Supplementary Table 1

GI number	Protein Length	BLASTCLUST cluster number	Transposons analyzed in this work	Phylum	Organism	Count per organism	Taxonomy
196183795	398	24	ISC1-1_CC	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
297547772	366	62	ISC1-1_KR	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
166086237	380	4	ISC1-1_MA	Cyanobacteria	Microcystis aeruginosa NIES-843	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa NIES-843
432001730	426	12	ISC2-1_AF	Firmicutes	Anoxybacillus flavithermus TNO-09.006	6	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus
769148683	470	72	ISC2-1_AH	Firmicutes	Anaerostipes hadrus	6	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus
516257699	427	21	ISC2-1_GS	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
433669275	419	126	ISC2-1_HH	Firmicutes	Halobacteroides halobius DSM 5150	3	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Halobacteroides,Halobacteroides halobius
297550215	429	8	ISC2-1_KR	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
805378795	438	3	ISC2-1_ML	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
126627116	447	11	ISC2-1_MS	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
291580488	427	54	ISC2-1_NH	Proteobacteria	Nitrosococcus halophilus Nc 4	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
528102090	429	19	ISC2-1_SM	Proteobacteria	Salipiger mucosus DSM 16094	4	Bacteria,Proteobacteria,Alphaproteobacteria,Rhodobacterales,Rhodobacteraceae,Salipiger,Salipiger mucosus
564132996	416	13	ISC2-1_YF	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1
658102102	450	48	ISC2Y-1_CH	Firmicutes	Clostridium haemolyticum NCTC 9693	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium haemolyticum
851246344	429	1		Euryarchaeota	Methanosarcina	2	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina
851247265	374	1		Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris

851246032	412	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241515	414	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241545	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241616	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851243101	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851240625	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851239624	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851240934	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241705	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241756	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851242384	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851238877	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241492	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851240156	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851242228	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris

851243919	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851239942	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241713	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851242838	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851239344	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851242567	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241676	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851245052	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241227	427	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851244192	429	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851243768	430	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
919167324	433	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851238328	448	1	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
805378796	457	1	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
851298689	426	1	Euryarchaeota	Methanosarcina sp. 1.H.A.2.2	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 1.H.A.2.2

851257057	426	1	Euryarchaeota	Methanosarcina sp. 1.H.T.1A.1	1	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 1.H.T.1A.1
851275145	426	1	Euryarchaeota	Methanosarcina sp. 2.H.T.1A.15	1	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.T.1A.15
851296580	426	1	Euryarchaeota	Methanosarcina sp. 2.H.T.1A.6	1	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.T.1A.6
851310953	421	1	Euryarchaeota	Methanosarcina sp. 2.H.T.1A.8	1	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.T.1A.8
805341356	414	1	Euryarchaeota	Methanosarcina sp. WH1	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WH1
851245944	427	1	Euryarchaeota	Methanosarcina sp. WH1	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WH1
851242202	429	1	Euryarchaeota	Methanosarcina sp. WH1	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WH1
851295935	427	1	Euryarchaeota	Methanosarcina sp. WWM596	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WWM596
493671516	423	2	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
915401517	409	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493721134	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493719933	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493719194	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493718356	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493721283	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493721103	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
493720167	423	2	Cyanobacteria	Arthrospira maxima	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima
209494659	402	2	Cyanobacteria	Arthrospira maxima CS-328	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima,Arthrospira maxima CS-328

493671654	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
493675308	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
493674113	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
493672300	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
493671246	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
504042804	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
493672164	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
504040676	423	2	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
375328713	402	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
375324714	402	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
890649894	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
495332043	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
890650142	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
495327223	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
495331526	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
495332312	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
495326132	423	2	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
809069684	423	2	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091
809068281	423	2	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091
809073352	423	2	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091

851246686	420	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851243214	438	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851240484	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851242080	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241805	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241077	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851239015	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851243036	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241624	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851241674	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851238917	439	3	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
805378300	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805379011	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805378884	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289

805378537	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805377617	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805379346	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805378765	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805377559	438	3	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
814871849	438	3	Euryarchaeota	Methanosarcina sp. 1.H.A.2.2	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 1.H.A.2.2
851298865	439	3	Euryarchaeota	Methanosarcina sp. 1.H.A.2.2	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 1.H.A.2.2
814724486	438	3	Euryarchaeota	Methanosarcina sp. 2.H.A.1B.4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.A.1B.4
851309945	439	3	Euryarchaeota	Methanosarcina sp. 2.H.A.1B.4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.A.1B.4
779874673	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
754188235	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488888475	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
501224371	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
779880012	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488856157	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
490387313	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa

488844531	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
817700858	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488848557	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
817698218	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488886060	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488880825	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
640537249	365	4	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
815963769	351	4	Cyanobacteria	Microcystis aeruginosa NIES-2549	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa NIES-2549
917762543	365	4	Cyanobacteria	Microcystis panniformis	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis
917762473	365	4	Cyanobacteria	Microcystis panniformis	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis
917763954	365	4	Cyanobacteria	Microcystis panniformis	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis
917762695	365	4	Cyanobacteria	Microcystis panniformis	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis
917761925	365	4	Cyanobacteria	Microcystis panniformis	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis
117530342	382	4	Viruses	Microcystis aeruginosa phage Ma-LMM01	1	Viruses,dsDNA viruses, no RNA stage,Caudovirales,Myoviridae,unassigned Myoviridae,Microcystis aeruginosa phage Ma-LMM01
525337077	365	4	Viruses	Microcystis phage MaMV-DC	1	Viruses,dsDNA viruses, no RNA stage,Caudovirales,Myoviridae,unclassified Myoviridae,Microcystis phage MaMV-DC
647622615	423	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
737176139	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
489712947	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
737199151	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii

737185631	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
503204504	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
737186250	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
737198348	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
737174679	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
737179446	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
511762573	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
489707312	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
647622816	442	5	Firmicutes	Lactobacillus delbrueckii	13	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii
495738552	442	5	Firmicutes	Lactobacillus equicursoris	3	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equicursoris
497243645	442	5	Firmicutes	Lactobacillus equicursoris	3	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equicursoris
495738712	442	5	Firmicutes	Lactobacillus equicursoris	3	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equicursoris
909655295	173	6	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488836987	177	6	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488855489	177	6	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488857866	177	6	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
159030839	177	6	Cyanobacteria	Microcystis aeruginosa PCC 7806	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 7806
389767976	177	6	Cyanobacteria	Microcystis aeruginosa PCC 7941	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 7941
389800064	164	6	Cyanobacteria	Microcystis aeruginosa PCC 9807	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 9807

389802092	177	6	Cyanobacteria	Microcystis aeruginosa PCC 9807	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 9807
917763287	164	6	Cyanobacteria	Microcystis panniformis	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis
389834663	177	6	Cyanobacteria	Microcystis sp. T1-4	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis sp. T1-4
489796450	421	7	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
736986416	453	7	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
736994528	453	7	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
736988255	453	7	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
489802478	453	7	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
490700428	453	7	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
574962803	452	7	Firmicutes	Lactobacillus salivarius cp400	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius,Lactobacillus salivarius cp400
334307204	452	7	Firmicutes	Lactobacillus salivarius NIAS840	2	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius,Lactobacillus salivarius NIAS840
380343618	452	7	Firmicutes	Lactobacillus salivarius SMXD51	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius,Lactobacillus salivarius SMXD51
495179012	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495190859	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495198001	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495197686	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495192414	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495184282	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495181058	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer

495182429	429	8	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
504896402	425	9	Cyanobacteria	Anabaena sp. 90	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena sp. 90
764892656	382	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
516414605	419	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
493210787	424	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
493207436	425	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
493212482	425	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
516414312	425	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
493208735	425	9	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
585119765	404	9	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
755618581	419	10	Firmicutes	Anoxybacillus ayderensis	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus ayderensis
765537962	409	10	Firmicutes	Anoxybacillus sp. ATCC BAA-2555	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus sp. ATCC BAA-2555
503962154	419	10	Firmicutes	Geobacillus	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus
514404880	406	10	Firmicutes	Geobacillus kaustophilus GBlys	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus kaustophilus,Geobacillus kaustophilus GBlys
544911901	420	10	Firmicutes	Geobacillus sp. A8	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus sp. A8
836606303	412	10	Firmicutes	Geobacillus sp. ZGt-1	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus sp. ZGt-1
902597013	409	10	Firmicutes	Geobacillus stearothermophilus	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus stearothermophilus
902592849	419	10	Firmicutes	Geobacillus stearothermophilus	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus stearothermophilus
618754134	417	10	Firmicutes	Geobacillus thermoleovorans B23	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus thermoleovorans group,Geobacillus thermoleovorans,Geobacillus thermoleovorans B23
517216644	434	11	Proteobacteria	Marinobacter lipolyticus	4	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter lipolyticus

517214180	436	11	Proteobacteria	Marinobacter lipolyticus	4	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter lipolyticus
494593180	434	11	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
494591835	434	11	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
738230227	434	11	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
494592943	434	11	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
494592612	434	11	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
755615045	426	12	Firmicutes	Anoxybacillus ayderensis	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus ayderensis
755177284	438	12	Firmicutes	Anoxybacillus ayderensis	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus ayderensis
491030539	426	12	Firmicutes	Anoxybacillus flavithermus	6	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus
491027649	426	12	Firmicutes	Anoxybacillus flavithermus	6	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus
493364910	426	12	Firmicutes	Anoxybacillus flavithermus	6	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus
491030759	434	12	Firmicutes	Anoxybacillus flavithermus	6	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus
544660233	426	12	Firmicutes	Anoxybacillus sp. SK3-4	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus sp. SK3-4
917405157	404	13	Firmicutes	Youngiibacter fragilis	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis
917405158	404	13	Firmicutes	Youngiibacter fragilis	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis
917405134	404	13	Firmicutes	Youngiibacter fragilis	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis
750625864	404	13	Firmicutes	Youngiibacter fragilis	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis
564132572	416	13	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1

564132569	416	13	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1
564133424	416	13	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1
524001916	414	14	Proteobacteria	Parasutterella excrementihominis CAG:233	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,environmental samples,Parasutterella excrementihominis CAG:233
496140621	414	14	Proteobacteria	Parasutterella excrementihominis	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis
496140300	414	14	Proteobacteria	Parasutterella excrementihominis	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis
748638366	398	14	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
302858730	411	14	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
496086763	414	14	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
524280884	396	14	Proteobacteria	Proteobacteria bacterium CAG:139	1	Bacteria,Proteobacteria,environmental samples,Proteobacteria bacterium CAG:139
815716624	414	14	Proteobacteria	Acinetobacter sp. N54.MGS-139	1	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Moraxellaceae,Acinetobacter,Acinetobacter sp. N54.MGS-139
740164447	400	15	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis
740163468	400	15	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis
740163470	400	15	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis
740164133	400	15	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis

404657206	390	15	Proteobacteria	Sutterella wadsworthensis 2_1_59BFAA	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis,Sutterella wadsworthensis 2_1_59BFAA
404658376	390	15	Proteobacteria	Sutterella wadsworthensis 2_1_59BFAA	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis,Sutterella wadsworthensis 2_1_59BFAA
404658162	390	15	Proteobacteria	Sutterella wadsworthensis 2_1_59BFAA	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis,Sutterella wadsworthensis 2_1_59BFAA
404657559	390	15	Proteobacteria	Sutterella wadsworthensis 2_1_59BFAA	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis,Sutterella wadsworthensis 2_1_59BFAA
696533158	437	16	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
752487288	437	16	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
696533105	437	16	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
752487569	437	16	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
749188410	440	16	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
169408891	440	16	Firmicutes	Clostridium botulinum A3 str. Loch Maree	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum,Clostridium botulinum A,Clostridium botulinum A3 str. Loch Maree
229260342	445	16	Firmicutes	Clostridium botulinum Ba4 str. 657	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum,Clostridium botulinum B,Clostridium botulinum Ba4 str. 657
493720362	379	17	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
493671347	380	17	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
493718402	380	17	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
493670882	379	17	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
375323701	350	17	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
375324149	351	17	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
890645632	379	17	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005

493575037	136	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493576568	146	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493574048	146	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493574420	153	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493574344	154	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493576467	155	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493575899	155	18	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
544688317	429	19	Proteobacteria	Salipiger mucosus	4	Bacteria,Proteobacteria,Alphaproteobacteria,Rhodobacterales,Rhodobacteraceae,Salipiger,Salipiger mucosus
739512799	429	19	Proteobacteria	Salipiger mucosus	4	Bacteria,Proteobacteria,Alphaproteobacteria,Rhodobacterales,Rhodobacteraceae,Salipiger,Salipiger mucosus
739511681	429	19	Proteobacteria	Salipiger mucosus	4	Bacteria,Proteobacteria,Alphaproteobacteria,Rhodobacterales,Rhodobacteraceae,Salipiger,Salipiger mucosus
528096348	396	19	Proteobacteria	Salipiger mucosus DSM 16094	2	Bacteria,Proteobacteria,Alphaproteobacteria,Rhodobacterales,Rhodobacteraceae,Salipiger,Salipiger mucosus,Salipiger mucosus DSM 16094
528101823	396	19	Proteobacteria	Salipiger mucosus DSM 16094	2	Bacteria,Proteobacteria,Alphaproteobacteria,Rhodobacterales,Rhodobacteraceae,Salipiger,Salipiger mucosus,Salipiger mucosus DSM 16094
513846822	253	20	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
754187657	253	20	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
488839845	253	20	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
490262043	253	20	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
763155486	267	20	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
166088064	239	20	Cyanobacteria	Microcystis aeruginosa NIES-843	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa NIES-843
516259361	427	21	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105

516259032	427	21	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
516257403	444	21	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
516257346	460	21	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
750141485	429	22	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495191494	429	22	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
750138303	429	22	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297550437	451	22	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
297556221	451	22	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
737470902	433	23	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
737472716	433	23	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
737471974	434	23	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
737471968	434	23	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
737470939	434	23	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
763348503	361	24	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
493036497	395	24	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
493031176	396	24	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196180960	433	24	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
511077203	384	25	Firmicutes	Firmicutes bacterium M10-2	5	Bacteria,Firmicutes,unclassified Firmicutes sensu stricto,unclassified Firmicutes sensu stricto (miscellaneous),Firmicutes bacterium M10-2

737132088	404	25	Firmicutes	Firmicutes bacterium M10-2	5	Bacteria,Firmicutes,unclassified Firmicutes sensu stricto,unclassified Firmicutes sensu stricto (miscellaneous),Firmicutes bacterium M10-2
737132074	404	25	Firmicutes	Firmicutes bacterium M10-2	5	Bacteria,Firmicutes,unclassified Firmicutes sensu stricto,unclassified Firmicutes sensu stricto (miscellaneous),Firmicutes bacterium M10-2
507803517	416	25	Firmicutes	Firmicutes bacterium M10-2	5	Bacteria,Firmicutes,unclassified Firmicutes sensu stricto,unclassified Firmicutes sensu stricto (miscellaneous),Firmicutes bacterium M10-2
507803696	416	25	Firmicutes	Firmicutes bacterium M10-2	5	Bacteria,Firmicutes,unclassified Firmicutes sensu stricto,unclassified Firmicutes sensu stricto (miscellaneous),Firmicutes bacterium M10-2
494521216	379	26	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
546219268	379	26	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
546208388	379	26	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
546232739	379	26	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
494515958	379	26	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
251771045	513	27	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
251771513	517	27	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
251771487	517	27	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
251770992	517	27	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
530562619	471	28	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
530560308	475	28	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II

530563372	475	28	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
530562068	475	28	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
916888290	456	29	Proteobacteria	Burkholderia sp. BT03	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia sp. BT03
576726017	469	29	Proteobacteria	Burkholderia sp. BT03	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia sp. BT03
916323178	456	29	Proteobacteria	Burkholderia terrae	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia terrae
389936164	469	29	Proteobacteria	Burkholderia terrae BS001	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia terrae,Burkholderia terrae BS001
251772633	443	30	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
251771704	456	30	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
251773312	456	30	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
251771591	456	30	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
916345279	452	31	Proteobacteria	Marinobacter lipolyticus	4	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter lipolyticus
494592450	434	31	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
494591841	434	31	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
494590156	434	31	Proteobacteria	Marinobacter sp. ELB17	9	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter sp. ELB17
502735286	449	32	Proteobacteria	Allochromatium vinosum	5	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Allochromatium,Allochromatium vinosum
502735669	449	32	Proteobacteria	Allochromatium vinosum	5	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Allochromatium,Allochromatium vinosum
502736417	449	32	Proteobacteria	Allochromatium vinosum	5	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Allochromatium,Allochromatium vinosum

502735804	449	32	Proteobacteria	Allochromatium vinosum	5	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Allochromatium,Allochromatium vinosum
489801486	434	33	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
763126085	440	33	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
736994526	442	33	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
334307171	434	33	Firmicutes	Lactobacillus salivarius NIAS840	2	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius,Lactobacillus salivarius NIAS840
495198391	429	34	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495182125	429	34	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
750138239	430	34	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297556095	429	34	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
78499555	425	35	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
504041472	425	35	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
504041485	429	35	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
737767765	429	35	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
357264392	427	36	Cyanobacteria	Crocosphaera watsonii WH 0003	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0003
543527372	401	36	Cyanobacteria	Crocosphaera watsonii WH 0005	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0005
543431877	401	36	Cyanobacteria	Crocosphaera watsonii WH 0401	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0401
67855965	401	36	Cyanobacteria	Crocosphaera watsonii WH 8501	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 8501
516255434	382	37	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105

516258864	382	37	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
516255175	382	37	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
516255773	384	37	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
302859443	283	38	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
302860852	289	38	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
748637811	289	38	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
914924593	290	38	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
919167262	226	39	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851247240	239	39	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
919167320	255	39	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851265821	239	39	Euryarchaeota	Methanosarcina sp. 2.H.T.1A.3	2	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.T.1A.3
750682808	195	40	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
738948966	195	40	Cyanobacteria	Planktothrix mougeotii	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix mougeotii
763056272	195	40	Cyanobacteria	Planktothrix prolifica	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix prolifica
763054849	182	40	Cyanobacteria	Planktothrix rubescens	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix rubescens

493575083	138	41	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493575284	152	41	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493574247	155	41	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493574266	167	41	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
500121981	464	42	Proteobacteria	Polaromonas naphthalenivorans	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas naphthalenivorans
752729499	464	42	Proteobacteria	Polaromonas naphthalenivorans	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas naphthalenivorans
120593573	481	42	Proteobacteria	Polaromonas naphthalenivorans CJ2	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas naphthalenivorans,Polaromonas naphthalenivorans CJ2
506389042	471	43	Firmicutes	Caldicellulosiruptor bescii	3	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor bescii
506389071	471	43	Firmicutes	Caldicellulosiruptor bescii	3	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor bescii
503194714	471	43	Firmicutes	Caldicellulosiruptor kronotskyensis	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor kronotskyensis
736843511	437	44	Firmicutes	[Clostridium] cellulosi	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Ruminococcaceae,Ruminiclostridium,[Clostridium] cellulosi
753833833	437	44	Firmicutes	Thermoanaerobacterium thermosaccharolyticum	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Thermoanaerobacterium,Thermoanaerobacterium thermosaccharolyticum
433293862	470	44	Firmicutes	Thermoanaerobacterium thermosaccharolyticum M0795	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Thermoanaerobacterium,Thermoanaerobacterium thermosaccharolyticum,Thermoanaerobacterium thermosaccharolyticum M0795
654919971	462	45	Proteobacteria	Burkholderia sp. UYPR1.413	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia sp. UYPR1.413

494863071	462	45	Proteobacteria	Burkholderia terrae	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia terrae
494862862	462	45	Proteobacteria	Burkholderia terrae	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia terrae
753797603	434	46	Actinobacteria	Nocardiopsis dassonvillei	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis dassonvillei
296847451	459	46	Actinobacteria	Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis dassonvillei,Nocardiopsis dassonvillei subsp. dassonvillei,Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111
738643828	434	46	Actinobacteria	Nocardiopsis sp. CNS639	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis sp. CNS639
550534946	450	47	Firmicutes	Peptoclostridium difficile	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptostreptococcaceae,Peptoclostridium,Peptoclostridium difficile
497580664	450	47	Firmicutes	Peptoclostridium difficile	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptostreptococcaceae,Peptoclostridium,Peptoclostridium difficile
545016077	451	47	Firmicutes	Peptoclostridium difficile	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptostreptococcaceae,Peptoclostridium,Peptoclostridium difficile
746229982	450	48	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
80159829	450	48	Viruses	Clostridium phage c-st	1	Viruses,dsDNA viruses, no RNA stage,Caudovirales,Myoviridae,unclassified Myoviridae,Clostridium phage c-st
738341286	427	49	Proteobacteria	Methylobacter whittenburyi	5	Bacteria,Proteobacteria,Gammaproteobacteria,Methylococcales,Methylococcaceae,Methylobacter,Methylobacter whittenburyi
738340993	440	49	Proteobacteria	Methylobacter whittenburyi	5	Bacteria,Proteobacteria,Gammaproteobacteria,Methylococcales,Methylococcaceae,Methylobacter,Methylobacter whittenburyi
738341565	450	49	Proteobacteria	Methylobacter whittenburyi	5	Bacteria,Proteobacteria,Gammaproteobacteria,Methylococcales,Methylococcaceae,Methylobacter,Methylobacter whittenburyi
829063323	401	50	Proteobacteria	Pseudomonas fluorescens	2	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Pseudomonadaceae,Pseudomonas,Pseudomonas fluorescens group,Pseudomonas fluorescens
829063102	402	50	Proteobacteria	Pseudomonas fluorescens	2	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Pseudomonadaceae,Pseudomonas,Pseudomonas fluorescens group,Pseudomonas fluorescens
655196732	446	50	Proteobacteria	Pseudomonas sp. Ant30-3	1	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Pseudomonadaceae,Pseudomonas,Pseudomonas sp. Ant30-3

815714495	436	51	Proteobacteria	Burkholderia sp. K4410.MGS-135	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia sp. K4410.MGS-135
512681223	442	51	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis
491573834	442	51	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis
495180193	438	52	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495197591	438	52	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495183374	438	52	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495616745	427	53	Firmicutes	Alicyclobacillus acidocaldarius	2	Bacteria,Firmicutes,Bacilli,Bacillales,Alicyclobacillaceae,Alicyclobacillus,Alicyclobacillus acidocaldarius
502515787	427	53	Firmicutes	Alicyclobacillus acidocaldarius	2	Bacteria,Firmicutes,Bacilli,Bacillales,Alicyclobacillaceae,Alicyclobacillus,Alicyclobacillus acidocaldarius
218238652	392	53	Firmicutes	Alicyclobacillus acidocaldarius LAA1	1	Bacteria,Firmicutes,Bacilli,Bacillales,Alicyclobacillaceae,Alicyclobacillus,Alicyclobacillus acidocaldarius,Alicyclobacillus acidocaldarius LAA1
502797744	427	54	Proteobacteria	Nitrosococcus halophilus	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
502797830	427	54	Proteobacteria	Nitrosococcus halophilus	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
851243218	427	55	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851243168	427	55	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851238757	427	55	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
829601212	424	56	Firmicutes	Enterococcus cecorum	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Enterococcaceae,Enterococcus,Enterococcus cecorum
829619121	424	56	Firmicutes	Enterococcus cecorum	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Enterococcaceae,Enterococcus,Enterococcus cecorum
829617565	424	56	Firmicutes	Enterococcus cecorum	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Enterococcaceae,Enterococcus,Enterococcus cecorum
491578877	415	57	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis
740163595	415	57	Proteobacteria	Sutterella wadsworthensis	8	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis

404658355	421	57	Proteobacteria	Sutterella wadsworthensis 2_1_59BFAA	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis,Sutterella wadsworthensis 2_1_59BFAA
504783188	418	58	Firmicutes	Exiguobacterium antarcticum	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family XII. Incertae Sedis,Exiguobacterium,Exiguobacterium antarcticum
652434556	418	58	Firmicutes	Exiguobacterium antarcticum	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family XII. Incertae Sedis,Exiguobacterium,Exiguobacterium antarcticum
501338645	418	58	Firmicutes	Exiguobacterium sibiricum	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family XII. Incertae Sedis,Exiguobacterium,Exiguobacterium sibiricum
763347204	386	59	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
763349918	386	59	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196182137	355	59	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
750140500	347	60	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
918699177	371	60	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297552337	377	60	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
516414495	359	61	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
585121494	337	61	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
585123623	368	61	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
918699864	354	62	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297554830	354	62	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963

495465212	358	63	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
764922063	366	63	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
332353334	352	63	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
738948808	364	64	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
738948126	364	64	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
750682874	365	64	Cyanobacteria	Planktothrix agardhii	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix agardhii
750138734	309	65	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
750143836	309	65	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
750143729	309	65	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
655460771	284	66	Thermotogae	Pseudothermotoga elfii	2	Bacteria,Thermotogae,Thermotogae,Thermotogales,Thermotogaceae,Pseudothermotoga,Pseudothermotoga elfii
908396443	272	66	Thermotogae	Pseudothermotoga lettingae	2	Bacteria,Thermotogae,Thermotogae,Thermotogales,Thermotogaceae,Pseudothermotoga,Pseudothermotoga lettingae
157315178	302	66	Thermotogae	Pseudothermotoga lettingae TMO	2	Bacteria,Thermotogae,Thermotogae,Thermotogales,Thermotogaceae,Pseudothermotoga,Pseudothermotoga lettingae,Pseudothermotoga lettingae TMO
524002790	170	67	Proteobacteria	Parasutterella excrementihominis CAG:233	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,environmental samples,Parasutterella excrementihominis CAG:233
329570285	185	67	Proteobacteria	Parasutterella excrementihominis YIT 11859	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis,Parasutterella excrementihominis YIT 11859
329574454	192	67	Proteobacteria	Parasutterella excrementihominis YIT 11859	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis,Parasutterella excrementihominis YIT 11859
852264045	62	68	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
881034106	65	68	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
357265126	56	68	Cyanobacteria	Crocosphaera watsonii WH 0003	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0003

737209489	483	69	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
669953820	532	69	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
750571318	449	70	Proteobacteria	Thiorhodospira sibirica	1	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Ectothiorhodospiraceae,Thiorhodospira,Thiorhodospira sibirica
349789229	474	70	Proteobacteria	Thiorhodospira sibirica ATCC 700588	1	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Ectothiorhodospiraceae,Thiorhodospira,Thiorhodospira sibirica,Thiorhodospira sibirica ATCC 700588
763349759	428	71	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196179674	471	71	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
769143982	470	72	Firmicutes	Anaerostipes hadrus	6	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus
763351214	445	73	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196178243	468	73	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
916890216	453	74	Proteobacteria	Candidatus Contendobacter odensis	2	Bacteria,Proteobacteria,Gammaproteobacteria,unclassified Gammaproteobacteria,Competibacteraceae,Candidatus Contendobacter,Candidatus Contendobacter odensis
577004633	466	74	Proteobacteria	Candidatus Contendobacter odensis Run_B_J11	2	Bacteria,Proteobacteria,Gammaproteobacteria,unclassified Gammaproteobacteria,Competibacteraceae,Candidatus Contendobacter,Candidatus Contendobacter odensis,Candidatus Contendobacter odensis Run_B_J11
499805501	465	75	Proteobacteria	Polaromonas sp. JS666	3	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas sp. JS666
499805580	465	75	Proteobacteria	Polaromonas sp. JS666	3	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas sp. JS666
503547932	463	76	Firmicutes	Mahella australiensis	3	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family IV. Incertae Sedis,Mahella,Mahella australiensis

503548020	463	76	Firmicutes	Mahella australiensis	3	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family IV. Incertae Sedis,Mahella,Mahella australiensis
757645062	463	77	Proteobacteria	Cupriavidus necator	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Cupriavidus,Cupriavidus necator
757647489	463	77	Proteobacteria	Cupriavidus necator	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Cupriavidus,Cupriavidus necator
506219084	459	78	Firmicutes	Ammonifex degensii	4	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Moorella group,Ammonifex,Ammonifex degensii
502569059	459	78	Firmicutes	Ammonifex degensii	4	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Moorella group,Ammonifex,Ammonifex degensii
910241805	457	79	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
516354009	457	79	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
737567486	443	80	Proteobacteria	Halomonas sp. GFAJ-1	2	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas sp. GFAJ-1
359298001	456	80	Proteobacteria	Halomonas sp. GFAJ-1	2	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas sp. GFAJ-1
495014271	456	81	Proteobacteria	Burkholderia sp. BT03	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia sp. BT03
494852515	456	81	Proteobacteria	Burkholderia terrae	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia terrae
750139499	413	82	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297556617	455	82	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
564807354	454	83	Firmicutes	Lactobacillus equi	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equi
640591377	454	83	Firmicutes	Lactobacillus equi	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equi
759968300	451	84	Actinobacteria	Streptosporangium roseum	3	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Streptosporangiaceae,Streptosporangium,Streptosporangium roseum
270508069	422	84	Actinobacteria	Streptosporangium roseum DSM 43021	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Streptosporangiaceae,Streptosporangium,Streptosporangium roseum,Streptosporangium roseum DSM 43021

771679752	436	85	Proteobacteria	Burkholderiaceae bacterium 16	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,unclassified Burkholderiaceae,Burkholderiaceae bacterium 16
919130721	449	85	Proteobacteria	Burkholderiaceae bacterium 16	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,unclassified Burkholderiaceae,Burkholderiaceae bacterium 16
825931341	433	86	Firmicutes	Aneurinibacillus tyrosinisolvens	5	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus tyrosinisolvens
825903244	448	86	Firmicutes	Aneurinibacillus tyrosinisolvens	5	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus tyrosinisolvens
763351071	426	87	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196178332	444	87	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
750171232	434	88	Proteobacteria	Halomonas jeotgali	2	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas jeotgali
648414493	443	88	Proteobacteria	Halomonas jeotgali	2	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas jeotgali
753813890	443	89	Fibrobacteres/Acic	Chloracidobacterium thermophilum	1	Bacteria,Fibrobacteres/Acidobacteria group,Acidobacteria,unclassified Acidobacteria,Acidobacteria subdivision 4,Chloracidobacterium,Chloracidobacterium thermophilum
347587148	430	89	Fibrobacteres/Acic	Chloracidobacterium thermophilum B	2	Bacteria,Fibrobacteres/Acidobacteria group,Acidobacteria,unclassified Acidobacteria,Acidobacteria subdivision 4,Chloracidobacterium,Chloracidobacterium thermophilum,Chloracidobacterium thermophilum B
749999474	419	90	Firmicutes	Anaerostipes hadrus	6	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus
429177907	442	90	Firmicutes	Anaerostipes hadrus DSM 3319	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus,Anaerostipes hadrus DSM 3319
807125388	420	91	Actinobacteria	Streptomyces sp. WM6386	2	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. WM6386
808101633	442	91	Actinobacteria	Streptomyces sp. WM6386	2	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. WM6386
490089111	420	92	Actinobacteria	Streptomyces viridochromogenes	2	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces viridochromogenes

918018082	442	92	Actinobacteria	Streptomyces viridochromogenes	2	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces viridochromogenes
728895995	440	93	Thermotogae	Fervidobacterium islandicum	3	Bacteria,Thermotogae,Thermotogae,Thermotogales,Fervidobacteriaceae,Fervidobacterium,Fervidobacterium islandicum
701166555	440	93	Thermotogae	Fervidobacterium islandicum	3	Bacteria,Thermotogae,Thermotogae,Thermotogales,Fervidobacteriaceae,Fervidobacterium,Fervidobacterium islandicum
636809000	439	94	Proteobacteria	Desulfotignum balticum	1	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfobacterales,Desulfobacteraceae,Desulfotignum,Desulfotignum balticum
748753481	439	94	Proteobacteria	Desulfotignum phosphitoxidans	1	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfobacterales,Desulfobacteraceae,Desulfotignum,Desulfotignum phosphitoxidans
495179088	438	95	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495195117	438	95	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
502958892	438	96	Euryarchaeota	Methanohalobium evestigatum	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanohalobium,Methanohalobium evestigatum
502959717	438	96	Euryarchaeota	Methanohalobium evestigatum	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanohalobium,Methanohalobium evestigatum
759742382	416	97	Actinobacteria	Streptomyces fulvoviolaceus	3	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces fulvoviolaceus
918372180	438	97	Actinobacteria	Streptomyces fulvoviolaceus	3	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces fulvoviolaceus
750144026	416	98	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297548145	437	98	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
916314723	425	99	Actinobacteria	Nocardiopsis ganjiahuensis	2	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis ganjiahuensis
516166536	436	99	Actinobacteria	Nocardiopsis ganjiahuensis	2	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis ganjiahuensis
665590333	435	100	Actinobacteria	Streptosporangium roseum	3	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Streptosporangiaceae,Streptosporangium,Streptosporangium roseum

502652377	435	100	Actinobacteria	Streptosporangium roseum	3	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Streptosporangiaceae,Streptosporangium,Streptosporangium roseum
750139029	394	101	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297555563	433	101	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
918699346	430	102	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495185044	432	102	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495195481	432	103	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495194584	432	103	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
503945474	432	104	Actinobacteria	Streptomyces bingchenggensis	3	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces bingchenggensis
503945237	432	104	Actinobacteria	Streptomyces bingchenggensis	3	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces bingchenggensis
851241801	432	105	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
851246091	432	105	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
669952828	430	106	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
737210774	431	106	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
738341504	413	107	Proteobacteria	Methylobacter whittenburyi	5	Bacteria,Proteobacteria,Gammaproteobacteria,Methylococcales,Methylococcaceae,Methylobacter,Methylobacter whittenburyi
738341074	431	107	Proteobacteria	Methylobacter whittenburyi	5	Bacteria,Proteobacteria,Gammaproteobacteria,Methylococcales,Methylococcaceae,Methylobacter,Methylobacter whittenburyi
505030549	427	108	Cyanobacteria	Anabaena cylindrica	1	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena cylindrica
746138950	431	108	Cyanobacteria	Aphanizomenon flos-aquae	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Aphanizomenon,Aphanizomenon flos-aquae

119457943	410	109	Cyanobacteria	Lyngbya sp. PCC 8106	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Lyngbya,Lyngbya sp. PCC 8106
748637106	431	109	Cyanobacteria	Lyngbya sp. PCC 8106	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Lyngbya,Lyngbya sp. PCC 8106
835374448	428	110	Firmicutes	Peptococcaceae bacterium CEB3	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,unclassified Peptococcaceae,Peptococcaceae bacterium CEB3
836679806	431	110	Firmicutes	Peptococcaceae bacterium CEB3	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,unclassified Peptococcaceae,Peptococcaceae bacterium CEB3
495180525	429	111	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495188438	429	111	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495183321	429	112	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495182844	429	112	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
763346502	396	113	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196182912	428	113	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
510930751	427	114	Firmicutes	Enterococcus cecorum	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Enterococcaceae,Enterococcus,Enterococcus cecorum
510929983	428	114	Firmicutes	Enterococcus cecorum	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Enterococcaceae,Enterococcus,Enterococcus cecorum
502797459	427	115	Proteobacteria	Nitrosococcus halophilus	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
502796854	427	115	Proteobacteria	Nitrosococcus halophilus	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
515519056	427	116	Cyanobacteria	Anabaena sp. PCC 7108	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena sp. PCC 7108
746136581	427	116	Cyanobacteria	Aphanizomenon flos-aquae	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Aphanizomenon,Aphanizomenon flos-aquae
763349672	427	117	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196179772	386	117	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420

851315043	427	118	Euryarchaeota	Methanosarcina sp. MTP4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. MTP4
851314722	427	118	Euryarchaeota	Methanosarcina sp. MTP4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. MTP4
908629034	412	119	Proteobacteria	Nitrosococcus watsonii	1	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus watsonii
299540414	426	119	Proteobacteria	Nitrosococcus watsonii C-113	1	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus watsonii,Nitrosococcus watsonii C-113
497231916	425	120	Cyanobacteria	Cyanothece	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece
495553706	425	120	Cyanobacteria	Cyanothece sp. CCY0110	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. CCY0110
498160676	425	121	Cyanobacteria	Acaryochloris sp. CCMEE 5410	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Acaryochloris,Acaryochloris sp. CCMEE 5410
498160623	425	121	Cyanobacteria	Acaryochloris sp. CCMEE 5410	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Acaryochloris,Acaryochloris sp. CCMEE 5410
797212860	425	122	Cyanobacteria	Tolypothrix sp. PCC 7601	1	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix sp. PCC 7601
515883449	425	122	Cyanobacteria	Mastigocladopsis repens	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladopsis,Mastigocladopsis repens
750139055	419	123	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297555630	421	123	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
524087929	421	124	Firmicutes	Clostridium sp. CAG:678	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,environmental samples,Clostridium sp. CAG:678
524087941	421	124	Firmicutes	Clostridium sp. CAG:678	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,environmental samples,Clostridium sp. CAG:678
750139018	398	125	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
297555535	419	125	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
505140114	419	126	Firmicutes	Halobacteroides halobius	3	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Halobacteroides,Halobacteroides halobius
507043497	415	127	Firmicutes	Bacillus	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus

228768623	374	127	Firmicutes	Bacillus pseudomycoides DSM 12442	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus pseudomycoides,Bacillus pseudomycoides DSM 12442
769213283	400	128	Firmicutes	[Eubacterium] cellulosolvens	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Eubacteriaceae,Eubacterium,[Eubacterium] cellulosolvens
389313404	412	128	Firmicutes	[Eubacterium] cellulosolvens 6	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Eubacteriaceae,Eubacterium,[Eubacterium] cellulosolvens,[Eubacterium] cellulosolvens 6
752581329	397	129	Firmicutes	Finegoldia magna	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptoniphilaceae,Finegoldia,Finegoldia magna
167832304	410	129	Firmicutes	Finegoldia magna ATCC 29328	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptoniphilaceae,Finegoldia,Finegoldia magna,Finegoldia magna ATCC 29328
502959635	401	130	Euryarchaeota	Methanohalobium evestigatum	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanohalobium,Methanohalobium evestigatum
502959253	407	130	Euryarchaeota	Methanohalobium evestigatum	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanohalobium,Methanohalobium evestigatum
515872749	389	131	Cyanobacteria	Spirulina subsalsa	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Spirulina,Spirulina subsalsa
515872123	406	131	Cyanobacteria	Spirulina subsalsa	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Spirulina,Spirulina subsalsa
504040543	401	132	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
504042800	401	132	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
851273483	392	133	Euryarchaeota	Methanosarcina horonobensis	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina horonobensis
805382013	399	133	Euryarchaeota	Methanosarcina horonobensis HB-1 = JCM 15518	2	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina horonobensis,Methanosarcina horonobensis HB-1 = JCM 15518
763346534	372	134	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
493031181	396	134	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
763352824	395	135	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196176410	381	135	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420

297555693	380	136	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
297547678	392	136	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
506219980	387	137	Firmicutes	Ammonifex degensii	4	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Moorella group,Ammonifex,Ammonifex degensii
506218806	388	137	Firmicutes	Ammonifex degensii	4	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Moorella group,Ammonifex,Ammonifex degensii
753958558	386	138	Cyanobacteria	Acaryochloris marina	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Acaryochloris,Acaryochloris marina
158310350	387	138	Cyanobacteria	Acaryochloris marina MBIC11017	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Acaryochloris,Acaryochloris marina,Acaryochloris marina MBIC11017
916320797	367	139	Cyanobacteria	Microcoleus sp. PCC 7113	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Microcoleus,Microcoleus sp. PCC 7113
428250446	384	139	Cyanobacteria	Microcoleus sp. PCC 7113	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Microcoleus,Microcoleus sp. PCC 7113
546224917	363	140	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
852262173	381	140	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
428255037	362	141	Cyanobacteria	Microcoleus sp. PCC 7113	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Microcoleus,Microcoleus sp. PCC 7113
754157869	376	141	Cyanobacteria	Microcoleus sp. PCC 7113	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Microcoleus,Microcoleus sp. PCC 7113
808795645	367	142	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
497470778	367	142	Cyanobacteria	Lyngbya sp. PCC 8106	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Lyngbya,Lyngbya sp. PCC 8106
503086269	365	143	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
503086059	365	143	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
196187591	360	144	Cyanobacteria	Synechococcus sp. PCC 7335	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 7335
740177457	361	144	Cyanobacteria	Synechococcus sp. PCC 7335	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 7335

764924346	360	145	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
332349483	349	145	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
493675647	346	146	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
78499557	353	146	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
655939361	339	147	Firmicutes	Thermicanus aegyptius	2	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family X. Incertae Sedis,Thermicanus,Thermicanus aegyptius
918099252	353	147	Firmicutes	Thermicanus aegyptius	2	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family X. Incertae Sedis,Thermicanus,Thermicanus aegyptius
753769621	343	148	Firmicutes	Pelotomaculum thermopropionicum	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Pelotomaculum,Pelotomaculum thermopropionicum
146272595	347	148	Firmicutes	Pelotomaculum thermopropionicum SI	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Pelotomaculum,Pelotomaculum thermopropionicum,Pelotomaculum thermopropionicum SI
753864852	335	149	Cyanobacteria	Stanieria cyanosphaera	1	Bacteria,Cyanobacteria,Pleurocapsales,Stanieria,Stanieria cyanosphaera
428272038	344	149	Cyanobacteria	Stanieria cyanosphaera PCC 7437	1	Bacteria,Cyanobacteria,Pleurocapsales,Stanieria,Stanieria cyanosphaera,Stanieria cyanosphaera PCC 7437
209492096	342	150	Cyanobacteria	Arthrospira maxima CS-328	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima,Arthrospira maxima CS-328
585308822	342	150	Cyanobacteria	Arthrospira sp. PCC 8005	13	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. PCC 8005
493671064	337	151	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
209494675	341	151	Cyanobacteria	Arthrospira maxima CS-328	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima,Arthrospira maxima CS-328
851319314	318	152	Euryarchaeota	Methanosarcina sp. MTP4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. MTP4
919162612	339	152	Euryarchaeota	Methanosarcina sp. MTP4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. MTP4
764922807	292	153	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
332352197	314	153	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L

542056062	307	154	Firmicutes	Aneurinibacillus aneurinilyticus ATCC 12856	1	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus aneurinilyticus,Aneurinibacillus aneurinilyticus ATCC 12856
917807473	307	154	Firmicutes	Aneurinibacillus migulanus	2	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus migulanus
805377875	264	155	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
805380095	287	155	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
515489461	283	156	Cyanobacteria	Prochlorothrix hollandica	3	Bacteria,Cyanobacteria,Prochlorales,Prochlorotrichaceae,Prochlorothrix,Prochlorothrix hollandica
817120015	286	156	Cyanobacteria	Prochlorothrix hollandica	3	Bacteria,Cyanobacteria,Prochlorales,Prochlorotrichaceae,Prochlorothrix,Prochlorothrix hollandica
763349797	274	157	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196179633	282	157	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
432000681	248	158	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
432000885	265	158	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
765303279	244	159	Proteobacteria	Halomonas meridiana	3	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas meridiana
765303089	244	159	Proteobacteria	Halomonas meridiana	3	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas meridiana
917394967	232	160	Cyanobacteria	Lyngbya aestuarii	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Lyngbya,Lyngbya aestuarii
550818364	238	160	Cyanobacteria	Lyngbya aestuarii BL J	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Lyngbya,Lyngbya aestuarii,Lyngbya aestuarii BL J
119463775	213	161	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
585120262	236	161	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414

493574041	211	162	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493574162	229	162	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
564132583	221	163	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1
564132560	222	163	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1
763349321	221	164	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
196180073	201	164	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
119461580	190	165	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
119461928	192	165	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
918383514	173	166	Proteobacteria	Pseudomonas aeruginosa	2	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Pseudomonadaceae,Pseudomonas,Pseudomonas aeruginosa group,Pseudomonas aeruginosa
565901635	173	166	Proteobacteria	Pseudomonas aeruginosa	2	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Pseudomonadaceae,Pseudomonas,Pseudomonas aeruginosa group,Pseudomonas aeruginosa
516414460	170	167	Cyanobacteria	Nodularia spumigena	9	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena
119465516	172	167	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
805337294	151	168	Euryarchaeota	Methanosarcina sp. WWM596	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WWM596
919167038	164	168	Euryarchaeota	Methanosarcina sp. WWM596	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WWM596
431999653	157	169	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006

432001846	158	169	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
488871377	137	170	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
718249451	136	170	Cyanobacteria	Microcystis aeruginosa NIES-44	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa NIES-44
851241503	123	171	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
805377642	116	171	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
852264147	118	172	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
543532946	110	172	Cyanobacteria	Crocosphaera watsonii WH 0402	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0402
302860576	103	173	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
302860570	106	173	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
763117502	99	174	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
763117432	99	174	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
442790464	92	175	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
736937830	96	175	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
491028078	91	176	Firmicutes	Anoxybacillus flavithermus	6	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus
432001960	90	176	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
442789060	88	177	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106

736939038	90	177	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
494521156	82	178	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
852265072	82	178	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
750682809	75	179	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
738948968	75	179	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
297141331	771	180	Firmicutes	[Bacillus] selenitireducens MLS10	2	Bacteria,Firmicutes,Bacilli,Bacillales,Sporolactobacillaceae,unclassified Sporolactobacillaceae,[Bacillus] selenitireducens,[Bacillus] selenitireducens MLS10
512057519	549	181	Actinobacteria	Streptomyces sp. HGB0020	2	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. HGB0020
517101236	523	182	Chlamydiae/Verru	Verrucomicrobium sp. 3C	4	Bacteria,Chlamydiae/Verrucomicrobia group,Verrucomicrobia,Verrucomicrobiae,Verrucomicrobiales,Verrucomicrobiaceae,Verrucomicrobium,Verrucomicrobium sp. 3C
474489591	516	183	Proteobacteria	Desulfotignum phosphitoxidans DSM 13687	1	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfobacterales,Desulfobacteraceae,Desulfotignum,Desulfotignum phosphitoxidans,Desulfotignum phosphitoxidans DSM 13687
769144095	507	184	Firmicutes	Anaerostipes hadrus	6	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus
503547901	497	185	Firmicutes	Mahella australiensis	3	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family IV. Incertae Sedis,Mahella,Mahella australiensis
805378337	497	186	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
251773297	494	187	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
739495022	492	188	Firmicutes	Selenomonas sp. FC4001	3	Bacteria,Firmicutes,Negativicutes,Selenomonadales,Veillonellaceae,Selenomonas,Selenomonas sp. FC4001
530929108	487	189	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
500122049	477	190	Proteobacteria	Polaromonas naphthalenivorans	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas naphthalenivorans
524427328	477	191	Firmicutes	Clostridium sp. CAG:265	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,environmental samples,Clostridium sp. CAG:265

530561424	477	192	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
648405926	477	193	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
655958159	477	194	Proteobacteria	Azohydromonas australica	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Alcaligenaceae,Azohydromonas,Azohydromonas australica
530562869	476	195	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
754582141	476	196	Fibrobacteres/Acic	Pyrinomonas methylaliphatogenes	2	Bacteria,Fibrobacteres/Acidobacteria group,Acidobacteria,unclassified Acidobacteria,Acidobacteria subdivision 4,Pyrinomonas,Pyrinomonas methylaliphatogenes
297157261	475	197	Actinobacteria	Streptomyces bingchenggensis BCW-1	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces bingchenggensis,Streptomyces bingchenggensis BCW-1
530562102	475	198	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
530559506	474	199	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
917662534	474	200	Firmicutes	Thermincola ferriacetica	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Thermincola,Thermincola ferriacetica
516257677	472	201	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
530563573	472	202	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
251771088	471	203	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
501634530	471	204	Proteobacteria	Acidithiobacillus ferrooxidans	2	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrooxidans
503167716	471	205	Firmicutes	Caldicellulosiruptor hydrothermalis	2	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor hydrothermalis
503796304	471	206	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans

196183095	470	207	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
654777069	470	208	Proteobacteria	Burkholderia mimosarum	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia mimosarum
740686785	470	209	Proteobacteria	Acidithiobacillus caldus	3	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus caldus
516144719	469	210	Actinobacteria	Nocardiopsis kunsanensis	3	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis kunsanensis
516255311	469	211	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
737978609	468	212	Proteobacteria	Burkholderia glathei	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia glathei
671571726	467	213	Firmicutes	Oribacterium sp. FC2011	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Oribacterium,Oribacterium sp. FC2011
549495638	466	214	Proteobacteria	Ralstonia pickettii	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Ralstonia,Ralstonia pickettii
740240025	466	215	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
251771163	465	216	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
648401347	465	217	Cyanobacteria	Calothrix sp. PCC 7103	6	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix sp. PCC 7103
836700638	464	218	Proteobacteria	Burkholderia glathei	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia glathei
491458270	462	219	Actinobacteria	Streptomyces pristinaespiralis	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces pristinaespiralis
780112544	462	220	Proteobacteria	Thioploca ingrica	2	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thioploca,Thioploca ingrica
218172972	461	221	Cyanobacteria	Cyanothece sp. PCC 7424	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7424
740252799	461	222	Proteobacteria	Thiobacillus prosperus	1	Bacteria,Proteobacteria,Gammaproteobacteria,unclassified Gammaproteobacteria,Thiobacillus prosperus
515355474	460	223	Cyanobacteria	Fischerella muscicola	1	Bacteria,Cyanobacteria,Stigonematales,Fischerella,Fischerella muscicola
495182297	459	224	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer

500125461	459	225	Proteobacteria	Polaromonas naphthalenivorans	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas naphthalenivorans
530927150	459	226	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
530927885	459	227	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
917481455	459	228	Firmicutes	Paenibacillus wynnii	1	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Paenibacillus,Paenibacillus wynnii
490176289	458	229	Proteobacteria	Desulfobacter postgatei	2	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfobacterales,Desulfobacteraceae,Desulfobacter,Desulfobacter postgatei
502796490	458	230	Proteobacteria	Nitrosococcus halophilus	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
737207500	458	231	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
829809554	458	232	Proteobacteria	Diaphorobacter sp. J5-51	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Diaphorobacter,Diaphorobacter sp. J5-51
915471230	458	233	Proteobacteria	Burkholderia ambifaria	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia cepacia complex,Burkholderia ambifaria
505042970	457	234	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina
516353909	457	235	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
549628277	457	236	Proteobacteria	Ralstonia pickettii	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Ralstonia,Ralstonia pickettii
654753328	457	237	Proteobacteria	Burkholderia nodosa	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia nodosa
910080418	457	238	Firmicutes	Anaerostipes hadrus	6	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus
910240999	457	239	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
910241764	457	240	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
496658392	456	241	Firmicutes	Coprobacillus sp. 3_3_56FAA	2	Bacteria,Firmicutes,Erysipelotrichia,Erysipelotrichales,Erysipelotrichaceae,Coprobacillus,Coprobacillus sp. 3_3_56FAA
503796369	456	242	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans

516352542	456	243	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
736413103	456	244	Proteobacteria	Candidatus Contendobacter odensis	2	Bacteria,Proteobacteria,Gammaproteobacteria,unclassified Gammaproteobacteria,Competibacteraceae,Candidatus Contendobacter,Candidatus Contendobacter odensis
759564206	456	245	Proteobacteria	Burkholderia oxyphila	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia oxyphila
916987011	456	246	Proteobacteria	Achromobacter sp. DH1f	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Alcaligenaceae,Achromobacter,Achromobacter sp. DH1f
749554550	455	247	Proteobacteria	Halomonas salina	1	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas salina
501633885	454	248	Proteobacteria	Acidithiobacillus ferrooxidans	2	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrooxidans
488782245	453	249	Bacteroidetes/Chl	Microscilla marina	1	Bacteria,Bacteroidetes/Chlorobi group,Bacteroidetes,Cytophagia,Cytophagales,Cytophagaceae,Microscilla,Microscilla marina
517126235	453	250	Proteobacteria	Cupriavidus sp. UYPR2.512	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Cupriavidus,Cupriavidus sp. UYPR2.512
702616456	453	251	Actinobacteria	Streptomyces virginiae	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces virginiae
914619641	453	252	Firmicutes	Lactobacillus agilis	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus agilis
120596178	452	253	Proteobacteria	Polaromonas naphthalenivorans CJ2	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas naphthalenivorans,Polaromonas naphthalenivorans CJ2
291529497	452	254	Firmicutes	Eubacterium rectale M104/1	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Eubacteriaceae,Eubacterium,Eubacterium rectale,Eubacterium rectale M104/1
517100800	451	255	Chlamydiae/Verru	Verrucomicrobium sp. 3C	4	Bacteria,Chlamydiae/Verrucomicrobia group,Verrucomicrobia,Verrucomicrobiae,Verrucomicrobiales,Verrucomicrobiaceae,Verrucomicrobium,Verrucomicrobium sp. 3C
651374235	451	256	Firmicutes	Caldanaerobius polysaccharolyticus	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Caldanaerobius,Caldanaerobius polysaccharolyticus
916576584	450	257	Actinobacteria	Streptomyces sp. HGB0020	2	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. HGB0020
490173387	449	258	Proteobacteria	Desulfobacter postgatei	2	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfobacterales,Desulfobacteraceae,Desulfobacter,Desulfobacter postgatei

502734885	449	259	Proteobacteria	Allochromatium vinosum	5	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Allochromatium,Allochromatium vinosum
851245734	449	260	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
916325889	449	261	Actinobacteria	Nocardiopsis gilva	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis gilva
494100423	448	262	Proteobacteria	Thiorhodococcus drewsii	1	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Thiorhodococcus,Thiorhodococcus drewsii
497835978	448	263	Proteobacteria	SAR324 cluster bacterium JCVI-SC AAA005	2	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,unclassified Deltaproteobacteria,SAR324 cluster,SAR324 cluster bacterium JCVI-SC AAA005
571050767	448	264	environmental san	uncultured bacterium Contig26	1	Bacteria,environmental samples,uncultured bacterium Contig26
640592508	448	265	Firmicutes	Lactobacillus equi	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equi
662066808	448	266	Firmicutes	Clostridium botulinum	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium botulinum
737612985	448	267	Proteobacteria	Halomonas sp. TG39a	1	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas sp. TG39a
740584636	448	268	Actinobacteria	Brachybacterium phenoliresistens	1	Bacteria,Actinobacteria,Actinobacteria,Micrococcales,Dermabacteraceae,Brachybacterium,Brachybacterium phenoliresistens
520868253	446	269	Proteobacteria	Pseudomonas stutzeri	1	Bacteria,Proteobacteria,Gammaproteobacteria,Pseudomonadales,Pseudomonadaceae,Pseudomonas,Pseudomonas stutzeri group,Pseudomonas stutzeri subgroup,Pseudomonas stutzeri
640591712	446	270	Firmicutes	Lactobacillus equi	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equi
851270337	446	271	Euryarchaeota	Methanosarcina horonobensis	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina horonobensis
495010668	445	272	Proteobacteria	Burkholderia sp. BT03	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia sp. BT03
503043082	445	273	Firmicutes	Acetohalobium arabaticum	4	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Acetohalobium,Acetohalobium arabaticum
738539867	445	274	Cyanobacteria	Myxosarcina sp. GI1	1	Bacteria,Cyanobacteria,Pleurocapsales,Myxosarcina,Myxosarcina sp. GI1
763349453	445	275	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
495454362	444	276	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
495466178	444	277	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens

506389025	443	278	Firmicutes	Caldicellulosiruptor bescii	3	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor bescii
516360165	443	279	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
771520715	443	280	Firmicutes	Caldicellulosiruptor sp. Wai35.B1	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor sp. Wai35.B1
516350411	442	281	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
764526366	442	282	Proteobacteria	Thioalkalimicrobium microaerophilum	1	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Piscirickettsiaceae,Thioalkalimicrobium,Thioalkalimicrobium microaerophilum
917194967	442	283	Actinobacteria	Streptomyces sp. NRRL F-525	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. NRRL F-525
495188212	441	284	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
516352019	441	285	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
780103597	441	286	Proteobacteria	Thioploca ingrica	2	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thioploca,Thioploca ingrica
917378057	441	287	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
495185167	440	288	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
516355684	439	289	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
754583666	439	290	Fibrobacteres/Acic	Pyrinomonas methylaliphatogenes	2	Bacteria,Fibrobacteres/Acidobacteria group,Acidobacteria,unclassified Acidobacteria,Acidobacteria subdivision 4,Pyrinomonas,Pyrinomonas methylaliphatogenes
916793994	439	291	Proteobacteria	Campylobacter fetus	1	Bacteria,Proteobacteria,delta/epsilon subdivisions,Epsilonproteobacteria,Campylobacterales,Campylobacteraceae,Campylobacter,Campylobacter fetus
917219793	439	292	Actinobacteria	Streptomyces violaceoruber	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces violaceoruber
918439172	439	293	Cyanobacteria	Tolypothrix campylonemoides	6	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix campylonemoides
495193778	438	294	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer

501164377	438	295	Thermotogae	Petrotoga mobilis	3	Bacteria,Thermotogae,Thermotogae,Petrotogales,Petrotogaceae,Petrotoga,Petrotoga mobilis
504988195	438	296	Cyanobacteria	Oscillatoria nigro-viridis	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria nigro-viridis
665859048	438	297	Actinobacteria	Streptomyces roseochromogenus	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces roseochromogenus
495179835	437	298	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
748817658	437	299	Firmicutes	Bacillus sp. REN51N	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus sp. REN51N
495179135	436	300	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
501164645	436	301	Thermotogae	Petrotoga mobilis	3	Bacteria,Thermotogae,Thermotogae,Petrotogales,Petrotogaceae,Petrotoga,Petrotoga mobilis
516184175	436	302	Actinobacteria	Nocardiopsis lucentensis	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis lucentensis
723287658	436	303	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
723288870	436	304	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
818877501	436	305	unclassified Bacter	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWB1_49_7	1	Bacteria,unclassified Bacteria,Microgenomates,unclassified Microgenomates,Microgenomates (Gottesmanbacteria) bacterium GW2011_GWB1_49_7
564812736	435	306	Firmicutes	Lactobacillus equi	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equi
664394896	435	307	Actinobacteria	Streptosporangium amethystogenes	2	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Streptosporangiaceae,Streptosporangium,Streptosporangium amethystogenes
736402546	435	308	Firmicutes	Clostridiales bacterium DRI-13	4	Bacteria,Firmicutes,Clostridia,Clostridiales,unclassified Clostridiales,unclassified Clostridiales (miscellaneous),Clostridiales bacterium DRI-13
737473603	435	309	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
836681294	435	310	Firmicutes	Peptococcaceae bacterium CEB3	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,unclassified Peptococcaceae,Peptococcaceae bacterium CEB3
516143664	434	311	Actinobacteria	Nocardiopsis kunsanensis	3	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis kunsanensis
737472691	434	312	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti

505041320	433	313	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina
657933271	433	314	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
749573854	433	315	Proteobacteria	Geoalkalibacter subterraneus	3	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfuromonadales,Geobacteraceae,Geoalkalibacter,Geoalkalibacter subterraneus
759564135	433	316	Proteobacteria	Burkholderia oxyphila	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Burkholderia oxyphila
763126099	433	317	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
889959964	433	318	Cyanobacteria	Scytonema tolypothrichoides	2	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema tolypothrichoides
916921277	433	319	Firmicutes	Lactobacillus equi	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equi
495192221	432	320	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
736504009	432	321	Actinobacteria	Actinomadura rifamycini	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Thermomonosporaceae,Actinomadura,Actinomadura rifamycini
763475824	432	322	Firmicutes	Peptoclostridium difficile	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptostreptococcaceae,Peptoclostridium,Peptoclostridium difficile
496349795	431	323	Chlamydiae/Verru	Methylacidiphilum fumariolicum	1	Bacteria,Chlamydiae/Verrucomicrobia group,Verrucomicrobia,unclassified Verrucomicrobia,Methylacidiphilales,Methylacidiphilaceae,Methylacidiphilum,Methylacidiphilum fumariolicum
505037441	431	324	Cyanobacteria	Halothece sp. PCC 7418	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Halothece cluster,Halothece,Halothece sp. PCC 7418
703021414	431	325	Actinobacteria	Actinomadura madurae	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Thermomonosporaceae,Actinomadura,Actinomadura madurae
723282587	431	326	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
737210766	431	327	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
764393758	431	328	Proteobacteria	Raoultella ornithinolytica	1	Bacteria,Proteobacteria,Gammaproteobacteria,Enterobacteriales,Enterobacteriaceae,Raoultella,Raoultella ornithinolytica
880798139	431	329	Cyanobacteria	Moorea bouillonii PNG5-198	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea bouillonii,Moorea bouillonii PNG5-198

504992636	430	330	Cyanobacteria	Oscillatoria nigro-viridis	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria nigro-viridis
505023946	430	331	Cyanobacteria	Cylindrospermum stagnale	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Cylindrospermum,Cylindrospermum stagnale
656263327	430	332	Euryarchaeota	euryarchaeote SCGC AAA261-G15	1	Archaea,Euryarchaeota,unclassified Euryarchaeota,unclassified Euryarchaeota (miscellaneous),euryarchaeote SCGC AAA261-G15
657934620	430	333	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
821562027	430	334	Proteobacteria	Microvirga sp. JC119	1	Bacteria,Proteobacteria,Alphaproteobacteria,Rhizobiales,Methylobacteriaceae,Microvirga,Microvirga sp. JC119
916738862	430	335	Nitrospirae	Thermodesulfovibrio islandicus	1	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Thermodesulfovibrio,Thermodesulfovibrio islandicus
495179751	429	336	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495186450	429	337	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495198645	429	338	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
495461888	429	339	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
495466227	429	340	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
750554050	429	341	Actinobacteria	Streptomyces acidiscabies	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces acidiscabies
495459261	428	342	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
495466254	428	343	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
518327680	428	344	Cyanobacteria	Calothrix sp. PCC 7103	6	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix sp. PCC 7103
648407024	428	345	Cyanobacteria	Oscillatoria sp. PCC 10802	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria sp. PCC 10802
723284236	428	346	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
764673158	428	347	Cyanobacteria	Mastigocladus laminosus	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladus,Mastigocladus laminosus
493029926	427	348	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
494598848	427	349	Cyanobacteria	Kamptonema	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Kamptonema

495453270	427	350	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
495465906	427	351	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
499309054	427	352	Cyanobacteria	Nostoc sp. PCC 7120	3	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nostoc,Nostoc sp. PCC 7120
499635620	427	353	Cyanobacteria	Anabaena variabilis	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena variabilis
499636046	427	354	Cyanobacteria	Anabaena variabilis	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena variabilis
502797006	427	355	Proteobacteria	Nitrosococcus halophilus	7	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus halophilus
503088871	427	356	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
504893952	427	357	Cyanobacteria	Anabaena sp. 90	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena sp. 90
505014506	427	358	Cyanobacteria	Crinalium epipsammum	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Crinalium,Crinalium epipsammum
515883076	427	359	Cyanobacteria	Stigonematales	1	Bacteria,Cyanobacteria,Stigonematales
515883518	427	360	Cyanobacteria	Mastigocladopsis repens	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladopsis,Mastigocladopsis repens
516256579	427	361	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
517100807	427	362	Chlamydiae/Verru	Verrucomicrobium sp. 3C	4	Bacteria,Chlamydiae/Verrucomicrobia group,Verrucomicrobia,Verrucomicrobiae,Verrucomicrobiales,Verrucomicrobiaceae,Verrucomicrobium,Verrucomicrobium sp. 3C
518324846	427	363	Cyanobacteria	Calothrix sp. PCC 7103	6	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix sp. PCC 7103
652319815	427	364	Cyanobacteria	Fischerella sp. PCC 9431	3	Bacteria,Cyanobacteria,Stigonematales,Fischerella,Fischerella sp. PCC 9431
652324245	427	365	Cyanobacteria	Fischerella sp. PCC 9431	3	Bacteria,Cyanobacteria,Stigonematales,Fischerella,Fischerella sp. PCC 9431
653226247	427	366	Firmicutes	Lachnospira multipara	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Lachnospira,Lachnospira multipara
654350231	427	367	Cyanobacteria	Mastigocoleus testarum	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocoleus,Mastigocoleus testarum
654617757	427	368	Cyanobacteria	Dolichospermum circinale	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Dolichospermum,Dolichospermum circinale
657929237	427	369	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
657932534	427	370	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
657932541	427	371	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
748134943	427	372	Cyanobacteria	Scytonema millei	2	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema millei

763350561	427	373	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
829618566	427	374	Firmicutes	Enterococcus cecorum	6	Bacteria,Firmicutes,Bacilli,Lactobacillales,Enterococcaceae,Enterococcus,Enterococcus cecorum
917001966	427	375	Firmicutes	Selenomonas sp. FC4001	3	Bacteria,Firmicutes,Negativicutes,Selenomonadales,Veillonellaceae,Selenomonas,Selenomonas sp. FC4001
504964918	426	376	Cyanobacteria	Oscillatoria acuminata	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria acuminata
505041099	426	377	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina
518326274	426	378	Cyanobacteria	Calothrix sp. PCC 7103	6	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix sp. PCC 7103
521982550	426	379	Chlamydiae/Verru	Verrucomicrobium sp. 3C	4	Bacteria,Chlamydiae/Verrucomicrobia group,Verrucomicrobia,Verrucomicrobiae,Verrucomicrobiales,Verrucomicrobiaceae,Verrucomicrobium,Verrucomicrobium sp. 3C
657931854	426	380	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
737839666	426	381	Proteobacteria	Cupriavidus basilensis	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Cupriavidus,Cupriavidus basilensis
749573752	426	382	Proteobacteria	Geoalkalibacter subterraneus	3	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfuromonadales,Geobacteraceae,Geoalkalibacter,Geoalkalibacter subterraneus
808795150	426	383	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
339834277	425	384	Proteobacteria	Acidithiobacillus sp. GGI-221	3	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus sp. GGI-221
495462176	425	385	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
503198332	425	386	Firmicutes	Caldicellulosiruptor	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor
504938402	425	387	Cyanobacteria	Synechococcus sp. PCC 6312	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 6312
517887110	425	388	Actinobacteria	Streptomyces prunicolor	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces prunicolor
652400688	425	389	Cyanobacteria	Planktothrix prolifica	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix prolifica
751564179	425	390	Cyanobacteria	Tolypothrix campylonemoides	6	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix campylonemoides
751565661	425	391	Cyanobacteria	Tolypothrix campylonemoides	6	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix campylonemoides

759990428	425	392	Actinobacteria	Streptomyces xylophagus	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces xylophagus
771515678	425	393	Firmicutes	Caldicellulosiruptor sp. Rt8.B8	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor sp. Rt8.B8
808794842	425	394	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
917397795	425	395	Firmicutes	Lactobacillus composti	8	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti
291529631	424	396	Firmicutes	Eubacterium rectale M104/1	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Eubacteriaceae,Eubacterium,Eubacterium rectale,Eubacterium rectale M104/1
493558269	424	397	Cyanobacteria	Xenococcus sp. PCC 7305	1	Bacteria,Cyanobacteria,Pleurocapsales,Xenococcus,Xenococcus sp. PCC 7305
496658465	424	398	Firmicutes	Coprobacillus sp. 3_3_56FAA	2	Bacteria,Firmicutes,Erysipelotrichia,Erysipelotrichales,Erysipelotrichaceae,Coprobacillus,Coprobacillus sp. 3_3_56FAA
501355452	424	399	Proteobacteria	Acidithiobacillus caldus	3	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus caldus
503100072	424	400	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
504891042	424	401	Cyanobacteria	Anabaena sp. 90	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena sp. 90
504975991	424	402	Cyanobacteria	Chroococcidiopsis thermalis	2	Bacteria,Cyanobacteria,Pleurocapsales,Chroococcidiopsis,Chroococcidiopsis thermalis
504975996	424	403	Cyanobacteria	Chroococcidiopsis thermalis	2	Bacteria,Cyanobacteria,Pleurocapsales,Chroococcidiopsis,Chroococcidiopsis thermalis
504992576	424	404	Cyanobacteria	Oscillatoria nigro-viridis	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria nigro-viridis
505015454	424	405	Cyanobacteria	Crinalium epipsammum	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Crinalium,Crinalium epipsammum
647307155	424	406	Firmicutes	Caldicoprobacter oshimai	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Caldicoprobacteraceae,Caldicoprobacter,Caldicoprobacter oshimai
647308279	424	407	Firmicutes	Caldicoprobacter oshimai	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Caldicoprobacteraceae,Caldicoprobacter,Caldicoprobacter oshimai
654353688	424	408	Cyanobacteria	Mastigocoleus testarum	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocoleus,Mastigocoleus testarum
657936925	424	409	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
751568033	424	410	Cyanobacteria	Tolypothrix campylonemoides	6	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix campylonemoides
769148495	424	411	Firmicutes	Anaerostipes hadrus	6	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Anaerostipes,Anaerostipes hadrus

494595516	423	412	Cyanobacteria	Kamptonema	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Kamptonema
494595821	423	413	Cyanobacteria	Kamptonema	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Kamptonema
495466012	423	414	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
501575717	423	415	Thermotogae	Thermosipho africanus	1	Bacteria,Thermotogae,Thermotogae,Thermotogales,Fervidobacteriaceae,Thermosipho,Thermosipho africanus
516255251	423	416	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
530553011	423	417	Euryarchaeota	Thermoplasmatales archaeon E-plasma	1	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,environmental samples,Thermoplasmatales archaeon E-plasma
657931856	423	418	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
740261246	423	419	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
489446257	422	420	Firmicutes	Bacillus methanolicus	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus methanolicus
501164742	422	421	Thermotogae	Petrotoga mobilis	3	Bacteria,Thermotogae,Thermotogae,Petrotogales,Petrotogaceae,Petrotoga,Petrotoga mobilis
664071344	422	422	Actinobacteria	Streptomyces fulvoviolaceus	3	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces fulvoviolaceus
739495030	422	423	Firmicutes	Selenomonas sp. FC4001	3	Bacteria,Firmicutes,Negativicutes,Selenomonadales,Veillonellaceae,Selenomonas,Selenomonas sp. FC4001
916618137	422	424	Firmicutes	Lactobacillus harbinensis	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus harbinensis
736402181	421	425	Firmicutes	Clostridiales bacterium DRI-13	4	Bacteria,Firmicutes,Clostridia,Clostridiales,unclassified Clostridiales,unclassified Clostridiales (miscellaneous),Clostridiales bacterium DRI-13
499649188	420	426	Proteobacteria	Pseudoalteromonas haloplanktis	1	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Pseudoalteromonadaceae,Pseudoalteromonas,Pseudoalteromonas haloplanktis
495460520	419	427	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
495464380	419	428	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
497357338	419	429	Firmicutes	Paenibacillus	1	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Paenibacillus
505140419	419	430	Firmicutes	Halobacteroides halobius	3	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Halobacteroides,Halobacteroides halobius
545380023	419	431	Firmicutes	Aneurinibacillus aneurinilyticus	1	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus aneurinilyticus

551011564	419	432	Firmicutes	Butyrivibrio fibrisolvens	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Butyrivibrio,Butyrivibrio fibrisolvens
759011080	419	433	Firmicutes	Aneurinibacillus migulanus	2	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus migulanus
503042356	418	434	Firmicutes	Acetohalobium arabaticum	4	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Acetohalobium,Acetohalobium arabaticum
504987354	418	435	Cyanobacteria	Oscillatoria nigro-viridis	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria nigro-viridis
521044455	418	436	Firmicutes	Sulfobacillus thermosulfidooxidans	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiales incertae sedis,Clostridiales Family XVII. Incertae Sedis,Sulfobacillus,Sulfobacillus thermosulfidooxidans
657218740	418	437	Firmicutes	Exiguobacterium oxidotolerans	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family XII. Incertae Sedis,Exiguobacterium,Exiguobacterium oxidotolerans
495197893	417	438	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
502938756	417	439	Firmicutes	[Bacillus] selenitireducens	1	Bacteria,Firmicutes,Bacilli,Bacillales,Sporolactobacillaceae,unclassified Sporolactobacillaceae,[Bacillus] selenitireducens
503769081	417	440	Proteobacteria	Acidithiobacillus caldus	3	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus caldus
517533367	417	441	Firmicutes	Anaeromusa acidaminophila	1	Bacteria,Firmicutes,Negativicutes,Selenomonadales,Veillonellaceae,Anaeromusa,Anaeromusa acidaminophila
737452652	415	442	Firmicutes	Bacillus sp. UNC322MFChir4.1	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus sp. UNC322MFChir4.1
406985418	414	443	environmental san	uncultured bacterium	1	Bacteria,environmental samples,uncultured bacterium
657936249	414	444	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
723287744	414	445	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
738422043	414	446	Firmicutes	Mitsuokella jalaludinii	1	Bacteria,Firmicutes,Negativicutes,Selenomonadales,Veillonellaceae,Mitsuokella,Mitsuokella jalaludinii
739503114	414	447	Firmicutes	Selenomonas ruminantium	1	Bacteria,Firmicutes,Negativicutes,Selenomonadales,Veillonellaceae,Selenomonas,Selenomonas ruminantium
656255040	413	448	Firmicutes	Oribacterium sp. NK2B42	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Oribacterium,Oribacterium sp. NK2B42
746610513	413	449	Firmicutes	Clostridium argentinense	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Clostridium,Clostridium argentinense

701167301	412	450	Thermotogae	Fervidobacterium islandicum	3	Bacteria,Thermotogae,Thermotogae,Thermotogales,Fervidobacteriaceae,Fervidobacterium,Fervidobacterium islandicum
769138930	412	451	Firmicutes	Oribacterium sp. FC2011	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Oribacterium,Oribacterium sp. FC2011
297555359	411	452	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
521043078	411	453	Firmicutes	Sulfobacillus thermosulfidooxidans	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiales incertae sedis,Clostridiales Family XVII. Incertae Sedis,Sulfobacillus,Sulfobacillus thermosulfidooxidans
734921353	411	454	Firmicutes	Desulfosporosinus sp. BICA1-9	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfosporosinus,Desulfosporosinus sp. BICA1-9
734927385	411	455	Firmicutes	Desulfosporosinus sp. BICA1-9	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfosporosinus,Desulfosporosinus sp. BICA1-9
736253160	411	456	Firmicutes	Bacillus sp. FJAT-14578	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus sp. FJAT-14578
518905354	410	457	Firmicutes	Bacillus sp. 123MFChir2	2	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus sp. 123MFChir2
518907476	410	458	Firmicutes	Bacillus sp. 123MFChir2	2	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Bacillus,Bacillus sp. 123MFChir2
524566620	410	459	Firmicutes	Firmicutes bacterium CAG:227	1	Bacteria,Firmicutes,environmental samples,Firmicutes bacterium CAG:227
764672287	410	460	Cyanobacteria	Mastigocladus laminosus	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladus,Mastigocladus laminosus
916839822	409	461	Firmicutes	Hungatella hathewayi	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Hungatella,Hungatella hathewayi
501427288	408	462	Firmicutes	Natranaerobius thermophilus	1	Bacteria,Firmicutes,Clostridia,Natranaerobiales,Natranaerobiaceae,Natranaerobius,Natranaerobius thermophilus
739163742	408	463	Proteobacteria	Psychromonas aquimarina	1	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Psychromonadaceae,Psychromonas,Psychromonas aquimarina
502959917	407	464	Euryarchaeota	Methanohalobium evestigatum	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanohalobium,Methanohalobium evestigatum
495125196	406	465	Bacteroidetes/Chl	Bacteroides dorei	1	Bacteria,Bacteroidetes/Chlorobi group,Bacteroidetes,Bacteroidia,Bacteroidales,Bacteroidaceae,Bacteroides,Bacteroides dorei
769922130	404	466	Cyanobacteria	Chroococcales cyanobacterium CENA595	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,unclassified Chroococcales,Chroococcales cyanobacterium CENA595
916282232	402	467	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina

297547519	401	468	Chloroflexi	Ktedonobacter racemifer DSM 44963	15	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer,Ktedonobacter racemifer DSM 44963
517215449	400	469	Proteobacteria	Marinobacter lipolyticus	4	Bacteria,Proteobacteria,Gammaproteobacteria,Alteromonadales,Alteromonadaceae,Marinobacter,Marinobacter lipolyticus
769158866	400	470	Firmicutes	Oribacterium sp. NK2B42	2	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,Oribacterium,Oribacterium sp. NK2B42
750641437	398	471	Proteobacteria	SAR324 cluster bacterium JCVI-SC AAA005	2	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,unclassified Deltaproteobacteria,SAR324 cluster,SAR324 cluster bacterium JCVI-SC AAA005
78499553	394	472	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
504963642	394	473	Cyanobacteria	Oscillatoria acuminata	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria acuminata
357260773	393	474	Cyanobacteria	Crocosphaera watsonii WH 0003	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0003
251772193	392	475	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
657199754	391	476	Cyanobacteria	Acaryochloris sp. CCMEE 5410	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Acaryochloris,Acaryochloris sp. CCMEE 5410
505011639	390	477	Cyanobacteria	Calothrix parietina	1	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix parietina
504963785	389	478	Cyanobacteria	Oscillatoria acuminata	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria acuminata
503587794	388	479	Firmicutes	Desulfotomaculum kuznetsovii	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfotomaculum,Desulfotomaculum kuznetsovii
505037351	385	480	Cyanobacteria	Halothece sp. PCC 7418	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Halothece cluster,Halothece,Halothece sp. PCC 7418
518337458	382	481	Cyanobacteria	Pleurocapsa sp. PCC 7319	2	Bacteria,Cyanobacteria,Pleurocapsales,Pleurocapsa,Pleurocapsa sp. PCC 7319
763347217	381	482	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
910241426	381	483	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
518326653	380	484	Cyanobacteria	Calothrix sp. PCC 7103	6	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix sp. PCC 7103
494517852	379	485	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii

332351493	378	486	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
493504336	377	487	Cyanobacteria	Synechococcus sp. PCC 7335	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 7335
751569099	376	488	Cyanobacteria	Tolypothrix campylonemoides	6	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix campylonemoides
915593086	374	489	Cyanobacteria	Acaryochloris sp. CCMEE 5410	4	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Acaryochloris,Acaryochloris sp. CCMEE 5410
332351757	373	490	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
503088683	373	491	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
898219347	372	492	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
493500461	371	493	Cyanobacteria	Synechococcus sp. PCC 7335	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 7335
504891808	371	494	Cyanobacteria	Anabaena sp. 90	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena sp. 90
515886569	371	495	Cyanobacteria	Mastigocladopsis repens	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladopsis,Mastigocladopsis repens
516257744	371	496	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
740253778	371	497	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
300496752	370	498	Firmicutes	Lactobacillus delbrueckii subsp. bulgaricus PB2003/044-T3-4	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii,Lactobacillus delbrueckii subsp. bulgaricus,Lactobacillus delbrueckii subsp. bulgaricus PB2003/044-T3-4
515389315	370	499	Cyanobacteria	Chlorogloeopsis fritschii	2	Bacteria,Cyanobacteria,Stigonematales,Chlorogloeopsis,Chlorogloeopsis fritschii
518333149	370	500	Cyanobacteria	Pleurocapsa sp. PCC 7319	2	Bacteria,Cyanobacteria,Pleurocapsales,Pleurocapsa,Pleurocapsa sp. PCC 7319
653153939	370	501	Cyanobacteria	Aphanizomenon flos-aquae	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Aphanizomenon,Aphanizomenon flos-aquae
755140659	370	502	Cyanobacteria	Anabaena sp. PCC 7108	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Anabaena,Anabaena sp. PCC 7108
493028331	368	503	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
493031658	368	504	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
493034793	368	505	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes

504995984	368	506	Cyanobacteria	Microcoleus sp. PCC 7113	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Microcoleus,Microcoleus sp. PCC 7113
530560580	368	507	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
759781475	367	508	Actinobacteria	Streptomyces bingchenggensis	3	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces bingchenggensis
428689568	366	509	Cyanobacteria	Halothece sp. PCC 7418	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Halothece cluster,Halothece,Halothece sp. PCC 7418
657932748	366	510	Cyanobacteria	[Scytonema hofmanni] UTEX B 1581	10	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,[Scytonema hofmanni] UTEX B 1581
493574625	365	511	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
493576687	365	512	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
503085700	365	513	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
505040939	365	514	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina
505041852	365	515	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina
505043997	365	516	Cyanobacteria	Dactylococcopsis salina	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Dactylococcopsis,Dactylococcopsis salina
515389462	365	517	Cyanobacteria	Chlorogloeopsis fritschii	2	Bacteria,Cyanobacteria,Stigonematales,Chlorogloeopsis,Chlorogloeopsis fritschii
648408069	365	518	Cyanobacteria	Prochlorothrix hollandica	3	Bacteria,Cyanobacteria,Prochlorales,Prochlorotrichaceae,Prochlorothrix,Prochlorothrix hollandica
652402791	365	519	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
723294073	365	520	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
505016981	364	521	Cyanobacteria	Crinalium epipsammum	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Crinalium,Crinalium epipsammum
515887458	364	522	Cyanobacteria	Mastigocladopsis repens	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladopsis,Mastigocladopsis repens
530558821	364	523	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
530928824	364	524	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'

764673423	364	525	Cyanobacteria	Mastigocladus laminosus	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladus,Mastigocladus laminosus
764953316	364	526	Cyanobacteria	Nostoc sp. PCC 7120	3	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nostoc,Nostoc sp. PCC 7120
917147043	364	527	Actinobacteria	Streptosporangium amethystogenes	2	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Streptosporangiaceae,Streptosporangium,Streptosporangium amethystogenes
495462462	360	528	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
723290517	360	529	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
917665054	359	530	Firmicutes	Thermincola ferriacetica	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Thermincola,Thermincola ferriacetica
654348331	358	531	Cyanobacteria	Mastigocoleus testarum	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocoleus,Mastigocoleus testarum
908671001	358	532	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
653151509	357	533	Cyanobacteria	Aphanizomenon flos-aquae	4	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Aphanizomenon,Aphanizomenon flos-aquae
654348422	357	534	Cyanobacteria	Mastigocoleus testarum	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocoleus,Mastigocoleus testarum
703193438	357	535	Cyanobacteria	Spirulina subsalsa	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Spirulina,Spirulina subsalsa
530558823	355	536	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
654100737	353	537	Firmicutes	Desulfovirgula thermocuniculi	2	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Desulfovirgula,Desulfovirgula thermocuniculi
751571642	352	538	Cyanobacteria	Tolypothrix campylonemoides	6	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix campylonemoides
723281300	351	539	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
737210796	351	540	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
915329395	351	541	Cyanobacteria	Synechococcus sp. PCC 7335	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 7335
517015347	349	542	Firmicutes	Desulfitobacterium hafniense	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfitobacterium,Desulfitobacterium hafniense
516359258	348	543	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
738590047	344	544	Proteobacteria	Nitrosococcus oceani	1	Bacteria,Proteobacteria,Gammaproteobacteria,Chromatiales,Chromatiaceae,Nitrosococcus,Nitrosococcus oceani

740235865	344	545	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
551153509	343	546	unclassified Bacter	Poribacteria bacterium WGA-3G	1	Bacteria,unclassified Bacteria,Poribacteria,Poribacteria bacterium WGA-3G
917662527	343	547	Firmicutes	Thermincola ferriacetica	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Thermincola,Thermincola ferriacetica
805384334	342	548	Euryarchaeota	Methanosarcina horonobensis HB-1 = JCM 15518	2	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina horonobensis,Methanosarcina horonobensis HB-1 = JCM 15518
515861153	341	549	Cyanobacteria	Leptolyngbya boryana	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Leptolyngbya,Leptolyngbya boryana
889965630	341	550	Cyanobacteria	Scytonema tolypothrichoides	2	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema tolypothrichoides
404657552	340	551	Proteobacteria	Sutterella wadsworthensis 2_1_59BFAA	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella wadsworthensis,Sutterella wadsworthensis 2_1_59BFAA
517015328	340	552	Firmicutes	Desulfitobacterium hafniense	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfitobacterium,Desulfitobacterium hafniense
517015320	339	553	Firmicutes	Desulfitobacterium hafniense	3	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfitobacterium,Desulfitobacterium hafniense
521041825	339	554	Firmicutes	Sulfobacillus thermosulfidooxidans	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiales incertae sedis,Clostridiales Family XVII. Incertae Sedis,Sulfobacillus,Sulfobacillus thermosulfidooxidans
521051118	339	555	unclassified Bacter	Candidatus Poribacteria sp. WGA-4E	1	Bacteria,unclassified Bacteria,Poribacteria,Candidatus Poribacteria sp. WGA-4E
503167640	338	556	Firmicutes	Caldicellulosiruptor hydrothermalis	2	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacterales Family III. Incertae Sedis,Caldicellulosiruptor,Caldicellulosiruptor hydrothermalis
851307650	338	557	Euryarchaeota	Methanosarcina sp. 2.H.A.1B.4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.A.1B.4
428001463	337	558	Cyanobacteria	Oscillatoria acuminata PCC 6304	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Oscillatoria,Oscillatoria acuminata,Oscillatoria acuminata PCC 6304
495475865	337	559	Cyanobacteria	Microcystis sp. T1-4	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis sp. T1-4
496140048	336	560	Proteobacteria	Parasutterella excrementihominis	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis
516257779	336	561	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105

588475866	335	562	Firmicutes	Lactobacillus composti DSM 18527 = JCM 14202	3	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti,Lactobacillus composti DSM 18527 = JCM 14202
919167216	333	563	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
332349884	332	564	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
654624416	331	565	Cyanobacteria	Dolichospermum circinale	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Dolichospermum,Dolichospermum circinale
196178704	327	566	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
736399397	326	567	Firmicutes	Clostridiales bacterium DRI-13	4	Bacteria,Firmicutes,Clostridia,Clostridiales,unclassified Clostridiales,unclassified Clostridiales (miscellaneous),Clostridiales bacterium DRI-13
917128556	325	568	Actinobacteria	Streptomyces	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces
17135565	323	569	Cyanobacteria	Nostoc sp. PCC 7120	3	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nostoc,Nostoc sp. PCC 7120
898215951	323	570	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
917059029	322	571	Firmicutes	Erysipelotrichaceae bacterium NK3D112	1	Bacteria,Firmicutes,Erysipelotrichia,Erysipelotrichales,Erysipelotrichaceae,unclassified Erysipelotrichaceae,unclassified Erysipelotrichaceae (miscellaneous),Erysipelotrichaceae bacterium NK3D112
750683094	321	572	Cyanobacteria	Planktothrix mougeotii	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix mougeotii
490700480	318	573	Firmicutes	Lactobacillus salivarius	11	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus salivarius
764667589	316	574	Cyanobacteria	Mastigocladus laminosus	4	Bacteria,Cyanobacteria,Stigonematales,Mastigocladus,Mastigocladus laminosus
919167264	316	575	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
763349201	313	576	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
737769353	312	577	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
880798173	310	578	Cyanobacteria	Moorea bouillonii PNG5-198	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea bouillonii,Moorea bouillonii PNG5-198
516757976	307	579	Firmicutes	Desulfurispora thermophila	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,Desulfurispora,Desulfurispora thermophila

727076115	307	580	Firmicutes	Anoxybacillus sp. BCO1	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus sp. BCO1
917359539	307	581	Firmicutes	Clostridiales bacterium DRI-13	4	Bacteria,Firmicutes,Clostridia,Clostridiales,unclassified Clostridiales,unclassified Clostridiales (miscellaneous),Clostridiales bacterium DRI-13
737120430	305	582	Firmicutes	Desulfovirgula thermocuniculi	2	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Desulfovirgula,Desulfovirgula thermocuniculi
919167308	304	583	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
763282104	303	584	Proteobacteria	Succinimonas amylolytica	1	Bacteria,Proteobacteria,Gammaproteobacteria,Aeromonadales,Succinivibrionaceae,Succinimonas,Succinimonas amylolytica
312281242	301	585	Firmicutes	Lactobacillus delbrueckii subsp. bulgaricus ND02	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus delbrueckii,Lactobacillus delbrueckii subsp. bulgaricus,Lactobacillus delbrueckii subsp. bulgaricus ND02
763057626	300	586	Cyanobacteria	Planktothrix prolifica	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix prolifica
493535324	299	587	Thermotogae	Mesotoga infera	1	Bacteria,Thermotogae,Thermotogae,Kosmotogales,Kosmotogaceae,Mesotoga,Mesotoga infera
499805551	299	588	Proteobacteria	Polaromonas sp. JS666	3	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Comamonadaceae,Polaromonas,Polaromonas sp. JS666
919167330	295	589	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
196179440	292	590	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
124514584	291	591	Nitrospirae	Leptospirillum rubarum	2	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group II,Leptospirillum rubarum
588476658	289	592	Firmicutes	Lactobacillus composti DSM 18527 = JCM 14202	3	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti,Lactobacillus composti DSM 18527 = JCM 14202
902595239	289	593	Firmicutes	Geobacillus stearothermophilus	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Geobacillus,Geobacillus stearothermophilus
496087940	287	594	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47

334181048	283	595	Firmicutes	Caldalkalibacillus thermarum TA2.A1	2	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Caldalkalibacillus,Caldalkalibacillus thermarum,Caldalkalibacillus thermarum TA2.A1
809070817	280	596	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091
814727436	278	597	Euryarchaeota	Methanosarcina sp. 2.H.A.1B.4	4	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.A.1B.4
124514585	276	598	Nitrospirae	Leptospirillum rubarum	2	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group II,Leptospirillum rubarum
332351076	276	599	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
196187499	275	600	Cyanobacteria	Synechococcus sp. PCC 7335	6	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Synechococcus,Synechococcus sp. PCC 7335
648259526	271	601	Firmicutes	Sulfobacillus thermosulfidooxidans	4	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiales incertae sedis,Clostridiales Family XVII. Incertae Sedis,Sulfobacillus,Sulfobacillus thermosulfidooxidans
339836119	270	602	Proteobacteria	Acidithiobacillus sp. GGI-221	3	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus sp. GGI-221
530557143	270	603	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
558532298	269	604	Actinobacteria	Streptomyces roseochromogenus subsp. oscitans DS 12.976	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces roseochromogenus,Streptomyces roseochromogenus subsp. oscitans,Streptomyces roseochromogenus subsp. oscitans DS 12.976
655460615	265	605	Thermotogae	Pseudothermotoga elfii	2	Bacteria,Thermotogae,Thermotogae,Thermotogales,Thermotogaceae,Pseudothermotoga,Pseudothermotoga elfii
119463013	263	606	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
302858720	263	607	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
530929278	263	608	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
406714585	261	609	Cyanobacteria	Arthrospira platensis C1	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis,Arthrospira platensis C1

763116037	260	610	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
196181015	257	611	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
530558507	252	612	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
898209016	252	613	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
918699942	252	614	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
916344013	251	615	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
543515433	250	616	Cyanobacteria	Crocosphaera watsonii WH 8502	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 8502
851263164	246	617	Euryarchaeota	Methanosarcina sp. 2.H.T.1A.3	2	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. 2.H.T.1A.3
652325204	245	618	Cyanobacteria	Fischerella sp. PCC 9431	3	Bacteria,Cyanobacteria,Stigonematales,Fischerella,Fischerella sp. PCC 9431
738947798	245	619	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
750138933	242	620	Chloroflexi	Ktedonobacter racemifer	52	Bacteria,Chloroflexi,Ktedonobacteria,Ktedonobacterales,Ktedonobacteraceae,Ktedonobacter,Ktedonobacter racemifer
908628614	241	621	Firmicutes	Acetohalobium arabaticum	4	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Acetohalobium,Acetohalobium arabaticum
119463753	239	622	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
260864875	234	623	Firmicutes	Ammonifex degensii KC4	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Moorella group,Ammonifex,Ammonifex degensii,Ammonifex degensii KC4
917378091	234	624	Proteobacteria	Acidithiobacillus ferrivorans	11	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus ferrivorans
738378477	233	625	Tenericutes	Mollicutes bacterium HR2	1	Bacteria,Tenericutes,Mollicutes,unclassified Mollicutes,unclassified Mollicutes (miscellaneous),Mollicutes bacterium HR2
919167253	231	626	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris

332351060	230	627	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
357261355	228	628	Cyanobacteria	Crocosphaera watsonii WH 0003	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0003
157313573	227	629	Thermotogae	Pseudothermotoga lettingae TMO	2	Bacteria,Thermotogae,Thermotogae,Thermotogales,Thermotogaceae,Pseudothermotoga,Pseudothermotoga lettingae,Pseudothermotoga lettingae TMO
251771570	224	630	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
302858718	224	631	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
196180239	223	632	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
723287742	223	633	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
179352487	222	634	Firmicutes	Natranaerobius thermophilus JW/NM-WN-LF	1	Bacteria,Firmicutes,Clostridia,Natranaerobiales,Natranaerobiaceae,Natranaerobius,Natranaerobius thermophilus,Natranaerobius thermophilus JW/NM-WN-LF
917775145	220	635	Cyanobacteria	Scytonema millei	2	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema millei
919167263	218	636	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
119461613	214	637	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
914401554	214	638	Cyanobacteria	Microcystis panniformis FACHB-1757	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis panniformis,Microcystis panniformis FACHB-1757
16611907	212	639	cellular organisms	Taxus wallichiana var. chinensis	1	Eukaryota,Viridiplantae,Streptophyta,Streptophytina,Embryophyta,Tracheophyta,Euphyllophyta,Spermatophyta,Acrogymnospermae,Pinidae,Cupressales,Taxaceae,Taxus,Taxus wallichiana,Taxus wallichiana var. chinensis
378599067	208	640	Proteobacteria	Sutterella parvirubra YIT 11816	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella parvirubra,Sutterella parvirubra YIT 11816

316895289	207	641	Firmicutes	Lachnospiraceae bacterium 5_1_63FAA	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Lachnospiraceae,unclassified Lachnospiraceae,Lachnospiraceae bacterium 5_1_63FAA
737152716	206	642	Cyanobacteria	Fischerella sp. PCC 9605	1	Bacteria,Cyanobacteria,Stigonematales,Fischerella,Fischerella sp. PCC 9605
763117433	206	643	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
302859206	205	644	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
543532102	205	645	Cyanobacteria	Crocosphaera watsonii WH 0402	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0402
564135307	205	646	Firmicutes	Youngiibacter fragilis 232.1	7	Bacteria,Firmicutes,Clostridia,Clostridiales,Clostridiaceae,Youngiibacter,Youngiibacter fragilis,Youngiibacter fragilis 232.1
918374422	204	647	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
546230530	203	648	Cyanobacteria	Crocosphaera watsonii	14	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii
805338714	203	649	Euryarchaeota	Methanosarcina sp. WWM596	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WWM596
428237825	202	650	Cyanobacteria	Calothrix sp. PCC 6303	1	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix parietina,Calothrix sp. PCC 6303
916309170	202	651	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
291570420	201	652	Cyanobacteria	Arthrospira platensis NIES-39	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis,Arthrospira platensis NIES-39
516358073	200	653	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
78499559	197	654	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
916309171	197	655	Cyanobacteria	Geitlerinema sp. PCC 7105	18	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Geitlerinema,Geitlerinema sp. PCC 7105
916344012	196	656	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
516356583	192	657	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
825911310	191	658	Firmicutes	Aneurinibacillus tyrosinisolvens	5	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus tyrosinisolvens

306985451	187	659	Cyanobacteria	Cyanothece sp. PCC 7822	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Cyanothece,Cyanothece sp. PCC 7822
516146108	187	660	Actinobacteria	Nocardiopsis kunsanensis	3	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis kunsanensis
763155591	187	661	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
908628613	187	662	Firmicutes	Acetohalobium arabaticum	4	Bacteria,Firmicutes,Clostridia,Halanaerobiales,Halobacteroidaceae,Acetohalobium,Acetohalobium arabaticum
763117162	186	663	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
209491336	184	664	Cyanobacteria	Arthrospira maxima CS-328	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima,Arthrospira maxima CS-328
916968425	183	665	Firmicutes	Sporolactobacillus terrae	1	Bacteria,Firmicutes,Bacilli,Bacillales,Sporolactobacillaceae,Sporolactobacillus,Sporolactobacillus terrae
209491231	180	666	Cyanobacteria	Arthrospira maxima CS-328	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira maxima,Arthrospira maxima CS-328
332351061	180	667	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
431999864	179	668	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
765303043	177	669	Proteobacteria	Halomonas meridiana	3	Bacteria,Proteobacteria,Gammaproteobacteria,Oceanospirillales,Halomonadaceae,Halomonas,Halomonas meridiana
825857133	177	670	Firmicutes	Aneurinibacillus tyrosinisolvens	5	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus tyrosinisolvens
805377640	176	671	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
917312938	175	672	Actinobacteria	Streptomyces sp. NRRL F-5140	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. NRRL F-5140
763155413	174	673	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
500832884	173	674	Thermotogae	Pseudothermotoga lettingae	2	Bacteria,Thermotogae,Thermotogae,Thermotogales,Thermotogaceae,Pseudothermotoga,Pseudothermotoga lettingae
517209446	173	675	Cyanobacteria	filamentous cyanobacterium ESFC-1	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,unclassified Oscillatoriales,filamentous cyanobacterium ESFC-1

530927867	173	676	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
763054851	171	677	Cyanobacteria	Planktothrix rubescens	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix rubescens
805377641	168	678	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
119462723	164	679	Cyanobacteria	Nodularia spumigena CCY9414	12	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Nodularia,Nodularia spumigena,Nodularia spumigena CCY9414
297143449	161	680	Firmicutes	[Bacillus] selenitireducens MLS10	2	Bacteria,Firmicutes,Bacilli,Bacillales,Sporolactobacillaceae,unclassified Sporolactobacillaceae,[Bacillus] selenitireducens,[Bacillus] selenitireducens MLS10
442790558	161	681	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
530557142	161	682	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
332351077	160	683	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
488892048	160	684	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
530560466	160	685	Euryarchaeota	Ferroplasma sp. Type II	16	Archaea,Euryarchaeota,Thermoplasmata,Thermoplasmatales,Ferroplasmaceae,Ferroplasma,environmental samples,Ferroplasma sp. Type II
737791031	157	686	Cyanobacteria	Arthrospira	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira
779875597	157	687	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
495466059	156	688	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
898216031	156	689	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
334181047	154	690	Firmicutes	Caldalkalibacillus thermarum TA2.A1	2	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Caldalkalibacillus,Caldalkalibacillus thermarum,Caldalkalibacillus thermarum TA2.A1
389829748	153	691	Cyanobacteria	Microcystis aeruginosa PCC 9809	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 9809
406713030	153	692	Cyanobacteria	Arthrospira platensis C1	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis,Arthrospira platensis C1

753833694	153	693	Firmicutes	Thermoanaerobacter wiegelii	1	Bacteria,Firmicutes,Clostridia,Thermoanaerobacterales,Thermoanaerobacteraceae,Thermoanaerobacter,Thermoanaerobacter wiegelii
805377874	151	694	Euryarchaeota	Methanosarcina lacustris Z-7289	17	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris,Methanosarcina lacustris Z-7289
159030837	150	695	Cyanobacteria	Microcystis aeruginosa PCC 7806	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 7806
851249382	150	696	Euryarchaeota	Methanosarcina	2	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina
543515434	149	697	Cyanobacteria	Crocosphaera watsonii WH 8502	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 8502
543532038	149	698	Cyanobacteria	Crocosphaera watsonii WH 0402	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0402
744449740	149	699	Cyanobacteria	Tolypothrix bouteillei VB521301	1	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei,Tolypothrix bouteillei VB521301
329571287	148	700	Proteobacteria	Parasutterella excrementihominis YIT 11859	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis,Parasutterella excrementihominis YIT 11859
329571288	147	701	Proteobacteria	Parasutterella excrementihominis YIT 11859	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis,Parasutterella excrementihominis YIT 11859
750683093	147	702	Cyanobacteria	Planktothrix mougeotii	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix mougeotii
809069588	143	703	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091
898209176	143	704	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
196181246	142	705	Cyanobacteria	Coleofasciculus chthonoplastes PCC 7420	16	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes,Coleofasciculus chthonoplastes PCC 7420
748630019	140	706	Cyanobacteria	Microcoleus vaginatus	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Microcoleus,Microcoleus vaginatus
442790478	139	707	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
332349885	138	708	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L

783187507	136	709	Firmicutes	Peptococcaceae bacterium BRH_c23	1	Bacteria,Firmicutes,Clostridia,Clostridiales,Peptococcaceae,unclassified Peptococcaceae,Peptococcaceae bacterium BRH_c23
302859777	135	710	Proteobacteria	Burkholderiales bacterium 1_1_47	14	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,unclassified Burkholderiales,unclassified Burkholderiales (miscellaneous),Burkholderiales bacterium 1_1_47
851296135	135	711	Euryarchaeota	Methanosarcina sp. WWM596	5	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina sp. WWM596
919167354	134	712	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
78499563	133	713	Cyanobacteria	Arthrospira platensis	20	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis
357263981	132	714	Cyanobacteria	Crocosphaera watsonii WH 0003	5	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Crocosphaera,Crocosphaera watsonii,Crocosphaera watsonii WH 0003
919167307	132	715	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
530929275	130	716	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
915406150	130	717	Proteobacteria	Parasutterella excrementihominis	4	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis
442790313	122	718	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
432002280	118	719	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
817701219	114	720	Cyanobacteria	Microcystis aeruginosa	35	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa
329570321	110	721	Proteobacteria	Parasutterella excrementihominis YIT 11859	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis,Parasutterella excrementihominis YIT 11859
518324131	110	722	Cyanobacteria	Calothrix sp. PCC 7103	6	Bacteria,Cyanobacteria,Nostocales,Rivulariaceae,Calothrix,Calothrix sp. PCC 7103
516042537	109	723	Firmicutes	Amphibacillus jilinensis	1	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Amphibacillus,Amphibacillus jilinensis

329571485	108	724	Proteobacteria	Parasutterella excrementihominis YIT 11859	6	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Parasutterella,Parasutterella excrementihominis,Parasutterella excrementihominis YIT 11859
516150425	107	725	Actinobacteria	Nocardiopsis valliformis	1	Bacteria,Actinobacteria,Actinobacteria,Streptosporangiales,Nocardiopsaceae,Nocardiopsis,Nocardiopsis valliformis
809072688	107	726	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091
493037492	106	727	Cyanobacteria	Coleofasciculus chthonoplastes	25	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Coleofasciculus,Coleofasciculus chthonoplastes
378597560	105	728	Proteobacteria	Sutterella parvirubra YIT 11816	2	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Sutterellaceae,Sutterella,Sutterella parvirubra,Sutterella parvirubra YIT 11816
652435818	105	729	Firmicutes	Exiguobacterium antarcticum	3	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillales incertae sedis,Bacillales Family XII. Incertae Sedis,Exiguobacterium,Exiguobacterium antarcticum
908364976	105	730	Proteobacteria	Candidatus Burkholderia kirkii	1	Bacteria,Proteobacteria,Betaproteobacteria,Burkholderiales,Burkholderiaceae,Burkholderia,Candidatus Burkholderia kirkii
588475865	104	731	Firmicutes	Lactobacillus composti DSM 18527 = JCM 14202	3	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus composti,Lactobacillus composti DSM 18527 = JCM 14202
386780378	103	732	unclassified seque	uncultured microorganism	1	unclassified sequences,environmental samples,uncultured microorganism
339833897	102	733	Proteobacteria	Acidithiobacillus sp. GGI-221	3	Bacteria,Proteobacteria,Gammaproteobacteria,Acidithiobacillales,Acidithiobacillaceae,Acidithiobacillus,Acidithiobacillus sp. GGI-221
919167331	102	734	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
723292966	99	735	Proteobacteria	Candidatus Thiomargarita nelsonii	10	Bacteria,Proteobacteria,Gammaproteobacteria,Thiotrichales,Thiotrichaceae,Thiomargarita,Candidatus Thiomargarita nelsonii
495461462	98	736	Cyanobacteria	Moorea producens	19	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens
738948970	97	737	Cyanobacteria	Planktothrix	8	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix
809068062	97	738	Cyanobacteria	Arthrospira sp. TJSD091	7	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira sp. TJSD091
347588852	94	739	Fibrobacteres/Aci	Chloracidobacterium thermophilum B	2	Bacteria,Fibrobacteres/Acidobacteria group,Acidobacteria,unclassified Acidobacteria,Acidobacteria subdivision 4,Chloracidobacterium,Chloracidobacterium thermophilum,Chloracidobacterium thermophilum B

664453855	94	740	Actinobacteria	Streptomyces sp. NRRL S-1824	1	Bacteria,Actinobacteria,Actinobacteria,Streptomycetales,Streptomycetaceae,Streptomyces,Streptomyces sp. NRRL S-1824
749573730	94	741	Proteobacteria	Geoalkalibacter subterraneus	3	Bacteria,Proteobacteria,delta/epsilon subdivisions,Deltaproteobacteria,Desulfuromonadales,Geobacteraceae,Geoalkalibacter,Geoalkalibacter subterraneus
919167215	93	742	Euryarchaeota	Methanosarcina lacustris	60	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina lacustris
432001269	92	743	Firmicutes	Anoxybacillus flavithermus TNO-09.006	8	Bacteria,Firmicutes,Bacilli,Bacillales,Bacillaceae,Anoxybacillus,Anoxybacillus flavithermus,Anoxybacillus flavithermus TNO-09.006
530928122	92	744	Nitrospirae	Leptospirillum sp. Group IV 'UBA BS'	8	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group IV,Leptospirillum sp. Group IV 'UBA BS'
825923929	89	745	Firmicutes	Aneurinibacillus tyrosinisolvens	5	Bacteria,Firmicutes,Bacilli,Bacillales,Paenibacillaceae,Aneurinibacillus group,Aneurinibacillus,Aneurinibacillus tyrosinisolvens
898220383	89	746	Cyanobacteria	Limnoraphis robusta	9	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Limnoraphis,Limnoraphis robusta
442790314	88	747	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
919175030	87	748	Euryarchaeota	Methanosarcina horonobensis	3	Archaea,Euryarchaeota,Methanomicrobia,Methanosarcinales,Methanosarcinaceae,Methanosarcina,Methanosarcina horonobensis
516353505	86	749	Cyanobacteria	Scytonema hofmanni	13	Bacteria,Cyanobacteria,Nostocales,Scytonemataceae,Scytonema,Scytonema hofmanni
754794025	85	750	Cyanobacteria	Planktothrix agardhii	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix agardhii
407874586	82	751	Firmicutes	Lactobacillus equicursoris 66c	1	Bacteria,Firmicutes,Bacilli,Lactobacillales,Lactobacillaceae,Lactobacillus,Lactobacillus equicursoris,Lactobacillus equicursoris 66c
389833116	75	752	Cyanobacteria	Microcystis aeruginosa PCC 9809	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Microcystis,Microcystis aeruginosa,Microcystis aeruginosa PCC 9809
442787585	75	753	Cyanobacteria	Gloeocapsa sp. PCC 73106	24	Bacteria,Cyanobacteria,Oscillatoriophycideae,Chroococcales,Gloeocapsa,Gloeocapsa sp. PCC 73106
910241825	75	754	Cyanobacteria	Tolypothrix bouteillei	9	Bacteria,Cyanobacteria,Nostocales,Microchaetaceae,Tolypothrix,Tolypothrix bouteillei
577004405	74	755	Proteobacteria	Candidatus Contendobacter odensis Run_B_J11	2	Bacteria,Proteobacteria,Gammaproteobacteria,unclassified Gammaproteobacteria,Competibacteraceae,Candidatus Contendobacter,Candidatus Contendobacter odensis,Candidatus Contendobacter odensis Run_B_J11

658298958	67	756	Cyanobacteria	Planktothrix agardhii NIVA-CYA 126/8	1	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Planktothrix,Planktothrix agardhii,Planktothrix agardhii NIVA-CYA 126/8
251773296	66	757	Nitrospirae	Leptospirillum ferrodiazotrophum	14	Bacteria,Nitrospirae,Nitrospira,Nitrospirales,Nitrospiraceae,Leptospirillum,Leptospirillum sp. Group III,Leptospirillum ferrodiazotrophum
752561796	62	758	Cyanobacteria	Cylindrospermum stagnale	2	Bacteria,Cyanobacteria,Nostocales,Nostocaceae,Cylindrospermum,Cylindrospermum stagnale
332353787	61	759	Cyanobacteria	Moorea producens 3L	12	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Moorea,Moorea producens,Moorea producens 3L
406710894	56	760	Cyanobacteria	Arthrospira platensis C1	3	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis,Arthrospira platensis C1
291567395	51	761	Cyanobacteria	Arthrospira platensis NIES-39	2	Bacteria,Cyanobacteria,Oscillatoriophycideae,Oscillatoriales,Arthrospira,Arthrospira platensis,Arthrospira platensis NIES-39

Supplementary Table 2

Genome	Phylum	COG3513 (Cas9)	pfam14239 (RRxRR or ISC)	COG0675 (IS605, TnpB)	COG1943 (Y1 tyrosine recombinase)	COG2452 (Serine transposase)
Acidilobus_saccharovorans_345_15_uid5	Acidilobales	0	0	1	0	2
Caldisphaera_lagunensis_DSM_15908_ui	Acidilobales	0	0	0	0	0
Aeropyrum_camini_SY1___JCM_12091_u	Desulfurococcales	0	0	1	0	1
Aeropyrum_pernix_K1_uid57757	Desulfurococcales	0	0	1	0	0
Desulfurococcus_fermentans_DSM_1653	Desulfurococcales	0	0	1	0	0
Desulfurococcus_kamchatkensis_1221n_	Desulfurococcales	0	0	8	1	17
Desulfurococcus_mucosus_DSM_2162_ui	Desulfurococcales	0	0	6	0	2
Ignicoccus_hospitalis_KIN4_I_uid58365	Desulfurococcales	0	0	0	0	0
Ignisphaera_aggregans_DSM_17230_uid5	Desulfurococcales	0	0	3	0	0
Staphylothermus_hellenicus_DSM_12710	Desulfurococcales	0	0	6	0	2
Staphylothermus_marinus_F1_uid58719	Desulfurococcales	0	0	5	0	1
Thermogladius_1633_uid167488	Desulfurococcales	0	0	4	0	5
Thermosphaera_aggregans_DSM_11486_	Desulfurococcales	0	0	1	0	2
Hyperthermus_butylicus_DSM_5456_uid	Desulfurococcales	0	0	1	0	0
Pyrolobus_fumarii_1A_uid73415	Desulfurococcales	0	0	1	0	0
Fervidicoccus_fontis_Kam940_uid162201	Fervidicoccales	0	0	1	0	0
Acidianus_hospitalis_W1_uid66875	Sulfolobales	0	0	17	0	8
Metallosphaera_cuprina_Ar_4_uid66329	Sulfolobales	0	0	1	0	0
Metallosphaera_sedula_DSM_5348_uid5	Sulfolobales	0	0	4	1	2
Sulfolobus_acidocaldarius_DSM_639_uid	Sulfolobales	0	0	5	0	2
Sulfolobus_acidocaldarius_N8_uid189027	Sulfolobales	0	0	5	0	2
Sulfolobus_acidocaldarius_Ron12_I_uid1	Sulfolobales	0	0	5	0	2
Sulfolobus_acidocaldarius_SUSAZ_uid232	Sulfolobales	0	0	4	0	0
Sulfolobus_islandicus_HVE10_4_uid1620	Sulfolobales	0	0	23	4	2
Sulfolobus_islandicus_L_D_8_5_uid43679	Sulfolobales	0	0	14	6	15
Sulfolobus_islandicus_L_S_2_15_uid5887	Sulfolobales	0	0	13	7	10
Sulfolobus_islandicus_LAL14_1_uid19721	Sulfolobales	0	0	12	4	0
Sulfolobus_islandicus_M_14_25_uid5884	Sulfolobales	0	0	5	2	2
Sulfolobus_islandicus_M_16_27_uid5885	Sulfolobales	0	0	6	2	0
Sulfolobus_islandicus_M_16_4_uid58841	Sulfolobales	0	0	13	4	3
Sulfolobus_islandicus_REY15A_uid162071	Sulfolobales	0	0	30	7	2
Sulfolobus_islandicus_Y_G_57_14_uid58	Sulfolobales	0	0	22	0	26
Sulfolobus_islandicus_Y_N_15_51_uid58	Sulfolobales	0	0	21	0	35
Sulfolobus_solfataricus_98_2_uid167998	Sulfolobales	0	0	23	1	20
Sulfolobus_solfataricus_P2_uid57721	Sulfolobales	0	0	42	2	40
Sulfolobus_tokodaii_7_uid57807	Sulfolobales	0	0	20	7	8
Thermofilum_pendens_Hrk_5_uid58563	Thermoproteales	0	0	0	0	0
Thermofilum_1910b_uid215374	Thermoproteales	0	0	0	0	0
Caldivirga_maquilingensis_IC_167_uid58	Thermoproteales	0	0	5	0	2
Pyrobaculum_aerophilum_IM2_uid57727	Thermoproteales	0	0	5	0	0
Pyrobaculum_arsenaticum_DSM_13514_	Thermoproteales	0	0	1	0	0
Pyrobaculum_calidifontis_JCM_11548_ui	Thermoproteales	0	0	3	0	0
Pyrobaculum_islandicum_DSM_4184_uid	Thermoproteales	0	0	41	0	0
Pyrobaculum_neutrophilum_V24Sta_uid	Thermoproteales	0	0	6	0	0
Pyrobaculum_oguniense_TE7_uid84411	Thermoproteales	0	0	3	0	0
Pyrobaculum_1860_uid82379	Thermoproteales	0	0	10	0	0
Thermoproteus_tenax_Kra_1_uid74443	Thermoproteales	0	0	9	0	0
Thermoproteus_uzoniensis_768_20_uid6	Thermoproteales	0	0	1	0	0
Vulcanisaeta_distributa_DSM_14429_uid	Thermoproteales	0	0	2	0	0
Vulcanisaeta_moutnovskia_768_28_uid6	Thermoproteales	0	0	10	1	0
Archaeoglobus_fulgidus_DSM_4304_uid5	Archaeoglobi	0	0	0	0	0

Archaeoglobus_profundus_DSM_5631_ui	Archaeoglobi	0	0	9	1	2
Archaeoglobus_sulfaticallidus_PM70_1_u	Archaeoglobi	0	0	15	3	0
Archaeoglobus_veneficus_SNP6_uid6526	Archaeoglobi	0	0	3	0	0
Ferroglobus_placidus_DSM_10642_uid40	Archaeoglobi	0	0	1	0	2
Halalkalicoccus_jeotgali_B3_uid50305	Halobacteria	0	0	3	1	0
Haloarcula_hispanica_ATCC_33960_uid7	Halobacteria	0	0	4	1	0
Haloarcula_hispanica_N601_uid230920	Halobacteria	0	0	5	1	0
Haloarcula_marismortui_ATCC_43049_ui	Halobacteria	0	0	13	2	0
Halobacterium_salinarum_R1_uid61571	Halobacteria	0	0	12	4	0
Halobacterium_NRC_1_uid57769	Halobacteria	0	0	10	4	0
Haloferax_mediterranei_ATCC_33500_ui	Halobacteria	0	0	6	1	0
Haloferax_volcanii_DS2_uid46845	Halobacteria	0	0	7	2	0
Halogeometricum_borinquense_DSM_11	Halobacteria	0	0	16	2	0
Halomicrobium_mukohataei_DSM_1228	Halobacteria	0	0	8	3	0
Halopiger_xanaduensis_SH_6_uid68105	Halobacteria	0	0	1	0	0
Haloquadratum_walsbyi_C23_uid162019	Halobacteria	0	0	5	0	0
Haloquadratum_walsbyi_DSM_16790_ui	Halobacteria	0	0	21	1	2
Halorhabdus_tiamatea_SARL4B_uid2140	Halobacteria	0	0	23	4	0
Halorhabdus_utahensis_DSM_12940_uid	Halobacteria	0	0	9	1	0
Halorubrum_lacusprofundi_ATCC_49239_	Halobacteria	0	0	23	9	0
Haloterrigena_turkmenica_DSM_5511_ui	Halobacteria	0	0	7	0	0
Halovivax_ruber_XH_70_uid184819	Halobacteria	0	0	5	1	0
Natrialba_magadii_ATCC_43099_uid4624	Halobacteria	0	0	21	1	2
Natrinema_pellirubrum_DSM_15624_uid	Halobacteria	0	0	18	1	0
Natrinema_J7_uid171337	Halobacteria	0	0	3	0	0
Natronobacterium_gregoryi_SP2_uid744	Halobacteria	0	0	10	2	0
Natronococcus_occultus_SP4_uid184863	Halobacteria	0	0	13	0	0
Natronomonas_moolapensis_8_8_11_uid	Halobacteria	0	0	15	4	0
Natronomonas_pharaonis_DSM_2160_ui	Halobacteria	0	0	36	3	0
Salinarchaeum_laminariae_Harcht_Bsk1_	Halobacteria	0	0	0	0	0
Methanobacterium_AL_21_uid63623	Methanobacteria	0	0	0	0	0
Methanobacterium_MB1_uid231690	Methanobacteria	0	0	0	0	0
Methanobacterium_SWAN_1_uid67359	Methanobacteria	0	0	0	0	0
Methanobrevibacter_ruminantium_M1_	Methanobacteria	0	0	0	0	0
Methanobrevibacter_smithii_ATCC_3506	Methanobacteria	0	0	1	0	0
Methanobrevibacter_AbM4_uid206516	Methanobacteria	0	0	0	0	0
Methanosphaera_stadtmanae_DSM_309	Methanobacteria	0	0	1	0	0
Methanothermobacter_marburgensis_M	Methanobacteria	0	0	0	0	0
Methanothermobacter_thermautotrophi	Methanobacteria	0	0	0	0	0
Methanothermus_fervidus_DSM_2088_u	Methanobacteria	0	0	1	0	0
Methanocaldococcus_fervens_AG86_uid	Methanococci	0	0	1	0	2
Methanocaldococcus_infernus_ME_uid4	Methanococci	0	0	0	0	0
Methanocaldococcus_jannaschii_DSM_2	Methanococci	0	0	3	0	2
Methanocaldococcus_FS406_22_uid4249	Methanococci	0	0	9	1	2
Methanocaldococcus_vulcanius_M7_uid4	Methanococci	0	0	2	0	0
Methanotorris_igneus_Kol_5_uid67321	Methanococci	0	0	10	0	8
Methanococcus_aeolicus_Nankai_3_uid5	Methanococci	0	0	3	0	0
Methanococcus_maripaludis_C5_uid5874	Methanococci	0	0	0	0	0
Methanococcus_maripaludis_C6_uid5894	Methanococci	0	0	0	0	0
Methanococcus_maripaludis_C7_uid5884	Methanococci	0	0	0	0	0
Methanococcus_maripaludis_S2_uid5803	Methanococci	0	0	0	0	0
Methanococcus_maripaludis_X1_uid7072	Methanococci	0	0	0	0	0
Methanococcus_vannielii_SB_uid58767	Methanococci	0	0	0	0	0
Methanococcus_voltae_A3_uid49529	Methanococci	0	0	0	0	0
Methanothermococcus_okinawensis_IH1	Methanococci	0	0	1	0	0
Methanocella_arvoryzae_MRE50_uid616	Methanomicrobia	0	0	0	0	0

Methanocella_conradii_HZ254_uid15791	Methanomicrobia	0	0	10	2	0
Methanocella_paludicola_SANAE_uid428	Methanomicrobia	0	0	0	0	0
Methanocorpusculum_labreanum_Z_uid5	Methanomicrobia	0	0	0	0	0
Methanoculleus_bourgensis_MS2_uid171	Methanomicrobia	0	0	12	0	0
Methanoculleus_marisnigri_JR1_uid5856	Methanomicrobia	0	0	0	0	0
Methanoplanus_petrolearius_DSM_1157	Methanomicrobia	0	0	1	0	1
Methanoregula_boonei_6A8_uid58815	Methanomicrobia	0	0	1	0	0
Methanoregula_formicicum_SMSP_uid18	Methanomicrobia	0	0	0	0	1
Methanosphaerula_palustris_E1_9c_uid5	Methanomicrobia	0	0	0	0	0
Methanospirillum_hungatei_JF_1_uid581	Methanomicrobia	0	0	0	0	0
Methanosaeta_concilii_GP6_uid66207	Methanomicrobia	0	0	40	6	0
Methanosaeta_harundinacea_6Ac_uid81	Methanomicrobia	0	0	8	1	0
Methanosaeta_thermophila_PT_uid5846	Methanomicrobia	0	0	2	0	0
Methanococcoides_burtonii_DSM_6242_	Methanomicrobia	0	0	4	0	0
Methanohalobium_evestigatum_Z_7303_	Methanomicrobia	0	5	60	2	6
Methanohalophilus_mahii_DSM_5219_ui	Methanomicrobia	0	0	4	0	0
Methanolobus_psychrophilus_R15_uid17	Methanomicrobia	0	0	16	2	0
Methanomethylovorans_hollandica_DSM	Methanomicrobia	0	0	18	3	0
Methanosalsum_zhilinae_DSM_4017_uid	Methanomicrobia	0	0	5	1	0
Methanosarcina_acetivorans_C2A_uid57	Methanomicrobia	0	0	6	2	0
Methanosarcina_barkeri_Fusaro_uid5771	Methanomicrobia	0	0	16	20	0
Methanosarcina_mazei_Go1_uid57893	Methanomicrobia	0	0	5	14	0
Methanosarcina_mazei_Tuc01_uid19018	Methanomicrobia	0	0	1	3	0
Methanomassiliicoccus_Mx1_Issoire_uid	Methanomicrobia	0	0	0	0	0
Methanopyrus_kandleri_AV19_uid57883	Methanopyri	0	0	1	0	0
Pyrococcus_abyssi_GE5_uid62903	Thermococci	0	0	3	0	2
Pyrococcus_furiosus_COM1_uid169620	Thermococci	0	0	5	0	2
Pyrococcus_furiosus_DSM_3638_uid5787	Thermococci	0	0	6	0	5
Pyrococcus_horikoshii_OT3_uid57753	Thermococci	0	0	2	0	0
Pyrococcus_NA2_uid66551	Thermococci	0	0	3	1	4
Pyrococcus_ST04_uid167261	Thermococci	0	0	3	0	4
Pyrococcus_yayanosii_CH1_uid68281	Thermococci	0	0	4	2	2
Thermococcus_barophilus_MP_uid54733	Thermococci	0	0	5	0	0
Thermococcus_gammatolerans_EJ3_uid5	Thermococci	0	0	0	0	0
Thermococcus_kodakarensis_KOD1_uid5	Thermococci	0	0	6	1	4
Thermococcus_litoralis_DSM_5473_uid8	Thermococci	0	0	12	1	10
Thermococcus_onnurineus_NA1_uid5904	Thermococci	0	0	1	0	0
Thermococcus_sibiricus_MM_739_uid59	Thermococci	0	0	6	1	4
Thermococcus_4557_uid70841	Thermococci	0	0	1	0	0
Thermococcus_AM4_uid54735	Thermococci	0	0	4	0	2
Thermococcus_CL1_uid168259	Thermococci	0	0	2	0	2
Ferroplasma_acidarmanus_fer1_uid5409	Thermoplasmata	0	0	11	1	0
Picrophilus_torridus_DSM_9790_uid5804	Thermoplasmata	0	0	0	0	0
Thermoplasma_acidophilum_DSM_1728_	Thermoplasmata	0	0	5	1	2
Thermoplasma_volcanium_GSS1_uid577	Thermoplasmata	0	0	14	3	4
Thermoplasmatales_archaeon_BRNA1_ui	Thermoplasmata	0	0	0	0	0
Aciduliprofundum_boonei_T469_uid4333	unclassified Euryarch	0	0	0	0	0
Aciduliprofundum_MAR08_339_uid1844	unclassified Euryarch	0	0	0	0	0
archaeon_Mx1201_uid196597	unclassified Euryarch	0	0	1	0	0
Candidatus_Korarchaeum_cryptofilum_O	Korarchaeota	0	0	4	0	2
Nanoarchaeum_equitans_Kin4_M_uid58	Nanoarchaeota	0	0	0	0	0
Cenarchaeum_symbiosum_A_uid61411	Thaumarchaeota	0	0	0	0	0
Candidatus_Nitrosopumilus_koreensis_A	Thaumarchaeota	0	0	1	0	0
Candidatus_Nitrosopumilus_AR2_uid176	Thaumarchaeota	0	0	0	0	0
Nitrosopumilus_maritimus_SCM1_uid58	Thaumarchaeota	0	0	0	0	0
Candidatus_Nitrososphaera_gargensis_G	Thaumarchaeota	0	0	41	3	0

Candidatus_Caldiarchaeum_subterraneu	Thaumarchaeota	0	0	0	0	1
halophilic_archaeon_DL31_uid72619	unclassified Archaea	0	0	21	1	0
Acidimicrobium_ferrooxidans_DSM_1033	Actinobacteria	0	0	1	0	3
Acidimicrobidae_bacterium_YM16_304_	Actinobacteria	0	0	0	5	0
Arcanobacterium_haemolyticum_DSM_2	Actinobacteria	0	0	0	0	2
Mobiluncus_curtisii_ATCC_43063_uid496	Actinobacteria	0	0	0	0	1
Catenulispora_acidiphila_DSM_44928_ui	Actinobacteria	0	0	1	0	1
Corynebacterium_argentoratense_DSM_	Actinobacteria	0	0	0	0	0
Corynebacterium_aurimucosum_ATCC_7	Actinobacteria	0	0	0	0	0
Corynebacterium_callunae_DSM_20147_	Actinobacteria	0	0	0	0	0
Corynebacterium_diphtheriae_241_uid83	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_31A_uid84	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_BH8_uid84	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_C7__beta_	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_CDCE_839	Actinobacteria	0	0	0	0	0
Corynebacterium_diphtheriae_HC01_uid8	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_HC02_uid8	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_HC03_uid8	Actinobacteria	0	0	0	0	0
Corynebacterium_diphtheriae_HC04_uid8	Actinobacteria	0	0	0	0	0
Corynebacterium_diphtheriae_INCA_402_	Actinobacteria	0	0	0	0	0
Corynebacterium_diphtheriae_NCTC_131	Actinobacteria	1	0	0	0	0
Corynebacterium_diphtheriae_PW8_uid8	Actinobacteria	0	0	0	0	0
Corynebacterium_diphtheriae_VA01_uid8	Actinobacteria	1	0	0	0	0
Corynebacterium_efficiens_YS_314_uid62	Actinobacteria	0	0	0	0	1
Corynebacterium_glutamicum_ATCC_130	Actinobacteria	0	0	0	0	0
Corynebacterium_glutamicum_ATCC_130	Actinobacteria	0	0	0	0	0
Corynebacterium_glutamicum_ATCC_130	Actinobacteria	0	0	0	0	0
Corynebacterium_glutamicum_MB001_ui	Actinobacteria	0	0	0	0	0
Corynebacterium_glutamicum_R_uid5889	Actinobacteria	0	0	0	0	0
Corynebacterium_glutamicum_SCgG1_ui	Actinobacteria	0	0	0	0	0
Corynebacterium_glutamicum_SCgG2_ui	Actinobacteria	0	0	0	0	0
Corynebacterium_halotolerans_YIM_7009	Actinobacteria	0	0	0	0	0
Corynebacterium_jeikeium_K411_uid5839	Actinobacteria	0	0	0	0	0
Corynebacterium_kroppenstedtii_DSM_4	Actinobacteria	0	0	0	0	0
Corynebacterium_maris_DSM_45190_uid	Actinobacteria	0	0	2	0	0
Corynebacterium_pseudotuberculosis_1_	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_10	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_25	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_26	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_3_	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_31	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_31	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_42	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_C2	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_CII	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_Cp	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_FR	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_I19	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_P5	Actinobacteria	0	0	0	0	0
Corynebacterium_pseudotuberculosis_PA	Actinobacteria	0	0	0	0	0
Corynebacterium_resistens_DSM_45100_	Actinobacteria	0	0	0	0	0
Corynebacterium_terpenotabidum_Y_11_	Actinobacteria	0	0	0	0	2
Corynebacterium_ulcerans_0102_uid1698	Actinobacteria	0	0	0	0	0
Corynebacterium_ulcerans_809_uid15965	Actinobacteria	0	0	0	0	0
Corynebacterium_ulcerans_BR_AD22_uid	Actinobacteria	0	0	0	0	0
Corynebacterium_urealyticum_DSM_7109	Actinobacteria	0	0	0	0	0

Corynebacterium_urealyticum_DSM_711	Actinobacteria	0	0	0	0	0
Corynebacterium_variabile_DSM_44702_	Actinobacteria	0	0	0	0	0
Gordonia_bronchialis_DSM_43247_uid41	Actinobacteria	0	0	0	0	0
Gordonia_polyisoprenivorans_VH2_uid86	Actinobacteria	0	0	1	0	0
Gordonia_KTR9_uid174812	Actinobacteria	0	0	0	0	0
Amycolicicoccus_subflavus_DQS3_9A1_u	Actinobacteria	0	0	4	0	8
Mycobacterium_avium_104_uid57693	Actinobacteria	0	0	1	1	0
Mycobacterium_avium_paratuberculosis_	Actinobacteria	0	0	0	0	0
Mycobacterium_avium_paratuberculosis_	Actinobacteria	0	0	0	0	0
Mycobacterium_indicus_pranii_MTCC_95	Actinobacteria	0	0	0	0	0
Mycobacterium_intracellulare_ATCC_139	Actinobacteria	0	0	0	0	0
Mycobacterium_intracellulare_MOTT_02	Actinobacteria	0	0	0	0	0
Mycobacterium_intracellulare_MOTT_64	Actinobacteria	0	0	1	0	0
Mycobacterium_yongonense_05_1390_u	Actinobacteria	0	0	2	0	0
Mycobacterium_abscessus_uid61613	Actinobacteria	0	0	0	0	0
Mycobacterium_abscessus_bolletii_5059	Actinobacteria	0	0	3	0	5
Mycobacterium_massiliense_GO_06_uid	Actinobacteria	0	0	0	0	0
Mycobacterium_chubuense_NBB4_uid16	Actinobacteria	0	0	0	0	0
Mycobacterium_gilvum_PYR_GCK_uid59	Actinobacteria	0	0	3	2	0
Mycobacterium_gilvum_Spyr1_uid61403	Actinobacteria	0	0	0	0	0
Mycobacterium_kansasii_ATCC_12478_u	Actinobacteria	0	0	1	0	2
Mycobacterium_leprae_Br4923_uid5929	Actinobacteria	0	0	0	0	0
Mycobacterium_leprae_TN_uid57697	Actinobacteria	0	0	0	0	0
Mycobacterium_liflandii_128FXT_uid590	Actinobacteria	0	0	0	1	0
Mycobacterium_marinum_M_uid59423	Actinobacteria	0	0	0	1	0
Mycobacterium_VKM_Ac_1815D_uid199	Actinobacteria	0	0	0	0	0
Mycobacterium_rhodesiae_NBB3_uid751	Actinobacteria	0	0	1	0	0
Mycobacterium_smegmatis_JS623_uid18	Actinobacteria	0	0	3	0	0
Mycobacterium_smegmatis_MC2_155_u	Actinobacteria	0	0	0	0	0
Mycobacterium_smegmatis_MC2_155_u	Actinobacteria	0	0	0	0	0
Mycobacterium_JDM601_uid67369	Actinobacteria	0	0	0	0	0
Mycobacterium_JLS_uid58489	Actinobacteria	0	0	0	0	0
Mycobacterium_KMS_uid58491	Actinobacteria	0	0	0	0	0
Mycobacterium_MCS_uid58465	Actinobacteria	0	0	0	0	0
Mycobacterium_MOTT36Y_uid164001	Actinobacteria	0	0	1	0	0
Mycobacterium_africanum_GM041182_	Actinobacteria	0	0	5	0	12
Mycobacterium_bovis_AF2122_97_uid57	Actinobacteria	0	0	6	0	12
Mycobacterium_bovis_BCG_Korea_1168	Actinobacteria	0	0	6	0	12
Mycobacterium_bovis_BCG_Mexico_uid8	Actinobacteria	0	0	6	0	12
Mycobacterium_bovis_BCG_Pasteur_117	Actinobacteria	0	0	6	0	12
Mycobacterium_bovis_BCG_Tokyo_172_	Actinobacteria	0	0	6	0	12
Mycobacterium_canettii_CIPT_14001005	Actinobacteria	0	0	8	0	10
Mycobacterium_canettii_CIPT_14006000	Actinobacteria	0	0	8	0	10
Mycobacterium_canettii_CIPT_14007000	Actinobacteria	0	0	7	0	6
Mycobacterium_canettii_CIPT_14007001	Actinobacteria	0	0	6	0	12
Mycobacterium_canettii_CIPT_14007001	Actinobacteria	0	0	4	1	0
Mycobacterium_tuberculosis_uid185758	Actinobacteria	0	0	7	0	12
Mycobacterium_tuberculosis_CAS_NITR2	Actinobacteria	0	0	4	0	8
Mycobacterium_tuberculosis_CCDC5079_	Actinobacteria	0	0	5	0	12
Mycobacterium_tuberculosis_CCDC5079_	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_CCDC5180_	Actinobacteria	0	0	4	0	12
Mycobacterium_tuberculosis_CDC1551_	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_CTRI_2_uid	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_EAI5_uid21	Actinobacteria	0	0	5	0	12
Mycobacterium_tuberculosis_EAI5_NITR	Actinobacteria	0	0	6	0	10
Mycobacterium_tuberculosis_F11_uid58	Actinobacteria	0	0	6	0	12

Mycobacterium_tuberculosis_H37Ra_uid	Actinobacteria	0	0	5	0	12
Mycobacterium_tuberculosis_H37Rv_uid	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_H37Rv_uid	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_KZN_1435_	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_KZN_4207_	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_KZN_605_	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_RGTB327_	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_RGTB423_	Actinobacteria	0	0	3	0	10
Mycobacterium_tuberculosis_Beijing_NIT	Actinobacteria	0	0	6	0	12
Mycobacterium_tuberculosis_Erdman___	Actinobacteria	0	0	7	0	12
Mycobacterium_tuberculosis_Haarlem_	Actinobacteria	0	0	7	0	12
Mycobacterium_tuberculosis_Haarlem3_	Actinobacteria	0	0	6	0	11
Mycobacterium_tuberculosis_UT205_uid	Actinobacteria	0	0	6	0	12
Mycobacterium_ulcerans_Agy99_uid629	Actinobacteria	0	0	0	1	0
Mycobacterium_vanbaalenii_PYR_1_uid5	Actinobacteria	0	0	2	1	0
Nocardia_brasiliensis_ATCC_700358_uid	Actinobacteria	0	0	1	0	1
Nocardia_cyriacigeorgica_GUH_2_uid893	Actinobacteria	0	0	2	0	1
Nocardia_farcinica_IFM_10152_uid58203	Actinobacteria	0	0	2	0	1
Rhodococcus_equi_103S_uid60171	Actinobacteria	0	0	0	0	1
Rhodococcus_erythropolis_CCM2595_uid	Actinobacteria	0	0	0	0	1
Rhodococcus_erythropolis_PR4_uid5901	Actinobacteria	0	0	0	0	2
Rhodococcus_jostii_RHA1_uid58325	Actinobacteria	0	0	18	2	1
Rhodococcus_opacus_B4_uid13791	Actinobacteria	0	0	11	1	3
Rhodococcus_pyridinivorans_SB3094_uid	Actinobacteria	0	0	0	0	1
Segniliparus_rotundus_DSM_44985_uid4	Actinobacteria	0	0	0	0	0
Tsukamurella_paurometabola_DSM_201	Actinobacteria	0	0	0	0	1
Acidothermus_cellulolyticus_11B_uid585	Actinobacteria	1	0	0	0	2
Frankia_alni_ACN14a_uid58695	Actinobacteria	0	0	3	0	3
Frankia_CcI3_uid58397	Actinobacteria	0	0	11	3	9
Frankia_EAN1pec_uid58367	Actinobacteria	0	0	30	8	10
Frankia_EuI1c_uid42615	Actinobacteria	0	0	0	0	1
Frankia_symbiont_of_Datisca_glomerata_	Actinobacteria	0	0	1	0	1
Blastococcus_saxobsidens_DD2_uid89391	Actinobacteria	0	0	2	0	0
Geodermatophilus_obscurus_DSM_4316	Actinobacteria	0	0	0	0	0
Modestobacter_marinus_uid167487	Actinobacteria	0	0	0	0	0
Nakamurella_multipartita_DSM_44233_u	Actinobacteria	0	0	0	0	1
Stackebrandtia_nassauensis_DSM_44728_	Actinobacteria	0	0	3	0	2
Kineococcus_radiotolerans_SRS30216_ui	Actinobacteria	0	0	0	0	0
Beutenbergia_cavernae_DSM_12333_uid	Actinobacteria	0	0	0	0	0
_Cellvibrio__gilvus_ATCC_13127_uid6814	Actinobacteria	0	0	0	0	2
Cellulomonas_fimi_ATCC_484_uid66779	Actinobacteria	0	0	0	0	1
Cellulomonas_flavigena_DSM_20109_uid	Actinobacteria	0	0	0	0	1
Brachybacterium_faecium_DSM_4810_ui	Actinobacteria	0	0	0	0	1
Kytococcus_sedentarius_DSM_20547_uid	Actinobacteria	0	0	0	0	0
Intrasporangium_calvum_DSM_43043_ui	Actinobacteria	0	0	0	0	2
Jonesia_denitrificans_DSM_20603_uid59	Actinobacteria	0	0	0	0	1
Clavibacter_michiganensis_NCPPB_382_u	Actinobacteria	0	0	0	0	0
Clavibacter_michiganensis_nebraskensis_	Actinobacteria	0	0	0	0	0
Clavibacter_michiganensis_sepedonicus_	Actinobacteria	0	0	0	0	1
Leifsonia_xyli_cynodontis_DSM_46306_u	Actinobacteria	0	0	0	0	0
Leifsonia_xyli_CTCB07_uid57759	Actinobacteria	0	0	0	0	0
Microbacterium_testaceum_StLB037_uid	Actinobacteria	0	0	0	0	0
Arthrobacter_arilaitensis_Re117_uid5350	Actinobacteria	0	0	0	0	1
Arthrobacter_aurescens_TC1_uid58109	Actinobacteria	0	0	0	0	0
Arthrobacter_chlorophenolicus_A6_uid5	Actinobacteria	0	0	0	0	0
Arthrobacter_phenanthrenivorans_Sphe3	Actinobacteria	0	0	0	0	0

Arthrobacter_FB24_uid58141	Actinobacteria	0	0	0	0	0
Arthrobacter_nitroguajacolicus_Rue61a_	Actinobacteria	0	0	0	0	0
Kocuria_rhizophila_DC2201_uid59099	Actinobacteria	0	0	0	0	0
Micrococcus_luteus_NCTC_2665_uid590	Actinobacteria	0	0	0	0	0
Renibacterium_salmoninarum_ATCC_332	Actinobacteria	0	0	0	2	0
Rothia_dentocariosa_ATCC_17931_uid49	Actinobacteria	0	0	0	0	0
Rothia_mucilaginosa_uid43093	Actinobacteria	0	0	0	0	0
Isoptericola_variabilis_225_uid67501	Actinobacteria	0	0	0	0	1
Xylanimonas_cellulosilytica_DSM_15894_	Actinobacteria	0	0	1	0	2
Sanguibacter_keddieii_DSM_10542_uid4	Actinobacteria	0	0	0	0	1
Tropheryma_whipplei_Twist_uid57705	Actinobacteria	0	0	0	0	0
Tropheryma_whipplei_TW08_27_uid579	Actinobacteria	0	0	0	0	0
Actinoplanes_friuliensis_DSM_7358_uid2	Actinobacteria	0	0	6	2	2
Actinoplanes_missouriensis_431_uid1581	Actinobacteria	0	0	1	0	1
Actinoplanes_N902_109_uid202219	Actinobacteria	0	0	0	0	2
Actinoplanes_SE50_110_uid162333	Actinobacteria	0	0	0	0	2
Micromonospora_aurantiaca_ATCC_2702	Actinobacteria	0	0	1	0	4
Micromonospora_L5_uid45895	Actinobacteria	0	0	1	0	2
Salinispora_arenicola_CNS_205_uid5865	Actinobacteria	0	0	0	0	2
Salinispora_tropica_CNB_440_uid58565	Actinobacteria	0	0	0	0	2
Verrucosispora_maris_AB_18_032_uid66	Actinobacteria	0	0	0	0	2
Kribbella_flavida_DSM_17836_uid43465	Actinobacteria	0	0	1	0	1
Nocardioides_JS614_uid58149	Actinobacteria	0	0	1	0	0
Microlunatus_phosphovorus_NM_1_uid6	Actinobacteria	0	0	0	0	0
Propionibacterium_acidipropionici_ATCC_	Actinobacteria	0	0	0	0	2
Propionibacterium_acnes_266_uid16205	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_6609_uid1621	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_ATCC_11828_	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_C1_uid176501	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_HL096PA1_uid	Actinobacteria	0	0	0	0	1
Propionibacterium_acnes_KPA171202_ui	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_SK137_uid480	Actinobacteria	0	0	0	0	1
Propionibacterium_acnes_TypeIA2_P_acr	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_TypeIA2_P_acr	Actinobacteria	0	0	0	0	0
Propionibacterium_acnes_TypeIA2_P_acr	Actinobacteria	0	0	0	0	0
Propionibacterium_avidum_44067_uid19	Actinobacteria	0	0	0	0	0
Propionibacterium_freudenreichii_sherm	Actinobacteria	0	0	0	0	0
Propionibacterium_propionicum_F0230a_	Actinobacteria	0	0	0	0	0
Actinosynnema_mirum_DSM_43827_uid	Actinobacteria	0	0	0	0	1
Amycolatopsis_mediterranei_RB_uid216	Actinobacteria	0	0	0	0	1
Amycolatopsis_mediterranei_S699_uid15	Actinobacteria	0	0	0	0	1
Amycolatopsis_mediterranei_S699_uid17	Actinobacteria	0	0	0	0	1
Amycolatopsis_mediterranei_U32_uid50	Actinobacteria	0	0	0	0	1
Amycolatopsis_orientalis_HCCB10007_ui	Actinobacteria	0	0	0	0	1
Pseudonocardia_dioxanivorans_CB1190_	Actinobacteria	0	0	0	0	1
Saccharomonospora_viridis_DSM_43017_	Actinobacteria	0	0	0	0	1
Saccharopolyspora_erythraea_NRRL_233	Actinobacteria	0	0	13	1	2
Saccharothrix_espanaensis_DSM_44229_	Actinobacteria	0	0	0	0	1
Thermobispora_bispora_DSM_43833_uid	Actinobacteria	0	0	0	0	2
Kitasatospora_setae_KM_6054_uid77027	Actinobacteria	0	0	0	0	2
Streptomyces_albus_J1074_uid196849	Actinobacteria	0	0	2	1	1
Streptomyces_avermitilis_MA_4680_uid	Actinobacteria	0	0	5	2	1
Streptomyces_bingchenggensis_BCW_1_	Actinobacteria	0	3	13	3	1
Streptomyces_cattleya_NRRL_8057___D	Actinobacteria	0	0	0	0	1
Streptomyces_cattleya_NRRL_8057_uid7	Actinobacteria	0	0	0	0	1
Streptomyces_coelicolor_A3_2__uid5780	Actinobacteria	0	0	5	0	1

Streptomyces_collinus_Tu_365_uid21442	Actinobacteria	0	0	0	0	1
Streptomyces_davawensis_JCM_4913_ui	Actinobacteria	0	0	12	3	3
Streptomyces_flavogriseus_ATCC_33331_	Actinobacteria	0	0	1	0	1
Streptomyces_fulvissimus_DSM_40593_u	Actinobacteria	0	0	0	0	1
Streptomyces_griseus_NBRC_13350_uid5	Actinobacteria	0	0	1	0	1
Streptomyces_hygroscopicus_jinggangen	Actinobacteria	0	0	0	0	1
Streptomyces_hygroscopicus_jinggangen	Actinobacteria	0	0	0	0	1
Streptomyces_rapamycinicus_NRRL_5491	Actinobacteria	0	0	10	0	1
Streptomyces_scabiei_87_22_uid46531	Actinobacteria	0	0	5	0	1
Streptomyces_PAMC26508_uid197217	Actinobacteria	0	0	0	0	1
Streptomyces_SirexAA_E_uid72627	Actinobacteria	0	0	0	0	1
Streptomyces_venezuelae_ATCC_10712_	Actinobacteria	0	0	0	0	1
Streptomyces_violaceusniger_Tu_4113_u	Actinobacteria	0	0	19	2	1
Nocardiopsis_alba_ATCC_BAA_2165_uid1	Actinobacteria	0	0	1	0	8
Nocardiopsis_dassonvillei_DSM_43111_u	Actinobacteria	0	1	10	1	2
Thermobifida_fusca_YX_uid57703	Actinobacteria	0	0	3	2	2
Streptosporangium_roseum_DSM_43021_	Actinobacteria	0	2	9	3	4
Thermomonospora_curvata_DSM_43183_	Actinobacteria	0	0	0	0	2
Bifidobacterium_adolescentis_ATCC_157	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_ATCC_25527_	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_AD011_	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_ATCC_2	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_B420_ui	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_BB_12_	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_Bi_07_ui	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_Bl_04_ui	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_Bl12_ui	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_BLC1_ui	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_CNCM_I	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_DSM_10	Actinobacteria	0	0	0	0	0
Bifidobacterium_animalis_lactis_V9_uid1	Actinobacteria	0	0	0	0	0
Bifidobacterium_asteroides_PRL2011_uid	Actinobacteria	0	0	0	0	0
Bifidobacterium_bifidum_BGN4_uid1679	Actinobacteria	0	0	0	0	0
Bifidobacterium_bifidum_PRL2010_uid59	Actinobacteria	0	0	0	0	0
Bifidobacterium_bifidum_S17_uid59545	Actinobacteria	1	0	0	0	0
Bifidobacterium_breve_ACS_071_V_Sch8	Actinobacteria	0	0	0	0	0
Bifidobacterium_breve_UCC2003_uid193	Actinobacteria	0	0	1	0	0
Bifidobacterium_dentium_Bd1_uid43091	Actinobacteria	1	0	0	0	0
Bifidobacterium_longum_DJO10A_uid58	Actinobacteria	1	0	1	0	1
Bifidobacterium_longum_NCC2705_uid57	Actinobacteria	0	0	0	0	0
Bifidobacterium_longum_infantis_157F_	Actinobacteria	0	0	1	0	0
Bifidobacterium_longum_infantis_ATCC_	Actinobacteria	0	0	7	1	2
Bifidobacterium_longum_infantis_ATCC_	Actinobacteria	0	0	7	1	2
Bifidobacterium_longum_BBMN68_uid60	Actinobacteria	0	0	0	0	0
Bifidobacterium_longum_F8_uid197184	Actinobacteria	0	0	0	0	0
Bifidobacterium_longum_JCM_1217_uid	Actinobacteria	0	0	4	0	1
Bifidobacterium_longum_JDM301_uid49	Actinobacteria	0	0	2	0	2
Bifidobacterium_longum_KACC_91563_ui	Actinobacteria	1	0	1	0	0
Bifidobacterium_thermophilum_RBL67_u	Actinobacteria	0	0	0	0	0
Gardnerella_vaginalis_409_05_uid43211	Actinobacteria	0	0	0	0	0
Gardnerella_vaginalis_ATCC_14019_uid5	Actinobacteria	0	0	0	0	0
Gardnerella_vaginalis_HMP9231_uid162	Actinobacteria	0	0	0	0	0
Adlercreutzia_equolifaciens_DSM_19450_	Actinobacteria	0	0	1	0	0
Atopobium_parvulum_DSM_20469_uid5	Actinobacteria	0	0	0	0	0
Coriobacterium_glomerans_PW2_uid657	Actinobacteria	1	0	0	0	0
Cryptobacterium_curtum_DSM_15641_ui	Actinobacteria	0	0	0	0	0

Eggerthella_lenta_DSM_2243_uid59079	Actinobacteria	0	0	0	0	1
Eggerthella_YY7918_uid68707	Actinobacteria	1	0	0	0	2
Gordonibacter_pamelaeae_7_10_1_b_ui	Actinobacteria	1	0	0	2	1
Olsenella_uli_DSM_7084_uid51367	Actinobacteria	1	0	0	0	0
Slackia_heliotrinireducens_DSM_20476_	Actinobacteria	0	0	0	3	0
Rubrobacter_xylanophilus_DSM_9941_ui	Actinobacteria	0	0	0	0	1
Conexibacter_woesei_DSM_14684_uid43	Actinobacteria	0	0	0	0	1
Aquifex_aeolicus_VF5_uid57765	Aquificae	0	0	3	0	0
Hydrogenobacter_thermophilus_TK_6_ui	Aquificae	0	0	9	1	1
Hydrogenobacter_thermophilus_TK_6_ui	Aquificae	0	0	8	1	1
Hydrogenobaculum_HO_uid190882	Aquificae	0	0	4	0	0
Hydrogenobaculum_SN_uid46251	Aquificae	0	0	3	0	0
Hydrogenobaculum_Y04AAS1_uid58857	Aquificae	0	0	4	0	0
Thermocrinis_albus_DSM_14484_uid462	Aquificae	0	0	5	1	0
Desulfurobacterium_thermolithotrophum	Aquificae	0	0	19	1	5
Thermovibrio_ammonificans_HB_1_uid6	Aquificae	0	0	1	0	0
Persephonella_marina_EX_H1_uid58119	Aquificae	0	0	0	0	0
Sulfurihydrogenibium_azorense_Az_Fu1_	Aquificae	0	0	12	0	0
Sulfurihydrogenibium_YO3AOP1_uid5885	Aquificae	0	0	9	1	1
Chthonomonas_calidirosea_T49_uid2086	Armatimonadetes	0	0	3	0	1
Rhodothermus_marinus_DSM_4252_uid4	Bacteroidetes/Chloro	0	0	3	1	0
Rhodothermus_marinus_SG0_5JP17_172_	Bacteroidetes/Chloro	0	0	11	1	2
Salinibacter_ruber_DSM_13855_uid5851	Bacteroidetes/Chloro	0	0	7	2	0
Salinibacter_ruber_M8_uid47323	Bacteroidetes/Chloro	0	0	9	2	0
Bacteroides_fragilis_638R_uid84217	Bacteroidetes/Chloro	1	0	0	0	0
Bacteroides_fragilis_NCTC_9343_uid5763	Bacteroidetes/Chloro	1	0	0	0	0
Bacteroides_fragilis_YCH46_uid58195	Bacteroidetes/Chloro	0	0	0	0	1
Bacteroides_helcogenes_P_36_108_uid6	Bacteroidetes/Chloro	0	0	0	0	0
Bacteroides_salanitronis_DSM_18170_ui	Bacteroidetes/Chloro	0	0	0	1	0
Bacteroides_thetaiotaomicron_VPI_5482_	Bacteroidetes/Chloro	0	0	0	0	0
Bacteroides_vulgatus_ATCC_8482_uid58	Bacteroidetes/Chloro	0	0	0	0	1
Bacteroides_xylanisolvens_XB1A_uid1971	Bacteroidetes/Chloro	0	0	0	2	0
Odoribacter_splanchnicus_DSM_20712_u	Bacteroidetes/Chloro	0	0	1	1	1
Paludibacter_propionicigenes_WB4_uid6	Bacteroidetes/Chloro	0	0	0	5	0
Parabacteroides_distasonis_ATCC_8503_	Bacteroidetes/Chloro	0	0	0	0	0
Porphyromonas_asaccharolytica_DSM_2	Bacteroidetes/Chloro	0	0	0	2	0
Porphyromonas_gingivalis_ATCC_33277_	Bacteroidetes/Chloro	0	0	0	0	0
Porphyromonas_gingivalis_TDC60_uid67	Bacteroidetes/Chloro	0	0	0	0	0
Porphyromonas_gingivalis_W83_uid5764	Bacteroidetes/Chloro	0	0	0	0	1
Tannerella_forsythia_ATCC_43037_uid83	Bacteroidetes/Chloro	0	0	0	1	0
Prevotella_dentalis_DSM_3688_uid18481	Bacteroidetes/Chloro	0	0	0	0	0
Prevotella_denticola_F0289_uid65091	Bacteroidetes/Chloro	0	0	0	0	0
Prevotella_intermedia_17_uid163151	Bacteroidetes/Chloro	1	0	0	0	0
Prevotella_melaninogenica_ATCC_25845_	Bacteroidetes/Chloro	0	0	0	1	0
Prevotella_ruminicola_23_uid47507	Bacteroidetes/Chloro	1	0	0	3	0
Prevotella_oral_taxon_299_F0039_uid45	Bacteroidetes/Chloro	0	0	0	0	0
Alistipes_finegoldii_DSM_17242_uid1681	Bacteroidetes/Chloro	0	0	0	0	1
Alistipes_shahii_WAL_8301_uid197175	Bacteroidetes/Chloro	0	0	0	0	0
Candidatus_Azobacteroides_pseudotrich	Bacteroidetes/Chloro	0	0	0	0	0
Bacteroides_CF50_uid222805	Bacteroidetes/Chloro	1	0	0	1	0
Belliella_baltica_DSM_15883_uid168182	Bacteroidetes/Chloro	1	0	0	2	0
Cyclobacterium_marinum_DSM_745_uid	Bacteroidetes/Chloro	0	0	0	3	0
Echinicola_vietnamensis_DSM_17526_ui	Bacteroidetes/Chloro	0	0	0	4	0
Cytophaga_hutchinsonii_ATCC_33406_ui	Bacteroidetes/Chloro	0	0	0	5	0
Dyadobacter_fermentans_DSM_18053_u	Bacteroidetes/Chloro	0	0	0	1	0
Emticicia_oligotrophica_DSM_17448_uid	Bacteroidetes/Chloro	0	0	0	5	0

Fibrella_aestuarina_uid178352	Bacteroidetes/Chloro	0	0	2	0	0
Flexibacter_litoralis_DSM_6794_uid16825	Bacteroidetes/Chloro	0	0	1	6	0
Leadbetterella_byssophila_DSM_17132_u	Bacteroidetes/Chloro	0	0	1	2	0
Runella_slithyformis_DSM_19594_uid683	Bacteroidetes/Chloro	0	0	0	6	0
Spirosoma_linguale_DSM_74_uid43413	Bacteroidetes/Chloro	0	0	0	7	0
Marivirga_tractuosa_DSM_4126_uid6083	Bacteroidetes/Chloro	0	0	0	1	0
Blattabacterium__Cryptocercus_punctula	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Blaberus_giganteus__u	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Blatta_orientalis__Tara	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Blattella_germanica__B	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Mastotermes_darwinie	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Nauphoeta_cinerea__u	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Panesthia_angustipenn	Bacteroidetes/Chloro	0	0	0	0	0
Blattabacterium__Periplaneta_americana	Bacteroidetes/Chloro	0	0	0	0	0
Fluviicola_taffensis_DSM_16823_uid6527	Bacteroidetes/Chloro	1	0	0	4	0
Owenweeksia_hongkongensis_DSM_1736	Bacteroidetes/Chloro	0	0	0	3	0
Aequorivita_sublithincola_DSM_14238_u	Bacteroidetes/Chloro	0	0	0	1	0
Capnocytophaga_canimorsus_Cc5_uid707	Bacteroidetes/Chloro	1	0	0	0	0
Capnocytophaga_ochracea_DSM_7271_u	Bacteroidetes/Chloro	0	0	0	0	0
Cellulophaga_algicola_DSM_14237_uid62	Bacteroidetes/Chloro	0	0	0	5	0
Cellulophaga_lytica_DSM_7489_uid63401	Bacteroidetes/Chloro	0	0	0	0	0
Croceibacter_atlanticus_HTCC2559_uid49	Bacteroidetes/Chloro	0	0	0	0	0
Flavobacterium_branchiophilum_FL_15_u	Bacteroidetes/Chloro	1	0	1	4	0
Flavobacterium_columnare_ATCC_49512_	Bacteroidetes/Chloro	1	0	0	1	0
Flavobacterium_indicum_GPTSA100_9_ui	Bacteroidetes/Chloro	0	0	0	1	0
Flavobacterium_johnsoniae_UW101_uid5	Bacteroidetes/Chloro	0	0	0	6	0
Flavobacterium_psychrophilum_JIP02_86	Bacteroidetes/Chloro	1	0	0	0	0
Gramella_forsetii_KT0803_uid58881	Bacteroidetes/Chloro	0	0	0	1	0
Krokinobacter_4H_3_7_5_uid66593	Bacteroidetes/Chloro	0	0	0	0	0
Lacinutrix_5H_3_7_4_uid68067	Bacteroidetes/Chloro	0	0	0	0	0
Flavobacteriales_bacterium_HTCC2170_u	Bacteroidetes/Chloro	0	0	0	0	0
Muricauda_ruestringensis_DSM_13258_u	Bacteroidetes/Chloro	0	0	1	0	0
Persicivirga_dokdonensis_DSW_6_uid186	Bacteroidetes/Chloro	0	0	0	2	0
Ornithobacterium_rhinotracheale_DSM_1	Bacteroidetes/Chloro	1	0	0	0	0
Polaribacter_MED152_uid54207	Bacteroidetes/Chloro	0	0	0	0	0
Psychroflexus_torquis_ATCC_700755_uid	Bacteroidetes/Chloro	1	0	0	8	0
Riemerella_anatipestifer_ATCC_11845___	Bacteroidetes/Chloro	1	0	0	0	0
Riemerella_anatipestifer_ATCC_11845___	Bacteroidetes/Chloro	0	0	0	0	0
Riemerella_anatipestifer_RA_CH_1_uid17	Bacteroidetes/Chloro	1	0	0	0	0
Riemerella_anatipestifer_RA_CH_2_uid18	Bacteroidetes/Chloro	1	0	0	0	0
Riemerella_anatipestifer_RA_GD_uid1620	Bacteroidetes/Chloro	1	0	0	0	0
Robiginitalea_biformata_HTCC2501_uid5	Bacteroidetes/Chloro	0	0	0	0	0
Flavobacteriaceae_bacterium_3519_10_u	Bacteroidetes/Chloro	0	0	0	1	0
Weeksella_virosa_DSM_16922_uid63627	Bacteroidetes/Chloro	1	0	0	0	0
Zobellia_galactanivorans_uid70621	Bacteroidetes/Chloro	0	0	0	2	0
Zunongwangia_profunda_SM_A87_uid48	Bacteroidetes/Chloro	1	0	2	0	0
Candidatus_Sulcia_muelleri_CARI_uid525	Bacteroidetes/Chloro	0	0	0	0	0
Candidatus_Sulcia_muelleri_DMIN_uid47	Bacteroidetes/Chloro	0	0	0	0	0
Candidatus_Sulcia_muelleri_GWSS_uid58	Bacteroidetes/Chloro	0	0	0	0	0
Candidatus_Sulcia_muelleri_SMDSEM_uid	Bacteroidetes/Chloro	0	0	0	0	0
Candidatus_Sulcia_muelleri_Sulcia_ALF_u	Bacteroidetes/Chloro	0	0	0	0	0
Candidatus_Uzinura_diaspidicola_ASNER_	Bacteroidetes/Chloro	0	0	0	0	0
Chitinophaga_pinensis_DSM_2588_uid59	Bacteroidetes/Chloro	0	0	0	0	0
Niastella_koreensis_GR20_10_uid83125	Bacteroidetes/Chloro	0	0	0	1	1
Haliscomenobacter_hydrossis_DSM_1100	Bacteroidetes/Chloro	0	0	0	6	0
Saprospira_grandis_Lewin_uid89375	Bacteroidetes/Chloro	0	0	0	1	0

Pedobacter_heparinus_DSM_2366_uid59	Bacteroidetes/Chlor	0	0	0	0	0
Pedobacter_saltans_DSM_12145_uid613	Bacteroidetes/Chlor	0	0	0	3	0
Solitalea_canadensis_DSM_3403_uid817	Bacteroidetes/Chlor	0	0	0	2	0
Sphingobacterium_21_uid64755	Bacteroidetes/Chlor	0	0	0	0	0
Candidatus_Amoebophilus_asiaticus_5a2	Bacteroidetes/Chlor	0	0	0	8	0
Cardinium_endosymbiont_cEper1_of_En	Bacteroidetes/Chlor	0	0	0	0	0
Chlorobaculum_parvum_NCIB_8327_uid5	Bacteroidetes/Chlor	0	0	0	3	0
Chlorobium_tepidum_TLS_uid57897	Bacteroidetes/Chlor	0	0	0	0	0
Chlorobium_chlorochromatii_CaD3_uid5	Bacteroidetes/Chlor	0	0	0	3	0
Chlorobium_limicola_DSM_245_uid5812	Bacteroidetes/Chlor	0	0	0	5	0
Chlorobium_phaeobacteroides_BS1_uid5	Bacteroidetes/Chlor	0	0	0	6	0
Chlorobium_phaeobacteroides_DSM_266	Bacteroidetes/Chlor	0	0	0	15	0
Chlorobium_phaeovibrioides_DSM_265_	Bacteroidetes/Chlor	0	0	0	2	0
Chlorobium_luteolum_DSM_273_uid581	Bacteroidetes/Chlor	0	0	0	0	0
Pelodictyon_phaeoclathratiforme_BU_1_	Bacteroidetes/Chlor	0	0	0	5	0
Chloroherpeton_thalassium_ATCC_35110	Bacteroidetes/Chlor	0	0	0	0	0
Prosthecochloris_aestuarii_DSM_271_uid	Bacteroidetes/Chlor	0	0	0	4	0
Ignavibacterium_album_JCM_16511_uid1	Bacteroidetes/Chlor	1	0	0	7	0
Melioribacter_roseus_P3M_uid170941	Bacteroidetes/Chlor	0	0	0	2	0
Caldisericum_exile_AZM16c01_uid15817	Caldiserica	0	0	2	0	1
Chlamydia_muridarum_Nigg_uid57785	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_pecorum_P787_uid221292	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_pecorum_PV3056_3_uid2212	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_pecorum_W73_uid221291	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_pecorum_E58_uid66295	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_pneumoniae_AR39_uid57	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_pneumoniae_CWL029_ui	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_pneumoniae_J138_uid57	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_pneumoniae_LPCoLN_uid	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_pneumoniae_TW_183_ui	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_01DC11_uid1595	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_01DC12_uid179070	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_02DC15_uid1595	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_08DC60_uid1595	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_6BC_uid159845	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_6BC_uid63621	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_84_55_uid175571	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_C19_98_uid1595	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_CP3_uid175578	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_GR9_uid175572	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_M56_uid175576	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_Mat116_uid1890	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_MN_uid175573	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_NJ1_uid175579	Chlamydiae/Verruco	0	0	0	0	0
Chlamydophila_psittaci_RD1_uid162063	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_VS225_uid175574	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_WC_uid175577	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_psittaci_WS_RT_E30_uid1755	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid216090	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_434_Bu_uid6163	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_A_363_uid1967	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_A_5291_uid1967	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid196771	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_A_HAR_13_uid5	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_A2497_uid1598	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_A2497_uid1599	Chlamydiae/Verruco	0	0	0	0	0

Chlamydia_trachomatis_B_Jali20_OT_uid	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_B_TZ1A828_OT_	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_C_TW_3_uid232	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_D_SotonD1_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_D_SotonD5_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_D_SotonD6_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_D_UW_3_CX_ui	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_D_EC_uid159881	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_D_LC_uid159879	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_E_11023_uid161	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_E_150_uid16140	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_E_Bour_uid1967	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid196776	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_E_SotonE8_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_E_SW3_uid1674	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid196778	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_F_SW4_uid1674	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_F_SW5_uid1674	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_G_11074_uid161	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_G_11222_uid161	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_G_9301_uid161	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_G_9768_uid161	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_G_SotonG1_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_Ia_SotonIa1_uid	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid196781	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_IU824_uid19371	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_IU888_uid19371	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_J_6276tet1_uid2	Chlamydiae/Verruco	0	0	1	1	0
Chlamydia_trachomatis_K_SotonK1_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L1_115_uid1967	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid196800	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L1_224_uid1967	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L1_440_LN_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2_25667R_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2_434_Bu_i__u	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2_434_Bu_f__u	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_795_uid196	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_8200_07_ui	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Ams1_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Ams2_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Ams3_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Ams4_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Ams5_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Canada1_ui	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_Canada2_ui	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_CV204_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_uid196789	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_UCH_1_pro	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2b_UCH_2_uid	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L2c_uid68843	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_L3_404_LN_uid1	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_RC_F_s_342_uid	Chlamydiae/Verruco	0	0	1	1	0
Chlamydia_trachomatis_RC_F_s_852_uid	Chlamydiae/Verruco	0	0	1	1	0
Chlamydia_trachomatis_RC_F_69_uid213	Chlamydiae/Verruco	0	0	0	0	0
Chlamydia_trachomatis_RC_J_s_122_uid	Chlamydiae/Verruco	0	0	1	1	0
Chlamydia_trachomatis_RC_J_943_uid21	Chlamydiae/Verruco	0	0	0	0	0

Chlamydia_trachomatis_RC_J_953_uid21	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydia_trachomatis_RC_J_966_uid21	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydia_trachomatis_RC_J_971_uid21	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydia_trachomatis_RC_L2_s_3_uid2	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydia_trachomatis_RC_L2_s_46_uid	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydia_trachomatis_RC_L2_55_uid21	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydia_trachomatis_Sweden2_uid161	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydophila_abortus_S26_3_uid57963	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydophila_caviae_GPIC_uid57783	Chlamydiae/Verrucor	0	0	0	0	0
Chlamydophila_felis_Fe_C_56_uid57971	Chlamydiae/Verrucor	0	0	0	0	0
Candidatus_Protochlamydia_amoebophil	Chlamydiae/Verrucor	0	0	0	0	0
Parachlamydia_acanthamoebae_UV7_uid	Chlamydiae/Verrucor	0	0	1	0	2
Simkania_negevensis_Z_uid68451	Chlamydiae/Verrucor	0	0	0	0	0
Waddlia_chondrophila_WSU_86_1044_ui	Chlamydiae/Verrucor	0	0	0	0	0
Opitutus_terrae_PB90_1_uid58965	Chlamydiae/Verrucor	0	0	0	3	0
Coraliomargarita_akajimensis_DSM_4522	Chlamydiae/Verrucor	0	0	0	1	0
Methylacidiphilum_infernorum_V4_uid5	Chlamydiae/Verrucor	0	0	15	0	6
Akkermansia_muciniphila_ATCC_BAA_83	Chlamydiae/Verrucor	1	0	0	2	0
Anaerolinea_thermophila_UNI_1_uid622	Chloroflexi	0	0	0	1	0
Caldilinea_aerophila_DSM_14535___NBR	Chloroflexi	0	0	0	1	2
Chloroflexus_aggregans_DSM_9485_uid5	Chloroflexi	0	0	13	13	0
Chloroflexus_aurantiacus_J_10_fl_uid576	Chloroflexi	0	0	0	2	2
Chloroflexus_Y_400_fl_uid59085	Chloroflexi	0	0	1	2	2
Roseiflexus_castenholzii_DSM_13941_uic	Chloroflexi	0	0	2	3	1
Roseiflexus_RS_1_uid58523	Chloroflexi	0	0	0	2	1
Herpetosiphon_aurantiacus_DSM_785_ui	Chloroflexi	0	0	4	1	0
Dehalococcoides_ethenogenes_195_uid5	Chloroflexi	0	0	0	0	0
Dehalococcoides_mccartyi_BTF08_uid19	Chloroflexi	0	0	0	0	0
Dehalococcoides_mccartyi_DCMB5_uid1	Chloroflexi	0	0	0	0	0
Dehalococcoides_mccartyi_GY50_uid230	Chloroflexi	0	0	0	0	0
Dehalococcoides_BAV1_uid58477	Chloroflexi	0	0	0	0	0
Dehalococcoides_CBDB1_uid58413	Chloroflexi	0	0	0	0	0
Dehalococcoides_GT_uid42115	Chloroflexi	0	0	0	0	0
Dehalococcoides_VS_uid42393	Chloroflexi	0	0	0	0	0
Dehalogenimonas_lykanthroporepellens_	Chloroflexi	0	0	0	0	0
Sphaerobacter_thermophilus_DSM_2074	Chloroflexi	0	0	0	1	1
Thermomicrobium_roseum_DSM_5159_	Chloroflexi	0	0	0	0	1
Desulfurispirillum_indicum_S5_uid45897	Chrysiogenetes	0	0	0	0	0
Gloeobacter_JS_uid225602	Cyanobacteria	0	0	9	2	0
Gloeobacter_violaceus_PCC_7421_uid58	Cyanobacteria	0	0	3	0	0
Anabaena_cylindrica_PCC_7122_uid1833	Cyanobacteria	0	1	7	5	0
Anabaena_90_uid179383	Cyanobacteria	0	4	23	7	2
Anabaena_variabilis_ATCC_29413_uid58	Cyanobacteria	0	2	16	4	1
Cylindrospermum_stagnale_PCC_7417_ui	Cyanobacteria	0	2	34	2	6
Nostoc_punctiforme_PCC_73102_uid577	Cyanobacteria	0	1	3	2	0
Nostoc_PCC_7107_uid182932	Cyanobacteria	0	0	3	6	0
Nostoc_PCC_7120_uid57803	Cyanobacteria	0	2	29	11	3
Nostoc_PCC_7524_uid182933	Cyanobacteria	0	0	12	9	0
_Nostoc_azollae__0708_uid49725	Cyanobacteria	0	0	1	1	0
Calothrix_PCC_6303_uid183109	Cyanobacteria	0	1	22	2	0
Calothrix_PCC_7507_uid182930	Cyanobacteria	0	1	5	9	1
Rivularia_PCC_7116_uid182929	Cyanobacteria	0	0	17	17	1
Acaryochloris_marina_MBIC11017_uid58	Cyanobacteria	0	1	3	5	0
cyanobacterium_UCYN_A_uid43697	Cyanobacteria	0	0	0	0	0
Chamaesiphon_PCC_6605_uid183005	Cyanobacteria	0	0	10	4	5
Cyanobacterium_PCC_10605_uid183340	Cyanobacteria	0	0	27	11	0

Cyanobacterium_stanieri_PCC_7202_uid1	Cyanobacteria	0	0	31	4	0
Cyanobium_gracile_PCC_6307_uid18293	Cyanobacteria	0	0	0	0	0
Cyanothece_ATCC_51142_uid59013	Cyanobacteria	0	1	8	5	2
Cyanothece_PCC_7424_uid59025	Cyanobacteria	0	1	52	13	6
Cyanothece_PCC_7425_uid59435	Cyanobacteria	0	0	5	0	0
Cyanothece_PCC_7822_uid52547	Cyanobacteria	0	7	32	5	1
Cyanothece_PCC_8801_uid59027	Cyanobacteria	0	0	33	12	2
Cyanothece_PCC_8802_uid59143	Cyanobacteria	0	0	25	8	5
Dactylococcopsis_salina_PCC_8305_uid1	Cyanobacteria	0	6	23	1	5
Gloeocapsa_PCC_7428_uid183112	Cyanobacteria	0	0	4	3	0
Halothece_PCC_7418_uid183338	Cyanobacteria	0	4	42	7	9
Microcystis_aeruginosa_NIES_843_uid59	Cyanobacteria	0	3	107	14	11
Synechococcus_elongatus_PCC_6301_uid	Cyanobacteria	0	0	1	0	0
Synechococcus_elongatus_PCC_7942_uid	Cyanobacteria	0	0	1	0	0
Synechococcus_CC9311_uid58123	Cyanobacteria	0	0	0	0	0
Synechococcus_CC9605_uid58319	Cyanobacteria	0	0	0	0	0
Synechococcus_CC9902_uid58323	Cyanobacteria	0	0	0	0	0
Synechococcus_JA_2_3B_a_2_13__uid58	Cyanobacteria	0	0	72	1	2
Synechococcus_JA_3_3Ab_uid58535	Cyanobacteria	0	0	48	16	20
Synechococcus_PCC_6312_uid182934	Cyanobacteria	0	1	1	3	0
Synechococcus_PCC_7002_uid59137	Cyanobacteria	0	0	2	0	0
Synechococcus_PCC_7502_uid183008	Cyanobacteria	0	0	0	1	0
Synechococcus_RCC307_uid61609	Cyanobacteria	0	0	0	0	0
Synechococcus_WH_7803_uid61607	Cyanobacteria	0	0	0	0	0
Synechococcus_WH_8102_uid61581	Cyanobacteria	0	0	0	0	0
Synechocystis_PCC_6803_uid159873	Cyanobacteria	0	0	1	0	0
Synechocystis_PCC_6803_uid189748	Cyanobacteria	0	0	1	0	0
Synechocystis_PCC_6803_uid57659	Cyanobacteria	0	0	1	0	0
Synechocystis_PCC_6803_substr__GT_I_	Cyanobacteria	0	0	1	0	0
Synechocystis_PCC_6803_substr__GT_I_	Cyanobacteria	0	0	1	0	0
Synechocystis_PCC_6803_substr__PCC_N	Cyanobacteria	0	0	1	0	0
Thermosynechococcus_elongatus_BP_1_	Cyanobacteria	0	0	35	12	0
Thermosynechococcus_NK55_uid231517	Cyanobacteria	0	0	0	0	0
Arthrospira_platensis_NIES_39_uid19717	Cyanobacteria	0	9	52	10	6
Crinalium_epipsammum_PCC_9333_uid1	Cyanobacteria	0	3	40	9	8
Geitlerinema_PCC_7407_uid183007	Cyanobacteria	0	0	21	5	0
Leptolyngbya_PCC_7376_uid182928	Cyanobacteria	0	0	0	2	0
Microcoleus_PCC_7113_uid183114	Cyanobacteria	0	3	13	2	0
Oscillatoria_acuminata_PCC_6304_uid18	Cyanobacteria	0	4	18	2	2
Oscillatoria_PCC_7112_uid183110	Cyanobacteria	0	4	76	14	8
Pseudanabaena_PCC_7367_uid183004	Cyanobacteria	0	0	0	2	0
Trichodesmium_erythraeum_IMS101_uid	Cyanobacteria	0	0	11	5	3
Chroococcidiopsis_thermalis_PCC_7203_	Cyanobacteria	0	2	7	4	0
Pleurocapsa_PCC_7327_uid183006	Cyanobacteria	0	0	13	8	1
Stanieria_cyanosphaera_PCC_7437_uid1	Cyanobacteria	0	1	37	13	3
Prochlorococcus_marinus_AS9601_uid58	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_MIT_9211_uid	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_MIT_9215_uid	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_MIT_9301_uid	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_MIT_9303_uid	Cyanobacteria	0	0	0	6	0
Prochlorococcus_marinus_MIT_9312_uid	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_MIT_9313_uid	Cyanobacteria	0	0	0	5	0
Prochlorococcus_marinus_MIT_9515_uid	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_NATL1A_uid58	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_NATL2A_uid58	Cyanobacteria	0	0	0	0	0
Prochlorococcus_marinus_CCMP1375_ui	Cyanobacteria	0	0	0	0	0

Prochlorococcus_marinus_pastoris_CCM	Cyanobacteria	0	0	0	0	0
Calditerrivibrio_nitroreducens_DSM_196	Deferribacteres	0	0	2	2	0
Deferribacter_desulfuricans_SSM1_uid46	Deferribacteres	0	0	17	17	0
Denitrovibrio_acetiphilus_DSM_12809_ui	Deferribacteres	0	0	0	1	1
Flexistipes_sinusarabici_DSM_4947_uid6	Deferribacteres	0	0	0	3	0
Deinococcus_deserti_VCD115_uid58615	Deinococcus-Thermu	0	0	0	0	1
Deinococcus_geothermalis_DSM_11300_	Deinococcus-Thermu	0	0	8	1	1
Deinococcus_gobiensis_I_0_uid162509	Deinococcus-Thermu	0	0	1	0	0
Deinococcus_maricopensis_DSM_21211_	Deinococcus-Thermu	0	0	0	0	0
Deinococcus_peraridilitoris_DSM_19664_	Deinococcus-Thermu	0	0	0	0	1
Deinococcus_proteolyticus_MRP_uid633	Deinococcus-Thermu	0	0	1	0	0
Deinococcus_radiodurans_R1_uid57665	Deinococcus-Thermu	0	0	9	9	0
Truepera_radiovictrix_DSM_17093_uid49	Deinococcus-Thermu	0	0	6	11	0
Marinithermus_hydrothermalis_DSM_14	Deinococcus-Thermu	0	0	3	0	1
Meiothermus_ruber_DSM_1279_uid1985	Deinococcus-Thermu	0	0	2	2	0
Meiothermus_ruber_DSM_1279_uid4666	Deinococcus-Thermu	0	0	2	2	0
Meiothermus_silvanus_DSM_9946_uid49	Deinococcus-Thermu	0	0	14	3	0
Oceanithermus_profundus_DSM_14977_	Deinococcus-Thermu	0	0	0	2	0
Thermus_oshimai_JL_2_uid178948	Deinococcus-Thermu	0	0	2	0	0
Thermus_scotoductus_SA_01_uid62273	Deinococcus-Thermu	0	0	2	0	1
Thermus_CCB_US3_UF1_uid81197	Deinococcus-Thermu	0	0	1	0	0
Thermus_thermophilus_HB27_uid58033	Deinococcus-Thermu	0	0	3	0	0
Thermus_thermophilus_HB8_uid58223	Deinococcus-Thermu	0	0	2	0	1
Thermus_thermophilus_JL_18_uid16212	Deinococcus-Thermu	0	0	4	0	0
Thermus_thermophilus_SG0_5JP17_16_u	Deinococcus-Thermu	0	0	7	0	0
Dictyoglomus_thermophilum_H_6_12_ui	Dictyoglomi	0	0	0	0	0
Dictyoglomus_turgidum_DSM_6724_uid5	Dictyoglomi	0	0	0	0	0
Elusimicrobium_minutum_Pei191_uid58	Elusimicrobia	1	0	0	1	0
uncultured_Termite_group_1_bacterium_	Elusimicrobia	2	0	0	0	0
Acidobacterium_capsulatum_ATCC_5119	Fibrobacteres/Acido	0	0	0	3	1
Granulicella_mallensis_MP5ACTX8_uid49	Fibrobacteres/Acido	0	0	0	4	0
Acidobacterium_MP5ACTX9_uid50551	Fibrobacteres/Acido	0	0	0	3	1
Terriglobus_roseus_DSM_18391_uid1681	Fibrobacteres/Acido	0	0	0	5	1
Terriglobus_saanensis_SP1PR4_uid53251	Fibrobacteres/Acido	0	0	0	1	1
Candidatus_Solibacter_usitatus_Ellin6076	Fibrobacteres/Acido	0	0	0	4	0
Candidatus_Chloracidobacterium_thermo	Fibrobacteres/Acido	0	1	27	4	7
Candidatus_Koribacter_versatilis_Ellin345	Fibrobacteres/Acido	0	0	0	4	1
Fibrobacter_succinogenes_S85_uid16191	Fibrobacteres/Acido	1	0	0	0	0
Fibrobacter_succinogenes_S85_uid41169	Fibrobacteres/Acido	1	0	0	0	0
Alicyclobacillus_acidocaldarius_DSM_446	Bacilli	0	1	3	0	2
Alicyclobacillus_acidocaldarius_Tc_4_1_u	Bacilli	0	0	12	0	12
Kyrpidia_tusciae_DSM_2912_uid48361	Bacilli	0	0	28	2	19
Amphibacillus_xylanus_NBRC_15112_uid	Bacilli	0	0	4	1	0
Anoxybacillus_flavithermus_WK1_uid591	Bacilli	0	0	20	0	4
Bacillus_cellulosilyticus_DSM_2522_uid4	Bacilli	0	0	0	3	0
Bacillus_anthracis_A0248_uid59385	Bacilli	0	0	6	0	0
Bacillus_anthracis_Ames_uid57909	Bacilli	0	0	4	0	0
Bacillus_anthracis__Ames_Ancestor__uid	Bacilli	0	0	7	0	0
Bacillus_anthracis_CDC_684_uid59303	Bacilli	0	0	9	0	0
Bacillus_anthracis_H9401_uid162021	Bacilli	0	0	9	0	0
Bacillus_anthracis_Sterne_uid58091	Bacilli	0	0	5	0	0
Bacillus_cereus_03BB102_uid59299	Bacilli	0	0	14	0	1
Bacillus_cereus_AH187_uid58753	Bacilli	0	0	8	0	0
Bacillus_cereus_AH820_uid58751	Bacilli	0	0	8	0	0
Bacillus_cereus_ATCC_10987_uid57673	Bacilli	0	0	9	1	0
Bacillus_cereus_ATCC_14579_uid57975	Bacilli	0	0	5	5	0

Bacillus_cereus_B4264_uid58757	Bacilli	0	0	4	1	0
Bacillus_cereus_biovar_anthracis_CI_uid	Bacilli	0	0	9	0	0
Bacillus_cereus_E33L_uid58103	Bacilli	0	0	17	0	0
Bacillus_cereus_F837_76_uid83611	Bacilli	0	0	9	0	1
Bacillus_cereus_FRI_35_uid173403	Bacilli	0	0	13	2	0
Bacillus_cereus_G9842_uid58759	Bacilli	0	0	7	1	0
Bacillus_cereus_NC7401_uid82815	Bacilli	0	0	8	0	0
Bacillus_cereus_Q1_uid58529	Bacilli	0	0	11	2	1
Bacillus_cytotoxicus_NVH_391_98_uid58	Bacilli	0	0	4	0	0
Bacillus_thuringiensis_Bt407_uid177931	Bacilli	0	0	5	0	0
Bacillus_thuringiensis_HD_771_uid17337	Bacilli	0	0	10	0	0
Bacillus_thuringiensis_HD_789_uid17386	Bacilli	0	0	4	0	2
Bacillus_thuringiensis_MC28_uid176369	Bacilli	0	0	7	0	0
Bacillus_thuringiensis_serovar_chinensis_	Bacilli	0	0	11	3	1
Bacillus_thuringiensis_serovar_finitimus_	Bacilli	0	0	14	2	1
Bacillus_thuringiensis_serovar_konkukian	Bacilli	0	0	11	0	0
Bacillus_thuringiensis_BMB171_uid49135	Bacilli	0	0	9	1	0
Bacillus_thuringiensis_serovar_kurstaki_	Bacilli	0	0	5	0	1
Bacillus_thuringiensis_serovar_IS5056_ui	Bacilli	0	0	17	6	1
Bacillus_thuringiensis_Al_Hakam_uid587	Bacilli	0	0	7	0	1
Bacillus_thuringiensis_YBT_1518_uid2294	Bacilli	0	0	9	11	1
Bacillus_toyonensis_BCT_7112_uid22721	Bacilli	0	0	2	0	0
Bacillus_weihenstephanensis_KBAB4_uid	Bacilli	0	0	5	0	0
Bacillus_clausii_KSM_K16_uid58237	Bacilli	0	0	2	4	0
Bacillus_coagulans_2_6_uid68053	Bacilli	0	0	11	0	0
Bacillus_coagulans_36D1_uid54335	Bacilli	0	0	8	0	0
Bacillus_halodurans_C_125_uid57791	Bacilli	0	0	0	8	0
Bacillus_infantis_NRRL_B_14911_uid222	Bacilli	0	0	0	2	0
Bacillus_megaterium_DSM319_uid48371	Bacilli	0	0	0	0	0
Bacillus_megaterium_QM_B1551_uid158	Bacilli	0	0	1	0	0
Bacillus_megaterium_WSH_002_uid1598	Bacilli	0	0	1	1	0
Bacillus_pseudofirmus_OF4_uid45847	Bacilli	0	0	3	4	0
Bacillus_pumilus_SAFR_032_uid59017	Bacilli	0	0	0	0	0
Bacillus_selenitireducens_MLS10_uid495	Bacilli	0	3	12	1	0
Bacillus_1NLA3E_uid81841	Bacilli	0	0	15	2	0
Bacillus_JS_uid162189	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_CC178_uid22	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_IT_45_uid181	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_LFB112_uid2	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_LL3_uid1581	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_DSM_7_uid5	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_FZB42_uid58	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_A	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_C	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_N	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_U	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_U	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_U	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_plantarum_Y	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_TA208_uid15	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_XH7_uid1588	Bacilli	0	0	0	0	0
Bacillus_amyloliquefaciens_Y2_uid16519	Bacilli	0	0	0	0	0
Bacillus_atrophaeus_1942_uid59887	Bacilli	0	0	0	0	0
Bacillus_licheniformis_9945A_uid207072	Bacilli	0	0	0	0	0
Bacillus_licheniformis_ATCC_14580_uid5	Bacilli	0	0	0	0	0
Bacillus_licheniformis_DSM_13___ATCC_	Bacilli	0	0	0	0	0

Bacillus_subtilis_BSn5_uid62463	Bacilli	0	0	0	0	0
Bacillus_subtilis_PY79_uid229877	Bacilli	0	0	0	0	0
Bacillus_subtilis_QB928_uid173926	Bacilli	0	0	0	0	0
Bacillus_subtilis_natto_BEST195_uid1830	Bacilli	0	0	0	0	0
Bacillus_subtilis_spizizenii_W23_uid51879	Bacilli	0	0	0	0	0
Bacillus_subtilis_spizizenii_TU_B_10_uid7	Bacilli	0	0	0	0	0
Bacillus_subtilis_168_uid57675	Bacilli	0	0	0	0	0
Bacillus_subtilis_BAB_1_uid195461	Bacilli	0	0	0	0	0
Bacillus_subtilis_BSP1_uid184010	Bacilli	0	0	0	0	0
Bacillus_subtilis_6051_HGW_uid193706	Bacilli	0	0	0	0	0
Bacillus_subtilis_RO_NN_1_uid158879	Bacilli	0	0	0	0	0
Bacillus_subtilis_XF_1_uid189187	Bacilli	0	0	0	0	0
Geobacillus_kaustophilus_HTA426_uid58	Bacilli	0	0	13	3	0
Geobacillus_C56_T3_uid49467	Bacilli	0	0	5	1	0
Geobacillus_HH01_uid188479	Bacilli	0	0	9	2	0
Geobacillus_JF8_uid215234	Bacilli	1	0	7	5	0
Geobacillus_WCH70_uid59045	Bacilli	0	0	67	8	0
Geobacillus_Y4_1MC1_uid55779	Bacilli	0	0	1	0	0
Geobacillus_Y412MC52_uid55381	Bacilli	0	0	13	0	0
Geobacillus_Y412MC61_uid41171	Bacilli	0	0	12	0	0
Geobacillus_thermodenitrificans_NG80_2	Bacilli	0	0	1	1	0
Geobacillus_thermoglucosidasius_C56_YS	Bacilli	0	0	1	0	0
Geobacillus_thermoleovorans_CCB_US3_	Bacilli	0	1	20	3	0
Halobacillus_halophilus_DSM_2266_uid1	Bacilli	0	0	16	2	0
Lysinibacillus_sphaericus_C3_41_uid5894	Bacilli	0	0	1	0	1
Oceanobacillus_iheyensis_HTE831_uid578	Bacilli	0	0	0	2	0
Exiguobacterium_antarcticum_B7_uid176	Bacilli	0	1	4	1	0
Exiguobacterium_sibiricum_255_15_uid5	Bacilli	0	1	14	3	0
Exiguobacterium_AT1b_uid59093	Bacilli	0	0	3	0	0
Exiguobacterium_MH3_uid227425	Bacilli	0	0	0	0	0
Listeria_innocua_Clip11262_uid61567	Bacilli	1	0	0	0	0
Listeria_ivanovii_PAM_55_uid73473	Bacilli	0	0	0	0	0
Listeria_monocytogenes_La111_uid19376	Bacilli	0	0	0	0	0
Listeria_monocytogenes_07PF0776_uid1	Bacilli	0	0	0	0	0
Listeria_monocytogenes_uid43671	Bacilli	0	0	0	0	0
Listeria_monocytogenes_08_5923_uid43	Bacilli	0	0	0	0	0
Listeria_monocytogenes_10403S_uid5446	Bacilli	1	0	0	0	0
Listeria_monocytogenes_ATCC_19117_ui	Bacilli	0	0	0	0	0
Listeria_monocytogenes_EGD_uid223288	Bacilli	1	0	0	0	0
Listeria_monocytogenes_EGD_e_uid6158	Bacilli	0	0	0	0	0
Listeria_monocytogenes_Finland_1998_u	Bacilli	0	0	0	0	0
Listeria_monocytogenes_FSL_R2_561_uic	Bacilli	0	0	0	0	0
Listeria_monocytogenes_HCC23_uid5920	Bacilli	0	0	0	0	0
Listeria_monocytogenes_J0161_uid54459	Bacilli	1	0	0	0	0
Listeria_monocytogenes_J1_220_uid1797	Bacilli	0	0	0	0	0
Listeria_monocytogenes_J1816_uid17973	Bacilli	0	0	0	0	0
Listeria_monocytogenes_L312_uid175768	Bacilli	0	0	0	0	0
Listeria_monocytogenes_serotype_4a_L9	Bacilli	0	0	0	0	0
Listeria_monocytogenes_M7_uid162131	Bacilli	0	0	0	0	0
Listeria_monocytogenes_N53_1_uid1937	Bacilli	0	0	0	0	0
Listeria_monocytogenes_Clip80459_uid5	Bacilli	0	0	0	0	0
Listeria_monocytogenes_serotype_4b_F2	Bacilli	0	0	0	0	0
Listeria_monocytogenes_serotype_4b_LL	Bacilli	0	0	0	0	0
Listeria_monocytogenes_serotype_7_SLC	Bacilli	1	0	0	0	0
Listeria_monocytogenes_SLCC2372_uid1	Bacilli	0	0	0	0	0
Listeria_monocytogenes_SLCC2376_uid1	Bacilli	0	0	0	0	0

Listeria_monocytogenes_SLCC2378_uid17	Bacilli	0	0	0	0	0
Listeria_monocytogenes_SLCC2479_uid17	Bacilli	0	0	0	0	0
Listeria_monocytogenes_SLCC2540_uid17	Bacilli	1	0	0	0	0
Listeria_monocytogenes_serotype_1_2b_	Bacilli	1	0	0	0	0
Listeria_monocytogenes_SLCC5850_uid17	Bacilli	1	0	0	0	0
Listeria_monocytogenes_SLCC7179_uid17	Bacilli	0	0	0	0	0
Listeria_seeligeri_serovar_1_2b_SLCC395	Bacilli	0	0	0	0	0
Listeria_welshimeri_serovar_6b_SLCC533	Bacilli	0	0	0	0	0
Brevibacillus_brevis_NBRC_100599_uid59	Bacilli	0	0	5	3	0
Paenibacillus_larvae_04_309_uid232355	Bacilli	0	0	8	4	0
Paenibacillus_mucilaginosus_3016_uid89	Bacilli	0	0	0	0	0
Paenibacillus_mucilaginosus_K02_uid162	Bacilli	0	0	0	0	0
Paenibacillus_mucilaginosus_KNP414_uid	Bacilli	0	0	0	0	0
Paenibacillus_polymyxa_CR1_uid231659	Bacilli	0	0	0	1	0
Paenibacillus_polymyxa_E681_uid53477	Bacilli	0	0	0	0	0
Paenibacillus_polymyxa_M1_uid162159	Bacilli	0	0	3	1	0
Paenibacillus_polymyxa_SC2_uid59583	Bacilli	0	0	8	0	0
Paenibacillus_JDR_2_uid59021	Bacilli	0	0	0	0	0
Paenibacillus_Y412MC10_uid41127	Bacilli	0	0	1	2	0
Paenibacillus_terrae_HPL_003_uid82371	Bacilli	0	0	1	1	0
Thermobacillus_composti_KWC4_uid740	Bacilli	0	0	0	0	0
Solibacillus_silvestris_StLB046_uid168516	Bacilli	0	0	0	0	0
Macrococcus_caseolyticus_JCSC5402_uid	Bacilli	0	0	0	0	0
Staphylococcus_aureus_04_02981_uid16	Bacilli	0	0	0	0	0
Staphylococcus_aureus_08BA02176_uid1	Bacilli	0	0	0	0	0
Staphylococcus_aureus_Bmb9393_uid21	Bacilli	0	0	0	5	0
Staphylococcus_aureus_CC45_uid209174	Bacilli	0	0	0	0	0
Staphylococcus_aureus_M1_uid197263	Bacilli	0	0	0	4	0
Staphylococcus_aureus_RF122_uid57661	Bacilli	0	0	0	0	0
Staphylococcus_aureus_11819_97_uid15	Bacilli	0	0	0	2	0
Staphylococcus_aureus_55_2053_uid559	Bacilli	0	0	0	0	0
Staphylococcus_aureus_6850_uid217772	Bacilli	0	0	0	7	0
Staphylococcus_aureus_COL_uid57797	Bacilli	0	0	0	1	0
Staphylococcus_aureus_ECT_R_2_uid159	Bacilli	0	0	0	0	0
Staphylococcus_aureus_ED133_uid15968	Bacilli	0	0	0	0	0
Staphylococcus_aureus_ED98_uid41455	Bacilli	0	0	0	0	0
Staphylococcus_aureus_HO_5096_0412_	Bacilli	0	0	0	6	0
Staphylococcus_aureus_JH1_uid58457	Bacilli	0	0	0	0	0
Staphylococcus_aureus_JH9_uid58455	Bacilli	0	0	0	0	0
Staphylococcus_aureus_JKD6159_uid159	Bacilli	0	0	0	0	0
Staphylococcus_aureus_LGA251_uid1593	Bacilli	0	0	0	0	0
Staphylococcus_aureus_M013_uid88065	Bacilli	0	0	0	7	0
Staphylococcus_aureus_MRSA252_uid57	Bacilli	0	0	0	0	0
Staphylococcus_aureus_MSHR1132_uid8	Bacilli	0	0	0	0	0
Staphylococcus_aureus_MSSA476_uid57	Bacilli	0	0	0	0	0
Staphylococcus_aureus_Mu3_uid58817	Bacilli	0	0	0	0	0
Staphylococcus_aureus_Mu50_uid57835	Bacilli	0	0	0	0	0
Staphylococcus_aureus_MW2_uid57903	Bacilli	0	0	0	1	0
Staphylococcus_aureus_N315_uid57837	Bacilli	0	0	0	0	0
Staphylococcus_aureus_NCTC_8325_uid5	Bacilli	0	0	0	1	0
Staphylococcus_aureus_SA40_uid221289	Bacilli	0	0	0	7	0
Staphylococcus_aureus_SA957_uid22128	Bacilli	0	0	0	7	0
Staphylococcus_aureus_ST228_10388_ui	Bacilli	0	0	0	0	0
Staphylococcus_aureus_ST228_10497_ui	Bacilli	0	0	0	0	0
Staphylococcus_aureus_ST228_15532_ui	Bacilli	0	0	0	0	0
Staphylococcus_aureus_ST228_16035_ui	Bacilli	0	0	0	0	0

Staphylococcus_aureus_ST228_18412_ui	Bacilli	0	0	0	0	0
Staphylococcus_aureus_uid193758	Bacilli	0	0	0	0	0
Staphylococcus_aureus_uid193759	Bacilli	0	0	0	0	0
Staphylococcus_aureus_uid193761	Bacilli	0	0	0	0	0
Staphylococcus_aureus_ST398_uid15924	Bacilli	0	0	0	0	0
Staphylococcus_aureus_71193_uid16214	Bacilli	0	0	0	0	0
Staphylococcus_aureus_CN1_uid217769	Bacilli	0	0	0	1	0
Staphylococcus_aureus_JKD6008_uid159	Bacilli	0	0	0	2	0
Staphylococcus_aureus_Newman_uid588	Bacilli	0	0	0	2	0
Staphylococcus_aureus_T0131_uid15986	Bacilli	0	0	0	2	0
Staphylococcus_aureus_TCH60_uid15985	Bacilli	0	0	0	0	0
Staphylococcus_aureus_TW20_uid15924	Bacilli	0	0	0	4	0
Staphylococcus_aureus_USA300_FPR375	Bacilli	0	0	0	2	0
Staphylococcus_aureus_USA300_TCH151	Bacilli	0	0	0	2	0
Staphylococcus_aureus_VC40_uid88071	Bacilli	0	0	0	2	0
Staphylococcus_aureus_Z172_uid225604	Bacilli	0	0	0	4	0
Staphylococcus_carnosus_TM300_uid594	Bacilli	0	0	1	0	0
Staphylococcus_epidermidis_ATCC_1222	Bacilli	0	0	0	4	0
Staphylococcus_epidermidis_RP62A_uid5	Bacilli	0	0	0	3	0
Staphylococcus_haemolyticus_JCSC1435_	Bacilli	0	0	0	2	0
Staphylococcus_lugdunensis_HKU09_01_	Bacilli	0	0	0	1	0
Staphylococcus_lugdunensis_N920143_ui	Bacilli	0	0	0	1	0
Staphylococcus_pasteuri_SP1_uid226267	Bacilli	1	0	1	1	0
Staphylococcus_pseudintermedius_ED99_	Bacilli	1	0	0	0	0
Staphylococcus_pseudintermedius_HKU1	Bacilli	0	0	0	0	0
Staphylococcus_saprophyticus_ATCC_15	Bacilli	0	0	1	0	0
Staphylococcus_warneri_SG1_uid187059	Bacilli	0	0	0	0	0
Aerococcus_urinae_ACS_120_V_Col10a_	Bacilli	0	0	0	0	0
Carnobacterium_maltaromaticum_LMA2	Bacilli	0	0	0	0	0
Carnobacterium_17_4_uid65789	Bacilli	0	0	0	0	0
Carnobacterium_WN1359_uid225603	Bacilli	0	0	0	0	0
Enterococcus_casseliflavus_EC20_uid556	Bacilli	0	0	1	0	0
Enterococcus_faecalis_D32_uid171261	Bacilli	1	0	1	0	0
Enterococcus_faecalis_OG1RF_uid54927	Bacilli	1	0	1	0	0
Enterococcus_faecalis_Symbioflor_1_uid	Bacilli	0	0	1	2	0
Enterococcus_faecalis_V583_uid57669	Bacilli	0	0	1	1	0
Enterococcus_faecium_Aus0004_uid8702	Bacilli	0	0	2	1	0
Enterococcus_faecium_Aus0085_uid2144	Bacilli	0	0	5	5	0
Enterococcus_faecium_DO_uid55353	Bacilli	0	0	2	1	0
Enterococcus_faecium_NRRL_B_2354_ui	Bacilli	0	0	1	1	0
Enterococcus_hirae_ATCC_9790_uid7061	Bacilli	1	0	1	0	0
Enterococcus_mundtii_QU_25_uid22942	Bacilli	1	0	4	1	1
Enterococcus_7L76_uid197170	Bacilli	1	0	1	0	0
Melissococcus_plutonius_ATCC_35311_u	Bacilli	0	0	0	0	0
Melissococcus_plutonius_DAT561_uid89	Bacilli	0	0	0	0	0
Tetragenococcus_halophilus_uid74441	Bacilli	0	0	2	7	0
Lactobacillus_acidophilus_30SC_uid6360	Bacilli	0	0	6	3	0
Lactobacillus_acidophilus_La_14_uid2014	Bacilli	0	0	7	0	0
Lactobacillus_acidophilus_NCFM_uid576	Bacilli	0	0	5	0	0
Lactobacillus_amylovorus_GRL_1112_uid	Bacilli	0	0	17	5	0
Lactobacillus_amylovorus_GRL1118_uid1	Bacilli	0	0	8	6	0
Lactobacillus_brevis_ATCC_367_uid5798	Bacilli	0	0	0	0	0
Lactobacillus_brevis_KB290_uid195560	Bacilli	0	0	0	0	0
Lactobacillus_buchneri_uid73657	Bacilli	1	0	0	0	0
Lactobacillus_buchneri_NRRL_B_30929_	Bacilli	1	0	0	0	0
Lactobacillus_casei_ATCC_334_uid57985	Bacilli	0	0	0	0	0

Lactobacillus_casei_BD_II_uid162119	Bacilli	1	0	0	0	0
Lactobacillus_casei_BL23_uid59237	Bacilli	1	0	0	0	0
Lactobacillus_casei_LC2W_uid162121	Bacilli	1	0	0	0	0
Lactobacillus_casei_LOCK919_uid210959	Bacilli	1	0	0	0	0
Lactobacillus_casei_Zhang_uid50673	Bacilli	1	0	0	0	0
Lactobacillus_casei_W56_uid178736	Bacilli	1	0	0	0	0
Lactobacillus_paracasei_8700_2_uid5529	Bacilli	1	0	0	0	0
Lactobacillus_crispatus_ST1_uid48359	Bacilli	0	0	10	0	13
Lactobacillus_delbrueckii_bulgaricus_203	Bacilli	1	0	9	0	2
Lactobacillus_delbrueckii_bulgaricus_ATC	Bacilli	0	1	2	0	1
Lactobacillus_delbrueckii_bulgaricus_ATC	Bacilli	0	1	3	0	1
Lactobacillus_delbrueckii_bulgaricus_ND	Bacilli	0	2	20	3	12
Lactobacillus_fermentum_CECT_5716_ui	Bacilli	0	0	10	0	0
Lactobacillus_fermentum_F6_uid203391	Bacilli	0	0	43	41	0
Lactobacillus_fermentum_IFO_3956_uid5	Bacilli	0	0	9	10	0
Lactobacillus_gasseri_ATCC_33323_uid57	Bacilli	0	0	0	0	0
Lactobacillus_helveticus_CNRZ32_uid212	Bacilli	0	0	0	0	0
Lactobacillus_helveticus_DPC_4571_uid5	Bacilli	0	0	31	0	7
Lactobacillus_helveticus_H10_uid162017	Bacilli	0	0	29	1	1
Lactobacillus_helveticus_R0052_uid1744	Bacilli	0	0	27	0	2
Lactobacillus_johnsonii_DPC_6026_uid16	Bacilli	1	0	5	1	0
Lactobacillus_johnsonii_FI9785_uid41735	Bacilli	0	0	3	1	0
Lactobacillus_johnsonii_N6_2_uid229876	Bacilli	0	0	5	2	0
Lactobacillus_johnsonii_NCC_533_uid580	Bacilli	0	0	2	1	0
Lactobacillus_kefiranofaciens_ZW3_uid6	Bacilli	0	0	16	3	11
Lactobacillus_plantarum_16_uid209042	Bacilli	0	0	0	0	0
Lactobacillus_plantarum_JDM1_uid59361	Bacilli	0	0	0	0	0
Lactobacillus_plantarum_P8_uid203333	Bacilli	0	0	0	0	0
Lactobacillus_plantarum_ST_III_uid53537	Bacilli	0	0	0	0	0
Lactobacillus_plantarum_WCFS1_uid6291	Bacilli	0	0	0	0	0
Lactobacillus_plantarum_ZJ316_uid1886	Bacilli	1	0	0	0	0
Lactobacillus_reuteri_DSM_20016_uid58	Bacilli	0	0	5	19	0
Lactobacillus_reuteri_I5007_uid208677	Bacilli	0	0	6	7	0
Lactobacillus_reuteri_JCM_1112_uid5887	Bacilli	0	0	5	19	0
Lactobacillus_reuteri_SD2112_uid55357	Bacilli	0	0	17	18	0
Lactobacillus_reuteri_TD1_uid213089	Bacilli	0	0	3	3	0
Lactobacillus_rhamnosus_ATCC_8530_ui	Bacilli	0	0	3	0	3
Lactobacillus_rhamnosus_GG_uid161983	Bacilli	1	0	2	0	0
Lactobacillus_rhamnosus_GG_uid59313	Bacilli	1	0	2	0	0
Lactobacillus_rhamnosus_Lc_705_uid593	Bacilli	0	0	3	0	2
Lactobacillus_rhamnosus_LOCK900_uid2	Bacilli	1	0	5	0	4
Lactobacillus_rhamnosus_LOCK908_uid2	Bacilli	0	0	3	0	3
Lactobacillus_ruminis_ATCC_27782_uid7	Bacilli	0	0	8	6	0
Lactobacillus_sakei_23K_uid58281	Bacilli	0	0	0	0	0
Lactobacillus_salivarius_CECT_5713_uid1	Bacilli	1	0	3	0	0
Lactobacillus_salivarius_UCC118_uid5823	Bacilli	1	0	3	3	0
Lactobacillus_sanfranciscensis_TMW_1_1	Bacilli	1	0	10	9	0
Pediococcus_claussenii_ATCC_BAA_344_	Bacilli	0	0	0	0	0
Pediococcus_pentosaceus_ATCC_25745_	Bacilli	0	0	0	0	0
Pediococcus_pentosaceus_SL4_uid22721	Bacilli	1	0	0	0	0
Leuconostoc_carnosum_JB16_uid176371	Bacilli	0	0	0	0	0
Leuconostoc_citreum_KM20_uid58481	Bacilli	0	0	0	0	0
Leuconostoc_gasicomitatum_LMG_1881	Bacilli	0	0	0	0	0
Leuconostoc_gelidum_JB7_uid175682	Bacilli	1	0	0	0	0
Leuconostoc_kimchii_IMSNU_11154_uid	Bacilli	0	0	0	1	0
Leuconostoc_mesenteroides_ATCC_8293_	Bacilli	0	0	0	0	0

Leuconostoc_mesenteroides_J18_uid843	Bacilli	0	0	0	0	0
Leuconostoc_C2_uid68743	Bacilli	0	0	0	1	0
Oenococcus_oeni_PSU_1_uid59417	Bacilli	0	0	0	0	0
Weissella_koreensis_KACC_15510_uid68	Bacilli	0	0	0	0	0
Lactococcus_garvieae_ATCC_49156_uid7	Bacilli	0	0	0	0	0
Lactococcus_garvieae_Lg2_uid161935	Bacilli	0	0	0	0	0
Lactococcus_lactis_cremoris_A76_uid160	Bacilli	0	0	0	0	0
Lactococcus_lactis_cremoris_KW2_uid21	Bacilli	0	0	0	0	0
Lactococcus_lactis_cremoris_MG1363_ui	Bacilli	0	0	0	0	0
Lactococcus_lactis_cremoris_NZ9000_uid	Bacilli	0	0	0	0	0
Lactococcus_lactis_cremoris_SK11_uid57	Bacilli	0	0	0	0	0
Lactococcus_lactis_cremoris_UC509_9_ui	Bacilli	0	0	0	0	0
Lactococcus_lactis_CV56_uid160253	Bacilli	0	0	0	0	0
Lactococcus_lactis_Il1403_uid57671	Bacilli	0	0	0	0	0
Lactococcus_lactis_IO_1_uid192185	Bacilli	0	0	0	0	0
Lactococcus_lactis_KF147_uid42831	Bacilli	0	0	0	0	0
Lactococcus_lactis_KLDS_4_0325_uid225	Bacilli	0	0	0	0	0
Streptococcus_agalactiae_2_22_uid2022	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_09mas018883_	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_GD201008_00	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_ILRI005_uid20	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_ILRI112_uid20	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_SA20_06_uid1	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_A909_uid5793	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_NEM316_uid6	Bacilli	1	0	0	0	0
Streptococcus_agalactiae_2603V_R_uid5	Bacilli	1	0	0	0	0
Streptococcus_anginosus_C1051_uid218	Bacilli	1	0	0	0	0
Streptococcus_anginosus_C238_uid2180	Bacilli	0	0	0	0	0
Streptococcus_constellatus_pharyngis_C1	Bacilli	0	0	0	0	0
Streptococcus_constellatus_pharyngis_C	Bacilli	0	0	0	0	0
Streptococcus_constellatus_pharyngis_C	Bacilli	0	0	0	0	0
Streptococcus_intermedius_B196_uid218	Bacilli	1	0	0	0	0
Streptococcus_intermedius_C270_uid217	Bacilli	0	0	0	0	0
Streptococcus_intermedius_JTH08_uid16	Bacilli	0	0	0	0	0
Streptococcus_dysgalactiae_equisimilis_1	Bacilli	0	0	0	1	0
Streptococcus_dysgalactiae_equisimilis_	Bacilli	1	0	0	0	0
Streptococcus_dysgalactiae_equisimilis_	Bacilli	1	0	0	0	0
Streptococcus_dysgalactiae_equisimilis_	Bacilli	1	0	0	0	0
Streptococcus_dysgalactiae_equisimilis_	Bacilli	1	0	0	0	0
Streptococcus_equi_4047_uid59259	Bacilli	0	0	0	2	0
Streptococcus_equi_zooepidemicus_uid5	Bacilli	0	0	0	0	0
Streptococcus_equi_zooepidemicus_ATC	Bacilli	0	0	0	8	0
Streptococcus_equi_zooepidemicus_MG	Bacilli	1	0	0	2	0
Streptococcus_gallolyticus_ATCC_43143_	Bacilli	2	0	0	0	0
Streptococcus_gallolyticus_ATCC_BAA_2	Bacilli	1	0	0	0	0
Streptococcus_gallolyticus_UCN34_uid46	Bacilli	2	0	0	0	0
Streptococcus_gordonii_Challis_substr__	Bacilli	1	0	0	0	0
Streptococcus_infantarius_CJ18_uid8703	Bacilli	1	0	0	0	0
Streptococcus_iniae_SF1_uid206041	Bacilli	1	0	0	5	0
Streptococcus_lutetiensis_033_uid21339	Bacilli	1	0	0	0	0
Streptococcus_macedonicus_ACA_DC_19	Bacilli	1	0	0	0	0
Streptococcus_mitis_B6_uid46097	Bacilli	0	0	0	4	0
Streptococcus_mutans_GS_5_uid169223	Bacilli	1	0	0	4	0
Streptococcus_mutans_LJ23_uid162197	Bacilli	1	0	0	1	0
Streptococcus_mutans_NN2025_uid4635	Bacilli	1	0	0	1	0
Streptococcus_mutans_UA159_uid57947	Bacilli	1	0	0	2	0

Streptococcus_oligofermentans_AS_1_30	Bacilli	0	0	0	0	0
Streptococcus_oralis_Uo5_uid65449	Bacilli	0	0	0	0	0
Streptococcus_parasanguinis_ATCC_1591	Bacilli	0	0	0	2	0
Streptococcus_parasanguinis_FW213_uid	Bacilli	0	0	0	4	0
Streptococcus_parauberis_KCTC_11537_	Bacilli	0	0	0	2	0
Streptococcus_pasteurianus_ATCC_4314	Bacilli	1	0	0	1	0
Streptococcus_pneumoniae_670_6B_uid	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_70585_uid5	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_A026_uid22	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_AP200_uid5	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_ATCC_70066	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_CGSP14_uid	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_D39_uid585	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_G54_uid591	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_gamPNI0373	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_Hungary19A	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_INV104_uid1	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_INV200_uid1	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_JJA_uid5912	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_OXC141_uid	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_P1031_uid5	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_R6_uid5785	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_SPN034156_	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_SPN034183_	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_SPN994038_	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_SPN994039_	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_SPNA45_uid	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_ST556_uid1	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_Taiwan19F_	Bacilli	0	0	0	0	0
Streptococcus_pneumoniae_TCH8431_1	Bacilli	0	0	0	1	0
Streptococcus_pneumoniae_TIGR4_uid57	Bacilli	0	0	0	2	0
Streptococcus_pseudopneumoniae_IS74	Bacilli	0	0	0	1	0
Streptococcus_pyogenes_A20_uid178106	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_HSC5_uid21297	Bacilli	0	0	0	0	0
Streptococcus_pyogenes_MGAS1882_uid	Bacilli	1	0	0	1	0
Streptococcus_pyogenes_M1_476_uid19	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_M1_GAS_uid57	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS5005_uid	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS2096_uid	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS9429_uid	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS8232_uid	Bacilli	0	0	0	0	0
Streptococcus_pyogenes_MGAS10270_ui	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS6180_uid	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS315_uid5	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_SSI_1_uid5789	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_MGAS10750_ui	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_NZ131_uid590	Bacilli	1	0	0	0	0
Streptococcus_pyogenes_Manfredo_uid5	Bacilli	0	0	0	0	0
Streptococcus_pyogenes_Alab49_uid162	Bacilli	0	0	0	0	0
Streptococcus_pyogenes_MGAS15252_ui	Bacilli	1	0	0	1	0
Streptococcus_pyogenes_MGAS10394_ui	Bacilli	0	0	0	0	0
Streptococcus_salivarius_CCHSS3_uid704	Bacilli	0	0	0	19	0
Streptococcus_salivarius_JIM8777_uid16	Bacilli	1	0	0	3	0
Streptococcus_sanguinis_SK36_uid58381	Bacilli	0	0	0	0	0
Streptococcus_I_G2_uid224251	Bacilli	1	0	0	0	0
Streptococcus_I_P16_uid224252	Bacilli	0	0	0	0	0

Streptococcus_suis_05ZYH33_uid58663	Bacilli	0	0	0	4	0
Streptococcus_suis_98HAH33_uid58665	Bacilli	0	0	0	4	0
Streptococcus_suis_A7_uid162111	Bacilli	0	0	0	5	0
Streptococcus_suis_BM407_uid59321	Bacilli	0	0	0	2	0
Streptococcus_suis_D12_uid162127	Bacilli	0	0	0	5	0
Streptococcus_suis_D9_uid162125	Bacilli	1	0	0	3	0
Streptococcus_suis_GZ1_uid161937	Bacilli	0	0	0	5	0
Streptococcus_suis_JS14_uid162095	Bacilli	0	0	0	5	0
Streptococcus_suis_P1_7_uid32235	Bacilli	0	0	0	2	0
Streptococcus_suis_S735_uid174333	Bacilli	0	0	0	4	0
Streptococcus_suis_SC070731_uid193769	Bacilli	0	0	0	1	0
Streptococcus_suis_SC84_uid59323	Bacilli	0	0	0	2	0
Streptococcus_suis_SS12_uid162123	Bacilli	0	0	0	5	0
Streptococcus_suis_ST1_uid167482	Bacilli	1	0	0	41	0
Streptococcus_suis_ST3_uid66327	Bacilli	1	0	0	2	0
Streptococcus_suis_T15_uid226112	Bacilli	0	0	0	2	0
Streptococcus_suis_TL13_uid203123	Bacilli	0	0	0	2	0
Streptococcus_thermophilus_CNRZ1066_	Bacilli	1	0	0	3	0
Streptococcus_thermophilus_JIM_8232_u	Bacilli	1	0	0	3	0
Streptococcus_thermophilus_LMD_9_uid	Bacilli	2	0	0	2	0
Streptococcus_thermophilus_LMG_18311	Bacilli	1	0	0	2	0
Streptococcus_thermophilus_MN_ZLW_0	Bacilli	2	0	0	0	0
Streptococcus_thermophilus_ND03_uid16	Bacilli	2	0	0	0	0
Streptococcus_uberis_0140J_uid57959	Bacilli	0	0	0	0	0
Alkaliphilus_metalliredigens_QYMF_uid58	Clostridia	0	0	3	10	0
Alkaliphilus_oremlandii_OhILAs_uid58495	Clostridia	0	0	0	0	0
Candidatus_Arthromitus_SFB_mouse_Jap	Clostridia	0	0	0	0	0
Candidatus_Arthromitus_SFB_mouse_Yit_	Clostridia	0	0	0	0	0
Candidatus_Arthromitus_SFB_rat_Yit_uid	Clostridia	0	0	0	0	0
Clostridium_acetobutylicum_ATCC_824_u	Clostridia	0	0	0	1	0
Clostridium_acetobutylicum_DSM_1731_	Clostridia	0	0	0	1	0
Clostridium_acetobutylicum_EA_2018_ui	Clostridia	0	0	0	1	0
Clostridium_acidurici_9a_uid176126	Clostridia	0	0	10	3	4
Clostridium_autoethanogenum_DSM_100	Clostridia	0	0	1	2	0
Clostridium_beijerinckii_NCIMB_8052_ui	Clostridia	0	0	0	0	0
Clostridium_botulinum_A_ATCC_19397_u	Clostridia	0	0	0	0	0
Clostridium_botulinum_A_ATCC_3502_ui	Clostridia	0	0	0	0	0
Clostridium_botulinum_A_Hall_uid58931	Clostridia	0	0	0	0	0
Clostridium_botulinum_A2_Kyoto_uid592	Clostridia	0	0	0	0	0
Clostridium_botulinum_A3_Loch_Maree_	Clostridia	0	1	3	2	0
Clostridium_botulinum_B_Eklund_17B_ui	Clostridia	0	0	0	0	0
Clostridium_botulinum_B1_Okra_uid5914	Clostridia	0	0	5	0	0
Clostridium_botulinum_Ba4_657_uid5917	Clostridia	0	1	8	3	1
Clostridium_botulinum_BKT015925_uid66	Clostridia	0	0	7	0	4
Clostridium_botulinum_E3_Alaska_E43_u	Clostridia	0	0	1	0	1
Clostridium_botulinum_F_230613_uid159	Clostridia	0	0	1	0	0
Clostridium_botulinum_F_Langeland_uid5	Clostridia	0	0	0	0	0
Clostridium_botulinum_H04402_065_uid	Clostridia	0	0	2	0	0
Clostridium_cellulolyticum_H10_uid58709	Clostridia	1	0	1	10	0
Clostridium_cellulovorans_743B_uid5150	Clostridia	0	0	0	13	0
Clostridium_clariflavum_DSM_19732_uid	Clostridia	0	0	0	10	0
Clostridium_kluyveri_DSM_555_uid58885	Clostridia	0	0	3	2	1
Clostridium_kluyveri_NBRC_12016_uid59	Clostridia	0	0	3	2	0
Clostridium_ljungdahlii_DSM_13528_uid5	Clostridia	0	0	1	0	0
Clostridium_novyi_NT_uid58643	Clostridia	0	0	0	0	0
Clostridium_pasteurianum_BC1_uid20147	Clostridia	0	0	6	2	0

Clostridium_perfringens_ATCC_13124_ui	Clostridia	0	0	3	0	0
Clostridium_perfringens_13_uid57681	Clostridia	0	0	7	3	0
Clostridium_phytofermentans_ISDg_uid5	Clostridia	0	0	3	0	0
Clostridium_saccharobutylicum_DSM_13	Clostridia	0	0	3	0	4
Clostridium_cf__saccharolyticum_K10_ui	Clostridia	0	0	0	2	0
Clostridium_saccharolyticum_WM1_uid5	Clostridia	0	0	0	5	0
Clostridium_saccharoperbutylacetonicum	Clostridia	0	0	1	0	0
Clostridium_BNL1100_uid84307	Clostridia	0	0	1	0	0
Clostridium_SY8519_uid68705	Clostridia	0	0	1	0	0
Clostridium_tetani_12124569_uid227214	Clostridia	0	0	0	4	0
Clostridium_tetani_E88_uid57683	Clostridia	0	0	6	8	0
Clostridium_thermocellum_ATCC_27405_	Clostridia	0	0	0	2	0
Clostridium_thermocellum_DSM_1313_u	Clostridia	0	0	0	11	0
Anaerococcus_prevotii_DSM_20548_uid5	Clostridia	0	0	0	0	0
Finegoldia_magna_ATCC_29328_uid5886	Clostridia	1	1	9	3	0
Sulfobacillus_acidophilus_DSM_10332_ui	Clostridia	0	0	1	1	1
Sulfobacillus_acidophilus_TPY_uid68841	Clostridia	0	0	1	0	0
Thermaerobacter_marianensis_DSM_128	Clostridia	0	0	0	0	1
Symbiobacterium_thermophilum_IAM_1	Clostridia	0	0	0	0	0
Acetobacterium_woodii_DSM_1030_uid8	Clostridia	0	0	0	1	0
Eubacterium_eligens_ATCC_27750_uid59	Clostridia	0	0	1	2	0
Eubacterium_limosum_KIST612_uid5977	Clostridia	0	0	4	0	0
Eubacterium_rectale_ATCC_33656_uid59	Clostridia	1	0	1	0	2
Eubacterium_rectale_uid197161	Clostridia	0	0	1	0	2
Eubacterium_rectale_uid197162	Clostridia	0	2	5	1	0
Eubacterium_siraeum_uid197160	Clostridia	0	0	0	1	0
Eubacterium_siraeum_V10Sc8a_uid1971	Clostridia	0	0	0	0	0
Heliobacterium_modesticaldum_Ice1_uid	Clostridia	0	0	6	0	2
_Ruminococcus__obeum_uid197165	Clostridia	0	0	1	0	0
_Ruminococcus__torques_uid197166	Clostridia	0	0	1	0	0
Butyrivibrio_fibrisolvens_uid197155	Clostridia	1	0	0	1	0
Butyrivibrio_proteoclasticus_B316_uid51	Clostridia	0	0	10	9	1
Clostridium_lentocellum_DSM_5427_uid	Clostridia	0	0	0	1	0
Coprococcus_catus_GD_7_uid197174	Clostridia	1	1	3	2	0
Coprococcus_ART55_1_uid197176	Clostridia	0	0	0	0	0
Roseburia_hominis_A2_183_uid73419	Clostridia	0	0	0	7	0
Roseburia_intestinalis_uid197164	Clostridia	1	0	0	2	0
Roseburia_intestinalis_XB6B4_uid197179	Clostridia	0	0	0	1	0
Oscillibacter_valericigenes_uid73895	Clostridia	0	0	0	0	0
Candidatus_Desulforudis_audaxviator_M	Clostridia	0	1	9	4	4
Dehalobacter_CF_uid177714	Clostridia	0	0	0	1	0
Dehalobacter_11DCA_uid177715	Clostridia	0	0	0	0	0
Desulfitobacterium_dehalogenans_ATCC_	Clostridia	0	0	0	0	0
Desulfitobacterium_dichloroeliminans_L	Clostridia	0	0	0	0	0
Desulfitobacterium_hafniense_DCB_2_ui	Clostridia	0	0	2	3	0
Desulfitobacterium_hafniense_Y51_uid5	Clostridia	0	0	2	4	0
Desulfosporosinus_acidiphilus_SJ4_uid15	Clostridia	0	0	0	1	0
Desulfosporosinus_meridiei_DSM_13257_	Clostridia	0	0	0	1	0
Desulfosporosinus_orientis_DSM_765_ui	Clostridia	0	0	0	0	0
Desulfotomaculum_acetoxidans_DSM_77	Clostridia	0	0	28	13	7
Desulfotomaculum_carboxydivorans_CO_	Clostridia	0	0	14	1	9
Desulfotomaculum_gibsoniae_DSM_7213	Clostridia	0	0	10	14	3
Desulfotomaculum_kuznetsovii_DSM_61	Clostridia	0	1	19	1	20
Desulfotomaculum_reducens_MI_1_uid5	Clostridia	0	0	1	1	0
Desulfotomaculum_ruminis_DSM_2154_	Clostridia	0	0	0	1	0
Pelotomaculum_thermopropionicum_SI_	Clostridia	0	1	1	4	0

Syntrophobotulus_glycolicus_DSM_8271_	Clostridia	0	0	0	0	0
Thermincola_potens_JR_uid48823	Clostridia	0	0	0	0	1
Filifactor_alocis_ATCC_35896_uid46625	Clostridia	1	0	0	9	0
Clostridium_difficile_630_uid57679	Clostridia	0	0	10	3	0
Clostridium_difficile_BI1_uid158363	Clostridia	0	0	22	8	2
Clostridium_difficile_CD196_uid41017	Clostridia	0	0	17	0	0
Clostridium_difficile_R20291_uid40921	Clostridia	0	0	16	0	0
_Clostridium__sticklandii_uid59585	Clostridia	0	0	2	0	1
Ethanoligenens_harbinense_YUAN_3_uid	Clostridia	0	0	1	4	0
Faecalibacterium_prausnitzii_L2_6_uid19	Clostridia	0	0	0	1	0
Faecalibacterium_prausnitzii_uid197157	Clostridia	0	0	0	1	0
Ruminococcus_albus_7_uid51721	Clostridia	0	0	11	4	0
Ruminococcus_bromii_uid197158	Clostridia	0	0	0	1	0
Ruminococcus_champanellensis_18P13_	Clostridia	0	0	1	0	0
Ruminococcus_uid197156	Clostridia	0	0	5	1	0
Clostridium_stercorarium_DSM_8532_ui	Clostridia	0	0	0	0	0
Clostridium_stercorarium_DSM_8532_ui	Clostridia	0	0	0	0	0
Syntrophomonas_wolfei_Goettingen_uid	Clostridia	0	0	0	6	0
Syntrophothermus_lipocalidus_DSM_126	Clostridia	0	0	0	0	0
butyrate_producing_bacterium_SM4_1_	Clostridia	0	0	1	0	0
butyrate_producing_bacterium_SS3_4_ui	Clostridia	0	0	1	2	0
butyrate_producing_bacterium_SSC_2_ui	Clostridia	0	0	4	2	0
Clostridiales_genomosp__BVAB3_UPII9_	Clostridia	0	0	4	2	0
Halanaerobium_hydrogeniformans_uid6	Clostridia	0	0	5	3	0
Halanaerobium_praevalens_DSM_2228_	Clostridia	0	0	4	6	0
Halothermothrix_orenii_H_168_uid5858	Clostridia	0	0	0	0	0
Acetohalobium_arabaticum_DSM_5501_	Clostridia	0	2	22	4	1
Halobacteroides_halobius_DSM_5150_ui	Clostridia	0	3	2	0	0
Natranaerobius_thermophilus_JW_NM_	Clostridia	0	1	3	2	0
Thermoanaerobacter_tengcongensis_MB	Clostridia	0	0	15	1	12
Carboxydothermus_hydrogenoformans_Z	Clostridia	0	0	8	2	0
Ammonifex_degensii_KC4_uid41053	Clostridia	0	5	51	4	24
Moorella_thermoacetica_ATCC_39073_ui	Clostridia	0	0	0	0	0
Tepidanaerobacter_Re1_uid66873	Clostridia	0	0	0	1	0
Tepidanaerobacter_acetatoxydans_Re1_	Clostridia	0	0	0	1	0
Thermacetogenium_phaeum_DSM_1227	Clostridia	0	0	10	3	5
Thermoanaerobacter_brockii_finnii_Ako_	Clostridia	0	0	8	1	2
Thermoanaerobacter_italicus_Ab9_uid46	Clostridia	0	0	2	0	0
Thermoanaerobacter_mathranii_A3_uid4	Clostridia	0	0	0	0	0
Thermoanaerobacter_pseudethanolicus_	Clostridia	0	0	9	1	7
Thermoanaerobacter_X513_uid53065	Clostridia	0	0	4	0	1
Thermoanaerobacter_X514_uid58589	Clostridia	0	0	4	0	3
Thermoanaerobacter_wiegelii_Rt8_B1_ui	Clostridia	0	0	3	2	1
Caldicellulosiruptor_bescii_DSM_6725_ui	Clostridia	0	3	10	4	1
Caldicellulosiruptor_hydrothermalis_108_	Clostridia	0	2	8	1	2
Caldicellulosiruptor_kristjanssonii_177R1	Clostridia	0	1	14	2	3
Caldicellulosiruptor_kronotskyensis_2002	Clostridia	0	1	8	1	3
Caldicellulosiruptor_lactoaceticus_6A_ui	Clostridia	0	1	11	4	2
Caldicellulosiruptor_obsidiansis_OB47_ui	Clostridia	0	0	17	3	0
Caldicellulosiruptor_owensensis_OL_uid6	Clostridia	0	0	0	1	0
Caldicellulosiruptor_saccharolyticus_DSM	Clostridia	0	0	9	2	7
Thermoanaerobacterium_thermosacchar	Clostridia	0	0	4	2	0
Thermoanaerobacterium_thermosacchar	Clostridia	0	1	0	1	0
Thermoanaerobacterium_xylanolyticum_	Clostridia	0	0	0	6	0
Thermosediminibacter_oceani_DSM_166	Clostridia	0	0	0	0	1
Mahella_australiensis_50_1_BON_uid669	Clostridia	0	3	3	0	0

Coprothermobacter_proteolyticus_DSM_	Clostridia	0	0	0	0	0
Thermodesulfobium_narugense_DSM_14	Clostridia	0	0	0	0	0
Erysipelothrix_rhusiopathiae_Fujisawa_ui	Erysipelotrichia	0	0	0	0	0
Erysipelothrix_rhusiopathiae_SY1027_uid	Erysipelotrichia	0	0	0	0	0
Eubacterium_cylindroides_T2_87_uid197	Erysipelotrichia	0	0	0	0	0
Acholeplasma_laidlawii_PG_8A_uid58901	Mollicutes	0	0	0	0	0
Candidatus_Phytoplasma_mali_uid59087	Mollicutes	0	0	0	0	0
Candidatus_Phytoplasma_australiense_ui	Mollicutes	0	0	0	0	0
Strawberry_lethal_yellows_phytoplasma_	Mollicutes	0	0	0	0	0
Candidatus_Phytoplasma_solani_284_09_	Mollicutes	0	0	0	0	0
Aster_yellows_witches_broom_phytoplas	Mollicutes	0	0	0	0	0
Onion_yellows_phytoplasma_OY_M_uid5	Mollicutes	0	0	0	0	0
Mesoplasma_florum_L1_uid58055	Mollicutes	0	0	0	0	0
Mesoplasma_florum_W37_uid224253	Mollicutes	0	0	0	0	0
Spiroplasma_apis_B31_uid230613	Mollicutes	1	0	0	0	0
Spiroplasma_chrysopicola_DF_1_uid2050	Mollicutes	0	0	0	0	0
Spiroplasma_diminutum_CUAS_1_uid212	Mollicutes	0	0	0	0	0
Spiroplasma_syrphidicola_EA_1_uid2050	Mollicutes	1	0	0	0	0
Spiroplasma_taiwanense_CT_1_uid21297	Mollicutes	0	0	0	0	0
Candidatus_Mycoplasma_haemolamae_P	Mollicutes	0	0	0	0	0
Candidatus_Mycoplasma_haemominutu	Mollicutes	0	0	0	0	0
Mycoplasma_agalactiae_uid46679	Mollicutes	0	0	0	0	0
Mycoplasma_agalactiae_PG2_uid61619	Mollicutes	0	0	0	0	0
Mycoplasma_arthritidis_158L3_1_uid580	Mollicutes	0	0	0	0	0
Mycoplasma_bovis_HB0801_uid168665	Mollicutes	0	0	0	0	0
Mycoplasma_bovis_Hubei_1_uid68691	Mollicutes	0	0	0	0	0
Mycoplasma_bovis_PG45_uid60859	Mollicutes	0	0	0	0	0
Mycoplasma_conjunctivae_uid59325	Mollicutes	0	0	0	0	0
Mycoplasma_crocodyli_MP145_uid47087	Mollicutes	0	0	0	0	0
Mycoplasma_cynos_C142_uid184824	Mollicutes	1	0	0	0	0
Mycoplasma_fermentans_JER_uid53543	Mollicutes	0	0	0	0	0
Mycoplasma_fermentans_M64_uid62099	Mollicutes	0	0	0	0	0
Mycoplasma_fermentans_PG18_uid1971	Mollicutes	0	0	0	0	0
Mycoplasma_gallisepticum_CA06_2006_	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_NC06_2006_	Mollicutes	0	0	0	0	0
Mycoplasma_gallisepticum_NC08_2008_	Mollicutes	0	0	0	0	0
Mycoplasma_gallisepticum_NC95_13295_	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_NC96_1596_	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_NY01_2001_	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_S6_uid20052	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_F_uid162001	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_R_high__uid1	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_R_low__uid5	Mollicutes	1	0	0	0	0
Mycoplasma_gallisepticum_VA94_7994_	Mollicutes	0	0	0	0	0
Mycoplasma_gallisepticum_WI01_2001_	Mollicutes	1	0	0	0	0
Mycoplasma_genitalium_G37_uid57707	Mollicutes	0	0	0	0	0
Mycoplasma_genitalium_M2288_uid173	Mollicutes	0	0	0	0	0
Mycoplasma_genitalium_M2321_uid173	Mollicutes	0	0	0	0	0
Mycoplasma_genitalium_M6282_uid173	Mollicutes	0	0	0	0	0
Mycoplasma_genitalium_M6320_uid173	Mollicutes	0	0	0	0	0
Mycoplasma_haemocanis_Illinois_uid823	Mollicutes	0	0	0	0	0
Mycoplasma_haemofelis_Ohio2_uid1620	Mollicutes	0	0	0	0	0
Mycoplasma_haemofelis_Langford_1_uid	Mollicutes	0	0	0	0	0
Mycoplasma_hominis_ATCC_23114_uid4	Mollicutes	0	0	0	0	0
Mycoplasma_hyopneumoniae_168_uid1	Mollicutes	0	0	0	0	0
Mycoplasma_hyopneumoniae_168_L_uid	Mollicutes	0	0	0	0	0

Mycoplasma_hyopneumoniae_232_uid5	Mollicutes	0	0	0	0	0
Mycoplasma_hyopneumoniae_7422_uid	Mollicutes	0	0	0	0	0
Mycoplasma_hyopneumoniae_7448_uid	Mollicutes	0	0	0	0	0
Mycoplasma_hyopneumoniae_J_uid5805	Mollicutes	0	0	0	0	0
Mycoplasma_hyorhinis_DBS_1050_uid22	Mollicutes	0	0	0	0	0
Mycoplasma_hyorhinis_GDL_1_uid87003	Mollicutes	0	0	0	0	0
Mycoplasma_hyorhinis_HUB_1_uid51695	Mollicutes	0	0	0	0	0
Mycoplasma_hyorhinis_MCLD_uid16208	Mollicutes	0	0	0	0	0
Mycoplasma_hyorhinis_SK76_uid181997	Mollicutes	0	0	0	0	0
Mycoplasma_mobile_163K_uid58077	Mollicutes	1	0	0	0	0
Mycoplasma_capricolum_ATCC_27343_u	Mollicutes	0	0	0	0	0
Mycoplasma_leachii_99_014_6_uid1620	Mollicutes	0	0	0	0	0
Mycoplasma_leachii_PG50_uid60849	Mollicutes	0	0	0	0	0
Mycoplasma_mycoides_capri_LC_95010_	Mollicutes	0	0	0	0	0
Mycoplasma_mycoides_SC_Gladysdale_u	Mollicutes	0	0	0	0	0
Mycoplasma_mycoides_SC_PG1_uid5803	Mollicutes	0	0	0	0	0
Mycoplasma_ovis_Michigan_uid232247	Mollicutes	0	0	0	0	0
Mycoplasma_parvum_Indiana_uid22337	Mollicutes	0	0	0	0	0
Mycoplasma_penetrans_HF_2_uid57729	Mollicutes	0	0	0	0	0
Mycoplasma_pneumoniae_309_uid8549	Mollicutes	0	0	0	0	0
Mycoplasma_pneumoniae_FH_uid16202	Mollicutes	0	0	0	0	0
Mycoplasma_pneumoniae_M129_uid577	Mollicutes	0	0	0	0	0
Mycoplasma_pneumoniae_M129_B7_uid	Mollicutes	0	0	0	0	0
Mycoplasma_pulmonis_UAB_CTIP_uid61	Mollicutes	0	0	0	0	0
Mycoplasma_putrefaciens_KS1_uid72481	Mollicutes	0	0	0	0	0
Mycoplasma_putrefaciens_Mput9231_ui	Mollicutes	0	0	0	0	0
Mycoplasma_suis_KI3806_uid63665	Mollicutes	0	0	0	0	0
Mycoplasma_suis_Illinois_uid61897	Mollicutes	0	0	0	0	0
Mycoplasma_synoviae_53_uid58061	Mollicutes	1	0	0	0	0
Mycoplasma_wenyonii_Massachusetts_u	Mollicutes	0	0	0	0	0
Ureaplasma_parvum_serovar_3_ATCC_2	Mollicutes	0	0	0	0	0
Ureaplasma_parvum_serovar_3_ATCC_7	Mollicutes	0	0	0	0	0
Ureaplasma_urealyticum_serovar_10_AT	Mollicutes	0	0	0	0	0
Acidaminococcus_fermentans_DSM_207	Negativicutes	0	0	1	1	0
Acidaminococcus_intestini_RyC_MR95_u	Negativicutes	1	0	0	1	1
Megamonas_hypermegale_uid197163	Negativicutes	0	0	0	2	0
Megasphaera_elsdenii_DSM_20460_uid7	Negativicutes	0	0	14	0	0
Selenomonas_ruminantium_lactilytica_T	Negativicutes	0	0	13	0	11
Selenomonas_sputigena_ATCC_35185_ui	Negativicutes	0	0	0	6	0
Veillonella_parvula_DSM_2008_uid41927	Negativicutes	0	0	0	0	0
Fusobacterium_4_8_uid205051	Fusobacteria	0	0	8	1	0
Fusobacterium_nucleatum_ATCC_25586_	Fusobacteria	0	0	0	2	0
Fusobacterium_3_1_36A2_uid55995	Fusobacteria	1	0	0	7	0
Ilyobacter_polytropus_DSM_2926_uid59	Fusobacteria	1	0	0	2	0
Leptotrichia_buccalis_C_1013_b_uid5921	Fusobacteria	0	0	7	3	0
Sebaldella_termitidis_ATCC_33386_uid41	Fusobacteria	0	0	0	2	0
Streptobacillus_moniliformis_DSM_1211	Fusobacteria	1	0	0	1	0
Gemmatimonas_aurantiaca_T_27_uid58	Gemmatimonadetes	0	0	0	0	0
Leptospirillum_ferrooxidans_C2_3_uid15	Nitrospirae	0	0	12	6	1
Leptospirillum_ferriphilum_ML_04_uid17	Nitrospirae	0	0	0	0	1
Candidatus_Nitrospira_defluvii_uid51175	Nitrospirae	0	0	0	2	2
Thermodesulfovibrio_yellowstonii_DSM_	Nitrospirae	0	0	1	0	0
Phycisphaera_mikurensis_NBRC_102666_	Phycisphaerae	0	0	0	5	0
Isosphaera_pallida_ATCC_43644_uid622	Planctomycetia	0	0	0	1	0
Pirellula_staleyi_DSM_6068_uid43209	Planctomycetia	0	0	0	3	1
Planctomyces_brasiliensis_DSM_5305_ui	Planctomycetia	0	0	0	6	0

Planctomyces_limnophilus_DSM_3776_ui	Planctomycetia	0	0	0	5	0
Rhodopirellula_baltica_SH_1_uid61589	Planctomycetia	0	0	0	4	0
Singulisphaera_acidiphila_DSM_18658_ui	Planctomycetia	0	0	0	1	0
Asticcacaulis_excentricus_CB_48_uid556	Alphaproteobacteria	0	0	0	0	0
Brevundimonas_subvibrioides_ATCC_152	Alphaproteobacteria	0	0	0	0	0
Caulobacter_segnis_ATCC_21756_uid417	Alphaproteobacteria	0	0	0	0	1
Caulobacter_K31_uid58551	Alphaproteobacteria	0	0	0	1	0
Caulobacter_crescentus_CB15_uid57891	Alphaproteobacteria	0	0	0	1	1
Caulobacter_crescentus_NA1000_uid593	Alphaproteobacteria	0	0	0	1	1
Phenylobacterium_zucineum_HLK1_uid5	Alphaproteobacteria	0	0	0	0	0
Magnetococcus_MC_1_uid57833	Alphaproteobacteria	0	0	0	2	0
Parvularcula_bermudensis_HTCC2503_ui	Alphaproteobacteria	0	0	0	0	0
Bartonella_australis_Aust_NH1_uid18995	Alphaproteobacteria	0	0	0	0	0
Bartonella_bacilliformis_KC583_uid58533	Alphaproteobacteria	0	0	0	0	0
Bartonella_clarridgeiae_73_uid62131	Alphaproteobacteria	0	0	0	0	0
Bartonella_grahamii_as4aup_uid59405	Alphaproteobacteria	0	0	0	0	0
Bartonella_henselae_Houston_1_uid5774	Alphaproteobacteria	0	0	0	0	0
Bartonella_quintana_RM_11_uid174512	Alphaproteobacteria	0	0	0	0	0
Bartonella_quintana_Toulouse_uid57635	Alphaproteobacteria	0	0	0	0	0
Bartonella_tribocorum_CIP_105476_uid5	Alphaproteobacteria	0	0	0	0	0
Bartonella_vinsonii_berkhoffii_Winnie_ui	Alphaproteobacteria	0	0	0	0	0
Beijerinckia_indica_ATCC_9039_uid59057	Alphaproteobacteria	0	0	0	0	0
Methylocella_silvestris_BL2_uid59433	Alphaproteobacteria	0	0	0	0	0
Bradyrhizobium_japonicum_USDA_110_u	Alphaproteobacteria	0	0	0	0	0
Bradyrhizobium_japonicum_USDA_6_uid	Alphaproteobacteria	0	0	0	0	0
Agromonas_oligotrophica_S58_uid19218	Alphaproteobacteria	0	0	0	1	0
Bradyrhizobium_BTAi1_uid58505	Alphaproteobacteria	0	0	0	3	1
Bradyrhizobium_ORS_278_uid58941	Alphaproteobacteria	0	0	0	2	0
Bradyrhizobium_S23321_uid158167	Alphaproteobacteria	0	0	0	0	1
Nitrobacter_hamburgensis_X14_uid5829	Alphaproteobacteria	0	0	0	1	0
Nitrobacter_winogradskyi_Nb_255_uid58	Alphaproteobacteria	0	0	0	0	1
Oligotropha_carboxidovorans_OM4_uid1	Alphaproteobacteria	0	0	0	0	0
Oligotropha_carboxidovorans_OM5_uid7	Alphaproteobacteria	0	0	0	0	0
Oligotropha_carboxidovorans_OM5_uid5	Alphaproteobacteria	0	0	0	0	0
Rhodopseudomonas_palustris_BisA53_ui	Alphaproteobacteria	0	0	0	1	0
Rhodopseudomonas_palustris_BisB18_ui	Alphaproteobacteria	1	0	0	4	0
Rhodopseudomonas_palustris_BisB5_uid	Alphaproteobacteria	1	0	0	1	0
Rhodopseudomonas_palustris_CGA009_u	Alphaproteobacteria	0	0	0	0	0
Rhodopseudomonas_palustris_DX_1_uid	Alphaproteobacteria	0	0	0	1	0
Rhodopseudomonas_palustris_HaA2_uid	Alphaproteobacteria	0	0	0	1	0
Rhodopseudomonas_palustris_TIE_1_uid	Alphaproteobacteria	0	0	0	0	0
Brucella_abortus_A13334_uid83615	Alphaproteobacteria	0	0	0	0	0
Brucella_abortus_bv__1_9_941_uid5801	Alphaproteobacteria	0	0	0	0	0
Brucella_abortus_S19_uid58873	Alphaproteobacteria	0	0	0	0	0
Brucella_melitensis_biovar_Abortus_230	Alphaproteobacteria	0	0	0	0	0
Brucella_canis_ATCC_23365_uid59009	Alphaproteobacteria	0	0	0	0	0
Brucella_canis_HSK_A52141_uid83613	Alphaproteobacteria	0	0	0	0	0
Brucella_ceti_TE10759_12_uid229880	Alphaproteobacteria	0	0	0	0	0
Brucella_ceti_TE28753_12_uid229879	Alphaproteobacteria	0	0	0	0	0
Brucella_melitensis_bv__1_16M_uid5773	Alphaproteobacteria	0	0	0	0	0
Brucella_melitensis_ATCC_23457_uid592	Alphaproteobacteria	0	0	0	0	0
Brucella_melitensis_M28_uid158857	Alphaproteobacteria	0	0	0	0	0
Brucella_melitensis_M5_90_uid158855	Alphaproteobacteria	0	0	0	0	0
Brucella_melitensis_NI_uid158853	Alphaproteobacteria	0	0	0	0	0
Brucella_microti_CCM_4915_uid59319	Alphaproteobacteria	0	0	0	0	0
Brucella_ovis_ATCC_25840_uid58113	Alphaproteobacteria	0	0	0	0	0

Brucella_pinnipedialis_B2_94_uid71131	Alphaproteobacteria	0	0	0	0	0
Brucella_suis_1330_uid159871	Alphaproteobacteria	0	0	0	0	0
Brucella_suis_1330_uid57927	Alphaproteobacteria	0	0	0	0	0
Brucella_suis_ATCC_23445_uid59015	Alphaproteobacteria	0	0	0	0	0
Brucella_suis_VBI22_uid83617	Alphaproteobacteria	0	0	0	0	0
Ochrobactrum_anthropi_ATCC_49188_ui	Alphaproteobacteria	0	0	0	0	0
Hyphomicrobium_denitrificans_1NES1_ui	Alphaproteobacteria	0	0	0	0	0
Hyphomicrobium_denitrificans_ATCC_51	Alphaproteobacteria	0	0	0	0	0
Hyphomicrobium_nitrativorans_NL23_ui	Alphaproteobacteria	0	0	0	0	0
Hyphomicrobium_MC1_uid68453	Alphaproteobacteria	0	0	0	0	0
Pelagibacterium_halotolerans_B2_uid743	Alphaproteobacteria	0	0	0	0	0
Rhodomicrobium_vannielii_ATCC_17100_	Alphaproteobacteria	0	0	0	0	0
Methylobacterium_extorquens_AM1_uid	Alphaproteobacteria	0	0	3	0	0
Methylobacterium_chloromethanicum_C	Alphaproteobacteria	0	0	0	0	0
Methylobacterium_extorquens_DM4_uid	Alphaproteobacteria	0	0	0	0	0
Methylobacterium_extorquens_PA1_uid5	Alphaproteobacteria	0	0	0	0	0
Methylobacterium_nodulans_ORS_2060_	Alphaproteobacteria	0	0	1	1	0
Methylobacterium_populi_BJ001_uid589	Alphaproteobacteria	0	0	2	0	0
Methylobacterium_radiotolerans_JCM_2	Alphaproteobacteria	0	0	0	0	0
Methylobacterium_4_46_uid58843	Alphaproteobacteria	0	0	0	0	0
Methylocystis_SC2_uid174072	Alphaproteobacteria	0	0	0	0	0
Chelativorans_BNC1_uid58069	Alphaproteobacteria	0	0	0	0	0
Mesorhizobium_australicum_WSM2073_	Alphaproteobacteria	0	0	0	0	0
Mesorhizobium_ciceri_biovar_biserrulae_	Alphaproteobacteria	0	0	0	1	0
Mesorhizobium_loti_MAFF303099_uid57	Alphaproteobacteria	0	0	0	4	0
Mesorhizobium_opportunistum_WSM20	Alphaproteobacteria	0	0	0	0	0
Candidatus_Liberibacter_americanus_Sa	Alphaproteobacteria	0	0	0	0	0
Candidatus_Liberibacter_asiaticus_gxpsy_	Alphaproteobacteria	0	0	0	0	0
Candidatus_Liberibacter_asiaticus_psy62_	Alphaproteobacteria	0	0	0	0	0
Candidatus_Liberibacter_solanacearum_	Alphaproteobacteria	0	0	0	0	0
bacterium_BT_1_uid184079	Alphaproteobacteria	0	0	0	0	0
Agrobacterium_H13_3_uid63403	Alphaproteobacteria	0	0	0	0	0
Agrobacterium_fabrum_C58_uid57865	Alphaproteobacteria	0	0	0	0	0
Agrobacterium_radiobacter_K84_uid582	Alphaproteobacteria	0	0	0	0	0
Agrobacterium_vitis_S4_uid58249	Alphaproteobacteria	0	0	0	0	0
Rhizobium_etli_bv__mimosae_Mim1_uid	Alphaproteobacteria	0	0	0	0	0
Rhizobium_etli_CFN_42_uid58377	Alphaproteobacteria	0	0	0	0	0
Rhizobium_etli_CIAT_652_uid59115	Alphaproteobacteria	0	0	0	0	0
Rhizobium_leguminosarum_bv__trifolii_	Alphaproteobacteria	0	0	0	0	0
Rhizobium_leguminosarum_bv__trifolii_	Alphaproteobacteria	0	0	0	0	0
Rhizobium_leguminosarum_bv__viciae_3	Alphaproteobacteria	0	0	0	0	0
Rhizobium_IRBG74_uid222820	Alphaproteobacteria	0	0	0	0	0
Rhizobium_tropici_CIAT_899_uid185179	Alphaproteobacteria	0	0	0	4	0
Sinorhizobium_fredii_HH103_uid86865	Alphaproteobacteria	0	0	0	1	0
Rhizobium_NGR234_uid59081	Alphaproteobacteria	0	0	0	4	0
Sinorhizobium_fredii_USDA_257_uid168	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_medicae_WSM419_uid58	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_1021_uid57603	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_2011_uid193772	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_AK83_uid52607	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_BL225C_uid5260	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_GR4_uid184823	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_Rm41_uid17637	Alphaproteobacteria	0	0	0	0	0
Sinorhizobium_meliloti_SM11_uid15968	Alphaproteobacteria	0	0	0	0	0
Parvibaculum_lavamentivorans_DS_1_ui	Alphaproteobacteria	1	0	0	0	0
Candidatus_Hodgkinia_cicadicola_Dsem_	Alphaproteobacteria	0	0	0	0	0

Azorhizobium_caulinodans_ORS_571_uid	Alphaproteobacteria	0	0	0	0	0
Starkeya_novella_DSM_506_uid48815	Alphaproteobacteria	0	0	0	0	0
Xanthobacter_autotrophicus_Py2_uid584	Alphaproteobacteria	0	0	0	0	0
Hirschia_baltica_ATCC_49814_uid59365	Alphaproteobacteria	0	0	0	0	0
Hyphomonas_neptunium_ATCC_15444_u	Alphaproteobacteria	0	0	0	0	0
Maricaulis_maris_MCS10_uid58689	Alphaproteobacteria	0	0	0	0	0
Dinoroseobacter_shibae_DFL_12_uid587	Alphaproteobacteria	1	0	0	0	0
Jannaschia_CCS1_uid58147	Alphaproteobacteria	0	0	1	0	0
Ketogulonicigenium_vulgare_WSH_001_u	Alphaproteobacteria	0	0	0	0	0
Ketogulonicigenium_vulgare_Y25_uid595	Alphaproteobacteria	0	0	0	0	0
Leisingera_methylohalidivorans_DSM_14	Alphaproteobacteria	0	0	0	0	0
Octadecabacter_antarcticus_307_uid547	Alphaproteobacteria	0	0	0	15	0
Octadecabacter_arcticus_238_uid54699	Alphaproteobacteria	0	0	0	39	0
Paracoccus_aminophilus_JCM_7686_uid2	Alphaproteobacteria	0	0	0	0	0
Paracoccus_denitrificans_PD1222_uid581	Alphaproteobacteria	0	0	0	1	0
Phaeobacter_gallaeciensis_2_10_uid5471	Alphaproteobacteria	0	0	0	0	0
Phaeobacter_gallaeciensis_DSM_26640_u	Alphaproteobacteria	0	0	0	0	0
Phaeobacter_gallaeciensis_DSM_17395_u	Alphaproteobacteria	0	0	0	0	0
Pseudovibrio_FO_BEG1_uid82373	Alphaproteobacteria	0	0	0	0	0
Rhodobacter_capsulatus_SB_1003_uid47	Alphaproteobacteria	0	0	0	0	0
Rhodobacter_sphaeroides_2_4_1_uid576	Alphaproteobacteria	0	0	0	0	0
Rhodobacter_sphaeroides_ATCC_17025_	Alphaproteobacteria	0	0	0	0	0
Rhodobacter_sphaeroides_ATCC_17029_	Alphaproteobacteria	0	0	0	0	0
Rhodobacter_sphaeroides_KD131_uid592	Alphaproteobacteria	0	0	0	0	0
Roseobacter_denitrificans_OCh_114_uid5	Alphaproteobacteria	0	0	0	0	0
Roseobacter_litoralis_Och_149_uid54719	Alphaproteobacteria	0	0	0	1	0
Ruegeria_pomeroyi_DSS_3_uid57863	Alphaproteobacteria	0	0	0	1	0
Ruegeria_TM1040_uid58193	Alphaproteobacteria	0	0	0	0	0
Acetobacter_pasteurianus_386B_uid2144	Alphaproteobacteria	0	0	2	0	0
Acetobacter_pasteurianus_IFO_3283_01_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_01_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_03_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_07_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_12_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_22_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_26_	Alphaproteobacteria	0	0	1	0	0
Acetobacter_pasteurianus_IFO_3283_32_	Alphaproteobacteria	0	0	1	0	0
Acidiphilium_cryptum_JF_5_uid58447	Alphaproteobacteria	0	0	3	1	1
Acidiphilium_multivorum_AIU301_uid633	Alphaproteobacteria	0	0	0	0	0
Gluconacetobacter_diazotrophicus_PAl_5	Alphaproteobacteria	1	0	0	0	0
Gluconacetobacter_diazotrophicus_PAl_5	Alphaproteobacteria	1	0	0	0	0
Gluconacetobacter_xylinus_NBRC_3288_	Alphaproteobacteria	0	0	0	0	0
Gluconobacter_oxydans_621H_uid58239	Alphaproteobacteria	0	0	0	0	0
Gluconobacter_oxydans_H24_uid179202	Alphaproteobacteria	0	0	0	0	0
Granulibacter_bethesdensis_CGDNIH1_ui	Alphaproteobacteria	0	0	0	0	0
Azospirillum_brasilense_Sp245_uid16216	Alphaproteobacteria	0	0	0	0	0
Azospirillum_lipoferum_4B_uid82343	Alphaproteobacteria	0	0	1	0	0
Azospirillum_B510_uid46085	Alphaproteobacteria	1	0	0	0	1
Thalassobaculum_L2_uid182483	Alphaproteobacteria	0	0	0	0	0
Magnetospirillum_gryphiswaldense_MSR_	Alphaproteobacteria	0	0	0	0	0
Magnetospirillum_magneticum_AMB_1_	Alphaproteobacteria	0	0	0	0	0
Rhodospirillum_centenum_SW_uid58805	Alphaproteobacteria	0	0	0	0	0
Rhodospirillum_photometricum_uid1590	Alphaproteobacteria	0	0	0	0	0
Rhodospirillum_rubrum_ATCC_11170_uic	Alphaproteobacteria	1	0	0	1	0
Rhodospirillum_rubrum_F11_uid162149	Alphaproteobacteria	1	0	0	0	0
Tistrella_mobilis_KA081020_065_uid1674	Alphaproteobacteria	1	0	0	0	0

Anaplasma_centrale_Israel_uid42155	Alphaproteobacteria	0	0	0	0	0
Anaplasma_marginale_Dawn_uid226994	Alphaproteobacteria	0	0	0	0	0
Anaplasma_marginale_Florida_uid58577	Alphaproteobacteria	0	0	0	0	0
Anaplasma_marginale_Gypsy_Plains_uid2	Alphaproteobacteria	0	0	0	0	0
Anaplasma_marginale_Maries_uid57629	Alphaproteobacteria	0	0	0	0	0
Anaplasma_phagocytophilum_Dog2_uid2	Alphaproteobacteria	0	0	0	0	0
Anaplasma_phagocytophilum_HZ_uid579	Alphaproteobacteria	0	0	0	0	0
Anaplasma_phagocytophilum_HZ2_uid21	Alphaproteobacteria	0	0	0	0	0
Anaplasma_phagocytophilum_JM_uid213	Alphaproteobacteria	0	0	0	0	0
Ehrlichia_canis_Jake_uid58071	Alphaproteobacteria	0	0	0	0	0
Ehrlichia_chaffeensis_Arkansas_uid57933	Alphaproteobacteria	0	0	0	0	0
Ehrlichia_muris_AS145_uid232250	Alphaproteobacteria	0	0	0	0	0
Ehrlichia_ruminantium_Gardel_uid58245	Alphaproteobacteria	0	0	0	0	0
Ehrlichia_ruminantium_Welgevonden_ui	Alphaproteobacteria	0	0	0	0	0
Ehrlichia_ruminantium_Welgevonden_ui	Alphaproteobacteria	0	0	0	0	0
Neorickettsia_risticii_Illinois_uid58889	Alphaproteobacteria	0	0	0	0	0
Neorickettsia_sennetsu_Miyayama_uid57	Alphaproteobacteria	0	0	0	0	0
Wolbachia_endosymbiont_TRS_of_Brugi	Alphaproteobacteria	0	0	0	0	0
Wolbachia_endosymbiont_of_Culex_quin	Alphaproteobacteria	0	0	0	0	0
Wolbachia_endosymbiont_of_Drosophila	Alphaproteobacteria	0	0	0	0	0
Wolbachia_endosymbiont_of_Drosophila	Alphaproteobacteria	0	0	0	0	0
Wolbachia_endosymbiont_of_Drosophila	Alphaproteobacteria	0	0	0	0	0
Wolbachia_endosymbiont_of_Onchocer	Alphaproteobacteria	0	0	0	0	0
Wolbachia_wRi_uid59371	Alphaproteobacteria	0	0	0	0	0
Candidatus_Midichloria_mitochondrii_Iri	Alphaproteobacteria	0	0	0	0	0
Orientia_tsutsugamushi_Boryong_uid616	Alphaproteobacteria	0	0	0	0	0
Orientia_tsutsugamushi_Ikeda_uid58869	Alphaproteobacteria	0	0	0	0	0
Rickettsia_bellii_OSU_85_389_uid58681	Alphaproteobacteria	0	0	0	0	0
Rickettsia_bellii_RML369_C_uid58405	Alphaproteobacteria	0	0	0	0	0
Rickettsia_canadensis_CA410_uid88063	Alphaproteobacteria	0	0	0	3	0
Rickettsia_canadensis_McKiel_uid58159	Alphaproteobacteria	0	0	0	7	0
Candidatus_Rickettsia_amblyommii_GAT_	Alphaproteobacteria	0	0	0	0	0
Rickettsia_africae_ESF_5_uid58799	Alphaproteobacteria	0	0	0	0	0
Rickettsia_akari_Hartford_uid58161	Alphaproteobacteria	0	0	0	12	0
Rickettsia_australis_Cutlack_uid158039	Alphaproteobacteria	0	0	0	21	0
Rickettsia_conorii_Malish_7_uid57633	Alphaproteobacteria	0	0	0	0	0
Rickettsia_felis_URRWXCal2_uid58331	Alphaproteobacteria	0	0	0	0	0
Rickettsia_heilongjiangensis_054_uid708	Alphaproteobacteria	0	0	0	0	0
Rickettsia_japonica_YH_uid73963	Alphaproteobacteria	0	0	0	0	0
Rickettsia_massiliae_MTU5_uid58801	Alphaproteobacteria	0	0	0	11	0
Rickettsia_massiliae_AZT80_uid86751	Alphaproteobacteria	0	0	0	0	0
Rickettsia_montanensis_OSU_85_930_ui	Alphaproteobacteria	0	0	0	0	0
Rickettsia_parkeri_Portsmouth_uid15804	Alphaproteobacteria	0	0	0	0	0
Rickettsia_peacockii_Rustic_uid59301	Alphaproteobacteria	0	0	0	0	0
Rickettsia_philipii_364D_uid89383	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rhipicephali_3_7_female6_CW	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Arizona_uid86655	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Brazil_uid88069	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Colombia_uid86653	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Hauke_uid86659	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Hino_uid86657	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Hlp_2_uid88067	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii_Iowa_uid58961	Alphaproteobacteria	0	0	0	0	0
Rickettsia_rickettsii__Sheila_Smith__uid5	Alphaproteobacteria	0	0	0	0	0
Rickettsia_slovaca_13_B_uid82369	Alphaproteobacteria	0	0	0	0	0
Rickettsia_slovaca_D_CWPP_uid158159	Alphaproteobacteria	0	0	0	0	0

Rickettsia_prowazekii_Breinl_uid196851	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_BuV67_CWPP_uid	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_Chernikova_uid15	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_Dachau_uid15805	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_GvV257_uid15805	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_Katsinyian_uid158	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_Madrid_E_uid615	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_NMRC_Madrid_E_	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_Rp22_uid161945	Alphaproteobacteria	0	0	0	0	0
Rickettsia_prowazekii_RpGvF24_uid1580	Alphaproteobacteria	0	0	0	0	0
Rickettsia_typhi_B9991CWPP_uid158357	Alphaproteobacteria	0	0	0	0	0
Rickettsia_typhi_TH1527_uid158161	Alphaproteobacteria	0	0	0	0	0
Rickettsia_typhi_Wilmington_uid58063	Alphaproteobacteria	0	0	0	0	0
Erythrobacter_litoralis_HTCC2594_uid58	Alphaproteobacteria	0	0	0	0	0
Novosphingobium_aromaticivorans_DSM	Alphaproteobacteria	0	0	0	0	0
Novosphingobium_PP1Y_uid67383	Alphaproteobacteria	0	0	0	1	0
Sphingobium_chlorophenolicum_L_1_uid	Alphaproteobacteria	0	0	0	0	0
Sphingobium_japonicum_UT26S_uid4707	Alphaproteobacteria	0	0	0	0	0
Sphingobium_SYK_6_uid73353	Alphaproteobacteria	0	0	0	0	0
Sphingomonas_MM_1_uid193771	Alphaproteobacteria	1	0	0	0	0
Sphingomonas_wittichii_RW1_uid58691	Alphaproteobacteria	0	0	0	0	0
Sphingopyxis_alaskensis_RB2256_uid583	Alphaproteobacteria	0	0	0	0	0
Zymomonas_mobilis_ATCC_10988_uid55	Alphaproteobacteria	0	0	0	0	0
Zymomonas_mobilis_ATCC_29191_uid17	Alphaproteobacteria	0	0	0	0	0
Zymomonas_mobilis_NCIMB_11163_uid4	Alphaproteobacteria	0	0	0	0	0
Zymomonas_mobilis_CP4___NRRL_B_14	Alphaproteobacteria	0	0	0	0	0
Zymomonas_mobilis_ZM4_uid58095	Alphaproteobacteria	0	0	0	0	0
Zymomonas_mobilis_pomaceae_ATCC_2	Alphaproteobacteria	0	0	0	0	0
Micavibrio_aeruginosavorus_ARL_13_uid	Alphaproteobacteria	0	0	0	0	0
Micavibrio_EPB_uid194120	Alphaproteobacteria	0	0	0	0	0
Polymorphum_gilvum_SL003B_26A1_uid	Alphaproteobacteria	0	0	0	0	0
alpha_proteobacterium_HIMB5_uid1757	Alphaproteobacteria	0	0	0	0	0
alpha_proteobacterium_HIMB59_uid175	Alphaproteobacteria	0	0	0	0	0
Candidatus_Pelagibacter_IMCC9063_uid	Alphaproteobacteria	0	0	0	0	0
Candidatus_Pelagibacter_ubique_HTCC1	Alphaproteobacteria	0	0	0	0	0
Candidatus_Puniceispirillum_marinum_I	Alphaproteobacteria	1	0	0	0	0
Achromobacter_xylosoxidans_A8_uid598	Betaproteobacteria	0	0	0	0	0
Achromobacter_xylosoxidans_NBRC_151	Betaproteobacteria	0	0	0	0	0
Achromobacter_xylosoxidans_uid205255	Betaproteobacteria	0	0	0	0	0
Advenella_kashmirensis_WT001_uid8085	Betaproteobacteria	0	0	0	0	0
Bordetella_avium_197N_uid61563	Betaproteobacteria	0	0	0	0	0
Bordetella_bronchiseptica_253_uid17891	Betaproteobacteria	0	0	0	1	0
Bordetella_bronchiseptica_MO149_uid17	Betaproteobacteria	0	0	0	1	0
Bordetella_bronchiseptica_RB50_uid5761	Betaproteobacteria	0	0	0	1	0
Bordetella_parapertussis_12822_uid5761	Betaproteobacteria	0	0	0	1	0
Bordetella_parapertussis_Bpp5_uid17751	Betaproteobacteria	0	0	0	1	0
Bordetella_parapertussis_18323_uid1755	Betaproteobacteria	0	0	0	0	0
Bordetella_pertussis_CS_uid158859	Betaproteobacteria	0	0	0	0	0
Bordetella_pertussis_Tohama_I_uid5761	Betaproteobacteria	0	0	0	0	0
Bordetella_petrii_uid61631	Betaproteobacteria	0	0	0	0	0
Pusillimonas_T7_7_uid66391	Betaproteobacteria	0	0	0	0	0
Taylorella_asinigenitalis_14_45_uid1971	Betaproteobacteria	0	0	0	0	0
Taylorella_asinigenitalis_MCE3_uid73771	Betaproteobacteria	0	0	0	0	0
Taylorella_equigenitalis_14_56_uid19719	Betaproteobacteria	0	0	0	0	0
Taylorella_equigenitalis_ATCC_35865_ui	Betaproteobacteria	0	0	0	0	0
Taylorella_equigenitalis_MCE9_uid62103	Betaproteobacteria	0	0	0	0	0

Burkholderia_ambifaria_AMMD_uid5830	Betaproteobacteria	0	0	11	0	0
Burkholderia_ambifaria_MC40_6_uid587	Betaproteobacteria	0	0	11	0	0
Burkholderia_cenocepacia_AU_1054_uid	Betaproteobacteria	0	0	8	0	0
Burkholderia_cenocepacia_HI2424_uid58	Betaproteobacteria	0	0	8	0	0
Burkholderia_cenocepacia_J2315_uid579	Betaproteobacteria	0	0	0	0	0
Burkholderia_cenocepacia_MC0_3_uid58	Betaproteobacteria	0	0	4	0	0
Burkholderia_cepacia_GG4_uid173858	Betaproteobacteria	0	0	1	0	0
Burkholderia_383_uid58073	Betaproteobacteria	0	0	2	0	0
Burkholderia_multivorans_ATCC_17616_	Betaproteobacteria	0	0	0	0	0
Burkholderia_multivorans_ATCC_17616_	Betaproteobacteria	0	0	0	0	0
Burkholderia_vietnamiensis_G4_uid5807	Betaproteobacteria	0	0	0	0	0
Burkholderia_gladioli_BSR3_uid66301	Betaproteobacteria	0	0	0	0	0
Burkholderia_glumae_BGR1_uid59397	Betaproteobacteria	0	0	0	0	0
Burkholderia_phenoliruptrix_BR3459a_ui	Betaproteobacteria	0	0	1	2	0
Burkholderia_phymatum_STM815_uid58	Betaproteobacteria	0	0	0	2	0
Burkholderia_phytofirmans_PsJN_uid587	Betaproteobacteria	0	0	1	1	0
Burkholderia_rhizoxinica_HKI_454_uid60	Betaproteobacteria	0	0	1	0	0
Burkholderia_CCGE1001_uid42975	Betaproteobacteria	0	0	0	2	0
Burkholderia_CCGE1002_uid42523	Betaproteobacteria	0	0	0	2	0
Burkholderia_CCGE1003_uid46253	Betaproteobacteria	0	0	0	1	1
Burkholderia_KJ006_uid165871	Betaproteobacteria	0	0	0	0	0
Burkholderia_RPE64_uid205541	Betaproteobacteria	0	0	0	1	0
Burkholderia_YI23_uid81081	Betaproteobacteria	0	0	0	1	0
Burkholderia_xenovorans_LB400_uid578	Betaproteobacteria	0	0	0	1	1
Burkholderia_mallei_ATCC_23344_uid57	Betaproteobacteria	0	0	0	0	0
Burkholderia_mallei_NCTC_10229_uid58	Betaproteobacteria	0	0	0	0	0
Burkholderia_mallei_NCTC_10247_uid58	Betaproteobacteria	0	0	0	0	0
Burkholderia_mallei_SAVP1_uid58387	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_1026b_uid16	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_1106a_uid58	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_1710b_uid58	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_668_uid5838	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_BPC006_uid1	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_K96243_uid5	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_MSHR305_ui	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_MSHR346_ui	Betaproteobacteria	0	0	0	0	0
Burkholderia_pseudomallei_NCTC_13179	Betaproteobacteria	0	0	0	0	0
Burkholderia_thailandensis_E264_uid580	Betaproteobacteria	0	0	0	0	0
Burkholderia_thailandensis_MSMB121_ui	Betaproteobacteria	0	0	0	0	0
Cupriavidus_metallidurans_CH34_uid578	Betaproteobacteria	0	0	0	1	0
Cupriavidus_necator_N_1_uid68689	Betaproteobacteria	0	0	21	12	0
Ralstonia_eutropha_H16_uid62925	Betaproteobacteria	0	0	1	1	0
Ralstonia_eutropha_JMP134_uid58047	Betaproteobacteria	0	0	0	1	0
Cupriavidus_taiwanensis_LMG_19424_ui	Betaproteobacteria	0	0	0	1	0
Pandoraea_pnomenusa_3kgm_uid22987	Betaproteobacteria	0	0	0	1	0
Pandoraea_RB_44_uid231151	Betaproteobacteria	0	0	0	1	0
Polynucleobacter_necessarius_asymbioti	Betaproteobacteria	0	0	0	1	0
Polynucleobacter_necessarius_STIR1_uid	Betaproteobacteria	0	0	0	0	0
Ralstonia_pickettii_12D_uid58859	Betaproteobacteria	0	0	0	1	1
Ralstonia_pickettii_12J_uid58737	Betaproteobacteria	0	0	0	1	1
Ralstonia_solanacearum_CFBP2957_uid5	Betaproteobacteria	0	0	0	1	0
Ralstonia_solanacearum_CMR15_uid227	Betaproteobacteria	0	0	0	1	0
Ralstonia_solanacearum_FQY_4_f_uid19	Betaproteobacteria	0	0	0	1	0
Ralstonia_solanacearum_GMI1000_uid57	Betaproteobacteria	0	0	0	1	0
Ralstonia_solanacearum_Po82_uid16213	Betaproteobacteria	0	0	0	1	0
Ralstonia_solanacearum_PSI07_uid50539	Betaproteobacteria	0	0	0	1	0

Acidovorax_avenae_ATCC_19860_uid424	Betaproteobacteria	1	0	0	1	0
Acidovorax_citrulli_AAC00_1_uid58429	Betaproteobacteria	0	0	0	1	0
Acidovorax_ebreus_TPSY_uid59233	Betaproteobacteria	1	0	0	1	0
Acidovorax_JS42_uid58427	Betaproteobacteria	0	0	0	1	0
Acidovorax_KKS102_uid176500	Betaproteobacteria	0	0	0	1	0
Rhodoferax_ferrireducens_T118_uid5835	Betaproteobacteria	0	0	0	1	0
Alicycliphilus_denitrificans_BC_uid49953	Betaproteobacteria	1	0	0	1	0
Alicycliphilus_denitrificans_K601_uid663	Betaproteobacteria	1	0	0	1	0
Comamonadaceae_bacterium_CR_uid22	Betaproteobacteria	0	0	1	6	1
Comamonas_testosteroni_CNB_2_uid62	Betaproteobacteria	0	0	0	1	0
Delftia_acidovorans_SPH_1_uid58703	Betaproteobacteria	0	0	0	1	0
Delftia_Cs1_4_uid67319	Betaproteobacteria	0	0	0	1	0
Polaromonas_naphthalenivorans_CJ2_ui	Betaproteobacteria	0	5	16	2	2
Polaromonas_JS666_uid58207	Betaproteobacteria	0	3	1	1	0
Ramlibacter_tataouinensis_TTB310_uid6	Betaproteobacteria	0	0	0	1	0
Variovorax_paradoxus_B4_uid218005	Betaproteobacteria	0	0	0	1	1
Variovorax_paradoxus_EPS_uid62107	Betaproteobacteria	0	0	0	1	0
Variovorax_paradoxus_S110_uid59437	Betaproteobacteria	0	0	0	1	0
Verminephrobacter_eiseniae_EF01_2_ui	Betaproteobacteria	1	0	0	1	0
Candidatus_Zinderia_insecticola_CARI_ui	Betaproteobacteria	0	0	0	0	0
Collimonas_fungivorans_Ter331_uid7079	Betaproteobacteria	0	0	0	2	0
Herbaspirillum_seropedicae_SmR1_uid50	Betaproteobacteria	0	0	0	1	1
Herminiimonas_arsenicoxydans_uid5829	Betaproteobacteria	0	0	0	1	0
Janthinobacterium_Marseille_uid58603	Betaproteobacteria	0	0	0	1	0
Leptothrix_cholodnii_SP_6_uid58971	Betaproteobacteria	0	0	0	1	1
Methylibium_petroleiphilum_PM1_uid58	Betaproteobacteria	0	0	0	1	0
Rubrivivax_gelatinosus_IL144_uid158163	Betaproteobacteria	0	0	0	0	1
Thiomonas_3As_uid178369	Betaproteobacteria	0	0	2	0	0
Thiomonas_intermedia_K12_uid48825	Betaproteobacteria	0	0	5	1	0
Gallionella_capsiferriformans_ES_2_uid5	Betaproteobacteria	0	0	0	1	0
Sideroxydans_lithotrophicus_ES_1_uid46	Betaproteobacteria	0	0	0	1	0
Sulfuricella_denitrificans_skB26_uid1702	Betaproteobacteria	0	0	0	0	0
Thiobacillus_denitrificans_ATCC_25259_u	Betaproteobacteria	0	0	0	2	0
Methylobacillus_flagellatus_KT_uid58049	Betaproteobacteria	0	0	0	1	0
Methylotenera_mobilis_JLW8_uid59373	Betaproteobacteria	0	0	0	0	0
Methylotenera_301_uid49469	Betaproteobacteria	0	0	0	2	0
Methylovorus_glucosetrophus_SIP3_4_ui	Betaproteobacteria	0	0	0	0	0
Methylovorus_MP688_uid60723	Betaproteobacteria	0	0	0	0	0
Chromobacterium_violaceum_ATCC_124	Betaproteobacteria	0	0	0	1	0
Laribacter_hongkongensis_HLHK9_uid59	Betaproteobacteria	0	0	0	0	0
Neisseria_gonorrhoeae_FA_1090_uid576	Betaproteobacteria	0	0	0	1	0
Neisseria_gonorrhoeae_NCCP11945_uid5	Betaproteobacteria	0	0	0	1	0
Neisseria_gonorrhoeae_TCDC_NG08107_	Betaproteobacteria	0	0	0	1	0
Neisseria_lactamica_020_06_uid60851	Betaproteobacteria	1	0	0	1	0
Neisseria_meningitidis_alpha14_uid6164	Betaproteobacteria	1	0	0	1	0
Neisseria_meningitidis_G2136_uid16208	Betaproteobacteria	0	0	0	4	0
Neisseria_meningitidis_M01_240149_uid	Betaproteobacteria	0	0	0	4	0
Neisseria_meningitidis_M01_240355_uid	Betaproteobacteria	0	0	1	3	0
Neisseria_meningitidis_M04_240196_uid	Betaproteobacteria	0	0	0	2	0
Neisseria_meningitidis_NZ_05_33_uid16	Betaproteobacteria	0	0	0	4	0
Neisseria_meningitidis_Z2491_uid57819	Betaproteobacteria	1	0	0	2	0
Neisseria_meningitidis_alpha710_uid161	Betaproteobacteria	0	0	0	4	0
Neisseria_meningitidis_H44_76_uid1620	Betaproteobacteria	0	0	0	1	0
Neisseria_meningitidis_MC58_uid57817	Betaproteobacteria	0	0	0	1	0
Neisseria_meningitidis_053442_uid58587	Betaproteobacteria	1	0	0	2	0
Neisseria_meningitidis_8013_uid161967	Betaproteobacteria	1	0	0	4	0

Neisseria_meningitidis_FAM18_uid57825	Betaproteobacteria	0	0	0	3	0
Neisseria_meningitidis_WUE_2594_uid16	Betaproteobacteria	1	0	0	4	0
Pseudogulbenkiania_NH8B_uid73423	Betaproteobacteria	0	0	0	0	0
Nitrosomonas_europaea_ATCC_19718_ui	Betaproteobacteria	0	0	0	1	0
Nitrosomonas_eutropha_C91_uid58363	Betaproteobacteria	0	0	0	0	0
Nitrosomonas_AL212_uid55727	Betaproteobacteria	1	0	0	8	0
Nitrosomonas_Is79A3_uid68745	Betaproteobacteria	0	0	0	5	0
Nitrosospira_multiformis_ATCC_25196_u	Betaproteobacteria	0	0	0	0	0
Aromatoleum_aromaticum_EbN1_uid582	Betaproteobacteria	0	0	2	8	0
Azoarcus_BH72_uid61603	Betaproteobacteria	0	0	0	0	0
Azoarcus_KH32C_uid193704	Betaproteobacteria	0	0	0	0	1
Dechlorosoma_suillum_PS_uid81439	Betaproteobacteria	0	0	0	0	0
Dechloromonas_aromatica_RCB_uid5802	Betaproteobacteria	0	0	0	0	0
Thauera_MZ1T_uid58987	Betaproteobacteria	0	0	0	1	0
Candidatus_Accumulibacter_phosphatis_	Betaproteobacteria	0	0	0	4	0
Candidatus_Nasuia_deltocephalinicola_N	Betaproteobacteria	0	0	0	0	0
syncytium_symbiont_of_Diaphorina_citri_	Betaproteobacteria	0	0	0	0	0
Candidatus_Tremblaya_phenacola_PAVE_	Betaproteobacteria	0	0	0	0	0
Candidatus_Tremblaya_princeps_PCIT_ui	Betaproteobacteria	0	0	0	0	0
Candidatus_Tremblaya_princeps_PCVAL_	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_crithic	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_crithic	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_desou	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_galatii	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_oncop	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_blasto	Betaproteobacteria	0	0	0	0	0
Candidatus_Kinetoplastibacterium_blasto	Betaproteobacteria	0	0	0	0	0
beta_proteobacterium_CB_uid191340	Betaproteobacteria	0	0	0	1	0
Bacteriovorax_marinus_SJ_uid82341	delta/epsilon subdivi	0	0	0	1	1
Bdellovibrio_bacteriovorus_HD100_uid61	delta/epsilon subdivi	0	0	0	3	0
Bdellovibrio_bacteriovorus_Tiberius_uid1	delta/epsilon subdivi	0	0	0	1	0
Bdellovibrio_exovorus_JSS_uid194119	delta/epsilon subdivi	1	0	0	2	0
Desulfarculus_baarsii_DSM_2075_uid513	delta/epsilon subdivi	0	0	0	0	0
Desulfatibacillum_alkenivorans_AK_01_ui	delta/epsilon subdivi	0	0	0	13	0
Desulfobacterium_autotrophicum_HRM2	delta/epsilon subdivi	0	0	1	3	0
Desulfobacula_toluolica_Tol2_uid175777	delta/epsilon subdivi	0	0	0	1	0
Desulfococcus_oleovorans_Hxd3_uid587	delta/epsilon subdivi	0	0	0	4	0
Desulfobulbus_propionicus_DSM_2032_u	delta/epsilon subdivi	0	0	0	5	0
Desulfocapsa_sulfexigens_DSM_10523_ui	delta/epsilon subdivi	0	0	0	3	0
Desulfotalea_psychrophila_LSv54_uid581	delta/epsilon subdivi	0	0	0	0	0
Desulfurivibrio_alkaliphilus_AHT2_uid494	delta/epsilon subdivi	0	0	0	2	0
Desulfohalobium_retbaense_DSM_5692_	delta/epsilon subdivi	0	0	0	2	0
Desulfomicrobium_baculatum_DSM_402	delta/epsilon subdivi	0	0	0	2	0
Desulfovibrio_aespoeensis_Aspo_2_uid42	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_africanus_Walvis_Bay_uid6	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_alaskensis_G20_uid57941	delta/epsilon subdivi	0	0	0	1	0
Desulfovibrio_desulfuricans_ND132_uid6	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_desulfuricans_ATCC_27774	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_gigas_DSM_1382_uid2212	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_hydrothermalis_AM13___	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_magneticus_RS_1_uid5930	delta/epsilon subdivi	0	0	0	2	0
Desulfovibrio_piezophilus_C1TLV30_uid1	delta/epsilon subdivi	0	0	0	4	0
Desulfovibrio_salexigens_DSM_2638_uid	delta/epsilon subdivi	0	0	0	0	0
Desulfovibrio_vulgaris_DP4_uid58679	delta/epsilon subdivi	0	0	1	0	0
Desulfovibrio_vulgaris_RCH1_uid161961	delta/epsilon subdivi	0	0	1	0	0
Desulfovibrio_vulgaris_Hildenborough_ui	delta/epsilon subdivi	0	0	1	0	0

Desulfovibrio_vulgaris__Miyazaki_F__uid	delta/epsilon subdivi	0	0	0	0	0
Lawsonia_intracellularis_N343_uid18659	delta/epsilon subdivi	0	0	0	0	0
Lawsonia_intracellularis_PHE_MN1_00_u	delta/epsilon subdivi	0	0	0	0	0
Hippea_maritima_DSM_10411_uid65267	delta/epsilon subdivi	0	0	1	4	0
Geobacter_bemidjiensis_Bem_uid58749	delta/epsilon subdivi	0	0	0	5	0
Geobacter_FRC_32_uid58543	delta/epsilon subdivi	0	0	0	6	0
Geobacter_lovleyi_SZ_uid58713	delta/epsilon subdivi	0	0	0	1	0
Geobacter_metallireducens_GS_15_uid5	delta/epsilon subdivi	0	0	0	1	0
Geobacter_M18_uid55771	delta/epsilon subdivi	0	0	0	3	0
Geobacter_M21_uid59037	delta/epsilon subdivi	0	0	0	3	0
Geobacter_sulfurreducens_KN400_uid16	delta/epsilon subdivi	0	0	0	5	0
Geobacter_sulfurreducens_PCA_uid5774	delta/epsilon subdivi	0	0	0	5	0
Geobacter_uraniireducens_Rf4_uid58475	delta/epsilon subdivi	0	0	0	14	0
Pelobacter_carbinolicus_DSM_2380_uid5	delta/epsilon subdivi	0	0	0	6	0
Pelobacter_propionicus_DSM_2379_uid5	delta/epsilon subdivi	0	0	1	3	0
Stigmatella_aurantiaca_DW4_3_1_uid15	delta/epsilon subdivi	0	0	0	0	0
Anaeromyxobacter_dehalogenans_2CP_1	delta/epsilon subdivi	0	0	0	6	0
Anaeromyxobacter_dehalogenans_2CP_	delta/epsilon subdivi	0	0	0	5	0
Anaeromyxobacter_Fw109_5_uid58755	delta/epsilon subdivi	0	0	1	4	0
Anaeromyxobacter_K_uid58953	delta/epsilon subdivi	0	0	0	4	0
Corallococcus_coralloides_DSM_2259_ui	delta/epsilon subdivi	0	0	0	0	0
Myxococcus_fulvus_HW_1_uid68443	delta/epsilon subdivi	0	0	1	0	2
Myxococcus_stipitatus_DSM_14675_uid1	delta/epsilon subdivi	0	0	0	0	0
Myxococcus_xanthus_DK_1622_uid5800	delta/epsilon subdivi	0	0	0	0	2
Haliangium_ochraceum_DSM_14365_uid	delta/epsilon subdivi	0	0	0	1	0
Sorangium_cellulosum__So_ce_56__uid6	delta/epsilon subdivi	0	0	0	1	0
Sorangium_cellulosum_So0157_2_uid21	delta/epsilon subdivi	0	0	0	1	0
Desulfobacca_acetoxidans_DSM_11109_	delta/epsilon subdivi	0	0	0	4	3
Desulfomonile_tiedjei_DSM_6799_uid16	delta/epsilon subdivi	0	0	0	5	0
Syntrophus_aciditrophicus_SB_uid58539	delta/epsilon subdivi	0	0	0	0	0
Syntrophobacter_fumaroxidans_MPOB_u	delta/epsilon subdivi	0	0	0	1	1
delta_proteobacterium_BABL1_uid23071	delta/epsilon subdivi	0	0	1	0	0
Arcobacter_butzleri_7h1h_uid200766	delta/epsilon subdivi	0	0	0	0	0
Arcobacter_butzleri_ED_1_uid158699	delta/epsilon subdivi	0	0	0	0	0
Arcobacter_butzleri_RM4018_uid58557	delta/epsilon subdivi	0	0	0	0	0
Arcobacter_nitrofigilis_DSM_7299_uid49	delta/epsilon subdivi	0	0	0	1	0
Arcobacter_L_uid158135	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_coli_15_537360_uid2261	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_coli_76339_uid217050	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_coli_CVM_N29710_uid21	delta/epsilon subdivi	0	0	1	0	0
Campylobacter_concisus_13826_uid5866	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_curvus_525_92_uid5866	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_fetus_82_40_uid58545	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_hominis_ATCC_BAA_381_	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_jejuni_4031_uid222817	delta/epsilon subdivi	1	0	0	0	0
Campylobacter_jejuni_RM1221_uid5789	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_jejuni_doylei_269_97_ui	delta/epsilon subdivi	1	0	3	0	0
Campylobacter_jejuni_00_2425_uid2193	delta/epsilon subdivi	1	0	1	0	0
Campylobacter_jejuni_00_2426_uid2193	delta/epsilon subdivi	1	0	1	0	0
Campylobacter_jejuni_00_2538_uid2193	delta/epsilon subdivi	1	0	1	0	0
Campylobacter_jejuni_00_2544_uid2193	delta/epsilon subdivi	1	0	2	0	1
Campylobacter_jejuni_81116_uid58771	delta/epsilon subdivi	1	0	0	0	0
Campylobacter_jejuni_81_176_uid58503	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_jejuni_IA3902_uid159531	delta/epsilon subdivi	1	0	0	0	0
Campylobacter_jejuni_ICDCCJ07001_uid6	delta/epsilon subdivi	0	0	1	0	0
Campylobacter_jejuni_M1_uid159535	delta/epsilon subdivi	1	0	0	0	0

Campylobacter_jejuni_NCTC_11168___A	delta/epsilon subdivi	1	0	0	0	0
Campylobacter_jejuni_NCTC_11168_BN1	delta/epsilon subdivi	1	0	0	0	0
Campylobacter_jejuni_PT14_uid176499	delta/epsilon subdivi	1	0	1	0	0
Campylobacter_jejuni_S3_uid159533	delta/epsilon subdivi	0	0	1	0	0
Campylobacter_lari_RM2100_uid58115	delta/epsilon subdivi	0	0	0	0	0
Campylobacter_03_427_uid226993	delta/epsilon subdivi	0	0	0	0	0
Sulfurospirillum_barnesii_SES_3_uid1681	delta/epsilon subdivi	0	0	0	2	0
Sulfurospirillum_deleyianum_DSM_6946_	delta/epsilon subdivi	0	0	0	1	0
Helicobacter_acinonychis_Sheeba_uid58	delta/epsilon subdivi	0	0	2	4	0
Helicobacter_bizzozeronii_CIII_1_uid6814	delta/epsilon subdivi	0	0	5	2	3
Helicobacter_cetorum_MIT_00_7128_uid	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_cetorum_MIT_99_5656_uid	delta/epsilon subdivi	0	0	24	23	0
Helicobacter_cinaedi_ATCC_BAA_847_ui	delta/epsilon subdivi	1	0	0	0	0
Helicobacter_cinaedi_PAGU611_uid1622	delta/epsilon subdivi	1	0	0	0	0
Helicobacter_felis_ATCC_49179_uid6140	delta/epsilon subdivi	0	0	3	0	1
Helicobacter_heilmannii_ASB1_4_uid182	delta/epsilon subdivi	0	0	12	4	1
Helicobacter_hepaticus_ATCC_51449_uid	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_mustelae_12198_uid46647	delta/epsilon subdivi	1	0	0	0	0
Helicobacter_pylori_26695_uid178201	delta/epsilon subdivi	0	0	7	7	0
Helicobacter_pylori_26695_uid57787	delta/epsilon subdivi	0	0	5	7	0
Helicobacter_pylori_35A_uid49903	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_51_uid161925	delta/epsilon subdivi	0	0	1	0	1
Helicobacter_pylori_uid159983	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_83_uid161153	delta/epsilon subdivi	0	0	2	1	0
Helicobacter_pylori_908_uid159985	delta/epsilon subdivi	0	0	2	1	0
Helicobacter_pylori_2017_uid161151	delta/epsilon subdivi	0	0	2	1	0
Helicobacter_pylori_2018_uid161159	delta/epsilon subdivi	0	0	2	1	0
Helicobacter_pylori_Aklavik117_uid1822	delta/epsilon subdivi	0	0	2	0	1
Helicobacter_pylori_Aklavik86_uid18220	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_B38_uid59415	delta/epsilon subdivi	0	0	5	0	5
Helicobacter_pylori_B8_uid49873	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_BM012A_uid229744	delta/epsilon subdivi	0	0	9	1	9
Helicobacter_pylori_BM012S_uid229881	delta/epsilon subdivi	0	0	9	1	9
Helicobacter_pylori_Cuz20_uid159987	delta/epsilon subdivi	0	0	4	1	1
Helicobacter_pylori_ELS37_uid158157	delta/epsilon subdivi	0	0	9	7	1
Helicobacter_pylori_F16_uid161145	delta/epsilon subdivi	0	0	3	0	2
Helicobacter_pylori_F30_uid159991	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_F32_uid161139	delta/epsilon subdivi	0	0	2	1	0
Helicobacter_pylori_F57_uid161143	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_G27_uid59305	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_Gambia94_24_uid15	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_HPAG1_uid58517	delta/epsilon subdivi	0	0	3	0	1
Helicobacter_pylori_HUP_B14_uid16221	delta/epsilon subdivi	0	0	2	1	1
Helicobacter_pylori_India7_uid161149	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_J99_uid57789	delta/epsilon subdivi	0	0	1	1	0
Helicobacter_pylori_Lithuania75_uid1594	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_OK113_uid193715	delta/epsilon subdivi	0	0	2	0	1
Helicobacter_pylori_OK310_uid193716	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_P12_uid59327	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_PeCan18_uid162211	delta/epsilon subdivi	0	0	2	2	0
Helicobacter_pylori_PeCan4_uid53539	delta/epsilon subdivi	0	0	2	1	0
Helicobacter_pylori_Puno120_uid159611	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_Puno135_uid161157	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_Rif1_uid178202	delta/epsilon subdivi	0	0	7	7	0
Helicobacter_pylori_Rif2_uid178203	delta/epsilon subdivi	0	0	7	7	0
Helicobacter_pylori_Sat464_uid159467	delta/epsilon subdivi	0	0	2	0	1

Helicobacter_pylori_Shi112_uid162207	delta/epsilon subdivi	0	0	7	2	5
Helicobacter_pylori_Shi169_uid162209	delta/epsilon subdivi	0	0	8	0	6
Helicobacter_pylori_Shi417_uid162205	delta/epsilon subdivi	0	0	2	0	0
Helicobacter_pylori_Shi470_uid59165	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_SJM180_uid53541	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_SNT49_uid159615	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_SouthAfrica20_uid21	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_SouthAfrica7_uid15	delta/epsilon subdivi	0	0	5	5	0
Helicobacter_pylori_UM032_uid203025	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_UM037_uid203027	delta/epsilon subdivi	0	0	5	0	0
Helicobacter_pylori_UM066_uid203028	delta/epsilon subdivi	0	0	0	0	0
Helicobacter_pylori_UM298_uid213226	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_UM299_uid203026	delta/epsilon subdivi	0	0	1	0	0
Helicobacter_pylori_v225d_uid159639	delta/epsilon subdivi	0	0	0	1	0
Helicobacter_pylori_XZ274_uid165869	delta/epsilon subdivi	0	0	4	0	3
uncultured_Sulfuricurvum_RIFRC_1_uid1	delta/epsilon subdivi	0	0	0	2	0
Sulfuricurvum_kujiense_DSM_16994_uid	delta/epsilon subdivi	0	0	0	3	0
Sulfurimonas_autotrophica_DSM_16294_	delta/epsilon subdivi	0	0	0	1	0
Sulfurimonas_denitrificans_DSM_1251_u	delta/epsilon subdivi	0	0	0	5	0
Wolinella_succinogenes_DSM_1740_uid6	delta/epsilon subdivi	2	0	0	0	0
Nitratifractor_salsuginis_DSM_16511_uid	delta/epsilon subdivi	1	0	0	9	0
Nautilia_profundicola_AmH_uid59345	delta/epsilon subdivi	0	0	0	1	0
Nitratiruptor_SB155_2_uid58861	delta/epsilon subdivi	0	0	0	0	0
Sulfurovum_NBC37_1_uid58863	delta/epsilon subdivi	0	0	0	8	0
Acidithiobacillus_caldus_SM_1_uid70791	Gammaproteobacter	0	3	5	1	0
Acidithiobacillus_ferrivorans_SS3_uid673	Gammaproteobacter	0	2	1	0	0
Acidithiobacillus_ferrooxidans_ATCC_232	Gammaproteobacter	0	2	6	0	5
Acidithiobacillus_ferrooxidans_ATCC_539	Gammaproteobacter	0	0	0	0	0
Aeromonas_hydrophila_ML09_119_uid2	Gammaproteobacter	0	0	0	1	0
Aeromonas_hydrophila_ATCC_7966_uid5	Gammaproteobacter	0	0	0	0	0
Aeromonas_salmonicida_A449_uid58631	Gammaproteobacter	0	0	0	1	0
Aeromonas_veronii_B565_uid66323	Gammaproteobacter	0	0	0	0	0
Oceanimonas_GK1_uid81627	Gammaproteobacter	0	0	0	1	0
Tolumonas_auensis_DSM_9187_uid5939	Gammaproteobacter	0	0	0	0	0
Alteromonas_macleodii_AltDE1_uid1790	Gammaproteobacter	0	0	0	0	0
Alteromonas_macleodii_ATCC_27126_ui	Gammaproteobacter	0	0	0	1	0
Alteromonas_macleodii__Aegean_Sea_M	Gammaproteobacter	0	0	0	0	0
Alteromonas_macleodii__Balearic_Sea_A	Gammaproteobacter	0	0	0	1	0
Alteromonas_macleodii__Black_Sea_11_	Gammaproteobacter	0	0	0	1	0
Alteromonas_macleodii__Deep_ecotype_	Gammaproteobacter	0	0	0	0	0
Alteromonas_macleodii__English_Chann	Gammaproteobacter	0	0	0	0	0
Alteromonas_macleodii__English_Chann	Gammaproteobacter	0	0	0	1	0
Alteromonas_macleodii__Ionian_Sea_U4_	Gammaproteobacter	0	0	1	0	0
Alteromonas_macleodii__Ionian_Sea_U7_	Gammaproteobacter	0	0	1	0	0
Alteromonas_macleodii__Ionian_Sea_U8_	Gammaproteobacter	0	0	1	0	0
Alteromonas_macleodii__Ionian_Sea_U	Gammaproteobacter	0	0	0	0	0
Alteromonas_macleodii__Ionian_Sea_U	Gammaproteobacter	0	0	0	0	0
Alteromonas_SN2_uid67349	Gammaproteobacter	0	0	1	0	0
Glaciecola_nitratireducens_FR1064_uid7	Gammaproteobacter	0	0	0	1	0
Glaciecola_psychrophila_170_uid193711	Gammaproteobacter	0	0	0	2	0
Glaciecola_4H_3_7_YE_5_uid66595	Gammaproteobacter	0	0	0	0	0
Marinobacter_adhaerens_HP15_uid1620	Gammaproteobacter	0	0	0	0	0
Marinobacter_aquaeolei_VT8_uid59419	Gammaproteobacter	0	0	2	1	0
Marinobacter_hydrocarbonoclasticus_AT	Gammaproteobacter	0	0	0	0	0
Marinobacter_BSs20148_uid171995	Gammaproteobacter	0	0	0	1	0
Saccharophagus_degradans_2_40_uid57	Gammaproteobacter	0	0	0	0	0

Teredinibacter_turnerae_T7901_uid5926	Gammaproteobacter	0	0	0	0	0
Colwellia_psychrerythraea_34H_uid5785	Gammaproteobacter	0	0	0	3	1
Ferrimonas_balearica_DSM_9799_uid533	Gammaproteobacter	0	0	0	1	0
Idiomarina_loihiensis_GSL_199_uid20525	Gammaproteobacter	0	0	0	1	0
Idiomarina_loihiensis_L2TR_uid58087	Gammaproteobacter	0	0	0	1	0
Pseudoalteromonas_atlantica_T6c_uid58	Gammaproteobacter	0	0	0	0	0
Pseudoalteromonas_haloplanktis_TAC12	Gammaproteobacter	0	1	4	3	0
Pseudoalteromonas_SM9913_uid61247	Gammaproteobacter	0	0	0	2	0
Psychromonas_ingrahamii_37_uid58521	Gammaproteobacter	0	0	2	4	0
Psychromonas_CNPT3_uid54249	Gammaproteobacter	0	0	0	0	0
Shewanella_amazonensis_SB2B_uid5825	Gammaproteobacter	0	0	0	9	0
Shewanella_baltica_BA175_uid52601	Gammaproteobacter	0	0	0	1	0
Shewanella_baltica_OS117_uid162025	Gammaproteobacter	0	0	0	0	0
Shewanella_baltica_OS155_uid58259	Gammaproteobacter	0	0	0	0	0
Shewanella_baltica_OS185_uid58743	Gammaproteobacter	0	0	0	2	0
Shewanella_baltica_OS195_uid58261	Gammaproteobacter	0	0	0	0	0
Shewanella_baltica_OS223_uid58775	Gammaproteobacter	0	0	0	0	0
Shewanella_baltica_OS678_uid50553	Gammaproteobacter	0	0	0	0	0
Shewanella_denitrificans_OS217_uid582	Gammaproteobacter	0	0	0	0	0
Shewanella_frigidimarina_NCIMB_400_ui	Gammaproteobacter	0	0	0	0	0
Shewanella_halifaxensis_HAW_EB4_uid5	Gammaproteobacter	0	0	0	0	0
Shewanella_loihica_PV_4_uid58349	Gammaproteobacter	0	0	0	0	0
Shewanella_oneidensis_MR_1_uid57949	Gammaproteobacter	0	0	0	1	0
Shewanella_pealeana_ATCC_700345_uid	Gammaproteobacter	0	0	0	1	0
Shewanella_piezotolerans_WP3_uid5874	Gammaproteobacter	0	0	0	1	0
Shewanella_putrefaciens_200_uid161927	Gammaproteobacter	0	0	2	1	0
Shewanella_putrefaciens_CN_32_uid582	Gammaproteobacter	0	0	0	0	0
Shewanella_sediminis_HAW_EB3_uid588	Gammaproteobacter	0	0	0	1	0
Shewanella_ANA_3_uid58347	Gammaproteobacter	0	0	4	2	0
Shewanella_MR_4_uid58345	Gammaproteobacter	0	0	0	4	0
Shewanella_MR_7_uid58343	Gammaproteobacter	0	0	0	0	0
Shewanella_W3_18_1_uid58341	Gammaproteobacter	0	0	0	0	0
Shewanella_violacea_DSS12_uid47085	Gammaproteobacter	0	0	0	1	0
Shewanella_woodyi_ATCC_51908_uid587	Gammaproteobacter	0	0	0	11	0
Dichelobacter_nodosus_VCS1703A_uid57	Gammaproteobacter	0	0	2	3	0
Allochromatium_vinosum_DSM_180_uid	Gammaproteobacter	0	5	2	2	0
Nitrosococcus_halophilus_Nc4_uid46803	Gammaproteobacter	0	7	24	13	4
Nitrosococcus_oceani_ATCC_19707_uid5	Gammaproteobacter	0	0	22	5	0
Nitrosococcus_watsonii_C_113_uid50331	Gammaproteobacter	0	1	5	3	0
Thiocystis_violascens_DSM_198_uid7402	Gammaproteobacter	0	0	3	7	2
Thioflavicoccus_mobilis_8321_uid184343	Gammaproteobacter	0	0	0	10	0
Alkalilimnicola_ehrlichii_MLHE_1_uid584	Gammaproteobacter	0	0	0	1	0
Halorhodospira_halophila_SL1_uid58473	Gammaproteobacter	0	0	1	0	0
Ectothiorhodospiraceae_bacterium_M19_	Gammaproteobacter	0	0	0	1	0
Spiribacter_UAH_SP71_uid226111	Gammaproteobacter	0	0	0	0	0
Thioalkalivibrio_nitratireducens_DSM_14	Gammaproteobacter	0	0	0	4	0
Thioalkalivibrio_K90mix_uid46181	Gammaproteobacter	0	0	2	9	0
Thioalkalivibrio_sulfidophilus_HL_EbGr7_	Gammaproteobacter	0	0	0	5	0
Halothiobacillus_neapolitanus_c2_uid413	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_Ak__Acyrthosiphon	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_APS__Acyrthosipho	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_5A__Acyrthosiphon	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_JF98__Acyrthosiph	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_JF99__Acyrthosiph	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_LL01__Acyrthosiph	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_TLW03__Acyrthosi	Gammaproteobacter	0	0	0	0	0

Buchnera_aphidicola_Tuc7__Acyrthosiph	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_Bp__Baizongia_pist	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_Cc__Cinara_cedri__	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola__Cinara_tujafilina__	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_Sg__Schizaphis_gra	Gammaproteobacter	0	0	0	0	0
Buchnera_aphidicola_Ua__Uroleucon_a	Gammaproteobacter	0	0	0	0	0
Candidatus_Moranella_endobia_PCIT_uid	Gammaproteobacter	0	0	0	0	0
Candidatus_Moranella_endobia_PCVAL_	Gammaproteobacter	0	0	0	0	0
Candidatus_Riesia_pediculicola_USDA_ui	Gammaproteobacter	0	0	0	0	0
Citrobacter_koseri_ATCC_BAA_895_uid5	Gammaproteobacter	0	0	0	1	0
Citrobacter_rodentium_ICC168_uid4308	Gammaproteobacter	0	0	0	1	0
Cronobacter_sakazakii_ATCC_BAA_894_	Gammaproteobacter	0	0	0	0	0
Cronobacter_sakazakii_45402_uid231516	Gammaproteobacter	0	0	0	1	0
Cronobacter_sakazakii_ES15_uid167045	Gammaproteobacter	0	0	0	1	0
Cronobacter_sakazakii_Sp291_uid189241	Gammaproteobacter	0	0	0	0	0
Cronobacter_turicensis_z3032_uid40821	Gammaproteobacter	0	0	0	0	0
Dickeya_dadantii_3937_uid52537	Gammaproteobacter	0	0	0	5	0
Dickeya_dadantii_Ech586_uid42519	Gammaproteobacter	0	0	0	1	0
Dickeya_dadantii_Ech703_uid59363	Gammaproteobacter	0	0	0	0	0
Dickeya_zeae_Ech1591_uid59297	Gammaproteobacter	0	0	0	0	0
Edwardsiella_ictaluri_93_146_uid59403	Gammaproteobacter	0	0	5	4	0
Edwardsiella_tarda_C07_087_uid193773	Gammaproteobacter	0	0	0	1	0
Edwardsiella_tarda_EIB202_uid41819	Gammaproteobacter	0	0	0	0	0
Edwardsiella_tarda_FL6_60_uid159657	Gammaproteobacter	0	0	0	1	0
Enterobacter_aerogenes_EA1509E_uid18	Gammaproteobacter	0	0	0	1	0
Enterobacter_aerogenes_KCTC_2190_uid	Gammaproteobacter	0	0	1	3	0
Enterobacter_asburiae_LF7a_uid72793	Gammaproteobacter	0	0	0	0	0
Enterobacter_cloacae_EcWSU1_uid8073	Gammaproteobacter	0	0	0	0	0
Enterobacter_cloacae_ATCC_13047_uid4	Gammaproteobacter	0	0	0	1	0
Enterobacter_cloacae_ENHKU01_uid172	Gammaproteobacter	0	0	0	0	0
Enterobacter_cloacae_NCTC_9394_uid19	Gammaproteobacter	0	0	0	1	0
Enterobacter_cloacae_dissolvens_SDM_u	Gammaproteobacter	0	0	0	0	0
Enterobacter_cloacae_SCF1_uid59969	Gammaproteobacter	0	0	0	1	0
Enterobacter_638_uid58727	Gammaproteobacter	0	0	0	0	0
Enterobacter_R4_368_uid208672	Gammaproteobacter	0	0	0	1	0
Erwinia_amylovora_ATCC_49946_uid469	Gammaproteobacter	0	0	0	0	0
Erwinia_amylovora_CFBP1430_uid46839	Gammaproteobacter	0	0	0	0	0
Erwinia_billingiae_Eb661_uid50547	Gammaproteobacter	0	0	0	0	0
Erwinia_pyrifoliae_DSM_12163_uid1596	Gammaproteobacter	0	0	0	0	0
Erwinia_pyrifoliae_Ep1_96_uid40659	Gammaproteobacter	0	0	0	0	0
Erwinia_Ejp617_uid159955	Gammaproteobacter	0	0	0	0	0
Erwinia_tasmaniensis_Et1_99_uid59029	Gammaproteobacter	0	0	0	0	0
Escherichia_coli_536_uid58531	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_55989_uid59383	Gammaproteobacter	0	0	3	4	0
Escherichia_coli_ABU_83972_uid161975	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_APEC_O1_uid58623	Gammaproteobacter	0	0	0	2	0
Escherichia_coli_APEC_O78_uid187277	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_B_REL606_uid58803	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_BL21_DE3__uid161947	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_BL21_DE3__uid161949	Gammaproteobacter	0	0	1	0	0
Escherichia_coli__BL21_Gold_DE3_pLysS_	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_ATCC_8739_uid58783	Gammaproteobacter	0	0	2	0	0
Escherichia_coli_CFT073_uid57915	Gammaproteobacter	0	0	2	20	0
Escherichia_coli_DH1_uid161951	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_DH1_uid162051	Gammaproteobacter	0	0	1	2	0
Escherichia_coli_E24377A_uid58395	Gammaproteobacter	0	0	3	1	0

Escherichia_coli_ED1a_uid59379	Gammaproteobacter	0	0	1	3	0
Escherichia_coli_ETEC_H10407_uid16199	Gammaproteobacter	0	0	2	0	0
Escherichia_coli_HS_uid58393	Gammaproteobacter	0	0	2	1	0
Escherichia_coli_IAI1_uid59377	Gammaproteobacter	0	0	3	3	0
Escherichia_coli_IAI39_uid59381	Gammaproteobacter	0	0	1	2	0
Escherichia_coli_IHE3034_uid162007	Gammaproteobacter	0	0	0	1	0
Escherichia_coli_JJ1886_uid226103	Gammaproteobacter	0	0	1	3	0
Escherichia_coli_BW2952_uid59391	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_K_12_substr__DH10B_ui	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_K_12_substr__MDS42_u	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_K_12_substr__MG1655_	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_K_12_substr__W3110_u	Gammaproteobacter	0	0	1	0	0
Escherichia_coli_KO11FL_uid162099	Gammaproteobacter	0	0	4	3	0
Escherichia_coli_KO11FL_uid52593	Gammaproteobacter	0	0	4	2	0
Escherichia_coli_LF82_uid161965	Gammaproteobacter	0	0	1	2	0
Escherichia_coli_LY180_uid219461	Gammaproteobacter	0	0	4	3	0
Escherichia_coli_NA114_uid162139	Gammaproteobacter	0	0	1	1	0
Escherichia_coli_O103_H2_12009_uid41	Gammaproteobacter	0	0	2	1	0
Escherichia_coli_O104_H4_2009EL_2050_	Gammaproteobacter	0	0	3	3	0
Escherichia_coli_O104_H4_2009EL_2071_	Gammaproteobacter	0	0	3	3	0
Escherichia_coli_O104_H4_2011C_3493_	Gammaproteobacter	0	0	3	3	0
Escherichia_coli_O111_H__11128_uid41	Gammaproteobacter	0	0	3	1	0
Escherichia_coli_O127_H6_E2348_69_uic	Gammaproteobacter	0	0	1	8	0
Escherichia_coli_O157_H7_EC4115_uid5	Gammaproteobacter	0	0	2	1	0
Escherichia_coli_O157_H7_EDL933_uid57	Gammaproteobacter	0	0	2	1	0
Escherichia_coli_O157_H7_Sakai_uid577	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_O157_H7_TW14359_uid	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_O26_H11_11368_uid41	Gammaproteobacter	0	0	3	2	0
Escherichia_coli_042_uid161985	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_O55_H7_CB9615_uid46	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_O55_H7_RM12579_uid1	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_O7_K1_CE10_uid162115	Gammaproteobacter	0	0	2	1	0
Escherichia_coli_O83_H1_NRG_857C_uid	Gammaproteobacter	0	0	1	2	0
Escherichia_coli_P12b_uid162061	Gammaproteobacter	0	0	3	5	0
Escherichia_coli_PMV_1_uid219679	Gammaproteobacter	0	0	0	1	0
Escherichia_coli_S88_uid62979	Gammaproteobacter	0	0	0	1	0
Escherichia_coli_SE11_uid59425	Gammaproteobacter	0	0	4	0	0
Escherichia_coli_SE15_uid161939	Gammaproteobacter	0	0	1	1	0
Escherichia_coli_SMS_3_5_uid58919	Gammaproteobacter	0	0	2	1	0
Escherichia_coli__clone_D_i14__uid1620	Gammaproteobacter	0	0	2	2	0
Escherichia_coli__clone_D_i2__uid16204	Gammaproteobacter	0	0	2	2	0
Escherichia_coli_UM146_uid162043	Gammaproteobacter	0	0	0	1	0
Escherichia_coli_UMN026_uid62981	Gammaproteobacter	0	0	3	6	0
Escherichia_coli_UMNK88_uid161991	Gammaproteobacter	0	0	3	0	0
Escherichia_coli_UTI89_uid58541	Gammaproteobacter	0	0	0	1	0
Escherichia_coli_W_uid162011	Gammaproteobacter	0	0	4	0	0
Escherichia_coli_W_uid162101	Gammaproteobacter	0	0	4	3	0
Escherichia_coli_Xuzhou21_uid163995	Gammaproteobacter	0	0	2	2	0
Escherichia_fergusonii_ATCC_35469_uid5	Gammaproteobacter	0	0	1	1	0
Klebsiella_oxytoca_E718_uid170256	Gammaproteobacter	0	0	1	3	0
Klebsiella_oxytoca_KCTC_1686_uid83159	Gammaproteobacter	0	0	1	4	0
Klebsiella_pneumoniae_uid203334	Gammaproteobacter	0	0	2	2	0
Klebsiella_pneumoniae_342_uid59145	Gammaproteobacter	0	0	0	0	0
Klebsiella_pneumoniae_CG43_uid223021	Gammaproteobacter	0	0	0	0	0
Klebsiella_pneumoniae_JM45_uid215235	Gammaproteobacter	0	0	0	0	0
Klebsiella_pneumoniae_KCTC_2242_uid1	Gammaproteobacter	0	0	0	0	0

Klebsiella_pneumoniae_1084_uid174151	Gammaproteobacter	0	0	0	0	0
Klebsiella_pneumoniae_HS11286_uid843	Gammaproteobacter	0	0	0	0	0
Klebsiella_pneumoniae_MGH_78578_uid	Gammaproteobacter	0	0	0	0	0
Klebsiella_pneumoniae_NTUH_K2044_ui	Gammaproteobacter	0	0	0	0	0
Klebsiella_variicola_At_22_uid42113	Gammaproteobacter	0	0	0	0	0
Morganella_morganii_KT_uid180867	Gammaproteobacter	0	0	0	1	0
Pantoea_ananatis_AJ13355_uid162073	Gammaproteobacter	0	0	0	0	0
Pantoea_ananatis_LMG_20103_uid46807	Gammaproteobacter	0	0	0	0	0
Pantoea_ananatis_uid86861	Gammaproteobacter	0	0	0	0	0
Pantoea_ananatis_PA13_uid162181	Gammaproteobacter	0	0	0	0	0
Pantoea_At_9b_uid55845	Gammaproteobacter	0	0	0	0	0
Pantoea_vagans_C9_1_uid49871	Gammaproteobacter	0	0	0	0	0
Pectobacterium_atrosepticum_SCRI1043_	Gammaproteobacter	0	0	0	1	0
Pectobacterium_carotovorum_PC1_uid5	Gammaproteobacter	0	0	0	0	0
Pectobacterium_carotovorum_PCC21_ui	Gammaproteobacter	0	0	0	0	0
Pectobacterium_SCC3193_uid193707	Gammaproteobacter	0	0	0	2	0
Pectobacterium_wasabiae_WPP163_uid4	Gammaproteobacter	0	0	0	3	0
Photorhabdus_asymbiotica_ATCC_43949_	Gammaproteobacter	0	0	1	2	0
Photorhabdus_luminescens_laumondii_T	Gammaproteobacter	0	0	1	8	0
Proteus_mirabilis_BB2000_uid214430	Gammaproteobacter	0	0	11	9	0
Proteus_mirabilis_HI4320_uid61599	Gammaproteobacter	0	0	13	14	0
Providencia_stuartii_MRSN_2154_uid162	Gammaproteobacter	0	0	0	1	0
Rahnella_aquatilis_CIP_78_65___ATCC_3	Gammaproteobacter	0	0	0	10	0
Rahnella_aquatilis_HX2_uid158049	Gammaproteobacter	0	0	0	0	0
Rahnella_Y9602_uid62715	Gammaproteobacter	0	0	0	0	0
Raoultella_ornithinolytica_B6_uid198431	Gammaproteobacter	0	0	1	0	0
Salmonella_bongori_Sbon_167_uid21308	Gammaproteobacter	0	0	3	5	0
Salmonella_bongori_NCTC_12419_uid701	Gammaproteobacter	0	0	1	2	0
Salmonella_enterica_arizonae_serovar_6	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_4_5_12_i__	Gammaproteobacter	0	0	1	9	0
Salmonella_enterica_serovar_Agona_242	Gammaproteobacter	0	0	1	0	0
Salmonella_enterica_serovar_Agona_SL4	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Bareilly_CF	Gammaproteobacter	0	0	1	0	0
Salmonella_enterica_serovar_Bovismorbi	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Choleraesu	Gammaproteobacter	0	0	1	1	0
Salmonella_enterica_Serovar_Cubana_CF	Gammaproteobacter	0	0	0	1	0
Salmonella_enterica_serovar_Dublin_CT_	Gammaproteobacter	0	0	0	1	0
Salmonella_enterica_serovar_Enteritidis_	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Gallinarum_	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Gallinarum_	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Gallinarum_	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_Serovar_Heidelberg_	Gammaproteobacter	0	0	0	4	0
Salmonella_enterica_serovar_Heidelberg_	Gammaproteobacter	0	0	0	4	0
Salmonella_enterica_serovar_Heidelberg_	Gammaproteobacter	0	0	0	4	0
Salmonella_enterica_serovar_Heidelberg_	Gammaproteobacter	0	0	0	4	0
Salmonella_enterica_serovar_Javiana_CF	Gammaproteobacter	0	0	1	2	0
Salmonella_enterica_serovar_Newport_S	Gammaproteobacter	0	0	1	0	0
Salmonella_enterica_serovar_Newport_	Gammaproteobacter	0	0	2	0	0
Salmonella_enterica_serovar_Paratyphi_	Gammaproteobacter	0	0	1	7	0
Salmonella_enterica_serovar_Paratyphi_	Gammaproteobacter	0	0	1	7	0
Salmonella_enterica_serovar_Paratyphi_	Gammaproteobacter	0	0	0	7	0
Salmonella_enterica_serovar_Paratyphi_	Gammaproteobacter	0	0	0	1	0
Salmonella_enterica_serovar_Pullorum_S	Gammaproteobacter	0	0	0	1	0
Salmonella_enterica_serovar_Schwarzen	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Thompson_	Gammaproteobacter	0	0	0	0	0
Salmonella_enterica_serovar_Typhi_CT1	Gammaproteobacter	0	0	1	27	0

Salmonella_enterica_serovar_Typhi_P_st	Gammaproteobacter	0	0	1	26	0
Salmonella_enterica_serovar_Typhi_Ty21	Gammaproteobacter	0	0	1	27	0
Salmonella_enterica_serovar_Typhi_Ty2_	Gammaproteobacter	0	0	1	27	0
Salmonella_enterica_Serovar_Typhimuri	Gammaproteobacter	0	0	0	8	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	2	11	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	6	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	8	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	8	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	10	0
Salmonella_typhimurium_DT104_uid223	Gammaproteobacter	0	0	0	12	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	7	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	6	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	7	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	9	0
Salmonella_enterica_serovar_Typhimuriu	Gammaproteobacter	0	0	1	7	0
Serratia_liquefaciens_ATCC_27592_uid21	Gammaproteobacter	0	0	0	0	0
Serratia_marcescens_FGI94_uid185180	Gammaproteobacter	0	0	0	0	0
Serratia_marcescens_WW4_uid188478	Gammaproteobacter	0	0	0	0	0
Serratia_odorifera_4Rx13_uid42253	Gammaproteobacter	0	0	0	0	0
Serratia_plymuthica_AS9_uid67313	Gammaproteobacter	0	0	0	0	0
Serratia_plymuthica_S13_uid210642	Gammaproteobacter	0	0	1	1	0
Serratia_proteamaculans_568_uid58725	Gammaproteobacter	0	0	3	0	0
Serratia_AS12_uid67315	Gammaproteobacter	0	0	0	0	0
Serratia_AS13_uid162065	Gammaproteobacter	0	0	0	0	0
Serratia_ATCC_39006_uid218470	Gammaproteobacter	0	0	0	1	0
Serratia_symbiotica__Cinara_cedri__uid8	Gammaproteobacter	0	0	0	0	0
Shigella_boydii_CDC_3083_94_uid58415	Gammaproteobacter	0	0	2	0	0
Shigella_boydii_Sb227_uid58215	Gammaproteobacter	0	0	1	0	0
Shigella_dysenteriae_1617_uid229875	Gammaproteobacter	0	0	1	2	0
Shigella_dysenteriae_Sd197_uid58213	Gammaproteobacter	0	0	1	1	0
Shigella_flexneri_2002017_uid159233	Gammaproteobacter	0	0	3	1	0
Shigella_flexneri_2a_2457T_uid57991	Gammaproteobacter	0	0	2	0	0
Shigella_flexneri_2a_301_uid62907	Gammaproteobacter	0	0	0	0	0
Shigella_flexneri_5_8401_uid58583	Gammaproteobacter	0	0	3	0	0
Shigella_sonnei_53G_uid84383	Gammaproteobacter	0	0	3	2	0
Shigella_sonnei_Ss046_uid58217	Gammaproteobacter	0	0	3	0	0
Escherichia_blattae_DSM_4481_uid1650	Gammaproteobacter	0	0	1	2	0
Sodalis_glossinidius__morsitans__uid585	Gammaproteobacter	0	0	0	0	0
Candidatus_Blochmannia_chromaiodes_	Gammaproteobacter	0	0	0	0	0
Candidatus_Blochmannia_floridanus_uid	Gammaproteobacter	0	0	0	0	0
Candidatus_Blochmannia_pennsylvanicus	Gammaproteobacter	0	0	0	0	0
Candidatus_Blochmannia_vafer_BVAF_ui	Gammaproteobacter	0	0	0	0	0
Candidatus_Hamiltonella_defensa_5AT__	Gammaproteobacter	0	0	0	0	0
secondary_endosymbiont_of_Ctenarytai	Gammaproteobacter	0	0	0	0	0
secondary_endosymbiont_of_Heteropsyll	Gammaproteobacter	0	0	0	0	0
Enterobacteriaceae_bacterium_FGI_57_u	Gammaproteobacter	0	0	0	0	0
Wigglesworthia_glossinidia_endosymbio	Gammaproteobacter	0	0	0	0	0
Wigglesworthia_glossinidia_endosymbio	Gammaproteobacter	0	0	0	0	0
Xenorhabdus_bovienii_SS_2004_uid4634	Gammaproteobacter	0	0	0	3	0
Xenorhabdus_nematophila_ATCC_19061_	Gammaproteobacter	0	0	7	10	0
Yersinia_enterocolitica_8081_uid57741	Gammaproteobacter	0	0	0	4	0
Yersinia_enterocolitica_palearctica_105_	Gammaproteobacter	0	0	0	0	0
Yersinia_enterocolitica_palearctica_Y11_	Gammaproteobacter	0	0	0	0	0
Yersinia_pestis_A1122_uid158119	Gammaproteobacter	0	0	0	67	0
Yersinia_pestis_Angola_uid58485	Gammaproteobacter	0	0	0	101	0
Yersinia_pestis_Antiqua_uid58607	Gammaproteobacter	0	0	0	67	0

Yersinia_pestis_CO92_uid57621	Gammaproteobacter	0	0	0	66	0
Yersinia_pestis_D106004_uid158071	Gammaproteobacter	0	0	0	59	0
Yersinia_pestis_D182038_uid158073	Gammaproteobacter	0	0	0	64	0
Yersinia_pestis_KIM_10_uid57875	Gammaproteobacter	0	0	0	53	0
Yersinia_pestis_Nepal516_uid58609	Gammaproteobacter	0	0	0	64	0
Yersinia_pestis_Pestoides_F_uid58619	Gammaproteobacter	0	0	0	56	0
Yersinia_pestis_biovar_Microtus_91001_	Gammaproteobacter	0	0	0	48	0
Yersinia_pestis_biovar_Medievalis_Harbi	Gammaproteobacter	0	0	0	61	0
Yersinia_pestis_Z176003_uid47317	Gammaproteobacter	0	0	0	63	0
Yersinia_pseudotuberculosis_IP_31758_u	Gammaproteobacter	0	0	0	15	0
Yersinia_pseudotuberculosis_IP_32953_u	Gammaproteobacter	0	0	0	5	0
Yersinia_pseudotuberculosis_PB1__uid59	Gammaproteobacter	0	0	0	2	0
Yersinia_pseudotuberculosis_YPIII_uid591	Gammaproteobacter	0	0	0	14	0
Coxiella_burnetii_CbuG_Q212_uid58893	Gammaproteobacter	0	0	0	2	0
Coxiella_burnetii_CbuK_Q154_uid58895	Gammaproteobacter	0	0	0	2	0
Coxiella_burnetii_Dugway_5J108_111_ui	Gammaproteobacter	0	0	0	2	0
Coxiella_burnetii_RSA_331_uid58637	Gammaproteobacter	0	0	0	0	0
Coxiella_burnetii_RSA_493_uid57631	Gammaproteobacter	0	0	0	0	0
Legionella_longbeachae_NSW150_uid46	Gammaproteobacter	0	0	0	0	0
Legionella_pneumophila_2300_99_Alcoy_	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_ATCC_43290_ui	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_Corby_uid5873	Gammaproteobacter	0	0	0	2	0
Legionella_pneumophila_Lens_uid58209	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_Paris_uid58211	Gammaproteobacter	1	0	0	5	0
Legionella_pneumophila_Lorraine_uid17	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_uid170534	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_Philadelphia_1_	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_Philadelphia_1_	Gammaproteobacter	0	0	0	1	0
Legionella_pneumophila_Thunder_Bay_u	Gammaproteobacter	0	0	0	1	0
Methylococcus_capsulatus_Bath_uid576	Gammaproteobacter	0	0	0	1	0
Methylomicrobium_alcaliphilum_uid7711	Gammaproteobacter	0	0	0	5	0
Methylomonas_methanica_MC09_uid67	Gammaproteobacter	0	0	0	13	0
Alcanivorax_borkumensis_SK2_uid58169	Gammaproteobacter	0	0	0	0	0
Alcanivorax_dieselolei_B5_uid176364	Gammaproteobacter	0	0	0	4	0
Kangiella_koreensis_DSM_16069_uid592	Gammaproteobacter	0	0	0	0	0
Hahella_chejuensis_KCTC_2396_uid5848	Gammaproteobacter	0	0	0	3	0
Chromohalobacter_salexigens_DSM_304	Gammaproteobacter	0	0	1	0	0
Halomonas_elongata_DSM_2581_uid527	Gammaproteobacter	0	0	0	0	0
Candidatus_Portiera_aleyrodidarum_BT_	Gammaproteobacter	0	0	0	0	0
Candidatus_Portiera_aleyrodidarum_BT_	Gammaproteobacter	0	0	0	0	0
Candidatus_Portiera_aleyrodidarum_BT_	Gammaproteobacter	0	0	0	0	0
Candidatus_Portiera_aleyrodidarum_BT_	Gammaproteobacter	0	0	0	0	0
Candidatus_Portiera_aleyrodidarum_TV_	Gammaproteobacter	0	0	0	0	0
Marinomonas_mediterranea_MMB_1_ui	Gammaproteobacter	0	0	0	1	0
Marinomonas_posidonica_IVIA_Po_181_	Gammaproteobacter	0	0	0	1	0
Marinomonas_MWYL1_uid58715	Gammaproteobacter	0	0	0	3	0
Thalassolituus_oleivorans_MIL_1_uid195	Gammaproteobacter	0	0	0	2	0
Actinobacillus_pleuropneumoniae_serov	Gammaproteobacter	0	0	0	1	0
Actinobacillus_pleuropneumoniae_serov	Gammaproteobacter	0	0	0	1	0
Actinobacillus_pleuropneumoniae_serov	Gammaproteobacter	0	0	0	1	0
Actinobacillus_succinogenes_130Z_uid58	Gammaproteobacter	1	0	0	1	0
Actinobacillus_suis_H91_0380_uid17636	Gammaproteobacter	1	0	0	4	0
Aggregatibacter_actinomycetemcomitan	Gammaproteobacter	0	0	0	2	0
Aggregatibacter_actinomycetemcomitan	Gammaproteobacter	0	0	0	0	0
Aggregatibacter_aphrophilus_NJ8700_ui	Gammaproteobacter	0	0	0	2	0
Mannheimia_succiniciproducens_MBEL5	Gammaproteobacter	0	0	0	2	0

Bibersteinia_trehalosi_192_uid193709	Gammaproteobacter	1	0	1	4	0
Gallibacterium_anatis_UMN179_uid6656	Gammaproteobacter	0	0	17	5	0
Haemophilus_ducreyi_35000HP_uid5762	Gammaproteobacter	0	0	0	0	0
Haemophilus_influenzae_10810_uid8664	Gammaproteobacter	0	0	0	0	0
Haemophilus_influenzae_86_028NP_uid5	Gammaproteobacter	0	0	0	0	0
Haemophilus_influenzae_F3031_uid6212	Gammaproteobacter	0	0	0	0	0
Haemophilus_influenzae_F3047_uid6209	Gammaproteobacter	0	0	1	0	0
Haemophilus_influenzae_KR494_uid2193	Gammaproteobacter	0	0	1	3	0
Haemophilus_influenzae_PittEE_uid5859	Gammaproteobacter	0	0	1	0	0
Haemophilus_influenzae_PittGG_uid5859	Gammaproteobacter	0	0	0	1	0
Haemophilus_influenzae_R2846_uid1619	Gammaproteobacter	0	0	0	0	0
Haemophilus_influenzae_R2866_uid1619	Gammaproteobacter	0	0	1	0	0
Haemophilus_influenzae_Rd_KW20_uid5	Gammaproteobacter	0	0	0	1	0
Haemophilus_parainfluenzae_T3T1_uid72	Gammaproteobacter	1	0	0	0	0
Haemophilus_parasuis_SH0165_uid5927	Gammaproteobacter	0	0	0	2	0
Haemophilus_parasuis_ZJ0906_uid20911	Gammaproteobacter	0	0	0	1	0
Haemophilus_somnus_129PT_uid57929	Gammaproteobacter	0	0	5	2	0
Haemophilus_somnus_2336_uid57979	Gammaproteobacter	0	0	4	4	0
Mannheimia_haemolytica_D153_uid2123	Gammaproteobacter	0	0	1	2	0
Mannheimia_haemolytica_D171_uid2123	Gammaproteobacter	0	0	0	2	0
Mannheimia_haemolytica_D174_uid2123	Gammaproteobacter	0	0	1	2	0
Mannheimia_haemolytica_M42548_uid1	Gammaproteobacter	0	0	3	4	0
Mannheimia_haemolytica_USDA_ARS_US	Gammaproteobacter	0	0	1	3	0
Mannheimia_haemolytica_USDA_ARS_SA	Gammaproteobacter	0	0	2	4	0
Mannheimia_haemolytica_USMARC_228	Gammaproteobacter	0	0	3	5	0
Pasteurella_multocida_36950_uid86887	Gammaproteobacter	0	0	0	7	0
Pasteurella_multocida_3480_uid161955	Gammaproteobacter	0	0	0	0	0
Pasteurella_multocida_HN06_uid156881	Gammaproteobacter	0	0	0	1	0
Pasteurella_multocida_Pm70_uid57627	Gammaproteobacter	1	0	0	0	0
Acinetobacter_baumannii_1656_2_uid15	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_AB0057_uid59	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_AB307_0294_	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_ACICU_uid587	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_ATCC_17978_	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_AYE_uid61637	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_BJAB07104_ui	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_BJAB0715_uid	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_BJAB0868_uid	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_D1279779_uid	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_MDR_TJ_uid1	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_MDR_ZJ06_ui	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_SDF_uid61601	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_TCDC_AB0715	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_TYTH_1_uid17	Gammaproteobacter	0	0	0	0	0
Acinetobacter_baumannii_ZW85_1_uid2	Gammaproteobacter	0	0	0	0	0
Acinetobacter_calcoaceticus_PHEA_2_ui	Gammaproteobacter	0	0	0	0	0
Acinetobacter_oleivorans_DR1_uid50119	Gammaproteobacter	0	0	0	0	0
Acinetobacter_ADP1_uid61597	Gammaproteobacter	0	0	0	0	0
Moraxella_catarrhalis_BBH18_uid48809	Gammaproteobacter	0	0	0	1	0
Psychrobacter_arcticus_273_4_uid58021	Gammaproteobacter	0	0	0	1	0
Psychrobacter_cryohalolentis_K5_uid583	Gammaproteobacter	0	0	1	1	0
Psychrobacter_G_uid210641	Gammaproteobacter	0	0	1	0	0
Psychrobacter_PRwf_1_uid58459	Gammaproteobacter	0	0	19	0	0
Azotobacter_vinelandii_CA_uid198829	Gammaproteobacter	0	0	5	2	0
Azotobacter_vinelandii_CA6_uid198830	Gammaproteobacter	0	0	5	2	0
Azotobacter_vinelandii_DJ_uid57597	Gammaproteobacter	0	0	5	2	0

Cellvibrio_japonicus_Ueda107_uid59139	Gammaproteobacter	0	0	0	0	0
Pseudomonas_aeruginosa_B136_33_uid1	Gammaproteobacter	0	0	0	0	2
Pseudomonas_aeruginosa_DK2_uid16899	Gammaproteobacter	0	0	0	2	0
Pseudomonas_aeruginosa_LES431_uid23	Gammaproteobacter	0	0	0	2	0
Pseudomonas_aeruginosa_LESB58_uid59	Gammaproteobacter	0	0	0	2	0
Pseudomonas_aeruginosa_M18_uid16208	Gammaproteobacter	0	0	0	2	2
Pseudomonas_aeruginosa_MTB_uid2311	Gammaproteobacter	0	0	0	2	0
Pseudomonas_aeruginosa_NCGM2_S1_ui	Gammaproteobacter	0	0	0	1	0
Pseudomonas_aeruginosa_PA1_uid22893	Gammaproteobacter	0	0	0	0	0
Pseudomonas_aeruginosa_PA1R_uid2289	Gammaproteobacter	0	0	0	0	0
Pseudomonas_aeruginosa_PA7_uid58627	Gammaproteobacter	0	0	0	2	0
Pseudomonas_aeruginosa_PAO1_uid5794	Gammaproteobacter	0	0	0	2	0
Pseudomonas_aeruginosa_RP73_uid2093	Gammaproteobacter	0	0	0	2	1
Pseudomonas_aeruginosa_SCV20265_uid	Gammaproteobacter	0	0	0	0	0
Pseudomonas_aeruginosa_UCBPP_PA14_	Gammaproteobacter	0	0	0	0	0
Pseudomonas_mendocina_NK_01_uid662	Gammaproteobacter	0	0	0	1	1
Pseudomonas_mendocina_ymp_uid5872	Gammaproteobacter	0	0	0	2	1
Pseudomonas_resinovorans_NBRC_10655	Gammaproteobacter	0	0	0	4	0
Pseudomonas_brassicacearum_NFM421_	Gammaproteobacter	0	0	0	2	0
Pseudomonas_entomophila_L48_uid5863	Gammaproteobacter	0	0	0	3	0
Pseudomonas_fluorescens_A506_uid165	Gammaproteobacter	0	0	0	1	0
Pseudomonas_fluorescens_F113_uid8703	Gammaproteobacter	0	0	0	3	0
Pseudomonas_fluorescens_Pf0_1_uid575	Gammaproteobacter	0	0	0	0	0
Pseudomonas_fluorescens_SBW25_uid15	Gammaproteobacter	0	0	0	4	0
Pseudomonas_poae_RE_1_1_14_uid1884	Gammaproteobacter	0	0	0	2	0
Pseudomonas_fluorescens_CHA0_uid203	Gammaproteobacter	0	0	0	0	0
Pseudomonas_fluorescens_Pf_5_uid5793	Gammaproteobacter	0	0	0	0	0
Pseudomonas_denitrificans_ATCC_13867	Gammaproteobacter	0	0	0	2	0
Pseudomonas_fulva_12_X_uid67351	Gammaproteobacter	0	0	0	3	0
Pseudomonas_monteilii_SB3078_uid2322	Gammaproteobacter	0	0	0	2	0
Pseudomonas_monteilii_SB3101_uid2322	Gammaproteobacter	0	0	0	2	0
Pseudomonas_putida_BIRD_1_uid162055	Gammaproteobacter	0	0	0	3	0
Pseudomonas_putida_DOT_T1E_uid1712	Gammaproteobacter	0	0	0	1	0
Pseudomonas_putida_F1_uid58355	Gammaproteobacter	0	0	0	3	0
Pseudomonas_putida_GB_1_uid58735	Gammaproteobacter	0	0	0	3	0
Pseudomonas_putida_H8234_uid208673	Gammaproteobacter	0	0	0	4	0
Pseudomonas_putida_HB3267_uid184078	Gammaproteobacter	0	0	0	4	0
Pseudomonas_putida_KT2440_uid57843	Gammaproteobacter	0	0	0	2	0
Pseudomonas_putida_NBRC_14164_uid2	Gammaproteobacter	0	0	0	2	0
Pseudomonas_ND6_uid167583	Gammaproteobacter	0	0	0	2	0
Pseudomonas_putida_S16_uid68747	Gammaproteobacter	0	0	0	1	0
Pseudomonas_putida_W619_uid58651	Gammaproteobacter	0	0	0	2	0
Pseudomonas_TKP_uid232248	Gammaproteobacter	0	0	0	1	0
Pseudomonas_putida_UW4_uid182733	Gammaproteobacter	0	0	0	3	0
Pseudomonas_VLB120_uid226717	Gammaproteobacter	0	0	0	1	0
Pseudomonas_stutzeri_A1501_uid58641	Gammaproteobacter	0	0	0	1	0
Pseudomonas_stutzeri_ATCC_17588___L	Gammaproteobacter	0	0	0	0	0
Pseudomonas_stutzeri_CCUG_29243_uid	Gammaproteobacter	0	0	1	0	0
Pseudomonas_stutzeri_DSM_10701_uid1	Gammaproteobacter	0	0	0	4	0
Pseudomonas_stutzeri_DSM_4166_uid16	Gammaproteobacter	0	0	0	0	0
Pseudomonas_stutzeri_RCH2_uid184342	Gammaproteobacter	0	0	0	1	0
Pseudomonas_syringae_B728a_uid57931	Gammaproteobacter	0	0	0	2	0
Pseudomonas_syringae_phaseolicola_144	Gammaproteobacter	0	0	0	2	0
Pseudomonas_syringae_tomato_DC3000_	Gammaproteobacter	0	0	0	1	0
Francisella_noatunensis_orientalis_LADL_	Gammaproteobacter	0	0	0	0	0
Francisella_noatunensis_orientalis_Toba_	Gammaproteobacter	0	0	0	0	0

Francisella_cf__novicida_3523_uid16210	Gammaproteobacter	1	0	0	0	0
Francisella_cf__novicida_Fx1_uid162105	Gammaproteobacter	0	0	1	1	0
Francisella_novicida_U112_uid58499	Gammaproteobacter	1	0	1	2	0
Francisella_philomiragia_ATCC_25017_ui	Gammaproteobacter	0	0	1	2	0
Francisella_TX077308_uid68321	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_holarctica_F92_uid	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_holarctica_FSC200_	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_holarctica_FTNF00	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_holarctica_LVS_uid	Gammaproteobacter	1	0	0	0	0
Francisella_tularensis_holarctica_OSU18_	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_mediasiatica_FSC1	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_FSC198_uid58693	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_NE061598_uid161	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_SCHU_S4_uid5758	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_TI0902_uid89373	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_TIGB03_uid89379	Gammaproteobacter	0	0	0	0	0
Francisella_tularensis_WY96_3418_uid58	Gammaproteobacter	1	0	0	0	0
Cycloclasticus_P1_uid176368	Gammaproteobacter	0	0	0	2	0
Cycloclasticus_zancles_7_ME_uid214092	Gammaproteobacter	0	0	0	3	0
Methylophaga_JAM7_uid162949	Gammaproteobacter	0	0	0	1	0
Methylophaga_JAM1_uid162947	Gammaproteobacter	0	0	0	0	0
Thioalkalimicrobium_cyclicum_ALM1_uid	Gammaproteobacter	0	0	0	0	0
Thiomicrospira_crunogena_XCL_2_uid581	Gammaproteobacter	0	0	0	0	0
Baumannia_cicadellinicola_Hc__Homaloc	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_CE_isolate_	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_CS_isolate_	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_DC_uid213	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_HT_isolate	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_PC_isolate_	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_uid58773	Gammaproteobacter	0	0	0	0	0
Candidatus_Carsonella_ruddii_HC_isolate	Gammaproteobacter	0	0	0	0	0
Simiduia_agarivorans_SA1_uid177713	Gammaproteobacter	0	0	0	3	0
Candidatus_Vesicomyosocius_okutanii_H	Gammaproteobacter	0	0	0	0	0
Candidatus_Ruthia_magnifica_Cm__Caly	Gammaproteobacter	0	0	0	0	0
gamma_proteobacterium_HdN1_uid5163	Gammaproteobacter	1	0	6	3	0
Vibrio_fischeri_ES114_uid58163	Gammaproteobacter	0	0	0	0	0
Vibrio_fischeri_MJ11_uid58907	Gammaproteobacter	0	0	0	0	0
Aliivibrio_salmonicida_LFI1238_uid59251	Gammaproteobacter	0	0	0	0	0
Photobacterium_profundum_SS9_uid629	Gammaproteobacter	0	0	0	28	0
Listonella_anguillarum_M3_uid217771	Gammaproteobacter	0	0	0	0	0
Vibrio_anguillarum_775_uid68057	Gammaproteobacter	0	0	0	0	0
Vibrio_cholerae_LMA3984_4_uid159541	Gammaproteobacter	0	0	0	1	0
Vibrio_cholerae_M66_2_uid59355	Gammaproteobacter	0	0	0	4	0
Vibrio_cholerae_IEC224_uid89389	Gammaproteobacter	0	0	0	4	0
Vibrio_cholerae_MJ_1236_uid59387	Gammaproteobacter	0	0	0	4	0
Vibrio_cholerae_O1_biovar_El_Tor_N169	Gammaproteobacter	0	0	0	4	0
Vibrio_cholerae_O1_2010EL_1786_uid78	Gammaproteobacter	0	0	0	4	0
Vibrio_cholerae_O395_uid58425	Gammaproteobacter	0	0	0	7	0
Vibrio_cholerae_O395_uid159869	Gammaproteobacter	0	0	0	7	0
Vibrio_furnissii_NCTC_11218_uid82347	Gammaproteobacter	0	0	0	0	0
Vibrio_alginolyticus_NBRC_15630___ATC	Gammaproteobacter	0	0	0	9	0
Vibrio_harveyi_ATCC_BAA_1116_uid2184	Gammaproteobacter	0	0	0	0	0
Vibrio_harveyi_ATCC_BAA_1116_uid589	Gammaproteobacter	0	0	0	0	0
Vibrio_parahaemolyticus_BB22OP_uid18	Gammaproteobacter	0	0	0	0	0
Vibrio_parahaemolyticus_O1_K33_CDC_	Gammaproteobacter	4	0	0	0	0
Vibrio_parahaemolyticus_RIMD_2210633	Gammaproteobacter	0	0	0	0	0

Vibrio_nigripulchritudo_SnF1_uid222819	Gammaproteobacter	0	0	0	0	0
Vibrio_EJY3_uid83161	Gammaproteobacter	0	0	0	0	0
Vibrio_Ex25_uid41601	Gammaproteobacter	0	0	0	0	0
Vibrio_splendidus_LGP32_uid59353	Gammaproteobacter	0	0	0	0	0
Vibrio_vulnificus_CMCP6_uid62909	Gammaproteobacter	0	0	0	0	0
Vibrio_vulnificus_MO6_24_O_uid62243	Gammaproteobacter	0	0	0	0	0
Vibrio_vulnificus_YJ016_uid58007	Gammaproteobacter	0	0	0	0	0
Frateuria_aurantia_DSM_6220_uid81775	Gammaproteobacter	0	0	0	0	0
Pseudoxanthomonas_spadix_BD_a59_uid	Gammaproteobacter	0	0	0	4	0
Pseudoxanthomonas_suwonensis_11_1_	Gammaproteobacter	0	0	0	3	0
Rhodanobacter_2APBS1_uid74431	Gammaproteobacter	0	0	0	5	0
Stenotrophomonas_maltophilia_D457_ui	Gammaproteobacter	0	0	0	3	0
Stenotrophomonas_maltophilia_JV3_uid	Gammaproteobacter	0	0	0	5	0
Stenotrophomonas_maltophilia_K279a_u	Gammaproteobacter	0	0	0	4	0
Stenotrophomonas_maltophilia_R551_3_	Gammaproteobacter	0	0	0	5	0
Xanthomonas_albilineans_GPE_PC73_uid	Gammaproteobacter	0	0	0	0	0
Xanthomonas_axonopodis_citrumelo_F1_	Gammaproteobacter	0	0	0	1	0
Xanthomonas_axonopodis_Xac29_1_uid1	Gammaproteobacter	0	0	0	1	0
Xanthomonas_campestris_8004_uid5759	Gammaproteobacter	0	0	0	1	0
Xanthomonas_campestris_ATCC_33913_	Gammaproteobacter	0	0	0	1	0
Xanthomonas_campestris_uid61643	Gammaproteobacter	0	0	0	2	0
Xanthomonas_campestris_raphani_756C_	Gammaproteobacter	0	0	0	2	0
Xanthomonas_axonopodis_citri_306_uid	Gammaproteobacter	0	0	0	1	0
Xanthomonas_citri_Aw12879_uid194444	Gammaproteobacter	0	0	1	1	0
Xanthomonas_campestris_vesicatoria_85	Gammaproteobacter	0	0	0	3	0
Xanthomonas_oryzae_KACC_10331_uid5	Gammaproteobacter	0	0	0	1	0
Xanthomonas_oryzae_MAFF_311018_uid	Gammaproteobacter	0	0	0	1	0
Xanthomonas_oryzae_PXO99A_uid59131	Gammaproteobacter	0	0	0	1	0
Xanthomonas_oryzae_oryzicola_BLS256_	Gammaproteobacter	0	0	0	1	0
Xylella_fastidiosa_9a5c_uid57849	Gammaproteobacter	0	0	1	0	4
Xylella_fastidiosa_M12_uid58763	Gammaproteobacter	0	0	3	0	4
Xylella_fastidiosa_M23_uid58809	Gammaproteobacter	0	0	3	1	1
Xylella_fastidiosa_GB514_uid162023	Gammaproteobacter	0	0	2	0	2
Xylella_fastidiosa_Temecula1_uid57869	Gammaproteobacter	0	0	0	0	0
Brachyspira_hyodysenteriae_WA1_uid59	Spirochaetes	0	0	0	0	1
Brachyspira_intermedia_PWS_A_uid1583	Spirochaetes	0	0	0	0	1
Brachyspira_murdochii_DSM_12563_uid	Spirochaetes	0	0	0	0	1
Brachyspira_pilosicoli_95_1000_uid5060	Spirochaetes	0	0	0	0	0
Brachyspira_pilosicoli_B2904_uid175255	Spirochaetes	0	0	0	0	0
Brachyspira_pilosicoli_P43_6_78_uid184	Spirochaetes	0	0	0	0	0
Brachyspira_pilosicoli_WesB_uid175256	Spirochaetes	0	0	0	0	0
Leptospira_biflexa_serovar_Patoc__Pato	Spirochaetes	0	0	0	0	0
Leptospira_biflexa_serovar_Patoc__Pato	Spirochaetes	0	0	0	0	0
Leptospira_borgpetersenii_serovar_Hardj	Spirochaetes	0	0	0	0	0
Leptospira_borgpetersenii_serovar_Hardj	Spirochaetes	0	0	0	0	0
Leptospira_interrogans_serovar_Copenha	Spirochaetes	0	0	0	0	0
Leptospira_interrogans_serovar_Lai_566	Spirochaetes	0	0	0	0	0
Leptospira_interrogans_serovar_Lai_IPA	Spirochaetes	0	0	0	0	0
Turneriella_parva_DSM_21527_uid16832	Spirochaetes	0	0	0	3	0
Borrelia_afzelii_HLJ01_uid177930	Spirochaetes	0	0	0	0	0
Borrelia_afzelii_PKo_uid58653	Spirochaetes	0	0	2	0	0
Borrelia_afzelii_PKo_uid159867	Spirochaetes	0	0	3	1	0
Borrelia_garinii_PBi_uid58125	Spirochaetes	0	0	0	0	0
Borrelia_bissettii_DN127_uid71231	Spirochaetes	0	0	1	0	0
Borrelia_burgdorferi_B31_uid57581	Spirochaetes	0	0	0	0	0
Borrelia_burgdorferi_CA382_uid214794	Spirochaetes	0	0	0	0	0

Borrelia_burgdorferi_JD1_uid161197	Spirochaetes	0	0	2	0	0
Borrelia_burgdorferi_N40_uid161241	Spirochaetes	0	0	3	0	0
Borrelia_burgdorferi_ZS7_uid59429	Spirochaetes	0	0	0	0	0
Borrelia_garinii_BgVir_uid162165	Spirochaetes	0	0	0	0	0
Borrelia_garinii_NMJW1_uid177081	Spirochaetes	0	0	0	0	0
Borrelia_crocidurae_Achema_uid162335	Spirochaetes	0	0	2	2	0
Borrelia_duttonii_Ly_uid58791	Spirochaetes	0	0	5	1	0
Borrelia_hermsii_DAH_uid59225	Spirochaetes	0	0	0	0	0
Borrelia_miyamotoi_LB_2001_uid215233	Spirochaetes	0	0	0	0	0
Borrelia_recurrentis_A1_uid58793	Spirochaetes	0	0	1	1	0
Borrelia_turicatae_91E135_uid58311	Spirochaetes	0	0	0	0	0
Spirochaeta_coccoides_DSM_17374_uid6	Spirochaetes	0	0	2	0	2
Spirochaeta_Buddy_uid63633	Spirochaetes	1	0	0	1	0
Sphaerochaeta_pleomorpha_Grapes_uid	Spirochaetes	0	0	0	1	0
Spirochaeta_africana_DSM_8902_uid817	Spirochaetes	0	0	0	0	0
Spirochaeta_smaragdinae_DSM_11293_u	Spirochaetes	0	0	0	0	0
Spirochaeta_thermophila_DSM_6192_uid	Spirochaetes	0	0	0	0	0
Spirochaeta_thermophila_DSM_6578_uid	Spirochaetes	0	0	0	0	0
Treponema_azotonutricium_ZAS_9_uid6	Spirochaetes	0	0	0	0	0
Treponema_brennaborense_DSM_12168	Spirochaetes	0	0	0	0	1
Spirochaeta_caldaria_DSM_7334_uid687	Spirochaetes	0	0	0	0	0
Treponema_denticola_ATCC_35405_uid5	Spirochaetes	1	0	0	0	0
Treponema_pallidum_Fribourg_Blanc_uid	Spirochaetes	0	0	0	0	0
Treponema_pallidum_DAL_1_uid87065	Spirochaetes	0	0	0	0	0
Treponema_pallidum_SS14_uid58977	Spirochaetes	0	0	0	0	0
Treponema_pallidum_Chicago_uid15954	Spirochaetes	0	0	0	0	0
Treponema_pallidum_Mexico_A_uid176	Spirochaetes	0	0	0	0	0
Treponema_pallidum_Nichols_uid208669	Spirochaetes	0	0	0	0	0
Treponema_pallidum_Nichols_uid57585	Spirochaetes	0	0	0	0	0
Treponema_pallidum_pertenue_CDC2_ui	Spirochaetes	0	0	0	0	0
Treponema_pallidum_pertenue_Gauthier	Spirochaetes	0	0	0	0	0
Treponema_pallidum_pertenue_SamoaD	Spirochaetes	0	0	0	0	0
Treponema_paraluiscuniculi_Cuniculi_A_	Spirochaetes	0	0	0	0	0
Treponema_pedis_T_A4_uid215715	Spirochaetes	1	0	0	0	0
Treponema_primitia_ZAS_2_uid67367	Spirochaetes	0	0	0	2	0
Treponema_succinifaciens_DSM_2489_ui	Spirochaetes	0	0	0	0	0
Aminobacterium_colombiense_DSM_122	Synergistetes	0	0	0	1	0
Anaerobaculum_mobile_DSM_13181_uid	Synergistetes	0	0	0	1	0
Synergistetes_bacterium_SGP1_uid19718	Synergistetes	0	0	0	0	0
Thermanaerovibrio_acidaminovorans_DS	Synergistetes	0	0	0	0	0
Thermovirga_lienii_DSM_17291_uid7712	Synergistetes	0	0	2	1	0
Thermodesulfatator_indicus_DSM_15286	Thermodesulfobacte	0	0	0	17	0
Thermodesulfobacterium_OPB45_uid682	Thermodesulfobacte	0	0	0	1	0
Fervidobacterium_nodosum_Rt17_B1_ui	Thermotogae	0	0	1	0	0
Fervidobacterium_pennivorans_DSM_90	Thermotogae	0	0	1	0	0
Kosmotoga_olearia_TBF_19_5_1_uid592	Thermotogae	0	0	0	2	0
Marinitoga_piezophila_KA3_uid81629	Thermotogae	0	0	0	0	0
Mesotoga_prima_MesG1_Ag_4_2_uid52	Thermotogae	0	0	0	1	0
Petrotoga_mobilis_SJ95_uid58747	Thermotogae	0	3	5	0	0
Thermosipho_africanus_TCF52B_uid5909	Thermotogae	0	1	4	3	0
Thermosipho_melanesiensis_BI429_uid5	Thermotogae	0	0	0	0	0
Thermotoga_lettingae_TMO_uid58419	Thermotogae	0	3	2	1	0
Thermotoga_maritima_MSB8_uid179902	Thermotogae	0	0	8	3	0
Thermotoga_maritima_MSB8_uid202924	Thermotogae	0	0	9	3	0
Thermotoga_maritima_MSB8_uid57723	Thermotogae	0	0	9	3	0
Thermotoga_naphthophila_RKU_10_uid4	Thermotogae	0	0	7	4	0

Thermotoga_neapolitana_DSM_4359_uid	Thermotogae	0	0	5	0	0
Thermotoga_petrophila_RKU_1_uid5865	Thermotogae	0	0	6	2	0
Thermotoga_RQ2_uid58935	Thermotogae	0	0	8	3	0
Thermotoga_thermarum_DSM_5069_uid	Thermotogae	0	0	0	0	0
Candidatus_Methylomirabilis_oxyfera_ui	unclassified Bacteria	0	0	0	2	1
candidate_division_SR1_bacterium_RAAC	unclassified Bacteria	0	0	0	0	0
candidate_division_WWE3_bacterium_R	unclassified Bacteria	0	0	0	0	0
Candidatus_Saccharibacteria_bacterium_	unclassified Bacteria	0	0	0	2	0
Candidatus_Saccharobacterium_alaburge	unclassified Bacteria	0	0	0	0	0
Candidatus_Cloacamonas_acidaminovora	unclassified Bacteria	0	0	0	3	0
Thermobaculum_terrenum_ATCC_BAA_7	unclassified Bacteria	0	0	0	0	1
Halyomorpha_halys_symbiont_uid22282	unclassified Bacteria	0	0	0	0	0

Supplementary Table 3

Note : Only hits with Probability (Prpbab) >50% indicated

GI number	**297550215**	**297547772**	**71910582**	**750144021**
Protein	**IscB2**	**IscB1**	**Cas9**	**TnpB**
Organism	Ktedonobacter racemifer DSM 493	Ktedonobacter racemifer DSM 44963	Streptococcus pyogenes MGAS5005	Ktedonobacter racemifer DSM 44963
pfam14239 RRXRR, RRXRR protein	Probab=100%; Score=573	Probab=100%; Score=573	Probab=74%; Score=46	Probab=52%; Score=30
cd09643, Csn1 (Cas9)	Probab=99.67 %; Score=177	Probab=99.67%; Score=177	Probab=100%; Score=1537	n/a
pfam02075, RuvC	Probab=92%; Score=41	Probab=92%; Score=41	n/a	n/a
cd00529, RuvC_resolvase, Holliday junction resolvases	n/a	n/a	n/a	Probab=92%; Score=35
pfam01385 OrfB_IS605	n/a	n/a	n/a	Probab=100%; Score=195
COG0675 Transposase and inactivated derivatives	n/a	n/a	n/a	Probab=100%; Score=310

Supplemental Figure 1. DNA (IG format) and protein (Fasta format) sequences of all new transposons reported in the manuscript.

```
; Ktedonobacter racemifer DSM 44963; 7 copies, ~99% identical to the consensus
; This transposon is inserted at the GT|GG target site (no target site duplications)
; Palindrome at pos 7-27: CCCCATGCCTAAAGGCAGGGG
;                         ==== ====>  <========
; Palindrome in the 3' terminus at pos 1531-1580:
;tail 1531                                          1580
;  Q: TGCGCCATGCTCCTCCCCATGGCTAAAGCCAGGGGTCCCCGCATGGCGCA
;     ||||||||||     ||| |||||  ||||| |||     ||||||||||
;  S: TGCGCCATGCGGGGACCCCTGGCTTTAGCCATGGGGAGGAGCATGGCGCA
ISC2-1_KR
CAGGTACCCCATGCCTAAAGGCAGGGGCTTGTGAAAGCAAGCTCGGACCTGTCCAGACTT
AGCCATGGGCCTTCTGCGCGAGGCAGGAGGTTATCAGGCTACGATAGAGGAGAAGTGTTC
AAGTTCCTACCTACAGGTGCGTGCCAGCCGGTAGCTCTAGAATCTCTGGGTTAAACAGCA
AAGCGGGGTCTATGCAGTGCTCAGGGAAAAGTACCGCCCTCTATCATTGTCGAGGCAAAC
ATTACCCTGGAAACAGGAGGCTCAACGTGAGCAATGTTTTTGTGATTGATAGTGACTATA
AACCTTTAAATCCGGTGCATCCAGGACACGCGAGGCGCTTGCTCAGGCAAGGGAAAGCAG
CCGTGTTTAGACGGTATCCGTTTACCATTGTGCTCAAACGGGTGGTAGAACAGCCAGAGG
TACAACCCTTGCACCTCAAGCTCGATCCAGGCAGTAAAACGACGGGAATTGCCCTGGTGA
ACGACACCAACGGCAAAATTGTGTTCGCGGCTGAACTCTCACATCGAGGGCATGCAATTA
AAGACAGTCTTGATAGTCGTCGTGCAAGTCGCCAGGGGCGTAGGCAGCGTAAAACACGCT
ACCGCAAGCCGCGATTTGACAATCGACGGAGGAAGAAGGGATGGTTGCCACCATCGTTAG
AAAGTCGCCTTGCCAACATTCTGACGTGGGTAGCTCGCCTGTGTCGATATGCTCCCATTG
CCACTCTCAGTCAGGAGCTTGTGAAGTTTGATATGCAATTGATGGAGAATCCCGACATTG
CAGGTGTGGAATACCAGCAAGGAACCTTGCAAGGCTATGAGGTCAGGGAATACTTGCTGG
AAAAATGGGAACGCACGTGTGCCTATTGTGGCAAACAAGATGTCCCGCTTCAGGTAGAGC
ATATCCATCCACGTGCCCGTAGTGGTACGAACAGGATGAGCAATCTTACCTTGGCGTGCG
AAGCATGCAATACTGCCAAAGGCACTCAGGAGATCGAAGTCTTCTTGAAAAAGAAACCTG
ACGTGCTCAAGCGTCTTCTCGCTCAGGTCAAAAAGCCACTCAAGGATGCCAGCGCTGTCA
ATAGCACACGATGTGCTTTGCTCGAACGGCTGAAAGCTCTCGGCTTGCCTGTCGAGTGTG
GGAGCGGTGGATTGACGAAGTTTAATCGTACCACGCGAGGACTCCCCAAAACCCACTGGC
TCGATGCAGCTTGCGTAGGCAAGAGCACGCCTGATGTGCTTTTGCAGAAGGGAGTCATCC
CACTGCGCATCAAAGCGACAGGGCATGGGAGGAGGCAAATGTGTGTGCCTGACAAGTATG
GATTCCCGAAGCAGCACAAAGAGCGCAAAAAGACATTTCTTGGGTATCAAACGGGTGATC
TGGTCAAAGCCATCACGCCCAAAGGAACATTTGAAGGACGGATAGCCATTCGTCATCGGC
CTTCATTCCGACTGGAGAAGGTCGATATTCACCCCAAATATATGCGTTGTGTGCAACGAT
CCGATGGCTATGAGTATACACAGAAAGGAGTGCGCCATGCTCCTCCCCATGGCTAAAGCC
AGGGGTCCCCGCATGGCGCAATTTTTAGAT
; Ktedonobacter_racemifer_DSM_44963; 3 copies, 99% identical to the consensus
; This transposon is inserted into the GT|GA target site (no duplications).
; Palindrome at pos 7-27: CCCCGGTTTGAAAACCGGGG
;                         ========>  <========
; Palindrome at pos 1533-1578:
; tail 1533                                      1578
;   Q: CGCCATGCTCCTCCCCATGGCTAAAGCCAGGGGTCCCCGCATGGCG
;      ||||||||     ||| |||||  ||||| |||     ||||||||
;   S: CGCCATGCGGGGACCCCTGGCTTTAGCCATGGGGAGGAGCATGGCG
ISC2-2_KR
CATGGACCCCGGTTTGAAAACCGGGGCTTGCAAGAAGTTTGAACGCTTCTTGTAACCCCCAACGGTTGGC
AAGCTGAAACATGACCAGATCCAGCCACCGCTCTTCTTCGGAGGAGCGATGGGGCTACGTTATCAGGAAG
TGTCAACGTTCGTACCGGAGGATGCGCGGCCAGTCTTCCGCTCTACAACCAGCAGGTTAAACAGACCGTG
GGTATAGTCAGTGCTTGCTGGATGTACCGCCTGATAACATCATCGAGGCCACCATCACCCGAGCAATCGG
AGGCTCTGAAAGGAGCAAGCACATGAGCCACGTTTTTGTCATCGATGCCAACAAGCAACCGCTCAATCCG
GTCCATCCTGCAAGGGCACGCGTATTGCTCTCGCAAGGGAAGGCGGCAGTACTGAAACGCTTTCCTTTTA
CCATCATCCTCAACGTTGCGATAGATGCTCCAGTCGTTGAAGAACTGCGGATCAAGATTGACCCAGGCTC
AAAGACCACAGGCATAGCTCTCGTCAACGACCAGTCGGGTGAAGTCGTCTTTGCGGCTGAACTCCATCAT
CGTGGAGCAAAGATCAAAGAGGCGCTCGATGATCGAAGAGCCGTCAGATATTCACGACGCCGACGCCATA
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CACGCTACAGAAAAGCGAGATGGCAGAATCGGAGGCGACGCGAGGGCTGGTTGCCGCCATCGCTTACTAG
CAGGATCAGCAATGTACTGACCTGGGTGAAGCGTCTGCGCAACCTTTGCCCGATCACAGCAATGAGCATG
GAGCTCGTGAAGTTTGATATGCAAGCGATGGAGAACCCCGATATCCAGGGATGGGAGTATCAACAAGGCA
CACTGGCAGGCTATGAACTCCGTGAGTACCTGCTAGAGAAGTGGAACCGAATGTGCGCGTATTGCGGCAA
GGGCAATGTCCCTTTGCAAGTGGAGCACATTGTGCCTCGTGCCAACAAGGGCACGCATCGCGTCAGTAAC
TTGACGCTCGCATGCGAGAAGTGTAACCAGGCCAAGGGAACCCAGGACATCAAAGACTTTCTCAAGAAGA
AACCAGCGATGCTCAAGCACATTCTTGCTCAGGCAAAAGCCCCGCTCAACGATGCCGCAGCGGTCAATGC
CACCCGTTGGGAGTTGTTCAGAGGGCTACAAGCGTTAGGGCTGCCAATCGAATGTGGTTCTGGCGGGTTA
ACGAAGTACAACAGGACGACACGTGAGCTTCCAAAAACGCACTGGATAGACGCGGCGTGTGTCGGTCAGA
GCACTCCTGAGTACCTGAACACCACAGGGATCTCTTCCTTGCTGATCACGGCGACGGGCTATGGCAAGAG
ACAACTGTGTGGCGTAGATAAGCATGGTTTTCCTCAGCGCCATCGACAACGCAAAAAGGTGCATCATGGG
TATCAGACGGGCGATCTGGTGCGAGCGGTAGTACCAGAGGGATTTGCGGCAGCGGGGAGACATGTGGGGC
GCGTCTTAGCACGAGCAACGGGATCGTTTGATCTGAGAACCGCACGTGGGCGCATAGAAGGAGTCCCTGT
GCGCTATTGTCGTCCTCTTCATCGCAATGATGGATATAGCTACCACAGCACGAGAGGCGGCAATTCCTCC
CCGCTCTAAAGAGGCGGGGCTTCCTTGCCGCTTCTCTGT
; Ktedonobacter racemifer DSM 44963; two 91% identical copies
; This transposon is inserted into GT|GA target (no duplications)
; Common ends with IS605B-3_KR
; Terminal palindromes:
; head  8                  28
;    Q: CCCCACGCATGAATGCGGGGG
;       ||||-|||||  ||||| |||
;    S: CCCC-CGCATTCATGCGTGGG
;
; tail  1661            1680
;    Q: CCCATGGGTGAACCCAGGGG
;       ||| |||||  ||||| |||
;    S: CCCCTGGGTTCACCCATGGG
ISC2-3_KR
CAACGATCCCCACGCATGAATGCGGGGGCTTGTCCCTTGTGTTGATGCCGTCTTCGTTGTCCAGCCGAGG
TACCAGAGCCCGCAGGCAAGGCGCTGATTGGTACCAGCGTTGCGCTCGTCACGACACCTCGTTGTGCTTC
CTCAGCAGCGAGCGCTGTCGCTCAGCGTTAAAAGCACCCGTCGGGGTACGGGTCGGTGCGTTGAGCCGAA
CAAGCGAGAGCAACACCGGCGAGGGGAGCGTCCTGAGTCAGCCTGCTCAGGACCGTTACACAGCCCGGTA
ACGGGGCCCTCACACGAGGGAAACGAAAGGAGTCACCCATGGTGTTTGTGCTCGACAGATACAAAAAGCC
GCTCATGCCCTGTACCCCCAGACGTGCACGCCTCCTGCTCGCACGCAAGCGGGCGGTGGTCCACCGGCTC
AGCCCCTTCACGATCCGTCTCAAGGACCGCAGCGTCCAGCAGAGCACGCTGCAACCGGTGGCGCTCAAGA
TCGATCCTGGCGCAAAAACCACGGGCCTGGCCCTGGCGCGGGTGGAGGAGACCAGCGAGGGAGAGGTGCA
CCACGCGCTGCACCTGGCCGAACTCTCCCACCGAGGAGAGGAGGTCCGCGACCGACTGCGCAAACGGGCC
GGGTATCGACGCCGGAGGCGTTCGACCAACCTGCGCTATCGGCCGGCGCGCTTCCTCAACCGCCGTCGAG
CGCCTGGCTGGCTCCCGCCGTCCCTGCGCTCACGCATCGACAATGTCCTGTCCTGGGGCAGGCGCTATCA
GCGCTGGGTTCCGCTGGTGCGCATCGCGGTGGAGCGCGTGAAGTTCGACACGCAGCTCTTGCAGCAACCA
GAGATCTCCGGGGTCGAGTACCAGCGCGGGGAACTGGCCGGTTGGGAAGTGCGCGCCTATCTCCTGGAGA
AGTTCGGGCGCAGGTGCGTGTACTGCGGGCGCACGGACACGCCCTTCGAGTTGGACCATATCCAGCCGCG
CAGTCGGGGTGGTTCCAACCGCGTGTCGAATCTGGCGCTCAGTTGCCACACGTGCAATGCCGCCAAGGGG
GAGCGCACCGCCGCGGAGTTCGGCCATCCCGAAGTGGCCGCCCAGGCGAAGCAGCCGTTGCGGGACACGG
CGGCGGTCAACGCCACCCGCTACGCGCTCTGTGACGAACTGCGCACGCTGGACCTGCCGCTCACCACCTG
GAGCGGCGGACGCACGAGATGGAACCGGGCGCGCTTCTCGATCCCCAAGACGCACGCGCTGGATGCCCTG
TGCGTGGGGGAGGTGGCGGGAGTCAAGGTGGGTGCGCACCAGGCCCTGGCCATCACAGCCACGGGTCGGG
GTCGCTACAGCCGCACGAATGTCGACGAGTCGGGCTTTCCGGTTGGCTCCTTGATGCGCCGCAAGCAGGT
CCTGGGAATCAAAACGGGGGACCGGGTGCGGGCCATGGTTCCGGAAGGGTTTGCGGCGCAGGGGACCCAT
ACCGGGCGCATCGCCGTGCGCGCGAACAAGCACTTTCGCATGGGCAAGGTGCAGGGGATTCCTGCGCGAT
TTTGCCGGGTGCTCCAACTGGCCGACGGCTACGACTATGCTGTGGTGGCAACGACCTTGCAGGGATGACG
GACCGAGGAGCCCCCTCCCCTGCCACCAGGAAAGGAACGCCTGCTTCCTCCCCATGGGTGAACCCAGGGG
CATCCGCAGGCCGAATGAGGT
; Ktedonobacter racemifer DSM 44963; two 97% identical copies
; This transposon is inserted into GT|GA target (no duplications).
; Terminal palindromes:
; head  24                                           68
;    Q: GGGGCTTGTGG--GAGACTACCCTGAGTGGTCTTGGCTGCGAGCCCC
```

```
;       ||||||:|::|--:||||:||:| |:||:||||:--|::|:||||||
;    S: GGGGCTCGCAGCCAAGACCACTCAGGGTAGTCTC--CCACAAGCCCC
;
; tail  1634                                        1680
;    Q: GGCGGCACTTCCTCCCCAGGCGTGAACGCC-GGGGCTTCCGTGCCGCC
;       ||||||||     ||||-|||||  |||||-||||     ||||||||
;    S: GGCGGCACGGAAGCCCC-GGCGTTCACGCCTGGGGAGGAAGTGCCGCC
;
ISC2-4_KR
CAGCGACCCCACCGGTAAACCGGGGGGCTTGTGGGAGACTACCCTGAGTGGTCTTGGCTGCGAGCCCCGA
TGCTGACCAGCCCCCGGTGTGCTCGCACACCGGAGCCGTTCAGAAGGAGCGCGAAAAAGCAGACCCTGGA
GTGGCTTTTCCAGCTCCCGGCTCTTTAATTGCTCAGTTAAACAGGTTGATGGGGTGTCCAAAGCCAGTGC
TGAGCAAAGATCGCCGCTTCTGACACCCGGGCGAGGAAAACATTACCGTTCGTGTGTGCTGGACAGGAAG
GCGCACACCAACGCGATGCCTCATTACGAGGCCCCCGCAAGGGGAGAACAGGAACAAAACCATGTCGCGT
GTATTGATTGTGGATGCAGAGCGCAGGCCGCTCATGCCCTGCACTCCTGCCCGCGCCCGTCTTCTGCTCA
AGGCGGGCAAGGCAGCCATCTTGCGTCGCTTTCCCTTTGTGCTGATTTTGCGCGAGGCGAGGCCAGAGGC
CGTGGTGGAGCCGCTGCGCGTCAAACTCGATCCTGGGTCCAAAACCAGCGGGATTGCCGTGCTCCATGAA
CAATCAGGTGAGGTGATGTGGGCGGCGGAGCTGACTCATCGAAGCACGCCGCTTCGCGAGGCGCTCGCGA
AGCGGCGTGCTGTGCGCCGATCTCGACGCAGCCGCCATACCCGCTACCGTGCGGCACGGTTTGCCAATCG
GAGGCGGCCCAAAGGGTGGCTCGCGCCCTCGCTTGAGAGTCGCGTGCTTCACCTGCTGACCTGGGTCAAG
CGCCTGTCCCGCTGGTGTCCGGTTGGCGCGCTCTCCTTGGAACTCGTGCGCTTTGATCTGGCGTTGCTGC
AGAACCCTTCCATTGAGGAGGTCGAATACCAACGCGGAACCTTGTGGGGAACGGAAGTACGCCAGTATCT
GCTCGACAAATGGCAGCATCGATGCACATATTGCCAGGCGAGCGAGGTGCCATTGGAAATCGACCATGTG
TCTCCCCGTTCGAAAGGTGGATCGCATCGCATCGCAAATCTCGTCATCGCGTGTCGGCCCTGCAACCAAG
CCAAAGGCGATCAACCCCTTGAGTCCTTTCTGGCAAACCGACCAGACGTGCTCGCTCGCGTGCAGGTGCA
GCGTCGCGCCCCACTGCATGATGCAGCGGCGGTCAACAGCACGCGGTGGCAGCTGTATGAGCGCCTCAAA
GCCCTTGATTTGCCGGTCGAGACGGGGTCTGGCGGTCTGACTAAGTGGAACCGACAAAGCCGAAACCTTC
CGAAGACCCACTGGATCGATGCCGCATGCACAGGGCGATCAACGCCAGAACGCCTCCAGATCCGGCATGT
TCGTCCCTGGCTGATTCAGGCACAGGGGCGGCAGGCTCGTCGCATGGTCAATGTGGATAAACGGGGGTTC
CCGCGAGGAAAAGCCAAAGGACCCAGCGGCATCTGCGGATTGAGGACAGGCGATCTGGTCCGTGCGGTGG
TCACGAAAGGCAAGAAGATCGGCACCTATGTCGGGCGTGTGGCGATCAAGTCGGATGGGTACTTGAAACT
GACAGGGCGTCCGTTCGGCATGGTCGAGGGAATTCACGCACGATATTGTCGGCCGGTCCATCGCAACGAT
GGCTACGCTTACGCGCAAGGAGAGGCGGCACTTCCTCCCCAGGCGTGAACGCCGGGGCTTCCGTGCCGCC
GTTTGGT
; Ktedonobacter racemifer DSM 44963; 2 copies (99.5% identical)
; Codes for Cas9H and Y1 TPase (overlapped ORFs).
; Its 35-bp 5'-terminus is similar to the one in IS605B-1_ME.
; Terminal palindromes:
;     head               24 47
;  Q: CAGTGGCTTCTTCGGAAGTCACTG
;     |||||:||||:  :||||:|||||
;  S: CAGTGACTTCCGAAGAAGCCACTG
;
;     tail                                   1936 1982
;  Q: GCGGCAATTCATCCACGAAG-CTGAAGACTTCGCGGTTTTCTTGCCGC
;     |||||||   | ||:|||||-||  ||-|||||:|| |   |||||||
;  S: GCGGCAAGAAAACCGCGAAGTCTTCAG-CTTCGTGGATGAATTGCCGC
;
ISC2Y-1_KR
GAACTACCACTGAGCTGAAGACGCAGTGGCTTCTTCGGAAGTCACTGAAGACGCAGACCAGGAGCTTCTT
CGGAAGCTTGAGTTCACCAGACTCGTTTCCAGAAATGGGAACAGCGTTCGATTGGTCATGACACCTGCGG
TTGACGCATCAGACCGCTGCTCTGTCGCTGAGGGTTAAGTAGGCTTGAGGAAAGGGCCGGTGCTCTCAGC
GCAAAAAGCCTTTTGAACACTGTCGAGATGAAGCCGGATTCCCTTCGTGGTCACAGCGAAGGGATACGCA
CCACCCGGCGCTTGCCGGAGCATTTTCCGAAAGGAGTTTTCTATGAACGTCGTCTACGTCCTCTCGTCGG
AGAGAACACCATTAATGCCCTGTCAACCTGCCATTGCGAGGTTGTTGCTGAAACAAGGAAAAGCAAAGGT
GAGGCATCGAACGCCCTTTACGATTCAGCTTCTCGCACAGCCAGAGCACGTGTACACACAACTGCTGACC
CATGGCGTTGATACGGGAAGTTCCATAATCGGATCAGCCGTGGCTAATGAGCATGGACACGTCGTGTATC
TTTCGGAAGTCGAGATACGCAATGATATTGCAAACACTATGAAGGAACGAGCGAGAGCACGCCGCAATCG
TCGTCAACGCAAGACACGCTATCGCCCTGCTCGCTGGCTCAATCGCAAGAAATCGATCAAAACTGGACGC
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TTCTCGCCCACCATGAGAAGCAAGATTGATACTCATCTGCGAGAAATTCGCTTTATACGGTCATTGCTGC
CCATCACGTCTACGATACTAGAAACAGGCTCATTTGATCCTCATGCACTCAGAAATCCTGAAGTCCTGCA
AAAGAAGTGGCTCTACCAGAGGGGCATCAACTACGGTTTTGCCAATACCAAAGCCTATGTGCTCACACGA
GACGGCTACCTCTGTCAGCAGTGCAAAGGGAAGTCAAAGGACCGACGGCTTGAAGTTCACCACATCATCT
TCAGAAGTCGAAATGGAAGCGATGAGGAAGCGAATTTACTCACTCTCTGCAAAACTTGTCATGATGGACT
CCATGCAGGCACCATCACCCTGAAACTCACAGGCAAGAAAAAGGGAACCTTGCAACATGCGACCCAGATG
AATAGCATCCGCACTCAGTTACTCAAGCGTGTTGAGGCAGAGGAAACCTGGGGCTTTGTCACCAAAGAGC
ATCGTCTTCTGGTAGGACTCCCCAAAGAGCATATCTTTGATGCAGCCGTGATTGCAACACGAGGAGTGAA
GCCAACCTTCTATACCACGAGCGTGCTCTCAAAACGCTGTGTGTCAGATGGAGATTACAAACAAACGAAA
GGAAAACACGGTCAACAACGAGTGAACACAGGCAAGATCATGGGATTTCGCAAGTTTGATAAGGTGTACT
ATTTGGGGAAGGAGTACTTTATCAAGGGGAGAATGTCTACCGGCTACGCGATCCTCATGGACATTGACGG
CAACAAAATTGAGTTCAAACCACTTCCCAAGTTTGACAAAATGAAGAGAGTAAGTGCACGTTCATCATGG
ATGATGAAACAAAGAACCACGCCAAATTCCTCATTCTCTATCACCTCATCTTTGTCTGCAAGTGCAGGAA
AAAACGTTTGATGCGCTCTGGAGATGAGACAAAAAGGATATTCGAGGTCATTGCAACACAATCAGACGTT
TCCTTTGAGACGATGGAGGTGGACAAGGATCATATTCACTGCCTAGTAAAAAGCGAACCGAGGATAGCAC
CACTCGCGATAGTACGAAGGTTAAAGCAAGAATCGACTCTTCAGCTTTGGCAGATGTACGAAGATGAATT
GAGAAGACACTTTTGGAAGGAAAGGACATTCTGGAGCGATGGATACTTCTGCCGTACCGTTGGCGATGCA
AGTCAGGGAACAAGACGCCAGTACATTGAGGATCAAGGGTGAGGTGCGGCAATTCATCCACGAAGCTGAA
GACTTCGCGGTTTTCTTGCCGCCTTTCCTAT
; Ktedonobacter racemifer DSM 44963; 4 copies ~98.5% identical to the consensus
; GT|AA target site (no duplications).
; This transposon is nonautonomous; it codes for the C-truncated Y1 TPase and Cas9H.
; ISC2Y-2_KR is 74% identical to ISC2Y-1_KR.
;
; Terminal palindromes:
; head 19 52
; Q: AGCTGAAGACGCAGCGGCTTCTTCGGAAGTCGTCGGGTCTGCGGTT
;    |:|:| |||| |::||:||||:  :||||:||::| |||| |:|:|
; S: AACCGCAGACCCGACGACTTCCGAAGAAGCCGCTGCGTCTTCAGCT
;
; tail 1940 1991
;
; Q: GGAGCGGCG-TTCATCCACGAGG-CTGAAGACCTCGTGGTTTTCTCGCCGCTCC
;    |||||||||-   | ||||||||-||  ||-||||||||- |   |||||||||
; S: GGAGCGGCGAGAAAACCACGAGGTCTTCAG-CCTCGTGG-ATGAACGCCGCTCC
;
ISC2Y-2_KR
GTGAACTACCACTGAGCTGAAGACGCAGCGGCTTCTTCGGAAGTCGTCGGGTCTGCGGTTTGGGAGCTTT
TTAGGAAGCTCAAGTTCACCAGACTCCTCATCAGAAATGATGAGACCGTTTGAAAGGTCATGACACCTGC
GGTTGACGCATCAGACCGCTGCTCTGTCGCCTGGGTTTAAGTAGGGCTGAGGAAAGGCCCGGTGATCCAG
GTGCAAAAAGCCTTTTGAACACTGTCGAGATGAGGTCGGATTCCCTGCATGGTCACAGTGCAGGGATACG
CATCACCCGGCGCTTGCCGGAGCATTTTTCCGAAAGGAATCGTCTGAACATGGTCTATGTCCTCTCACCA
GATAGGACGCCGCTTATGCCTTGCTCTGCTGCGATTGCCCGTTTGTTGCTCAAAGAGGGAAAGGCCAAAG
TCGTCCGCAGAACCCCTTTTACGATCAAGTTGTCTGTACAGCCAGAGCGTACCTACACCCAACCCTTGAC
CTTGGGAGTGGATACCGGGAGTGCGGTGATTGGTTCGGCTGTCGCGGATGAACAGGGCAGCATCTTGTAT
CTTTCTGAAGTGGAAGTGCGCAATGATATTGCCACGACGATGAAAGAACGAGCCACCCATCGTCGAGATC
GCCGCAACCGAAAGACACGCTATCGGCCTGCACGCTGGTTACATCGAAGGAATTCCATCAAGACTGGGCG
ATTCTCCCCAACCATGAGAAGCAAGATCGACGCCCATCTGCGAGAAATCCACTTTGCGCACTCCTTGTTG
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TTTCGTAGCCAACACGGAAGCGATGAGGAAAGCAAGCTCTTGACGCTCTGCAAGACCTGTCATGATGCCC
TTCACGCTGGGACTATTCCCCTCAAGCGCACCGGAAAGAAAAAAGGGGATTTGCTGCACGCGACCCAGAT
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CATCGATTGCTTGCGGGTTTGCCCAAAGAACATTGTTTTGACGCGGCCATGATTGCGACACGCGGAAATC
GGCCTGTTTTCCAGATACAAACGGTGTTTGTCAAGAAATGCATTCCAGATGGAGAGTATCAGCAAACCAA
AGGAAAGCGAAGCGAGCAACGGATCCCGACAGGAAAAATCCAGGGATGCGCGCAAATGCGACAAAGTGCG
TTATCGAGGTCAGGAATACTTTATCAAAGGGCGTATGTCTACTGGTTATGCTATTTTGATGATGATAGAC
GGGAAAAAGGTCGATTTGAAACCCATTCCCAAGTTTGAGAAGATGAAGAGAGTGAGTGCGCGATCCTCAT
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; Geitlerinema sp. PCC 7105; 10 copies
; GT|GG target site (no duplications).
; palindrome at pos 8-38: CCGCCGTCAAGCCTGTTGGCTATGACGGGGG
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; palindrome at pos 1560-1629:
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;     |||||||     ||||||:||-|||| :: ||||-||:||||||     |||||||
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; Geitlerinema sp. PCC 7105;
;  GT|GG target site (no duplications)
; 2A and 2B are 91% identical to each other
; FRAGMENT 12422 -> 10705
;gi|442995890|gb|ANFQ01000137.1|
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; Geitlerinema sp. PCC 7105
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;  Coleofasciculus chthonoplastes PCC 7420; 4 identical copies
;  TT|GG target site (no duplications).
;  Palindrome at pos 7-34: CCCCACGCTACTAACGTGGAGCGTGGGG
;                          =========          =========
;  The 3'-terminal palindrome at pos 1353-1383:
;  tail 1353                       1383
;    Q: TACTTCGTTGAGGTCGGAGTCCCACGAGGTA
;       |||:|||| |:: || || ::| ||||:|||
;    S: TACCTCGTGGGACTCCGACCTCAACGAAGTA
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;  TT|GA target site (no duplications).
;  Palindrome at pos 7-36: ccctgacttagctatcgcttgaagtcaggg
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;  The 3'-terminal palindrome at pos 1421-1462:
;  tail 1421 1462
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; GT|GA target sites (no duplications).
; Terminal palindromes:
; head 8                 27
;   Q: CCCTCGACTGAAGTCGAAGG
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;   S: CCTTCGACTTCAGTCGAGGG
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;  tail 1522                            1555
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; Target site N|ATGA
; consensus
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; Microcystis aeruginosa NIES-843
; consensus from 46 copies
; N|ATGA target site
; Terminal palindromes:
; head   10 33
; S: TCGCCG-CCGTAAAACGGACGGCGA
;    ||||||-||||   ||||-||||||
; Q: TCGCCGTCCGTTTTACGG-CGGCGA
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TGTGCTAATATTTAACAGCAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAATTTTCG
; Nitrosococcus halophilus Nc 4
; consensus sequence from 4 99% copies
; head1             14 58
; S: CTAACTCATTCTCCAAGTTCGTCCTGAACTTTCCGAATGAGTTGG
;    |:|||||||||   ||||||:   :||||||   |||||||||:|
; Q: CCAACTCATTCGGAAAGTTCAGGACGAACTTGGAGAATGAGTTAG
;
; tail              54 64
; S: TGCGCTGCGCA
;    ||||| |||||
; Q: TGCGCAGCGCA
ISC2-1_NH
GTTGAGTCGTCGCCTAACTCATTCTCCAAGTTCGTCCTGAACTTTCCGAATGAGTTGGTTGGCTCAACCA
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;  Halomonas meridiana strain R1t3
;  It has a common 3' terminus with IS605B-1_HM
;  conceptual consensus
; head               8 27
; S: CCCCCGCCTGAAGGCGGGAG
;    |:|||||||  |||||||:|
; Q: CTCCCGCCTTCAGGCGGGGG
;
; tail              24 43
; S: CCCGGCGCTAAAGCACCGGG
;    |||||:|||  |||:|||||
; Q: CCCGGTGCTTTAGCGCCGGG
;
ISC2-1_HM
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; Halomonas meridiana strain R1t3
; gi|764088103|gb|JZEM01000040.1| 11370 -> 12688
; N|ATGA target site
;
; common 3' terminus with ISC2-1_HM
; imperfect terminal palindromes:
; head  9 30
; Q: TCCCCTCCCTAAAGGAAGGAGA
;    ||:|||:|||  |||:|||:||
; S: TCTCCTTCCTTTAGGGAGGGGA
;
; tail  1278 1298
; Q: CCCCGCCCTAAAAGGACGGGG
;    |||||:|||   |||:|||||
; S: CCCCGTCCTTTTAGGGCGGGG
;
IS605B-1_HM
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; Marinobacter sp. ELB17
; 5 copies ~94% identical to the consensus
; shares its 3' end with IS605B-1_MS
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; the consensus is 71% identical to ISC2-1_HM
; The N[transposon]ATGA targets are found based on comparison
; to Marinobacter sp. BSs20148
ISC2-1_MS
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CTGGAAGACTGGGATCACGCTGGCGAAAGGTAAAGCGCCGAAGGTTCCGGTCGCCGCGCAAGCGGGAGCC
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ACAGGAAAAACGAGTCGCGCTGACGCACGACGCGCTATCCCTCCCCGACCTGAAGGACGGGGTATCCCGC
GCAAAATG
; Marinobacter sp. ELB17
; 3 copies >92% identical to each other
; The N|ATGA target site
ISC2-2_MS
GTCAACTACCCCGCCGTGAACGACGGGGCTTGTAGAGAACACCCTACACGCCAAGTTGACCAGGGAAAGC
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; Ktedonobacter racemifer DSM 44963
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; FRAGMENT 1448433 -> 1447073
; gi|297546893|gb|ADVG01000004.1|
; shares both termini and target with ISC2-1_KR
; Terminal palindromes:
; head  9 29
; CCCCATGGCGAAAGCCA-GGGG
; |||| ||||    |||| ||||
; CCCC-TGGCTTTCGCCATGGGG
;
; tail 1315 1344
; CCATGTCTAAACCCAGGGGTCCACGCATGG
; |||||: |::||||  ||||::| :|||||
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IS605B-1_KR
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; consensus from 4 copies
; common 3' terminus with ISC2-2_KR
; Terminal palindromes:
; head  1 36
; CTGAAGCTCCCCGCGCTAAAGCGACGGGGGTTCCAG
; |||:|:|:|||  ||||  ||||  |||:|:|:|||
; CTGGAACCCCCGTCGCTTTAGCGCGGGGAGCTTCAG
;
; tail  1777 1821
; GCGGCGATTCATCCCCGG-CATCAATGACCGGGGCTTTCTCGCCGC
; |||||||   | ||||||-|||::|||-|||||| |   |||||||
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IS605B-2_KR
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CGTTCTCTGTAA
; the consensus was derived from 6 copies >99% identical to it
; common ends with ISC2-3_KR
; Terminal palindromes:
;
; head  11 30
; CCCATCGCTGAAGCGAGGGG
; ||| |||||  ||||| |||
; CCCCTCGCTTCAGCGATGGG
;
; tail  1430 1474
; CGCCTGCTTCCTCCCCGCGTTTGAAAACG-GGGGCATCCGCAGGCG
; |||||||   : |||| |||||  ||||| |||| :   |||||||
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IS605B-3_KR
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CCCCTCCGTTGCCCCACTCCGACAAGGAACGCCTGCTTCCTCCCCGCGTTTGAAAACGGGGGCATCCGCA
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; Ktedonobacter racemifer DSM 44963
; the consensus was derived from 3 copies ~97% identical to it.
; Terminal palindromes:
;  head 9                  29
;    Q: CCCCCACATTGAATGTGGGGG
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;    S: CCCCCACATTCAATGTGGGGG
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;  tail 1296                    1323
;    Q: GGGCAAGGGAAGCCACCCTTCCTAGCCC
;       |||| |||:|:| :: |:|:||| ||||
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ISC1-1_KR
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TCCTGTCCAAGTGGGGAAGGAGCATCTCTACCAACTCTTGCGAGAGATGGGACTCACCCTACATCTGCGT
GAGGGCTGGCAGACGAAGGAGCTTCGAGAGCAGCATGGCCTCAAAAAGACGAAGAGCAAGTCGAAGCAGT
CCTTTGAGTCGCATGCGGTGGATAGTTGGGTGCTCGCAGCCTCGATCAGTGGGGCGGAGCACCCCACCTG
CACCCGTCTGTGGTACATGGTGCCAGCCATCTTGCATCGTCGCCAACTCCATCGTTTGCAAGCGTCAAAG
GGAGGCGTGCGCAAGCCCTATGGGGGAACCCGCTCATTGGGCGTGAAACGGGGAACCCTTGTCGAGCACA
AGAAATACGGACGCTGTACCGTCGGCGGAGTTGACCGCAAGCGAAACACCATCAGCTTGCACGAATACAG
AACGAACACACGACTCACGCAAGCAGCGAAAGTGGAGACCTGTCGAGTCTTGACCTGGCTGTCTTGGCGC
TCCTGGTTGATCAGAGGAAAGCACACATCGTCAAAGGGCAAGGGAAGCCACCCTTCCTAGCCCCAACAAA
GGAACGCCTGT
; Oceanimonas smirnovii ATCC BAA-899
; 3 copies, ~97% identity to the consensus
; N|ATGA target site
;
; terminal palindromes:
; head 9-28
; Q: CCCCTCCCTAAAGGAAGGGG
;    |||||:|||  |||:|||||
; S: CCCCTTCCTTTAGGGAGGGG
;
; tail 1272-1292
; Q: CCCCGCCCTAAAAGGACGGGG
;    |||||:|||   |||:|||||
; S: CCCCGTCCTTTTAGGGCGGGG
;
IS605B-1_OS
TTGACTGCACCCCTCCCTAAAGGAAGGGGATTCCCAATTCACCGAGAACCGGACACGGAGACTGGCCCCA
TGCCGCTTACATTCTCTCCAAGGGCTAACACCGCCAGCCCGGCGGCTTTAATGTTTGTCGCGGCGTTGAT
GTCGCGGTCATGGTGTGCACCACATTCGGGGCAGTCCCATTTTCTGACCGACAACGGCAGCGACGACAAG
GTATGCCCGCAACCCGAACAGCGTTTGGAGCTGGGGAACCACTGGTCAATGGCGACCAGTGAGCGACCGG
CCCATTCTGCCTTGTACGCCAACTGGCGCACGAACTCGCCCCAGCCTGCATCGGCAATGGCTTTGCTCAG
TTTCGGGTTGCGGATCATGTTTTTCACATTCAGGGATTCGACGCAGATCACTTGGTTCTCGTTAATCAGT
CTGCGGGACAGCTTGTGCAAGTTGTCCTGTCGGCAATCGGAGATCTTGGCGTGAAGTTTCGCCACCTTCT
GCCGGGCCTTGGCGCGGTTGGCCGAGCCGAGCTTTTTCTTGCTCAGTCGGCGCTGTGCCTTGGCCAGTCT
GGCGGCGTATTTCGCGGTATGGCGGGGATTGCCGACCCGTTCACCCTGGTCGGTGATAAACAGATCTGTC
AGGCCCAGATCAATGCCGGTCATGTTGGGAGTAACCGGCAGTTTGCCGGGCGCGAACTCACACAGGCAGC
TCACAAAGTAACGGCCTGCCGAGTCCTTGGAAACGGTCACGGTACTGGGGTCGCCGGGCAGTTCACGGCT
CCAGCGAATATTCAGCGGGGTTTTGCTCTTGGCCAGGTACAGCTTGCCGTCCCGGTATTTGAAGGCCGAG
CGGGTGAACTCCGCCGACTGGCGGTGCCGCTTGTGCTTAAATACCGGGTACTTGGCACGGCCTTCAAAGA
AATTTTTGAAGGCGGTTTGCTGGTGGCGCAGGCATTGCTGCAAGGGCACACACGACACCTCAGACAGAAA
```

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CGCCAGCTCAGGATCTTTCTTGAGTTCGGTCAGCCGGGCGTTAGCGCCAACGTAGCCGATTTTTTGCTGA
CGCAGCTCAAAAGCATCAGTACGCCAGCGCAGTATCGCGTTATAGACAAAACGCACACAACCGAAGGTCT
GAGCCAACAGCTCAGTCTGTTCGGGTGTCGGGTAAAACCGATATTTATAAGCGCGTTTTGTCATGCGCTT
AGTTTAGTAAACCACTGTATAGATAACCAGTTTAAAAGGAGAGGCGGGAACAGGGGCGGCTGACGCCGCC
GTGCTATCCCTCCCCGCCCTAAAAGGACGGGGTTTCCCGCGCAAAATTG
;  Methanosarcina lacustris Z-7289
; 12 full-length copies 96% identical to the consensus
; GT|GA target, basen on ISC2-1N_ML and cross-genome comparisons
; ISC2-1N1_ML - related nonautonomous family
ISC2-1_ML
CAACTACCCGCCAATAAATTGGCAGGCATGTAATATTGCTTCGGTTGACCAGCTTAAGTATTAATTTACT
ACGTTGGATTTGTCATAACACCTGCAGGTGCTTCCTCAGCTTGTAGCTCTGTTGTATAATATTAAAAGTT
CTGTAGGGTAGGAACGGTGTATTATGCTTAACAAGCATTTCCAACATTAGCGAGAGGAGACACGAAAGTG
CGTTACCGGAAGCAGGATTCATCTTACTTCTGAGATCGGAGAAATCCAATTATGATCTTTGTATTAAACA
AAAACAAACAACCGTTAAGCCCCTGTCATTCAGCAGTTGCCAGAAAATTGCTTAAAACAGGAAAAGCGGT
TATTCATAAAAAATATCCATTCACAATTCGACTAAAAGAGTTGAAAAATTCCGAAAATAAAGCTGAATTC
CGATTAAAAATAGACTATGGAAGCCGACACACAGGTTTAGCTATCTTAAATGGTTCTAAAGTAATTGGGC
TTGCTCAAATCCATCACAAAACCAGTATTAAAAGCAATATGGATAGCCGCAGAGCAATGCGGAGAACTCG
ACGAAATAGAACAACCAGGTATAGAAAACCCAGATTCAACAACAGAAAACGAAAAGAAGGTTGGCTTCCC
CCATCCCTGCAAAGCAGGGTAGACAACATCCAAAATTGGGTTAATAGACTGCAAAAACTGTGTCCTTTGA
CTCATATTTCGTATGAAAATGCCAAATTTGATACCCAGCTAATGCAAAATCCTGAAATTTCAGGTATTGA
ATATCAGCAAGGAGAACTTCAGGGGTATGAAGTTAGGGAATATTTGCTTGAAAAATGGAATAGAAAATGT
GCATATTGCGGAGCAGAAAATGTTCCGCTTGAAATAGAACATATCATACCAAAAGCAAGACATGGAACGA
GCAGAGTTTCCAATTTAACATTAGCTTGCAGAACTTGCAATGAAGCAAAAGGAACTAAGACAGCAGAAGA
ATTTGGGTATCCTGATATTCAAAAACAAGCAAGAATACCACTGAGGGATGCTACACTTGTCACAGCTACA
CGATGGAAAGTCTACAATGTTCTTGCAGAAACTGGACTTGAAGTCGAATGTGGCACAGGTGCAAGGACGA
AGATGAATAGAATCAGGTTGAATCTACCCAAAGATCATCATTTTGATGCAATTTGTGTTGGTGCTTCAAC
ACCAGATAAAATAATATTCAAAACAAATTCAGTACTTCACATAAAAGCAAAAGGTAGAGGATCACATTGC
AGAACCAATCTTGATAAGTACGGATTTCCTAGAGGGTATCTGAGTAGACAAAAGAGTTTCTTTGGATTCC
AGACAGGAGATATTGTTAAAGCGGTTGTTCCGAAAGGAAAATACAAAGGAATTCATTTTGGTGCTGTAGC
TTGTAGAAAAACAGGTTATTTTGATATTAAAAATAAAGAAGGTGTTAGAATAGGGCAGGGAATTAATCAT
AAATATTGCAATATTTTGAGTAGAGCAGATGGATACGAATATGCCACAGAGCATTTGGAAGTTGACGGAA
TTCCTCCTACGACTGAAGTCATAGGCATCCTTCCTTAATTTATCGT
; Methanosarcina lacustris Z-7289
; 38 copies ~99% identical to the consensus
; gt|ga target
ISC2-1N1_ML
CAACTACCCGTCACTAAAGTGGCAGGCATGTAATAGTGCCCCGGTTGACCAGCCTTAGTCTTAATTGACT
ACGTTGGAAATGTCATGATACCTGCGAATGCTTCCTCAGTTTGTAGCTCTATCGTGTAGCATTAAAAGTC
CTGAGAGGTAGGGGCGGTGTGTTACACATAACAAGCATATCCAACATTGGCGAGAGGAGATACGAAAGTA
CGTTACCTGCGGAGGAAACTCGTTTCCAAAGCAGAGTGGAGAAATCCAAACATGAAAGGAATGCCAGAAA
ATTGACGGCATTCCTCTCATGACTAAAGTCAAAAGCATCCTGCCTTATTTTTTCGT
; Clostridium haemolyticum NCTC 9693 plasmid p1Ch9693
; JENX01000125
; GT|AA target
ISC2Y-1_CH
CAACTGCCAACTACCCTAAAGGGTAGTGGCTTGTAAGAAATTGCAAGTCGGTTGAATAGCCTAAGTCTTA
AATGACTACGATTATTAAGAATATATAGGTACTTCAAGATACTTCTCTAGTCTTGAACACTACGCTTTAA
CATTAAACATTTCTGATGGCAGGAAAAGTGTGTTAAAGATACAAAACCTTTTTAATCATTGGCGAAGAGA
ACTTACCACCGAAAGGTGAGGTTAAATTATCTGAAAGGATTAAATTTTATGGTATATGTAATAGATATTA
ATGGGAATCCATTAATGCCAACAAATGAAGCAAAAGCAAGAAAACTTTTAAAGAATAAGAAAGCGATAGT
TAAAGAGTTAAAACCATTTACTGTTCAATTAAATTATGAAACTAGTAATTATACTCAAAGAATAACTTTA
GGAATTGATAGTGGATATTTGAATATAGGTTTTAGTGCAATAACTGATAAGAAAGAATTAATAGTTGGTG
AAGTTAAACTTCTTCAAGGAATAAAAGATAGAATACAAGAAAAAGCAATGTATAGAAGGCAAAGAAGAAA
TAGATTGAGATATAGAAAAGCTAGATGGAATAATAGAACCAAAAGTAAGCACAAAGGTTGGTTAGCACCT
AGCTTACAACATAAATTAGATAGTCATATTAAATTTATTGATAGTTTATATAATGTACTACCTATAACAA
AATGCGTTGTAGAAATAGCAAATTTTGATATACAGAAAATCAAAAACCCTAATATAAGTGGTGAAGAATA
TCAGCAAGGAGAAATGATGGGGTTCTGGAACTTAAGAGAGTACATTCTTCATAGAGATAATCACAAATGT
CAAAATCCTAATTGTAAAAATAAGTCTAAAGAACAGATTTTAGAAATTCATCATATTAAGTATAGAAGTG
```

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AAGGTGGTTCAGATAGTCCTAACAATTTAATTACACTTTGTAGTAAATGCCATACTTCACCTAACCATAA
AAAAGGTAAATTTCTTTATGATTGGTGCATAAATGGAAAAAAAGTTAGAGGATTTAAAGATGCTACTTTT
ATGAGCATGATAAGATGGTATTTAATTAATACTCTTAAAGAAAAACACAGTAACATTTCAATAACCTATG
GCTATATAACTAAAAATCATAGAATTACACATAAAATTAAAAAAACACATTATAATGATGCATTTGCGAT
AGCAAAAGGAATTAATCAAATTAGAAATAATGATATATTTAATGTATCGCAGGCAAGAAGGAATAATCGG
TCTTTAGAAAAGTTTTATGATTGTAAAATAATAGATGTTAGAACTGGTAATAAGGTTTCAGGTGGAGACT
TAAACTGTGGAAGAAGGACTAGAAATAAAAACCATAGTACAGAAAACCTTAGAATTTATAGAGGTGAGAA
GATTTCAAAAGGTCAAAGAAGAATTAGAAAACAAAAATATTTCTATCAGCCAAATGATTTAGTTAGATAT
GAGGGTAAGATTTATACAGTAAAAGGAAGCCAAAATGGTGGTAAATATGTTGCACTTAAAGAGATTAAAA
AAGTGCCTAAAGTGGATTTATTAACACCTTATAAATTCCAAAAAGGATTTGTTTATGAAATATATAAGTA
AAAATCATAGTAAATTTTTATTAATGACACATTTGATATTTGTTTGTAAGTATAGAAAAAAGTTATTAAT
AAGACTTGGTGATGATATTAAAAAACTGTTTTATGCAATAGCAGAAGAAAAAGATTTAAATATAATAGAA
ATGGAAGTAGGCAAAGATCACATCCATTTATTAGTTCAATATTCTCCAACGCAATCAATATTGCAGATTG
TAAGATGGTTTAAACAAATTTCTACTTATAGGGTTTGGAGAGTTGGTAAAACCCAATACTATTTAAATAA
TCATTTTTGGCAAGAAAGAACTTTTTGGAGTGATGGATATTTTGCCTGTAGTATTGGTAAAGTGAGTAAA
GAAACAATAGAAAAATATATACAGCAACAAGGGTAAAAACAATTCATCACCTACCCTAAAGGGTACGTGT
TTTCTTGTTAATGTATTAT
; Anoxybacillus flavithermus TNO-09.006
; 6 copies ~97% identical to the consensus
; GT|GA target site
; 66% identical to ISC2-1_ML in archaea (71% protein identity).
; common termini with IS605B-1_AF:
; IS605B-1_AF    1 CAACTACCCAACGACTAAAGCTGTGGGCTTGCAACTCCC 39
;                  |||| ||||||:||||||||:::||||||||:|| :|||
; ISC2-1_AF      1 CAACAACCCAATGACTAAAGTCATGGGCTTGTAAGCCCC 39
;
; IS605B-1_AF 1305 TTCCTCCCCATGCTTGAAAGCAGGGGTTTCC-TGCGTGA 1342
;                  |||||||||:|||:|:||:|||||||:||||-|||||:|
; ISC2-1_AF   1528 TTCCTCCCCGTGCCTAAAGGCAGGGGCTTCCTTGCGTAA 1566
;
;  Terminal palindromes:
;  head  3 32
;  ACAA-CCCAATGACTAAAGTCA-TGGGCTTGT
;  |||| |||| ||||  |||||| |||| ||||
;  ACAAGCCCA-TGACTTTAGTCATTGGG-TTGT
;
;  tail 1534 1553
;  CCCGTGCCTAAAGGCAGGGG
;  ||| |||||  ||||| |||
;  CCCCTGCCTTTAGGCACGGG
;
ISC2-1_AF
CAACAACCCAATGACTAAAGTCATGGGCTTGTAAGCCCCATGTTGACCAGACCAAGGCTTGAAACAGAGC
CTACGTTATAGATGTCATGACACGTTCGGGTGCTTCTCCAGCCCGTTCCTCTGTCGTGCAAGGTTAAACA
AGCGTGGTGGGTAGCGCTAGTGTCTTGCACATAACAAGCATCTATAACATGGTCGAGGAGAATATGACCT
GCTTTATGCAGAGGAAAGGGGAGAACCCTATGGTTTTTGTGTTAGACACAAACAAACGTCCGCTTGCTCC
TTGTCACGAAGCAGTTGCAAGAAAGCTGTTGAAACAAGGGAAGGCGGCGATTTACAGGCGATTTCCATTT
ACCATCATCTTGAAAAAATCAGTAGACGAATCAGAAATTAAAGCAACATATCGGCTAAAAATCGACTATG
GAAGCAGGCATACAGGATTAGCGATTTTGCGAGGACAAGAAGTGGTATGGTTAGGGCAACTTGACCATCG
CACAGACATCAAGGAAAGAATAGATAAAAGGCGTGCTTTTCGTCGAGCAAGACGAAATCGAAAAACAAGA
TACAGAAAACCACGCTTTCTGAACCGCAAGCGAAAGGAGGGGTGGTTGCCACCATCGCTAGAGAGTCGTG
TGCAAAATATCCAAACATGGGTGGACCGTCTAAAGAAGATATGCCCGATTGGGCATATATCGTACGAGAA
CGCAAAGTTTGACACGCAACTCATGCGAAATCCTGAAATCAATGGTGTAGAGTATCAACAAGGCACGCTA
CAAGGATATGAAGTACGGGAGTATTTGCTTGAAAAGTTTGGGCGGAAGTGTTGTTATTGCGGAAAAGAAA
ATGTTCCACTTGAAGTGGAGCATATCATTCCAAAATCGAGAGGTGGAACAGACCGAGTGGATAACCTATG
TCTTGCCTGTCATGACTGTAATCAGCGCAAAGGAAGTAAGACAGCAGAAGAATTCGGGTATCCGCACATT
CAAAAAATGGTCAAAGAAACCCTAAAGGATACAAGTGCTATCAAACTCGACAGATGGAAAGTGTATGAAG
TGTTAAAGCAGACAGGATGCGATGTCGAGTGTGGAACAGGTGCACGAACAAAAATGAATCGTATTCGTTT
AGGCTTGCCGAAAACACACTATTTTGACGCTTGTTGTGTAGGCGAAAGCACACCACTCCACTTGCATTTC
```

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AAAACAAAAGAAGTGTTATTTATCAAGGCAAAAGGGCGTGGTAGTCGCTCTCGTACAAACCTAGATAGAT
ATGGCTTCCCAAGAGGTTATCTTGCAAGACAAAAATTCTTCTTTGGTTTTCAAACAGGGGACATGGTTAA
GGCTGTTGTCCCAAGAGGGAAATATCAAGGCGTTTGGTTTGGCGAAGTCGCATGTAGAAAGACTGGAAGT
TTCGATATTAAAGGCAAGGACGGAAAGCGTATCGCACAAGGAATAAATTATAGATATGTCCAAGTCATTC
AGCGATTTGACGGATATGCTTATGGAAAGGGGGTGGCGGAACTTGCGTAAGGTGCAATTCCTCCCCGTGC
CTAAAGGCAGGGGCTTCCTTGCGTAAGTTTCGT
; 3 copies, 99%; GT|GA target site
; common termini with ISC2-1_AF:
; IS605B-1_AF    1 CAACTACCCAACGACTAAAGCTGTGGGCTTGCAACTCCC 39
;                  |||| ||||||:||||||||:::||||||||:|| :|||
; ISC2-1_AF      1 CAACAACCCAATGACTAAAGTCATGGGCTTGTAAGCCCC 39
;
; IS605B-1_AF 1305 TTCCTCCCCATGCTTGAAAGCAGGGGTTTCC-TGCGTGA 1342
;                  |||||||||:|||:|:||:|||||||:||||-|||||:|
; ISC2-1_AF   1528 TTCCTCCCCGTGCCTAAAGGCAGGGGCTTCCTTGCGTAA 1566
;
; Terminal palindromes:
; head  27 52
; GCTTGCAACTCCCCAGAAGTGCAAGC
; ||||||| :||:  :||: |||||||
; GCTTGCACTTCTGGGGAGTTGCAAGC
;
; tail  1311 1330
; CCCATGCTTGAAAGCAGGGG
; ||| |||||  ||||| |||
; CCCCTGCTTTCAAGCATGGG
;
IS605B-1_AF
caactacccaacgactaaagctgtgggcttgcaactccccagaagtgcaagcggatgttatcctccttcc
ttcacttggggttgcatcagggcaggttgacaactacccaacgacgcaggtcatgcctgtgtcgttcctt
caacgatgtactcgattccttttcgttgaaggttcatggcaccaattcggtcatcgtttgaggtatatcc
gcatgttcgacaacaaaacgtgtgcgttttcttatttcggtttgctttctctgtatgtccgcattttgga
catgtttgggatgtgtatgttgggtctaccacaatcactttggctcggtgtttgtgtgctttgtactcga
tttttgtcttaaatcataaaacgcccaagataccatttcataccgatggttaacggacacttttttctgt
tctttggcgaacacctgttaaatcctctaacacaaacagcgtgttcttaccataacgctcaacgagtgcc
ttactgatgcaatggttgacatcttgcatccaacggttttctcgttgaccgatttctttaatcttctac
gagcagacggagtttgctttttttgtagttgtctgcggagttgtttatactttgctcgtttgtgtttgat
gtgtctacctttgaaaaataacgtctgtccgtttgaatcataaacagtcgcaagaaaatttacacccata
tctacgccaaccacttggcaaatgtgatgaaggtttgcttcttccatttctttggatacagggatatgga
gaaaccacttttgatgtttattcactaactttgctgttccaaacgtccatgttccgtcgaaatacgtttc
aagttctttcgtttgaaaaggaactttgattcgtccttctaacgtattgatggaaaacaaccctttggtt
aggctgtaatctcgattaaaaacgaggtctatttgcggtttttaaacgcaatctgacaacgcttatgtc
cattggtttggttggttttatatttgcaatcaccgtttttaacacagactgcgccatttgagattttaa
gccaaatgtagagcgaagtttgcggtacgtcatcttgtgaagtttggcttgcacaagggtgttttctttg
tatatcacttccgacaccgcattgcacgcatcacgatatgcttgcatcgtttttgaagaagttgttcct
gttcagatgtcggtaaaatttaatttttgctgttaaagtcaatttcatgtcctcaccacctttcactaa
ttttattttatattttttagcgaaaaataaacaaaaaaacgcattcctccccatgcttgaaagcagggg
tttcctgcgtgattaatcat
; Anaerostipes hadrus strain PEL 85
; Its protein was found among most distant ones from the original set
; 2 copies 97% identical to each other
; Terminal imperfect palindromes:
; head             9 29
; CTCGGCCATTGAATAACCGGG
; |:|||::||| |||::|||:|
; CCCGGTTATTCAATGGCCGAG
;
; tail          1760 1782
; TCTCGGTCATTGAATGGCAGAGA
```

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; |||| |:|||| ||||:| ||||
; TCTCTGCCATTCAATGACCGAGA
;
; termini are similar to these in IS605B-1_AH and IS605B-2_AH
ISC2-1_AH
GTCAGCTTCTCGGCCATTGAATAACCGGGCATGCAAAGAAGTGTGCAAAGTTATTACATAGTCCCCGAAA
GGGCGAGCTGACTAGACTCAGCGCAAGGGAATCCATTTTTGTTGGATACTGAGTGCTACGTCCCAGATAT
CAATACCCGACCCGGTGGTACCCTAGCCGGGAACAGGGTTCAGGCAACGGATGTCTTTCAGGAGAAGAAA
ACACTGACCTGGAGCAAGAAGTATCTGGAACATTGTCGAAGGGTGATCACTCCCATCCGGGAGAGCAGGA
CTTTTGTGTACCTGCTATTACAATACAAGGAGGACCAGCCATGAGCGTATTCGTGGTAGGGCTGAACGGA
TGCCGGCTGATGCCTACATCTGAGAGAAAAGCCCGTTTATTGCTAAAACATGGGAAAGCTTCTGTTTATC
GGAAGGTCCCATTTACCATAAAACTGAATTATAAGACAGGCAGTACGACACAATCTGGCTATCTAGGGAT
CGATACTGGATCACAGCATATCGGAGTATCCGTTGTCCGTGAAGATGGAACAGTCTTACATAAAGAAGAG
ATCGGTCTGAGAGATTCCATGAGTAAAAGAAAACTGATGCAGTCAAGGGCTTCCTCAAGAAGAGGAAGAC
GTCATCGAAAGACCAGATACCGTCATCCCAAATGGAGACCAAAAGCCAAACGTGTCTATTGTGAGATTCC
AGACCGAAAGGGAAGGCACTGGAAGAAAAAAGAGATCACGTTCGCATCCAAACGGGCGAAAGGGTGGCTT
CCGCCATCGCTGCAGTCAAAGACAGATCATCATATCTGGTGGATCAAAAAGCTGCAGGATCTTCTTCCAG
AGGGATACCGTCTTTCGATCGAGCTTGGCCGTTTCGATCCGGCAAGATTGAAAGATCCGGAGATCCATGG
AGAACTGTACCAGAAAGGACCACAGTATGACTATGAAAATGTCCGAGCTTATGTTCTCAATCGTGACAGA
TATACTTGTCAGGTATGTGGGAAGAAAGGCGGAAAACTGCATGTACACCATATCCTGTACCGGAGTCATG
GAGCGACCGATGATCCACAATATATGGCTACGGTGTGCAGCGATTGCCATAACACGGAGAACCATCAACA
GGGAGGCATTCTCTATCAGTGGATGCAGAAGCAGAAGAAATTCACCAGAGGACTGAGAGATGCCACCTTC
ATGAACATCTTACGGAAACGTCTGATAGAAGCATTCCCAGGAGCAACGTTTACCTATGGAAATATCACAA
AGGCAGACCGTGAGAGATTAAGACTTCCAAAAAGTCATGGAAATGATGCGACTGCGATCGCTATCGTAAA
GACTGGGATCATGACAGTAAAAGATAAAGAACCCGTGATCTATATCCAGCAGGTCCGAAGAAAGAAACGT
TCTTTACATGAGGAAACTCCGAGAAAAGGACGTAAGGAACCAAACCGTAAAGCTTCACGATATGATAAGA
ACACGAAAGCAGTCACTGTTACGAAAAGGAAGAATAAGAAGAAGATAACGATCACTGGCTGTCTGTTCGA
TCGTGTAGAGTTGAATGGAAAGAAGGGATGGATCTCTGGCTTTACTGATAAGTCCTGTTATGTAAAAGAT
GAGAATGACCAATATATCCGGACATCTCCAAAATACAAACAGGTCAGTCTGTCAAAACTCAAGATTTTGC
ATCATTGTGGGAACTGGGCGATAGGAGCAAGGCAATCCCTTGGAAAGGGATGATGGCTCAAAAGAGCCTC
CTGCTTTCATCTCGGTCATTGAATGGCAGAGAATTCCCGCAGAATATCTTAA
; Anaerostipes hadrus strain PEL 85
; Terminal imperfect palindromes (identical at both ends):
;
;    head  9 29
; Q: CTCGGTCATTGAATGGCCGAG
;    |||||:|||| ||||:|||||
; S: CTCGGCCATTCAATGACCGAG
;
;    tail 2022 2042
; Q: CTCGGTCATTGAATGGCCGAG
;    |||||:|||| ||||:|||||
; S: CTCGGCCATTCAATGACCGAG
;
IS605B-1_AH
GTGAACTACTCGGTCATTGAATGGCCGAGCATCCGGAGATACTCTTTACAAACAATTTCCGAACTTAGAG
AAATGAGACCAGACTGCATGTATCGTACCATCTAGAAACATCTCTTTTCAGACAGTCCGGATACGGTCAT
GCCGTACCAAGACAGTGGTAGTTCCTATGTTCCATATGACTGGGCAGGCTCATGTTTCAGGTTACACACC
TGATCTTGGGACCGCTTTTTATATGGATGCTGCTTTTTTATAAGCACTGCATCTGTCCGCGTAGATCTGA
CGCAATGCTTCCTGTAGTTTTTTATGCTGATACTCATATTTTTTACTGACCGCAAGGATCTCTTTATCAT
TCGCACGTTCCTTGATATTTACGGAAGCATTATGATCTGCATCATCCTCATGTCCACAGCAGGTACATTT
GAACGCCTTATCTTTACGATTATCTGCATCCAGATTTCCACATACCGGACATACCTGACTGGTGAAGTCC
GGAACAACTTCCATAAAGTCATAGCCTTTCCAGTTTAATGTGATCATCAGCTTCTGTTGAAGTTTTCCTC
TCGCAAACATGGAAAGCTTTCCATTGGCTTTCTTACTTTTGTTGAATTCACGGATATCCAGTTTTTCCAG
AACCGTCATCGTATTCTTTGCCAGATCGTTAAGATAAGAACTGACAGCTTTTTTGATCTCCTGATCGAGC
ATCTGATAATAATGCCGTTTCTTTCGATATGGGACTTCCATAGTCTGCATCATATGTTCCAGCTGATCCA
CCTTCTGGATGAGAGAACGTCTCACATCCTCGGAAAGATCATGACTGTGCAGGTAATGGCAGATCTTACG
CTTTTTATTTCTCAGATCAGATAGTTCTGCAAAGGCAGTCTCCACTTCCTCATGATAGAAATCGATCACC
CGCTTCATAGATCCAACATGTCGTCCGTCAGAAGCATAGAGAGCATCCGTGATCCCGGTATCAACACCGA
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TATAAGTATCTACGGCAGGCTTTTCACGTTTTACGGTATAAGACCATCCGATCCGGAGAACAGGACCACG
CATCTGTAACATGACAGTCCCGCCCAGTCGATTCGCTTCGATCTTATGCAGAGAATGTCTGCTCGTATCG
ATCGGGACTGCGATCCTCTTTCCGCCAGTAGGATCAGAGATCGTGATCACATAGGGCATGACGGTATCTG
TTGACTTTTCCAGTCTCATGAGTCTGGAATCCAGAGGGATTGATACATTACGTAGTTCCGGAACTTTATA
CTCGATAGATCTGGCAGCATAAGCATCCAGAAATCGCACACGGATGTCATAAAACTCTGCATCTGTCATC
GCAGATAATTTCTTCGCACATTCCTTATGGAATTTTTGTCCGATCTTGTTCATCGTCTGGATCATATCAG
TGCGGGATCTGCCCATGATATACATAGCGAACAATACCTTTGACTTTGCAAAGATCCCGAATCCGTCAGC
GATCATATCCAGACGGATGTTATCTAACCGGTTGGATAAGTGAGTAACTGCAACATCGAACGCATTCTGA
CAAAAAGCAGAGTTGATCCCTTTCGGACGGTTCGTCTTTTCCAGTCTTCGTATCTGCGAATCTTTCTTGT
CATTCTTTACGATCTGAAAGAATATAGAAGTTTCCTGATCCAGAAGCCGTATGTTATGATTCACGAGCTT
GATGAACAGTCTCTGCATTTCTTTTAGAGCAGAGCGTTTCTGTACATTCGGTGTTCCATACAAGAAAACA
CTTTTGGTAACGGATGTCTGAAATTCACTGTCTTTTCTGCGTCTTGCCTTTGGCATATAGAACTTTCTCC
TTTCTGTAGGTTTTCTTTCACTATAAATATGAGATATTTTAGAAAAAATAAAAATCATATATAAGAAAAT
GATTCTAGATAATTAGGACTCTAGCCTCTCGGTTATCCATATGAGAATTGTTCGTAAAAACAGAGAAAAA
GCAATGTTTATGCAGTTTATATCATATACACACAGTCATGCTTTTTATCGGTCGCTTTCATCTCGGTCAT
TGAATGGCCGAGGATTCCCGCTCTGCTTTCCTAA
; Anaerostipes hadrus strain PEL 85
; Terminal imperfect palindromes:
; head  9 29
; Q: CTCGGCAATTGAATTACCGCG
;    | |||:|||| ||||:||| |
; S: CGCGGTAATTCAATTGCCGAG
;
; tail 1881 1901
; Q: CTCGTCAATTGAATTACCGAG
;    |||| :|||| ||||: ||||
; S: CTCGGTAATTCAATTGACGAG
;
IS605B-2_AH
GTGAACTACTCGGCAATTGAATTACCGCGCATCTGAAGAAGAACCTCAAACACTCATGTAAAACCATTCC
GATTCTTTTGAAAAGAACCCATCTTATGTGCGAGCGCATAAGACAGAGAGCTTCCCATCGGAACAGTCCG
GATACGGTCATGCCATACCAGGACAGCGGTAGTTCCTATGACCCGTAGTTCCGGCATCTACACAGCTTTC
GCTGCGATTTACGATACCATCCCTTGCGGGTGCTGCTTTTTAAATCGTTTGTTCTGTTCCATATAATAAC
CCTTAAGGGCATTTTGAAGACCTTTCCCGTATCTGTGCTTTTCACAGATATCCATCAGATCTTTGTTTAC
TGCACGTTCCCGGATATTAATGCTTCCTACATGGTCTGCATCATCTTCATAACCGCAGCAAGTACACCTG
AACTTCTTTCCGTCTCGGTTTGCTCTGTCCAGGTTACCGCATACTGGGCAGACCTGGCTGGTAAACTCAG
GAGCTACCTCAATGAAGTCATATCCTTTCCAGTTCAGTGCCCTCATCAGTGCTTCCTGTGTCTTGCCACG
GGCAAAGCAGGAAAACATCCCGTTTACTTTACGGCTCTTCTTGAATTCTTTTATATCAAGACGCTCGATA
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; Halobacteroides halobius DSM 5150
; Belongs to a small group distant from others
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; Two 98% identical copies
; Target site is not clear
; Terminal imperfect palindromes:
; head  5 71
; AGCTATGAAACAG-CTTATAAAATCCTAACTAATGCTATTTAAAGTTAGGTAAAACTGTTTCGTTGCT
; ||| |:|||||||-:|||:  ||:::||| ||::::|| |||:::||  :|-||:|||||||:| |||
; AGCAACGAAACAGTTTTACCTAACTTTAAATAGCATTAGTTAGGATTTTAT-AAGCTGTTTCATAGCT
; tail  1745 1790
; CTGTTTAT--AAACCTAT----AAGTAGTTTTAAATAGGTTTTTATAAGCAG
; |||:||||--||||||||----|| || ||----|||||--|||||||:|||
; CTGCTTATAAAAACCTATTTAAAACTACTT----ATAGG--TTTATAAACAG
;
ISC2-1_HH
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ATAAACCTATAAGTAGTTTTAAATAGGTTTTTATAAGCAGG
; Archaea, Methanosarcina lacustris Z-7289
; consensus was derived from 10 copies that are ~97% identical to it
; GT|GA target site
; It shares common termini with IS605B-1_ML:
; IS605B-1_ML 2 AACTACCCCTCCCTAAAACTTTCGCTTAATAGCTCAAGTTTTTGAGGACGGAGCTT 57
;               ||:||||||||||||||||:|||:|:|||::|||||:||||||||||| |||||||
; ISC2-2_ML   2 AATTACCCCTCCCTAAAACCTTCACCTAACGGCTCAGGTTTTTGAGGAAGGAGCTT 57
;
; IS605B-1_ML 1275 TGACGCTCTCATCTCCCACCTGTCCAATCCGGTAGAACCGGATTGTCCGAGGAAGGAGTCTTCCCGCT 1342
;                  |||||| :|| ||:|||||||||:|   |||||:|:: | |:| |||-|||||||||:|||-|||:|||
; ISC2-2_ML   1608 TGACGCATTCCTCCCCCACCTGCCATTTCCGGCAAGCCGGAAATGT-CGAGGAAGGGGTC-TCCTGCT 1673
;
; Terminal palindromes:
; head    8 52
; CCCTCCCTAAAACCTTCACCTAACGGCTCAGGTTTTTGAGGAAGG
; ||:|||::|||| |:| | |:: ::| | |:| ||||::|||:||
; CCTTCCTCAAAAACCTGAGCCGTTAGGTGAAGGTTTTAGGGAGGG
;
; tail 1620 1664
; CCCCCACCT-GCCATTTCCGGCAAGCCGGAAATGTCGAGGAAGGGG
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GAT
; Archaea, Methanosarcina lacustris Z-7289
; derived from 14 copies ~98% identical to it
; GT|AAA target site
; It shares common terminal parts with ISC2-2_ML:
; IS605B-1_ML 2 AACTACCCCTCCCTAAAACTTTCGCTTAATAGCTCAAGTTTTTGAGGACGGAGCTT 57
;               ||:||||||||||||||||:|||:|:|||::|||||:||||||||||| |||||||
; ISC2-2_ML   2 AATTACCCCTCCCTAAAACCTTCACCTAACGGCTCAGGTTTTTGAGGAAGGAGCTT 57
;
; IS605B-1_ML 1275 TGACGCTCTCATCTCCCACCTGTCCAATCCGGTAGAACCGGATTGTCCGAGGAAGGAGTCTTCCCGCT 1342
;                  |||||| :|| ||:||||||||:|   |||||:|:: | |:| |||-|||||||||:|||-|||:|||
; ISC2-2_ML   1608 TGACGCATTCCTCCCCCACCTGCCATTTCCGGCAAGCCGGAAATGT-CGAGGAAGGGGTC-TCCTGCT 1673
;
; Terminal palindromes:
; head  12 43
; CCCTAAAACTTTCGCTTAATAGCTCAAGTTTTTGAG
; |:| |||||||  |||    |||  ||||||| |:|
; CTCAAAAACTTGAGCTATTAAGCGAAAGTTTTAGGG
;
; tail 1287 1332
; CTCCCACCT-GTCCAATCCGGTAGAACCGGATTGTCCGAGGAAGGAG
; ||||: |||-|  |||||||||   |||||||||  | ||| :||||
; CTCCTTCCTCGGACAATCCGGTTCTACCGGATTGGAC-AGGTGGGAG
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; CP003548
; Nostoc sp. PCC 7107, complete genome
; 4 copies (3 are 100% identical)
; N|TTCA
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; Coleofasciculus chthonoplastes PCC 7420
; FRAGMENT 27308 -> 22901
; gi|193882179|gb|ABRS01000127.1|
; contains insertion of mobile group 2 intron (RT-maturade-HMH)
IS605-1_CC
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; Coleofasciculus chthonoplastes PCC 7420
; FRAGMENT 44903 -> 48819
; gi|193882172|gb|ABRS01000134.1|
; Genome contains 3 copies: 2 copies are 99.95% identical to each and contain
; the mobile group2 intron at the same position; the third copy does not
; have this insertion.
; Terminal palindromes:
; head   18 49
; TTCCCCGACTTCAGCGATAGC--AAGTCGGGGAA
; |||||||||||--|| || ||--|||||||||||
; TTCCCCGACTT--GCTATCGCTGAAGTCGGGGAA
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; tail  3882 3910
; ACAGCGACTTCAACAAAGT--AAGTCGCTGT
; ||||||||||--||   ||--||||||||||
; ACAGCGACTT--ACTTTGTTGAAGTCGCTGT
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; Methanohalobium evestigatum Z-7303
; Consensus was derived from 6 copies ~ 94% identical to it.
; It codes for TnpB (pos 1277-48).
; This transposon shares its 34-bp 5’-terminus with ISC2Y-1_KR and ISC2Y-2_KR.
; The shared region contains an imperfect palindrome (pos 9-31). The
; 3’-terminal palindrome is at position 1330-1354.
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; gi|126630642|gb|AAXY01000001.1| 229256 -> 227033
; It is inserted just upstream the ACTG target site.
; Its 3'-terminus is simialr to that in ISC2-1_MS:
; IS605B-1_MS  1372 1413
; ISC2-1_MS    1641 1682
; Q: CGCGCTATCCTTCCCCGCCCTGAAGGGCGAGGTTTGCCGCGC
;    ||||||||||:|||||| ||||||||:||:||| | ||||||
; S: CGCGCTATCCCTCCCCGACCTGAAGGACGGGGTATCCCGCGC
;
; Terminal imperfect palindromes:
; head  11 56
; Q: TCCCCGCCCTCTT-GCTTCGCTCGTCGCTACGCGAAAAGGACGGGGA
;    ||||||:|||:||-|| | ||     || | ||-||:|||:||||||
; S: TCCCCGTCCTTTTCGCGTAGCGACGAGCGAAGC-AAGAGGGCGGGGA
;
; tail  1384 1403
; Q: CCCCGCCCTGAAGGGCGAGG
;    ||:||||||  ||||||:||
; S: CCTCGCCCTTCAGGGCGGGG
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Protein sequences encoded by the reported transposons (FASTA format).

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MTKRAYKYRFYPTPEQAELLAQTFGCVRFVYNSILRWRTDAFYQRQEKVGYVGANARLTELKKDPELAFL
SEVSSVPLQQCLRHQQTAFKNFFEGRAKYPVFKSKRHRQSAEFTRSAFKYRDGKLYLAKSKTPLNIRWSR
ELPGEPSTVTVSKDSAGRYFVSCLCEFEPSKLPVTSNMTGIDLGLKDLFITDQGERVGNPRHTAKYAARL
AKAQRRLSKKKLGSANRAKARQKVAKLHAKISDCRQDNLHKLSRRLINENQVICVESLKVKNMIRNPTLS
KAIADAGWGEFVRQLAYKAEWGGRSLVAIDQWFPSSKRCSGCGHTLSSLPLTVRKWNCPECGANHDRDHN
AATNIKAAGLAVLALGENVSGMASV
>ISC2-1_MS Marinobacter sp. ELB17
MSVFVLDRRKHPLMPCTERRARLLLDRGRAVVVRAYPFTIRLKDRTGGITQPVRIKIDPGSKTTGIAVVR
ENGQKQHVLALMELAHRGRQISKSLEQRRAFRRRRRNQLRYRAPRFLNRTKPKGWLAPSLQHRVDTTKSL
VNRLRSLVPVVSISQELVRFDTQKMENPEVSGVEYQQGTLLGYEVREYLLEKWGRECAYCTDKDTPLQIE
HIDPKANGGSNRISNLTLACRPCNQEKDRKSLVSFFATSKRLKNHQARLDRILKQCKKPLRDASAVNSTR
WALYQTLKQTGLPVEVGTGGRTKFNRCRLRIPKTHALDAACVGEVEIVEGWDVPTLAIKATGRGSYKRTR
LTKHGFPRGYLMRQKQVQGFQTGDMVRAVVPTGTKAGTWLGRVAVRKTGSFNIQTNSGAIQGISHRHCVL
TQRADGYGYHIQPNQRKEEGDRKNESR
>IS605B-3_KR    Ktedonobacter racemifer DSM 493
MKQTIIAKLKLHTTSEQLAQLRNLQLAYRDALNYVSRYAFEHGKMSSKRRLQEGTYQELRVLYALPAQMA
CSVPRQVGATYKGLWTKYKKHAASRKAGVTKKRYKGLDQPPRYLSPTVTYQQGRDYGFKTEQRVSVLTLS
GRLILPYSGYERHVALIEQGTSIGTAQLWYDQRKKRFYLLVALSLELPDPEPGDLPQVVGVDVGRRYLAV
TSTTTGSGDPLFFLGKEAVAQADHYTRLRKRLQQKGTRGAMRKVRAIEQRERRLKAETNHCISKRIIHRH
PASLIGLEELTDIRERTKPKKHRRTKQGKSSELVSPKQRRENRRRSQWSFAQLQAMIAYKAMLAGSVAIK
VDADYSSQACPRCGHTARANRPGKGLVFVCQNCHYTLHADLVGARNLVLRTLLVWQDWARTGLLSVAPDT
SDSEAKAARLSRYAELRWSPDASPSLQRWGH
>ISC2-4_KR Ktedonobacter racemifer DSM 493
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WVKRLSRWCPVGALSLELVRFDLALLQNPSIEEVEYQRGTLWGTEVRQYLLDKWQHRCTYCQASEVPLEI
DHVSPRSKGGSHRIANLVIACRPCNQAKGDQPLESFLANRPDVLARVQVQRRAPLHDAAAVNSTRWQLYE
RLKALDLPVETGSGGLTKWNRQSRNLPKTHWIDAACTGRSTPERLQIRHVRPWLIQAQGRQARRMVNVDK
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RNDGYAYAQGEAALPPQA
>ISC1-1_KR Ktedonobacter racemifer DSM 493
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LRTILPFTDVVVEDVQAVTRKGKGGTWNGSFSPVQVGKEHLYQLLREMGLTLHLREGWQTKELREQHGLK
KTKSKSKQSFESHAVDSWVLAASISGAEHPTCTRLWYMVPAILHRRQLHRLQASKGGVRKPYGGTRSLGV
KRGTLVEHKKYGRCTVGGVDRKRNTISLHEYRTNTRLTQAAKVETCRVLTWLSWRSWLIRGKHTSSKGKG
SHPS
>IS605B-1_OS    Oceanimonas smirnovii ATCC BAA-899
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SEVSCVPLQQCLRHQQTAFKNFFEGRAKYPVFKHKRHRQSAEFTRSAFKYRDGKLYLAKSKTPLNIRWSR
ELPGDPSTVTVSKDSAGRYFVSCLCEFAPGKLPVTPNMTGIDLGLTDLFITDQGERVGNPRHTAKYAARL
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KAIADAGWGEFVRQLAYKAEWAGRSLVAIDQWFPSSKRCSGCGHTLSSLPLSVRKWDCPECGAHHDRDIN
AATNIKAAGLAVLALGENVSGMGPVSVSGSR
>ISC2-1_ML Methanosarcina lacustris Z-7289
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```
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QKLCPLTHISYENAKFDTQLMQNPEISGIEYQQGELQGYEVREYLLEKWNRKCAYCGAENVPLEIEHIIP
KARHGTSRVSNLTLACRTCNEAKGTKTAEEFGYPDIQKQARIPLRDATLVTATRWKVYNVLAETGLEVEC
GTGARTKMNRIRLNLPKDHHFDAICVGASTPDKIIFKTNSVLHIKAKGRGSHCRTNLDKYGFPRGYLSRQ
KSFFGFQTGDIVKAVVPKGKYKGIHFGAVACRKTGYFDIKNKEGVRIGQGINHKYCNILSRADGYEYATE
HLEVDGIPPTTEVIGILP
>ISC2Y-1_CH-IscB Clostridium haemolyticum NCTC 9693 plasmid p1Ch9693
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KKELIVGEVKLLQGIKDRIQEKAMYRRQRRNRLRYRKARWNNRTKSKHKGWLAPSLQHKLDSHIKFIDSL
YNVLPITKCVVEIANFDIQKIKNPNISGEEYQQGEMMGFWNLREYILHRDNHKCQNPNCKNKSKEQILEI
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SNISITYGYITKNHRITHKIKKTHYNDAFAIAKGINQIRNNDIFNVSQARRNNRSLEKFYDCKIIDVRTG
NKVSGGDLNCGRRTRNKNHSTENLRIYRGEKISKGQRRIRKQKYFYQPNDLVRYEGKIYTVKGSQNGGKY
VALKEIKKVPKVDLLTPYKFQKGFVYEIYK
>ISC2Y-1_CH-IscA Clostridium haemolyticum NCTC 9693 plasmid p1Ch9693
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SILQIVRWFKQISTYRVWRVGKTQYYLNNHFWQERTFWSDGYFACSIGKVSKETIEKYIQQQG
>ISC2-1_AF Anoxybacillus flavithermus TNO-09.006
MVEENMTCFMQRKGENPMVFVLDTNKRPLAPCHEAVARKLLKQGKAAIYRRFPFTIILKKSVDESEIKAT
YRLKIDYGSRHTGLAILRGQEVVWLGQLDHRTDIKERIDKRRAFRRARRNRKTRYRKPRFLNRKRKEGWL
PPSLESRVQNIQTWVDRLKKICPIGHISYENAKFDTQLMRNPEINGVEYQQGTLQGYEVREYLLEKFGRK
CCYCGKENVPLEVEHIIPKSRGGTDRVDNLCLACHDCNQRKGSKTAEEFGYPHIQKMVKETLKDTSAIKL
DRWKVYEVLKQTGCDVECGTGARTKMNRIRLGLPKTHYFDACCVGESTPLHLHFKTKEVLFIKAKGRGSR
SRTNLDRYGFPRGYLARQKFFFGFQTGDMVKAVVPRGKYQGVWFGEVACRKTGSFDIKGKDGKRIAQGIN
YRYVQVIQRFDGYAYGKGVAELA
>IS605B-1_AF     Anoxybacillus flavithermus TNO-09.006
MINHAGNPCFQAWGGMRFFVYFSLKKYKIKLVKGGEDMKLTLTAKIKILPTSEQEQLLQKTMQAYRDACN
AVSEVIYKENTLVQAKLHKMTYRKLRSTFGLKSQMAQSVLKTVIAKYKTNQTNGHKRCQIAFKKPQIDLV
FNRDYSLTKGLFSINTLEGRIKVPFQTKELETYFDGTWTFGTAKLVNKHQKWFLHIPVSKEMEEANLHHI
CQVVGVDMGVNFLATVYDSNGQTLFFKGRHIKHKRAKYKQLRRQLQKKQTPSARRRLKKIGQRENRWMQD
VNHCISKALVERYGKNTLFVLEDLTGVRQRTEKVSVNHRYEMVSWAFYDLRQKIEYKAHKHRAKVIVVDP
TYTSQTCPKCGHTEKANRNKKTHTFCCRTCGYTSNDDRIGAMNLQRKGIEYIVEGTTQA
>ISC2-1_AH Anaerostipes hadrus
MSVFVVGLNGCRLMPTSERKARLLLKHGKASVYRKVPFTIKLNYKTGSTTQSGYLGIDTGSQHIGVSVVR
EDGTVLHKEEIGLRDSMSKRKLMQSRASSRRGRRHRKTRYRHPKWRPKAKRVYCEIPDRKGRHWKKKEIT
FASKRAKGWLPPSLQSKTDHHIWWIKKLQDLLPEGYRLSIELGRFDPARLKDPEIHGELYQKGPQYDYEN
VRAYVLNRDRYTCQVCGKKGGKLHVHHILYRSHGATDDPQYMATVCSDCHNTENHQQGGILYQWMQKQKK
FTRGLRDATFMNILRKRLIEAFPGATFTYGNITKADRERLRLPKSHGNDATAIAIVKTGIMTVKDKEPVI
YIQQVRRKKRSLHEETPRKGRKEPNRKASRYDKNTKAVTVTKRKNKKKITITGCLFDRVELNGKKGWISG
FTDKSCYVKDENDQYIRTSPKYKQVSLSKLKILHHCGNWAIGARQSLGKG
>IS605B-1_AH     Anaerostipes hadrus
MIFIFSKISHIYSERKPTERRKFYMPKARRRKDSEFQTSVTKSVFLYGTPNVQKRSALKEMQRLFIKLVN
HNIRLLDQETSIFFQIVKNDKKDSQIRRLEKTNRPKGINSAFCQNAFDVAVTHLSNRLDNIRLDMIADGF
GIFAKSKVLFAMYIMGRSRTDMIQTMNKIGQKFHKECAKKLSAMTDAEFYDIRVRFLDAYAARSIEYKVP
ELRNVSIPLDSRLMRLEKSTDTVMPYVITISDPTGGKRIAVPIDTSRHSLHKIEANRLGGTVMLQMRGPV
LRIGWSYTVKREKPAVDTYIGVDTGITDALYASDGRHVGSMKRVIDFYHEEVETAFAELSDLRNKKRKIC
HYLHSHDLSEDVRRSLIQKVDQLEHMMQTMEVPYRKKRHYYQMLDQEIKKAVSSYLNDLAKNTMTVLEKL
DIREFNKSKKANGKLSMFARGKLQQKLMITLNWKGYDFMEVVPDFTSQVCPVCGNLDADNRKDKAFKCTC
CGHEDDADHNASVNIKERANDKEILAVSKKYEYQHKKLQEALRQIYADRCSAYKKAASI
>IS605B-2_AH     Anaerostipes hadrus
MARAYRRKDSTFETSPVKSVFLYGEPNKAKLHLLSRMQQRFCELANENIRTICETDGLFLQLVKNDKKDS
VVRKLEKQFRPAGLNSAFCQAAFDYAFTRLSNRINTIRKDMYAEDQTIFTQSKVLFAMSLMRQSKKEMSA
VMKDLANRKNGRNISFYKDCADTLDSLDEDEFRFLMQELVDSYAVHTAEYRIPHISRTEVPLDSRLMRIE
ESADIKAPYVISVTDPFNRNKRFIVPLNTSRHSLHKIKSNKMAGSVFVCVKNGNLRVGWAYTRSVKQPKT
SVIRGVDTGITDVFHTSDGNAIGSMKPVLDFYHSTVEPSFAGLSDLRNKKRSISHYLRHHKALPEDVRRS
LIQKMDRLDEMMQTMNAPYRKKRRYYGLLDQEIRKSVTGYMDGLKRDTLTVIERLDIKEFKKSRKVNGMF
SCFARGKTQEALMRALNWKGYDFIEVAPEFTSQVCPVCGNLDRANRDGKKFRCTCCGYEDDADHVGSINI
RERAVNKDLMDICEKHRYGKGLQNALKGYYMEQNKRFKKQHPQGMVS
```

```
>ISC2-1_HH Halobacteroides halobius DSM 5150
MILRQRREVPIMEVAEMPNKYAFVLDSKGKLLDPTKSKKAWYLIRKGKASLVEEYPLIIKLKREVPKDQV
NSDKLILGIDDGTKKVGFALVQKCQTKNKVLFKAVMEQRQDVSKKMEERRGYRRYRRSHKRYRPARFDNR
SSSKRKGRIPPSILQKKQAILRVVNKLKKYIRIDKIVLEDVSIDIRKLTEGRELYNWEYQESNRLDENLR
KATLYRDDCTCQLCGTTETMLHAHHIMPRRDGGADSIYNLITLCKACHKDKVDNNEYQYKDQFLAIIDSK
ELSDLKSASHVMQGKTWLRDKLSKIAQLEITSGGNTANKRIDYEIEKSHSNDAICTTGLLPVDNIDDIKE
YYIKPLRKKSKAKIKELKCFRQRDLVKYTKRNGETYTGYITSLRIKNNKYNSKVCNFSTLKGKIFRGYGF
RNLTLLNRPKGLMIV
>ISC2-2_ML Methanosarcina lacustris Z-7289
MLVFVINQNKKPLMPCKPSKARKLLQAGKAKVVRNTPFTIKLLFGSSGYTQPVIAGMDTGSKVVGCAAIA
NGKVLYQSEIYLRENVSKKMEQRKMYRRTRRGRKTRYRPARFDNRGNSRREGRLAPSIKSKLESHFREKR
FVESLLPVTGWKVELASFDIHKITNPEVSGVGYQEGDLKGFYNVKAYVLDRDGYTCQHCMGKSKDSRLHC
HHIVFRSQKGSDAPENLITLCETCHKALHNGEFKLSGNKSKTKHATEIGILKSQIRKSGWSFAETFGYET
KYRREQVLKLLKTHYFDAVAICCRDDQKVEVEDSVFLKRNVPAGDYQQRRGKRSEKKIPTGKLFGLRKFD
LVKTENGIGFIRGKRSSGYFSISDIFGNKISDSVNVKKKCRRLSARSTTLVQMVQMTHSSPTCHFRQAGN
VEEGVSC
>IS605B-1_ML    Methanosarcina lacustris Z-7289
MLRGNRYRIYPNKEQKALMEKHFGSCRFVYNKLLEIKSLMYKKFRISLSEFDLNNHLLVLKEVYPWLKEV
NAGALQQASRNLNKAFTNFFNFGFGYPQKKKKKDHHFSFQIPQHYSLDTSISKVLLPKFGWIKVKMHREI
SKGSLKTITISRTPTGKYYISFLTNDGEKLPEKQEFSHATLIGIDVGVTTFATLSTGEKIDNPKFLKNSL
ERLKCLQIRVSKKVKGSKNRRKAVYKLTKIHEKISNQRHDFQHKVSNRLISENQAIAVETLNIKGLKKNH
KLAQVISDSAWYSFVLKLTYKAEWVGKTILKIGMFEPSSKTCNVCGYKLKELSLDIREWQCPDCKNTHDR
DINAAINIKKIAVGTTV
>IS605-1_NS-TnpB Nostoc sp. PCC 7107
MTFRLYPNEKTELILRYHRKLHKDLYNAAVNNRFNQYKIYNHKVDYFEQQNCLPAFKDVWVEYKELPSHA
LQATLKRVDFAFERWFKGLGKRPRFKSIRHYSGWTYPDCAGFKVESEGENGYLNLSKIGRIQMRGQALGW
GKSTTCTIVYRNSKWYASITVDVLDQALKPKVLPVGAIGIDLGCKAALSITDGENHQQIDAPKFLRNAEQ
KIKKASKEKRRKRAPNRNKKIKASRRYKKAQSKVTKLVRKVGNQRQNWVHQVAAEIVSGNSFVATEKLEV
KNMTSKAKKGKRKKQKAGLNKSILDVAFGMLRNTIKYKVEQIGGVFVEVPTKKVKPSQTCPKCGHQHKKT
LDIRVHNCVVCGYVQDRDIAAAEVMLYWSKGTLPGLGTSLVVAESPSSPTSTGKRKQSGSMRQLGAKKRQ
KSTEKLAKNELGDVETHSSGEANCG
>IS605-1_NS-Y1  Nostoc sp. PCC 7107
MLSRKGSHAVFSIHLHFVFITKYRKKVITAPILERMHEIFANICIKTNCILVEFSGEEDHVHLLVDYHPD
NNISDFTSSLKSASSRVIRKEFKEHIEKFYWKPLFWSSSYYVASSGGAPIDQLRQYIKEQDAPTE
>IS605B-1_ME    (1277..48) TnpB
MYLTQKNHLRADKQTYETLKRLTKLSKNLYNFTLYTIRQYFFNYGKYLNKNTAYHTVKENENYRLMPSQV
AQNTVETVDGSMKSFFKLLDKKRKGEYEKPVSLPKYLDKDGNFICTFKKDQLKVIDDKIRLSLGPEYGRT
YGTRYLYFKIPDNIIGQYINQVRIVPKYKGRWFEIEFVYHEDGEIAELDYNSHLSIDLGVDNFATCVTTS
GTAFILDGRGIKSYNRWWNKEKSRLQSVYDKQNVDDGIKMDRFSNKRFWKINDFMNQCVNHIVKHCLENR
IGNIVIGEMKEIKQEQNIGKKNTQNFQTIPFARFKQKLASKCEYHGIKYHEVDEAYTSKVDALALEPIRK
HKKYLGKRPKRGIFQSSTGRLINADINGALNILRKVIGDSLAGITDSGDVNSPGRIRLSR
```

Supplemental Figure 2.

***ISC2-1_KR* transposon is inserted into the middle point of the GTGG target site without any target site duplications.** In the pairwise alignments of three repeats (Rep1, Rep2, and Rep3) harboring copies of *ISC2-1_KR* with the sequences of the corresponding copies of the repeats free of the transposon insertions, the *ISC2-1_KR* sequences are in red, while the identified GTGG target site sequences are in green. The internal parts of *ISC2-1_KR* copies are marked by ‘N’s. In the alignments, coordinates of the corresponding sequences in GenBank are indicated in the top sections, The Rep1 and Rep2 insertion-free sequences are replaced by their consensus sequences.

1. Insertion of *ISC2-1_KR* into Rep1

```
S: Rep1 (consensus from 3 copies))        1  144
Q: gi|297545792|gb|ADVG01000005.1|    517283  515550
Identity = 88%

S: CTCACCCGTATTACAGTAGAACANGCGTTCTCATTCATGAGAACCGCAGTGCATAAGAAGGCAGAGCAGG
   ||||||||||||||||||||||| ||||||||:| |:||||||||||||:||||||||||| | ||||||
Q: CTCACCCGTATTACAGTAGAACATGCGTTCTCGTACGTGAGAACCGCAGCGCATAAGAAGGGATAGCAGG

S: GT--------------------------------------------------------------------
   ||
Q: GTCAGGTACCTCATGCCTAAAGGCAGGGGCTTGTGAAAGCAAGCTCGGACCTGTCCAGACTTAGCCATGG

S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

S: ----------------------------------------------------GGATGTTGAGTCGCTCCA
                                                       |||||||||||| |||||
Q: GCTCCTCCCCATGGCTAAAGCCAGGGGTCCCCGTATGGCGCAATTTTTAGATGGATGTTGAGTCCCTCCA

S: TCCTTCCTGCTCTGCTGGCACTGCACGTGCAACAGATAGAGCCTGGCTCTCTGT
   :|| ||||| | |||||||:||||||||||||:||||:||||:|||||||||||
Q: CCCATCCTGGTATGCTGGCGCTGCACGTGCAATAGATGGAGCTTGGCTCTCTGT
```

2. Insertion of *ISC2-1_KR* into Rep2

```
S: Rep2 (consensus from 10 copies)         1 144
Q: gi|297554026|gb|ADVG01000001.1|    2707943 2709664
Identity = 87%

S: TGAGACGCACCGTTGCAAGCACGGGCGGCACCCTSGTCGAAGTTCCCACACGCACGACGGCGCTGAGCCA
   ||||||||||||||||||||||||||||||:||| :||||||||||||||||||||||:|| || ||:||
Q: TGAGACGCACCGTTGCAAGCACGGGCGGCATCCTCATCGAAGTTCCCACACGCACGACAGCCCTCAGTCA

S: AT--------------------------------------------------------------------
   :|
Q: GTCAGGAACCCCATGCCTAAAGGCAGGGGCTTGCGTAAGTAAGCCTGGACCTGACCAGTCTCAGCCAGAG

S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

S: ----------------------------------------GGTGTCATGGCTGTGGCAAGCGGGTCAAGA
                                           ||||:||||||||:|||||| :||||||:|
Q: GTCTAAAGCCAGGGGTCCCCGCATTGCGCAATTTTATGATGGTGCCATGGCTGCGGCAAGAAGGTCAAAA

S: AGCCGCTYTCTCAGCGCTGGCAYCAGTGCGCATGTGGCGTGG
   |||||||+||:|||||||||||+|||||:|| ||||||||||
Q: AGCCGCTCTCCCAGCGCTGGCACCAGTGTGCCTGTGGCGTGG
```

3. Insertion of *ISC2-1_KR* into Rep3

```
S:      gi|297546893|gb|ADVG01000004.1|       512487 512623   (Rep3, only one copy)
Q:      gi|297549204|gb|ADVG01000003.1|      1807417 1805686
Identity = 92%


S: ATGCTATGTTCCCATAAAGATCATTCACGATCCCCCGTCCATCTGCTGATGGAAGACGATTACCAACGAG
   |||||||||||:||||||||||:||||||||||||||||||||||||||||||||||||| ||||||||:
Q: ATGCTATGTTCTCATAAAGATCGTTCACGATCCCCCGTCCATCTGCTGATGGAAGACGATGACCAACGAA

S: AC--------------------------------------------------------------------
   ::
Q: GTCAGGAACCCCATGCCTAAAGGCAGGGGCTTGCGTAAGTAAGCCTGGACCTGACCAGTCTCAGCCAGAG


S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN


S: ---------------------------------------------------------GGTGAAAGGAGAT
   ---------------------------------------------------------|||||||||||||
Q: TCCTCCCCATGTCTAAAGCCAGGGGTCCCCGCATTGCGCAATTTTATGATGGTGAATGGTGAAAGGAGAT

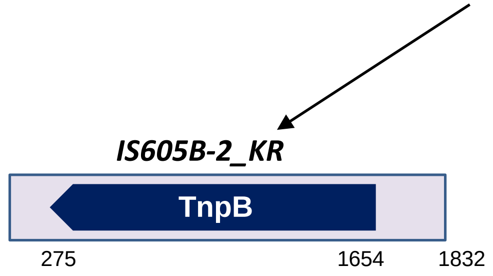
S: GCCCATGACCGATGCGTTCTCGCGGACCAGCACACGAAACTCCAAATGGATC
   :||||||||||||||||||||||||:||||:||:|||||||||||:||||||
Q: ACCCATGACCGATGCGTTCTCGCGGGCCAGTACGCGAAACTCCAAGTGGATC
```

Supplemental Figure 3. The *ISC2-2_KR* and *IS605B-2_KR* transposons have similar 3'-terminal regions. A, The Censor map of 8 regions similar to the 64-bp 3'-terminus of the *ISC2-2_KR* consensus sequence (positions 1588-1651). B, The 1832-bp consensus sequence of the *IS605B-2_KR* transposon was obtained based on multiple alignment of expanded DNA sequences of the eight regions similar to the *ISC2-2_KR* terminus. It contains one ORF encoding the TnpB protein (pos. 1654-275). Although this protein was not similar to CDD (NCBI BLAST), it is similar to a number of TnpB proteins encoded by transposons annotated in ISfinder (www-is.biotoul.fr) as members of the *IS200/IS605* superfamily. The best BLASTP hit was to TnpB encoded by the *ISCbt* transposon (E=8e-33). The proper classification of this protein was also supported by HHpred. It contains the OrfB/TnpB and Zn-ribbon (deactivated cysteines) domains. C, Pairwise alignment of the similar 3'-termini of the *IS605B-2_KR* and *ISC2-2_KR* transposons.

A)

```
gi|297545792|gb|ADVG01000005.1|  561089 561150  ISC2-2_KR    1588 1651    d   0.8154
gi|297554026|gb|ADVG01000001.1| 1548921 1548982 ISC2-2_KR    1588 1651    c   0.8154
gi|297554026|gb|ADVG01000001.1| 2166815 2166876 ISC2-2_KR    1588 1651    c   0.8154
gi|297549204|gb|ADVG01000003.1| 1191713 1191774 ISC2-2_KR    1588 1651    d   0.8154
gi|297546893|gb|ADVG01000004.1| 1576276 1576337 ISC2-2_KR    1588 1651    c   0.8308
gi|297546893|gb|ADVG01000004.1| 2626842 2626903 ISC2-2_KR    1588 1651    d   0.7969
gi|297551548|gb|ADVG01000002.1| 1958579 1958640 ISC2-2_KR    1588 1651    c   0.7969
gi|297554026|gb|ADVG01000001.1|  307670 307731  ISC2-2_KR    1588 1651    c   0.7778
```

B)



C)

```
IS605B-2_KR     1773 1832
TwoNucs-2_KR    1595 1653    Identity = 77%
Q: AGAGGCGGCGATTCATCCCCGGCATCAATGACCGGGGCTTTCTCGCCGCGTTCTCTGTAA
   |||||||||:|||| |||||| : | || :: ||||||||:||:|||||-||||||||:|
S: AGAGGCGGCAATTCCTCCCCGCTCTAAAGAGGCGGGGCTTCCTTGCCGC-TTCTCTGTGA
```

Supplemental Figure 4.

A, Censor map of *ISC1-1_MA* transposons in the *Microcystis aeruginosa NIES-843* genome. First three collumns: GenBank accession number and coordinates of DNA regions significantly similar to the *ISC1-1_MA* consensus sequence. Columns 5-6 show coordinates of the consensus part similar to the corresponding GenBank region. In the column 7, “d” and “c” mark the orientation of the GenBank regions (d - direct, c – complementary). The DNA identity and Censor scores are listed in columns 8 and 9. Four copies of the transposon, including two with internal deletions are shaded in gray. **B**, Pairwise alignment of similar 3’-termini in *ISC1-1_MA* and *IS605B-1_MA*. The ATGA target sites are in bold. **C**, Pairwise alignments of DNA sequences of the *ISC1-1_MA*-containing locus, 70-bp flanks, with orthologous loci free of the inserted transposon identified in *Microcystis aeruginosa 9717*. The GenBank accession numbers and loci positions are listed above the alignment. The inserted transposon sequence is in red; its target site is in blue. The transposon’s internal portion is schematically marked by “N”s. **D**, Map of two copies of *ISC1-1_MA* in the *M. aeruginosa 9717* genome. Each of the 140-bp loci harboring the transposon is aligned with its ortholog identified in the *M. aeruginosa NIES-843* genome. **E**, Pairwise alignment of twelve 140-bp loci harboring the *IS605B-1_MA* transposons in *M. aeruginosa NIES-843* with their transposon-free orthologs identified in *M. aeruginosa 9717*. The transposon and target sites sequences are in red and blue, respectively.

A) Map of *ISC1-1_MA* copies in the *Microcystis aeruginosa NIES-843* genome

AP009552	54468	54513	ISC1-1_MA	1321	1376	c	0.8776	82
AP009552	496061	496107	ISC1-1_MA	1320	1376	c	0.8800	84
AP009552	875264	875302	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	**974217**	**975592**	**ISC1-1_MA**	**1**	**1376**	**c**	**1.0000**	**4128**
AP009552	1245946	1245984	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	1250298	1250336	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	1380060	1380098	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	1415903	1415941	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	1439543	1439581	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	1482146	1482184	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	1594189	1594227	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	1600904	1600940	ISC1-1_MA	1341	1376	c	0.8649	72
AP009552	2071377	2071415	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	2107139	2107177	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	2257893	2257947	ISC1-1_MA	1319	1374	c	0.8772	112
AP009552	2352189	2352226	ISC1-1_MA	1341	1376	d	0.8947	80
AP009552	2494260	2494298	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	2667744	2667782	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	2681387	2681425	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	**2687565**	**2687842**	**ISC1-1_MA**	**1099**	**1376**	**c**	**0.9640**	**764**
AP009552	**2688337**	**2689277**	**ISC1-1_MA**	**1**	**941**	**c**	**0.9447**	**2458**
AP009552	2942200	2942238	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	2964062	2964100	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	3181176	3181214	ISC1-1_MA	1338	1376	c	0.8750	78
AP009552	3427549	3427587	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	3443118	3443156	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	3477923	3477961	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	3709177	3709215	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	3711190	3711228	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	3834187	3834225	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	3870195	3870233	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	3906002	3906048	ISC1-1_MA	1320	1376	c	0.8800	84
AP009552	3912540	3912578	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	4164055	4164093	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	**4504686**	**4506060**	**ISC1-1_MA**	**1**	**1376**	**d**	**0.9884**	**4012**
AP009552	4574961	4575006	ISC1-1_MA	1321	1376	c	0.8776	82
AP009552	4688372	4688410	ISC1-1_MA	1338	1376	c	0.8500	72
AP009552	4693539	4693584	ISC1-1_MA	1321	1376	d	0.8776	82
AP009552	4916791	4916829	ISC1-1_MA	1338	1376	d	0.8500	72
AP009552	5031160	5031198	ISC1-1_MA	1338	1376	d	0.8500	72

AP009552	5230157	5230202	ISC1-1_MA	1321	1376	d	0.8776	82
AP009552	5506665	5506711	ISC1-1_MA	1320	1376	c	0.8800	84
AP009552	**5688487**	**5688736**	**ISC1-1_MA**	**1127**	**1376**	**c**	**0.9520**	**666**
AP009552	**5688737**	**5688928**	**ISC1-1_MA**	**1**	**192**	**c**	**0.9635**	**526**
AP009552	5800782	5800828	ISC1-1_MA	1320	1376	d	0.8800	84

B) The *ISC1-1_MA* and *IS605B-1_MA* transposons have similar 3'-termini.

```
ISC1-1_MA      1321 1376
IS605B-1_MA      1280 1325     Identity = 88%

S: 1321 aaagccgccctccgctatcgctaaa-gggcggggtttcagacccatttttcgatga 1376
        |||||||||----------|-||||- ||||||||||||||||||  ||||||||||
Q: 1280 aaagccgcc----------g-taaaacggcggggtttcagacccaaattttcgatga 1325
```

C) *ISC1-1_MA*

```
Microcystis aeruginosa NIES-843 DNA (complete genome)
Microcystis aeruginosa 9717 (WGS project CAII01000000)

Locus 1:
Q: AP009552                          4504616 4506130
S: gi|389720214|emb|CAII01000056.1|   5228    5371

Q: CTATCTTTTGTAGTCGATCGAGGGGGACAGGGATTATAATGCCCTTAGCCTAGCGTAGCAAGGGATAATT
   |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
S: CTATCTTTTGTAGTCGATCGAGGGGGACAGGGATTATAATGCCCTTAGCCTAGCCTAGCAAGGGATAATT

Q: GTCACTAACCCCGCCCTAAAAGCGACGGAGCTTGCCTAGACCAATTTAGGCGACGCAAGTAGAGACTACC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: TTAGCAAGATTCAGTTAATTCGTCGTTCTAACGGTTTAATTGTTTCTCGCTAACTTATATAAAGCCGCCC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: TCCGTTATCGCTAAAGGGCGGGTTTCAGACCCATTTTTTCAATGACCGGACTAAGTATCGATCGCCAGAA
   -----------------------------------------|||||||||||||||||||||||||||||
S: -----------------------------------------ATGACCGGACTAAGTATCGATCGCCAGAA

Q: AAAAAAGCATAAACAGGGCCAAACAAAAGCTGATAGTCCCCCGCT
   |||||||||||||||||||||||||||||||||||||||||||||
S: AAAAAAGCATAAACAGGGCCAAACAAAAGCTGATAGTCCCCCGCT
```

D)

```
Microcystis aeruginosa 9717 WGS project CAII01000000
Microcystis aeruginosa NIES-843 DNA, complete genome

gi|389715910|emb|CAII01000642.1|   12639 14010   ISC1-1_MA        1 1372    c   0.96
gi|389718374|emb|CAII01000290.1|   21575 22945   ISC1-1_MA        1 1372    c   0.96

Locus 1:
Q: 389715910    14080   12572
S: AP009552     2477064 2477200

Q: ATCTCGGAAAACCAGACAATAAACAACGGCTTCTTTGTGCTTCTCAACAGCGAACACCAGCTATATCGTC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||---
S: ATCTCGGAAAACCAGACAATAAACAACGGCTTCTTTGTGCTTCTCAACAGCGAACATCAGCTATATC---
```

```
Q: ACTAACCCCGCCCTAAAAGGGACGGGGCTTGCCTAAACCAATTTAGGCGACGCAAGTAGAGACTACCGCA
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: GCAAGATTCAGTTAATTCGTCGTTCTAACGGTTTAATTGTTTCTCACTAACTCATATAAAGCCGCCCTCC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: GCTATCGCTAAAGGGCGGGGTTTCAGACCCAGTTTTTCAATGAAAATTCTCAGAACCCAAACCCTGCGCG
   ---------------------------------------|||||||||||||||||||||||||||||||
S: ---------------------------------------ATGAAAATTCTCAGAACCCAAACCCTGCGCG

Q: GTCCCAACTACTGGAGTATTCGTCGCGACAAGCTCATTG
   |||||||||||||||||||||||||||||||||||||||
S: GTCCCAACTACTGGAGTATTCGTCGCGACAAGCTCATTG


Locus 2:
Q: 389718374   23015   21505
S: AP009552    2390880 2391019

Q: GTAGCGATCGAGTTGCCAGCAGCCCACCTCGCGACGTAAGATAACAGCAAAACTGTCCCGGATTTTCCCT
   |||||||||||||||||||||||||||||:||||| |||||||||||||||||||:|| :||||||||||
S: GTAGCGATCGAGTTGCCAGCAGCCCACCTTGCGACCTAAGATAACAGCAAAACTGCCCGAGATTTTCCCT

Q: GTCACTAACCCCGCCCTAAAAGGGACGGGGCTTGCCTAGACCAATTTAGGCGACGCAAGTAGAGACTACC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: TTAGTAAGATTCAGTTAATTCGTCGTTCTAACGGTTTAATTGTTTCTCACTAACTTGTATAAAGCCGCCC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: TCCGTTATCGCTAAAGGGCGGGTTTCAGACCCAGTTTTTCGATGAGTGATCAAATCCTTTCTTCCCTCTC
   -----------------------------------------|||||||||||||||||||||||||||||
S: -----------------------------------------ATGAGTGATCAAATCCTTTCTTCCCTCTC

Q: CCTAGAACAAAAACGACAAAACCTGCGCCACCAAAGGCGAT
   |||:|||||||||||||||||||||||||||||||||||||
S: CCTGGAACAAAAACGACAAAACCTGCGCCACCAAAGGCGAT
==========================================================================
```

E)

IS605B-1_MA transposon is inserted at the N|ATGA target sites.

S: Loci with inserted copies of *IS605B-1_MA* are from the *Microcystis aeruginosa NIES-843* DNA, complete genome;
Q: Orthologous loci without the transposon insertions are from *Microcystis aeruginosa 9717* WGS project CAII01000000.

```
Locus 1:
S: AP009552                           497455  495991
Q: gi|389716044|emb|CAII01000622.1|   9241    9384

S: TTCTGGTTCCCGACAATCGGCCGGCAAAGAACTAAGATCAAGATCAAGGAATCCCCTACCGTTAAAGCTG
   ||||:||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Q: TTCTAGTTCCCGACAATCGGCCGGCAAAGAACTAAGATCAAGATCAAGCAATCCCCTACCGTTAAAGCTG

S: TTGACATCCTCACCGCCGTAAAACGGACGGCGATTCCCAAACCTCACGATTTGAGTTTCTGCTTCTTTCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------
```

```
S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGCGCTAGTATTTAACGGTAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAATTTTCGATGAAATTA
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAAATTA

S: CCCCGTCTTGCCACTTTAATCATTGGTCTGAGCTTTATTTTCGGATTAATGTTGTGGTTAGTCAA
   ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: CCCCGTCTTGCCGCTTTAATCATTGGTCTGAGCTTTATTTTCGGATTAATGTTGTGGTTAGTCAA


Locus 2:
S: AP009552                           3297568 3296112
Q: gi|389717700|emb|CAII01000397.1|   13166   13301

S: ATGAATTGTCTTTAACCCAGCCAAGAAATTGCTTTTCGGCACTACTGCCGGTAACACATCTAGGAAAACT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Q: ATGAATTGTCTTTAACCCAGCCAAGAAATTGCTTTTCGGCACTACTGCCGGTAACACATCTAGGGAAACT

S: TTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTAGGTTTCTGCTTCTTTCCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GTTCTAATATTTAACAGTAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAAATTTCCGATGAAAAAA
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAAAAAA

S: TATATTGACAATCAAACCAATAAATGATAGAGGGAGATAAATCCCCTGTTGCCAGGG
   ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Q: TATATTGACAATCAAACCAATAAATGATATAGGGAGATAAATCCCCTGTTGCCAGGG

Locus 3:
S: AP009552                           2045725 2044261
Q: gi|389719931|emb|CAII01000092.1|   2994    2851

S: AACTTTAACCAGTATGAAACGAGCGGGGGCCGATTTGATTTTGACCTATTTTGCTGCCGATGTGGCATTA
   ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: AACTTTAATCAGTATGAAACGAGCGGGGGCCGATTTGATTTTGACCTATTTTGCTGCCGATGTGGCATTA

S: TTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTAGGTTTCTGCTTCTTTCCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCGCTAAGATTTAACAGCAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAAATTTCCGATGAAACAG
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAAACAG

S: GAAAGCCGATTTTAGGGTTTTTGCCAGCGAAATTGATAGACATTATCCTGCGCTCCCCATACCTG
   |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Q: GAAAGCCGATTTTAGGGTTTTTGCCAGCGAAATTGATAGAAATTATCCTGCGCTCCCCATACCTG


Locus 4:
S: AP009552                           2436022 2434556
Q: gi|389715322|emb|CAII01000736.1|   476     333

S: ATGCCTAATGGAAGACTAACCTACAAGCGAGGAGAGATATGGTGGGTCGATCTGAAACCCGTTGTTGGTC
   |||||||||||||||||||||||:|||||||||||||| |||||||||||||||||||||||| |||||:
Q: ATGCCTAATGGAAGACTAACCTATAAGCGAGGAGAGATCTGGTGGGTCGATCTGAAACCCGTTCTTGGTT

S: TTGACATCCTCGCCGCCGTAAAACGGACGGCGATTCCCAAACCTCACGATTTGGGTTTCTGCTTCTTTCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------
```

```
S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: ATGTGCTAAGATTTAACAGCAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAAATTTTCGATGAAAC
   ---------------------------------------------------------------|||||||
Q: ---------------------------------------------------------------ATGAAAC

S: CGATAAAGAACGCCCTTGCCTGATTTTACAAAACGATATGGGCAATCAAAATGGAACAACGACAATA
   ||||||||||||:|||||||||||||||||||||||||| ||||||||||||||||||||||||:||
Q: CGATAAAGAACGTCCTTGCCTGATTTTACAAAACGATATTGGCAATCAAAATGGAACAACGACAGTA

Locus 5:
S: AP009552                          5554110 5552646
Q: gi|389716977|emb|CAII01000497.1|  3824    3681

S: CGTCGATCGATCTTGAGGGACTTTGGCGGACATATAGCATTTATATTTGAGTTGTGGACATTTTGCTGGA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: CGTCGATCGATCTTGAGGGACTTTGGCGGACATATAGCATTTATATTTGAGTTGTGGACATTTTGCTGGA

S: TTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTAGGTTTCTGCTTCTTTCCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCGCTAAGATTTAACAGCAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAAATTTCCGATGATTTTA
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGATTTTA

S: GATTTTGGCTGGATTGGCGGAGTAGAAGGCAATTGGCGAAAATATAAAGCTCCCCGACAATTTTA
   ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Q: GATTTTGGCTGGATTGGCGGATTAGAAGGCAATTGGCGAAAATATAAAGCTCCCCGACAATTTTA

Locus 6:
S: AP009552                          2696486 2695021
Q: gi|389720349|emb|CAII01000032.1|  739     882

S: CTGCGGATTGGATGGTACTTTGGCACTGAGCGGTTTGAGTCAGAGGGTGAGTTTTTCCGAGTCACGATTG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: CTGCGGATTGGATGGTACTTTGGCACTGAGCGGTTTGAGTCAGAGGGTGAGTTTTTCCGAGTCACGATTG

S: TTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTGGGTTTCTGCTTCTTTCCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGCGCTAGTATTTAACAGCAAAGCCGCCGTAAAACGGCGGGGTTTCAGACCCAAAATTTCCGATGATGCA
   --------------------------------------------------------------||||||||
Q: --------------------------------------------------------------ATGATGCA

S: ATCTATCGGTAGAACGATCGGACATCAATAAAGAAATTACAGCCAACTTTGTAGAATGAAGTACAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: ATCTATCGGTAGAACGATCGGACATCAATAAAGAAATTACAGCCAACTTTGTAGAATGAAGTACAG

Locus 7:
S: AP009552                                  1595582 1594119
Q: gi|389720472|emb|CAII01000016.1|          3854    3997

S: CAGCAAGATTTATCGAGAGTTTTCGCCTCAGTTTTCGGTGTGGAATTATTTTCTCTTGACAAGGATTAAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: CAGCAAGATTTATCGAGAGTTTTCGCCTCAGTTTTCGGTGTGGAATTATTTTCTCTTGACAAGGATTAAC

S: TTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTAGGTTTCTGCTTCTGTCCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------
```

```
S: GTGCTAATATTTAACAGTAAAGCCGTCGTAGAACGACGGGGTTTCAGACCCAAATTTTCGATGAGCGATC
   ------------------------------------------------------------||||||||||
Q: ------------------------------------------------------------ATGAGCGATC

S: GCAAAGACCCAGAAAAACTCGCCGCGGAAAATAGGGACGATAACCCCGAAAATAACGGTAAAAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: GCAAAGACCCAGAAAAACTCGCCGCGGAAAATAGGGACGATAACCCCGAAAATAACGGTAAAAC



Locus 8:
S: AP009552                          3832830 3834295
Q: gi|389717915|emb|CAII01000359.1|   783     926

S: AACTGGTCACAACTTGTCGTAAAGTGAAATAGGACTGACCAGTGCCACCGATTTTGATTAGCAAACTCCC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: AACTGGTCACAACTTGTCGTAAAGTGAAATAGGACTGACCAGTGCCACCGATTTTGATTAGCAAACTCCC

S: TTGACATCCTCGCCGCCGTAAAACGGACGGCGATTCCCAAACCTCACGATTTGGGTTTCTGCTTCTTTCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: ATGTGCTAATATTTAACAGTAAAGCCGTCGTAGAACGACGGGGTTTCAGACCCAAATTTTCGATGATTCA
   --------------------------------------------------------------||||||||
Q: --------------------------------------------------------------ATGATTCA

S: TCAACCCCCGGCGGGGACAAGGGATTTATTACCCCTAGAAGTTACCCAAAAAGGCTGGATTAACGA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: TCAACCCCCGGCGGGGACAAGGGATTTATTACCCCTAGAAGTTACCCAAAAAGGCTGGATTAACGA

Locus 9:
S: AP009552                          3707822 3709285
Q: gi|389715687|emb|CAII01000677.1|   2350    2493

S: TAAAAGAGCC-TTTTTCGGCAATAATCTGGCTATTTTTCCCCTAGCTAACCACTATATTGATCAATCGCC
   ||||||||||-|||||||||||:||||||||||-|||||||||||||||||:||||||||||||||||||
Q: TAAAAGAGCCTTTTTTCGGCAACAATCTGGCTA-TTTTCCCCTAGCTAACCGCTATATTGATCAATCGCC

S: TTTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTAGGTTTCTGCTTCTTTCC
   |---------------------------------------------------------------------
Q: T---------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGTTCTAATATTTAACAGTAAAGCCGTCGTAGAACGACGGGGTTTCAGACCCAAATTTTCGATGAATCAT
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAATCAT

S: CCTTACTCTTGGATCGAGGATAGCTTAAAAACCCTCCATCGGGCCAATTGGTATCGAAGGGTTAA
   ||||||||||||||:||||||||||||||||||||||||||||||:|||||||||||||||||||
Q: CCTTACTCTTGGATTGAGGATAGCTTAAAAACCCTCCATCGGGCCGATTGGTATCGAAGGGTTAA

Locus 10:
S: AP009552                          4162699 4164153
Q: gi|389717603|emb|CAII01000408.1|   4219    4352

S: GGGAGGTTTGAGTATCTGTACCCATAGATTACCCAAAGGTTTCCAATCAGGATGCAATCTAGATGACAAA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: GGGAGGTTTGAGTATCTGTACCCATAGATTACCCAAAGGTTTCCAATCAGGATGCAATCTAGATGACAAA

S: TTGACATCCTCACCGCCGTAAACGGACGGTGATTCCCAAACCTCACGATTTAGGTTTCTGCTTCTTTCCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------
```

```
S: TGTTCTAATATTTAACAGTAAAGCCGTCGTAGAACGACGGGGTTTCAGACCCAAATTTTCGATGAGCAAT
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAGCAAT

S: TTTCTCAGATAGCGATCGCAGGGCGATCAGTGAGGGGTTTGTACTAAAATGTCCA
   ||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Q: TTTCTCAGATAGCGATCGCAGGGCGATCGGTGAGGGGTTTGTACTAAAATGTCCA



Locus 11:
S: AP009552                          3476567 3478031
Q: gi|389715256|emb|CAII01000763.1|  157     14

S: CTGGATCCAGCAGCACCCCGCCGCCACAAATTTCTGCTGCTGACAGGTTCGGCAAGAGTCTCACGCTAGA
   |||||||||||||:|||||||||||||||||| |||||||||||||||||||||||||:|||||||||||
Q: CTGGATCCAGCAGTACCCCGCCGCCACAAATTGCTGCTGCTGACAGGTTCGGCAAGAGCCTCACGCTAGA

S: TTGACATCCTCGCCGCCGTAAAACGGACGGCGATTCCCAAACCTCACGATTTGGGTTTCTGCTTCTTTCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGTGCTAATATTTAACAGTAAAGCCGTCGTAGAACGACGGGGTTTCAGACCCAAATTTTCGATGAGTAGG
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAGTAGG

S: TATTTGATCCTAGATTCTCTGTTCAGATCATACCGGAATCAGTGACCAAAATCAGTTATCAGTAA
   |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: TATTTGATACTAGATTCTCTGTTCAGATCATACCGGAATCAGTGACCAAAATCAGTTATCAGTAA

Locus 12:
S: AP009552                          4915435 4916893
Q: gi|389718924|emb|CAII01000228.1|  3415    3278

S: TGGGGACGGAAAAAATCCATTTCGATGACCGCAACAGGCCCGGGCCGCTTTGATAAAAGTGAAAAAGTG
   |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Q: TGGGGACGGAAAAAATCCCTTTCGATGACCGCAACAGGCCCGGGCCGCTTTGATAAAAGTGAAAAAGTG

S: TTGACATCCTCGCCGCCGTAAAACGGACGGCGATTCCCAAACCTCACGATTTGGGTTTCTGCTTCTTTCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGTGCTAATATTTAACAGTAAAGCCGTCGTAGAACGACGGGGTTTCAGACCCAAATTTTCGATGAGGGAT
   -------------------------------------------------------------|||||||||
Q: -------------------------------------------------------------ATGAGGGAT

S: GATTAATTGTCAAGAAAAGCTAACATTAGTTGACCGAAAATTTGGGTACAAGCCCCGCC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Q: GATTAATTGTCAAGAAAAGCTAACATTAGTTGACCGAAAATTTGGGTACAAGCCCCGCC

====================================================================
```

Supplemental Figure 5.

Identification of exact target sites and transposon’s ends by pairwise alignments of concatenated sequences flanking transposon’s copies with sequences of orthologous loci free of the transposon’s insertions.

A, Two140-bp concatenated sequences of 70-bp regions flanking each of two copies of *ISC2-1_ML* in *Methanosarcina lacustris Z-7289* (Archaea) are aligned with sequences of their orthologous loci found in *Methanosarcina sp. WWM596* and *Methanosarcina sp. WH1* genomes*.*

B, Six 280-bp concatenated sequences of 140-bp regions flanking each of six copies of *ISC2-1_AF* in *Anoxybacillus flavithermus TNO-09.006* (Proteobacteria) are aligned with sequences of their orthologous loci identified in different strains of *Anoxybacillus flavithermus*.

C, Two 280-bp concatenated sequences of 140-bp regions flanking each of two copies of *IS605B-1_AF* in *Anoxybacillus flavithermus TNO-09.006* are aligned with sequences of their orthologous loci identified in different strains of *Anoxybacillus flavithermus*. In all pairwise alignments, red arrows indicate positions of transposons inserted in the concatenated flanking sequences (queries); left and right dinucleotides of the GTGA target sites are in green and purple

A) Queries: concatenated 70-bp flanks of two *ISC2-1_ML* copies in the *Methanosarcina lacustris Z-7289* genome

Copy 1:

Methanosarcina sp. WWM596, complete genome
Sequence ID: gb|CP009503.1| Length: 4137337 Number of Matches: 1

```
   Score      Expect    Identities      Gaps     Strand   Frame
161 bits(87)  2e-36()  126/144(88%)  5/144(3%)  Plus/Plus
Query  1        GACAGGCTGCTGCTCGGCAGTGTGGCTGAAAATGTTGTAAGGCACTGCAAGGTACCGGTA  60
                |||||||||||||||||||| ||||| |||||   |||  ||||||||||||| ||||||
Sbjct  2257167  GACAGGCTGCTGCTCGGCAGCGTGGCAGAAAAAACTGTCCGGCACTGCAAGGTGCCGGTA  2257226

                            ⬇
Query  61       ATGATTGTGAGTGAAAAATGCAGAACCTGAGGCAGAGAGCTCGAAAAATCACATTCAACC  116
                ||||||||:|||||||| |||||||||||||||| |||  ||||||||||||||||||||
Sbjct  2257227  ATGATTGTAAGTGAAAAGTGCAGAACCTGAGGCAAAGA-ATCGAAAAATCACATTCAACC  2257285

Query  117      TCAGGTTTTATCTTCTGCACCTG  140
                |||||||||| |||||||||| |||
Sbjct  2257286  TCAGGTTTTGATCTTCTGCATCTG  2257309
```

Copy 2:

Methanosarcina sp. WH1, complete genome
Sequence ID: gb|CP009504.1| Length: 3914091 Number of Matches: 1

```
    Score      Expect     Identities      Gaps      Strand    Frame
202 bits(109)  1e-48()   133/144(92%)  4/144(2%)  Plus/Minus
Query  1       ACCGAAGCGTACCTCCGAATCGAAGGCTTCGGATTTCCGGGATATACTACCATTTCTTCC  60
               ||||||||||||||||| ||||||||||||||||||||||||||||  ||||||||||||
Sbjct  974349  ACCGAAGCGTACCTCCGGATCGAAGGCTTCGGATTTCCGGGATATATAACCATTTCTTCC  974290

                           ⬇
Query  61      GTAATAGGCAGTGAAACATCAAAAAACTCTGGCAGAATAAAACCCCCGTTACTCTTAAGC  116
               ||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Sbjct  974289  GTAATAGGCAGTGAAACATCAAAAAACTCTGGCAGAATAAAACCCCCTTTAATCTTAAGC  974230

Query  117     AAAGCTTCCAGTTACTTTGCTTAA  140
               |||||||| ||||||||||| |||
Sbjct  974229  AAAGCTTCAAGTTACTTTGCATAA  974206
```

==

B) Queries: concatenated 140-bp flanks of six *ISC2-1_AF* copies in the *Anoxybacillus flavithermus TNO-09.006* genome

Copy1:

Anoxybacillus flavithermus subsp. yunnanensis str. E13 Contig33, whole genome shotgun sequence
Sequence ID: gb|AVGH01000033.1| Length: 311501

```
Query  1      TAGCCAAAGGAGAAGCTGTCCACCCGAAAGAAGGCGAAGAAGTGAAACGTAAGCCGGTGA  60
              |||||||||||||||| || || |||||||||||||||||||||||||| ||||||||||
Sbjct  97885  TAGCCAAAGGAGAAGCGGTTCATCCGAAAGAAGGCGAAGAAGTGAAACGCAAGCCGGTGA  97826

Query  61     AAAAAGCGGTGGAAGTCGGCCGAAATGATCCGTGCCCATGCGGAAGCGGAAAAAAATATA  120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  97825  AAAAAGCGGTGGAAGTCGGCCGAAATGATCCGTGCCCGTGCGGAAGCGGAAAAAAATATA  97766

Query  121    AACATTGTTGCGGACGATAAGTGAGGGATATTCCCTCGCTTTCGTTATGTTGCGTACGCC  176
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||| ||||
Sbjct  97765  AACATTGTTGCGGACGATAAGTGAGGGATGTTCCCTCGCTTTCGTTATGTTGCGTCCGCC  97706

Query  177    GAGATGTTTACATACAATAATGGTTGAGGTGAAGGACATGATCGATTTAGTAGAAATTAA  236
              |||| |||| |||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  97705  GAGACGTTTGCATACAATAATGGTTGAGGTGAAGGACATGATTGATTTAGTAGAAATTAA  97646

Query  237    GCAAGAGCTTGAAAAAATGGCTAAGCGATTAGTGGATATTAGGG  280
              |||||||||||||||||||||||||||||||| |||||||||||
Sbjct  97645  GCAAGAGCTTGAAAAAATGGCTAAGCGATTAGCGGATATTAGGG  97602
```

Copy2:

Anoxybacillus flavithermus NBRC 109594 DNA, contig: 0021, whole genome shotgun sequence
Sequence ID: dbj|BARH01000021.1 | Length: 52818 Number of Matches: 1

Score	Expect	Identities	Gaps	Strand	Frame
477 bits(258)	3e-131()	276/284(97%)	4/284(1%)	Plus/Plus	

```
Query  1      CGTCGAGAGTTTCCGCATGCTGAGCACTTATATATTGATAAAATGTATCGTGAAGTCGCA  60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  33077  CGTCGAGAGTTTCCGCATGCCGAGCACTTATATATTGATAAAATGTATCGTGAAGTCGCA  33136

Query  61     GCAGCTCCGAAGCATCATATTGCGGTCGTGTTATTAAGTGCAAATATCGATGTACACGCA  120
              ||||| |||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  33137  GCAGCCCCGAAGCATCATATTGCGGTCGTGTTATTAAGTGCAAACATCGATGTACACGCA  33196

Query  121    CAATATTTATAGAAAGTTGTGTGATCGTTGTGAAAGTTGTCTATATGTACACGCCATTAT  176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  33197  CAATATTTATAGAAAGTTGTGTGATCGTTGTGAAAGTTGTCTATATGTACACGCCATTAT  33256

Query  177    GTGGAACATGTCAAGTGGCAAGTCGTATGGTTGATGTACTTGAGCAGTTATTGCCATCTG  236
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  33257  GTGGAACATGTCAAGTGGCAAGTCGAATGGTTGATGTACTTGAGCAGTTATTGCCATCTG  33316

Query  237    TTACATTTGAACGTCAAGATTTAAACTACGTGCCGGACAAAGCG  280
              ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  33317  TTACATTTGAACGTCAAGATTTAAACTACGTGCCGGACAAAGCG  33360
```

Copy3:

Anoxybacillus flavithermus NBRC 109594 DNA, contig: 0021, whole genome shotgun sequence
Sequence ID: dbj|BARH01000021.1|Length: 52818Number of Matches: 1

Score	Expect	Identities	Gaps	Strand	Frame
472 bits(255)	2e-129()	275/284(97%)	4/284(1%)	Plus/Plus	

```
Query  1      TCATACGCCAATCAACATCATTGCGAAAAAACGTGAGGCAGCGCAAGCACTAATTGAAGC  60
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  31532  TCATACGCCAATCAACATCATTGCGAAAAAGCGTGAGGCAGCGCAAGCACTAATTGAAGC  31591

Query  61     TGAACGATATGTTGTGTAATAATGGAAGTACCAGACGCATCGTCTGGTACTTTCTGTTTG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  31592  TGAACGATATGTTGTGTAATAATGGAAGTACCAGACGCATCGTCTGGTACTTTCTCTTTG  31651

                                   ⬇
Query  121    TTATATTGTGTATAGATGAGGTGAGAAGATGGTAACATTTTATTGGTATCCAAAGTGCGG  176
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  31652  TTATATTGTGCATAGATGAGGTGAGAAGATGGTAACATTTTATTGGTATCCAAAATGCGG  31711

Query  177    CACATGTCGCAAAGCAAAAAAATGGCTAGATGACAACAACATTTCTGTGCAAGCGATACA  236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  31712  CACATGTCGCAAAGCAAAAAAATGGCTAGATGACAACAACATTTCTGTGCAAGCGATACA  31771

Query  237    TATTGTTGAGCAGCCTCCGTCAAAAGAGCAGTTGCGGACGTTAT  280
              ||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  31772  TATTGTTGAACAGCCTCCGTCAAAAGAGCAGTTGCGGACGTTAT  31815
```

Copy4:

Anoxybacillus flavithermus AK1 seq_num_004, whole genome shotgun sequence
Sequence ID: gb|APCD01000004.1|Length: 184270Number of Matches: 2

Score	Expect	Identities	Gaps	Strand	Frame
259 bits(140)	1e-65()	158/166(95%)	4/166(2%)	Plus/Plus	

```
                                     ⬇
Query  119    GTGACGGGCGGTTATATGGAAAGTGAACCGTTTTGCGTATATATACCAGAGCGCATGAGG  174
              |||||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  13902  GTGACGGGCGATTATATGGAAAGTGAACCGTTTTGCGTATATATACCAGGGCGCATGAGG  13961

Query  175    GAAAAAGGGGAATCCCAAACCGTGTTCGCTTAACGCGAGCGTGGTTTGGGATGATGTATA  234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  13962  GAAAAAGGGGAATCCCAAACCGTGTTCGCTTAACGCGAGCGTGGTTTGGGATGATGTACA  14021

Query  235    ATTAAAAATCAAAGTTATCTGGATCTGGACCGATGCGACGGTTTTC  280
              ||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  14022  ATTAAAAATCAAAGTTATCTGGATCTGGACCGATGCGGCGGTTTTC  14067
```

Copy5:

Anoxybacillus flavithermus AK1 seq_num_001, whole genome shotgun sequence
Sequence ID: gb|APCD01000001.1|Length: 336904Number of Matches: 1

Score	Expect	Identities	Gaps	Strand	Frame
388 bits(210)	2e-104()	245/261(94%)	5/261(1%)	Plus/Minus	

```
Query  25      TATCTTGTCACTGTTCTGACAAATATGCACGTCCTTGCATTTCTAATATCAAATA-GATA  83
               |||||||||||  ||| |||||| ||| ||||||||||||||| ||||| ||||| ||||
Sbjct  173278  TATCTTGTCACCATTCAGACAAACATGTACGTCCTTGCATTTCCAATATGAAATAAGATA  173219

                                                                         ⬇
Query  84      GTATATACGATATAAGGTATACAAGGAGGTGGAAAAATGGCAAAAGTACAAATTAAAGTG  140
               ||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Sbjct  173218  GTATATACGATATAAGGTATACAAGGAGGTGGAAAAATGACGAAAGTACAAATTAAAGTG  173159

Query  141     ATGGATAATGGTTCATTTCGTGTAACCGGCGATGTCGAATTAATTGACATGGAAGGAAAC  199
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173158  ATGGATAATGGTTCATTTCGTGTAACCGGCGATGTCGAATTAATTGACATGGAAGGAAAC  173099

Query  200     AAGTTCGAAACAAAAGAAACGTTTTCTCTCTGTCGTTGCGGGCTCTCACAAAACATGCCG  259
               ||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  173098  AAGTTTGAAACAAAAGAAACGTTTTCTCTCTGTCGTTGTGGGCTCTCACAAAACATGCCG  173039

Query  260     TTTTGTGATGCAGCCCATAAA  280
               |||||||||||||||||||||
Sbjct  173038  TTTTGTGATGCAGCCCATAAA  173018
```

Copy6:

Anoxybacillus flavithermus NBRC 109594 DNA, contig: 0009, whole genome shotgun sequence
Sequence ID: dbj|BARH01000009.1|Length: 172593Number of Matches: 1

Score	Expect	Identities	Gaps	Strand	Frame
488 bits(264)	2e-134()	278/284(98%)	4/284(1%)	Plus/Plus	

Features:

```
Query  1       AAACGAACCGATTGAACAAAAACGCATTCGTCAGCTTATCaaaaaaaTTCAAGCATATAA  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  146430  AAACGAACCGATTGAACAAAAACGCATTCGTCAGCTTATCAAAAAAATTCAAGCATATAA  146489

Query  61      CGAATGGCTGATGGCGCATCCACGCTATGAGACAGTCATCATTCCGATCGGTGACGGAAT  120
               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  146490  CGAATGGCTGATGGCGCATCCACGTTATGAGACAGTCATCATTCCGATCGGTGACGGAAT  146549
                                     ⬇
Query  121     GGCGATATCGAGAAAACGAGGTGAATAGAATGAAAAAACCAGAATTGCTTGTTACGCCAA  176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  146550  GGCGATATCGAGAAAACGAGGTGAATAGAATGAAAAAACCAGAATTGCTTGTTACGCCAA  146609

Query  177     CGAGCGTGGCGCATATTGAACAACTCGCACAAGCAGGAGCGAATGCTGTCATCATTGGTG  236
               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  146610  CGAGCGTGGCGCATATTGAACAACTCGCACAAGCAGGAGCGAATGCCGTCATCATTGGTG  146669

Query  237     AACAACGGTACGGCTTGCGTTTAGCAGGTGAGTTTTCACGTCAA  280
               ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  146670  AACAACGGTACGGCTTGCGTTTAGCAGGTGAGTTTTCACGTCAA  146713


=================================================================
```

C) Queries: concatenated 140-bp flanks of two *IS605B-1_AF* copies in the *Anoxybacillus flavithermus TNO-09.006* genome

Copy1:

Anoxybacillus flavithermus AK1 seq_num_018, whole genome shotgun sequence
Sequence ID: gb|APCD01000018.1|Length: 51524Number of Matches: 1

Score	Expect	Identities	Gaps	Strand	Frame
483 bits(261)	2e-132()	277/284(98%)	4/284(1%)	Plus/Minus	

```
Query  1      ATTAAAATGACGTTTGCTTTTTCTTTTGCTAAGTGAAAAGCAACAGAGGAGCCAACAATT  60
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  48080  ATTAAAATGACGTTTGCTTTTTCTTTTGCTAAGTGAAAGGCAACAGAGGAGCCAACAATT  48021

Query  61     CCACCGCCAATGACGATATAACGATTCATCGTTTACACCTTTCCTTTTCGTGATACTGTA  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  48020  CCACCGCCAATGACGATATAACGATTCATCGTTTACACCTTTCCTTTTCGTGATACTGTA  47961
                                    ⬇
Query  121    TCATTACGATAACATAGGACGTGAAAAAAGCAAGGGTCTTCCCTTGCCTTTTAATAAAAC  176
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Sbjct  47960  TCATTACGATAACATAGGACATGAAAAAAGCAAGGGTCTTCCCTTGCCTTTTAATAAAAC  47901

Query  177    CATTTTGCCATTTCATAATATAATGGCATGCCGATTGTTAAGTTAAATGGGAAGGTGAGC  236
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  47900  CATTTTGCCATTTCATAATATAAGGGCATGCCGATTGTTAAGTTAAATGGGAAGGTGAGC  47841

Query  237    CCGAGCGCCATGCCGAGATAAATAGCAGGGTTTGCTTCTGGAAC  280
              ||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  47840  CCGAGCGCCATGCCGAGATAAATTGCAGGGTTTGCTTCTGGAAC  47797
```

Copy2:

Anoxybacillus flavithermus WK1, complete genome
Sequence ID: gb|CP000922.1|Length: 2846746Number of Matches: 1

Score	Expect	Identities	Gaps	Strand	Frame
466 bits(252)	2e-128()	274/284(96%)	4/284(1%)	Plus/Minus	

```
Query  1        CGTCGAGAGTTTCCGCATGCTGAGCACTTATATATTGATAAAATGTATCGTGAAGTCGCA  60
                ||||||||||||||||||| ||||||||| |||||||||||||||||||||||||| |||
Sbjct  2450942  CGTCGAGAGTTTCCGCATGCCGAGCACTTGTATATTGATAAAATGTATCGTGAAGTGGCA  2450883

Query  61       GCAGCTCCGAAGCATCATATTGCGGTCGTGTTATTAAGTGCAAATATCGATGTACACGCA  120
                ||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  2450882  GCAGCCCCGAAGCATCATATTGCGGTCGTGTTATTAAGTGCAAACATCGATGTACACGCA  2450823

                                      ⬇
Query  121      CAATATTTATAGAAAGTTGTGTGATCGTTGTGAAAGTTGTCTATATGTACACGCCATTAT  176
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2450822  CAATATTTATAGAAAGTTGTGTGATCGTTGTGAAAGTTGTCTATATGTACACGCCATTAT  2450763

Query  177      GTGGAACATGTCAAGTGGCAAGTCGTATGGTTGATGTACTTGAGCAGTTATTGCCATCTG  236
                ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  2450762  GTGGAACATGTCAAGTGGCAAGTCGAATGGTTGATGTACTTGAGCAGTTATTGCCATCTG  2450703

Query  237      TTACATTTGAACGTCAAGATTTAAACTACGTGCCGGACAAAGCG  280
                ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2450702  TTACATTTGAACGTCAAGATTTAAACTACGTGCCGGACAAAGCG  2450659
```

Supplemental Figure 6. The *ISC2-1_MS* (A, B), *ISC2-2_MS* (C, D) , *ISC2-1_HM* (E, F) and *IS605B-1_MS* (G) transposons are inserted at 5'-N|ATGA-3' target sites ("I" indicates the exact position of the insertions, which are not accompanied by the target site duplications). (A,D,E) – maps of copies of the transposons. (B,D,F,G) – pairwise alignments of DNA sequences of the transposon's copies expanded 70-bp (B,D), 210-bp (F), 140-bp (G) in both directions with orthologous loci free of the inserted transposons identified in genomes of *Marinobacter sp. BSs20148* (B, D, G) and *Halomonas sp. TD01*(F). The inserted transposon's sequences are in red; their target sites are in blue.

A) Map of *ISC2-1_MS* in the *Marinobacter sp. ELB17* genome (WGS assembly):

```
gi|126627097|gb|AAXY01000028.1|   15628 17319   ISC2-1_MS       1 1692    c   0.9368
gi|126627372|gb|AAXY01000023.1|   14080 15773   ISC2-1_MS       1 1692    c   0.9504
gi|126627643|gb|AAXY01000019.1|   51520 53211   ISC2-1_MS       1 1692    d   0.9379
gi|126627941|gb|AAXY01000015.1|   18509 20202   ISC2-1_MS       1 1692    d   0.9191
gi|126628706|gb|AAXY01000008.1|   89245 90929   ISC2-1_MS       1 1692    c   0.9478
```

B) Pairwise alignment of the expanded five copies of *ISC2-1_MS* (70-bp in both directions) with their transposon-free orthologs identified in *Marinobacter sp. BSs20148* (complete genome, GenBank CP003735)

```
Q: gi|126627097|gb|AAXY01000028.1|     15558 17389   c
S: CP003735                          2460492 2460635 d

Q: TATTATCAGTGACTTTTTTAGCCGTCGGCGCGAACTCAGGCGCCAATCAGCCAAAACGGAGTAAATGGAC
   |||||||||||||||||||||||:||||||:||||||||||||||||:||||||||||||||||||||||
S: TATTATCAGTGACTTTTTTAGCCATCGGCGTGAACTCAGGCGCCAATTAGCCAAAACGGAGTAAATGGAC

Q: GTCAACTACCCCGCCCTAAAGGACGGGGCTTGTAGAGAACACCCTGCAGGCCAGGTTGACCAGGGAAAGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

   NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
   ----------------------------------------------------------------------

Q: ACAGGGAAAACGAGTCGCGCTGACGCACGACGCGCTATCCCTCCCCGCCCTGAAGGGCGGGGTATCCCGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: GCAAAATGATGAAAGTTCTCGTTACCGGCGGTGCCGGCTACATTGGCAGCCACGTCGTGCGCCAGTTGGC
   --------|||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:||||
S: --------ATGAAAGTTCTCGTTACCGGCGGTGCCGGCTACATTGGCAGCCACGTTGTGCGCCAGCTGGC

Q: TGCTGCAGGCCA
   |||||| |||||
S: TGCTGCCGGCCA


Q: gi|126627372|gb|AAXY01000023.1|   14010 15843   c
S: CP003735                        2624061 2624204 c

Q: AATGTGGGGTGTCGGATTTGGAGTGTATAATACTGGAACTTGTGGCAATTACCTAGGGAACCGCTCCAAC
   ||||||| |:||: :||||||||||||||||||||||| |||||||||||||||||||||||||||||||
S: AATGTGGTGCGTTTAATTTGGAGTGTATAATACTGGAAATTGTGGCAATTACCTAGGGAACCGCTCCAAC

Q: GTCAACTACCCCGCCCTAAAGGACGGGGCTTGTTAGAGAACACCCTGCAAGCCAGGTTGACCAGGGAAAG
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: GACAGGAAAAACGAGTCGCGCTAACGCACGACGCGCTATCCCTCCCCGACCTGAAGGACGGGGGTATCCC
   ----------------------------------------------------------------------
```

```
S: ----------------------------------------------------------------------

Q: GCGCAAAATGATGAAACGCACCGCATTCTTTCTGTCAGACGGAACAGGCCTGACTGCCGAAGGGCTAGGA
   ----------||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
S: ----------ATGAAACGCACCGCATTCTTTCTGTCAGACGGAACAGGCCTGACTGCCGAAGGGCTAGGA

Q: CACGCGCTGCTGGC
   ||||||||||| ||
S: CACGCGCTGCTTGC



Q: gi|126627643|gb|AAXY01000019.1|   51450 53281   d
S: CP003735                        2701480 2701623 c

Q: GTCGGGATGACAACAAAGATCCGTCCATTCACTGACCAGCACTATAAAACGGACAGGAGATTACAGCGCC
   |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
S: GTCGGGATGAAAACAAAGATCCGTCCATTCACTGACCAGCACTATAAAACGGACAGGAGATTACAGCGCC

Q: GTCAACTACCCCGCCCTAAAGGACGGAGCTTGTAGAGAACACCCTGCAAGCCAGGTTGACCAGGGAAAGT
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------


Q: ACAGGAAAAACGAGTCGCGCTGACGCACGACGCGCTATCCCTCCCCGCCCTGAAGGACGGGGTATCCCGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: GCAAAATGATGACGGACATCCAACAAACGGTATACGTGGTTGAAGACGACGAAGCGGTGCGCGATTCACT
   --------||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
S: --------ATGACGGACATCCAACAAACGGTATACGTGGTTGAAGACGACGAAGCGGTGCGCGATTCACT

Q: GGAGTTGTTGCT
   ||||:||:||||
S: GGAGCTGCTGCT


Q: gi|126627941|gb|AAXY01000015.1|   18439 20272    d
S: CP003735                        1573673 1573816  c

Q: AGCTGACCGAGTTCCAGAGCAACGCGGCTCGACTGCAGCAGCAGCGTGCTGACATTGAGGCCATGTAGGC
   |||||||||||||:||| ||||: :||| || :|||:||||||||:|||||||||||||||||||||:||
S: AGCTGACCGAGTTTCAGCGCAATCTGGCGCGTTTGCGGCAGCAGCATGCTGACATTGAGGCCATGTAAGC

Q: GTCAACTACCCCGCCCTGAAGGACGGGGCTTGTAGAAAACACCCTGCAAGCCAGGTTGACCAGGGAAAGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------


Q: AGACAGGGAACACGAGTCGCGCTGACGCACGACGCGCACTCCCTCCCCGACCTGAAGGACGGGGTATCCC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: GCGCAAAATGATGAATGTGGGTGTTAAGCGTTCCGGGGGTGGCGGGCAGATCGCCATTCTTGGAGCGGGT
   ----------|||| ||::||:||||||||||:|||||:|||||||||||||||||||||||||||||||
S: ----------ATGACTGCAGGCGTTAAGCGTTTCGGGGATGGCGGGCAGATCGCCATTCTTGGAGCGGGT

Q: TCAATGGGGCGGCT
   ||||||||||||||
S: TCAATGGGGCGGCT


=========================================================================
```

C) Map of *ISC2-2_MS* in the *Marinobacter sp. ELB17* genome (WGS assembly):

```
gi|126628107|gb|AAXY01000013.1|   14326 16017   ISC2-2_MS             1 1692    d   1.0000
gi|126630264|gb|AAXY01000002.1|  157923 159614  ISC2-2_MS             1 1692    d   0.9451
gi|126628706|gb|AAXY01000008.1|   96459 98150   ISC2-2_MS             1 1692    d   0.9149
```

D) Pairwise alignment of the expanded three copies of *ISC2-2_MS* (70-bp in both directions) with their transposon-free orthologs identified in *Marinobacter sp. BSs20148* (complete genome, GenBank CP003735)

```
Q: gi|126628107|gb|AAXY01000013.1|   14256 16087   d
S: CP003735                        2223718 2223861 d

Q: CTCTACGTGGACATCCGTAATAGCCCATAACCGGGTCACCATGAAAGTGGTTAAAACAACAAAGGTACCC
   ||||||||||||||||||||:|||||||||||||||||||||:|| ||||||||||||||||||||||||
S: CTCTACGTGGACATCCGTAACAGCCCATAACCGGGTCACCATAAACGTGGTTAAAACAACAAAGGTACCC

Q: GTCAACTACCCCGCCGTGAACGACGGGGCTTGTAGAGAACACCCTACACGCCAAGTTGACCAGGGAAAGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CAGGAAAGTCTGTCGTGCTAACGCACGACGCGCACTCCCTCCCCGACCTAAAAGGACGGGGTTTCCCGCG
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CAAAATCGATGATAAAAAAACGCTTGAGTGAATCATCGGCCAAGCCTTTTAACCACTTATTTTGCGCTGC
   --------||||||||||||||||:||:|: |||||:|||| :||:|||||||||||||:|||||||:||
S: --------ATGATAAAAAAACGCTCGAATACATCATTGGCCCGGCTTTTTAACCACTTACTTTGCGCCGC

Q: TGCCATCGGCTT
   : |||| |||||
S: CTCCATAGGCTT


Q: gi|126630264|gb|AAXY01000002.1|  157853 159684  d
S: CP003735                        1010890 1011033 c

Q: TACCTATAACTGCTCAGCGGGCACACAGTATCCGCAATAGTAATGTTCACTGACTATTTTAGGGCAAATT
   ||||||:||||||||||||||||||||||||||||||: ||: |||||||| ||||||||||||||||||
S: TACCTACAACTGCTCAGCGGGCACACAGTATCCGCAACCGTGCTGTTCACTCACTATTTTAGGGCAAATT

Q: GTCAACTACCCCGCCGTGAACGACGGGGCTTGTAGAGAACACCCTACACGCCAAGTTGACCAGGGAAAGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CAGGAAAGTCTGTCGTGCTAACGCACGACGCGCACTCCCTCCCCGACCCAAAAGGACGGGGTTTCCCGCG
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CAAAATCGATGATACTTCAAGATTCCGTAGTTGCAATTACCGGCGGTGGCCAGGGTTTGGGGCGCGCCAT
   --------||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
S: --------ATGATACTTCAAGATTCCGTAGTTGCAATTACTGGCGGTGGCCAGGGTTTGGGGCGCGCCAT

Q: GGCTGAATTTCT
   ||||||||||||
S: GGCTGAATTTCT
```

```
Q: gi|126628706|gb|AAXY01000008.1|   96389 98220   d
S: CP003735                         694454 694597  c

Q: TTCTATTCTGGCAGGCAGACGCTGCGGCACGCTGGGTTATGAAACACTTCTTATCAACTGGGCTTTAACG
   |||||||||||||||||||||||||||||||||||||||||| ||||||:|||:||||||||||||||||
S: TTCTATTCTGGCAGGCAGACGCTGCGGCACGCTGGGTTATGACACACTTTTTACCAACTGGGCTTTAACG

Q: GTCAACTACCCCGCCGTGAACGACGGGGCTTGTAGAGAGCACCCTACACGCCAGGTTGACCAGGGAAAGC
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CAGGAAAGTCTGTCGTGCTAACGCACGACGCGCTATCCCTCCCCGACCTAAAAGGACGGGGTTTCCCGCG
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CAAAATCGATGAAAATTCTTCAGGCGCTGCCAGCGCTGCACAGTGGTGGTGTAGAGCGGGGTACCGTCGA
   --------||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
S: --------ATGAAAATTCTTCAGGCGCTGCCAGCGCTGCACAGTGGCGGTGTAGAGCGGGGTACCGTCGA

Q: ATTCGCCAGACA
   ||||||||||||
S: ATTCGCCAGACA


===========================================================================
```

E) Map of *ISC2-1_HM* in the *Halomonas meridiana strain R1t3* genome (WGS assembly):

```
gi|764088526|gb|JZEM01000028.1|   27448 29182   ISC2-1_HM       1 1735    c   1.0000
```

F) Pairwise alignment of the expanded *ISC2-1_HM* (210-bp in both directions) with the transposon-free orthologous locus identified in the *Halomonas sp. TD01* genome (GenBank AFQW01000013):

```
gi|764088526|gb|JZEM01000028.1|   29392 27238
AFQW01000013                     103642 103223
I=79%

Q: TGAAGAGGGGTGGCAGCTTGATAGCGAACTATTAAACTACGACGGGACCACCCGGCATGCCTGGAGCGAC
   ||| ||||| |||||||| :|||  ||::||||: ||||:||:|| |:|||||| ||||||||||||||:
S: TGATGAGGGCTGGCAGCTGAATACAGAGTTATTGCACTATGATGGCATCACCCGTCATGCCTGGAGCGAT

Q: ACCCACGTAGTGTTGCAGCAGCCCCCTCAGCGTATGGAAGCCTCCCGAATGGATGTATGGCTGGATGACA
   :|| | :: ||::| |||||||| ||:|||||:|| || ||:|| || ||||||||||||||||||||:|
S: GCCGAGACCGTACTTCAGCAGCCGCCCCAGCGCATTGACGCTTCACGCATGGATGTATGGCTGGATGATA

Q: GCCAAGTCCGTTTAACCAACAACGTGCGCGGCGTTCATCCGCCGGCCACCCGTTCCCCTTAGGAGTCGCG
   ||||::||||:||||||||||||||||||||||||||||||||||||||:|||||||  |||||||||||
S: GCCAGATCCGCTTAACCAACAACGTGCGCGGCGTTCATCCGCCGGCCACTCGTTCCCAGTAGGAGTCGCG

Q: GTCAACTACCCCCGCCTGAAGGCGGGAGCTTGTGACAACAAGCCCGGTTGACCAGGGAGAGCGGTAGCCA
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: TCACTTTACACCCTTCACCCACCTAACAGGAGGAGCGGGACAGGCGGTGGCGTAACCCAGTCGCCCTGCG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

Q: GGCGACGCGCTATCCCTCCCGGCGCTAAAGCACCGGGTTTCTCGCGCAAAATCTGATGAATGCTCTAATC
   -------------------------------------------------------|||||:||||| ||:
Q: -------------------------------------------------------ATGAACGCTCTCATT

Q: CGCACTGCACTTCTTGCCCTAGCCGTGCCGCTTGTCACAATTGCACTGCCTGT---AGCGGCA-------
   ||||| |||||::|:|||---------------------|||||:||:||::|---|||||||-------
Q: CGCACGGCACTCTTCGCC---------------------ATTGCGCTACCCATCTCAGCGGCAGCGCTTC
```

```
Q: -----------CAAAACCAAGCGCCTATTCATGTGGAGGCCGACCGGTTAGACCTTGACCAACGAGCAGG
   -----------||||:|||||| ||::|  | ||:|||||:||||| |||||:||:||:|||||||||||
Q: CGGTCATGGCGCAAAGCCAAGCCCCCGTAGAAGTAGAGGCTGACCGTTTAGATCTCGATCAACGAGCAGG

Q: GACAGCCGTGTACACCGGTAACGTTGACATTCGCCAAGGCAATATGCAGCTACGCGGAGAGCGTGTCGAA
    || |||||:||: ||||||||||:||:||||| ||:|||||||||||:||:||||| || ||:||:|||
Q: CACCGCCGTATATTCCGGTAACGTCGATATTCGACAGGGCAATATGCAACTGCGCGGCGATCGCGTTGAA

Q: ATTCAG
   ||||||
Q: ATTCAG

=========================================================================
```

G)

```
IS605B-1_MS    Marinobacter sp. ELB17
CP003735       Marinobacter sp. BSs2014

gi|126630642|gb|AAXY01000001.1|  228656 226964
CP003735                        3812492 3812767

Q: AATCGAGATCTTCCGCAGTACCCATACCCTTGCCGTATTTGAGCCGGTACTTAACCACCACGGCAGACAA
   |||||||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||||||
S: AATCGAGATCTTCCGCAATACCCATGCCCTTGCCGTATTTGAGCCGGTACTTAACCACCACGGCAGACAA

Q: AACCAGCAGCAAAATCCCGATAACAGCCGCGAAAACACCGGTTATAGGTACAATCATATTCAGTCCTGTT
   |||||||||||||||:|||||||||||||||||||||||||||||||||| |||||||||||||||||||
S: AACCAGCAGCAAAATTCCGATAACAGCCGCGAAAACACCGGTTATAGGTAAAATCATATTCAGTCCTGTT

Q: GTTGACATCCTCCCCGCCCTCTTGCTTCGCTCGTCGCTACGCGAAAAGGACGGGGATTCCTACGGCGATT
   |---------------------------------------------------------------------
S: G---------------------------------------------------------------------

Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: TATATCCATCCACATTCAAGAGCAAGGACGGCTACGCCGTCCGCGCTATCCTTCCCCGCCCTGAAGGGCG
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: AGGTTTGCCGCGCACTGGATCAATGAACTGCCCGCGCAGGCCATGCCTGCGTCGCCGACAAGTGACGGAA
   ------------------||||||||||||||||||||||||||||:||||||||||||||||:||||||
S: ------------------ATCAATGAACTGCCCGCGCAGGCCATGCCCGCGTCGCCGACAAGTAACGGAA

Q: GCAACCTCACTGTGCCTTACTTTCACCCAGCTCGGCAATTGCCTTGGCCATAGCGCTGTGGCAGCGCGCG
   ||:| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
S: GCGAACTCACTGTGCCTTACTTTCACCCAGCTCGGCAATTGCCTTGGCCATAGCGCTGTGGCAGCGCGCG

Q: ATCAGTTCGGGTA
   |||||||||||||
S: ATCAGTTCGGGTA


gi|126629570|gb|AAXY01000004.1|   24028 22228
CP003735                        3449151 3449496

Q: CGCCGTTGGATGAACGTATGCAGATGAGTGCACCACGGGCGTAACCCCGTCAATTTGGTAACACGGCATA
   |||||||||||||||||||||:||||:||||||||| |||||||||||||||||||||||||||||||||
S: CGCCGTTGGATGAACGTATGCGGATGGGTGCACCACCGGCGTAACCCCGTCAATTTGGTAACACGGCATA

Q: AAACTCCCCTGACTGA------------------------------------------------------
   ||||||:||| || :|------------------------------------------------------
S: AAACTCTCCTCACAAAGTCGTTCTTTTTAACTTAAAGACTATTTTATGTATCAAAACCTGGCGAAGACAT

Q: -----------------ACACTAACGTTTATTTCACGAGTTCTGAGAGCTCAAGTTTAAACACAAGATAC
   -----------------||:|| :|||||||||:||||||::|||||||| ||:||||||||||||||||
S: AAAACACCCATATCGAGACGCTCGCGTTTATTTTACGAGTCTTGAGAGCTAAAATTTAAACACAAGATAC

Q: ACTTGACATCCTCCCCGCCCTGAAGGATAGGGATTCCTGCTGCGCTCAGGCGTGGCATTGAGCCATCCCT
   ||--------------------------------------------------------------------
S: AC--------------------------------------------------------------------
```

```
Q: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
   ----------------------------------------------------------------------
S: ----------------------------------------------------------------------

Q: CTGCGATGTCCGCGCTATTCATCCCCGGCCTGAAGGCCGAGGTTTTCCGCGCATTCCGATAAAAATCAGA
   ----------------------------------------------------------||||||||||||
S: ----------------------------------------------------------ATAAAAATCAGA

Q: AATCTGCGAGCACTGCTACACTGAAAAATCAAACGTGATACAAAAATTCATTATTCTTACCCTTGACCGG
   |||||||||||||||||| |||||||||:||||||||||||||||||||||:||| ||:|||||||||||
S: AATCTGCGAGCACTGCTAAACTGAAAAACCAAACGTGATACAAAAATTCATCATTATTGCCCTTGACCGG

Q: TATCAATTAAAACCTATACTCTTTCGTTAAAACAAACAAGGTAAAACACCGC
   ||||||||||||||||||||||||||||||||||||||| ::||||||||||
S: TATCAATTAAAACCTATACTCTTTCGTTAAAACAAACAACACAAAACACCGC
```

Supplemental Figure 7. Phylogenetic tree of IscA and TnpA Y1 transposases (Figure 5 in the main text) in the Newick format.

(IS6051_HP:0.49198042,IS6051_FP:0.13809583,(((IS6051_BSp:0.06225530,IS6051_EH:0.15633384)1.000000:0.45066912,(ISC2Y1_CS:0.57003179,ISC2Y1_EC:0.34822821)0.985870:0.15712019)0.999967:0.25729340,(((IS6051_MM:0.27944804,IS6051_MZ:0.37157052)0.999982:0.25286451,((IS6051_VB:0.91205125,ISC2Y1_KR:0.58815167)0.615112:0.10188805,(IS6051_BC:0.38657671,IS6051_RI:0.61253716)0.598364:0.08737726)0.975325:0.10002596)0.999975:0.17520367,(IS6051_BMT2:0.37145949,(ISC2Y1_AA:0.27958692,(ISC2Y1_CH:0.24760373,ISC2Y1_MA:0.34666893)0.489115:0.05390627)0.797239:0.05027554)0.391616:0.02395123)0.994942:0.16202732)1.000000:0.32875794);

Supplementary Figure 8. IscB tree in Newick format.

The tree was reconstructed by FastTree program ("-gamma –wag" options). A multiple alignment of IscB sequences was filtered with homogeneity threshold of 0.5 and gap occurrence threshold of 0.5, prior to tree reconstruction. This tree is schematically shown in Figure 6.

```
(((495188212__Ktedonobacter_racemifer:0.19300,((495179135__Ktedonobacter_racemifer:0.12942,(49518
0525__Ktedonobacter_racemifer:0.08376,(((495182844__Ktedonobacter_racemifer:0.04845,(495186450__K
tedonobacter_racemifer:0.03647,(495182297__Ktedonobacter_racemifer:0.03740,297550215__Ktedonobact
er_racemifer__ISC2_1_KR:0.02308)0.755:0.01382)0.879:0.00016)0.870:0.01068,(297550437__Ktedonobact
er_racemifer_DSM_44963:0.03114,495179751__Ktedonobacter_racemifer:0.08685)0.593:0.00015)0.762:0.0
0601,(495185167__Ktedonobacter_racemifer:0.02509,495198645__Ktedonobacter_racemifer:0.07922)0.852
:0.01641)0.753:0.00932)0.948:0.04370)0.610:0.00346,(495180193__Ktedonobacter_racemifer_ISC2-
2_KR:0.10813,495179835__Ktedonobacter_racemifer:0.11304)0.752:0.04938)0.755:0.03002)0.806:0.02684
,(497835978__SAR324_cluster_bacterium_JCVI_SC_AAA005:0.24021,(((889959964__Scytonema_tolypothrich
oides:0.09715,((516355684__Scytonema_hofmanni:0.06903,516352019__Scytonema_hofmanni:0.04646)0.949
:0.03444,(((499309054__Nostoc_sp_PCC_7120:0.02422,499635620__Anabaena_variabilis:0.06516)0.970:0.
05181,(((652319815__Fischerella_sp_PCC_9431:0.01562,(652324245__Fischerella_sp_PCC_9431:0.03503,5
15883076__Stigonematales:0.00523)0.873:0.01260)0.293:0.00560,(((657929237__Scytonema_hofmanni_UTE
X_B_1581:0.05748,504893952__Anabaena_sp_90:0.02890)0.805:0.01185,((515519056__Anabaena_sp_PCC_710
8:0.05269,(654617757__Dolichospermum_circinale:0.06352,505030549__Anabaena_cylindrica:0.01798)0.6
48:0.02666)0.500:0.01269,(499636046__Anabaena_variabilis:0.07563,(657931854__Scytonema_hofmanni_U
TEX_B_1581:0.02794,657932534__Scytonema_hofmanni_UTEX_B_1581:0.02196)0.904:0.02067)0.587:0.00015)
0.916:0.02047)0.838:0.01257,657932541__Scytonema_hofmanni_UTEX_B_1581:0.06562)0.776:0.00714)0.404
:0.00711,(748134943__Scytonema_millei:0.06170,505023946__Cylindrospermum_stagnale:0.07076)0.459:0
.01077)0.643:0.01847)0.740:0.00891,(518327680__Calothrix_sp_PCC_7103:0.06344,(518326274__Calothri
x_sp_PCC_7103:0.02512,518324846__Calothrix_sp_PCC_7103:0.04734)0.963:0.04578)0.856:0.02462)0.883:
0.01911)0.828:0.01381)0.946:0.03608,(503088871__Cyanothece_sp_PCC_7822:0.10915,196179674__Coleofa
sciculus_chthonoplastes_PCC_7420:0.08667)0.448:0.01983)0.908:0.02787,(648407024__Oscillatoria_sp_
PCC_10802:0.07550,(78499555__Arthrospira_platensis:0.16053,528102090__Salipiger_mucosus_DSM_16094
__ISC2_1_SM:0.12324)0.685:0.00885)0.898:0.02360)0.706:0.00527)0.819:0.01501)0.697:0.00462,((((669
952828__Acidithiobacillus_ferrivorans:0.10571,((501355452__Acidithiobacillus_caldus:0.02501,33983
4277__Acidithiobacillus_sp_GGI_221:0.04500)0.954:0.06206,(521982550__Verrucomicrobium_sp_3C:0.060
33,517100807__Verrucomicrobium_sp_3C:0.03902)0.911:0.04201)0.129:0.02369)0.969:0.06654,(501164377
__Petrotoga_mobilis:0.15158,749573752__Geoalkalibacter_subterraneus:0.06351)0.847:0.03228)0.775:0
.02862,(((((502796854__Nitrosococcus_halophilus:0.04511,(299540414__Nitrosococcus_watsonii_C_113:
0.04757,291580488__Nitrosococcus_halophilus_Nc_4__ISC2_1_NH:0.03642)0.734:0.00654)0.572:0.01306,5
02797006__Nitrosococcus_halophilus:0.05095)1.000:0.10210,(738341074__Methylobacter_whittenburyi:0
.13739,(723287658__Candidatus_Thiomargarita_nelsonii:0.02771,723288870__Candidatus_Thiomargarita_
nelsonii:0.02492)0.966:0.06371)0.723:0.03113)0.000:0.00014,(723284236__Candidatus_Thiomargarita_n
elsonii:0.02476,723282587__Candidatus_Thiomargarita_nelsonii:0.02241)0.999:0.09617)0.757:0.00695,
(764393758__Raoultella_ornithinolytica:0.18169,(502796490__Nitrosococcus_halophilus:0.15357,74957
3854__Geoalkalibacter_subterraneus:0.06735)0.865:0.03459)0.187:0.01848)0.747:0.00768)0.897:0.0292
4,(((491573834__Sutterella_wadsworthensis:0.16265,((495179088__Ktedonobacter_racemifer:0.03750,49
5193778__Ktedonobacter_racemifer:0.11288)1.000:0.20018,((((((750554050__Streptomyces_acidiscabies
:0.05151,(503945237__Streptomyces_bingchenggensis:0.09643,916325889__Nocardiopsis_gilva:0.10456)0
.601:0.01145)0.861:0.02015,(296847451__Nocardiopsis_dassonvillei_DSM_43111:0.16249,((516143664__N
ocardiopsis_kunsanensis:0.08561,((516144719__Nocardiopsis_kunsanensis:0.12550,516166536__Nocardio
psis_ganjiahuensis:0.06269)0.700:0.01734,516184175__Nocardiopsis_lucentensis:0.10244)0.768:0.0192
3)0.922:0.02785,736504009__Actinomadura_rifamycini:0.14695)0.773:0.01649)0.947:0.03544)0.780:0.02
095,703021414__Actinomadura_madurae:0.13264)0.628:0.00394,(270508069__Streptosporangium_roseum_DS
M_43021:0.06926,(502652377__Streptosporangium_roseum:0.05196,664394896__Streptosporangium_amethys
togenes:0.04746)0.466:0.01455)0.721:0.01375)0.929:0.04116,(491458270__Streptomyces_pristinaespira
lis:0.12817,(702616456__Streptomyces_virginiae:0.24876,((((759742382__Streptomyces_fulvoviolaceus
:0.02252,(759990428__Streptomyces_xylophagus:0.04084,(517887110__Streptomyces_prunicolor:0.02712,
917194967__Streptomyces_sp_NRRL_F_525:0.05729)0.462:0.01789)0.886:0.02391)0.947:0.02982,807125388
__Streptomyces_sp_WM6386:0.03576)0.383:0.00538,917219793__Streptomyces_violaceoruber:0.07968)0.88
7:0.02041,(490089111__Streptomyces_viridochromogenes:0.13695,(916576584__Streptomyces_sp_HGB0020:
0.00015,512057519__Streptomyces_sp_HGB0020:0.00598)0.953:0.04596)0.568:0.01243)0.284:0.03157)0.84
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:0.01775)0.839:0.01706)0.890:0.01815)0.991:0.08101,(493558269__Xenococcus_sp_PCC_7305:0.12559,(50
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:0.02295,((657933271__Scytonema_hofmanni_UTEX_B_1581:0.04762,(504992636__Oscillatoria_nigro_virid
is:0.09100,657934620__Scytonema_hofmanni_UTEX_B_1581:0.09630)0.751:0.01238)0.724:0.00991,50498819
5__Oscillatoria_nigro_viridis:0.05118)0.974:0.04841)0.863:0.02742)0.750:0.00016)0.856:0.01311)0.4
31:0.00582)0.807:0.00913);
```

Supplemental Figure 9.

The TnpB of *IS605* and *IS605B* transposons are targeted by the mobile group II introns

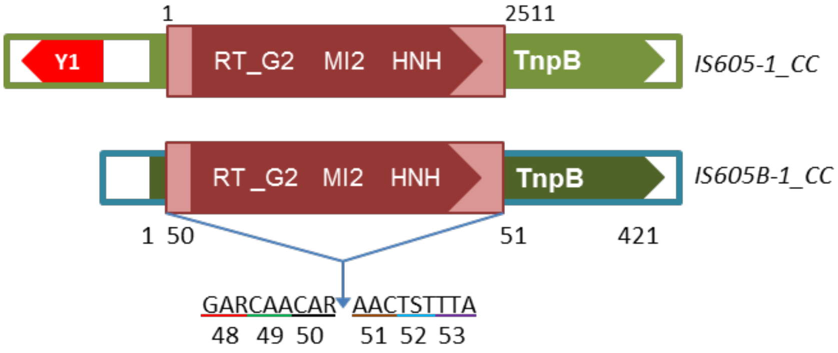

Figure S9A. Target site-specific insertions of identical copies of a 2511-bp mobile group 2 intron into TnpB-coding ORFs in the *IS605-1_CC* and *IS605B-1_CC* transposons. The transposons orientation was changed according to the orientations of the ORFs coding for the TnpB and RT_G2-MI2-HNH proteins. Amino acid positions of the encoded TnpB proteins corresponds to the TnpB protein encoded by the *IS605-1_NP* transposon. RT_G2, MI2, and HNH are the reverse transcriptase, RNA-binding maturase, and homing HNH endonuclease domains. TnpB-coding ORFs in *IS605-1_CC* and *IS605B-1_CC* transposons are only 60% identical to each other; there is no significant similarity between the remaining parts of these transposons.

In the *C. chthonoplastes PCC 7420* genome, we identified a 72-bp region that is ~86% identical to the 3'-sequence of ISC1-2_CC (Fig. S6A). In line with the findings reported in our paper, this region is the 3'-terminal portion of a *IS605*-like transposon: the 3' end of a TnpA gene is situated 25-bp upstream of this region, and the TnpB gene, which is transcribed in the opposite orientation, is located ~2.8-kb upstream of TnpA. This transposon, *IS605-1_CC*, is present in the *C. chtonoplastes* genome as a single copy; therefore its 5'-terminus cannot be defined without additional DNA sequences of similar transposons from other species. Using the TnpB gene sequence as a query in a BLASTN search against the bacterial sequences in GenBank, we found that the genomes of the cyanobacteria *Anabaena cylindrica PCC 7122* and *Nostoc sp. PCC 7107* contain, respectively, 2 and 4 sequences ~70% identical to the query. As a result, we identified two transposons, *IS605-1_AC* (2 copies 99.7% identical to each other) and *IS605-1_NS* (4 copies, including 3 copies 100% identical to each other). Based on the comparison of the TnpB ORFs in these two transposons with their homolog from *C. chthonoplastes*, we found that the latter is disrupted by a 2511-bp insertion that encodes a 600-aa protein that consists of a reverse transcriptase (RT_G2 family), a GIIM maturase and a HNH homing endonuclease which are the hallmarks of bacterial mobile group II introns {Lambowitz, 2011 #50} (Fig. S6A, S6B).

In addition to the identified insertion of the 2511-bp retroelement in the *IS605-1_CC* transposon, the *C. chthonoplastes* genome contains two copies of the same element that are 100% identical to each other and differ from the inserted copy by a single nucleotide substitution. Surprisingly, these two copies are inserted into the same position in another TnpB gene of an *IS605B-1_CC* transposon. The genome contains three nearly identical copies of this transposon. The transposon encodes a TnpB protein that is only 58% identical to TnpB in *IS605-1_CC*. One of these copies contains an intact TnpB gene whereas in the two other copies this genes is disrupted by the Group II intron insertions. All three insertions reside precisely at the same position between codons encoding EQQ and NC/SL amino acids (between aa-positions 50 and 51 in TnpB from *IS605-1_NS*). Given that the “empty” copy of *IS605B-1_CC* and the two copies containing the mobile intron are nearly identical, comparison of these transposons does not allow one to determine whether both insertions occurred recently and independently at the same target site in two identical copies or it was actually only one insertion followed by transposition of the “composite” *IS605B-1_CC* transposon. However, given the low DNA identity between *IS605-1_CC* and *IS605B-1_CC* (~60% between the TnpB genes), it is clear that nearly identical 2511-bp copies of the mobile intron were integrated independently into the GARCAACAR|AACTSTTA target site (Fig. S6A).

Due to the target-site specificity, the orientation of both ORFs, coding for TnpB and RT-HNH, is the same. Preliminary analysis reveals many other examples of insertion of mobile group II RT-HNH introns, distantly related to the one reported here, into different positions of TnpB genes (data not shown). Thus, the HNH nuclease domain present in Cas9 and IscB might have been originally contributed by a mobile group II intron inserted into a TnpB gene.

```
gi|193882179 22972 CCGCTATCCCTCCTCACCCTCCTGAGCCTGCGAAGGATCTGCTGAGGGTGAGGACTCTCGCGAACT-CGTTGA 22901
                   || |||||||||::||||||||||||||||||||||||||||||||||||::| ||| |||||| |-|| |||
    ISC1-2_CC 1412 CCTCTATCCCTCTCCACCCTCCTGAGCCTGCGAAGGATCTGCTGAGGGTGGAGTCTCACGCGAAATACGATGA 1484
```

Figure S9B. Pairwise alignment of the 73-bp 3’-terminus of *ISC1-2_CC* (bottom sequence) with a 72-bp sequence identified in the C. chthonoplastes PCC 7420 genome (top sequence).

```
IS605-1_CC       1 4399
IS605-1_AC       1 1921    Identity = 0.704

S: ATGAACTACCCAGCCCTA-----CTTCG-TTGAGGTCTGGGTTTCTACAACC------------------
   ||||||||||:----|||-----|||||-||||: |  :|||||||||| ||------------------
Q: ATGAACTACCT----CTAGTTAGCTTCGCTTGAACTAGAGGTTTCTACATCCTCTAGTTTGTTATTAGCA

S: -----------AGACCAGTATGACTATGTTTCTGACGCTTCACTTGTCCTAGTTGCTTCATGCTTCCTGT
   -----------|||--------------|||:||||||||| :|| :|||||||||:||||||||||:|:
Q: AAGTCCCCTTGAGA--------------TTTTTGACGCTTCTTTTCCCCTAGTTGCCTCATGCTTCCCGC

S: TTGCTTACGCTTACAGGTTTCTGAAGTAGAGCTAGAGACATCAGCGTCTGCGAGGCTCGTTCCAAACCCC
   || :||:||------||| : |||||||||||:|||:| ||||||||||:||||||| ||||| ||||||
Q: TTTTTTGCG------GGTGCGTGAAGTAGAGCCAGAAAGATCAGCGTCTACGAGGCTAGTTCCTAACCCC

S: GGTAGAATTCCTAATGCCCACAAAAGCATTACTAGAGCAGCGGCTAAATCCCTATCCATTTCGAGTCCAC
   ||||||:| |||  ||||||  ||||||| ||:  ||||||:|| | ||||||:|||    |: ::||||
Q: GGTAGAGTGCCTTTTGCCCAATAAAGCATGACCTCAGCAGCAGCAATATCCCTGTCCTGAACATACCCAC

S: ATTCATGGCAATGGTGAACTCTTTCATCTAAGGTCTTTTTGGCTTGGTTTCCGCATTTAGGGCAGGTCTG
   |  ||: ||| ||:||  ||| ||:||| |: ||:||:|||  :||:||||||||||| ||:|||||:||
Q: AAACACCGCACTGATGCTCTCGTTTATCGAGTGTTTTCTTGTGCTGATTTCCGCATTTTGGACAGGTTTG

S: AGATGGTTTCACTTTGCGAGTAGGAACCTCTACAAAAACCCCACCAGCGTTTTTTACTTTGTACTCAATC
   |   |||||:|||| :||:|| ||:||:||:||:||:|| ||||||:: | ||:|||||||||:|:|||
Q: ACTAGGTTTTACTTGACGGGTTGGGACTTCCACGAAGACACCACCAATTTGTTCTACTTTGTATTTAATA

S: GCTGACCTTAGCATCCCCATACCTACGTCTAAGATGGATTTATTTAGCCCAGCCTTTTGCTTTTTGCGTT
   | || :|| |||||||| | |||:||||| |::|| ||||||||||:||||||:||||||||||||||:|
Q: GATGCTCTAAGCATCCCAAAACCCACGTCAAGAATTGATTTATTTAACCCAGCTTTTTGCTTTTTGCGCT

S: TGCCTTTTTTGGAAGAGCGGGTCATTTTAGAGACTTCTAGTTTTTCCGTAGCAACGAAGCTATTACAGCT
   |:|||||:|| |    :| :||||| ||   :||||||||||||||||| ||||:||||||||||| ||:
Q: TACCTTTCTTCGCTTTACTAGTCATATTCTTAACTTCTAGTTTTTCCGTTGCAATGAAGCTATTACTGCC

S: AACAATGTCTGTTGCTACTTGGTGTACCCAATTCTGACGCTGATTAGCTAC-CTTACGGGTTACTTTGCT
   :|: || |||::||| |||||:||||||||:|::|||||:|||||||| ||-| |:|-|::|| |||:||
Q: GATTATTTCTACTGCAACTTGATGTACCCAGTCTTGACGTTGATTAGCAACTCGTGC-GACTAGTTTACT

S: AATCTTGGCTTGGGTCTTTTTCCACCGATTAGAAGCTTTCTGTTTTTTTCTTCTGTTAGGAGGTCTTTTC
   ||::|| :||||||::||||| :|:|  :|||||||:||   |||||| :||||:|| || |  | |||
Q: AACTTTCACTTGGGCTTTTTTATATCTTCTAGAAGCCTTGATTTTTTTGTTTCTATTTGGTGCGCGTTTA

S: CGACGTTTTCCCTTAGAAAGACGCTTAATTTTGGCTTCAGCTTTTCGCAAAAACTTAGGAGCTTCAATGA
   || | :||::||||||||:  : :||:|||||   ||||||  |||   ||||||||||:|| |||||
Q: CGTCTCTTCTCCTTAGAAGCTTTTTTGATTTTCTGTTCAGCAATTCTATAAAACTTAGGGGCATCAATTT

S: AAGAATGATTTTCTCCATCAGTTATTGCTAACGCTGACTTGCACCCAAAATCGATACCAACTGAACCAA-
   :  :|||||||||:||:||:|| |||| |||:|||||:||:||||| |||||:|| || ||:| |||||-
Q: GTTGATGATTTTCCCCGTCGGTAATTGATAATGCTGATTTACACCCTAAATCAATTCCTACCGCACCAAT

S: -----AATCTGTTTGTCTCGTTGCCGCCTGTAATTCAGTTATATTAACGGTTATACTGGCATACCATTTT
   -----|| :| || ||:|::  ||:  || ||| ------|:|||||| ||||||  |||:||||||||
Q: GGGTAAAGTTTTTGGTTTTAGGGCTTGCTCTAAA------ACATTAACTGTTATAGAGGCGTACCATTTG

S: CTATTGCGATAAACAATAGTGCAGGTCGTTGGAGTTCCCCAGATA-CGGGCTTTGCCGCGCATCTGGATT
   |:||||||| |||||||||||||:|| || ||  |:|||||-|||-: |||||  ||:|||||:||:||:
Q: CCATTGCGAAAAACAATAGTGCAAGTAGTAGGTTTCCCCCA-ATATTTGGCTTGTCCACGCATTTGAATC
```

```
S: GAGCCAATCTTAGCTAACTCTAGATAACCGTTATCACCCGTTGTATGTACCTTCCAGCCTGTTTTACTTG
     ||||||:||:| ||: |::||||| ||:|| ||:||  | |  | |||:||  | || |:   |::||
Q: TTGCCAATTTTGGATAGATTCAGATACCCATTCTCGCCATTAGATTCTACTTTAAACCCAGCAGAATCTG

S: GATAAGTCCATCCAGAATAATGTTTAATTGACTTATATTTGGGTCGCTTTGCTAAACCCTTAAACCAACG
   |||| |||||:|| ||||||||::|:|||||:||: ||:|:|| ||:||  |:|| ||:||||||||:||
Q: GATATGTCCACCCCGAATAATGCCTGATTGATTTGAATCTAGGACGTTTACCCAACCCTTTAAACCAGCG

S: ATTAAATGCGTAATCGACACGCTTTAAAGTGGCTTGTAGAGTCATGG-----AATTGCATTCTTTGTACT
    |:||| ||: ||||:|| ||||||||||| ||:||||:||-|||||-----||----::||||||||:|
Q: TTCAAAAGCAAAATCAACCCGCTTTAAAGTCGCCTGTAAAG-CATGGCTAGGAA----GCTCTTTGTATT
                                 1176
S: CTGTCCAAACTTCTTTAAAAGCCGGTAAAGAGTTATTAAACTCAACGAGACTGTCACCAGTCCCCCTGGT
   ||::|||:||||||||||| ||:||:||| |:||------------------------------------
Q: CTACCCAGACTTCTTTAAACGCTGGCAAACAATT------------------------------------

S: CTTCAAAACCGTGCGTGAAAGTTTCCTCTCACACGGCTCCTCAACGATAAGGTGCAAGTCATGCATACCT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CATTACCCATTTGTCCTCGACTCTTTCGAGCCTTTTGGTGAGCTTAGGCTTGGCACTGTTACAGCCAGAT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGATTGCCGAGACTGCCATCTGTGACGGTCTTTGTGTCATGGCAATGTCTATGTAGAAGCTGCCAATTAT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CGTAGAAATCCTTTCCACCTTGCGACTTAGGGATTCTGTGGTCAACTTCCATCACATCGTTTTCACGGAA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AATTAATCCGCAGTGAGTACATTTCCCTTTTTGCTTCTTCAACAATGTTGCCAGTGTCTTAGGCATTTCA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGGTTGTTACCCATTCTTGAACTCCAATAAACCAAGTTGCCGTTGTATGGGGACGATTCGCCCTTAACCT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTACATAGCGCTTAATTGGTGTTTCGCTATGTTTTAGTAACCGCGTAGGGTTATTACCTTTTTGCCTGGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGCGAATACCCAGTTGTCGCCGTCTATGGATTGCCAATACTTCTTTGACACCCATCCCCCGGATTTTTTG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGGTGTCGGCGCTTTGCCCAAGCTCTGAGCTTCTGGTACATGAGGTAATCTTGGTCACAGTAAGCCACCT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TACTTACTTGTGTTGCGTAGTAGTTAGCCCATCCCCGAATAATCGGGTTCAGTTTCTTAATTAGCGCCAC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTGTGGTGCATTCCTGTGGGCGTTGATAACTTCCGCAATCTGTTCGTAGTGTACCTTCTGCTTATCCTTG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTTGGGGTGATGATTGGTTTTATTCCTAGCGCTCTTCCATATTTGTCTTTTCCAGAGTGGTATTTACCCA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTTTGTATTGACGTATATTGAAGCCAAGGAAATCAAATCCTGGCTGTTCTTGTTCATACGGGTTGAGGGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GTGAGCAAGTCTTGTTTTGCTAGGTTTTAGTTCCAAACCCATGTCTTTCAACCATTCCTGGATTATATCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTGCCACTTTGGACGATGGTTAAGTCTTCGTGGAGAATCACGAAGTCGTCGGCATATCTGATCACGGATG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------
```

```
S: GAGGATAGAATGTCTTCTTTACCCCATTTTCAGAGTATCCCCGTTTTGGGAATACCCTTTTGATTAGATT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTCCATCCCGTGGAGGGCAATGTTTGCTAGTAACGGAGAAATGACCCCGCCCTGTGGCGTTCCCTCAGTT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GTTGGAAACAACTGCTTTGCGTCCATCACTCCCCCTTTTAACCATGCTCGGATTTGACGGCGTATGGTAG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGAATGTATTTAATTTTCTTAGCAGTGCTTTATGGTCGATTTGGTCAAAGCATTTAGCAATATCGGCATC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AAGGACATATTTGCCCTTAAACCTAATTGTGTCATATATAGCCTGAACCGCATCGTGACATGAGCGTCCG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGTCTGAAACCGTATGAGTTGGCTTCAAATCGCGCTTCCCATTCTGGCTCTAGTGCCAGTTTGACAAGTG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTTGCAAAGCTCGGTCTTTCATTGTCGGGATGCCTAAAGGTCTTTTCTCCTCCTTTCCGGGTTTGGGAAT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CCATACTCGCCTGGTTGGAGCGACCTTTGAACATAGTTTTAGATTTTCAACCAAGATGAGACGTTGCTTT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGGGTCAGTGACTTAACACCATCCACACCTGCCGTCTTCTTACCTTGATTGTCTTGGGTAACCCGGCGAA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CCGAGAGACATTTTGCTGCCCAGGACTTCATCAGCATCTTTTGGAGTCTGCGAGTCATTTTCACATCGCC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: ACGCTGAGAGGCTCGATAGATTCTCTTCTGCAACTTGTAGACTTTACGCTCTAGTTTTTGCCAGGGTATT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCCTTCCATTCCATCGTAGTCTTTAAACTCGCTTTAGACATTTGTATTGCTACTTAAGACTCTATCTTTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTTATCATCGTGAGTCTGTTGGCGTATCCCTCTTATTAGTAGAGAGCGTTAGCTTCTGACTCAATCTTTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTCCCATTGCTTGCGGTTGGCACCTACTCAGGCATCGACCTGACTGAGAGCATAAGGGAGGTTATCTCGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TCCTGATAGCCATTGTTTGAACTTTTAGGATGGTACTATCCACCGGGTTTATAGGGAGTACAAGTTGGTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AACAACAAAATTGCCAACCCCTGATTTCCTGTGCCTTTTGGCTCCAGTGTGTCAGCCTTATTACACTGGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TCTTCGTAACGATGGTTCAGTCGTACCTTCGTATTCCTATCCATGAGTTCTTGCTCGATGGTTGCCGGAT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TAGGCTTCCAGCATTGCCACCTTTCACCCCCGCTTTAGGCTTTGATAACCAGTCTCAAACCTAGGGGACA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AGGTTTTAAAAACCCTGGCTCTGTGTGCTTTTACTCCTGTACTTAGAGAGTAGGACTTGAGAGTTTGCTT
   ----------------------------------------------------------------------
```

```
Q: ----------------------------------------------------------------------

S: TCTCTCACCTACATGGCTATCAAGTTGTCAAGGTTCAGACCTTGCAGGTAATCCTCTATCCATTTCAGGA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------
                            3688
S: ATAGTTTCTACCTAACGATTCGCACTTGTTGCTCGAAGTAGTCAACGCTATGGTTGAACTTCTGGTACTG
   -------------------------|||||||||:||:||:||||| :|:|||||:|||||:||:||:||
Q: -------------------------TTGTTGCTCAAAATAATCAACCTTGTGGTTAAACTTTTGATATTG

S: GGTAAACCGATTACAGACAGCAGCGTTGTACAGGTCTTTGTGCAACTTACGGTGATACCGCAATGTCTGC
   ||||||:| :|||: ||| ||:|||||: |:|:|||||||||:||||| |||||||||||||||-|:||
Q: GGTAAATCTGTTATTGACTGCGGCGTTAAATAAGTCTTTGTGTAACTTTCGGTGATACCGCAAT-TTTGA

S: TTTTGCT-TTTTATTGGGGTATAGCCGAAAATTTACACGTCTTGTTGGCATCGC-----TGTTCCCTC--
   ||: |:|-|:| ||| ||:||||:|||:||| |:|:|||||| :|:| ||: |:-----| | |||||--
Q: TTCAGTTGTCTGATTTGGATATAACCGGAAAGTCATACGTCTGATCGCCACAGTAAATATTTACCCTCTG

S: --------CTGTTACACT--TAAGGTAA--CAGATTCAGGTGAGGGTATGTCAAGTGAAAGCTAGAAAAG
   --------||||||: :|--||| :|||--:|||: |:||----||| |||||||||:  ||| | ||||
Q: TTTAAAATCTGTTATTTTATTAATATAAATTAGACACGGG----GGTTTGTCAAGTGGTTGCTCGTAAAG

S: GTTCGCACTCTGTATTTTCTGTTCAACTGCATATAGTATTTGTAACTAAATACAGGCGCAAGATTATTAC
   |:||:||| |||||||:|||:|||| ||:||: | :|||||||:||||||||| |: : ||:|| ||||
Q: GCTCACACGCTGTATTCTCTATTCACCTACACTTTATATTTGTGACTAAATACCGAAAGAAAATAATTAA

S: AGTGGGAATGTTACAGAGATTACATGAAGTGCTTGCCAATGTTTGTATTAAGACAAAGTGTCGGTTAGTA
    |:   |||::|: |:||| |:||:||::| :|||| |||:|:||:|||||||| || ||:  :||||||
Q: TGCTCCAATACTGGAAAGAATGCACGAGATTTTTGCAAATATCTGCATTAAGACTAACTGCATATTAGTA

S: GAGTTTTCAGGAGAAGCTGACCATGTACATCTATTAGTAGACTTTCATCCTGACAACAATTTATCATCTC
   |||||||| || |||   ||:||:|| |||:||:|:||:|||| |||:||||||||:|||-----||:||
Q: GAGTTTTCTGGTGAACAAGATCACGTTCATTTACTGGTGGACTATCACCCTGACAATAAT-----ATTTC

S: TAATTGG-----TAGTATGAAGTCTGCATCTAGTCGAATCATCAGAAAAGACTTTGCTGCTCAACTGTCA
   |:|||  -----|||| |:||:|||||   |||:||:||:||: | ||||| |||:-------------|
Q: TGATTTTACATCTAGTTTAAAATCTGCTAGTAGCCGGATTATTCGTAAAGAATTTA-------------A

S: AAAAC-------------TTATACTAAGTCGGCATTTTGGTCGGGTTCTTATTATGTTGCGTCTACTGGC
   |:|||-------------||||   ||::| |: |||||||| :|:|| |||||||| ||:|| | |||:
Q: AGAACATATTGATAAATTTTATTGGAAACCTGTCTTTTGGTCTAGCTCGTATTATGTGGCATCAAGTGGT

S: GGTGCGCCTATTGAGAGAATTAAGGC-TTACATCAAATCACAAGACGCACCCA-----------------
   |||||||| |||||-|:||:|||::|- ||:||:||:  |||||||||||| |-----------------
Q: GGTGCGCCAATTGA-AAAACTAAAACAATATATTAAGGAACAAGACGCACCAACGAAGTAAATAGAATAG

S: -AAAATTGATTGCCTCCGTTCCTCCGGCAAT---CCGCTATCCCTCCTCACCCTCCTGAGCCTGCGAAGG
   -||:||||:||:::|:||:|:| |:-|||||---||||| |  |:|||-|||||------------| ||
Q: AAAGATTGGTTATTTTCGCTTCACT-GCAATAACCCGCTCTAACCCCT-ACCCT------------ATGG

S: ATCTGCTGAGGGTGAGGACTCTCGCGA
   :| :::|||||||::||||| :|||||
Q: GTACATTGAGGGTAGGGACTGCCGCGA
```

Figure S9C. Pairwise alignment of the 4399-bp *ISC1-2_CC* transposon containing the insertion of the mobile group 2 retroelement (shown in bold) with a *IS605-1_AC* transposon identified in the *Anabaena cylindrica PCC 7122* genome.

```
IS605-1_CC             1176 64
IS605-1_AC_TnpB          51 419
Identity = 0.7027

S:1176 NSLPAFKEVWTEYKECNSMTLQATLKRVDYAFNRWFKGLAKRPKYKSIKHYSGWTYPSKTGWKVHTTGDN 967
       N LPAFKEVW EYKE  S  LQATLKRVD+AF RWFKGL:KRP++KSI+HYSGWTYP   G+KV + G+N
Q:  51 NCLPAFKEVWVEYKELPSHALQATLKRVDFAFERWFKGLGKRPRFKSIRHYSGWTYPDSAGFKVESNGEN 120

S: 966 GYLELAKIGSIQMRGKARIWGTPTTCTIVYRNRKWYASITVNITELQAATRQTDFGSVGIDFGCKSALAI 757
       GYL L+KIG IQMRG+A+ WG PTTCTIV+RN KWYASITVN+ E     +    G+VGID GCKSAL+I
```

```
Q: 121 GYLNLSKIGKIQMRGQAKYWGKPTTCTIVFRNGKWYASITVNVLEQALKPKTLPIGAVGIDLGCKSALSI 190

S: 756 TDGENHSFIEAPKFLRKAEAKIKRLSKGKRRKRPPNRRKKQKASNRWKKTQAKISKVTRKVANQRQNWVH 547
       TDGENH  I+APKF R AE KIK+ SK KRRKR PNR KK KAS R+KK Q K+SK+  +VANQRQ+WVH
Q: 191 TDGENHQQIDAPKFYRIAEQKIKKASKEKRRKRAPNRNKKIKASRRYKKAQVKVSKLVARVANQRQDWVH 260

S: 546 QVATDIVSCNSFVATEKLEVSKMTRSSKKGKRKKQKAGLNKSILDVGMGMLRSAIEYKVKNAGGVFVEVP 337
       QVA +I+  NSF+ATEKLEV  MT  +KKGKRKKQKAGLNKSILDVG GMLR++I+YKV+  GGVFVEVP
Q: 261 QVAVEIIGSNSFIATEKLEVKNMTSKAKKGKRKKQKAGLNKSILDVGFGMLRASIKYKVEQIGGVFVEVP 330

S: 336 TRKVKPSQTCPKCGNQAKKTLDERVHHCHECGLEMDRDLAAALVMLLWALGILPGFGTSLADADVSSSTS 127
       TR+VKPSQTCPKCGNQ KKTLD+R H C  CG   DRD+AAA VML WA G LPG GTSL DAD+S STS
Q: 331 TRQVKPSQTCPKCGNQHKKTLDKREHQCGVCGYVQDRDIAAAEVMLYWAKGTLPGLGTSLVDADLSGSTS 400

S: 126 ETCKRKQTGSMKQLGQVKRQK 64
        T--RK+ GSM+QLG+ KRQK
Q: 401 RT--RKKAGSMRQLGEKKRQK 419


IS605-1_CC         3837 3688
IS605-1_AC_TnpB       1 50
Identity = 0.7800

S: 3837 VNFRLYPNKKQKQTLRYHRKLHKDLYNAAVCNRFTQYQKFNHSVDYFEQQ 3688
        + FRLYPN+  +  LRYHRKLHKDL+NAAV NRFTQYQKFNH VDYFEQQ
Q:    1 MTFRLYPNQTTESKLRYHRKLHKDLFNAAVNNRFTQYQKFNHKVDYFEQQ 50
```

D)

```
IS605-1_CC       1 4399
IS605-1_NS       1 1919
Identity = 0.6996

S: ATGAACTACCCAGCCCT-ACTTCG-TTGAGGTCTGGGTTTCTACAACC----------------------
   ||||||||||||   :|-:|||||-:|||: | |||||||||||| ||----------------------
Q: ATGAACTACCCACAATTGGCTTCGCCTGAACTGTGGGTTTCTACATCCCCCAGTTCGTTTTTAGCGAGTT

S: -------AGACCAGTATGACTATGTTTCTGACGCTTCACTTGTCCTAGTTGCTTCATGCTTCCTGTTTGC
   -------|||--------------|||:|| |||||| ::  :|||||||||:||||   ||| | ||||
Q: TTTCTGTAGA--------------TTTTTGTCGCTTCTTCGCCCCTAGTTGCCTCATCGATCCAGATTGC

S: TTACGCTTACAGGTTTCTGAAGTAGAGCTAGA-GACATCAGCGTCTGCGAGGCTCGTTCCAAACCCCGGT
   |||||||||| :||   || :| ||||||||:-|||-|| ||| ||:||||||| ||||| |||||||||
Q: TTACGCTTACCAGTAGATGTGGGAGAGCTAGGCGAC-TCTGCGACTACGAGGCTAGTTCCTAACCCCGGT

S: AGAATTCCTAATGCCCACAAAAGCATTACTAGAGCAGCGGCTAAATCCCTATCCATTTCGAGTCCACATT
   |||:| |||   | |||  |||||||||||  :|||||:|| | ||||||||||  : || :|||:||
Q: AGAGTACCTTTAGACCAATAAAGCATTACTTCGGCAGCAGCAATATCCCTATCCTGCACGTATCCGCAAA

S: CATGGCAATGGTGAACTCTTTCATCTAAGGTCTTTTTGGCTTGGTTTCCGCATTTAGGGCAGGTCTGAGA
   ||  :|||| :|||||||   :||| |::||:|||||:  |||:|  ||:||:|| ||:|||||:|||
Q: CAACACAATTATGAACTCGAATATCAAGAGTTTTTTTATGTTGATGACCACACTTCGGACAGGTTTGACT

S: TGGTTTCACTTTGCGAGTAGGAACCTCTACAAAAACCCCACCAGCGTTTTTTACTTTGTACTCAATCGC-
    ||:||:||||| :  || |||||:|||||||| || ||||||:: | :|: ||||||||||::|| |:-
Q: AGGCTTTACTTTCTTCGTTGGAACTTCTACAAATACACCACCAATTTGCTCAACTTTGTACTTGATGGTA

S: ---TGACCTTAGCATCCCCATACCTACGTCTAAGATGGATTTATTTAGCCCAGCCTTTTGCTTTTTGCGT
   ---:||----|||||:|| | | | ||:||||: || ||:|||||:||:|| ||:|||||||||||:||:
Q: TTGCGA----AGCATTCCAAAAGCAACATCTAGTATTGACTTATTCAGTCCTGCTTTTTGCTTTTTACGC

S: TTGCCTTTTTTGGAAGAGCGGGTCATTTTAGAGACTTCTAGTTTTTCCGTAGCAACGAAGCTATTACAGC
   ||||||||:|| |    :| :||||| ||    |||||||||||||| || |||||||||||||||| ||
Q: TTGCCTTTCTTTGCTTTACTAGTCATGTTTTTACTTCTAGTTTTTCAGTCGCAACGAAGCTATTACCGC

S: TAACAATGTCTGTTGCTACTTGGTGTACCCAATTCTGACGCTGATTAGCTACCTTACGGGTTACTTTGCT
   | ||||| ||||:|||||||||:||||||||:||:|| | :|||||| | ||:|||||:::|| :||: |
Q: TTACAATTTCTGCTGCTACTTGATGTACCCAGTTTTGTCTTTGATTACCAACTTTACGAACTAGCTTAGT

S: AATCTTGGCTTGGGTCTTTTTCCACCGATTAGAAGCTTTCTGTTTTTTTCTTCTGTTAGGAGGTCTTTTC
   ||:||| | |||||::||||| :|:|| :||||||||||   |||||| :||||:|| || |  | |||
Q: AACCTTTGATTGGGCTTTTTTATATCGTCTAGAAGCTTTAATTTTTTTGTTTCTATTTGGTGCGCGTTTA
```

```
S: CGACGTTTTCCCTTAGAAAGACGCTTAATTTTGGCTTCAGCTTTTCGCAAAAACTTAGGAGCTTCAATGA
   || | :||::||||||||:  : :||:|||||   |||||| |||| ||||||||||||||| ||:||
Q: CGCCTCTTCTCCTTAGAAGCTTTTTTGATTTTCTGTTCAGCATTTCTCAAAAACTTAGGAGCATCGATTT

S: AAGAATGATTTTCTCCATCAGTTATTGCTAACGCTGACTTGCACCCAAAATCGATACCAACTGAACCAAA
   :  :||||||:|||||||| || |||| |||:|||| :||:|| || ||:||:|||||||:|| |||||-
Q: GTTGATGATTCTCTCCATCCGTAATTGATAATGCTGCTTTACAACCTAAGTCAATACCAATTGCACCAA-

S: ATCTG----------------------TTTGTCTCGTTGCCGCCTGTAATTCAGTTATATTAACGGTTAT
   --|||----------------------|| |||| |:-------------------|:||:|||:|| ||
Q: --CTGGTAGAACTTTAGGCTTTAATGCTTGGTCTAGC-------------------ACATCAACAGTAAT

S: ACTGGCATACCATTTTCTATTGCGATAAACAATAGTGCAGGTCGTTGGAGTTCCCCAGATACGGGCTTTG
   |   ||:|||||||| ||||||||||||||:||||||||:|| ||||:  | |||||: :  ::||:|
Q: AGATGCGTACCATTTACTATTGCGATAAACGATAGTGCAAGTAGTTGATTTACCCCAACCCAAAGCCTGC

S: CCGCGCATCTGGATTGAGCCAATCTTAGCTAACTCTAGATAACCGTTATCACCCGTTGTATGTACCTTCC
   || ||||||||:||  : |||||:|||| :|: |: ||||| ||||| ||:||: : |  | |||:||
Q: CCCCGCATCTGAATACGTCCAATTTTAGACAGATTGAGATATCCGTTTTCGCCTTCAGATTCTACTTTAA

S: AGCCTGTTTTACTTGGATAAGTCCATCCAGAATAATGTTTAATTGACTTATATTTGGGTCGCTTTGCTAA
   |:||||: : :::|||||||||||||||| |||||||||:||||||||||| ||:| || |||||  |||:
Q: AACCTGCACAGTCTGGATAAGTCCATCCTGAATAATGTCTAATTGACTTAAATCTCGGACGCTTACCTAG

S: ACCCTTAAACCAACGATTAAATGCGTAATCGACACGCTTTAAAGTGGCTTGTAGAGTCATGGAATTGCAT
    ||:|||||||||||| |:||||||: ||||:|||||:||||| || |||||:||-----------|||||
Q: CCCTTTAAACCAACGCTCAAATGCAAAATCAACACGTTTTAATGTTGCTTGCAG-----------TGCAT

S: -----------TCTTTGTACTCTGTCCAAACTTCTTTAAAAGCCGGTAAAGAGTTATTAAACTCAACGAG
   -----------||||||||||||::|||||| |||||||| ||:||:||| |:||---------------
Q: GGCTGGGAAGTTCTTTGTACTCTACCCAAACATCTTTAAATGCTGGCAAACAATT---------------

S: ACTGTCACCAGTCCCCCTGGTCTTCAAAACCGTGCGTGAAAGTTTCCTCTCACACGGCTCCTCAACGATA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AGGTGCAAGTCATGCATACCTCATTACCCATTTGTCCTCGACTCTTTCGAGCCTTTTGGTGAGCTTAGGC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTGGCACTGTTACAGCCAGATTGATTGCCGAGACTGCCATCTGTGACGGTCTTTGTGTCATGGCAATGTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TATGTAGAAGCTGCCAATTATCGTAGAAATCCTTTCCACCTTGCGACTTAGGGATTCTGTGGTCAACTTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CATCACATCGTTTTCACGGAAAATTAATCCGCAGTGAGTACATTTCCCTTTTTGCTTCTTCAACAATGTT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCCAGTGTCTTAGGCATTTCAGGGTTGTTACCCATTCTTGAACTCCAATAAACCAAGTTGCCGTTGTATG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGGACGATTCGCCCTTAACCTTTACATAGCGCTTAATTGGTGTTTCGCTATGTTTTAGTAACCGCGTAGG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GTTATTACCTTTTTGCCTGGTTGCGAATACCCAGTTGTCGCCGTCTATGGATTGCCAATACTTCTTTGAC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: ACCCATCCCCCGGATTTTTTGGGGTGTCGGCGCTTTGCCCAAGCTCTGAGCTTCTGGTACATGAGGTAAT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTTGGTCACAGTAAGCCACCTTACTTACTTGTGTTGCGTAGTAGTTAGCCCATCCCCGAATAATCGGGTT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CAGTTTCTTAATTAGCGCCACTTGTGGTGCATTCCTGTGGGCGTTGATAACTTCCGCAATCTGTTCGTAG
   ----------------------------------------------------------------------
```

```
Q: ----------------------------------------------------------------------

S: TGTACCTTCTGCTTATCCTTGCTTGGGGTGATGATTGGTTTTATTCCTAGCGCTCTTCCATATTTGTCTT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTCCAGAGTGGTATTTACCCACTTTGTATTGACGTATATTGAAGCCAAGGAAATCAAATCCTGGCTGTTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TTGTTCATACGGGTTGAGGGTGTGAGCAAGTCTTGTTTTGCTAGGTTTTAGTTCCAAACCCATGTCTTTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AACCATTCCTGGATTATATCCTTGCCACTTTGGACGATGGTTAAGTCTTCGTGGAGAATCACGAAGTCGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CGGCATATCTGATCACGGATGGAGGATAGAATGTCTTCTTTACCCCATTTTCAGAGTATCCCCGTTTTGG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GAATACCCTTTTGATTAGATTTTCCATCCCGTGGAGGGCAATGTTTGCTAGTAACGGAGAAATGACCCCG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CCCTGTGGCGTTCCCTCAGTTGTTGGAAACAACTGCTTTGCGTCCATCACTCCCCCTTTTAACCATGCTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GGATTTGACGGCGTATGGTAGGGAATGTATTTAATTTTCTTAGCAGTGCTTTATGGTCGATTTGGTCAAA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCATTTAGCAATATCGGCATCAAGGACATATTTGCCCTTAAACCTAATTGTGTCATATATAGCCTGAACC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCATCGTGACATGAGCGTCCGGGTCTGAAACCGTATGAGTTGGCTTCAAATCGCGCTTCCCATTCTGGCT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTAGTGCCAGTTTGACAAGTGCTTGCAAAGCTCGGTCTTTCATTGTCGGGATGCCTAAAGGTCTTTTCTC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTCCTTTCCGGGTTTGGGAATCCATACTCGCCTGGTTGGAGCGACCTTTGAACATAGTTTTAGATTTTCA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: ACCAAGATGAGACGTTGCTTTGGGGTCAGTGACTTAACACCATCCACACCTGCCGTCTTCTTACCTTGAT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGTCTTGGGTAACCCGGCGAACCGAGAGACATTTTGCTGCCCAGGACTTCATCAGCATCTTTTGGAGTCT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCGAGTCATTTTCACATCGCCACGCTGAGAGGCTCGATAGATTCTCTTCTGCAACTTGTAGACTTTACGC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TCTAGTTTTTGCCAGGGTATTGCCTTCCATTCCATCGTAGTCTTTAAACTCGCTTTAGACATTTGTATTG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTACTTAAGACTCTATCTTTCCTTATCATCGTGAGTCTGTTGGCGTATCCCTCTTATTAGTAGAGAGCGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TAGCTTCTGACTCAATCTTTCCTCCCATTGCTTGCGGTTGGCACCTACTCAGGCATCGACCTGACTGAGA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GCATAAGGGAGGTTATCTCGTTCCTGATAGCCATTGTTTGAACTTTTAGGATGGTACTATCCACCGGGTT
```

```
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TATAGGGAGTACAAGTTGGTCAACAACAAAATTGCCAACCCCTGATTTCCTGTGCCTTTTGGCTCCAGTG
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: TGTCAGCCTTATTACACTGGTTCTTCGTAACGATGGTTCAGTCGTACCTTCGTATTCCTATCCATGAGTT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CTTGCTCGATGGTTGCCGGATTAGGCTTCCAGCATTGCCACCTTTCACCCCCGCTTTAGGCTTTGATAAC
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: CAGTCTCAAACCTAGGGGACAAGGTTTTAAAAACCCTGGCTCTGTGTGCTTTTACTCCTGTACTTAGAGA
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: GTAGGACTTGAGAGTTTGCTTTCTCTCACCTACATGGCTATCAAGTTGTCAAGGTTCAGACCTTGCAGGT
   ----------------------------------------------------------------------
Q: ----------------------------------------------------------------------

S: AATCCTCTATCCATTTCAGGAATAGTTTCTACCTAACGATTCGCACTTGTTGCTCGAAGTAGTCAACGCT
   ----------------------------------------------:||||||||:||:||:||||| :|
Q: ----------------------------------------------CTGTTGCTCAAAATAATCAACTTT

S: ATGGTTGAACTTCTGGTACTGGGTAAACCGATTACAGACAGCAGCGTTGTACAGGTCTTTGTGCAACTTA
   :||:||: |  |:| ||||||| ||||:| :|||:  || ||:||:|||||||:|||:||||| |:|||
Q: GTGATTATAGATTTTGTACTGGTTAAATCTGTTATTTACTGCGGCATTGTACAAGTCCTTGTGGAGCTTT

S: CGGTGATACCGCAATGTCTGCTTTTGCTTT-TTATTGGGGTATAGCCGAAAATTTACACGTCTTGTTGGC
   |||||||||||||| :|-|: ||: |:|||-|::|| |||||||:||||||| |:|: |||||||||| |
Q: CGGTGATACCGCAAAAT-TAATTCAGTTTTCTCGTTTGGGTATAACCGAAAAGTCATTCGTCTTGTTGCC

S: ATCG-------CTGTTCCCTCC------------TGTTACACTTAAGGTAACAGATTCAGGTGAGGGTA-
   |: |-------:||||:|||||------------|:|||  |  || ::|||:||: |------|| ||-
Q: ACAGGCTGTTTTTGTTTCCTCCAAAAATCTGGTATATTAATCAGAATACAACGGACAC------GGCTAC

S: -TGTCAAGTGAAAGCTAGAAAAGGTTCGCACTCTGTATTTTCTGTTCAACTGCATATAGTATTTGTAACT
   -||||||:||    || | ||||| ||:||| |||| ||||||:|||| :|:||| | || |||:| |||
Q: TTGTCAAATGCTTTCTCGTAAAGGGTCACACGCTGTTTTTTCTATTCACTTACATTTCGTTTTTATTACT

S: AAATACAGGCGCAAGATTATTACAGTGGGAATGTTACAGAGATTACATGAAGTGCTTGCCAATGTTTGTA
   ||:||: |  : ||::| ||||| |::  ||| :|  ||||: |:||:||::| :|||| |||:||||:|
Q: AAGTATCGTAAAAAAGTAATTACCGCACCAATCCTTGAGAGGATGCACGAGATTTTTGCAAATATTTGCA

S: TTAAGACAAAGTGTCGGTTAGTAGAGTTTTCAGGAGAAGCTGACCATGTACATCTATTAGTAGACTTTCA
   ||||:|| || ||:   ||:|| ||:||:||||| ||||  |||||||||||:||:|:||:|||| |||
Q: TTAAAACTAATTGCATTTTGGTTGAATTCTCAGGTGAAGAAGACCATGTACATTTACTGGTGGACTATCA

S: TCCTGACAACAATTTATC-------ATCTCTAATTGGTAGTATGAAGTCTGCATCTAGTCGAATCATCAG
   :|| ||||||||| | ||-------|:|||||:||-------|:||:|||||   |||| |::||||: |
Q: CCCAGACAACAATATTTCTGACTTTACCTCTAGTT-------TAAAATCTGCTAGTAGTAGGGTCATTCG

S: AAAAGACTTTGCTGCTCAACTGTCAAAAACTTATACT--AAGTCGGCATTTTGGTCGGGTTCTTATTATG
    ||||| |||:  |  ||--|:|::|||| || ||||--||::|  ::|||||||| :|:|| |||||||
Q: TAAAGAATTTAAGGAGCA--TATTGAAAAGTTTTACTGGAAACCTTTGTTTTGGTCTAGCTCGTATTATG

S: TTGCGTCTACTGGCGGTGCGCCTATTGAGAGAATTAAGGCTTACATCAAATCACAAGACGCACCCA----
   | ||||| | ||||||:||:|| |||||  :| |||:|   ||:||:|||  :|||||:||||| |----
Q: TAGCGTCAAGTGGCGGCGCACCGATTGATCAACTTAGGCAATATATTAAAGAGCAAGATGCACCGACCGA

S: --AAA-----ATTGATTGCCTCCGTTCC--TCCGGCAATCCGCT---ATCCCTCCTCACCCTCCTGAGCC
   --|||-----||||:||:::|||::|:|--|||:::||:|||||---||||||----||||| ||:|| -
Q: ATAAATATGGATTGGTTATTTCCACTTCGTTCCAATAACCCGCTCCGATCCCT----ACCCTACTAAGA-

S: TGCGAAGGATCTGCTGAGGGTGAGGACTCTCGCGA
   ------------|:|||||||::||||| :|||||
Q: ------------GTTGAGGGTAGGGACTGCCGCGA
```

Fig. S9E)

```
IS605-1_CC           1176 64
IS605-1_NS_TnpB        51 421
Identity = 0.6900

S: 1176 NSLPAFKEVWTEYKECNSMTLQATLKRVDYAFNRWFKGLAKRPKYKSIKHYSGWTYPSKTGWKVHTTGDN 967
        N LPAFK+VW EYKE  S  LQATLKRVD+AF RWFKGL:KRP++KSI+HYSGWTYP   G+KV + G+N
Q:   51 NCLPAFKDVWVEYKELPSHALQATLKRVDFAFERWFKGLGKRPRFKSIRHYSGWTYPDCAGFKVESEGEN 120

S: 966 GYLELAKIGSIQMRGKARIWGTPTTCTIVYRNRKWYASITVNITELQAATRQTDFGSVGIDFGCKSALAI 757
       GYL L+KIG IQMRG+A  WG  TTCTIVYRN KWYASITV++ +     +    G++GID GCK+AL+I
Q: 121 GYLNLSKIGRIQMRGQALGWGKSTTCTIVYRNSKWYASITVDVLDQALKPKVLPVGAIGIDLGCKAALSI 190

S: 756 TDGENHSFIEAPKFLRKAEAKIKRLSKGKRRKRPPNRRKKQKASNRWKKTQAKISKVTRKVANQRQNWVH 547
       TDGENH  I+APKFLR AE KIK+ SK KRRKR PNR KK KAS R+KK Q+K++K+ RKV:NQRQNWVH
Q: 191 TDGENHQQIDAPKFLRNAEQKIKKASKEKRRKRAPNRNKKIKASRRYKKAQSKVTKLVRKVGNQRQNWVH 260

S: 546 QVATDIVSCNSFVATEKLEVSKMTRSSKKGKRKKQKAGLNKSILDVGMGMLRSAIEYKVKNAGGVFVEVP 337
       QVA +IVS NSFVATEKLEV  MT  +KKGKRKKQKAGLNKSILDV: GMLR+ I+YKV+  GGVFVEVP
Q: 261 QVAAEIVSGNSFVATEKLEVKNMTSKAKKGKRKKQKAGLNKSILDVAFGMLRNTIKYKVEQIGGVFVEVP 330

S: 336 TRKVKPSQTCPKCGNQAKKTLDERVHHCHECGLEMDRDLAAALVMLLWALGILPGFGTSLADADVSSSTS 127
       T+KVKPSQTCPKCG+Q KKTLD RVH+C  CG   DRD+AAA VML W+ G LPG GTSL  A+  SS +
Q: 331 TKKVKPSQTCPKCGHQHKKTLDIRVHNCVVCGYVQDRDIAAAEVMLYWSKGTLPGLGTSLVVAESPSSPT 400

S: 126 ETCKRKQTGSMKQLGQVKRQK 64
        T KRKQ+GSM+QLG  KRQK
Q: 401 STGKRKQSGSMRQLGAKKRQK 421

IS605-1_CC         3837 3688
IS605-1_NS_TnpB       1 50
Identity = 0.7400

S: 3837 VNFRLYPNKKQKQTLRYHRKLHKDLYNAAVCNRFTQYQKFNHSVDYFEQQ 3688
        + FRLYPN+K +  LRYHRKLHKDLYNAAV NRF QY+ +NH VDYFEQQ
Q:    1 MTFRLYPNEKTELILRYHRKLHKDLYNAAVNNRFNQYKIYNHKVDYFEQQ 50
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