

Description of Additional Supplementary Files:

Supplementary Dataset 1: Genome annotation, transcriptome and proteome analysis results of strain 892

Supplementary Dataset 2: Genome annotation, transcriptome and proteome analysis results of strain 913

Supplementary Dataset 3: Sequence percent identity between exo-fucosidases in strain 892

Supplementary Dataset 4: Sequence percent identity between exo-fucosidases in strain 913

Supplementary Dataset 5: Wilcoxon rank sum test results comparing transcripts per cell in each PUL and carbon source.

Supplementary Dataset 6: Detected fucosidases in Planctomycetota, Verrucomicrobia and Bacteroidota genomes.

Supplementary Dataset 7: Reciprocal best match blast of GH168 encoded in genomes from Planctomycetota, Verrucomicrobia and Bacteroidota.

Supplementary Dataset 8: Alphafold-predicted structure of the enzyme Fun168D

Supplementary Dataset 9: Alphafold-predicted structure of the enzyme 913_05635 from strain 913

Supplementary Dataset 10: Alphafold-predicted structure of the enzyme 892_06289 from strain 892

Supplementary Dataset 11: Alphafold-predicted structure of the enzyme 913_01189 from strain 913

Supplementary Dataset 12: Alphafold-predicted structure of the enzyme 892_06282 from strain 892