Supporting Materials

Table S1 Wastewater-fed plastisphere metagenome-assembled genome (MAG) summary. bac=bin average coverage.

Name	Lineage	N50 (bp)	Size (bp)	FT bac	XL bac	HDPE bac	PET bac
MAG1	c_Pacebacteria; g_UBA4124	747129	1091364	0.01	0.14	0.15	0.19
MAG2	f_Chitinophagaceae; g_Chitinimonas sp.	45685	4555148	0.76	1.9	2.28	1.97
MAG3	g_Cutibacterium; s_Cutibacterium acnes	21296	2437512	0.24	0.78	0.06	0.08
MAG4	f_Hyphomonadaceae; g_UBA7672 sp.	6830	3378324	0.16	0.93	0.97	1.29
MAG5	f_Nevskiaceae; g_SCVA01 sp.	4375	3553933	1.07	0.97	2.06	0.74
MAG6	f_Ketobacteraceae	16805	5025262	19.65	0.15	1.28	2
MAG7	c_Pacebacteria; g_UBA10103	697513	744096	2.41	0.03	0.11	0.5
MAG8	g_Pseudomonas; s_Pseudomonas sp003052585	4311	3545691	3.07	0.53	0.74	0.6
MAG9	f_Cellvibrionaceae; g_Cellvibrio sp.	234835	5076046	0.06	0.87	1.18	1.39
MAG10	f_Peribacteraceae	4379	2138433	0.11	0.14	0.13	0.19
MAG11	f_Bdellowibrionaceae; g_Ga0074139 sp.	38151	3612311	0.51	0.01	0.04	0.05
MAG12	f_Bdellowibrionaceae; g_Ga0074139 sp.	10581	1772549	0.44	1.44	2.52	1.11
MAG13	g_Sphingobium; s_Sphingobium xenophagum	11216	3811294	0.02	0.16	0.21	0.26
MAG14	g_Sphingopyxis; s_Sphingopyxis sp 001468395	19609	3771052	0.19	0.97	1.77	0.91
MAG15	f_Chitinophagaceae; g_Ferruginibacter sp.	2984	3010089	0.06	0.26	0.58	0.46
MAG16	f_Hyphomonadaceae; g_SWB02 sp.	4467	2443752	2.29	0.15	0.29	0.47
MAG17	c_Alphaproteobacteria; g_SZUA-430; s_SZUA-4330	47775	2372065	0.04	0.26	0.3	0.33
MAG18	f_Micavibrionaceae	414428	606713	1.15	0.06	0.15	0.12

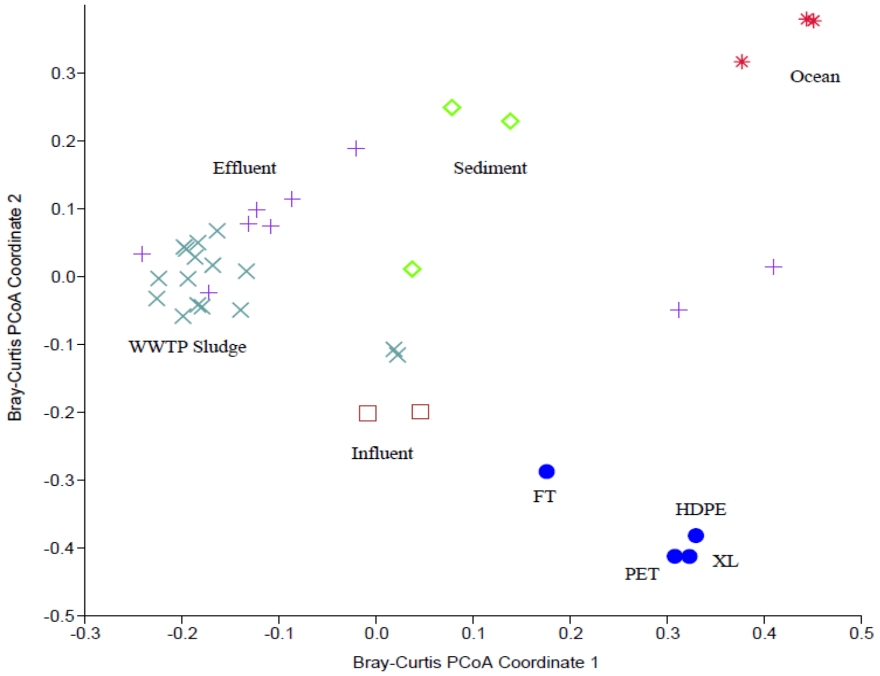
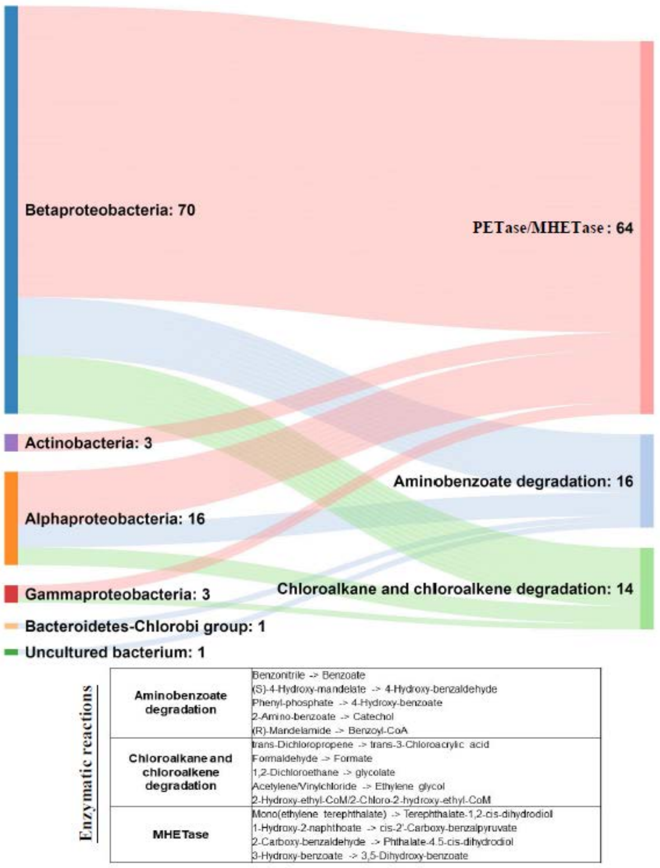


Fig. S1 Comparisons of the plastisphere resistomes with the other environments.



Aminobenzoate degradation	Benzonitrile -> Benzoate (S)-4-Hydroxy-mandelate -> 4-Hydroxy-benzaldehyde Phenyl-phosphate -> 4-Hydroxy-benzoate 2-Amino-benzoate -> Catechol (R)-Mandelamide -> Benzoyl-CoA
Chloroalkane and chloroalkene degradation	trans-Dichloropropene -> trans-3-Chloroacrylic acid Formaldehyde -> Formate 1,2-Dichloroethane -> glycolate Acetylene/Vinylchloride -> Ethylene glycol 2-Hydroxy-ethyl-CoM/2-Chloro-2-hydroxy-ethyl-CoM
MHETase	Mono(ethylene terephthalate) -> Terephthalate-1,2-cis-dihydrodiol 1-Hydroxy-2-naphthoate -> cis-2'-Carboxy-benzalpyruvate 2-Carboxy-benzaldehyde -> Phthalate-4.5-cis-dihydrodiol 3-Hydroxy-benzoate -> 3,5-Dihydroxy-benzoate

Fig. S2 Plastic-degrading evidence suggested by metagenomics analyses.

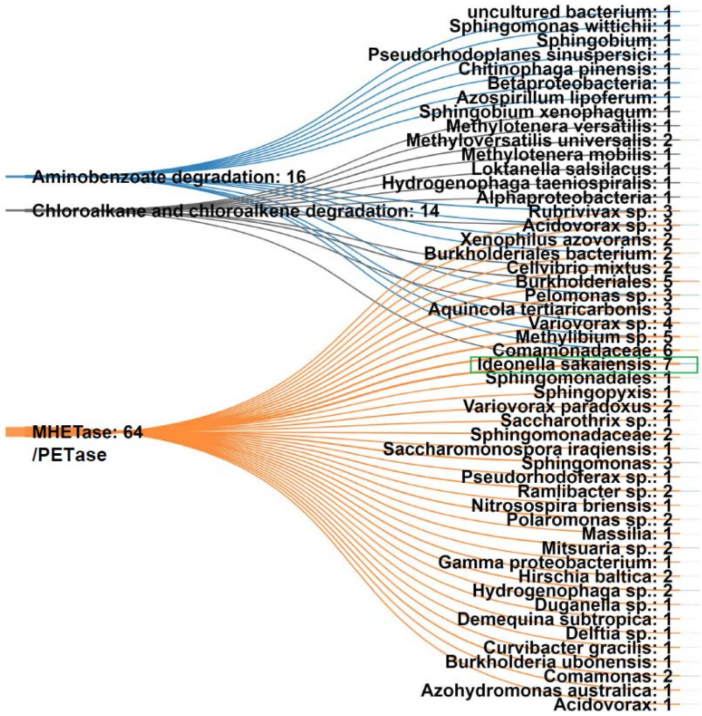


Fig. S3 Taxonomic hosts and plastic degrading pathways identified using Kaiju.

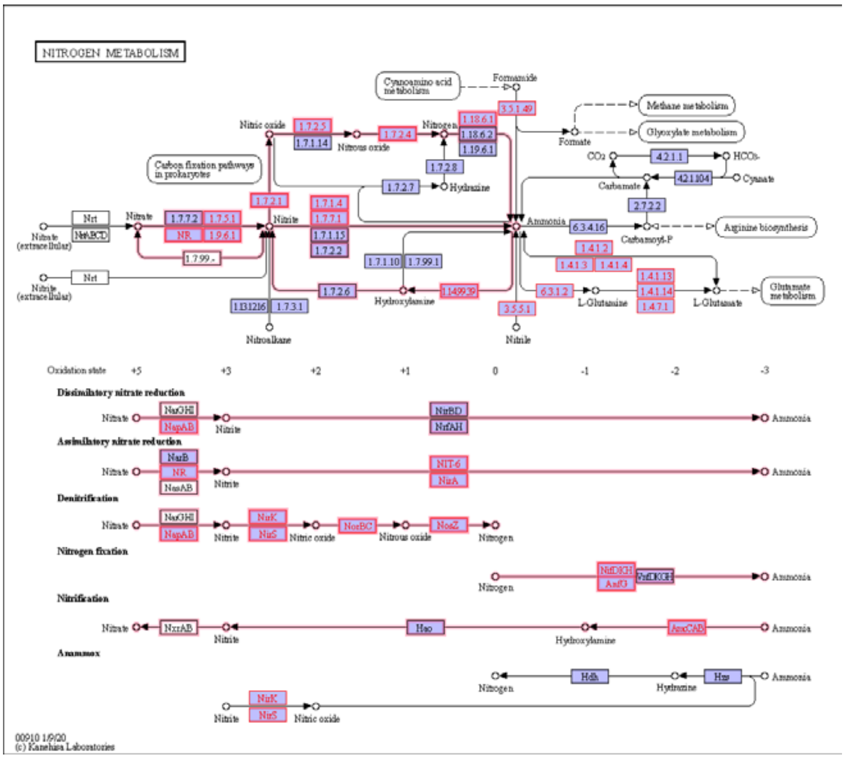


Fig. S4 The nitrogen metabolism identified using metagenomics contigs. The EC number identified in this study is red-coded.

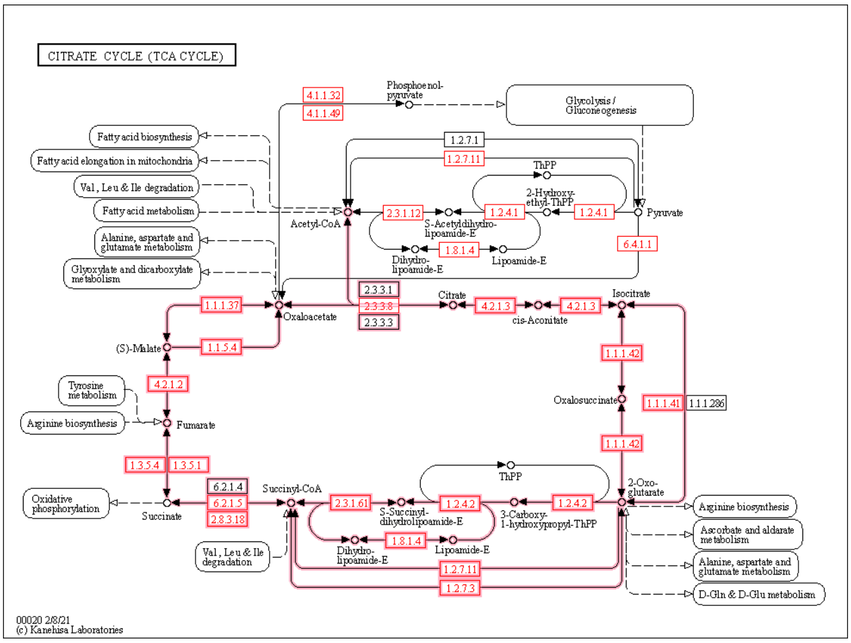


Fig. S5 The TCA metabolism (carbon) identified using metagenomics contigs. The EC number identified in this study is red-coded.

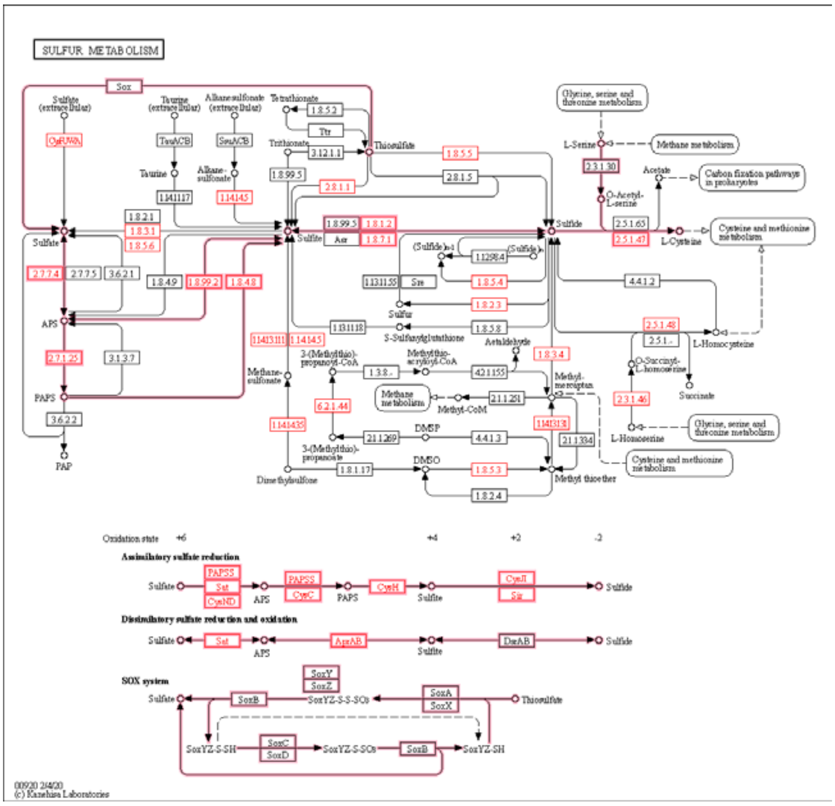


Fig. S6 The sulfur metabolism (KEGG Mapper) identified using metagenomics contigs. The EC number identified in this study is red-coded.

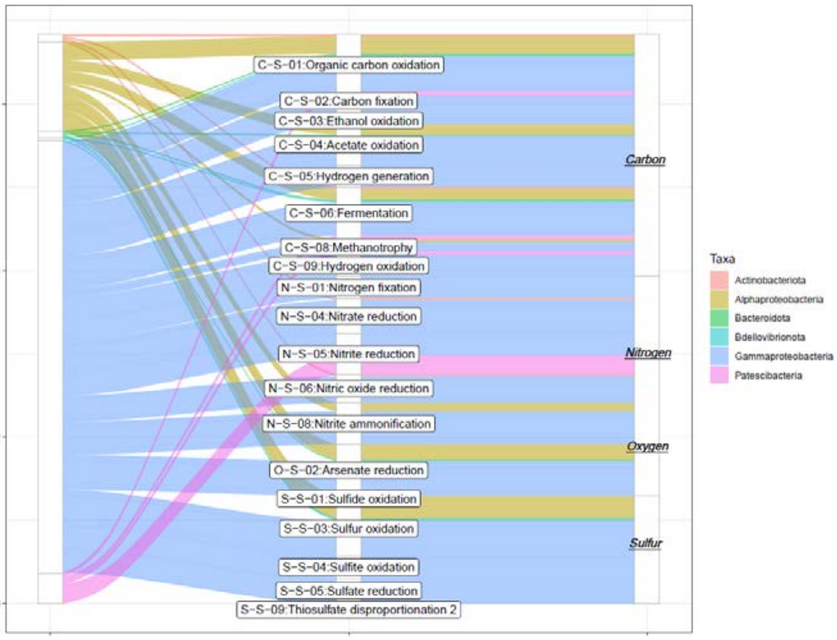


Fig. S7 The metabolisms annotated by METABOLIC. Colors indicate taxa information.

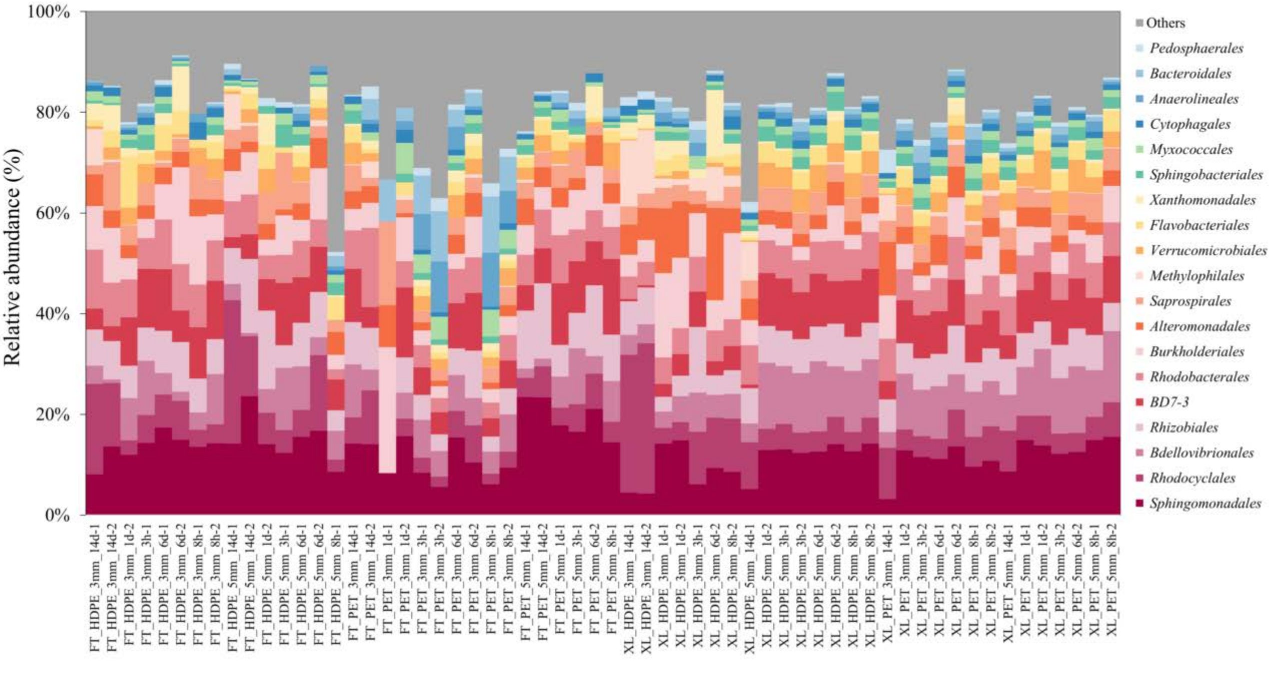


Fig. S8 The 60 amplicon sequencing samples’ OTU annotated at the order level.