



Supplementary 16: Maximum likelihood phylogenetic tree of [NiFe]-hydrogenase gene sequences obtained from our MAGS (n=304) and representative genomes from the GTDB. Branches and reference gene labels are coloured according to the group of [NiFe]-hydrogenase, including the novel group 1m [NiFe]-hydrogenase described in this paper (magenta). Bootstrap values >90% are depicted as filled circles on branches; 1000 ultrafast bootstrap iterations were applied.