Methods:

Metagenomic sequencing was performed at the Ramaciotti Centre for Genomics (UNSW, Sydney) on a NovaSeq X Plus 10B (2x150bp; Illumina).

Raw reads were first quality controlled using fastp v0.23.41, then go reads error correction using the Bayesian – Hammer as implemented in SPAdes v4.0.02. Resultant corrected reads were assembled using Megahit v1.2.93; only contigs over 1kb were retained for gene prediction. Parallelized version of Prodigal -- pprodigal was used for gene prediction; non-redundant genes (protein translations) were generated using CD-HIT v4.8.14, with parameters setting as -c 0.9 -M 0 -T 0 -l 20 -G 0 -aS 0.9 -g 0. KEGG Orthology and pathway analysis was performed using KofamKOALA5 (KofamScan v 1.3.0 with the latest KOfam database v2024-08-29). CAZy analysis was performed using DIAMOND v2.1.96 to align the non-redundant genes against the latest CAZyDB database (v2024-07-24). Resultant tables (reads count per sample) including KO, pathway and CAZy were generated using CoverM7(https://github.com/wwood/CoverM).

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