unclassified	27148
s__unclassified	27149
s__unclassified	27150
s__unclassified	27151
s__unclassified	27152
s__unclassified	27153
s__unclassified	27154
s__unclassified	27157
s__unclassified	27160
s__unclassified	27161
s__unclassified	27163
s__unclassified	27164
s__unclassified	27166
s__unclassified	27170
s__unclassified	27171
s__unclassified	27172
s__unclassified	27173
s__unclassified	27174
s__unclassified	27175
s__unclassified	27176
s__unclassified	27178
s__unclassified	27180
s__unclassified	27181
s__unclassified	27182
s__unclassified	27184
s__unclassified	27185
s__unclassified	27186
s__unclassified	27191
s__unclassified	27192
s__unclassified	27194
s__unclassified	27195
s__unclassified	27197

EF686600.1 gg_id:247858 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6866
EU469255.1 gg_id:297622 Speke's gazelle feces clone SP3_h06_1 EU469
EU453520.1 gg_id:343276 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU453
EU170433.1 gg_id:240700 Clostridium sp. str. W72 EU170
FJ365004.1 gg_id:366702 feces adult twins and mothers; TS1 clone TS1_a01g01 FJ3650
DQ793719.1 gg_id:185168 human fecal clone RL246_aai76b08 DQ793
EU463106.1 gg_id:294065 naked mole-rat feces clone molerat_aai70a01 EU463
AB307643.1 gg_id:268556 clay wall used Japanese traditional buildings clone B42 AB307
DQ800879.1 gg_id:198184 human fecal clone RL183_aao04f08 DQ800
EU457334.1 gg_id:331013 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80 EU457
EF400652.1 gg_id:210777 human fecal clone SJTU_E_16_56 EF4006
DQ015580.1 gg_id:131378 mouse cecum clone M3_g06_2 DQ015
DQ394651.1 gg_id:155932 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
DQ808780.1 gg_id:190703 human fecal clone RL243_aai85b07 DQ808
FJ366863.1 gg_id:357503 feces adult twins and mothers; TS27 clone TS27_a04g03 FJ3668
EU843786.1 gg_id:343476 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU509268.1 gg_id:263766 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46h08 EU509
AM693109.2 gg_id:525997 Microbial level alterations overall gastrointestinal microbiota diarrhoea-predominar AM693
EF404038.1 gg_id:213124 human fecal clone SJTU_C_03_83 EF4040
EF603287.1 gg_id:231021 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6032
GQ449055.1 gg_id:561879 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_ GQ449
EF409954.1 gg_id:211472 Isolation equol-producing fecal clone QE4 EF4099
EU470456.1 gg_id:297964 Grevy's zebra feces clone GZ_aaa02h03 EU470
AY916351.1 gg_id:113822 human stool clone D036 AY9163
FJ364575.1 gg_id:361644 feces adult twins and mothers; TS15 clone TS15_a04e11 FJ3645
AF376224.1 gg_id:50072 ckncm320-B3-25 clone AF3762
EU775897.1 gg_id:330061 Horse feces clone horsem_aai93d07 EU7758
DQ800561.1 gg_id:178571 human fecal clone RL183_aah29g05 DQ800
DQ905474.1 gg_id:170185 human fecal clone 014-b10 DQ905
DQ803929.1 gg_id:189820 human fecal clone RL200_aai60a09 DQ803
EU764469.1 gg_id:311864 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B EU7644
EU469193.1 gg_id:291668 Speke's gazelle feces clone SP3_h03_1 EU469
EU468601.1 gg_id:302588 okapi feces clone OK1_g10_1 EU468
FJ673780.1 gg_id:527976 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
GQ175446.1 gg_id:566899 Chicken intestinal microbiota modulations various feed supplementations DGGE an GQ175
AY854329.1 gg_id:110824 herbivore gastrointestinal tract clone Thompsons41 AY8543
EU461148.1 gg_id:294246 hamadryas baboon feces clone BAZ_aah89b06 EU461
EU508360.1 gg_id:271519 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03g03 EU5083
DQ237939.1 gg_id:143881 influence fumarate disodium on ruminal metabolism goats goat rumen clone M2 DQ237
FJ368475.1 gg_id:362854 feces adult twins and mothers; TS3 clone TS3_a04g11 FJ3684
EU761698.1 gg_id:338035 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU7616

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	1	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	27199
s__unclassified	27201
s__unclassified	27202
s__unclassified	27212
s__unclassified	27214
s__unclassified	27215
s__unclassified	27217
s__unclassified	27226
s__unclassified	27227
s__unclassified	27228
s__unclassified	27229
s__unclassified	27230
s__unclassified	27231
s__unclassified	27232
s__unclassified	27233
s__unclassified	27234
s__unclassified	27235
s__unclassified	27236
s__unclassified	27240
s__unclassified	27241
s__unclassified	27242
s__unclassified	27243
s__unclassified	27244
s__unclassified	27247
s__unclassified	27248
s__unclassified	27250
s__unclassified	27252
s__unclassified	27253
s__unclassified	27254
s__unclassified	27255
s__unclassified	27256
s__unclassified	27260
s__unclassified	27261
s__unclassified	27262
s__unclassified	27263
s__unclassified	27264
s__unclassified	27265
s__unclassified	27268
s__unclassified	27276
s__unclassified	27279
s__unclassified	27280

DQ800732.1 gg_id:176290 human fecal clone RL183_aao02g01 DQ800
EF434360.1 gg_id:208911 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
AB234454.1 gg_id:146455 termite gut homogenate clone MgMjD-029 AB2344
DQ673514.1 gg_id:161997 rumen fluid clone GRC49 DQ673
EU842855.1 gg_id:352007 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8428
EU381669.1 gg_id:263881 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid p EU3816
AY980635.1 gg_id:122955 human rectum mucosal biopsy clone LL09 AY9806
DQ809631.1 gg_id:196782 human fecal clone RL184_aan81g10 DQ809
EU472112.1 gg_id:287351 francois langur feces clone FL_1aaa04a01 EU4721
EF402506.1 gg_id:210552 human fecal clone SJTU_B_08_85 EF4025
FJ366734.1 gg_id:367775 feces adult twins and mothers; TS27 clone TS27_a03c04 FJ3667
GU304571.1 gg_id:548654 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
EU468515.1 gg_id:292708 okapi feces clone OK1_f10 EU4685
EF603304.1 gg_id:230751 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6033
GQ502533.1 gg_id:574604 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
EU506537.1 gg_id:266214 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03f04 EU5065
EU794307.1 gg_id:346705 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L25 EU7943
EU794105.1 gg_id:345871 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_W46 EU7941
DQ014883.1 gg_id:130110 mouse cecum clone M1_h02_3 DQ014
GU174108.1 gg_id:592004 Microbial Bactrian camel estimated rumen clone XJC79 GU174
EU842993.1 gg_id:308786 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8429
AB234478.1 gg_id:146871 termite gut homogenate clone MgMjW-23 AB2344
FJ366107.1 gg_id:364527 feces adult twins and mothers; TS25 clone TS25_a02g07 FJ3661
DQ815960.1 gg_id:169219 mouse cecum clone aab24h04 DQ815
EU504849.1 gg_id:270413 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03c03 EU5048
EU511174.1 gg_id:270030 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal03h04 EU5111
DQ793285.1 gg_id:189122 human fecal clone RL199_aaj41g04 DQ793
EU887972.1 gg_id:323591 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
DQ804871.1 gg_id:187847 human fecal clone RL385_aao81h01 DQ804
FJ371344.1 gg_id:370052 feces adult twins and mothers; TS6 clone TS6_a03h02 FJ3713
EU006164.1 gg_id:236225 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0061
DQ798670.1 gg_id:199475 human fecal clone RL181_aan99g11 DQ798
EF603268.1 gg_id:232658 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
DQ809981.1 gg_id:175170 human fecal clone RL184_aao66f07 DQ809
DQ795049.1 gg_id:178859 human fecal clone RL310_aam39e10 DQ795
FJ367663.1 gg_id:369320 feces adult twins and mothers; TS2 clone TS2_a02b03 FJ3676
EU453675.1 gg_id:313431 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4536
AY986321.1 gg_id:121129 human stool clone D715 AY9863
GQ897679.1 gg_id:559659 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU774417.1 gg_id:309482 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai14 EU7744
EU463401.1 gg_id:299759 domesticated horse feces clone horsem_aai93c02 EU4634

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	27283
s__unclassified	27287
s__unclassified	27289
s__unclassified	27301
s__unclassified	27302
s__unclassified	27303
s__unclassified	27305
s__unclassified	27313
s__unclassified	27317
s__unclassified	27319
s__unclassified	27325
s__unclassified	27329
s__unclassified	27339
s__unclassified	27352
s__unclassified	27357
s__unclassified	27361
s__unclassified	27371
s__unclassified	27390
s__unclassified	27421
s__unclassified	27427
s__unclassified	27428
s__unclassified	27430
s__unclassified	27433
s__unclassified	27434
s__unclassified	27435
s__unclassified	27448
s__unclassified	27458
s__unclassified	27465
s__unclassified	27470
s__unclassified	27472
s__unclassified	27488
s__unclassified	27495
s__unclassified	27506
s__unclassified	27511
s__unclassified	27517
s__unclassified	27525
s__unclassified	27527
s__unclassified	27528
s__unclassified	27530
s__unclassified	27546
s__unclassified	27548

EU773222.1 gg_id:349444 BigHorn sheep feces clone BH1_aao25h06 EU773
DQ796716.1 gg_id:184287 human fecal clone RL179_aao53e11 DQ796
EF445157.1 gg_id:216557 rabbit cecum clone NED1A10 EF4451
GU304029.1 gg_id:590712 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
DQ673580.1 gg_id:171848 rumen fluid clone GRC115 DQ673
EU465584.1 gg_id:296437 argali sheep feces clone AS1_aao38f10.Contig1 EU465
FJ880813.1 gg_id:437273 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU461017.1 gg_id:302744 red kangaroo feces clone KO1_aai42d09 EU461
EU470386.1 gg_id:293477 Grevy's zebra feces clone GZ_aaa02e11 EU470
EU382005.1 gg_id:272899 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
GU303495.1 gg_id:582952 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU470037.1 gg_id:303164 trancaspain urial feces clone TU1_aaa03b09 EU470
DQ801064.1 gg_id:193895 human fecal clone RL387_aao91f04 DQ801
EU250958.1 gg_id:363509 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU250
DQ793756.1 gg_id:188225 human fecal clone RL246_aai76g11 DQ793
AB185540.1 gg_id:104439 rumen clone F23-D09 AB185
EU464078.1 gg_id:303244 reticulated giraffe feces clone gir_aah93b06 EU464
EU469077.1 gg_id:296415 Speke's gazelle feces clone SP3_a12 EU469
EU462596.1 gg_id:295615 Sumatran orangutan feces clone orang2_aai65h01 EU462
EU506620.1 gg_id:258946 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53e02 EU506
EF096988.1 gg_id:198512 mouse cecum clone SWPT13_aaa03g08 EF0969
EU842961.1 gg_id:315150 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU466444.1 gg_id:287377 bighorn sheep feces clone BH2_aao23g10 EU466
FJ681223.1 gg_id:528725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
EU842439.1 gg_id:340770 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EU794257.1 gg_id:344025 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J17 EU794
AB198524.1 gg_id:135518 termite gut wall fraction clone RsW02-034 AB198
EF454875.2 gg_id:221978 termite hindgut clone 290cost002-P3L-568 EF4548
EU465567.1 gg_id:299012 argali sheep feces clone AS1_aao37h07.Contig1 EU465
AY858483.2 gg_id:109604 gastrointestinal tract eland clone ELAND_3 AY8584
EU794310.1 gg_id:307291 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P3 EU7943
AB185579.1 gg_id:103145 rumen clone F24-A06 AB185
EU794264.1 gg_id:354632 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L34 EU794
AF050582.1 gg_id:16073 contaminated aquifer clone WCHB1-54 AF0505
EU794192.1 gg_id:323910 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_E02 EU7941
AM183003.1 gg_id:251289 and its spatial composts compost clone SMA17 AM183
EU844610.1 gg_id:311446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8446
AB009176.1 gg_id:16063 rumen clone RFN17 bacterium AB009
EU775199.1 gg_id:329360 Reticulated giraffe feces clone gir_aah94d12 EU775
DQ801076.1 gg_id:176718 human fecal clone RL387_aao91g09 DQ801
EU794129.1 gg_id:356245 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AE6 EU7941

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	1	1	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	0	0	0	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	1	0	0	0	0	0	1
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	27551
s__unclassified	27558
s__unclassified	27576
s__unclassified	27588
s__unclassified	27592
s__unclassified	27612
s__unclassified	27616
s__unclassified	27621
s__unclassified	27626
s__unclassified	27629
s__unclassified	27635
s__unclassified	27639
s__unclassified	27648
s__unclassified	27649
s__unclassified	27654
s__unclassified	27674
s__unclassified	27704
s__unclassified	27705
s__unclassified	27709
s__unclassified	27711
s__unclassified	27723
s__unclassified	27731
s__unclassified	27743
s__unclassified	27746
s__unclassified	27760
s__unclassified	27761
s__unclassified	27766
s__unclassified	27783
s__unclassified	27793
s__unclassified	27795
s__unclassified	27798
s__unclassified	27799
s__unclassified	27809
s__unclassified	27830
s__unclassified	27834
s__unclassified	27844
s__unclassified	27846
s__unclassified	27851
s__unclassified	27853
s__unclassified	27860
s__unclassified	27880

GQ402104.1 gg_id:512146 alpacas and sheep forestomach clone ALP8 GQ402
EU474824.1 gg_id:300854 takin feces clone TAK_aaa02g06 EU474
EU774438.1 gg_id:342510 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1 EU774
EU844076.1 gg_id:354499 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU794087.1 gg_id:312992 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_U43 EU794
EU773732.1 gg_id:346413 Cheetah feces clone CE3_aai05h11 EU773
DQ394632.1 gg_id:151144 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ394634.1 gg_id:151267 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU794085.1 gg_id:314757 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_Z35 EU794
EU471995.1 gg_id:298553 francois langur feces clone FL_1aaa03c03 EU471
AB233996.1 gg_id:156549 anaerobic reactor clone B-3 AB233
GQ451308.1 gg_id:592857 Fecal Yunnan snub-nosed monkey feces clone J325 GQ451
EU453210.1 gg_id:349798 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU453
EU844645.1 gg_id:339252 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU794156.1 gg_id:349201 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L42 EU794
AB198484.1 gg_id:135720 termite gut wall fraction clone RsW01-056 AB198
EU466282.1 gg_id:289200 bighorn sheep feces clone BH2_aao21c11 EU466
GU454868.1 gg_id:518493 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
EU461091.1 gg_id:301917 red kangaroo feces clone KO1_aai44a02 EU461
EU468985.1 gg_id:301716 Speke's gazelle feces clone SP2_d07_1 EU468
GU174133.1 gg_id:551562 Microbial Bactrian camel estimated rumen clone XJC124 GU174
EU844169.1 gg_id:326767 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU461512.1 gg_id:303394 black rhinoceros feces clone RH_aaj91c12 EU461
EU462243.1 gg_id:299441 chimpanzee feces clone CHIMP1_aaj38c11 EU462
AB185776.1 gg_id:105514 rumen clone U29-D05 AB185
EU762139.1 gg_id:307647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU468725.1 gg_id:290201 okapi feces clone OK2_g04_1 EU468
EU794278.1 gg_id:325883 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H46 EU794
EU509875.1 gg_id:270519 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak22h11 EU509
DQ797051.1 gg_id:199149 human fecal clone RL386_aao86c11 DQ797
EU850568.1 gg_id:303584 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF379 EU850
EU381809.1 gg_id:273552 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ681730.1 gg_id:522625 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ681667.1 gg_id:517931 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
EU773299.1 gg_id:329112 BigHorn sheep feces clone BHSD_aaa04e12 EU773
EU464400.1 gg_id:295056 hamadryas baboon feces clone AFBAB_aai04d05 EU464
DQ808758.1 gg_id:177437 human fecal clone RL239_aaj12h05 DQ808
EU469314.1 gg_id:293987 Speke's gazelle feces clone SP3_h03_3 EU469
FJ681337.1 gg_id:518060 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ456148.1 gg_id:157036 pre-adolescent turkey cecum clone CFT29A2 DQ456
EU776470.1 gg_id:340210 Red Kangaroo feces clone KO2_aai17e12 EU776

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	0	1	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae

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

s__unclassified	27881
s__unclassified	27882
s__unclassified	27883
s__unclassified	27887
s__unclassified	27895
s__unclassified	27897
s__unclassified	27901
s__unclassified	27921
s__unclassified	27926
s__unclassified	27945
s__unclassified	27951
s__unclassified	27957
s__unclassified	27979
s__unclassified	27983
s__unclassified	27985
s__unclassified	28000
s__unclassified	28005
s__unclassified	28006
s__unclassified	28017
s__unclassified	28023
s__unclassified	28029
s__unclassified	28033
s__unclassified	28041
s__unclassified	28057
s__unclassified	28060
s__unclassified	28064
s__unclassified	28066
s__unclassified	28072
s__unclassified	28076
s__unclassified	28078
s__unclassified	28086
s__unclassified	28089
s__unclassified	28094
s__unclassified	28113
s__unclassified	28114
s__unclassified	28118
s__unclassified	28134
s__unclassified	28144
s__unclassified	28154
s__unclassified	28167
s__unclassified	28168

EU775007.1 gg_id:318972 Francois Langur feces clone FL_1aaa04e03 EU775
FJ366012.1 gg_id:366309 feces adult twins and mothers; TS25 clone TS25_a01f12 FJ3660
GQ449144.1 gg_id:511242 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ449
EU773276.1 gg_id:349695 BigHorn sheep feces clone BH2_aao22h09 EU773
EU771349.1 gg_id:321127 Asiatic elephant feces clone AE2_aaa02h02 EU771
EU776451.1 gg_id:354054 Red Kangaroo feces clone KO2_aai17g04 EU776
EU844199.1 gg_id:304015 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU472419.1 gg_id:293879 Angola colobus feces clone EAC_1aaa03d10 EU472
DQ801138.1 gg_id:181671 human fecal clone RL387_aao92g09 DQ801
EU776342.1 gg_id:320831 Red Kangaroo feces clone KO1_aai42g11 EU776
EF686635.1 gg_id:237134 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC1 EF6866
EU465539.1 gg_id:289774 argali sheep feces clone AS1_aao37c02.Contig1 EU465
EU464112.1 gg_id:296798 reticulated giraffe feces clone gir_aah93h11 EU464
AF050581.1 gg_id:16062 contaminated aquifer clone WCHB1-49 AF050
EU470437.1 gg_id:289438 Grevy's zebra feces clone GZ_aaa03g08 EU470
EU843153.1 gg_id:353179 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463648.1 gg_id:288212 domesticated horse feces clone horsej_aai90d05 EU463
EU773265.1 gg_id:333820 BigHorn sheep feces clone BHSD_aaa03a03 EU773
EU470173.1 gg_id:292016 trancaspain urial feces clone TU2_aaa03h02 EU470
EU794179.1 gg_id:331046 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_A15 EU794
EU470148.1 gg_id:300089 trancaspain urial feces clone TU2_aaa02b09 EU470
EU470366.1 gg_id:287724 Grevy's zebra feces clone GZ_aaa01d12 EU470
GQ502523.1 gg_id:583328 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
DQ805504.1 gg_id:187508 human fecal clone RL203_aai63e04 DQ805
EU458486.1 gg_id:291270 spotted hyena feces clone HY2_h02 EU458
EU772024.1 gg_id:335757 Argali sheep feces clone AS2_aao36e09 EU772
GQ451202.1 gg_id:578310 Fecal Yunnan snub-nosed monkey feces clone J52 GQ451
GQ448531.1 gg_id:594107 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU779127.1 gg_id:328671 Trancaspian Urial feces clone TU2_aaa02e08 EU779
DQ801040.1 gg_id:196502 human fecal clone RL387_aao91c07 DQ801
AB192042.1 gg_id:142583 termite gut homogenate clone M1NP1-42 AB192
AB198499.1 gg_id:135452 termite gut wall fraction clone RsW01-073 AB198
EF686609.1 gg_id:239644 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC9 EF6866
EU468734.1 gg_id:297952 okapi feces clone OK3_b09 EU468
FJ366638.1 gg_id:362693 feces adult twins and mothers; TS27 clone TS27_a02a10 FJ3666
GQ448437.1 gg_id:547348 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ684375.1 gg_id:528722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
EU772128.1 gg_id:337202 Argali sheep feces clone AS2_aao36f02 EU772
EU779349.1 gg_id:344615 Somali Wild Ass feces clone WA_aaa04g06 EU779
FJ680570.1 gg_id:522248 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU844036.1 gg_id:344137 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	1	0	1	1
0	1	0	0	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	1	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Ruminococcaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae
o__Clostridiales	f__Sulfobacillaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Sulfobacillus
g__Thermaerobacter
g__Thermaerobacter
g__Thermaerobacter
g__Thermaerobacter
g__Thermaerobacter
g__Thermaerobacter
g__unclassified
g__unclassified
g__YNPFFP6
g__YNPFFP6
g__YNPFFP6
g__YNPFFP6
g__YNPFFP6

s__unclassified	28172
s__unclassified	28176
s__unclassified	28178
s__unclassified	28183
s__unclassified	28186
s__unclassified	28188
s__unclassified	28189
s__unclassified	28200
s__unclassified	70482
s__Sulfobacillus acidophilus	48617
s__Sulfobacillus acidophilus	49147
s__Sulfobacillus benefaciens	49778
s__Sulfobacillus thermosulfidooxidans	49089
s__Sulfobacillus thermosulfidooxidans	49788
s__unclassified	48210
s__unclassified	48216
s__unclassified	48233
s__unclassified	48278
s__unclassified	48432
s__unclassified	48458
s__unclassified	48666
s__unclassified	48677
s__unclassified	48928
s__unclassified	48940
s__unclassified	49538
s__unclassified	49761
s__unclassified	49844
s__unclassified	49886
s__Thermaerobacter subterraneus	49695
s__unclassified	48674
s__unclassified	49162
s__unclassified	49164
s__unclassified	49251
s__unclassified	49369
s__unclassified	48349
s__unclassified	48624
s__unclassified	48283
s__unclassified	48543
s__unclassified	48636
s__unclassified	48810
s__unclassified	49814

FJ680572.1 gg_id:528121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU794263.1 gg_id:326926 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_J18 EU7942
EU794233.1 gg_id:346556 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AF12 EU7942
EU509795.1 gg_id:264941 cecal contents Mus musculus strain C57BL/6J; WD11 clone WD11_aak21b06 EU5097
GQ898040.1 gg_id:552448 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
EU466218.1 gg_id:290974 bighorn sheep feces clone BH1_aao28c02 EU4662
EU466103.1 gg_id:296496 bighorn sheep feces clone BH1_aao25h04 EU4661
EU470320.1 gg_id:297021 Grevy's zebra feces clone GZ_aaa04h11 EU4703
EU468812.1 gg_id:291161 okapi feces clone OK3_g06_2 EU4688
EF088287.1 gg_id:190918 Sulfobacillus acidophilus str. 1 EF0882
AY007665.2 gg_id:33263 Sulfobacillus yellowstonensis str. YTF-1 AY0076
EU495236.1 gg_id:275497 Sulfobacillus benefaciens str. MT606 EU4952
EU499919.1 gg_id:279555 Sulfobacillus thermosulfidooxidans str. N19-50-01 EU4999
U75648.1 gg_id:14342 Sulfobacillus thermosulfidooxidans str. BC1 U75648
EF612374.1 gg_id:236874 historic semiarid lead-zinc site mine tailings clone K6-C04 EF6123
EU419196.1 gg_id:264046 Sulfobacillus acidophilus str. DK-I15/45 EU4191
AY079150.1 gg_id:60544 Sulfobacillus sibiricus str. N1 AY0791
EU419151.1 gg_id:270741 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
DQ464142.1 gg_id:157528 acid mine drainage clone D3-5 DQ464
EF612378.1 gg_id:244429 historic semiarid lead-zinc site mine tailings clone K6-C81 EF6123
DQ834229.1 gg_id:164112 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National DQ834
AM749742.1 gg_id:246891 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
EF612379.1 gg_id:250416 historic semiarid lead-zinc site mine tailings clone K6-C107 EF6123
EU419149.1 gg_id:273033 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
EU419137.1 gg_id:275460 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
DQ464143.1 gg_id:157541 acid mine drainage clone D3-28 DQ464
AY805540.1 gg_id:108883 thermophilic bioleaching clone JTC05 AY8055
EU419152.1 gg_id:266474 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
NR_028814.1 gg_id:583050 Thermaerobacter subterraneus str. C21; ATCC BAA-137 NR_028
AB061441.1 gg_id:50462 Thermaerobacter nagasakiensis str. JCM 11223 AB0614
AB454087.1 gg_id:323069 Thermaerobacter sp. str. Ni80 AB4540
EU214629.1 gg_id:331773 Thermaerobacter subterraneus ir-12 EU2146
AY936496.1 gg_id:114490 Thermaerobacter riparius str. KW1 AY9364
AB011495.1 gg_id:13721 Thermaerobacter marianensis AB0114
AB254790.1 gg_id:160816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
DQ234653.1 gg_id:143589 subsurface water clone DR546BH1103001SAD85 DQ234
AF465653.1 gg_id:25424 G+C Gram-positive clone YNPRH70A AF4656
EF612375.1 gg_id:255886 historic semiarid lead-zinc site mine tailings clone K6-C05 EF6123
AF391988.1 gg_id:27433 thermal soil clone YNPFFP9 AF3919
EU419144.1 gg_id:275922 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU4191
AM749765.1 gg_id:240376 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749

0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	1	1	1
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	1	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	0	1	0	0	0	0	0	0

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

o__Clostridiales	f__Symbiobacteriaceae
o__Clostridiales	f__Symbiobacteriaceae
o__Clostridiales	f__Symbiobacteriaceae
o__Clostridiales	f__Symbiobacteriaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Syntrophomonadaceae
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis

g__Symbiobacterium
g__Symbiobacterium
g__Symbiobacterium
g__unclassified
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__Syntrophomonas
g__unclassified
g__unclassified
g__unclassified
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium
g__Thermoanaerobacterium

s__Symbiobacterium thermophilum	49734
s__unclassified	49267
s__unclassified	49595
s__unclassified	49310
s__Syntrophomonas erecta	49077
s__Syntrophomonas wolfei	48459
s__unclassified	48305
s__unclassified	48309
s__unclassified	48476
s__unclassified	48480
s__unclassified	48496
s__unclassified	48653
s__unclassified	48663
s__unclassified	48769
s__unclassified	48858
s__unclassified	48887
s__unclassified	49055
s__unclassified	49056
s__unclassified	49270
s__unclassified	49274
s__unclassified	49276
s__unclassified	49344
s__unclassified	49421
s__unclassified	49453
s__unclassified	49477
s__unclassified	49573
s__unclassified	49693
s__unclassified	49881
s__unclassified	48366
s__unclassified	48631
s__unclassified	48915
s__Thermoanaerobacterium saccharolyticum	48260
s__Thermoanaerobacterium saccharolyticum	48816
s__Thermoanaerobacterium saccharolyticum	49101
s__Thermoanaerobacterium saccharolyticum	49412
s__Thermoanaerobacterium saccharolyticum	49460
s__Thermoanaerobacterium saccharolyticum	49703
s__Thermoanaerobacterium saccharolyticum	49843
s__unclassified	48403
s__unclassified	49269
s__unclassified	49618

AP006840.1 gg_id:129187 Symbiobacterium thermophilum IAM 14863 str. IAM14863 AP006
AB361629.1 gg_id:243859 Symbiobacterium sp. str. KY38 AB361
AB455238.1 gg_id:322976 Symbiobacterium sp. str. KY46 AB455
AB455239.1 gg_id:344098 Symbiobacterium sp. str. KA13 AB455
DQ112187.1 gg_id:132753 Syntrophomonas sporosyntrophas str. Y4-1 DQ112
FJ799130.1 gg_id:559105 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AF050586.1 gg_id:13690 contaminated aquifer clone WCHB1-82 AF050
AF482445.1 gg_id:77471 granular sludge clone R5p27 AF482
DQ984666.1 gg_id:257916 Anaerobic degradation unsaturated or saturated long chain fatty acids (LCFA) preser DQ984
AY290767.1 gg_id:87293 Syntrophomonas curvata str. GB8-1 AY290
AB252683.1 gg_id:172658 and activities propionate-oxidizing that affected propionate concentration anaerobic AB252
AB186861.1 gg_id:103994 polychlorinated dioxin dechlorinating microcosm clone TSBW01 AB186
AB248633.1 gg_id:146259 mesophilic anaerobic butyrate-degrading reactor clone BHB04 AB248
EF559161.1 gg_id:217350 mesophilic anaerobic digester clone G35_D8_L_B_A02 EF5591
AM947547.1 gg_id:259682 Minor changes detected microbial structure and after three week thermophilic dige AM947
CR933176.1 gg_id:110152 Evry municipal wastewater treatment plant clone 008H01_B_SD_P15 CR933
AB248623.1 gg_id:149149 mesophilic anaerobic butyrate-degrading reactor clone BLB01 AB248
FJ799160.1 gg_id:511304 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AB234271.1 gg_id:150183 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
X99980.1 gg_id:13689 Thermosyntropha lipolytica str. JW265 X99980
DQ339710.1 gg_id:208155 assessment complex microbial degrading long chain fatty acids (LCFA) methanogeni DQ339
DQ080135.1 gg_id:137138 reductive dechlorination 2345-tetrachlorobiphenyl three s: evidence involvement D DQ080
AB192059.1 gg_id:141089 termite gut homogenate clone M1PL1-18 AB192
AB248632.1 gg_id:145683 mesophilic anaerobic butyrate-degrading reactor clone BHB03 AB248
AB234008.1 gg_id:154827 anaerobic reactor clone B-15 AB234
NR_028910.1 gg_id:552212 Pelospora glutarica str. WoGl3; DSM 6652 NR_02
EF515712.1 gg_id:222308 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
FJ799131.1 gg_id:510041 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
AB274497.1 gg_id:203894 packed-bed reactor clone CFB-8 AB274
AB021305.1 gg_id:13691 Syntrophothermus lipocalidus str. TGB-C1 AB021
AB539943.1 gg_id:567072 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
X76743.1 gg_id:13762 Clostridium thermoamylolyticum str. DSM2335 X76743
AY350594.2 gg_id:221143 Thermoanaerobacterium aciditolerans str. 761-119 AY350
EU999016.1 gg_id:322435 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
FJ268955.1 gg_id:356922 Thermoanaerobacterium saccharolyticum str. B6A FJ2689
EU563363.1 gg_id:272616 Thermoanaerobacterium saccharolyticum str. D22 EU563
FM999998.1 gg_id:532726 Thermoanaerobacterium sp. PO-2009 FM999
L09172.1 gg_id:13755 Thermoanaerobacterium xylanolyticum str. LXIIT L09172
AY140670.1 gg_id:59208 Thermoanaerobacterium bryantii str. mel9 AY140
AY331143.1 gg_id:106330 Mahella australiensis str. 50-1-BON AY331
AF247003.1 gg_id:27592 Thermoanaerobacterium thermosaccharolyticum str. D120-70 AF247

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	0	1	0	0	0	1	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__Thermoanaerobacterium
g__Acidaminococcus
g__Acidaminococcus
g__Acidaminococcus
g__Acidaminococcus
g__Acidaminococcus
g__Anaeroglobus
g__Anaerospora
g__Anaerospora
g__Anaerospora
g__Desulfosporomusa
g__Desulfosporomusa
g__Desulfosporomusa
g__Desulfosporomusa
g__Desulfosporomusa
g__Desulfosporomusa
g__Desulfosporomusa
g__Desulfosporomusa
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister

s__unclassified	49893
s__Acidaminococcus fermentans	50245
s__Acidaminococcus fermentans	50272
s__Acidaminococcus fermentans	50535
s__Acidaminococcus intestini	50571
s__unclassified	50834
s__unclassified	50482
s__Anaerospora hongkongensis	50927
s__unclassified	50142
s__unclassified	50647
s__Desulfosporomusa polytropa	50530
s__unclassified	50137
s__unclassified	50211
s__unclassified	50394
s__unclassified	50486
s__unclassified	50672
s__unclassified	50673
s__unclassified	50712
s__Dialister invisus	50107
s__Dialister invisus	50213
s__Dialister invisus	50408
s__Dialister invisus	50519
s__Dialister invisus	50578
s__Dialister invisus	50804
s__Dialister invisus	50828
s__Dialister invisus	50958
s__Dialister micraerophilus	50124
s__Dialister pneumosintes	50428
s__unclassified	49995
s__unclassified	50024
s__unclassified	50045
s__unclassified	50054
s__unclassified	50132
s__unclassified	50135
s__unclassified	50150
s__unclassified	50151
s__unclassified	50162
s__unclassified	50221
s__unclassified	50224
s__unclassified	50258
s__unclassified	50275

EF507903.1 gg_id:239939 Caldanaerobium fijiensis str. JW/YJL-F3 EF5079
EF060090.1 gg_id:199473 Acidaminococcus fermentans str. ADV 6092.03 EF0600
EF060091.1 gg_id:176163 Acidaminococcus fermentans str. ADV 1338.05 EF0600
EU728758.1 gg_id:337187 Acidaminococcus sp. str. DJF_RP55 EU7287
EF028685.1 gg_id:199297 Acidaminococcus intestinalis str. LBN 321 EF0286
EU773566.1 gg_id:307454 Goeldi's Marmoset feces clone CAL_b10_1 EU7735
NR_028812.1 gg_id:539819 Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 4477 NR_028
AY372050.1 gg_id:94360 Anaerospora hongkongensis str. HKU15 AY3720
AY728067.1 gg_id:104334 decayed velvetleaf seed clone S1-6-CL2 AY7280
DQ816346.1 gg_id:172987 mouse cecum clone aaa80f06 DQ816
EU981222.1 gg_id:340874 sulfate reducing living bench scale aquifer packed bed clone A7_FB EU9812
AB288880.1 gg_id:201846 termite gut homogenate clone BOf1-11 AB2888
EF454547.2 gg_id:224315 termite hindgut clone 290cost002-P3L-2304 EF4545
FJ542917.1 gg_id:510013 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
AM158322.1 gg_id:156235 Sporomusa rhizae str. RS AM158
AJ279799.1 gg_id:21147 Sporomusa malonica str. DSM 5090 Type AJ2797
AJ279801.1 gg_id:25868 Sporomusa sphaeroides str. DSM 2875 Type AJ2798
NR_025415.1 gg_id:541895 Sporomusa acidovorans str. DSM 3132 NR_025
GQ047238.1 gg_id:466398 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010d GQ047
FJ372052.1 gg_id:364054 feces adult twins and mothers; TS9 clone TS9_a01c02 FJ3720
DQ794346.1 gg_id:187487 human fecal clone RL197_aah86a07 DQ794
EU762181.1 gg_id:340520 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU7621
DQ803760.1 gg_id:180927 human fecal clone RL200_aai58a11 DQ803
NZ_ACIM02000001.1 gg_id:470239 Dialister invisus str. DSM 15470 NZ_AC
FJ370202.1 gg_id:369002 feces adult twins and mothers; TS56 clone TS56_a01g01 FJ3702
FJ363905.1 gg_id:358364 feces adult twins and mothers; TS14 clone TS14_a04g03 FJ3639
AF473837.2 gg_id:136415 Dialister micraerophilus str. ADV 04.01 AF4738
U13040.1 gg_id:13826 Dialister pneumosintes str. SC3D U13040
FM872697.1 gg_id:365104 occupant source house floor dust clone FA02F02 FM872
EU461194.1 gg_id:290748 hamadryas baboon feces clone BAZ_aah90c07 EU4611
DQ071524.1 gg_id:229365 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCc32 DQ071
FJ364585.1 gg_id:363398 feces adult twins and mothers; TS15 clone TS15_a04g01 FJ3645
FJ833261.1 gg_id:512439 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q302_40H05 FJ8332
FJ832358.1 gg_id:593767 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_87G11 FJ8323
DQ326331.1 gg_id:145728 Metagenomic gut microbiome healthy human stool clone C320 DQ326
EU464320.1 gg_id:293799 hamadryas baboon feces clone AFBAB_aai02f07 EU4643
FJ834270.1 gg_id:564560 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_63G08 FJ8342
AY850119.1 gg_id:109904 Dialister sp. str. ADV 1053.03 AY8501
EU773545.1 gg_id:349811 Goeldi's Marmoset feces clone CAL_e11 EU7735
EU764686.1 gg_id:325573 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7646
DQ353930.1 gg_id:145968 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z83 DQ353

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	0	1	1	1	0	1	1	0	0
1	1	1	1	0	1	1	1	0	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Dialister
g__Megamonas
g__Megamonas
g__Megamonas
g__Megamonas
g__Megamonas
g__Megamonas
g__Megasphaera
g__Megasphaera
g__Megasphaera
g__Megasphaera
g__Megasphaera
g__Megasphaera
g__Megasphaera
g__Mitsuokella
g__Mitsuokella
g__Mitsuokella
g__Mitsuokella
g__Mitsuokella
g__Mitsuokella
g__Mitsuokella
g__Pectinatus

s__unclassified	50284
s__unclassified	50380
s__unclassified	50397
s__unclassified	50398
s__unclassified	50504
s__unclassified	50555
s__unclassified	50563
s__unclassified	50585
s__unclassified	50679
s__unclassified	50692
s__unclassified	50700
s__unclassified	50732
s__unclassified	50821
s__unclassified	50844
s__unclassified	50849
s__unclassified	50913
s__unclassified	50929
s__unclassified	50936
s__unclassified	50966
s__unclassified	70164
s__Megamonas hypermegale	50296
s__Megamonas hypermegale	50352
s__Megamonas hypermegale	50404
s__Megamonas hypermegale	50513
s__unclassified	50340
s__unclassified	50546
s__Megasphaera elsdenii	50065
s__Megasphaera elsdenii	50192
s__Megasphaera elsdenii	50500
s__Megasphaera elsdenii	50903
s__unclassified	50264
s__unclassified	50599
s__unclassified	50877
s__Mitsuokella multacida	50023
s__Mitsuokella multacida	50058
s__unclassified	50242
s__unclassified	50490
s__unclassified	50770
s__unclassified	50842
s__unclassified	50964
s__unclassified	50025

DQ796597.1 gg_id:184999 human fecal clone RL179aan75f02 DQ796
EU009830.1 gg_id:240947 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_M8 EU0098
EU464269.1 gg_id:287863 hamadryas baboon feces clone AFBAB_aai01d11 EU4642
DQ325965.1 gg_id:148937 Metagenomic gut microbiome healthy human stool clone B855 DQ325
AY958942.1 gg_id:128228 Microbes on human vaginal epithelium clone rRNA169 AY9589
DQ809210.1 gg_id:196169 human fecal clone RL308_aal83d11 DQ809
GQ014629.1 gg_id:495037 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw762b GQ014
GQ156497.1 gg_id:590051 Human gut microbiome adopts alternative state bowel transplantation ileum intesti GQ156
DQ353912.1 gg_id:146557 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z25 DQ353
FJ833651.1 gg_id:563580 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_64H08 FJ8336
DQ325967.1 gg_id:146807 Metagenomic gut microbiome healthy human stool clone B859 DQ325
GQ082178.1 gg_id:382947 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ082
DQ325932.1 gg_id:150078 Metagenomic gut microbiome healthy human stool clone B792 DQ325
NR_028862.1 gg_id:585826 Allisonella histaminiformans str. MR2; DSM 15230 NR_028
EU009856.1 gg_id:255834 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_X48 EU0098
FJ832445.1 gg_id:582014 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q101_25A04 FJ8324
EU475193.1 gg_id:295381 bonobo feces clone BNO_aaa01c01 EU4751
AY959160.1 gg_id:130495 Microbes on human vaginal epithelium clone rRNA387 AY9591
FJ832730.1 gg_id:562702 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q101_38F05 FJ8327
EU775402.1 gg_id:342839 Western lowland gorilla feces clone GOR_aag73e12 EU7754
DQ071435.1 gg_id:228821 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw4 DQ071
FJ489245.1 gg_id:513909 Megamonas hypermegale str. ABXD_AE27 FJ4892
DQ071446.1 gg_id:228113 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw1 DQ071
NR_025514.1 gg_id:552592 Megamonas hypermegale str. DSM 1672 NR_025
EU465518.1 gg_id:287786 lion feces clone LI3_aah78g03 EU4655
EU939429.1 gg_id:343257 Fecal wild pygmy loris feces clone WF16S_275 EU9394
U95029.1 gg_id:53032 Megasphaera elsdenii str. S3 U95029
AY038996.1 gg_id:24370 Megasphaera elsdenii str. YJ-4 AY0389
DQ905695.1 gg_id:170226 human fecal clone 014C-G12 DQ905
DQ904992.1 gg_id:170296 human fecal clone 002-g5 DQ904
DQ278866.1 gg_id:151623 Megasphaera sp. TrE9262 DQ278
DQ904832.1 gg_id:168912 human fecal clone 001C-a6 DQ904
DQ904811.1 gg_id:173152 human fecal clone 001B-g7 DQ904
ABWK02000005.1 gg_id:579171 Mitsuokella multacida str. DSM 20544 ABWK0
NZ_ABWK02000010.1 gg_id:470692 Mitsuokella multacida str. DSM 20544 NZ_AB
AY985193.1 gg_id:119553 human stool clone C039 AY9851
DQ325931.1 gg_id:148483 Metagenomic gut microbiome healthy human stool clone B785 DQ325
AY982411.1 gg_id:117325 human sigmoid colon mucosal biopsy clone MK92 AY9824
AY977807.1 gg_id:123930 human cecum mucosal biopsy clone LE93 AY9778
NR_028840.1 gg_id:590732 Mitsuokella jalaludinii str. M9; DSM 13811 NR_028
DQ223731.1 gg_id:140868 Pectinatus haikarae str. VTT E-88329; DSM 16980 DQ223

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Phascolarctobacterium
g__Propionispora
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas

s__unclassified	50028
s__unclassified	50044
s__unclassified	50196
s__unclassified	50235
s__unclassified	50321
s__unclassified	50493
s__unclassified	50561
s__unclassified	50628
s__unclassified	50655
s__unclassified	50696
s__unclassified	50698
s__unclassified	50733
s__unclassified	50755
s__unclassified	50894
s__unclassified	50799
s__Selenomonas noxia	50437
s__Selenomonas noxia	50556
s__Selenomonas noxia	50912
s__Selenomonas ruminantium	50018
s__Selenomonas ruminantium	50055
s__Selenomonas ruminantium	50244
s__Selenomonas ruminantium	50405
s__Selenomonas ruminantium	50528
s__Selenomonas ruminantium	50787
s__Selenomonas ruminantium	50884
s__Selenomonas ruminantium	50898
s__Selenomonas ruminantium	50932
s__Selenomonas sputigena	50351
s__Selenomonas sputigena	50859
s__unclassified	50022
s__unclassified	50074
s__unclassified	50122
s__unclassified	50147
s__unclassified	50197
s__unclassified	50205
s__unclassified	50324
s__unclassified	50445
s__unclassified	50457
s__unclassified	50469
s__unclassified	50544
s__unclassified	50553

GQ492364.1 gg_id:556835 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ491916.1 gg_id:591490 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ366265.1 gg_id:370318 feces adult twins and mothers; TS25 clone TS25_a04f05 FJ3662
EF404155.1 gg_id:206419 human fecal clone SJTU_C_05_48 EF4041
GQ493381.1 gg_id:587536 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ368136.1 gg_id:357831 feces adult twins and mothers; TS30 clone TS30_a04f02 FJ3681
DQ805306.1 gg_id:183098 human fecal clone RL249_aaj84h07 DQ805
GQ492054.1 gg_id:594375 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ362702.1 gg_id:367004 feces adult twins and mothers; TS13 clone TS13_a02b03 FJ3627
EU009791.1 gg_id:255530 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_A48 EU009
EF400225.1 gg_id:212456 human fecal clone SJTU_E_10_50 EF4002
X72867.1 gg_id:13860 Phascolarctobacterium faecium X72867
GQ492591.1 gg_id:575113 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU009762.1 gg_id:239970 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_AC19 EU009
NR_025418.1 gg_id:559721 Propionispora vibrioides str. FKBS1; DSM 13305 NR_02
AY878646.1 gg_id:112413 Selenomonas noxia str. AIP 45-92 AY8786
AY947498.2 gg_id:114498 subgingival plaque clone OH4A AY9474
AY878645.1 gg_id:111934 Selenomonas noxia str. AIP 518-78 AY8786
AF161581.1 gg_id:13799 Selenomonas ruminantium str. K2 AF1615
EU381812.1 gg_id:276744 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
AY685145.1 gg_id:99746 Selenomonas ruminantium L6 AY6851
EU327399.1 gg_id:237808 Selenomonas ruminantium str. LongL1 EU3273
AB198429.1 gg_id:257094 Selenomonas ruminantium str. S36 AB1984
DQ673518.1 gg_id:165042 rumen fluid clone GRC53 DQ673
EF112197.1 gg_id:178224 Selenomonas ruminantium str. 65 EF1121
AB003379.1 gg_id:13812 Selenomonas ruminantium str.JCM6582 AB0033
AF001774.1 gg_id:13813 rumen clone RFP7 AF0017
ACKP02000033.1 gg_id:589013 Selenomonas sputigena str. ATCC 35185 ACKP0
AF373023.1 gg_id:17310 Selenomonas sputigena str. ATCC35185 AF3730
EF195237.1 gg_id:180877 Selenomonas sp. str. MCB2 EF1952
AY685142.1 gg_id:99281 Selenomonas ruminantium M40 AY6851
AY207052.1 gg_id:83279 human mouth clone P2PA_80 AY2070
AF287790.1 gg_id:23591 human subgingival plaque clone DM071 AF2877
NR_028796.1 gg_id:550364 Selenomonas noxia str. ATCC 43541 NR_02
EU669564.1 gg_id:292356 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O EU6695
AY349403.1 gg_id:93019 human oral cavity clone FT050 AY3494
DQ673510.1 gg_id:168649 rumen fluid clone GRC45 DQ673
AM419977.1 gg_id:252996 Noma subgingival plaque clone 101H05(oral) AM419
AF538861.1 gg_id:59529 Selenomonas sp. oral clone P4PA_36 P2 AF5388
AY878647.1 gg_id:112215 Selenomonas sp. str. AIP 308-97 AY8786
FM873718.1 gg_id:368850 occupant source house mattress dust clone MA03E01 FM873

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Selenomonas
g__Sporotalea
g__Thermosinus
g__Thermosinus
g__Thermosinus
g__Thermosinus
g__Thermosinus
g__Thermosinus
g__Thermosinus
g__Thermosinus
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	50562
s__unclassified	50590
s__unclassified	50629
s__unclassified	50670
s__unclassified	50671
s__unclassified	50674
s__unclassified	50728
s__unclassified	50744
s__unclassified	50751
s__unclassified	50800
s__unclassified	50820
s__unclassified	50824
s__unclassified	50826
s__unclassified	50836
s__unclassified	50907
s__unclassified	50693
s__Thermosinus carboxydivorans	50727
s__unclassified	50077
s__unclassified	50109
s__unclassified	50247
s__unclassified	50396
s__unclassified	50577
s__unclassified	50593
s__unclassified	50666
s__unclassified	49989
s__unclassified	49991
s__unclassified	49997
s__unclassified	50000
s__unclassified	50002
s__unclassified	50003
s__unclassified	50008
s__unclassified	50009
s__unclassified	50020
s__unclassified	50047
s__unclassified	50056
s__unclassified	50063
s__unclassified	50075
s__unclassified	50080
s__unclassified	50083
s__unclassified	50088
s__unclassified	50094

DQ003636.1 gg_id:120969 human mouth clone MB3_C41 DQ003
AY349409.1 gg_id:92349 human oral cavity clone JI021 AY3494
AM420026.1 gg_id:254272 Noma subgingival plaque clone 201F02(oral) AM420
GU302661.1 gg_id:586155 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU850496.1 gg_id:329400 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF265 EU8504
AY278627.1 gg_id:86707 Selenomonas genomosp. C1 AY2786
AM420028.1 gg_id:252936 Noma subgingival plaque clone 201F04(oral) AM420
AY341820.1 gg_id:92263 Selenomonas genomosp. P5 AY3418
AM419959.1 gg_id:241050 Noma subgingival plaque clone 101C02(oral) AM419
GQ006802.1 gg_id:502861 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87h08c GQ006
GQ006643.1 gg_id:503020 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86a02c GQ006
AM420074.1 gg_id:238385 Noma subgingival plaque clone 301F12(oral) AM420
EU669566.1 gg_id:295019 Profiles Root Caries Elderly Patients supragingival plaque tooth root surface clone O(EU6695
AM420113.1 gg_id:240321 Noma subgingival plaque clone 303G10(oral) AM420
DQ394645.1 gg_id:155308 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
DQ145536.1 gg_id:141405 Geosinus fermentans str. R7 DQ145
NZ_AAWL01000001.1 gg_id:192281 Thermosinus carboxydivorans str. Nor1 NZ_AA
AJ009486.1 gg_id:13842 TCB-transforming consortium clone SJA-112 AJ0094
DQ125719.1 gg_id:134207 uranium contaminated soil clone AKAU3815 DQ125
AF275913.1 gg_id:72075 anaerobic digestor clone AA01 AF2759
AB195907.1 gg_id:109195 Anaerobic sludge clone N39 AB1959
AB486682.1 gg_id:559077 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4866
EU864464.1 gg_id:310615 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU8644
AB240309.1 gg_id:141751 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AB487569.1 gg_id:571451 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4875
FJ673072.1 gg_id:516219 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AB486151.1 gg_id:586628 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4861
FJ683262.1 gg_id:512213 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU843176.1 gg_id:304446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8431
AJ006980.1 gg_id:13862 Succinispira mobilis str. 19gly1 AJ0069
EU344280.1 gg_id:273405 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
FJ683898.1 gg_id:521321 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
AF407698.1 gg_id:60600 Great Artesian Basin clone G07 AF4076
FJ880994.1 gg_id:405629 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
NR_025298.1 gg_id:575973 Anaeroarcus burkinensis str. DSM 6283 NR_025
FJ676048.1 gg_id:530548 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
GQ038559.1 gg_id:383518 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
AY244964.1 gg_id:84451 cow rumen clone BS10 AY2449
FJ799146.1 gg_id:583522 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
FJ672960.1 gg_id:519106 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ801441.1 gg_id:198328 human fecal clone RL388_aao95e11 DQ801

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	1	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

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

s__unclassified	50099
s__unclassified	50106
s__unclassified	50108
s__unclassified	50114
s__unclassified	50116
s__unclassified	50128
s__unclassified	50129
s__unclassified	50141
s__unclassified	50143
s__unclassified	50145
s__unclassified	50149
s__unclassified	50160
s__unclassified	50165
s__unclassified	50167
s__unclassified	50190
s__unclassified	50202
s__unclassified	50214
s__unclassified	50216
s__unclassified	50218
s__unclassified	50227
s__unclassified	50229
s__unclassified	50236
s__unclassified	50239
s__unclassified	50254
s__unclassified	50257
s__unclassified	50270
s__unclassified	50273
s__unclassified	50274
s__unclassified	50276
s__unclassified	50278
s__unclassified	50293
s__unclassified	50298
s__unclassified	50304
s__unclassified	50305
s__unclassified	50314
s__unclassified	50316
s__unclassified	50317
s__unclassified	50318
s__unclassified	50320
s__unclassified	50328
s__unclassified	50329

FJ678610.1 gg_id:522237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ832386.1 gg_id:533799 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q401_22F03 FJ8323
EU775040.1 gg_id:351818 Francois Langur feces clone FL_2aaa04b12 EU775
AB487852.1 gg_id:548067 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR AB487
FJ681608.1 gg_id:517653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
FJ386549.1 gg_id:364845 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ834254.1 gg_id:575321 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_14F02 FJ8342
EU773455.1 gg_id:328240 Black lemur feces clone BKLE_g09_1 EU773
DQ833299.1 gg_id:170560 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed DQ833
FJ684672.1 gg_id:532119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ678209.1 gg_id:528615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
AY684401.2 gg_id:110815 mucosal biopsies human intestine clone HuAC20 AY684
AB486629.1 gg_id:577345 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU531895.1 gg_id:263067 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AF071415.1 gg_id:13851 Anaeromusa acidaminophila str. DSM 3853 AF071
EU469036.1 gg_id:303124 Speke's gazelle feces clone SP2_c09_3 EU469
DQ824735.1 gg_id:179447 human fecal clone RL185_aaj72d08 DQ824
FJ683901.1 gg_id:521470 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
GU304004.1 gg_id:549795 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
FJ673979.1 gg_id:516340 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
DQ833301.1 gg_id:164274 Anaerobic Reductive Dechlorination Vinyl Chloride ly Enriched Bachman Aquifer Sed DQ833
FJ682035.1 gg_id:525023 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU307091.1 gg_id:251142 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
AB034135.1 gg_id:48795 rumen clone 4C28d-2 AB034
DQ904885.1 gg_id:163607 human fecal clone 001C-f2 DQ904
GQ005015.1 gg_id:504647 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65h1 GQ005
FJ676618.1 gg_id:532032 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
FJ678334.1 gg_id:527813 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
AB486685.1 gg_id:572648 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
FJ678463.1 gg_id:527603 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6784
EU845665.1 gg_id:336552 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ682745.1 gg_id:527983 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ684630.1 gg_id:514989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
EU774198.1 gg_id:346793 Chimpanzee feces clone CHIMP1_aaj39c11 EU774
EU307090.1 gg_id:243204 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU307
EU775009.1 gg_id:316336 Francois Langur feces clone FL_2aaa02b05 EU775
EU747937.1 gg_id:337267 neotropical folivorous flying bird adult hoatzin crop clone hoa13_77E10 EU747
DQ310746.1 gg_id:199797 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC DQ310
AY995255.1 gg_id:123766 human vagina clone FX8B2-5 AY995
AY667269.1 gg_id:103280 TCE-dechlorinating groundwater clone TANB127 AY667
FJ674118.1 gg_id:518615 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

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

s__unclassified	50334
s__unclassified	50339
s__unclassified	50343
s__unclassified	50367
s__unclassified	50369
s__unclassified	50403
s__unclassified	50409
s__unclassified	50416
s__unclassified	50417
s__unclassified	50427
s__unclassified	50429
s__unclassified	50431
s__unclassified	50440
s__unclassified	50458
s__unclassified	50463
s__unclassified	50467
s__unclassified	50472
s__unclassified	50476
s__unclassified	50489
s__unclassified	50505
s__unclassified	50514
s__unclassified	50515
s__unclassified	50520
s__unclassified	50522
s__unclassified	50527
s__unclassified	50543
s__unclassified	50564
s__unclassified	50570
s__unclassified	50575
s__unclassified	50576
s__unclassified	50579
s__unclassified	50580
s__unclassified	50584
s__unclassified	50591
s__unclassified	50592
s__unclassified	50594
s__unclassified	50603
s__unclassified	50615
s__unclassified	50617
s__unclassified	50618
s__unclassified	50620

GQ179679.1 gg_id:455949 Heterogeneity vaginal microbial within individuals vagina clone VE44F01 GQ179
FJ678138.1 gg_id:521053 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
FJ678575.1 gg_id:531578 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
FJ682764.1 gg_id:518322 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
AY672080.2 gg_id:149234 Microbial on patients stomatitis and healthy biofilm denture wearers clone DWE10 AY672
DQ217599.1 gg_id:139963 Zymophilus raffinosivorans str. VTT E-90406; DSM 20765; ATCC 496 DQ217
FJ673355.1 gg_id:525608 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ679306.1 gg_id:520520 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6793
FJ372095.1 gg_id:363046 feces adult twins and mothers; TS9 clone TS9_a01f12 FJ3720
AB034141.1 gg_id:28188 rumen clone 3C28d-10 AB034
AY985859.1 gg_id:117810 human stool clone D133 AY985
DQ113674.1 gg_id:132784 dog colon clone C2-26 DQ113
AB185750.1 gg_id:103463 rumen clone U29-B01 AB185
GU303125.1 gg_id:570205 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU842705.1 gg_id:318812 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ674045.1 gg_id:521328 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
AB034079.1 gg_id:51519 rumen clone 3C3d-10 AB034
FJ680777.1 gg_id:510572 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
EU747918.1 gg_id:346208 neotropical folivorous flying bird adult hoatzin crop clone hoa12_26B04 EU747
FJ673180.1 gg_id:514372 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AB486409.1 gg_id:546268 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AF371705.1 gg_id:45688 swine intestine clone p-286-a3 AF371
AB486202.1 gg_id:575498 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
FJ684083.1 gg_id:520119 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6840
AJ009494.1 gg_id:13843 anaerobic TCB-transforming consortium clone SJA-143 AJ0094
GQ060518.1 gg_id:462753 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02g03 GQ060
GQ451274.1 gg_id:514095 Fecal Yunnan snub-nosed monkey feces clone J269 GQ451
AF357557.1 gg_id:72198 mpn-isolate group 9 AF357
AF371701.1 gg_id:34987 swine intestine clone p-2365-55G5 AF371
AB198438.1 gg_id:237356 Selenomonas ruminantium str. S206 AB198
AF473834.1 gg_id:38606 Megasphaera micronuciformis str. AIP 412.00; CIP 107280 AF473
EU382011.1 gg_id:268506 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU794209.1 gg_id:334383 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O30 EU794
EU475011.1 gg_id:296159 red river hog feces clone RRH_aaa03c07 EU475
FJ674071.1 gg_id:521929 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ372342.1 gg_id:368157 feces adult twins and mothers; TS9 clone TS9_a04e03 FJ3723
EF063619.1 gg_id:193173 Microbial ecology autotrophic denitrifying anaerobic methanogenic UASB reactor clo EF0636
DQ223729.1 gg_id:140753 Megasphaera sueciensis str. VTT E-97791 DQ223
EU779137.1 gg_id:354926 Trancaspian Urial feces clone TU1_aaa03b10 EU779
FN563256.1 gg_id:554464 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
EU747978.1 gg_id:349584 neotropical folivorous flying bird adult hoatzin crop clone hoa13_48H06 EU747

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	0	0	1	0	1	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	1	1	1	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	1	1	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	1	1	0	0	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	1	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

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

s__unclassified	50621
s__unclassified	50624
s__unclassified	50632
s__unclassified	50643
s__unclassified	50646
s__unclassified	50653
s__unclassified	50656
s__unclassified	50661
s__unclassified	50667
s__unclassified	50668
s__unclassified	50678
s__unclassified	50687
s__unclassified	50690
s__unclassified	50691
s__unclassified	50702
s__unclassified	50730
s__unclassified	50735
s__unclassified	50739
s__unclassified	50745
s__unclassified	50748
s__unclassified	50794
s__unclassified	50808
s__unclassified	50813
s__unclassified	50817
s__unclassified	50827
s__unclassified	50831
s__unclassified	50832
s__unclassified	50835
s__unclassified	50837
s__unclassified	50840
s__unclassified	50845
s__unclassified	50862
s__unclassified	50866
s__unclassified	50868
s__unclassified	50869
s__unclassified	50871
s__unclassified	50872
s__unclassified	50885
s__unclassified	50897
s__unclassified	50902
s__unclassified	50910

CU920189.1 gg_id:572427 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
AB486952.1 gg_id:541359 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
AY959093.1 gg_id:131417 Microbes on human vaginal epithelium clone rRNA320 AY959(
FJ675815.1 gg_id:531229 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ678660.1 gg_id:519991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ673588.1 gg_id:526829 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ673153.1 gg_id:529494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
AB198425.1 gg_id:246110 Selenomonas ruminantium str. S2 AB198
EU850607.1 gg_id:334117 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF440 EU850
AB034134.1 gg_id:42912 rumen clone 4C28d-6 AB034
AB218316.1 gg_id:148501 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgB-66 AB218
AY958931.1 gg_id:153751 Microbes on human vaginal epithelium clone rRNA158 AY958
GQ004077.1 gg_id:505586 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu68d0 GQ004
AB486076.1 gg_id:569899 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
AB487430.1 gg_id:540748 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
FJ682840.1 gg_id:520575 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
FJ393127.1 gg_id:362899 Fusing Biology Engineering Improve Power Output Microbial Fuel Cells microbial fuel FJ3931
U81750.2 gg_id:13861 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHB04 U8175
FJ833201.1 gg_id:594131 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q102_39G05 FJ8332
FJ673713.1 gg_id:524216 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
GQ006579.1 gg_id:503085 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85b11c GQ006
FJ386554.1 gg_id:369923 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ673625.1 gg_id:530256 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EF399619.1 gg_id:206942 human fecal clone SJTU_E_01_29 EF3996
EU009839.1 gg_id:254812 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Q48 EU009
EU234118.1 gg_id:252011 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU234
AB198432.1 gg_id:242601 Selenomonas ruminantium str. S109 AB198
DQ295866.1 gg_id:191985 Pelosinus fermentans str. UFO1 DQ295
FJ172883.1 gg_id:352391 Qinghai Yak Ruminal and Fungi China rumen clone RB-2F2 FJ1728
FJ680477.1 gg_id:523055 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ682404.1 gg_id:513552 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
AB486876.1 gg_id:578241 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB486
EU259482.1 gg_id:241086 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC106 EU259
AY981016.1 gg_id:116502 human rectum mucosal biopsy clone V190 AY981(
FJ680012.1 gg_id:515217 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6800
FJ677302.1 gg_id:528220 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
DQ795993.1 gg_id:188086 human fecal clone RL202_aai50a03 DQ795
GU214167.1 gg_id:593991 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
DQ777892.2 gg_id:166356 rat feces clone R-1170 DQ777
AB034191.1 gg_id:38984 Anaerovibrio lipolyticus str. ATCC 33276 AB034
EU748414.1 gg_id:328699 neotropical folivorous flying bird adult hoatzin crop clone hoa5_08h08 EU748

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
1	0	1	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	1	1	1	0	0	0	1	1	1
0	0	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	0	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella

s__unclassified	50917
s__unclassified	50918
s__unclassified	50922
s__unclassified	50933
s__unclassified	50938
s__unclassified	50939
s__unclassified	50940
s__unclassified	50945
s__unclassified	50950
s__unclassified	50953
s__unclassified	50959
s__unclassified	52942
s__unclassified	53942
s__unclassified	49990
s__unclassified	50005
s__unclassified	50016
s__unclassified	50026
s__unclassified	50029
s__unclassified	50032
s__unclassified	50043
s__unclassified	50046
s__unclassified	50069
s__unclassified	50073
s__unclassified	50105
s__unclassified	50161
s__unclassified	50164
s__unclassified	50198
s__unclassified	50203
s__unclassified	50210
s__unclassified	50217
s__unclassified	50223
s__unclassified	50248
s__unclassified	50281
s__unclassified	50303
s__unclassified	50347
s__unclassified	50354
s__unclassified	50366
s__unclassified	50379
s__unclassified	50400
s__unclassified	50407
s__unclassified	50426

AJ229233.1 gg_id:16834 anoxic bulk soil flooded rice microcosm clone BSV90 clone AJ2292
AY244972.1 gg_id:83021 cow rumen clone BS18 AY2449
FJ683141.1 gg_id:528857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
NR_029357.1 gg_id:547456 Propionispira arboris str. 12B4; DSM 2179 NR_02
GQ004964.1 gg_id:504698 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu65d0 GQ004
EU344158.1 gg_id:260291 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ825568.1 gg_id:559706 Microbial during start-up mesophilic biogas plant clone 21_BS5_39 FJ8255
AB198435.1 gg_id:236008 Selenomonas ruminantium str. S150 AB198
AB486785.1 gg_id:541916 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EU461059.1 gg_id:288601 red kangaroo feces clone KO1_aai43d02 EU461
DQ168841.1 gg_id:154690 Fermentative biohydrogen production heated anaerobic sludge clone J25 DQ168
EU468247.1 gg_id:290103 domesticated horse feces clone horsej_h07 EU468
EU463594.1 gg_id:302001 domesticated horse feces clone horsej_aai89d11 EU463
GQ102701.1 gg_id:458599 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ102
EU096495.1 gg_id:253506 Veillonella sp. 18 EU096
GQ073513.1 gg_id:403167 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073
GQ006562.1 gg_id:503102 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85a06c GQ006
AY514996.1 gg_id:99976 Veillonella rodentium str. ATCC 17743 AY514
GQ073646.1 gg_id:458617 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ073
GQ086352.1 gg_id:443529 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ086
GQ074436.1 gg_id:406819 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162 GQ074
GQ010293.1 gg_id:499375 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
GQ114701.1 gg_id:381455 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ114
FJ558085.1 gg_id:528199 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EF434331.1 gg_id:210713 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
GQ091818.1 gg_id:411006 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
EF515580.1 gg_id:218801 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
GQ338722.1 gg_id:573384 and function human intestinal microbiota ileostomy effluent healthy patient clone A GQ338
EU460862.1 gg_id:301827 short-beaked echidna feces clone ECH_aai39e05 EU460
GQ101329.1 gg_id:453095 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw493 GQ101
GQ006752.1 gg_id:502912 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87c06c GQ006
GQ022064.1 gg_id:487605 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
FJ374768.1 gg_id:585419 Veillonella sp. str. S101 FJ3747
GQ109121.1 gg_id:448078 Topographical and Temporal Human Skin Microbiome skin palm clone nbw608f12c1 GQ109
GQ031217.1 gg_id:422979 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ031
GQ055579.1 gg_id:381881 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1117e GQ055
GQ011614.1 gg_id:498054 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw794c0 GQ011
GQ113791.1 gg_id:414090 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
GQ030037.1 gg_id:437122 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866c0 GQ030
AY995768.1 gg_id:119118 Veillonella atypica str. ATCC 17744 AY995
GQ030108.1 gg_id:459734 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw867c0 GQ030

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	1	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella

s__unclassified	50433
s__unclassified	50448
s__unclassified	50455
s__unclassified	50461
s__unclassified	50464
s__unclassified	50466
s__unclassified	50471
s__unclassified	50492
s__unclassified	50502
s__unclassified	50508
s__unclassified	50517
s__unclassified	50531
s__unclassified	50538
s__unclassified	50565
s__unclassified	50569
s__unclassified	50588
s__unclassified	50611
s__unclassified	50613
s__unclassified	50639
s__unclassified	50651
s__unclassified	50663
s__unclassified	50697
s__unclassified	50701
s__unclassified	50707
s__unclassified	50721
s__unclassified	50725
s__unclassified	50750
s__unclassified	50780
s__unclassified	50793
s__unclassified	50802
s__unclassified	50811
s__unclassified	50855
s__unclassified	50883
s__unclassified	50901
s__unclassified	50915
s__unclassified	50916
s__unclassified	50920
s__unclassified	50925
s__unclassified	50956
s__Veillonella dispar	49996
s__Veillonella dispar	50017

GQ048471.1 gg_id:389670 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu51 GQ048
AY244769.1 gg_id:85594 Veillonella montpellierensis str. 2001-112662 AY2447
GQ005879.1 gg_id:503784 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu97g GQ005
GQ006870.1 gg_id:502794 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88g07c GQ006
GQ113854.1 gg_id:375581 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
AM697482.1 gg_id:219084 sequencing libraries indoor dust clone BF0001D097 AM697
GQ016366.1 gg_id:493301 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
DQ346420.2 gg_id:145149 individual-specific oral microflora during initial colonization enamel human mouth; ir DQ346
GQ073330.1 gg_id:427426 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207g06c1 GQ073
AY995769.1 gg_id:127371 Veillonella parvula str. ATCC 17745 AY9957
GQ022740.1 gg_id:486930 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
AF186072.1 gg_id:13824 Veillonella criceti str. ATCC17747 AF186
GQ113989.1 gg_id:468332 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ088982.1 gg_id:465651 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
GQ114846.1 gg_id:374291 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ075584.1 gg_id:437044 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ073254.1 gg_id:420928 Topographical and Temporal Human Skin Microbiome skin palm clone nbw206h05c GQ073
X84007.1 gg_id:13822 Veillonella atypica str. DSM 20739 X84007
GQ019382.1 gg_id:490287 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189d GQ019
GQ030048.1 gg_id:430534 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw866d0 GQ030
EU774885.1 gg_id:329844 Short-beaked Echidna feces clone ECH_aai40g10 EU7748
GQ101667.1 gg_id:404939 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497g11c GQ101
GQ071993.1 gg_id:459656 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190h04 GQ071
GQ005607.1 gg_id:504056 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ005
EU774889.1 gg_id:324786 Short-beaked Echidna feces clone ECH_aai38d06 EU7748
GQ006690.1 gg_id:502974 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86e02c GQ006
GQ114743.1 gg_id:381926 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ113658.1 gg_id:405229 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
EF185167.1 gg_id:192322 Veillonella dentocariosa str. RBV106 EF1851
AY355140.1 gg_id:95347 Veillonella caviae str. DSM 20738 AY3551
GQ006838.1 gg_id:502826 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu88d03c GQ006
GQ114136.1 gg_id:439586 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ101225.1 gg_id:420790 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ048453.1 gg_id:429982 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu51 GQ048
GQ031800.1 gg_id:464887 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
GQ000861.1 gg_id:469425 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ101676.1 gg_id:458976 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497h10 GQ101
GQ019421.1 gg_id:490247 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu189g GQ019
FJ558100.1 gg_id:517047 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
GQ027279.1 gg_id:416279 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ073269.1 gg_id:467872 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207a10c1 GQ073

0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	1	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	0	1	1	0	0	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae

g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella

s__Veillonella dispar	50038
s__Veillonella dispar	50052
s__Veillonella dispar	50062
s__Veillonella dispar	50076
s__Veillonella dispar	50119
s__Veillonella dispar	50134
s__Veillonella dispar	50159
s__Veillonella dispar	50187
s__Veillonella dispar	50265
s__Veillonella dispar	50283
s__Veillonella dispar	50290
s__Veillonella dispar	50294
s__Veillonella dispar	50308
s__Veillonella dispar	50309
s__Veillonella dispar	50337
s__Veillonella dispar	50341
s__Veillonella dispar	50346
s__Veillonella dispar	50375
s__Veillonella dispar	50498
s__Veillonella dispar	50499
s__Veillonella dispar	50503
s__Veillonella dispar	50539
s__Veillonella dispar	50557
s__Veillonella dispar	50574
s__Veillonella dispar	50607
s__Veillonella dispar	50641
s__Veillonella dispar	50676
s__Veillonella dispar	50740
s__Veillonella dispar	50757
s__Veillonella dispar	50761
s__Veillonella dispar	50768
s__Veillonella dispar	50773
s__Veillonella dispar	50790
s__Veillonella dispar	50863
s__Veillonella dispar	50876
s__Veillonella dispar	50946
s__Veillonella montpellierensis	50654
s__Veillonella parvula	49992
s__Veillonella parvula	50131
s__Veillonella parvula	50139
s__Veillonella parvula	50185

GQ081299.1 gg_id:452838 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ081
GQ027242.1 gg_id:430526 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
GQ054340.1 gg_id:386212 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
GQ113978.1 gg_id:387664 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ026752.1 gg_id:424674 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ026
GQ012701.1 gg_id:496965 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ012
GQ012679.1 gg_id:496988 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ012
GQ073407.1 gg_id:468068 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208f10c1 GQ073
GQ032582.1 gg_id:375502 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ073344.1 gg_id:393528 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h08c! GQ073
GQ076880.1 gg_id:400365 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ032461.1 gg_id:463442 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ073357.1 gg_id:459514 Topographical and Temporal Human Skin Microbiome skin palm clone nbw208b01c! GQ073
GQ057614.1 gg_id:372040 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
GQ073343.1 gg_id:395352 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207h07c! GQ073
GQ114938.1 gg_id:377847 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685c03 GQ114
GQ054349.1 gg_id:409913 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
GQ073109.1 gg_id:378037 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205b12c! GQ073
GQ032236.1 gg_id:433236 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ073722.1 gg_id:412083 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ073
GQ012772.1 gg_id:496894 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ012
GQ076847.1 gg_id:408841 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1154 GQ076
GQ033104.1 gg_id:434692 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ033
GQ027285.1 gg_id:428376 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
GQ032864.1 gg_id:466022 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ032144.1 gg_id:465685 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ032547.1 gg_id:383330 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ032561.1 gg_id:379283 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ032526.1 gg_id:443459 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ027702.1 gg_id:462502 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ027
GQ009508.1 gg_id:500157 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
GQ054356.1 gg_id:383423 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1108 GQ054
GQ016840.1 gg_id:492829 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw826b0 GQ016
GQ076950.1 gg_id:377262 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
AF439639.1 gg_id:25275 Veillonella dispar str. ATCC 17748 AF4396
X84006.1 gg_id:13820 Veillonella dispar str. DSM 20735 X84006
AF473836.1 gg_id:26894 Veillonella montpellierensis str. ADV 281.99 AF4738
GQ006633.1 gg_id:503031 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85g12c GQ006
GQ087817.1 gg_id:375551 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw359b0 GQ087
GQ073137.1 gg_id:388944 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205e07c1 GQ073
GQ086284.1 gg_id:422736 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Clostridiales	f__Veillonellaceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Desulfitobacterales	f__Desulfitobacteraceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae

g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Veillonella
g__Desulfitobacter
g__Desulfitobacter
g__Desulfitobacter
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Halanaerobium
g__Halothermothrix
g__unclassified
g__unclassified

s__Veillonella parvula	50234
s__Veillonella parvula	50253
s__Veillonella parvula	50289
s__Veillonella parvula	50312
s__Veillonella parvula	50313
s__Veillonella parvula	50355
s__Veillonella parvula	50385
s__Veillonella parvula	50434
s__Veillonella parvula	50439
s__Veillonella parvula	50596
s__Veillonella parvula	50610
s__Veillonella parvula	50614
s__Veillonella parvula	50660
s__Veillonella parvula	50720
s__Veillonella parvula	50726
s__Veillonella parvula	50764
s__Veillonella parvula	50772
s__Veillonella parvula	50788
s__Veillonella parvula	50852
s__Veillonella parvula	50921
s__Veillonella parvula	50947
s__Veillonella ratti	50121
s__Veillonella ratti	50175
s__Veillonella ratti	50682
s__unclassified	48585
s__unclassified	48751
s__unclassified	49081
s__unclassified	48326
s__unclassified	48487
s__unclassified	48786
s__unclassified	48997
s__unclassified	49043
s__unclassified	49194
s__unclassified	49257
s__unclassified	49795
s__unclassified	49825
s__unclassified	49926
s__unclassified	52643
s__Halothermothrix orenii	52689
s__unclassified	51896
s__unclassified	51927

EU766448.1 gg_id:328607 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
GQ047868.1 gg_id:451862 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ047
AM179906.1 gg_id:148234 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G3-1 AM179
GQ006791.1 gg_id:502872 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87g04c GQ006
AY947495.2 gg_id:114821 subgingival plaque clone OH1A AY947
AF439641.1 gg_id:35224 Veillonella atypica str. ATCC 17744 AF439
GQ027353.1 gg_id:421354 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
EF510493.1 gg_id:217660 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5104
GQ032280.1 gg_id:370470 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
GQ074330.1 gg_id:430796 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161f GQ074
GQ084875.1 gg_id:431117 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
GQ086120.1 gg_id:463770 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ086
GQ114042.1 gg_id:373803 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ114
GQ086092.1 gg_id:404253 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ086
GQ114025.1 gg_id:385911 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clo GQ114
AF439640.1 gg_id:30716 Veillonella parvula str. CIP 60.1 AF439
EF510428.1 gg_id:218682 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5104
GQ027272.1 gg_id:457673 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ027
GQ006604.1 gg_id:503059 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85e02c GQ006
GQ072552.1 gg_id:374904 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
FJ557333.1 gg_id:518743 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5573
FJ369852.1 gg_id:361643 feces adult twins and mothers; TS55 clone TS55_a01e08 FJ3698
FJ369825.1 gg_id:357386 feces adult twins and mothers; TS55 clone TS55_a01c04 FJ3698
FJ370053.1 gg_id:358239 feces adult twins and mothers; TS55 clone TS55_a03h07 FJ3700
AB478008.1 gg_id:576201 Microbial aquifer subsurface accretionary prism Japan geothermal groundwater clo AB478
AY538171.1 gg_id:98963 Desulfitobacter alkalitolerans str. Sk.kt5 AY538
FJ638550.1 gg_id:570010 Temperature dependent succession sulfate reducing muddy southwestern Taiwan h FJ6385
DQ230961.1 gg_id:142730 subsurface water clone DR938CH110701SACH36 DQ230
EU639075.1 gg_id:306415 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic EU639
DQ413080.1 gg_id:153409 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
GQ502520.1 gg_id:542395 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
DQ988278.1 gg_id:192181 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with DQ988
EU638492.1 gg_id:319720 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic EU638
AB118592.1 gg_id:93438 Endosymbiont 'TC1' Trimyema compressum clone TC1 AB118
FJ712502.1 gg_id:526485 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) FJ7125
AB439298.1 gg_id:541578 and microbial oils produced Asia petroleum crude oil (Daqing) imported China clone AB439
EU981271.1 gg_id:353812 sulfate reducing living bench scale aquifer column water clone E9_SW EU981
U32594.1 gg_id:14315 Halanaerobium acetethylicum str. EIGI; DSM 3532 U3259
L22016.1 gg_id:14309 Halothermothrix orenii L22016
X89072.1 gg_id:14311 Halocella cellulolsilytica str. DSM 7362 X89072
L22890.1 gg_id:14313 Halanaerobium salsuginis str. VS-752 L22890

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halanaerobiaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__Halanaerobiales	f__Halobacteroidaceae
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__MBA08	f__unclassified
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Anaerobrancaceae
o__Natranaerobiales	f__Contubernalisaceae
o__Natranaerobiales	f__Contubernalisaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Acetohalobium
g__Acetohalobium
g__Halanaerobacter
g__Halanaerobacter
g__Halanaerobacter
g__Natroniella
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__A55_D21
g__A55_D21
g__Anaerobranca
g__Dethiobacter
g__Dethiobacter
g__Dethiobacter
g__KF-Gitt2-16
g__KF-Gitt2-16
g__Candidatus Contubernalis
g__Candidatus Contubernalis

s__unclassified	51985
s__unclassified	52092
s__unclassified	52100
s__unclassified	52324
s__unclassified	52333
s__unclassified	52347
s__unclassified	52462
s__unclassified	52771
s__unclassified	52794
s__unclassified	52909
s__Acetohalobium arabaticum	52173
s__unclassified	52096
s__Halanaerobacter lacunarum	52766
s__unclassified	52720
s__unclassified	52930
s__unclassified	52006
s__unclassified	51823
s__unclassified	52385
s__unclassified	52740
s__unclassified	58009
s__unclassified	58152
s__unclassified	58153
s__unclassified	58275
s__unclassified	58306
s__unclassified	58322
s__unclassified	58422
s__unclassified	58679
s__unclassified	58715
s__unclassified	58865
s__unclassified	58107
s__unclassified	58541
s__unclassified	48910
s__unclassified	49384
s__unclassified	49154
s__unclassified	48591
s__unclassified	48716
s__unclassified	49474
s__unclassified	48240
s__unclassified	49859
s__unclassified	48519
s__unclassified	48602

EF585982.1 gg_id:247996 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_A EF5859
EF558989.1 gg_id:244525 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5589
EU869420.1 gg_id:316746 Microbial hypersaline Sidi Ameur water Himalatt Salt Lake Algerian Sahara clone ARD EU8694
EU245629.1 gg_id:249184 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-H0 EU2456
EF559026.1 gg_id:238840 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
EF106374.1 gg_id:201587 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2 EF1063
EU245738.1 gg_id:255254 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M5-F07 EU2457
EF106367.1 gg_id:202585 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2 EF1063
FJ202891.1 gg_id:320426 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
AM947558.1 gg_id:264238 Minor changes detected microbial structure and after three week thermophilic dige AM947
X89077.1 gg_id:14308 Acetohalobium arabaticum X89077
NR_028804.1 gg_id:581342 Selenihalanaerobacter shriftii str. DSSE-1; ATCC BAA-73 NR_028
EF459724.1 gg_id:219578 Prokaryotic Hypersaline Inland Turkey Tuz Lake (hypersaline) clone 4-62B EF4597
EU327343.1 gg_id:288770 Halobacteroides sp. str. 6SANG EU3273
X89074.1 gg_id:14301 Halobacteroides halobius str. DSM 5150 X89074
GU452712.1 gg_id:525021 Natroniella sp. str. AHT18 GU452
X89073.1 gg_id:14302 Orenia marismortui str. DSM 5156 X89073
Y18485.1 gg_id:69790 Orenia salinaria str. SG3902 Y18485
EU245188.1 gg_id:242318 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-G09 EU2451
EF559012.1 gg_id:250397 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
AM947554.1 gg_id:270282 Minor changes detected microbial structure and after three week thermophilic dige AM947
EF586067.1 gg_id:246373 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EF558957.1 gg_id:238729 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5589
EF586053.1 gg_id:257232 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF5860
EU878323.1 gg_id:567033 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
EU639242.1 gg_id:313846 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6392
FN436027.1 gg_id:539789 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN4360
AM947555.1 gg_id:266221 Minor changes detected microbial structure and after three week thermophilic dige AM947
EF559059.1 gg_id:243394 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
EF586029.1 gg_id:252533 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_ EF5860
EF559123.1 gg_id:226234 mesophilic anaerobic digester clone C35_D63_H_B_F12 EF5591
EF559004.1 gg_id:248896 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
EF586046.1 gg_id:241887 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF5860
GU455299.1 gg_id:522555 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
EU358734.1 gg_id:312486 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
EF422412.2 gg_id:224884 Dethiobacter alkaliphilus str. AHT1 EF4224
AF507887.1 gg_id:62675 Mono Lake at depth 35m station 6 July 2000 clone ML635J-4 AF5078
AJ295640.1 gg_id:31598 uranium mill tailing clone KF-Gitt2-16 AJ2956
AJ582199.1 gg_id:93440 soil near uranium mill tailings clone Gitt-GS-113 AJ5821
DQ432150.1 gg_id:156668 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Fazda sediment clone DQ432
AF507888.1 gg_id:55772 Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C AF5078

0	0	1	0	0	0	0	0	0	1	1	0	0
0	1	1	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Natranaerobiales	f__Contubernalisaceae
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__ML1228J-1
o__Natranaerobiales	f__Natranaerobiaceae
o__Natranaerobiales	f__Natranaerobiaceae
o__Natranaerobiales	f__Natranaerobiaceae
o__Natranaerobiales	f__Natranaerobiaceae
o__Natranaerobiales	f__YAB3B13
o__Natranaerobiales	f__YAB3B13
o__Natranaerobiales	f__YAB3B13
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__OPB54	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified

g__Candidatus Contubernalis
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Natranaerobius
g__Natranaerobius
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	48978
s__unclassified	48259
s__unclassified	48347
s__unclassified	48694
s__unclassified	48899
s__unclassified	49044
s__unclassified	49306
s__unclassified	49496
s__unclassified	49818
s__unclassified	49842
s__unclassified	49911
s__unclassified	49971
s__Natranaerobius thermophilus	49841
s__unclassified	48980
s__unclassified	48467
s__unclassified	49674
s__unclassified	48331
s__unclassified	48832
s__unclassified	48927
s__unclassified	57869
s__unclassified	57951
s__unclassified	58111
s__unclassified	58131
s__unclassified	58141
s__unclassified	58187
s__unclassified	58228
s__unclassified	58383
s__unclassified	58492
s__unclassified	58501
s__unclassified	58669
s__unclassified	58734
s__unclassified	58842
s__unclassified	57855
s__unclassified	57892
s__unclassified	58318
s__unclassified	57814
s__unclassified	57836
s__unclassified	57896
s__unclassified	57921
s__unclassified	57932
s__unclassified	57946

AJ853529.1 gg_id:110524 landfill leachate clone GZKB35 AJ8535
GQ848216.1 gg_id:544950 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
EU878335.1 gg_id:554328 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
DQ206412.1 gg_id:139538 microbial mediates arsenate reduction soda lake water clone ML-AsS-10 DQ206
DQ837275.1 gg_id:244602 Archaeal and pristine National Park Spain Donana coastal aquifer clone 56S_1B_61 DQ837
FJ203016.1 gg_id:351673 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
GQ848219.1 gg_id:541684 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
EU812988.1 gg_id:341763 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-N EU8129
EU592468.1 gg_id:573525 Seasonal changes Salton Sea hypersaline sediment clone SSS47A EU5924
GU083673.1 gg_id:542800 Microorganism Xiarinur soda lake sediment clone x269 GU083
GQ848204.1 gg_id:588856 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
AF454298.1 gg_id:63836 Bacillus sp. clone ML1228J-1 AF4542
NZ_ABKR01000005.1 gg_id:261070 Natranaerobius thermophilus str. JW/NM-WN-LF NZ_AB
AJ271451.1 gg_id:73970 Natronoanaerobium halophilum G-M14CH-4 AJ2714
AJ271450.1 gg_id:23520 Natronoanaerobium salstagnum O-M12SP-2 AJ2714
AJ271452.1 gg_id:72206 Natronoanaerobium aggerbacterium G-M16NWC-4 AJ2714
DQ354747.1 gg_id:155876 subsurface water clone MS149BH1062003_30 DQ354
AB539949.1 gg_id:571087 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB5399
DQ088759.1 gg_id:132063 0.7 1.4 kmbls sctn cntnntl crst cln BE325FW032701CTS_hl1-69 DQ088
EU250948.1 gg_id:358480 degraded cellulose lindane NSC-7 NFC-7 grown 50 degrees Celsius compost compose EU2509
AY330127.1 gg_id:95976 methanogenic landfill leachate bioreactor clone AC039 AY3301
DQ125604.1 gg_id:134479 uranium contaminated soil clone AKAU3609 DQ125
GQ402678.1 gg_id:512997 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ125579.1 gg_id:132342 uranium contaminated soil clone AKAU3574 DQ125
DQ125547.1 gg_id:129508 uranium contaminated soil clone AKAU3523 DQ125
DQ887916.1 gg_id:168335 thermophilic anaerobic solid waste bioreactor clone GHB3B06 DQ887
DQ125708.1 gg_id:133296 uranium contaminated soil clone AKAU3802 DQ125
FJ381977.1 gg_id:583118 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT FJ3819
EF585978.1 gg_id:246509 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_A EF5859
AY330129.1 gg_id:95835 methanogenic landfill leachate bioreactor clone AC007 AY3301
DQ887936.1 gg_id:169354 thermophilic anaerobic solid waste bioreactor clone GMB4H09 DQ887
AB274500.1 gg_id:215152 packed-bed reactor clone CFB-11 AB2745
DQ125736.1 gg_id:134788 uranium contaminated soil clone AKAU3845 DQ125
EU887985.1 gg_id:339192 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
AM947551.1 gg_id:260695 Minor changes detected microbial structure and after three week thermophilic dige AM947
FJ985789.1 gg_id:451463 depths Colombia South America soil 0-10 m depth former landfill clone -1 FJ9857
FJ985786.1 gg_id:402134 depths Colombia South America soil 5 m depth former landfill clone C5-11 FJ9857
CU919747.1 gg_id:567508 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU919791.1 gg_id:534056 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AY684074.1 gg_id:133964 methanogenic enrichment 'MRE50' clone MRE50b10 AY6840
CU919182.1 gg_id:566892 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	1	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	0	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0

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

o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__SHA-98	f__unclassified
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfC
g__sfD
g__sfD
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Caldicellulosiruptor

s__unclassified	58048
s__unclassified	58052
s__unclassified	58077
s__unclassified	58105
s__unclassified	58108
s__unclassified	58236
s__unclassified	58239
s__unclassified	58265
s__unclassified	58292
s__unclassified	58372
s__unclassified	58432
s__unclassified	58483
s__unclassified	58487
s__unclassified	58582
s__unclassified	58624
s__unclassified	58642
s__unclassified	58657
s__unclassified	58724
s__unclassified	58729
s__unclassified	58746
s__unclassified	58771
s__unclassified	58843
s__unclassified	49004
s__unclassified	49253
s__unclassified	49735
s__unclassified	49907
s__unclassified	49979
s__unclassified	58430
s__unclassified	58708
s__unclassified	58793
s__unclassified	57872
s__unclassified	58519
s__Anaerocellum thermophilum	49360
s__Caldicellulosiruptor saccharolyticus	48938
s__unclassified	48495
s__unclassified	48540
s__unclassified	48557
s__unclassified	48567
s__unclassified	48781
s__unclassified	48854
s__unclassified	49143

CU922852.1 gg_id:538720 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
AY684093.1 gg_id:131483 methanogenic enrichment 'MRE50' clone MRE50b17 AY684
CU927811.1 gg_id:560195 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
AY684100.1 gg_id:131930 methanogenic enrichment 'MRE50' clone MRE50b22 AY684
AY684090.1 gg_id:130626 methanogenic enrichment 'MRE50' clone MRE50b08 AY684
CT573824.1 gg_id:150758 Evry municipal wastewater treatment plant clone 013H11_B_SD_P15 CT573
AY526502.1 gg_id:136583 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone D3 AY526
CU919826.1 gg_id:551199 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU919394.1 gg_id:554083 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
EU639084.1 gg_id:320495 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU638947.1 gg_id:342798 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EF559227.1 gg_id:222005 mesophilic anaerobic digester clone A35_D28_H_B_B01 EF559
CU919273.1 gg_id:572645 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918907.1 gg_id:539546 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AB434894.1 gg_id:277048 Effect temperature on microbial glucose-degrading methanogenic consortium under AB434
EU878344.1 gg_id:593716 Investigation factors influencing production large-scale municipal biogas plant therm EU878
EF198048.1 gg_id:185617 Microbial structures mesophilic and methanogenic consortia anaerobic thermophilic EF198
EU639113.1 gg_id:306099 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
AB374111.1 gg_id:246025 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
CR933199.1 gg_id:110387 Evry municipal wastewater treatment plant clone 008A06_B_SD_P15 CR933
CU919263.1 gg_id:549429 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918937.1 gg_id:549084 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU921330.1 gg_id:570394 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
DQ899892.1 gg_id:257323 structure receiving long-term augmentations chromium contaminated wastes landfi DQ899
DQ018807.1 gg_id:132376 anaerobic swine lagoon clone C-131 DQ018
AB234270.1 gg_id:145732 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
DQ018815.1 gg_id:132872 Unq Mcrbl Anrbc Swn Lgns anrbc swn lgn cln C-146 DQ018
EF586045.1 gg_id:245235 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D15_ EF586
EF586061.1 gg_id:243276 Methanol-assimilating anaerobic solid waste digester fed methanol clone M55_D21_ EF586
EF559043.1 gg_id:238463 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF559
AB234000.1 gg_id:152360 anaerobic reactor clone B-7 AB234
FN563383.1 gg_id:578169 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
NC_012034.1 gg_id:471220 Anaerocellum thermophilum str. DSM 6725 NC_01
CP000679.1 gg_id:224527 Caldicellulosiruptor saccharolyticus str. DSM 8903 CP000
EF100909.1 gg_id:193269 Caldicellulosiruptor kronotskiensis str. 2002 EF100
U80596.1 gg_id:16088 Caldicellulosiruptor owensensis str. OL U8059
L35151.1 gg_id:16089 Caldicellulosiruptor sp. str. Rt8B.4 L35151
EF100907.1 gg_id:181163 Caldicellulosiruptor kristjanssonii str. 117 EF100
AJ004811.1 gg_id:16095 Caldicellulosiruptor kristjanssonii str. I77R1B AJ0048
L09183.1 gg_id:16093 Thermoanaerobacter cellulolyticus str. NA 10B L09183
FJ189575.1 gg_id:351375 digester anaerobic sludge clone EUB_54 FJ1895

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	1	0
0	1	0	1	0	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	1
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	1	1	1	1	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Caldicellulosiruptoraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae

g__Caldicellulosiruptor
g__Caldicellulosiruptor
g__Ammonifex
g__Ammonifex
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Caldanaerobacter
g__Carboxydothermus
g__Carboxydothermus
g__Carboxydothermus
g__Carboxydothermus
g__Moorella
g__Moorella
g__Moorella
g__Moorella
g__Moorella
g__Tepidanaerobacter
g__Thermacetogenium
g__Thermacetogenium
g__Thermacetogenium
g__Thermacetogenium
g__Thermacetogenium
g__Thermacetogenium
g__Thermacetogenium
g__Thermacetogenium
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter

s__unclassified	49701
s__unclassified	49986
s__unclassified	54968
s__unclassified	56145
s__Caldanaerobacter subterraneus	55285
s__Caldanaerobacter subterraneus	55882
s__unclassified	55124
s__unclassified	55376
s__unclassified	55641
s__unclassified	56021
s__unclassified	56022
s__unclassified	56043
s__unclassified	56129
s__unclassified	56298
s__Carboxydothermus hydrogenoformans	48627
s__unclassified	48277
s__unclassified	48890
s__unclassified	48953
s__unclassified	48801
s__unclassified	48992
s__unclassified	49261
s__unclassified	49627
s__unclassified	49889
s__unclassified	55886
s__unclassified	55104
s__unclassified	55215
s__unclassified	56029
s__unclassified	56100
s__unclassified	56257
s__unclassified	56275
s__unclassified	56296
s__unclassified	56338
s__Thermoanaerobacter ethanolicus	54928
s__Thermoanaerobacter ethanolicus	55923
s__Thermoanaerobacter ethanolicus	56291
s__Thermoanaerobacter mathranii	55699
s__Thermoanaerobacter sp. X514	56089
s__Thermoanaerobacter uzonensis	55083
s__unclassified	54987
s__unclassified	55012
s__unclassified	55267

EF100908.1 gg_id:185074 Caldicellulosiruptor hydrothermalis str. 108 EF1009
DQ152922.1 gg_id:139369 Caldicellulosiruptor sp. str. YI5 DQ152
CP001785.1 gg_id:521670 Ammonifex degensii str. KC4 CP0017
EF554597.1 gg_id:233108 Fervidomicrobium thiophilum str. SR EF5545
NC_003869.1 gg_id:471376 Thermoanaerobacter tengcongensis MB4 str. MB4T NC_00
AF174484.1 gg_id:39044 Carboxydibrachium pacificum str. JM AF1744
EU109461.1 gg_id:237130 Thermoanaerobacter subterraneus str. S2302 EU1094
AF212925.1 gg_id:26976 Thermoanaerobacter yonseiensis str. KB1 AF2129
EF554599.1 gg_id:234626 Thermoanaerobacter subterraneus str. 2707 EF5545
EF195126.1 gg_id:175440 Caldanaerobacter hydrothermalis str. K67 EF1951
FJ189534.1 gg_id:349650 digester anaerobic sludge clone EUB_13 FJ1895
EF554598.1 gg_id:232884 Thermoanaerobacter subterraneus str. SP47 EF5545
AY278483.1 gg_id:87364 Thermoanaerobacter keratinophilus str. 2KXI AY2784
DQ115806.1 gg_id:134076 Thermoanaerobacter tengcongensis str. 185y2 DQ115
CP000141.1 gg_id:140847 Carboxydothermus hydrogenoformans str. Z-2901 CP0001
U76363.1 gg_id:13728 Thermoterrabacterium ferrireducens U76363
U76364.1 gg_id:13730 Thermoterrabacterium ferrireducens U76364
EF542810.1 gg_id:218099 Carboxydothermus siderophilus str. 1315 EF5428
AF487538.1 gg_id:82633 Moorella mulderi str. TMS AF4875
EU638616.1 gg_id:334086 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6386
AY684084.1 gg_id:153109 first genome data rice I methanogens combination cultivation and techniques metha AY6840
FJ189582.1 gg_id:324196 digester anaerobic sludge clone EUB_61 FJ1895
EU638454.1 gg_id:309145 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6384
AB222053.1 gg_id:137796 Clostridium sp. str. EBR-02E-0600 AB2220
AB020336.1 gg_id:13717 Thermacetogenium phaeum str. PB AB0203
EF559057.1 gg_id:243312 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
DQ647145.1 gg_id:257640 Microbial structure -temperature oil-field produced water Troll formations North Se DQ647
EF558950.1 gg_id:246613 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5589
EU386162.1 gg_id:265020 Thermacetogenium sp. str. Sp3 EU3861
AB332113.1 gg_id:246435 Continuous cultivation and structure thermophilc propionate-degrading microbial co AB3321
DQ097678.2 gg_id:134576 oil field clone B11_otu13 DQ097
DQ887938.1 gg_id:165206 thermophilic anaerobic solid waste bioreactor clone GMB4F03 DQ887
AF542519.1 gg_id:59095 Thermoanaerobacter ethanolicus str. X521 AF5425
AF542521.1 gg_id:59098 Thermoanaerobacter ethanolicus str. X524 AF5425
DQ128182.1 gg_id:138446 Thermoanaerobacter ethanolicus 3 DQ128
AY701757.1 gg_id:106184 Thermoanaerobacter sp. str. AIP 504.99 AY7017
NC_010321.1 gg_id:259585 Thermoanaerobacter pseudethanolicus 33223 str. ATCC 33223; 39E NC_010
EU262599.1 gg_id:240738 Thermoanaerobacter inferii str. AK15 EU2625
L09167.1 gg_id:13780 Thermoanaerobacter thermocopriae str. JT-3T L09167
DQ128177.1 gg_id:137851 Thermoanaerobacter ethanolicus 6 DQ128
DQ128183.1 gg_id:202453 Thermoanaerobacter ethanolicus 2 DQ128

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	0	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

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

o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacteraceae
o__Thermoanaerobacterales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Thermoanaerobacterales	f__Thermoanaerobacterales Family III. Incertae Sedis
o__Thermoanaerobacterales	f__Thermodesulfobiaceae
o__Thermoanaerobacterales	f__Thermodesulfobiaceae
o__Thermoanaerobacterales	f__Thermodesulfobiaceae
o__Thermoanaerobacterales	f__Thermodesulfobiaceae
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified
o__Thermoanaerobacterales	f__unclassified

g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__Thermoanaerobacter
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Thermovenabulum
g__Thermovenabulum
g__Coprothermobacter
g__Coprothermobacter
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfC
g__sfD
g__sfE

s__unclassified	55527
s__unclassified	55753
s__unclassified	55874
s__unclassified	55905
s__unclassified	56127
s__unclassified	56213
s__unclassified	56277
s__unclassified	48351
s__unclassified	48711
s__unclassified	49690
s__unclassified	55098
s__unclassified	55315
s__unclassified	55444
s__unclassified	55488
s__unclassified	55535
s__unclassified	55687
s__unclassified	55730
s__unclassified	55797
s__unclassified	55976
s__unclassified	56061
s__unclassified	56088
s__unclassified	56212
s__unclassified	56249
s__unclassified	56269
s__unclassified	55035
s__unclassified	55358
s__unclassified	55123
s__unclassified	55936
s__unclassified	55659
s__unclassified	55852
s__unclassified	48743
s__unclassified	49458
s__unclassified	49578
s__unclassified	49297
s__unclassified	49655
s__unclassified	49668
s__unclassified	48878
s__unclassified	49086
s__unclassified	49681
s__unclassified	48502
s__unclassified	49577

DQ128178.1 gg_id:137799 Thermoanaerobacter ethanolicus 1 DQ128
NR_029301.1 gg_id:574119 Thermoanaerobacter wiegelii str. Rt8.B1; DSM 10319 NR_02
DQ128181.1 gg_id:137863 Thermoanaerobacter ethanolicus 4 DQ128
L09160.1 gg_id:13765 Thermoanaerobacter kivui L09160
DQ681066.1 gg_id:163311 Thermoanaerobacter wiegelii str. B5 DQ681
AF234164.1 gg_id:29733 Thermoanaerobacter sulfurigignens str. JW/SL826T AF234
L09164.1 gg_id:13789 Thermoanaerobacter ethanolicus ATCC 33223 str. 39E L09164
EU731003.1 gg_id:338174 single-species ecosystem deep within Earth fracture water borehole MP104 level 10 EU731
FJ712408.1 gg_id:523660 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
EU730994.1 gg_id:353154 single-species ecosystem deep within Earth fracture water borehole MP104 level 10 EU730
EU419136.1 gg_id:267107 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
FJ748761.1 gg_id:545194 Thermoanaerobacter sp. str. RH0804 FJ7487
AB062280.1 gg_id:20457 Thermanaeromonas toyohensis str. ToBE AB062
DQ887945.1 gg_id:168959 thermophilic anaerobic solid waste bioreactor clone GMB4H08 DQ887
AY216596.1 gg_id:85134 Thermoanaerobacter subterraneus str. OCA1 AY216
AB374119.1 gg_id:250276 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
EU638335.1 gg_id:348663 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
FJ638536.1 gg_id:572985 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AB374120.1 gg_id:243918 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
AB434897.1 gg_id:271632 Effect temperature on microbial glucose-degrading methanogenic consortium under AB434
AE013109.1 gg_id:66678 Thermoanaerobacter tengcongensis str. MB4 AE013
AB374132.1 gg_id:243488 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
AB374117.1 gg_id:238691 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
AB374134.1 gg_id:256314 Effect temperature on microbial glucose-degrading methanogenic consortium under AB374
DQ097675.2 gg_id:134191 oil field clone B5_otu10 DQ097
AY703479.1 gg_id:138789 Thermosediminibacter litoriperuensis str. JW/YJL-1230-2 AY703
EU638920.1 gg_id:316096 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU639339.1 gg_id:323523 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EF174273.1 gg_id:190840 direct activated sludge compost maturation stage clone H42-814 EF1742
CU920710.1 gg_id:539239 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
DQ079649.1 gg_id:137457 deep terrestrial subsurface fluid-filled fracture clone EV818FW062101BH4MD9 DQ079
AB260059.1 gg_id:179484 Microbial black exposed hot ridge flank crustal fluids Black rust formation on boreho AB260
AB300079.1 gg_id:220063 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A AB300
AM777947.1 gg_id:237589 nonsaline . Influence pore-size filters determination structure alkaline groundwater AM777
DQ088764.1 gg_id:133580 subsurface clone BE325FW032701CTS_hole1-27 DQ088
DQ088772.1 gg_id:131486 subsurface clone BE325FW032701CTS_hole1-1 DQ088
AB426224.1 gg_id:275227 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
EF632928.1 gg_id:246403 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
FJ203601.1 gg_id:339359 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
AB539950.1 gg_id:517375 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
DQ256302.1 gg_id:142791 subsurface water clone EV818BHEB6102702SAFF42 DQ256

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Clostridia
k__Bacteria	k__Bacteria	p__Firmicutes	c__Thermolithobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria

o__Thermoanaerobacterales	f__unclassified
o__TIBE07	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__Thermolithobacterales	f__Thermolithobacteraceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae

g__sfF
g__sfA
g__sfA
g__sfA
g__Thermolithobacter
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Cetobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium

s__unclassified	52477
s__unclassified	49242
s__unclassified	58815
s__unclassified	58817
s__Thermolithobacter ferrireducens	48413
s__Cetobacterium somerae	71897
s__Cetobacterium somerae	72134
s__Cetobacterium somerae	72290
s__Cetobacterium somerae	72371
s__Cetobacterium somerae	72759
s__Cetobacterium somerae	72796
s__Cetobacterium somerae	72881
s__Cetobacterium somerae	72953
s__Cetobacterium somerae	73107
s__unclassified	72010
s__unclassified	72017
s__unclassified	72161
s__unclassified	72337
s__unclassified	72383
s__unclassified	72422
s__unclassified	72433
s__unclassified	72499
s__unclassified	72551
s__unclassified	72604
s__unclassified	72661
s__unclassified	72684
s__unclassified	72697
s__unclassified	72763
s__unclassified	72983
s__unclassified	72996
s__unclassified	73004
s__Fusobacterium canifelinum	71860
s__Fusobacterium equinum	73103
s__Fusobacterium necrophorum	72284
s__Fusobacterium necrophorum	73083
s__unclassified	71840
s__unclassified	71980
s__unclassified	72012
s__unclassified	72035
s__unclassified	72093
s__unclassified	72103

AJ431236.1 gg_id:79101 Cytophaga sp. str. BHI60-57B AJ4312
EF585979.1 gg_id:257911 Methanol-assimilating anaerobic solid waste digester fed methanol clone B55_K_B_/ EF5859
EF559068.1 gg_id:252254 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF5590
AM947532.1 gg_id:265589 Minor changes detected microbial structure and after three week thermophilic dige AM947
AF282252.1 gg_id:17524 Ferribacter thermoautotrophicus str. JW/JH-Fiji-2 AF2822
DQ815026.1 gg_id:169250 zebrafish digestive tract clone aab49a06 DQ815
DQ815290.1 gg_id:171837 zebrafish digestive tract clone aab52g10 DQ815
DQ815286.1 gg_id:171805 zebrafish digestive tract clone aab52g04 DQ815
DQ815110.1 gg_id:173268 zebrafish digestive tract clone aab50b10 DQ815
DQ815013.1 gg_id:161980 zebrafish digestive tract clone aab56g09 DQ815
AM179923.1 gg_id:145422 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G15-: AM179
DQ815269.1 gg_id:172292 zebrafish digestive tract clone aab52e06 DQ815
DQ815170.1 gg_id:168343 zebrafish digestive tract clone aab51a08 DQ815
DQ815292.1 gg_id:170458 zebrafish digestive tract clone aab52h02 DQ815
EU460633.1 gg_id:297393 polar bear feces clone PB2_aai23f09 EU460
EU460497.1 gg_id:293496 polar bear feces clone PB2_aai21g01 EU460
DQ815229.1 gg_id:164983 zebrafish digestive tract clone aab51h04 DQ815
EU460618.1 gg_id:287660 polar bear feces clone PB2_aai23e02 EU460
EU460666.1 gg_id:296915 polar bear feces clone PB2_aai24b06 EU460
X78419.1 gg_id:11302 Cetobacterium ceti X78419
EU460449.1 gg_id:296950 polar bear feces clone PB2_aai21a07 EU460
EU460631.1 gg_id:298501 polar bear feces clone PB2_aai23f07 EU460
EU460679.1 gg_id:297037 polar bear feces clone PB2_aai24c12 EU460
EU460629.1 gg_id:293351 polar bear feces clone PB2_aai23f05 EU460
GU293194.1 gg_id:562985 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EU460532.1 gg_id:297473 polar bear feces clone PB2_aai22c03 EU460
EU460361.1 gg_id:297672 polar bear feces clone PB1_aai27c07 EU460
EU460550.1 gg_id:291093 polar bear feces clone PB2_aai22e07 EU460
EU460627.1 gg_id:291261 polar bear feces clone PB2_aai23f02 EU460
EU460489.1 gg_id:294813 polar bear feces clone PB2_aai21f01 EU460
EU460637.1 gg_id:298087 polar bear feces clone PB2_aai23g02 EU460
NR_025679.1 gg_id:554906 Fusobacterium canifelinum str. RMA 12708; CCUG 49735 Q11 NR_02
AJ295750.1 gg_id:34266 Fusobacterium equinum str. horse VPB 4027 AJ2957
X74408.1 gg_id:11309 Fusobacterium necrophorum str. B FnS-40 X74408
X74407.1 gg_id:11305 Fusobacterium necrophorum str. AB FnS-1 X74407
FJ471661.1 gg_id:524898 Fusobacterium nucleatum str. ChDC F319 FJ4716
GQ004485.1 gg_id:505177 Topographical and Temporal Human Skin Microbiome skin nare clone nbu59b02c1 GQ004
EU772809.1 gg_id:306442 Bush dog feces clone bdog1_aai77h07 EU7728
AF543300.1 gg_id:58280 Fusobacterium nucleatum str. ChDC OS50 AF5433
GQ448468.1 gg_id:511044 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_2wks_gr GQ448
AF481217.1 gg_id:68347 Fusobacterium nucleatum str. E9_12 AF4812

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
1	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	1	1	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria

o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae

g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__Fusobacterium
g__J2-29
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia

s__unclassified	72145
s__unclassified	72172
s__unclassified	72325
s__unclassified	72396
s__unclassified	72435
s__unclassified	72473
s__unclassified	72496
s__unclassified	72615
s__unclassified	72628
s__unclassified	72741
s__unclassified	72786
s__unclassified	72979
s__unclassified	73063
s__unclassified	73076
s__unclassified	73082
s__unclassified	73098
s__unclassified	72430
s__Leptotrichia buccalis	72462
s__Leptotrichia hofstadii	72051
s__Leptotrichia trevisanii	72862
s__unclassified	71902
s__unclassified	71919
s__unclassified	71985
s__unclassified	72079
s__unclassified	72091
s__unclassified	72178
s__unclassified	72216
s__unclassified	72263
s__unclassified	72275
s__unclassified	72280
s__unclassified	72313
s__unclassified	72333
s__unclassified	72405
s__unclassified	72408
s__unclassified	72439
s__unclassified	72441
s__unclassified	72461
s__unclassified	72497
s__unclassified	72612
s__unclassified	72614
s__unclassified	72626

FJ959515.1 gg_id:550936 bottlenose dolphin upper respiratory tract blowhole clone D896_106 FJ9595
NZ_ACET01000043.1 gg_id:470433 Fusobacterium gonidiaformans str. ATCC 25563 NZ_AC
FJ471649.1 gg_id:529903 Fusobacterium nucleatum str. ChDC F290 FJ4716
GQ091870.1 gg_id:449592 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ091
GQ113263.1 gg_id:375228 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
FJ978721.1 gg_id:408384 feces clone CL_F_417 FJ9787
EU774026.1 gg_id:308389 Cheetah feces clone CE3_aai08d02 EU774
EF089177.1 gg_id:185041 Fusobacterium nucleatum str. Ulm 14 EF0891
FJ978724.1 gg_id:381867 feces clone CL_F_422 FJ9787
FJ978541.1 gg_id:427042 feces clone CL_F_080 FJ9785
FJ471639.2 gg_id:514347 Fusobacterium nucleatum str. ChDC F113 FJ4716
GQ088072.1 gg_id:459200 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ088
FJ471673.1 gg_id:520375 Fusobacterium periodonticum str. ChDC F334 FJ4716
DQ440563.1 gg_id:156573 Fusobacterium nucleatum str. Ulm DQ440
GQ087757.1 gg_id:395408 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
GQ014795.1 gg_id:494871 Topographical and Temporal Human Skin Microbiome skin palm clone nbw764c09c1 GQ014
FJ978525.1 gg_id:468118 feces clone CL_F_056 FJ9785
CP001685.1 gg_id:529857 Leptotrichia buccalis C-1013-b str. DSM 1135 CP001
FJ577251.2 gg_id:568972 Leptotrichia hofstadii str. F0254 FJ5772
AF206305.1 gg_id:71541 Leptotrichia trevisanii AF206
AY134896.1 gg_id:59574 oral periodontitis clone EX103 AY1348
AM420035.1 gg_id:241454 Noma subgingival plaque clone 201G10(oral) AM420
CP001685.1 gg_id:529859 Leptotrichia buccalis C-1013-b str. DSM 1135 CP001
GQ129984.1 gg_id:399980 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
AY207053.1 gg_id:83573 human mouth clone P2PB_51 AY207
AF432138.1 gg_id:31235 tongue dorsum scrapings clone FP036 AF432
GQ000682.1 gg_id:469247 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ000882.1 gg_id:469447 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
AY349385.1 gg_id:92131 human oral cavity clone GT020 AY349
FJ976353.1 gg_id:578509 Interindividual healthy human oral microbiota mouth clone 12BB57 FJ9763
AM420193.1 gg_id:258023 Noma subgingival plaque clone 502D06(oral) AM420
GQ016176.1 gg_id:493491 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
FJ577259.2 gg_id:566658 Leptotrichia goodfellowii str. F0264 FJ5772
AY029803.1 gg_id:70629 Leptotrichia hofstadii str. LB23 AY0298
AF287814.1 gg_id:38061 human subgingival plaque clone F138 AF2878
GQ032449.1 gg_id:403062 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
AF385571.1 gg_id:70038 crevicular epithelial cells clone EI013 AF3855
GQ016227.1 gg_id:493440 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
EU137409.1 gg_id:267538 Bartonella-positive fleas: and assembly patterns Oropsylla hirsuta (prairie dog flea) C EU1374
NZ_ACVB02000014.1 gg_id:484462 Leptotrichia hofstadii str. F0254 NZ_AC
AM420110.1 gg_id:256867 Noma subgingival plaque clone 303F08(oral) AM420

1	1	1	0	1	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__Fusobacteria	c__Fusobacteria
k__Bacteria	k__Bacteria	p__GAL15	c__unclassified
k__Bacteria	k__Bacteria	p__GAL15	c__unclassified
k__Bacteria	k__Bacteria	p__GAL15	c__unclassified
k__Bacteria	k__Bacteria	p__GAL15	c__unclassified
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes

o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__Fusobacteriales	f__Fusobacteriaceae
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae

g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Leptotrichia
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Propionigenium
g__Sebaldella
g__Sebaldella
g__Sneathia
g__Sneathia
g__Sneathia
g__Streptobacillus
g__Streptobacillus
g__u114
g__u114
g__unclassified
g__sfA
g__sfA
g__sfB
g__sfC
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas

s__unclassified	72639
s__unclassified	72642
s__unclassified	72717
s__unclassified	72875
s__unclassified	72959
s__unclassified	73088
s__Propionigenium maris	72998
s__unclassified	72106
s__unclassified	72289
s__unclassified	72359
s__unclassified	72364
s__unclassified	72374
s__unclassified	72540
s__unclassified	72665
s__unclassified	72825
s__unclassified	72962
s__unclassified	73079
s__Sebaldella termitidis	73020
s__unclassified	72784
s__Leptotrichia amnionii	71971
s__Leptotrichia amnionii	72986
s__unclassified	72728
s__Streptobacillus moniliformis	72846
s__unclassified	72676
s__unclassified	72608
s__unclassified	72938
s__unclassified	71997
s__unclassified	55914
s__unclassified	56193
s__unclassified	56117
s__unclassified	55568
s__unclassified	57787
s__unclassified	57835
s__unclassified	57859
s__unclassified	57878
s__unclassified	57891
s__unclassified	57960
s__unclassified	57969
s__unclassified	57988
s__unclassified	58102
s__unclassified	58136

GQ070510.1 gg_id:399174 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ070
GQ111263.1 gg_id:375876 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
GQ032233.1 gg_id:381314 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ032
GQ422731.1 gg_id:555711 Leptotrichia sp. oral taxon 225 str. FEA2 GQ422
GQ000663.1 gg_id:469228 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GU086183.1 gg_id:593385 Leptotrichia shahii str. PW1036 GU086
NR_026243.1 gg_id:557791 Propionigenium maris str. 10succ1; DSM 9537 NR_02
EU236316.1 gg_id:296908 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1bD2 EU2363
X54275.1 gg_id:11301 Propionigenium modestum X54275
AJ877255.1 gg_id:112138 Ilyobacter psychrophilus str. FQ50 AJ8772
AJ307980.1 gg_id:52873 Ilyobacter insuetus str. DSM 6831 T AJ3079
Y16799.1 gg_id:42042 Propionigenium maris str. DSL-1 Y16799
FJ264772.1 gg_id:324952 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2647
FJ717186.1 gg_id:510621 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
FJ717188.1 gg_id:558150 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7171
EU052253.1 gg_id:240997 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
AY770718.1 gg_id:110394 Fusobacteria sea urchin Paracentrotus lividus clone PlS49 AY7707
CP001739.1 gg_id:518403 Sebaldella termitidis str. ATCC 33386 CP0017
EF608534.1 gg_id:228694 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
EF218611.1 gg_id:212738 Leptotrichia amnionii str. CCUG 51847 EF2186
AY078425.1 gg_id:29566 Leptotrichia amnionii str. AMN-1 AY0784
AJ344093.1 gg_id:58542 Sneathia sanguinegens str. CCUG 41628T AJ3440
AB330759.1 gg_id:236558 Streptobacillus moniliformis str. KWG2 AB3307
GQ072215.1 gg_id:447942 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw193e1 GQ072
GQ850557.1 gg_id:591820 surface water northern Bering Sea clone u114 GQ850
FJ456795.1 gg_id:545014 microbiota two Antarctic notothenioid fish species intestinal flora clone A007_NCI FJ4567
DQ206413.1 gg_id:139839 microbial mediates arsenate reduction soda lake water clone ML-AsS-15 DQ206
EU044321.1 gg_id:256629 uences structure fosters richness subtropical Altamaha Ohopee River Valley inland d EU0443
EF019213.1 gg_id:213629 aspen rhizosphere clone Amb_16S_1909 EF0192
DQ490008.1 gg_id:158907 Microbial Great Boiling Spring sediment hot spring; temperature 80 C clone GBS_L1_ DQ490
EU134698.1 gg_id:255244 tallgrass prarie soil clone FFCH14117 EU1346
FM873495.1 gg_id:363705 occupant source house floor dust clone FD04E09 FM873
EF018217.1 gg_id:216704 aspen rhizosphere clone Amb_16S_564 EF0182
EF540422.1 gg_id:220442 oil-shale semi-coke solid waste clone MK51 EF5404
GQ113134.1 gg_id:433730 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw675f0 GQ113
EU283562.1 gg_id:278836 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1853 EU2835
FJ444672.1 gg_id:591271 Cotton Rhizosphere cotton rhizosphere clone 2y-23 FJ4446
AB240260.1 gg_id:142399 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB2402
DQ640655.1 gg_id:234041 full-scale EBPR sludge clone Skagenf3 DQ640
GQ090575.1 gg_id:440096 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ090
AB234279.1 gg_id:146305 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	1	0	0	0	0	0	1
0	0	1	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes

o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae

g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__Gemmatimonas
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	58143
s__unclassified	58170
s__unclassified	58200
s__unclassified	58216
s__unclassified	58350
s__unclassified	58391
s__unclassified	58423
s__unclassified	58431
s__unclassified	58549
s__unclassified	58585
s__unclassified	58659
s__unclassified	58673
s__unclassified	57806
s__unclassified	57810
s__unclassified	57822
s__unclassified	57824
s__unclassified	57839
s__unclassified	57864
s__unclassified	57887
s__unclassified	57920
s__unclassified	57943
s__unclassified	57957
s__unclassified	58037
s__unclassified	58074
s__unclassified	58076
s__unclassified	58096
s__unclassified	58097
s__unclassified	58119
s__unclassified	58120
s__unclassified	58123
s__unclassified	58129
s__unclassified	58130
s__unclassified	58149
s__unclassified	58156
s__unclassified	58159
s__unclassified	58174
s__unclassified	58175
s__unclassified	58182
s__unclassified	58188
s__unclassified	58199
s__unclassified	58232

AF432648.1 gg_id:104785 lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Pro AF4326
EF157193.1 gg_id:243247 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
EF018812.1 gg_id:214676 aspen rhizosphere clone Amb_16S_1283 EF0188
FJ478758.1 gg_id:512313 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EF203205.1 gg_id:207957 phylotypes sediments Lake Kastoria Greece sediment clone Kas174B EF2032
AF432635.1 gg_id:99232 lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Prod AF4326
DQ067025.1 gg_id:133200 Lake Washington sediment clone pLW-82 DQ067
FJ536876.1 gg_id:587747 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5368
DQ520169.1 gg_id:160270 shal China sequences hypertrophic freshwater lake clone ML-5-110.2 DQ520
EF018312.1 gg_id:207648 aspen rhizosphere clone Amb_16S_675 EF0183
AF545649.1 gg_id:72899 shortgrass steppe soil (Stunner series fine loamy over sandy Ustic Calciargid) under Bc AF5456
AY218696.1 gg_id:81623 penguin droppings sediments clone KD8-87 AY2186
AB426207.1 gg_id:264973 -situ identification study benzene-degrading s under methanogenic condition anaerc AB4262
EU979110.1 gg_id:336425 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU9791
DQ906809.1 gg_id:239203 Oman subsurface soil clone 5B-5 DQ906
EF516323.1 gg_id:225306 grassland soil clone FCPT668 EF5163
EF019647.1 gg_id:215970 aspen rhizosphere clone Elev_16S_798 EF0196
DQ067020.1 gg_id:129424 Lake Washington sediment clone pLW-79 DQ067
FJ479207.1 gg_id:588566 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EF019081.1 gg_id:204271 aspen rhizosphere clone Amb_16S_1670 EF0190
FJ152750.1 gg_id:339480 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
EU044086.1 gg_id:237353 fluences structure fosters richness subtropical Altamaha Ohopee River Valley inland EU0440
EU193066.1 gg_id:360943 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
AM934748.1 gg_id:549433 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY921939.1 gg_id:114406 farm soil clone AKYG583 AY9219
EU881263.1 gg_id:329628 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU8812
AY922055.1 gg_id:114310 farm soil clone AKYG703 AY9220
AY921712.1 gg_id:112987 farm soil clone AKYG963 AY9217
AY921894.1 gg_id:114101 farm soil clone AKYG1555 AY9218
EF612383.1 gg_id:237047 historic semiarid lead-zinc mine tailings site soil clone OS-C17 EF6123
AY395378.1 gg_id:103904 pasture soil clone EB1059 AY3953
AY192277.1 gg_id:79951 Rocky Mountain alpine soil clone W2a-1F AY1922
GU359099.1 gg_id:518957 rhizosphere soil peanut clone 2G11 GU359
DQ906907.1 gg_id:253096 Oman subsurface soil clone 12B-7 DQ906
EU801865.1 gg_id:314599 It's all ranking aquatic Chesapeake Bay MD clone 3C003242 EU8018
FJ746162.1 gg_id:512463 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
EF020040.1 gg_id:211950 aspen rhizosphere clone Elev_16S_1437 EF0200
FJ230809.1 gg_id:325203 Microclimate and limits photosynthesis cyanobacteria Northern Australia hypolithic s FJ2308
AB257644.1 gg_id:259192 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
AY921918.1 gg_id:113407 farm soil clone AKYG1585 AY9219
EU283563.1 gg_id:279650 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1336 EU2835

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	0	0	0	0	0	0	0	1
1	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	1	0	1	1	1
1	0	1	0	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes

o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__Gemmatimonadales	f__Gemmatimonadaceae
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	58233
s__unclassified	58285
s__unclassified	58298
s__unclassified	58313
s__unclassified	58314
s__unclassified	58330
s__unclassified	58370
s__unclassified	58401
s__unclassified	58402
s__unclassified	58418
s__unclassified	58474
s__unclassified	58480
s__unclassified	58493
s__unclassified	58526
s__unclassified	58527
s__unclassified	58535
s__unclassified	58557
s__unclassified	58558
s__unclassified	58567
s__unclassified	58586
s__unclassified	58614
s__unclassified	58619
s__unclassified	58625
s__unclassified	58658
s__unclassified	58660
s__unclassified	58665
s__unclassified	58672
s__unclassified	58676
s__unclassified	58703
s__unclassified	58705
s__unclassified	58760
s__unclassified	58798
s__unclassified	58805
s__unclassified	58864
s__unclassified	58866
s__unclassified	58871
s__unclassified	58877
s__unclassified	57916
s__unclassified	57928
s__unclassified	57993
s__unclassified	58004

EU134840.1 gg_id:249299 tallgrass prarie soil clone FFCH11609 EU1348
AY913252.1 gg_id:112876 forest soil clone DUNssu032 (+2C) (OTU#201) AY9132
AB257643.1 gg_id:265561 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
EU652636.1 gg_id:277713 Seasonal variation microbial Yel Sea sediment clone D8S-116 EU6526
EU048610.1 gg_id:254529 Microbial surface marine sediment Xisha Trough South China Sea clone MD2902-B3 EU0486
AY922130.1 gg_id:114403 farm soil clone AKYH466 AY9221
AY673312.1 gg_id:110882 Gemmatimonadetes Ellin7146 AY6733
FJ479068.1 gg_id:560811 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
AY922123.1 gg_id:113603 farm soil clone AKYH1517 AY9221
EF020045.1 gg_id:207989 aspen rhizosphere clone Elev_16S_1446 EF0200
AY921994.1 gg_id:112986 farm soil clone AKYG1838 AY9219
GQ396903.1 gg_id:557467 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
AY921912.1 gg_id:114146 farm soil clone AKYG1614 AY9219
EU676443.1 gg_id:289924 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals- EU6764
EF018145.1 gg_id:208048 aspen rhizosphere clone Amb_16S_479 EF0181
GU205280.1 gg_id:516178 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
FJ152768.1 gg_id:335807 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AY289480.1 gg_id:90194 soil clone ABS-650 AY2894
GQ113661.1 gg_id:384470 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
EF516935.1 gg_id:219517 grassland soil clone FCPN548 EF5169
EU193059.1 gg_id:360637 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU1930
DQ532275.1 gg_id:168856 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EF688378.1 gg_id:250371 soil clone F6-84 EF6883
AY921776.1 gg_id:113308 farm soil clone AKYG961 AY9217
EU234231.1 gg_id:242383 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
EU881123.1 gg_id:308062 Karst region primary forest soil clone KPF200711-086 EU8811
DQ067019.1 gg_id:128235 Lake Washington sediment clone pLW-78 DQ067
EU134880.1 gg_id:249280 tallgrass prarie soil clone FFCH2651 EU1348
DQ833499.1 gg_id:166488 detected analyses depth sediment Guanting Reservoir clone 69-18 DQ833
AY921771.1 gg_id:113042 farm soil clone AKYG666 AY9217
EF492900.1 gg_id:246196 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EU134828.1 gg_id:249948 tallgrass prarie soil clone FFCH6230 EU1348
EU861901.1 gg_id:325238 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
FJ755752.1 gg_id:565312 vertical archaeal water and Lake Taihu sediment clone LT-SB-B6 FJ7557
AY218678.1 gg_id:82251 penguin droppings sediments clone KD8-105 AY2186
AY921899.1 gg_id:114389 farm soil clone AKYG781 AY9218
DQ906808.1 gg_id:243477 Oman subsurface soil clone 5B-4 DQ906
GQ263232.1 gg_id:590444 Structure Simulated Level Waste Site simulated level waste site clone F3_42X GQ263
FJ444711.1 gg_id:511297 Cotton Rhizosphere cotton rhizosphere clone 3y-46 FJ4447
GQ263030.1 gg_id:576743 Structure Simulated Level Waste Site simulated level waste site clone F2_153X GQ263
EF174264.1 gg_id:197816 direct activated 4th maturation stage sludge clone F37-814 EF1742

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	1	0	1	1	0	0
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	0	0	0
1	1	1	0	1	1	1	1	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfC
g__sfC
g__sfC
g__sfC
g__sfC
g__sfC
g__sfD
g__sfD
g__sfD
g__sfD
g__sfD
g__sfD
g__sfD
g__sfD
g__sfE
g__sfE

s__unclassified	58073
s__unclassified	58094
s__unclassified	58124
s__unclassified	58220
s__unclassified	58323
s__unclassified	58360
s__unclassified	58374
s__unclassified	58459
s__unclassified	58518
s__unclassified	58571
s__unclassified	58598
s__unclassified	58725
s__unclassified	58833
s__unclassified	57790
s__unclassified	57987
s__unclassified	58212
s__unclassified	58429
s__unclassified	58436
s__unclassified	58644
s__unclassified	58664
s__unclassified	58687
s__unclassified	58852
s__unclassified	58853
s__unclassified	58133
s__unclassified	58138
s__unclassified	58248
s__unclassified	58294
s__unclassified	58320
s__unclassified	58482
s__unclassified	58650
s__unclassified	58694
s__unclassified	57930
s__unclassified	57963
s__unclassified	58100
s__unclassified	58234
s__unclassified	58359
s__unclassified	58540
s__unclassified	58807
s__unclassified	58860
s__unclassified	58137
s__unclassified	58185

EU037358.2 gg_id:277360 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
GQ263154.1 gg_id:579054 Structure Simulated Level Waste Site simulated level waste site clone F3_100X GQ263
GQ397033.1 gg_id:586289 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
GQ262951.1 gg_id:563031 Structure Simulated Level Waste Site simulated level waste site clone F1_87X2 GQ262
EU979063.1 gg_id:344838 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
EF157266.1 gg_id:248780 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
FJ152642.1 gg_id:312327 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
GQ263158.1 gg_id:553767 Structure Simulated Level Waste Site simulated level waste site clone F3_106X GQ263
AM935432.1 gg_id:550147 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
GQ262827.1 gg_id:584041 Structure Simulated Level Waste Site simulated level waste site clone F1_15X2 GQ262
GQ263089.1 gg_id:593457 Structure Simulated Level Waste Site simulated level waste site clone F2_39X GQ263
GQ263091.1 gg_id:561233 Structure Simulated Level Waste Site simulated level waste site clone F2_41X GQ263
GQ262961.1 gg_id:538070 Structure Simulated Level Waste Site simulated level waste site clone F1_92X GQ262
FJ425592.1 gg_id:363208 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl FJ4255
DQ300602.1 gg_id:147735 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static DQ300
GQ346931.1 gg_id:591890 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ346
DQ295242.1 gg_id:148154 Fragments Six Marine Planktonic Antarctic sea water clone Ant4D5 DQ295
AJ567595.1 gg_id:89477 deep-sea sediment clone MBAE42 AJ5675
EU287180.1 gg_id:251953 Pacific arctic surface sediment clone P13-87 EU287
EU374078.1 gg_id:276624 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
AM997489.1 gg_id:548429 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
FJ205357.1 gg_id:512804 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
AM935228.1 gg_id:574770 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU652634.1 gg_id:277772 Seasonal variation microbial Yel Sea sediment clone A8S-129 EU652
FJ746291.1 gg_id:572935 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
AY592149.1 gg_id:106730 marine ANAMMOX sediment clone AY592149 AY592
EU287420.1 gg_id:244505 Pacific arctic surface sediment clone S26-120 EU287
AF186415.1 gg_id:11593 sponge symbiont clone PAUC43f AF186
FJ024313.1 gg_id:359471 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I FJ0243
AB294923.1 gg_id:226129 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB294
AF286033.1 gg_id:37339 saltmarsh clone LCP-68 AF286
EU979085.1 gg_id:308997 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
FJ444650.1 gg_id:560438 Cotton Rhizosphere cotton rhizosphere clone 2h-20 FJ4446
EF540395.1 gg_id:225607 oil-shale semi-coke solid waste clone 1_11MK EF5403
EU134894.1 gg_id:248455 tallgrass prarie soil clone FFCH6442 EU1348
EU134893.1 gg_id:239710 tallgrass prarie soil clone FFCH12021 EU1348
EU193063.1 gg_id:369973 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
AY921663.1 gg_id:113478 farm soil clone AKYH1024 AY9216
AY493976.1 gg_id:136870 Fingerprinting aggregates soil clone 5 AY4939
DQ431899.1 gg_id:208663 microorganisms catalyzing nitrogen removal and organic matter metabolism perme DQ431
EU491861.1 gg_id:270789 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918

0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	1	1	0	0	0	0	0	1
1	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	0	1	1
0	1	1	1	1	1	1	0	0	0	0	1	1
1	1	1	0	1	1	1	1	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	1	1	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__Gemmatimonadetes	c__Gemmatimonadetes
k__Bacteria	k__Bacteria	p__GN02	c__BB34
k__Bacteria	k__Bacteria	p__GN02	c__BB34
k__Bacteria	k__Bacteria	p__GN02	c__BB34

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__sfE
g__sfE
g__sfE
g__sfE
g__sfF
g__sfF
g__sfF
g__sfF
g__sfF
g__sfG
g__sfG
g__sfG
g__sfG
g__sfG
g__sfH
g__sfH
g__sfH
g__sfH
g__sfH
g__sfI
g__sfI
g__sfI
g__sfI
g__sfJ
g__sfJ
g__sfK
g__sfK
g__sfL
g__sfL
g__sfM
g__sfM
g__sfN
g__sfO
g__sfP
g__sfQ
g__sfR
g__sfS
g__sfT
g__sfA
g__sfA
g__sfA

s__unclassified	58229
s__unclassified	58464
s__unclassified	58499
s__unclassified	58785
s__unclassified	57958
s__unclassified	58214
s__unclassified	58246
s__unclassified	58728
s__unclassified	58772
s__unclassified	57851
s__unclassified	57956
s__unclassified	58104
s__unclassified	58534
s__unclassified	58663
s__unclassified	57841
s__unclassified	57934
s__unclassified	58287
s__unclassified	58343
s__unclassified	58604
s__unclassified	57965
s__unclassified	58028
s__unclassified	58086
s__unclassified	58163
s__unclassified	58089
s__unclassified	58223
s__unclassified	57925
s__unclassified	58281
s__unclassified	58399
s__unclassified	58450
s__unclassified	57982
s__unclassified	58766
s__unclassified	57830
s__unclassified	58059
s__unclassified	58390
s__unclassified	57818
s__unclassified	58142
s__unclassified	58753
s__unclassified	58327
s__unclassified	74871
s__unclassified	75300
s__unclassified	75751

FJ152644.1 gg_id:322198 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
EU134886.1 gg_id:254415 tallgrass prarie soil clone FFCH1365 EU1348
EU134854.1 gg_id:240326 tallgrass prarie soil clone FFCH14573 EU1348
AY921936.1 gg_id:113023 farm soil clone AKYG548 AY9219
AJ347028.1 gg_id:60181 sponge symbiont clone TK19 AJ3470
GU118643.1 gg_id:557462 Threatened Corals Provide Microbial Habitats clone Mfav_E13 GU118
GU118605.1 gg_id:565653 Threatened Corals Provide Microbial Habitats clone Mfav_L08 GU118
GU118693.1 gg_id:544625 Threatened Corals Provide Microbial Habitats clone Mfav_D05 GU118
GU118648.1 gg_id:586196 Threatened Corals Provide Microbial Habitats clone Mfav_H20 GU118
GQ095375.1 gg_id:443417 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
EF516463.1 gg_id:218620 grassland soil clone FCPU694 EF5164
EF516718.1 gg_id:217803 grassland soil clone FCPU461 EF5167
EU289488.1 gg_id:254895 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AY921785.1 gg_id:113624 farm soil clone AKYH1201 AY9217
FJ152619.1 gg_id:356469 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FJ152871.1 gg_id:322098 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
FJ152673.1 gg_id:342606 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
GU083675.1 gg_id:585141 Microorganism Xiarinur soda lake sediment clone x271 GU083
EU374077.1 gg_id:267176 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU3740
GQ143755.1 gg_id:373545 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
AF317745.1 gg_id:136926 Nullarbor cave clone wb1_A18 AF3177
AM943577.1 gg_id:269262 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hyper AM943
AY592110.1 gg_id:99079 marine ANAMMOX sediment clone AY592110 AY5921
GQ262856.1 gg_id:554991 Structure Simulated Level Waste Site simulated level waste site clone F1_32X2 GQ262
DQ906881.1 gg_id:241659 Oman subsurface soil clone 11B-8 DQ906
EU682493.1 gg_id:530814 Four Primer Sets Detecting Anammox s estuary sediment Mai Po Nature Reserve clo EU6824
EU652631.1 gg_id:277923 Seasonal variation microbial Yel Sea sediment clone C8S-21 EU6526
EU245438.1 gg_id:237565 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-F03 EU2454
EU369136.1 gg_id:304950 libraries oyster shell clone MBIOS-20 EU3691
EU219931.1 gg_id:247892 study prokaryotic approach landfill soil 5.5 ft. depth clone C6B EU2199
EU369154.1 gg_id:317743 libraries oyster shell clone MBHOS-05 EU3691
EF125397.1 gg_id:182109 soil naked tidal flat sediment near mangrove clone MSB-1C5 EF1253
AB491850.1 gg_id:542631 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac AB4918
EU134887.1 gg_id:252091 tallgrass prarie soil clone FFCH15678 EU1348
EU134863.1 gg_id:255390 tallgrass prarie soil clone FFCH17465 EU1348
GU056071.1 gg_id:579069 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
FJ152883.1 gg_id:351400 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
AB250557.1 gg_id:160916 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #2-2 AB2505
EU283598.1 gg_id:279155 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A406 EU2835
FJ205371.1 gg_id:510313 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
EU700157.1 gg_id:288295 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU15 EU7001

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	1	0	0	0	0	0	1	1	1	0
0	0	0	1	0	0	0	0	0	1	1	1	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__GN02	c__GKS2-174
k__Bacteria	k__Bacteria	p__GN02	c__GKS2-174
k__Bacteria	k__Bacteria	p__GN02	c__GN07
k__Bacteria	k__Bacteria	p__GN02	c__GN07
k__Bacteria	k__Bacteria	p__GN02	c__GN08
k__Bacteria	k__Bacteria	p__GN02	c__unclassified
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN02	c__VC12-cl04
k__Bacteria	k__Bacteria	p__GN04	c__5bav_B12
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__GN15
k__Bacteria	k__Bacteria	p__GN04	c__MSB-5A5
k__Bacteria	k__Bacteria	p__GN04	c__MSB-5A5
k__Bacteria	k__Bacteria	p__GN04	c__MSB-5A5
k__Bacteria	k__Bacteria	p__GN04	c__MSB-5A5
k__Bacteria	k__Bacteria	p__GN04	c__MSB-5A5
k__Bacteria	k__Bacteria	p__GN06	c__KSB3
k__Bacteria	k__Bacteria	p__GN06	c__unclassified
k__Bacteria	k__Bacteria	p__GN06	c__unclassified
k__Bacteria	k__Bacteria	p__GN06	c__unclassified
k__Bacteria	k__Bacteria	p__GN06	c__unclassified
k__Bacteria	k__Bacteria	p__GN06	c__unclassified
k__Bacteria	k__Bacteria	p__GN06	c__unclassified
k__Bacteria	k__Bacteria	p__GN1	c__unclassified
k__Bacteria	k__Bacteria	p__GN1	c__unclassified
k__Bacteria	k__Bacteria	p__GN1	c__unclassified
k__Bacteria	k__Bacteria	p__GN1	c__unclassified

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfD
g__sfE
g__sfF
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	74813
s__unclassified	75546
s__unclassified	74959
s__unclassified	75458
s__unclassified	75617
s__unclassified	74814
s__unclassified	74988
s__unclassified	75011
s__unclassified	75015
s__unclassified	75154
s__unclassified	75247
s__unclassified	75437
s__unclassified	75668
s__unclassified	75690
s__unclassified	75844
s__unclassified	75905
s__unclassified	58818
s__unclassified	58197
s__unclassified	58626
s__unclassified	58433
s__unclassified	58583
s__unclassified	58280
s__unclassified	58396
s__unclassified	58756
s__unclassified	58795
s__unclassified	57942
s__unclassified	58573
s__unclassified	57970
s__unclassified	58225
s__unclassified	58338
s__unclassified	52125
s__unclassified	52015
s__unclassified	52460
s__unclassified	51930
s__unclassified	52611
s__unclassified	52840
s__unclassified	52920
s__unclassified	51869
s__unclassified	52115
s__unclassified	52193
s__unclassified	52219

AF507713.1 gg_id:65673 forest soil clone S166 AF507
EU491859.1 gg_id:264825 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ347441.1 gg_id:581615 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
DQ234160.2 gg_id:144617 determined library mangrove clone DS076 DQ234
DQ329577.1 gg_id:159133 Guerrero Negro hypersaline microbial mat clone 05D2Z07 DQ329
DQ397339.1 gg_id:159241 Guerrero Negro hypersaline microbial mat clone 02D2Z08 DQ397
AB192119.1 gg_id:142691 termite gut homogenate clone M2PT2-27 AB192
FJ791860.1 gg_id:571248 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7918
AY197400.1 gg_id:86409 Guaymas Basin hydrothermal vent sediments clone B02R018 AY197
FJ959985.1 gg_id:579816 bottlenose dolphin upper respiratory tract blowhole clone D940_045 FJ9599
AB232534.1 gg_id:154098 Prokaryotic gills deep-sea hydrothermal vent shrimp gill Alvinocaris longirostris clone AB232
EU052256.1 gg_id:256207 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
AF367482.1 gg_id:17620 deep-sea hydrothermal vent clone VC1.2-cl02 AF367
GQ349327.1 gg_id:562277 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU265935.1 gg_id:537633 transition and zone within near-shore anoxic basin: Nitinat Lake depth 20 m clone Ni EU265
EU101198.1 gg_id:237363 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
GU061180.1 gg_id:585963 Evaluation culturing methods cultivate previously Yel Sea intertidal beach surface se GU061
EU245804.1 gg_id:257757 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-F03 EU245
DQ330597.1 gg_id:159245 Guerrero Negro hypersaline microbial mat clone 09D2Z91 DQ330
FJ712458.1 gg_id:523166 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
EU385807.1 gg_id:258358 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU245526.1 gg_id:256848 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-F08 EU245
FJ810558.1 gg_id:405181 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
FJ416124.1 gg_id:357229 sediments sediment station NEC5 Northern Bering Sea clone 115O3 FJ4161
EU542519.1 gg_id:273867 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
DQ811954.1 gg_id:162191 mangrove soil clone MSB-5A5 DQ811
EU487916.1 gg_id:564815 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EF203188.1 gg_id:204759 phylotypes sediments Lake Kastoria Greece sediment clone Kas139B EF2031
EU048677.1 gg_id:254199 and archaeal surface marine sediment Slope South China Sea clone MD2896-B18 EU048
EU487964.1 gg_id:573020 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EU245855.1 gg_id:256405 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M7-C07 EU245
DQ329580.1 gg_id:159470 Guerrero Negro hypersaline microbial mat clone 062DZ43 DQ329
DQ154831.1 gg_id:138844 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
GQ246356.1 gg_id:548387 Temporal and spatial China North Yel Sea sediments clone Cm1-19 GQ246
FJ264777.1 gg_id:340190 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
FM165273.1 gg_id:566144 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
FJ264598.1 gg_id:317416 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2645
EU246145.1 gg_id:257436 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-C07 EU246
EU245601.1 gg_id:257385 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-E09 EU245
DQ329606.1 gg_id:159400 Guerrero Negro hypersaline microbial mat clone 04D2Z65 DQ329
DQ329608.1 gg_id:159092 Guerrero Negro hypersaline microbial mat clone 05D2Z01 DQ329

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	1	0	0	0
0	1	0	0	1	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	1	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__GN1	c__unclassified
k__Bacteria	k__Bacteria	p__GN12	c__unclassified
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__RB384
k__Bacteria	k__Bacteria	p__GOUTA4	c__unclassified
k__Bacteria	k__Bacteria	p__HDBW-WB69	c__unclassified
k__Bacteria	k__Bacteria	p__HDBW-WB69	c__unclassified
k__Bacteria	k__Bacteria	p__HDBW-WB69	c__unclassified
k__Bacteria	k__Bacteria	p__Hyd24-12	c__unclassified
k__Bacteria	k__Bacteria	p__Hyd24-12	c__unclassified
k__Bacteria	k__Bacteria	p__Hyd24-12	c__WM88
k__Bacteria	k__Bacteria	p__Hyd24-12	c__WM88
k__Bacteria	k__Bacteria	p__Hyd24-12	c__WM88
k__Bacteria	k__Bacteria	p__Hyd24-12	c__WM88
k__Bacteria	k__Bacteria	p__Hyd24-12	c__WM88
k__Bacteria	k__Bacteria	p__KSB1	c__GW-22
k__Bacteria	k__Bacteria	p__KSB1	c__GW-22
k__Bacteria	k__Bacteria	p__KSB1	c__GW-22
k__Bacteria	k__Bacteria	p__KSB1	c__GW-22
k__Bacteria	k__Bacteria	p__KSB1	c__GW-22
k__Bacteria	k__Bacteria	p__KSB1	c__GW-22
k__Bacteria	k__Bacteria	p__KSB1	c__MSB-5B5
k__Bacteria	k__Bacteria	p__KSB1	c__MSB-5B5
k__Bacteria	k__Bacteria	p__KSB1	c__MSB-5B5
k__Bacteria	k__Bacteria	p__KSB1	c__MSB-5B5
k__Bacteria	k__Bacteria	p__KSB1	c__Ucn15732
k__Bacteria	k__Bacteria	p__KSB1	c__unclassified
k__Bacteria	k__Bacteria	p__LCP-89	c__unclassified
k__Bacteria	k__Bacteria	p__LCP-89	c__unclassified
k__Bacteria	k__Bacteria	p__LCP-89	c__unclassified
k__Bacteria	k__Bacteria	p__LCP-89	c__unclassified
k__Bacteria	k__Bacteria	p__LCP-89	c__unclassified
k__Bacteria	k__Bacteria	p__LCP-89	c__unclassified
k__Bacteria	k__Bacteria	p__LD1	c__unclassified
k__Bacteria	k__Bacteria	p__LD1	c__unclassified
k__Bacteria	k__Bacteria	p__LD1	c__unclassified

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB

s__unclassified	52916
s__unclassified	58069
s__unclassified	53040
s__unclassified	53054
s__unclassified	53288
s__unclassified	53335
s__unclassified	53423
s__unclassified	53432
s__unclassified	53721
s__unclassified	53359
s__unclassified	51337
s__unclassified	51581
s__unclassified	51276
s__unclassified	58249
s__unclassified	58521
s__unclassified	57833
s__unclassified	57952
s__unclassified	58140
s__unclassified	58695
s__unclassified	57889
s__unclassified	57800
s__unclassified	58274
s__unclassified	58503
s__unclassified	58765
s__unclassified	58378
s__unclassified	58062
s__unclassified	57821
s__unclassified	58164
s__unclassified	58341
s__unclassified	58447
s__unclassified	58049
s__unclassified	58258
s__unclassified	57799
s__unclassified	57903
s__unclassified	58161
s__unclassified	58434
s__unclassified	58584
s__unclassified	58713
s__unclassified	58083
s__unclassified	58670
s__unclassified	58563

DQ329610.1 gg_id:159257 Guerrero Negro hypersaline microbial mat clone 062DZ28 DQ329
GQ472356.1 gg_id:546599 Microbial Dongping Lake lake sediment clone 3S4-17 GQ472
EU134901.1 gg_id:255924 tallgrass prarie soil clone FFCH3687 EU134
AB300086.1 gg_id:225464 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone A AB300
EU134900.1 gg_id:248928 tallgrass prarie soil clone FFCH18260 EU134
FJ901586.1 gg_id:567970 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita FJ9015
AB240362.1 gg_id:143463 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB240
EU134904.1 gg_id:249081 tallgrass prarie soil clone FFCH18804 EU134
AY050577.1 gg_id:106690 MCB-contaminated groundwater-treating reactor clone GOUTA4 AY050
AJ543759.1 gg_id:95866 anoxic sediment Lake Cadagno clone 49 AJ5437
FJ746261.1 gg_id:567096 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
AB237732.1 gg_id:139838 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB237
EU386097.1 gg_id:261462 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EF688196.1 gg_id:351571 Detection microbial sludge anaerobic wastewater treatment system clone 4E1_cons EF6881
FJ645694.1 gg_id:550022 Microbial dynamics during -temperature biotreatment PCP-contaminated wastestrea FJ6456
EU622292.1 gg_id:298479 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv EU622
DQ415793.1 gg_id:158359 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
EF602489.1 gg_id:233633 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EF687508.1 gg_id:283688 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6875
GQ249498.1 gg_id:562766 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor GQ249
DQ329567.1 gg_id:159197 Guerrero Negro hypersaline microbial mat clone 08D2Z50 DQ329
DQ329541.1 gg_id:159505 Guerrero Negro hypersaline microbial mat clone 05D2Z11 DQ329
EU246164.1 gg_id:237663 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E12 EU246
DQ329542.1 gg_id:159334 Guerrero Negro hypersaline microbial mat clone 05D2Z93 DQ329
EU407206.1 gg_id:273907 household biogas digester clone GW-22 EU407
EU246196.1 gg_id:246894 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-B01 EU246
FJ484771.1 gg_id:566342 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4847
FJ484430.1 gg_id:513424 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
FJ712497.1 gg_id:529594 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
DQ811937.1 gg_id:162879 mangrove soil clone MSB-5B5 DQ811
EU617724.1 gg_id:346244 Seasonal variation microbial Yel Sea sediment clone C13S-9 EU617
AM086123.1 gg_id:149924 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone c AM086
FJ712479.1 gg_id:532343 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
EU386122.1 gg_id:261859 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
AF286032.1 gg_id:26077 saltmarsh clone LCP-89 AF286
FJ716412.1 gg_id:562251 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
EU048684.1 gg_id:246605 and archaeal surface marine sediment Slope South China Sea clone MD2896-B27 EU048
FJ716279.1 gg_id:551134 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
GU363012.1 gg_id:532990 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU363
AY114321.1 gg_id:63785 anoxic marine sediment clone LD1-PA32 AY114
EU487944.1 gg_id:562517 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	1	1	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	0	0	0	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__Lentisphaerae
k__Bacteria	k__Bacteria	p__Lentisphaerae	c__unclassified
k__Bacteria	k__Bacteria	p__MD2896-B26	c__unclassified
k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1
k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1
k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1
k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1

o__Lentisphaerales	f__Lentisphaeraceae
o__Lentisphaerales	f__Lentisphaeraceae
o__Lentisphaerales	f__Lentisphaeraceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Victivallales	f__Victivallaceae
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__Z20	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__Lentisphaera
g__Lentisphaera
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Victivallis
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfC
g__sfD
g__sfD
g__sfE
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB

s__Lentisphaera araneosa	54262
s__unclassified	54602
s__unclassified	54142
s__unclassified	54064
s__unclassified	54077
s__unclassified	54124
s__unclassified	54132
s__unclassified	54174
s__unclassified	54180
s__unclassified	54357
s__unclassified	54373
s__unclassified	54374
s__unclassified	54429
s__unclassified	54501
s__unclassified	54542
s__unclassified	54620
s__unclassified	54745
s__unclassified	54775
s__unclassified	54825
s__unclassified	54911
s__unclassified	54912
s__Victivallis vadensis	54676
s__unclassified	54060
s__unclassified	54281
s__unclassified	54586
s__unclassified	54639
s__unclassified	54496
s__unclassified	54646
s__unclassified	54834
s__unclassified	54017
s__unclassified	54538
s__unclassified	54561
s__unclassified	54480
s__unclassified	54557
s__unclassified	54444
s__unclassified	54363
s__unclassified	58316
s__unclassified	74692
s__unclassified	75450
s__unclassified	75090
s__unclassified	75815

NR_027571.1 gg_id:568139 Lentisphaera araneosa HTCC2155 str. HTCC2155; ATCC BAA-859 NR_02
EU050936.1 gg_id:237639 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_46 EU050
EU617881.1 gg_id:308950 Seasonal variation microbial Yel Sea sediment clone C13S-64 EU617
EU373977.1 gg_id:275456 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
DQ903989.1 gg_id:243625 Cytophaga sp. PRPR22 DQ903
AB189358.1 gg_id:113979 cold seep sediment clone JT75-104 AB189
AJ431234.1 gg_id:79161 Cytophaga sp. str. Dex80-43 AJ4312
CU918294.1 gg_id:575335 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU236367.1 gg_id:299835 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91E2 EU236
GU302469.1 gg_id:552105 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
FJ172855.1 gg_id:349140 Qinghai Yak Ruminal and Fungi China rumen clone RB-3G5 FJ1728
DQ067008.1 gg_id:131533 Lake Washington sediment clone pLW-89 DQ067
FJ172836.1 gg_id:306087 Qinghai Yak Ruminal and Fungi China rumen clone RB-4D9 FJ1728
AB062771.1 gg_id:32071 termite gut homogenate clone BCf1-10 AB062
EU885059.1 gg_id:323370 microbial hindgut chamber Pomacanthus sexstriatus GI tract clone A2F3 EU885
EU491122.1 gg_id:266959 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
U81755.2 gg_id:1542 anaerobic digestor clone vadinHB65 U8175
AB009200.1 gg_id:14576 rumen clone RFN44 AB009
EU491130.1 gg_id:265874 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU850520.1 gg_id:342488 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF297 EU850
EF092196.1 gg_id:274447 Persistent Axinella corrugata Lentisphaerae clone Ax29_B12 EF0921
NZ_ABDE01000031.1 gg_id:235858 Victivallis vadensis str. ATCC BAA-548 NZ_AB
FJ833297.1 gg_id:551530 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A3Q401_04D01 FJ8332
EU462436.1 gg_id:290815 Sumatran orangutan feces clone orang1_aai54e09 EU462
DQ353908.1 gg_id:148459 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z20 DQ353
EU465080.1 gg_id:288148 African elephant feces clone AFYEL_aaj67g06 EU465
CU920558.1 gg_id:551462 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
CU924053.1 gg_id:571561 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EU459524.1 gg_id:287575 capybara feces clone CAP_aah99b07 EU459
AJ536842.1 gg_id:97002 chemocline clone 362 AJ5368
FJ755755.1 gg_id:563388 vertical archaeal water and Lake Taihu sediment clone LT-SB-B11 FJ7557
EU050937.1 gg_id:255593 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_35 EU050
GU196208.1 gg_id:584283 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
EF602493.1 gg_id:233246 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
AJ431235.1 gg_id:79502 Cytophaga sp. str. Dex80-64 AJ4312
AY553939.1 gg_id:113934 Baltimore Harbor sediment clone FA6 AY553
EU048683.1 gg_id:251056 and archaeal surface marine sediment Slope South China Sea clone MD2896-B26 EU048
GQ246316.1 gg_id:511355 Temporal and spatial China North Yel Sea sediments clone Sd1-35 GQ246
GU180194.1 gg_id:547075 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU385673.1 gg_id:265544 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
DQ521806.1 gg_id:160216 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	1	0	1	0	0	0
0	1	0	0	0	0	0	1	0	1	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1
k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1
k__Bacteria	k__Bacteria	p__MSBL6	c__AT425_EubG1
k__Bacteria	k__Bacteria	p__MSBL6	c__KB1
k__Bacteria	k__Bacteria	p__MSBL6	c__KB1
k__Bacteria	k__Bacteria	p__MSBL6	c__KB1
k__Bacteria	k__Bacteria	p__MSBL6	c__KB1
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__MVP-15	c__unclassified
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__12-24
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__NC10	c__wb1-A12
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__JH-WHS47	f__unclassified
o__JH-WHS47	f__unclassified
o__JH-WHS47	f__unclassified
o__JH-WHS47	f__unclassified
o__JH-WHS47	f__unclassified
o__Methylomirabiliales	f__Methylomirabiliaceae
o__Methylomirabiliales	f__Methylomirabiliaceae
o__Methylomirabiliales	f__Methylomirabiliaceae
o__Methylomirabiliales	f__Methylomirabiliaceae
o__Methylomirabiliales	f__Methylomirabiliaceae
o__MIZ17	f__unclassified
o__MIZ17	f__unclassified
o__MIZ17	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__Nitrospirales	f__FW
o__Nitrospirales	f__FW
o__Nitrospirales	f__FW
o__Nitrospirales	f__FW

g__sfC
g__sfC
g__sfD
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__Candidatus Methylomirabilis
g__Candidatus Methylomirabilis
g__Candidatus Methylomirabilis
g__Candidatus Methylomirabilis
g__Candidatus Methylomirabilis
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__4-29
g__4-29
g__4-29
g__4-29

s__unclassified	75000
s__unclassified	75796
s__unclassified	74651
s__unclassified	74676
s__unclassified	74732
s__unclassified	75166
s__unclassified	75595
s__unclassified	53017
s__unclassified	53315
s__unclassified	53504
s__unclassified	53595
s__unclassified	53637
s__unclassified	53644
s__unclassified	53686
s__unclassified	53800
s__unclassified	53602
s__unclassified	53345
s__unclassified	58394
s__unclassified	58411
s__unclassified	58648
s__unclassified	58803
s__unclassified	58847
s__unclassified	58203
s__unclassified	58397
s__unclassified	58510
s__unclassified	58653
s__unclassified	58750
s__unclassified	58277
s__unclassified	58485
s__unclassified	58517
s__unclassified	57788
s__unclassified	58000
s__unclassified	58126
s__unclassified	58245
s__unclassified	58532
s__unclassified	58600
s__unclassified	58709
s__unclassified	52181
s__unclassified	52278
s__unclassified	52469
s__unclassified	52470

EU542528.1 gg_id:269354 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
EU181498.1 gg_id:251185 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
DQ521805.1 gg_id:160462 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
EF106489.1 gg_id:202958 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2 EF1064
AJ133617.1 gg_id:1688 brine sediment clone KTK 32 AJ1336
EU246019.1 gg_id:246314 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-F02 EU246
FN393496.1 gg_id:552766 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1H1 FN393
GU390826.1 gg_id:526942 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
AJ536840.1 gg_id:95720 chemocline clone 331 AJ5368
AB539947.1 gg_id:569847 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB539
CU921965.1 gg_id:554874 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
AY570581.1 gg_id:108459 -temperature biodegraded Canadian oil reservoir clone PL-11B10 AY570
GU476613.1 gg_id:515032 microbial biogas fermentation enrichment clone BBMC-13 GU476
FJ462041.1 gg_id:580192 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
DQ354746.1 gg_id:152989 subsurface water clone MS149BH1062003_13 DQ354
GU196193.1 gg_id:591769 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
EU844484.1 gg_id:335853 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ748807.1 gg_id:578422 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estua FJ7488
AJ519650.1 gg_id:75874 uranium mill tailings soil sample clone Sh765B-TzT-35 AJ5196
AB426199.1 gg_id:274653 -situ identification study benzene-degrading s under methanogenic condition anaer AB426
AB486305.1 gg_id:538794 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBAR AB486
EF492972.1 gg_id:257902 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AF351214.1 gg_id:71271 coal tar-contaminated groundwater clone 12-24 AF351
FJ621558.1 gg_id:561816 Enrichment and detection denitrifying methanotrophic NC10 phylum eutrophic fresh FJ6215
DQ837250.1 gg_id:239257 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_43 DQ837
FJ907182.1 gg_id:573993 Enrichment anoxic methane utilizing denitrification (AnMUD) microorganisms mixed FJ9071
DQ369742.1 gg_id:156874 microbial consortium couples oxidation denitrification anaerobic methane oxidation DQ369
AB179508.1 gg_id:105296 sedimentary rock clone MIZ17 AB179
DQ906849.1 gg_id:250973 Oman subsurface soil clone 10A-11 DQ906
DQ906843.1 gg_id:244437 Oman subsurface soil clone 7C-23 DQ906
FJ205220.1 gg_id:556077 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
AM991185.1 gg_id:278069 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
EU491416.1 gg_id:260370 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
EU491462.1 gg_id:269959 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
AY177763.1 gg_id:79044 vadose clone 5G01 AY177
AF317743.1 gg_id:136988 Nullarbor cave clone wb1_A12 AF317
EU373968.1 gg_id:273635 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU373
EU335184.1 gg_id:242324 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
AF351231.1 gg_id:42281 upgradient coal tar waste-contaminated groundwater clone 4-29 sp. AF351
GU208486.1 gg_id:589700 Study on Sediment Dongping Lake sediment clone Shs2-20 GU208
DQ138963.1 gg_id:138815 rice straw paddy soil clone JG118 DQ138

1	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira

o__Nitrospirales	f__FW
o__Nitrospirales	f__FW
o__Nitrospirales	f__FW
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Leptospirillaceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae

g__GOUTA7
g__GOUTA7
g__GOUTA7
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__Leptospirillum
g__JG37-AG-70
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira

s__unclassified	52132
s__unclassified	52304
s__unclassified	52509
s__Leptospirillum ferriphilum	51954
s__Leptospirillum ferriphilum	52024
s__Leptospirillum ferriphilum	52696
s__Leptospirillum ferriphilum	52868
s__Leptospirillum ferrodiazotrophum	51889
s__Leptospirillum ferrodiazotrophum	51895
s__Leptospirillum ferrodiazotrophum	52128
s__Leptospirillum ferrodiazotrophum	52155
s__Leptospirillum ferrodiazotrophum	52213
s__Leptospirillum ferrodiazotrophum	52288
s__Leptospirillum ferrodiazotrophum	52337
s__Leptospirillum ferrodiazotrophum	52339
s__Leptospirillum ferrodiazotrophum	52371
s__Leptospirillum ferrodiazotrophum	52552
s__Leptospirillum ferrodiazotrophum	52592
s__Leptospirillum ferrooxidans	51851
s__Leptospirillum ferrooxidans	51920
s__Leptospirillum ferrooxidans	52246
s__Leptospirillum ferrooxidans	52282
s__Leptospirillum ferrooxidans	52350
s__Leptospirillum ferrooxidans	52631
s__Leptospirillum ferrooxidans	52722
s__unclassified	51980
s__unclassified	52095
s__unclassified	52662
s__unclassified	52459
s__Nitrospira sp.	52790
s__unclassified	51775
s__unclassified	51809
s__unclassified	51835
s__unclassified	51850
s__unclassified	51905
s__unclassified	51908
s__unclassified	51926
s__unclassified	51948
s__unclassified	52041
s__unclassified	52051
s__unclassified	52059

AY050579.1 gg_id:28363 MCB-contaminated groundwater-treating reactor clone GOUTA7 AY0505
AF523973.1 gg_id:63250 forested wetland clone FW13 AF5239
DQ138964.1 gg_id:138554 rice straw paddy soil clone JG325 DQ138
AF356831.1 gg_id:50647 Leptospirillum ferriphilum str. Warwick AF3568
EU733647.1 gg_id:319964 Leptospirillum ferriphilum str. YTW315 EU7336
GU168010.1 gg_id:584037 Leptospirillum ferriphilum GU168
DQ451017.1 gg_id:156803 Leptospirillum ferriphilum str. GX DQ451
DQ464149.1 gg_id:157346 acid mine drainage clone D1-90 DQ464
AF544226.1 gg_id:58150 acid mine drainage clone ASL9 AF5442
AB254780.1 gg_id:159816 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB2547
EU372645.1 gg_id:564896 Evaluation Leptospirillum spp. Rio Tinto basin model interest biohydrometallurgy wa EU3726
DQ328622.1 gg_id:149323 microorganisms populating site extreme acid mine drainage sediment clone H50 DQ328
FJ228338.1 gg_id:347059 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur FJ2283
DQ464151.1 gg_id:158060 acid mine drainage clone D1-95 DQ464
EF409845.1 gg_id:211316 acid mine drainage clone FKBZ-53-06 EF4098
AF543509.1 gg_id:56204 acid mine drainage clone BA33 AF5435
FJ228276.1 gg_id:344157 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur FJ2282
FJ228310.1 gg_id:311765 sulfate-reducing enriched during bioremediation experiment sediments (Brandenbur FJ2283
AF356835.1 gg_id:24590 Leptospirillum ferrooxidans str. Chil-Lf2 AF3568
AF356833.1 gg_id:41859 Leptospirillum ferrooxidans str. BCT2 AF3568
X86776.1 gg_id:1509 Leptospirillum ferrooxidans str. L15 DSM 2705 X86776
GU168016.1 gg_id:565828 Leptospirillum ferrooxidans GU168
AF356839.1 gg_id:39980 Leptospirillum ferrooxidans str. Sy AF3568
AY952274.1 gg_id:153665 Leptospirillum ferrooxidans AY9522
EF025338.1 gg_id:191142 Leptospirillum ferriphilum str. ZTS EF0253
DQ659194.1 gg_id:221094 acid mine drainage clone DBS-Clone19 DQ659
GU168013.1 gg_id:571763 Leptospirillum ferriphilum GU168
DQ223208.1 gg_id:143919 subsurface water clone EV221H2111601SAH4 DQ223
EF018100.1 gg_id:203943 aspen rhizosphere clone Amb_16S_432 EF0181
AF155154.1 gg_id:1493 Nitrospira cf. moscoviensis str. SBR2016 AF1551
AJ617918.1 gg_id:110103 oxic-anoxic interphase flooded paddy soil clone D023010 AJ6179
AY555798.1 gg_id:106808 Bor Khlueng hot spring clone PK287 AY5557
EU287071.1 gg_id:237590 Pacific arctic surface sediment clone B78-107 EU2870
AM997652.1 gg_id:542056 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EU803576.1 gg_id:332256 It's all ranking aquatic Lake Gatun clone 5C231165 EU8035
GQ249372.1 gg_id:583840 Research on biodiversity sludge bioflim Biological Aeration Filter clone B14 GQ249
DQ814725.1 gg_id:173004 zebrafish digestive tract clone aaa35h01 DQ814
AJ617920.1 gg_id:109789 oxic-anoxic interphase flooded paddy soil clone D023011 AJ6179
AY921743.1 gg_id:114282 farm soil clone AKYG586 AY9217
EU491464.1 gg_id:276859 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
DQ128338.2 gg_id:183441 conventional tillage soil clone HSB CT52_D06 DQ128

0	1	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira

o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Nitrospiraceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae

g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__Nitrospira
g__unclassified
g__unclassified
g__BD2-6
g__BD2-6
g__BD2-6
g__BD2-6
g__BD2-6
g__BD2-6
g__Candidatus Magnetobacterium
g__DCE29
g__DCE29

s__unclassified	52061
s__unclassified	52149
s__unclassified	52179
s__unclassified	52215
s__unclassified	52225
s__unclassified	52232
s__unclassified	52245
s__unclassified	52375
s__unclassified	52381
s__unclassified	52499
s__unclassified	52507
s__unclassified	52514
s__unclassified	52526
s__unclassified	52558
s__unclassified	52603
s__unclassified	52622
s__unclassified	52646
s__unclassified	52687
s__unclassified	52690
s__unclassified	52692
s__unclassified	52719
s__unclassified	52736
s__unclassified	52763
s__unclassified	52775
s__unclassified	52803
s__unclassified	52809
s__unclassified	52850
s__unclassified	52857
s__unclassified	52872
s__unclassified	52917
s__unclassified	52321
s__unclassified	52410
s__unclassified	51826
s__unclassified	51829
s__unclassified	52175
s__unclassified	52340
s__unclassified	52373
s__unclassified	52928
s__unclassified	52281
s__unclassified	51862
s__unclassified	52283

DQ811892.1 gg_id:166567 mangrove soil clone MSB-3C1 DQ811
FJ535097.1 gg_id:511523 microbial colonizing walls Karstic Slovenia cave wall biofilm clone 2PJM17 FJ5350
EU035954.2 gg_id:316621 Insight microbial structure Norwegian deep-water Desmacidon sponge deep-sea cor EU035
GU118642.1 gg_id:549595 Threatened Corals Provide Microbial Habitats clone Mfav_D14 GU118
EF492939.1 gg_id:257467 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
GQ848453.1 gg_id:588843 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
GQ500804.1 gg_id:586905 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
EF594048.1 gg_id:234702 mixed granule anammox reactor clone KIST-JJY015 EF5940
AY921494.2 gg_id:153641 Changes soils rice field soil clone AP19 AY9214
AY493911.1 gg_id:136740 Fingerprinting aggregates soil clone 1183 AY4939
NR_029287.1 gg_id:554350 Nitrospira moscoviensis str. NSP M-1; DSM 10035 NR_02
DQ451477.1 gg_id:156598 forest soil clone FAC38 DQ451
EU287156.1 gg_id:246040 Pacific arctic surface sediment clone P13-63 EU287
AJ863251.1 gg_id:120977 poplar tree microcosm bulk soil flooded clone 21BSF62 AJ8632
AJ617917.1 gg_id:111105 oxic-anoxic interphase flooded paddy soil clone D02307 AJ6179
GQ214107.1 gg_id:536771 China loess clone P859 GQ214
AB176700.1 gg_id:102911 subsurface geothermal water clone HAuD-LB/2-23 AB176
CU466688.1 gg_id:309217 Evry wastewater treatment plant anoxic basin clone CU466
AY921873.1 gg_id:113562 farm soil clone AKYG388 AY9218
AJ617919.1 gg_id:110431 oxic-anoxic interphase flooded paddy soil clone D14423 AJ6179
AY328715.1 gg_id:88698 drinking water system simulator clone DSSD16 AY3287
EF612393.1 gg_id:246188 historic semiarid lead-zinc mine tailings site soil clone OS-C76 EF6123
FJ529312.1 gg_id:570363 Evidence vertical transmission symbionts adult embryo Caribbean sponge Svenzea ze FJ5293
EF092255.1 gg_id:260626 Persistent Axinella corrugata Nitrospira clone MAx27_C6 EF0922
EU652665.1 gg_id:279215 Seasonal variation microbial Yel Sea sediment clone D8S-37 EU652
DQ058679.1 gg_id:139106 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit DQ058
AF317764.1 gg_id:136664 Nullarbor cave clone wb1_F07 AF317
EU491363.1 gg_id:274991 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
GQ472347.1 gg_id:545624 Microbial Dongping Lake lake sediment clone 3C2-9 GQ472
EF562103.1 gg_id:243273 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum EF5621
AJ863252.1 gg_id:123055 poplar tree microcosm bulk soil flooded clone 21BSF5 AJ8632
EF019030.1 gg_id:210132 aspen rhizosphere clone Amb_16S_1574 EF0190
AB015536.1 gg_id:150698 deep-sea sediments depths clone BD2-6 AB015
FJ416081.1 gg_id:368981 sediments sediment station NEC5 Northern Bering Sea clone 009K2 FJ4160
GQ357017.1 gg_id:582662 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_ GQ357
EU491391.1 gg_id:269847 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
EU734917.1 gg_id:307509 assemblages sediment station DBSE Northern Bering Sea clone 008A10 EU734
EU925847.1 gg_id:329091 sediments sediment station DBS1 northern Bering Sea clone 038E63 EU925
EU780676.1 gg_id:304501 magnetic-enriched magnetotactic Miyun reservoir Beijing China fresh water sedimer EU780
DQ478745.1 gg_id:157587 UASB reactor treating brewery wastewater clone CLONG59 DQ478
AB179690.1 gg_id:101911 groundwater 0.2 m-captured fraction clone KNA6-EB14 AB179

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	0	0	0	0	0	0	1
0	1	1	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__Nitrospirae	c__Nitrospira
k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__GN13

o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__Nitrospirales	f__Thermodesulfovibrionaceae
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified

g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__GOUTA19
g__HB118
g__HB118
g__LCP-6
g__LCP-6
g__LCP-6
g__LCP-6
g__LCP-6
g__LCP-6
g__LCP-6
g__LCP-6
g__LCP-6
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__Thermodesulfovibrio
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB

s__unclassified	51981
s__unclassified	52091
s__unclassified	52489
s__unclassified	52513
s__unclassified	52606
s__unclassified	52614
s__unclassified	52623
s__unclassified	52626
s__unclassified	52670
s__unclassified	52911
s__unclassified	52476
s__unclassified	52781
s__unclassified	51859
s__unclassified	51861
s__unclassified	52326
s__unclassified	52420
s__unclassified	52551
s__unclassified	52743
s__unclassified	52795
s__unclassified	52885
s__unclassified	52891
s__Thermodesulfovibrio yellowstonii	51845
s__Thermodesulfovibrio yellowstonii	52021
s__unclassified	51843
s__unclassified	51969
s__unclassified	52060
s__unclassified	52165
s__unclassified	52248
s__unclassified	52621
s__unclassified	52831
s__unclassified	52889
s__unclassified	52922
s__unclassified	52251
s__unclassified	52481
s__unclassified	52875
s__unclassified	57907
s__unclassified	57918
s__unclassified	58016
s__unclassified	58799
s__unclassified	58822
s__unclassified	58144

AB240355.1 gg_id:143990 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
GU208344.1 gg_id:555144 Study on Sediment Dongping Lake sediment clone Tds3-9 GU208
AB240285.1 gg_id:142177 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
GQ402751.1 gg_id:513871 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ755775.1 gg_id:581592 vertical archaeal water and Lake Taihu sediment clone LT-SB-B104 FJ7557
GQ402791.1 gg_id:572073 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ450806.1 gg_id:160776 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ395024.1 gg_id:151318 harbor sediment clone VHS-B5-55 DQ395
DQ138962.1 gg_id:138089 rice straw paddy soil clone JG131 DQ138
EU617719.1 gg_id:331634 Seasonal variation microbial Yel Sea sediment clone A13S-27 EU617
GU208367.1 gg_id:565006 Study on Sediment Dongping Lake sediment clone Td1-7 GU208
EF648166.1 gg_id:238866 dynamics during produced water treatment aerobic activated sludge clone XJ134 EF6481
DQ354748.1 gg_id:155453 subsurface water clone MS149BH1062003_38 DQ354
FJ484454.1 gg_id:540847 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
AF286037.1 gg_id:51852 mercury and PCB contaminated saltmarsh sediment clone LCP-6 LCP-6 AF286
DQ811894.1 gg_id:171789 mangrove soil clone MSB-3B5 DQ811
DQ833491.1 gg_id:167800 detected analyses depth sediment Guanting Reservoir clone 35-52 DQ833
FJ902311.1 gg_id:558620 phreatic limestone sinkholes northeastern Mexico biomat rock outcrop cenote La Pal FJ9023
EU592458.1 gg_id:594158 Seasonal changes Salton Sea hypersaline sediment clone SSS22N EU592
DQ811893.1 gg_id:167447 mangrove soil clone MSB-4D12 DQ811
FJ485017.1 gg_id:512051 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
CP001147.1 gg_id:336962 Thermodesulfovibrio yellowstonii str. DSM 11347 CP001
AB231858.1 gg_id:138300 Thermodesulfovibrio yellowstonii str. YP87 AB2318
EF081294.1 gg_id:188164 Thermodesulfovibrio sp. str. Hbr5 EF0812
GQ844371.1 gg_id:584184 Microbial anoxic tank full-scale water treatment plant influent produced wastewate GQ844
FJ638591.1 gg_id:511823 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AB231857.1 gg_id:200798 Thermodesulfovibrio sp. str. TDV AB2318
X96726.1 gg_id:1523 Thermodesulfovibrio islandicus str. R1ha3 X96726
EF205565.1 gg_id:208106 among geographically regions central Tibet geothermal spring mat clone TP17 EF2055
AB183860.1 gg_id:99703 deep aquifer Great Artesian Basin clone GAB-B04 AB1838
AF255602.1 gg_id:27466 Nitrospira sp. str. SRI-237 AF2556
AB021302.1 gg_id:1530 Thermodesulfovibrio sp. str. TGE-P1 AB0213
AY947906.1 gg_id:143270 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
GU289667.1 gg_id:526213 Moderately thermophilic magnetotactic Nevada USA hot springs clone HSMV-1 GU289
EU735733.1 gg_id:320307 Biological Arsenic Remediation Project Groundwater Aquifer soil clone C_I55 EU7357
FJ497655.1 gg_id:590984 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
DQ640738.1 gg_id:232235 full-scale EBPR sludge clone Skagen116 DQ640
FM213079.1 gg_id:568248 Biodiversity and shifts assessment biology tools Biotrickling treating loads biotricklin FM213
FJ497309.1 gg_id:540736 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
FJ516826.1 gg_id:552017 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s FJ5168
EF520619.1 gg_id:235051 structure lakes: what controls ? acid-impacted lake clone ACK-BTH02-32 EF5206

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__GN13
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__NKB19	c__unclassified
k__Bacteria	k__Bacteria	p__O1aA90	c__unclassified
k__Bacteria	k__Bacteria	p__OP1	c__GAL35
k__Bacteria	k__Bacteria	p__OP1	c__GAL35
k__Bacteria	k__Bacteria	p__OP1	c__OP1
k__Bacteria	k__Bacteria	p__OP11	c__OP11-1
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-2
k__Bacteria	k__Bacteria	p__OP11	c__OP11-3
k__Bacteria	k__Bacteria	p__OP11	c__OP11-3
k__Bacteria	k__Bacteria	p__OP11	c__OP11-4
k__Bacteria	k__Bacteria	p__OP11	c__OP11-4
k__Bacteria	k__Bacteria	p__OP11	c__unclassified
k__Bacteria	k__Bacteria	p__OP11	c__unclassified
k__Bacteria	k__Bacteria	p__OP11	c__WCHB1-64
k__Bacteria	k__Bacteria	p__OP11	c__WCHB1-64
k__Bacteria	k__Bacteria	p__OP11	c__WCHB1-64
k__Bacteria	k__Bacteria	p__OP11	c__WCHB1-64
k__Bacteria	k__Bacteria	p__OP11	c__WCHB1-64
k__Bacteria	k__Bacteria	p__OP11	c__WCHB1-64

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__BB36	f__unclassified
o__KD3-145	f__unclassified
o__KD3-145	f__unclassified
o__KD3-145	f__unclassified
o__KD3-145	f__unclassified
o__WCHB1-07	f__unclassified
o__WCHB1-07	f__unclassified
o__WCHB1-07	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__J-1	f__unclassified
o__RCP1-27	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__d153	f__unclassified
o__d153	f__unclassified
o__d153	f__unclassified
o__K2-4-19	f__unclassified
o__K2-4-19	f__unclassified
o__K2-4-19	f__unclassified

g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfC
g__sfD
g__sfE
g__sfF
g__sfG
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfB
g__sfC
g__sfA
g__sfB
g__sfC

s__unclassified	58407
s__unclassified	58686
s__unclassified	57900
s__unclassified	57944
s__unclassified	58289
s__unclassified	58809
s__unclassified	57879
s__unclassified	58186
s__unclassified	58297
s__unclassified	58449
s__unclassified	58005
s__unclassified	58722
s__unclassified	58875
s__unclassified	51880
s__unclassified	58601
s__unclassified	57858
s__unclassified	58015
s__unclassified	51705
s__unclassified	58530
s__unclassified	58278
s__unclassified	51590
s__unclassified	74806
s__unclassified	75170
s__unclassified	75602
s__unclassified	75894
s__unclassified	75688
s__unclassified	75539
s__unclassified	75565
s__unclassified	75845
s__unclassified	74758
s__unclassified	75301
s__unclassified	75868
s__unclassified	75204
s__unclassified	75691
s__unclassified	75340
s__unclassified	75876
s__unclassified	74894
s__unclassified	74983
s__unclassified	75890
s__unclassified	75885
s__unclassified	75174

GU208454.1 gg_id:562764 Study on Sediment Dongping Lake sediment clone Fr2-1 GU208
CU921757.1 gg_id:574695 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
DQ395545.1 gg_id:154578 deep-sea octacoral clone ctg_CGOCA85 DQ395
GU302451.1 gg_id:546200 Spatial structure and activity sedimentary microbial underlying Beggiatoa spp. mat h GU302
FJ497634.1 gg_id:570634 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
FJ497567.1 gg_id:539167 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
GQ246342.1 gg_id:566822 Temporal and spatial China North Yel Sea sediments clone Cm1-5 GQ246
EU617857.1 gg_id:306314 Seasonal variation microbial Yel Sea sediment clone C13S-3 EU617
FJ769506.1 gg_id:514019 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7695
EU245141.1 gg_id:238328 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-H0 EU245
GQ848462.1 gg_id:591704 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
EU491069.1 gg_id:263387 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
EU385825.1 gg_id:269047 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3858
EU591656.1 gg_id:275968 Microbial Ecology Focused-Pulsed Electric Field Sludge Pretreatment Methanogenic EU591
AJ306780.1 gg_id:66921 DCP degrading consortium clone SHA-100 AJ3067
DQ067040.1 gg_id:132726 Lake Washington sediment clone pLW-99 DQ067
GU118009.1 gg_id:554824 Threatened Corals Provide Microbial Habitats clone Apal_G06 GU118
AY193179.1 gg_id:80983 thermal spring mat clone O1aA90 AY193
EU635936.1 gg_id:278503 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EU635935.1 gg_id:278911 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EU924242.1 gg_id:310156 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU924
DQ404838.1 gg_id:202174 contaminated sediment clone 655967 DQ404
FJ189542.1 gg_id:340415 digester anaerobic sludge clone EUB_21 FJ1895
AY218580.1 gg_id:82092 penguin droppings sediments clone KD2-26 AY218
AY218586.1 gg_id:82149 penguin droppings sediments clone KD2-5 AY218
AY188303.1 gg_id:80684 marine? clone KD3-145 AY188
EU542445.1 gg_id:264265 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
AY188301.1 gg_id:99822 marine? clone KD2-44 AY188
AF050600.1 gg_id:10566 contaminated aquifer clone WCHB1-07 AF050
EF019888.1 gg_id:210172 aspen rhizosphere clone Elev_16S_1253 EF0198
EU386078.1 gg_id:269947 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EF019157.1 gg_id:206209 aspen rhizosphere clone Amb_16S_1804 EF0191
EU134976.1 gg_id:255464 tallgrass prarie soil clone FFCH9932 EU134
FJ479589.1 gg_id:509215 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
DQ298014.1 gg_id:142268 Microbial hydrocarbon contaminated soil clone UB12 DQ298
AF422676.1 gg_id:42849 TCE-sediment clone d153 AF422
CU924193.1 gg_id:534077 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
FJ710771.1 gg_id:593853 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
GQ356089.1 gg_id:556282 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU050864.1 gg_id:253554 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_10 EU050
EU386076.1 gg_id:274390 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386

1	0	0	1	1	0	1	0	1	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	1	0	1	1
1	1	1	1	1	1	1	0	0	1	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__BD4-9
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__koll11
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__PBS-25
k__Bacteria	k__Bacteria	p__OP3	c__unclassified
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1

o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__kpj58rc
o__GIF10	f__unclassified
o__GIF10	f__unclassified
o__GIF10	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfC
g__sfD
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfB
g__sfA
g__sfB
g__sfC
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfD
g__sfE
g__sfF
g__sfG
g__sfH
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	52301
s__unclassified	52399
s__unclassified	52450
s__unclassified	52495
s__unclassified	52768
s__unclassified	52828
s__unclassified	52504
s__unclassified	52206
s__unclassified	52185
s__unclassified	51911
s__unclassified	51983
s__unclassified	52135
s__unclassified	52138
s__unclassified	52223
s__unclassified	52296
s__unclassified	52485
s__unclassified	52597
s__unclassified	52617
s__unclassified	52919
s__unclassified	52290
s__unclassified	52874
s__unclassified	52678
s__unclassified	52634
s__unclassified	52668
s__unclassified	52274
s__unclassified	51974
s__unclassified	52303
s__unclassified	52106
s__unclassified	52227
s__unclassified	52083
s__unclassified	52046
s__unclassified	52609
s__unclassified	52675
s__unclassified	52739
s__unclassified	52156
s__unclassified	52556
s__unclassified	53117
s__unclassified	53193
s__unclassified	53367
s__unclassified	53405
s__unclassified	53463

EU386072.1 gg_id:264190 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EU386007.1 gg_id:266385 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
AB015559.1 gg_id:1665 deep-sea sediment clone BD4-9 AB015
EU385777.1 gg_id:271294 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
FJ746242.1 gg_id:511521 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU386085.1 gg_id:258248 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ356152.1 gg_id:575286 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU385765.1 gg_id:266542 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU385956.1 gg_id:271229 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU800499.1 gg_id:331078 It's all ranking aquatic Delaware Bay NJ clone 2C228620 EU800
AM997403.1 gg_id:534821 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AM991275.1 gg_id:279473 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
DQ676354.1 gg_id:226121 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AM997371.1 gg_id:538271 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AF507707.1 gg_id:65679 forest soil clone S042 AF507
AY661975.1 gg_id:137070 uranium-contaminated groundwater clone 300E2-C09 AY661
EU491175.1 gg_id:264161 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AM997579.1 gg_id:552101 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
GU208411.1 gg_id:592150 Study on Sediment Dongping Lake sediment clone Fh2-22 GU208
AY667264.1 gg_id:102531 TCE-dechlorinating groundwater clone TANB84 AY667
DQ837261.1 gg_id:238430 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_70 DQ837
AB232806.1 gg_id:138097 Microbial mesophilic chemostat cultivation propionate-degrading methanogenic con AB232
EF019262.1 gg_id:204198 aspen rhizosphere clone Elev_16S_444 EF0192
AB294344.1 gg_id:211556 Microbial structure deep coal seem groundwater stream clone SWB33 AB294
EU881347.1 gg_id:317758 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU881
EU491266.1 gg_id:274405 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU373974.1 gg_id:272286 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
FJ901639.1 gg_id:509494 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita FJ9016
FJ901656.1 gg_id:593533 phreatic limestone sinkholes northeastern Mexico biomat 30m deep cenote La Palita FJ9016
EU385757.1 gg_id:266325 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
DQ676379.1 gg_id:225089 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
GQ356163.1 gg_id:534717 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EF032777.1 gg_id:176040 cyanobacterial mat in lava cave clone HAVOmat111 EF0327
FJ719059.1 gg_id:517884 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_G0 FJ7190
AB294345.1 gg_id:204818 Microbial structure deep coal seem groundwater stream clone SWB34 AB294
AY850293.1 gg_id:137151 depending on what microbial treatment present soil clone w3 AY850
AJ704718.1 gg_id:109302 marine sediment clone HMMVPog-54 AJ7047
EU048680.1 gg_id:252470 and archaeal surface marine sediment Slope South China Sea clone MD2896-B22 EU048
EU385872.1 gg_id:263088 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AY704402.1 gg_id:112300 oceanic crust clone FS142-68B-02 AY704
GQ143758.1 gg_id:395003 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	1	0	0	0	1	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	0	1	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	1	1	0	1	0	1	0	0	1
1	1	1	1	1	1	1	1	0	1	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_1
k__Bacteria	k__Bacteria	p__OP8	c__OP8_2
k__Bacteria	k__Bacteria	p__OP8	c__OP8_2
k__Bacteria	k__Bacteria	p__OP8	c__OP8_2
k__Bacteria	k__Bacteria	p__OP8	c__OP8_2
k__Bacteria	k__Bacteria	p__OP8	c__unclassified
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1

o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__HMMVPog-54	f__unclassified
o__OPB95	f__unclassified
o__SHA-124	f__unclassified
o__SHA-124	f__unclassified
o__SHA-124	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__BA021	f__unclassified
o__BA021	f__unclassified
o__BA021	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfA
g__sfB
g__sfC
g__sfD
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	53481
s__unclassified	53482
s__unclassified	53544
s__unclassified	53560
s__unclassified	53582
s__unclassified	53590
s__unclassified	53623
s__unclassified	53707
s__unclassified	53751
s__unclassified	53775
s__unclassified	53828
s__unclassified	53835
s__unclassified	53880
s__unclassified	53903
s__unclassified	53372
s__unclassified	53779
s__unclassified	53107
s__unclassified	53556
s__unclassified	53049
s__unclassified	53350
s__unclassified	53469
s__unclassified	53246
s__unclassified	53577
s__unclassified	52946
s__unclassified	53700
s__unclassified	53680
s__unclassified	53915
s__unclassified	53924
s__unclassified	53170
s__unclassified	53788
s__unclassified	53938
s__unclassified	52955
s__unclassified	53002
s__unclassified	53084
s__unclassified	53101
s__unclassified	53256
s__unclassified	53275
s__unclassified	53404
s__unclassified	53519
s__unclassified	53588
s__unclassified	53654

EU385778.1 gg_id:265533 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU385676.1 gg_id:260694 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU181480.1 gg_id:249848 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
EU245272.1 gg_id:252038 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B04 EU245
AB177161.1 gg_id:133316 seafloor methane hydrate clone ODP1230B18.23 AB177
EU385795.1 gg_id:269229 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
FJ746322.1 gg_id:551173 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7463
DQ811948.1 gg_id:170025 mangrove soil clone MSB-4A8 DQ811
EU385934.1 gg_id:277377 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AB177172.1 gg_id:130540 seafloor methane hydrate clone ODP1230B20.28 AB177
EU385742.1 gg_id:266551 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU488093.1 gg_id:559670 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
DQ811949.1 gg_id:169350 mangrove soil clone MSB-3A8 DQ811
EU592453.1 gg_id:563387 Seasonal changes Salton Sea hypersaline sediment clone SSS83N EU592
EU245470.1 gg_id:252775 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-A0 EU245
EU245402.1 gg_id:238714 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-C0 EU245
FJ873297.1 gg_id:538899 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8732
FJ461971.1 gg_id:510303 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4619
DQ067009.1 gg_id:134526 Lake Washington sediment clone pLW-103 DQ067
EU399664.1 gg_id:273972 and localization microbial consortium full-scale granular activated carbon anaerobic EU399
AJ583209.1 gg_id:95059 radioactive site ground water clone S15B-MN72 AJ5832
AJ249097.1 gg_id:53679 DCP-dechlorinating consortium clone SHA-89 AJ2490
AY221615.1 gg_id:89676 metal and hydrocarbon contaminated soil clone HS9-75 AY2216
AF419691.1 gg_id:70520 Guaymas Basin hydrothermal sediment clone C1_B017 AF4196
EU290738.1 gg_id:257532 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
FJ755774.1 gg_id:592094 vertical archaeal water and Lake Taihu sediment clone LT-SB-B88 FJ7557
AF449263.1 gg_id:61847 Riftia pachyptila's tube clone R76-B102 AF4492
CR933160.1 gg_id:110989 Evry municipal wastewater treatment plant clone 009E07_B_SD_P15 CR9331
EU721812.1 gg_id:575401 microbial production water Alaskan mesothermic petroleum reservoir two methods EU7218
EU358736.1 gg_id:315354 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
EF559206.1 gg_id:225664 mesophilic anaerobic digester clone A35_D28_L_B_A04 EF5592
AM745221.1 gg_id:295808 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AF419693.1 gg_id:74279 Guaymas Basin hydrothermal sediment clone C1_B023 AF4196
AB300125.1 gg_id:224659 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
AJ535219.1 gg_id:77784 marine sediment above hydrate ridge clone Hyd01-10 division AJ5352
AM745133.1 gg_id:289184 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
AY542196.1 gg_id:112789 Gulf Mexico seafloor sediments clone GoM HDB-04 AY5421
AB525465.1 gg_id:586929 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed AB5254
AB189340.1 gg_id:113184 cold seep sediment clone JT58-14 AB1893
FJ712453.1 gg_id:530784 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
AF419682.1 gg_id:72683 Guaymas Basin hydrothermal sediment clone CS_B013 AF4196

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__JS1
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__OP9	c__OPB46
k__Bacteria	k__Bacteria	p__PAUC34f	c__unclassified
k__Bacteria	k__Bacteria	p__PAUC34f	c__unclassified
k__Bacteria	k__Bacteria	p__PAUC34f	c__unclassified
k__Bacteria	k__Bacteria	p__PAUC34f	c__unclassified
k__Bacteria	k__Bacteria	p__PAUC34f	c__unclassified
k__Bacteria	k__Bacteria	p__PAUC34f	c__unclassified
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27

o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__SB-45	f__unclassified
o__OPB72	f__TIBD11
o__OPB72	f__TIBD11
o__OPB72	f__TIBD11
o__OPB72	f__TIBD11
o__OPB72	f__TIBD11
o__OPB72	f__TIBD11
o__OPB72	f__unclassified
o__OPB72	f__unclassified
o__SHA-1	f__unclassified
o__SHA-1	f__unclassified
o__SHA-1	f__unclassified
o__SHA-1	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__CL500-15	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfD
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfC
g__sfD
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	53682
s__unclassified	53770
s__unclassified	53905
s__unclassified	53956
s__unclassified	53963
s__unclassified	55064
s__unclassified	55117
s__unclassified	55576
s__unclassified	55834
s__unclassified	56086
s__unclassified	56359
s__unclassified	55559
s__unclassified	55729
s__unclassified	55218
s__unclassified	55393
s__unclassified	55546
s__unclassified	56382
s__unclassified	58453
s__unclassified	58851
s__unclassified	57834
s__unclassified	58116
s__unclassified	58195
s__unclassified	58469
s__unclassified	52076
s__unclassified	52300
s__unclassified	52327
s__unclassified	52393
s__unclassified	52471
s__unclassified	52641
s__unclassified	52660
s__unclassified	52821
s__unclassified	52863
s__unclassified	52078
s__unclassified	52081
s__unclassified	52157
s__unclassified	52257
s__unclassified	51881
s__unclassified	51978
s__unclassified	52068
s__unclassified	52413
s__unclassified	52446

AY592418.1 gg_id:100189 deep-sea mud volcano clone Amsterdam-2B-61; BC20-2B-61 AY5924
AB300107.1 gg_id:223917 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB300
EU386091.1 gg_id:273192 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EU290732.1 gg_id:242377 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
AF154105.1 gg_id:13713 hydrocarbon seep sediment clone GCA018 AF154
EU639265.1 gg_id:335164 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
CU919953.1 gg_id:542554 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU919427.1 gg_id:541379 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU920257.1 gg_id:539233 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EF559042.1 gg_id:249738 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF559
EF558973.1 gg_id:248313 Microbial functional groups solid waste digestor stable isotope probing thermophilic EF558
EU635950.1 gg_id:278345 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
AF027082.1 gg_id:1654 hot spring clone OPB47 AF027
AJ306782.1 gg_id:66918 DCP-dechlorinating consortium clone SHA-1 AJ3067
AB195912.1 gg_id:109200 Anaerobic sludge clone N10 AB195
CU925213.1 gg_id:561559 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
AB195913.1 gg_id:109201 Anaerobic sludge clone N16 AB195
GU118564.1 gg_id:592392 Threatened Corals Provide Microbial Habitats clone Mfav_F21 GU118
AY485295.1 gg_id:106114 marine sponge clone 232 AY485
AY627378.1 gg_id:103111 marine clone AY627378 AY627
GQ349157.1 gg_id:575293 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
FJ746128.1 gg_id:539443 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7461
EF076099.1 gg_id:238478 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF076
EU617889.1 gg_id:327521 Seasonal variation microbial Yel Sea sediment clone D13S-68 EU617
FJ208807.1 gg_id:307010 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
FJ208813.1 gg_id:305954 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
GQ348002.1 gg_id:540414 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ208832.1 gg_id:332638 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
DQ058681.1 gg_id:139290 Identification biofilm and bulk s nonchlorinated model system: detection large nitrit DQ058
BX294710.2 gg_id:84726 aerobic basin clone CY0ARA025G12 BX294
EF575301.1 gg_id:227921 site S25 near Coco's Island marine clone S25_1645 EF5753
FJ485411.1 gg_id:509346 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4854
EU236408.1 gg_id:290327 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E7 EU236
EF208657.1 gg_id:201142 Vertical and horizontal structure microbial sandy carbonate sediment clone CI35cm.2 EF2086
GQ246374.1 gg_id:577122 Temporal and spatial China North Yel Sea sediments clone Cm1-37 GQ246
AM997498.1 gg_id:560658 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
FJ208809.1 gg_id:352790 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
L10943.1 gg_id:2910 Marine sp. (aggregate agg27) generated fragment L10943
EU478627.1 gg_id:339005 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
AY907752.1 gg_id:137332 identification picoplankton contrasting waters Arabian Sea water clone A314014 AY9077
AM997936.1 gg_id:548511 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__agg27
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__C6
k__Bacteria	k__Bacteria	p__Planctomycetes	c__FFCH393
k__Bacteria	k__Bacteria	p__Planctomycetes	c__FFCH393
k__Bacteria	k__Bacteria	p__Planctomycetes	c__FFCH393
k__Bacteria	k__Bacteria	p__Planctomycetes	c__FFCH393
k__Bacteria	k__Bacteria	p__Planctomycetes	c__FFCH393
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Koll-18
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Koll-18
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Koll-18
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae

o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__OM190	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Kueneniaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae

g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfD
g__sfD
g__sfE
g__sfF
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfC
g__sfD
g__sfD
g__sfA
g__sfA
g__sfB
g__sfC
g__sfD
g__sfA
g__sfB
g__sfC
g__Candidatus Anammoxoglobus
g__Candidatus Brocadia
g__Candidatus Brocadia
g__Candidatus Brocadia
g__Candidatus Jettenia
g__Candidatus Jettenia
g__Candidatus Kuenenia
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua

s__unclassified	52578
s__unclassified	52674
s__unclassified	52776
s__unclassified	52150
s__unclassified	52271
s__unclassified	52273
s__unclassified	52555
s__unclassified	52214
s__unclassified	52528
s__unclassified	52557
s__unclassified	52750
s__unclassified	52388
s__unclassified	51971
s__unclassified	51839
s__unclassified	52037
s__unclassified	52445
s__unclassified	51917
s__unclassified	52836
s__unclassified	52294
s__unclassified	52900
s__unclassified	52127
s__unclassified	52906
s__unclassified	52230
s__unclassified	52587
s__unclassified	52810
s__unclassified	51970
s__unclassified	52700
s__unclassified	51674
s__unclassified	51127
s__unclassified	51440
s__unclassified	53871
s__unclassified	53137
s__unclassified	53309
s__unclassified	53561
s__unclassified	53095
s__unclassified	53466
s__unclassified	53887
s__Candidatus Scalindua brodae	53465
s__Candidatus Scalindua brodae	53580
s__Candidatus Scalindua marina	53210
s__Candidatus Scalindua marina	53505

FJ652534.1 gg_id:570506 aerobic and anaerobic ammonia-oxidizing marine sponges Atlantic Ocean water colur FJ6525
DQ513072.1 gg_id:160383 Microbial life fluids ridge flank crustal fluid clone FS266-6B-03 DQ513
EF092217.1 gg_id:270621 Persistent Axinella corrugata clone B255_19a EF0922
FJ208822.1 gg_id:333159 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
FJ208814.1 gg_id:336106 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
FJ208815.1 gg_id:318107 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2088
EF516837.1 gg_id:223894 grassland soil clone FCPS655 EF5168
GQ349982.1 gg_id:579975 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
DQ513105.1 gg_id:161200 Microbial life fluids ridge flank crustal fluid clone FS275-24B-03 DQ513
EU373996.1 gg_id:270915 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU373
EU491188.1 gg_id:266276 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU478635.1 gg_id:332383 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EF645945.1 gg_id:242961 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6459
GU118095.1 gg_id:584707 Threatened Corals Provide Microbial Habitats clone Apal_E05 GU118
EU050872.1 gg_id:237785 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_05 EU050
DQ070801.1 gg_id:147446 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
CU917688.1 gg_id:569653 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
AM056027.1 gg_id:137533 anammox wastewater treatment plant AM056
AM490671.1 gg_id:550928 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AY266450.1 gg_id:85294 Baltimore Harbor sediment clone B4 AY2664
EU478641.1 gg_id:338211 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
FN396716.1 gg_id:565403 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN3967
EU135126.1 gg_id:257290 tallgrass prarie soil clone FFCH12905 EU1351
FJ444691.1 gg_id:565666 Cotton Rhizosphere cotton rhizosphere clone 3h-166 FJ4446
FJ905739.1 gg_id:535979 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F106b FJ9057
GQ339140.1 gg_id:527968 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
EU617888.1 gg_id:353402 Seasonal variation microbial Yel Sea sediment clone D13S-58 EU6178
EU638793.1 gg_id:340317 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6387
GQ347619.1 gg_id:580887 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF314425.1 gg_id:39505 aerobic phosphorus-removal ecosystem clone PHOS-HE93 AF3144
EU478694.1 gg_id:312765 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
FJ710640.1 gg_id:513938 Abundance and microbial long-term operated anammox reactors initiated inocula upi FJ7106
FJ710627.1 gg_id:534693 Abundance and microbial long-term operated anammox reactors initiated inocula upi FJ7106
GQ356125.1 gg_id:576581 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU661858.1 gg_id:292847 and kinetic research ammonia mixed sludge anaerobic ammonium oxidation reactor EU6618
AB057453.1 gg_id:28149 Planctomycete clone KSU-1 AB0574
GQ175284.1 gg_id:578161 nitrogen removal reactors lab scale SBR inorganic medium and glucose influence org GQ175
AY254883.1 gg_id:102606 rotating biological contactor clone EN 8 AY2548
AY257181.1 gg_id:92388 Candidatus Scalindua sorokinii AY2571
DQ386151.1 gg_id:206446 Anaerobic Ammonium Oxidizing Marine Widespread Occurrence but sea water Gulli DQ386
EF602038.1 gg_id:296196 Anammox marine sediments: cell numbers potential anammox activity and pore nutr EF6020

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Kueneniae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__ODP123
k__Bacteria	k__Bacteria	p__Planctomycetes	c__ODP123
k__Bacteria	k__Bacteria	p__Planctomycetes	c__ODP123
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae

o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__Kueneniales	f__Scalinduaceae
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__Phycisphaeraceae
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified

g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__Candidatus Scalindua
g__sfA
g__sfA
g__sfB
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB

s__Candidatus Scalindua marina	53695
s__Candidatus Scalindua wagneri	52968
s__Candidatus Scalindua wagneri	53290
s__unclassified	52954
s__unclassified	52976
s__unclassified	52986
s__unclassified	53041
s__unclassified	53067
s__unclassified	53068
s__unclassified	53314
s__unclassified	53328
s__unclassified	53399
s__unclassified	53417
s__unclassified	53452
s__unclassified	53585
s__unclassified	53630
s__unclassified	53739
s__unclassified	53778
s__unclassified	53797
s__unclassified	53810
s__unclassified	53881
s__unclassified	52365
s__unclassified	52861
s__unclassified	52001
s__unclassified	54168
s__unclassified	54190
s__unclassified	54423
s__unclassified	54427
s__unclassified	54645
s__unclassified	54660
s__unclassified	54794
s__unclassified	54249
s__unclassified	54438
s__unclassified	54467
s__unclassified	54574
s__unclassified	54623
s__unclassified	54636
s__unclassified	54688
s__unclassified	54808
s__unclassified	54905
s__unclassified	54075

EU142947.1 gg_id:324638 Enrichment and two marine anammox involved nitrogen gas production anaerobic a EU142
AB300486.1 gg_id:219357 Detection Activity and Anammox Genes Coastal Marine Sediments Japan intertidal s AB300
AB281489.1 gg_id:194829 anaerobic ammonium-oxidizing planctomycete JMK-2 AB281
EU478593.1 gg_id:324123 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU039861.1 gg_id:316215 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478626.1 gg_id:345186 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU478620.1 gg_id:307226 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU478663.1 gg_id:308582 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
GQ350985.1 gg_id:588411 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU039851.1 gg_id:334236 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478595.1 gg_id:335981 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
DQ869384.1 gg_id:173040 evidence broad anaerobic ammonium-oxidizing freshwater and marine sediments B DQ869
EU039841.1 gg_id:338086 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478687.1 gg_id:306841 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU039858.1 gg_id:318377 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU039856.1 gg_id:305926 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
GQ143786.1 gg_id:381880 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
EU478661.1 gg_id:328021 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
EU039855.1 gg_id:347502 Anaerobic Ammonium Oxidation Anammox Oxygen Minimum Zone Northern upper EU039
EU478664.1 gg_id:307650 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU478
DQ534739.1 gg_id:229398 Anaerobic ammonium oxidation contributes significantly nitrogen loss Peruvian oxy DQ534
EU385873.1 gg_id:258876 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU385800.1 gg_id:262268 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
AB177204.1 gg_id:131205 seafloor methane hydrate clone ODP1230B31.20 AB177
EU050874.1 gg_id:239076 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_21 EU050
AB474364.1 gg_id:554768 Phycisphaera mikrensis str. NBRC 102668 AB474
FJ516779.1 gg_id:569736 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5167
EU236426.1 gg_id:302876 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92H6 EU236
FJ202723.1 gg_id:356606 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
EU491354.1 gg_id:261113 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
AF445715.1 gg_id:44762 Planctomycetales clone SM2B12 AF445
DQ811901.1 gg_id:173711 mangrove soil clone MSB-4A3 DQ811
EF632950.1 gg_id:252359 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
AY344414.1 gg_id:91792 Lake Kauhako surface clone K2-S-7 AY344
FJ205228.1 gg_id:533393 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
EU135058.1 gg_id:239668 tallgrass prarie soil clone FFCH1059 EU135
FJ205225.1 gg_id:568694 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
EU801770.1 gg_id:341049 It's all ranking aquatic Chesapeake Bay MD clone 3C003141 EU801
FJ626886.1 gg_id:510050 Identification Phytodetritus Degrading Microbial Sublittoral Gulf Mexico Sands ocean FJ6268
EU135079.1 gg_id:247437 tallgrass prarie soil clone FFCH3889 EU135
AB430337.1 gg_id:276470 Removal Nitrogen Compounds Coupling Anoxic Ammonium Oxidation and Nitrate Re AB430

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Phycisphaerae
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Phycisphaerales	f__unclassified
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae

g__sfB
g__sfC
g__sfC
g__sfD
g__sfD
g__sfE
g__sfE
g__sfF
g__sfG
g__sfH
g__sfI
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__Gemmata
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	54425
s__unclassified	54208
s__unclassified	54705
s__unclassified	54451
s__unclassified	54508
s__unclassified	54332
s__unclassified	54731
s__unclassified	54874
s__unclassified	54657
s__unclassified	54005
s__unclassified	54536
s__unclassified	56417
s__unclassified	56453
s__unclassified	56486
s__unclassified	56543
s__unclassified	56562
s__unclassified	56809
s__unclassified	56996
s__unclassified	57025
s__unclassified	57057
s__unclassified	57065
s__unclassified	57241
s__unclassified	57307
s__unclassified	57360
s__unclassified	57564
s__unclassified	57689
s__unclassified	56570
s__unclassified	56649
s__unclassified	56663
s__unclassified	56702
s__unclassified	56735
s__unclassified	56761
s__unclassified	56788
s__unclassified	56797
s__unclassified	56807
s__unclassified	56858
s__unclassified	56875
s__unclassified	56892
s__unclassified	56929
s__unclassified	57015
s__unclassified	57040

AB434262.1 gg_id:340702 Effect concentration on treatment non-woven biomass carrier sludge taken anammc AB434
DQ351812.1 gg_id:146588 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EU236371.1 gg_id:294838 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg9F4 EU236
AM086132.1 gg_id:145659 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone (AM086
FJ612210.1 gg_id:561975 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.3.10 FJ6122
DQ396220.1 gg_id:151370 deep-sea octacoral clone ctg_NISA377 DQ396
DQ513014.1 gg_id:160569 Microbial life fluids ridge flank crustal fluid clone FS140-16B-02 DQ513
AY162125.1 gg_id:135863 Cultivating Sargasso Sea clone GMD15D02 AY162
EF574227.1 gg_id:231309 site S25 near Coco's Island marine clone S25_571 EF5742
EF632831.1 gg_id:237452 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) sedir EF6328
AY957928.1 gg_id:115016 drinking water biofilm clone B3NR69D13 AY957
EU135121.1 gg_id:248077 tallgrass prarie soil clone FFCH5834 EU135
DQ450805.1 gg_id:200837 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EU662552.1 gg_id:553506 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU662
EF515938.1 gg_id:218719 grassland soil clone FCPP573 EF515
FJ901683.1 gg_id:591480 phreatic limestone sinkholes northeastern Mexico biomat sediment cenote La Palita (FJ9016
GU359065.1 gg_id:531410 rhizosphere soil peanut clone 1S21 GU359
AF407717.1 gg_id:201735 microbial Australia's Great Artesian Basin 52 deg. C brown filament clone B16 AF407
GQ356133.1 gg_id:566719 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EU881297.1 gg_id:304737 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU881
AF312220.1 gg_id:199817 -based BTX-catabolizing microbial African sandy soil South Africa: KwaZulu-Natal Pro AF312
EF580964.1 gg_id:277693 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM1 EF5809
AF121889.1 gg_id:200587 analyses sulfidogenic and phenol-degrading microbial consortia 2-bromophenol-deh AF1218
DQ521520.1 gg_id:202207 Antarctic lake ice cover clone ANTLV2_E09 DQ521
AJ616270.1 gg_id:202670 and seasonal changes planctomycetales biofilms river biofilm clone DEL26 AJ6162
AB240380.1 gg_id:201941 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
EF516039.1 gg_id:225108 grassland soil clone FCPN712 EF5160
EF125955.1 gg_id:581157 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose EF1259
FJ232661.1 gg_id:308368 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
AB486233.1 gg_id:540991 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
EU135254.1 gg_id:255557 tallgrass prarie soil clone FFCH8636 EU135
FJ479411.1 gg_id:572242 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EU135178.1 gg_id:237749 tallgrass prarie soil clone FFCH7061 EU135
FJ232680.1 gg_id:333924 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
AY963421.1 gg_id:203044 analyses structures soils evergreen broad-leaved forests south-west China soil clone AY9634
FJ479427.1 gg_id:586523 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF580956.1 gg_id:279355 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM9 EF5809
DQ413078.1 gg_id:201687 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU881243.1 gg_id:312527 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EU135175.1 gg_id:248027 tallgrass prarie soil clone FFCH6996 EU135
EU044117.1 gg_id:239077 luences structure fosters richness subtropical Altamaha Ohopee River Valley inland c EU044

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Gemmataceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Gemmatales	f__Isosphaeraceae
o__Planctomycetales	f__Planctomycetaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Isosphaera
g__Isosphaera
g__Isosphaera
g__Singulisphaera
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__A17

s__unclassified	57048
s__unclassified	57093
s__unclassified	57119
s__unclassified	57159
s__unclassified	57216
s__unclassified	57223
s__unclassified	57260
s__unclassified	57317
s__unclassified	57399
s__unclassified	57416
s__unclassified	57430
s__unclassified	57485
s__unclassified	57495
s__unclassified	57553
s__unclassified	57652
s__unclassified	57701
s__unclassified	56407
s__unclassified	56595
s__unclassified	57308
s__Singulisphaera acidiphila	56720
s__unclassified	56484
s__unclassified	56605
s__unclassified	56614
s__unclassified	56625
s__unclassified	56933
s__unclassified	56987
s__unclassified	57001
s__unclassified	57010
s__unclassified	57017
s__unclassified	57019
s__unclassified	57146
s__unclassified	57247
s__unclassified	57359
s__unclassified	57462
s__unclassified	57576
s__unclassified	57583
s__unclassified	57591
s__unclassified	57616
s__unclassified	57630
s__unclassified	57718
s__unclassified	56442

CU921500.1 gg_id:549231 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
EU135265.1 gg_id:236310 tallgrass prarie soil clone FFCH18216 EU135
EU135274.1 gg_id:242459 tallgrass prarie soil clone FFCH18590 EU135
EU881267.1 gg_id:321885 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
FJ612288.1 gg_id:576167 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.14 FJ6122
FJ466217.1 gg_id:563036 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
FJ536899.1 gg_id:590906 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5368
FJ203423.1 gg_id:331911 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
EU135107.1 gg_id:249175 tallgrass prarie soil clone FFCH2726 EU135
FJ232673.1 gg_id:325828 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2326
EF516153.1 gg_id:220916 grassland soil clone FCPN669 EF5161
GQ093878.1 gg_id:397840 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ652504.1 gg_id:593106 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-38 FJ6525
EF019897.1 gg_id:205038 aspen rhizosphere clone Elev_16S_1264 EF0198
EU881193.1 gg_id:326719 Karst region natural restoration land soil clone KNR200711-121 EU881
EU135245.1 gg_id:250454 tallgrass prarie soil clone FFCH17044 EU135
AJ231195.1 gg_id:2884 Isosphaera pallida AJ2311
DQ814661.1 gg_id:201392 Reciprocal Gut Microbiota Transplants Zebrafish and Mice Germ-free Recipients Hos DQ814
DQ814734.1 gg_id:200402 Reciprocal Gut Microbiota Transplants Zebrafish and Mice Germ-free Recipients Hos DQ814
AM902526.1 gg_id:250059 Singulisphaera acidiphila str. PO2 AM902
AY234528.1 gg_id:112330 soil isolate Ellin5111 AY2345
GQ402671.1 gg_id:552820 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB238776.1 gg_id:146076 shal subsurface Sarobetsu Mire peat soil clone HSM-SS-013 AB238
GQ264465.1 gg_id:545566 Structure Simulated Level Waste Site simulated level waste site clone WW3_167 GQ264
DQ986200.1 gg_id:186517 planctomycete member Isosphaera genus freshwater aquarium Isosphaera-like str. DQ986
EU669616.1 gg_id:340209 soil clone S22-2 EU669
EU289510.1 gg_id:246083 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU289
AJ252623.1 gg_id:20352 agricultural soil clone SC-I-20 AJ2526
EF515969.1 gg_id:220676 grassland soil clone FCPP710 EF5159
AB254788.1 gg_id:160585 Biogenic Fe-oxyhydroxides nodules (takashikozo) encrusted iron-oxide reducing sedi AB254
AJ867920.1 gg_id:202171 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone C8 AJ8679
EU861926.1 gg_id:345379 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
EF019037.1 gg_id:215283 aspen rhizosphere clone Amb_16S_1586 EF0190
X81959.1 gg_id:2877 Isophaera sp. str. 640 X81959
DQ532192.1 gg_id:170729 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
AJ292683.1 gg_id:27191 PCB-polluted soil clone 2112 AJ2926
X81958.1 gg_id:2879 Isophaera sp. str. 666 X81958
EF492942.1 gg_id:249037 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
AF465649.1 gg_id:35108 planctomycete clone YNPRH1A AF4656
EF516492.1 gg_id:222936 grassland soil clone FCPS404 EF5164
EU335237.1 gg_id:241588 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335

0	0	0	0	0	0	0	0	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	1	0	0	1	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	0	1
0	1	0	0	1	0	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	1	0	0
0	0	0	0	1	0	1	0	0	0	1	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	1	1	1	0	1	1	0	1
0	0	0	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

g__A17
g__A17
g__A17
g__A17
g__A17
g__A17
g__A17
g__A17
g__A17
g__A17
g__Blastopirellula
g__Blastopirellula
g__Blastopirellula
g__Pirellula
g__Pirellula
g__Pirellula
g__Pirellula
g__Pirellula
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces

s__unclassified	56549
s__unclassified	56611
s__unclassified	56664
s__unclassified	56733
s__unclassified	56736
s__unclassified	56938
s__unclassified	57151
s__unclassified	57330
s__unclassified	57698
s__unclassified	57702
s__Blastopirellula marina	56971
s__unclassified	56905
s__unclassified	57520
s__Pirellula staleyi	57607
s__unclassified	56511
s__unclassified	56784
s__unclassified	56923
s__unclassified	57626
s__Planctomyces brasiliensis	57234
s__Planctomyces limnophilus	56589
s__Planctomyces maris	56922
s__unclassified	56388
s__unclassified	56401
s__unclassified	56434
s__unclassified	56529
s__unclassified	56588
s__unclassified	56646
s__unclassified	56651
s__unclassified	56684
s__unclassified	56717
s__unclassified	56746
s__unclassified	56753
s__unclassified	56785
s__unclassified	56790
s__unclassified	56800
s__unclassified	56902
s__unclassified	56909
s__unclassified	56920
s__unclassified	56973
s__unclassified	57006
s__unclassified	57008

EU135036.1 gg_id:241400 tallgrass prarie soil clone FFCH5359 EU135
EU135064.1 gg_id:252536 tallgrass prarie soil clone FFCH11875 EU135
FJ478520.1 gg_id:513639 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AF234700.1 gg_id:35556 sludge clone A25 AF2347
GQ356088.1 gg_id:542965 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EF516829.1 gg_id:219667 grassland soil clone FCPN696 EF5168
EU135135.1 gg_id:235394 tallgrass prarie soil clone FFCH1662 EU135
EU589315.1 gg_id:273690 China Ningxia rice paddy field soil clone 2_H12 EU5893
AF234760.1 gg_id:33376 sludge clone A17 AF2347
FJ232659.1 gg_id:322102 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
FJ543069.1 gg_id:531452 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
X86391.1 gg_id:2815 Pirellula sp. str. AGA/M12 X86391
GQ264007.1 gg_id:509308 Structure Simulated Level Waste Site simulated level waste site clone WC3_03 GQ264
M34126.1 gg_id:2826 Pirellula staleyi M3412
AM902592.1 gg_id:245810 Acidobacteria and Planctomycetes radioactive mineral Central Alps Austria subsurfa AM902
AJ616292.1 gg_id:107831 river biofilm clone DEL77 AJ6162
EU135081.1 gg_id:257073 tallgrass prarie soil clone FFCH2281 EU135
AJ252628.1 gg_id:28765 agricultural soil clone SC-I-28 AJ2526
AF513967.1 gg_id:62476 planctomycete clone LA4-B40N AF5139
X62911.1 gg_id:2845 Planctomyces limnophilus X62911
GQ850548.1 gg_id:568227 surface water northern Bering Sea clone u78 GQ850
AJ231186.1 gg_id:2859 Planctomyces sp. str. 248 AJ2311
EF019893.1 gg_id:207109 aspen rhizosphere clone Elev_16S_1259 EF0198
AJ616272.1 gg_id:106693 river biofilm clone DEL30 AJ6162
EU236333.1 gg_id:288195 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2A6 EU2363
AB286452.1 gg_id:205500 Reducing production and domination comamonadaceae reducing oxygen supply was AB2864
EU703485.1 gg_id:385507 lakes on Eastern Tin Plateau freshwater lake altitude 4279 masl clone XZZLH76 EU7034
GQ264049.1 gg_id:532634 Structure Simulated Level Waste Site simulated level waste site clone WC3_146 GQ264
EU135201.1 gg_id:246619 tallgrass prarie soil clone FFCH11725 EU135
EU135291.1 gg_id:243965 tallgrass prarie soil clone FFCH3333 EU135
FJ232636.1 gg_id:318175 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
GU118118.1 gg_id:577627 Threatened Corals Provide Microbial Habitats clone Apal_L16 GU118
GQ093884.1 gg_id:415267 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
DQ256391.1 gg_id:143227 Cloning and microorganism genes alkaline soil clone pGXAR2 DQ256
EF580936.1 gg_id:278198 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4 EF5809
GQ202636.1 gg_id:576162 RFLP two library insect-resistant trans-genic and its control soil conventional cotton GQ202
FJ232624.1 gg_id:325188 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
FJ236055.1 gg_id:356355 three Parisian treatment plants approaches drinking water clone Joinville4 FJ2360
AJ576406.1 gg_id:105661 midgut homogenate Pachnoda ephippiata larva clone PeM40 AJ5764
GQ264445.1 gg_id:591299 Structure Simulated Level Waste Site simulated level waste site clone WW3_146 GQ264
AJ231185.1 gg_id:2863 Planctomyces sp. str. 423 AJ2311

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	0	0	0	0	0	1	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	0	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Planctomyces
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula

s__unclassified	57047
s__unclassified	57049
s__unclassified	57060
s__unclassified	57124
s__unclassified	57170
s__unclassified	57179
s__unclassified	57219
s__unclassified	57230
s__unclassified	57277
s__unclassified	57305
s__unclassified	57336
s__unclassified	57345
s__unclassified	57357
s__unclassified	57443
s__unclassified	57450
s__unclassified	57535
s__unclassified	57541
s__unclassified	57555
s__unclassified	57572
s__unclassified	57602
s__unclassified	57612
s__unclassified	57635
s__unclassified	57643
s__unclassified	57672
s__unclassified	57676
s__unclassified	57688
s__unclassified	57744
s__unclassified	57748
s__unclassified	57756
s__Rhodopirellula baltica	56540
s__Rhodopirellula baltica	56734
s__Rhodopirellula baltica	56854
s__Rhodopirellula baltica	56872
s__Rhodopirellula baltica	57468
s__Rhodopirellula baltica	57621
s__unclassified	56406
s__unclassified	56424
s__unclassified	56519
s__unclassified	56523
s__unclassified	56535
s__unclassified	56604

AF029079.1 gg_id:2853 Planctomyces complete clone 7F15 AF029
EU332801.1 gg_id:368930 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU332
FJ232625.1 gg_id:337721 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
X81954.1 gg_id:2868 Planctomyces sp. str. 658 X81954
GQ487909.1 gg_id:585391 Microbial metal soil polluted heavy metals clone T1-58 GQ487
DQ228417.1 gg_id:199905 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU979049.1 gg_id:308618 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
AJ252614.1 gg_id:46917 agricultural soil clone SC-I-11 AJ2526
EF157243.1 gg_id:255306 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
GQ488002.1 gg_id:533542 Microbial metal soil polluted heavy metals clone V8-4 GQ488
FJ624888.1 gg_id:509799 Influence lead contamination on boreal pine forest soil clone HF_C_15 FJ6248
GQ994843.1 gg_id:588567 planctomycete bloom eutrophic and simulated blooms algal microcosms lake sedim GQ994
FJ542938.1 gg_id:517269 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU491846.1 gg_id:270163 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GQ487907.1 gg_id:589189 Microbial metal soil polluted heavy metals clone T1-42 GQ487
FJ437980.1 gg_id:545573 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
EU617893.1 gg_id:314251 Seasonal variation microbial Yel Sea sediment clone D13S-21 EU617
DQ815011.1 gg_id:162552 zebrafish digestive tract clone aab56g07 DQ815
FJ542891.1 gg_id:521367 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
GQ263999.1 gg_id:558118 Structure Simulated Level Waste Site simulated level waste site clone WC2_93 GQ263
GU183590.1 gg_id:556104 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a GU183
GQ009454.1 gg_id:500211 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AJ616260.1 gg_id:101336 river biofilm clone DEL04 AJ6162
BX294907.2 gg_id:84917 anaerobic digester clone CY0ARA056H03 BX2949
AY532587.1 gg_id:102577 uranium-contaminated aquifer clone 1013-28-CG52 AY5325
AY328798.1 gg_id:88168 drinking water system simulator clone DSSD101 AY3287
FJ230918.1 gg_id:339412 under Level Antibiotic Selection Pressures river water clone F45 FJ2309
DQ395915.1 gg_id:152923 deep-sea octacoral clone ctg_CGOF043 DQ395
GQ402618.1 gg_id:512701 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF589344.1 gg_id:231022 Rhodopirellula baltica str. OJF17 EF5893
EF421452.1 gg_id:211974 Rhodopirellula baltica str. OJF14 EF4214
EF421451.1 gg_id:215170 Rhodopirellula baltica str. OJF13 EF4214
EF589343.1 gg_id:227672 Rhodopirellula baltica str. OJF16 EF5893
EF012748.1 gg_id:192974 Rhodopirellula baltica str. OJF4 EF0127
EF012749.1 gg_id:180732 Rhodopirellula baltica str. OJF5 EF0127
EU236437.1 gg_id:297164 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg63H3 EU2364
AM259894.1 gg_id:212998 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-09 AM259
EU236342.1 gg_id:295035 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2H2 EU2363
FJ624356.1 gg_id:440418 Rhodopirellula sp. str. SM50 FJ6243
DQ640663.1 gg_id:233756 full-scale EBPR sludge clone Skagenf17 DQ640
FJ624322.1 gg_id:448778 Rhodopirellula sp. str. CS14 FJ6243

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	1	1	1	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	0	1	1	1	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	0	0	1
0	0	0	1	1	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__Rhodopirellula
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	56608
s__unclassified	56626
s__unclassified	56637
s__unclassified	56655
s__unclassified	56676
s__unclassified	56704
s__unclassified	56710
s__unclassified	56731
s__unclassified	56748
s__unclassified	56770
s__unclassified	56865
s__unclassified	56908
s__unclassified	56974
s__unclassified	56978
s__unclassified	57012
s__unclassified	57131
s__unclassified	57168
s__unclassified	57218
s__unclassified	57226
s__unclassified	57264
s__unclassified	57315
s__unclassified	57363
s__unclassified	57379
s__unclassified	57385
s__unclassified	57428
s__unclassified	57466
s__unclassified	57486
s__unclassified	57593
s__unclassified	57615
s__unclassified	57625
s__unclassified	57683
s__unclassified	57732
s__unclassified	57753
s__unclassified	57766
s__unclassified	52474
s__unclassified	52773
s__unclassified	54011
s__unclassified	54021
s__unclassified	54027
s__unclassified	54031
s__unclassified	54036

GU305724.1 gg_id:558514 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
X81942.1 gg_id:2801 Pirellula sp. str. 302 X81942
EU249951.1 gg_id:245163 Polyphasic description Pocillopora seawater adjacent Pacillopora meandrina coral co EU2499
EF157256.1 gg_id:245908 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
FJ624353.1 gg_id:418512 Rhodopirellula sp. str. SM44 FJ6243
DQ986201.1 gg_id:190032 Pirellula sp. OJF3 DQ986
EF012750.1 gg_id:184921 Rhodopirellula baltica str. OJF6 EF0127
X81939.1 gg_id:2767 Pirellula sp. str. 140 X81939
EU812984.1 gg_id:323488 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
DQ499312.1 gg_id:159626 acidic cave snottite biofilm clone CV73 DQ499
GQ246290.1 gg_id:512628 Temporal and spatial China North Yel Sea sediments clone Sd1-9 GQ246
EU246802.1 gg_id:240923 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
AJ616261.1 gg_id:101508 river biofilm clone DEL05 AJ6162
AY907796.1 gg_id:136912 identification picoplankton contrasting waters Arabian Sea water clone A714001 AY9077
AB294955.1 gg_id:222378 -dependent & analyses hydrothermal system off Taketomi Island Japan microbial ma AB2949
GU061671.1 gg_id:549851 and function microbial mesoscale eddy perturbations South China Sea clone CE2-DC GU061
DQ903990.1 gg_id:235788 Microbes Hawaiian Marine Sponge Suberites zeteki USA: Oahu Hawaii clone PRPR39 DQ903
X81940.1 gg_id:2783 Pirellula sp. str. 516 X81940
FJ624355.1 gg_id:399640 Rhodopirellula sp. str. SM49 FJ6243
EF574895.1 gg_id:233369 site S25 near Coco's Island marine clone S25_1239 EF5748
FJ623363.1 gg_id:583343 Efficient polyhydroxyalkanoates production waste-activated submitted process seque FJ6233
FJ624354.1 gg_id:395015 Rhodopirellula sp. str. SM48 FJ6243
GU061406.1 gg_id:569946 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m GU061
EU037330.2 gg_id:269075 structure landfill sediments receiving long-term augmentations wastes chromium co EU0373
X81943.1 gg_id:2800 Pirellula sp. str. 382 X81943
X81941.1 gg_id:2787 Pirellula sp. str. 158 X81941
X81945.1 gg_id:2793 Pirellula sp. str. 139 X81945
FJ624364.1 gg_id:421926 Rhodopirellula sp. str. SM23 FJ6243
GQ302560.1 gg_id:542353 prokaryotic sediment Shawan methods cold spring clone sw-xj213 GQ302
EU703306.1 gg_id:435220 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH106 EU7033
AJ431347.1 gg_id:40268 Greenland:Ikka Fjord clone AJ4313
AF468237.1 gg_id:80863 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKCH2Br2-9 AF4682
EU491585.1 gg_id:271404 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU4915
FJ624347.1 gg_id:400480 Rhodopirellula baltica str. SH155 IFAM 1436 FJ6243
FJ205295.1 gg_id:557224 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
EU050866.1 gg_id:237562 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_87 EU0508
FJ485080.1 gg_id:560755 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
FJ197610.1 gg_id:338655 deep Pacific Ocean and Eastern Mediterranean Sea sediment clone ALVIN29a_5E_FL FJ1976
GQ143793.1 gg_id:403814 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
GQ339128.1 gg_id:517627 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
AB177200.1 gg_id:137395 seafloor methane hydrate clone ODP1230B30.13 AB1772

0	0	1	0	0	1	1	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

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

s__unclassified	54041
s__unclassified	54052
s__unclassified	54063
s__unclassified	54072
s__unclassified	54073
s__unclassified	54087
s__unclassified	54089
s__unclassified	54096
s__unclassified	54099
s__unclassified	54116
s__unclassified	54140
s__unclassified	54149
s__unclassified	54157
s__unclassified	54159
s__unclassified	54162
s__unclassified	54170
s__unclassified	54192
s__unclassified	54230
s__unclassified	54234
s__unclassified	54236
s__unclassified	54251
s__unclassified	54269
s__unclassified	54277
s__unclassified	54300
s__unclassified	54301
s__unclassified	54316
s__unclassified	54318
s__unclassified	54322
s__unclassified	54324
s__unclassified	54326
s__unclassified	54337
s__unclassified	54341
s__unclassified	54348
s__unclassified	54351
s__unclassified	54379
s__unclassified	54393
s__unclassified	54403
s__unclassified	54404
s__unclassified	54424
s__unclassified	54440
s__unclassified	54454

DQ676328.1 gg_id:219735 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AY921874.1 gg_id:114298 farm soil clone AKYG1711 AY9218
GU444061.1 gg_id:523807 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
DQ206406.1 gg_id:139615 microbial mediates arsenate reduction soda lake water clone ML--10 DQ206
AM997881.1 gg_id:576223 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EF516155.1 gg_id:227320 grassland soil clone FCPT723 EF5161
AB530247.1 gg_id:544394 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB530
AF507705.1 gg_id:65683 forest soil clone S165 AF5077
DQ450803.1 gg_id:161593 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
FJ746253.1 gg_id:510156 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU048670.1 gg_id:257221 and archaeal surface marine sediment Slope South China Sea clone MD2896-B10 EU048
FJ873309.1 gg_id:562253 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8733
EF688380.1 gg_id:237185 soil clone F6-89 EF6883
EU245970.1 gg_id:250462 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-H0 EU2459
GU322886.1 gg_id:548781 Metaproteomics -temperature anaerobic granular sludge cultivated temperatures c GU322
GQ246434.1 gg_id:594302 Temporal and spatial China North Yel Sea sediments clone Ld1-39 GQ246
AY493903.1 gg_id:136324 Fingerprinting aggregates soil clone 1430 AY4939
FJ264747.1 gg_id:311487 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
CU923200.1 gg_id:550970 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
GQ246448.1 gg_id:576923 Temporal and spatial China North Yel Sea sediments clone Ld1-53 GQ246
AF507704.1 gg_id:55354 forest soil clone C167 AF5077
AY963300.1 gg_id:156060 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
EU386080.1 gg_id:262812 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
FJ479214.1 gg_id:543366 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
U81656.2 gg_id:2794 anaerobic digestor clone vadinBA30 U8165
EF019225.1 gg_id:210216 aspen rhizosphere clone Elev_16S_394 EF0192
FJ712480.1 gg_id:518323 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
FJ638603.1 gg_id:576295 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6386
EU622299.1 gg_id:296920 syntrophic partnerships deep-sea vents direct cell capture and metagenomics Eel Riv EU622
EF019958.1 gg_id:215591 aspen rhizosphere clone Elev_16S_1337 EF0199
EU245568.1 gg_id:248646 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B0 EU2455
EU135296.1 gg_id:244874 tallgrass prarie soil clone FFCH4400 EU135
EU135033.1 gg_id:235601 tallgrass prarie soil clone FFCH5199 EU135
EF516309.1 gg_id:223655 grassland soil clone FCPT556 EF5163
EU245782.1 gg_id:251795 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-C0 EU2457
FJ264744.1 gg_id:327743 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
EU385736.1 gg_id:271883 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU3857
AF423302.1 gg_id:35667 soil clone 96-2 AF4233
EU245905.1 gg_id:258094 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-A0 EU2459
DQ329791.1 gg_id:159475 Guerrero Negro hypersaline microbial mat clone 05D2Z14 DQ329
EF612394.1 gg_id:255351 historic semiarid lead-zinc mine tailings site soil clone OS-C18 EF6123

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	0	0	0	0	1	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

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

s__unclassified	54456
s__unclassified	54477
s__unclassified	54488
s__unclassified	54494
s__unclassified	54540
s__unclassified	54553
s__unclassified	54559
s__unclassified	54562
s__unclassified	54572
s__unclassified	54582
s__unclassified	54587
s__unclassified	54594
s__unclassified	54631
s__unclassified	54653
s__unclassified	54654
s__unclassified	54692
s__unclassified	54702
s__unclassified	54708
s__unclassified	54733
s__unclassified	54755
s__unclassified	54756
s__unclassified	54787
s__unclassified	54839
s__unclassified	54842
s__unclassified	54855
s__unclassified	54859
s__unclassified	54869
s__unclassified	54894
s__unclassified	54898
s__unclassified	54909
s__unclassified	56393
s__unclassified	56402
s__unclassified	56414
s__unclassified	56440
s__unclassified	56446
s__unclassified	56447
s__unclassified	56459
s__unclassified	56472
s__unclassified	56506
s__unclassified	56507
s__unclassified	56524

EU386028.1 gg_id:265434 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
EU385723.1 gg_id:262361 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
CU919054.1 gg_id:548383 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
EU786130.1 gg_id:556144 cotton rhizosphere soil clone 3H-211 EU786
EF018222.1 gg_id:203959 aspen rhizosphere clone Amb_16S_572 EF0182
EU385921.1 gg_id:264090 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU385781.1 gg_id:268863 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
FJ485338.1 gg_id:571346 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
EF540419.1 gg_id:220924 oil-shale semi-coke solid waste clone MK11 EF5404
EF032768.1 gg_id:181593 cyanobacterial mat in lava cave clone HAVOmat68 EF0327
EU245501.1 gg_id:245089 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-D0 EU245
AB177155.1 gg_id:136191 seafloor methane hydrate clone ODP1230B16.23 AB177
GQ844339.1 gg_id:543377 Microbial full-scale produced water treatment plant biofilm anoxic tank clone BB-B5 GQ844
GQ472311.1 gg_id:573896 Microbial Dongping Lake lake sediment clone 2B3-12 GQ472
FJ748808.1 gg_id:585249 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estua FJ7488
GQ143768.1 gg_id:454105 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
EU386008.1 gg_id:273669 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
DQ811900.1 gg_id:163946 mangrove soil clone MSB-5C12 DQ811
FJ545451.1 gg_id:508778 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-19 FJ5454
EU245488.1 gg_id:235811 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M2-B0 EU245
EF208700.1 gg_id:200413 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
EF516637.1 gg_id:225058 grassland soil clone FCPS673 EF5166
AJ292685.1 gg_id:44216 PCB-polluted soil clone WD283 AJ2926
FJ444683.1 gg_id:588682 Cotton Rhizosphere cotton rhizosphere clone 2y-55 FJ4446
GU056117.1 gg_id:554003 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
FN563400.1 gg_id:556620 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
EF018678.1 gg_id:211992 aspen rhizosphere clone Amb_16S_968 EF0186
EF515994.1 gg_id:219383 grassland soil clone FCPT539 EF5159
EU181513.1 gg_id:237389 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
EF019563.1 gg_id:214259 aspen rhizosphere clone Elev_16S_1077 EF0195
EU491712.1 gg_id:272697 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ232638.1 gg_id:347560 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
FJ712491.1 gg_id:510851 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
GQ356165.1 gg_id:573216 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
FJ478514.1 gg_id:544225 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
FJ232658.1 gg_id:353016 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
EU491293.1 gg_id:271990 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU135104.1 gg_id:243304 tallgrass prarie soil clone FFCH17847 EU135
EU374014.1 gg_id:271620 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
AY592336.1 gg_id:104089 deep-sea mud volcano clone Amsterdam-1B-32; BC20-1B-32 AY5923
FJ203528.1 gg_id:337295 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035

0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	0	1	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	1	1	1
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	0	1	1	1	0	0	0
0	0	0	0	0	0	0	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

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

s__unclassified	56528
s__unclassified	56564
s__unclassified	56594
s__unclassified	56596
s__unclassified	56643
s__unclassified	56680
s__unclassified	56682
s__unclassified	56694
s__unclassified	56719
s__unclassified	56743
s__unclassified	56759
s__unclassified	56760
s__unclassified	56765
s__unclassified	56771
s__unclassified	56780
s__unclassified	56819
s__unclassified	56827
s__unclassified	56836
s__unclassified	56837
s__unclassified	56838
s__unclassified	56840
s__unclassified	56851
s__unclassified	56864
s__unclassified	56867
s__unclassified	56869
s__unclassified	56885
s__unclassified	56887
s__unclassified	56888
s__unclassified	56890
s__unclassified	56894
s__unclassified	56916
s__unclassified	56921
s__unclassified	56926
s__unclassified	56946
s__unclassified	56956
s__unclassified	56960
s__unclassified	56964
s__unclassified	57004
s__unclassified	57011
s__unclassified	57021
s__unclassified	57027

GU118069.1 gg_id:568055 Threatened Corals Provide Microbial Habitats clone Apal_G07 GU118
FJ712558.1 gg_id:516943 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
GU118019.1 gg_id:592923 Threatened Corals Provide Microbial Habitats clone Apal_F10 GU118
AY913229.1 gg_id:113272 forest soil clone DUNssu001 (+1B) (OTU#209) AY913
GU118132.1 gg_id:588256 Threatened Corals Provide Microbial Habitats clone Apal_N24 GU118
DQ289921.1 gg_id:165216 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ873317.1 gg_id:512846 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8733
GQ356148.1 gg_id:571807 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
FJ516887.1 gg_id:535958 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5168
EU843071.1 gg_id:348461 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
FJ652501.1 gg_id:582419 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-33 FJ6525
AY114326.1 gg_id:71342 anoxic marine sediment clone LD1-PA40 AY1143
EU491864.1 gg_id:259028 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4918
FJ203614.1 gg_id:306565 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
FJ203304.1 gg_id:323269 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ232644.1 gg_id:337297 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2326
DQ396219.1 gg_id:152458 deep-sea octacoral clone ctg_NISA190 DQ396
EF573103.1 gg_id:229876 Coco's Island site 23 marine clone S23_1202 EF5731
GQ487912.1 gg_id:578134 Microbial metal soil polluted heavy metals clone T1-103 GQ487
FJ205299.1 gg_id:548823 Prokaryotic deep-sea region East Lau Spreading Centre active hydrothermal field sedi FJ2052
FJ203110.1 gg_id:337594 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
EU734992.1 gg_id:341990 assemblages sediment station DBSE Northern Bering Sea clone 086B35 EU734
FJ203078.1 gg_id:355875 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
GQ356114.1 gg_id:512540 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
AB486712.1 gg_id:589011 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR AB486
EF123574.1 gg_id:249219 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbe EF1235
EF125439.1 gg_id:179213 mangrove soil clone MSB-2E1 EF1254
GQ340148.1 gg_id:586939 Prokaryotic Marathonas Reservoir Greece water column clone B07-89-BAC GQ340
AM774187.1 gg_id:278832 lineages Planctomycetes densely colonize alkaline gut soil-feeding termites (Cubiter AM774
AB192132.1 gg_id:202625 termite gut homogenate clone M1NP1-64 AB192
AM086149.1 gg_id:149208 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
GU369884.1 gg_id:518971 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AF234735.1 gg_id:50882 sludge clone A8 AF2347
EF020031.1 gg_id:216224 aspen rhizosphere clone Elev_16S_1426 EF0200
CU926663.1 gg_id:535989 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
EF125452.1 gg_id:190111 mangrove soil clone MSB-2F5 EF1254
GU118783.1 gg_id:558104 Threatened Corals Provide Microbial Habitats clone Mfra_K07 GU118
GQ340267.1 gg_id:579129 Prokaryotic Marathonas Reservoir Greece water column clone A08-139-BAC GQ340
AJ306767.1 gg_id:66932 DCP-dechlorinating consortium clone SHA-87 AJ3067
FJ203428.1 gg_id:327231 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
EF516721.1 gg_id:218584 grassland soil clone FCPU585 EF5167

0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	1	0	0
1	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	1	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	1	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae

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

s__unclassified	57029
s__unclassified	57037
s__unclassified	57059
s__unclassified	57070
s__unclassified	57088
s__unclassified	57117
s__unclassified	57134
s__unclassified	57143
s__unclassified	57158
s__unclassified	57160
s__unclassified	57176
s__unclassified	57187
s__unclassified	57206
s__unclassified	57211
s__unclassified	57239
s__unclassified	57240
s__unclassified	57251
s__unclassified	57286
s__unclassified	57294
s__unclassified	57303
s__unclassified	57343
s__unclassified	57346
s__unclassified	57354
s__unclassified	57370
s__unclassified	57372
s__unclassified	57398
s__unclassified	57488
s__unclassified	57494
s__unclassified	57513
s__unclassified	57514
s__unclassified	57521
s__unclassified	57527
s__unclassified	57529
s__unclassified	57552
s__unclassified	57574
s__unclassified	57588
s__unclassified	57613
s__unclassified	57623
s__unclassified	57631
s__unclassified	57679
s__unclassified	57710

AF027058.1 gg_id:2799 hot spring clone OPB6 AF027(
EU245214.1 gg_id:237911 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-B12 EU245
DQ329768.1 gg_id:201435 Guerrero Negro hypersaline microbial mat clone 02D2Z12 DQ329
EU386107.1 gg_id:265536 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
DQ070794.1 gg_id:147997 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
FJ203440.1 gg_id:321503 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
AB486437.1 gg_id:552968 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB486
GU302676.1 gg_id:533316 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ232648.1 gg_id:323064 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
EU135213.1 gg_id:244630 tallgrass prarie soil clone FFCH13721 EU135
GQ214098.1 gg_id:562881 China loess clone P818 GQ214
EF540354.1 gg_id:225493 oil-shale semi-coke solid waste clone 24B_MJK EF5403
AY704401.1 gg_id:112006 oceanic crust clone FS142-21B-02 AY704
FJ232639.1 gg_id:332829 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
GU118848.1 gg_id:532921 Threatened Corals Provide Microbial Habitats clone Mfra_N03 GU118
AJ390475.1 gg_id:200304 lineages (sub)division level detected signature nucleotide-targeted recovery genes b AJ3904
DQ404806.1 gg_id:155344 contaminated sediment clone 661261 DQ404
EF205581.1 gg_id:214356 among geographically regions central Tibet geothermal spring mat clone TP5 EF2055
GU118276.1 gg_id:548121 Threatened Corals Provide Microbial Habitats clone Dstr_C07 GU118
FJ232651.1 gg_id:351648 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
DQ404633.1 gg_id:152343 contaminated sediment clone 656078 DQ404
EF125406.1 gg_id:178940 soil naked tidal flat sediment near mangrove clone MSB-1E4 EF1254
FJ203554.1 gg_id:342344 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EF208715.1 gg_id:200049 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
DQ289931.1 gg_id:170286 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EF208689.1 gg_id:200911 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.FC EF2086
AB240225.1 gg_id:142901 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
AB270056.1 gg_id:170512 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
AJ290182.1 gg_id:200064 and seasonal changes planctomycetales biofilms extracted river biofilm s clone DSP2 AJ2901
EU381635.1 gg_id:264273 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EF419414.1 gg_id:204219 Substantial alterations cutaneous biota psoriatic lesions human skin clone 6P2-75 EF4194
FJ516944.1 gg_id:509690 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
FJ542842.1 gg_id:525666 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
X81948.1 gg_id:2823 Pirellula str. 670 X81948
GQ246406.1 gg_id:536385 Temporal and spatial China North Yel Sea sediments clone Ld1-11 GQ246
DQ289943.1 gg_id:168811 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
EU488313.1 gg_id:555142 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ232657.1 gg_id:342256 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludg FJ2326
AY225652.1 gg_id:96259 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-38 AY2256
FJ437939.1 gg_id:544528 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
DQ070834.1 gg_id:150611 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	1	1	1	0	0	0
0	1	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	1	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	1	1	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__Planctomycea
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__PW285
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Planctomycetes	c__vadinHA49
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__Planctomycetales	f__Planctomycetaceae
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__unclassified	f__unclassified
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfC
g__sfD
g__sfA
g__sfA
g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__sfB
g__sfC
g__sfC
g__sfD
g__sfE
g__sfF
g__sfG
g__Asticcacaulis
g__Asticcacaulis
g__Asticcacaulis
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas

s__unclassified	57716
s__unclassified	57722
s__unclassified	57726
s__unclassified	57757
s__unclassified	57765
s__unclassified	57768
s__unclassified	57769
s__unclassified	57776
s__unclassified	57779
s__unclassified	51857
s__unclassified	52346
s__unclassified	52522
s__unclassified	52682
s__unclassified	52429
s__unclassified	52521
s__unclassified	52869
s__unclassified	52011
s__unclassified	52948
s__unclassified	53357
s__unclassified	53361
s__unclassified	53811
s__unclassified	52959
s__unclassified	53066
s__unclassified	53498
s__unclassified	53858
s__unclassified	53171
s__unclassified	53400
s__unclassified	52569
s__unclassified	52014
s__unclassified	51754
s__unclassified	52454
s__Asticcacaulis biprosthecium	59419
s__Asticcacaulis biprosthecium	60053
s__Asticcacaulis excentricus	59110
s__Brevundimonas alba	58878
s__Brevundimonas diminuta	58940
s__Brevundimonas diminuta	58971
s__Brevundimonas diminuta	58987
s__Brevundimonas diminuta	59016
s__Brevundimonas diminuta	59071
s__Brevundimonas diminuta	59132

CT574224.1 gg_id:154335 evidence planctomycete Evry municipal wastewater treatment plant clone 029B06_F CT5742
FJ542996.1 gg_id:514874 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EU734986.1 gg_id:353483 assemblages sediment station DBSE Northern Bering Sea clone 080B24 EU7349
EU491549.1 gg_id:269000 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU4915
FJ172792.1 gg_id:344848 Qinghai Yak Ruminal and Fungi China rumen clone RB-2C12 FJ1727
FJ203088.1 gg_id:312705 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
EF494313.1 gg_id:224266 Nunnock River granitic landscape clone NR.4.006 EF4943
DQ984569.1 gg_id:245832 Mt. Nan-Jen soil clone IFD_124 DQ984
AB355065.1 gg_id:252268 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB3550
EF515912.1 gg_id:217349 grassland soil clone FCPO648 EF5159
AB487699.1 gg_id:588740 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4876
FJ208839.1 gg_id:351437 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2088
GQ402727.1 gg_id:545813 Accessing microbial biodiversity and metabolic potential tropical -based approach pe GQ402
FJ905699.1 gg_id:513469 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F13b FJ9056
FJ652511.1 gg_id:586795 aerobic and anaerobic ammonia-oxidizing sponges marine sponge clone ML-Pla-24 FJ6525
FJ208828.1 gg_id:315617 Enrichment ANAMMOX Wastewater Treatment Plants Korea and Their Activity sludge FJ2088
EU621897.1 gg_id:274014 and kinetic research ammonia mixed anaerobic ammonium oxidation reactor seedec EU6218
CU920107.1 gg_id:537364 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
FJ374260.1 gg_id:359089 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3742
AB234544.1 gg_id:145313 termite gut homogenate clone MgMjD-104 AB2345
AB234542.1 gg_id:149255 termite gut homogenate clone MgMjR-038 AB2345
EF032767.1 gg_id:178484 cyanobacterial mat in lava cave clone HAVOmat22 EF0327
AB252879.1 gg_id:171614 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 018 AB2528
EU881130.1 gg_id:329424 Karst region primary forest soil clone KPF200711-199 EU8811
EU135304.1 gg_id:244428 tallgrass prarie soil clone FFCH773 EU1353
GU119349.1 gg_id:579236 Threatened Corals Provide Microbial Habitats reef water clone Reef_L13 GU119
GQ348014.1 gg_id:555348 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EF032766.1 gg_id:189073 cyanobacterial mat in lava cave clone HAVOmat101 EF0327
EU617890.1 gg_id:309328 Seasonal variation microbial Yel Sea sediment clone D13S-65 EU6178
EU135137.1 gg_id:242995 tallgrass prarie soil clone FFCH15608 EU1351
EU478637.1 gg_id:324136 microdiversity study anammox Candidatus Scalindua phylotype marine oxygen minir EU4786
AY947993.1 gg_id:143867 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9479
AJ247193.1 gg_id:25580 Asticcacaulis biprosthecium str. DSM 4723(T) AJ2471
AB016610.1 gg_id:5563 Asticcacaulis excentricus str. ATCC15261 AB0166
AF296688.1 gg_id:23972 Brevundimonas alba str. H12C5 AF2966
FJ950569.1 gg_id:436320 Brevundimonas diminuta str. c82 FJ9505
EU536433.1 gg_id:281870 profile human microbiota antecubital fossa (inner elbow) skin clone nbt213g08 EU5364
FJ658350.1 gg_id:568324 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6583
DQ335215.1 gg_id:145289 Brevundimonas terrae str. KSL-145 DQ335
EU465068.1 gg_id:294281 African elephant feces clone AFYEL_aaj67e11 EU4650
FJ950592.1 gg_id:424138 Brevundimonas diminuta str. c94 FJ9505

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	1	0	1	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	1	1	1	1	1	0	0	1	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	1	1	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae

g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas

s__Brevundimonas diminuta	59158
s__Brevundimonas diminuta	59195
s__Brevundimonas diminuta	59196
s__Brevundimonas diminuta	59207
s__Brevundimonas diminuta	59241
s__Brevundimonas diminuta	59251
s__Brevundimonas diminuta	59284
s__Brevundimonas diminuta	59294
s__Brevundimonas diminuta	59317
s__Brevundimonas diminuta	59360
s__Brevundimonas diminuta	59463
s__Brevundimonas diminuta	59487
s__Brevundimonas diminuta	59733
s__Brevundimonas diminuta	59736
s__Brevundimonas diminuta	59834
s__Brevundimonas diminuta	59960
s__Brevundimonas diminuta	60065
s__Brevundimonas diminuta	60080
s__Brevundimonas diminuta	60156
s__Brevundimonas mediterranea	59914
s__Brevundimonas mediterranea	60200
s__unclassified	58902
s__unclassified	58918
s__unclassified	58932
s__unclassified	58942
s__unclassified	58957
s__unclassified	58982
s__unclassified	59003
s__unclassified	59012
s__unclassified	59062
s__unclassified	59122
s__unclassified	59162
s__unclassified	59178
s__unclassified	59266
s__unclassified	59343
s__unclassified	59437
s__unclassified	59455
s__unclassified	59502
s__unclassified	59529
s__unclassified	59542
s__unclassified	59548

EU434547.1 gg_id:262017 Brevundimonas diminuta str. b76 EU4345
EU465065.1 gg_id:301063 African elephant feces clone AFYEL_aaj67e08 EU4650
EU434576.1 gg_id:262199 Brevundimonas diminuta str. b108 EU4345
EU464720.1 gg_id:297700 Hartmann's mountain zebra feces clone AFZEB_aaj69f09 EU4647
FJ658310.1 gg_id:535144 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6583
FJ658395.1 gg_id:540941 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6583
EU434570.1 gg_id:265057 Brevundimonas diminuta str. b77 EU4345
EU464980.1 gg_id:290745 African elephant feces clone AFYEL_aaj66b08 EU4649
DQ824709.1 gg_id:183605 human fecal clone RL185_aaj72b02 DQ824
FJ657857.1 gg_id:537717 Metalworking Fluids and Aerosols Metallurgy Plant metalworking fluid clone Winter_ FJ6578
EU535556.1 gg_id:284254 profile human microbiota antecubital fossa (inner elbow) skin clone nbt27b12 EU5355
GQ280032.1 gg_id:588010 Brevundimonas sp. str. BJ-22 GQ280
FJ658136.1 gg_id:543663 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6581
EU434575.1 gg_id:258759 Brevundimonas diminuta str. b124 EU4345
AB021415.1 gg_id:5595 Brevundimonas diminuta str. IAM 12691T AB0214
EU465159.1 gg_id:296763 African elephant feces clone AFYEL_aaj68h07 EU4651
FN433035.1 gg_id:559314 Brevundimonas terrae CCM24B FN4330
EU434509.1 gg_id:268353 Brevundimonas diminuta str. b215 EU4345
EU464952.1 gg_id:291623 African elephant feces clone AFYEL_aaj65f11 EU4649
AJ244706.1 gg_id:109577 Brevundimonas mediterranea str. V4.BO.18 LMG 22801 = MM_2367 AJ2447
AJ244707.1 gg_id:109696 Brevundimonas mediterranea str. V4.BE.56 LMG 22802 = MM_3001 AJ2447
AM402981.1 gg_id:162149 Brevundimonas sp. str. JO26 AM402
AY971369.1 gg_id:115361 Brevundimonas kwangchunensis str. KSL-110 AY9713
EU834791.1 gg_id:585677 Microbiology Aerobic Phosphorus Removal Process aerobic phosphorus-removing se EU8347
EF363713.1 gg_id:204302 Brevundimonas lenta str. DS-18 EF3637
GU321351.1 gg_id:547657 Brevundimonas sp. str. NMC11 GU321
AM412000.1 gg_id:198378 Brevundimonas nasdae Z66zhy AM412
AY328801.1 gg_id:90161 drinking water OR9 AY3288
EF157195.1 gg_id:241110 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AY169433.1 gg_id:82124 Brevundimonas vesicularis AY1694
AJ227782.1 gg_id:5579 Brevundimonas bacteroides str. CB7 AJ2277
AJ227797.1 gg_id:5583 Brevundimonas sp. str. FWC40 AJ2277
AJ227781.1 gg_id:5611 Brevundimonas vesicularis str. LMG 11141 AJ2277
AY293404.1 gg_id:87601 travertine terrace Yellowstone Hot Springs clone SM2A11 AY2934
EF546433.1 gg_id:219465 Brevundimonas nasdae str. P1 EF5464
EU182863.1 gg_id:247068 Brachybacterium sp. str. MH35 EU1828
DQ825663.1 gg_id:162728 Brevundimonas sp. str. 5420S-28 DQ825
AY328842.1 gg_id:89703 drinking water MB11 AY3288
AJ227786.1 gg_id:53033 Brevundimonas intermedia str. ATCC 15262(T) AJ2277
EU636022.1 gg_id:278329 Antarctic str. N97 EU6360
EU182890.1 gg_id:250309 Brevundimonas sp. str. MH62 EU1828

0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	1	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	0	1	1	0	1	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	1	1	1	0	1	1	1	1	1	0	0	1
0	0	0	0	0	1	1	0	1	0	0	0	1
0	1	1	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	1	0	0	0	0
0	1	1	1	0	1	1	1	1	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	0	1	1	1	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	1	1	1	1	0	0	1
1	1	1	1	0	1	1	1	1	0	1	1	0
0	0	0	1	0	1	1	1	1	1	0	0	1
0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	1	0	0	0	0	0
0	1	0	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	1	0	1	1	1
0	1	1	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	0	0	1	0	1	0	0
1	0	1	0	0	1	1	1	0	0	0	1	1
0	0	0	1	0	0	1	0	0	0	0	0	0
0	1	1	1	1	0	0	0	0	0	1	0	0
0	1	1	1	0	1	1	1	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae

g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Brevundimonas
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Caulobacter
g__Mycoplana
g__Mycoplana
g__Phenylobacterium
g__Phenylobacterium
g__Phenylobacterium
g__Phenylobacterium
g__Phenylobacterium
g__Phenylobacterium

s__unclassified	59557
s__unclassified	59603
s__unclassified	59611
s__unclassified	59617
s__unclassified	59622
s__unclassified	59671
s__unclassified	59715
s__unclassified	59740
s__unclassified	59831
s__unclassified	59875
s__unclassified	59975
s__unclassified	60072
s__unclassified	60088
s__unclassified	60100
s__unclassified	60119
s__unclassified	60145
s__unclassified	60166
s__unclassified	60193
s__Caulobacter fusiformis	59445
s__Caulobacter fusiformis	60060
s__Caulobacter henricii	59296
s__Caulobacter vibrioides	59857
s__unclassified	58905
s__unclassified	59230
s__unclassified	59271
s__unclassified	59321
s__unclassified	59515
s__unclassified	59666
s__unclassified	59668
s__unclassified	59749
s__unclassified	59959
s__unclassified	60074
s__unclassified	60090
s__unclassified	58959
s__unclassified	59318
s__unclassified	59011
s__unclassified	59336
s__unclassified	59570
s__unclassified	59660
s__unclassified	59849
s__unclassified	59997

EU143355.1 gg_id:238339 Brevundimonas sp. str. J22 EU143
EU580513.1 gg_id:543062 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret EU580
AJ007808.1 gg_id:5626 Brevundimonas variabilis str. ACM 5107 (T) AJ0078
AB426562.1 gg_id:270554 Brevundimonas sp. str. HINF004 AB4265
DQ372984.1 gg_id:152214 Brevundimonas sp. str. EMB102 DQ372
AY328835.1 gg_id:89630 drinking water MA26 AY3288
EU379308.1 gg_id:274963 Brevundimonas intermedia str. 6R-J-7d EU3793
AJ007802.1 gg_id:5568 Brevundimonas intermedia str. ACM 2608 (T) AJ0078
AJ227784.1 gg_id:5617 Brevundimonas subvibrioides str. CB81 AJ2277
AJ495803.1 gg_id:63466 Brevundimonas sp. p22P AJ4958
AJ227783.1 gg_id:43186 Brevundimonas variabilis str. ATCC 15255 (T) AJ2277
EU434579.1 gg_id:266190 Brevundimonas aurantiaca str. e12 EU4345
AM183353.1 gg_id:167639 Brevundimonas sp. 1228-1II AM183
AB447548.1 gg_id:316703 Brevundimonas sp. str. SUWAF011 AB4475
DQ981459.1 gg_id:203778 Brevundimonas sp. SB4 DQ981
DQ442520.1 gg_id:191932 Streptomyces longisporoflavus str. NRRL ISP-5165T DQ442
FN397631.1 gg_id:452397 Brevundimonas sp. str. CM 272 FN3976
DQ413152.1 gg_id:152156 Brevundimonas sp. str. EMB 68 DQ413
AJ007803.1 gg_id:5518 Caulobacter fusiformis str. ACM 5108 (T) AJ0078
AB008533.1 gg_id:5557 Caulobacter fusiformis str. ATCC15257 AB0085
AJ007805.1 gg_id:5560 Caulobacter henricii str. ACM 5105 (T) AJ0078
AE005673.1 gg_id:209341 Caulobacter crescentus str. CB15 AE0056
AM921622.1 gg_id:248395 Caulobacter henricii PhyCEm-80 AM921
EF515958.1 gg_id:221595 grassland soil clone FCPT664 EF5159
DQ124680.1 gg_id:154386 Caulobacter tundrae str. Z-0024 DQ124
AF523036.1 gg_id:89365 natural mineral water clone D-1 AF5230
EU730905.1 gg_id:352383 Caulobacter vibrioides str. 156 EU7309
DQ532299.1 gg_id:164042 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
AY512823.1 gg_id:106146 Caulobacter vibrioides str. S13 AY5128
AB271055.1 gg_id:165771 Caulobacter ginsengisoli str. Gsoil 317 AB2710
AM940947.1 gg_id:278226 Caulobacter sp. ECN-2008 AM940
DQ404656.1 gg_id:151101 contaminated sediment clone 654987 DQ404
GQ396801.1 gg_id:538121 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
FN556568.1 gg_id:518192 Brevundimonas sp. str. JW23.4a FN5565
EU434505.1 gg_id:263790 Brevundimonas bullata str. b350 EU4345
DQ501309.1 gg_id:199553 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
AY234477.1 gg_id:112129 soil isolate Ellin5060 AY2344
FJ197848.1 gg_id:313604 Brevundimonas sp. 39(2008) str. 39 FJ1978
AJ717391.1 gg_id:111099 Phenylobacterium falsum str. AC49 AJ7173
AJ582031.1 gg_id:93768 soil near uranium mill tailings clone JG36-GS-63 AJ5820
AY921824.1 gg_id:114202 farm soil clone AKYG696 AY9218

0	0	0	1	0	0	0	0	0	0	1	1	0
0	0	0	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	1	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	1	0	0	0	0	1
0	1	1	1	1	1	1	0	0	0	0	1	0
1	0	0	1	1	1	1	0	1	0	1	1	1
1	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	1	1	0
0	1	1	1	1	0	1	0	0	0	1	0	0
0	1	1	0	1	0	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	1	0	1	0	0
0	0	0	0	0	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	1	0	0	0	0
1	0	0	0	0	0	1	1	1	1	1	0	1
0	0	0	0	0	0	1	0	1	0	1	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	1	0	0	0	1	0	1
0	0	0	0	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	1
1	0	0	0	1	1	1	1	0	0	0	1	1
0	0	0	0	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Caulobacterales	f__Caulobacteraceae
o__Kiloniellales	f__Kiloniellaceae

g__Phenylobacterium
g__Phenylobacterium
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Kiloniella

s__unclassified	60112
s__unclassified	60194
s__unclassified	58929
s__unclassified	58958
s__unclassified	58960
s__unclassified	58980
s__unclassified	58981
s__unclassified	58991
s__unclassified	59058
s__unclassified	59098
s__unclassified	59103
s__unclassified	59135
s__unclassified	59179
s__unclassified	59200
s__unclassified	59202
s__unclassified	59263
s__unclassified	59286
s__unclassified	59299
s__unclassified	59385
s__unclassified	59400
s__unclassified	59421
s__unclassified	59507
s__unclassified	59523
s__unclassified	59573
s__unclassified	59596
s__unclassified	59605
s__unclassified	59673
s__unclassified	59685
s__unclassified	59703
s__unclassified	59755
s__unclassified	59760
s__unclassified	59766
s__unclassified	59790
s__unclassified	59910
s__unclassified	60050
s__unclassified	60058
s__unclassified	60069
s__unclassified	60071
s__unclassified	60098
s__unclassified	60187
s__unclassified	59633

GQ002488.1 gg_id:507172 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
AJ292592.1 gg_id:49162 PCB-polluted soil clone WD225 AJ2925
DQ202243.1 gg_id:140164 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo DQ202
GQ402724.1 gg_id:551851 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AB473899.1 gg_id:554330 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB4738
D49422.1 gg_id:5594 Brevundimonas diminuta str. IFO 3140 D49422
DQ984595.1 gg_id:240075 Mt. Nan-Jen litterfall clone IYF98 DQ984
GQ402558.1 gg_id:592079 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ177484.1 gg_id:139814 Brevundimonas sp. str. Tibet-IK73 DQ177
EF516954.1 gg_id:226283 grassland soil clone FCPT726 EF5169
AJ292595.1 gg_id:30983 PCB-polluted soil clone WD233 AJ2925
AF289151.1 gg_id:70005 freshwater clone PRD01a003B AF2891
EU730914.1 gg_id:335822 Brevundimonas diminuta str. 207 EU7309
EU445215.1 gg_id:565413 Isolation Weight Forest Topsoil Metagenomic tropical forest topsoil clone R36 EU4452
GU118509.1 gg_id:573233 Threatened Corals Provide Microbial Habitats clone Gven_K20 GU118
DQ532251.1 gg_id:168212 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
GU169058.1 gg_id:570254 Biofilms formed on substances: response f conditions and carbon concentrations sy GU169
FJ979845.1 gg_id:402409 Caulobacter sp. str. tsz12 FJ9798
AM697237.1 gg_id:227434 sequencing libraries indoor dust clone BF0001C078 AM697
AY922007.1 gg_id:113237 farm soil clone AKYG412 AY9220
GU118288.1 gg_id:568445 Threatened Corals Provide Microbial Habitats clone Dstr_G22 GU118
GQ402816.1 gg_id:589382 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU202832.1 gg_id:317304 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU2028
EU434454.1 gg_id:264269 Brevundimonas diminuta str. a229 EU4344
DQ177483.1 gg_id:140010 Brevundimonas sp. str. Tibet-IK53 DQ177
GU118656.1 gg_id:575957 Threatened Corals Provide Microbial Habitats clone Mfav_J15 GU118
DQ532201.1 gg_id:171288 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
EU881329.1 gg_id:324088 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
EF520395.1 gg_id:235185 structure lakes: what controls ? acid-impacted lake clone ADK-BTe02-51 EF5203
EU784736.1 gg_id:336351 Brevundimonas sp. str. E8 EU7847
AY569007.1 gg_id:103285 Nitrobacteria hamadaniensis str. 104 AY5690
AB167225.1 gg_id:107935 Brevundimonas diminuta str. c66 AB1672
EF520409.1 gg_id:231965 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-54 EF5204
GQ402771.1 gg_id:587634 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
GU118170.1 gg_id:560087 Threatened Corals Provide Microbial Habitats clone Dstr_P10 GU118
AB473919.1 gg_id:573162 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB4739
EU665093.1 gg_id:547599 Soil are Changed Agricultural Practices agricultural soil clone Plot22-C12 EU6650
AB374373.1 gg_id:272478 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
AB167229.1 gg_id:107937 Brevundimonas diminuta str. c79 AB1672
AY734246.1 gg_id:133283 spring water of alpine karst aquifer clone SDKAS1_2 AY7342
DQ167245.1 gg_id:138986 Kopriimonas byunsanensis str. KOPRI 13522 DQ167

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	1	1	0
0	0	0	1	0	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	0	1	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	1	1	1	1	1	1	0	1
0	0	0	1	1	1	1	1	0	0	0	1	0
1	1	1	0	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	1	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
1	1	1	0	1	0	1	1	1	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
1	1	1	1	1	1	1	1	0	0	1	1	1
0	1	0	1	0	1	0	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	1	1	1	1	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kiloniellales	f__Kiloniellaceae
o__Kordiimonadales	f__Kordiimonadaceae
o__Kordiimonadales	f__Kordiimonadaceae
o__Kordiimonadales	f__Kordiimonadaceae
o__Kordiimonadales	f__Kordiimonadaceae
o__Kordiimonadales	f__Kordiimonadaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae

g__Kiloniella
g__Thalassospira
g__Thalassospira
g__Thalassospira
g__Thalassospira
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Kordiimonas
g__Kordiimonas
g__unclassified
g__unclassified
g__unclassified
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus

s__unclassified	59784
s__Thalassospira xiamenensis	59277
s__Thalassospira xiamenensis	59510
s__unclassified	59427
s__unclassified	59568
s__unclassified	58969
s__unclassified	59104
s__unclassified	59170
s__unclassified	59187
s__unclassified	59220
s__unclassified	59265
s__unclassified	59308
s__unclassified	59365
s__unclassified	59371
s__unclassified	59683
s__unclassified	59799
s__unclassified	59804
s__unclassified	60158
s__unclassified	61263
s__unclassified	60915
s__unclassified	60971
s__unclassified	60344
s__unclassified	60681
s__unclassified	61264
s__magnetic coccus MP17	53415
s__magnetic coccus MP17	53486
s__magnetic coccus MP17	53773
s__Magnetococcus sp. MC-1	53064
s__unclassified	53026
s__unclassified	53073
s__unclassified	53099
s__unclassified	53131
s__unclassified	53154
s__unclassified	53159
s__unclassified	53188
s__unclassified	53220
s__unclassified	53343
s__unclassified	53455
s__unclassified	53500
s__unclassified	53522
s__unclassified	53805

AM749667.1 gg_id:566744 Kiloniella laminariae str. LD81 AM749
EF437150.1 gg_id:208597 Thalassospira nitroreducens str. TN1 EF4371
FJ210804.1 gg_id:346096 Thalassospira sp. str. QDHT-08 FJ2108
AB373113.1 gg_id:277271 Thalassospira sp. str. N5EA13-1A AB3731
AB373114.1 gg_id:265832 Thalassospira sp. str. G12-1 AB3731
AF358664.1 gg_id:35557 Thalassospira lucentensis AF3586
FJ202650.1 gg_id:316411 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
AB006768.1 gg_id:4594 Terasakiella pusilla str. IFO13613 AB0067
AY922191.1 gg_id:112927 whalefall clone 131616 AY9221
EF092208.1 gg_id:260078 Persistent Axinella corrugata clone Ax36_F7 EF0922
AJ633974.1 gg_id:114828 host's accessory nidamental gland clone 6ANG531 AJ6339
EF629835.1 gg_id:258350 Changes marine Mycale laxissima on transfer aqua sponge tissue EF6298
AY922227.1 gg_id:113991 whalefall clone 131732 AY9222
GQ169074.1 gg_id:592716 Thalassospira lucentensis str. TVGB18 GQ169
AY162078.1 gg_id:135758 Cultivating Sargasso Sea clone GMD37B4 AY1620
EU880514.1 gg_id:352101 Thalassospira lucentensis str. P44 EU8805
FJ952806.1 gg_id:399348 Thalassospira sp. str. 2ta2 FJ9528
AF143826.1 gg_id:25696 hydrocarbon-degrading consortium clone 4-Org1-58 AF1438
GU118853.1 gg_id:541338 Threatened Corals Provide Microbial Habitats clone Mfra_C21 GU118
EU268103.1 gg_id:254391 summer Dalian and Liaodong bay determined sea water clone L0603 EU2681
AY682384.1 gg_id:100730 Parvulomonas gwangyangensis str. GW14-5 AY6823
DQ917818.1 gg_id:221237 Microbial profiles bleached and wild-type Muricea elongata Kordiimonas clone BME DQ917
GU119022.1 gg_id:554110 Threatened Corals Provide Microbial Habitats clone Past_K19 GU119
EU287361.1 gg_id:252140 Pacific arctic surface sediment clone S26-61 EU2873
AB537162.1 gg_id:517870 Preparation single species magnetotactic multiple-displacement sediment water we AB5371
X81185.1 gg_id:11274 magnetic coccus MP17 str. TB24 X81185
X61607.1 gg_id:11262 magnetic coccus MP17 X61607
AAAN03000028.1 gg_id:130031 Magnetococcus sp. str. MC-1 AAAN0
DQ785314.1 gg_id:166095 magnetotactic sediments Jiaozhou Bay sediment clone QH-1 DQ785
EF371486.1 gg_id:214607 magnetotactic China Jiaozhou Bay clone M-40 EF3714
EF379386.1 gg_id:211078 magnetotactic China Jiaozhou Bay clone XSE-4 EF3793
AJ863157.1 gg_id:111324 marine microcosm clone CF24 AJ8631
GQ468519.1 gg_id:540513 Temporal variation magnetotactic two freshwater microcosms fresh water sedimen GQ468
Y13213.1 gg_id:11268 magnetic coccus MP17 str. pa19 Y13213
AJ863155.1 gg_id:109702 freshwater microcosm clone CF22 AJ8631
Y13210.1 gg_id:11281 Magnetic strain clone rj517 Y13210
X81184.1 gg_id:11271 magnetic coccus MP17 str. CS981 X81184
X81182.1 gg_id:11270 magnetic coccus MP17 str. CS92 X81182
EU570899.1 gg_id:543851 transition and zone within near-shore anoxic basin: Nitinat Lake depth 13 m clone Ni EU5708
EF370485.1 gg_id:205086 Morphology and wild type magnetotactic Miyun reservoir near Beijing China fresh w: EF3704
EF371485.1 gg_id:212269 magnetotactic China Jiaozhou Bay clone M-52 EF3714

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	1	0	1	0	0	0
0	0	0	0	0	1	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Magnetococcales	f__Magnetococcaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Parvularculales	f__Parvularculaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Aurantimonadaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae

g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Magnetococcus
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Parvularcula
g__Aurantimonas
g__Aurantimonas
g__Aurantimonas
g__Aurantimonas
g__Aurantimonas
g__Aurantimonas
g__Aurantimonas
g__Aurantimonas
g__Fulvimarina
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella

s__unclassified	53813
s__unclassified	53866
s__unclassified	53874
s__unclassified	53902
s__unclassified	53966
s__unclassified	60238
s__unclassified	60320
s__unclassified	60499
s__unclassified	60664
s__unclassified	60939
s__unclassified	61011
s__unclassified	61247
s__unclassified	61251
s__unclassified	62742
s__unclassified	62857
s__Aurantimonas altamirensis	61622
s__Aurantimonas altamirensis	62183
s__Aurantimonas coralicida	61502
s__Aurantimonas manganoxydans	62356
s__Aurantimonas manganoxydans	62503
s__Aurantimonas manganoxydans	62504
s__unclassified	61801
s__unclassified	62921
s__Fulvimarina pelagi	61844
s__unclassified	61826
s__unclassified	61888
s__unclassified	61921
s__unclassified	61941
s__unclassified	61967
s__unclassified	62342
s__unclassified	62443
s__unclassified	62621
s__unclassified	62689
s__unclassified	62856
s__unclassified	62935
s__Bartonella bacilliformis	61846
s__Bartonella clarridgeiae	61576
s__Bartonella elizabethae	62149
s__Bartonella elizabethae	62843
s__Bartonella grahamii	61673
s__Bartonella grahamii	61827

X81183.1 gg_id:11265 magnetic coccus MP17 str. TB12 X81183
EF371491.1 gg_id:209788 magnetotactic China Jiaozhou Bay clone M-67 EF3714
Y13208.1 gg_id:11266 Magnetic strain clone rj53 Y13208
Y13212.1 gg_id:11267 magnetic coccus MP17 str. pa11 Y13212
GQ468507.1 gg_id:593515 Temporal variation magnetotactic two freshwater microcosms fresh water sedimen GQ468
AY328711.1 gg_id:88630 drinking water system simulator clone DSSD12 AY3287
GQ500720.1 gg_id:561524 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
AF544015.1 gg_id:111917 Parvularcula bermudensis str. HTCC2503 AF5440
AY625140.1 gg_id:104892 perchloroethylene-contaminated ground water clone I-6 AY6251
AM934846.1 gg_id:544221 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
FM242322.1 gg_id:318593 sequences sediment clone 63 T9d-oil FM242
EF530680.1 gg_id:226147 Extremely acidic pendulous biofilms Frasassi cave system Italy microbial biofilm clone EF5306
AY193164.1 gg_id:80157 marine tidal mat clone BTM11 AY1931
GU370118.1 gg_id:530853 Rhodovulum sulfidophilum str. P721(3) GU370
EF173322.1 gg_id:185425 Sinorhizobium sp. MKI8 EF1733
EU544515.1 gg_id:272510 Aurantimonas altamirensis str. IFP14.1 EU5445
EU442518.1 gg_id:275257 Aurantimonas altamirensis str. NML 070722 LSPQ no. ID089387 EU4425
EF512716.1 gg_id:218585 Aurantimonas coralicida str. JL661 EF5127
AY178863.1 gg_id:77748 Fulvimarina litoralis str. HTCC2156 AY1788
AJ508755.1 gg_id:110301 marine str. V4.MO.18 AJ5087
AJ508754.1 gg_id:110412 marine str. V4.MO.17 AJ5087
EF423363.1 gg_id:206636 Aurantimonas sp. str. N1 EF4233
EF373540.1 gg_id:206133 Aurantimonas kwangyangensis str. CW5 EF3735
AY178861.1 gg_id:77696 Fulvimarina pelagi str. HTCC2615 AY1788
GQ009485.1 gg_id:500180 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AM746691.1 gg_id:241968 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A13 AM746
FJ357425.1 gg_id:363192 Aurantimonas sp. str. YIM J01 FJ3574
FM872739.1 gg_id:365130 occupant source house floor dust clone FB01C04 FM872
EF489025.1 gg_id:221997 Bacillus sp. str. HB01085 EF4890
FM872541.1 gg_id:368575 occupant source house floor dust clone FA01H06 FM872
FN421693.1 gg_id:536202 proteogenomics physiology phyllosphere soybean clone 3_E11 FN4216
GQ115503.1 gg_id:421082 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw686f02 GQ115
AB257635.1 gg_id:262792 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
GQ009554.1 gg_id:500111 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
DQ883810.1 gg_id:164020 Aerobacter ureolyica str. 5715S-12 DQ883
Z70003.1 gg_id:5472 Bartonella bacilliformis str. LA6.3 Z70003
X89208.1 gg_id:5476 Bartonella sp str. ATCC 51734 X89208
AB246808.1 gg_id:149483 Bartonella elizabethae str. Q-4 AB2468
AB246801.2 gg_id:147120 Bartonella elizabethae str. R-5 AB2468
AB440632.1 gg_id:338719 Bartonella sp. str. Fuji 18-1 AB4406
AB242293.1 gg_id:141840 Bartonella sp. str. Fuji 12-1 AB2422

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	0	1
1	1	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae
o__Rhizobiales	f__Bartonellaceae

g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella
g__Bartonella

s__Bartonella grahamii	62028
s__Bartonella grahamii	62265
s__Bartonella grahamii	62306
s__Bartonella grahamii	62481
s__Bartonella grahamii	62932
s__Bartonella henselae	62510
s__Bartonella henselae	62710
s__Bartonella henselae	62904
s__Bartonella queenslandensis	61815
s__Bartonella queenslandensis	62753
s__Bartonella queenslandensis	62765
s__Bartonella quintana	62507
s__Bartonella schoenbuchensis	62762
s__Bartonella washoensis	61420
s__Bartonella washoensis	61704
s__Bartonella washoensis	62017
s__Candidatus Bartonella rudakovii	61797
s__unclassified	61381
s__unclassified	61456
s__unclassified	61469
s__unclassified	61528
s__unclassified	61741
s__unclassified	61860
s__unclassified	61866
s__unclassified	61868
s__unclassified	61972
s__unclassified	61993
s__unclassified	62035
s__unclassified	62066
s__unclassified	62091
s__unclassified	62112
s__unclassified	62137
s__unclassified	62156
s__unclassified	62202
s__unclassified	62216
s__unclassified	62250
s__unclassified	62398
s__unclassified	62554
s__unclassified	62633
s__unclassified	62720
s__unclassified	62855

NR_029367.1 gg_id:588047 Bartonella taylorii str. M6; NCTC 12861 NR_02
AB426635.1 gg_id:259103 Bartonella grahamii str. Cg4263alb AB426
AB426630.1 gg_id:276614 Bartonella grahamii str. Hokkaido 48-1 AB426
AB529507.1 gg_id:594215 Bartonella grahamii str. cg147up AB529
AB529498.1 gg_id:578474 Bartonella grahamii str. Korea 4-1 AB529
AY513504.1 gg_id:103693 Bartonella henselae str. 882_ANT5 AY513
U87831.1 gg_id:5492 aortic heart valve patient with endocarditis clone v9 U8783
Z11684.1 gg_id:5473 Bartonella henselae str. BA-TF Z11684
EU111755.1 gg_id:273803 Bartonella queenslandensis str. AUST/NH5 EU111
EU111749.1 gg_id:270242 Bartonella rattiaustraliensis str. AUST/NH4 EU111
EU111754.1 gg_id:263406 Bartonella queenslandensis str. AUST/NH12 EU111
NC_005955.1 gg_id:129029 Bartonella quintana str. Toulouse NC_00
AJ278187.1 gg_id:25998 Bartonella schoenbuchensis str. R1 AJ2781
AB519061.1 gg_id:550137 Bartonella washoensis str. DR1-1 AB519
AB519065.1 gg_id:548080 Bartonella washoensis str. SR25-1 AB519
AB519062.1 gg_id:548956 Bartonella washoensis str. DR3-1 AB519
EF682085.1 gg_id:331242 'Candidatus rudakovii' detected voles Western Siberia Candidatus Bartonella rudakov EF682
AF293389.1 gg_id:49049 Bartonella capreoli str. IBS 193 AF293
FJ177634.1 gg_id:353598 Bartonella sp. str. HMD-3 FJ1776
EU294521.1 gg_id:244723 Bartonella volans str. FSq-1 EU294
Z70001.1 gg_id:5501 Bartonella sp str. R-phy2 Z70001
EF616480.1 gg_id:249397 Bartonella silvicola str. Cul-9 BAA-1453 EF6164
AB292597.1 gg_id:211030 Bartonella washoensis str. Sb944nv AB292
Z70005.1 gg_id:5475 Bartonella sp str. R-phy1 Z70005
Z70008.1 gg_id:5483 Bartonella sp str. C5rat Z70008
EU111759.1 gg_id:268319 Bartonella coopersplainensis str. AUST/NH20 EU111
AF204274.1 gg_id:46747 Bartonella birtlesii str. 325 AF2042
X89110.1 gg_id:5486 Wolbachia melophagi str. MO6 X89110
Z70004.1 gg_id:5484 Bartonella sp str. C7rat Z70004
DQ645425.1 gg_id:161188 Bartonella henselae str. M7SHD DQ645
AY370186.1 gg_id:103856 ground up bee tissues clone pAJ208 AY370
Z70006.1 gg_id:5498 Bartonella sp str. C1phy Z70006
EU111752.1 gg_id:260102 Bartonella rattiaustraliensis str. AUST/NH14 EU111
AY515119.1 gg_id:100507 Bartonella phoceensis str. 16120 AY515
NR_029368.1 gg_id:541643 Bartonella doshiae str. R18; NCTC 12862 NR_02
AY254309.1 gg_id:104973 Bartonella chomelii AY2543
L01260.1 gg_id:5502 Bartonella elizabethae L01260
DQ538394.1 gg_id:227943 Bartonella australis str. Aust/NH1 DQ538
AY515118.1 gg_id:100352 Bartonella rattimassiliensis str. 16115 AY515
AJ002139.1 gg_id:5462 Bartonella alsatica str. 382 AJ0021
NR_029366.1 gg_id:571234 Bartonella grahamii str. V2; NCTC 12860 NR_02

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Beijerinckiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

g__Beijerinckia
g__Beijerinckia
g__Beijerinckia
g__Beijerinckia
g__Beijerinckia
g__Chelatococcus
g__Methylocella
g__Methylocella
g__Methylocella
g__Methylocella
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia

s__Beijerinckia indica	58919
s__Beijerinckia indica	59399
s__unclassified	59000
s__unclassified	59166
s__unclassified	59504
s__unclassified	59811
s__Methylocella palustris	59460
s__Methylocella palustris	59631
s__Methylocella silvestris	59616
s__Methylocella tundrae	59376
s__unclassified	58925
s__unclassified	58927
s__unclassified	59113
s__unclassified	59257
s__unclassified	59258
s__unclassified	59260
s__unclassified	59380
s__unclassified	59386
s__unclassified	59468
s__unclassified	59501
s__unclassified	59752
s__unclassified	59778
s__unclassified	59823
s__unclassified	59872
s__unclassified	59940
s__unclassified	59943
s__unclassified	59977
s__unclassified	60021
s__Afipia broomeae	59989
s__Afipia felis	59348
s__Afipia genosp. 1	60086
s__Afipia genosp. 1	60094
s__Afipia genosp. 1	60118
s__unclassified	58906
s__unclassified	58935
s__unclassified	59009
s__unclassified	59018
s__unclassified	59039
s__unclassified	59219
s__unclassified	59340
s__unclassified	59650

AB119197.1 gg_id:106044 Beijerinckia indica str. ATCC 9036 AB119
AB119199.1 gg_id:106358 Beijerinckia indica str. ATCC 19361 AB119
AJ563932.1 gg_id:100451 Beijerinckia mobilis str. DSM 2326 AJ5639
AB119210.1 gg_id:106197 Beijerinckia sp. str. TB16 AB119
AB119203.1 gg_id:101664 Beijerinckia sp. str. TB9 AB119
EF584507.1 gg_id:232942 Chelatococcus daeguensis str. K106 EF5845
AM162441.1 gg_id:155035 and situ identification acidic sphagnum peat bog clone B56 AM162
AJ563926.1 gg_id:104947 Methylocella palustris str. Ch3 AJ5639
CP001280.1 gg_id:527956 Methylocella silvestris str. BL2 CP001
AJ555244.1 gg_id:83530 Methylocella tundrae str. T4 AJ5552
DQ450165.1 gg_id:155167 (Uruguay) Atlantic coastal lagoon clone R7C54 DQ450
EU131038.1 gg_id:252176 alkaline China coal mine soil clone SIP CM24 EU131
GQ402592.1 gg_id:584864 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ719048.1 gg_id:530044 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_D0 FJ7190
EF064161.1 gg_id:225511 Microbial sediment bottom AMD pool acid mine drainage clone Sed3 EF0641
X97076.1 gg_id:4762 peat bog clone TM9 X97076
EU133271.1 gg_id:246401 tallgrass prarie soil clone FFCH2375 EU133
AF407384.1 gg_id:27469 MCB-contaminated groundwater-treating reactor clone RB7C5 AF4073
FM253682.1 gg_id:348953 Rock gold mine unusually microbial biofilm clone H09-2 FM253
AF200697.1 gg_id:32333 13C- extracted 13C-methanol exposed soil clone UP3 proteobacterium AF2006
AB119198.1 gg_id:106192 Beijerinckia derxii str. ATCC 49361 AB119
FM253655.1 gg_id:349812 Rock gold mine unusually microbial biofilm clone E02-2 FM253
FN433469.1 gg_id:562500 Methylocapsa sp. str. KYG FN4334
CU926994.1 gg_id:551719 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
DQ837242.1 gg_id:252587 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_23 DQ837
GU205295.1 gg_id:524604 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
AY913393.1 gg_id:112985 forest soil clone DUNssu187 (-7A) (OTU#034) AY9133
DQ451456.1 gg_id:156677 forest soil clone FAC17 DQ451
U87759.1 gg_id:4967 Afipia broomeae str. F186 U87759
AY513503.1 gg_id:103555 Afipia felis str. 2002033830 AY5135
U87764.1 gg_id:4964 Afipia genosp. 2 str. G8965 U87764
EU499727.1 gg_id:276997 Field-based laboratory stable isotope probing surveys identities both aerobic and an EU499
GQ032540.1 gg_id:375131 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ032
DQ222224.1 gg_id:140520 Bradyrhizobium sp. str. CCBAU 71283012 DQ222
AY568510.1 gg_id:102699 Afipia massiliensis str. NW-12 AY5685
AY029562.1 gg_id:58038 Afipia massiliensis str. 34633; CIP 107022; CCUG 45153 AY0295
AY547290.1 gg_id:99065 Bradyrhizobium sp. str. CCBAU 7128301 AY5472
AF288304.1 gg_id:41002 Afipia birgiae str. 34632 AF2883
AB099659.1 gg_id:77914 Oligotropha carboxidovorans str. S23 AB0996
FJ193001.1 gg_id:304744 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1930
FJ165544.1 gg_id:559211 Microbially-enhanced Dissolution Karst Carbonates microbial biofilm Sonterra #8 well FJ1655

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	0	0	0	1	1	1	0	0	0
1	0	0	1	0	0	0	0	0	0	0	0	0
1	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	0	1
0	0	0	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Afipia
g__Balneimonas
g__Balneimonas
g__Balneimonas
g__Balneimonas
g__Balneimonas
g__Balneimonas
g__Balneimonas
g__Balneimonas
g__Blastobacter
g__Blastobacter
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bosea
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium

s__unclassified	59772
s__unclassified	59851
s__unclassified	60042
s__unclassified	60137
s__unclassified	60141
s__unclassified	60154
s__unclassified	59109
s__unclassified	59155
s__unclassified	59743
s__unclassified	59753
s__unclassified	59758
s__unclassified	59775
s__unclassified	59930
s__unclassified	59970
s__Bradyrhizobium sp. BTAi1	59433
s__unclassified	59107
s__Bosea vestrisii	60083
s__unclassified	58889
s__unclassified	59019
s__unclassified	59163
s__unclassified	59322
s__unclassified	59377
s__unclassified	59378
s__unclassified	59475
s__unclassified	59522
s__unclassified	59544
s__unclassified	59712
s__unclassified	59797
s__unclassified	59852
s__unclassified	59935
s__unclassified	59945
s__unclassified	60182
s__Bradyrhizobium canariense	58976
s__Bradyrhizobium canariense	58985
s__Bradyrhizobium canariense	58995
s__Bradyrhizobium canariense	59059
s__Bradyrhizobium canariense	59432
s__Bradyrhizobium elkanii	58910
s__Bradyrhizobium elkanii	58946
s__Bradyrhizobium elkanii	58984
s__Bradyrhizobium elkanii	58993

AY238503.1 gg_id:92573 Bradyrhizobium sp. str. 1 AY2385
AJ295483.1 gg_id:40221 rape rhizosphere clone wr0024 AJ2954
U87761.1 gg_id:4971 Afipia broomeae str. G5958 U8776
AY568503.2 gg_id:106979 Afipia broomeae str. C-12 AY5685
EF203409.1 gg_id:261125 Bradyrhizobium sp. str. URBM1 EF2034
EF520400.1 gg_id:231834 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-40 EF5204
EU308573.1 gg_id:243951 Deinococcus sp. str. 4A4 EU3085
DQ838529.1 gg_id:161809 Methylobacterium sp. str. WSM3686 DQ838
AJ871433.1 gg_id:111252 Chelatococcus asaccharovorans CP141b AJ8714
DQ298340.1 gg_id:151224 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FM160634.1 gg_id:292268 Microvirga sp. PCA19 PCA 19 FM160
AB098515.2 gg_id:78887 Balneimonas flocculans str. TFB AB0985
GQ103792.1 gg_id:446977 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ103
AY776209.1 gg_id:108377 Methylobacterium sp. str. AC72a AY7762
AF338176.1 gg_id:68816 Blastobacter denitrificans str. IFAM 1005; LMG 8443 AF3381
X66025.1 gg_id:5058 Blastobacter denitrificans str. LMG 8443 X66025
AF288306.1 gg_id:24179 Bosea vestrisii str. 34635 AF2883
GU377117.1 gg_id:526769 Afipia sp. str. sptzw29 GU377
EU325943.1 gg_id:255748 Bosea sp. str. fei-4-9 EU3259
DQ377760.1 gg_id:153195 Bosea sp. PD 19 DQ377
AJ968692.1 gg_id:165499 Bosea sp. str. STM 358 AJ9686
AJ250796.1 gg_id:4822 Bosea thiooxidans str. DSM 9653 AJ2507
DQ104985.1 gg_id:136035 Bosea thiooxidans str. JS 11 DQ104
EU730912.1 gg_id:324973 Bosea thiooxidans str. 187 EU7309
AJ250797.1 gg_id:4823 Bosea thiooxidans str. RpPI5-VS AJ2507
DQ303323.1 gg_id:149709 Bosea sp. TM19_7 DQ303
EF114681.1 gg_id:194437 Bosea sp. str. SJH07 EF1146
AF288307.1 gg_id:27298 Bosea massiliensis str. 34649 AF2883
EU130951.1 gg_id:243491 Afipia sp. BAC312 EU1309
AF288309.1 gg_id:47211 Bosea massiliensis str. 63287 AF2883
EU584530.1 gg_id:263418 Afipia sp. str. Everest-gws-91 EU5845
NR_028787.1 gg_id:583653 Bosea minatitlanensis str. AMX51; DSM 13099 NR_028
EU561082.1 gg_id:273777 Bradyrhizobium sp. str. CTFI54 EU5610
FJ390904.1 gg_id:589546 Bradyrhizobium canariense str. SEMIA 928 FJ3909
GQ899183.1 gg_id:569090 Bradyrhizobium canariense str. L-2 GQ899
EU561083.1 gg_id:273925 Bradyrhizobium sp. str. CTFI410 EU5610
EU420082.1 gg_id:569322 Bradyrhizobium canariense str. Cy-1 EU4200
AY649429.1 gg_id:99495 Bradyrhizobium elkanii str. BR2001 AY6494
EU170546.1 gg_id:251540 Bradyrhizobium elkanii str. CCBAA 05065 EU1705
FJ192710.1 gg_id:319167 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1927
AY904753.1 gg_id:111860 Bradyrhizobium elkanii str. SEMIA 6148 AY9047

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	1	0	1	1	0	0	0	1	0	0
0	0	1	1	0	1	1	0	0	0	1	0	0
0	0	0	1	0	1	1	0	0	0	1	0	0
0	0	0	1	0	1	0	0	0	0	1	0	0
1	1	0	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	0	0	0	0	1	1
1	1	0	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	1	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
1	1	1	0	1	0	1	0	0	0	0	0	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium

s__Bradyrhizobium elkanii	58996
s__Bradyrhizobium elkanii	59074
s__Bradyrhizobium elkanii	59176
s__Bradyrhizobium elkanii	59180
s__Bradyrhizobium elkanii	59313
s__Bradyrhizobium elkanii	59374
s__Bradyrhizobium elkanii	59491
s__Bradyrhizobium elkanii	59499
s__Bradyrhizobium elkanii	59651
s__Bradyrhizobium elkanii	59690
s__Bradyrhizobium elkanii	59701
s__Bradyrhizobium elkanii	59706
s__Bradyrhizobium elkanii	59719
s__Bradyrhizobium elkanii	59774
s__Bradyrhizobium elkanii	59803
s__Bradyrhizobium elkanii	59809
s__Bradyrhizobium elkanii	59814
s__Bradyrhizobium elkanii	59898
s__Bradyrhizobium elkanii	59949
s__Bradyrhizobium elkanii	60036
s__Bradyrhizobium elkanii	60162
s__Bradyrhizobium elkanii	60185
s__Bradyrhizobium elkanii	60198
s__Bradyrhizobium yuanmingense	59006
s__Bradyrhizobium yuanmingense	59199
s__Bradyrhizobium yuanmingense	59226
s__Bradyrhizobium yuanmingense	59335
s__Bradyrhizobium yuanmingense	59430
s__Bradyrhizobium yuanmingense	59458
s__Bradyrhizobium yuanmingense	59646
s__Bradyrhizobium yuanmingense	59788
s__Bradyrhizobium yuanmingense	60068
s__Bradyrhizobium yuanmingense	60171
s__unclassified	58899
s__unclassified	58907
s__unclassified	58936
s__unclassified	58943
s__unclassified	58944
s__unclassified	58966
s__unclassified	59045
s__unclassified	59068

FJ418920.1 gg_id:362396 Bradyrhizobium sp. str. PC28 FJ4189
U35000.3 gg_id:4946 Bradyrhizobium elkanii str. USDA 76 U3500
AY904788.1 gg_id:112273 Bradyrhizobium elkanii str. SEMIA 6425 AY9047
AY904762.1 gg_id:111745 Bradyrhizobium elkanii str. SEMIA 6160 AY9047
AF417554.1 gg_id:21176 Bradyrhizobium elkanii str. DASA37005 AF4175
AF208516.1 gg_id:55735 Bradyrhizobium elkanii str. USDA 46 AF2085
FJ193395.1 gg_id:328559 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1933
DQ786801.1 gg_id:169640 Bradyrhizobium elkanii str. HaE4 DQ786
FJ193017.1 gg_id:353693 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1930
AF417553.1 gg_id:49609 Bradyrhizobium elkanii str. DASA38001 AF4175
AY904736.1 gg_id:112163 Bradyrhizobium elkanii str. SEMIA 696 AY9047
AY904748.1 gg_id:112153 Bradyrhizobium elkanii str. SEMIA 6100 AY9047
FJ193380.1 gg_id:324669 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1933
AF417556.1 gg_id:44293 Bradyrhizobium elkanii str. DASA35013 AF4175
GQ129847.1 gg_id:465190 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
EU399711.1 gg_id:271806 Bradyrhizobium elkanii str. CCBAU 05041 EU3997
AY039016.1 gg_id:64297 Bradyrhizobium sp. ORS3260 str. ORS 3260 AY0390
AF417555.1 gg_id:21431 Bradyrhizobium elkanii str. DASA35011 AF4175
AY904744.1 gg_id:111950 Bradyrhizobium elkanii str. SEMIA 6028 AY9047
EU170551.1 gg_id:242313 Bradyrhizobium elkanii str. CCBAU 23109 EU1705
AY649433.1 gg_id:103679 Bradyrhizobium elkanii str. BR3279 AY6494
AY904789.1 gg_id:112254 Bradyrhizobium elkanii str. SEMIA 6440 AY9047
FJ192573.1 gg_id:321198 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1925
FJ540914.1 gg_id:586787 Bradyrhizobium yuanmingense str. DTB8 FJ5409
FJ540920.1 gg_id:578473 Bradyrhizobium yuanmingense str. DTC5 FJ5409
AF417549.1 gg_id:20737 Bradyrhizobium japonicum str. DASA24015 AF4175
AY904774.1 gg_id:111573 Bradyrhizobium japonicum str. SEMIA 6319 AY9047
AF193818.1 gg_id:49866 Bradyrhizobium yuanmingense str. B071 AF1938
FJ540960.1 gg_id:585297 Bradyrhizobium yuanmingense str. TSC9 FJ5409
AF417548.1 gg_id:45495 Bradyrhizobium japonicum str. DASA03183 AF4175
EF070133.1 gg_id:196710 Bradyrhizobium yuanmingense str. CCBAU 43022 EF0701
EF061098.1 gg_id:183640 Bradyrhizobium yuanmingense str. CCBAU 45079 EF0610
AY649439.1 gg_id:104594 Bradyrhizobium japonicum str. BR3267 AY6494
AY162036.1 gg_id:135634 Cultivating soil clone PI_GH1.1.B1 AY1620
AF417543.1 gg_id:71773 Bradyrhizobium japonicum str. DASA12006 AF4175
DQ303328.1 gg_id:146763 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
DQ133341.1 gg_id:137967 Bradyrhizobium liaoningense str. GXD1 DQ133
DQ786798.1 gg_id:168591 Bradyrhizobium liaoningense str. DdE3 DQ786
AB240363.1 gg_id:144998 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
AF239843.2 gg_id:32699 Bradyrhizobium japonicum str. PRY40 AF2398
EF221623.1 gg_id:207870 Bradyrhizobium sp. str. JR008 EF2216

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	1	0	1	0	1	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	0	1	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	0	0
0	1	1	0	1	0	1	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	0	0	1
0	0	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	0	0	0	0	0	0	1
0	0	0	0	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	0	0	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium

s__unclassified	59091
s__unclassified	59129
s__unclassified	59143
s__unclassified	59146
s__unclassified	59148
s__unclassified	59159
s__unclassified	59171
s__unclassified	59177
s__unclassified	59183
s__unclassified	59210
s__unclassified	59214
s__unclassified	59232
s__unclassified	59270
s__unclassified	59283
s__unclassified	59293
s__unclassified	59310
s__unclassified	59366
s__unclassified	59402
s__unclassified	59414
s__unclassified	59448
s__unclassified	59486
s__unclassified	59503
s__unclassified	59513
s__unclassified	59520
s__unclassified	59528
s__unclassified	59574
s__unclassified	59575
s__unclassified	59576
s__unclassified	59625
s__unclassified	59636
s__unclassified	59669
s__unclassified	59726
s__unclassified	59737
s__unclassified	59805
s__unclassified	59817
s__unclassified	59862
s__unclassified	59889
s__unclassified	59896
s__unclassified	59902
s__unclassified	59909
s__unclassified	59973

DQ303347.1 gg_id:147207 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
DQ303349.1 gg_id:149227 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
U69636.1 gg_id:4932 Bradyrhizobium lupini str. FN 13 (USDA 3505) U69636
AY904778.1 gg_id:112228 Bradyrhizobium elkanii str. SEMIA 6387 AY9047
AY904757.1 gg_id:112271 Bradyrhizobium japonicum str. SEMIA 6155 AY9047
DQ303324.1 gg_id:147536 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EU145989.1 gg_id:236262 Bradyrhizobium liaoningense str. CCBAU 83684 EU1459
EU170561.1 gg_id:245983 Bradyrhizobium elkanii str. CCBAU 41236 EU1705
EU399713.1 gg_id:258733 Bradyrhizobium japonicum str. CCBAU 43170 EU3997
AF417544.1 gg_id:32002 Bradyrhizobium japonicum str. DASA12007 AF4175
GQ181045.1 gg_id:563588 Bradyrhizobium elkanii str. LN5 GQ181
DQ303376.1 gg_id:145414 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AF417542.1 gg_id:23765 Bradyrhizobium japonicum str. DASA02010 AF4175
EU561080.1 gg_id:266287 Bradyrhizobium sp. str. CTFI47 EU5610
FJ025097.1 gg_id:348667 Bradyrhizobium japonicum str. SEMIA 6153 FJ0250
EF394156.1 gg_id:210105 Bradyrhizobium japonicum str. CCBAU 65068 EF3941
FJ390914.1 gg_id:591406 Bradyrhizobium japonicum str. SEMIA 512 FJ3909
AB195987.1 gg_id:132401 Bradyrhizobium elkanii str. MF834 AB1959
X70403.1 gg_id:4945 Bradyrhizobium sp str. LMG 9566 X70403
AB179515.1 gg_id:100954 sedimentary rock clone MIZ24 AB1795
AF363138.1 gg_id:24680 Bradyrhizobium japonicum str. MSDJ G94 AF3631
EF394146.1 gg_id:214964 Bradyrhizobium japonicum str. CCBAU 53135 EF3941
FJ418696.1 gg_id:364095 Bradyrhizobium japonicum str. CCBAU 33175 FJ4186
AY904746.1 gg_id:111411 Bradyrhizobium elkanii str. SEMIA 6069 AY9047
DQ517956.1 gg_id:159686 Bradyrhizobium japonicum str. HHL-01 DQ517
GQ181034.1 gg_id:510301 Bradyrhizobium elkanii str. LNW14 GQ181
EU133476.1 gg_id:237433 tallgrass prarie soil clone FFCH17074 EU1334
EF070138.1 gg_id:195443 Bradyrhizobium liaoningense str. CCBAU 33158 EF0701
DQ303346.1 gg_id:145143 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AY904756.1 gg_id:112304 Bradyrhizobium japonicum str. SEMIA 6152 AY9047
DQ303348.1 gg_id:147522 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AF239844.2 gg_id:51967 Bradyrhizobium japonicum str. PRY42 AF2398
AY568513.2 gg_id:103141 Bradyrhizobium elkanii str. NW-6 AY5685
DQ303379.1 gg_id:146676 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EU335263.1 gg_id:257149 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
DQ303343.1 gg_id:148707 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
DQ303364.1 gg_id:148890 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EF512281.1 gg_id:223867 Bradyrhizobium japonicum str. CCBAU 45002 EF5122
AF363135.1 gg_id:18027 Bradyrhizobium japonicum str. MSDJ 5697 AF3631
EF394151.1 gg_id:211052 Bradyrhizobium japonicum str. CCBAU 65619 EF3941
DQ786799.1 gg_id:170123 Bradyrhizobium liaoningense str. BqE4 DQ786

0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	0	1	0	1	1	0	1	0
0	1	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	0	0	1
1	0	0	1	0	0	0	0	0	0	0	0	1
0	1	0	0	0	1	1	0	0	0	0	0	1
1	0	0	1	0	0	0	0	0	0	0	0	1
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	0	0	1	0	0	0	0	0	0	0	1
0	1	0	0	1	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Bradyrhizobium
g__Methylobacterium
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Nitrobacter
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas

s__unclassified	59983
s__unclassified	59986
s__unclassified	60000
s__unclassified	60019
s__unclassified	60025
s__unclassified	60038
s__unclassified	60056
s__unclassified	60067
s__unclassified	60084
s__unclassified	60101
s__unclassified	60133
s__unclassified	60147
s__unclassified	60172
s__unclassified	60184
s__unclassified	60188
s__unclassified	60189
s__unclassified	59190
s__Nitrobacter alkalicus	59688
s__Nitrobacter alkalicus	60161
s__Nitrobacter hamburgensis	59911
s__Nitrobacter vulgaris	60134
s__unclassified	59044
s__unclassified	59075
s__unclassified	59131
s__unclassified	59191
s__unclassified	59227
s__unclassified	59808
s__unclassified	59864
s__Afipia genosp. 4	59157
s__Afipia genosp. 4	59274
s__Rhodopseudomonas oryzae	59505
s__unclassified	58967
s__unclassified	59025
s__unclassified	59077
s__unclassified	59184
s__unclassified	59218
s__unclassified	59346
s__unclassified	59441
s__unclassified	59550
s__unclassified	59553
s__unclassified	59615

FJ390900.1 gg_id:545943 Bradyrhizobium liaoningense str. SEMIA 5062 FJ3909
DQ303374.1 gg_id:146501 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EU074195.1 gg_id:250401 Bradyrhizobium liaoningense str. CCBAU 03282 EU074
DQ303326.1 gg_id:149079 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AF417541.1 gg_id:54256 Bradyrhizobium japonicum str. DASA02007 AF4175
AF363133.1 gg_id:37117 Bradyrhizobium japonicum str. MSDJ 5718 AF363
AY599677.1 gg_id:104113 fungal ascocarp clone Cl-19-TB8-II AY5996
AF417545.1 gg_id:49277 Bradyrhizobium japonicum str. THA7 AF4175
EU333380.1 gg_id:268064 Bradyrhizobium japonicum RLA09 EU3333
EU083497.1 gg_id:240912 Evidence Carboxylation During Degradation Hexadecane Denitrifying Consortium he EU083
DQ303335.1 gg_id:148648 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
AY904773.1 gg_id:111438 Bradyrhizobium elkanii str. SEMIA 6208 AY9047
EF018750.1 gg_id:211106 aspen rhizosphere clone Amb_16S_1209 EF0187
DQ517958.1 gg_id:160432 Bradyrhizobium sp. str. HMS-O1 DQ517
EF019158.1 gg_id:204406 aspen rhizosphere clone Amb_16S_1805 EF0191
U69637.1 gg_id:4921 Bradyrhizobium lupini str. KM50 90 (USDA 3514) U69637
NC_010725.1 gg_id:289367 Methylobacterium populi str. BJ001 NC_01
AF069958.1 gg_id:111772 Nitrobacter alkalicus str. AN4 AF0699
AF069957.1 gg_id:73775 Nitrobacter alkalicus str. AN2 AF0699
NC_007964.1 gg_id:156705 Nitrobacter hamburgensis str. X14 NC_00
AM292301.1 gg_id:254106 Nitrobacter vulgaris str. BB3 AM292
AY055796.1 gg_id:17737 Nitrobacter winogradskyi str. ATCC 14123 AY0557
AM286382.1 gg_id:220346 Nitrobacter vulgaris str. K55 AM286
AY055798.1 gg_id:56503 Nitrobacter sp. str. KB212 AY0557
EU528247.1 gg_id:284778 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
L11661.1 gg_id:4840 Nitrobacter winogradskyi str. W L11661
AM286390.1 gg_id:223530 Nitrobacter vulgaris str. 329 AM286
L11662.1 gg_id:4842 Nitrobacter sp str. LL L11662
AF529115.1 gg_id:62406 trichloroethene-contaminated site clone FTLM116 proteobacterium AF5291
AB241411.1 gg_id:223626 Rhodopseudomonas lichen O5 AB2414
AB196356.1 gg_id:109667 Rhodopseudomonas palustris str. LW-RE AB1963
AF487428.1 gg_id:68786 Rhodopseudomonas palustris str. Wai1S1 AF4874
U09829.1 gg_id:4878 marine sediment clone JAP850 Rochelle U09829
X87279.1 gg_id:4854 Rhodopseudomonas palustris str. DSM 126 X87279
EU018457.1 gg_id:252635 Rhodobacter sphaeroides PSB07-19 EU0184
CP000463.1 gg_id:183860 Rhodopseudomonas palustris str. BisA53 CP0004
AB167545.1 gg_id:100949 Rhodopseudomonas palustris str. KP0014 FERMP-19432 AB1675
AJ968691.1 gg_id:166553 Rhodopseudomonas sp. 1416ri str. ORS 1416 AJ9686
CP000301.1 gg_id:153177 Rhodopseudomonas palustris str. BisB18 CP0003
EF515308.1 gg_id:224099 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22f08 EF5153
AB167544.1 gg_id:100793 Rhodopseudomonas palustris str. KP0003 FERMP-19430 AB1675

0	1	0	0	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	1	0	0	0	0
0	1	0	0	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	1	0	0	0	0
0	1	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	0	0	1
0	1	0	1	1	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	0	0	1
0	0	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__Rhodopseudomonas
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	59661
s__unclassified	59713
s__unclassified	59761
s__unclassified	59855
s__unclassified	59868
s__unclassified	59880
s__unclassified	59957
s__unclassified	60116
s__unclassified	60190
s__unclassified	58917
s__unclassified	58926
s__unclassified	58948
s__unclassified	58977
s__unclassified	58990
s__unclassified	58998
s__unclassified	59017
s__unclassified	59021
s__unclassified	59027
s__unclassified	59048
s__unclassified	59089
s__unclassified	59117
s__unclassified	59127
s__unclassified	59141
s__unclassified	59161
s__unclassified	59228
s__unclassified	59242
s__unclassified	59264
s__unclassified	59268
s__unclassified	59273
s__unclassified	59278
s__unclassified	59289
s__unclassified	59291
s__unclassified	59330
s__unclassified	59349
s__unclassified	59355
s__unclassified	59357
s__unclassified	59359
s__unclassified	59370
s__unclassified	59416
s__unclassified	59454
s__unclassified	59457

EU221585.1 gg_id:253925 Rhodopseudomonas palustris str. DX-1 EU221
AF509907.1 gg_id:111553 Bradyrhizobium sp. str. CMI23 AF509
AB079634.1 gg_id:62340 Rhodopseudomonas palustris VA2-2 AB079
L11664.1 gg_id:4866 Rhodopseudomonas palustris L11664
DQ126338.1 gg_id:138381 Rhodopseudomonas sp. str. PSB-O DQ126
EU531568.1 gg_id:514717 Rhodopseudomonas palustris str. J EU531
EU018458.1 gg_id:248384 Rhodopseudomonas palustris PSB07-21 EU018
GQ036328.1 gg_id:384524 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362h08c1 GQ036
DQ984578.1 gg_id:245601 Mt. Nan-Jen litterfall clone IYF09 DQ984
DQ497243.1 gg_id:157613 Chelatococcus sp DQ497
GQ421849.1 gg_id:550491 Microvirga sp. str. 5420S-16 GQ421
FJ025099.1 gg_id:308491 Bradyrhizobium japonicum str. SEMIA 6396 FJ0250
AY904750.1 gg_id:112390 Bradyrhizobium japonicum str. SEMIA 6144 AY904
AJ009451.1 gg_id:4819 anaerobic TCB-transforming consortium clone SJA-9 AJ0094
EF121353.1 gg_id:216650 microbiota uninfected and Rickettsia-infected colonized cat fleas Ctenocephalides fel EF1213
EU861833.1 gg_id:309753 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
FJ478995.1 gg_id:579612 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
FJ025100.1 gg_id:309477 Bradyrhizobium japonicum str. SEMIA 6154 FJ0251
GU455366.1 gg_id:523224 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AM412118.1 gg_id:247879 Chelatococcus sp. str. P-117 AM412
EU256461.1 gg_id:256534 Bradyrhizobium sp. str. CCBAU 85044 EU256
AM990457.1 gg_id:279499 Chelatococcus sp. str. I-21 AM990
DQ303342.1 gg_id:150032 Dynamic during maturation Tuber magnatum Pico ascoma Bradyrhizobium clone TM DQ303
EF394148.1 gg_id:205693 Bradyrhizobium japonicum str. CCBAU 43277 EF3941
X87272.1 gg_id:4980 Bradyrhizobium japonicum str. DSM 30131 T X87272
AF530465.1 gg_id:61023 Bradyrhizobium japonicum JZ1 AF5304
DQ129309.1 gg_id:138424 microarray level air two cities Texas urban aerosol clone AKIW763 DQ129
EU276558.1 gg_id:362293 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU276
AF417550.1 gg_id:48037 Bradyrhizobium japonicum str. DASA01059 AF4175
EF018822.1 gg_id:204655 aspen rhizosphere clone Amb_16S_1300 EF0188
FJ716001.1 gg_id:579890 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AY345540.1 gg_id:91124 Lake Wai'ele'ele water clone LWSR-28 AY3455
GQ129955.1 gg_id:434250 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
AF417547.2 gg_id:33185 Bradyrhizobium japonicum str. DASA38025 AF4175
GQ389009.1 gg_id:587997 quality deterioration drinking system during serious red water outbreak clone J57 GQ389
DQ432334.1 gg_id:156941 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W DQ432
EF394142.1 gg_id:204550 Bradyrhizobium japonicum str. CCBAU 41267 EF3941
AY649440.1 gg_id:99283 Bradyrhizobium japonicum str. BR3288 AY6494
AB187010.1 gg_id:101203 Suiyo seamount hydrothermal vent water 0.2micro-m filterable fraction clone SSM-M AB187
AB195991.1 gg_id:130287 Bradyrhizobium japonicum str. MH615 AB195
AJ867909.1 gg_id:143411 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone B6 AJ8679

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	0	0	0	1	0	1
0	0	0	1	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	1	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	1	1	0	0	0	1	0	1
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	1	0	1
1	0	0	0	1	1	1	0	0	0	1	0	0
1	0	0	1	1	1	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	1	0	0
0	1	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
1	0	0	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	1	0	0
0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae

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

s__unclassified	59476
s__unclassified	59480
s__unclassified	59497
s__unclassified	59508
s__unclassified	59524
s__unclassified	59531
s__unclassified	59532
s__unclassified	59533
s__unclassified	59583
s__unclassified	59586
s__unclassified	59630
s__unclassified	59637
s__unclassified	59657
s__unclassified	59659
s__unclassified	59664
s__unclassified	59697
s__unclassified	59745
s__unclassified	59756
s__unclassified	59771
s__unclassified	59777
s__unclassified	59780
s__unclassified	59789
s__unclassified	59806
s__unclassified	59844
s__unclassified	59871
s__unclassified	59878
s__unclassified	59886
s__unclassified	59888
s__unclassified	59913
s__unclassified	59920
s__unclassified	59925
s__unclassified	59947
s__unclassified	59965
s__unclassified	59985
s__unclassified	60017
s__unclassified	60034
s__unclassified	60049
s__unclassified	60075
s__unclassified	60078
s__unclassified	60087
s__unclassified	60129

AJ968693.1 gg_id:167720 Bosea sp. str. ORS 1414 AJ9686
EU878006.2 gg_id:576097 Salinarimonas rosea str. YIM YD3 EU878
GQ103050.1 gg_id:397383 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
FJ479132.1 gg_id:512302 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
AM292299.1 gg_id:242856 Nitrobacter hamburgensis str. Y AM292
AB195986.1 gg_id:128373 Bradyrhizobium canariense str. MH547 AB195
EU029133.1 gg_id:244029 Deinococcus sp. str. 5A4 EU029
AM411919.1 gg_id:253138 Bradyrhizobium sp. str. P-44 AM411
AB300992.1 gg_id:223242 Bradyrhizobium iriomotense str. EK05 (= NBRC 102520) AB300
EF394144.1 gg_id:214300 Bradyrhizobium japonicum str. CCBAU 53152 EF3941
AY963315.1 gg_id:154614 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
AB426223.1 gg_id:263163 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AJ785294.1 gg_id:211869 Rhizobiales genosp. AL ARRI 185 AJ7852
CU927551.1 gg_id:545730 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
DQ351924.1 gg_id:173105 manganese oxidation soil clone JH-GY18 DQ351
AF417552.1 gg_id:27428 Bradyrhizobium japonicum str. DASA37011 AF417
AY372184.1 gg_id:94343 Bradyrhizobium betae str. PL7HG1 AY372
EF516928.1 gg_id:222831 grassland soil clone FCPN762 EF5169
AF208509.1 gg_id:56515 Bradyrhizobium japonicum str. USDA 129 AF2085
AY904764.1 gg_id:112297 Bradyrhizobium japonicum str. SEMIA 6163 AY904
FJ382130.1 gg_id:582075 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
AF417551.1 gg_id:45827 Bradyrhizobium japonicum str. DASA37026 AF417
AY904758.1 gg_id:112060 Bradyrhizobium japonicum str. SEMIA 6156 AY904
FJ528273.1 gg_id:573764 Bradyrhizobium sp. str. Mf253 FJ5282
AF234889.2 gg_id:77279 Bradyrhizobium japonicum str. SEMIA 5080 AF2348
AY904765.1 gg_id:112064 Bradyrhizobium japonicum str. SEMIA 6164 AY904
FJ382683.1 gg_id:510366 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3826
AY904743.1 gg_id:111821 Bradyrhizobium japonicum str. SEMIA 6002 AY904
AF502220.1 gg_id:55851 EBPR sludge lab scale clone HP1B78 AF5022
EF032655.1 gg_id:198655 structure riverine biofilms river biofilm clone SepB-6 EF0326
FJ380996.1 gg_id:549917 Bradyrhizobium sp. str. BQN4T-01d FJ3809
AY178079.1 gg_id:100322 Bradyrhizobium sp. Cmey1 Cmey 1 AY178
AY904732.1 gg_id:111515 Bradyrhizobium japonicum str. SEMIA 656 AY904
AF409021.1 gg_id:98929 Bradyrhizobium sp. str. Ellin179 AF409
D13430.1 gg_id:4937 Bradyrhizobium japonicum str. USDA 110 D13430
AB220164.1 gg_id:153145 Bradyrhizobium sp. QC1 AB220
AF508112.1 gg_id:66234 Bosea thiooxidans TJ1 AF508
GU377100.1 gg_id:514335 Balneimonas sp. str. sptzw09 GU377
AY169423.1 gg_id:81409 Bradyrhizobium japonicum AY1694
D78366.1 gg_id:5055 Agromonas oligotrophica str. JCM1494 D78366
GQ389186.1 gg_id:582505 quality deterioration drinking system during serious red water outbreak clone D59 GQ389

0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	0	1	1
0	1	0	0	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	1	0	1
0	1	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	0	0	0	0	0	0	0
1	0	0	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	1	0	1
0	0	0	1	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Bradyrhizobiaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Brucella
g__Brucella
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Ochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__Pseudochrobactrum
g__unclassified

s__unclassified	60130
s__unclassified	60132
s__unclassified	60136
s__unclassified	60177
s__unclassified	60558
s__unclassified	62393
s__unclassified	62562
s__Ochrobactrum grignonense	61953
s__Ochrobactrum intermedium	61842
s__Ochrobactrum intermedium	61854
s__Ochrobactrum intermedium	61906
s__Ochrobactrum intermedium	62289
s__unclassified	61464
s__unclassified	61639
s__unclassified	61667
s__unclassified	61720
s__unclassified	61926
s__unclassified	62062
s__unclassified	62169
s__unclassified	62189
s__unclassified	62197
s__unclassified	62217
s__unclassified	62229
s__unclassified	62331
s__unclassified	62355
s__unclassified	62385
s__unclassified	62619
s__unclassified	62713
s__unclassified	62737
s__unclassified	62806
s__unclassified	62872
s__Pseudochrobactrum saccharolyticum	62386
s__unclassified	61440
s__unclassified	61519
s__unclassified	61889
s__unclassified	62053
s__unclassified	62138
s__unclassified	62602
s__unclassified	62772
s__unclassified	62840
s__unclassified	61380

AF408978.1 gg_id:99637 Bradyrhizobium sp. str. Ellin136 AF408
AF417546.1 gg_id:68929 Bradyrhizobium japonicum str. DASA03066 AF417
GQ848213.1 gg_id:586303 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
AY904786.1 gg_id:111454 Bradyrhizobium japonicum str. SEMIA 6420 AY904
AM990460.1 gg_id:277676 Chelatococcus sp. str. TKE5A AM990
L37584.1 gg_id:5189 Brucella canis L37584
X13695.1 gg_id:5204 Brucella melitensis biovar Abortus str. 11-19 X13695
EU165529.1 gg_id:255878 Ochrobactrum sp. str. MI9.3 EU165
U70978.1 gg_id:5195 Ochrobactrum anthropi str. LMG 3301 U70978
AF526513.2 gg_id:57487 Ochrobactrum intermedium ADV14 AF5265
EU352765.1 gg_id:265442 Ochrobactrum anthropi str. NK 2.T-3 EU352
AB120120.1 gg_id:94870 Ochrobactrum anthropi AB120
AB091758.1 gg_id:59527 Ochrobactrum tritici AS1 AB091
AM490617.1 gg_id:247109 Ochrobactrum anthropi str. DSM 7216 AM490
FJ984528.1 gg_id:451696 Ochrobactrum haemophilum str. NBSL23 FJ9845
AF229848.1 gg_id:31117 Ochrobactrum sp. str. PR17 AF2298
AF229879.1 gg_id:24208 Ochrobactrum sp. str. 4FB13 AF2298
FJ859687.2 gg_id:536560 Ochrobactrum pseudogrignonense str. BIHB 340 FJ8596
DQ112028.1 gg_id:130527 Ochrobactrum anthropi str. T1 DQ112
AM084018.1 gg_id:140347 Ochrobactrum sp. str. R-25055 AM084
AM490612.1 gg_id:249691 Ochrobactrum anthropi str. LMG 401 AM490
AJ550273.2 gg_id:90730 Ochrobactrum sp. TK14 AJ5502
DQ295875.1 gg_id:142896 Ochrobactrum sp. str. CDB2 DQ295
EU370421.1 gg_id:271876 Ochrobactrum sp. str. 45C2 EU370
EU352762.1 gg_id:268033 Ochrobactrum tritici str. NK 2.X-2 EU352
DQ133574.1 gg_id:139474 Ochrobactrum sp. str. LJJS1-2 DQ133
EF028152.1 gg_id:179539 Ochrobactrum sp. str. xll-3 EF0281
EU399793.1 gg_id:272191 Ochrobactrum anthropi str. PV2Z2 EU399
AM411061.1 gg_id:175969 Ochrobactrum cytisi str. 43(25)zhy AM411
GQ203110.1 gg_id:585971 Ochrobactrum pseudogrignonense str. 4-4DEP GQ203
AY917134.1 gg_id:113673 Ochrobactrum anthropi CYP2004 AY917
AM180484.1 gg_id:145855 Pseudochrobactrum saccharolyticum str. CCUG 33852 AM180
GQ451252.1 gg_id:534015 Fecal Yunnan snub-nosed monkey feces clone J187 GQ451
GQ451321.1 gg_id:510928 Fecal Yunnan snub-nosed monkey feces clone J346 GQ451
FJ950551.1 gg_id:415870 Pseudochrobactrum saccharolyticum str. c299 FJ9505
FJ493040.1 gg_id:589752 Pseudochrobactrum asaccharolyticum str. 2G-2 FJ4930
AM263420.1 gg_id:161116 Pseudochrobactrum kiredjianae str. CCUG 49584 AM263
FM872511.1 gg_id:365772 occupant source house floor dust clone FA01D11 FM872
GQ451230.1 gg_id:564278 Fecal Yunnan snub-nosed monkey feces clone J145 GQ451
FJ950554.1 gg_id:407459 Pseudochrobactrum asaccharolyticum str. c72 FJ9505
FJ950543.1 gg_id:417632 Ochrobactrum grignonense str. c15 FJ9505

0	0	0	1	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	1	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	1	1	0	0	1
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Brucellaceae
o__Rhizobiales	f__Cohaesibacteraceae
o__Rhizobiales	f__Cohaesibacteraceae
o__Rhizobiales	f__Cohaesibacteraceae
o__Rhizobiales	f__Cohaesibacteraceae
o__Rhizobiales	f__Cohaesibacteraceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Cohaesibacter
g__Cohaesibacter
g__Cohaesibacter
g__Cohaesibacter
g__unclassified
g__Blastochloris
g__Blastochloris
g__Blastochloris
g__Blastochloris
g__Blastochloris
g__Blastochloris
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia

s__unclassified	61482
s__unclassified	61727
s__unclassified	61859
s__unclassified	61994
s__unclassified	62100
s__unclassified	62291
s__unclassified	62296
s__unclassified	62329
s__unclassified	62382
s__unclassified	62495
s__unclassified	62848
s__unclassified	62885
s__unclassified	62926
s__unclassified	61561
s__unclassified	62301
s__unclassified	62543
s__unclassified	62770
s__unclassified	62313
s__Blastochloris viridis	59707
s__Blastochloris viridis	59798
s__Blastochloris viridis	59893
s__unclassified	59362
s__unclassified	59691
s__unclassified	59810
s__Candidatus Devosia euplotis	60350
s__unclassified	60239
s__unclassified	60240
s__unclassified	60292
s__unclassified	60328
s__unclassified	60364
s__unclassified	60386
s__unclassified	60416
s__unclassified	60462
s__unclassified	60472
s__unclassified	60512
s__unclassified	60514
s__unclassified	60552
s__unclassified	60569
s__unclassified	60580
s__unclassified	60606
s__unclassified	60609

AJ920029.1 gg_id:114742 Ochrobactrum shiyianus str. WSH-W04 AJ9200
DQ365923.2 gg_id:155200 Ochrobactrum pseudintermedium str. ADV43 DQ365
AY914071.1 gg_id:113751 Ochrobactrum sp. R-3 AY9140
AB369864.1 gg_id:253214 Pseudochrobactrum glaciale str. KMM 3858 (= Pi 26) AB3698
AM114407.1 gg_id:151281 Ochrobactrum anthropi str. CCUG 34735 AM114
FJ887929.1 gg_id:551972 Ochrobactrum intermedium str. AR9 FJ8879
AF526514.2 gg_id:62908 Ochrobactrum intermedium ADV21 AF5265
EU352758.1 gg_id:271007 Ochrobactrum intermedium str. NK 2.HA-1 EU3527
GQ280047.1 gg_id:591634 Ochrobactrum intermedium str. BJ-37 GQ280
AF526515.2 gg_id:62909 Ochrobactrum intermedium ADV24 AF5265
AF515675.1 gg_id:77381 Ochrobactrum sp. YYS-2002 AF5156
AJ519939.1 gg_id:76582 Ochrobactrum gallinifaecis str. Iso 196 AJ5199
AM041247.1 gg_id:133461 Ochrobactrum aqua-oryzae str. MTCC 4195 AM041
FJ202509.1 gg_id:345537 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
DQ446093.2 gg_id:172411 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid DQ446
GU118085.1 gg_id:560738 Threatened Corals Provide Microbial Habitats clone Apal_L09 GU118
FJ202721.1 gg_id:319280 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
GU118071.1 gg_id:567305 Threatened Corals Provide Microbial Habitats clone Apal_M03 GU118
D25314.1 gg_id:4687 Blastochloris viridis str. ATCC19567 D25314
AM502287.1 gg_id:261580 Blastochloris gulmargensis str. JA248 AM502
AF084509.1 gg_id:200193 Blastochloris viridis str. B9 AF0845
AJ401203.1 gg_id:78031 Blastochloris sp. AT2101 AJ4012
AY117148.1 gg_id:63558 Blastochloris sulfoviridis str. OK3G7 AY1171
AJ012089.1 gg_id:4711 Blastochloris sulfoviridis str. ToP1 AJ0120
AJ548824.1 gg_id:82396 Candidatus Devosia euplotis str. CAMP4.4 AJ5488
EU589260.1 gg_id:260684 China Ningxia rice paddy field soil clone 1_C6 EU5892
EF433460.1 gg_id:212196 Devosia sp. str. IPL15 EF4334
EU812979.1 gg_id:311842 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
EF540476.1 gg_id:224522 Devosia sp. 6_4V EF5404
FJ807418.1 gg_id:550842 Presence and iron oxidizing landfill leachate impacted groundwater surface water int FJ8074
EU362140.1 gg_id:355188 and Mesquite Flats Site Death Valley dune sand clone 11 EU3621
DQ125710.1 gg_id:130155 uranium contaminated soil clone AKAU3805 DQ125
EF612399.1 gg_id:255206 historic semiarid lead-zinc mine tailings site soil clone OS-C20 EF6123
GQ396877.1 gg_id:573755 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
AY512822.1 gg_id:105993 Devosia riboflavina AY5128
DQ279337.1 gg_id:144518 Dynamic during maturation Tuber magnatum Pico ascoma Xanthomonas clone TM1 DQ279
EF067859.1 gg_id:174315 Devosia terrae str. DCY11 EF0678
FN421512.1 gg_id:573013 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 12_F07 FN4215
EU289427.1 gg_id:245814 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
GQ472390.1 gg_id:544772 Microbial Dongping Lake lake sediment clone 4D3-5 GQ472
FM253613.1 gg_id:333986 Rock gold mine unusually microbial biofilm clone F07-1 FM253

0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	1	0	0	1	0	1
0	0	0	0	0	1	0	0	0	0	0	0	1
0	1	0	1	1	1	1	0	1	0	1	1	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	1	1	1
0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	1
0	0	0	1	1	0	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae

g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Devosia
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium

s__unclassified	60635
s__unclassified	60702
s__unclassified	60710
s__unclassified	60784
s__unclassified	60809
s__unclassified	60868
s__unclassified	60901
s__unclassified	60969
s__unclassified	60980
s__unclassified	61005
s__unclassified	61008
s__unclassified	61027
s__unclassified	61078
s__unclassified	61084
s__unclassified	61085
s__unclassified	61112
s__unclassified	61126
s__unclassified	61135
s__unclassified	61228
s__unclassified	61256
s__unclassified	61285
s__unclassified	61304
s__unclassified	61332
s__unclassified	61334
s__unclassified	61335
s__unclassified	61342
s__unclassified	61350
s__Hyphomicrobium facile	59262
s__Hyphomicrobium methylovorum	59562
s__Hyphomicrobium methylovorum	59644
s__Hyphomicrobium methylovorum	59801
s__Hyphomicrobium sulfonivorans	58898
s__Hyphomicrobium zavarzinii	59552
s__Hyphomicrobium zavarzinii	59881
s__unclassified	58912
s__unclassified	58915
s__unclassified	59057
s__unclassified	59125
s__unclassified	59150
s__unclassified	59154
s__unclassified	59168

AB361068.1 gg_id:249524 Devosia yakushimanensis str. Yak96B AB361
GQ006663.1 gg_id:502999 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu86b10c GQ006
FN594684.1 gg_id:559356 and arsenic mobilization rock biofilms ancient biofilom gold mine Zloty Stok clone f1- FN594
EF018449.1 gg_id:215447 aspen rhizosphere clone Amb_16S_1074 EF0184
GQ263214.1 gg_id:581749 Structure Simulated Level Waste Site simulated level waste site clone F3_19X GQ263
EU709017.1 gg_id:301593 Devosia sp. str. B2 EU709
FJ560749.1 gg_id:550691 Prosthecomicrobium mishustinii str. 17 FJ5607
EF540486.1 gg_id:227483 Devosia sp. c4M EF5404
AM293857.1 gg_id:237298 Devosia subaequoris str. HST3-14 AM293
GU444083.1 gg_id:516056 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
EF540440.1 gg_id:224543 oil-shale semi-coke solid waste clone PK_X EF5404
CU927436.1 gg_id:573246 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
FM872901.1 gg_id:365288 occupant source house floor dust clone FB04D08 FM872
EF575560.1 gg_id:232353 Devosia sp. str. BD-c194 EF5755
AY921786.1 gg_id:114008 farm soil clone AKYG1666 AY9217
EU344945.1 gg_id:273185 Hepialus gonggaensis guts equalized library larval gut clone Hg5-35 EU344
GQ264021.1 gg_id:540672 Structure Simulated Level Waste Site simulated level waste site clone WC3_112 GQ264
AJ318163.1 gg_id:25284 Waste-gas biofilter clone BIri24 AJ3181
AY695724.1 gg_id:107598 USA: New Mexico Carlsbad Lechuguilla Cave Rainbow Room clone RR3A4 AY695
GQ263858.1 gg_id:565555 Structure Simulated Level Waste Site simulated level waste site clone WC2_101 GQ263
EU937979.1 gg_id:332501 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
CU918672.1 gg_id:552248 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
GQ396880.1 gg_id:560208 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
DQ814270.1 gg_id:163314 zebrafish digestive tract clone aab66c07 DQ814
EU133360.1 gg_id:257399 tallgrass prarie soil clone FFCH11455 EU133
DQ248307.1 gg_id:142990 carbon tetrachloride contaminated soil clone TF11 DQ248
GQ093782.1 gg_id:453654 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
Y14309.1 gg_id:4622 Hyphomicrobium facile str. H-526 Y14309
FM877980.1 gg_id:553425 Microbial iron redox cycling circumneutral-pH groundwater seep Hyphomicrobium c FM877
Y14307.1 gg_id:4627 Hyphomicrobium methylovorum str. DSM 5458 Y14307
AB016812.1 gg_id:4626 Hyphomicrobium methylovorum str. MBIC3196 AB0168
AF235089.1 gg_id:29178 Hyphomicrobium sulfonivorans str. S1; ATCC BAA-113; DSM 13863 AF235
FJ536921.1 gg_id:594171 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5369
Y14305.1 gg_id:4632 Hyphomicrobium zavarzinii str. ZV-622 Y14305
AB252934.1 gg_id:167855 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 225 AB252
EF019299.1 gg_id:210886 aspen rhizosphere clone Elev_16S_489 EF0192
AF198623.1 gg_id:47454 Hyphomicrobium chloromethanicum str. CM2 AF1986
AF234719.1 gg_id:52859 sludge clone A27b AF2347
AY328655.1 gg_id:88846 drinking water system simulator clone DSSF33 AY3286
Y14302.1 gg_id:4636 Hyphomicrobium vulgare str. IFAM MC-750 ATCC 27500 Y14302
DQ814327.1 gg_id:172883 zebrafish digestive tract clone aab67a09 DQ814

0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	1	0	1	1	0
0	1	0	1	1	0	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	1	0	0	1	1	1
0	0	0	1	1	0	1	0	0	0	1	0	1
1	1	0	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	1	1	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	1	1	1
1	1	0	1	0	1	0	1	1	0	1	1	1
0	0	0	1	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	0	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae

g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Hyphomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium
g__Pedomicrobium

s__unclassified	59194
s__unclassified	59240
s__unclassified	59309
s__unclassified	59327
s__unclassified	59381
s__unclassified	59412
s__unclassified	59474
s__unclassified	59483
s__unclassified	59489
s__unclassified	59514
s__unclassified	59519
s__unclassified	59538
s__unclassified	59539
s__unclassified	59609
s__unclassified	59647
s__unclassified	59652
s__unclassified	59653
s__unclassified	59667
s__unclassified	59711
s__unclassified	59730
s__unclassified	59800
s__unclassified	59843
s__unclassified	59926
s__unclassified	59937
s__unclassified	59953
s__unclassified	59954
s__unclassified	59998
s__unclassified	60002
s__unclassified	60055
s__unclassified	60126
s__unclassified	60135
s__Pedomicrobium australicum	59509
s__unclassified	59005
s__unclassified	59100
s__unclassified	59307
s__unclassified	59418
s__unclassified	59484
s__unclassified	59555
s__unclassified	59759
s__unclassified	59813
s__unclassified	59919

AY957933.1 gg_id:115024 drinking water biofilm clone B3NR69D18 AY9579
Y14303.1 gg_id:4630 Hyphomicrobium hollandicum str. IFAM KB-677 Y14303
Y14304.1 gg_id:4635 Hyphomicrobium aestuarii str. DSM 1564 Y14304
CU918149.1 gg_id:539592 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AY328697.1 gg_id:88935 drinking water system simulator clone DSSF75 AY3286
AY328659.1 gg_id:89720 drinking water system simulator clone DSSF37 AY3286
AF097815.2 gg_id:4640 activated sludge clone 49520 AF0978
AF279787.1 gg_id:26693 Hyphomicrobium sp. str. PMC AF2797
AY328635.1 gg_id:89164 drinking water system simulator clone DSSF12 AY3286
AY328650.1 gg_id:90267 drinking water system simulator clone DSSF27 AY3286
GQ500789.1 gg_id:573659 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
X53182.1 gg_id:34344 Hyphomicrobium vulgare str. MC-750 X53182
GQ263780.1 gg_id:558638 Structure Simulated Level Waste Site simulated level waste site clone WC1_b17 GQ263
CU918043.1 gg_id:568017 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AF097824.2 gg_id:4624 activated sludge clone 4953 AF0978
DQ814766.1 gg_id:172128 zebrafish digestive tract clone aab53a04 DQ814
CU920885.1 gg_id:547603 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
GQ264377.1 gg_id:513073 Structure Simulated Level Waste Site simulated level waste site clone WW2_57 GQ264
AY328683.1 gg_id:88276 drinking water system simulator clone DSSF61 AY3286
DQ815221.1 gg_id:168134 zebrafish digestive tract clone aab51g05 DQ815
FM253620.1 gg_id:324555 Rock gold mine unusually microbial biofilm clone G04-1 FM253
Y14308.1 gg_id:4619 Hyphomicrobium denitrificans str. DSM 1869 Y14308
GQ500820.1 gg_id:591347 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
FJ152725.1 gg_id:336999 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
GQ281066.1 gg_id:586097 Hyphomicrobium facile str. NBCS23 GQ281
GQ500792.1 gg_id:579761 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
EF019856.1 gg_id:207848 aspen rhizosphere clone Elev_16S_1214 EF0198
FJ439830.1 gg_id:550289 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M2 FJ4398
AY328674.1 gg_id:90421 drinking water system simulator clone DSSF52 AY3286
EF125445.1 gg_id:198749 mangrove soil clone MSB-2E9 EF1254
DQ814141.1 gg_id:172266 zebrafish digestive tract clone aab60d07 DQ814
GU269548.1 gg_id:579387 Pedomicrobium ferrugineum str. ATCC 33119 GU269
GQ339120.1 gg_id:529888 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
GQ264219.1 gg_id:585537 Structure Simulated Level Waste Site simulated level waste site clone WW1_b13 GQ264
FJ478816.1 gg_id:573426 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
FJ479530.1 gg_id:554597 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
AY921654.1 gg_id:113465 farm soil clone AKYG1791 AY9216
FJ478521.1 gg_id:556996 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
GU269549.1 gg_id:571598 Pedomicrobium manganicum str. ATCC 33121 GU269
EF019229.1 gg_id:207866 aspen rhizosphere clone Elev_16S_398 EF0192
EU644219.1 gg_id:285061 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	0
0	1	0	1	1	1	1	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	1	1	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae

g__Pedomicrobium
g__Rhodomicrobium
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes

s__unclassified	60127
s__unclassified	60584
s__Rhodoplanes elegans	59292
s__Rhodoplanes elegans	59863
s__Rhodoplanes elegans	60117
s__unclassified	51142
s__unclassified	51455
s__unclassified	58884
s__unclassified	58887
s__unclassified	58992
s__unclassified	59047
s__unclassified	59055
s__unclassified	59063
s__unclassified	59116
s__unclassified	59126
s__unclassified	59182
s__unclassified	59208
s__unclassified	59216
s__unclassified	59224
s__unclassified	59236
s__unclassified	59249
s__unclassified	59253
s__unclassified	59312
s__unclassified	59315
s__unclassified	59324
s__unclassified	59326
s__unclassified	59329
s__unclassified	59344
s__unclassified	59393
s__unclassified	59403
s__unclassified	59408
s__unclassified	59431
s__unclassified	59459
s__unclassified	59527
s__unclassified	59537
s__unclassified	59546
s__unclassified	59581
s__unclassified	59592
s__unclassified	59629
s__unclassified	59641
s__unclassified	59645

EU335234.1 gg_id:240757 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EF153296.1 gg_id:187340 Rhodomicrobium sp. str. ShRmc01 EF1532
EF650482.1 gg_id:238973 Rhodocista sp. str. GP-7 EF6504
D25313.1 gg_id:4680 Rhodoplanes roseus str. 941 D25313
AM712913.1 gg_id:247905 Rhodoplanes piscinae str. JA266 AM712
EF019983.1 gg_id:212484 aspen rhizosphere clone Elev_16S_1370 EF0199
EU133616.1 gg_id:254348 tallgrass prarie soil clone FFCH2026 EU1336
EU335329.1 gg_id:245987 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
AY921820.1 gg_id:113474 farm soil clone AKYG712 AY9218
AY922092.1 gg_id:114396 farm soil clone AKYH1064 AY9220
EF018397.1 gg_id:208293 aspen rhizosphere clone Amb_16S_1010 EF0183
GQ263521.1 gg_id:534454 Structure Simulated Level Waste Site simulated level waste site clone FW2_47B GQ263
EU335450.1 gg_id:235975 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EF020096.1 gg_id:210974 aspen rhizosphere clone Elev_16S_1506 EF0200
GQ500727.1 gg_id:576799 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
AY622245.1 gg_id:107444 subsurface soil clone B-L17 AY6222
FJ479010.1 gg_id:561693 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ625323.1 gg_id:570840 Influence lead contamination on boreal pine forest soil clone HF_M_20 FJ6253
EF019513.1 gg_id:207374 aspen rhizosphere clone Elev_16S_1015 EF0195
EF032737.1 gg_id:179877 cyanobacterial mat in lava cave clone HAVOmat148 EF0327
EF018835.1 gg_id:215423 aspen rhizosphere clone Amb_16S_1316 EF0188
AY234497.1 gg_id:111439 soil isolate Ellin5080 AY2344
EU937846.1 gg_id:315986 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9378
AY921720.1 gg_id:113725 farm soil clone AKYH1040 AY9217
FJ807419.1 gg_id:570413 Presence and iron oxidizing landfill leachate impacted groundwater surface water int FJ8074
EF020128.1 gg_id:215872 aspen rhizosphere clone Elev_16S_1545 EF0201
DQ537531.1 gg_id:163571 manganese oxidation soil clone JH-GY22 DQ537
FJ152854.1 gg_id:316335 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
DQ984560.1 gg_id:237595 Mt. Nan-Jen soil clone IFD_31 DQ984
AY326602.1 gg_id:136172 Amazon soil clone 711-1 AY3266
AJ581617.1 gg_id:93792 soil near uranium mill tailings clone KCM-C-24 AJ5816
FJ479160.1 gg_id:551343 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
FJ479575.1 gg_id:585582 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
AB286367.1 gg_id:204919 Reducing production and domination comamonadaceae reducing oxygen supply was AB2863
EF018437.1 gg_id:212776 aspen rhizosphere clone Amb_16S_1057 EF0184
AY395414.1 gg_id:105676 pasture soil clone EB1095 AY3954
EF019188.1 gg_id:208963 aspen rhizosphere clone Amb_16S_1857 EF0191
DQ451455.1 gg_id:156816 forest soil clone FAC16 DQ451
EU133294.1 gg_id:251152 tallgrass prarie soil clone FFCH12843 EU1332
AY913382.1 gg_id:113588 forest soil clone DUNssu176 (-7A) (OTU#160) AY9133
AY963313.1 gg_id:151184 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	1	1	0
1	1	1	0	0	1	0	1	1	1	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	1	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	1
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae

g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__Rhodoplanes
g__unclassified

s__unclassified	59658
s__unclassified	59674
s__unclassified	59676
s__unclassified	59695
s__unclassified	59699
s__unclassified	59702
s__unclassified	59720
s__unclassified	59731
s__unclassified	59734
s__unclassified	59744
s__unclassified	59769
s__unclassified	59776
s__unclassified	59783
s__unclassified	59818
s__unclassified	59829
s__unclassified	59838
s__unclassified	59866
s__unclassified	59873
s__unclassified	59874
s__unclassified	59901
s__unclassified	59921
s__unclassified	59931
s__unclassified	59956
s__unclassified	59966
s__unclassified	59967
s__unclassified	59978
s__unclassified	59991
s__unclassified	60013
s__unclassified	60032
s__unclassified	60048
s__unclassified	60054
s__unclassified	60057
s__unclassified	60073
s__unclassified	60114
s__unclassified	60128
s__unclassified	60160
s__unclassified	60181
s__unclassified	60211
s__unclassified	60414
s__unclassified	62359
s__unclassified	58885

GQ262926.1 gg_id:566311 Structure Simulated Level Waste Site simulated level waste site clone F1_73X GQ262
DQ837247.1 gg_id:244310 Archaeal and pristine National Park Spain Donana coastal aquifer clone 49S1_2B_37 DQ837
FJ478974.1 gg_id:584077 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EF540400.1 gg_id:217826 oil-shale semi-coke solid waste clone 4_24MK EF5404
AY724055.2 gg_id:111888 soil clone DUNssu006 AY724
AB121773.1 gg_id:98457 Bradyrhizobium sp. str. Shinshu-th2 AB121
AY921846.1 gg_id:114139 farm soil clone AKYG1898 AY921
GQ397068.1 gg_id:575164 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
EU335327.1 gg_id:250714 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
AJ810382.1 gg_id:159481 Rhizobiales genosp. AB CsBT10/2 AJ8103
EU429497.1 gg_id:544454 producing pigmented colonies aerosol and soil remote glaciated areas (Antarctica Al EU429
EF516064.1 gg_id:218539 grassland soil clone FCPS586 EF516
GU444101.1 gg_id:515709 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
GQ402598.1 gg_id:566207 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF018075.1 gg_id:211128 aspen rhizosphere clone Amb_16S_400 EF018
DQ404666.1 gg_id:152904 contaminated sediment clone 654997 DQ404
EU644207.1 gg_id:282627 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
GQ264285.1 gg_id:555816 Structure Simulated Level Waste Site simulated level waste site clone WW2_06 GQ264
EF019849.1 gg_id:205156 aspen rhizosphere clone Elev_16S_1206 EF0198
DQ125920.1 gg_id:136171 uranium contaminated soil clone AKAU4191 DQ125
EU669630.1 gg_id:314708 soil clone S22-33 EU669
EF020062.1 gg_id:213736 aspen rhizosphere clone Elev_16S_1469 EF020
AY426439.1 gg_id:101471 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B14 AY4264
EF018152.1 gg_id:216748 aspen rhizosphere clone Amb_16S_487 EF0181
CU918797.1 gg_id:534993 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU133549.1 gg_id:253944 tallgrass prarie soil clone FFCH2918 EU133
AB240329.1 gg_id:144888 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
GQ264159.1 gg_id:584598 Structure Simulated Level Waste Site simulated level waste site clone WW1_a15 GQ264
GQ263836.1 gg_id:592746 Structure Simulated Level Waste Site simulated level waste site clone WC1_b83 GQ263
EU289423.1 gg_id:256335 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
GQ500841.1 gg_id:546305 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
EF019976.1 gg_id:206188 aspen rhizosphere clone Elev_16S_1362 EF019
EU335194.1 gg_id:256477 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
GQ093920.1 gg_id:452881 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EU289515.1 gg_id:256361 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU289
EF520408.1 gg_id:228499 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-5 EF5204
AY921875.1 gg_id:112834 farm soil clone AKYH1162 AY921
EU133623.1 gg_id:254308 tallgrass prarie soil clone FFCH929 EU133
EU881166.1 gg_id:317632 Karst region primary forest soil clone KPF200711-134 EU881
DQ125603.1 gg_id:136238 uranium contaminated soil clone AKAU3608 DQ125
DQ269121.1 gg_id:191415 marine macro-alga surface clone DPC255 DQ269

1	1	0	1	1	1	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	0	0
1	0	0	1	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	0	1	1	0	0	0	1	1	1
0	1	1	1	1	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	1	1
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	1
0	0	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	1	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
0	1	1	1	1	1	1	0	0	0	1	1	1
0	1	0	1	1	1	1	0	0	0	1	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Hyphomicrobiaceae

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

s__unclassified	58911
s__unclassified	58933
s__unclassified	58983
s__unclassified	59007
s__unclassified	59029
s__unclassified	59083
s__unclassified	59095
s__unclassified	59192
s__unclassified	59209
s__unclassified	59213
s__unclassified	59248
s__unclassified	59252
s__unclassified	59288
s__unclassified	59337
s__unclassified	59352
s__unclassified	59388
s__unclassified	59391
s__unclassified	59471
s__unclassified	59479
s__unclassified	59563
s__unclassified	59587
s__unclassified	59735
s__unclassified	59768
s__unclassified	59828
s__unclassified	59842
s__unclassified	59846
s__unclassified	59961
s__unclassified	60006
s__unclassified	60012
s__unclassified	60109
s__unclassified	60124
s__unclassified	60153
s__unclassified	60165
s__unclassified	60183
s__unclassified	60216
s__unclassified	60466
s__unclassified	60686
s__unclassified	60761
s__unclassified	60801
s__unclassified	60872
s__unclassified	61216

EU703268.1 gg_id:547851 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
AB240517.1 gg_id:141913 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
EF520393.1 gg_id:233793 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-93 EF5203
AY934488.1 gg_id:138039 Hyphomicrobium sp. str. WG6 AY9344
GQ397055.1 gg_id:583185 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
AM934937.1 gg_id:572993 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
EU491418.1 gg_id:263450 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
AM935138.1 gg_id:564931 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
GQ264131.1 gg_id:588269 Structure Simulated Level Waste Site simulated level waste site clone WC3_68 GQ264
EU881135.1 gg_id:318155 Karst region primary forest soil clone KPF200711-156 EU881
DQ413077.1 gg_id:151855 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
EU491437.1 gg_id:274058 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
GQ263776.1 gg_id:579939 Structure Simulated Level Waste Site simulated level waste site clone WC1_b11 GQ263
AM889180.1 gg_id:579421 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an AM889
EU491407.1 gg_id:260794 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
Y14313.1 gg_id:4638 Filomicrobium fusiforme str. DSM 5304 Y14313
FJ203575.1 gg_id:338671 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
CU927236.1 gg_id:567895 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
DQ860029.1 gg_id:248682 anchovy intestinal microflora clone F1W DQ860
FM242368.1 gg_id:305774 sequences sediment clone 64 T9d+oil FM242
GQ264526.1 gg_id:589466 Structure Simulated Level Waste Site simulated level waste site clone WW3_80 GQ264
DQ125521.1 gg_id:136194 uranium contaminated soil clone AKAU3482 DQ125
FM253663.1 gg_id:344787 Rock gold mine unusually microbial biofilm clone F01-2 FM253
EU488066.1 gg_id:552142 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EU491718.1 gg_id:262760 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
GU362945.1 gg_id:572272 and archaeal biogeochemical cycling genes within Qiongdongnan basin Sea: pilot stu GU362
EU491544.1 gg_id:260534 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
CU926506.1 gg_id:549098 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FM872754.1 gg_id:363198 occupant source house floor dust clone FB01E01 FM872
EU246798.1 gg_id:256471 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
AB453748.1 gg_id:550276 Sulfur-Oxidizing Deep-sea Sponges deep-sea Poecilosclerida sponge clone GM-BSS-B AB453
AB487448.1 gg_id:574086 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
EF117253.1 gg_id:178313 Hyphomicrobium sp. str. SLG5B-19 EF1172
FJ264674.1 gg_id:306677 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
AB099999.1 gg_id:150659 Microbial dead chimney structures systems Mid-Okinawa Trough and Indian Ocean F AB0999
EF018886.1 gg_id:205881 aspen rhizosphere clone Amb_16S_1374 EF0188
EU753663.1 gg_id:353953 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753
EF540511.1 gg_id:226508 Devosia sp. 4_C16_46 EF5405
AM162442.1 gg_id:156227 and situ identification acidic sphagnum peat bog clone B60 AM162
EU335176.1 gg_id:238442 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
EF644804.1 gg_id:303233 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6448

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	1	1	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	1	1	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	0
0	1	0	0	1	1	1	1	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	1	0	0	0	0	1	0	1
0	1	0	1	1	1	1	1	1	0	1	1	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Hyphomicrobiaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae

g__unclassified
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium

s__unclassified	61239
s__Methylobacterium adhaesivum	58879
s__Methylobacterium adhaesivum	59087
s__Methylobacterium aquaticum	59331
s__Methylobacterium brachiatum	59648
s__Methylobacterium fujisawaense	58973
s__Methylobacterium fujisawaense	59786
s__Methylobacterium fujisawaense	59890
s__Methylobacterium fujisawaense	60014
s__Methylobacterium hispanicum	59139
s__Methylobacterium hispanicum	59700
s__Methylobacterium hispanicum	59979
s__Methylobacterium isbiliense	59438
s__Methylobacterium komagatae	59056
s__Methylobacterium komagatae	59259
s__Methylobacterium komagatae	59420
s__Methylobacterium komagatae	59903
s__Methylobacterium komagatae	59939
s__Methylobacterium nodulans	59723
s__Methylobacterium organophilum	59962
s__Methylobacterium organophilum	60082
s__Methylobacterium podarium	59185
s__Methylobacterium populi	59040
s__Methylobacterium populi	59917
s__Methylobacterium radiotolerans	58923
s__Methylobacterium radiotolerans	59422
s__Methylobacterium radiotolerans	59456
s__Methylobacterium radiotolerans	59607
s__Methylobacterium radiotolerans	59796
s__Methylobacterium radiotolerans	59916
s__Methylobacterium radiotolerans	60111
s__Methylobacterium thiocyanatum	59061
s__Methylobacterium zatmanii	59102
s__Methylobacterium zatmanii	59212
s__Methylobacterium zatmanii	59718
s__Methylobacterium zatmanii	60144
s__unclassified	58886
s__unclassified	58896
s__unclassified	58947
s__unclassified	58954
s__unclassified	58961

EF020326.1 gg_id:203923 aspen rhizosphere clone Elev_16S_1905 EF0203
FJ157965.1 gg_id:583678 Methylobacterium sp. str. 5a.1.5 FJ1579
AB220073.1 gg_id:131580 Methylobacterium sp. str. PB20 AB2200
AJ635303.1 gg_id:106826 Methylobacterium aquaticum str. GR16 AJ6353
AB252205.1 gg_id:238917 Methylobacterium brachiatum str. Hojyo2 AB2522
EF116592.1 gg_id:190418 Methylobacterium fujisawaense str. TNAU14 EF1165
FJ382176.1 gg_id:574655 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
GQ181028.1 gg_id:588577 Methylobacterium fujisawaense str. LNW7 GQ181
EF015477.1 gg_id:189399 Methylobacterium fujisawaense str. MP1 EF0154
EU379265.1 gg_id:266548 Methylobacterium hispanicum str. 2N-2A EU3792
EU867320.1 gg_id:581205 Methylobacterium hispanicum str. CCGE2229 EU8673
EU379303.1 gg_id:259601 Methylobacterium hispanicum str. 6R-J-4b EU3793
AJ888240.1 gg_id:132019 Methylobacterium sp. str. AR25 AJ8882
AY169421.1 gg_id:81189 Methylobacterium fujisawaense AY1694
GQ113305.1 gg_id:404095 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
FJ593719.1 gg_id:528281 midgut tropical caterpillars fed on diets egg clone 298EGG8 FJ5937
AB252202.1 gg_id:250748 Methylobacterium persicinum str. 002-165 AB2522
AB252201.1 gg_id:237732 Methylobacterium komagatae str. 002-079 AB2522
NZ_ABIP01000058.1 gg_id:251181 Methylobacterium nodulans str. ORS 2060 NZ_AB
EF019402.1 gg_id:208196 aspen rhizosphere clone Elev_16S_637 EF0194
AB024616.1 gg_id:4808 Methylobacterium sp. str. MBIC4305 MIF2 AB0246
AY468364.1 gg_id:99777 Methylobacterium podarium str. FM3 AY4683
ABFR01000001.1 gg_id:238083 Methylobacterium populi str. BJ001 ABFR01
NC_010725.1 gg_id:289369 Methylobacterium populi str. BJ001 NC_010
GU294326.1 gg_id:574537 Methylobacterium radiotolerans str. 5310 GU294
AB175637.1 gg_id:152031 Methylobacterium organophilum str. DSM 760 AB1756
GQ077459.1 gg_id:411824 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1209a(GQ077
EU730904.1 gg_id:305729 Methylobacterium fujisawaense str. 151 EU7309
NC_010505.1 gg_id:264722 Methylobacterium radiotolerans str. JCM 2831 NC_010
GQ281074.1 gg_id:545132 Methylobacterium radiotolerans str. NBCS05 GQ281
AB175641.1 gg_id:154811 Methylobacterium radiotolerans str. IAM 12098 AB1756
AB175646.1 gg_id:151826 Methylobacterium thiocyanatum str. DSM 11490 AB1756
GQ281068.1 gg_id:543707 Methylobacterium extorquens str. NBCS12 GQ281
D32230.1 gg_id:4776 Methylobacterium zatmanii str. JCM 2819 D32230
AB175647.1 gg_id:150755 Methylobacterium zatmanii str. DSM 5688 AB1756
GU294335.1 gg_id:543270 Methylobacterium zatmanii str. 6012 GU294
EF682985.1 gg_id:242745 Eastern Mediterranean atmosphere clone F13_9A_FL EF6829
GQ084916.1 gg_id:374179 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
U58018.1 gg_id:4788 Methylobacterium thiocyanatum str. ALL/SCN-P U58018
AY741725.1 gg_id:101778 Methylobacterium sp. str. SKJH-20 AY7417
DQ507203.1 gg_id:159608 Methylobacterium sp. str. K611B DQ507

0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	1	0	0
0	0	0	1	0	1	0	0	0	0	1	0	0
0	0	0	1	0	1	0	0	0	0	1	0	0
0	0	0	1	0	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	1	1	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae

g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium

s__unclassified	58962
s__unclassified	59004
s__unclassified	59097
s__unclassified	59114
s__unclassified	59128
s__unclassified	59172
s__unclassified	59193
s__unclassified	59222
s__unclassified	59243
s__unclassified	59247
s__unclassified	59302
s__unclassified	59404
s__unclassified	59410
s__unclassified	59415
s__unclassified	59417
s__unclassified	59423
s__unclassified	59493
s__unclassified	59534
s__unclassified	59547
s__unclassified	59549
s__unclassified	59551
s__unclassified	59560
s__unclassified	59571
s__unclassified	59591
s__unclassified	59620
s__unclassified	59632
s__unclassified	59663
s__unclassified	59684
s__unclassified	59710
s__unclassified	59717
s__unclassified	59725
s__unclassified	59754
s__unclassified	59757
s__unclassified	59791
s__unclassified	59793
s__unclassified	59904
s__unclassified	59915
s__unclassified	59968
s__unclassified	59976
s__unclassified	59984
s__unclassified	59994

GQ004577.1 gg_id:505086 Topographical and Temporal Human Skin Microbiome skin nare clone nbu60b03c1 GQ004
EF116586.1 gg_id:178333 Methylobacterium thiocyanatum str. TNAU8 EF1165
AY436812.1 gg_id:105470 Methylobacterium sp. str. ST4.9 AY4368
AY616142.1 gg_id:110238 Methylobacterium radiotolerans str. P AY6161
EU528225.1 gg_id:284643 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU5282
AB220086.1 gg_id:134057 Methylobacterium sp. str. PB140 AB2200
AB175635.1 gg_id:154997 Methylobacterium lusitanum str. NCIMB 13779 AB1756
GQ002387.1 gg_id:507275 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176g11 GQ002
AY838487.1 gg_id:109372 fruiting body Pleurotus eryngii clone PE31 AY8384
EU379312.1 gg_id:277255 Methylobacterium fujisawaense str. 7RN-5A EU3793
M95654.1 gg_id:4785 Methylobacterium sp str. PK-1 M9565
EF015479.1 gg_id:196467 Methylobacterium lusitanum str. MP2 EF0154
DQ339624.1 gg_id:146461 Methylobacterium sp. str. Ens25 DQ339
EF116591.1 gg_id:177690 Methylobacterium aminovorans str. TNAU13 EF1165
AM910532.1 gg_id:268349 Methylobacterium aminovorans str. F13 AM910
GQ008625.1 gg_id:501040 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ008
NR_029082.1 gg_id:584448 Methylobacterium populi BJ001 str. BJ001; ATCC BAA-705; NCIMB 13946 NR_029
AF198624.1 gg_id:52319 Methylobacterium chloromethanicum str. CM4 AF1986
EF116585.1 gg_id:191242 Methylobacterium thiocyanatum str. TNAU7 EF1165
NZ_ABEX01000007.1 gg_id:239664 Methylobacterium chloromethanicum str. CM4 NZ_AB
EF015478.1 gg_id:187464 Methylobacterium aquamaris str. MRT EF0154
AY366072.1 gg_id:93863 Methylobacterium extorquens str. UCM B-3368 AY3660
AF267912.1 gg_id:43152 Methylobacterium extorquens str. DSM 13060 F AF2679
EF116584.1 gg_id:190499 Methylobacterium suomiense str. TNAU4 EF1165
EF116583.1 gg_id:180676 Methylobacterium populi str. TNAU3 EF1165
FJ225120.1 gg_id:332818 Methylobacterium sp. str. DDW-1 FJ2251
DQ223682.1 gg_id:161482 Methylobacterium sp. zf-IVRht11 DQ223
EF426729.1 gg_id:204294 Methylobacterium sp. PMB02 EF4267
AB252208.1 gg_id:253017 Methylobacterium tardum str. RB677 AB2522
AY365229.1 gg_id:93518 Methylobacterium extorquens str. UCM B-3362 AY3652
AB252209.1 gg_id:246889 Methylobacterium gregens str. RB678 AB2522
GQ002395.1 gg_id:507267 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu176h08 GQ002
AB369041.1 gg_id:555620 and microbial oils produced Asia petroleum crude oil (Qatar Land Light) clone PT-QTL AB3690
EU250227.1 gg_id:249628 acid mine drainage clone GXDC-13 EU2502
AB220102.1 gg_id:138655 Methylobacterium sp. str. PB236 AB2201
FJ192175.1 gg_id:329760 Genetic inventory 'KSC-PHSF' spacecraft assembly clean room during Phoenix missior FJ1921
EF116582.1 gg_id:182127 Methylobacterium populi str. TNAU1 EF1165
AY741717.1 gg_id:105899 Methylobacterium sp. str. SKJH-15 AY7417
D32228.1 gg_id:4786 Methylobacterium rhodesianum str. JCM 2810 D32228
AJ851087.1 gg_id:112210 Methylobacterium variabile str. GR3 AJ8510
GQ059305.1 gg_id:374704 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ059

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylobacteriaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae

g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__Methylobacterium
g__unclassified
g__unclassified
g__unclassified
g__Methylocystis
g__Methylocystis
g__Methylocystis
g__Methylocystis
g__Methylocystis
g__Methylocystis
g__Methylopila
g__Methylopila
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Methylosinus
g__Pleomorphomonas
g__Pleomorphomonas
g__Pleomorphomonas
g__Pleomorphomonas
g__Pleomorphomonas
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	60039
s__unclassified	60079
s__unclassified	60093
s__unclassified	60131
s__unclassified	60159
s__unclassified	60168
s__unclassified	60186
s__unclassified	58964
s__unclassified	59238
s__unclassified	59323
s__Methylocystis parvus	59250
s__Methylocystis parvus	59624
s__Methylocystis parvus	59678
s__unclassified	59164
s__unclassified	59746
s__unclassified	60123
s__unclassified	59347
s__unclassified	59469
s__Methylosinus sporium	58970
s__Methylosinus sporium	59623
s__Methylosinus sporium	59826
s__Methylosinus sporium	60142
s__Methylosinus trichosporium	59305
s__Methylosinus trichosporium	59812
s__unclassified	59704
s__unclassified	59724
s__unclassified	59879
s__unclassified	60070
s__unclassified	60077
s__Pleomorphomonas oryzae	58963
s__Pleomorphomonas oryzae	59662
s__Pleomorphomonas oryzae	59833
s__unclassified	59111
s__unclassified	59751
s__unclassified	58890
s__unclassified	59106
s__unclassified	59285
s__unclassified	59465
s__unclassified	59518
s__unclassified	59643
s__unclassified	59748

AY569289.1 gg_id:102246 pink microbial mat clone YJQ-13 AY569
DQ471331.1 gg_id:157883 Methylobacterium jeotgali str. S2R03-9 DQ471
AF409010.1 gg_id:102764 Methylobacterium sp. str. Ellin168 AF409
Z23159.1 gg_id:4797 Methylobacterium sp. str. PC30.44 (pale pink colony type) Z23159
AB252204.1 gg_id:312016 Methylobacterium sp. Hojyo1 AB252
D32229.1 gg_id:4784 Methylobacterium rhodinum str. JCM 2811 D3222
DQ129299.1 gg_id:138274 microarray level air two cities Texas urban aerosol clone AKIW886 DQ129
DQ532273.1 gg_id:164604 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
FJ193768.1 gg_id:341095 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1937
EU289454.1 gg_id:256447 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU289
AF107461.1 gg_id:32547 Methylosinus pucelana str. MTS AF107
AJ458508.1 gg_id:64197 Methylocystis parvus str. 57 AJ4585
AF150805.1 gg_id:4738 Methylocystis parvus AF150
DQ852349.1 gg_id:176777 Methylocystis sp. str. m1511 DQ852
AJ458510.1 gg_id:72367 Methylocystis sp. str. 50/54 AJ4585
AJ458467.1 gg_id:64230 Methylocystis sp. str. 495/4 AJ4584
FJ502233.3 gg_id:558957 Methylopila sp. str. JZL-4 FJ5022
DQ404188.1 gg_id:212879 Schlegelia plantiphila str. S1 DQ404
AB007842.1 gg_id:58407 methylotroph str. Hohenstaufen AB007
M95665.1 gg_id:4737 Methylosinus sporium M9566
AJ458495.1 gg_id:111428 Methylosinus sporium str. KS16a AJ4584
M95664.1 gg_id:4735 Methylosinus sp str. LAC M9566
AJ458481.1 gg_id:64219 Methylosinus trichosporium str. 33/1 AJ4584
AF150804.1 gg_id:4739 Methylosinus trichosporium AF150
L20845.1 gg_id:4736 methanotrophic str. IMV B-3060 L20845
AJ458483.1 gg_id:64217 Methylocystis sp. str. Pi5/4 AJ4584
AY921958.1 gg_id:113362 farm soil clone AKYG1554 AY921
AJ431385.2 gg_id:64234 Methylosinus trichosporium str. KS21 AJ4313
AY922142.1 gg_id:113005 farm soil clone AKYH643 AY922
EF515258.1 gg_id:224728 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22a11 EF5152
AY297803.1 gg_id:89669 waterlogged archaeological wood clone pACH83 AY297
EF515279.1 gg_id:220495 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22c11 EF5152
CU924338.1 gg_id:560880 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AB127972.1 gg_id:101532 Kaistina koreensis str. Y9 AB127
GQ060654.1 gg_id:467965 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03g03 GQ060
GQ064493.1 gg_id:418162 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ064
AJ458504.1 gg_id:64202 Methylocystis sp. str. F10V2a AJ4585
AB095950.1 gg_id:87497 Ancalomicrobium adetum AB095
AJ458500.1 gg_id:64205 Methylocystis sp. str. 10 AJ4585
GQ055294.1 gg_id:371984 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1113d GQ055
CU925731.1 gg_id:548842 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925

0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	1	1	0	1
1	1	0	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	0	1	0	0	0	1	0	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Methylocystaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Nordellaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Nordella
g__Ahrensia
g__Ahrensia
g__Ahrensia
g__Ahrensia
g__Aminobacter
g__Aminobacter
g__Aquamicrobium
g__Chelativorans
g__Chelativorans
g__Chelativorans
g__Chelativorans
g__Chelativorans
g__Defluvibacter
g__Defluvibacter

s__unclassified	59802
s__unclassified	59882
s__unclassified	59948
s__unclassified	59974
s__unclassified	59993
s__unclassified	60029
s__unclassified	60178
s__unclassified	61070
s__unclassified	61231
s__unclassified	61396
s__unclassified	61501
s__unclassified	61557
s__unclassified	61765
s__unclassified	61891
s__unclassified	62045
s__unclassified	62171
s__unclassified	62281
s__unclassified	62307
s__unclassified	62365
s__unclassified	62368
s__unclassified	62486
s__unclassified	62519
s__unclassified	62544
s__unclassified	62648
s__unclassified	62654
s__unclassified	62852
s__unclassified	62889
s__unclassified	61796
s__unclassified	62121
s__unclassified	62631
s__unclassified	62845
s__unclassified	61800
s__unclassified	62074
s__unclassified	61478
s__Chelativorans multitrophicus	61995
s__Chelativorans multitrophicus	62395
s__unclassified	61662
s__unclassified	62163
s__unclassified	62766
s__unclassified	61776
s__unclassified	62815

DQ202244.1 gg_id:140112 Enrichment s Type II Methane-Oxidizing Inhabiting Northern Peatlands peatland clo DQ202
GQ221762.1 gg_id:582735 Prosthecomicrobium hirschii str. 6 GQ221
AM162434.1 gg_id:156044 and situ identification acidic sphagnum peat bog clone B112 AM162
AY138237.1 gg_id:107461 human stomach biopsy clone Sto3-1 AY138
AJ458473.1 gg_id:56422 Methylocystis echinoides str. IMET 10491 AJ4584
GQ402774.1 gg_id:537864 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AM283543.1 gg_id:165785 Methylocystis heyerii str. H2 AM283
FJ478572.1 gg_id:541918 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU979087.1 gg_id:304412 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
GU208455.1 gg_id:591539 Study on Sediment Dongping Lake sediment clone Fr1-9 GU208
GQ500824.1 gg_id:540718 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
GQ500812.1 gg_id:556729 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
AM934956.1 gg_id:546522 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
FJ755762.1 gg_id:552837 vertical archaeal water and Lake Taihu sediment clone LT-SB-B39 FJ7557
CU923583.1 gg_id:566212 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
FJ542854.1 gg_id:530919 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
CU921271.1 gg_id:550854 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
CU926316.1 gg_id:532947 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
EF019602.1 gg_id:214638 aspen rhizosphere clone Elev_16S_1127 EF0196
AY921960.1 gg_id:113860 farm soil clone AKYG1560 AY921
FM874050.1 gg_id:362109 occupant source house mattress dust clone MB05G07 FM874
EF032656.1 gg_id:182489 structure riverine biofilms river biofilm clone SepB-8 EF0326
EU589298.1 gg_id:272318 China Ningxia rice paddy field soil clone 2_D3 EU589
GQ093788.1 gg_id:382544 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EF590055.2 gg_id:230239 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5900
AF370880.1 gg_id:66822 Nordella oligomobilis str. N21 AF3708
DQ984605.1 gg_id:236172 LY oil-contaminated soil clone LYC075 DQ984
AJ582085.1 gg_id:102514 Ahrensia sp. DFL-33 AJ5820
AJ582087.1 gg_id:95153 Ahrensia sp. DFL-44 AJ5820
AJ582086.1 gg_id:94505 Ahrensia sp. DFL-42 AJ5820
AJ582084.1 gg_id:95110 Ahrensia sp. DFL-13 AJ5820
L20802.1 gg_id:5138 Aminobacter ciceronei str. ER2 L20802
DQ196478.1 gg_id:139758 Aminobacter sp. str. MI-p2a DQ196
GQ254285.1 gg_id:544184 Aquamicrobium sp. str. H15 GQ254
FJ167676.1 gg_id:307902 Chelatovorus multitrophus str. LPM-6 FJ1676
EF457242.1 gg_id:237931 Chelatovorus oligotrophus str. LPM4 EF4572
GU111569.1 gg_id:537767 Nitratireductor sp. str. SL014B-25A2 GU111
EF157205.1 gg_id:249985 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
EU564843.1 gg_id:267825 Nitratireductor sp. str. CC-MHSW-5 EU5648
EU281628.1 gg_id:243131 Bacillus sp. B2(2007b) str. B2 EU281
EU024398.2 gg_id:238204 Isolation cyclohexylalkyltetralin degradation sediments marine sediment clone WBI3 EU024

0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	0	0	1
1	1	1	1	1	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	0	1	1	0	1	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	1	0	0	0	1	0	0
1	1	0	0	1	1	1	0	0	0	1	0	0
0	0	1	1	1	1	0	0	0	0	1	0	1
1	0	0	1	0	1	1	0	0	0	0	0	1
0	1	1	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	1	0	1	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	1	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae

g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium

s__Mesorhizobium albiziae	61517
s__Mesorhizobium alhagi	61423
s__Mesorhizobium ciceri	61394
s__Mesorhizobium ciceri	61556
s__Mesorhizobium ciceri	61792
s__Mesorhizobium ciceri	62410
s__Mesorhizobium huakuii	61513
s__Mesorhizobium huakuii	61652
s__Mesorhizobium huakuii	61813
s__Mesorhizobium huakuii	61986
s__Mesorhizobium huakuii	62104
s__Mesorhizobium huakuii	62283
s__Mesorhizobium huakuii	62528
s__Mesorhizobium huakuii	62601
s__Mesorhizobium temperatum	61471
s__Mesorhizobium temperatum	61643
s__Mesorhizobium temperatum	61936
s__Mesorhizobium temperatum	62059
s__Mesorhizobium temperatum	62792
s__unclassified	61389
s__unclassified	61496
s__unclassified	61550
s__unclassified	61589
s__unclassified	61600
s__unclassified	61618
s__unclassified	61739
s__unclassified	61753
s__unclassified	61867
s__unclassified	61892
s__unclassified	61908
s__unclassified	61911
s__unclassified	61931
s__unclassified	61938
s__unclassified	61979
s__unclassified	62000
s__unclassified	62031
s__unclassified	62032
s__unclassified	62046
s__unclassified	62054
s__unclassified	62090
s__unclassified	62114

DQ311089.1 gg_id:149931 Mesorhizobium sp. str. CCBAU 61156 DQ311
GU201842.1 gg_id:516545 Rhizobium leguminosarum str. Qtx-1 GU201
AJ487829.1 gg_id:66200 Mesorhizobium ciceri str. Rch9816 AJ4878
FM209490.1 gg_id:314928 Mesorhizobium ciceri str. TS56 FM209
U07934.1 gg_id:5127 Mesorhizobium ciceri str. UPM-Ca7 U07934
X67230.1 gg_id:5122 Mesorhizobium loti str. LMG 4284 X67230
EU256435.1 gg_id:251597 Mesorhizobium plurifarium str. CCBAU 85060 EU2564
EF061111.1 gg_id:186691 Mesorhizobium huakuii str. CCBAU 25053 EF0611
EF061107.1 gg_id:198842 Mesorhizobium amorphae str. CCBAU 45122 EF0611
GU083820.1 gg_id:593690 Mesorhizobium amorphae str. DBT14 GU083
DQ310706.1 gg_id:186218 Mesorhizobium loti str. U261 DQ310
EF061108.1 gg_id:184949 Mesorhizobium amorphae str. CCBAU 25161 EF0611
EF061106.1 gg_id:194940 Mesorhizobium amorphae str. CCBAU 45139 EF0611
EU399717.1 gg_id:273591 Mesorhizobium huakuii str. CCBAU 03094 EU3997
EU849580.1 gg_id:554748 Mesorhizobium sp. str. CCNWYC132 EU8495
EU410952.1 gg_id:276865 Mesorhizobium temperatum str. CCNWSX0012-2 EU4109
AY195843.1 gg_id:82201 Mesorhizobium mediterraneum str. PECA03 AY1958
EU074171.1 gg_id:253654 Mesorhizobium mediterraneum str. CCBAU 01409 EU0741
AF508208.1 gg_id:102422 Mesorhizobium temperadae str. CCBAU 11018; SDW 018 AF5082
AY725261.1 gg_id:136815 decayed velvetleaf seed clone S1-4-CL6 AY7252
FJ234902.1 gg_id:352327 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl FJ2349
AF410897.1 gg_id:20161 Mesorhizobium sp. str. Lo7-12 AF4108
FJ550306.1 gg_id:512978 Mesorhizobium tianshanense str. BIHB 4151 FJ5503
FJ025121.1 gg_id:324436 Mesorhizobium tianshanense str. SEMIA 3012 FJ0251
EU707156.1 gg_id:290008 Mesorhizobium tianshanense str. CCBAU 15528 EU7071
Z94807.1 gg_id:5084 Mesorhizobium genosp. T str. BDV5908 Z94807
DQ407284.1 gg_id:156049 Mesorhizobium tianshanense str. RCAN08 DQ407
GQ500629.1 gg_id:558777 Mesorhizobium sp. str. S948 GQ500
FJ544261.1 gg_id:580951 Mesorhizobium sp. str. CA17 FJ5442
DQ100068.1 gg_id:135924 Mesorhizobium plurifarium str. CCBAU 51276 DQ100
AY922072.1 gg_id:113594 farm soil clone AKYG882 AY9220
FJ025123.1 gg_id:306937 Mesorhizobium amorphae str. SEMIA 849 FJ0251
AF325770.1 gg_id:47902 Rhizobium sp. str. TM-5 AF3257
AY688622.1 gg_id:136093 Mesorhizobium plurifarium str. Sp42 AY6886
DQ859034.1 gg_id:204637 Mesorhizobium plurifarium str. ORS 3324 DQ859
FJ550307.1 gg_id:548722 Mesorhizobium tianshanense str. BIHB 4154 FJ5503
D14514.1 gg_id:5142 Mesorhizobium loti str. ATCC33669 D14514
EU256441.1 gg_id:248289 Mesorhizobium loti str. CCBAU 85068 EU2564
D14511.1 gg_id:5149 Rhizobium sp str. TAL 1148 D14511
GQ088394.1 gg_id:443339 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
AF508207.1 gg_id:102269 Mesorhizobium nortea str. CCBAU 11014; SDW 014 AF5082

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	1	1
0	1	1	1	1	1	1	1	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	1	0	0	1	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	1	1
0	0	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae

g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Mesorhizobium
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Nitratireductor
g__Parvibaculum
g__Parvibaculum
g__Parvibaculum
g__Parvibaculum

s__unclassified	62135
s__unclassified	62140
s__unclassified	62147
s__unclassified	62187
s__unclassified	62304
s__unclassified	62336
s__unclassified	62337
s__unclassified	62433
s__unclassified	62452
s__unclassified	62566
s__unclassified	62572
s__unclassified	62592
s__unclassified	62609
s__unclassified	62651
s__unclassified	62677
s__unclassified	62696
s__unclassified	62754
s__unclassified	62759
s__unclassified	62827
s__unclassified	62862
s__unclassified	62881
s__unclassified	62898
s__Nitratireductor aquibiodomus	61593
s__Nitratireductor aquibiodomus	61658
s__Nitratireductor aquibiodomus	61715
s__Nitratireductor aquibiodomus	61865
s__Nitratireductor aquibiodomus	61922
s__Nitratireductor aquibiodomus	62626
s__Nitratireductor aquibiodomus	62640
s__Nitratireductor aquibiodomus	62705
s__Nitratireductor aquibiodomus	62874
s__unclassified	61512
s__unclassified	61705
s__unclassified	62206
s__unclassified	62242
s__unclassified	62699
s__unclassified	62945
s__unclassified	60284
s__unclassified	60324
s__unclassified	60473
s__unclassified	60534

GQ221766.1 gg_id:575053 Prosthecomicrobium sp. str. ATCC 27825 GQ221
D13431.1 gg_id:5091 Mesorhizobium huakuii str. IFO15243 D13431
U50166.1 gg_id:5085 Mesorhizobium loti str. ICMP3153 USDA 3455 261 U50166
CU919824.1 gg_id:566028 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AB166876.1 gg_id:99830 Mesorhizobium sp. str. M01 AB1668
AF041447.1 gg_id:5146 Mesorhizobium tianshanense str. -1BS; USDA 3592 AF0414
AY195844.1 gg_id:81838 Mesorhizobium mediterraneum str. PECA20 AY1958
AF325769.1 gg_id:23504 Rhizobium sp. str. E-13 AF3257
AY490116.1 gg_id:109828 Mesorhizobium sp. str. lema-2 AY4901
FJ544258.1 gg_id:563420 Mesorhizobium sp. str. CA9 FJ5442
EU410950.1 gg_id:271237 Mesorhizobium amorphae str. CCNWGS0015-1 EU410
EU867314.1 gg_id:556935 Phyllobacterium sp. str. CCGE2278 EU8673
EU074176.1 gg_id:236357 Mesorhizobium ciceri str. CCBAU 01466 EU0741
AJ785293.1 gg_id:159531 Mesorhizobium genosp. AA Cs6145 AJ7852
Z94819.1 gg_id:5097 Mesorhizobium genosp. U str. BDV5514 Z94819
AY509218.1 gg_id:99286 Mesorhizobium loti str. S139 AY5092
EU256445.1 gg_id:235712 Mesorhizobium loti str. CCBAU 85074 EU2564
EU256442.1 gg_id:252097 Mesorhizobium mediterraneum str. CCBAU 85070 EU2564
EU074175.1 gg_id:240934 Mesorhizobium loti str. CCBAU 01465 EU0741
CU926186.1 gg_id:540566 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FJ542962.1 gg_id:511099 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
AJ295079.1 gg_id:74017 Mesorhizobium plurifarium str. ORS1096 (LMG 15298) AJ2950
EU874893.1 gg_id:308046 Mesorhizobium sp. W12 EU8748
CU915140.1 gg_id:466324 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
CU915133.1 gg_id:381876 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
EU440986.1 gg_id:317496 Nitratireductor aquibiodomus str. PR57-9 EU4409
EU874875.1 gg_id:344328 Mesorhizobium sp. W66 EU8748
CU915137.1 gg_id:413807 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
NR_025262.1 gg_id:570268 Nitratireductor aquibiodomus str. NL21; DSM 15645 NR_025
CU915181.1 gg_id:401720 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
AM498744.1 gg_id:254465 Nitratireductor kimnyeongense str. KY 101 = JBRI2113 AM498
CU915166.1 gg_id:423734 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
CU915156.1 gg_id:377929 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
CU915082.1 gg_id:409815 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU915
EU143347.2 gg_id:253753 Nitratireductor sp. str. J3 EU1433
DQ659453.1 gg_id:160997 Chelatobacter sp. Pht-3B DQ659
GU447302.1 gg_id:518497 Nitratireductor sp. str. C115 GU447
FJ182044.1 gg_id:313217 Parvibaculum sp. str. P31 FJ1820
DQ015855.1 gg_id:139871 Antarctic lake water clone WLB16-101 DQ015
FJ536887.1 gg_id:563896 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5368
AB186821.1 gg_id:101714 polychlorinated dioxin dechlorinating microcosm clone TSAC02 AB1868

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae

g__Parvibaculum
g__Parvibaculum
g__Parvibaculum
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Phyllobacterium
g__Pseudaminobacter
g__Pseudaminobacter
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	60563
s__unclassified	60842
s__unclassified	60882
s__Phyllobacterium ifriqiyense	62829
s__Phyllobacterium myrsinacearum	62454
s__Phyllobacterium myrsinacearum	62779
s__unclassified	61629
s__unclassified	61834
s__unclassified	62118
s__unclassified	62158
s__unclassified	62207
s__unclassified	62335
s__unclassified	62345
s__unclassified	62376
s__unclassified	62470
s__unclassified	62548
s__unclassified	62591
s__unclassified	62757
s__unclassified	62888
s__Pseudaminobacter salicylatoxidans	61433
s__unclassified	61852
s__unclassified	59032
s__unclassified	59488
s__unclassified	59554
s__unclassified	59595
s__unclassified	59785
s__unclassified	59891
s__unclassified	60215
s__unclassified	60233
s__unclassified	60252
s__unclassified	60277
s__unclassified	60299
s__unclassified	60305
s__unclassified	60316
s__unclassified	60319
s__unclassified	60333
s__unclassified	60345
s__unclassified	60347
s__unclassified	60371
s__unclassified	60408
s__unclassified	60428

FM242452.1 gg_id:311978 sequences sediment clone 9 T12d+oil FM242
AY387398.1 gg_id:101358 Parvibaculum lavamentivorans str. DS-1; DSM13023; NCIMB13966 AY3873
FN430653.1 gg_id:537152 Parvibaculum sp. str. MBNA2 FN4306
FJ154092.1 gg_id:333292 Phyllobacterium ifriqiyense str. CCNWGS0184 FJ1540
EU169165.1 gg_id:236290 Phyllobacterium myrsinacearum str. B65 EU1691
EU420076.1 gg_id:541971 Phyllobacterium myrsinacearum str. Sp-0 EU4200
AY636000.1 gg_id:104486 Phyllobacterium callistus str. CSC19 AY6360
DQ917820.1 gg_id:219107 Microbial profiles bleached and wild-type Muricea elongata Phyllobacterium clone B DQ917
FJ405362.1 gg_id:367932 Phyllobacterium myrsinacearum str. SPc FJ4053
EU169173.1 gg_id:253647 Phyllobacterium myrsinacearum str. B18 EU1691
AY785319.1 gg_id:144696 Phyllobacterium brassicacearum str. STM 196 AY7853
AJ011330.1 gg_id:5118 Phyllobacterium myrsinacearum HM35 AJ0113
EU928863.1 gg_id:345333 Phyllobacterium sp. str. T1018 EU9288
X98418.1 gg_id:5120 Nanobacterium sanguineum Seralab FBS batch 901045 X98418
AY785329.1 gg_id:142779 Phyllobacterium myrsinacearum str. STM 958 AY7853
EF364390.1 gg_id:225459 Phyllobacterium sp. str. Hue-5 EF3643
AY635999.1 gg_id:107799 Phyllobacterium callistus str. CSC32 AY6359
AY512821.1 gg_id:105844 Phyllobacterium myrsinacearum AY5128
GU257961.1 gg_id:593356 Bartonella elizabethae str. HXG-C15 GU257
AY331575.1 gg_id:91742 Pseudaminobacter sp. str. mp-1 AY3315
D32248.1 gg_id:5112 Thiobacillus sp. str. THI 051 D32248
FJ203076.1 gg_id:337809 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203650.1 gg_id:356370 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
GU118765.1 gg_id:542574 Threatened Corals Provide Microbial Habitats clone Mfra_M12 GU118
FJ203080.1 gg_id:338592 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203059.1 gg_id:303869 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203057.1 gg_id:350236 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
DQ396147.1 gg_id:155758 deep-sea octacoral clone ctg_NISA060 DQ396
AB099936.1 gg_id:79338 inactive deep-sea hydrothermal vent chimneys clone IheB2-3 AB0999
EU491659.1 gg_id:270912 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
AF358017.1 gg_id:26724 peat soil microcosm clone LO13.3 AF3580
EU491413.1 gg_id:269457 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU4914
EF572341.1 gg_id:228614 Coco's Island site 23 marine clone S23_440 EF5723
DQ351777.1 gg_id:147394 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
GQ250606.1 gg_id:545163 bulk sea water column Gulf Mexico clone GOM_WB10-41 GQ250
EU246807.1 gg_id:248919 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EU488046.1 gg_id:568753 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4880
FJ478659.1 gg_id:548335 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FM253615.1 gg_id:337543 Rock gold mine unusually microbial biofilm clone F09-1 FM253
EU735674.1 gg_id:343405 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU7356
AY913401.1 gg_id:113418 forest soil clone DUNssu195 (-7A) (OTU#173) AY9134

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	1	0	0	0	0
1	1	1	1	1	1	0	1	1	1	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	0	1	1	1	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae

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

s__unclassified	60434
s__unclassified	60440
s__unclassified	60501
s__unclassified	60505
s__unclassified	60530
s__unclassified	60535
s__unclassified	60545
s__unclassified	60549
s__unclassified	60624
s__unclassified	60642
s__unclassified	60654
s__unclassified	60655
s__unclassified	60656
s__unclassified	60660
s__unclassified	60712
s__unclassified	60716
s__unclassified	60727
s__unclassified	60757
s__unclassified	60778
s__unclassified	60781
s__unclassified	60824
s__unclassified	60830
s__unclassified	60853
s__unclassified	60861
s__unclassified	60885
s__unclassified	60890
s__unclassified	60930
s__unclassified	60932
s__unclassified	60958
s__unclassified	60965
s__unclassified	60978
s__unclassified	60993
s__unclassified	61018
s__unclassified	61020
s__unclassified	61033
s__unclassified	61035
s__unclassified	61068
s__unclassified	61105
s__unclassified	61123
s__unclassified	61140
s__unclassified	61157

AY923020.1 gg_id:114265 Sargasso Sea waters clone D92_92 AY923(
AY922026.1 gg_id:112779 farm soil clone AKYG492 AY922(
AY913262.1 gg_id:113787 forest soil clone DUNssu042 (-2A) (OTU#176) AY913
GQ263181.1 gg_id:510769 Structure Simulated Level Waste Site simulated level waste site clone F3_139X GQ263
EU881134.1 gg_id:308120 Karst region primary forest soil clone KPF200711-010 EU881
EU236381.1 gg_id:288220 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91H4 EU236
AY913338.1 gg_id:114183 forest soil clone DUNssu131 (+7A) (OTU#177) AY913
EF019626.1 gg_id:215375 aspen rhizosphere clone Elev_16S_770 EF0196
EU488067.1 gg_id:548592 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488(
FJ152813.1 gg_id:308393 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU386115.1 gg_id:270010 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
GQ262947.1 gg_id:549426 Structure Simulated Level Waste Site simulated level waste site clone F1_85X GQ262
AJ633940.1 gg_id:114727 host's accessory nidamental gland clone 52ANG2 AJ6339
EU386026.1 gg_id:272493 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386(
AY913351.1 gg_id:112770 forest soil clone DUNssu144 (+7A) (OTU#173) AY913
FJ479146.1 gg_id:588630 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
EU491428.1 gg_id:260972 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
DQ070827.1 gg_id:147965 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
GU369888.1 gg_id:529803 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AB491708.1 gg_id:559688 Microbial control lamina formation Crystal geyser central Utah travertine clone CG1(AB491
DQ814512.1 gg_id:161858 zebrafish digestive tract clone aaa30b10 DQ814
GQ262857.1 gg_id:567747 Structure Simulated Level Waste Site simulated level waste site clone F1_33X GQ262
EU491525.1 gg_id:271177 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4(EU491
AY162106.1 gg_id:150582 Cultivating Sargasso Sea clone GMD21A06 AY162
AY913263.1 gg_id:113892 forest soil clone DUNssu043 (-2A) (OTU#173) AY913
GQ262821.1 gg_id:534554 Structure Simulated Level Waste Site simulated level waste site clone F1_12X GQ262
EU735621.1 gg_id:339556 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
EU799979.1 gg_id:351580 It's all ranking aquatic Newport Harbour RI clone 1C227658 EU799
EU491596.1 gg_id:264919 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ745115.1 gg_id:575156 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
EU385898.1 gg_id:259577 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU181478.1 gg_id:245815 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
AF406520.1 gg_id:106379 complex marine community d at depth 200 m North Aegean Sea (Station 3) clone AE AF406
GQ262936.1 gg_id:575894 Structure Simulated Level Waste Site simulated level waste site clone F1_79X GQ262
AM936572.1 gg_id:547134 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
GU369924.1 gg_id:518338 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
AM936135.1 gg_id:553156 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
AM712634.1 gg_id:257971 Anderseniella baltica str. BA141 AM712
GU220743.1 gg_id:571033 Microbial mineralization and involved microbial Basin field temperature hydrotherm GU220
FJ152698.1 gg_id:346361 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
DQ334628.1 gg_id:176463 Impact metals on sediments heavy metal polluted marine sediment clone HB2-33-2 DQ334

0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	0	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	0	1	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	0	1	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	1	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	1	1	1	1
0	1	0	0	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	0	0	1	1	0	0	0	1
1	1	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae

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

s__unclassified	61166
s__unclassified	61174
s__unclassified	61177
s__unclassified	61187
s__unclassified	61212
s__unclassified	61241
s__unclassified	61258
s__unclassified	61266
s__unclassified	61274
s__unclassified	61300
s__unclassified	61330
s__unclassified	61331
s__unclassified	61370
s__unclassified	61415
s__unclassified	61489
s__unclassified	61504
s__unclassified	61525
s__unclassified	61531
s__unclassified	61584
s__unclassified	61592
s__unclassified	61598
s__unclassified	61606
s__unclassified	61625
s__unclassified	61700
s__unclassified	61709
s__unclassified	61710
s__unclassified	61729
s__unclassified	61779
s__unclassified	61806
s__unclassified	61833
s__unclassified	61863
s__unclassified	61872
s__unclassified	61882
s__unclassified	61923
s__unclassified	61966
s__unclassified	61975
s__unclassified	62025
s__unclassified	62065
s__unclassified	62067
s__unclassified	62087
s__unclassified	62102

EU236304.1 gg_id:289355 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a1A9 EU236
EF208711.1 gg_id:201560 Vertical and horizontal structure microbial sandy carbonate sediment clone Cl75cm.2 EF2087
EU881167.1 gg_id:342537 Karst region primary forest soil clone KPF200711-032 EU881
GQ347790.1 gg_id:592876 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AF382114.1 gg_id:79210 bacterioplankton clone ZA3318c AF382
FJ203577.1 gg_id:322591 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
GU118597.1 gg_id:581316 Threatened Corals Provide Microbial Habitats clone Mfav_F16 GU118
FJ152626.1 gg_id:304121 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FJ024326.1 gg_id:358115 Prokaryotic and their role biogeochemical cycling marine basalts basalt Juan de Fuca I FJ0243
DQ395471.1 gg_id:156247 deep-sea octacoral clone ctg_CGOAA69 DQ395
FJ203565.1 gg_id:315490 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EU491292.1 gg_id:276298 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
GQ848473.1 gg_id:538386 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ152991.1 gg_id:340224 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
GQ009791.1 gg_id:499876 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
DQ104986.1 gg_id:137534 Mesorhizobium sp. str. JS 12 DQ104
EU332813.1 gg_id:360547 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU3328
FJ167442.1 gg_id:342632 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
AB374372.1 gg_id:259747 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
FJ203570.1 gg_id:316649 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
AB246806.1 gg_id:146335 Mesorhizobium sp. str. Q-2 AB2468
DQ001642.1 gg_id:158376 Microbial seeps asphalt seep clone E101-27 DQ001
EF471634.1 gg_id:269321 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay EF4716
AF234721.1 gg_id:32754 sludge clone A7 AF2347
AJ864462.1 gg_id:109471 Mesorhizobium thiogangeticum str. SJT AJ8644
FJ674841.1 gg_id:529939 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6748
CU922361.1 gg_id:547097 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
AY598817.1 gg_id:105079 Hoeflea marina str. LMG 128 AY5988
NR_025411.1 gg_id:547162 Mesorhizobium chacoense str. PR5; DSM 17287 NR_02
GU118307.1 gg_id:538811 Threatened Corals Provide Microbial Habitats clone Dstr_L15 GU118
GU118284.1 gg_id:589090 Threatened Corals Provide Microbial Habitats clone Dstr_M18 GU118
AF280865.1 gg_id:72907 bioreactor clone mle1-44 AF2808
AB167198.1 gg_id:107911 Rhizobium sp. str. c19 AB167
AF150703.1 gg_id:24111 Elbe River snow isolate Iso26 Iso26_1389 AF1507
FJ670878.1 gg_id:524118 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6708
EF019808.1 gg_id:206948 aspen rhizosphere clone Elev_16S_999 EF0198
FJ152680.1 gg_id:332848 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FN436146.1 gg_id:554537 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
AY942778.1 gg_id:145164 but species richness marine sponge Cymbastela concentrica clone Cc173 AY9427
AM934887.1 gg_id:573454 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY690674.1 gg_id:99235 Mesorhizobium sp. str. GC08 AY6906

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	1	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	0	1	1	1	0	0	1
0	0	0	1	0	1	1	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Phyllobacteriaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium

s__unclassified	62133
s__unclassified	62165
s__unclassified	62188
s__unclassified	62194
s__unclassified	62210
s__unclassified	62235
s__unclassified	62263
s__unclassified	62284
s__unclassified	62285
s__unclassified	62372
s__unclassified	62415
s__unclassified	62431
s__unclassified	62440
s__unclassified	62506
s__unclassified	62532
s__unclassified	62538
s__unclassified	62540
s__unclassified	62545
s__unclassified	62553
s__unclassified	62561
s__unclassified	62582
s__unclassified	62604
s__unclassified	62608
s__unclassified	62644
s__unclassified	62706
s__unclassified	62745
s__unclassified	62763
s__unclassified	62814
s__unclassified	62819
s__Agrobacterium larrymoorei	61514
s__Agrobacterium larrymoorei	62567
s__Agrobacterium rubi	61649
s__Agrobacterium rubi	61693
s__Agrobacterium rubi	62512
s__Agrobacterium vitis	61808
s__Rhizobium sp. IRBG 74	61414
s__Rhizobium sp. IRBG 74	61648
s__Rhizobium sp. IRBG 74	61958
s__Rhizobium sp. IRBG 74	62030
s__Rhizobium sp. IRBG 74	62056
s__Rhizobium sp. IRBG 74	62164

FJ671319.1 gg_id:524448 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
AY332151.1 gg_id:100524 Mesorhizobium sp. str. GWS-SE-H103 AY3321
FJ671077.1 gg_id:519193 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
AB265157.1 gg_id:164464 Mesorhizobium sp. str. E11 AB2651
AJ318199.1 gg_id:73511 Waste-gas biofilter clone BIwii1 AJ3181
FJ542875.1 gg_id:521776 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
FJ203541.1 gg_id:316301 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata I FJ2035
GQ263841.1 gg_id:548137 Structure Simulated Level Waste Site simulated level waste site clone WC1_b89 GQ263
EU287328.1 gg_id:243907 Pacific arctic surface sediment clone S26-28 EU2873
FJ671628.1 gg_id:529153 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ675300.1 gg_id:527154 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6753
DQ860072.1 gg_id:170119 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone L9 DQ860
AY307924.1 gg_id:90640 Aminobacter sp. str. COX AY3079
EU236387.1 gg_id:287433 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92A11 EU2363
EU223941.1 gg_id:246412 -RFLP microbes Qinghai-Tin rail soil clone 56 EU2239
FJ671907.1 gg_id:514109 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
DQ814869.1 gg_id:162010 zebrafish digestive tract clone aab54f12 DQ814
GU454867.1 gg_id:523337 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
DQ364238.2 gg_id:157010 Rhizobium sp. str. WH2K DQ364
FJ542989.1 gg_id:528720 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
Y15403.1 gg_id:5113 Aquamicrobium defluvii str. DSM 11603 Y15403
DQ860063.1 gg_id:167582 Symbiotic aerobic anoxygenic phototrophic colonial tunicate clone C7 DQ860
FJ674998.1 gg_id:518661 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
FJ907162.1 gg_id:552671 Aminobacter sp. str. Sokolova FJ9071
FJ542969.1 gg_id:531912 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
AB257631.1 gg_id:267976 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
AY515416.1 gg_id:99884 bulk water German Wadden Sea May 1999 clone GWS-BW-H52M AY5154
AB257653.1 gg_id:273074 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
EU404018.1 gg_id:306709 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU4040
EU769196.1 gg_id:329286 velvetleaf seed clone S4-6-CL4 EU7691
Z30542.1 gg_id:5416 Agrobacterium larrymoorei str. 3-10 Z30542
D14503.1 gg_id:5409 Agrobacterium rubi str. IFO13261 D14503
X67228.1 gg_id:5430 Agrobacterium rubi str. LMG 156 X67228
D12787.1 gg_id:5414 Agrobacterium rubi str. IAM 13569 D12787
AJ389912.1 gg_id:33557 Agrobacterium vitis str. CFBP2736 AJ3899
DQ466575.1 gg_id:156733 Agrobacterium tumefaciens str. B8LH DQ466
FJ493020.1 gg_id:556421 Agrobacterium tumefaciens str. T0H5 FJ4930
EU295450.1 gg_id:241317 Agrobacterium sp. str. LKXJ-3 EU2954
AB208737.1 gg_id:115126 Agrobacterium sp. AEOC022 AB2087
DQ803328.1 gg_id:190446 human fecal clone RL311_aam24b01 DQ803
EU652866.1 gg_id:280086 Agrobacterium sp. str. ZY068 EU6528

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	1	1	1	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	0	1	1	1	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	0	0	0	0	0
0	1	0	1	1	0	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	0	0	0	1	1	1
0	0	0	1	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	1
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	1	0	0	0	1	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium

s__Rhizobium sp. IRBG 74	62192
s__Rhizobium sp. IRBG 74	62261
s__Rhizobium sp. IRBG 74	62334
s__Rhizobium sp. IRBG 74	62434
s__Rhizobium sp. IRBG 74	62442
s__Rhizobium sp. IRBG 74	62448
s__Rhizobium sp. IRBG 74	62467
s__Rhizobium sp. IRBG 74	62485
s__Rhizobium sp. IRBG 74	62508
s__Rhizobium sp. IRBG 74	62536
s__Rhizobium sp. IRBG 74	62700
s__Rhizobium sp. IRBG 74	62726
s__Rhizobium sp. IRBG 74	62897
s__Rhizobium sp. IRBG 74	62901
s__Rhizobium undicola	62186
s__unclassified	60848
s__unclassified	61392
s__unclassified	61404
s__unclassified	61422
s__unclassified	61484
s__unclassified	61535
s__unclassified	61554
s__unclassified	61595
s__unclassified	61602
s__unclassified	61666
s__unclassified	61785
s__unclassified	61805
s__unclassified	61840
s__unclassified	61944
s__unclassified	62012
s__unclassified	62092
s__unclassified	62093
s__unclassified	62108
s__unclassified	62142
s__unclassified	62184
s__unclassified	62236
s__unclassified	62272
s__unclassified	62300
s__unclassified	62311
s__unclassified	62319
s__unclassified	62322

EF152286.1 gg_id:179195 Rhizobium sp. str. sc-w EF1522
AY438103.1 gg_id:155955 Rhizobium sp. str. EGY AY4381
DQ119110.1 gg_id:134359 Zoogloea ramigera DQ119
GQ444136.1 gg_id:587424 Agrobacterium tumefaciens str. VKLR 01 GQ444
EF377321.1 gg_id:214126 Agrobacterium sp. str. CCBAU 10749 EF3773
AM157353.1 gg_id:142761 Agrobacterium tumefaciens AM157
DQ278905.1 gg_id:143494 Agrobacterium sp. str. 24DA-1 DQ278
EU022589.1 gg_id:330237 Agrobacterium tumefaciens str. KBA3RM1 EU0225
EF025327.1 gg_id:184622 Agrobacterium tumefaciens str. SREPS2 EF0253
DQ383276.2 gg_id:217367 Agrobacterium tumefaciens str. 7406 DQ383
DQ288946.1 gg_id:144288 Agrobacterium tumefaciens TG32 DQ288
GQ258493.1 gg_id:561134 Rhizobium galegae str. Ca2 GQ258
GQ169812.1 gg_id:577612 Agrobacterium tumefaciens str. B986 GQ169
EU295451.1 gg_id:242798 Agrobacterium sp. str. LKXJ-2 EU2954
DQ648579.1 gg_id:161239 Rhizobium undicola str. Liujia-81 DQ648
FN640463.1 gg_id:514145 Agrobacterium sp. str. ZX09 FN6404
DQ009494.1 gg_id:127447 Agrobacterium tumefaciens str. CCBAU 81181 DQ009
AB368996.1 gg_id:549668 and microbial oils produced Asia petroleum crude oil (Arabian Extra light) clone PT-A AB3689
AY353708.1 gg_id:92988 Azotobacter chroococcum str. DSM2286 AY3537
EF620435.1 gg_id:241441 Agrobacterium tumefaciens str. ISSDS-381 EF6204
EU256457.1 gg_id:254367 Agrobacterium tumefaciens str. CCBAU 85023 EU2564
EF102818.1 gg_id:253586 Agrobacterium tumefaciens str. G-1-22 EF1028
AY626383.1 gg_id:99992 Agrobacterium tumefaciens str. ICMP 369 AY6263
AF422644.1 gg_id:26211 TCE-sediment clone d035 AF4226
AJ295683.1 gg_id:26338 Agrobacterium tumefaciens str. IrT-JG-6 AJ2956
EU155875.1 gg_id:244531 Agrobacterium tumefaciens str. D6 EU1558
X73041.1 gg_id:5266 Blastobacter aggregatus str. IFAM 1003 X73041
GQ267695.1 gg_id:562519 Agrobacterium tumefaciens str. CCNWSX539 GQ267
FJ444745.1 gg_id:561714 Cotton Rhizosphere cotton rhizosphere clone 4y-57 FJ4447
AY576874.1 gg_id:101430 Agrobacterium tumefaciens str. BY6 AY5768
AB535700.1 gg_id:545894 Agrobacterium tumefaciens str. Pl.2-1 AB5357
EU834271.1 gg_id:315015 Agrobacterium tumefaciens str. DS54 EU8342
AJ306769.1 gg_id:66930 DCP-dechlorinating consortium clone SHA-91 AJ3067
DQ860031.1 gg_id:250206 anchovy intestinal microflora clone F1Y DQ860
AY048887.1 gg_id:33043 rhizosphere clone Q3-24C12 AY0488
AF239848.2 gg_id:47953 Bradyrhizobium japonicum str. PRY65 AF2398
DQ288890.1 gg_id:144720 Ensifer adhaerens DQ288
EU373406.1 gg_id:261377 Agrobacterium tumefaciens str. TPR09 EU3734
AY626382.1 gg_id:99841 Agrobacterium larrymoorei str. ICMP 15237 AY6263
AY568505.2 gg_id:107283 Agrobacterium tumefaciens str. C- AY5685
AJ389905.1 gg_id:34745 Agrobacterium tumefaciens str. Mushin6 AJ3899

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	1	0	0
0	0	1	0	1	0	0	1	1	1	1	0	1
0	0	1	1	1	0	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	0	0	0	0	1	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Agrobacterium
g__Candidatus Liberibacter
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Ensifer
g__Kaistia

s__unclassified	62352
s__unclassified	62403
s__unclassified	62589
s__unclassified	62598
s__unclassified	62646
s__unclassified	62660
s__unclassified	62661
s__unclassified	62676
s__unclassified	62681
s__unclassified	62736
s__unclassified	62839
s__unclassified	62878
s__unclassified	62899
s__Candidatus Liberibacter africanus	62086
s__Sinorhizobium kostiense	62695
s__Sinorhizobium saheli	61505
s__Sinorhizobium saheli	62728
s__Sinorhizobium terangae	61388
s__Sinorhizobium xinjiangense	61773
s__Sinorhizobium xinjiangense	61894
s__Sinorhizobium xinjiangense	62218
s__Sinorhizobium xinjiangense	62622
s__unclassified	61490
s__unclassified	61599
s__unclassified	61670
s__unclassified	61686
s__unclassified	61981
s__unclassified	62080
s__unclassified	62111
s__unclassified	62232
s__unclassified	62308
s__unclassified	62317
s__unclassified	62405
s__unclassified	62427
s__unclassified	62468
s__unclassified	62487
s__unclassified	62523
s__unclassified	62682
s__unclassified	62786
s__unclassified	62798
s__unclassified	59088

AF003374.1 gg_id:5424 Rhizobium sp. str. SH19312
AB362777.1 gg_id:244116 Agrobacterium sp. str. YT0023
D13294.1 gg_id:5417 Agrobacterium tumefaciens str. IAM 14141
AY826796.1 gg_id:111301 Agrobacterium vitis str. PHX1
AB508898.1 gg_id:587039 Agrobacterium sp. str. TSH97
EU221403.1 gg_id:255931 Agrobacterium tumefaciens str. H2P4
GU233958.1 gg_id:584818 Agrobacterium tumefaciens str. HM-1
EU373439.1 gg_id:269871 Agrobacterium tumefaciens str. YRR11
AY682683.2 gg_id:142056 Microbial biofilms corroding systems heating system clone 62
DQ357728.1 gg_id:580478 Agrobacterium sp. ULV1
AY221180.1 gg_id:79849 Agrobacterium tumefaciens EBRI 20
EU618037.1 gg_id:279343 Rhizobium sp. str. CCBAU 65813
FM209485.1 gg_id:323633 Agrobacterium tumefaciens str. OLJ36
L22533.1 gg_id:199880 Candidatus Liberibacter africanus str. Nelspruit
AM181747.1 gg_id:161523 Sinorhizobium kostiense str. LMG 19225
AY034028.1 gg_id:43724 Sinorhizobium kummerowiae str. CCBAU 71714
X68390.2 gg_id:5210 Sinorhizobium saheli str. LMG 7837
AJ295073.1 gg_id:25282 Sinorhizobium terangae str. ORS1244 (LMG 15317)
AF250353.1 gg_id:20311 Sinorhizobium xinjiangense str. Rx22
AF250354.1 gg_id:52806 Sinorhizobium xinjiangense str. CCBAU110
FJ418688.1 gg_id:366662 Sinorhizobium fredii str. CCBAU 21119
AF250377.1 gg_id:39113 Sinorhizobium xinjiangense str. CCBAU 830844
AF452129.1 gg_id:69312 Ensifer adhaerens str. LMG 20571
EU221356.1 gg_id:249920 Ensifer adhaerens str. J2S2
DQ786803.1 gg_id:169278 Sinorhizobium fredii str. SjzE4
EF437258.1 gg_id:254285 Sinorhizobium sp. str. RH18
FJ418687.1 gg_id:359351 Sinorhizobium fredii str. CCBAU 21111
EU301688.1 gg_id:235385 Ensifer adhaerens str. Y12B
AB433352.1 gg_id:272085 Sinorhizobium fredii str. USDA 194
AB433350.1 gg_id:265416 Sinorhizobium fredii str. USDA 192
EU930422.1 gg_id:351757 Sinorhizobium fredii str. 15067
FJ405371.1 gg_id:360590 Ensifer mexicanus str. CAF249
EF506205.1 gg_id:225990 Sinorhizobium fredii S24
EU139306.1 gg_id:235960 Sinorhizobium fredii str. CCBAU 43300
DQ786804.1 gg_id:163644 Sinorhizobium fredii str. SjzZ4
DQ411930.1 gg_id:193675 Ensifer mexicanum str. ITTG-R7
EU410949.1 gg_id:262494 Sinorhizobium xinjiangense str. CCNWGS0023-2
D12796.1 gg_id:5260 Sinorhizobium xinjiangense str. IAM 14142
D14516.1 gg_id:5217 Sinorhizobium fredii str. ATCC35423
DQ859043.1 gg_id:204451 Sinorhizobium sp. str. ORS 3411
EF592609.1 gg_id:232106 Kaistia soli str. 5YN9-8

AF0033
AB3627
D13294
AY8267
AB5088
EU2214
GU233
EU3734
AY6826
DQ357
AY2211
EU6180
FM209
L22533
AM181
AY0340
X68390
AJ2950
AF2503
AF2503
FJ4186
AF2503
AF4521
EU2213
DQ786
EF4372
FJ4186
EU3016
AB4333
AB4333
EU9304
FJ4053
EF5062
EU1393
DQ786
DQ411
EU4109
D12796
D14516
DQ859
EF5926

0	0	0	1	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	1	0	0	0
0	0	1	1	1	0	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	1	1	1	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	0	1	1	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Kaistia
g__Kaistia
g__Kaistia
g__Martelella
g__Martelella
g__Martelella
g__Mycoplana
g__Mycoplana
g__Mycoplana
g__Ochrobactrum
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium

s__unclassified	59434
s__unclassified	59638
s__unclassified	59859
s__Martelella mediterranea	62400
s__Martelella mediterranea	62679
s__unclassified	61442
s__Mycoplana peli	62040
s__unclassified	61885
s__unclassified	62647
s__Ochrobactrum intermedium	62483
s__Rhizobium etli	61809
s__Rhizobium etli	61830
s__Rhizobium etli	62323
s__Rhizobium etli	62784
s__Rhizobium etli	62939
s__Rhizobium galegae	61925
s__Rhizobium galegae	62460
s__Rhizobium galegae	62549
s__Rhizobium galegae	62552
s__Rhizobium galegae	62924
s__Rhizobium giardinii	61610
s__Rhizobium giardinii	62500
s__Rhizobium giardinii	62638
s__Rhizobium leguminosarum	61426
s__Rhizobium leguminosarum	61432
s__Rhizobium leguminosarum	61435
s__Rhizobium leguminosarum	61495
s__Rhizobium leguminosarum	61549
s__Rhizobium leguminosarum	61597
s__Rhizobium leguminosarum	61663
s__Rhizobium leguminosarum	61683
s__Rhizobium leguminosarum	61697
s__Rhizobium leguminosarum	61778
s__Rhizobium leguminosarum	61790
s__Rhizobium leguminosarum	61818
s__Rhizobium leguminosarum	61820
s__Rhizobium leguminosarum	61881
s__Rhizobium leguminosarum	61904
s__Rhizobium leguminosarum	61919
s__Rhizobium leguminosarum	61960
s__Rhizobium leguminosarum	61968

AM409365.1 gg_id:174460 Kaistia sp. str. B6-12 AM409
FJ542971.1 gg_id:527906 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
AM409364.1 gg_id:180502 Kaistia sp. str. B6-8 AM409
AY394871.1 gg_id:95247 Rhizobium sp. str. EPR 13 AY3948
DQ768630.1 gg_id:238108 Martelella mediterranea MARC4N DQ768
EF207562.1 gg_id:215523 mangrove system sediment EF2075
EU258744.1 gg_id:235404 Mycoplana peli str. AN419 EU2587
DQ419569.1 gg_id:153696 Rhizobium sp. str. -1 DQ419
EU256384.1 gg_id:245182 Sinorhizobium borbori str. DN316-1 EU2563
GU433460.1 gg_id:521715 Rhizobium multihospitium str. CCBAU 31043 GU433
AY221178.1 gg_id:80113 Rhizobium tropici EBRI 32 AY2211
AY221176.1 gg_id:79981 Rhizobium etli EBRI 21 AY2211
AY221177.1 gg_id:80442 Rhizobium etli EBRI 26 AY2211
U89820.1 gg_id:5300 Rhizobium mongolense str. USDA 1877 U89820
AY117636.1 gg_id:63517 Rhizobium etli str. PRF164 AY1176
AF511497.1 gg_id:87964 Rhizobium sp. str. Gls-3 AF5114
AF025853.1 gg_id:5454 Rhizobium galegae str. 59A2 AF0258
AY509213.1 gg_id:107491 Rhizobium galegae str. S163 AY5092
DQ267108.1 gg_id:143997 Rhizobium sp. str. CCBAU 45111-1 DQ267
AY775170.1 gg_id:107864 Rhizobium sp. str. CCBAU 23084 AY7751
EU256413.1 gg_id:248308 Rhizobium giardinii str. CCBAU 85014 EU2564
FJ445210.1 gg_id:547364 Rhizobium sp. str. CCNWGS0271 FJ4452
EU399693.1 gg_id:271840 Rhizobium giardinii str. CCBAU 01209 EU3996
U89826.1 gg_id:5357 Rhizobium leguminosarum bv. viciae str. USDA 2434 bv. U89826
FJ025091.1 gg_id:331780 Rhizobium leguminosarum str. SEMIA 3025 FJ0250
U29386.1 gg_id:5334 Rhizobium leguminosarum bv. viciae str. USDA 2370; ATCC 10004; SEMIA 032 U29386
FJ025089.1 gg_id:352984 Rhizobium leguminosarum str. SEMIA 388 FJ0250
DQ406712.1 gg_id:154460 Rhizobium leguminosarum str. RP422 DQ406
FJ449665.1 gg_id:551782 Rhizobium leguminosarum CCNWSX0855 FJ4496
AY491062.1 gg_id:112424 Rhizobium leguminosarum str. ICMP 14642 AY4910
EF525223.1 gg_id:224132 Rhizobium leguminosarum str. PB166 EF5252
FJ025094.1 gg_id:328736 Rhizobium leguminosarum str. SEMIA 2082 FJ0250
AY904729.1 gg_id:112447 Rhizobium leguminosarum str. SEMIA 222 AY9047
DQ835293.2 gg_id:171581 Rhizobium leguminosarum bv. viciae str. CCBAU 03321 DQ835
AY509900.1 gg_id:112446 Rhizobium leguminosarum str. ATCC 14480 AY5099
U89831.1 gg_id:5335 Rhizobium leguminosarum bv. viciae str. USDA 2508 U89831
AY904742.1 gg_id:112445 Rhizobium leguminosarum str. SEMIA 3007 AY9047
EU256416.1 gg_id:257453 Rhizobium leguminosarum str. CCBAU 85142 EU2564
EU637927.1 gg_id:548867 Rhizobium leguminosarum bv. viciae str. XtP1 EU6379
DQ989228.1 gg_id:186910 Rhizobium leguminosarum str. CCBAU 73374 DQ989
EU256418.1 gg_id:251645 Rhizobium leguminosarum str. CCBAU 85010 EU2564

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	1	0	0
0	0	0	0	0	0	0	1	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium

s__Rhizobium leguminosarum	61985
s__Rhizobium leguminosarum	61987
s__Rhizobium leguminosarum	62008
s__Rhizobium leguminosarum	62027
s__Rhizobium leguminosarum	62043
s__Rhizobium leguminosarum	62070
s__Rhizobium leguminosarum	62075
s__Rhizobium leguminosarum	62083
s__Rhizobium leguminosarum	62116
s__Rhizobium leguminosarum	62153
s__Rhizobium leguminosarum	62155
s__Rhizobium leguminosarum	62181
s__Rhizobium leguminosarum	62191
s__Rhizobium leguminosarum	62231
s__Rhizobium leguminosarum	62269
s__Rhizobium leguminosarum	62287
s__Rhizobium leguminosarum	62312
s__Rhizobium leguminosarum	62332
s__Rhizobium leguminosarum	62351
s__Rhizobium leguminosarum	62362
s__Rhizobium leguminosarum	62505
s__Rhizobium leguminosarum	62513
s__Rhizobium leguminosarum	62518
s__Rhizobium leguminosarum	62524
s__Rhizobium leguminosarum	62535
s__Rhizobium leguminosarum	62594
s__Rhizobium leguminosarum	62632
s__Rhizobium leguminosarum	62690
s__Rhizobium leguminosarum	62703
s__Rhizobium leguminosarum	62738
s__Rhizobium leguminosarum	62788
s__Rhizobium leguminosarum	62809
s__Rhizobium leguminosarum	62833
s__Rhizobium leguminosarum	62877
s__Rhizobium leguminosarum	62900
s__Rhizobium multihospitium	62666
s__Rhizobium multihospitium	62879
s__Rhizobium sullae	61679
s__Rhizobium sullae	61782
s__Rhizobium sullae	61961
s__Rhizobium sullae	62478

AY904740.1 gg_id:112421 Rhizobium leguminosarum str. SEMIA 2051
DQ786802.1 gg_id:164124 Rhizobium leguminosarum str. DdE4
DQ993270.1 gg_id:184444 Rhizobium leguminosarum str. CCBAU 43201
U89830.1 gg_id:5361 Rhizobium leguminosarum bv. viciae str. USDA 2501 bv.
EF525221.1 gg_id:225304 Rhizobium leguminosarum str. PB164
EU074196.1 gg_id:248930 Rhizobium leguminosarum str. CCBAU 03285
EF364380.1 gg_id:224417 Rhizobium leguminosarum str. Mad-3
EU329018.1 gg_id:248964 Rhizobium leguminosarum str. CCNWXJ0104
U89824.1 gg_id:5355 Rhizobium leguminosarum bv. viciae str. USDA 2377
FJ025087.1 gg_id:355511 Rhizobium leguminosarum str. SEMIA 344
EF634452.1 gg_id:279482 Rhizobium leguminosarum str. PP6
DQ989227.1 gg_id:196413 Rhizobium leguminosarum str. CCBAU 81422
DQ993269.1 gg_id:186689 Rhizobium leguminosarum str. CCBAU 61381
EU170564.1 gg_id:248471 Rhizobium leguminosarum str. CCBAU 71205
GQ118966.1 gg_id:414744 Rhizobium leguminosarum bv. viciae str. BKBLV17
GU083840.1 gg_id:581334 Rhizobium indigoferae str. ZY7-2
EU256422.1 gg_id:252040 Rhizobium leguminosarum str. CCBAU 85022
EU410946.1 gg_id:261545 Rhizobium leguminosarum str. CCNWSX0011-1
EF525222.1 gg_id:219478 Rhizobium leguminosarum str. PB165
FM209478.1 gg_id:322548 Rhizobium leguminosarum bv. viciae str. M14
EF364382.1 gg_id:221307 Rhizobium leguminosarum str. Mad-5
FJ787328.1 gg_id:566975 Rhizobium leguminosarum str. FB1
NZ_ABRA01002618.1 gg_id:541025 Rhizobium etli str. 8C-3
DQ835291.2 gg_id:166841 Rhizobium leguminosarum bv. viciae str. CCBAU 01253
EF525230.1 gg_id:219443 Rhizobium leguminosarum str. PB173
U89829.1 gg_id:5360 Rhizobium leguminosarum bv. viciae str. USDA 2498 bv.
DQ406707.1 gg_id:151503 Rhizobium leguminosarum str. RP399
EU730599.1 gg_id:292520 Rhizobium leguminosarum bv. viciae str. BIHB 1191
EF525228.1 gg_id:217795 Rhizobium leguminosarum str. PB171
U89827.1 gg_id:5358 Rhizobium leguminosarum bv. viciae str. USDA 2443 bv.
DQ993268.1 gg_id:178826 Rhizobium leguminosarum str. CCBAU 65102
AY946012.1 gg_id:114608 Rhizobium leguminosarum bv. phaseoli str. RRE6
EF525219.1 gg_id:218373 Rhizobium leguminosarum str. PB162
EF525231.1 gg_id:218153 Rhizobium leguminosarum str. PB180
EF525212.1 gg_id:226245 Rhizobium leguminosarum str. PB129
GQ246944.1 gg_id:564777 Rhizobium sp. str. PM25
EU748920.1 gg_id:303700 Rhizobium sp. str. ML96
AF417558.1 gg_id:49093 Rhizobium gallicum str. DASA12005
AF417557.1 gg_id:39270 Rhizobium gallicum str. DASA12020
AF239242.1 gg_id:41578 Rhizobium sp. YAS34
AF417559.1 gg_id:74262 Rhizobium gallicum str. DASA12010

AY904
DQ786
DQ993
U89830
EF5252
EU0741
EF3643
EU3290
U89824
FJ0250
EF6344
DQ989
DQ993
EU1705
GQ118
GU083
EU2564
EU4109
EF5252
FM209
EF3643
FJ7873
NZ_AB
DQ835
EF5252
U89829
DQ406
EU7305
EF5252
U89827
DQ993
AY9460
EF5252
EF5252
EF5252
GQ246
EU7489
AF4175
AF4175
AF2392
AF4175

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium

s__Rhizobium sullae	62556
s__Rhizobium sullae	62854
s__Rhizobium sullae	62912
s__unclassified	61385
s__unclassified	61400
s__unclassified	61418
s__unclassified	61445
s__unclassified	61447
s__unclassified	61454
s__unclassified	61472
s__unclassified	61479
s__unclassified	61483
s__unclassified	61485
s__unclassified	61487
s__unclassified	61494
s__unclassified	61497
s__unclassified	61508
s__unclassified	61516
s__unclassified	61527
s__unclassified	61537
s__unclassified	61560
s__unclassified	61562
s__unclassified	61572
s__unclassified	61582
s__unclassified	61587
s__unclassified	61616
s__unclassified	61628
s__unclassified	61635
s__unclassified	61669
s__unclassified	61680
s__unclassified	61682
s__unclassified	61713
s__unclassified	61714
s__unclassified	61717
s__unclassified	61733
s__unclassified	61748
s__unclassified	61752
s__unclassified	61761
s__unclassified	61764
s__unclassified	61774
s__unclassified	61794

AM922177.1 gg_id:235606 Rhizobium gallicum Sulf-70 AM922
AY509212.1 gg_id:107348 Rhizobium mongolense str. S110 AY5092
AF417561.1 gg_id:45894 Rhizobium gallicum str. DASA12024 AF4175
EU399924.1 gg_id:264788 Rhizobium tropici str. CAF333 EU3999
DQ422964.1 gg_id:155498 Sinorhizobium sp. str. Lv6.1Se DQ422
AB487888.1 gg_id:554002 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSSUR0 AB4878
EU420078.1 gg_id:563426 Agrobacterium rhizogenes str. Cy-0 EU4200
AY509210.1 gg_id:107049 Rhizobium etli str. S1 AY5092
GQ015299.1 gg_id:494367 Topographical and Temporal Human Skin Microbiome skin palm clone nbw766g05c1 GQ015
GQ015367.1 gg_id:494299 Topographical and Temporal Human Skin Microbiome skin palm clone nbw767e11c1 GQ015
EU399914.1 gg_id:275574 Rhizobium tropici str. CAF224 EU3999
GU129569.1 gg_id:583148 Rhizobium giardinii str. Qtx-3 GU129
EU694389.1 gg_id:299472 Rhizobium huautlense str. MI-7 EU6943
U89817.1 gg_id:5320 Rhizobium mongolense str. USDA 1844 U89817
D14515.1 gg_id:5330 Rhizobium sp str. OK-50 D14515
AJ810381.1 gg_id:159130 Rhizobium genosp. AK CsB1B3 AJ8103
GQ287633.1 gg_id:587508 Rhizobium tropici str. Sap110 GQ287
EF540480.1 gg_id:219212 Rhizobium sp. 8_4V EF5404
EU399716.1 gg_id:268493 Rhizobium giardinii str. CCBAU 83011 EU3997
EU881929.1 gg_id:346116 Rhizobium sp. str. DJA1 EU8819
FJ025131.1 gg_id:334111 Rhizobium tropici str. SEMIA 4088 FJ0251
GQ397032.1 gg_id:574749 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
DQ815117.1 gg_id:166290 zebrafish digestive tract clone aab50c07 DQ815
X67226.2 gg_id:5448 Rhizobium galegae str. LMG 6214 X67226
EU335452.1 gg_id:243842 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EU399916.1 gg_id:269266 Rhizobium tropici str. CAF226 EU3999
FJ405384.1 gg_id:358164 Rhizobium tropici str. CAF446 FJ4053
U89832.1 gg_id:5277 Rhizobium tropici str. CIAT 899; USDA 9030 U89832
EF515979.1 gg_id:225133 grassland soil clone FCPU446 EF5159
FJ821665.1 gg_id:562882 Rhizobium sp. str. M20 FJ8216
DQ406713.1 gg_id:154917 Rhizobium tropici str. RP261 DQ406
FJ405376.1 gg_id:369125 Rhizobium tropici str. CAF344 FJ4053
EU074168.1 gg_id:255982 Rhizobium galegae str. CCBAU 01393 EU0741
FJ405380.1 gg_id:370346 Rhizobium tropici str. CAF439 FJ4053
EU488741.1 gg_id:321329 Rhizobium tropici str. CFN 299 EU4887
FJ671671.1 gg_id:530568 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FJ528271.1 gg_id:573223 Rhizobium sp. str. Cs217 FJ5282
U71078.2 gg_id:5393 Rhizobium hainanense str. I66 U71078
AJ863373.1 gg_id:120422 poplar tree microcosm rhizosphere flooded clone 17RHF35 AJ8633
EU488743.1 gg_id:339515 Rhizobium tropici str. H12 EU4887
EU399925.1 gg_id:273473 Rhizobium tropici str. CAF336 EU3999

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	1	0	0
0	1	0	1	0	1	1	0	0	0	1	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	1	0	1	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	1	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	1	0	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	1	1	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	0	1	1	1	0	1	1	1	1	1
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	0	1
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	0	0	1	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	1	0	1	0	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	1	1	1	1	0	0	0	0	1	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium

s__unclassified	61795
s__unclassified	61810
s__unclassified	61811
s__unclassified	61816
s__unclassified	61839
s__unclassified	61855
s__unclassified	61858
s__unclassified	61887
s__unclassified	61913
s__unclassified	61917
s__unclassified	61928
s__unclassified	61933
s__unclassified	61943
s__unclassified	61950
s__unclassified	61963
s__unclassified	61969
s__unclassified	61977
s__unclassified	62004
s__unclassified	62009
s__unclassified	62011
s__unclassified	62037
s__unclassified	62038
s__unclassified	62039
s__unclassified	62049
s__unclassified	62055
s__unclassified	62085
s__unclassified	62094
s__unclassified	62095
s__unclassified	62115
s__unclassified	62128
s__unclassified	62129
s__unclassified	62131
s__unclassified	62143
s__unclassified	62144
s__unclassified	62161
s__unclassified	62209
s__unclassified	62219
s__unclassified	62223
s__unclassified	62234
s__unclassified	62238
s__unclassified	62241

DQ814312.1 gg_id:165661 zebrafish digestive tract clone aab66g09 DQ814
AF510387.1 gg_id:86899 Rhizobium sp. str. Phr-9 AF5103
AY688621.1 gg_id:132540 Rhizobium huautlense str. Se130 AY6886
FJ527681.1 gg_id:570278 Agrobacterium rhizogenes str. rif200811 FJ5276
EU256404.1 gg_id:243982 Rhizobium etli str. CCBAU 85039 EU2564
AF417565.1 gg_id:48790 Rhizobium leguminosarum str. DASA23052 AF4175
AY509217.1 gg_id:99135 Sinorhizobium fredii str. S150 AY5092
DQ490336.1 gg_id:157614 Representation heterotrophic isolates respective libraries recent Hawaiian (<300 yr DQ490
U38469.1 gg_id:5280 Rhizobium tropici str. USDA 2676 synonyms: CIAT 166 U38469
EF364372.1 gg_id:225279 Rhizobium sp. str. Alm-1 EF3643
AF025852.1 gg_id:5449 Rhizobium huautlense str. SO2 () AF0258
AB255067.1 gg_id:170340 corroded concrete clone IC-50 AB2550
EU344941.1 gg_id:262518 Hepialus gonggaensis guts equalized library larval gut clone Hg5-31 EU3449
GU214130.1 gg_id:586800 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
AY064414.2 gg_id:75987 Rhizobium sp. str. DCP1 AY0644
FJ405378.1 gg_id:369642 Rhizobium tropici str. CAF436 FJ4053
FJ154086.1 gg_id:338916 Rhizobium giardinii str. CCNW0174 FJ1540
DQ814224.1 gg_id:162443 zebrafish digestive tract clone aab65f01 DQ814
AF364068.1 gg_id:77604 Rhizobium indigoferae str. CCBAU 71042 AF3640
AY166841.1 gg_id:76567 Rhizobium tropici str. UPRM8033 AY1668
DQ337581.1 gg_id:149175 Rhizobium sp. BBTR4 DQ337
AF417564.1 gg_id:17261 Rhizobium leguminosarum str. DASA23046 AF4175
EU618036.1 gg_id:278997 Rhizobium sp. str. CCBAU 65810 EU6180
DQ337571.1 gg_id:149885 Rhizobium sp. CHNTR26 DQ337
DQ814410.1 gg_id:165081 zebrafish digestive tract clone aab68c07 DQ814
AJ864848.1 gg_id:131846 Rhizobium sp. J34 AJ8648
AY626396.1 gg_id:105525 Agrobacterium vitis str. ICMP 5960 AY6263
EU488749.1 gg_id:336323 Rhizobium tropici str. 233 EU4887
DQ532253.1 gg_id:166577 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
FJ405385.1 gg_id:366415 Agrobacterium rhizogenes str. CAF448 FJ4053
EU556969.3 gg_id:271487 Rhizobium sp. str. SL-1 EU5569
EF364377.1 gg_id:223771 Rhizobium sp. str. Alm-6 EF3643
GQ118964.1 gg_id:443148 Rhizobium tropici str. BKBLV5 GQ118
FJ675259.1 gg_id:513708 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FM209489.1 gg_id:310821 Agrobacterium rhizogenes str. TS54 FM209
EU133607.1 gg_id:240333 tallgrass prarie soil clone FFCH12734 EU1336
AY117624.1 gg_id:63521 Rhizobium tropici str. PRF93 AY1176
AM922184.1 gg_id:248062 Rhizobium sp. Sulf-536 AM922
CU927666.1 gg_id:555946 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
DQ100062.1 gg_id:132779 Rhizobium sp. str. CCBAU 43060 DQ100
FJ444645.1 gg_id:577522 Cotton Rhizosphere cotton rhizosphere clone 2h-14 FJ4446

0	0	1	1	0	1	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	1	0	1	1	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	1	0	1	0	0	0	0	1
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	1	1	0	1	1	1	0	1	1	1
0	1	1	1	0	1	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	0	1	0	0	1	0	1
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	0	1	1	1	1	0	1	0	1
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium

s__unclassified	62248
s__unclassified	62255
s__unclassified	62276
s__unclassified	62278
s__unclassified	62290
s__unclassified	62320
s__unclassified	62349
s__unclassified	62375
s__unclassified	62387
s__unclassified	62392
s__unclassified	62399
s__unclassified	62406
s__unclassified	62419
s__unclassified	62424
s__unclassified	62439
s__unclassified	62444
s__unclassified	62450
s__unclassified	62472
s__unclassified	62491
s__unclassified	62509
s__unclassified	62511
s__unclassified	62555
s__unclassified	62613
s__unclassified	62625
s__unclassified	62628
s__unclassified	62656
s__unclassified	62669
s__unclassified	62691
s__unclassified	62731
s__unclassified	62741
s__unclassified	62755
s__unclassified	62760
s__unclassified	62771
s__unclassified	62776
s__unclassified	62785
s__unclassified	62795
s__unclassified	62797
s__unclassified	62812
s__unclassified	62816
s__unclassified	62828
s__unclassified	62832

EF100519.1 gg_id:243157 Rhizobium sp. str. STM 4023 EF1005
EU344911.1 gg_id:267554 Hepialus gonggaensis guts equalized library larval gut clone Hg5-01 EU3449
U86344.1 gg_id:5267 Rhizobium giardinii str. H152 U86344
AM697248.1 gg_id:221087 sequencing libraries indoor dust clone BF0001C089 AM697
Z94803.1 gg_id:5364 Rhizobium genosp. R str. BDV5365 Z94803
GQ181047.1 gg_id:511579 Rhizobium lusitanum str. BLN7 GQ181
EF157275.1 gg_id:243829 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1572
AY034026.1 gg_id:31634 Rhizobium loessense str. CCBAU 7190B AY0340
AY117667.1 gg_id:63509 Rhizobium tropici str. PRF77 AY1176
EU399920.1 gg_id:264590 Rhizobium tropici str. CAF279 EU3999
CU927615.1 gg_id:567667 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
EU748922.1 gg_id:321970 Rhizobium sp. str. ML102 EU7489
EU488756.1 gg_id:313755 Rhizobium tropici str. H52 EU4887
FJ025129.1 gg_id:315875 Rhizobium sp. str. SEMIA 6411 FJ0251
AY064412.2 gg_id:76783 Rhizobium sp. str. DCP2 AY0644
AB233492.1 gg_id:205713 Amorphomonas oryzae str. B26 AB2334
EU867317.1 gg_id:586260 Rhizobium sp. str. CCGE2052 EU8673
U29387.1 gg_id:5389 Rhizobium sp str. RCR 3618D; USDA 2947 U29387
EU256433.1 gg_id:255837 Rhizobium cellulosilyticus str. CCBAU 85045 EU2564
DQ310471.1 gg_id:199327 Rhizobium sp. 28/2 DQ310
DQ984537.1 gg_id:256496 FD oil-contaminated soil clone FD_52 DQ984
AF417562.1 gg_id:24266 Rhizobium leguminosarum str. DASA23002 AF4175
AF510386.1 gg_id:87585 Rhizobium sp. str. vgs-11 AF5103
AB233494.1 gg_id:212299 Amorphomonas oryzae str. B47 AB2334
AF417563.1 gg_id:47187 Rhizobium leguminosarum str. DASA23111 AF4175
EU410948.1 gg_id:267876 Rhizobium giardinii str. CCNWGS0022 EU4109
AY117623.1 gg_id:63522 Rhizobium tropici str. PRF34 AY1176
FJ405382.1 gg_id:361567 Rhizobium tropici str. CAF443 FJ4053
Z79620.1 gg_id:5452 Rhizobium galegae str. NBIMTC 2246 Z79620
AY904747.1 gg_id:111491 Agrobacterium rhizogenes str. SEMIA 6070 AY9047
DQ303318.1 gg_id:150175 Dynamic during maturation Tuber magnatum Pico ascoma Rhizobium clone TM4_28 DQ303
EU600086.1 gg_id:276672 Pueraria montana var. lobata EU6000
AM697022.1 gg_id:217449 sequencing libraries indoor dust clone BF0001B048 AM697
EF522124.1 gg_id:220384 Agrobacterium rhizogenes str. CU10 EF5221
D11344.1 gg_id:5282 Rhizobium tropici str. IFO15247 D11344
GQ115602.1 gg_id:459244 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688b1 GQ115
AF260298.2 gg_id:77278 Rhizobium tropici str. PRF35 AF2602
FJ405375.1 gg_id:359783 Rhizobium tropici str. CAF341 FJ4053
EU488750.1 gg_id:322227 Rhizobium giardinii str. H152 EU4887
AF510382.1 gg_id:87256 Rhizobium sp. str. Kusp-1 AF5103
EU399714.1 gg_id:274169 Rhizobium tropici str. CCBAU 83795 EU3997

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	1	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	0	1
1	1	1	1	1	1	1	1	1	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	1	1
0	1	1	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	0	1	1	1	1	0	1	1	1
0	1	1	1	1	1	1	1	1	1	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	1	1	1	1	0	1	0	1	0	1
0	1	1	1	1	1	1	0	0	0	0	0	1
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	1	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	1	0	1	0	0
0	1	1	1	0	1	1	0	0	0	0	1	0
0	1	1	1	1	1	1	0	0	0	0	1	1
0	1	0	1	1	0	1	1	1	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae

g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Rhizobium
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Shinella
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium

s__unclassified	62864
s__unclassified	62866
s__unclassified	62870
s__unclassified	62873
s__unclassified	62875
s__unclassified	62883
s__unclassified	62886
s__unclassified	62917
s__unclassified	62942
s__Shinella granuli	61757
s__Shinella zoogloeoides	61409
s__Shinella zoogloeoides	61945
s__Shinella zoogloeoides	62213
s__unclassified	61405
s__unclassified	61905
s__unclassified	61907
s__unclassified	61932
s__unclassified	61935
s__unclassified	61954
s__unclassified	62001
s__unclassified	62048
s__unclassified	62201
s__unclassified	62389
s__unclassified	62522
s__unclassified	62616
s__unclassified	62909
s__unclassified	62914
s__unclassified	62933
s__Sinorhizobium arboris	61383
s__unclassified	61393
s__unclassified	61462
s__unclassified	61463
s__unclassified	61499
s__unclassified	61551
s__unclassified	61579
s__unclassified	61586
s__unclassified	61665
s__unclassified	61694
s__unclassified	61744
s__unclassified	61771
s__unclassified	61903

DQ993272.1 gg_id:193836 Rhizobium sp. str. CCBAU 43112 DQ993
EU584258.1 gg_id:352865 Rhizobium sp. str. ORS 3441 EU584
AY316683.1 gg_id:200464 Reichenowia parasiticae AY316
EF173321.1 gg_id:192524 Sinorhizobium sp. MKI7 EF1733
FJ517717.1 gg_id:560086 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e FJ5177
EU399935.1 gg_id:260090 Rhizobium tropici str. CAF438 EU399
D12788.1 gg_id:5289 Agrobacterium rhizogenes str. IAM 13570 D12788
EU399919.1 gg_id:276979 Rhizopus oryzae str. CAF276 EU399
DQ304797.1 gg_id:154037 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert India root clone C6 DQ304
AB187585.1 gg_id:104322 Granulella daejeonensis str. Ch06 AB187
EU723213.1 gg_id:334997 Shinella sp. str. NP526a EU723
FJ598327.1 gg_id:566021 Shinella sp. str. 2-9 FJ5983
EU346730.1 gg_id:267822 Shinella zoogloeoides str. BC026 EU346
AF502218.1 gg_id:55816 EBPR sludge lab scale clone HP1B02 AF502
GQ009804.1 gg_id:499861 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
DQ898296.1 gg_id:173668 Rhizobium sp. str. MTR-3A DQ898
EU104300.1 gg_id:345964 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
AB285481.1 gg_id:232448 Sulfolanivorax yambarensis str. MS4 AB285
FJ154090.1 gg_id:351849 Shinella kummerowiae str. CCNWGS0228 FJ1540
EF437254.1 gg_id:249079 Rhizobium sp. str. RZ6 EF4372
FN436071.1 gg_id:573545 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
FN555404.1 gg_id:511375 Sinorhizobium sp. I-Bh25-4 FN555
D14255.1 gg_id:5205 Zoogloea ramigera str. IAM12669 D14255
DQ984584.1 gg_id:256527 Mt. Nan-Jen litterfall clone IYF06 DQ984
DQ096644.1 gg_id:132981 Rhizobium sp. PIP4 str. PIP4; JCM 12219 DQ096
EU888002.1 gg_id:349041 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU888
DQ814239.1 gg_id:162359 zebrafish digestive tract clone aab65g10 DQ814
X74915.1 gg_id:5207 Shinella zoogloeoides str. ATCC 19623 X74915
AM181744.1 gg_id:160209 Sinorhizobium arboris str. LMG 14919 AM181
D14509.1 gg_id:5245 Sinorhizobium meliloti str. IAM12611 D14509
EU379945.1 gg_id:270061 Sinorhizobium meliloti str. CCBAU 83856 EU379
EF531326.1 gg_id:278035 Sinorhizobium meliloti str. AC-1 EF5313
GU433464.1 gg_id:517976 Sinorhizobium meliloti str. CCBAU 65887 GU433
EU256454.1 gg_id:253057 Sinorhizobium meliloti str. CCBAU 85101 EU256
EF634450.1 gg_id:278262 Sinorhizobium meliloti str. PP3 EF6344
DQ989230.1 gg_id:176599 Sinorhizobium meliloti str. CCBAU 81180 DQ989
AY904726.1 gg_id:111921 Sinorhizobium meliloti str. SEMIA 103 AY904
AM946566.1 gg_id:325210 Ensifer maghrebium str. ORS 1410 AM946
EU625296.1 gg_id:278661 Sinorhizobium meliloti str. 27 EU625
FJ025127.1 gg_id:351945 Sinorhizobium meliloti str. SEMIA 6162 FJ0251
EU545511.1 gg_id:342747 Sinorhizobium meliloti EU545

0	1	1	1	0	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	0	0	0	0	0	0	0	1
0	0	0	0	0	0	1	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	1	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	1	0	0	0	0
0	0	0	1	0	0	1	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	0	0	1	0	1	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	1	0	0	0	0
0	0	1	1	0	0	1	0	1	0	0	0	0
0	0	0	1	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	1	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhizobiaceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae

g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__Sinorhizobium
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Labrenzia
g__Labrenzia
g__Pannonibacter

s__unclassified	61947
s__unclassified	62132
s__unclassified	62175
s__unclassified	62198
s__unclassified	62260
s__unclassified	62293
s__unclassified	62298
s__unclassified	62383
s__unclassified	62402
s__unclassified	62502
s__unclassified	62517
s__unclassified	62527
s__unclassified	62547
s__unclassified	62551
s__unclassified	62569
s__unclassified	62860
s__unclassified	59747
s__unclassified	61386
s__unclassified	61507
s__unclassified	61615
s__unclassified	61721
s__unclassified	61824
s__unclassified	61841
s__unclassified	61924
s__unclassified	62026
s__unclassified	62068
s__unclassified	62076
s__unclassified	62123
s__unclassified	62154
s__unclassified	62193
s__unclassified	62270
s__unclassified	62338
s__unclassified	62447
s__unclassified	62629
s__unclassified	62721
s__unclassified	62767
s__unclassified	62783
s__unclassified	62847
s__Labrenzia aggregata	61869
s__unclassified	61601
s__Pannonibacter phragmitetus	61544

GU143694.1 gg_id:559023 Sinorhizobium medicae str. NisA-4 GU143
AB535696.1 gg_id:557105 Sinorhizobium medicae str. Cl.3-2 AB5356
EU379949.1 gg_id:261990 Sinorhizobium meliloti str. CCBAU 83575 EU3799
AY904727.1 gg_id:111751 Sinorhizobium meliloti str. SEMIA 134 AY9047
EU256452.1 gg_id:244861 Sinorhizobium meliloti str. CCBAU 85092 EU2564
AF533685.1 gg_id:61015 Sinorhizobium meliloti str. WSM1702 AF5336
AM946567.1 gg_id:343932 Ensifer xericitae str. ORS 1401 AM946
GU129566.1 gg_id:594144 Sinorhizobium meliloti str. Qtx-8-1 GU129
AB535703.1 gg_id:545858 Sinorhizobium medicae str. Pl.4-2 AB5357
AB015420.1 gg_id:34931 Sinorhizobium indiaensis str. Ra-3 AB0154
GQ452960.1 gg_id:572099 Sinorhizobium sp. str. DP10 GQ452
EU399794.1 gg_id:275434 Sinorhizobium meliloti str. SaTO3 EU3997
FJ821001.1 gg_id:512395 Sinorhizobium sp. str. PN21 FJ8210
DQ989229.1 gg_id:181509 Sinorhizobium fredii str. CCBAU 01348 DQ989
EF645800.1 gg_id:240354 Sinorhizobium meliloti str. 91532 EF6458
EF070136.1 gg_id:182386 Sinorhizobium meliloti str. CCBAU 05137 EF0701
AB017203.1 gg_id:50238 Prosthecomicrobium pneumaticum str. MBIC3489 AB017
EU488283.1 gg_id:551681 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ793198.1 gg_id:564313 Rhizobium sp. str. CAAS-2R FJ7931
CU920781.1 gg_id:563220 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EU488449.1 gg_id:570051 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU488300.1 gg_id:559383 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU488378.1 gg_id:565999 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU488368.1 gg_id:542279 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU488131.1 gg_id:534712 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4881
AB232339.2 gg_id:155467 Bartonella sp. str. TFC2 AB2323
EU488467.1 gg_id:553301 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EF540509.1 gg_id:219954 Rhizobium sp. 4_C16_39 EF5405
EF516927.1 gg_id:218154 grassland soil clone FCPP541 EF5169
EU488260.1 gg_id:547565 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
AY133103.1 gg_id:56163 TCE-contaminated site clone ccspost2147 AY1331
EU488463.1 gg_id:571469 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU488371.1 gg_id:534308 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
EU817493.1 gg_id:326733 Rhizobium sp. str. XJ-L72 EU8174
EF090606.1 gg_id:197918 Agrobacterium sp. str. Mei-QS6 EF0906
EU488459.1 gg_id:565076 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4884
EU488190.1 gg_id:543717 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4881
EU488204.1 gg_id:553575 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
NZ_AAUW01000023.1 gg_id:175858 Stappia aggregata str. IAM 12614 NZ_AA
DQ416553.1 gg_id:150935 s1cb108 DQ416
FJ493017.1 gg_id:535774 Pannonibacter phragmitetus str. T0AnH5 FJ4930

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	1	1	0	1	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	1	0	1	0	0	0	0	0
0	0	1	0	0	1	1	0	0	0	1	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	1	0	0	0	0	0
0	1	1	0	1	1	0	1	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	1	1	1	1	1	0	1	1	0
0	0	0	0	1	0	0	0	1	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobacteraceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__Rhodobiaceae
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified

g__Pannonibacter
g__Pannonibacter
g__Pseudovibrio
g__Pseudovibrio
g__Pseudovibrio
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Afifella
g__Afifella
g__Afifella
g__Afifella
g__Rhodobium
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__Pannonibacter phragmitetus	61633
s__unclassified	61718
s__unclassified	62823
s__unclassified	62863
s__unclassified	62882
s__unclassified	61410
s__unclassified	61460
s__unclassified	61503
s__unclassified	61515
s__unclassified	61653
s__unclassified	61660
s__unclassified	61728
s__unclassified	61770
s__unclassified	61783
s__unclassified	62010
s__unclassified	62036
s__unclassified	62160
s__unclassified	62182
s__unclassified	62396
s__unclassified	62550
s__unclassified	62574
s__unclassified	62667
s__unclassified	62811
s__unclassified	62887
s__Afifella marina	60542
s__Afifella marina	60815
s__unclassified	60973
s__unclassified	61098
s__Rhodobium orientis	59356
s__unclassified	58949
s__unclassified	59203
s__unclassified	59237
s__unclassified	59407
s__unclassified	59839
s__unclassified	58891
s__unclassified	58894
s__unclassified	58953
s__unclassified	58974
s__unclassified	58979
s__unclassified	59026
s__unclassified	59035

EU841534.1 gg_id:340002 Pannonibacter phragmitetus str. 224 EU841
EF608175.3 gg_id:535229 Pannonibacter sp. str. HT23 EF6081
AM990762.1 gg_id:279133 Pseudovibrio sp. MOLA 539 AM990
FJ169215.1 gg_id:342767 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
FJ169195.1 gg_id:321382 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1691
EU726271.1 gg_id:342195 Stappia sp. str. B106 EU726
EU581698.1 gg_id:275806 Rhodobacteraceae sp. MEBiC05064T marine sponge Geomun-Island South Korea EU581
DQ985041.1 gg_id:193166 Halomonas sp. str. JL1044 DQ985
EF101502.1 gg_id:194356 Stappia meyerae str. GA15 EF1015
EU167953.1 gg_id:269625 Stappia sp. str. 16-23 EU167
AY162083.1 gg_id:135498 Cultivating Sargasso Sea clone GMD37F4 AY162
FJ202909.1 gg_id:325677 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
AY628423.1 gg_id:99161 Stappia marina str. mano18 AY6284
D85832.1 gg_id:111501 Roseibium denhamense str. OCh 254 D85832
AY588950.1 gg_id:122223 Pacific Ocean deep sea sediment clone DE6.8 AY5889
EU168019.1 gg_id:269506 Stappia sp. str. 23-28 EU168
EU999013.1 gg_id:304551 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Foı EU999
DQ270709.1 gg_id:144694 Halomonas sp. B-3046 DQ270
GU199002.1 gg_id:593115 Mycoplana sp. str. G110 GU199
GU322907.1 gg_id:524664 Labrenzia sp. str. YC6927 GU322
EF101504.1 gg_id:185052 Stappia conradae str. MIO EF1015
DQ660386.1 gg_id:161779 Pseudovibrio sp. str. SPO723 DQ660
AJ889009.1 gg_id:139632 Stappia alba str. 5OM9 AJ8890
DQ416561.1 gg_id:151808 s1cb71 DQ416
DQ985044.1 gg_id:196145 Rhodopseudomonas sp. str. JL1015 DQ985
AM696707.1 gg_id:224191 Rhodobium marinum str. JA211 AM696
GU370102.1 gg_id:521541 Rhodopseudomonas sp. str. P530(9) GU370
EU445271.1 gg_id:272585 Rhodobium pfennigii str. AR 2102 EU445
AM180706.1 gg_id:161325 Rhodobium gokurnum str. JA 173 AM180
DQ532207.1 gg_id:166078 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
AB374392.1 gg_id:269733 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
AB257630.1 gg_id:273081 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abov AB2576
EU133571.1 gg_id:245274 tallgrass prarie soil clone FFCH4802 EU1335
FJ152795.1 gg_id:310212 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
DQ451507.1 gg_id:156833 forest soil clone FAC68 DQ451
AY862042.1 gg_id:112593 Washburn Spring 1 community clone WB1B012 AY8620
GQ093827.1 gg_id:452509 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ152772.1 gg_id:315470 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AF050531.1 gg_id:4714 contaminated aquifer clone WCHB1-55 AF0505
GQ402732.1 gg_id:538998 Accessing microbial biodiversity and metabolic potential tropical -based approach pı GQ402
EU104345.1 gg_id:338628 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1043

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	1	1	0	0	1	1	1
0	0	0	1	1	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	1	1	1	0	0	1	0	1
1	1	1	1	1	1	1	1	1	0	1	0	1
1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	0	0	0	1	0	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	59042
s__unclassified	59060
s__unclassified	59067
s__unclassified	59070
s__unclassified	59072
s__unclassified	59085
s__unclassified	59112
s__unclassified	59121
s__unclassified	59156
s__unclassified	59297
s__unclassified	59367
s__unclassified	59382
s__unclassified	59389
s__unclassified	59396
s__unclassified	59405
s__unclassified	59406
s__unclassified	59413
s__unclassified	59426
s__unclassified	59435
s__unclassified	59464
s__unclassified	59477
s__unclassified	59512
s__unclassified	59536
s__unclassified	59561
s__unclassified	59565
s__unclassified	59567
s__unclassified	59572
s__unclassified	59577
s__unclassified	59585
s__unclassified	59589
s__unclassified	59593
s__unclassified	59627
s__unclassified	59649
s__unclassified	59654
s__unclassified	59656
s__unclassified	59682
s__unclassified	59709
s__unclassified	59738
s__unclassified	59773
s__unclassified	59794
s__unclassified	59815

EU887986.1 gg_id:304250 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
AF200695.1 gg_id:51286 13C- extracted 13C-methanol exposed soil clone UP2 proteobacterium AF200
EF516292.1 gg_id:222685 grassland soil clone FCPT613 EF5162
EF465533.1 gg_id:225699 Pseudoxanthobacter soli str. CC-CC4 EF4655
GQ263890.1 gg_id:510008 Structure Simulated Level Waste Site simulated level waste site clone WC2_141 GQ263
EU881257.1 gg_id:332410 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
DQ984620.1 gg_id:257087 YK oil-contaminated soil clone YK_31 DQ984
GQ262949.1 gg_id:538739 Structure Simulated Level Waste Site simulated level waste site clone F1_86X GQ262
AJ229208.1 gg_id:25697 anoxic bulk soil flooded rice microcosm clone BSV56 clone AJ2292
AM162440.1 gg_id:155413 and situ identification acidic sphagnum peat bog clone B83 AM162
U87772.1 gg_id:4760 Afipia genosp. 6 str. G8665 U8777
EF020321.1 gg_id:207430 aspen rhizosphere clone Elev_16S_1897 EF0203
X97077.1 gg_id:4765 peat bog clone TM19 X97077
FJ380167.1 gg_id:360221 ornithogenic Ross Sea region Antarctica AB1 soil clone 13/1/8F FJ3801
AF358012.1 gg_id:29077 peat soil microcosm clone LO13.2 AF358
DQ129631.1 gg_id:137916 microarray level air two cities Texas urban aerosol clone AKIW856 DQ129
DQ823159.1 gg_id:162179 Techniques Microbial Studies Oregon Caves National Monument Quad 3 off trail clo DQ823
GQ350414.1 gg_id:586170 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EF516212.1 gg_id:225488 grassland soil clone FCPP499 EF5162
FJ152802.1 gg_id:308948 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1528
EU881153.1 gg_id:310925 Karst region primary forest soil clone KPF200711-196 EU881
GQ402664.1 gg_id:548721 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AM936498.1 gg_id:559544 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EF019286.1 gg_id:209662 aspen rhizosphere clone Elev_16S_473 EF0192
GQ402711.1 gg_id:546022 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
DQ451452.1 gg_id:156829 forest soil clone FAC13 DQ451
GQ097820.1 gg_id:417366 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw397h0 GQ097
AM935446.1 gg_id:547229 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
FM253652.1 gg_id:332834 Rock gold mine unusually microbial biofilm clone D06-2 FM253
EU861875.1 gg_id:338761 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
CU925666.1 gg_id:553033 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
CU926879.1 gg_id:567435 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
DQ813987.1 gg_id:162431 zebrafish digestive tract clone aab58b10 DQ813
AY913367.1 gg_id:137744 forest soil clone DUNssu160 (+7B) (OTU#170) AY9133
CU923391.1 gg_id:570766 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
GQ021391.1 gg_id:488276 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu27 GQ021
FJ658644.1 gg_id:555885 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Sum FJ6586
NR_025428.1 gg_id:548469 Chelatococcus asaccharovorans str. TE2 NR_02
GQ848214.1 gg_id:552413 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
FJ592562.1 gg_id:574090 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5925
AY792286.1 gg_id:124699 Humic Lake clone CrystalBog021H4 AY792

0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	0	0	0	1	0	1
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	1	1	1	1	0	0	0	1	1	1
0	0	0	0	1	0	0	0	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	1	1	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	1	0	0	0	0	0	0	0	0
0	1	1	1	1	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	1	0	0	0	0	0	0
0	0	0	1	1	0	1	0	0	0	0	1	1
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	59816
s__unclassified	59836
s__unclassified	59853
s__unclassified	59892
s__unclassified	59923
s__unclassified	59936
s__unclassified	59946
s__unclassified	59950
s__unclassified	59969
s__unclassified	59980
s__unclassified	59982
s__unclassified	60001
s__unclassified	60030
s__unclassified	60063
s__unclassified	60066
s__unclassified	60091
s__unclassified	60096
s__unclassified	60099
s__unclassified	60122
s__unclassified	60167
s__unclassified	60169
s__unclassified	60173
s__unclassified	60179
s__unclassified	60191
s__unclassified	60210
s__unclassified	60674
s__unclassified	60713
s__unclassified	60860
s__unclassified	61195
s__unclassified	61369
s__unclassified	61387
s__unclassified	61455
s__unclassified	61458
s__unclassified	61467
s__unclassified	61538
s__unclassified	61543
s__unclassified	61564
s__unclassified	61594
s__unclassified	61596
s__unclassified	61609
s__unclassified	61620

FJ478967.1 gg_id:586430 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
DQ129276.1 gg_id:137669 urban aerosol clone AKIW916 DQ129
FJ542954.1 gg_id:513048 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
FJ624896.1 gg_id:544990 Influence lead contamination on boreal pine forest soil clone HF_C_23 FJ6248
GQ065523.1 gg_id:452998 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw89d08(GQ065
AY212626.1 gg_id:106732 water 20 m upstream manure clone 175up AY2126
FM253660.1 gg_id:338715 Rock gold mine unusually microbial biofilm clone E09-2 FM253
DQ660884.1 gg_id:254810 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DCK-I-2 DQ660
AY921699.1 gg_id:113477 farm soil clone AKYG1801 AY9216
EU133586.1 gg_id:247599 tallgrass prarie soil clone FFCH5858 EU1335
AB240233.1 gg_id:144675 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU617827.1 gg_id:344447 Seasonal variation microbial Yel Sea sediment clone D13S-4 EU6178
EF079080.1 gg_id:252325 seeps sulfur-rich neutral pH ecosystem ochre-colored flocculent iron seep ditch fresh EF0790
EU050753.1 gg_id:256661 libraries sediment Kings Bay Svalbard Arctic clone ss1_B_08_05 EU0507
EF018669.1 gg_id:209579 aspen rhizosphere clone Amb_16S_956 EF0186
FM253680.1 gg_id:310692 Rock gold mine unusually microbial biofilm clone H07-2 FM253
AY921829.1 gg_id:114266 farm soil clone AKYH1529 AY9218
AM935046.1 gg_id:566962 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
GQ263215.1 gg_id:585259 Structure Simulated Level Waste Site simulated level waste site clone F3_22X GQ263
AY922106.1 gg_id:113801 farm soil clone AKYH1402 AY9221
GQ263169.1 gg_id:511500 Structure Simulated Level Waste Site simulated level waste site clone F3_121X GQ263
GU118725.1 gg_id:567929 Threatened Corals Provide Microbial Habitats clone Mfra_B11 GU118
GQ008167.1 gg_id:501498 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ008
DQ378213.1 gg_id:154041 oil-polluted soil clone F51_Pitesti DQ378
GQ263279.1 gg_id:534132 Structure Simulated Level Waste Site simulated level waste site clone FW1_a25 GQ263
DQ230971.1 gg_id:141437 subsurface water clone DR938CH110701SACH95 DQ230
GQ263757.1 gg_id:584708 Structure Simulated Level Waste Site simulated level waste site clone WC1_a78 GQ263
GQ263601.1 gg_id:589565 Structure Simulated Level Waste Site simulated level waste site clone FW3_155C GQ263
DQ097300.1 gg_id:161408 marine RS.Sph.026 DQ097
FJ998414.1 gg_id:390344 Amorphus sp. str. YIM D10 FJ9984
FJ477551.1 gg_id:509105 gut symbionts are tightly linked herbivory ants whole extracted single ant clone 83f FJ4775
FJ416098.1 gg_id:368583 sediments sediment station NEC5 Northern Bering Sea clone 061M64 FJ4160
FJ430076.1 gg_id:360023 Rhizobium sp. str. CCNWGS114 FJ4300
DQ454123.3 gg_id:229692 Rhizobium sp. str. J3-A127 DQ454
EF580937.1 gg_id:277780 Survey Microbial Freshwater Calcareous Mats freshwater calcareous mat clone CM4 EF5809
DQ113411.1 gg_id:143364 microflora ants genus Bartonella Tetraponera attenuata RT13 clone DQ113
GU118131.1 gg_id:535654 Threatened Corals Provide Microbial Habitats clone Apal_F11 GU118
FJ477662.1 gg_id:591010 gut symbionts are tightly linked herbivory ants whole extracted single ant clone UAB- FJ4776
EU056822.1 gg_id:354679 Rhizobium oryzae str. Alt 501 EU0568
DQ269119.1 gg_id:197574 marine macro-alga surface clone DPC247 DQ269
GQ199732.1 gg_id:591717 Mycoplana sp. str. 210_30 GQ199

0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	0	1	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	1	0	0	0	0	0	1	1
0	1	0	1	1	1	1	0	0	0	1	1	1
0	0	1	0	0	1	0	0	0	1	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0	0	0	1	1	1
1	1	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	1	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	1	0	0	1	1	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1	1	0	1	1	1
0	0	0	0	0	0	1	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified

g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA
g__sfA

s__unclassified	61627
s__unclassified	61645
s__unclassified	61707
s__unclassified	61724
s__unclassified	61775
s__unclassified	61798
s__unclassified	61802
s__unclassified	61807
s__unclassified	61814
s__unclassified	61829
s__unclassified	61850
s__unclassified	61851
s__unclassified	61870
s__unclassified	61980
s__unclassified	62002
s__unclassified	62016
s__unclassified	62029
s__unclassified	62060
s__unclassified	62180
s__unclassified	62203
s__unclassified	62240
s__unclassified	62262
s__unclassified	62288
s__unclassified	62318
s__unclassified	62360
s__unclassified	62388
s__unclassified	62414
s__unclassified	62421
s__unclassified	62441
s__unclassified	62453
s__unclassified	62492
s__unclassified	62563
s__unclassified	62620
s__unclassified	62649
s__unclassified	62664
s__unclassified	62684
s__unclassified	62687
s__unclassified	62718
s__unclassified	62775
s__unclassified	62782
s__unclassified	62794

FJ516967.1 gg_id:557392 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
FJ202935.1 gg_id:348688 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
FJ230932.1 gg_id:323791 under Level Antibiotic Selection Pressures river water clone F30 FJ2309
EU290679.1 gg_id:254474 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU290
EF125460.1 gg_id:176046 mangrove soil clone MSB-2G6 EF1254
EU022307.1 gg_id:256730 Mycoplana dimorpha str. DSM 7138 EU0223
AB476277.1 gg_id:567915 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB476
FJ203608.1 gg_id:318738 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
GU118008.1 gg_id:558255 Threatened Corals Provide Microbial Habitats clone Acer_O09 GU118
AM403234.1 gg_id:165611 Nitrate-reducing and Denitrifying Marine Aqua Biofilter marine aqua AM403
AJ318143.1 gg_id:46411 Waste-gas biofilter clone BIhii25 AJ3181
GQ093939.1 gg_id:462605 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
GQ033083.1 gg_id:432897 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ033
EF363715.1 gg_id:215874 Rhizobium soli str. DS-42 EF3637
GU118128.1 gg_id:548423 Threatened Corals Provide Microbial Habitats clone Apal_H04 GU118
GU118281.1 gg_id:563202 Threatened Corals Provide Microbial Habitats clone Dstr_J12 GU118
EU491593.1 gg_id:273684 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
AF423220.1 gg_id:51992 soil clone 1315-2 AF4232
FJ712592.1 gg_id:517638 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7125
AY642558.1 gg_id:155596 and carbonate precipitation giant microbialites ly alkaline Lake Van Turkey microbiali AY6425
GQ054602.1 gg_id:405655 Topographical and Temporal Human Skin Microbiome skin back clone nbw1092d01c GQ054
DQ917801.1 gg_id:217617 Microbial profiles bleached and wild-type Muricea elongata Mesorhizobium clone BI DQ917
AJ294417.1 gg_id:22665 Rhizobium sp. str. TCK AJ2944
EU246825.1 gg_id:240545 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EF532794.1 gg_id:221752 Mycoplana caeni str. K107 EF5327
GU369925.1 gg_id:525633 and mats vents Arc white microbial film on pebble aphotic zone shal hydrothermal v GU369
AM930452.1 gg_id:259822 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
EF649779.1 gg_id:244917 Rhizobium sp. str. J3-AN59 EF6497
DQ330994.1 gg_id:159335 Guerrero Negro hypersaline microbial mat clone 09D2Z18 DQ330
CU920079.1 gg_id:535750 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
AM697186.1 gg_id:223514 sequencing libraries indoor dust clone BF0001C027 AM697
GQ093897.1 gg_id:466355 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ425633.1 gg_id:365493 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata cl FJ4256
EU528264.1 gg_id:286797 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
GQ365715.1 gg_id:548464 Hoeflea sp. str. AY-2 GQ365
DQ289935.1 gg_id:167459 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
FJ193930.1 gg_id:340714 Genetic inventory 'KSC-Astrotek' spacecraft assembly clean room during DAWN missi FJ1939
FJ203409.1 gg_id:331011 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
AF359524.1 gg_id:38898 Alexandrium lusitanicum NEPCC 253 AF3595
U78037.1 gg_id:5136 Ophiactis balli symbiont U7803
EU753666.1 gg_id:306406 modern freshwater stromatolites Ruidera Pools Natural Park Spain dry stromatolite EU753

0	1	1	1	1	1	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	1	0	0	1	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	1	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
1	1	1	1	1	1	1	1	0	1	1	0	1
0	1	1	1	1	1	1	0	1	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	1	1	1	1	0	1	0	0	0	0	0
0	1	1	1	1	1	1	0	0	0	0	1	0
0	1	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	0	1	1	1	0	0	1	1	1
0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	0	0	1	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__unclassified
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhizobiales	f__Xanthobacteraceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae

g__sfA
g__sfA
g__sfB
g__sfB
g__sfB
g__Ancylobacter
g__Ancylobacter
g__Azorhizobium
g__Azorhizobium
g__Azorhizobium
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__Labrys
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__Xanthobacter
g__Xanthobacter
g__Xanthobacter
g__Xanthobacter
g__Xanthobacter
g__Hirschia
g__Hirschia
g__Hyphomonas
g__Hyphomonas
g__Hyphomonas
g__Hyphomonas
g__Hyphomonas

s__unclassified	62868
s__unclassified	62944
s__unclassified	59037
s__unclassified	59099
s__unclassified	59341
s__unclassified	58956
s__unclassified	59569
s__Azorhizobium caulinodans	59820
s__Azorhizobium doebereinerae	59361
s__unclassified	60018
s__Labrys methylaminiphilus	60432
s__unclassified	60258
s__unclassified	60285
s__unclassified	60337
s__unclassified	60481
s__unclassified	60486
s__unclassified	60627
s__unclassified	60767
s__unclassified	61119
s__unclassified	61192
s__unclassified	58916
s__unclassified	59053
s__unclassified	59101
s__unclassified	59452
s__unclassified	59579
s__unclassified	59621
s__unclassified	59665
s__unclassified	59693
s__unclassified	60596
s__unclassified	59115
s__unclassified	60052
s__Xanthobacter autotrophicus	59387
s__Xanthobacter flavus	59787
s__Xanthobacter flavus	59876
s__Hirschia baltica	60559
s__Hirschia baltica	60745
s__Hyphomonas jannaschiana	60685
s__Hyphomonas neptunium	60263
s__Hyphomonas neptunium	61329
s__unclassified	60392
s__unclassified	60483

AJ271901.1 gg_id:38159 Rhizobium sp. str. rob18 AJ2719
AF003376.1 gg_id:5163 Rhizobium sp. str. SH2672 AF0033
DQ103630.1 gg_id:132060 hypersaline endoevaporitic microbial mat clone E2aG02 DQ103
DQ103632.1 gg_id:150577 hypersaline endoevaporitic microbial mat clone E6aD10 DQ103
DQ103628.1 gg_id:150589 hypersaline endoevaporitic microbial mat clone E2aB07 DQ103
AF004845.1 gg_id:4722 Methylorhabdus multivorans str. DM13 AF0048
AY056830.1 gg_id:17276 Ancylobacter rudongensis str. AS1.1761 AY0568
X94200.1 gg_id:4704 Azorhizobium caulinodans str. ORS 571 X94200
AY904784.1 gg_id:111946 Azorhizobium sp. str. SEMIA 6402 AY9047
EU876663.1 gg_id:317195 Azorhizobium sp. str. pcnb-3 EU8766
AB236172.1 gg_id:148902 Labrys methylaminiphilus str. DSM16812 AB2361
FJ707292.1 gg_id:572030 Labrys wisconsinensis str. SRNK-1 FJ7072
AB236169.1 gg_id:147634 Labrys okinawaensis str. MAFF210191 AB2361
FJ478661.1 gg_id:543156 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EF019390.1 gg_id:209096 aspen rhizosphere clone Elev_16S_622 EF0193
AJ535707.1 gg_id:105233 Labrys monachus str. VKM-B1479 AJ5357
EF516667.1 gg_id:218772 grassland soil clone FCPT638 EF5166
AB236170.1 gg_id:149143 Labrys miyagiensis str. G24103 AB2361
EF516470.1 gg_id:224138 grassland soil clone FCPO739 EF5164
AB271044.1 gg_id:166471 Labrys ginsengisoli str. Gsoil 106 AB2710
DQ986319.1 gg_id:174214 Thiobacillus sp. str. S1 DQ986
GQ046109.1 gg_id:464010 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ046
AJ535709.1 gg_id:105545 Angulomicrobium amanitiforme str. NCIMB 1785 AJ5357
FJ588700.1 gg_id:541172 Starkeya sp. str. pcnb4 FJ5887
X94198.1 gg_id:4663 Xanthobacter agilis str. SA35 X94198
X99469.1 gg_id:4700 Xanthobacter tagetidis str. TagT2C X99469
EF540453.1 gg_id:221589 Ancylobacter sp. b1M EF5404
AM778407.1 gg_id:236974 Ancylobacter oxalaticus NS05 AM778
EU289458.1 gg_id:239819 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AJ306541.1 gg_id:68682 Xanthobacter sp. str. INA43/2-2 (DSM 11820) sewage sludge INA43/2-2 AJ3065
DQ533878.1 gg_id:231483 Xanthobacter flavus str. WM2814 DQ533
X94201.1 gg_id:4654 Xanthobacter autotrophicus str. 7c X94201
X94202.1 gg_id:4673 Xanthobacter flavus str. H4-14 X94202
AF399969.1 gg_id:62751 Xanthobacter aminoxidans str. 14a AF3999
AJ421782.1 gg_id:43442 Hirschia baltica str. DSM 5838T AJ4217
FM202386.1 gg_id:570096 Hirschia sp. str. GSW-2 FM202
AJ227814.1 gg_id:5865 Hyphomonas jannaschiana str. ATCC 33883 (T) AJ2278
CP000158.1 gg_id:162510 Hyphomonas neptunium str. ATCC 15444 CP0001
AF082795.1 gg_id:5870 Hyphomonas rosenbergii str. VP-6 AF0827
EF540362.1 gg_id:217590 oil-shale semi-coke solid waste clone 07B_MJK EF5403
NR_024937.1 gg_id:543637 Hyphomonas adhaerens str. MHS-3; ATCC 43965 NR_024

0	0	0	1	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	1	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	1
0	1	0	0	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	1	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	1	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	0	0
0	1	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae

g__Hyphomonas
g__Hyphomonas
g__Hyphomonas
g__Hyphomonas
g__Maricaulis
g__Maricaulis
g__Maricaulis
g__Maricaulis
g__Maricaulis
g__Maricaulis
g__Maricaulis
g__Oceanicaulis
g__Oceanicaulis
g__Oceanicaulis
g__Oceanicaulis
g__Oceanicaulis
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified
g__unclassified

s__unclassified	60792
s__unclassified	60900
s__unclassified	60972
s__unclassified	61124
s__Maricaulis maris	60478
s__Maricaulis maris	60597
s__Maricaulis virginensis	60849
s__Maricaulis virginensis	60862
s__unclassified	60469
s__unclassified	60611
s__unclassified	61202
s__Oceanicaulis alexandrii	61353
s__unclassified	60410
s__unclassified	60560
s__unclassified	60821
s__unclassified	61165
s__unclassified	60353
s__unclassified	60377
s__unclassified	60391
s__unclassified	60397
s__unclassified	60443
s__unclassified	60465
s__unclassified	60515
s__unclassified	60607
s__unclassified	60610
s__unclassified	60618
s__unclassified	60683
s__unclassified	60684
s__unclassified	60733
s__unclassified	60841
s__unclassified	60877
s__unclassified	60884
s__unclassified	60913
s__unclassified	60918
s__unclassified	60924
s__unclassified	60982
s__unclassified	61113
s__unclassified	61238
s__unclassified	61262
s__unclassified	61273
s__unclassified	61309

DQ396058.1 gg_id:151886 deep-sea octacoral clone ctg_NISA280 DQ396
DQ160243.2 gg_id:139361 Hyphomonas taiwanensis str. HYP1 DQ160
NR_024938.1 gg_id:572877 Hyphomonas johnsonii str. MHS-2; ATCC 43964 NR_02
AF082797.1 gg_id:5859 Hyphomonas oceanitis str. SCH-89 AF082
AJ007807.1 gg_id:5841 Maricaulis maris str. ACM 5106 (T) AJ0078
EU528177.1 gg_id:286163 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AJ301667.1 gg_id:26948 Maricaulis virginensis str. VC 5 AJ3016
DQ768642.1 gg_id:245137 Maricaulis virginensis MARC4M DQ768
FJ797347.1 gg_id:567500 Arenicola marina bioturbated mesocosm marine sediment clone 20 FJ7973
AY162105.1 gg_id:135262 Cultivating Sargasso Sea clone GMD21C01 AY162
NR_025323.1 gg_id:545614 Maricaulis parjimensis str. MCS 25; DSM 16078 NR_02
AJ309862.1 gg_id:40525 Oceanicaulis alexandrii str. C116-18 AJ3098
DQ644012.1 gg_id:236476 Production cyanobacterial toxin Microcystin disease corals black band diseased (BB DQ644
AY701470.1 gg_id:108547 dinoflagellate symbiont clone GCDE08_V AY701
AJ227811.1 gg_id:5847 Caulobacter sp. str. MCS33 AJ2278
GQ441337.1 gg_id:593605 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
FJ152756.1 gg_id:347767 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
DQ395426.1 gg_id:154213 deep-sea octacoral clone ctg_CGOAB48 DQ395
FJ203305.1 gg_id:307703 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
AB286621.1 gg_id:209532 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AF359547.1 gg_id:18991 Scrippsiella trochoidea NEPCC 15 AF359
AY942774.1 gg_id:148699 but species richness marine sponge Cymbastela concentrica clone Cc118 AY942
FJ497641.1 gg_id:542217 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4976
EU881181.1 gg_id:303607 Karst region natural restoration land soil clone KNR200711-027 EU881
AF234756.1 gg_id:18609 sludge clone S36 AF2347
GU118388.1 gg_id:538371 Threatened Corals Provide Microbial Habitats clone Gven_P10 GU118
EU196330.1 gg_id:244514 Investigation heterotrophic and autotrophic microbial perennial springs cold saline (EU196
EU245307.1 gg_id:241958 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-G02 EU245
DQ376579.1 gg_id:150962 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin DQ376
AB294313.1 gg_id:205348 Microbial structure deep coal seem groundwater stream clone SWB02 AB294
AY654758.1 gg_id:105062 Oculina mucus isolate 111 AY6547
AM990862.1 gg_id:278552 Caulobacter sp. MOLA 88 AM990
FM242321.1 gg_id:337659 sequences sediment clone 83 T9d-oil FM242
AJ578477.1 gg_id:102289 Woodsholea maritima str. CM251 AJ5784
AB286463.1 gg_id:208631 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
EF495229.1 gg_id:222908 Croceitomaculum antarcticum str. IMCC3195 EF4952
AJ617875.1 gg_id:110283 oxic-anoxic interphase flooded paddy soil clone D14429 AJ6178
FM242450.1 gg_id:332051 sequences sediment clone 21 T12d+oil FM242
EU665092.1 gg_id:571737 Soil are Changed Agricultural Practices agricultural soil clone Plot22-2G04 EU665
GQ500759.1 gg_id:590926 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Bio-Sep beads conta GQ500
FJ826144.1 gg_id:514038 Succession during spring Sea filtered surface sea water decay period after diatom blo FJ8261

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	1	0
1	0	0	0	0	0	1	1	0	1	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	1	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	1	1	1	1	0	0	1	0	1
0	0	0	1	1	0	0	0	0	0	0	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Hyphomonadaceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae

g__unclassified
g__unclassified
g__unclassified
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Amaricoccus
g__Antarctobacter
g__Catellibacterium
g__Dinoroseobacter
g__Dinoroseobacter
g__Dinoroseobacter
g__Haematobacter
g__Haematobacter
g__Jannaschia
g__Jannaschia
g__Jannaschia
g__Jannaschia
g__Jannaschia
g__Jannaschia
g__Ketogulonicigenium
g__Ketogulonicigenium
g__Ketogulonicigenium
g__Leisingera
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella

s__unclassified	61343
s__unclassified	61361
s__unclassified	61362
s__unclassified	60388
s__unclassified	60802
s__unclassified	61209
s__unclassified	61569
s__unclassified	61590
s__unclassified	61607
s__unclassified	61617
s__unclassified	61690
s__unclassified	61698
s__unclassified	62097
s__unclassified	62573
s__unclassified	62841
s__Antarctobacter heliothermus	61836
s__unclassified	61877
s__Dinoroseobacter shibae	62645
s__unclassified	61974
s__unclassified	62214
s__Haematobacter massiliensis	61518
s__Haematobacter massiliensis	61861
s__Jannaschia helgolandensis	61623
s__unclassified	61421
s__unclassified	61459
s__unclassified	62326
s__unclassified	62842
s__unclassified	62858
s__Ketogulonicigenium vulgare	62167
s__unclassified	61395
s__unclassified	62044
s__unclassified	61716
s__Loktanella salsilacus	62475
s__Loktanella tamlensis	62611
s__Loktanella vestfoldensis	61611
s__Loktanella vestfoldensis	61702
s__unclassified	61429
s__unclassified	61488
s__unclassified	61532
s__unclassified	61641
s__unclassified	61687

AY921760.1 gg_id:112748 farm soil clone AKYH1490 AY921
FJ516864.1 gg_id:565583 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s FJ5168
GU444088.1 gg_id:530619 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
EU491552.1 gg_id:263491 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR4C EU491
EU236280.1 gg_id:296183 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5aCo7 EU236
EU236341.1 gg_id:298881 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a2G5 EU236
EU104323.1 gg_id:309713 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
GQ441341.1 gg_id:581650 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
NR_026060.1 gg_id:570345 Amaricoccus tamworthensis str. Ben103; ACM 5097 NR_02
U88042.1 gg_id:5811 Amaricoccus macauensis str. Ben104 U8804
DQ130031.1 gg_id:151324 microbial biota normal forearm human skin clone GL97 DQ130
NR_029203.1 gg_id:580499 Amaricoccus veronensis str. Ben102; ACM 5098 NR_02
FJ152897.1 gg_id:336456 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
DQ346506.1 gg_id:154801 during composting libraries compost clone 2B22 DQ346
FJ152955.1 gg_id:323451 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
EF489005.1 gg_id:245310 Antarctobacter sp. str. TG22 EF489
EU053204.1 gg_id:246019 Catellibacterium terrae str. QMT-4 EU053
NC_009952.1 gg_id:250733 Dinoroseobacter shibae str. DFL 12 NC_00
FJ202183.1 gg_id:343990 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
DQ289933.1 gg_id:167723 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable Sh DQ289
AF452106.1 gg_id:62868 Rhodobacter massiliensis str. Framboise AF452
DQ342310.1 gg_id:205946 Haematobacter massiliensis str. H2443 DQ342
AJ534225.1 gg_id:75300 Jannaschia helgolandensis HEL-43 AJ5342
AM990650.1 gg_id:278279 culturable oligotrophic ocean (South Pacific Gyre) sea water AM990
AJ748747.1 gg_id:110922 Jannaschia rubra str. 4SM3 AJ7487
AY906862.1 gg_id:112620 Jannaschia sp. str. CL-SP26 AY9068
EF202612.1 gg_id:200932 Jannaschia donghaensis str. DSW-17 EF2026
DQ643999.1 gg_id:159971 Jannaschia pohangensis DQ643
EU034641.1 gg_id:253055 Ketogulonicigenium vulgare str. VC-2-2 EU034
DQ915605.1 gg_id:320216 Ketogulonicigenium robustum str. NRRL B-12627 DQ915
AF136849.1 gg_id:135903 Ketogulonicigenium vulgare str. DSM 4025 AF1368
AY005463.1 gg_id:45273 Leisingera methylohalidivorans str. MB2 AY0054
AJ582229.1 gg_id:93357 Loktanella salsilacus str. LMG 22002 AJ5822
DQ533555.1 gg_id:163668 Loktanella tamlensis str. SSW-27 DQ533
FJ172067.1 gg_id:327793 Microbial athalassohaline Tirez lagoon (Spain) water clone MJZ2 FJ1720
AJ582227.1 gg_id:94079 Loktanella vestfoldensis str. LMG 22006 AJ5822
AY576770.1 gg_id:138842 Ruegeria sp. str. 3X/A02/236 AY5767
AF173971.1 gg_id:73505 Roseobacter sp. str. KT1117 AF1739
FJ172062.1 gg_id:354977 Microbial athalassohaline Tirez lagoon (Spain) water clone MJW2 FJ1720
EF659438.1 gg_id:246665 within Poole Harbour seawater clone PH-F10 EF6594
AM691092.1 gg_id:220404 Rhodobacteraceae clone EG3 AM691

1	1	1	1	1	1	1	1	0	0	1	0	0
1	1	1	0	0	0	1	1	1	0	0	1	1
0	0	0	0	0	1	0	0	1	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	1	1	0	0	1	1	0
0	0	1	1	1	1	1	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	1	0	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae

g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Loktanella
g__Maribius
g__Marinovum
g__Marinovum
g__Marinovum
g__Marinovum
g__Marivita
g__Marivita
g__Marivita
g__Marivita
g__Marivita
g__Marivita
g__Methylarcula
g__Methylarcula
g__Methylarcula
g__Methylarcula
g__Nautella
g__Nautella
g__Nautella
g__Nautella
g__Nautella
g__Nautella
g__Nautella
g__Nautella
g__Nautella
g__Nereida
g__Oceanibulbus
g__Oceanibulbus
g__Oceanibulbus

s__unclassified	61703
s__unclassified	61743
s__unclassified	61768
s__unclassified	61939
s__unclassified	61940
s__unclassified	61976
s__unclassified	62042
s__unclassified	62098
s__unclassified	62254
s__unclassified	62346
s__unclassified	62430
s__unclassified	62756
s__unclassified	62835
s__unclassified	62801
s__Marinovum algicola	61613
s__Marinovum algicola	61990
s__unclassified	61784
s__unclassified	61832
s__unclassified	61577
s__unclassified	61952
s__unclassified	62005
s__unclassified	62058
s__unclassified	62294
s__unclassified	62850
s__Loktanella hongkongensis	61521
s__unclassified	61760
s__unclassified	61890
s__unclassified	61959
s__Nautella italica	62391
s__unclassified	61444
s__unclassified	61668
s__unclassified	61819
s__unclassified	61838
s__unclassified	62377
s__unclassified	62455
s__unclassified	62780
s__unclassified	62859
s__unclassified	62822
s__Oceanibulbus indolifex	62274
s__Oceanibulbus indolifex	62347
s__Oceanibulbus indolifex	62817

AJ505786.1 gg_id:61254 coastal sediment clone AJ5057
FJ152873.1 gg_id:328838 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1528
FJ716887.1 gg_id:510302 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7168
DQ397336.1 gg_id:153999 Thalassobius sp. str. UST050418-052 DQ397
GU061095.1 gg_id:592005 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone TFS- GU061
DQ344498.1 gg_id:145649 Loktanella koreensis str. GA2-M3 DQ344
AY167339.1 gg_id:81378 Roseobacter sp. str. ARK9990 AY1673
FJ203462.1 gg_id:307704 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
AJ505788.2 gg_id:61250 coastal sediment clone AJ5057
FJ889546.1 gg_id:563888 Phaeobacter sp. str. ZS356 FJ8895
AY654808.1 gg_id:103608 Oculina mucus isolate 78 AY6548
AY654838.1 gg_id:100870 Oculina mucus isolate 40 AY6548
AF170751.1 gg_id:5658 Roseobacter sp. str. QSSC9-8 AF1707
DQ514326.1 gg_id:161345 Maribius bermudensis str. B5-6 DQ514
AY162102.1 gg_id:135261 Cultivating Sargasso Sea clone GMD21D01 AY1621
X78313.1 gg_id:5670 Ruegeria algicola str. ATCC 51441ML4 X78313
AB491842.1 gg_id:557828 affiliation (Litopenaeus vannamei) Banyuwangi East Java microbial flocs floating brac AB4918
AJ633967.1 gg_id:114827 host's accessory nidamental gland clone T65ANG1 AJ6339
FJ716854.1 gg_id:541703 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7168
AJ295988.1 gg_id:26995 Ruegeria aff. gelatinovorans str. ch611 AJ2959
EU592330.1 gg_id:539299 Seasonal changes Salton Sea hypersaline water clone SSW55N EU5923
AY258078.1 gg_id:135688 Ruegeria sp. str. DG882 AY2580
AY344411.1 gg_id:91079 Lake Kauhako surface clone K2-S-32 AY3444
GU324080.1 gg_id:556772 Marivita sp. str. CB 1101 GU324
AY600300.1 gg_id:103542 Loktanella hongkongensis str. UST950701-009P AY6003
FN431787.1 gg_id:544367 Loktanella hongkongensis str. AMV3 AMV18 FN4317
AM983542.1 gg_id:537512 Loktanella pyoseonensis str. JJM85 AM983
EU143345.1 gg_id:252067 Loktanella sp. str. J20 EU1433
AM944522.1 gg_id:268667 Nautella italica str. R-28753 AM944
FJ202078.1 gg_id:310849 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
FJ202115.1 gg_id:343849 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
EU592375.1 gg_id:583983 Seasonal changes Salton Sea hypersaline water clone SSW89Au EU5923
EF092158.1 gg_id:267120 Persistent Axinella corrugata Roseobacter clone AC2_A2 EF0921
DQ675021.1 gg_id:162482 Pseudoruegeria aquimaris str. SW-255 DQ675
DQ917854.1 gg_id:219732 Microbial profiles bleached and wild-type Muricea elongata clone BME80 DQ917
FJ202604.1 gg_id:318096 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2026
FJ202395.1 gg_id:319436 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2023
DQ915613.1 gg_id:346324 Nereida ignava str. CECT5292 DQ915
DQ915614.1 gg_id:327289 Oceanibulbus indolifex str. DSM14862 DQ915
NR_027563.1 gg_id:544041 Oceanibulbus indolifex HEL-45 str. Hel-45; DSM 14862 NR_02
EU694388.1 gg_id:293008 Oceanibulbus indolifex str. D15 EU6943

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae

g__Oceanicola
g__Oceanicola
g__Oceanicola
g__Oceanicola
g__Oceanicola
g__Octadecabacter
g__Octadecabacter
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus

s__Oceanicola batsensis	62655
s__Oceanicola granulosus	62940
s__unclassified	62534
s__unclassified	62674
s__unclassified	62867
s__Octadecabacter antarcticus	61642
s__unclassified	61988
s__Methylarcula terricola	61755
s__Methylarcula terricola	61989
s__Paracoccus alcaliphilus	62258
s__Paracoccus alcaliphilus	62497
s__Paracoccus aminovorans	61909
s__Paracoccus aminovorans	62003
s__Paracoccus aminovorans	62521
s__Paracoccus aminovorans	62750
s__Paracoccus aminovorans	62769
s__Paracoccus denitrificans	61553
s__Paracoccus denitrificans	61895
s__Paracoccus denitrificans	62627
s__Paracoccus denitrificans	62837
s__Paracoccus marcusii	62018
s__Paracoccus marcusii	62435
s__Paracoccus marcusii	62657
s__Paracoccus solventivorans	61436
s__Paracoccus versutus	61691
s__Paracoccus versutus	61736
s__Paracoccus versutus	62420
s__Paracoccus versutus	62461
s__Paracoccus versutus	62936
s__Paracoccus yeei	62585
s__Paracoccus yeei	62831
s__Paracoccus zeaxanthinifaciens	61767
s__Paracoccus zeaxanthinifaciens	62333
s__Paracoccus zeaxanthinifaciens	62614
s__unclassified	61403
s__unclassified	61491
s__unclassified	61523
s__unclassified	61526
s__unclassified	61603
s__unclassified	61621
s__unclassified	61624

NZ_AAMO01000005.1 gg_id:146037 Oceanicola batsensis str. HTCC2597	NZ_AA
DQ915616.1 gg_id:305517 Oceanicola granulosus str. KCTC12143	DQ915
GQ250665.1 gg_id:544324 bulk sea water column Gulf Mexico clone GOM_WB10-7	GQ250
AB166982.1 gg_id:101280 Roseobacter sp. str. NT N37	AB166
FJ230846.1 gg_id:341497 marine str. SD7	FJ2308
FJ196062.1 gg_id:310847 Octadecabacter sp. str. ZS6-9	FJ1960
AB180384.1 gg_id:109216 Octadecabacter sp. str. No. 49	AB180
AF030437.1 gg_id:5737 Methylarcula terricola str. h37; VKM B-2160	AF0304
AF030436.1 gg_id:5762 Methylarcula terricola str. h1; VKM B-2159	AF0304
DQ402044.1 gg_id:150822 Paracoccus alcaliphilus str. mku-E2	DQ402
DQ469585.1 gg_id:158059 Paracoccus alcaliphilus str. Sty2-VH	DQ469
D32240.1 gg_id:5761 Paracoccus aminovorans str. JCM 7685	D3224
GQ497295.1 gg_id:552938 Paracoccus sp. str. KSL5401-001	GQ497
GU201846.1 gg_id:518236 Paracoccus aminophilus str. Zw-11	GU201
AY312056.1 gg_id:88947 Paracoccus sp. Ol18	AY312
AF376134.1 gg_id:24018 Paracoccus sp. str. T231	AF376
FM207553.1 gg_id:348847 Paracoccus denitrificans E4	FM207
FJ381982.1 gg_id:582190 Potentially pathogenic and air stem cell transplant winter hospital shower water BMT	FJ3819
EF070124.1 gg_id:190880 Paracoccus sp. TRP	EF0701
DQ539490.1 gg_id:169913 Paracoccus sp. SBRD2	DQ539
DQ270723.1 gg_id:142241 Pseudomonas sp. B-1015	DQ270
AF139992.1 gg_id:5771 Paracoccus marcusii str. ML-003	AF139
AJ582185.1 gg_id:93958 soil near uranium mill tailings clone Gitt-GS-149	AJ5821
AY014175.1 gg_id:47316 Paracoccus solventivorans str. ATCC 700252	AY014
FJ950555.1 gg_id:410450 Paracoccus versutus str. c75	FJ9505
EU434343.1 gg_id:275527 Paracoccus versutus str. a266	EU4343
DQ512861.1 gg_id:159464 Paracoccus sp. str. LW36	DQ512
AY004210.1 gg_id:28386 Paracoccus versutus str. kps	AY0042
EU434456.1 gg_id:276317 Paracoccus versutus str. a234	EU4344
FM872636.1 gg_id:369875 occupant source house floor dust clone FA04D10	FM872
AY014179.1 gg_id:46743 Paracoccus yeei str. G3060	AY014
GU108563.1 gg_id:545865 active chemolithoautotrophic prokaryotes sulfidic zone Black pelagic redoxcline dete	GU108
FJ713782.2 gg_id:571011 Paracoccus sp. str. DEH99	FJ7137
AB275604.1 gg_id:212709 Paracoccus kamogawaensis str. YSFL3	AB2756
AJ864466.1 gg_id:109475 Paracoccus pantotrophus str. JT001	AJ8644
GQ250442.1 gg_id:577514 Paracoccus sp. str. MJ17	GQ250
AB025189.1 gg_id:5770 Paracoccus sp. str. MBIC4018 HI7	AB025
DQ923133.1 gg_id:180344 Paracoccus halotolerans str. YIM 90738	DQ923
D32238.1 gg_id:5766 Paracoccus alcaliphilus str. JCM 7364	D32238
DQ108402.1 gg_id:137632 Paracoccus sp. Tibet-S9a3	DQ108
FJ842690.1 gg_id:576262 Paracoccus sp. str. NII-0918	FJ8426

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	1	1	0	1	0	0	0	0	1	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	0	1	0	1	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria

o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae
o__Rhodobacterales	f__Rhodobacteraceae

g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus
g__Paracoccus

s__unclassified	61637
s__unclassified	61788
s__unclassified	61821
s__unclassified	61893
s__unclassified	61946
s__unclassified	61965
s__unclassified	61973
s__unclassified	61984
s__unclassified	62015
s__unclassified	62022
s__unclassified	62072
s__unclassified	62077
s__unclassified	62082
s__unclassified	62126
s__unclassified	62178
s__unclassified	62204
s__unclassified	62220
s__unclassified	62221
s__unclassified	62256
s__unclassified	62267
s__unclassified	62280
s__unclassified	62328
s__unclassified	62348
s__unclassified	62358
s__unclassified	62371
s__unclassified	62401
s__unclassified	62476
s__unclassified	62581
s__unclassified	62642
s__unclassified	62672
s__unclassified	62697
s__unclassified	62719
s__unclassified	62733
s__unclassified	62734
s__unclassified	62791
s__unclassified	62820
s__unclassified	62830
s__unclassified	62846
s__unclassified	62890
s__unclassified	62916
s__unclassified	62928

EU341164.1 gg_id:238449 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU341
AY626831.1 gg_id:103986 Paracoccus sp. str. QD5-2-1 AY6268
AM697590.1 gg_id:225243 sequencing libraries indoor dust clone BF0002D101 AM697
DQ423482.1 gg_id:155546 Paracoccus sp. str. HN-182 DQ423
EU196530.1 gg_id:241681 Paracoccus sp. Ol18 EU1965
FJ670987.1 gg_id:527854 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6709
FJ675504.1 gg_id:532336 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
AM231051.1 gg_id:159385 Paracoccus sp. str. R-24342 AM231
AJ864463.1 gg_id:109472 Paracoccus thiocyanatus str. SST AJ8644
FJ675534.1 gg_id:519944 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
AY573045.1 gg_id:106521 Paracoccus sp. str. ARCTIC-P17 AY5730
AJ534231.1 gg_id:202277 Methylarcula sp. HEL-8 AJ5342
AB255110.1 gg_id:172587 corroded concrete clone SC-148 AB2551
FM874023.1 gg_id:370368 occupant source house mattress dust clone MB05C10 FM874
DQ116009.1 gg_id:130794 bovine teat canal clone D-64 DQ116
DQ337586.1 gg_id:150080 Paracoccus sp. BBTR62 DQ337
FJ774966.1 gg_id:559136 Symbionts Brown Planthopper (Homoptera: Delphacidae) symbiont Nilaparvata luger FJ7749
EU368762.1 gg_id:267622 Paracoccus sp. str. B61 Ydz-zz EU3687
DQ129626.1 gg_id:138528 microarray level air two cities Texas urban aerosol clone AKIW1050 DQ129
GQ129980.1 gg_id:370584 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
DQ532252.1 gg_id:165945 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space Ce DQ532
D32239.1 gg_id:5758 Paracoccus aminophilus str. JCM 7686 D32239
AB264130.1 gg_id:165184 Paracoccus sp. str. TDMA-10 AB2641
GQ260189.1 gg_id:588165 Paracoccus sp. str. 22-5 GQ260
D32241.1 gg_id:5779 Paracoccus kocurii str. JCM 7684 D32241
AM900779.1 gg_id:235419 Paracoccus sp. PA216 AM900
AY167832.1 gg_id:77519 Paracoccus sp. str. SAFR-029 AY1678
AB264129.1 gg_id:164471 Paracoccus sp. str. TDMA-8 AB2641
AM990798.1 gg_id:279292 Paracoccus sp. MOLA 22 AM990
EF157164.1 gg_id:237879 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
FJ267566.1 gg_id:323776 Paracoccus sp. str. II_Gauze_W_10_18 FJ2675
FJ658279.1 gg_id:570280 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6582
AB098589.1 gg_id:78216 Paracoccus sp. str. TUT1021 AB0985
AB185957.1 gg_id:265461 Paracoccus marinus str. KKL-A5 AB1859
DQ856507.1 gg_id:243813 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1I DQ856
GQ452286.1 gg_id:582083 Paracoccus sp. str. MU2A-22 GQ452
AJ580352.1 gg_id:107767 Paracoccus sp. BOG6 AJ5803
AB012914.1 gg_id:5765 Paracoccus sp. str. MBIC3345 Y4 AB0129
AM084041.1 gg_id:139889 Paracoccus sp. str. R-24616 AM084
AB024613.1 gg_id:5740 Paracoccus sp. str. MBIC1145 AB0246
FJ210812.1 gg_id:323743 Paracoccus sp. str. QDHT-17 FJ2108

0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	0	0	0	1	1	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria
k__Bacteria	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria