



**Additional File 19. Phylogeny of a *xoxF3* sequence retrieved from metagenome assembled genome *Methylothenera* ss03.**

Phylogenetic tree of *xoxF3* sequences retrieved from the MAG *Methylothenera* ss03. Reference gene sequences were selected from the NCBI nucleotide database. Only bootstrap values  $\geq 50\%$  (based on 500 replicates) are labelled at branch points. Alignments were produced at the amino acid level with the Muscle algorithm and phylogenetic trees were produced in Mega7 [70] with nucleotide sequence data using the neighbour-joining method. There was a total of 193 amino acid residues in the final dataset.