

Supplement to: G. E. Novakovsky, D. V. Dibrova, and A. Y. Mulkidjanian, Phylogenomic Analysis of Type 1 NADH:Quinone Oxidoreductase (ISSN 0006-2979, *Biochemistry (Moscow)*, 2016, Vol. 81, No. 7, pp. 770-784)

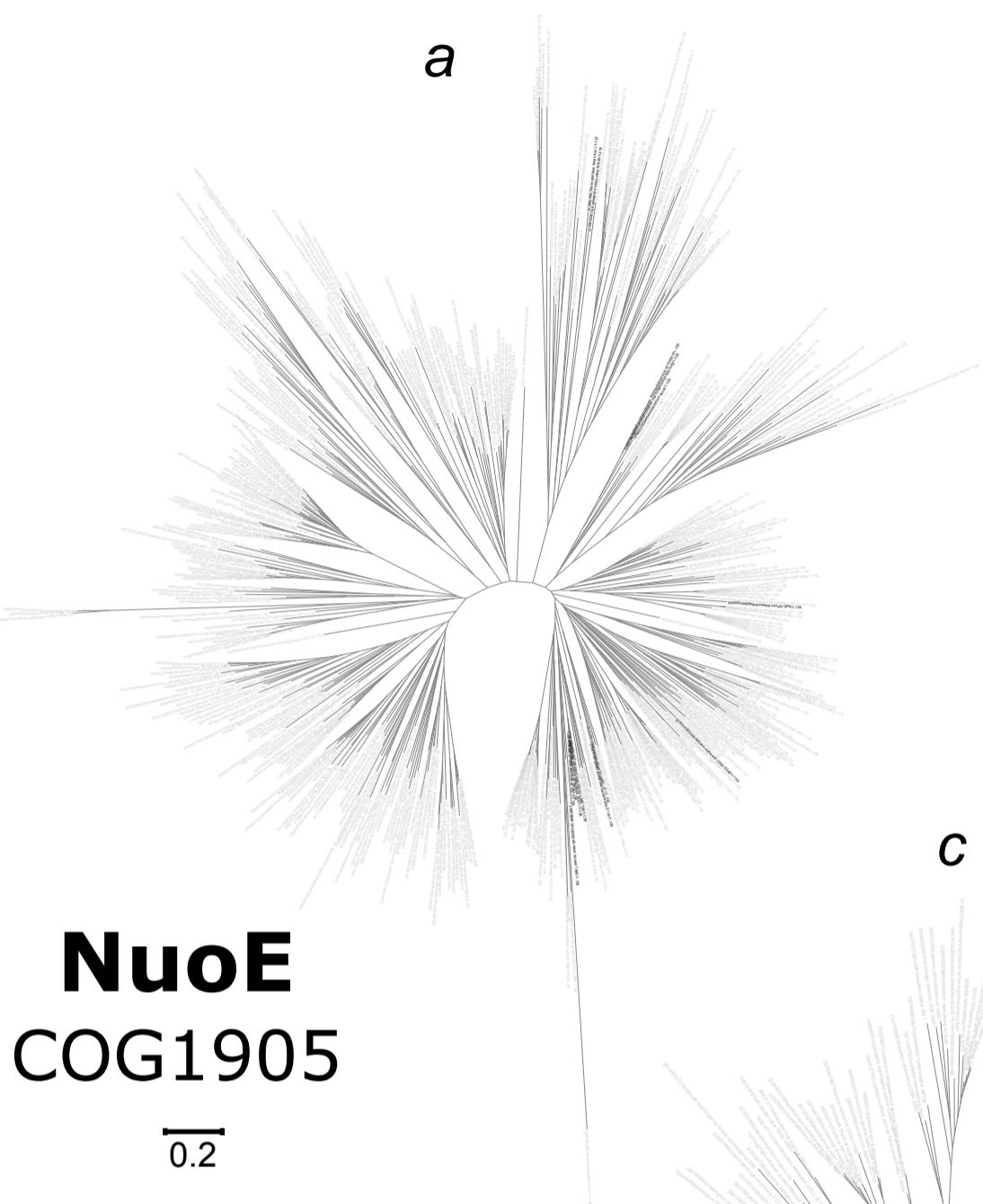
Fig. 2. Phylogenetic trees for subunits of the N-module. Archaeal sequences are rendered in black, and bacterial sequences are rendered in gray. a) Phylogenetic tree for the NuoE subunit; b) phylogenetic tree for the NuoF subunit; c) phylogenetic tree for the NuoG subunit.

Fig. 3. Separate clades with archaeal sequences from the trees of the N-module, see text for details; the bootstrap values are indicated.

Fig. 4. Phylogenetic trees for the subunits of the Q-module. The main archaeal clade, which is separated from bacterial sequences, is shown by gray ovals. Black arrows point to small archaeal clades from Thermoplasmatales, the clades with archaeal proteins from Halobacteria are shown with solid gray lines, and the clades of bacterial proteins from Thermotogae are marked with dashed arrows. a) Phylogenetic tree for the NuoB subunit; b) phylogenetic tree for the NuoC subunit; c) phylogenetic tree for the NuoD subunit.

Fig. 5. Phylogenetic trees for the subunits of the P-module. The main archaeal clade, which is separated from bacterial sequences, where present, is shown in a gray oval. The clades with archaeal proteins from Halobacteria are shown with solid gray lines and solid gray arrows. a) Phylogenetic tree for the NuoL/MnhA subunit (the part of this tree, which probably stands for NuoL clades, as shown by genomic neighborhood analysis, is marked with broken line); b) phylogenetic tree for the NuoM subunit; c) phylogenetic tree for the NuoN subunit; d) phylogenetic tree for the NuoH subunit.

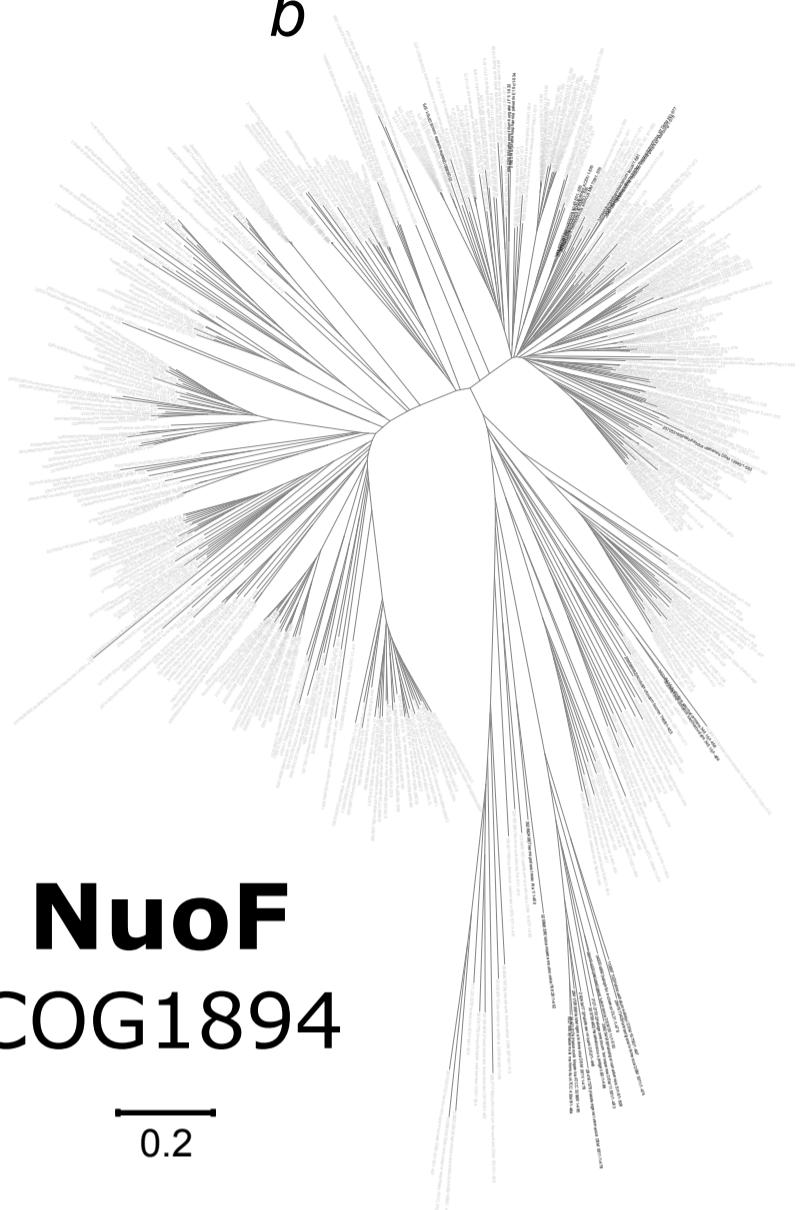
a



NuoE
COG1905

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0.2

b

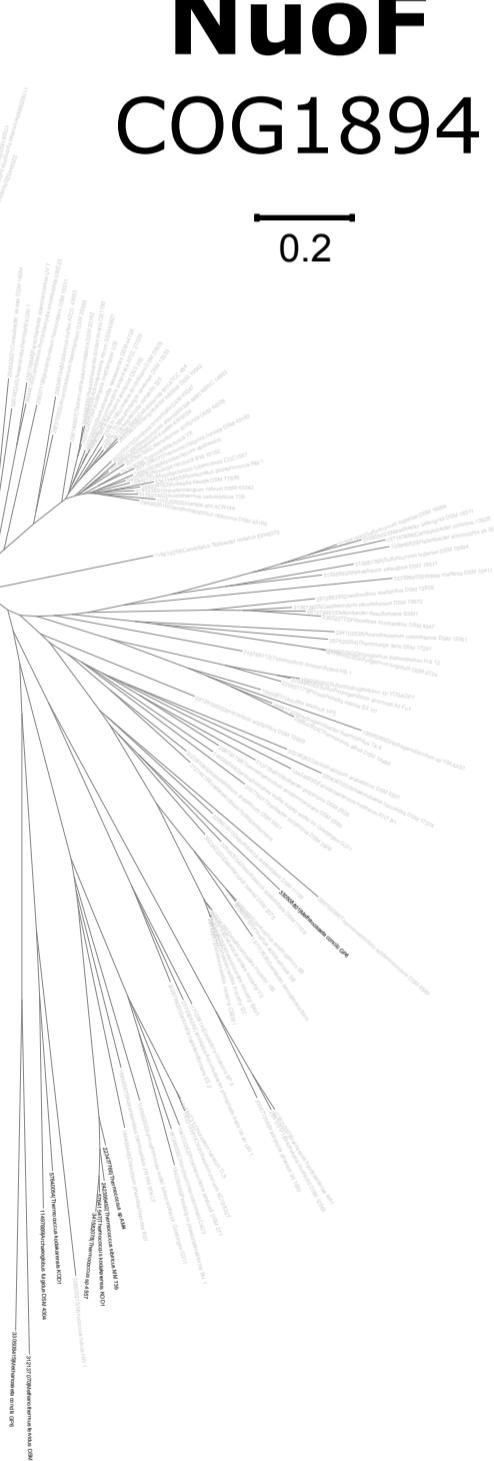


NuoF
COG1894

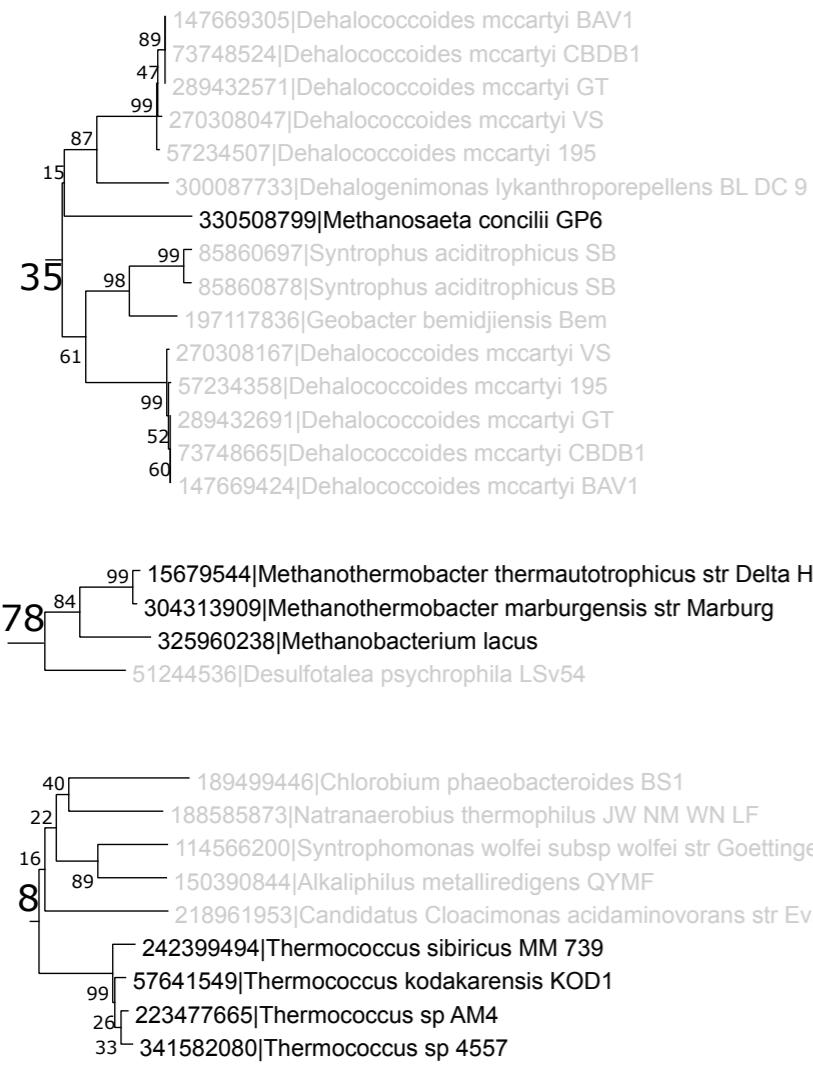
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NuoG
COG1034

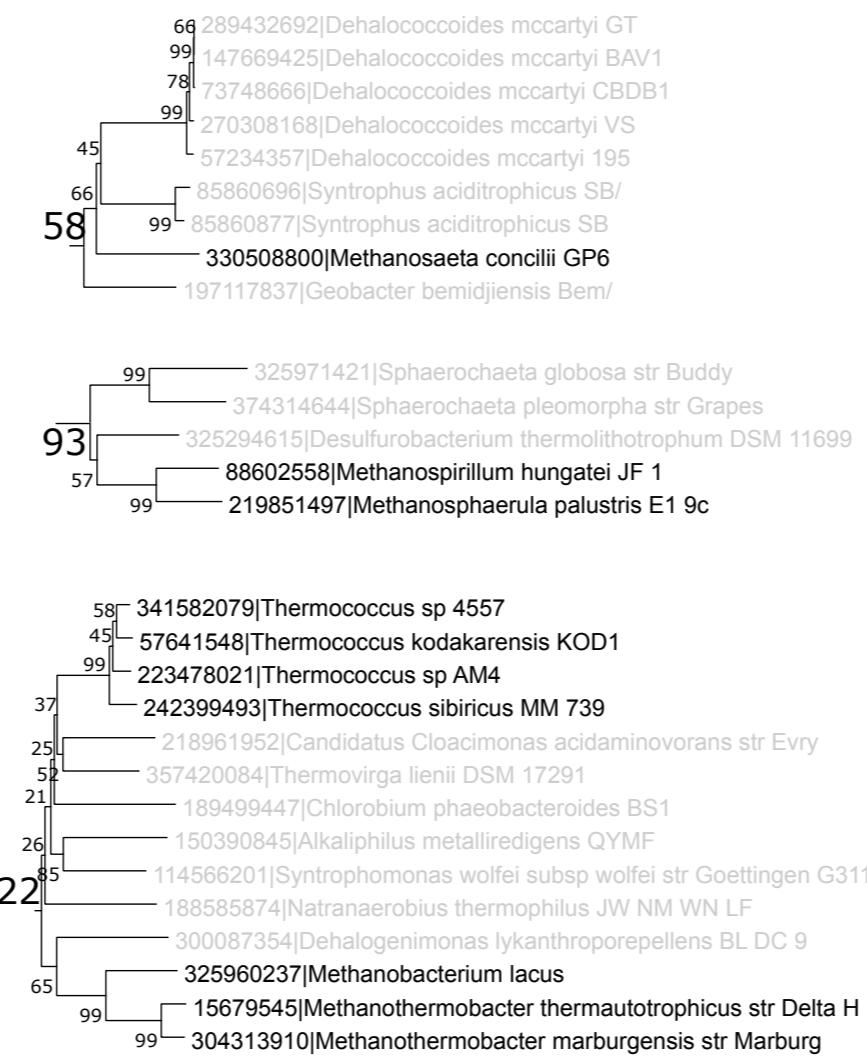
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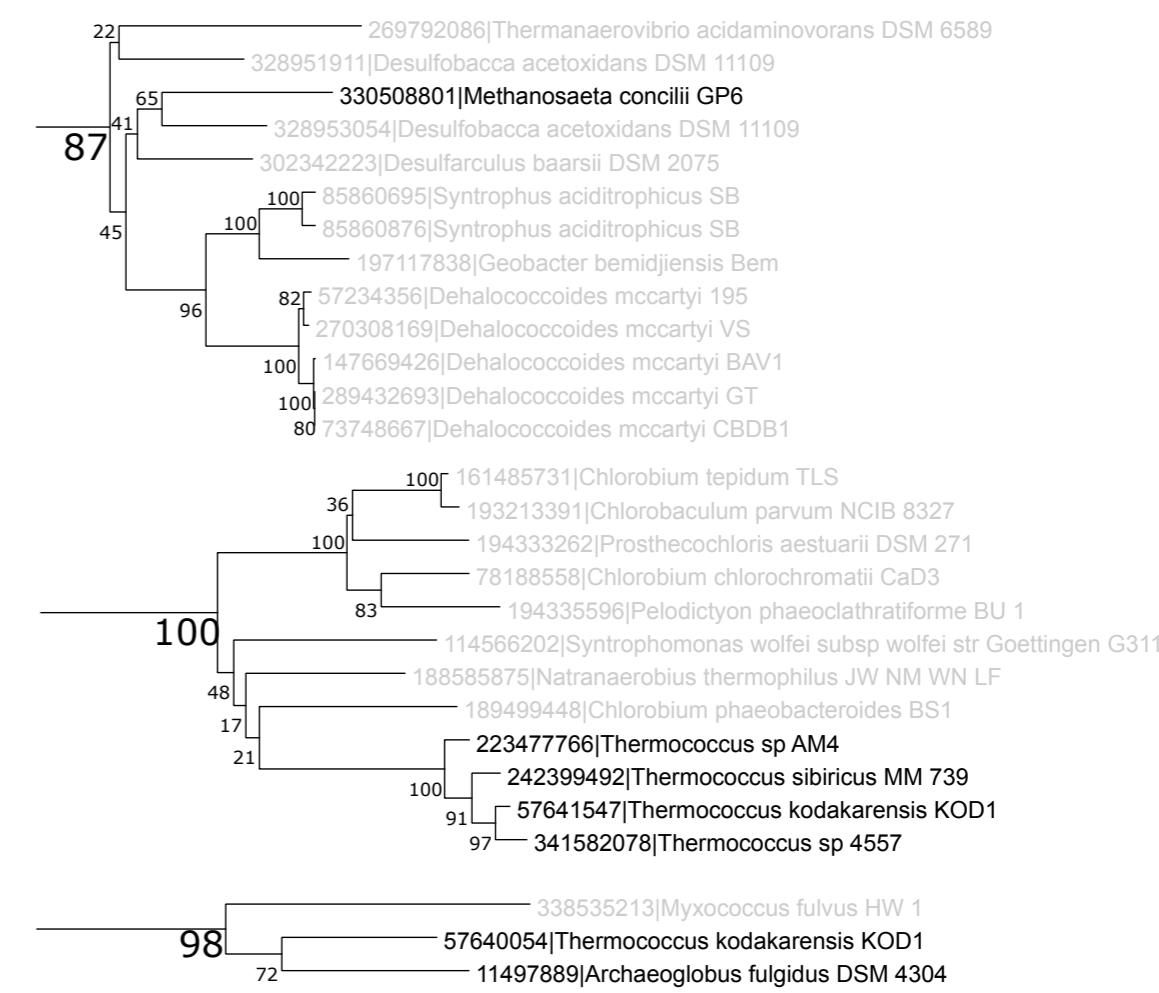
NuoE (COG1905)



NuoF (COG1894)



NuoG (COG1034)



0.2

0.2

0.2

