

Supplementary Figures

Fig. S1 Bayesian trees showing phylogenetic affiliations of 16S rRNA genes detected in unincubated and incubated KTLS sediment samples belonging to (a) *Thermus*, *Thermodesulfobacteria*, *Thermotogae*, *Dictyoglomi*, *Aquificae*, JS1, OP5, OP9 and OP11, (b) *Cyanobacteria*, *Verrucomicrobia*, *Acidobacteria*, *Planctomycetes*, *Actinobacteria*, *Chloroflexi*, *Deferribacteres*, *Spirochaetes*, *Bacteroides* and *Nitrospirae*, (c) *Firmicutes*, (d) *Proteobacteria* and (e) archaea. The detected sequences were labeled in boldface with the fraction of each in relation to the total screened clones in an individual library. The “unm” and digits starting from the fourth characters of the sequence name represent unincubated sediments and incubation temperature, respectively. Supporting values for branch nodes below 0.5 are not shown. The number attached with the referenced bar represents the substitutions per sequence position

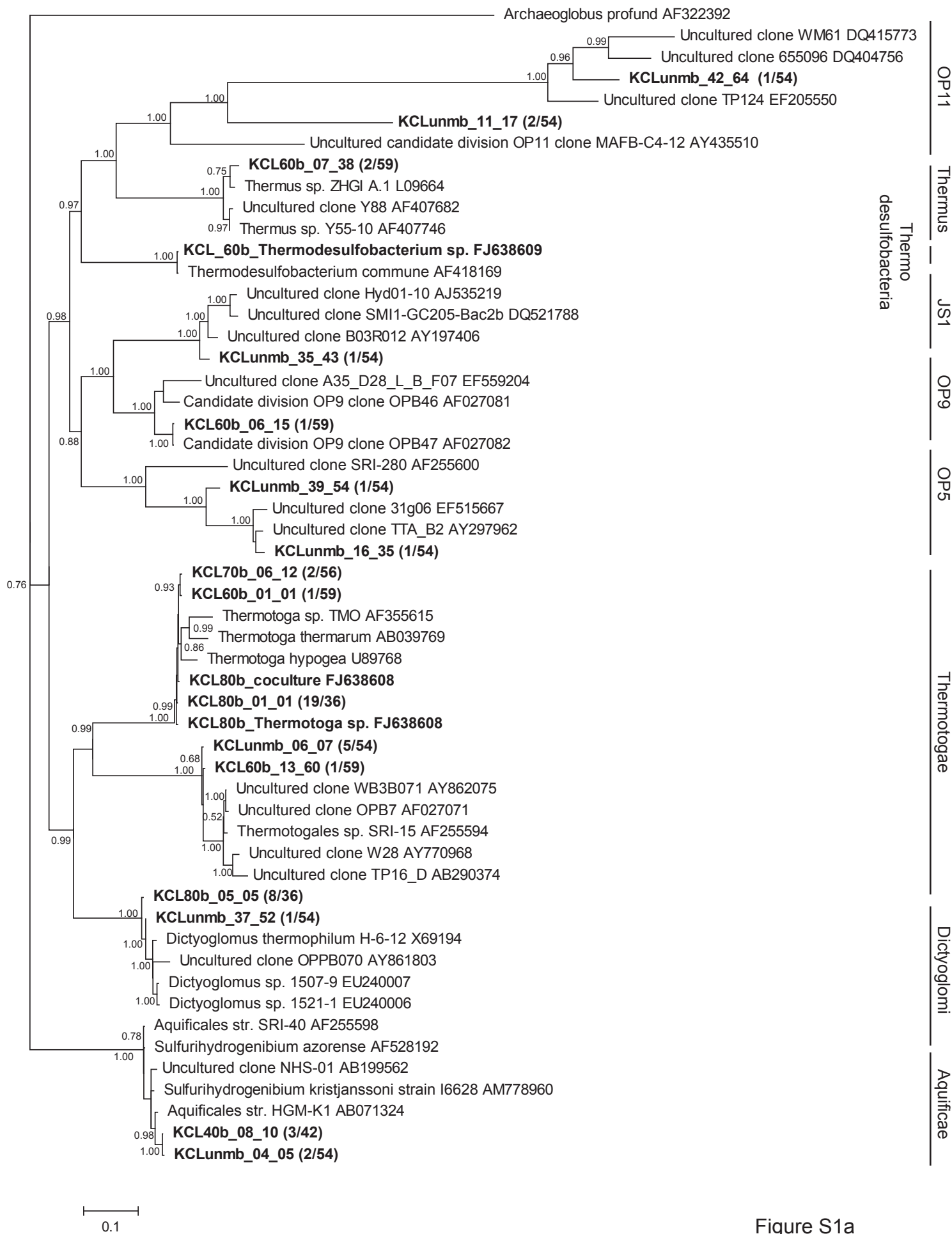


Figure S1a

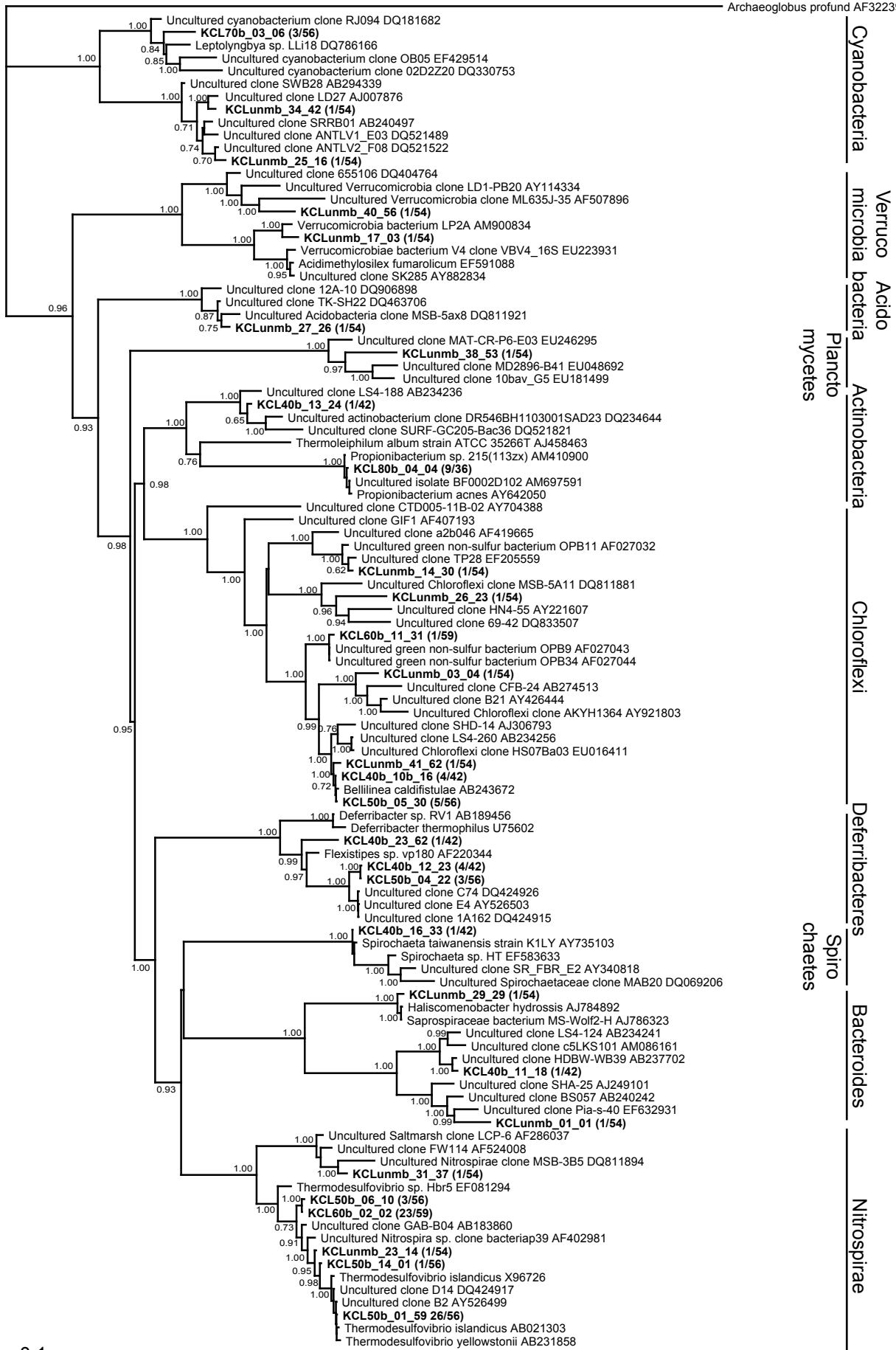
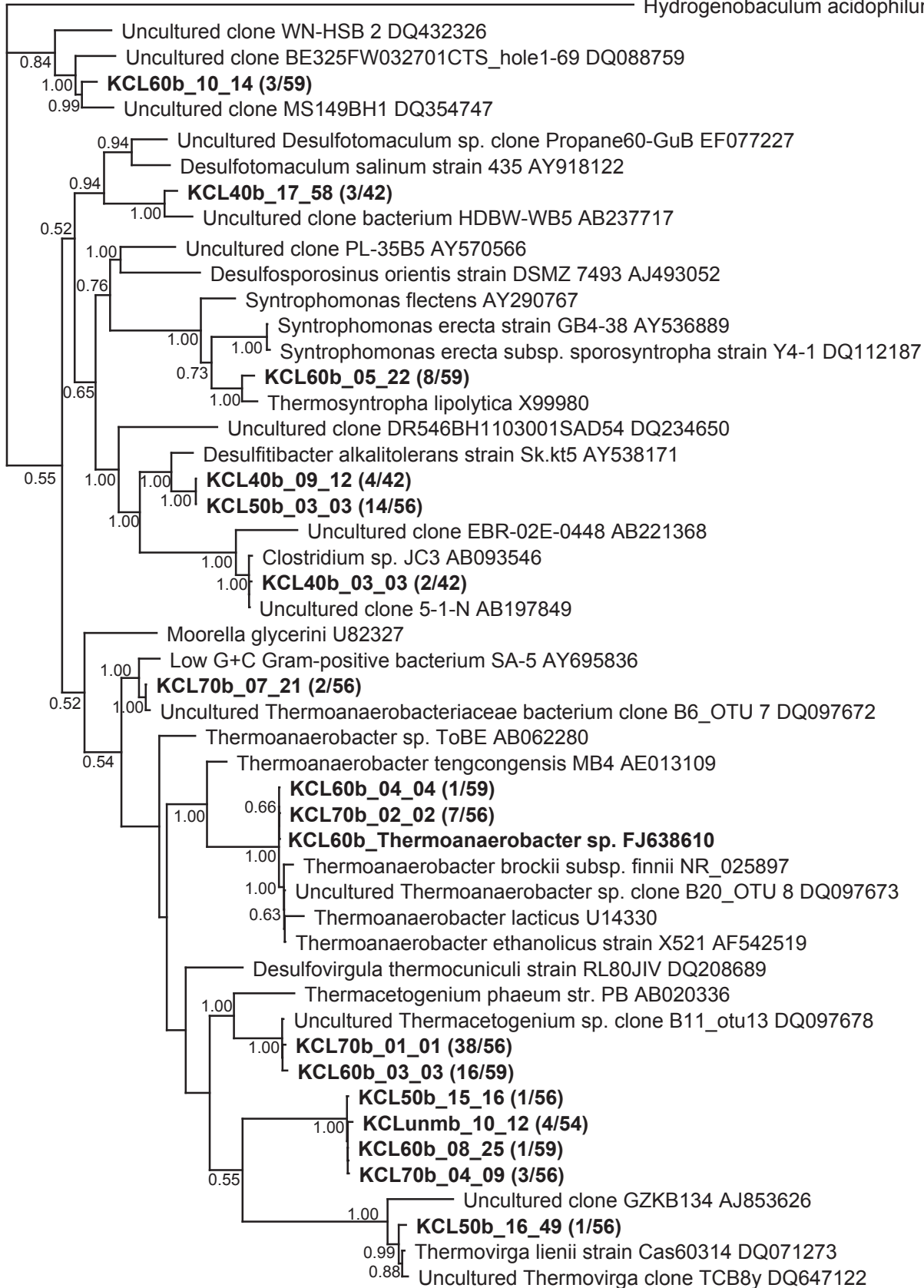


Figure S1b



Firmicutes

0.1

Figure S1c

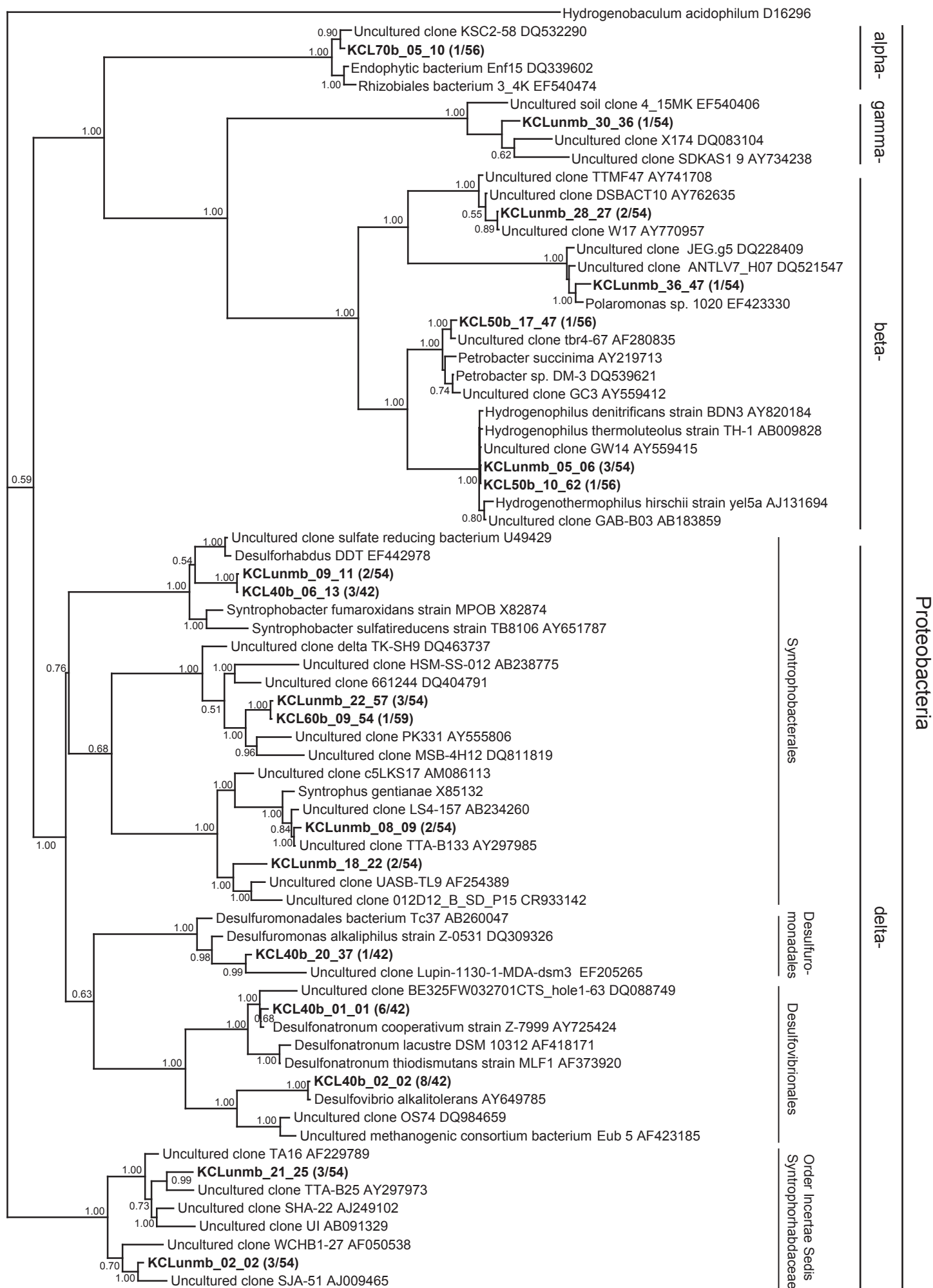


Figure S1d

