

16_k141_319369	Bacteria: 1.00	Proteobacteria: 1.00	NA	NA	NA	NA	Proteobacteria bacterium TMED61: 0.84
16_k141_339408	Bacteria: 1.00	Bacteroidetes: 0.86	no support	no support	no support	no support	no support
16_k141_392261	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
16_k141_414130	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 1.00	Rhodobacteraceae: 1.00	no support	no support
16_k141_506975	Bacteria: 1.00	Bacteroidetes: 0.76	Flavobacteriia: 0.76	Flavobacteriales: 0.76	no support	no support	no support
16_k141_552797	no support	no support	no support	no support	no support	no support	no support
16_k141_567513	Bacteria: 0.68	no support	no support	no support	no support	no support	no support
16_k141_580000	Eukaryota: 1.00	NA	Pelagophyceae: 0.51	Pelagomonadales: 0.51	NA	Aureococcus: 0.51	Aureococcus anophagefferens*: 0.51
16_k141_697129	Bacteria: 0.54	no support	no support	no support	no support	no support	no support
16_k141_698950	no support	no support	no support	no support	no support	no support	no support
16_k141_73806	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
16_k141_752405	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
16_k141_805129	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
16_k141_814350	Eukaryota: 1.00	NA	Pelagophyceae: 1.00	Pelagomonadales: 1.00	NA	Aureococcus: 1.00	Aureococcus anophagefferens*: 1.00
16_k141_884553	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
16_k141_91757	Bacteria: 1.00	Lentisphaerae: 0.76	Lentisphaeria: 0.70	Lentisphaerales: 0.58	Lentisphaeraceae: 0.58	no support	no support
16_k141_920012	Bacteria: 0.90	no support	no support	no support	no support	no support	no support
16_k141_982964	Bacteria: 0.63	no support	no support	no support	no support	no support	no support
17_k141_239172	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
17_k141_271030	Bacteria: 1.00	Lentisphaerae: 0.85	Lentisphaeria: 0.83	Lentisphaerales: 0.71	Lentisphaeraceae: 0.71	NA	Lentisphaeraceae bacterium*: 0.60
17_k141_336292	Bacteria: 1.00	Lentisphaerae: 0.83	Lentisphaeria: 0.66	Lentisphaerales: 0.64	Lentisphaeraceae: 0.64	no support	no support
17_k141_358034	Bacteria: 0.90	no support	no support	no support	no support	no support	no support
17_k141_389870	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
17_k141_434876	no support	no support	no support	no support	no support	no support	no support
17_k141_451521	Bacteria: 1.00	Actinobacteria: 0.80	no support	no support	no support	no support	no support
17_k141_462954	Bacteria: 1.00	Proteobacteria: 0.56	Gammaproteobacteria: 0.56	NA	NA	Candidatus Thioglobus: 0.56	Candidatus Thioglobus sp. NP1: 0.56
17_k141_540426	Bacteria: 1.00	Bacteroidetes: 0.92	Cytophagia: 0.92	no support	no support	no support	no support
17_k141_560283	Bacteria: 0.85	Proteobacteria: 0.85	Betaproteobacteria: 0.82	no support	no support	no support	no support
17_k141_565457	Bacteria: 0.92	no support	no support	no support	no support	no support	no support

17_k141_599502	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
17_k141_639123	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
17_k141_738967	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.64	no support	no support	no support	no support
17_k141_798470	Bacteria: 0.58	no support	no support	no support	no support	no support	no support
18_k141_133495	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
18_k141_186503	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
18_k141_252393	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 1.00	Rhodobacteraceae: 1.00	NA	Rhodobacteraceae bacterium: 1.00
18_k141_353367	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
18_k141_437839	Eukaryota: 1.00	NA	Pelagophyceae: 1.00	Pelagomonadales: 1.00	NA	Aureococcus: 1.00	Aureococcus anophagefferens*: 1.00
18_k141_554657	Bacteria: 0.81	Bacteroidetes: 0.74	no support	no support	no support	no support	no support
18_k141_673355	Bacteria: 1.00	Bacteroidetes: 0.91	no support	no support	no support	no support	no support
18_k141_700482	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
18_k141_80123	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
18_k141_865812	Bacteria: 1.00	Bacteroidetes: 0.88	no support	no support	no support	no support	no support
18_k141_898049	Eukaryota: 1.00	Chlorophyta: 1.00	Mamiellophyceae: 1.00	Mamiellales: 1.00	Bathycoccaceae: 1.00	Bathycoccus: 1.00	Bathycoccus prasinos*: 1.00
19_k141_179943	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	SAR86 cluster bacterium: 0.51
19_k141_288541	Bacteria: 1.00	Planctomycetes: 1.00	no support	no support	no support	no support	no support
19_k141_298365	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
19_k141_385876	Bacteria: 1.00	Planctomycetes: 1.00	no support	no support	no support	no support	no support
19_k141_392029	Bacteria: 0.93	Proteobacteria: 0.93	Alphaproteobacteria: 0.93	Pelagibacterales: 0.93	Pelagibacteraceae: 0.93	no support	no support
19_k141_399029	Bacteria: 1.00	Rhodothermaeota: 0.63	no support	no support	no support	no support	no support
19_k141_495976	Bacteria: 0.72	no support	no support	no support	no support	no support	no support
19_k141_524369	Bacteria: 1.00	Proteobacteria: 0.74	Alphaproteobacteria: 0.74	Rhodobacterales: 0.74	no support	no support	no support
19_k141_57710	Eukaryota: 1.00	NA	Pelagophyceae: 1.00	Pelagomonadales: 1.00	NA	Aureococcus: 1.00	Aureococcus anophagefferens*: 1.00
19_k141_674417	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
19_k141_757971	Bacteria: 1.00	Bacteroidetes: 0.85	Flavobacteriia: 0.85	Flavobacteriales: 0.85	no support	no support	no support
19_k141_860717	Bacteria: 1.00	Planctomycetes: 1.00	no support	no support	no support	no support	no support
19_k141_916416	Bacteria: 0.92	no support	no support	no support	no support	no support	no support
1_k141_110569	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_160480	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support

1_k141_178908	Bacteria: 0.90	Actinobacteria: 0.73	Actinomycetia: 0.73	Micrococcales: 0.73	Microbacteriaceae: 0.73	Microbacterium: 0.73	no support
1_k141_188434	Bacteria: 1.00	Proteobacteria: 0.56	no support	no support	no support	no support	no support
1_k141_188667	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
1_k141_202180	Bacteria: 0.89	Actinobacteria: 0.65	no support	no support	no support	no support	no support
1_k141_208982	Bacteria: 0.99	no support	no support	no support	no support	no support	no support
1_k141_210006	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_226966	Bacteria: 0.89	no support	no support	no support	no support	no support	no support
1_k141_253685	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_306129	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
1_k141_318982	Bacteria: 0.83	Actinobacteria: 0.68	no support	no support	no support	no support	no support
1_k141_328873	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_369165	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	SAR86 cluster bacterium: 0.71
1_k141_39786	Bacteria: 1.00	Proteobacteria: 0.94	Gammaproteobacteria: 0.87	no support	no support	no support	no support
1_k141_401067	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
1_k141_415862	Bacteria: 1.00	Proteobacteria: 0.81	Gammaproteobacteria: 0.81	no support	no support	no support	no support
1_k141_440756	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomicrobiales: 0.68	no support	no support	no support
1_k141_443738	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_4489	Bacteria: 1.00	Bacteroidetes: 0.99	Flavobacteriia: 0.83	Flavobacteriales: 0.81	Flavobacteriaceae: 0.81	NA	Flavobacteriaceae bacterium TMED208: 0.54
1_k141_455033	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_460960	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_481169	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Pelagibacterales: 1.00	Pelagibacteriaceae: 1.00	no support	no support
1_k141_497682	Bacteria: 1.00	Proteobacteria: 0.98	Gammaproteobacteria: 0.98	NA	NA	NA	Gammaproteobacteria bacterium TMED186: 0.76
1_k141_498695	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_49987	Bacteria: 0.95	Bacteroidetes: 0.82	no support	no support	no support	no support	no support
1_k141_516519	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_55460	Bacteria: 1.00	Proteobacteria: 0.77	Gammaproteobacteria: 0.77	NA	NA	NA	SAR86 cluster bacterium: 0.64
1_k141_557398	Bacteria: 1.00	Actinobacteria: 1.00	Acidimicrobiia: 0.70	NA	NA	NA	Acidimicrobiia bacterium: 0.70
1_k141_563953	Bacteria: 1.00	Actinobacteria: 0.99	Actinomycetia: 0.99	Micrococcales: 0.98	Microbacteriaceae: 0.98	Microbacterium: 0.98	no support
1_k141_588384	Bacteria: 0.94	Proteobacteria: 0.94	no support	no support	no support	no support	no support

1_k141_623915	Bacteria: 1.00	Proteobacteria: 1.00	Betaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_646012	Bacteria: 1.00	Rhodothermaeota: 0.87	NA	NA	NA	NA	Rhodothermaeota bacterium MED-G16: 0.55
1_k141_665714	Bacteria: 1.00	Proteobacteria: 0.69	Alphaproteobacteria: 0.69	no support	no support	no support	no support
1_k141_681347	Bacteria: 0.97	no support	no support	no support	no support	no support	no support
1_k141_690695	Bacteria: 0.95	Bacteroidetes: 0.86	no support	no support	no support	no support	no support
1_k141_709904	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_712452	Bacteria: 0.87	Actinobacteria: 0.87	no support	no support	no support	no support	no support
1_k141_714245	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_720556	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
1_k141_726662	Bacteria: 1.00	Actinobacteria: 0.90	no support	no support	no support	no support	no support
1_k141_73404	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_746314	Bacteria: 0.98	Proteobacteria: 0.92	Alphaproteobacteria: 0.92	Sphingomonadales: 0.92	Sphingomonadaceae: 0.91	Sphingomonas: 0.90	no support
1_k141_755953	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.57	no support	no support	no support	no support
1_k141_761992	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Pelagibacterales: 0.94	no support	no support	no support
1_k141_774024	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_783086	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_785748	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_83086	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
1_k141_843551	Bacteria: 0.88	Proteobacteria: 0.88	no support	no support	no support	no support	no support
1_k141_845589	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_8665	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_873093	Bacteria: 0.88	Bacteroidetes: 0.77	no support	no support	no support	no support	no support
1_k141_878817	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
1_k141_878846	Bacteria: 1.00	Proteobacteria: 0.96	Gammaproteobacteria: 0.65	NA	NA	NA	SAR86 cluster bacterium: 0.65
1_k141_895014	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
1_k141_954557	Bacteria: 0.87	no support	no support	no support	no support	no support	no support
1_k141_97664	no support	no support	no support	no support	no support	no support	no support
20_k141_173528	Bacteria: 0.71	Cyanobacteria: 0.71	NA	Synechococcales: 0.71	no support	no support	no support
20_k141_330210	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
20_k141_549731	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	SAR86 cluster bacterium: 0.91

20_k141_607934	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 0.68
20_k141_633824	Bacteria: 1.00	Bacteroidetes: 0.94	Flavobacteriia: 0.94	Flavobacteriales: 0.94	no support	no support	no support
20_k141_754708	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
20_k141_887530	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
21_k141_290075	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
21_k141_356839	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
21_k141_493080	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	no support	no support	no support	no support
21_k141_53160	Eukaryota: 1.00	Chlorophyta: 1.00	Mamiellophyceae: 1.00	Mamiellales: 1.00	Bathycoccaceae: 1.00	Bathycoccus: 1.00	Bathycoccus prasinos*: 1.00
21_k141_554987	Bacteria: 0.93	Cyanobacteria: 0.93	NA	Synechococcales: 0.93	Prochloraceae: 0.93	Prochlorococcus: 0.93	no support
21_k141_566531	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
21_k141_610497	no support	no support	no support	no support	no support	no support	no support
21_k141_627732	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Legionellales: 1.00	NA	NA	Legionellales bacterium: 1.00
21_k141_818310	Bacteria: 1.00	Bacteroidetes: 0.87	no support	no support	no support	no support	no support
21_k141_875102	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium TMED226: 0.82
22_k141_114585	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_12412	Bacteria: 1.00	Proteobacteria: 0.62	Alphaproteobacteria: 0.57	no support	no support	no support	no support
22_k141_126198	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_144797	Bacteria: 1.00	Actinobacteria: 0.92	Actinomycetia: 0.59	no support	no support	no support	no support
22_k141_157481	Bacteria: 0.54	no support	no support	no support	no support	no support	no support
22_k141_161416	Bacteria: 1.00	Actinobacteria: 1.00	Nitriliruptoria: 1.00	Euzebyales: 1.00	Euzebyaceae: 1.00	Euzebya: 1.00	no support
22_k141_172111	Bacteria: 1.00	Proteobacteria: 0.90	Gammaproteobacteria: 0.90	Cellvibrionales: 0.57	Porticoccaceae: 0.57	no support	no support
22_k141_175488	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_21204	Bacteria: 0.96	Proteobacteria: 0.96	Alphaproteobacteria: 0.96	Rhodobacterales: 0.96	Rhodobacteraceae: 0.96	no support	no support
22_k141_218930	Bacteria: 1.00	Bacteroidetes: 0.55	no support	no support	no support	no support	no support
22_k141_262217	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	no support	no support	no support
22_k141_280657	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.79	no support	no support	no support	no support
22_k141_280758	Bacteria: 1.00	Proteobacteria: 0.95	Alphaproteobacteria: 0.94	Rhodobacterales: 0.94	Rhodobacteraceae: 0.94	NA	Rhodobacteraceae bacterium: 0.86
22_k141_286225	Bacteria: 1.00	Bacteroidetes: 0.91	no support	no support	no support	no support	no support
22_k141_291662	Bacteria: 1.00	Bacteroidetes: 0.92	Flavobacteriia: 0.92	Flavobacteriales: 0.92	no support	no support	no support
22_k141_291818	Bacteria: 1.00	Bacteroidetes: 0.61	no support	no support	no support	no support	no support

22_k141_296647	Bacteria: 1.00	Bacteroidetes: 0.92	no support	no support	no support	no support	no support
22_k141_301027	Bacteria: 1.00	Bacteroidetes: 0.77	Flavobacteriia: 0.77	Flavobacteriales: 0.77	no support	no support	no support
22_k141_311775	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Cellvibrionales: 0.89	Porticocceae: 0.83	no support	no support
22_k141_319695	Bacteria: 0.94	Bacteroidetes: 0.94	no support	no support	no support	no support	no support
22_k141_332080	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.99	Cellvibrionales: 0.99	Porticocceae: 0.56	no support	no support
22_k141_336485	Bacteria: 1.00	Bacteroidetes: 0.54	no support	no support	no support	no support	no support
22_k141_342631	Bacteria: 0.96	Bacteroidetes: 0.96	Flavobacteriia: 0.96	Flavobacteriales: 0.96	no support	no support	no support
22_k141_354190	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	NA	NA	Flavobacteriales bacterium: 1.00
22_k141_356700	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_403570	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
22_k141_422854	Bacteria: 1.00	Bacteroidetes: 0.71	no support	no support	no support	no support	no support
22_k141_44723	Bacteria: 0.98	Proteobacteria: 0.81	Alphaproteobacteria: 0.78	Rhodobacterales: 0.78	Rhodobacteraceae: 0.71	Planktomarina: 0.57	no support
22_k141_467055	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Flavobacteriaceae: 1.00	NA	Flavobacteriaceae bacterium: 1.00
22_k141_470688	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 0.88	Flavobacteriales: 0.88	NA	NA	Flavobacteriales bacterium: 0.88
22_k141_477067	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 1.00	Rhodobacteraceae: 1.00	no support	no support
22_k141_490279	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_495890	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_510147	Bacteria: 0.99	Bacteroidetes: 0.99	Flavobacteriia: 0.53	Flavobacteriales: 0.53	NA	NA	Flavobacteriales bacterium: 0.53
22_k141_513461	no support	no support	no support	no support	no support	no support	no support
22_k141_515583	Bacteria: 0.85	no support	no support	no support	no support	no support	no support
22_k141_518137	Bacteria: 0.92	no support	no support	no support	no support	no support	no support
22_k141_518376	Bacteria: 1.00	Bacteroidetes: 0.95	Flavobacteriia: 0.95	Flavobacteriales: 0.95	no support	no support	no support
22_k141_537266	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_54015	Bacteria: 1.00	Bacteroidetes: 1.00	no support	no support	no support	no support	no support
22_k141_559517	Bacteria: 1.00	Bacteroidetes: 0.94	NA	NA	NA	NA	Bacteroidetes bacterium: 0.80
22_k141_564034	Bacteria: 1.00	Bacteroidetes: 0.65	Flavobacteriia: 0.61	Flavobacteriales: 0.61	no support	no support	no support
22_k141_572781	Bacteria: 1.00	Proteobacteria: 0.80	Alphaproteobacteria: 0.80	Rhodobacterales: 0.80	Rhodobacteraceae: 0.80	NA	Rhodobacteraceae bacterium: 0.80
22_k141_585394	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 1.00	Rhodobacteraceae: 1.00	NA	Rhodobacteraceae bacterium: 1.00
22_k141_588206	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_605048	Bacteria: 0.88	no support	no support	no support	no support	no support	no support

22_k141_610153	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 0.89
22_k141_628785	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_630754	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_638071	Bacteria: 1.00	Planctomycetes: 1.00	Phycisphaerae: 0.62	Phycisphaerales: 0.62	NA	NA	Phycisphaerales bacterium*: 0.62
22_k141_64415	Bacteria: 1.00	Proteobacteria: 0.92	Gammaproteobacteria: 0.92	no support	no support	no support	no support
22_k141_656692	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_65869	Bacteria: 0.82	no support	no support	no support	no support	no support	no support
22_k141_662416	Bacteria: 1.00	Bacteroidetes: 0.77	Flavobacteriia: 0.73	Flavobacteriales: 0.73	Cryomorphaceae: 0.50	NA	Cryomorphaceae bacterium: 0.50
22_k141_670722	Bacteria: 1.00	Bacteroidetes: 0.69	Flavobacteriia: 0.69	Flavobacteriales: 0.69	no support	no support	no support
22_k141_676685	Bacteria: 1.00	Bacteroidetes: 0.70	Flavobacteriia: 0.70	Flavobacteriales: 0.70	no support	no support	no support
22_k141_6928	Bacteria: 1.00	Bacteroidetes: 0.86	Flavobacteriia: 0.86	Flavobacteriales: 0.86	no support	no support	no support
22_k141_697813	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_716741	Bacteria: 1.00	Proteobacteria: 0.80	Gammaproteobacteria: 0.80	no support	no support	no support	no support
22_k141_734013	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodospirillales: 1.00	Rhodospirillaceae: 1.00	no support	no support
22_k141_744365	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Cellvibrionales: 1.00	Porticocaceae: 0.81	no support	no support
22_k141_765910	Bacteria: 1.00	Bacteroidetes: 0.94	Flavobacteriia: 0.94	Flavobacteriales: 0.94	no support	no support	no support
22_k141_807710	Bacteria: 1.00	Bacteroidetes: 0.73	Flavobacteriia: 0.64	Flavobacteriales: 0.64	NA	NA	Flavobacteriales bacterium: 0.52
22_k141_80919	Bacteria: 1.00	Bacteroidetes: 0.53	Flavobacteriia: 0.53	Flavobacteriales: 0.53	no support	no support	no support
22_k141_82869	Bacteria: 1.00	Bacteroidetes: 0.53	no support	no support	no support	no support	no support
22_k141_84523	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_86807	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
22_k141_89967	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
22_k141_95830	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
23_k141_10153	Bacteria: 1.00	Proteobacteria: 0.84	Gammaproteobacteria: 0.84	no support	no support	no support	no support
23_k141_110579	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	no support	no support	no support
23_k141_112504	Bacteria: 0.92	Proteobacteria: 0.92	Gammaproteobacteria: 0.92	no support	no support	no support	no support
23_k141_148276	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Oceanospirillales: 1.00	Oceanospirillaceae: 1.00	NA	Oceanospirillaceae bacterium: 1.00
23_k141_148952	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Pseudoalteromonadaceae: 1.00	Pseudoalteromonas: 1.00	no support
23_k141_158766	Bacteria: 1.00	Proteobacteria: 0.54	Betaproteobacteria: 0.54	no support	no support	no support	no support

23_k141_179779	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
23_k141_2370	Bacteria: 1.00	Bacteroidetes: 0.51	no support	no support	no support	no support	no support
23_k141_247444	Bacteria: 0.67	Cyanobacteria: 0.67	NA	Synechococcales: 0.67	no support	no support	no support
23_k141_28421	Bacteria: 0.93	no support	no support	no support	no support	no support	no support
23_k141_293657	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
23_k141_337458	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	SAR86 cluster bacterium: 0.61
23_k141_359393	Bacteria: 1.00	Bacteroidetes: 0.76	Flavobacteriia: 0.76	Flavobacteriales: 0.76	no support	no support	no support
23_k141_374042	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 0.86	Flavobacteriales: 0.86	Crocinitomicaceae: 0.83	no support	no support
23_k141_379353	Bacteria: 1.00	Bacteroidetes: 0.61	Flavobacteriia: 0.61	Flavobacteriales: 0.61	no support	no support	no support
23_k141_399777	Bacteria: 1.00	Bacteroidetes: 0.72	Flavobacteriia: 0.72	Flavobacteriales: 0.72	no support	no support	no support
23_k141_399967	Bacteria: 1.00	Proteobacteria: 0.93	Gammaproteobacteria: 0.93	NA	NA	NA	Gammaproteobacteria bacterium: 0.62
23_k141_406909	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
23_k141_453723	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Oceanospirillales: 1.00	no support	no support	no support
23_k141_457731	Bacteria: 0.96	no support	no support	no support	no support	no support	no support
23_k141_478074	Bacteria: 1.00	Bacteroidetes: 0.83	Flavobacteriia: 0.83	Flavobacteriales: 0.83	no support	no support	no support
23_k141_504782	Bacteria: 1.00	Proteobacteria: 1.00	NA	NA	NA	NA	Proteobacteria bacterium: 0.55
23_k141_537934	Bacteria: 1.00	Proteobacteria: 0.85	Gammaproteobacteria: 0.85	no support	no support	no support	no support
23_k141_538063	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
23_k141_549371	Bacteria: 1.00	Bacteroidetes: 0.81	Flavobacteriia: 0.81	no support	no support	no support	no support
23_k141_574308	Bacteria: 1.00	Actinobacteria: 1.00	Actinomycetia: 1.00	NA	NA	NA	Actinobacteria bacterium: 1.00
23_k141_584539	Bacteria: 1.00	Bacteroidetes: 1.00	no support	no support	no support	no support	no support
23_k141_589697	Bacteria: 1.00	Bacteroidetes: 0.57	Flavobacteriia: 0.57	Flavobacteriales: 0.57	no support	no support	no support
23_k141_605682	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 0.80	Rhodobacteraceae: 0.80	NA	Rhodobacteraceae bacterium: 0.80
23_k141_624169	Bacteria: 1.00	Bacteroidetes: 0.86	Flavobacteriia: 0.86	Flavobacteriales: 0.86	Flavobacteriaceae: 0.85	no support	no support
23_k141_647662	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
23_k141_683534	Bacteria: 1.00	Bacteroidetes: 0.75	Flavobacteriia: 0.71	Flavobacteriales: 0.71	no support	no support	no support
23_k141_716104	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Pseudoalteromonadaceae: 1.00	Pseudoalteromonas: 1.00	Pseudoalteromonas denitrificans: 0.88
23_k141_730969	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodospirillales: 1.00	Rhodospirillaceae: 1.00	no support	no support
23_k141_745178	Bacteria: 0.93	Planctomycetes: 0.87	NA	NA	NA	NA	Planctomycetes bacterium: 0.87
23_k141_753057	Bacteria: 1.00	Proteobacteria: 0.89	Gammaproteobacteria: 0.89	Cellvibrionales: 0.59	Porticocaceae: 0.59	no support	no support

23_k141_794766	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Cellvibrionales: 0.96	Porticoccaceae: 0.96	Porticoccus: 0.82	Porticoccus sp.*: 0.82
23_k141_815283	Bacteria: 1.00	Bacteroidetes: 0.67	Flavobacteriia: 0.67	Flavobacteriales: 0.56	NA	NA	Flavobacteriales bacterium: 0.56
24_k141_160455	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.98	Rhodobacterales: 0.98	no support	no support	no support
24_k141_171662	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
24_k141_191308	Bacteria: 1.00	Proteobacteria: 0.99	Gammaproteobacteria: 0.98	Alteromonadales: 0.95	Pseudoalteromonadaceae: 0.91	Pseudoalteromonas: 0.91	no support
24_k141_192790	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Cellvibrionales: 0.71	Porticoccaceae: 0.71	no support	no support
24_k141_208898	Bacteria: 0.99	Proteobacteria: 0.99	Gammaproteobacteria: 0.99	Alteromonadales: 0.94	Pseudoalteromonadaceae: 0.89	Pseudoalteromonas: 0.89	no support
24_k141_212920	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.76	Oceanospirillales: 0.76	no support	no support	no support
24_k141_223133	Bacteria: 0.96	Proteobacteria: 0.91	Alphaproteobacteria: 0.79	Rhodobacterales: 0.79	NA	NA	Rhodobacterales bacterium HTCC2255: 0.72
24_k141_225047	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 0.89	Pseudoalteromonadaceae: 0.74	Pseudoalteromonas: 0.74	no support
24_k141_229082	Bacteria: 0.87	no support	no support	no support	no support	no support	no support
24_k141_274140	Bacteria: 0.99	Bacteroidetes: 0.88	Flavobacteriia: 0.81	Flavobacteriales: 0.79	Flavobacteriaceae: 0.79	no support	no support
24_k141_286195	Bacteria: 1.00	Bacteroidetes: 0.83	Flavobacteriia: 0.83	Flavobacteriales: 0.83	Flavobacteriaceae: 0.61	no support	no support
24_k141_328670	no support	no support	no support	no support	no support	no support	no support
24_k141_345032	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Crocinitomicaceae: 1.00	Fluviicola: 1.00	Fluviicola sp.: 1.00
24_k141_357622	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 1.00	Rhodobacteraceae: 1.00	NA	Rhodobacteraceae bacterium: 0.94
24_k141_363920	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
24_k141_417363	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Flavobacteriaceae: 1.00	no support	no support
24_k141_421138	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
24_k141_428569	Bacteria: 0.96	Bacteroidetes: 0.96	Flavobacteriia: 0.57	Flavobacteriales: 0.57	no support	no support	no support
24_k141_454983	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
24_k141_46276	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Flavobacteriaceae: 0.98	no support	no support
24_k141_482584	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
24_k141_494523	Bacteria: 1.00	Bacteroidetes: 0.90	Flavobacteriia: 0.88	Flavobacteriales: 0.88	Flavobacteriaceae: 0.87	no support	no support
24_k141_508814	Bacteria: 1.00	Proteobacteria: 0.99	Gammaproteobacteria: 0.98	Alteromonadales: 0.86	Pseudoalteromonadaceae: 0.76	Pseudoalteromonas: 0.76	no support
24_k141_560063	Bacteria: 1.00	Bacteroidetes: 0.74	Flavobacteriia: 0.74	no support	no support	no support	no support
24_k141_576453	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
24_k141_621418	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
24_k141_625175	Bacteria: 0.93	Proteobacteria: 0.93	Alphaproteobacteria: 0.93	Rhodobacterales: 0.93	Rhodobacteraceae: 0.93	NA	Rhodobacteraceae bacterium: 0.93

24_k141_657725	Bacteria: 0.94	Proteobacteria: 0.94	Alphaproteobacteria: 0.94	Rhodobacterales: 0.89	Rhodobacteraceae: 0.89	NA	Rhodobacteraceae bacterium: 0.73
24_k141_681529	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
24_k141_695390	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
24_k141_708757	Bacteria: 1.00	Bacteroidetes: 0.60	Flavobacteriia: 0.60	Flavobacteriales: 0.60	NA	NA	Flavobacteriales bacterium: 0.60
24_k141_715393	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
24_k141_81428	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.98	Rhodobacterales: 0.91	no support	no support	no support
24_k141_89444	Bacteria: 1.00	Lentisphaerae: 0.93	Lentisphaeria: 0.93	Lentisphaerales: 0.93	Lentisphaeraceae: 0.93	NA	Lentisphaeraceae bacterium*: 0.64
2_k141_107175	Bacteria: 1.00	Proteobacteria: 0.95	Betaproteobacteria: 0.95	no support	no support	no support	no support
2_k141_231850	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
2_k141_258309	Bacteria: 0.93	Proteobacteria: 0.76	Gammaproteobacteria: 0.57	no support	no support	no support	no support
2_k141_2996	Bacteria: 1.00	Proteobacteria: 0.59	Gammaproteobacteria: 0.59	no support	no support	no support	no support
2_k141_353594	Bacteria: 0.92	Proteobacteria: 0.75	no support	no support	no support	no support	no support
2_k141_408943	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
2_k141_410077	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
2_k141_410135	Bacteria: 0.91	Actinobacteria: 0.91	no support	no support	no support	no support	no support
2_k141_501545	Bacteria: 0.92	Proteobacteria: 0.70	Gammaproteobacteria: 0.55	no support	no support	no support	no support
2_k141_568663	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
2_k141_600930	Bacteria: 0.63	Bacteroidetes: 0.58	Flavobacteriia: 0.58	Flavobacteriales: 0.58	NA	NA	Flavobacteriales bacterium: 0.58
2_k141_6427	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
2_k141_66582	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
2_k141_66913	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.64	no support	no support	no support	no support
2_k141_975062	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
3_k141_143843	Bacteria: 1.00	Proteobacteria: 0.81	Alphaproteobacteria: 0.79	Hyphomonadales: 0.79	Hyphomonadaceae: 0.79	Hyphomonas: 0.79	no support
3_k141_159802	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
3_k141_198040	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Alteromonadaceae: 1.00	Marinobacter: 1.00	no support
3_k141_250370	Bacteria: 1.00	Candidatus Marinimicrobia: 0.90	NA	NA	NA	NA	Candidatus Marinimicrobia bacterium: 0.90
3_k141_259586	NA	NA	NA	NA	NA	NA	uncultured organism MedDCM-OCT-S04-C478: 0.64
3_k141_292961	Bacteria: 1.00	Candidatus Marinimicrobia: 0.72	NA	NA	NA	NA	Candidatus Marinimicrobia bacterium: 0.72
3_k141_302629	Bacteria: 1.00	Actinobacteria: 0.89	Actinomycetia: 0.89	Micrococcales: 0.89	Microbacteriaceae: 0.89	Leifsonia: 0.89	Leifsonia sp.: 0.89

3_k141_429847	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 0.94	Myxococcales: 0.94	no support	no support	no support
3_k141_45958	Bacteria: 0.92	Proteobacteria: 0.80	Gammaproteobacteria: 0.80	Alteromonadales: 0.74	Alteromonadaceae: 0.74	Marinobacter: 0.74	no support
3_k141_467259	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	Sandaracinaceae: 0.50	NA	Sandaracinaceae bacterium*: 0.50
3_k141_486053	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 0.74
3_k141_503823	Bacteria: 1.00	Proteobacteria: 0.77	Gammaproteobacteria: 0.77	no support	no support	no support	no support
3_k141_593222	Bacteria: 0.92	Proteobacteria: 0.74	Gammaproteobacteria: 0.74	Alteromonadales: 0.72	Alteromonadaceae: 0.72	Marinobacter: 0.72	no support
3_k141_633769	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodospirillales: 1.00	no support	no support	no support
3_k141_6476	Bacteria: 1.00	Actinobacteria: 0.92	no support	no support	no support	no support	no support
3_k141_663669	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	no support	no support	no support
3_k141_66437	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
3_k141_687471	Bacteria: 1.00	Bacteroidetes: 0.86	Flavobacteriia: 0.86	Flavobacteriales: 0.86	no support	no support	no support
3_k141_714338	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.96	Hyphomicrobiales: 0.96	Aurantimonadaceae: 0.77	no support	no support
3_k141_731125	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
3_k141_784722	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
3_k141_789508	Bacteria: 1.00	Proteobacteria: 0.97	Alphaproteobacteria: 0.96	Hyphomonadales: 0.92	Hyphomonadaceae: 0.92	Hyphomonas: 0.84	no support
3_k141_830730	Bacteria: 1.00	Proteobacteria: 0.73	Alphaproteobacteria: 0.70	Sphingomonadales: 0.67	no support	no support	no support
3_k141_836045	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomicrobiales: 0.85	no support	no support	no support
3_k141_836609	Bacteria: 1.00	Proteobacteria: 0.99	Alphaproteobacteria: 0.99	Hyphomicrobiales: 0.94	Aurantimonadaceae: 0.94	no support	no support
3_k141_892661	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	no support	no support	no support
3_k141_936940	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
3_k141_938916	Bacteria: 0.89	Actinobacteria: 0.78	no support	no support	no support	no support	no support
4_k141_147618	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Oceanospirillales: 0.83	Alcanivoracaceae: 0.83	Alcanivorax: 0.83	no support
4_k141_161800	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 0.90
4_k141_253932	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
4_k141_268362	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.79	NA	NA	NA	Gammaproteobacteria bacterium: 0.79
4_k141_386327	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
4_k141_495312	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
4_k141_513089	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomicrobiales: 0.90	no support	no support	no support
4_k141_60506	Bacteria: 0.89	Proteobacteria: 0.89	Alphaproteobacteria: 0.89	no support	no support	no support	no support

4_k141_70679	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
4_k141_711263	Bacteria: 1.00	Proteobacteria: 0.95	Gammaproteobacteria: 0.95	Oceanospirillales: 0.95	Oleiphilaceae: 0.95	Oleiphilus: 0.95	no support
4_k141_855023	Bacteria: 1.00	Actinobacteria: 0.75	no support	no support	no support	no support	no support
4_k141_862362	Bacteria: 1.00	Proteobacteria: 1.00	NA	NA	NA	NA	Proteobacteria bacterium: 1.00
4_k141_866455	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	no support	no support	no support	no support
4_k141_89201	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
4_k141_950971	Bacteria: 0.87	Proteobacteria: 0.81	Gammaproteobacteria: 0.81	Alteromonadales: 0.65	Alteromonadaceae: 0.65	Marinobacter: 0.65	no support
4_k141_981843	Bacteria: 0.96	Proteobacteria: 0.96	Alphaproteobacteria: 0.96	Hyphomicrobiales: 0.96	no support	no support	no support
5_k141_1041368	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
5_k141_1052317	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
5_k141_1054409	Bacteria: 1.00	Proteobacteria: 0.96	Gammaproteobacteria: 0.96	no support	no support	no support	no support
5_k141_1082158	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Vibrionales: 1.00	no support	no support	no support
5_k141_1185582	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Pseudomonadales: 1.00	Pseudomonadaceae: 0.91	Pseudomonas: 0.91	no support
5_k141_1226140	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomicrobiales: 1.00	Rhodobiaceae: 1.00	NA	Rhodobiaceae bacterium*: 1.00
5_k141_141154	Bacteria: 1.00	Candidatus Marinimicrobia: 0.92	NA	NA	NA	NA	Candidatus Marinimicrobia bacterium: 0.92
5_k141_156088	Bacteria: 1.00	Rhodothermaeota: 0.65	no support	no support	no support	no support	no support
5_k141_164137	Bacteria: 0.89	Proteobacteria: 0.89	Alphaproteobacteria: 0.89	Maricaulales: 0.89	Maricaulaceae: 0.89	no support	no support
5_k141_181738	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
5_k141_251289	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomonadales: 1.00	Hyphomonadaceae*: 1.00	no support	no support
5_k141_25794	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Maricaulales: 0.93	Maricaulaceae: 0.93	Maricaulis: 0.82	no support
5_k141_409288	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
5_k141_442065	Bacteria: 1.00	Proteobacteria: 0.95	Gammaproteobacteria: 0.95	NA	NA	NA	Gammaproteobacteria bacterium: 0.95
5_k141_443192	Bacteria: 1.00	Proteobacteria: 0.93	Gammaproteobacteria: 0.93	no support	no support	no support	no support
5_k141_503021	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
5_k141_68513	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Pseudomonadales: 1.00	Pseudomonadaceae: 1.00	Pseudomonas: 0.65	no support
5_k141_780267	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 0.98	Flavobacteriales: 0.98	Flavobacteriaceae: 0.87	NA	Flavobacteriaceae bacterium: 0.87
5_k141_817973	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodospirillales: 1.00	no support	no support	no support
5_k141_833048	Bacteria: 1.00	Chloroflexi: 1.00	no support	no support	no support	no support	no support
5_k141_876822	Bacteria: 0.95	no support	no support	no support	no support	no support	no support
5_k141_918191	Bacteria: 1.00	Actinobacteria: 1.00	Actinomycetia: 1.00	Propionibacteriales: 0.81	Nocardioidaceae: 0.81	Pimelobacter: 0.72	Pimelobacter sp.*: 0.72

5_k141_924327	Bacteria: 1.00	NA	NA	NA	NA	NA	bacterium TMED46: 0.70
5_k141_928548	Bacteria: 0.72	Proteobacteria: 0.72	Gammaproteobacteria: 0.62	Vibrionales: 0.62	no support	no support	no support
5_k141_963588	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.96	NA	NA	NA	Gammaproteobacteria bacterium TMED257: 0.96
5_k141_990402	Bacteria: 0.96	Actinobacteria: 0.90	Actinomycetia: 0.90	no support	no support	no support	no support
6_k141_104421	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.64	no support	no support	no support	no support
6_k141_111942	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	no support	no support	no support
6_k141_159118	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	no support	no support	no support
6_k141_193528	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	no support	no support	no support
6_k141_196731	Bacteria: 0.96	Proteobacteria: 0.96	Alphaproteobacteria: 0.96	Rhodobacterales: 0.90	Rhodobacteraceae: 0.90	Ahrensia: 0.90	Ahrensia sp.: 0.90
6_k141_238268	Bacteria: 0.95	Proteobacteria: 0.95	Alphaproteobacteria: 0.81	Rhodobacterales: 0.55	Rhodobacteraceae: 0.55	Ahrensia: 0.55	Ahrensia sp.: 0.55
6_k141_266046	Bacteria: 1.00	Proteobacteria: 1.00	Deltaproteobacteria: 1.00	Myxococcales: 1.00	Sandaracinaceae: 0.70	NA	Sandaracinaceae bacterium*: 0.70
6_k141_279575	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.95	Rhodobacterales: 0.93	Rhodobacteraceae: 0.93	Ahrensia: 0.93	Ahrensia sp.: 0.93
6_k141_546	no support	no support	no support	no support	no support	no support	no support
6_k141_68143	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 0.99	Rhodospirillales: 0.90	no support	no support	no support
6_k141_8233	Bacteria: 1.00	Actinobacteria: 1.00	Nitriliruptoria: 1.00	Euzebyales: 1.00	Euzebyaceae: 1.00	Euzebya: 1.00	no support
6_k141_8774	Bacteria: 1.00	Proteobacteria: 0.96	Alphaproteobacteria: 0.96	Hyphomonadales: 0.94	Hyphomonadaceae*: 0.94	no support	no support
6_k141_97482	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomonadales: 1.00	Hyphomonadaceae*: 1.00	no support	no support
7_k141_141434	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
7_k141_155479	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Oceanospirillales: 0.98	Alcanivoracaceae: 0.98	Alcanivorax: 0.69	no support
7_k141_203753	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Vibrionales: 1.00	no support	no support	no support
7_k141_234494	Bacteria: 1.00	Proteobacteria: 0.98	Gammaproteobacteria: 0.98	Oceanospirillales: 0.81	Alcanivoracaceae: 0.81	Alcanivorax: 0.65	no support
7_k141_243606	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
7_k141_291656	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Oceanospirillales: 0.99	Alcanivoracaceae: 0.99	Alcanivorax: 0.74	no support
7_k141_334343	Bacteria: 0.99	Proteobacteria: 0.99	Alphaproteobacteria: 0.98	Rhodobacterales: 0.94	Rhodobacteraceae: 0.91	Sulfitobacter: 0.79	no support
7_k141_417033	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
7_k141_490004	Bacteria: 1.00	Proteobacteria: 0.88	Alphaproteobacteria: 0.88	Pelagibacterales: 0.88	NA	NA	Pelagibacterales bacterium SAG-MED32: 0.88
7_k141_496110	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Hyphomicrobiales: 1.00	Rhodobiaceae: 1.00	NA	Rhodobiaceae bacterium*: 1.00
7_k141_509836	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Oceanospirillales: 1.00	Alcanivoracaceae: 1.00	Alcanivorax: 0.61	no support
7_k141_548834	Bacteria: 1.00	Proteobacteria: 0.92	Gammaproteobacteria: 0.92	Oceanospirillales: 0.92	Alcanivoracaceae: 0.92	Alcanivorax: 0.84	no support

7_k141_586997	Bacteria: 1.00	Proteobacteria: 0.98	Alphaproteobacteria: 0.98	Rhodobacterales: 0.96	Rhodobacteraceae: 0.96	Sulfitobacter: 0.84	no support
7_k141_591226	Bacteria: 0.99	Proteobacteria: 0.99	Gammaproteobacteria: 0.99	Oceanospirillales: 0.92	Alcanivoracaceae: 0.92	Alcanivorax: 0.88	no support
7_k141_627629	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.94	Alteromonadales: 0.84	Alteromonadaceae: 0.84	Marinobacter: 0.84	no support
7_k141_745429	Bacteria: 1.00	Proteobacteria: 0.98	Alphaproteobacteria: 0.98	Rhodobacterales: 0.96	Rhodobacteraceae: 0.95	Sulfitobacter: 0.83	no support
7_k141_84381	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	Rhodobacterales: 0.92	Rhodobacteraceae: 0.91	Sulfitobacter: 0.76	no support
9_k141_1021009	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_1039522	Bacteria: 1.00	Proteobacteria: 0.94	Gammaproteobacteria: 0.94	Alteromonadales: 0.61	no support	no support	no support
9_k141_190102	Bacteria: 1.00	Candidatus Marinimicrobia: 0.70	NA	NA	NA	NA	Candidatus Marinimicrobia bacterium: 0.70
9_k141_208497	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.98	Oceanospirillales: 0.95	Alcanivoracaceae: 0.95	Alcanivorax: 0.72	no support
9_k141_284466	Bacteria: 1.00	no support	no support	no support	no support	no support	no support
9_k141_308801	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 0.91	Legionellales: 0.78	NA	NA	Legionellales bacterium: 0.78
9_k141_328917	Bacteria: 1.00	Chloroflexi: 1.00	NA	NA	NA	NA	Chloroflexi bacterium: 0.58
9_k141_352615	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Pseudoalteromonadaceae: 1.00	Pseudoalteromonas: 1.00	no support
9_k141_360001	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Pseudoalteromonadaceae: 0.70	Pseudoalteromonas: 0.61	no support
9_k141_371773	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 0.66
9_k141_379141	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
9_k141_425602	Bacteria: 1.00	Proteobacteria: 1.00	no support	no support	no support	no support	no support
9_k141_461938	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 0.93
9_k141_473766	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Pseudoalteromonadaceae: 0.74	no support	no support
9_k141_510210	Bacteria: 0.68	Actinobacteria: 0.68	no support	no support	no support	no support	no support
9_k141_535753	Bacteria: 1.00	Chloroflexi: 1.00	no support	no support	no support	no support	no support
9_k141_579011	Bacteria: 1.00	Proteobacteria: 0.62	no support	no support	no support	no support	no support
9_k141_580773	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_639864	Bacteria: 1.00	Actinobacteria: 0.99	Actinomycetia: 0.99	Propionibacteriales: 0.96	Nocardiodaceae: 0.96	Nocardioides: 0.96	no support
9_k141_685811	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_716922	Bacteria: 1.00	Proteobacteria: 1.00	Alphaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_726320	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	NA	NA	NA	Gammaproteobacteria bacterium: 1.00
9_k141_733915	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	Pseudoalteromonadaceae: 1.00	no support	no support
9_k141_749334	Bacteria: 1.00	Proteobacteria: 0.84	Gammaproteobacteria: 0.84	no support	no support	no support	no support

9_k141_796666	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_804910	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 0.57	Pseudoalteromonadaceae: 0.57	Pseudoalteromonas: 0.57	no support
9_k141_823203	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Flavobacteriaceae: 1.00	no support	no support
9_k141_82633	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Flavobacteriaceae: 1.00	Tenacibaculum: 0.63	Tenacibaculum soleae: 0.63
9_k141_833100	Bacteria: 1.00	Proteobacteria: 0.89	Gammaproteobacteria: 0.89	no support	no support	no support	no support
9_k141_84122	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_847541	Bacteria: 1.00	Proteobacteria: 0.91	Gammaproteobacteria: 0.91	no support	no support	no support	no support
9_k141_868470	Bacteria: 0.91	no support	no support	no support	no support	no support	no support
9_k141_870089	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	no support	no support	no support	no support
9_k141_919001	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Legionellales: 0.95	NA	NA	Legionellales bacterium: 0.95
9_k141_921415	Bacteria: 1.00	Proteobacteria: 1.00	Gammaproteobacteria: 1.00	Alteromonadales: 1.00	no support	no support	no support
9_k141_983411	Bacteria: 1.00	Bacteroidetes: 1.00	Flavobacteriia: 1.00	Flavobacteriales: 1.00	Flavobacteriaceae: 1.00	no support	no support

Appendix 6

Table S3: Showing known BGC pathway identified from the SAO non-redundant KS contigs and their percentage similarity

Contigs/region	BGC type	From location	To location	Most similar known cluster	Type	Similarity
10_k141_580458/Region 7.1	arylpolyene	6,400	49,981	APE Vf	Other	30%
10_k141_295956/Region 8.1	arylpolyene	1	1,814			
10_k141_849482/Region 13.1	arylpolyene	1	1,955	flexirubin	Polyketide	5%
10_k141_168623/Region 14.1	arylpolyene	1	3,184	flexirubin	Polyketide	11%
10_k141_569960/Region 19.1	arylpolyene	1	3,951	APE Vf	Other	15%
11_k141_956206/Region 25.1	arylpolyene	1	8,578	flexirubin	Polyketide	25%
11_k141_569222/Region 31.1	NRPS,T1PKS	1	36,118			
11_k141_203925/Region 32.1	PUFA,hgIE-KS	60,376	106,022	eicosapentaenoic acid	Other	66%
11_k141_389331/Region 45.1	T1PKS,NRPS	1	33,699			
13_k141_105401/Region 72.1	arylpolyene	1	3,024	flexirubin	Polyketide	13%
14_k141_1012099/Region 95.1	arylpolyene	1	4,671	flexirubin	Polyketide	8%
14_k141_223467/Region 104.1	arylpolyene	1	6,269	flexirubin	Polyketide	16%
14_k141_897973/Region 107.1	arylpolyene	1	2,186	APE Ec	Other	15%
14_k141_753018/Region 114.1	ladderane	1	2,582			
14_k141_1029109/Region 116.1	arylpolyene	1	3,314	APE Vf	Other	15%
15_k141_526901/Region 128.1	arylpolyene	1	3,163			
16_k141_697129/Region 134.1	T1PKS	1	14,790			
16_k141_920012/Region 135.1	arylpolyene	12,294	55,858	APE Vf	Other	40%
16_k141_392261/Region 136.1	arylpolyene	1	2,080			

16_k141_982964/Region 142.1	arylpolyene	1	8,748	APE Vf	Other	15%
17_k141_565457/Region 155.1	arylpolyene	187,459	231,040	APE Vf	Other	30%
17_k141_358034/Region 156.1	arylpolyene	7,209	50,772	APE Vf	Other	35%
17_k141_798470/Region 159.1	arylpolyene	1	3,575	APE Ec	Other	15%
18_k141_554657/Region 176.1	arylpolyene	1	3,204			
1_k141_73404/Region 194.1	arylpolyene	1	4,034			
1_k141_873093/Region 202.1	terpene	166,809	187,642	carotenoid	Terpene	42%
1_k141_873093/Region 202.2	T1PKS,NRPS	681,163	731,905			
1_k141_328873/Region 230.1	arylpolyene	1	1,769	APE Vf	Other	10%
1_k141_845589/Region 250.1	T1PKS	1	9,986			
22_k141_605048/Region 269.1	arylpolyene,resorcinol	162,351	208,418	flexirubin	Polyketide	13%
22_k141_336485/Region 276.1	arylpolyene,resorcinol	1	8,641	flexirubin	Polyketide	16%
22_k141_65869/Region 284.1	arylpolyene	371,576	417,912	flexirubin	Other	36%
22_k141_422854/Region 288.1	arylpolyene	1	4,367	flexirubin	Polyketide	8%
22_k141_470688/Region 311.1	arylpolyene	1	2,476	flexirubin	Polyketide	5%
22_k141_54015/Region 312.1	NRPS,T1PKS	1	12,344			
22_k141_559517/Region 325.1	NRPS	1	11,289			
22_k141_80919/Region 332.1	T3PKS	1	8,831			
22_k141_354190/Region 335.1	arylpolyene	1	2,460			
23_k141_716104/Region 348.1	arylpolyene	1	3,595	APE Vf	Other	15%
23_k141_549371/Region 349.1	T3PKS	1	2,036			
23_k141_453723/Region 359.1	arylpolyene	1	1,487			
24_k141_681529/Region 375.1	arylpolyene	1	3,368	APE Vf	Other	10%
24_k141_225047/Region 378.1	arylpolyene	2,427	24,274	APE Vf	Other	10%
24_k141_208898/Region 380.1	hglE- KS,T1PKS,PUFA	1	37,171	eicosapentaenoic acid-like compound	Other	18%
24_k141_560063/Region 386.1	T3PKS	1	2,541			
24_k141_708757/Region 387.1	arylpolyene	1	2,853	flexirubin	Polyketide	8%
24_k141_212920/Region 391.1	arylpolyene	1	2,484	APE Vf	Other	10%
24_k141_46276/Region 392.1	arylpolyene,resorcinol	1	23,289	flexirubin	Polyketide	44%
24_k141_345032/Region 394.1	arylpolyene	1	3,352	flexirubin	Polyketide	13%

24_k141_695390/Region 398.1	arylpolyene	1	10,359	APE Vf	Other	25%
24_k141_417363/Region 399.1	arylpolyene	1	8,227	flexirubin	Polyketide	25%
24_k141_328670/Region 400.1	arylpolyene	1	8,979	APE Vf	Other	15%
2_k141_501545/Region 412.1	resorcinol	73,959	115,107			
2_k141_353594/Region 413.1	hglE-KS,T1PKS	74,570	128,062	paulomycin	Other	3%
3_k141_633769/Region 427.1	arylpolyene	1	9,764			
3_k141_467259/Region 430.1	arylpolyene	1	4,134			
3_k141_663669/Region 434.1	arylpolyene	1	11,616			
3_k141_789508/Region 442.1	T1PKS,hglE-KS	213,391	264,848			
3_k141_892661/Region 449.1	ladderane	1	2,597			
5_k141_251289/Region 472.1	T1PKS	1	9,903			
5_k141_68513/Region 476.1	arylpolyene	1	2,041	APE Vf	Other	10%
5_k141_1185582/Region 486.1	arylpolyene	1	3,093			
6_k141_193528/Region 497.1	arylpolyene	1	3,876			
6_k141_159118/Region 499.1	arylpolyene	1	6,746	aryl polyenes	Other	22%
6_k141_266046/Region 500.1	hglE-KS	1	8,499			
6_k141_68143/Region 501.1	ectoine	89,601	99,999	ectoine	Other	80%
6_k141_97482/Region 503.1	hglE-KS,T1PKS	1	17,833			
6_k141_111942/Region 506.1	ladderane	1	6,760			
7_k141_627629/Region 513.1	T1PKS,NRPS	1	26,776			
7_k141_84381/Region 519.1	T1PKS	17,712	64,164			
7_k141_203753/Region 521.1	arylpolyene	1	1,901	APE Vf	Other	10%
7_k141_334343/Region 522.1	hserlactone	49,579	70,301			
9_k141_82633/Region 526.1	arylpolyene	1	4,367			
9_k141_84122/Region 529.1	arylpolyene	1	2,425	APE Vf	Other	10%
9_k141_733915/Region 540.1	arylpolyene	1	4,667	APE Vf	Other	15%
9_k141_868470/Region 544.1	T1PKS,NRPS	1	15,886			
9_k141_473766/Region 549.1	arylpolyene	1	2,051	APE Vf	Other	10%
9_k141_983411/Region 557.1	arylpolyene	1	17,309	flexirubin	Polyketide	33%
9_k141_823203/Region 558.1	T3PKS	1	7,838			

Appendix 7

Table S4: Showing known BGC pathway identified from the TARA non-redundant KS contigs and their percentage similarity

Contigs/region	BGC type	From location	To location	Most similar known cluster	Type	Similarity
TARA_ANE-k99_2692542/Region 22.1	arylpolyene	1	26,262	flexirubin	Polyketide	44%
TARA_ANE-k99_2888596/Region 26.1	NRPS	1	26,980			
TARA_ANE-k99_3002501/Region 27.1	T1PKS	1	22,133			
TARA_ANE-k99_3031332/Region 28.1	T1PKS	1	10,359			
TARA_ANE-k99_3872539/Region 35.1	arylpolyene	1	12,229			
TARA_ANE-k99_3964636/Region 37.1	T1PKS	1,931	39,463			
TARA_ANE-k99_4257134/Region 40.1	T1PKS	2,810	38,546			
TARA_ANE-k99_6730098/Region 59.1	arylpolyene	1	20,706			
TARA_ANE-k99_9620988/Region 80.1	T1PKS	1	12,545			
TARA_ANE-k99_11352568/Region 97.1	T1PKS	1	10,274			
TARA_ASE-k99_973679/Region 111.1	hgIE-KS,T1PKS	1	10,522			
TARA_ASE-k99_3319788/Region 123.1	NRPS,T1PKS	1	28,095			
TARA_ASE-k99_3539774/Region 125.1	arylpolyene	1	28,171	APE Vf	Other	25%
TARA_ASE-k99_4740099/Region 129.1	PUFA,T1PKS	1	10,518			
TARA_ASE-k99_6939433/Region 140.1	hgIE-KS	1	10,751			
TARA_ASW-k99_771653/Region 145.1	T1PKS	1	12,766			
TARA_ASW-k99_1259523/Region 148.1	terpene	8,457	29,605			
TARA_ASW-k99_1596744/Region 151.1	ladderane	1	22,194			
TARA_ASW-k99_1853689/Region 153.1	T1PKS	1	25,277			

TARA_ASW-k99_2069705/Region 157.1	T1PKS	1	25,955	berninamycin A	RiPP	26%
TARA_ASW-k99_2429447/Region 161.1	T3PKS	1	27,216			
TARA_ASW-k99_2555030/Region 162.1	arylpolyene	1	27,585			
TARA_ASW-k99_4841156/Region 180.1	arylpolyene	1,046	42,329			
TARA_ASW-k99_5140954/Region 183.1	T1PKS	1	16,672			
TARA_ASW-k99_5827606/Region 187.1	NRPS	1	11,047			
TARA_ASW-k99_6277563/Region 190.1	T1PKS	1	10,748			
TARA_ASW-k99_6302083/Region 191.1	T3PKS	1	19,574			
TARA_ASW-k99_7931438/Region 200.1	T1PKS	20,313	61,757			
TARA_ASW-k99_9390589/Region 216.1	hglE-KS	1	22,629			
TARA_ION-k99_2637854/Region 231.1	terpene	86,893	108,583			
TARA_ION-k99_2637854/Region 231.2	redox-cofactor	119,596	141,803	azinomycin B	NRP + Polyketide	4%
TARA_ION-k99_4336073/Region 239.1	RiPP-like	73,949	84,737			
TARA_ION-k99_4336073/Region 239.2	terpene	270,808	292,486			
TARA_ION-k99_4336073/Region 239.3	redox-cofactor	302,157	324,364	azinomycin B	NRP + Polyketide	4%
TARA_ION-k99_4828864/Region 244.1	T1PKS	1	28,582			
TARA_ION-k99_7062432/Region 261.1	arylpolyene	1	14,390			
TARA_ION-k99_8207243/Region 265.1	T1PKS	9,731	50,555			
TARA_ION-k99_8530172/Region 267.1	T1PKS	1	15,090			
TARA_ION-k99_8926338/Region 268.1	betalactone	3,627	27,955			
TARA_ION-k99_11168747/Region 278.1	NRPS,T1PKS	1	70,319	oxazolepoxidomycin A	Polyketide	13%
TARA_ION-k99_12523780/Region 284.1	hglE-KS	1	23,027			
TARA_ION-k99_14455400/Region 289.1	T1PKS	1	11,187			
TARA_IOS-k99_1812130/Region 301.1	T1PKS	1	11,145			
TARA_IOS-k99_3481211/Region 311.1	hglE-KS	1	28,651			
TARA_IOS-k99_5040029/Region 325.1	RiPP-like	29,169	40,065			
TARA_IOS-k99_5585544/Region 331.1	T1PKS	1	21,832			
TARA_IOS-k99_7245556/Region 343.1	arylpolyene	176	35,541			
TARA_IOS-k99_9531409/Region 354.1	T1PKS,NRPS	1	19,050			
TARA_IOS-k99_11608981/Region 366.1	T1PKS	1	11,032			
TARA_IOS-k99_12211857/Region 369.1	T1PKS	1	11,231			

TARA_IOS-k99_13206630/Region 372.1	arylpolylene	1	13,823			
TARA_MED-k99_829504/Region 404.1	T1PKS	1	12,785			
TARA_MED-k99_1413773/Region 421.1	arylpolylene	63,351	104,526	lactonamycin	Polyketide	3%
TARA_MED-k99_3702765/Region 482.1	arylpolylene	1	10,301	APE Vf	Other	10%
TARA_MED-k99_4407384/Region 493.1	hserlactone	36,722	57,456			
TARA_MED-k99_4997507/Region 505.1	arylpolylene	1	26,464			
TARA_MED-k99_5022155/Region 508.1	arylpolylene	1	11,550			
TARA_MED-k99_5205461/Region 511.1	RiPP-like	76,533	87,387			
TARA_MED-k99_5299240/Region 515.1	arylpolylene	1	17,684			
TARA_MED-k99_5879508/Region 525.1	T1PKS	1	33,433			
TARA_MED-k99_6432729/Region 533.1	T1PKS	38,099	64,987			
TARA_MED-k99_6609820/Region 536.1	hglE-KS	1	23,583			
TARA_MED-k99_7993022/Region 559.1	T1PKS	1	33,921			
TARA_MED-k99_9189128/Region 583.1	terpene	150,907	171,839			
TARA_MED-k99_9456448/Region 592.1	NRPS,T1PKS	1	15,666			
TARA_PON-k99_213996/Region 598.1	hglE-KS	1	10,050			
TARA_PON-k99_1011198/Region 601.1	NRPS	1	17,478			
TARA_PON-k99_1175079/Region 603.1	hglE-KS	9,261	45,539			
TARA_PON-k99_1231741/Region 604.1	NRPS	1	18,509	mycobactin	NRP + Polyketide	60%
TARA_PON-k99_1254868/Region 605.1	hglE-KS	1	27,700			
TARA_PON-k99_1570427/Region 609.1	arylpolylene	4,925	45,977			
TARA_PON-k99_2437080/Region 619.1	NRPS,T1PKS	1	15,286			
TARA_PON-k99_4118086/Region 632.1	T1PKS,NRPS	1	39,156			
TARA_PON-k99_4235523/Region 633.1	T1PKS	1	24,469			
TARA_PON-k99_4270088/Region 634.1	T1PKS	1	14,505			
TARA_PON-k99_5387792/Region 647.1	T1PKS	1	15,080			
TARA_PON-k99_5593556/Region 649.1	arylpolylene	32,011	73,213			
TARA_PON-k99_5958106/Region 653.1	arylpolylene,ladderane	1	22,722			
TARA_PON-k99_6842487/Region 660.1	arylpolylene	1	16,610			
TARA_PON-k99_7218854/Region 665.1	T1PKS	1	18,114	glycopeptidolipid	NRP	16%
TARA_PON-k99_7763728/Region 673.1	T1PKS	1	37,613			

TARA_PON-k99_8804150/Region 683.1	T1PKS	1	10,311	1-heptadecene	Polyketide:Modular type I	100%
TARA_PON-k99_9329632/Region 689.1	T1PKS	1	10,155			
TARA_PON-k99_9956518/Region 693.1	arylpolyene	1	34,284			
TARA_PON-k99_10334859/Region 697.1	RiPP-like	28,923	39,804			
TARA_PON-k99_11831479/Region 710.1	T1PKS,NRPS	1	62,748	chondrochloren A	NRP + Polyketide:Modular type I	22%
TARA_PON-k99_12794088/Region 718.1	terpene	7,532	28,335			
TARA_PON-k99_13894771/Region 725.1	arylpolyene	1	13,082	aryl polyenes	Other	22%
TARA_PON-k99_13954325/Region 726.1	T1PKS	1	18,322			
TARA_PON-k99_15561696/Region 741.1	T1PKS,hglE-KS	1	10,188	TP-1161	RiPP:Thiopeptide	12%
TARA_PON-k99_15758939/Region 743.1	T1PKS	1	22,183			
TARA_PSE-k99_775059/Region 753.1	hglE-KS	1	10,575			
TARA_PSE-k99_2030147/Region 765.1	NRPS	1	34,704	didemnin B / nordidemnin B / didemnin X / didemnin Y	Polyketide + NRP:Cyclic depsipeptide	45%
TARA_PSE-k99_2180720/Region 770.1	terpene	90,920	113,718			
TARA_PSE-k99_2180720/Region 770.2	proteusin	125,119	145,490			
TARA_PSE-k99_2493361/Region 775.1	T1PKS	105,550	153,184			
TARA_PSE-k99_2550615/Region 776.1	arylpolyene	1	11,246	APE Vf	Other	30%
TARA_PSE-k99_2558412/Region 778.1	T1PKS	7,343	53,744			
TARA_PSE-k99_6484808/Region 814.1	arylpolyene	1	21,719			
TARA_PSE-k99_9211891/Region 827.1	T1PKS	1	33,484			
TARA_PSE-k99_9266729/Region 828.1	arylpolyene	1	17,393	aryl polyenes	Other	16%
TARA_PSE-k99_9404822/Region 830.1	ladderane	1	13,789			
TARA_PSE-k99_10001996/Region 837.1	T1PKS	1	27,029			
TARA_PSE-k99_11445862/Region 851.1	arylpolyene	1	10,735			
TARA_PSE-k99_11687429/Region 852.1	T1PKS	1	32,146	vazabotide A	NRP	4%
TARA_PSE-k99_11941962/Region 855.1	T3PKS	34,625	75,677	ET-743	NRP:Beta-lactam	8%
TARA_PSE-k99_13046137/Region 864.1	arylpolyene	13,524	54,234	APE Vf	Other	50%
TARA_PSE-k99_13059475/Region 865.1	T1PKS	49,169	96,719	s56-p1	NRP	3%

TARA_PSE-k99_13248480/Region 869.1	NRPS	1	10,758			
TARA_PSE-k99_13335927/Region 871.1	arylpolyene	1	29,093	APE Vf	Other	40%
TARA_PSE-k99_14423699/Region 878.1	terpene	120,431	141,267	carotenoid	Terpene	42%
TARA_PSE-k99_14677836/Region 882.1	proteusin	1	12,587			
TARA_PSE-k99_14786034/Region 884.1	butyrolactone	7,402	20,827			
TARA_PSE-k99_16004998/Region 895.1	arylpolyene, resorcinol	1	38,120	flexirubin	Polyketide	8%
TARA_PSE-k99_16767245/Region 897.1	T1PKS	1	11,881			
TARA_PSE-k99_17406297/Region 904.1	arylpolyene	1	14,169	APE Ec	Other	15%
TARA_PSE-k99_18921703/Region 922.1	NRPS	1	11,723	didemnin B / nordidemnin B / didemnin X / didemnin Y	Polyketide + NRP:Cyclic depsipeptide	36%
TARA_PSE-k99_19871325/Region 934.1	arylpolyene	1	10,561	flexirubin	Polyketide	11%
TARA_PSE-k99_22430428/Region 955.1	NRPS, T1PKS	1	49,749	puwainaphycin F / minutissamide A	NRP	33%
TARA_PSE-k99_22441888/Region 956.1	NRPS	1,382	44,736	thalassospiramide A	NRP:Lipopeptide + Polyketide:Trans-AT type I	100%
TARA_PSE-k99_22651754/Region 957.1	NRPS, T1PKS	1	16,993	micacocidin	NRP:NRP siderophore + Polyketide:Modular type I + Polyketide:Iterative type I	20%
TARA_PSE-k99_22688052/Region 959.1	T1PKS	1	15,183			
TARA_PSE-k99_22709537/Region 960.1	T1PKS	1	20,351			
TARA_PSE-k99_24883498/Region 971.1	NRPS, T1PKS	1	15,348			
TARA_PSE-k99_25439984/Region 980.1	arylpolyene	47,604	91,157	APE Vf	Other	50%
TARA_PSE-k99_25631123/Region 984.1	arylpolyene	1	28,676	flexirubin	Polyketide	19%
TARA_PSE-k99_26181230/Region 990.1	terpene	16,324	32,186			
TARA_PSE-k99_26535095/Region 993.1	T1PKS	1	21,434			
TARA_PSE-k99_27046995/Region 995.1	arylpolyene	1	21,038	APE Ec	Other	10%
TARA_PSE-k99_28122088/Region 1003.1	T1PKS	1	30,344			
TARA_PSW-k99_58599/Region 1005.1	ladderane	1	38,932	TP-1161	RiPP:Thiopeptide	16%
TARA_PSW-k99_236712/Region 1008.1	T3PKS	273,400	314,494			
TARA_PSW-k99_236712/Region 1008.2	terpene	500,632	521,468	carotenoid	Terpene	57%

TARA_PSW-k99_934618/Region 1013.1	arylpolyene	1	11,869			
TARA_PSW-k99_937050/Region 1014.1	hglE-KS,T1PKS	16,802	69,586	eicoseicosapentaenoic acid	Other	15%
TARA_PSW-k99_2012911/Region 1027.1	NRPS,T1PKS	9,559	61,230			
TARA_PSW-k99_2415730/Region 1033.1	T1PKS	1	46,107			
TARA_PSW-k99_2714889/Region 1036.1	hserlactone	27,485	47,952			
TARA_PSW-k99_3002637/Region 1040.1	T1PKS,NRPS	1	46,731			
TARA_PSW-k99_3826268/Region 1054.1	T1PKS	1,041	33,110	funisamine	Polyketide	5%
TARA_PSW-k99_3907640/Region 1055.1	terpene	8,240	29,079	carotenoid	Terpene	28%
TARA_PSW-k99_3927251/Region 1057.1	T1PKS	11,745	52,824			
TARA_PSW-k99_4475253/Region 1060.1	T1PKS	1	43,645			
TARA_PSW-k99_5115786/Region 1071.1	arylpolyene	1	14,993			
TARA_PSW-k99_5373462/Region 1077.1	T1PKS	1	30,218			
TARA_PSW-k99_5716256/Region 1087.1	T1PKS	1	12,218			
TARA_PSW-k99_5945439/Region 1090.1	arylpolyene	1	19,978			
TARA_PSW-k99_6084385/Region 1092.1	betalactone	12,901	40,420	fengycin	NRP	13%
TARA_PSW-k99_6638563/Region 1102.1	terpene	4,785	25,789			
TARA_PSW-k99_6887639/Region 1113.1	hglE-KS,T1PKS	1	35,886	eicoseicosapentaenoic acid	Other	21%
TARA_PSW-k99_6997347/Region 1114.1	arylpolyene	1	15,874			
TARA_PSW-k99_7461075/Region 1121.1	NRPS	224	46,397	bacillaene	Polyketide + NRP	28%
TARA_PSW-k99_7461075/Region 1121.2	NRPS,T1PKS	55,123	99,761			
TARA_PSW-k99_7488810/Region 1122.1	terpene	49,071	66,284			
TARA_PSW-k99_7524880/Region 1123.1	T1PKS	1	31,670	phenalamide A2	NRP + Polyketide	25%
TARA_PSW-k99_7785607/Region 1127.1	arylpolyene	1	23,816			
TARA_PSW-k99_7966335/Region 1130.1	T1PKS	1	30,931			
TARA_PSW-k99_8083719/Region 1133.1	arylpolyene,RiPP-like	1	28,165			
TARA_PSW-k99_8235592/Region 1135.1	terpene	1	16,935			
TARA_PSW-k99_8428153/Region 1139.1	T1PKS	57,245	104,117			
TARA_PSW-k99_8942982/Region 1145.1	arylpolyene	117,114	158,352			
TARA_PSW-k99_9218994/Region 1149.1	hglE-KS,T1PKS	1	34,438			

TARA_PSW-k99_9502407/Region 1155.1	hserlactone,T1PKS,butyrolactone	16,576	75,506	thailanstatin A	NRP + Polyketide	10%
TARA_PSW-k99_9520575/Region 1156.1	T1PKS	1	31,142			
TARA_PSW-k99_9885307/Region 1161.1	RiPP-like	123,220	134,071			
TARA_PSW-k99_10292531/Region 1168.1	NRPS	37,211	63,407	micacocidin	NRP:NRP siderophore + Polyketide:Modular type I + Polyketide:Iterative type I	20%
TARA_PSW-k99_11124378/Region 1176.1	NRPS,T1PKS	1	32,096			
TARA_PSW-k99_11132354/Region 1177.1	T1PKS	26,669	55,796			
TARA_RED-k99_165427/Region 1179.1	T1PKS	1	44,666			
TARA_RED-k99_598896/Region 1186.1	arylpolyene	1	12,070			
TARA_RED-k99_1972275/Region 1222.1	T1PKS	1	14,296			
TARA_RED-k99_2043078/Region 1224.1	T1PKS	496,208	542,477			
TARA_RED-k99_2052333/Region 1225.1	arylpolyene	1	23,209			
TARA_RED-k99_2210738/Region 1227.1	terpene	83,356	104,408			
TARA_RED-k99_2529078/Region 1238.1	terpene	20,674	41,504			
TARA_RED-k99_2796487/Region 1246.1	hglE-KS	1	25,265			
TARA_RED-k99_3927568/Region 1270.1	lassopeptide	1,120	17,726			
TARA_RED-k99_3927568/Region 1270.2	lassopeptide	58,412	80,792			
TARA_RED-k99_3930265/Region 1271.1	T1PKS	1	32,947	oviedomycin	Polyketide:Type II	8%
TARA_RED-k99_4022104/Region 1272.1	RiPP-like	15,157	26,029			
TARA_RED-k99_4941388/Region 1293.1	hserlactone	32,380	52,994			
TARA_RED-k99_5017231/Region 1297.1	T1PKS	1	25,563	eicoseicosapentaenoic acid	Other	10%
TARA_RED-k99_5778951/Region 1308.1	T1PKS	1	16,817			
TARA_RED-k99_7992211/Region 1360.1	T1PKS	1	28,918	guadinomine	NRP + Polyketide	7%
TARA_RED-k99_8017624/Region 1362.1	T1PKS	1	19,939			
TARA_RED-k99_8701261/Region 1374.1	terpene	22,497	44,248			
TARA_RED-k99_9355052/Region 1383.1	arylpolyene	1	37,543			
TARA_ANW-k99_31938/Region 1392.1	T1PKS	1	11,964			
TARA_ANW-k99_426342/Region 1394.1	RiPP-like	1	7,387			

TARA_ANW- k99_1018361/Region 1399.1	hserlactone	1	18,955			
TARA_ANW- k99_2040536/Region 1411.1	NRPS	1	27,340			
TARA_ANW- k99_2931189/Region 1419.1	terpene,hglE-KS	1	17,323			
TARA_ANW- k99_3409679/Region 1423.1	T1PKS	1	15,796			
TARA_ANW- k99_3484098/Region 1424.1	arylpolyene	1	20,154			
TARA_ANW- k99_4094640/Region 1432.1	T3PKS	1	11,081			
TARA_ANW- k99_6319736/Region 1459.1	NRPS,T1PKS	1	46,187			
TARA_ANW- k99_6695559/Region 1463.1	T1PKS	1	11,561			
TARA_ANW- k99_6760279/Region 1464.1	arylpolyene	1	15,451			
TARA_ANW- k99_6797346/Region 1465.1	T1PKS	2,692	35,844			
TARA_ANW- k99_7068302/Region 1469.1	arylpolyene	16,001	41,743			
TARA_ANW- k99_7171645/Region 1470.1	arylpolyene	1	15,144			
TARA_ANW- k99_7836192/Region 1478.1	arylpolyene	1	49,520	APE Vf	Other	25%
TARA_ANW- k99_8234935/Region 1481.1	arylpolyene, resorcinol	1	28,112	flexirubin	Polyketide	66%
TARA_ANW- k99_9622640/Region 1494.1	ladderane, arylpolyene	1	13,696			
TARA_ANW- k99_9709422/Region 1497.1	T1PKS	1	12,580	eicoseicosapentaenoic acid	Other	21%
TARA_ANW- k99_10064631/Region 1501.1	T1PKS	1	13,120			
TARA_ANW- k99_11223962/Region 1508.1	T1PKS	1	25,756			
TARA_ANW- k99_11302352/Region 1510.1	T1PKS	1	13,861			
TARA_SOC-k99_17348/Region 1511.1	arylpolyene	1	12,814			

TARA_SOC-k99_48115/Region 1512.1	T3PKS	1	16,812			
TARA_SOC-k99_237486/Region 1515.1	arylpolyene	1	29,040			
TARA_SOC-k99_893914/Region 1524.1	arylpolyene	1	20,646	flexirubin	Polyketide	41%
TARA_SOC-k99_1216356/Region 1528.1	T3PKS	1	29,224			
TARA_SOC-k99_1784331/Region 1533.1	arylpolyene	1	13,234	flexirubin	Polyketide	16%
TARA_SOC-k99_1983783/Region 1536.1	terpene	1	14,013	carotenoid	Terpene	28%
TARA_SOC-k99_2535372/Region 1545.1	arylpolyene,T3PKS	1	20,896			
TARA_SOC-k99_3385775/Region 1553.1	arylpolyene	1	20,337			

Appendix 8

Table S5: Showing the distribution of known BGC pathway identified from the SAO non-redundant KS contigs and their percentage similarity

Contigs/region	BGC type	From location	To location	Most similar known cluster	Type	Similarity
1_k141_73404/Region 2.1	arylpolyene	1	4,034			
1_k141_873093/Region 10.1	terpene	166,809	187,642	carotenoid	Terpene	42%
1_k141_873093/Region 10.2	T1PKS,NRPS	681,163	731,905			
1_k141_328873/Region 39.1	arylpolyene	1	1,769	APE Vf	Other	10%
1_k141_845589/Region 60.1	T1PKS	1	9,986			
2_k141_501545/Region 67.1	resorcinol	73,959	115,107			
2_k141_353594/Region 69.1	hglE-KS,T1PKS	74,570	128,062	paulomycin	Other	3%
3_k141_96687/Region 95.1	T1PKS,hglE-KS	25,309	78,801	paulomycin	Other	3%
3_k141_702016/Region 97.1	resorcinol	73,959	115,107			
3_k141_633769/Region 107.1	arylpolyene	1	9,764			
3_k141_467259/Region 114.1	arylpolyene	1	4,134			
3_k141_808400/Region 122.1	arylpolyene	1	3,808			
3_k141_663669/Region 125.1	arylpolyene	1	11,616			
3_k141_789508/Region 136.1	T1PKS,hglE-KS	213,391	264,848			
3_k141_892661/Region 144.1	ladderane	1	2,597			
4_k141_912315/Region 168.1	arylpolyene	1	3,998			
5_k141_251289/Region 185.1	T1PKS	1	9,903			
5_k141_652315/Region 189.1	resorcinol	46,182	87,330			
5_k141_68513/Region 194.1	arylpolyene	1	2,041	APE Vf	Other	10%
5_k141_688086/Region 205.1	T1PKS,hglE-KS	26,083	79,575	paulomycin	Other	3%

5_k141_1185582/Region 212.1	arylpolyene	1	3,093			
5_k141_78374/Region 214.1	arylpolyene	1	9,904			
5_k141_610370/Region 223.1	T1PKS,hglE-KS	259,544	311,001			
5_k141_920741/Region 226.1	arylpolyene	1	4,645			
6_k141_50111/Region 228.1	arylpolyene	1	14,956			
6_k141_235002/Region 232.1	resorcinol	74,124	115,272			
6_k141_193528/Region 236.1	arylpolyene	1	3,876			
6_k141_265014/Region 237.1	arylpolyene	1	2,301			
6_k141_159118/Region 239.1	arylpolyene	1	6,746	aryl polyenes	Other	22%
6_k141_59400/Region 241.1	T1PKS,hglE-KS	26,083	79,575	paulomycin	Other	3%
6_k141_266046/Region 242.1	hglE-KS	1	8,499			
6_k141_68143/Region 244.1	ectoine	89,601	99,999	ectoine	Other	80%
6_k141_97482/Region 247.1	T1PKS,hglE-KS	1	17,833			
6_k141_111942/Region 250.1	ladderane	1	6,760			
6_k141_225096/Region 251.1	arylpolyene	1	37,391	APE Vf	Other	10%
7_k141_627629/Region 261.1	T1PKS,NRPS	1	26,776			
7_k141_84381/Region 271.1	T1PKS	17,712	64,164			
7_k141_203753/Region 276.1	arylpolyene	1	1,901	APE Vf	Other	10%
7_k141_334343/Region 277.1	hserlactone	49,579	70,301			
8_k141_535735/Region 282.1	arylpolyene	1	1,809			
8_k141_101970/Region 285.1	arylpolyene	1	7,498			
8_k141_471464/Region 287.1	arylpolyene	1	2,204	APE Vf	Other	20%
8_k141_281465/Region 298.1	terpene	4,286	25,290			
9_k141_82633/Region 321.1	arylpolyene	1	4,367			
9_k141_84122/Region 324.1	arylpolyene	1	2,425	APE Vf	Other	10%
9_k141_733915/Region 344.1	arylpolyene	1	4,667	APE Vf	Other	15%
9_k141_868470/Region 348.1	NRPS,T1PKS	1	15,886			
9_k141_473766/Region 355.1	arylpolyene	1	2,051	APE Vf	Other	10%
9_k141_22135/Region 361.1	T1PKS	1	11,467			
9_k141_983411/Region 367.1	arylpolyene	1	17,309	flexirubin	Polyketid e	33%

9_k141_823203/Region 368.1	T3PKS	1	7,838			
10_k141_680081/Region 370.1	arylpolyene	1	5,570	flexirubin	Polyketide	19%
10_k141_580458/Region 379.1	arylpolyene	6,400	49,981	APE Vf	Other	30%
10_k141_451084/Region 383.1	arylpolyene	1	3,710			
10_k141_295956/Region 384.1	arylpolyene	1	1,814			
10_k141_849482/Region 397.1	arylpolyene	1	1,955	flexirubin	Polyketide	5%
10_k141_168623/Region 399.1	arylpolyene	1	3,184	flexirubin	Polyketide	11%
10_k141_330940/Region 406.1	arylpolyene	1	5,763	flexirubin	Polyketide	13%
10_k141_904164/Region 407.1	T3PKS	1	10,754			
10_k141_569960/Region 411.1	arylpolyene	1	3,951	APE Vf	Other	15%
11_k141_956206/Region 419.1	arylpolyene	1	8,578	flexirubin	Polyketide	25%
11_k141_569222/Region 431.1	NRPS,T1PKS	1	36,118			
11_k141_203925/Region 432.1	PUFA,hglE-KS	60,376	106,022	eicosapentaenoic acid	Other	66%
11_k141_389331/Region 460.1	T1PKS,NRPS	1	33,699			
11_k141_813671/Region 464.1	T3PKS	1	4,477			
12_k141_1096211/Region 484.1	NRPS	100,883	132,197	chejuenolide A / chejuenolide B	Polyketide	15%
13_k141_100709/Region 509.1	hglE-KS,T1PKS	24,394	75,851			
13_k141_105401/Region 528.1	arylpolyene	1	3,024	flexirubin	Polyketide	13%
13_k141_839269/Region 540.1	arylpolyene	1	1,181			
13_k141_86176/Region 541.1	arylpolyene	1	4,338			
13_k141_211967/Region 544.1	T1PKS,hglE-KS	26,083	79,575	paulomycin	Other	3%
13_k141_742488/Region 551.1	resorcinol	73,959	115,107			
13_k141_39623/Region 553.1	T1PKS	1	20,047			
14_k141_399450/Region 578.1	T1PKS	31,333	77,902			
14_k141_1012099/Region 580.1	arylpolyene	1	4,671	flexirubin	Polyketide	8%

14_k141_771963/Region 589.1	resorcinol	73,932	115,080			
14_k141_223467/Region 595.1	arylpolyene	1	6,269	flexirubin	Polyketide	16%
14_k141_897973/Region 600.1	arylpolyene	1	2,186	APE Ec	Other	15%
14_k141_873357/Region 613.1	T1PKS,hglE-KS	26,083	79,575	paulomycin	Other	3%
14_k141_753018/Region 618.1	ladderane	1	2,582			
14_k141_1029109/Region 620.1	arylpolyene	1	3,314	APE Vf	Other	15%
14_k141_272023/Region 637.1	arylpolyene	1	2,552	flexirubin	Polyketide	11%
15_k141_759704/Region 654.1	arylpolyene	1	1,939	flexirubin	Polyketide	8%
15_k141_305974/Region 655.1	arylpolyene	1	1,619	flexirubin	Polyketide	8%
15_k141_526901/Region 662.1	arylpolyene	1	3,163			
15_k141_528765/Region 663.1	arylpolyene	1	4,033	flexirubin	Polyketide	13%
16_k141_697129/Region 679.1	T1PKS	1	14,790			
16_k141_502314/Region 680.1	arylpolyene	35,558	82,131	flexirubin	Polyketide	55%
16_k141_920012/Region 681.1	arylpolyene	12,294	55,858	APE Vf	Other	40%
16_k141_392261/Region 682.1	arylpolyene	1	2,080			
16_k141_284832/Region 691.1	T3PKS	74,197	115,300			
16_k141_982964/Region 703.1	arylpolyene	1	8,748	APE Vf	Other	15%
16_k141_44289/Region 712.1	arylpolyene	1	8,813	APE Vf	Other	10%
16_k141_294334/Region 713.1	arylpolyene	1	3,738	flexirubin	Polyketide	13%
16_k141_387750/Region 735.1	arylpolyene	1	33,881	APE Vf	Other	30%
17_k141_565457/Region 745.1	arylpolyene	187,459	231,040	APE Vf	Other	30%
17_k141_358034/Region 747.1	arylpolyene	7,209	50,772	APE Vf	Other	35%
17_k141_798470/Region 759.1	arylpolyene	1	3,575	APE Ec	Other	15%
17_k141_537429/Region 781.1	arylpolyene	1	4,004	APE Vf	Other	10%

17_k141_665540/Region 782.1	arylpolyene	1	2,456	flexirubin	Polyketide	13%
18_k141_875853/Region 818.1	T1PKS	17,595	64,164			
18_k141_554657/Region 823.1	arylpolyene	1	3,204			
18_k141_168703/Region 845.1	arylpolyene	1	17,174	APE Vf	Other	30%
19_k141_209518/Region 893.1	ladderane	1	2,663			
21_k141_98863/Region 928.1	T3PKS	1	8,723			
21_k141_327557/Region 958.1	resorcinol	73,959	115,107			
21_k141_957892/Region 962.1	T1PKS,hglE-KS	26,083	79,575	paulomycin	Other	3%
22_k141_605048/Region 977.1	arylpolyene,resorcino l	162,351	208,418	flexirubin	Polyketide	13%
22_k141_336485/Region 988.1	resorcinol,arylpolym e	1	8,641	flexirubin	Polyketide	16%
22_k141_275063/Region 996.1	resorcinol	3,074	27,493			
22_k141_65869/Region 1001.1	arylpolyene	371,576	417,912	flexirubin	Other	36%
22_k141_422854/Region 1006. 1	arylpolyene	1	4,367	flexirubin	Polyketide	8%
22_k141_28569/Region 1011.1	arylpolyene	1	6,773	APE Vf	Other	15%
22_k141_697585/Region 1020. 1	arylpolyene	1	1,387	flexirubin	Polyketide	5%
22_k141_470688/Region 1036. 1	arylpolyene	1	2,476	flexirubin	Polyketide	5%
22_k141_54015/Region 1037.1	NRPS,T1PKS	1	12,344			
22_k141_825735/Region 1038. 1	ladderane	1	4,998			
22_k141_54573/Region 1041.1	ectoine	87,239	97,637	ectoine	Other	80%
22_k141_222669/Region 1043. 1	arylpolyene	1	5,589			
22_k141_392020/Region 1053. 1	T1PKS	19,237	47,400			
22_k141_412564/Region 1057. 1	arylpolyene	1	3,610			
22_k141_559517/Region 1058. 1	NRPS	1	11,289			

22_k141_457442/Region 1064.1	arylpolyene	1	4,127			
22_k141_686181/Region 1065.1	arylpolyene	1	37,391	APE Vf	Other	10%
22_k141_80919/Region 1068.1	T3PKS	1	8,831			
22_k141_354190/Region 1071.1	arylpolyene	1	2,460			
23_k141_716104/Region 1095.1	arylpolyene	1	3,595	APE Vf	Other	15%
23_k141_549371/Region 1096.1	T3PKS	1	2,036			
23_k141_694466/Region 1097.1	arylpolyene	75,771	122,344	flexirubin	Polyketide	55%
23_k141_71496/Region 1111.1	NRPS	1	12,215			
23_k141_453723/Region 1121.1	arylpolyene	1	1,487			
23_k141_98389/Region 1128.1	T3PKS	1	9,743			
23_k141_602719/Region 1132.1	T3PKS	498,211	530,245			
23_k141_499467/Region 1138.1	arylpolyene	1	28,639	APE Vf	Other	10%
23_k141_187763/Region 1148.1	T3PKS	1	7,623			
24_k141_386724/Region 1156.1	T1PKS	1	7,190			
24_k141_681529/Region 1157.1	arylpolyene	1	3,368	APE Vf	Other	10%
24_k141_350974/Region 1161.1	arylpolyene	1	34,398	flexirubin	Polyketide	55%
24_k141_111922/Region 1166.1	T3PKS	1	3,867			
24_k141_462903/Region 1173.1	T3PKS	1	17,999			
24_k141_225047/Region 1177.1	arylpolyene	2,427	24,274	APE Vf	Other	10%

24_k141_614420/Region 1183.1	resorcinol	73,959	115,107			
24_k141_208898/Region 1184.1	hglE-KS,T1PKS,PUFA	1	37,171	eicosapentaenoic acid-like compound	Other	18%
24_k141_653222/Region 1197.1	arylpolyene	28,003	65,238	APE Vf	Other	10%
24_k141_560063/Region 1201.1	T3PKS	1	2,541			
24_k141_708757/Region 1203.1	arylpolyene	1	2,853	flexirubin	Polyketide	8%
24_k141_212920/Region 1216.1	arylpolyene	1	2,484	APE Vf	Other	10%
24_k141_46276/Region 1217.1	arylpolyene,resorcinol	1	23,289	flexirubin	Polyketide	44%
24_k141_325214/Region 1218.1	NRPS	1	12,113			
24_k141_230241/Region 1219.1	T1PKS,hglE-KS	26,083	69,203			
24_k141_345032/Region 1221.1	arylpolyene	1	3,352	flexirubin	Polyketide	13%
24_k141_471897/Region 1222.1	hglE-KS	82,396	106,393			
24_k141_695390/Region 1228.1	arylpolyene	1	10,359	APE Vf	Other	25%
24_k141_417363/Region 1231.1	arylpolyene	1	8,227	flexirubin	Polyketide	25%
24_k141_328670/Region 1234.1	arylpolyene	1	8,979	APE Vf	Other	15%
24_k141_639534/Region 1238.1	T3PKS	134,622	175,725			

Appendix 9

Table S6: Showing the medium to high quality MAGs with their respective taxonomic classification, completeness and contamination

MAG ID	Classification	Completeness	Contamination
200m S6			
Spring			
SAR324_204	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	88.65	0.84
Posei_205	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__Thalassarchaeum sp002495735	83.96	0.4
Verru_203	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	85.83	4.77
Acidi_207	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__S20-B6;s__S20-B6 sp002699725	85.31	3.85
Dehal_201	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA1328;s__	87.36	3.56
Gamma_204	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__	58.79	6.04
Dehal_202	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__	67.54	5.17
Verru_204	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1100;g__;s__	63.31	6.67
Acidi_208	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	83.1	2.99
Gamma_205	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	50.81	0

Gamma_206	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__	77.3	6.4
Gamma_207	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDSEA-S09-B13;s__REDSEA-S09-B13 sp002456995	84.76	3.66
Gamma_208	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA11791;s__	86.91	6.33
200m Winter S39			
Posei_222	d__Archaea;p__Thermoplasmatota;c__Poseidoniii;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__Thalassarchaeum sp002495735	83.16	0
Nitros_205	d__Bacteria;p__Nitrospinota;c__Nitrospina;o__Nitrospinales;f__Nitrospinaceae;g__LS-NOB;s__LS-NOB sp003545625	81.09	2.23
Posei_223	d__Archaea;p__Thermoplasmatota;c__Poseidoniii;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-P;s__	56.13	3.3
Posei_224	d__Archaea;p__Thermoplasmatota;c__Poseidoniii;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-O2;s__	58.51	1.6
Posei_225	d__Archaea;p__Thermoplasmatota;c__Poseidoniii;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-O1;s__MGIIb-O1 sp002498525	70.11	1.84
SAR324_214	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	90.07	3.69
Verru_216	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	97.75	0.81
Verru_217	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__ ;s__	76.12	2.99
SAR324_215	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__UBA8110;s__	61.81	1.73
Acidi_227	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__S20-B6;s__S20-B6 sp002699725	89.32	3.85
Posei_226	d__Archaea;p__Thermoplasmatota;c__Poseidoniii;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__	52.4	4.8
Verru_218	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1100;g__ ;s__	74.13	5.45
Posei_227	d__Archaea;p__Thermoplasmatota;c__Poseidoniii;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	72	6.89
Gamma_235	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__GCA-2726415;s__	75.44	3.05
Gamma_236	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Woeseiales;f__Woeseiaceae;g__GCA-002728725;s__	77.59	2.83
Gamma_237	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDSEA-S09-B13;s__REDSEA-S09-B13 sp002456995	96.65	1.83
Gamma_238	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__ ;s__	60.8	2.17
Acidi_228	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__TK06;g__UBA2110;s__UBA2110 sp002331465	72.98	5.57
Marin_207	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	90.11	0
Crenar_203	d__Archaea;p__Crenarchaeota;c__Nitrososphaeria;o__Nitrososphaerales;f__Nitrosopumilaceae;g__Nitrosopelagicus;s__	66.83	8.74
500m Spring S7			
Dehal_501	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__	66.97	4.36

Nitros_504	d__Bacteria;p__Nitrospinae;c__Nitrospinae;o__Nitrospinales;f__Nitrospinae;g__LS-NOB;s__LS-NOB sp003545625	92.47	7.34
SAR324_506	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__UBA8110;s__	83.94	2.52
Verru_503	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	83.56	2.4
Nitros_505	d__Bacteria;p__Nitrospinae;c__Nitrospinae;o__Nitrospinales;f__Nitrospinae;g__SCGCAA288-L16;s__	56.21	7.76
SAR324_507	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	91.26	0.84
Acidi_507	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__S20-B6;s__S20-B6 sp002699725	94.87	6.41
Posei_509	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__Thalassarchaeum sp002495735	82.36	0
Marin_505	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	90.11	1.1
Gamma_521	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__UBA11654;s__	59.88	2.01
Posei_510	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	69.73	0.29
Acidi_508	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__TK06;g__UBA2110;s__UBA2110 sp002331465	93.16	2.14
Gamma_522	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDSEA-S09-B13;s__REDSEA-S09-B13 sp002456995	82.62	1.83
Dehal_502	d__Bacteria;p__Chloroflexota;c__Dehalococcidia;o__SAR202;f__UBA826;g__UBA11996;s__	66.49	1.98
500m Winter S40			
SAR324_520	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	87.99	1.03
Planc_502	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__UBA1268;g__UBA1268;s__	55.15	1.25
Verru_516	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	79.94	8.61
Gemma_505	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__GCA-2718595;s__	63.49	2.81
Gamma_551	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__	91.11	0.68
Gamma_552	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__	63.07	1.7
Gamma_553	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__UBA11654;s__	55.27	5.69
Acidi_528	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	83.57	2.99
Bacte_503	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MAG-121220-bin8;s__	92.42	2.94
Gamma_554	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	67.85	0
Gamma_555	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Woeseiales;f__Woeseiaceae;g__GCA-002728725;s__	57.77	7.92
Gamma_556	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__GCA-2726415;s__	58.02	0.64
Planc_503	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__Mariniblastus;s__	77.1	2.35

**2600m Spring
S8**

Posei_d01	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-O1;s__MGIIb-O1 sp002498525	86.4	0
DG_d01	d__Bacteria;p__TA06_A;c__DG-26_A;o__f__g__s__	57.26	0.75
Gemma_d01	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__UBA1138 sp003447875	60.84	3.3
Gamma_d01	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA11791;s__	53.28	1.32
Posei_d02	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__MGIII;f__CG-Epi1;g__UBA8886;s__UBA8886 sp003193815	70.92	1.64
Planc_d01	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__s__	72.74	3.53
Gamma_d02	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__	84.71	2.89
SAR324_d01	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	90.42	0
Posei_d03	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__UBA60;s__UBA60 sp002503395	68.63	2.53
SAR324_d02	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__UBA8110;s__	56.2	5.93
Verru_d01	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1100;g__s__	65.21	8.91
SAR324_d03	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__	85.17	0
Dehal_d01	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__UBA9611 sp002746355	86.56	2.97
Gamma_d03	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__SAR86;f__SAR86;g__AEGEAN-183;s__	65.76	0.74
Gamma_d04	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__	94.78	1.83
Dehal_d02	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA9455;s__UBA9455 sp002313245	94.55	0
Dehal_d03	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__SAR202;f__UBA11138;g__UBA1123;s__UBA1123 sp002313895	86.33	4.95
Posei_d04	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	84.4	0.8
Gamma_d05	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	93.91	0
Acidi_d01	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	93.16	2.14
Gamma_d06	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__s__	98.23	0
Gamma_d07	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	58.35	0.78
Dehal_d04	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA11650;s__UBA11650 sp002401285	85.52	9.16
Marin_d01	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	86.81	1.1
Gamma_d08	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	54.78	0.35
Marin_d02	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__UBA8229;g__UBA8229;s__UBA8229 sp003535775	52.38	3.36

**2690m Winter
S37**

Gamma_d25	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__UBA9145 sp002731775	93.95	3.46
Gamma_d26	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Oleiphilaceae;g__Marinobacter;s__Marinobacter salarius	91.88	0.55
Posei_d16	d__Archaea;p__Thermoplasmata;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__ ;s__	65.01	1.14
Posei_d17	d__Archaea;p__Thermoplasmata;c__Poseidoniiia;o__MGIII;f__CG-Epi1;g__UBA8886;s__UBA8886 sp003193815	75.73	3.77
SAR324_d09	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	87.02	0
Posei_d18	d__Archaea;p__Thermoplasmata;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-O1;s__MGIIb-O1 sp002498525	85.6	0
Posei_d19	d__Archaea;p__Thermoplasmata;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__UBA60;s__UBA60 sp002503395	61.62	4.57
Dehal_d16	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA9455;s__UBA9455 sp002313245	65.75	0
Gemma_d06	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__UBA1138 sp003447875	91.75	4.4
Posei_d20	d__Archaea;p__Thermoplasmata;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__MGIIa-L1;s__	77.33	0.8
Gamma_d27	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__SAR86;f__SAR86;g__AEGEAN-183;s__	64.87	0.49
Bacte_d02	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__GCA-2700405;s__	67.36	1.23
Acidi_d05	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	95.44	2.14
Gamma_d28	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__ ;s__	59.42	1.06
Posei_d21	d__Archaea;p__Thermoplasmata;c__Poseidoniiia;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	81.2	0.8
Gamma_d29	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	91.92	0.66
Verru_d04	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	73.14	0
Gamma_d30	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__ ;s__	95.92	0.17
Verru_d05	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__ ;s__	89.58	4.25
Marin_d08	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__SCGC-AAA003-L08;f__ ;g__ ;s__	80.47	1.1
Marin_d09	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	86.81	0
SAR324_d10	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__	87.9	0
Dehal_d17	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__UBA9611 sp002746355	85.64	0.99

Appendix 10

Table S7: Showing the MAGs and their reference genomes ANI values

MAGs_ID	classification	fastani_reference	fastani_reference_radius	fastani_ani	fastani_af	closest_placement_reference	closest_placement_ani	closest_placement_af	aa_percent
200m spring 56									
SAR324_204	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	GCA_002082305.1	95.0	97.43	0.82	GCA_000213335.2	97.73	0.49	90.18
Verru_203	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	N/A	N/A	N/A	N/A	GCA_002299785.1	91.03	0.61	76.65
Acidi_207	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia; o__Microtrichales;f__MedAcidi-G1;g__S20-B6;s__S20-B6 sp002699725	GCA_002699725.1	95.0	97.26	0.89	GCA_002699725.1	97.26	0.89	74.31
Dehal_201	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA1328;s__	N/A	N/A	N/A	N/A	GCA_002501045.1	77.78	0.29	79.62
Gamma_204	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	56.71
Dehal_202	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	60.71
Verru_204	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1100;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	48.61
Acidi_208	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia; o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	N/A	N/A	N/A	N/A	GCA_002717365.1	78.98	0.36	76.15

Gamma_205	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	N/A	N/A	N/A	N/A	GCA_002698045.1	95.93	0.59	51.77
Gamma_206	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	71.13
Gamma_207	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDESA-S09-B13;s__REDESA-S09-B13 sp002456995	GCA_002456995.1	95.0	97.65	0.76	GCA_002456995.1	97.65	0.76	79.82
Gamma_208	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA11791;s__	N/A	N/A	N/A	N/A	GCA_002714255.1	93.61	0.61	79.88
Posei_205	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__Thalassarchaeum sp002495735	GCA_002495735.1	95.0	99.11	0.87	GCA_002495735.1	99.11	0.87	78.71
200m winter S39									
Acidi_227	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__MedAcidi-G1;g__S20-B6;s__S20-B6 sp002699725	GCA_002699725.1	95.0	97.15	0.86	GCA_002699725.1	97.15	0.86	79.38
Acidi_228	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__TK06;g__UBA2110;s__UBA2110 sp002331465	GCA_002331465.1	95.0	96.82	0.81	GCA_002331465.1	96.82	0.81	71.85
Marin_207	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	GCA_002715035.1	95.0	98.79	0.87	GCA_002715035.1	98.79	0.87	89.48
Gamma_237	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDESA-S09-B13;s__REDESA-S09-B13 sp002456995	GCA_002456995.1	95.0	97.57	0.82	GCA_002456995.1	97.57	0.82	95.93
SAR324_214	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	GCA_002082305.1	95.0	97.74	0.75	GCA_002082305.1	97.74	0.75	89.01
Nitros_205	d__Bacteria;p__Nitrospina;c__Nitrospina;o__Nitrospinales;f__Nitrospinaeae;g__LS-NOB;s__LS-NOB sp003545625	GCA_003545625.1	95.0	97.93	0.82	GCA_003545625.1	97.93	0.82	72.4
Verru_217	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	62.2
Verru_216	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	N/A	N/A	N/A	N/A	GCA_002299785.1	91.28	0.73	86.49
Verru_218	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1100;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	54.6
Gamma_236	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Woeseiales;f__Woeseiaceae;g__GCA-002728725;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	98.1
Gamma_235	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__GCA-2726415;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	73.99
Gamma_238	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	84.05
SAR324_215	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__UBA8110;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	62.26
Posei_222	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__Thalassarchaeum sp002495735	GCA_002495735.1	95.0	99.36	0.88	GCA_002495735.1	99.36	0.88	81.25
Posei_225	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-O1;s__MGIIb-O1 sp002498525	GCA_002498525.1	95.0	97.67	0.99	GCA_002498525.1	97.67	0.99	64.62
Posei_226	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__Thalassarchaeum;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	40.57
Posei_224	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-O2;s__	N/A	N/A	N/A	N/A	GCA_002499785.1	89.0	0.82	55.0
Posei_223	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIIb-P;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	44.63

Posei_227	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	70.69
Crenar_203	d__Archaea;p__Crenarchaeota;c__Nitrososphaeria;o__Nitrososphaerales;f__Nitrosopumilaceae;g__Nitrosopelagicus;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	55.82
500m spring S7										
Acidi_508	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__TK06;g__UBA2110;s__UBA2110 sp002331465	GCA_002331465.1	95.0	96.98	0.82	GCA_002331465.1	96.98	0.82	87.84	
Gamma_522	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDSEA-S09-B13;s__REDSEA-S09-B13 sp002456995	GCA_002456995.1	95.0	97.45	0.79	GCA_002456995.1	97.45	0.79	83.21	
Acidi_507	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__MedAcidi-G1;g__S20-B6;s__S20-B6 sp002699725	GCA_002699725.1	95.0	97.15	0.86	GCA_002699725.1	97.15	0.86	89.46	
Marin_505	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	GCA_002715035.1	95.0	98.64	0.88	GCA_002715035.1	98.64	0.88	89.29	
Nitros_504	d__Bacteria;p__Nitrospina;o__Nitrospina;c__Nitrospinales;f__Nitrospinaeae;g__LS-NOB;s__LS-NOB sp003545625	GCA_003545625.1	95.0	98.71	0.74	GCA_003545625.1	98.71	0.74	86.07	
SAR324_507	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	GCA_002082305.1	95.0	97.92	0.79	GCA_002082305.1	97.92	0.79	92.72	
Dehal_502	d__Bacteria;p__Chloroflexota;c__Dehalococcidia;o__SAR202;f__UBA826;g__UBA11996;s__	N/A	N/A	N/A	N/A	GCA_002708495.1	95.95	0.57	56.85	
Dehal_501	d__Bacteria;p__Chloroflexota;c__Dehalococcidia;o__UBA3495;f__UBA3495;g__UBA9611;s__	N/A	N/A	N/A	N/A	GCA_002730485.1	79.31	0.57	60.65	
Verru_503	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	N/A	N/A	N/A	N/A	GCA_002299785.1	90.79	0.58	68.77	
Gamma_521	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	78.33	
SAR324_506	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__UBA8110;s__	N/A	N/A	N/A	N/A	GCA_002707655.1	98.2	0.58	81.35	
Nitros_505	d__Bacteria;p__Nitrospina;o__Nitrospina;c__Nitrospinales;f__Nitrospinaeae;g__SCGAAA288-L16;s__	N/A	N/A	N/A	N/A	GCA_000372225.1	93.7	0.25	47.58	
Posei_509	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__Poseidoniales;f__Thalassosarchaeae;g__Thalassarchaeum;s__Thalassarchaeum sp002495735	GCA_002495735.1	95.0	99.38	0.89	GCA_002495735.1	99.38	0.89	80.43	
Posei_510	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	65.53	
500m winter S40										
SAR324_520	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	GCA_002082305.1	95.0	97.13	0.82	GCA_000213335.2	97.16	0.42	87.1	
Acidi_528	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	N/A	N/A	N/A	N/A	GCA_002717365.1	78.63	0.39	74.62	
Verru_516	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	N/A	N/A	N/A	N/A	GCA_002299785.1	90.79	0.61	74.54	
Planc_503	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__Mariniblastus;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	64.11	
Planc_502	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__UBA1268;g__UBA1268;s__	N/A	N/A	N/A	N/A	GCA_002862165.1	87.7	0.74	49.68	
Bacte_503	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MAG-121220-bin8;s__	N/A	N/A	N/A	N/A	GCA_002700465.1	77.83	0.39	83.49	

Gemma_505	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__GCA-2718595;s__	N/A	N/A	N/A	N/A	GCA_002718595.1	78.83	0.28	59.5
Gamma_552	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	63.43
Gamma_551	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	97.22
Gamma_554	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	N/A	N/A	N/A	N/A	GCA_002698045.1	96.08	0.54	59.56
Gamma_555	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Woeseiales;f__Woeseiaceae;g__GCA-002728725;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	62.54
Gamma_556	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__GCA-2726415;s__	N/A	N/A	N/A	N/A	GCA_002726415.1	77.53	0.18	53.35
Gamma_553	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	73.79
2600m spring S8									
Dehal_d01	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__UBA9611 sp002746355	GCA_002746355.1	95.0	99.25	0.94	GCA_002746355.1	99.25	0.94	80.28
Dehal_d02	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA9455;s__UBA9455 sp002313245	GCA_002313245.1	95.0	99.4	0.86	GCA_002313245.1	99.4	0.86	87.38
Gamma_d04	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__REDSEA-S09-B13;s__REDSEA-S09-B13 sp003447825	GCA_003447825.1	95.0	99.41	0.89	GCA_003447825.1	99.41	0.89	92.94
Dehal_d03	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__SAR202;f__UBA11138;g__UBA1123;s__UBA1123 sp002313895	GCA_002313895.1	95.0	99.52	0.89	GCA_002313895.1	99.52	0.89	76.33
Marin_d01	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	GCA_002715035.1	95.0	96.78	0.82	GCA_002715035.1	96.78	0.82	90.18
SAR324_d01	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	GCA_002082305.1	95.0	99.16	0.88	GCA_002082305.1	99.16	0.88	92.32
Dehal_d04	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA11650;s__UBA11650 sp002401285	GCA_002401285.1	95.0	98.7	0.68	GCA_002401285.1	98.7	0.68	70.04
Gemma_d01	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__UBA1138 sp003447875	GCA_003447875.1	95.0	98.79	0.91	GCA_003447875.1	98.79	0.91	53.85
Marin_d02	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__UBA8229;g__UBA8229;s__UBA8229 sp003535775	GCA_003535775.1	95.0	98.68	0.68	GCA_003535775.1	98.68	0.68	57.18
Acidi_d01	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	N/A	N/A	N/A	N/A	GCA_002717365.1	79.26	0.43	88.17
Verru_d01	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1100;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	51.01
Planc_d01	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	63.83
DG_d01	d__Bacteria;p__TA06_A;c__DG-26_A;o__f__g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	51.29
Gamma_d02	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	80.28
Gamma_d05	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	N/A	N/A	N/A	N/A	GCA_002698045.1	94.21	0.82	92.34
Gamma_d06	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	97.08
Gamma_d01	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA11791;s__	N/A	N/A	N/A	N/A	GCA_002714255.1	97.85	0.45	52.9
Gamma_d03	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__SAR86;f__SAR86;g__AEGEAN-183;s__	N/A	N/A	N/A	N/A	GCA_001628005.1	79.76	0.67	84.4

Gamma_d07	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	59.56
Gamma_d08	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	69.27
SAR324_d03	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	85.95
SAR324_d02	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__UBA8110;s__	N/A	N/A	N/A	N/A	GCA_002707655.1	N/A	N/A	N/A	44.84
Posei_d01	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__Poseidoniales;f__Thalassoarchaeaceae;g__MGIb-O1;s__MGIb-O1 sp002498525	GCA_002498525.1	95.0	98.4	0.98	GCA_002498525.1	98.4	0.98	0.98	83.7
Posei_d02	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__MGIII;f__CG-Epi1;g__UBA8886;s__UBA8886 sp003193815	GCA_003193815.1	95.0	95.39	0.67	GCA_003193815.1	95.39	0.67	0.67	62.33
Posei_d03	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__Poseidoniales;f__Poseidoniceae;g__UBA60;s__UBA60 sp002503395	GCA_002503395.1	95.0	96.97	0.93	GCA_002503395.1	96.97	0.93	0.93	63.41
Posei_d04	d__Archaea;p__Thermoplasmata;c__Poseidonii;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	N/A	N/A	N/A	N/A	GCA_002506485.1	91.89	0.73	0.73	81.07
2690m winter S37										
Dehal_d16	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA9455;s__UBA9455 sp002313245	GCA_002313245.1	95.0	98.91	0.87	GCA_002313245.1	98.91	0.87	0.87	55.52
SAR324_d09	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__Arctic96AD-7 sp002082305	GCA_002082305.1	95.0	99.1	0.89	GCA_002082305.1	99.1	0.89	0.89	89.15
Gamma_d25	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__UBA9145 sp002731775	GCA_002731775.1	95.0	98.6	0.79	GCA_002731775.1	98.6	0.79	0.79	97.28
Gamma_d26	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Oleiphilaceae;g__Marinobacter;s__Marinobacter salarius	GCF_000831005.1	95.0	98.67	0.95	GCF_000831005.1	98.67	0.95	0.95	93.89
Marin_d09	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__TCS55 sp002715035	GCA_002715035.1	95.0	96.74	0.8	GCA_002715035.1	96.74	0.8	0.8	88.65
Dehal_d17	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA3495;f__UBA3495;g__UBA9611;s__UBA9611 sp002746355	GCA_002746355.1	95.0	99.05	0.94	GCA_002746355.1	99.05	0.94	0.94	73.85
Gemma_d06	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__UBA1138 sp003447875	GCA_003447875.1	95.0	98.94	0.93	GCA_003447875.1	98.94	0.93	0.93	87.98
Acidi_d05	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichales;f__MedAcidi-G1;g__UBA9410;s__	N/A	N/A	N/A	N/A	GCA_002717365.1	79.16	0.44	0.44	89.17
Verru_d05	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	77.18
Verru_d04	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__	N/A	N/A	N/A	N/A	GCA_002299785.1	90.69	0.62	0.62	65.81
Bacte_d02	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__GCA-2700405;s__	N/A	N/A	N/A	N/A	GCA_002700405.1	81.92	0.58	0.58	90.62
Marin_d08	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__SCGC-AAA003-L08;f__g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	73.45
Gamma_d29	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__Thioglobus;s__	N/A	N/A	N/A	N/A	GCA_002698045.1	94.15	0.81	0.81	91.31
Gamma_d30	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiomicrospirales;f__Thioglobaceae;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	91.87
Gamma_d27	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__SAR86;f__SAR86;g__AEGEAN-183;s__	N/A	N/A	N/A	N/A	GCA_001628005.1	79.77	0.63	0.63	83.33
Gamma_d28	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA11654;f__UBA11654;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	84.4

SAR324_d10	d__Bacteria;p__SAR324;c__SAR324;o__SAR324;f__NAC60-12;g__Arctic96AD-7;s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	88.21
Posei_d19	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__UBA60;s__UBA60 sp002503395	GCA_002503395.1	95.0	96.83	0.97	GCA_002503395.1	96.83	0.97		50.02
Posei_d18	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Thalassosphaeraeae;g__MGIIb-O1;s__MGIIb-O1 sp002498525	GCA_002498525.1	95.0	98.37	0.97	GCA_002498525.1	98.37	0.97		83.72
Posei_d17	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__MGIII;f__CG-Epi1;g__UBA8886;s__UBA8886 sp003193815	GCA_003193815.1	95.0	96.02	0.69	GCA_003193815.1	96.02	0.69		64.97
Posei_d20	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__MGIIa-L1;s__	N/A	N/A	N/A	N/A	GCA_002499015.1	81.87	0.73		76.13
Posei_d16	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__Poseidoniales;f__Poseidoniaceae;g__s__	N/A	N/A	N/A	N/A	N/A	N/A	N/A		48.67
Posei_d21	d__Archaea;p__Thermoplasmatota;c__Poseidoniiia;o__MGIII;f__CG-Epi1;g__CG-Epi1;s__	N/A	N/A	N/A	N/A	GCA_002506485.1	91.84	0.74		79.61

Appendix 11

Table S8: The Southern Ocean MAGs and their BGC abundance

MAG_ID	Phylum	Region	Type	From	To	Most similar known cluster	Similarity
200m Spring							
Dehal_201	Chloroflexota	Region 340.1	terpene	1	1,567		
Dehal_202	Chloroflexota	Region 17.1	other	1	6,957		
		Region 61.1	terpene	1	4,852	hopene	15%
		Region 157.1	terpene	1	3,441		
		Region 608.1	terpene	1	1,557		
Gamma_204	Proteobacteria	Region 6.1	other	1	7,050		
Gamma_208	Proteobacteria	Region 216.1	betalactone	1	4,465		
Posei_205	Thermoplasmatota	Region 14.1	terpene	9,997	24,461		

SAR324_204	SAR324	Region 158.1	arylpolyene	1	5,621	APE Vf	Other	10%
		Region 258.1	PUFA	1	3,654			
		Region 292.1	T3PKS	1	3,239			
		Region 298.1	hglE-KS	1	3,136			
Verru_203	Verrucomicrobiota	Region 62.1	terpene	1	8,278			
		Region 134.1	terpene	1	5,632			
Verru_204	Verrucomicrobiota	Region 17.1	terpene	1	4,364			
		Region 183.1	terpene	1	2,334			
		Region 578.1	terpene	1	1,385			
		Region 799.1	ectoine	1	1,170			
		Region 861.1	terpene	1	1,124			
200m winter								
Acidi_228	Actinobacteriota	Region 127.1	other	1	6,379			
Gamma_237	Proteobacteria	Region 63.1	betalactone	1	15,291			
Nitros_205	Nitrospinota	Region 92.1	terpene	1	4,139			
		Region 188.1	RiPP-like	1	3,134			
		Region 458.1	terpene	1	1,884			
Posei_222	Thermoplasmatota	Region 34.1	terpene	1	14,411			
Posei_224	Thermoplasmatota	Region 5.1	terpene	1	10,670			
Posei_225	Thermoplasmatota	Region 99.1	terpene	1	4,222			
Posei_226	Thermoplasmatota	Region 225.1	terpene	1	1,768			
Posei_227	Thermoplasmatota	Region 3.1	terpene	4,092	21,629			
SAR324_214	SAR324	Region 3.1	T3PKS	9,389	32,131			
		Region 114.1	T1PKS,PUFA	1	7,587			
		Region 185.1	arylpolyene	1	5,177	APE Vf	Other	15%
		Region 265.1	hglE-KS	1	3,863			
Region 329.1	RiPP-like	1	3,150					
SAR324_215	SAR324	Region 35.1	arylpolyene	1	4,064	APE Vf	Other	15%
		Region 556.1	hglE-KS	1	1,517			
Verru_216	Verrucomicrobiota	Region 28.1	terpene	1	11,941			

		Region 39.1	terpene	1,890	16,773			
Verru_217	Verrucomicrobiota	Region 45.1	T3PKS	1	7,338			
		Region 134.1	terpene	1	5,423			
		Region 442.1	T1PKS	1	3,114			
		Region 506.1	terpene	1	2,896			
		Region 694.1	hglE-KS	1	2,365	heterocyst glycolipids	Other	28%
		Region 792.1	hglE-KS	1	2,128			
Verru_218	Verrucomicrobiota	Region 144.1	terpene	1	2,755			
		Region 152.1	terpene	1	2,737			
		Region 561.1	terpene	1	1,465			
500m Spring								
Acidi_507	Actinobacteriota	Region 272.1	NRPS	1	1,140			
Dehal_501	Chloroflexota	Region 24.1	other	1	5,408			
		Region 136.1	terpene	1	3,404			
		Region 457.1	terpene	1	1,899			
		Region 685.1	terpene	1	1,456			
Gamma_522	Proteobacteria	Region 104.1	ectoine	1	5,765			
Nitros_504	Nitrospinota	Region 55.1	terpene	1	9,723			
		Region 242.1	terpene	1	3,942			
		Region 303.1	RiPP-like	1	3,145			
Nitros_505	Nitrospinota	Region 5.1	betalactone	1	15,228			
		Region 56.1	RiPP-like	1	6,026			
Posei_509	Thermoplasmatota	Region 20.1	terpene	10,374	27,024			
Posei_510	Thermoplasmatota	Region 28.1	terpene	1	7,879			
SAR324_506	SAR324	Region 159.1	hglE-KS	1	4,614			
		Region 243.1	arylpolyene	1	3,718			
		Region 299.1	betalactone	1	3,240			
		Region 423.1	hglE-KS	1	2,557			
		Region 440.1	T1PKS	1	2,501			
		Region 851.1	arylpolyene	1	1,265			

SAR324_507	SAR324	Region 104.1	PUFA,T1PKS	1	7,588			
		Region 164.1	arylpolyene	1	5,373	APE Vf	Other	15%
		Region 276.1	hglE-KS	1	3,543			
		Region 298.1	T3PKS	1	3,271			
Verru_503	Verrucomicrobiota	Region 111.1	terpene	1	7,031			
		Region 240.1	terpene	1	4,833			
500m winter								
Bacte_503	Bacteroidota	Region 11.1	arylpolyene	1	34,972	flexirubin	Polyketide	58%
Gamma_552	Proteobacteria	Region 65.1	other	1	7,408			
Planc_502	Planctomycetota	Region 295.1	terpene	1	2,873			
		Region 414.1	hglE-KS	1	2,353			
		Region 432.1	terpene	1	2,285			
Planc_503	Planctomycetota	Region 74.1	terpene	1	9,041			
		Region 495.1	phosphonate	1	3,811			
		Region 597.1	arylpolyene	1	3,226			
SAR324_520	SAR324	Region 53.1	arylpolyene	1	8,032	APE Vf	Other	15%
		Region 82.1	T1PKS,PUFA	1	6,661			
		Region 230.1	arylpolyene	1	3,706			
		Region 276.1	T3PKS	1	3,382			
		Region 822.1	hglE-KS	1	1,082			
Verru_516	Verrucomicrobiota	Region 442.1	terpene	1	2,593			
		Region 604.1	terpene	1	2,013			
		Region 1187.1	terpene	1	1,025			
2600m spring								
Dehal_d01	Chloroflexota	Region 14.1	other	1	35,614			
		Region 19.1	terpene	19,396	33,252			
		Region 39.1	terpene	9,158	22,060			
Dehal_d02	Chloroflexota	Region 11.1	terpene	13,202	34,672	heme D1	Other	17%
Dehal_d03	Chloroflexota	Region 38.1	terpene	2,965	17,572			
		Region 193.1	terpene	1	6,795			
Dehal_d04	Chloroflexota	Region 20.1	terpene	1	13,760			

		Region 114.1	terpene	1	6,941			
DG_d01	TA06	Region 219.1	sactipeptide	1	3,202			
		Region 339.1	terpene	1	2,789			
		Region 430.1	ladderane	1	2,570			
		Region 487.1	T3PKS	1	2,417			
Gamma_d01	Proteobacteria	Region 313.1	ectoine	1	3,316			
Gamma_d02	Proteobacteria	Region 35.1	betalactone	1	14,478			
Gamma_d04	Proteobacteria	Region 38.1	betalactone	6,366	27,948			
Gamma_d08	Proteobacteria	Region 14.1	phosphonate	1	29,327			
Gemma_d01	Gemmatimonadota	Region 229.1	T1PKS,hglE-KS	1	4,105			
		Region 259.1	hglE-KS	1	3,835	heterocyst glycolipids	Other	28%
		Region 472.1	ranthipeptide	1	2,723			
		Region 538.1	T1PKS	1	2,509			
Planc_d01	Planctomycetota	Region 88.1	terpene	1	5,443			
Posei_d01	Thermoplasmatota	Region 17.1	terpene	4,692	25,367			
Posei_d02	Thermoplasmatota	Region 194.1	terpene	1	1,924			
Posei_d03	Thermoplasmatota	Region 42.1	terpene	1	6,630			
Posei_d04	Thermoplasmatota	Region 6.1	terpene	1	13,655			
SAR324_d01	SAR324	Region 6.1	T3PKS	1	22,743			
		Region 41.1	PUFA,T1PKS	1	15,217			
		Region 200.1	hglE-KS	1	3,944			
SAR324_d02	SAR324	Region 347.1	hglE-KS	1	1,909			
		Region 360.1	PUFA	1	1,896			
		Region 469.1	hglE-KS	1	1,696			
		Region 476.1	aryl polyene	1	1,688	aryl polyenes	Other	16%
		Region 871.1	aryl polyene	1	1,231			
		Region 1048.1	aryl polyene	1	1,099			
SAR324_d03	SAR324	Region 65.1	T3PKS	1	15,028			
		Region 71.1	aryl polyene	1	13,956	APE Vf	Other	20%

		Region 87.1	hglE- KS,PUFA	1	11,989	heterocyst glycolipids	Other	28%
Verru_d01	Verrucomicrobiota	Region 153.1	terpene	1	2,693			
		Region 293.1	terpene	1	2,114			
		Region 332.1	terpene	1	2,004			
		Region 1273.1	terpene	1	1,029			
2960m winter								
Bacte_d02	Bacteroidota	Region 10.1	terpene	1	11,223			
Dehal_d16	Chloroflexota	Region 133.1	terpene	1	4,557			
Dehal_d17	Chloroflexota	Region 15.1	other	1	17,248			
		Region 21.1	terpene	1	15,476			
		Region 151.1	terpene	1	6,979			
Gamma_d25	Proteobacteria	Region 216.1	terpene	1	3,817			
Gamma_d26	Proteobacteria	Region 14.1	ectoine	1	9,007			
		Region 16.1	betalactone	1	21,551			
		Region 69.1	siderophore	1	13,192	xanthoferrin	Other	28%
		Region 86.1	redox- cofactor	1	12,068	lankacidin C	NRP + Polyketide	13%
		Region 238.1	betalactone	1	5,310	fengycin	NRP	13%
		Region 465.1	betalactone	1	2,527			
Gamma_d28	Proteobacteria	Region 5.1	phosphonate	17,896	48,300			
Gemma_d06	Gemmatimonadota	Region 206.1	hglE- KS,T1PKS	1	6,323			
		Region 229.1	ranthipeptide	1	5,626			
Posei_d16	Thermoplasmatota	Region 283.1	terpene	1	1,903			
		Region 387.1	hglE-KS	1	1,551			
Posei_d17	Thermoplasmatota	Region 143.1	terpene	1	2,314			
Posei_d18	Thermoplasmatota	Region 26.1	terpene	1	20,648			
Posei_d19	Thermoplasmatota	Region 156.1	terpene	1	2,801			
		Region 424.1	terpene	1	1,589			
		Region 614.1	hglE-KS	1	1,230			
Posei_d20	Thermoplasmatota	Region 5.1	terpene	27,172	42,624			

		Region 33.1	T1PKS	1	16,443			
		Region 64.1	resorcinol	1	9,188			
SAR324_d09	SAR324	Region 3.1	T3PKS	10,842	33,584			
		Region 42.1	PUFA,T1PKS	1	15,056			
		Region 210.1	hglE-KS	1	3,881			
SAR324_d10	SAR324	Region 24.1	T3PKS	1	22,125			
		Region 70.1	arylpolyene	1	14,071	APE Vf	Other	25%
		Region 76.1	PUFA,T1PKS	1	13,513			
		Region 140.1	hglE-KS	1	6,699			
Verru_d04	Verrucomicrobiota	Region 40.1	terpene	1	16,291			
		Region 215.1	terpene	1	3,631			
Verru_d05	Verrucomicrobiota	Region 60.1	T3PKS	1	17,132			
		Region 68.1	terpene	1	16,075			
		Region 77.1	terpene	1	15,804			

Appendix 12

Table S9: The SO KS domain similarity to NaPDoS KS domain

Query id	Database match id	percent identity	align length	e-value	pathway product	domain class
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SAR324_507_s1	PfaC_Shewanella_PUFA	50	455	2.00E-123	polyunsaturated fatty acid	PUFA
SAR324_507_s2	PfaA_Shewanella_PUFA	28	459	6.00E-46	polyunsaturated fatty acid	PUFA
Gemma_d01_s2	PfaC_Shewanella_PUFA	48	274	5.00E-62	polyunsaturated fatty acid	PUFA
Gemma_d01_s2	PfaA_Shewanella_PUFA	36	293	1.00E-40	polyunsaturated fatty acid	PUFA
SAR324_d01_s1	PfaC_Shewanella_PUFA	50	462	5.00E-126	polyunsaturated fatty acid	PUFA
SAR324_d01_s2	PfaA_Shewanella_PUFA	28	459	5.00E-46	polyunsaturated fatty acid	PUFA
SAR324_214_w1	PfaC_Shewanella_PUFA	50	455	2.00E-123	polyunsaturated fatty acid	PUFA
SAR324_214_w2	PfaA_Shewanella_PUFA	28	459	8.00E-46	polyunsaturated fatty acid	PUFA
Verru_217_w	PfaA_Shewanella_PUFA	33	288	5.00E-38	polyunsaturated fatty acid	PUFA
Verru_217_w	PfaA_Shewanella_PUFA	47	60	1.00E-12	polyunsaturated fatty acid	PUFA
SAR_324_520_w1	PfaC_Shewanella_PUFA	52	413	7.00E-117	polyunsaturated fatty acid	PUFA
SAR324_520_w2	PfaA_Shewanella_PUFA	28	459	2.00E-44	polyunsaturated fatty acid	PUFA
SAR324_d09_w1	PfaC_Shewanella_PUFA	50	462	5.00E-126	polyunsaturated fatty acid	PUFA
SAR324_d09_w2	PfaA_Shewanella_PUFA	28	459	3.00E-46	polyunsaturated fatty acid	PUFA
Gemma_d06_w1	PfaC_Shewanella_PUFA	41	375	2.00E-65	polyunsaturated fatty acid	PUFA
Gemma_d06_w2	PfaA_Shewanella_PUFA	36	293	1.00E-40	polyunsaturated fatty acid	PUFA
Posei_d20_w1	ArsA_Azotobacter_PUFA	41	461	4.00E-76	alkylresorcinol	PUFA
Posei_d20_w2	AlnL_ACI88861_KSa	26	434	2.00E-16	alnumycin	typeII
SAR324_d10_w1	PfaC_Shewanella_PUFA	49	462	1.00E-118	polyunsaturated fatty acid	PUFA

SAR324_d10_w2	PfaA_Shewanella_PUFA	28	459	5.00E-45	polyunsaturated fatty acid	PUFA
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