

Anaerobic derivatives of mitochondria and peroxisomes in the free-living amoeba *Pelomyxa schiedti* revealed by single-cell genomics

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Additional file 2: Figures S1 – S6

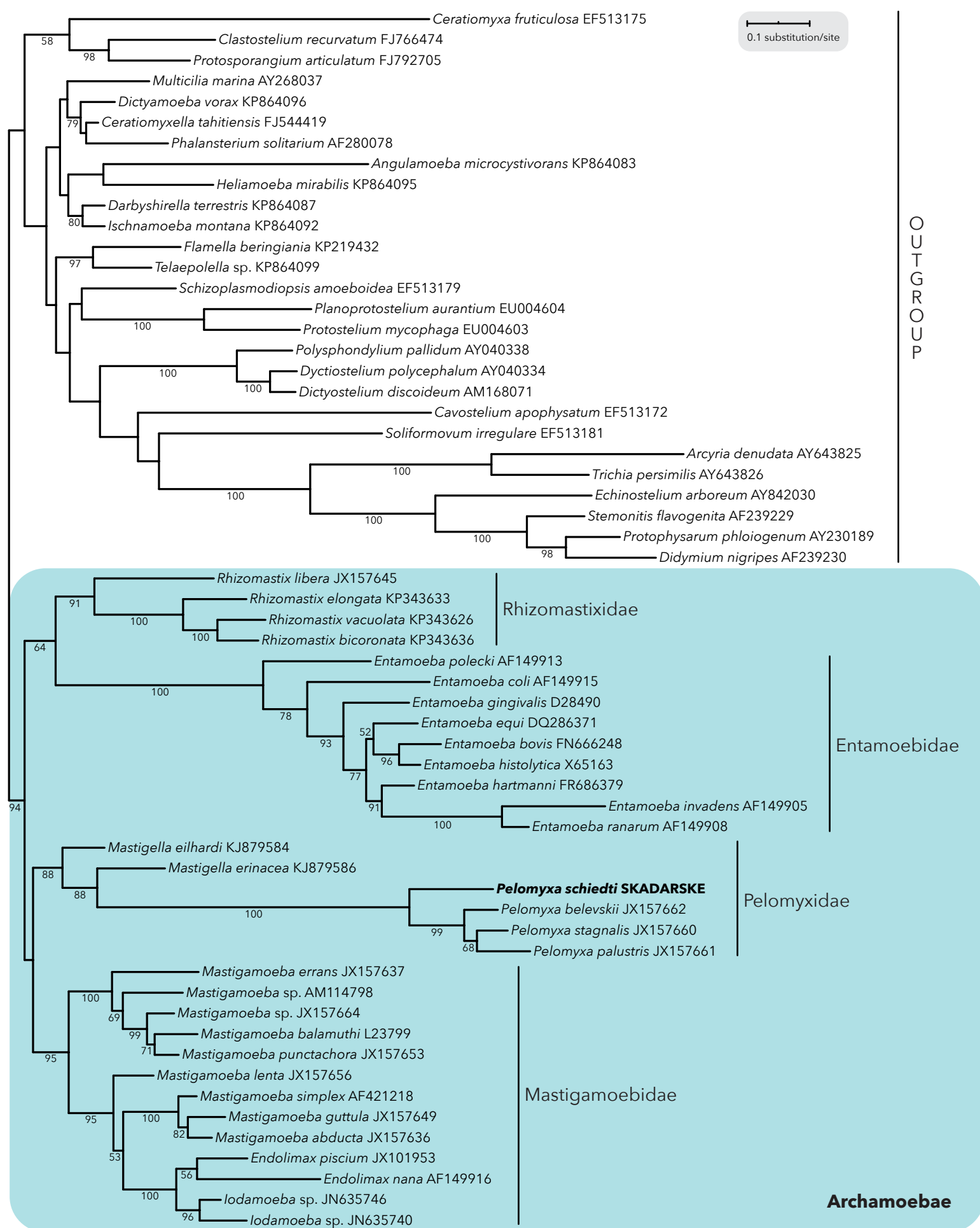


Fig. S1. Phylogenetic analysis of amoebozoan 18S rDNA. Maximum-likelihood tree places *Pelomyxa schiedti* in monophyletic Pelomyxidae group inside monophyletic Archamoebae. Standard bootstrap support values shown when $\geq 50\%$.

BUSCO Assessment Results

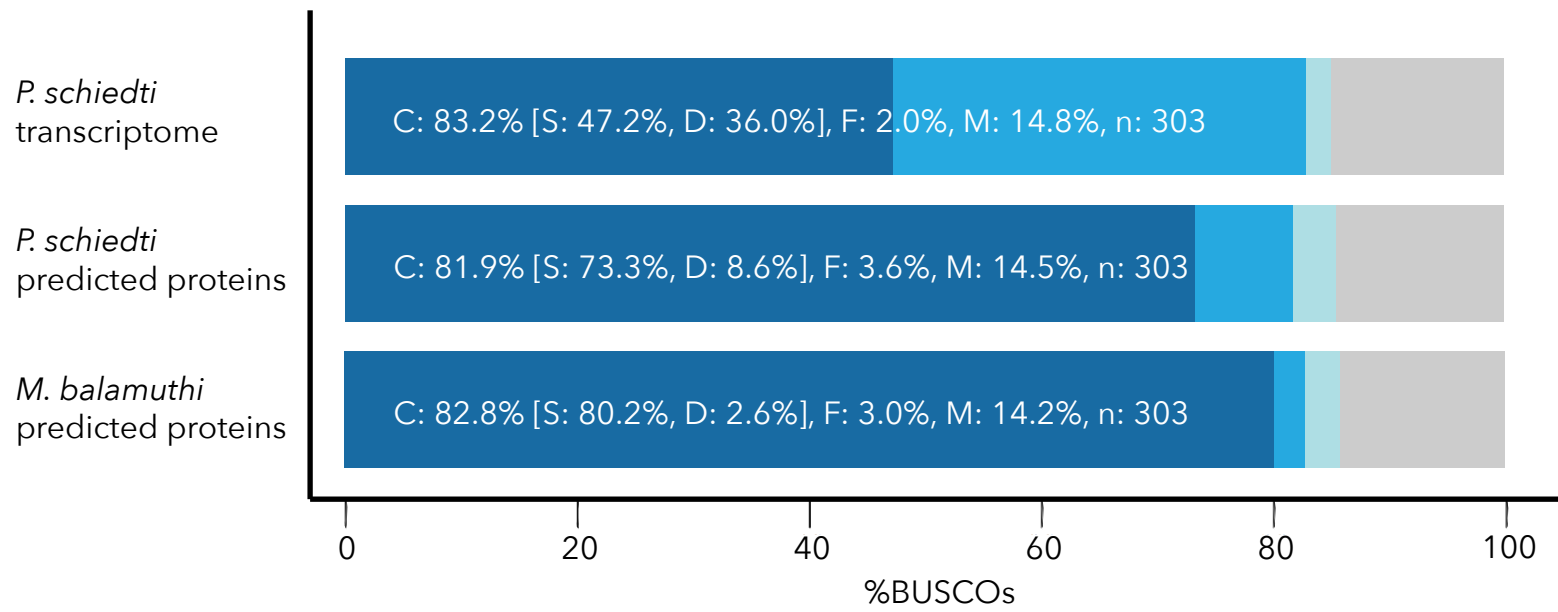
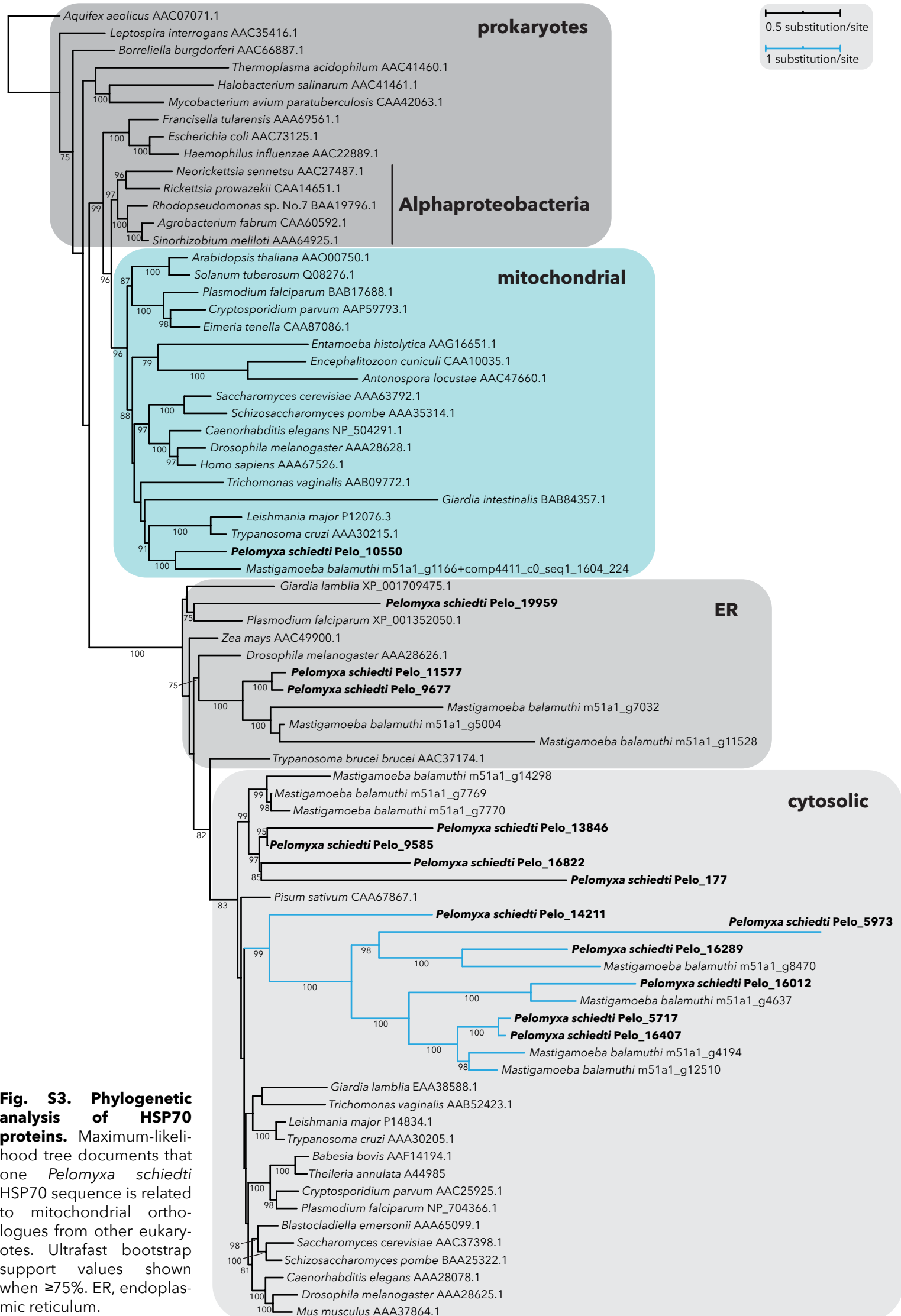


Fig. S2. BUSCO analysis of *Pelomyxa schiedti* transcriptome and predicted proteins. Completeness of *P. schiedti* datasets were assessed using odb9_eukaryota dataset and compared with completeness of predicted proteins from *Mastigamoeba balamuthi*.



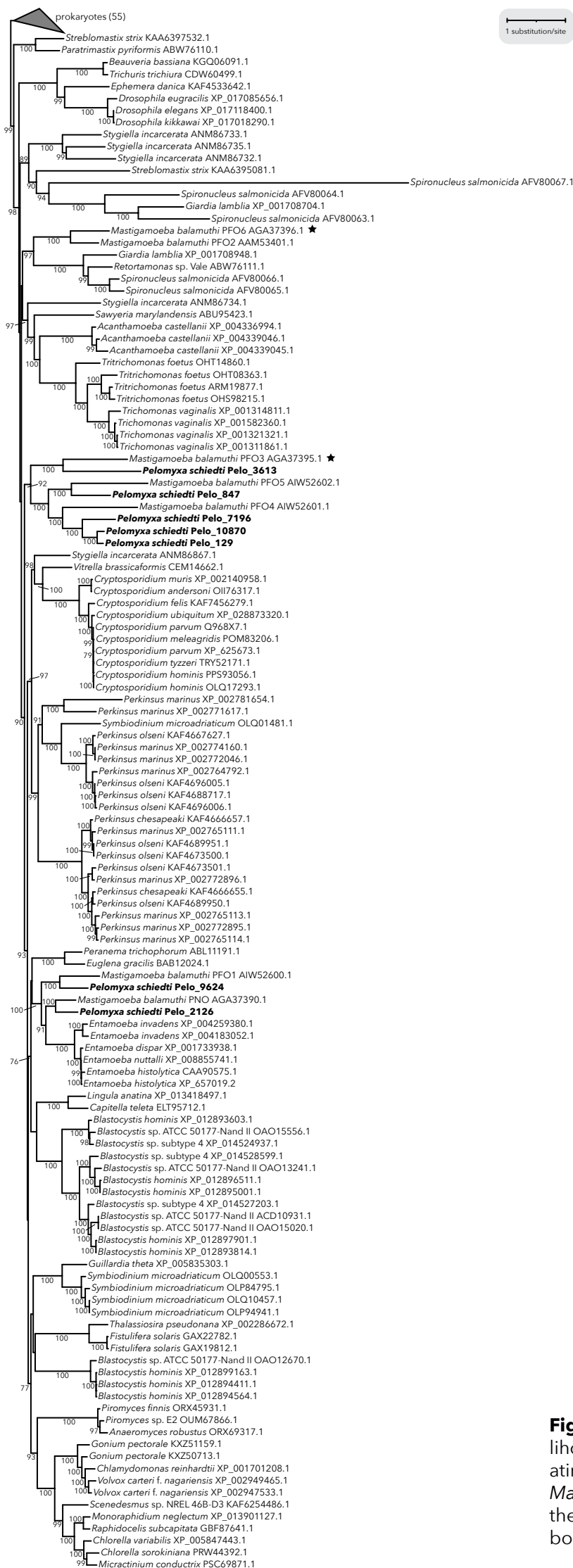


Fig. S4. Phylogenetic analysis of PFO enzymes. Maximum-likelihood phylogenetic tree identifies PFO version putatively operating in *Pelomyxa schiedti* MRO. Hydrogenosomal PFO copies of *Mastigamoeba balamuthi* marked with stars. Number in parentheses shows number of species in the collapsed clade. Ultrafast bootstrap support values shown when $\geq 75\%$.

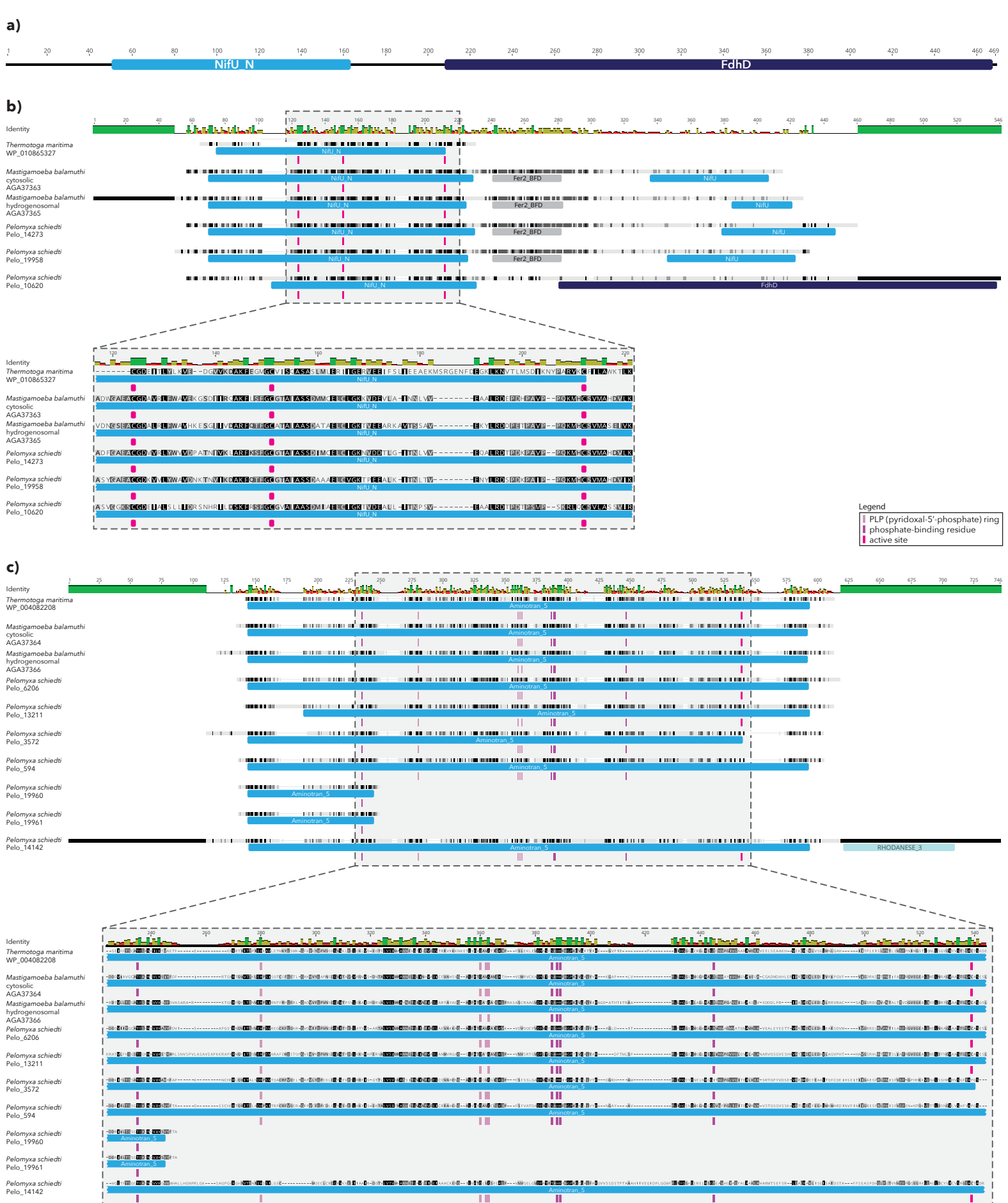


Fig. S5. Sequences of *Pelomyxa schiedti* components of NIF system. a) *P. schiedti* protein Pelo_10620, composed of NifU N-terminal domain fused to FdhD (formate dehydrogenase accessory sulfurtransferase) C-terminal domain, as determined by InterProScan. **b-c)** Sequence alignment of NifU (**b**) and NifS (**c**) proteins from *P. schiedti* and *Mastigamoeba balamuthi* in comparison with bacterial homologues from *Thermotoga maritima*. Amino acid residues necessary for function of NifU and NifS are labeled according to graphical legend.

