

Supporting information

Marine biodegradation mechanism of biodegradable plastics revealed by plastisphere analysis

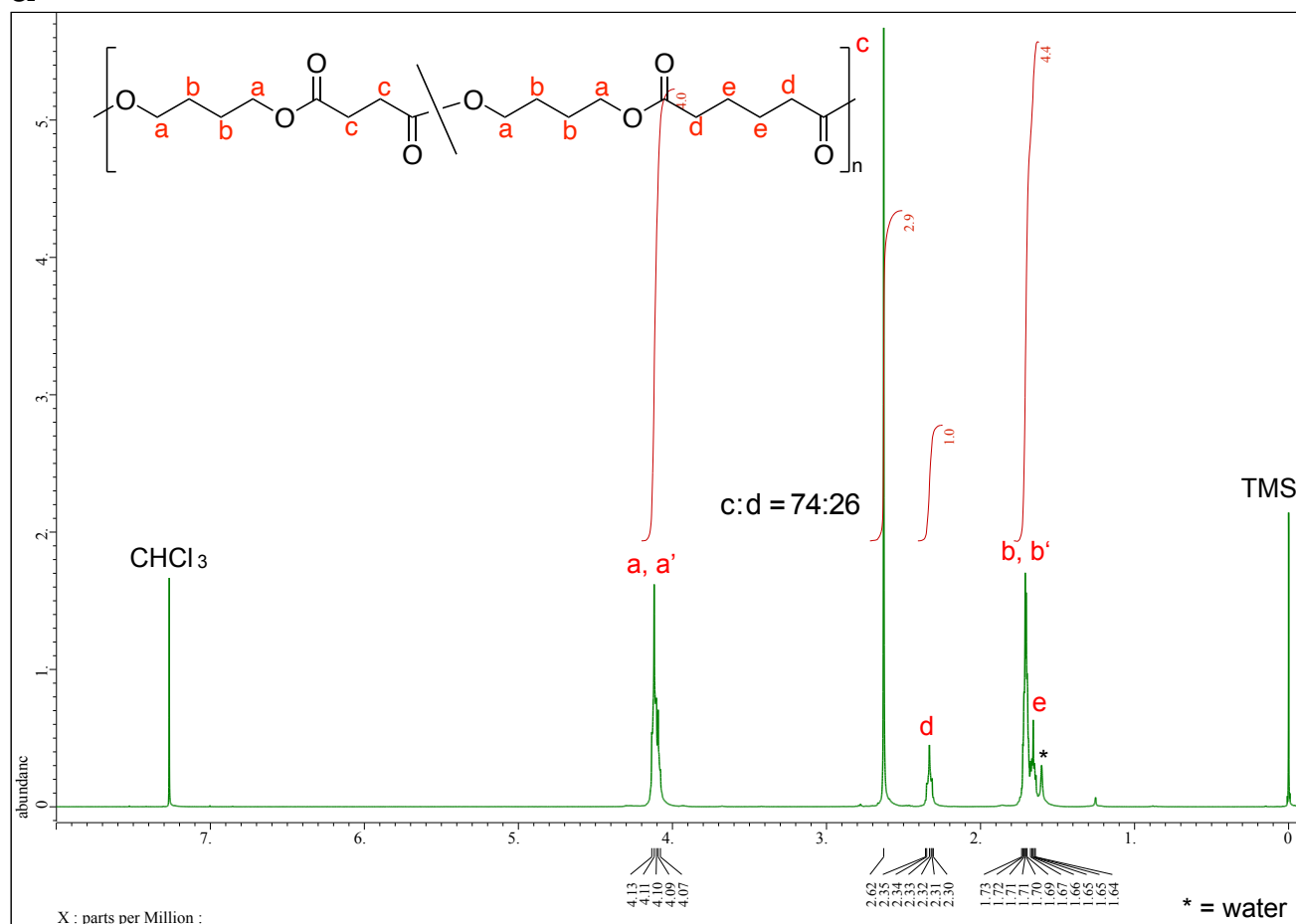
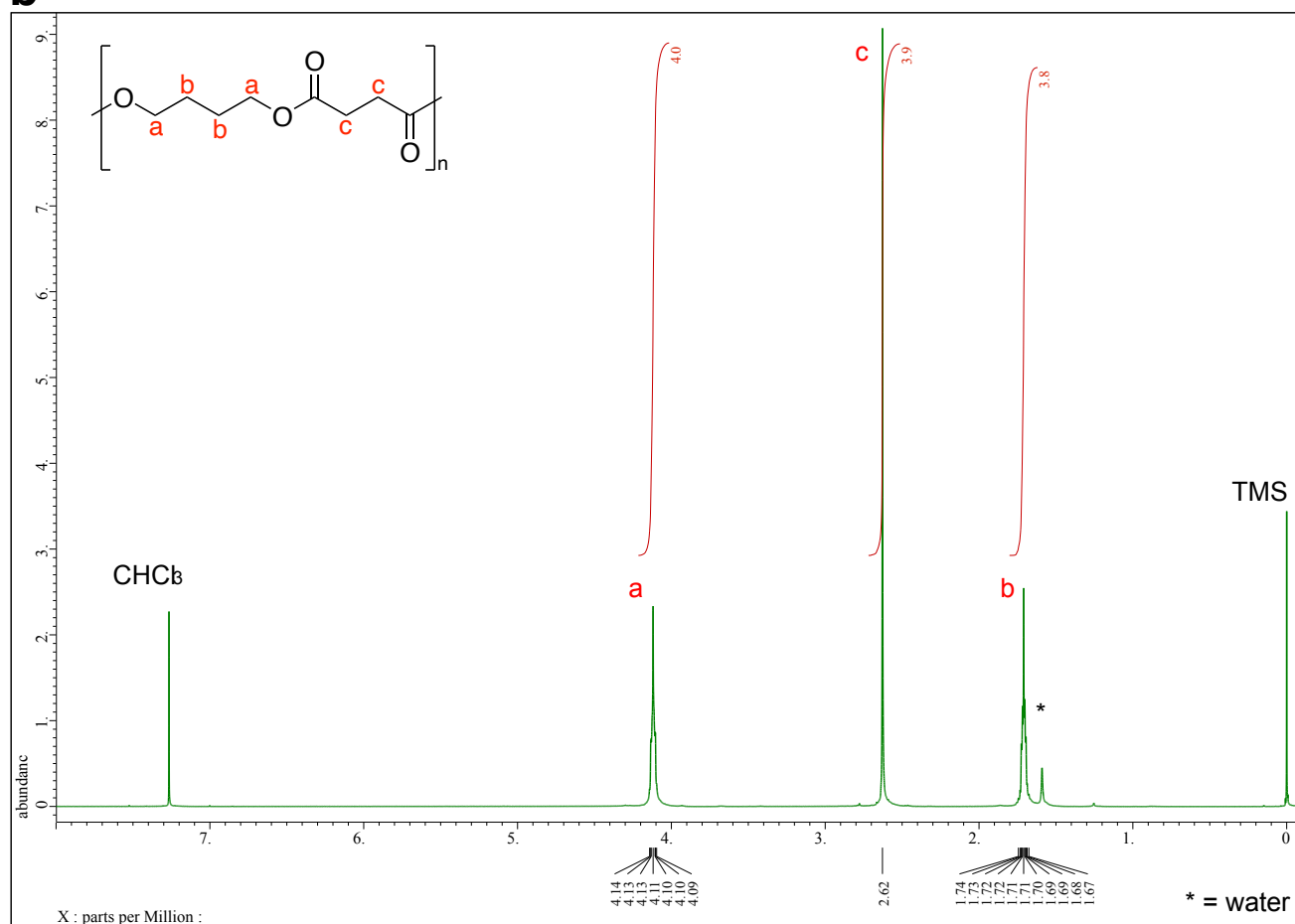
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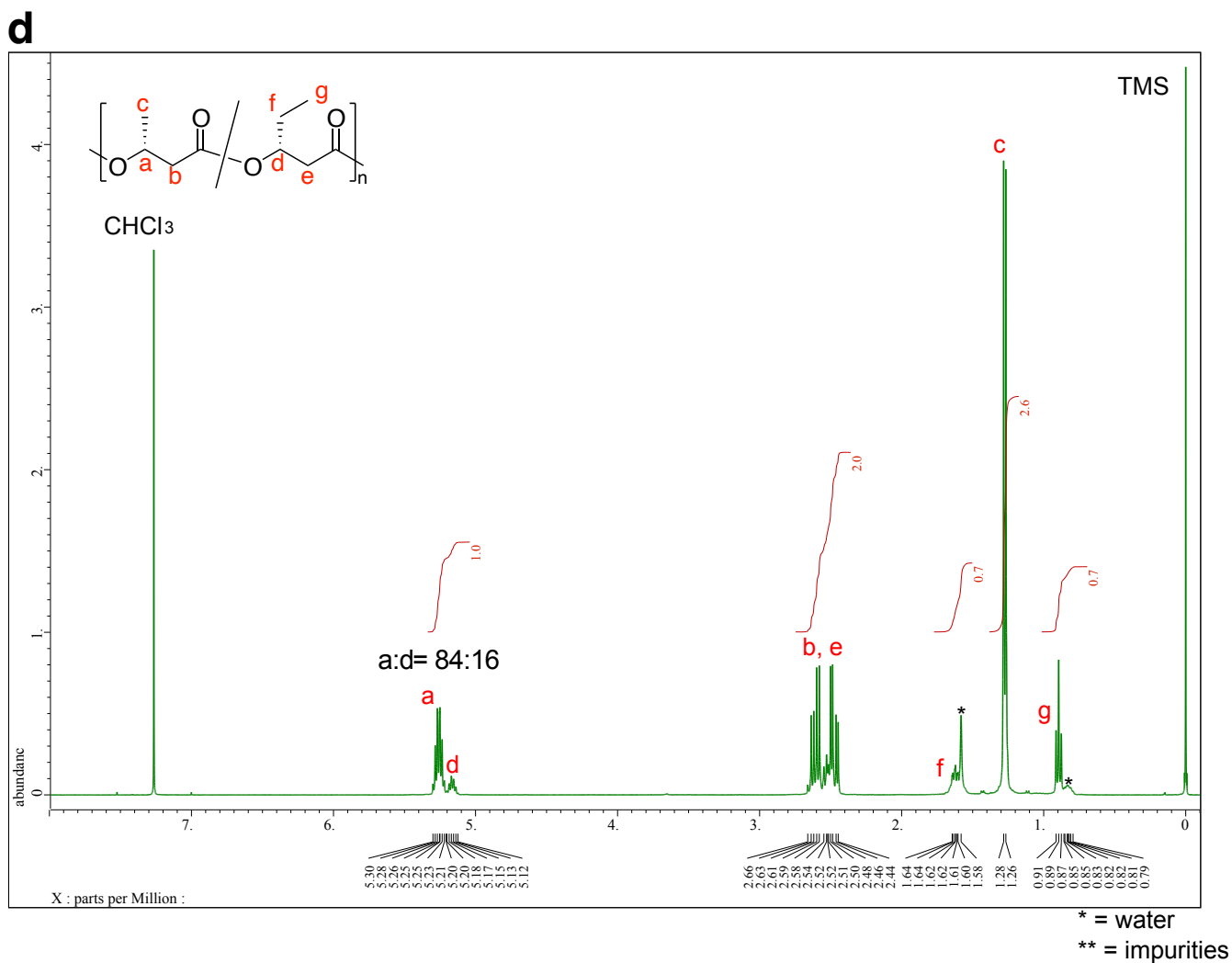
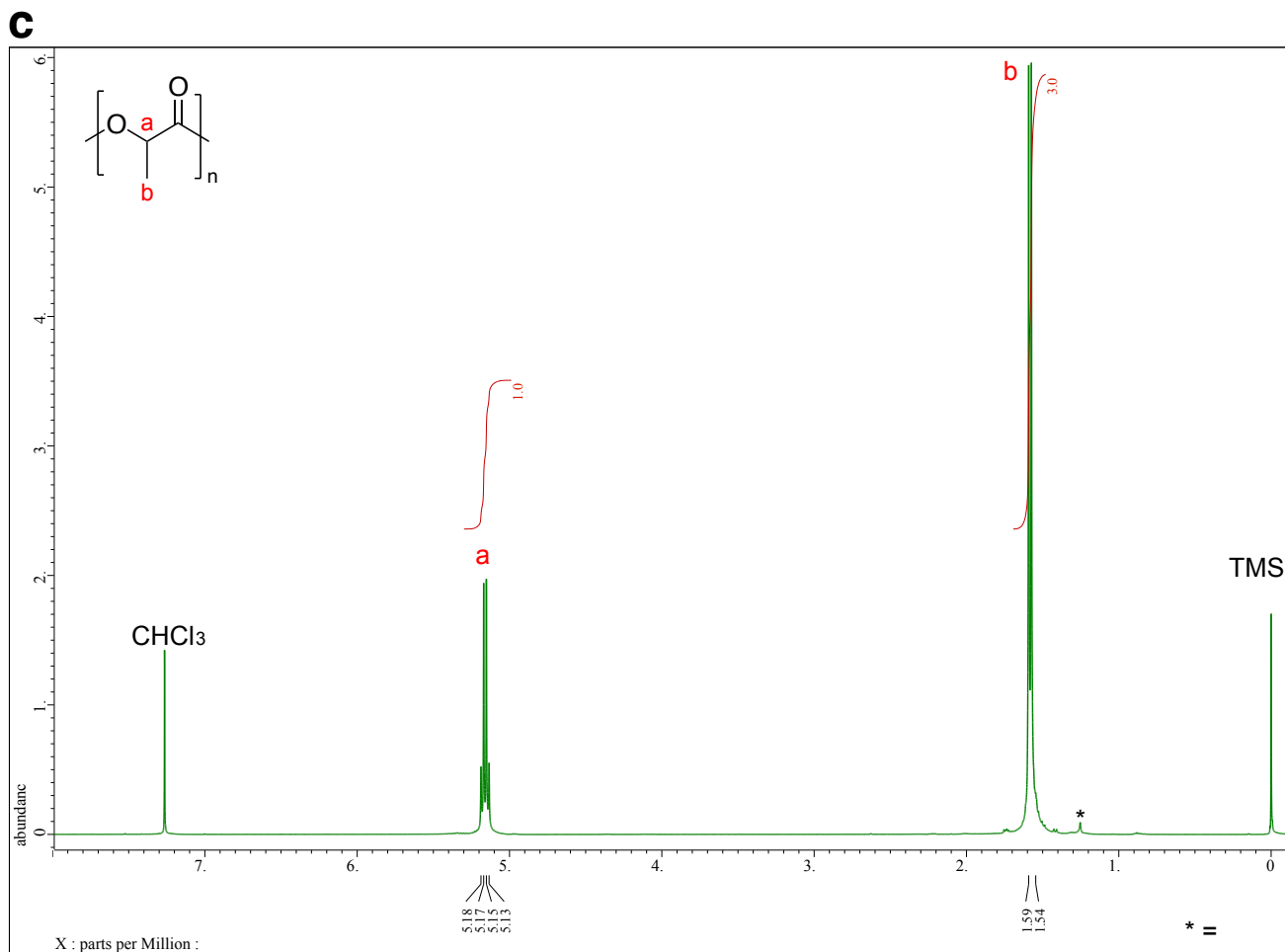
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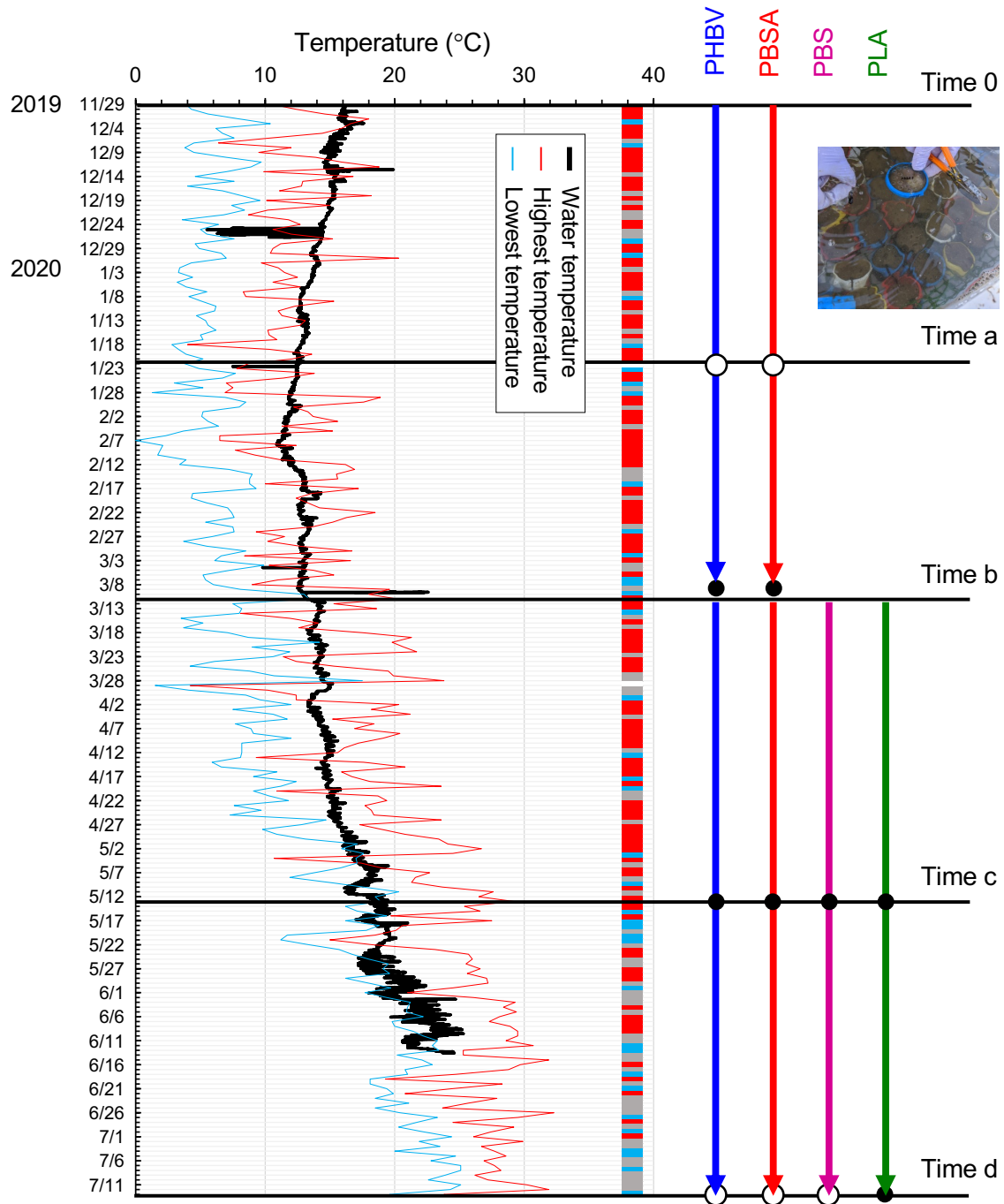
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a**b**

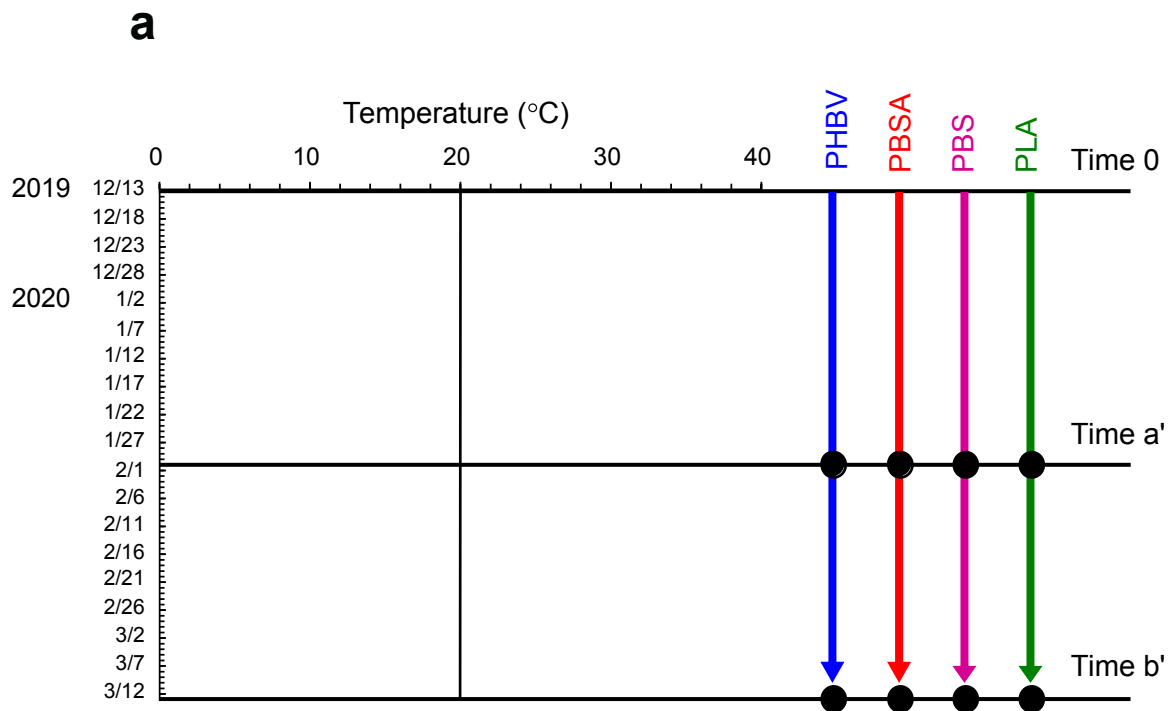


Supplementary Fig. 1 ¹H NMR spectra of PBSA (a), PBS (b), PLA (c), and PHBV (d) (400 MHz, 298 K, CDCl₃).

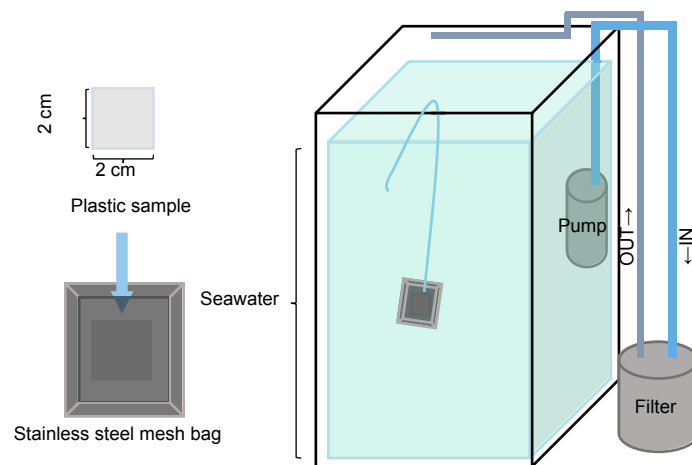


Supplementary Fig. 2 Water temperature and weather of experimental site.

On-site seawater temperature at the JAMSTEC quay and weather (highest and lowest temperature) in Yokohama city were shown in the left line graph. The logging of water temperature was accidentally stopped on 6/13/2020. The color of the bar shows the weather at noon (Red, sunny; Gray, Cloudy; Blue, rainy; White, snowy). Four different plastic films (PHBV, PBSA, PBS, and PLA) were soaked in the seawater for three months in winter (from Time 0 to b) and four months in spring (from Time b to d). DNA/RNAseq of plastisphere was performed for five samples (open circles), while only DNaseq was performed for the other samples (black dots).

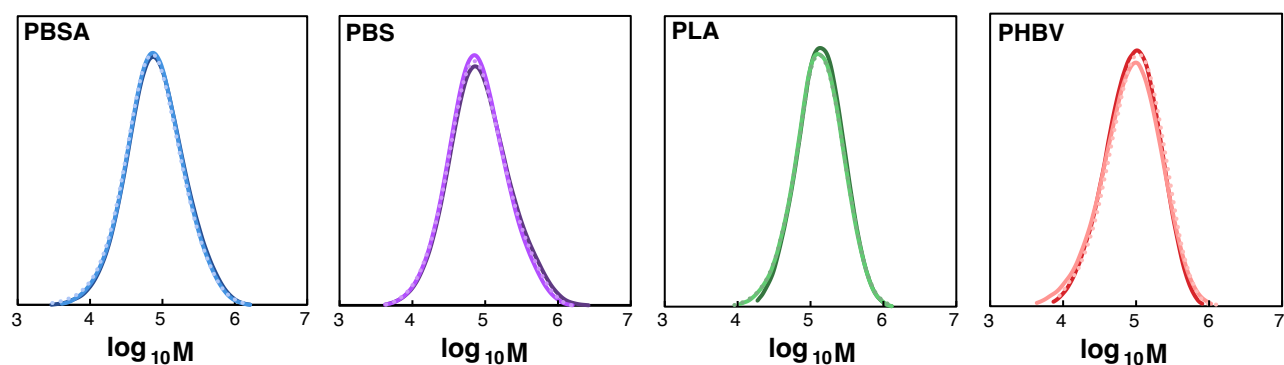
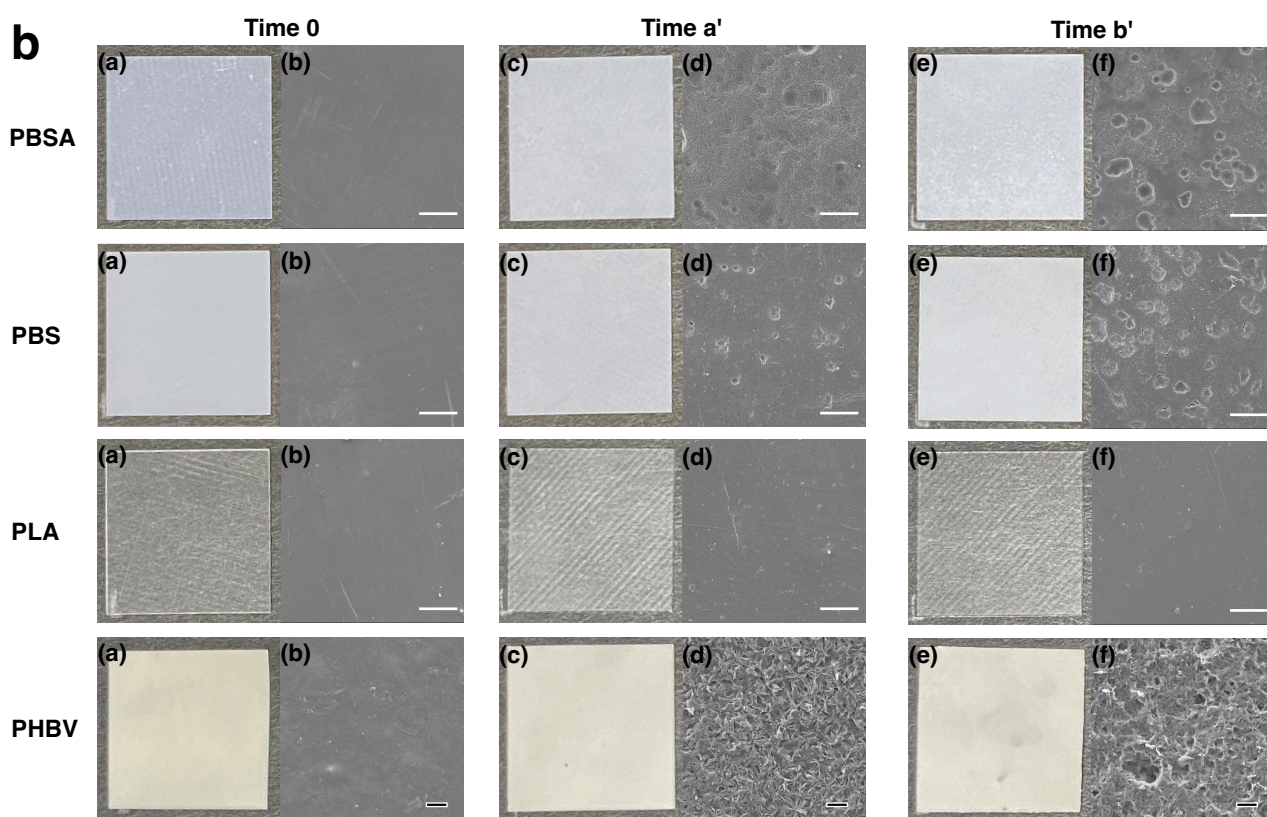


b



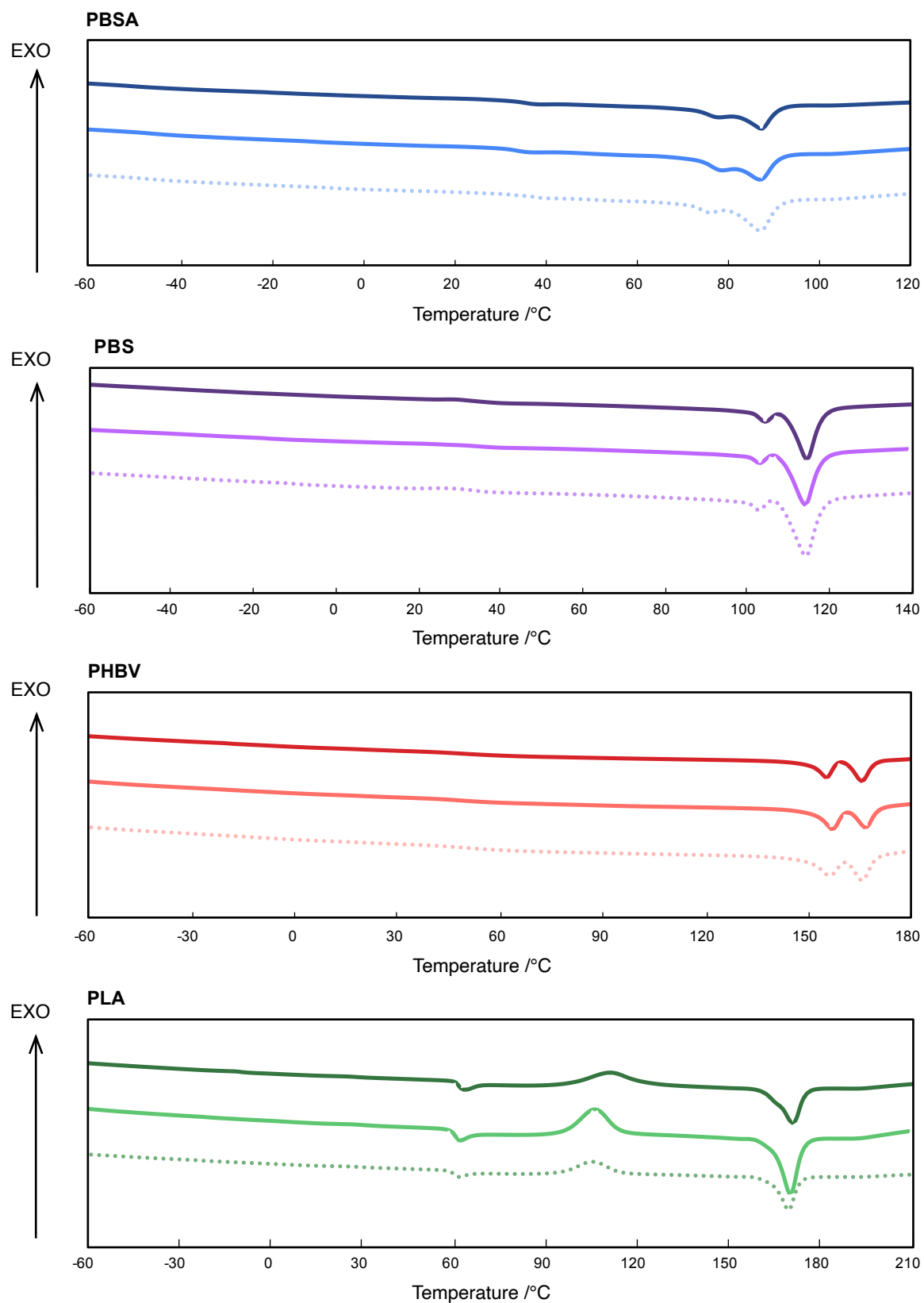
Supplementary Fig. 3 Experimental design of incubation within the seawater in the laboratory.

a Four different plastic films (PHBV, PBSA, PBS, and PLA) were soaked in the seawater corrected from the JAMSTEC quay for three months in the laboratory. DNaseqs of plastisphere were performed for the films (black dots). **b** Stainless steel mesh bags containing plastic films were incubated within the seawater in the laboratory.

a**b**

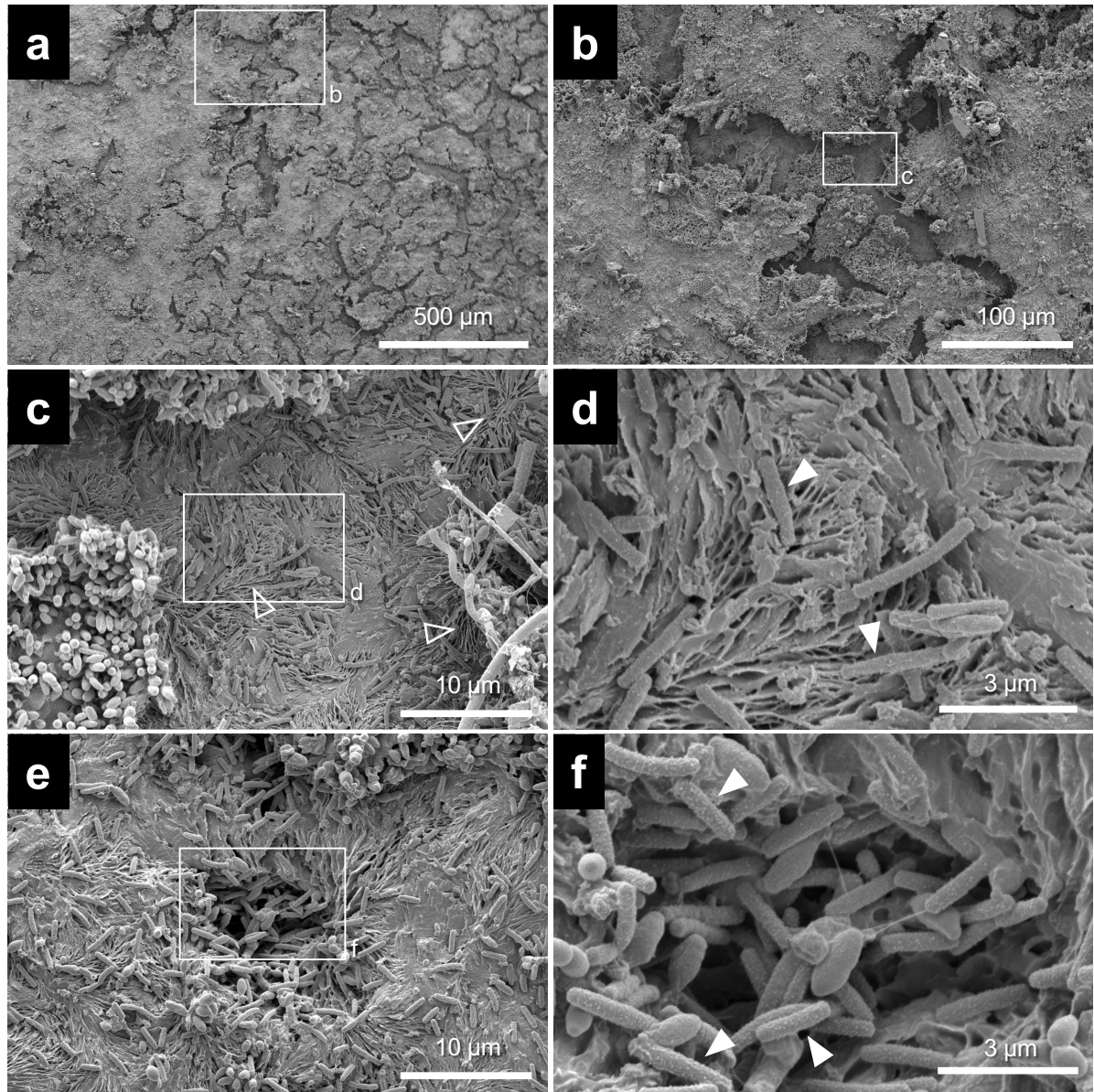
Supplementary Fig. 4 Biodegradability of PBSA, PBS, PLA, and PHBV in the seawater in the laboratory.

a Gel permeation chromatography (GPC) chromatogram of each film before (dark-colored lines) and after incubation for 1.5 months (light-colored lines) and 3 months (dot lines). **b** Macroscopic surface (a, c, e) and SEM (b, d, f) images of PBSA, PBS, PLA, and PHBV film before (Time 0, a, b) and after incubation for 1.5 months (Time a', c, d) and 3 months (Time b', e, f). White bars mean 100 μm . Black bars mean 10 μm .



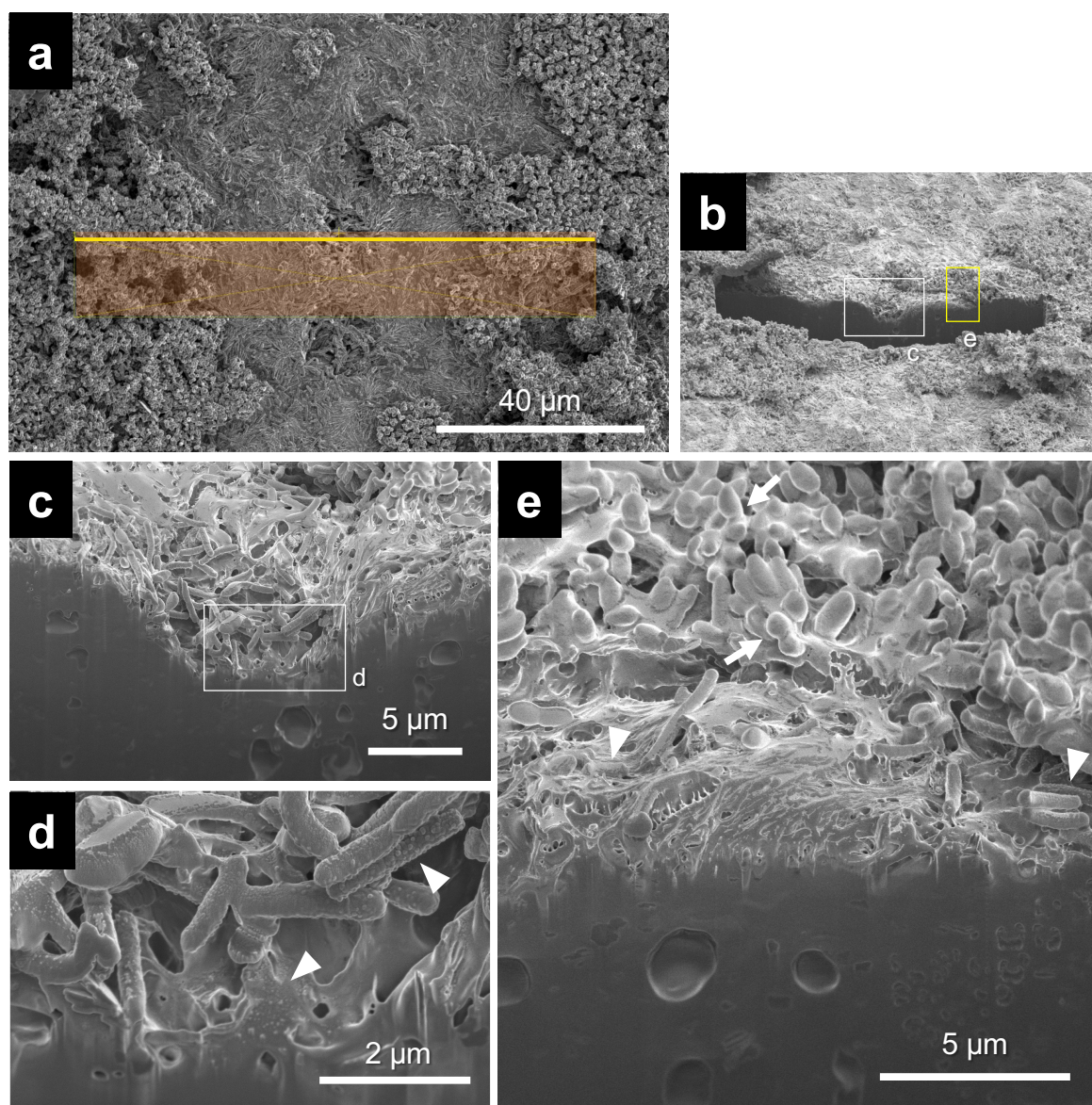
Supplementary Fig. 5 DSC charts of PBSA, PBS, PHBV and PLA in first cooling process at a rate of $10\text{ }^{\circ}\text{C} \cdot \text{min}^{-1}$.

The DSC charts of each polyester film before (dark-colored lines) and after incubation within the seawater in the natural environment for 2 months (light-colored lines) and 4 months (dot lines).



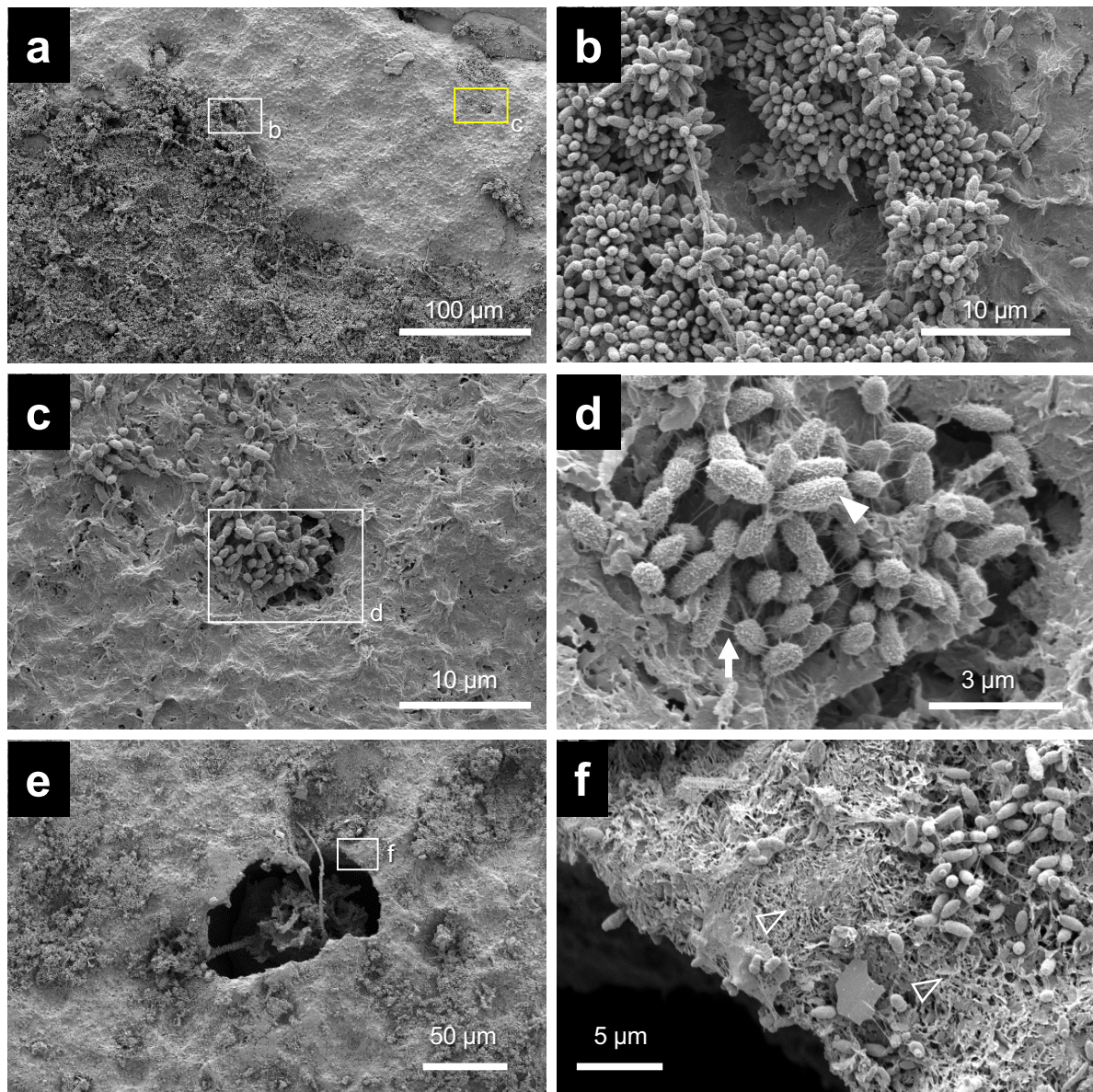
Supplementary Fig. 6 Magnified FE-SEM images for biofilms on the PHBV (1.5 month).

a An overview of the biofilm established on PHBV in the real marine environment at Time a. **b** Rectangle region in **a**. **c** Rectangle region in **b**. Magnified images of the biofilms. Open arrowheads in **c** The structure of PHBV that was partly degraded. **d** Rectangle region in **c**. **e** The area with the hole. **f** Rectangle region in **e**. Magnified microbial cell morphologies to correlate with PHBV degradation. Filled arrowheads indicate rod-shaped microbes with the secretion of vesicles frequently observed near the interface.



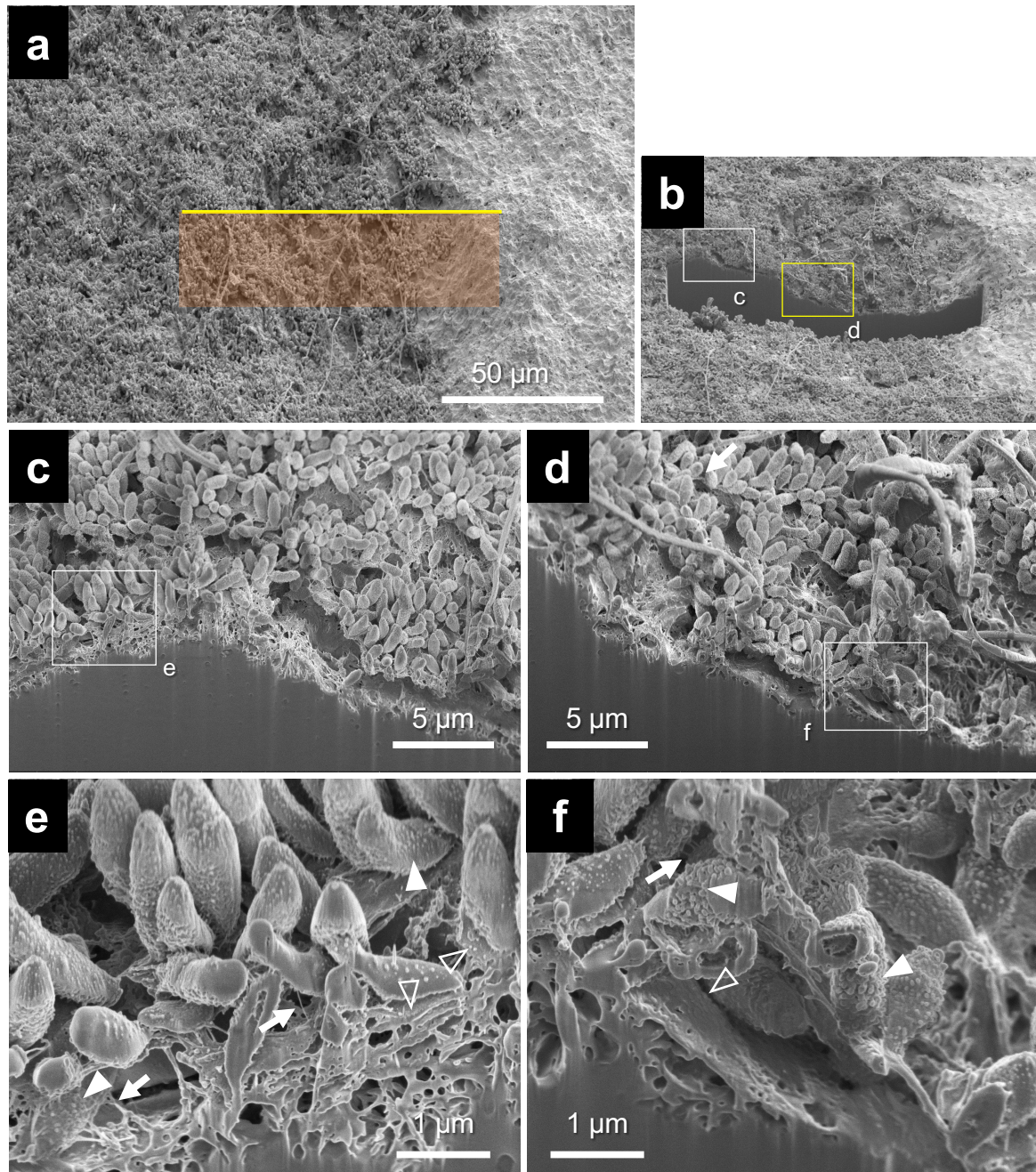
Supplementary Fig. 7 Cross-section FE-SEM images for biofilms on the PHBV (1.5 month) processed by a focused ion beam.

a The region to proceed to cut by a focused ion beam. **b** The image after cutting. **c** A cross-section image of biofilm to degrade PHBV film (white rectangle region in **b**). **d** A magnified image close to the PHBV-microbe interface. **e** A cross-section image of the region with the thick biofilm (yellow rectangle region in **b**). Arrowheads in **d** and **e** indicate rod-shaped microbes with the secretion of vesicles frequently observed near the interface. Arrows in **e** indicate slime-formed microbes that established slimy biofilm over the PHBV film.



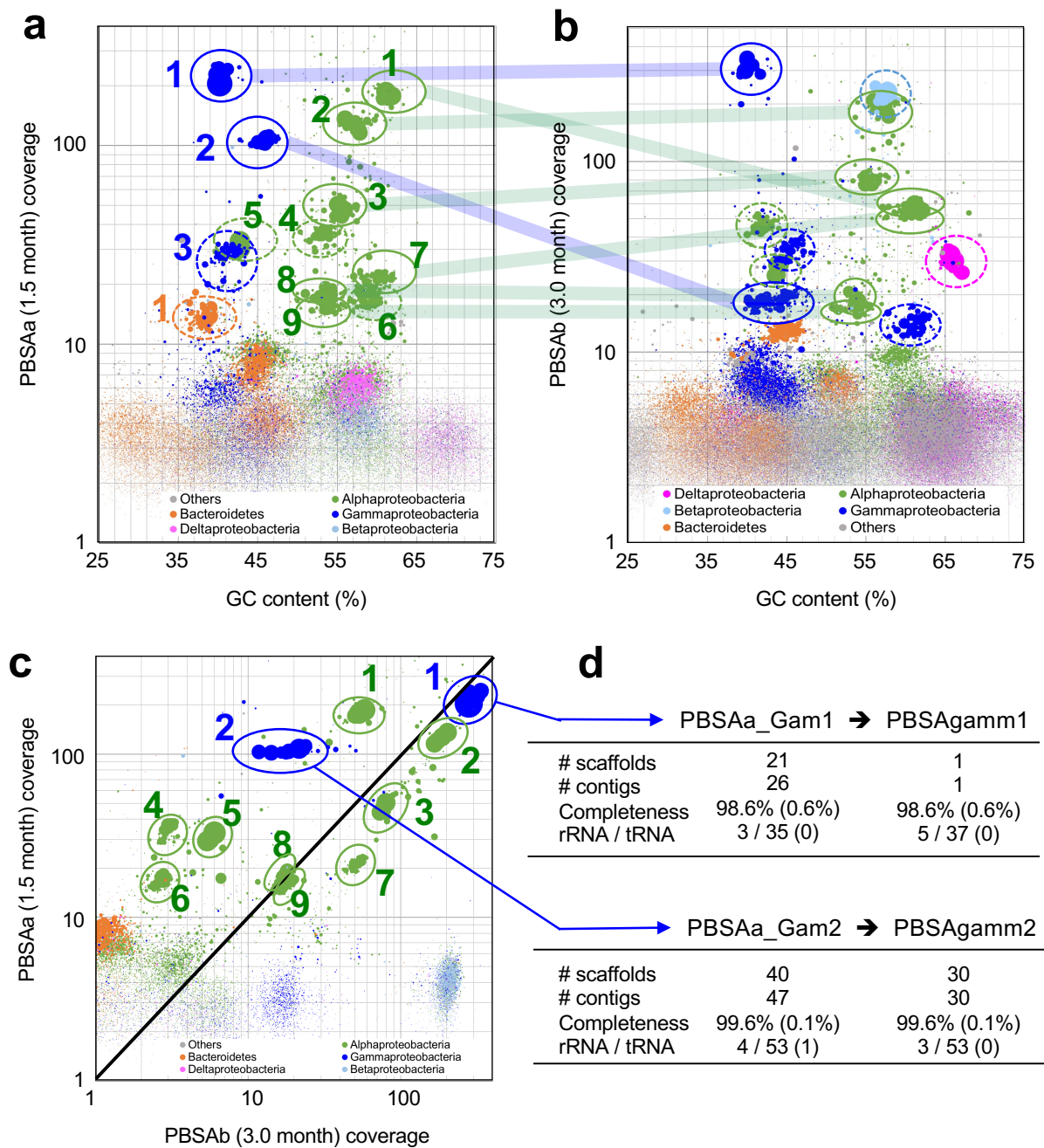
Supplementary Fig. 8 Magnified FE-SEM images for biofilms on the PBSA (1.5 month).

a An overview of the biofilm established on PBSA in the marine environment at Time a. **b and c** Rectangle region in **a**. Magnified images of the dense biofilm on the PBSA, and intact area with single-layer microcolony, respectively. **d** Rectangle region in **c**. A magnified image of biofilm to visualize microbial cell morphologies where dominant microbes secreted vesicles (filled arrowhead) and attached to the interface by using pili (arrow). **e** The area with the hole. **f** Rectangle region in **e**. The magnified image of the edge of the hole. Open arrowheads in **f** indicate the structure of PBSA that was partly degraded.



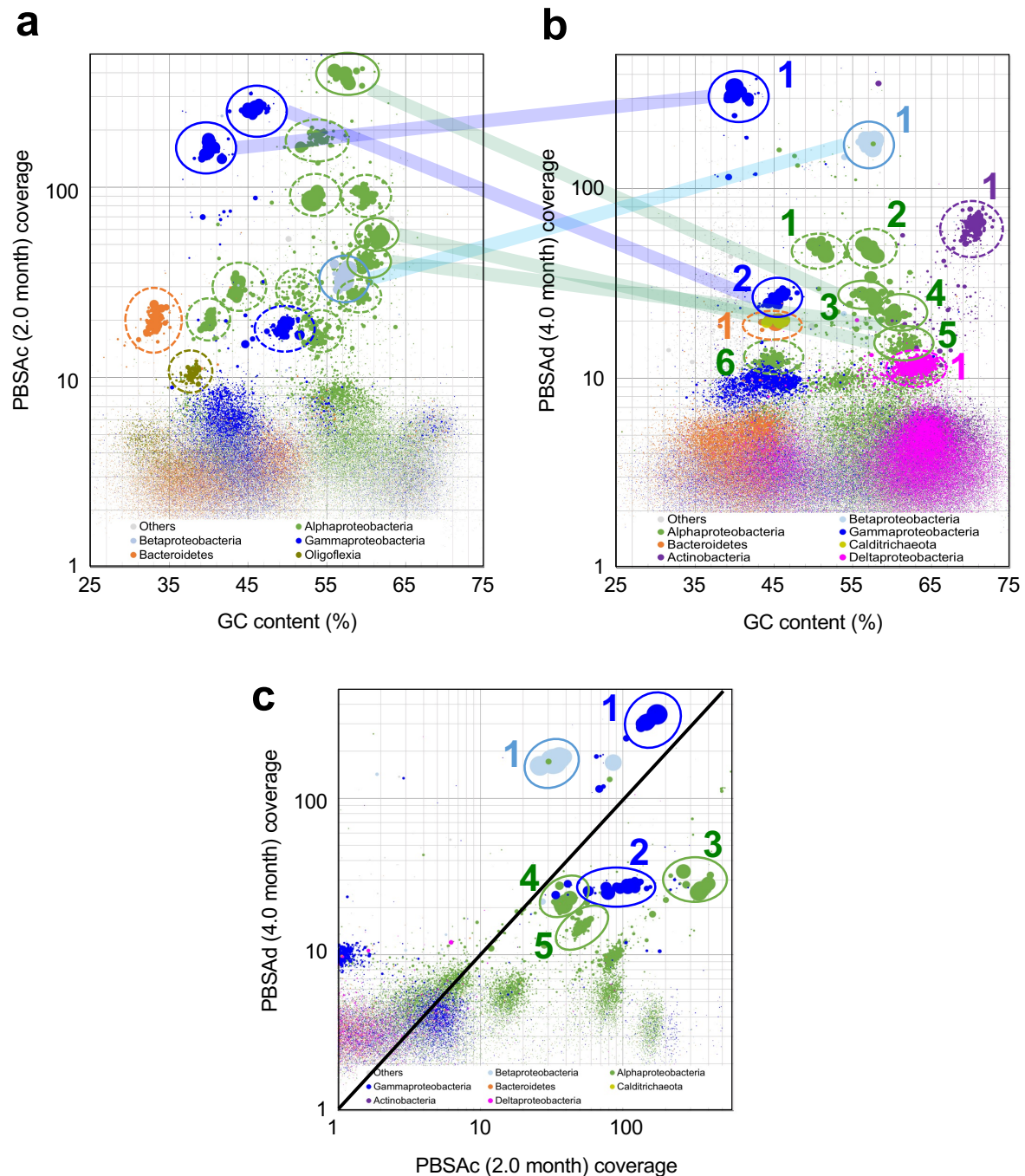
Supplementary Fig. 9 Cross-section FE-SEM images for biofilms on the PBSA (1.5 month) processed by a focused ion beam.

a The region to proceed to cut by a focused ion beam. **b** The image after cutting. **c** A cross-section image of biofilm to degrade PBSA film (white rectangle region in **b**). **d** A magnified image close to the PBSA-microbe interface (yellow rectangle region in **b**). **e** A cross-section image of the region with the thick biofilm (white rectangle region in **c**). **f** A cross-section image of the region with the thin biofilm (white rectangle region in **d**). Filled arrowheads in **e** and **f** indicate rod-shaped microbes with the secretion of vesicles frequently observed near the interface. Arrowheads in **e** and **f** indicate the structure of PBSA that was partly degraded. Arrows in **d**, **e**, and **f** indicate that microbes attached to the interface by using pili.



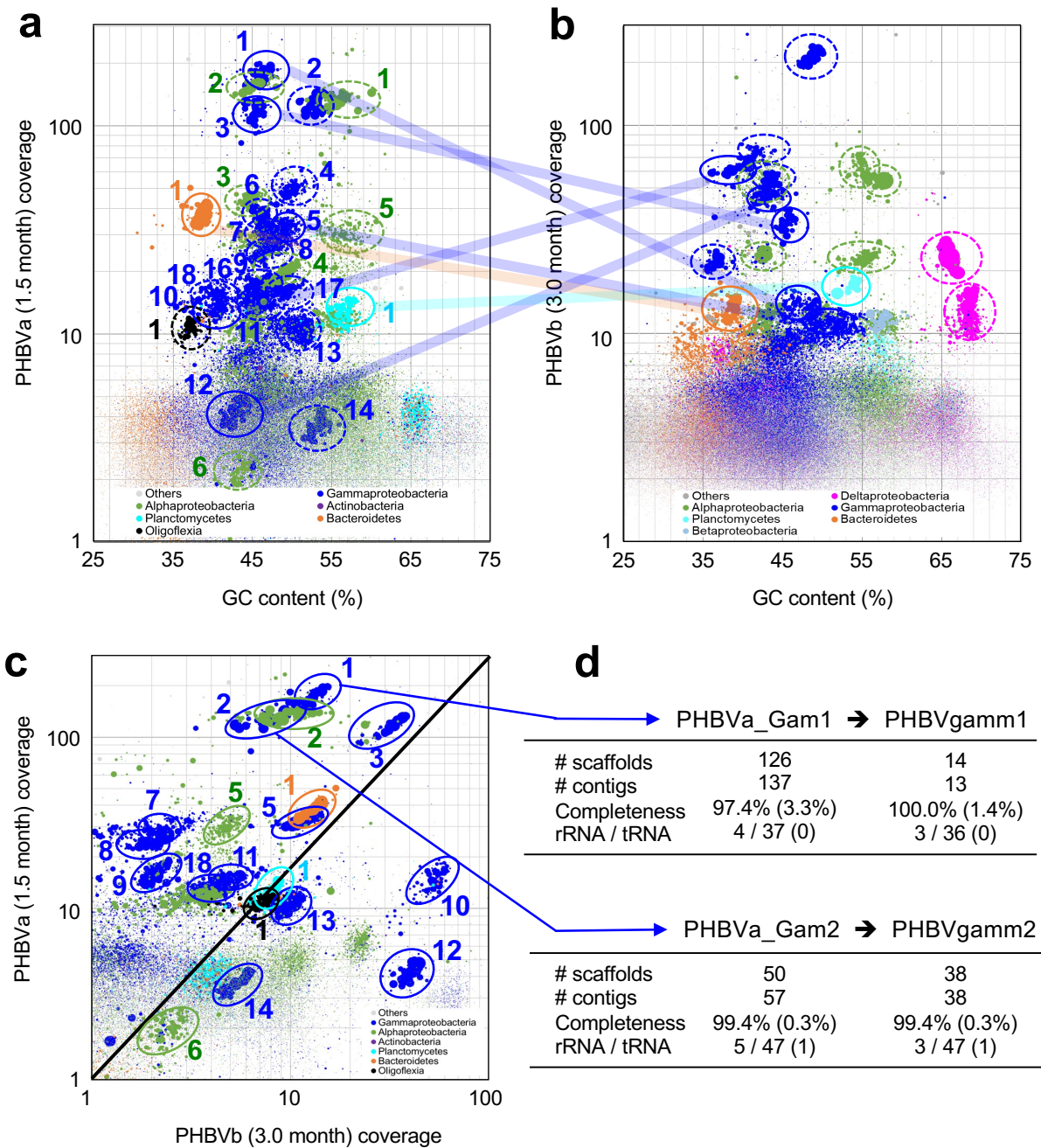
Supplementary Fig. 10 Metagenome-assembled genomes (MAGs) established from plastisphere PBSAa.

Genome clustering from the assembled scaffolds of metagenomic sequences of plastisphere PBSAa (**a**) and PBSAb (**b**) based on the mean coverage versus GC% plot. Colored circles indicate clusters of individual MAGs (solid line shown in both communities, broken line shown in one of them), while numbers shown near the circles correspond to the MAG IDs established from plastisphere PBSAa. MAGs were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis). The differential coverage plot between PBSAa and PBSAb plastisphere (**c**). Two dominant MAGs, PBSAa_Gam1 and PBSAa_Gam2, were manually refined to PBSAgamm1 and PBSAgamm2, respectively (**d**). The genome completeness was analyzed by Check M (contamination in parentheses). Number of rRNAs was analyzed by rRNAmmer, while number of tRNAs was analyzed by tRNAscan (number of missing number for amino acids in parentheses).



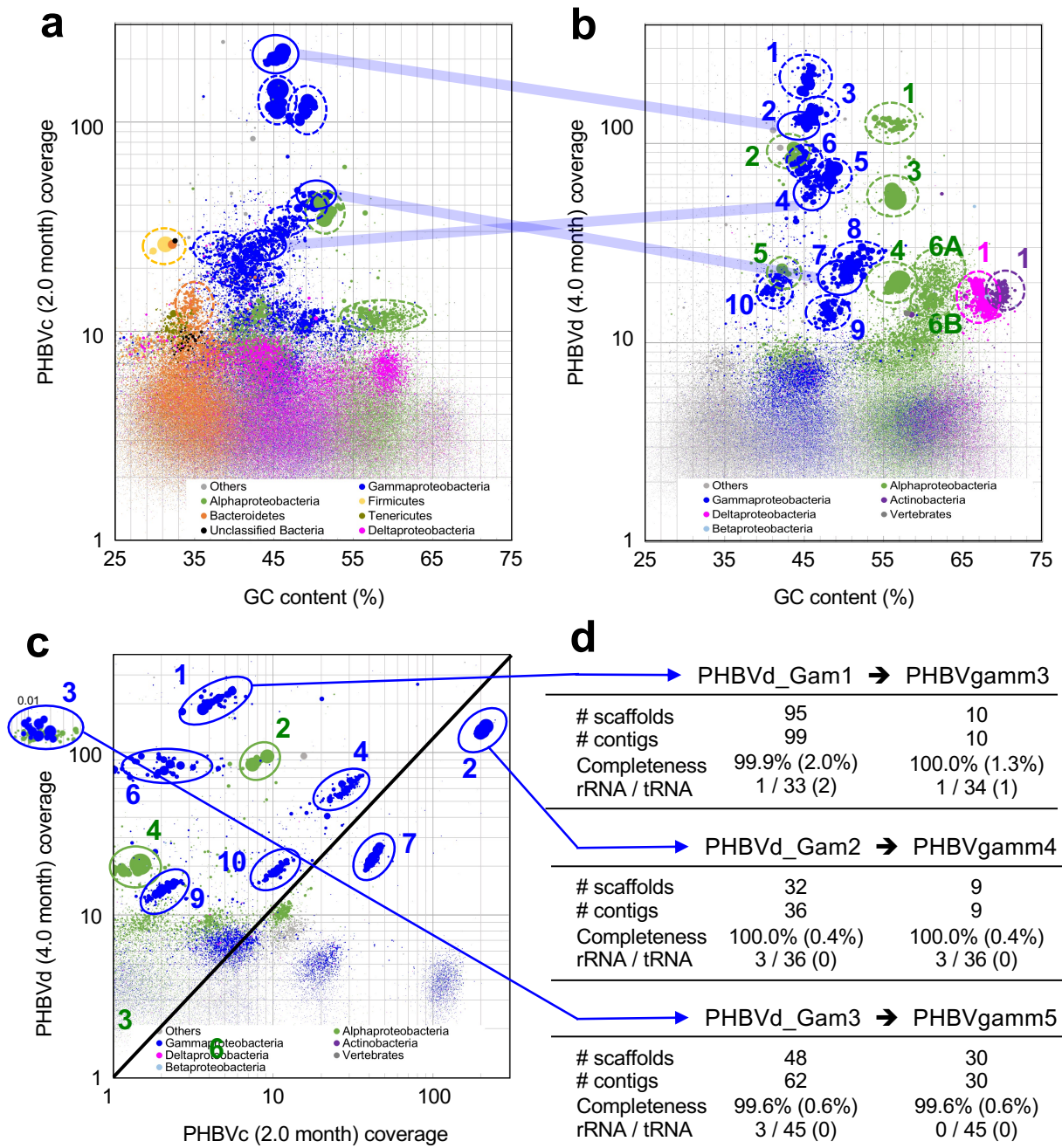
Supplementary Fig. 11 Metagenome-assembled genomes (MAGs) established from plastisphere PBSAd.

Genome clustering from the assembled scaffolds of metagenomic sequences of plastisphere PBSAc (**a**) and PBSAd (**b**) based on the mean coverage versus GC% plot. Colored circles indicate clusters of individual MAGs (solid line shown in both communities, broken line shown in one of them), while numbers shown near the circles correspond to the MAG IDs established from plastisphere PBSAd. MAGs were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis). The differential coverage plot between PBSAd and PBSAc plastisphere (**c**).



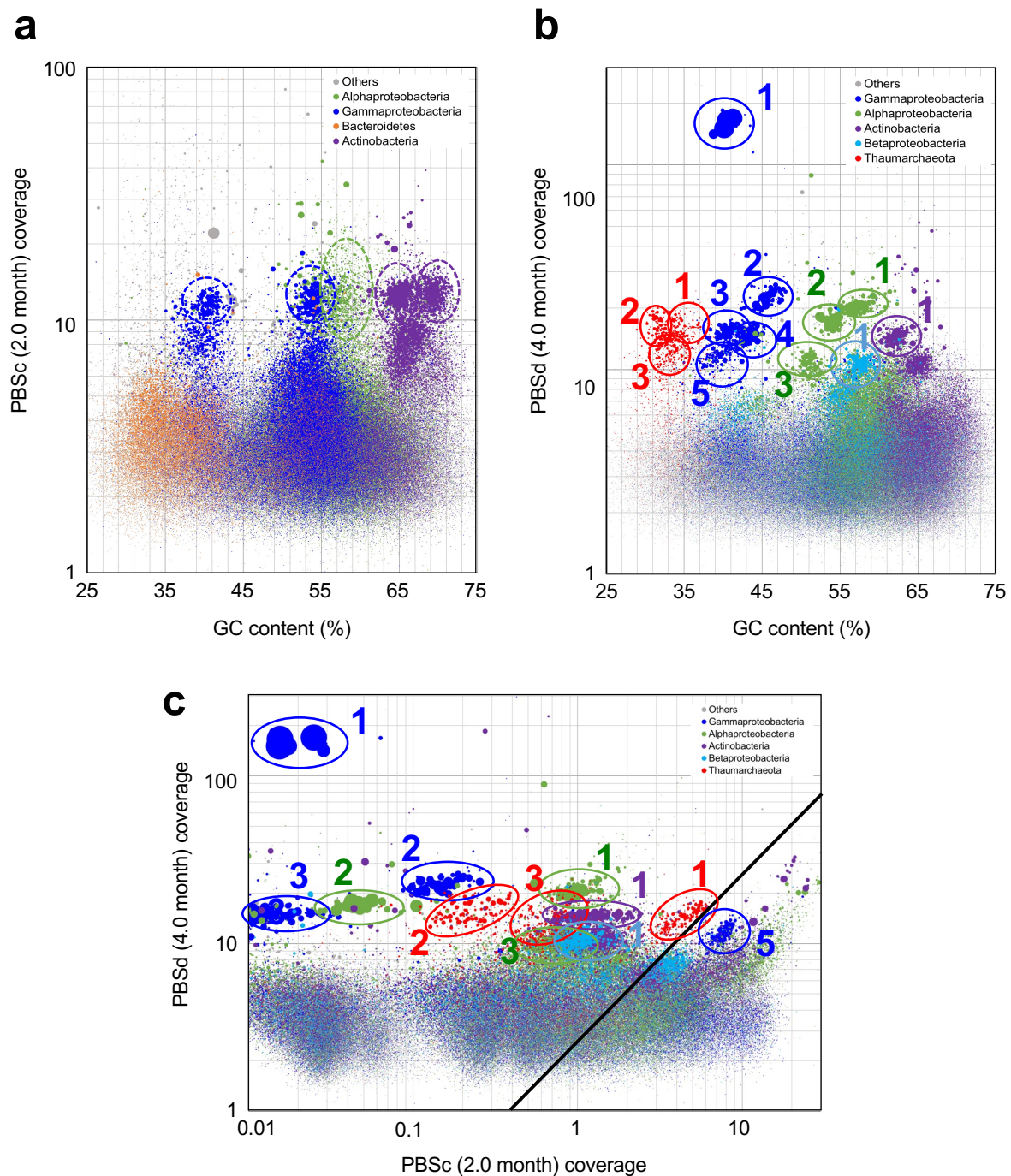
Supplementary Fig. 12 Metagenome-assembled genomes (MAGs) established from plastsphere PHBVa.

Genome clustering from the assembled scaffolds of metagenomic sequences of PHBVa (**a**) and PHBVb (**b**) based on the mean coverage versus GC% plot. Colored circles indicate clusters of individual MAGs (solid line shown in both communities, broken line shown in one of them), while numbers shown near the circles correspond to the MAG IDs established from PBSAa. MAGs were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis). The differential coverage plot between PHBVa and PHBVb (**c**). Two dominant MAGs, PHBVa_Gam1 and PHBVa_Gam2, were manually refined to PHBVgamm1 and PHBVgamm2, respectively (**d**). The genome completeness was analyzed by Check M (contamination in parentheses). The number of rRNAs was analyzed by rRNAmmer, while number of tRNAs was analyzed by tRNAscan (number of missing numbers for amino acids in parentheses).



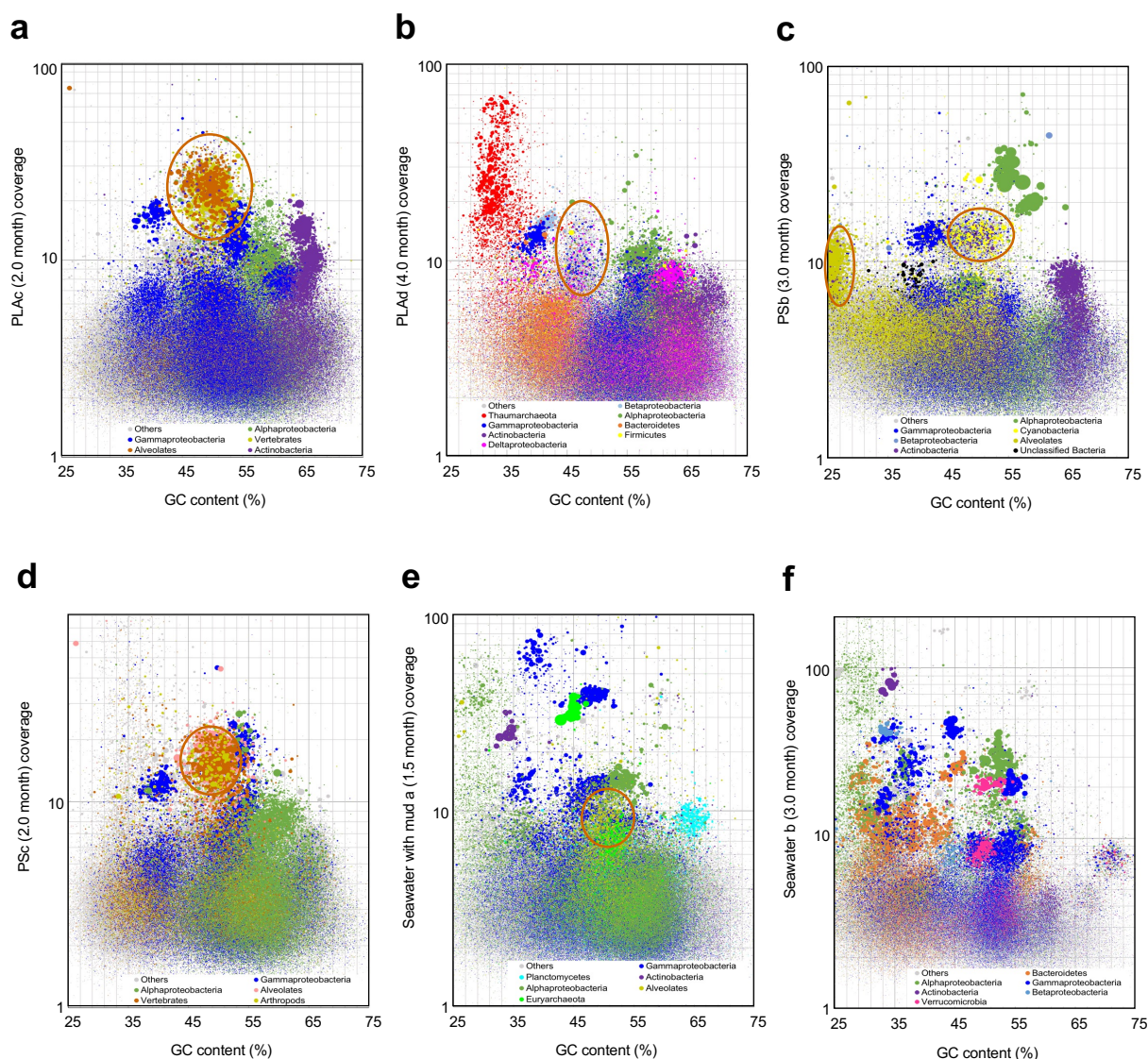
Supplementary Fig. 13 Metagenome-assembled genomes (MAGs) established from plastisphere PHBVd.

Genome clustering from the assembled scaffolds of metagenomic sequences of plastisphere PHBVc (**a**) and PHBVd (**b**) based on the mean coverage versus GC% plot. Colored circles indicate clusters of individual MAGs (solid line shown in both communities, broken line shown in one of them), while numbers shown near the circles correspond to the MAG IDs established from plastisphere PHBVd. MAGs were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis). The differential coverage plot between PHBVd and PHBVc plastisphere (**c**). Three dominant MAGs, PHBVd_Gam1, PHBVd_Gam2, and PHBVd_Gam3 were manually refined to PHBVgamm3, PHBVgamm4, and PHBVgamm5, respectively (**d**). The genome completeness was analyzed by Check M (contamination in parentheses). Number of rRNAs was analyzed by rRNAmmer, while number of tRNAs was analyzed by tRNAscan (number of missing number for amino acids in parentheses).



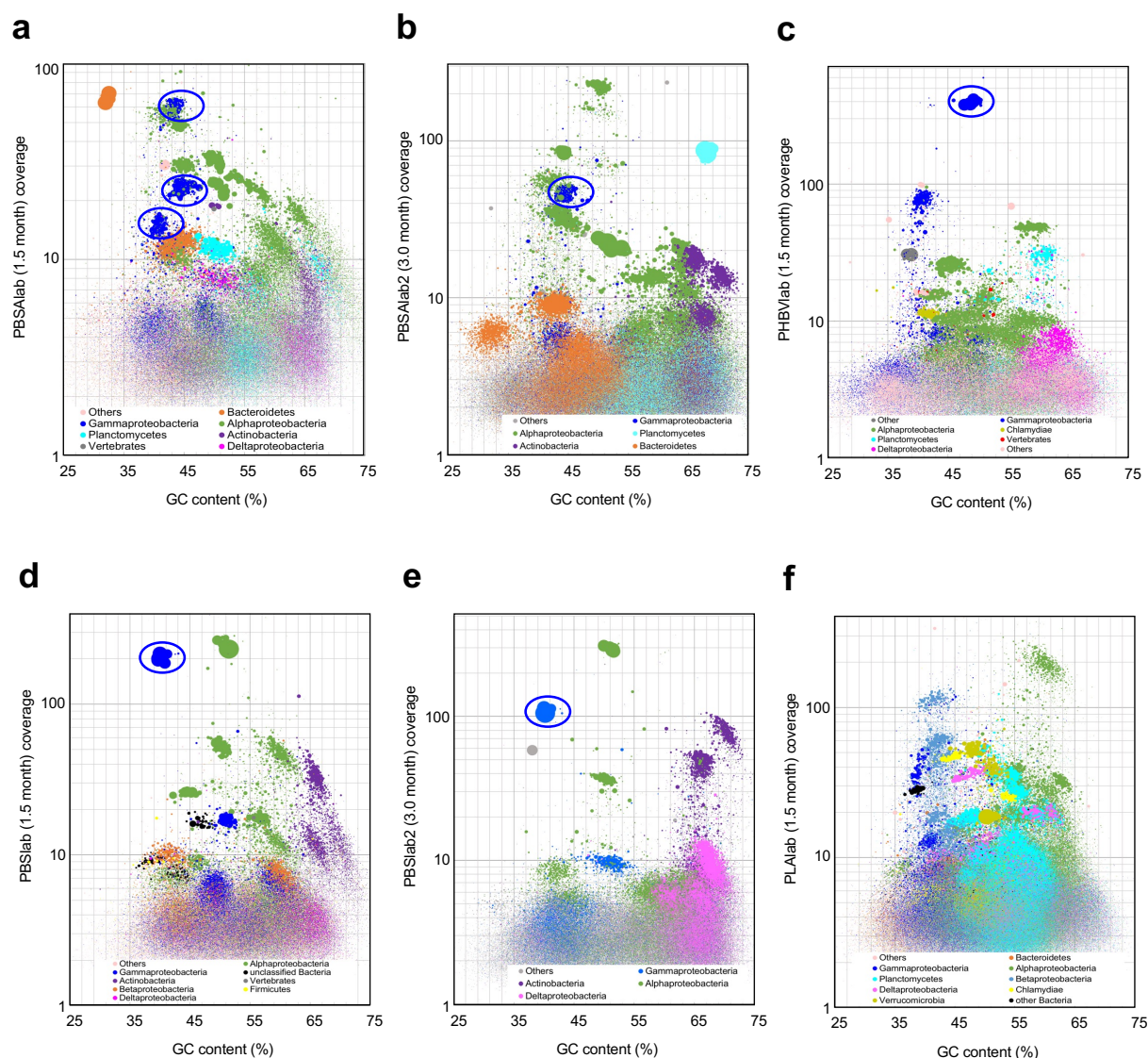
Supplementary Fig. 14 Metagenome-assembled genomes (MAGs) established from plastisphere PBSd.

Genome clustering from the assembled scaffolds of metagenomic sequences of plastisphere PBSd (**a**) and PBSd (**b**) based on the mean coverage versus GC% plot. Colored circles indicate clusters of individual MAGs, while numbers shown near the circles correspond to the MAG IDs established from plastisphere PBSd. MAGs were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis). The differential coverage plot between PBSd and PBSd plastisphere (**c**).



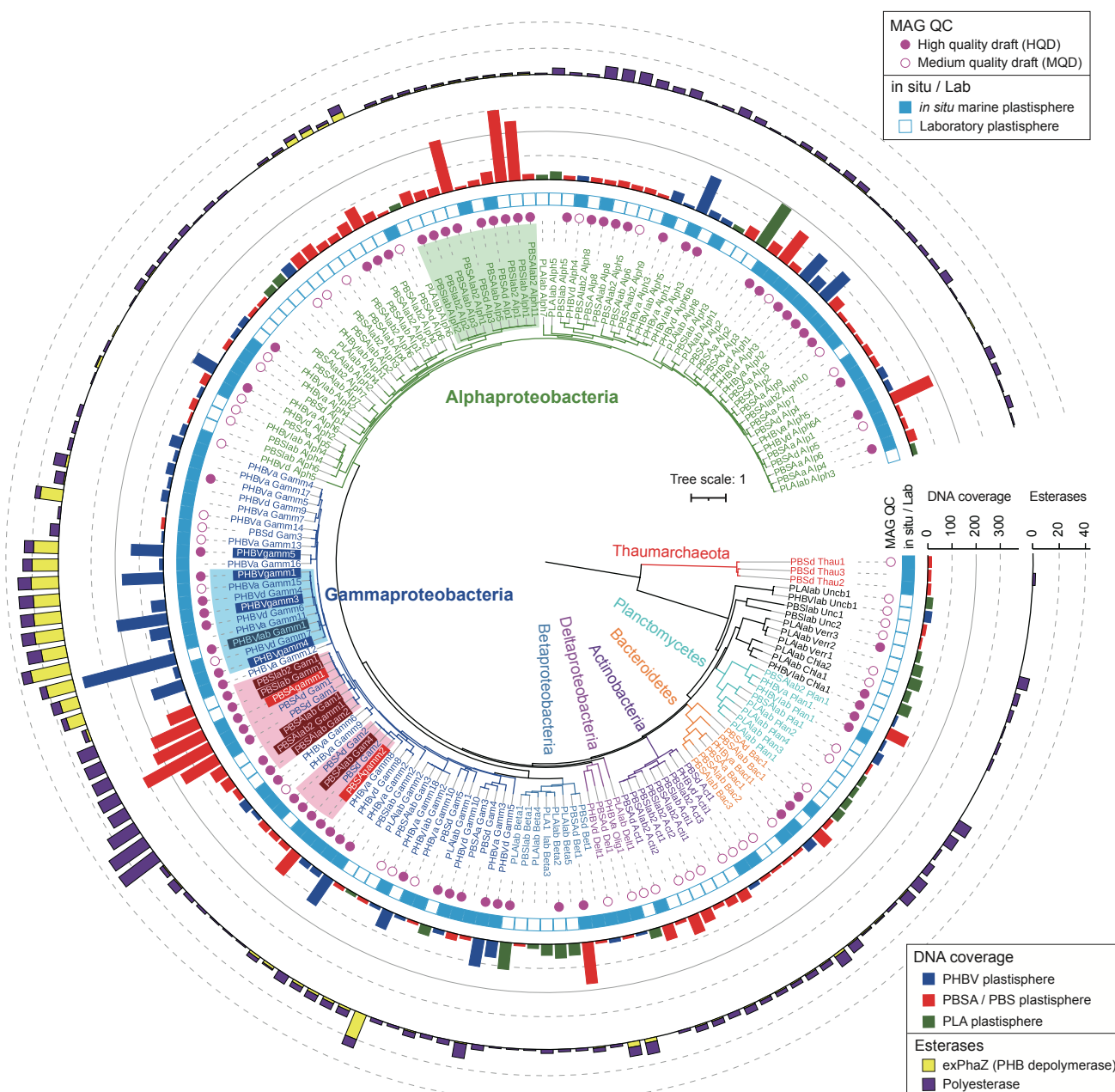
Supplementary Fig. 15 Metagenomic assembly for seawater microbial community and for plastisphere established on PLA and PS.

Genome clustering from the assembled scaffolds of metagenomic sequences of plastisphere PLAc (a), PLAd (b), PSb (c), PSc (d) and of microbial community in seawater (e, f) around the experimental site, based on the mean coverage versus GC% plot. Brown colored circles indicate genomic clusters of Eukaryote. Genomic clusters were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis).



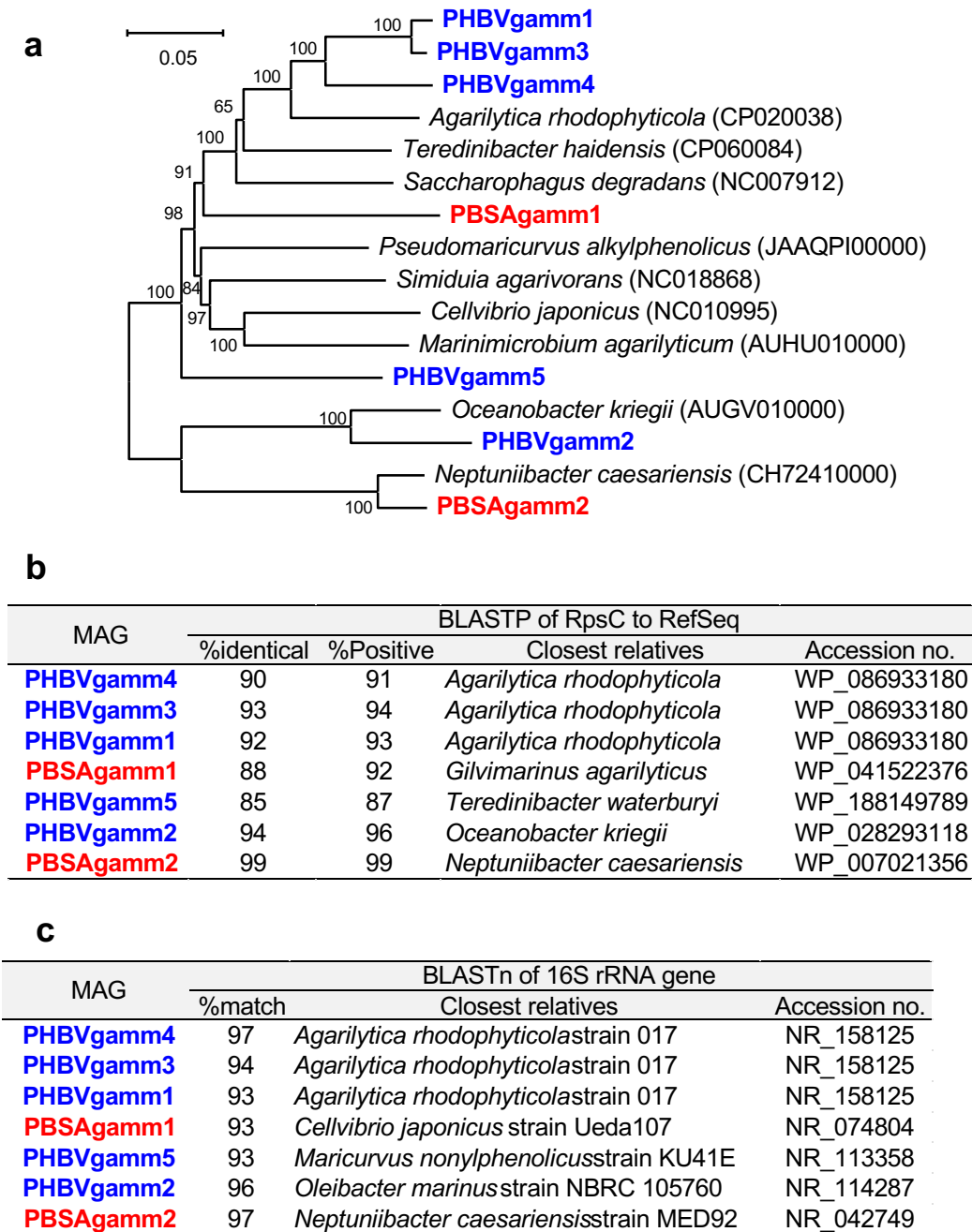
Supplementary Fig. 16 Metagenomic assembly for plastisphere established on PBSA, PHBV, PBS, and PLA during the laboratory experiment.

Genome clustering from the assembled scaffolds of metagenomic sequences of plastisphere PBSAlab (**a**), PBSAlab2 (**b**), PHBVlab (**c**), PBSlab (**d**), PBSlab2 (**e**), and PLAlab (**f**), based on the mean coverage versus GC% plot. Blue colored circles indicate clusters of MAGs correlated with the seven refined Gammaproteobacterial MAGs in this study. MAGs were identified using the estimated taxonomic classification (color of dots), length (size of dots), GC content (X-axis) and mean coverage of scaffold (Y-axis).



Supplementary Fig. 17 Phylogenomic tree of metagenome-assembled genomes (MAGs) generated from plastisphere metagenomes by laboratory and *in situ* marine environments.

Phylogenomic tree of MAGs generated from both *in situ* and laboratory plastispheres on PBSA, PBS, PHBV, and PLA was constructed by marker gene sets in CheckM argolism. MAG QC by MiMAG criteria is shown as purple circles near the MAG ID. Light blue boxes show MAGs either from *in situ* experiments (filled box) or laboratory experiments (open box). Seven manually refined MAGs and the related MAGs in laboratory plastisphere are shown as outline character in MAG ID. Average genome coverage of long contigs (>10,000 bp) for MAGs in each metagenomic libraries is shown as thick bar chart (blue bars for PHBV plastisphere, red bars for PBSA/PBS plastisphere, and green bars for PLA). Numbers of genes coding polyesterase (yellow) and extracellular PHB depolymerase (purple) for each MAG are shown as bar charts outside of coverage bars.



Supplementary Fig. 18 Phylogenomic tree and BLAST analyses of RpsC and 16S rRNA gene.

a Phylogenomic tree for refined Gammaproteobacterial MAGs with reference genomes was generated by using concatenated marker protein alignment generated in CheckM. **b** BLAST-P analysis of ribosomal protein S3 (RpsC) was performed with Refseq database as a reference. **c** BLAST-n analysis of 16S rRNA gene was performed with NCBI SSU/LSU dataset as a reference.

Supplementary Table 1. Molecular masses of film before and after incubation in the ocean.

Polyester	Before incubation		After incubation for 2		After incubation for 4	
	Mn	Mw/Mn	Mn	Mw/Mn	Mn	Mw/Mn
PBSA	5.8 x10 ⁴	2.5	5.9 x10 ⁴	2.6	6.0 x10 ⁴	2.4
PBS	6.3 x10 ⁴	2.8	6.3 x10 ⁴	2.7	6.1 x10 ⁴	2.4
PLA	6.1 x10 ⁴	1.9	5.7 x10 ⁴	1.8	5.7 x10 ⁴	1.8
PHBV	1.9 x10 ⁵	2.7	1.1 x10 ⁵	3.3	1.3 x10 ⁵	2.9

Supplementary Table 2. Mechanical properties of film before and after incubation in the ocean.

Polyester	Before incubation			After incubation for 2 months			After incubation for 4 months		
	Young's modulus (MPa)	Tensile strength (MPa)	Elongation at break (%)	Young's modulus (MPa)	Tensile strength (MPa)	Elongation at break (%)	Young's modulus (MPa)	Tensile strength (MPa)	Elongation at break (%)
PBSA	224±16	19.0±0.7	496±211	236±39	18.0±0.6	300±123	201±25	15.5±1.9	274±176
PBS	485±42	38.6±1.9	110±80	386±50	34.6±4.7	85±77	546±22	36.9±2.6	74±86
PLA	793±423	56.0±3.0	11.0±2.0	993±91	51.0±3.3	11±2.0	1384±90	58.1±5.3	8.0±1.0
PHBV	775±46	24.1±1.1	12.0±1.0	710±60	20.9±0.8	9.0±1.0	744±47	20.0±1.3	8.0±0.0

Supplementary Table 3. Thermal properties of film before and after incubation in the ocean.

Polyester	Before incubation			After incubation for 2 months				After incubation for 4 months				
	Tg(°C)	Tc(°C)	Tm(°C)	ΔH(J/g)	Tg(°C)	Tc(°C)	Tm(°C)	ΔH(J/g)	Tg(°C)	Tc(°C)	Tm(°C)	ΔH(J/g)
PBSA	ND	40.8	82.3	36.5	ND	41.8	86.2	32.3	ND	42.2	87.2	34.9
PBS	ND	77.8	114.6	60	ND	77.4	114.8	59.6	ND	77.4	114.7	55
PLA	62.4	109.7	170.5	41.9	62.2	106.2	170.4	41.7	61.8	105.9	169.7	42.2
PHBV	-20.3	97.8	165.8	42.1	-20.3	102.9	166.8	44.8	-17.5	101.1	165.9	45.2

Supplementary Table 4 Statistical parameters of metagenomic assemblies.

Community	Material	Time (month)	in situ or Lab.	mRNA seq	No. of DNA raw reads ^a	Reads Mapped ^a	% Mapped ^a	No. Scaffolds	Total Bases (bp)	Max contig size (bp)	No. contigs >1 kbp
PHBVa2 ^b											
PHBVa ^b	PHBV	1.5	in situ	No	28,224,562	23,101,043	81.8%	151,103	276,330,972	693,856	45,144
PHBVa-MAGs ^c				Yes	52,949,280	45,741,822	86.4%				
					32,851,773	62.0%	4.052	108,115,752	693,856	3,657	
PHBVb	PHBV	3.0	in situ	No	50,324,746	35,235,303	70.0%	210,757	368,009,959	800,046	68,344
PHBVc	PHBV	2.0	in situ	No	50,157,026	32,931,869	65.7%	225,135	302,919,830	1,340,725	63,861
PHBVd	PHBV	4.0	in situ	Yes	53,403,926	39,712,012	74.4%	186,768	277,559,977	1,651,231	49,854
PHBVd-MAGs ^c					30,815,927	57.7%	2.629	79,366,551	1,651,231	2,354	
PBSAa	PBSA	1.5	in situ	Yes	29,912,294	24,513,016	81.9%	51,666	114,567,031	1,184,025	17,919
PBSAa-MAGs ^c					21,619,755	72.3%	1,122	49,884,411	1,184,025	1,004	
PBSAb	PBSA	3.0	in situ	No	51,270,894	39,778,241	77.6%	158,978	250,263,011	987,546	51,611
PBSAc	PBSA	2.0	in situ	No	48,212,466	39,290,758	81.5%	107,339	172,196,546	1,244,643	28,255
PBSAd	PBSA	4.0	in situ	Yes	51,297,828	32,064,365	62.5%	210,371	263,529,181	966,928	53,044
PBSAd-MAGs ^c					23,300,164	45.4%	1.904	56,660,639	966,928	1,749	
PBSd	PBS	2.0	in situ	No	50,068,710	8,335,521	16.6%	278,084	246,144,596	169,697	50,751
PBSd	PBS	4.0	in situ	Yes	53,106,870	17,641,655	33.2%	296,524	302,164,159	925,872	59,851
PBSd-MAGs ^c					9,178,741	17.3%	2.909	49,250,054	925,872	2,559	
PLAc	PLA	2.0	in situ	No	58,008,978	15,167,197	26.1%	369,470	356,726,506	110,117	69,977
PLAd	PLA	4.0	in situ	No	50,600,398	10,888,738	21.5%	284,329	261,876,975	109,911	53,746
PSb	PS	3.0	in situ	No	33,415,252	10,301,285	30.8%	245,297	247,990,393	581,904	61,687
PSc	PS	2.0	in situ	No	44,277,582	10,546,193	23.8%	278,696	257,878,344	109,188	52,331
seawater a	seawater	1.5	in situ	No	88,294,004	15,323,360	17.4%	346,195	339,470,399	294,336	77,277
seawater mud b	seawater	3.0	in situ	No	45,992,884	20,705,581	45.0%	192,694	267,800,049	445,781	54,673
PHBVIab	PHBV	1.5	Lab.	No	33,909,090	26,531,370	79.1%	128,930	206,073,231	529,685	41,820
PBSAIIab	PBSA	1.5	Lab.	No	41,274,936	27,520,941	67.2%	145,117	227,273,087	834,644	40,095
PBSA13Iab2	PBSA	3.0	Lab.	No	30,972,462	22,541,977	72.8%	208,301	283,853,846	832,282	59,636
PBSIab	PBS	1.5	Lab.	No	41,524,606	25,687,669	61.9%	158,256	191,531,730	1,215,023	40,982
PBSIab2	PBS	3.0	Lab.	No	28,699,734	20,019,761	69.8%	177,377	226,249,958	1,183,905	54,174
PLAIIab	PLA	1.5	Lab.	No	136,633,524	77,740,761	56.9%	741,376	928,776,039	1,208,587	211,361
seawaterIab	seawater	1.5	Lab.	No	61,476,216	39,161,039	63.7%	271,019	398,196,820	911,343	82,177

^a Numbers of reads to perform mapping raw reads back to the assembled scaffolds (with length cutoff 0.7 and similarity cutoff 0.95).

^b For PHBV time a plastisphere, two metagenomic sequences were co-assembled to make scaffolds, and mapped to the scaffolds separately.

^c For samples with mRNAseq, statistical parameters only from MAG-associated scaffolds were also shown.

Supplementary Table 5 Summary of MAGs clustered from metagenomic assemblies of *in situ* plastispheres.

MAG ID ^a	RpsC-based frequency (%) ^b	Averaged DNA coverage ^c	mRNA read per one million mapped read ^d	Genome size (bp)	GC content (%)	Numbers of ORF	ESTHER- assigned ORF's	PHB depolymerase	Poly-esterase	Number of contigs	Number of scaffolds	N50 scaffold (bp)	Longest scaffold (bp)	Taxa ^f					
														MAG QC ^e	Phylum	Class	Order	family	genus
PBSd_Gam1	29.9	165.6	159,382	3,679,901	41%	3260	67	0	15	31	28	919,872	925,872	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellyvibrionaceae	Neptuniibacter
PBSd_Gam2	5.1	22.6	24,886	3,680,247	46%	3630	36	0	1	114	112	80,126	207,083	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitriinoclaeeae	
PBSd_Alpl1	5.0	20.5	17,127	8,250,262	57%	8662	92	1	4	403	350	58,654	245,009	HQD	Proteobacteria	Alphaproteobacteria	Geminicoccales	Rhodobacteriaceae	Planktotalea
PBSd_Alpl2	5.0	16.7	3,708	3,869,070	54%	3799	80	0	3	65	53	169,485	316,546	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Nitrosopurillaceae	Nitrosopurillus
PBSd_Tha2	3.1	15.6	226,617	1,411,850	33%	1904	8	0	0	147	129	19,958	44,473	LQD	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Cellyvibrionaceae	
PBSd_Gam3	3.3	15.3	14,510	3,296,942	41%	3152	40	0	2	99	94	60,326	161,466	MD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitrosopurillaceae	
PBSd_Tha1	2.7	14.7	175,462	1,378,793	34%	1927	8	0	0	303	264	8,936	35,599	MD	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrosopurillaceae	Nitrosopurillus
PBSd_Gam4	3.0	14.5	10,465	5,824,007	43%	5440	72	0	4	184	175	84,616	188,450	LQD	Proteobacteria	Gammaproteobacteria	UBA10353	UBA7415	
PBSd_Act1	4.1	14.4	7,725	7,626,238	62%	7378	160	1	4	587	509	28,281	115,125	MD	Actinobacteriota	Acidimicrobia	Acidimicrobiales	SZUA-35	SZUA-35
PBSd_Tha3	2.7	13.6	112,376	1,258,647	33%	1763	7	0	2	374	332	6,498	22,472	LQD	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrosopurillaceae	Nitrosopurillus
PBSd_Gam5	2.8	11.4	3,057	2,182,883	39%	2249	17	0	3	210	200	17,516	55,488	LQD	Proteobacteria	Gammaproteobacteria	UBA4575	UBA4575	
PBSd_Bet1	1.6	10.6	1,437	3,411,388	57%	3467	45	0	2	359	342	16,532	56,786	LQD	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	
PBSd_Alpl3	3.0	10.1	3,013	3,379,826	51%	3266	50	1	1	334	321	22,564	91,222	LQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAa_Gam1	23.1	227.5	316,133	3,680,327	40%	3257	71	0	16	26	21	460,864	1,184,025	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellyvibrionaceae	
PBSAagamm1			272,525	3,679,316	40%	3187	66	0	14	1	1	3,679,316	3,679,316		Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellyvibrionaceae	
PBSAa_Alpl1	20.6	179.3	49,991	3,308,539	61%	3202	51	0	5	40	35	446,993	699,388	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	59-46-T64
PBSAa_Gam2	14.9	146.2	20,890	3,703,417	57%	3716	69	1	4	71	66	444,717	532,418	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	Martiniibacter
PBSAa_Alpl2	12.3	109.3	246,340	3,730,535	46%	3618	37	0	1	47	40	255,983	596,634	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitriinoclaeeae	Neptuniibacter
PBSAagamm2			206,043	3,794,966	46%	3660	38	0	1	30	30	267,509	984,308	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitriinoclaeeae	Neptuniibacter
PBSAa_Alpl3	5.8	49.8	21,403	5,359,277	56%	5222	86	0	3	82	74	233,817	548,690	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	Pelagimonas
PBSAa_Alpl4	4.5	36.0	7,989	3,360,382	53%	3425	51	0	4	83	78	108,750	293,001	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	Cognatis himia
PBSAa_Alpl5	3.4	30.3	45,045	2,615,821	42%	2511	35	1	0	16	14	609,642	767,649	MD	Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	UBA1672
PBSAa_Gam3	3.3	27.3	5,957	3,403,912	41%	3222	78	0	3	137	131	61,718	135,755	HQD	Proteobacteria	Gammaproteobacteria	UBA10353	UBA7415	
PBSAa_Alpl7	2.8	23.3	7,257	3,646,916	60%	3629	75	0	1	221	153	53,485	150,327	MD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	UBA3069
PBSAa_Alpl8	2.2	18.4	10,491	2,854,400	54%	2716	58	0	9	48	43	102,559	321,878	HQD	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Hyphomicrobiaceae	Hyphomonas
PBSAa_Alpl6	2.0	17.0	3,927	3,666,811	59%	3759	67	0	1	254	156	62,038	219,557	LQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	Thalassobius
PBSAa_Alpl9	1.8	15.9	8,155	3,846,373	54%	3881	85	0	3	199	140	75,802	167,183	MD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	Planktotalea
PBSAa_Bac1	1.8	13.7	52,100	6,672,217	39%	5598	85	1	1	257	168	74,826	266,019	MD	Bacteroidia	Bacteroidia	Chitinophagales	Saprospiraceae	Aureispira
PBSAd_Gam1	32.3	308.9	389,824	3,681,281	40%	3263	71	0	16	38	35	279,637	640,106	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellyvibrionaceae	
PBSAd_Bet1	21.9	172.1	1,705	5,259,905	57%	4792	82	1	3	20	17	720,984	966,928	HQD	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	
PBSAd_Act1	7.7	63.3	218	4,850,554	70%	4719	93	1	4	303	261	46,899	148,935	MD	Actinobacteriota	Acidimicrobia	Acidimicrobiales	SZUA-35	SZUA-35
PBSAd_Alpl1	5.1	48.6	3,914	3,397,300	51%	3035	46	1	1	35	32	308,207	530,875	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAd_Alpl2	5.2	47.1	657	3,084,910	57%	3013	55	0	2	23	21	536,316	709,461	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	
PBSAd_Alpl3	3.0	27.8	676	3,605,426	57%	3613	69	1	4	70	59	324,949	462,461	MD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	
PBSAd_Gam2	3.0	27.0	59,219	3,490,073	45%	3369	32	0	3	54	48	170,552	299,081	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitriinoclaeeae	Martiniibacter
PBSAd_Alpl4	2.3	21.8	482	3,782,375	60%	3667	77	0	1	52	47	179,621	526,667	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	Neptuniibacter
PBSAd_Bac1	2.0	20.1	16,070	6,345,459	45%	5143	127	1	8	81	59	279,044	592,851	HQD	Calditrichia	Calditrichia	RBG-13-44-9	J042	UBA3069
PBSAd_Alpl5	1.8	15.2	345	3,313,242	61%	3365	53	0	4	218	171	37,815	140,877	MD	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteriaceae	
PBSAd_Alpl6	1.6	12.2	26,562	4,610,933	45%	4422	79	5	6	267	243	31,498	139,544	MD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	
PBSAd_De1	1.3	11.6	2,704	11,239,181	63%	9804	148	3	9	1017	911	19,889	127,860	LQD	Myxococcota	UBA727			

Supplementary Table 5 continued for plastisphere PHBVa.

MAG ID ^a	RpsC-based frequency (%) ^b	Averaged DNA coverage ^c	mRNA read per one million mapped read ^d	Genome size (bp)	GC content (%)	Numbers of ORF	ESTHER-assigned ORFs	PHB depolymerase	Poly-esterase	Number of contigs	Number of scaffolds	N50 scaffold (bp)	Longest scaffold (bp)	MAG QC ^e	Taxa ^f				
															Phylum	Class	Order	family	genus
PHBVa_Gam1	12.6	171.6	120,842	4,262,082	46%	3668	101	22	9	137	126	96,590	234,379	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agarivytica
PHBVgamm1			108,732	4,320,852	46%	3573	99	21	10	14	13	464,342	1,442,602						
PHBVa_Alp1	15.1	156.6	58,336	3,526,823	45%	3222	54	0	6	75	65	92,109	231,764	HQD	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Hyphomicrobiaceae	Hirschia
PHBVa_Alp2	11.4	136.3	22,951	4,791,574	56%	4677	92	0	2	109	97	101,097	255,140	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteriaceae	Pelagibonas
PHBVa_Gam2			209,185	3,541,384	53%	3173	38	2	1	57	50	158,628	361,422						
PHBVgamm2	10.7	129.5	178,772	3,589,484	53%	3125	38	2	1	38	38	199,609	367,494	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Saccharosphaerales, A	Oceanobacter
PHBVa_Gam3	9.0	115.0	47,941	4,570,814	45%	3990	99	1	11	104	89	98,292	259,041	HQD	Proteobacteria	Gammaproteobacteria	UBA10353	UBA7415	Arenicella
PHBVa_Gam4	4.0	48.7	30,143	4,155,562	50%	3790	58	0	3	330	279	29,814	103,219	LOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	GCA-2707785
PHBVa_Alp3	3.0	43.6	17,919	3,469,681	45%	3302	55	0	1	148	136	56,866	181,622	HQD	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Hyphomicrobiaceae	Hirschia
PHBVa_Bac1	3.4	37.1	35,785	6,637,954	39%	5485	84	1	1	185	119	117,704	386,490	HQD	Bacteroidia	Bacteroidia	Chitinophagales	Saprospiraceae	Aureispira
PHBVa_Gam6	2.8	33.8	24,905	4,593,365	46%	4237	76	1	3	46	42	215,493	690,495	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Sporichthyaceae	Oceanicoccus
PHBVa_Gam5	3.2	32.2	30,874	4,441,111	49%	3819	62	0	3	92	77	171,157	342,155	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	GCA-2707785
PHBVa_Gam7	2.6	29.6	21,358	4,108,098	48%	3875	59	1	7	359	327	22,660	89,583	LOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	GCA-2707785
PHBVa_Alp5	2.7	29.0	3,620	3,464,084	56%	3800	63	1	0	634	614	10,669	78,198	LOD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteriaceae	Epibacterium
PHBVa_Gam8	2.1	25.0	12,346	3,666,882	46%	3486	42	0	1	72	66	175,863	693,856	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitrospiraceae	Neptunomonas
PHBVa_Alp4	1.5	19.7	21,271	4,015,446	49%	3916	46	1	3	94	73	114,162	279,330	MOD	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Terrasakellaceae	Terrasakella
PHBVa_Gam17	1.3	16.3	11,081	4,192,559	49%	3795	62	0	3	302	264	46,470	121,119	LOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	GCA-2707785
PHBVa_Gam16	0.0	16.1	17,265	3,180,293	46%	2964	66	20	7	146	107	56,563	174,512	LOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	
PHBVa_Gam9	1.4	15.6	21,154	5,811,666	45%	5182	93	1	6	191	148	89,160	306,147	MOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Sporichthyaceae	
PHBVa_Gam18	0.8	13.7	9,867	4,541,327	41%	3993	101	2	5	231	184	40,188	144,334	MOD	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Kangiellicaceae	GCA-002733465
PHBVa_Gam11	1.0	13.7	26,991	4,176,949	46%	3672	121	38	7	366	285	37,128	283,726	LOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agarivytica
PHBVa_Gam10	1.5	13.6	12,741	2,926,949	39%	2587	71	20	7	197	188	27,037	129,149	MOD	Proteobacteria	Gammaproteobacteria	QZLD01	QZLE01	
PHBVa_Plan1	1.0	12.3	9,914	2,885,902	56%	2547	26	0	0	160	131	37,931	154,944	HQD	Planctomycetia	Phycisphaerae	Phycisphaerales	SM1A02	UBA1924
PHBVa_Olig1	0.8	10.6	1,811	2,553,718	37%	2428	26	0	0	120	107	42,002	137,223	MOD	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	UBA1609	
PHBVa_Gam13	0.9	9.9	9,746	4,407,078	51%	3912	78	0	7	48	43	274,108	658,540	MOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	UBA1124
PHBVa_Gam12	0.3	4.3	9,319	4,640,734	43%	4004	60	2	3	141	107	130,435	365,999	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	
PHBVa_Gam14	0.3	3.5	5,485	3,298,500	53%	2868	59	17	4	100	84	102,737	277,442	MOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	
PHBVa_Alp6	0.2	1.9	2,553	2,842,381	43%	2876	54	0	1	192	171	26,941	98,060	LOD	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Korarchaeaceae	GCA-2401685
PHBVa_Gam15	0.1	0.3	3,622	3,872,245	45%	3358	95	20	11	172	158	60,762	253,838	MOD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agarivytica

Supplementary Table 5 continued for plastisphere PHBvd.

MAG ID ^a	RpsC-based frequency (%) ^b	Averaged DNA coverage ^c	mRNA read per one million mapped read ^d	Genome size (bp)	GC content (%)	Numbers of ORF	ESTHER- assigned ORFs	PHB depolymerase	Poly-esterase	Number of contigs	Number of scaffolds	N50 scaffold (bp)	Longest scaffold (bp)	MAG QC ^e	Taxa ^f				
															Phylum	Class	Order	family	genus
PHBvd_Gam1	14.9	210.6	182,238	4,066,271	45%	3365	109	23	10	99	95	197,537	416,767	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agaritytica
PHBvGam3			130,529	4,107,637	45%	3274	105	22	10	10	10	775,086	1,509,955						
PHBvd_Gam2	9.7	134.5	53,080	3,453,275	45%	2924	70	13	4	36	32	603,584	774,499	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agaritytica
PHBvGam4			41,095	3,515,869	45%	2872	72	13	4	9	9	978,143	1,548,295						
PHBvd_Gam3	10.5	133.7	105,147	3,346,983	46%	2995	70	19	7	62	48	189,963	468,601	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	
PHBvGam5			74,174	3,407,865	46%	2935	70	19	7	30	30	345,501	554,887						
PHBvd_Alpl1	10.1	124.5	197	3,321,024	56%	3393	46	0	1	92	90	84,769	175,049	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteriaceae	Acetabacterium
PHBvd_Alpl2	6.3	95.6	43,531	2,503,170	43%	2432	33	0	0	25	24	661,166	669,445	HQD	Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	UBA1672
PHBvd_Gam6	5.9	81.4	96,800	4,012,246	45%	3393	98	19	11	78	75	122,949	319,321	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agaritytica
PHBvd_Gam5	5.0	68.2	38,729	4,698,842	48%	4068	107	0	4	45	43	192,179	877,294	HQD	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Marinicellaceae	Marinicella
PHBvd_Gam4	4.5	59.0	43,576	3,932,039	46%	3317	99	21	10	138	133	53,152	181,840	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agaritytica
PHBvd_Alpl3	4.2	54.6	213	3,829,835	56%	3762	61	0	1	15	15	753,061	1,651,231	HQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteriaceae	Halocythiobacter_B
PHBvd_Gam8	2.0	25.1	22,805	4,716,611	51%	4216	62	2	3	122	115	99,849	262,713	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Saccharosphaerales_A	Oceanobacter
PHBvd_Alpl6A	1.3	22.4	64	3,379,600	61%	3867	59	0	1	700	527	10,654	47,835	LQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteriaceae	Roseovarius
PHBvd_Alpl5	1.8	22.2	7,395	1,801,473	42%	1595	14	0	0	35	33	150,472	450,342	MQD	Proteobacteria	Alphaproteobacteria	Caedimonomadales	UBA9215	UBA9215
PHBvd_Gam7	1.6	21.9	9,633	3,889,404	50%	3383	88	14	7	82	74	123,232	497,375	MQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	Agaritytica
PHBvd_Alpl4	1.5	20.7	369	3,849,649	57%	3729	89	0	2	39	36	443,449	1,570,991	MQD	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Hyphomicrobiales	Henriciella
PHBvd_Alpl6B	3.1	20.6	92	2,967,299	62%	3341	50	0	1	632	530	9,092	99,002	LQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteriaceae	Albibacillus
PHBvd_Gam10	1.5	18.3	11,252	3,408,035	41%	3300	38	1	4	131	112	67,092	194,172	HQD	Proteobacteria	Gammaproteobacteria	UBA10353	UBA7415	
PHBvd_Act1	1.6	17.2	228	6,372,521	69%	6056	140	1	4	286	212	51,344	318,719	MQD	Actinobacteria	Acidimicrobia	Acidimicrobiales	SZUA-35	SZUA-35
PHBvd_De1	1.0	16.1	311	10,911,394	67%	8895	159	4	7	394	312	65,607	246,026	MQD	Myxococcota	Polyangia	Nannocystales	Nannocystaceae	
PHBvd_Gam9	1.2	14.1	7,211	4,906,880	48%	4325	79	2	9	136	123	88,232	314,401	LQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Celivibrionaceae	GCA-2707785

^a Seven active gammaproteoterial MAGs were manually refined, and the stats of the refined MAGs are shown below the original MAGs (orange colored).

^b Relative frequency within each plastisphere metagenome was calculated based on the coverage of rpsC genes for the MAGs per summed coverage of all rpsC genes in the metagenome. If rpsC gene was not coded in the MAG, the relative frequency was estimated from the averaged DNA coverage.

^c Averaged DNA coverage was calculated by averaged coverage of long scaffolds (>10 kbp) in each MAG.

^d Number of mRNA reads mapped to ORFs in each MAG was normalized per one million mapped mRNA reads to whole ORFs in the metagenome for each plastisphere RNAseq.

^e MAG QC was identified by MIMAG criteria that were shown in Supplementary Table S5. HQD, high quality draft; MQD, medium quality draft; LQD, low quality draft.

^f Taxonomy of each MAG was identified by GBD-B-tk program.

Supplementary Table 6 Summary of MAGs clustered from metagenomic assemblies of lab plastispheres.

MAG ID	Averaged DNA coverage ^a	Genome size (bp)	GC content (%)	Numbers of ORF	PHB depolymerase	Poly-esterase	Number of contigs	Number of scaffolds	N50 scaffold (bp)	Longest scaffold (bp)	MAG QC ^b	Taxa ^c				
												Phylum	Class	Order	family	genus
PBSlab_Alph1	245.8	3,449,783	51%	3063	1	1	25	22	318,961	1,215,023	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSlab_Gamm1	207.5	3,691,123	40%	3272	0	14	15	14	543,040	764,244	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellvibrionaceae	
PBSlab_Alph2	53.1	3,475,367	50%	3220	1	2	107	101	89,721	254,885	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSlab_Alph3	46.3	5,243,352	60%	5678	1	3	1170	716	13,842	56,643	LQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	
PBSlab_Act1	32.8	4,910,606	66%	5128	1	3	890	502	17,038	82,820	LQD	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	SZUA-35	SZUA-35
PBSlab_Alph4	25.4	2,343,035	44%	2306	2	1	27	20	240,864	376,695	MQD	Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	UBA1672
PBSlab_Alph5	17.2	3,616,088	57%	3591	0	2	133	76	98,958	330,808	HQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Henriciella
PBSlab_Gamm2	16.7	4,196,884	51%	3968	0	7	200	125	64,259	149,502	LQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	HTCC2089	UBA4582
PBSlab_Unc1	16.7	915,909	47%	921	0	0	59	41	36,066	138,113	MQD	Patescibacteria	Paceibacteria	UBA9983	UBA2163	OLB19
PBSlab_Beta1	10.2	2,471,495	42%	2592	0	1	538	422	8,965	30,435	LQD	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	Nitrosomonas
PBSlab_Unc2	9.1	720,211	39%	767	0	0	43	37	27,040	74,416	MQD	Patescibacteria	ABY1	UBA1544		
PBSlab_Alph6	9.0	1,534,012	46%	1746	0	1	232	174	11,361	36,336	LQD	Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	
PBSlab2_Alp1	297.4	3,441,880	51%	3047	1	1	17	17	441,823	665,840	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSlab2_Gam1	110.0	3,691,176	40%	3269	0	14	16	15	543,040	1,183,905	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellvibrionaceae	
PBSlab2_Act1	78.9	4,095,195	70%	4254	0	4	588	406	14,670	60,788	MQD	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	SZUA-35	SZUA-35
PBSlab2_Act2	51.7	4,135,838	66%	4036	1	5	314	207	54,651	119,102	MQD	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	SZUA-35	SZUA-35
PBSlab2_Act3	44.3	4,568,085	66%	4816	1	3	820	579	13,769	53,644	MQD	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	SZUA-35	SZUA-35
PBSlab2_Alp2	36.6	3,187,015	50%	2914	1	2	92	91	61,695	148,841	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAlab_Bac1	67.3	5,427,933	32%	4770	0	2	30	26	557,841	834,644	HQD	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Kordia
PBSAlab_Gam1	57.9	3,815,203	43%	3401	0	24	144	114	66,621	216,958	LQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellvibrionaceae	
PBSAlab_Alp2	55.6	2,925,311	42%	2895	0	0	456	346	14,308	56,503	MQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodomicrobiaceae	
PBSAlab_Alp1	49.0	4,423,455	44%	4167	4	3	108	79	120,661	231,901	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylogillaceae	
PBSAlab_Alp3	31.7	3,617,467	50%	3298	1	2	62	54	123,398	456,118	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAlab_Alp4	30.1	4,437,357	45%	4282	1	2	234	190	49,566	152,064	MQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAlab_Alp8	25.6	3,068,169	53%	2936	0	9	93	50	134,768	264,060	HQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hyphomonas
PBSAlab_Gam2	23.4	5,414,914	44%	4827	0	33	95	81	147,291	496,778	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellvibrionaceae	
PBSAlab_Alp5	23.4	3,435,019	51%	3089	1	1	43	34	300,271	475,939	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAlab_Gam4	23.4	3,729,265	45%	3553	0	2	30	30	215,037	362,691	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Nitrospiraceae	Neptunibacter
PBSAlab_Alp6	21.6	3,136,664	57%	3075	0	4	167	106	49,098	149,073	MQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia
PBSAlab_Alp7	17.2	3,579,823	64%	3747	0	3	535	334	16,380	51,949	LQD	Proteobacteria	Alphaproteobacteria	Minwuiaceae	Minwuiaceae	Minwui
PBSAlab_Gam3	15.0	4,327,662	41%	3849	2	5	231	183	40,034	128,313	MQD	Proteobacteria	Gammaproteobacteria	Enterobacterales	Kangielaceae	GCA-002733465
PBSAlab_Bac2	12.6	6,545,044	45%	5343	1	7	784	570	19,953	63,032	LQD	Bacteroidota	Bacteroidia	Chitinophagales	Saprospiraceae	Lewinella
PBSAlab_Bac3	11.3	9,805,420	43%	8156	2	9	1450	1068	14,474	65,588	MQD	Bacteroidota	Bacteroidia	Chitinophagales	Saprospiraceae	
PBSAlab_Pla1	11.2	7,203,590	50%	5967	0	11	382	294	38,721	171,811	MQD	Planctomycetota	Planctomycetes	Planctomycetales	Planctomycetaceae	Gimesia
PBSAlab2_Alp1	217.8	3,636,380	50%	3402	1	2	192	189	48,666	150,850	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAlab2_Alp2	86.9	4,430,241	44%	4162	4	3	86	62	187,893	493,381	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylogillaceae	
PBSAlab2_Plan1	85.0	3,807,608	68%	3061	0	0	21	16	509,649	786,985	HQD	Planctomycetota	Phycisphaerae	Phycisphaerales	SM1A02	UBA1926
PBSAlab2_Alp3	55.5	2,645,508	42%	2901	0	0	816	690	5,898	28,581	LQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodomicrobiaceae	
PBSAlab2_Gamm1	45.6	5,590,806	44%	5004	0	32	119	113	109,715	313,784	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellvibrionaceae	
PBSAlab2_Alp4	35.3	4,512,655	43%	4149	2	2	125	91	81,769	298,071	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylogillaceae	
PBSAlab2_Alp6	29.4	4,999,064	45%	4994	1	2	562	497	55,247	145,760	LQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylogillaceae	
PBSAlab2_Alp11	23.2	3,441,829	51%	3104	1	1	59	57	228,294	832,282	HQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	
PBSAlab2_Alp5	20.4	3,478,778	64%	3367	0	6	115	83	71,582	253,142	HQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	UBA7672
PBSAlab2_Alp8	20.0	3,142,411	54%	2951	0	9	17	15	338,455	597,831	HQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hyphomonas
PBSAlab2_Act1	17.6	4,786,913	66%	4837	1	3	535	361	20,318	85,803	MQD	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	SZUA-35	SZUA-35
PBSAlab2_Alp7	16.0	4,103,983	64%	3980	0	4	225	174	35,805	122,909	LQD	Proteobacteria	Alphaproteobacteria	Minwuiaceae	Minwuiaceae	Minwui
PBSAlab2_Act2	13.8	4,132,051	70%	4289	1	4	516	399	14,735	74,177	LQD	Actinobacteriota	Acidimicrobiia	Acidimicrobiales	SZUA-35	SZUA-35
PBSAlab2_Alp10	13.8	3,144,626	60%	3203	0	6	206	165	29,867	88,239	LQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Pseudococcicola
PBSAlab2_Alp9	13.0	3,004,181	57%	2956	0	6	186	160	35,784	79,877	LQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia
PHBVIab_Gamm1	393.9	3,634,917	49%	3067	21	5	41	37	225,967	490,056	HQD	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Cellvibrionaceae	Agarilitica
PHBVIab_Gamm2	77.6	4,519,051	41%	4015	2	5	395	319	25,600	138,839	HQD	Proteobacteria	Gammaproteobacteria	Enterobacterales	Kangielaceae	GCA-002733465
PHBVIab_Alp1	48.1	6,056,619	59%	5870	0	2	414	279	41,741	154,974	MQD	Proteobacteria	Alphaproteobacteria	Rhizobiales	Stappiaceae	Roseibium
PHBVIab_Uncb1	30.2	1,397,995	38%	1320	0	0	19	14	357,676	529,685	MQD	Dependentiae	Babeliae	Babeliales	Vermiphilaceae	
PHBVIab_Plan1	29.9	2,288,908	61%	2068	0	0	182	181	20,105	57,515	LQD	Planctomycetota	Phycisphaerae	Phycisphaerales	SM1A02	UBA1924
PHBVIab_Alp3	26.9	3,281,979	45%	3048	0	4	110	78	72,616	149,619	HQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia
PHBVIab_Alp2	25.1	3,491,024	45%	3424	0	3	117	95	80,873	288,502	HQD	Proteobacteria	Alphaproteobacteria	Sneathiellales	Sneathiellaceae	Sneathiella
PHBVIab_Alp4	15.7	2,795,802	43%	2795	0	2	129	118	72,468	172,584	MQD	Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	UBA1672
PHBVIab_Chla1	11.4	2,302,322	42%	2042	0	2	66	56	73,306	246,964	HQD	Verrucomicrobiota_A	Chlamydia	Parachlamydiales	Waddliaceae	Waddlia
PHBVIab_Alp5	10.6	3,220,661	45%	3179	0	2	224	171	36,209	156,239	LQD	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia
PLAlab_Alph1	195.9	5,040,314	60%	5833	1	3	1523	880	9,536	69,044	LQD	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	
PLAlab_Beta1	112.2	2,9														

Supplementary Table 7 Minimum Information about a Metagenome-Assembled Genome (MIMAG)

MAG Name	MAG classification	Completeness ^a	Contamination ^a	Heterogeneity ^a	No. of tRNAs	No. of tRNA missing	5 S	16 S	23 S	Marker Lineage ^a	No. Markers ^a	0 ^a	1 ^a	2 ^a	3+ ^a
PBSAgamm1	Refined MAG ^b	98.6	0.6	0.0	37	0	Y	Y	Y	c_Gammaproteobacteria	507	4	500	3	0
PBSAgamm2	Refined MAG ^b	99.6	0.1	0.0	53	0	Y	Y	Y	o_Oceanospirillales	529	1	526	2	0
PHBVgamm1	Refined MAG ^b	100.0	1.4	0.0	36	0	Y	Y	Y	c_Gammaproteobacteria	507	0	503	4	0
PHBVgamm2	Refined MAG ^b	99.4	0.3	0.0	47	1	Y	Y	Y	c_Gammaproteobacteria	505	2	501	1	1
PHBVgamm3	Refined MAG ^b	100.0	1.3	0.0	34	1	Y	N	N	c_Gammaproteobacteria	507	0	504	3	0
PHBVgamm4	Refined MAG ^b	100.0	0.4	0.0	36	0	Y	Y	Y	c_Gammaproteobacteria	507	1	505	1	0
PHBVgamm5	Refined MAG ^b	99.6	0.6	0.0	45	0	N	N	N	c_Gammaproteobacteria	451	1	448	2	0
PBSd_Act1	Medium Quality Draft	91.5	7.7	20.0	42	0	Y	N	N	k_Bacteria	171	17	137	13	4
PBSd_Al1	Medium Quality Draft	95.3	2.9	0.0	42	0	N	N	N	o_Rhodospirillales	336	11	309	15	1
PBSd_Al2	High Quality Draft	97.1	1.1	33.3	38	3	Y	N	N	f_Rhodobacteraceae	582	16	560	6	0
PBSd_Al3	Low Quality Draft	90.9	3.8	10.5	28	4	N	N	N	o_Rhizobiales	413	46	348	19	0
PBSd_Bet1	Low Quality Draft	92.1	3.9	41.7	28	3	Y	N	N	k_Bacteria	104	8	84	12	0
PBSd_Gam1	High Quality Draft	98.6	0.9	0.0	38	0	Y	Y	Y	c_Gammaproteobacteria	507	4	498	5	0
PBSd_Gam2	High Quality Draft	98.6	0.7	25.0	49	2	N	Y	N	o_Oceanospirillales	529	4	521	4	0
PBSd_Gam3	Medium Quality Draft	91.6	3.6	6.7	22	7	N	N	N	c_Gammaproteobacteria	507	47	445	15	0
PBSd_Gam4	Low Quality Draft	98.3	19.8	10.7	37	4	Y	N	N	k_Bacteria	104	1	75	28	0
PBSd_Gam5	Low Quality Draft	92.4	2.5	14.3	25	4	Y	N	N	c_Gammaproteobacteria	544	34	496	14	0
PBSd_Thau1	Medium Quality Draft	89.3	3.9	0.0	42	1	Y	N	N	k_Archaea	145	13	128	4	0
PBSd_Thau2	Low Quality Draft	86.7	8.7	35.7	38	3	Y	Y	Y	k_Archaea	145	22	113	8	2
PBSd_Thau3	Low Quality Draft	77.2	8.8	72.7	31	4	Y	N	N	k_Archaea	145	35	99	11	0
PBSAa_Al1	High Quality Draft	97.4	0.0	0.0	41	2	Y	N	N	f_Rhodobacteraceae	582	10	572	0	0
PBSAa_Al2	High Quality Draft	99.3	2.2	18.2	41	1	N	N	N	f_Rhodobacteraceae	616	3	602	11	0
PBSAa_Al3	High Quality Draft	99.4	1.2	0.0	40	1	Y	N	N	f_Rhodobacteraceae	654	2	647	4	1
PBSAa_Al4	High Quality Draft	99.3	0.7	100.0	38	2	Y	N	N	f_Rhodobacteraceae	582	3	576	3	0
PBSAa_Al5	Medium Quality Draft	94.8	0.6	0.0	32	1	Y	N	N	c_Alphaproteobacteria	349	15	332	2	0
PBSAa_Al6	Low Quality Draft	90.2	1.2	0.0	37	1	Y	N	N	f_Rhodobacteraceae	582	75	500	7	0
PBSAa_Al7	Medium Quality Draft	92.9	0.7	40.0	32	4	N	N	N	f_Rhodobacteraceae	582	56	521	5	0
PBSAa_Al8	High Quality Draft	98.1	0.0	100.0	31	2	N	N	N	c_Alphaproteobacteria	529	6	522	1	0
PBSAa_Al9	Medium Quality Draft	95.6	2.5	41.2	34	3	N	N	N	f_Rhodobacteraceae	582	29	536	17	0
PBSAa_Bac1	Medium Quality Draft	99.5	3.0	0.0	45	2	Y	N	N	p_Bacteroidetes	302	1	294	7	0
PBSAa_Gam1 ^b	High Quality Draft	98.6	0.6	0.0	35	0	Y	Y	Y	c_Gammaproteobacteria	507	4	500	3	0
PBSAa_Gam2 ^b	High Quality Draft	99.6	0.1	0.0	53	1	Y	Y	Y	o_Oceanospirillales	529	1	526	2	0
PBSAa_Gam3 ^b	High Quality Draft	98.2	0.6	0.0	37	0	Y	Y	Y	p_Proteobacteria	261	3	256	1	1
PBSAd_Act1	Medium Quality Draft	99.2	3.0	25.0	45	0	Y	N	N	k_Bacteria	171	1	166	4	0
PBSAd_Al1	High Quality Draft	99.9	0.4	0.0	39	1	Y	Y	N	o_Rhizobiales	413	1	410	2	0
PBSAd_Al2	High Quality Draft	97.1	0.0	0.0	36	1	N	N	N	f_Rhodobacteraceae	616	18	598	0	0
PBSAd_Al3	Medium Quality Draft	98.9	4.6	6.3	41	1	Y	N	N	f_Rhodobacteraceae	616	5	579	32	0
PBSAd_Al4	High Quality Draft	96.2	0.9	25.0	39	1	Y	N	N	f_Rhodobacteraceae	582	19	559	4	0
PBSAd_Al5	Medium Quality Draft	95.9	2.8	35.0	38	3	N	N	N	f_Rhodobacteraceae	582	30	532	20	0
PBSAd_Al6	Medium Quality Draft	93.1	1.3	0.0	41	3	N	Y	N	o_Rhizobiales	416	29	383	4	0
PBSAd_Bac1	High Quality Draft	96.6	1.1	0.0	36	1	N	N	N	k_Bacteria	147	4	142	1	0
PBSAd_Bet1	High Quality Draft	99.4	1.4	0.0	43	0	Y	Y	N	p_Proteobacteria	259	1	255	1	2
PBSAd_Del1	Low Quality Draft	87.8	12.9	3.6	80	1	Y	N	N	c_Deltaproteobacteria	247	29	198	16	4
PBSAd_Gam1	High Quality Draft	98.5	0.6	0.0	35	0	Y	Y	Y	c_Gammaproteobacteria	507	5	499	3	0
PBSAd_Gam2	High Quality Draft	99.6	0.9	0.0	53	0	Y	Y	Y	o_Oceanospirillales	529	1	524	4	0
PHBVa_Al1	High Quality Draft	99.6	0.3	33.3	35	0	Y	Y	Y	c_Alphaproteobacteria	529	2	524	3	0
PHBVa_Al2	High Quality Draft	99.0	1.4	0.0	44	1	Y	Y	Y	f_Rhodobacteraceae	654	5	641	8	0
PHBVa_Al3	High Quality Draft	98.1	1.1	62.5	32	1	N	N	N	c_Alphaproteobacteria	529	12	513	2	2
PHBVa_Al4	Medium Quality Draft	96.3	1.2	0.0	37	3	Y	N	N	o_Rhodospirillales	336	23	310	3	0
PHBVa_Al5	Low Quality Draft	87.5	6.0	74.3	42	0	Y	N	Y	f_Rhodobacteraceae	625	60	534	29	2
PHBVa_Al6	Low Quality Draft	86.5	2.2	14.3	27	6	N	N	N	c_Alphaproteobacteria	349	37	305	7	0
PHBVa_Bac1	High Quality Draft	99.5	2.0	0.0	48	1	Y	N	Y	p_Bacteroidetes	302	1	297	4	0
PHBVa_Gam1 ^b	High Quality Draft	97.4	3.3	80.0	37	0	Y	Y	Y	c_Gammaproteobacteria	507	8	479	20	0
PHBVa_Gam2 ^b	High Quality Draft	99.4	0.3	0.0	47	1	Y	Y	Y	c_Gammaproteobacteria	505	3	500	1	1
PHBVa_Gam3	High Quality Draft	98.8	0.0	0.0	40	1	N	N	N	p_Proteobacteria	261	2	259	0	0
PHBVa_Gam4	Low Quality Draft	90.4	1.2	33.3	28	5	N	N	N	c_Gammaproteobacteria	507	76	423	6	2
PHBVa_Gam5	High Quality Draft	98.6	1.6	42.9	33	4	N	N	N	c_Gammaproteobacteria	507	33	467	7	0
PHBVa_Gam6	High Quality Draft	100.0	2.0	0.0	35	2	N	N	N	c_Gammaproteobacteria	503	0	495	8	0
PHBVa_Gam7	Low Quality Draft	86.8	5.0	35.7	31	4	N	N	N	c_Gammaproteobacteria	507	71	408	28	0
PHBVa_Gam8	High Quality Draft	100.0	2.9	6.7	42	1	Y	N	N	o_Oceanospirillales	529	0	514	15	0
PHBVa_Gam9	Medium Quality Draft	98.6	4.9	10.0	34	3	Y	N	N	c_Gammaproteobacteria	503	9	474	20	0
PHBVa_Gam10	Medium Quality Draft	91.1	1.3	33.3	32	0	N	Y	Y	c_Gammaproteobacteria	544	36	502	6	0
PHBVa_Gam11	Low Quality Draft	91.9	7.5	16.7	34	1	Y	N	N	c_Gammaproteobacteria	507	60	411	36	0
PHBVa_Gam12	High Quality Draft	98.1	1.6	50.0	42	1	Y	Y	N	c_Gammaproteobacteria	507	8	493	6	0
PHBVa_Gam13	Medium Quality Draft	99.3	2.8	0.0	27	6	N	N	N	c_Gammaproteobacteria	507	5	492	9	1
PHBVa_Gam14	Medium Quality Draft	96.4	1.6	44.4	26	5	N	N	N	c_Gammaproteobacteria	507	25	473	9	0
PHBVa_Gam15	Medium Quality Draft	94.9	1.9	12.5	26	4	Y	N	N	c_Gammaproteobacteria	507	30	469	8	0
PHBVa_Gam16	Low Quality Draft	93.8	1.5	16.7	18	8	N	N	N	c_Gammaproteobacteria	507	50	451	6	0
PHBVa_Gam17	Low Quality Draft	68.9	1.9	100.0	14	11	N	N	N	k_Bacteria	104	55	47	2	0
PHBVa_Gam18	Medium Quality Draft	96.7	3.4	6.7	53	0	N	N	N	c_Gammaproteobacteria	312	10	287	15	0
PHBVa_Olig1	Medium Quality Draft	92.3	3.6	25.0	22	5	Y	N	N	k_Bacteria	182	21	157	4	0
PHBVa_Pla1	High Quality Draft	94.3	0.0	0.0	35	1	Y	N	N	k_Bacteria	143	5	138	0	0
PHBVd_Act1	Medium Quality Draft	97.0	3.4	0.0	43	0	N	N	N	k_Bacteria	171	5	161	5	0
PHBVd_Al1	High Quality Draft	98.9	0.5	50.0	33	2	Y	N	N	f_Rhodobacteraceae	617	7	608	2	0
PHBVd_Al2	High Quality Draft	94.8	0.4	0.0	32	1	Y	N	N	c_Alphaproteobacteria	349	15	333	1	0
PHBVd_Al3	High Quality Draft	99.3	0.7	0.0	36	1	Y	N	N	f_Rhodobacteraceae	617	3	608	6	0
PHBVd_Al4	Medium Quality Draft	99.0	1.6	0.0	36	4	Y	N	N	c_Alphaproteobacteria	529	5	519	4	1
PHBVd_Al5	Medium Quality Draft	95.2	0.0	0.0	35	3	Y	N	N	k_Bacteria	152	6	146	0	0
PHBVd_Al6A	Low Quality Draft	75.2	7.1	20.9	21	6	N	N	N	f_Rhodobacteraceae	654	164	449	40	1
PHBVd_Al6B	Low Quality Draft	57.3	14.5	28.6	9	14	N	N	N	k_Bacteria	104	32	50	19	3
PHBVd_Del1	Medium Quality Draft	94.3	2.7	0.0	44	0	N	N	N	c_Deltaproteobacteria	247	16	226	5	0
PHBVd_Gam1 ^b	High Quality Draft	99.9	2.0	62.5	33	2	Y	N	N	c_Gammaproteobacteria	507	1	498	8	0
PHBVd_Gam2 ^b	High Quality Draft	100.0	0.4	0.0	36	0	Y	Y	Y	c_Gammaproteobacteria	507	1	505	1	0
PHBVd_Gam3 ^b	High Quality Draft	99.6	0.6	0.0	45	0	Y	Y	Y	c_Gammaproteobacteria	451	1	448	2	0
PHBVd_Gam4	High Quality Draft	98.4	1.0	0.0	31	2	N	N	N	c_Gammaproteobacteria	507	16	487	4	0
PHBVd_Gam5	High Quality Draft	98.5	2.3	0.0	65	0	Y	N	Y	c_Gammaproteobacteria	481	7	465	9	0
PHBVd_Gam6	High Quality Draft	97.9	0.6	33.3	31	1	N	N	N	c_Gammaproteobacteria	507	20	484	3	0
PHBVd_Gam7	Medium Quality Draft	99.9	1.4	50.0	29	3	N	N	N	c_Gammaproteobacteria	507	2	501	4	0
PHBVd_Gam8	High Quality Draft	98.1	0.8	0.0	45	1	N	Y	N	c_Gammaproteobacteria	505	6	496	2	1
PHBVd_Gam9	Low Quality Draft	98.6	1.8	0.0	23	7	N	N	N	c_Gammaproteobacteria	507	8	491	8	0
PHBVd_Gam10	High Quality Draft	98.1	1.8	0.0	36	2	Y	N	N	p_Proteobacteria	261	6	250	5	0

Supplementary Table 7 Continued

MAG Name	MAG classification	Completeness ^a	Contamination ^a	Heterogeneity ^a	No. of tRNAs	No. of tRNA missing	5 S	16 S	23 S	Marker Lineage ^a	No. Markers ^a	0 ^a	1 ^a	2 ^a	3+ ^a
PBSlab_Act1	Low Quality Draft	95.5	22.5	40.9	45	1	Y	Y	N	k_Bacteria	104	4	54	36	10
PBSlab_Alp1	High Quality Draft	99.9	0.8	0.0	40	0	Y	Y	Y	o_Rhizobiales	413	1	409	3	0
PBSlab_Alp2	High Quality Draft	98.7	0.6	0.0	35	2	Y	N	N	o_Rhizobiales	413	6	405	2	0
PBSlab_Alp3	Low Quality Draft	87.4	1.7	14.3	38	0	Y	Y	Y	c_Alphaproteobacteria	388	41	340	7	0
PBSlab_Alp4	Medium Quality Draft	94.8	1.7	20.0	30	2	Y	N	N	c_Alphaproteobacteria	349	15	329	5	0
PBSlab_Alp5	High Quality Draft	97.1	2.9	0.0	34	1	Y	N	N	c_Alphaproteobacteria	529	19	492	18	0
PBSlab_Alp6	Low Quality Draft	69.3	1.3	20.0	17	8	N	N	N	c_Alphaproteobacteria	349	104	240	5	0
PBSlab_Bet1	Low Quality Draft	92.7	3.7	16.0	19	6	Y	N	N	c_Betaproteobacteria	413	31	357	25	0
PBSlab_Gam1	High Quality Draft	98.6	0.6	0.0	32	1	N	N	N	c_Gammaproteobacteria	507	4	500	3	0
PBSlab_Gam2	Low Quality Draft	94.8	4.5	0.0	28	4	N	N	N	c_Gammaproteobacteria	451	21	411	17	2
PBSlab_Unc1	Medium Quality Draft	68.0	1.0	0.0	32	3	Y	Y	N	k_Bacteria	151	40	110	1	0
PBSlab_Unc2	Medium Quality Draft	50.5	0.0	0.0	24	4	N	N	N	k_Bacteria	151	61	90	0	0
PBSlab2_Act1	Medium Quality Draft	93.2	3.4	11.1	40	1	Y	Y	Y	k_Bacteria	171	8	154	9	0
PBSlab2_Act2	Medium Quality Draft	98.0	2.7	20.0	41	0	Y	N	N	k_Bacteria	171	4	162	5	0
PBSlab2_Act3	Medium Quality Draft	90.6	2.6	0.0	38	0	Y	Y	Y	k_Bacteria	171	16	151	4	0
PBSlab2_Alp1	High Quality Draft	99.9	0.8	0.0	44	0	Y	Y	Y	o_Rhizobiales	413	1	409	3	0
PBSlab2_Alp2	High Quality Draft	98.5	0.9	50.0	35	1	Y	N	N	o_Rhizobiales	413	7	402	4	0
PBSlab2_Gam1	High Quality Draft	98.6	0.6	0.0	33	1	N	N	N	c_Gammaproteobacteria	507	4	500	3	0
PBSAlab_Alp1	High Quality Draft	98.5	2.3	0.0	37	1	N	N	N	o_Rhizobiales	416	5	404	7	0
PBSAlab_Alp2	Medium Quality Draft	89.8	0.8	33.3	31	1	N	N	N	o_Rhizobiales	416	41	372	3	0
PBSAlab_Alp3	High Quality Draft	99.1	3.4	18.2	39	1	N	N	N	o_Rhizobiales	413	6	396	11	0
PBSAlab_Alp4	Medium Quality Draft	94.0	3.0	0.0	36	3	N	N	N	o_Rhizobiales	416	21	385	10	0
PBSAlab_Alp5	High Quality Draft	96.4	0.6	0.0	37	0	N	N	N	o_Rhizobiales	413	12	399	2	0
PBSAlab_Alp6	Medium Quality Draft	92.3	2.2	0.0	35	1	N	N	N	c_Alphaproteobacteria	529	33	487	9	0
PBSAlab_Alp7	Low Quality Draft	80.5	3.2	8.3	28	5	N	N	N	c_Alphaproteobacteria	349	60	279	9	1
PBSAlab_Alp8	High Quality Draft	97.2	1.5	12.5	32	3	N	N	N	c_Alphaproteobacteria	529	14	507	8	0
PBSAlab_Bac1	High Quality Draft	99.6	1.6	0.0	55	0	N	N	N	s_algicola	571	2	559	10	0
PBSAlab_Bac2	Low Quality Draft	93.5	4.1	0.0	35	2	N	N	N	p_Bacteroidetes	300	14	276	10	0
PBSAlab_Bac3	Medium Quality Draft	94.1	3.1	18.2	30	1	N	N	N	p_Bacteroidetes	298	16	271	11	0
PBSAlab_Gam1	Low Quality Draft	97.2	0.9	0.0	23	5	N	N	N	c_Gammaproteobacteria	507	13	492	2	0
PBSAlab_Gam2	High Quality Draft	97.4	1.3	0.0	44	3	N	N	N	c_Gammaproteobacteria	507	8	493	5	1
PBSAlab_Gam3	Medium Quality Draft	94.1	1.6	0.0	46	0	N	N	N	c_Gammaproteobacteria	312	28	281	3	0
PBSAlab_Gam4	High Quality Draft	99.6	0.5	0.0	56	0	N	N	N	o_Oceanospirillales	529	20	507	2	0
PBSAlab_Pla1	Medium Quality Draft	98.9	6.9	12.5	57	0	N	N	N	k_Bacteria	146	1	139	5	1
PBSAlab2_Act1	Medium Quality Draft	94.9	3.4	0.0	38	1	Y	N	N	k_Bacteria	171	7	159	5	0
PBSAlab2_Act2	Low Quality Draft	84.5	1.4	0.0	44	1	Y	N	N	k_Bacteria	171	31	137	3	0
PBSAlab2_Alp1	High Quality Draft	99.0	0.9	50.0	36	3	Y	Y	N	o_Rhizobiales	413	6	403	4	0
PBSAlab2_Alp2	High Quality Draft	96.5	1.9	0.0	37	1	N	N	N	o_Rhizobiales	416	11	399	6	0
PBSAlab2_Alp3	Low Quality Draft	84.9	1.4	28.6	27	6	N	N	N	o_Rhizobiales	416	59	350	7	0
PBSAlab2_Alp4	High Quality Draft	97.6	1.5	0.0	37	2	N	N	N	o_Rhizobiales	416	8	403	5	0
PBSAlab2_Alp5	High Quality Draft	97.3	0.3	50.0	39	2	Y	N	N	c_Alphaproteobacteria	529	14	513	2	0
PBSAlab2_Alp6	Low Quality Draft	98.0	13.6	15.6	43	2	N	N	N	o_Rhizobiales	416	8	362	37	9
PBSAlab2_Alp7	Low Quality Draft	90.9	4.0	53.9	36	3	N	N	N	c_Alphaproteobacteria	349	24	312	13	0
PBSAlab2_Alp8	High Quality Draft	98.4	0.3	50.0	32	3	Y	N	N	c_Alphaproteobacteria	529	5	522	2	0
PBSAlab2_Alp9	Low Quality Draft	87.9	3.3	0.0	28	2	Y	Y	Y	c_Alphaproteobacteria	529	69	442	18	0
PBSAlab2_Alp10	Low Quality Draft	86.7	1.4	10.0	30	8	N	N	N	f_Rhodobacteraceae	654	99	545	10	0
PBSAlab2_Alp11	High Quality Draft	99.9	2.0	25.0	39	0	Y	N	N	o_Rhizobiales	413	1	406	5	1
PBSAlab2_Gam1	High Quality Draft	97.7	2.1	0.0	59	0	N	N	N	c_Gammaproteobacteria	507	8	491	7	1
PBSAlab2_Pla1	High Quality Draft	94.9	1.1	0.0	46	0	Y	Y	Y	k_Bacteria	143	5	137	1	0
PHBVIab_Alp1	Medium Quality Draft	94.8	0.5	0.0	36	3	N	N	N	o_Rhizobiales	484	22	460	2	0
PHBVIab_Alp2	High Quality Draft	95.3	1.9	0.0	31	1	N	N	N	c_Alphaproteobacteria	349	16	327	6	0
PHBVIab_Alp3	High Quality Draft	97.0	0.1	0.0	31	1	N	N	N	c_Alphaproteobacteria	529	11	517	1	0
PHBVIab_Alp4	Medium Quality Draft	95.0	5.3	9.1	34	0	Y	N	N	c_Alphaproteobacteria	349	15	312	22	0
PHBVIab_Alp5	Low Quality Draft	93.5	0.4	0.0	24	4	N	N	N	c_Alphaproteobacteria	529	48	478	3	0
PHBVIab_Ch1	High Quality Draft	97.5	0.7	0.0	32	2	N	N	N	k_Bacteria	230	6	223	1	0
PHBVIab_Gam1	High Quality Draft	100.0	1.9	0.0	35	1	Y	Y	Y	c_Gammaproteobacteria	507	0	502	4	1
PHBVIab_Gam2	High Quality Draft	98.8	1.4	25.0	41	1	Y	N	N	c_Gammaproteobacteria	312	3	305	4	0
PHBVIab_Pla1	Low Quality Draft	85.8	1.7	50.0	29	1	N	Y	Y	k_Bacteria	143	16	125	2	0
PHBVIab_Unc1	Medium Quality Draft	60.0	1.2	0.0	32	1	Y	N	N	k_Bacteria	338	112	223	3	0
PLAlab_Alp1	Low Quality Draft	82.7	2.6	66.7	39	1	N	N	N	c_Alphaproteobacteria	388	72	307	9	0
PLAlab_Alp2	Low Quality Draft	86.3	0.3	50.0	37	3	Y	N	N	c_Alphaproteobacteria	349	46	301	2	0
PLAlab_Alp3	Low Quality Draft	92.8	4.9	0.0	32	4	N	N	N	f_Rhodobacteraceae	582	35	522	24	1
PLAlab_Alp4	Low Quality Draft	85.8	0.4	0.0	19	6	N	N	N	o_Rhizobiales	416	56	359	1	0
PLAlab_Alp5	Low Quality Draft	79.5	7.8	2.3	44	2	N	N	N	c_Alphaproteobacteria	529	91	398	38	2
PLAlab_Alp6	Low Quality Draft	55.6	0.4	0.0	16	8	Y	N	N	o_Rhizobiales	413	182	230	1	0
PLAlab_Alp7	Low Quality Draft	76.8	5.6	0.0	23	8	Y	N	N	c_Alphaproteobacteria	388	106	267	14	1
PLAlab_Alp8	Low Quality Draft	83.9	9.7	2.9	36	1	N	N	N	c_Alphaproteobacteria	388	67	287	34	0
PLAlab_Bet1	High Quality Draft	96.5	0.7	25.0	31	1	Y	N	N	c_Betaproteobacteria	413	11	398	4	0
PLAlab_Bet2	High Quality Draft	98.9	0.5	50.0	34	1	N	N	N	c_Betaproteobacteria	413	6	405	2	0
PLAlab_Bet3	Low Quality Draft	91.3	5.0	0.0	25	5	N	N	N	c_Betaproteobacteria	413	36	352	25	0
PLAlab_Bet4	Low Quality Draft	92.1	49.4	26.0	32	5	N	N	N	k_Bacteria	103	6	46	40	11
PLAlab_Bet5	Low Quality Draft	83.5	41.0	77.4	18	8	Y	N	N	k_Bacteria	104	11	49	38	6
PLAlab_Ch1	High Quality Draft	96.0	0.7	0.0	35	2	Y	N	N	k_Bacteria	230	7	222	1	0
PLAlab_Ch2	Medium Quality Draft	94.4	0.0	0.0	31	2	Y	N	N	k_Bacteria	230	11	219	0	0
PLAlab_Del1	Medium Quality Draft	90.4	2.6	0.0	35	2	N	N	N	k_Bacteria	188	26	158	4	0
PLAlab_Gam1	High Quality Draft	99.3	3.0	7.7	36	2	N	N	N	c_Gammaproteobacteria	543	3	518	20	2
PLAlab_Gam2	Low Quality Draft	90.4	3.4	0.0	14	9	Y	N	N	c_Gammaproteobacteria	312	27	278	7	0
PLAlab_Pla1	Medium Quality Draft	91.1	4.6	11.1	34	1	Y	N	N	k_Bacteria	102	7	77	18	0
PLAlab_Pla2	Medium Quality Draft	91.7	3.3	0.0	49	1	Y	N	N	k_Bacteria	146	10	133	3	0
PLAlab_Pla3	Low Quality Draft	91.5	6.6	12.5	32	2	Y	N	N	k_Bacteria	140	28	104	8	0
PLAlab_Pla4	Low Quality Draft	77.9	0.0	0.0	27	3	Y	N	N	k_Bacteria	140	28	112	0	0
PLAlab_Unc1	Medium Quality Draft	55.7	1.2	0.0	29	3	N	Y	N	k_Bacteria	338	126	209	3	0
PLAlab_Ver1	Medium Quality Draft	98.3	9.9	96.4	34	3	N	N	N	k_Bacteria	104	1	75	28	0
PLAlab_Ver2	Low Quality Draft	86.2	1.4	0.0	31	4	N	N	N	k_Bacteria	230	50	178	2	0
PLAlab_Ver3	High Quality Draft	98.7	5.7	0.0	39	2	N	N	N	k_Bacteria	230	2	213	14	1

^a Genome completeness, contamination, and heterogeneity were analyzed by using CheckM software.^b Seven Gammaproteobacterial MAGs with high mRNA expression were manually refined.

Supplementary Table 8 Analysis of dDDH of the Gammaproteobacterial MAGs referred to refined seven MAGs.

MAGs ^a	Plastic sphere		Order	family	genus	GC%	Genome size (bp)	Genome completeness (%)	Reference refined MAGs						
	PHBVa	PHBVd							PBSAa	PBSAd	PBSd	PHBVgamm3	PHBVgamm1	PHBVgamm4	PBSAgamm1
PHBVgamm3			Pseudomonadales	Cellvibrionaceae	Agarilytica	45.4%	4,107,637	100.0	-	23.5	19.2	24.8	23.7	24.5	32.6
PHBVgamm1			Pseudomonadales	Cellvibrionaceae	Agarilytica	45.9%	4,320,852	100.0	23.5	-	19.9	24.5	20.1	20.7	30.0
PHBVd_Gam4			Pseudomonadales	Cellvibrionaceae	Agarilytica	46.0%	3,932,039	98.4	23.4	91.7	19.0	18.7	17.6	16.6	38.5
PHBVa_Gam15			Pseudomonadales	Cellvibrionaceae	Agarilytica	44.8%	3,872,245	94.9	25.4	24.4	19.0	18.7	23.2	20.7	63.9
PHBVd_Gam6			Pseudomonadales	Cellvibrionaceae	Agarilytica	45.1%	4,012,246	97.9	25.5	24.6	18.5	19.6	17.7	16.2	33.0
PHBVa_Gam11			Pseudomonadales	Cellvibrionaceae	Agarilytica	45.9%	4,176,949	91.9	18.4	18.5	18.9	20.1	17.4	18.4	43.0
PHBVd_Gam7			Pseudomonadales	Cellvibrionaceae	Agarilytica	50.1%	3,889,404	99.9	17.4	17.6	18.2	18.3	17.5	21.3	20.7
PHBVgamm4			Pseudomonadales	Cellvibrionaceae	Agarilytica	45.4%	3,515,869	100.0	19.2	19.9	-	31.3	25.5	25.1	19.8
PHBVa_Gam12			Pseudomonadales	Cellvibrionaceae		42.9%	4,640,734	98.1	18.7	22.6	19.3	21.0	19.6	20.5	19.5
PBSd_Gam1			Pseudomonadales	Cellvibrionaceae		40.5%	3,679,901	98.6	19.7	27.2	28.0	21.8	23.9	36.9	58.3
PBSAgamm1			Pseudomonadales	Cellvibrionaceae		40.2%	3,679,316	98.6	24.8	24.5	31.3	-	29.4	28.2	32.5
PBSAd_Gam1			Pseudomonadales	Cellvibrionaceae		40.2%	3,681,281	98.5	23.7	23.3	30.5	100.0	28.6	26.1	30.4
PBSd_Gam3			Pseudomonadales	Cellvibrionaceae		40.7%	3,296,942	91.6	16.2	16.7	15.9	17.6	16.9	16.6	66.4
PHBVa_Gam14			Pseudomonadales	Cellvibrionaceae		53.1%	3,298,500	96.4	21.2	23.1	18.8	17.7	19.2	22.1	20.4
PHBVa_Gam13			Pseudomonadales	Cellvibrionaceae	UBA1124	51.4%	4,407,078	99.3	16.5	16.7	24.1	17.6	16.6	16.9	16.8
PHBVa_Gam7			Pseudomonadales	Cellvibrionaceae	GCA-2707785	48.4%	4,108,098	86.8	17.0	17.4	17.6	16.9	18.4	18.1	19.0
PHBVd_Gam9			Pseudomonadales	Cellvibrionaceae	GCA-2707785	48.2%	4,906,880	98.6	18.8	18.1	19.7	16.1	17.8	16.8	18.4
PHBVa_Gam5			Pseudomonadales	Cellvibrionaceae	GCA-2707785	48.8%	4,441,111	98.6	17.3	17.2	17.8	19.6	18.7	17.3	20.3
PHBVa_Gam17			Pseudomonadales	Cellvibrionaceae	GCA-2707785	49.2%	4,192,559	68.9	21.2	19.3	15.9	21.3	23.0	19.6	23.5
PHBVa_Gam4			Pseudomonadales	Cellvibrionaceae	GCA-2707785	49.8%	4,155,562	90.4	17.6	16.7	18.4	19.8	18.5	19.4	18.4
PHBVa_Gam16			Pseudomonadales	Cellvibrionaceae		46.2%	3,180,293	93.8	26.9	17.2	22.6	25.1	88.0	18.9	28.0
PHBVgamm5			Pseudomonadales	Cellvibrionaceae		46.0%	3,407,865	99.6	23.7	20.1	25.5	29.4	-	23.5	24.3
PHBVa_Gam9			Pseudomonadales	Spongibacteraceae		45.5%	5,811,666	98.6	18.3	19.5	18.4	18.6	34.2	19.8	23.0
PHBVa_Gam6			Pseudomonadales	Spongibacteraceae		46.1%	4,593,365	100.0	17.3	18.0	16.7	14.8	16.4	16.4	16.6
PHBVgamm2			Pseudomonadales	Saccharospirillaceae_A	Oceanobacter	52.8%	3,589,484	99.4	24.5	20.7	25.1	28.2	23.5	-	20.4
PHBVd_Gam8			Pseudomonadales	Saccharospirillaceae_A	Oceanobacter	51.0%	4,716,611	98.1	26.9	27.6	27.3	36.0	21.5	21.0	18.8
PHBVa_Gam8			Pseudomonadales	Nitirincloaceae	Neptunomonas	46.3%	3,686,882	100.0	25.2	15.9	17.8	42.4	19.4	19.4	18.7
PBSAd_Gam2			Pseudomonadales	Nitirincloaceae	Neptunibacter	45.5%	3,490,073	99.6	21.8	20.1	19.7	35.1	23.4	19.7	45.4
PBSd_Gam2			Pseudomonadales	Nitirincloaceae	Neptunibacter	45.6%	3,680,247	98.6	33.1	30.5	17.9	29.4	21.7	19.0	99.7
PBSAgamm2			Pseudomonadales	Nitirincloaceae	Neptunibacter	45.6%	3,794,966	99.6	32.6	30.0	19.8	32.5	24.3	20.4	-
PHBVa_Gam18			Enterobacteriales	Kangiellaceae	GCA-002733465	40.9%	4,541,327	96.7	22.6	18.3	21.5	18.7	27.0	26.4	17.7
PHBVd_Gam5			Xanthomonadales	Marinicellaceae	Marinicella	48.0%	4,698,842	98.5	38.2	30.1	23.9	28.3	31.7	25.3	28.3
PBSd_Gam5					UBA4575	39.2%	2,182,883	92.4	32.2	30.9	30.2	29.2	31.5	45.9	48.8
PHBVa_Gam10					QZLD01	38.9%	2,926,949	91.1	18.4	23.4	25.3	24.9	30.8	32.4	30.5
PHBVa_Gam3					UBA10353	45.4%	4,570,814	98.8	16.2	18.3	22.1	21.7	30.2	35.3	24.7
PBSd_Gam4					UBA7415	43.3%	5,824,007	98.3	54.1	16.1	23.8	26.4	41.5	17.9	20.0
PBSAa_Gam3					UBA10353	41.2%	3,403,912	98.2	20.3	25.0	20.3	18.0	18.7	19.8	18.8
PHBVd_Gam10					UBA10353	41.1%	3,408,035	98.1	22.5	54.8	31.0	36.1	45.1	38.5	38.9

^a Refined seven MAGs are shown by bold letters. PHBV plastisphere-originated MAGs are blue letter, while PBSA plastisphere-originated MAGs are red color. Identical MAGs (dDDH >99%) are highlighted by yellow cells.

Supplementary Table 9 In house list of polyester degrading enzyme

In house ID	Esterase	Description	Size
4OYy_1_Chains_A_B_C_D_E_F_G_H_I_J_K_L_Cutinase_	Cutinase(PBAT)	<i>Humicola insolens</i> (34413)	194
5KXU_1_Chain_A_Proteinase_K_For_PLA_	ProteinaseK	<i>Engyodontium album</i> (37998)	279
6shn_A_	cutinase(PETase)	polyester hydrolase	312
A0A0K8PeT7	cutinase(PETase)	Poly(ethylene terephthalate) hydrolase OS=Ideonella sakaiensis	290
AAB02914	PHB	poly(3-hydroxybutyrate) depolymerase [Streptomyces exfoliatus]	488
AAB40611	PHB	poly(3-hydroxybutyrate) depolymerase [Alcaligenes faecalis]	635
ADV92526	Cutinase	cutinase 1 partial [Thermobifida cellosilytica]	262
AGX06818	PHB	poly(3-hydroxybutyrate) depolymerase [Bacillus infantis NRRL B-1491 1]	592
AMW89397	PolyEster	aryl esterase partial [Pseudomonas oleovorans]	181
BAA19791	PHB	poly(hydroxybutyrate depolymerase [Deiflia acidovorans]	494
BAA32541	PHB	poly(hydroxybutyrate depolymerase [Pseudomonas stutzeri]	576
BAB86909	Cutinase(PBS depoly)	PBS(A) depolymerase [Acidovorax delfieldii]	304
BAC15574	PHB	poly(3-hydroxybutyrate) depolymerase [Marinobacter sp. NK-1]	578
BAC67242	Cutinase	cutinase-like protein [Cryptococcus sp. S-2]	239
BAI99230	Cutinase(PBSA)	esterase [Thermobifida alba]	296
BAK48590	Cutinase	esterase [Thermobifida alba]	300
BAN51852	Cutinase	cutinase [Paraphoma sp. B47-9]	227
BAU59415	PHB	PHB depolymerase [Shewanella sp. JKCM-AJ-6 1A]	683
BAV72205	Cutinase(PBAT hyd)	PBAT hydrolase [Bacillus pumilus] If ESTHER= lipase_2 pseae6-q15x05 ==> Phaz7	215
BCL64964	Cutinase(PBAT hyd)	PBAT hydrolase [Rhodococcus sp.]	216
CAH17553	Cutinase(PBAT hyd)	BT-A-hydrolase 1 [Thermobifida fusca]	301
CAH17554	Cutinase(PBAT hyd)	BT-A-hydrolase 2 [Thermobifida fusca]	301
CAL82416	Cutinase(PBAT hyd)	putative secreted lipase [Clostridium botulinum A str. ATCC 3502]	480
CAL83600	Cutinase(PBAT hyd)	putative secreted lipase [Clostridium botulinum A str. ATCC 3502]	429
DAC80635	Cutinase(compost)	TPA_exp alpha/beta hydrolase [Streptomyces sp. SM14]	284
EFC94627	Cutinase(PBAT hyd)	Carboxylesterase partial [[Clostridium] pathway] DSM 13479]	414
EIW29778	Cutinase(PolyEster)	lipase [Pelosinus fermentans DSM 17108]	402
HEM19059.1	cutinase(PETase)	alpha/beta hydrolase_For_PET [Chloroflexi bacterium]	280
GHJ57577	PHB	poly(3-hydroxyalkanoic acid) depolymerase	434
P00590	Cutinase(PCL)	CUT11_FUSSO Cutinase 1 OS=Fusarium solani subsp. pisi	230
P12625	PHB	Poly(3-hydroxybutyrate) depolymerase Precursor [Rastonia pickettii]	488
P52956_1	Cutinase	Cutinase 1	213
pdb_1CEX_	Cutinase	A Chain A CUTINASE	214
pdb_1SVN_	Savinase	PLA degrading enzyme	318
pdb_2D80_	PHB	A Chain A PHB depolymerase_Talaromyces funiculosus	318
pdb_6OKL_	Ananain	PLA degrading enzyme	198
pdb_7CC4_	Cutinase	A Chain A Cutinase-like enzyme	198
tr_G9BY57_	cutinase(PETase)	G9BY57_9BACT LCC OS=uncultured bacterium	293
WP_197023848	PHB	PHB depolymerase family esterase [Microbubiter sp. HZ11]	438

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