



Figure S3 Coverage of M-Y reference genomes by draft metagenome assembly. Contigs from the M-Y draft metagenome assembly were aligned to the reference genomes of each species with BLASTn (Altschul *et al.* 1990) using the following parameters: ``-perc_identity 95 -evalue 1e-30 -word_size 50``. The restrictiveness of these parameters ensured that all alignments generated were greater than 70 bp. Left: The fraction of each reference genome covered by BLASTn alignments. Right: For each reference genome, the N50 length of draft contigs aligning to that genome.