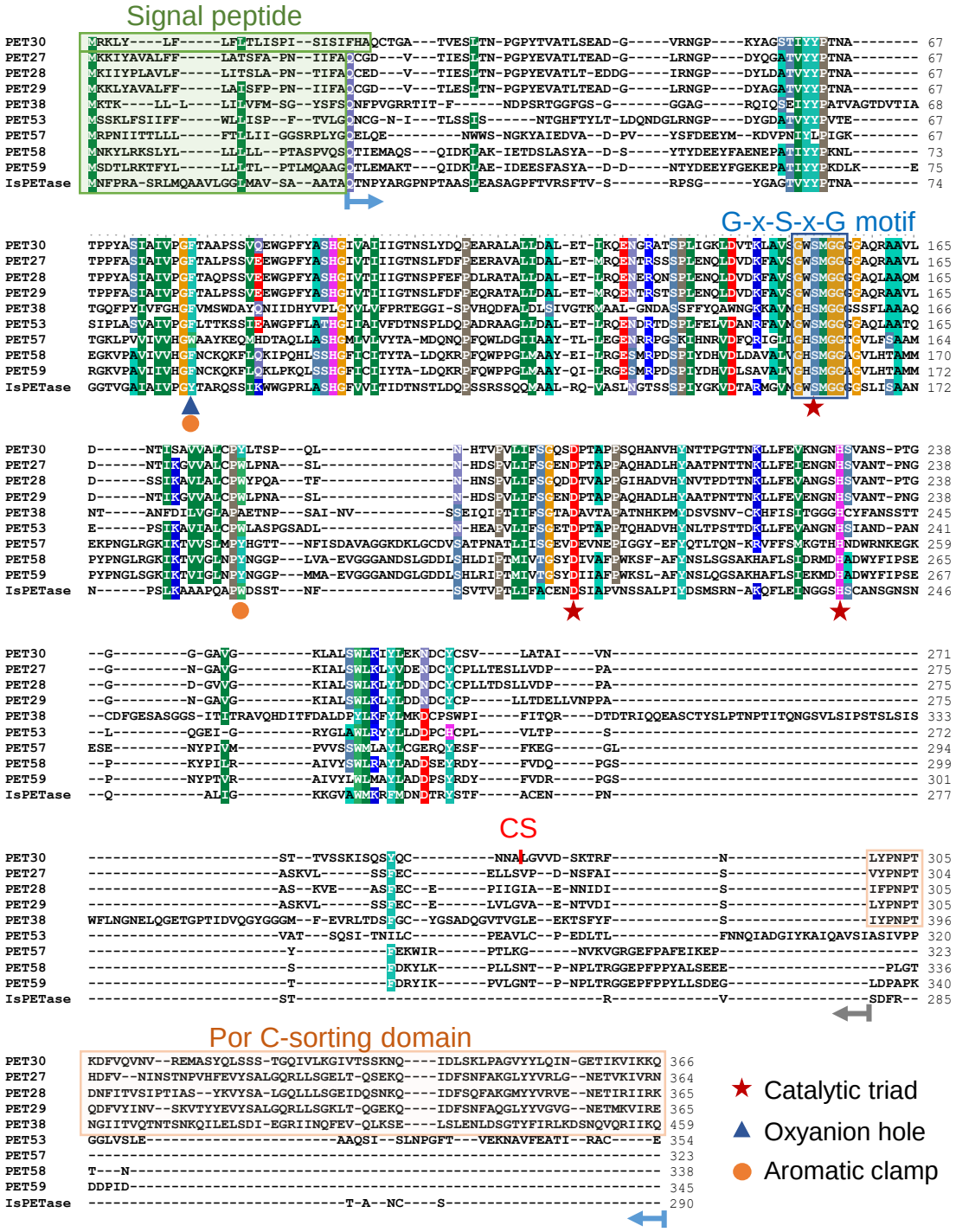

FIGURE S1: Amino acid alignment of 9 potential PETases affiliated with the Bacteroidetes phylum. The original sequences were used for the structural alignment and the alignment was constructed with T-Coffee. Alignment was visualized with Bioedit version 7.0.5. The IsPETase and the LCC were included for reasons of benchmarking. Blue arrows indicate the start and the end of the active PET27 and PET 30 clones. we introduced a methionine as the first aa of the protein sequences. The signal peptide deleted version of the enzymes was functionally verified. The red arrow labelled with CS indicates the predicted cleavage site of N-terminal PorC domain. The grey arrow indicates the C-terminus of the truncated version of PET30 (PET30Δ300-366), number indicates the position of amino acid). PET30Δ300-366 was active on PCL and BHET.

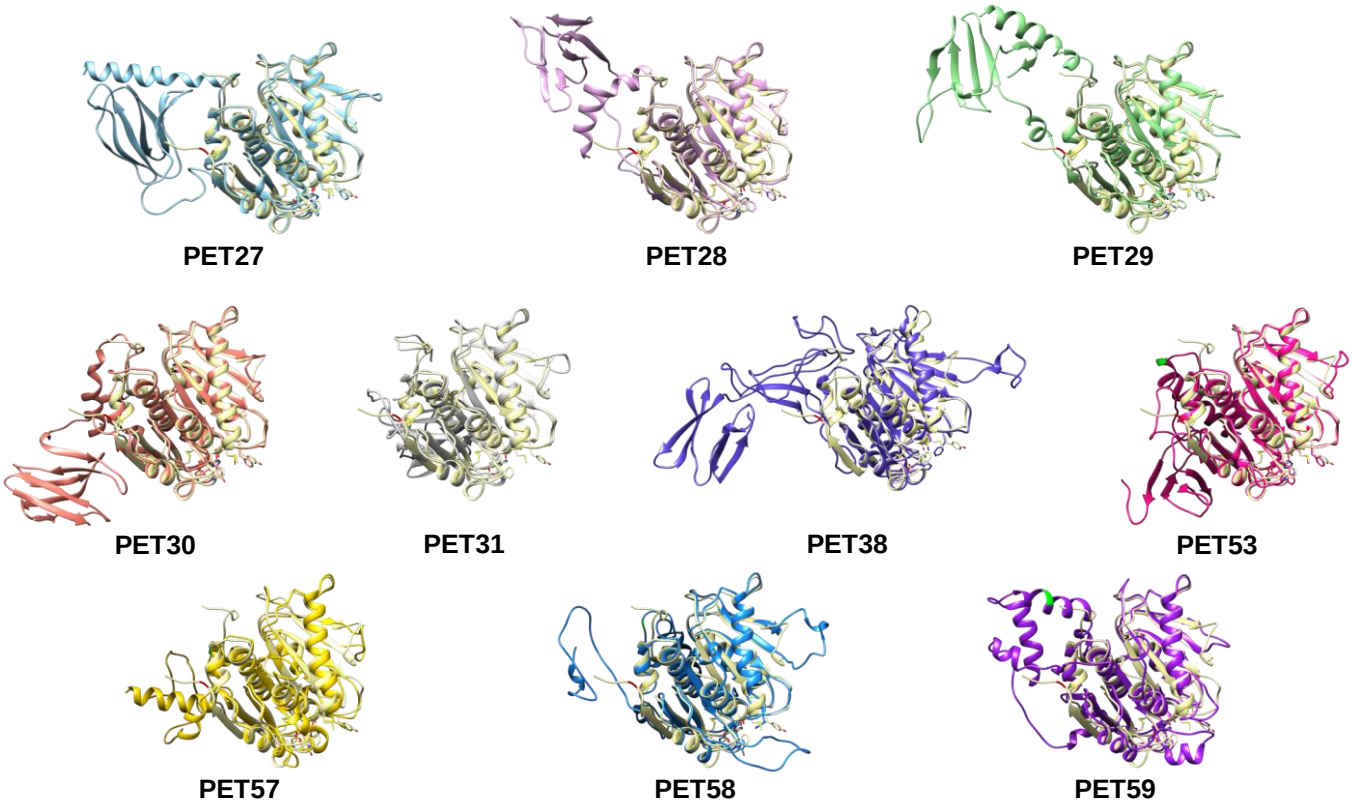

FIGURE S2: Structure prediction models of verified and predicted PETases affiliated with the phylum of the Bacteroidetes. 3D structures were modeled using the Robetta server using the IsPETase crystal structure (light yellow, 6QGC) as a backbone.

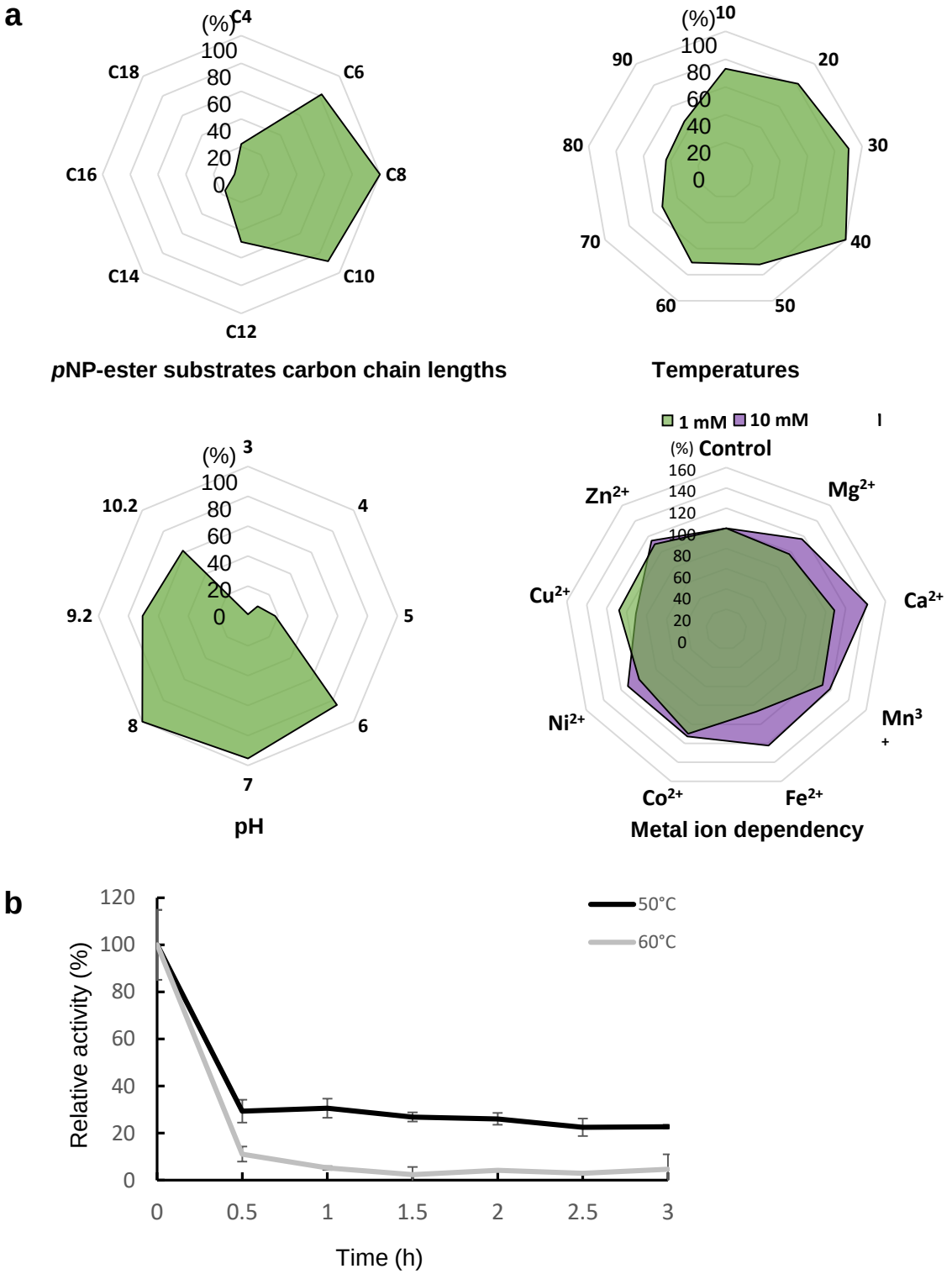

FIGURE S3: Biochemical characterization of PET27 and PET30 using various *p*NP-substrates. **a** For PET30, substrate preferences, temperature optimum, pH optimum and cofactor requirements were tested. All tests besides substrate preferences were carried out with *p*NP-octanoate. Data obtained with a *p*NP-assay are shown in net diagrams; **b** Thermostability of PET30. Data represent mean values of at least three independent measurements.

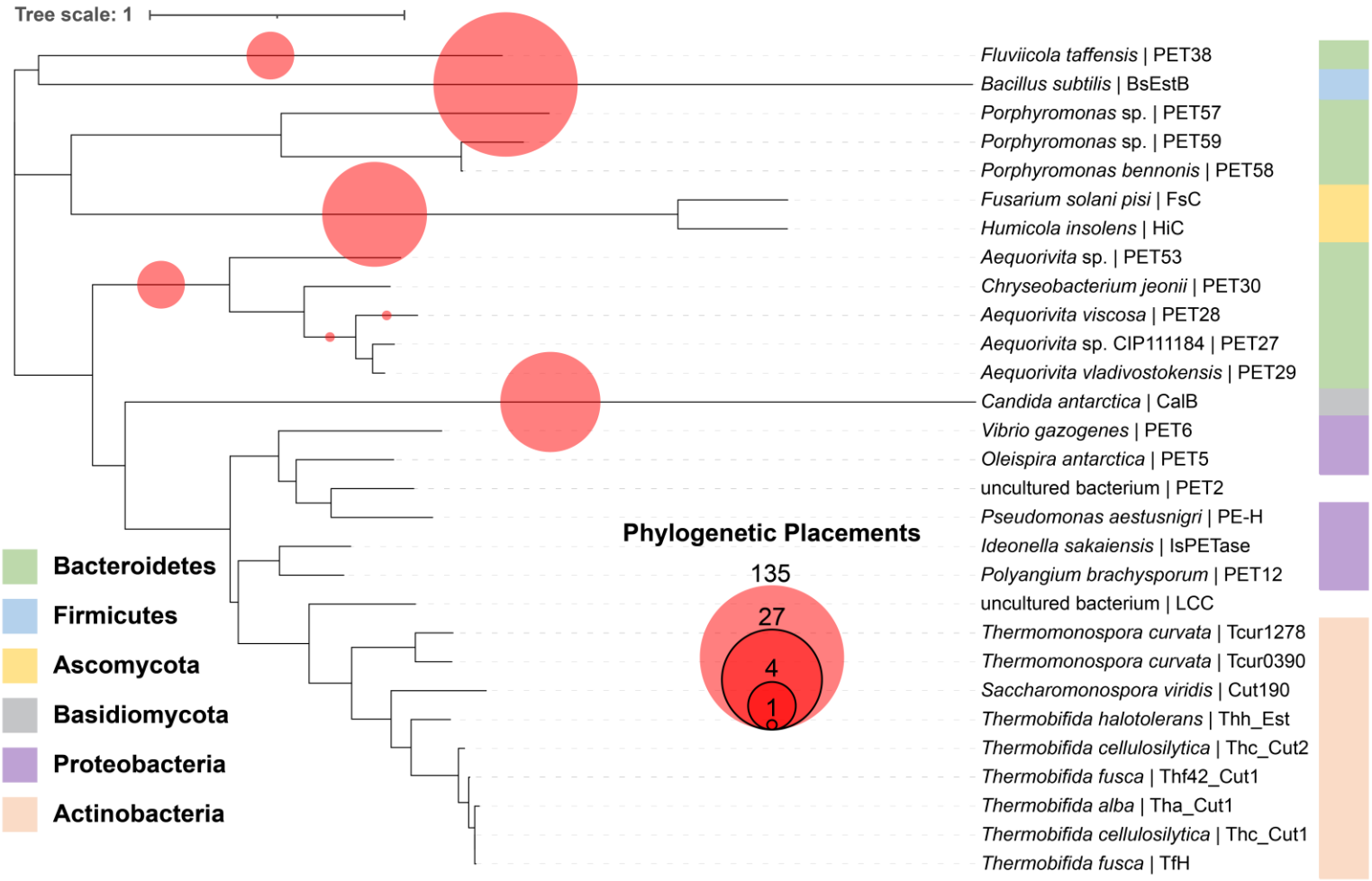

FIGURE S4: Phylogenetic placements of PETase homologs from Saanich Inlet MAGs to reference tree. Sequences from MAGs constructed using metagenomic reads at seven depths over the redoxcline of Saanich Inlet (NESAP) during Cruise 72 (SI072) on 12 August 2012 at station SI03 (latitude: 48.59166667° , longitude: -123.505°) mapped to the phylogenetic tree of 29 known and predicted PETase sequences shown in FIGURE 4. Light red circles represent the phylogenetic position and relative number of sequence hits from the concatenated set of medium plus quality MAGs. Sequence assignments performed using TreeSAPP and visualized with iTOL.

FIGURE S5: Phylogenetic placements and abundance of PETase homologs in two environmental metagenomes. Metagenomic sequence assemblies and metagenomic read abundances from four and seven depths over the redoxclines of the **a** Baltic Sea from samples taken on 26 October 2014 from at station TF0271 and **b** Saanich Inlet (NESAP) during Cruise 72 (SI072) on 12 August 2012 at station SI03 (latitude: 48.59166667°, longitude: -123.505°) mapped to the phylogenetic tree of 29 known and predicted PETase sequences shown in FIGURE 4. Light red circles represent the phylogenetic position and relative number of sequence hits from the concatenated set of SI072 metagenomic contigs; red bars indicate the relative abundance (TPM) of metagenomic reads matching metagenomic sequence hits from contigs at the cognate depth. Tree construction, sequence assignment, and abundance calculations performed using TreeSAPP and visualized with iTOL.

TABLE S1: Bacterial strains and plasmids used in this work.

Strain	Properties	Reference/source
E. coli DH5α	*supE*44 Δ*lacU*169 (Φ80 lac*Z* ΔM15) *hsdR*17 *recA*1 *endA*1 *gyrA*96 *thi*-1 *relA*1	Invitrogen (Karlsruhe, Germany)
E. coli BL21 (DE3)	F^-, *ompT*, *hsdS* B (r_B^- m_B^-) *gal*, *dcm*, λDE3	Novagen/Merck (Darmstadt, Germany)
E. coli SHuffle® T7	huA2 lacZ::T7 gene1 [lon] ompT ahpC gal λatt::pNEB3-r1-cDsbC (SpecR, lacIq) ΔtrxB sulA11 R(mcr-73::miniTn10--TetS)2 [dcm] R(zgb-210::Tn10 --TetS) endA1 Δgor Δ(mcrC-mrr)114::IS10	NEB (Frankfurt am Main, Germany)

Vector	Properties	Reference/source
pET21a(+)	Expression vector, *lacI*, Amp^R, T7-*lac*- promoter, C-terminal His_6-tag coding sequence	Novagen/Merck (Darmstadt, Germany)
pET21a(+)::PET27	1026 bp insert in pET21a(+) coding for PET27	This work
pET21a(+)::PET28	1029 bp insert in pET21a(+) coding for PET28	This work
pET21a(+)::PET29	1029 bp insert in pET21a(+) coding for PET29	This work
pET21a(+)::PET30	1032 bp insert in pET21a(+) coding for PET30	This work
pET21a(+)::PET30_ Δ300-366	831 bp insert in pET21a(+) coding for PET30, truncated protein lacking PorC	This work
pET21a(+)::PET38	1341 bp insert in pET21a(+) coding for PET38	This work
pET21a(+)::PET53	1072 bp insert in pET21a(+) coding for PET53	This work
pET21a(+)::PET57	969 bp insert in pET21a(+) coding for PET57	This work
pET21a(+)::PET58	1014 bp insert in pET21a(+) coding for PET58	This work
pET21a(+)::PET59	1035 bp insert in pET21a(+) coding for PET59	This work
pMAL-p4x::IsPETase	795 bp insert in pMAL-p4x coding for the wildtype IsPETase from *Ideonella sakaiensis*	This work

TABLE S2: Primers used in this work.

Primer	Sequence (5' → 3')	Length (bp)	Tm (°C)	Source
T7_prom	TAATACGACTCACTATAGGG	20	53	Eurofins MWG (Elsberg, Germany)
T7_term	CTAGTTATTGCTCAGCGGT	19	54	Eurofins MWG (Elsberg, Germany)
PET_for	ATATAGGCGCCAGCAACC	18	59	Novagen/Merck (Darmstadt, Germany)
PET_rev	TCCGGATATAGTTCCTC	17	52	Novagen/Merck (Darmstadt, Germany)

TABLE S3: Identifiers and GenBank entries employed in the phylogenetic clustering of PET active enzymes in FIGURE 4.

Name	GenBank or PDB entry	Phylogenetic Affiliation	Reference
BsEstB	ADH43200.1	*Bacillus subtilis* 4P3-11	Herrero Acero *et al*. 2011
CalB	4K6G_A	*Candida antarctica*	Andersen *et al*. 1999; Xie *et al*. 2014
Cut190	BAO42836.1	*Saccharomonospora viridis* AHK190	Kawai *et al*. 2014
FsC	1CEX	*Fusarium solani* pisi	Silva *et al*. 2005
HiC	4OYY	*Humicola insolens*	Ronkvist *et al*. 2009
IsPETase	GAP38373.1	*Ideonella sakaiensis* 201-F6	Yoshida *et al*. 2016
LCC	AEV21261.1	uncultured bacterium	Sulaiman *et al*. 2012
PE-H	A0A1H6AD45	*Pseudomonas aestusnigri* VGXO14T	Bollinger *et al*. 2020
PET2	C3RYL0	uncultured bacterium	
PET5	R4YKL9	*Oleispira antarctica* RB-8	Danso *et al*. 2018
PET6	A0A1Z2SIQ1	*Vibrio gazogenes*	
PET12	A0A0G3BI90	*Polyangium brachysporum*	
Tcur0390	WP_012850775.1	*Thermomonospora curvata* DSM43183	Wei *et al*. 2014
Tcur1278	WP_012851645.1	*Thermomonospora curvata* DSM43183	Chertkov *et al*. 2011
TfH	WP_011291330.1	*Thermobifida fusca* DSM43793	Müller *et al*. 2005
Thc_Cut1	ADV92526.1	*Thermobifida cellulosilytica* DSM44535	
Thc_Cut2	ADV92527.1	*Thermobifida cellulosilytica* DSM44535	Herrero Acero *et al*. 2011
Thf42_Cut1	ADV92528.1	*Thermobifida fusca* DSM44342	
Tha_Cut1	ADV92525.1	*Thermobifida alba* DSM43185	Ribitsch *et al*. 2012
Thh_Est	AFA45122.1	*Thermobifida halotolerans* DSM44931	

TABLE S4: Homologs of bacteroidetal PET27 and PET30 hydrolases in metagenomes.

Locus Tag	Gene ID	Genome Name (GREEN=Bacteroidetes; YELLOW=FCB)	NCBI Biosample Accession	Pubmed ID /GenBank entry
Ga0266410_112824	2790477168	*Aequorivita sp.* CPC67	SAMEA2621812	25999513
Ga0267287_12740	2786516536	*Marinimicrobia bacterium* SP4388	SAMEA2621812	25999513
Ga0214074_111348	2758370761	*Psychroflexus torquis* ATCC 700755	SAMN02603919	24391155 , 32431677
Ga0441744_095_43538_44635	2893010289	*Psychroflexus gondwanensis* ACAM 365	SAMN10790446	24391155, 32431677
Ga0452869_05_68007_69104	2890419200	*Brumimicrobium glaciale* IC156	SAMN10779751	24391155, 32431677
Ga0125537_104199	2776033716	*Altibacter lentus* JL2010	SAMN02988278	25342673
Ga0101260_1142	2663974789	*Bacteroidetes bacterium* SCGC AD-308-D03 - v2	SAMN06314724	373136
Ga0266415_110121	2790487960	*Aequorivita sp.* SAT106	SAMEA2620929	25999513
Ga0266677_12858	2778555477	*Flavobacteriaceae bacterium* SAT1509	SAMEA2620929	25999513
Ga0267170_100812	2814895288	*Gemmatimonadetes bacterium* RS373	SAMEA2620929	25999513
Ga0267250_100918	2786410539	*Marinimicrobia bacterium* RS418	SAMEA2620929	25999513
Ga0267252_10536	2786413511	*Marinimicrobia bacterium* RS816	SAMEA2620929	25999513
Ga0267252_10542	2786413517	*Marinimicrobia bacterium* RS816	SAMEA2620929	25999513
Ga0266410_112825	2769034576	*Aequorivita sp.* CPC68	SAMEA2621812	25999513
Ga0267287_12741	2767134878	*Marinimicrobia bacterium* SP4389	SAMEA2621812	25999513
Ga0214074_111349	2765235181	*Psychroflexus torquis* ATCC 700756	SAMN02603919	24391155 , 32431678
Ga0441744_095_43538_44636	2763335483	*Psychroflexus gondwanensis* ACAM 366	SAMN10790446	24391155, 32431677
Ga0452869_05_68007_69105	2761435786	*Brumimicrobium glaciale* IC157	SAMN10779751	24391155, 32431677
Ga0267200_1431	2786528832	*Marinimicrobia bacterium* EAC25	SAMEA2620855	25999513, 29337314
Ga0267200_1544	2786528992	*Marinimicrobia bacterium* EAC25	SAMEA2620855	25999513, 29337314
Ga0416765_13_4825_5925	2860314059	*Chryseobacterium sp.* 16F	SAMN14915977	25824943
PI23P_05397	639004873	*Polaribacter irgensii* 23-P	SAMN02436114	9542092 /NZ_CH724148.1
Aeqsu_2514	2509583556	*Aequorivita sublithincola* QSSC9-3, DSM 14238	SAMN02232006	28604660
Ga0266584_11073	2788314349	*Cryomorphaceae bacterium* CPC63	SAMEA2622923	25999513
Ga0266589_10312	2787698016	*Cytophagia bacterium* NAT375	SAMEA2622923	25999513
Ga0267262_14611	2786499724	*Marinimicrobia bacterium* SAT24	SAMEA2622923	25999513
Ga0267263_11113	2786500508	*Marinimicrobia bacterium* SAT2619	SAMEA2622923	25999513
Ga0267267_12326	2786498443	*Marinimicrobia bacterium* SP108	SAMEA2622923	25999513
Ga0267268_10328	2786441642	*Marinimicrobia bacterium* SP173	SAMEA2622923	25999513
Ga0267268_1112	2786442127	*Marinimicrobia bacterium* SP173	SAMEA2622923	25999513
Ga0267270_13120	2786484524	*Marinimicrobia bacterium* SP276	SAMEA2622923	25999513
Ga0267272_1173	2786478779	*Marinimicrobia bacterium* SP3060	SAMEA2622923	25999513
Ga0267273_13417	2786477564	*Marinimicrobia bacterium* SP3097	SAMEA2622923	25999513
Ga0267276_13625	2786480397	*Marinimicrobia bacterium* SP3117	SAMEA2622923	25999513
Ga0267279_10440	2786489803	*Marinimicrobia bacterium* SP328	SAMEA2622923	25999513
Ga0267280_12433	2786520859	*Marinimicrobia bacterium* SP359	SAMEA2622923	25999513
Ga0267282_10178	2786519018	*Marinimicrobia bacterium* SP4039	SAMEA2622923	25999513
Ga0063505_10623	2606052547	*Roseivirga seohaensis aquiponti* D-25	SAMN03145748	27107724/ JSVA01000000

Ga0267161_105313	2814952585	*Gemmatimonadetes bacterium* EAC635	SAMEA2623295	25999513
Ga0267164_1577	2814955360	*Gemmatimonadetes bacterium* NAT196	SAMEA2623295	25999513
Ga0267234_12226	2786460090	*Marinimicrobia bacterium* NAT495	SAMEA2623295	25999513
Ga0267237_1518	2786446587	*Marinimicrobia bacterium* NAT62	SAMEA2623295	25999513
Ga0267238_1416	2786464404	*Marinimicrobia bacterium* NAT74	SAMEA2623295	25999513
Ga0267239_13724	2786462435	*Marinimicrobia bacterium* NP104	SAMEA2623295	25999513
Ga0215720_101116	2756777030	*Marinirhabdus gelatinilytica* DSM 101478	SAMN08776299	QRAO00000000
Ga0266586_11614	2788308996	*Cryomorphaceae bacterium* SP53	SAMEA2619927	25999513
Ga0267165_10476	2814943193	*Gemmatimonadetes bacterium* NP105	SAMEA2619818	25999513
SCB49_04680	641143976	*Ulvibacter sp.* SCB49	SAMN02981237	ABCO00000000
G440DRAFT_00359	2524126300	*Aequorivita capsosiphonis* DSM 23843	SAMN02440880	AUBG00000000
Ga0266370_16423	2789796087	*Altibacter sp.* EAC109	SAMEA2619376	25999513
Ga0266560_154	2825980380	*Crocinitomicaceae bacterium* NAT165	SAMEA2619376	25999513
Ga0267217_1484	2786425266	*Marinimicrobia bacterium* MED806	SAMEA2619376	25999513
Ga0267217_16831	2786425767	*Marinimicrobia bacterium* MED806	SAMEA2619376	25999513
Ga0267218_1219	2786426885	*Marinimicrobia bacterium* MED808	SAMEA2619376	25999513
Ga0267219_10943	2786427199	*Marinimicrobia bacterium* MED812	SAMEA2619376	25999513
Ga0267220_10096	2786428744	*Marinimicrobia bacterium* MED829	SAMEA2619376	25999513
Ga0267220_10106	2786428754	*Marinimicrobia bacterium* MED829	SAMEA2619376	25999513
Ga0267224_14310	2786401069	*Marinimicrobia bacterium* NAT217	SAMEA2619376	25999513
Ga0267226_12918	2786404156	*Marinimicrobia bacterium* NAT220	SAMEA2619376	25999513
Ga0267227_13041	2786403315	*Marinimicrobia bacterium* NAT224	SAMEA2619376	25999513
Ga0267228_1422	2786399119	*Marinimicrobia bacterium* NAT230	SAMEA2619376	25999513
Ga0267208_10372	2786507568	*Marinimicrobia bacterium* MED586	SAMEA2619667	25999513
Ga0267208_10412	2786507636	*Marinimicrobia bacterium* MED586	SAMEA2619667	25999513
Ga0267209_1018	2786508441	*Marinimicrobia bacterium* MED589	SAMEA2619667	25999513
Ga0267212_106014	2786417419	*Marinimicrobia bacterium* MED648	SAMEA2619667	25999513
Ga0267212_10712	2786417608	*Marinimicrobia bacterium* MED648	SAMEA2619667	25999513
Ga0267212_110812	2786418228	*Marinimicrobia bacterium* MED648	SAMEA2619667	25999513
Ga0267213_15817	2786422578	*Marinimicrobia bacterium* MED757	SAMEA2619667	25999513
Ga0267214_1214	2786420423	*Marinimicrobia bacterium* MED764	SAMEA2619667	25999513
Ga0267214_12210	2786420472	*Marinimicrobia bacterium* MED764	SAMEA2619667	25999513
Ga0267214_1225	2786420467	*Marinimicrobia bacterium* MED764	SAMEA2619667	25999513
Ga0267214_14025	2786421083	*Marinimicrobia bacterium* MED764	SAMEA2619667	25999513
Ga0344934_2405	2839770976	*Dokdonia sinensis* SH27	SAMN10250232	32228747
Ga0441973_01_775875_776969	2890600833	*Ulvibacter sp.* KK4	SAMD00166796	32539909
LY87DRAFT_1302	2597312806	*Dokdonia sp.* Hel_I_5	SAMN05661066	32539909
Ga0267202_1226	2786524372	*Marinimicrobia bacterium* EAC649	SAMEA2620230	25999513
Ga0267202_13210	2786524561	*Marinimicrobia bacterium* EAC649	SAMEA2620230	25999513
Ga0267202_13216	2786524567	*Marinimicrobia bacterium* EAC649	SAMEA2620230	25999513
Ga0350409_3222	2848310855	*Psychroflexus sp.* MES1-P1E	SAMN08125772	PJBS00000000, CM009131
Ga0066802_10753	2623289129	*Aequorivita viscosa* DSM 26349	SAMN04487908	FQYV00000000
Ga0077144_1092	2641186029	*Chryseobacterium jeonii* DSM 17048	SAMN03145167	JSYL00000000
Ga0079842_10854	2668214597	*Aequorivita viscosa* CGMCC 1.11023	SAMN05216556	FNNS00000000

Ga0104531_1111	2676887423	*Chryseobacterium jeonii* DSM 17048	SAMN05421876	FOLA00000000
Ga0114183_10545	2656209723	*Roseivirga seohaensis* SW-152	SAMN04423148	28077207
Ga0170448_3258	2729662814	*Ulvibacter antarcticus* DSM 23424	SAMN06264851	REFC00000000
Ga0310487_0626	2799156613	*Roseivirga ehrenbergii* DSM 102268	SAMN10864729	SMGS00000000
Ga0336340_1074	2835308220	*Winogradskyella sp.* KYW1333	SAMN09667312	QPHL00000000
Ga0336670_2825	2837407865	*Aequorivita lipolytica* CIP 107455	SAMEA4644770	30225207
Ga0336672_3534	2835103747	*Aequorivita antarctica* CIP 107457	SAMEA4644771	PMC6139392
Ga0443045_01_3096381_3097484	2884436497	*Nonlabens sp.* Ci31	SAMN12697551	CP043633
pgond44_05165	2533771942	*Psychroflexus gondwanensis* ACAM 44	SAMN02471957	24391155
Ga0077372_102327	2628626758	*Aequorivita vladivostokensis* KMM 3516	SAMN03084320	JSVU00000000
Ga0114184_10616	2654412999	*Roseivirga echinicomitans* KMM 6058	SAMN04382068	LRDB00000000.1
Ga0248413_145580	2812952679	*Roseivirga ehrenbergii* KMM 6017	SAMN03084331	LQZQ00000000
Ga0373279_1152	2830035069	*Lewinella antarctica* DSM 105096	SAMN13172327	PMC6139392
Ga0336671_791	2835108492	*Aequorivita sp.* CIP 111184	SAMEA4704834	UEFQ00000000
Ga0399719_270	2836794304	*Aequorivita sp.* H23M31	SAMN10518960	CP034951
Ga0441974_01_521424_522518	2890652824	*Ulvibacter marinus* KCTC 32322T	SAMD00166797	BKCG00000000.1

TABLE S5: Metagenome-assembled genomes (MAGs) used for phylogenetic placements.

treesapp_placement	MAG_lineage
root_PET27_subcluster	
SI072_10m_bin.9_k147_132539_4|PETase|1_364	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Polaribacter;s__
Aequorivita viscosa | PET28*	
SI072_10m_bin.34_k147_89139_3|PETase|1_365	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__HC6-5;s__
root_Chryseobacterium-Aequorivita	
SI072_135m_bin.14_k147_139204_83|PETase|16_290	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__;s__
SI072_150m_bin.1_k147_56438_83|PETase|16_290	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__;s__
SI072_165m_bin.40_k147_203340_118|PETase|14_298	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__UBA1611;g__GCA-2722105;s__
SI072_200m_bin.13_k147_208574_82|PETase|16_290	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__;s__
Bacillus subtilis 4P3-11 | BsEstB	
SI072_10m_bin.1_k147_223144_6|PETase|15_183	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Halioglobus;s__Halioglobus
SI072_10m_bin.1_k147_332038_9|PETase|9_225	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Halioglobus;s__Halioglobus
SI072_10m_bin.1_k147_365569_11|PETase|145_380	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Halioglobus;s__Halioglobus
SI072_10m_bin.12_k147_180046_20|PETase|54_297	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Luminiphilus;s__
SI072_10m_bin.16_k147_254444_26|PETase|33_424	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MS024-2A;s__
SI072_10m_bin.2_k147_35430_4|PETase|429_704	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Luminiphilus;s__Luminiphilus
SI072_10m_bin.2_k147_357240_2|PETase|410_646	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Luminiphilus;s__Luminiphilus
SI072_10m_bin.22_k147_4742_1|PETase|53_353	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__Ilumatobacteraceae;g__Ilumatobacter_A;s__
SI072_10m_bin.23_k147_194206_9|PETase|104_392	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4421;s__
SI072_10m_bin.23_k147_329165_78|PETase|5_270	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4421;s__
SI072_10m_bin.23_k147_347650_2|PETase|5_344	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4421;s__
SI072_10m_bin.23_k147_364526_5|PETase|52_396	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4421;s__
SI072_10m_bin.25_k147_287642_3|PETase|125_397	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_10m_bin.25_k147_422157_2|PETase|10_280	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_10m_bin.25_k147_451486_1|PETase|9_234	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_10m_bin.25_k147_45177_3|PETase|115_269	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_10m_bin.29_k147_227285_2|PETase|25_188	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__SG8-40;g__UBA3031;s__UBA3031

SI072_10m_bin.30_k147_260225_1|PETase|46_297	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_10m_bin.33_k147_296917_6|PETase|126_384	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MS024-2A;s__MS024-2A
SI072_10m_bin.34_k147_413085_7|PETase|8_123	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__HC6-5;s__
SI072_10m_bin.36_k147_210176_4|PETase|10_311	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__SW10;s__SW10
SI072_10m_bin.36_k147_359242_4|PETase|4_253	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__SW10;s__SW10
SI072_10m_bin.38_k147_426643_8|PETase|96_356	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_10m_bin.38_k147_447566_2|PETase|8_215	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_10m_bin.41_k147_21880_4|PETase|45_174	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Emcibacteraceae;g__UBA4441;s__UBA4441
SI072_10m_bin.41_k147_309092_12|PETase|414_644	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Emcibacteraceae;g__UBA4441;s__UBA4441
SI072_10m_bin.42_k147_123332_2|PETase|92_341	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__HTCC2207
SI072_10m_bin.42_k147_45472_4|PETase|7_242	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__HTCC2207
SI072_10m_bin.46_k147_112644_3|PETase|27_230	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA10347;g__UBA10347;s__UBA10347
SI072_10m_bin.46_k147_387871_1|PETase|12_167	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA10347;g__UBA10347;s__UBA10347
SI072_10m_bin.48_k147_151632_15|PETase|13_278	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Puniceispirillales;f__Puniceispirillaceae;g__Puniceispirillum;s__Puniceispirillum
SI072_10m_bin.7_k147_262022_10|PETase|41_252	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__OM182;s__OM182
SI072_10m_bin.7_k147_422148_12|PETase|1_218	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__OM182;s__OM182
SI072_10m_bin.7_k147_425788_10|PETase|4_271	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__OM182;s__OM182
SI072_10m_bin.8_k147_122281_4|PETase|51_260	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__HTCC2207
SI072_10m_bin.8_k147_17292_2|PETase|5_235	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__HTCC2207
SI072_100m_bin.11_k147_416087_4|PETase|105_312	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_100m_bin.11_k147_639240_4|PETase|14_250	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_100m_bin.12_k147_105190_3|PETase|6_249	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA868;s__
SI072_100m_bin.12_k147_652179_13|PETase|7_238	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA868;s__
SI072_100m_bin.14_k147_106818_52|PETase|95_355	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__;g__;s__
SI072_100m_bin.15_k147_185881_16|PETase|5_327	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_100m_bin.15_k147_465775_19|PETase|120_340	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_100m_bin.21_k147_35136_5|PETase|158_404	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_100m_bin.21_k147_624616_48|PETase|2_255	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_100m_bin.22_k147_303806_46|PETase|371_625	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__UBA3125;s__

SI072_100m_bin.23_k147_158766_19|PETase|79_336	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_100m_bin.23_k147_624752_3|PETase|72_306	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_100m_bin.28_k147_369523_3|PETase|77_336	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_100m_bin.28_k147_474142_2|PETase|140_416	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_100m_bin.28_k147_629843_1|PETase|22_175	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9926;s__UBA9926
SI072_100m_bin.29_k147_248877_1|PETase|367_664	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MED-G11;s__
SI072_120m_bin.1_k147_176119_1|PETase|367_664	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MED-G11;s__
SI072_120m_bin.12_k147_354144_22|PETase|158_404	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_120m_bin.12_k147_57379_21|PETase|2_255	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_120m_bin.14_k147_602771_46|PETase|371_625	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__UBA3125;s__
SI072_120m_bin.15_k147_85463_16|PETase|77_336	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_120m_bin.16_k147_28024_4|PETase|14_250	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_120m_bin.16_k147_542838_24|PETase|105_312	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_120m_bin.16_k147_599139_11|PETase|6_286	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_120m_bin.17_k147_394027_11|PETase|120_340	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_120m_bin.17_k147_412563_16|PETase|5_327	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_120m_bin.18_k147_235104_107|PETase|29_245	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_120m_bin.18_k147_235104_26|PETase|117_269	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_120m_bin.18_k147_453093_5|PETase|8_210	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_120m_bin.22_k147_300658_2|PETase|66_395	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA868;s__
SI072_120m_bin.22_k147_615784_4|PETase|7_238	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA868;s__
SI072_120m_bin.22_k147_97393_6|PETase|6_249	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA868;s__
SI072_120m_bin.6_k147_235462_46|PETase|95_355	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__;g__;s__
SI072_120m_bin.9_k147_14753_3|PETase|337_632	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__;s__
SI072_135m_bin.1_k147_51144_6|PETase|337_632	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__;s__
SI072_135m_bin.11_k147_152116_2|PETase|60_336	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_135m_bin.13_k147_26518_18|PETase|8_210	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_135m_bin.13_k147_367812_45|PETase|117_269	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_135m_bin.13_k147_57094_1|PETase|29_245	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_135m_bin.15_k147_123971_1|PETase|105_312	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__;s__

SI072_135m_bin.15_k147_26021_3|PETase|3_287	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__;s__
SI072_135m_bin.18_k147_28018_7|PETase|367_664	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MED-G11;s__
SI072_135m_bin.19_k147_156290_17|PETase|371_625	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__UBA3125;s__
SI072_135m_bin.22_k147_237941_3|PETase|3_281	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_135m_bin.22_k147_504785_1|PETase|120_340	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_135m_bin.3_k147_29235_28|PETase|56_296	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__
SI072_135m_bin.6_k147_471414_30|PETase|121_282	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__
SI072_135m_bin.7_k147_447453_7|PETase|129_274	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__PS1;f__Thioglobaceae;g__Thioglobus;s__
SI072_135m_bin.9_k147_237701_2|PETase|19_270	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_135m_bin.9_k147_257023_4|PETase|48_298	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_135m_bin.9_k147_262667_5|PETase|12_219	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_135m_bin.9_k147_26268_2|PETase|41_277	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_135m_bin.9_k147_459505_4|PETase|15_306	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_135m_bin.9_k147_535345_3|PETase|120_269	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_150m_bin.12_k147_312361_141|PETase|121_282	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__
SI072_150m_bin.14_k147_200740_1|PETase|10_240	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_150m_bin.14_k147_240884_33|PETase|117_269	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_150m_bin.14_k147_255041_5|PETase|8_210	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_150m_bin.14_k147_342627_7|PETase|9_164	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_150m_bin.14_k147_427492_2|PETase|29_245	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_150m_bin.15_k147_233366_8|PETase|187_343	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__
SI072_150m_bin.15_k147_421088_11|PETase|56_296	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__
SI072_150m_bin.17_k147_324198_5|PETase|337_632	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__;s__
SI072_150m_bin.22_k147_184738_46|PETase|371_625	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__UBA3125;s__
SI072_150m_bin.8_k147_17710_1|PETase|15_317	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_150m_bin.8_k147_234353_3|PETase|40_272	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_150m_bin.8_k147_43933_5|PETase|19_270	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_150m_bin.8_k147_53041_3|PETase|48_298	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_150m_bin.8_k147_84014_2|PETase|12_219	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_165m_bin.10_k147_235737_46|PETase|119_275	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__UBA1611;g__GCA-2722105;s__

SI072_165m_bin.10_k147_404228_9|PETase|167_356	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__UBA1611;g__GCA-2722105;s__
SI072_165m_bin.13_k147_229427_474|PETase|126_289	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__Marinisomataceae;g__Marinisoma;s__Marinisoma
SI072_165m_bin.19_k147_230381_1|PETase|16_331	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__;s__
SI072_165m_bin.19_k147_679114_18|PETase|2_299	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__;s__
SI072_165m_bin.22_k147_351315_4|PETase|2_255	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_165m_bin.22_k147_431836_5|PETase|158_404	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__
SI072_165m_bin.25_k147_282140_12|PETase|367_664	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MED-G11;s__
SI072_165m_bin.29_k147_332037_7|PETase|181_367	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__;g__;s__
SI072_165m_bin.3_k147_693571_2|PETase|6_249	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__UBA868;s__
SI072_165m_bin.34_k147_254321_22|PETase|56_296	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__
SI072_165m_bin.34_k147_556770_20|PETase|169_357	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__TCS55;g__TCS55;s__
SI072_165m_bin.35_k147_359435_3|PETase|337_632	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__;s__
SI072_165m_bin.36_k147_514888_7|PETase|7_159	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Ga0077536;f__Ga0077536;g__UBA4457;s__
SI072_165m_bin.6_k147_283723_46|PETase|371_625	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__UBA3125;s__
SI072_165m_bin.8_k147_277730_5|PETase|8_210	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_165m_bin.8_k147_321440_10|PETase|117_269	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_165m_bin.8_k147_321440_91|PETase|29_245	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA9659;s__
SI072_165m_bin.9_k147_334686_15|PETase|60_336	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_200m_bin.1_k147_168882_133|PETase|121_282	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__
SI072_200m_bin.15_k147_47456_46|PETase|371_625	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__UBA3125;s__
SI072_200m_bin.16_k147_58230_10|PETase|31_194	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__
SI072_200m_bin.16_k147_71417_26|PETase|323_622	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__
SI072_200m_bin.16_k147_80826_11|PETase|108_264	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__
SI072_200m_bin.19_k147_137056_3|PETase|5_327	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_200m_bin.19_k147_194650_4|PETase|120_340	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_200m_bin.7_k147_216172_4|PETase|337_632	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__MedAcidi-G1;g__;s__
SI072_200m_bin.9_k147_111979_2|PETase|14_250	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_200m_bin.9_k147_201639_1|PETase|3_287	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__
SI072_200m_bin.9_k147_7371_1|PETase|105_312	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23;f__UBA6960;g__UBA1138;s__

root_Ascomycota

SI072_10m_bin.11_k147_305174_1|PETase|78_299	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Planktotalea;s__Planktotalea
SI072_10m_bin.14_k147_304693_3|PETase|16_240	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__MB11C04;g__MB11C04;s__
SI072_10m_bin.14_k147_391190_10|PETase|79_246	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__MB11C04;g__MB11C04;s__
SI072_10m_bin.16_k147_160894_12|PETase|125_369	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MS024-2A;s__
SI072_10m_bin.2_k147_205500_3|PETase|35_299	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Halieaceae;g__Luminiphilus;s__Luminiphilus
SI072_10m_bin.22_k147_352998_50|PETase|85_243	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__Ilumatobacteraceae;g__Ilumatobacter_A;s__
SI072_10m_bin.22_k147_411156_1|PETase|54_274	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__Ilumatobacteraceae;g__Ilumatobacter_A;s__
SI072_10m_bin.35_k147_50460_1|PETase|112_342	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Tateyamaria;s__
SI072_10m_bin.46_k147_150954_2|PETase|154_362	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA10347;g__UBA10347;s__UBA10347
SI072_100m_bin.14_k147_21249_7|PETase|272_402	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__;g__;s__
SI072_100m_bin.24_k147_375442_3|PETase|16_234	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA2165;g__GCA-2687515;s__
SI072_100m_bin.4_k147_183490_2|PETase|53_276	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__UBA6615;f__UBA6615;g__UBA8079;s__
SI072_100m_bin.4_k147_357294_2|PETase|141_363	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__UBA6615;f__UBA6615;g__UBA8079;s__
SI072_120m_bin.13_k147_312130_6|PETase|53_276	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__UBA6615;f__UBA6615;g__;s__
SI072_120m_bin.13_k147_527904_13|PETase|141_363	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__UBA6615;f__UBA6615;g__;s__
SI072_120m_bin.15_k147_477766_13|PETase|1_266	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_120m_bin.15_k147_91670_12|PETase|44_268	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_120m_bin.20_k147_47755_5|PETase|23_261	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__GCA-2731375;f__GCA-2731375;g__GCA-2731375;s__
SI072_120m_bin.24_k147_420423_9|PETase|16_234	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA2165;g__GCA-2687515;s__
SI072_120m_bin.6_k147_378796_3|PETase|272_405	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__;g__;s__
SI072_120m_bin.6_k147_549758_4|PETase|72_300	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__;g__;s__
SI072_135m_bin.11_k147_85417_2|PETase|44_268	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_135m_bin.8_k147_71679_4|PETase|4_260	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__UBA10353;f__LS-SOB;g__GCA-2726415;s__
SI072_135m_bin.9_k147_342930_1|PETase|22_284	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4582;s__
SI072_165m_bin.14_k147_463385_11|PETase|16_234	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA2165;g__GCA-2687515;s__
SI072_165m_bin.19_k147_832784_24|PETase|10_187	d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__;s__
SI072_165m_bin.40_k147_496763_2|PETase|54_255	d__Bacteria;p__Marinisomatota;c__Marinisomatia;o__Marinisomatales;f__UBA1611;g__GCA-2722105;s__
SI072_165m_bin.43_k147_571149_15|PETase|105_254	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__MB11C04;g__GCA-2730975;s__
SI072_165m_bin.43_k147_835100_6|PETase|50_272	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__MB11C04;g__GCA-2730975;s__
SI072_165m_bin.5_k147_415994_2|PETase|273_484	d__Bacteria;p__Planctomycetota;c__UBA8108;o__UBA1146;f__UBA1146;g__QNYK01;s__

SI072_165m_bin.9_k147_395191_12|PETase|1_266	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_165m_bin.9_k147_613913_12|PETase|44_267	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
Candida antarctica | CalB	
SI072_10m_bin.15_k147_138143_2|PETase|188_355	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Puniceispirillales;f__Puniceispirillaceae;g__UBA5951;s__
SI072_10m_bin.19_k147_29141_6|PETase|18_278	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__Opitutaceae;g__UBA6669;s__
SI072_10m_bin.19_k147_423886_9|PETase|20_242	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__Opitutaceae;g__UBA6669;s__
SI072_10m_bin.23_k147_129747_8|PETase|122_313	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__HTCC2089;g__UBA4421;s__
SI072_10m_bin.40_k147_315382_3|PETase|15_280	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__NS11-12g;f__UBA9320;g__UBA9320;s__
SI072_10m_bin.46_k147_254869_3|PETase|12_242	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__UBA10347;g__UBA10347;s__UBA10347
SI072_10m_bin.8_k147_134070_2|PETase|3_264	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Porticoccaceae;g__HTCC2207;s__HTCC2207
SI072_100m_bin.15_k147_46976_5|PETase|12_297	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_100m_bin.23_k147_210787_12|PETase|61_238	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_100m_bin.23_k147_351730_19|PETase|79_207	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_100m_bin.23_k147_445012_3|PETase|44_267	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_100m_bin.24_k147_108656_6|PETase|4_206	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA2165;g__GCA-2687515;s__
SI072_100m_bin.25_k147_648988_18|PETase|17_240	d__Bacteria;p__Latescibacterota;c__UBA2968;o__UBA8231;f__GCA-002724215;g__GCA-2724215;s__
SI072_120m_bin.11_k147_559876_11|PETase|17_240	d__Bacteria;p__Latescibacterota;c__UBA2968;o__UBA8231;f__GCA-002724215;g__GCA-2724215;s__
SI072_120m_bin.15_k147_423866_22|PETase|79_207	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_120m_bin.15_k147_575261_7|PETase|72_311	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_120m_bin.17_k147_302972_30|PETase|12_297	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_120m_bin.24_k147_479071_3|PETase|4_206	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA2165;g__GCA-2687515;s__
SI072_120m_bin.7_k147_527646_3|PETase|332_626	d__Bacteria;p__Chloroflexota;c__Dehalococcoidia;o__UBA1151;f__Bin127;g__UBA1328;s__
SI072_135m_bin.11_k147_242391_2|PETase|72_315	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_135m_bin.11_k147_74023_2|PETase|61_238	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_135m_bin.22_k147_270470_7|PETase|12_297	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudohongiellaceae;g__UBA9145;s__
SI072_165m_bin.14_k147_233497_8|PETase|4_206	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA2165;g__GCA-2687515;s__
SI072_165m_bin.21_k147_616435_71|PETase|101_339	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__MAG-121220-bin8;s__
SI072_165m_bin.4_k147_222839_5|PETase|2_283	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__UBA3470;g__;s__
SI072_165m_bin.9_k147_177213_17|PETase|72_311	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Pedosphaerales;f__UBA1096;g__UBA1096;s__
SI072_200m_bin.16_k147_86924_4|PETase|256_481	d__Bacteria;p__Marinisomatota;c__UBA8477;o__UBA8477;f__UBA8477;g__;s__

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