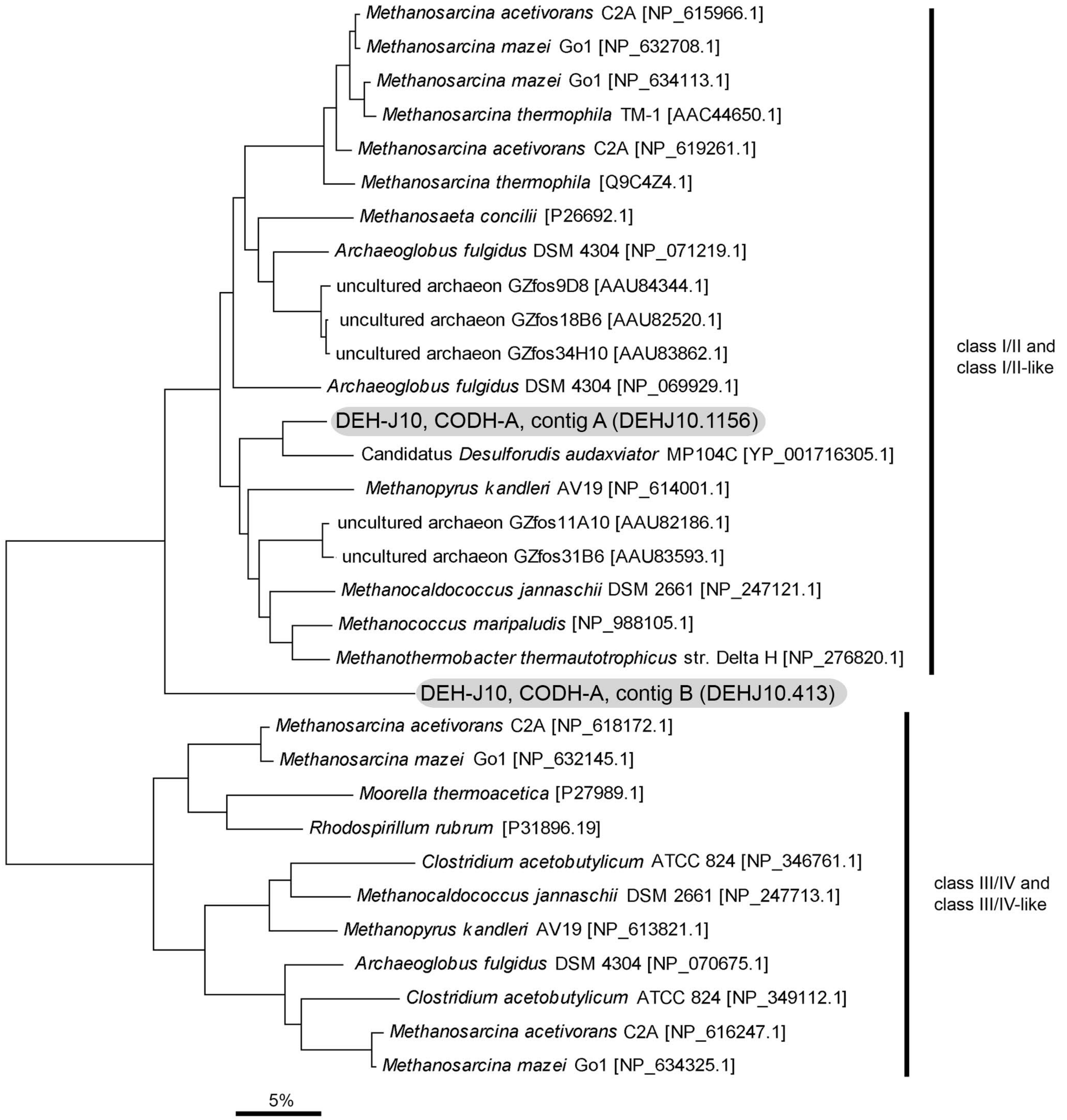
Supplementary Figure 2. Phylogenetic affiliations of the carbon monoxide dehydrogenase/acetyl-CoA decarbonylase-synthase (CODH/ACDS), alpha subunit protein sequences derived from single cell DEH-J10 in relation to other relevant alpha subunits from various bacteria and archaea. The phylogenetic analysis presented was performed with Mega5 using Maximum-Likelihood analysis and the Jones-Taylor-Thornton (JTT) substitution model. Phylogenies were also constructed using the Neighbour-Joining method, and both methods were also performed with and without trimming of overhanging ends of sequence alignments, yet these made no major differences to the overall phylogeny presented. Nomenclature of major sub-groups is based on Meyerdierks et al. 2005.* The scale bar represents 5% sequence divergence.



*Meyerdierks, A., Kube, M., Lombardot, T., Knittel, K., Bauer, M., Glöckner, F.O., Reinhardt, R., and R. Amann. Insights into the genomes of archaea mediating the anaerobic oxidation of methane. *Environ Microbiol* 7: 1937-1951.