

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: An analysis of completeness and contamination of all Metagenome Assembled 49 Genomes (MAGs) following the MAGpy annotation pipeline (Stewart et al. 2018 DOI: 50 10.1038/s41467-018-03317-6).

File Name: Supplementary Data 2

Description: An analysis of completeness and contamination of all MCL clusters from the network 55 analysis of contigs described in this study. Completeness and contamination were analysed following 56 the MAGpy annotation pipeline (Stewart et al. 2018 DOI: 10.1038/s41467-018-03317-6).

File Name: Supplementary Software

Description: All scripts used in this study, including commands for each program used. This includes 60 raw read QC, reference assembly, de novo contig assembly from non-mapping reads, Blobtools 61 analysis, taxonomical assignation, BUSCO and MAGPy analysis.