



**Supplementary Figure S10.** Phylogenetic analysis of 3,651 clusters with contamination  $\leq 0.10$  and completeness  $\geq 0.50$ . Taxonomic labels were assigned by GTDB (version 95) using GTDB-TK (version 1.3.0) with default parameters. FastTree (version 2.1.11) with default parameters was used to construct the tree based on the concatenated marker gene amino acid alignments created by CheckM (version 1.0.13). The tree was visualized in iTOL. Only the bacterial phyla were shown.