

Supplementary data legends

Table S1. Enrichment conditions along transfers (T1–T8)

Table S2. Metadata and list of amplicon sequence variants (ASVs) predicted as contaminants via the decontam software

Table S3. General metagenome-assembled genome (MAG) features and predicted taxonomy using GTDB-tk

Table S4. Genes encoding polyethylene terephthalate (PET)-transforming enzymes based on Kyoto Encyclopedia of Genes and Genomes (KEGG) annotation

Table S5. General features of predicted polyethylene terephthalate hydrolases (PETases)

Table S6. Genomic context of predicted polyethylene terephthalate hydrolases (PETases) in metagenome-assembled genome (MAG) PET_3 (*Amycolatopsis*)