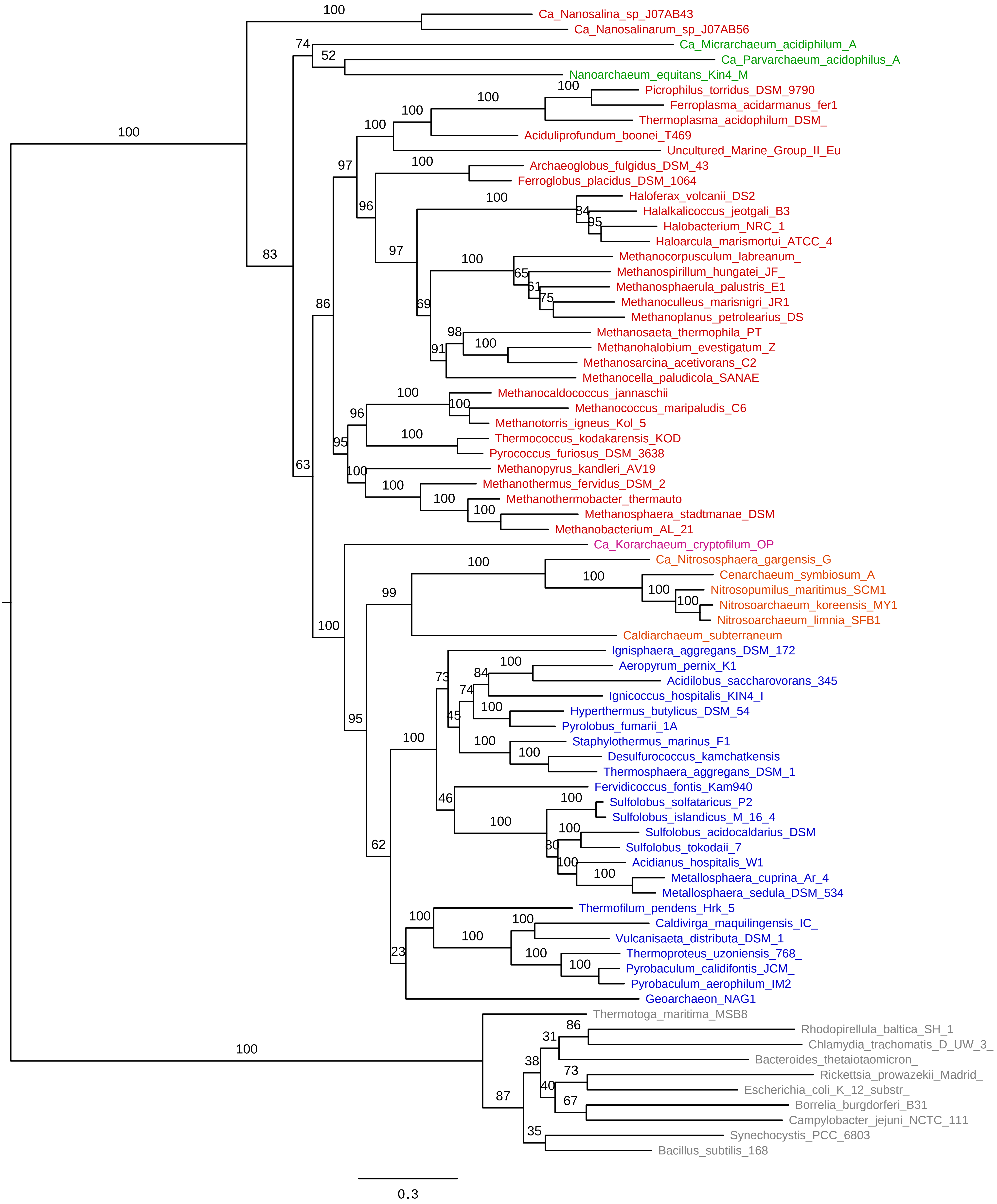
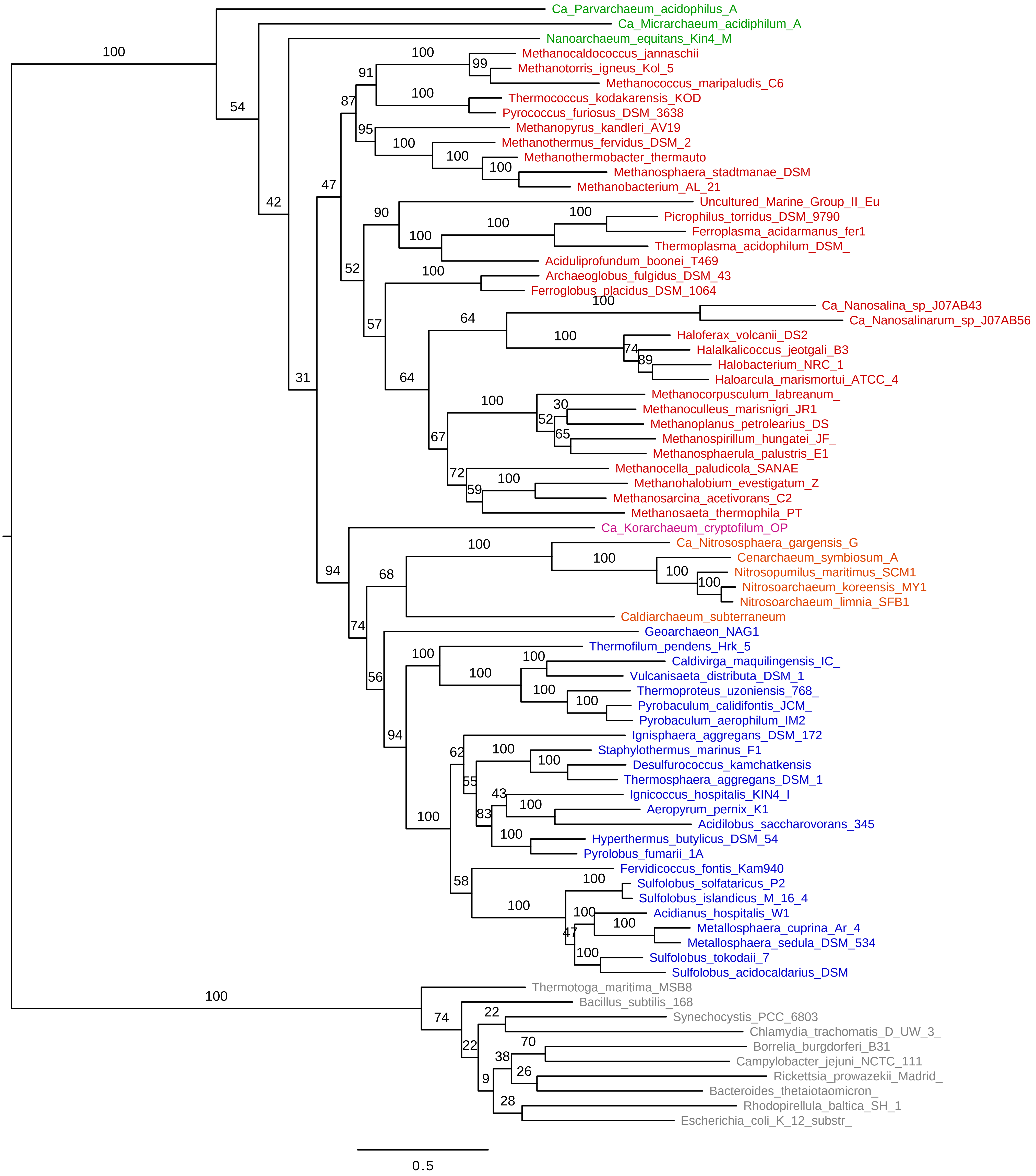
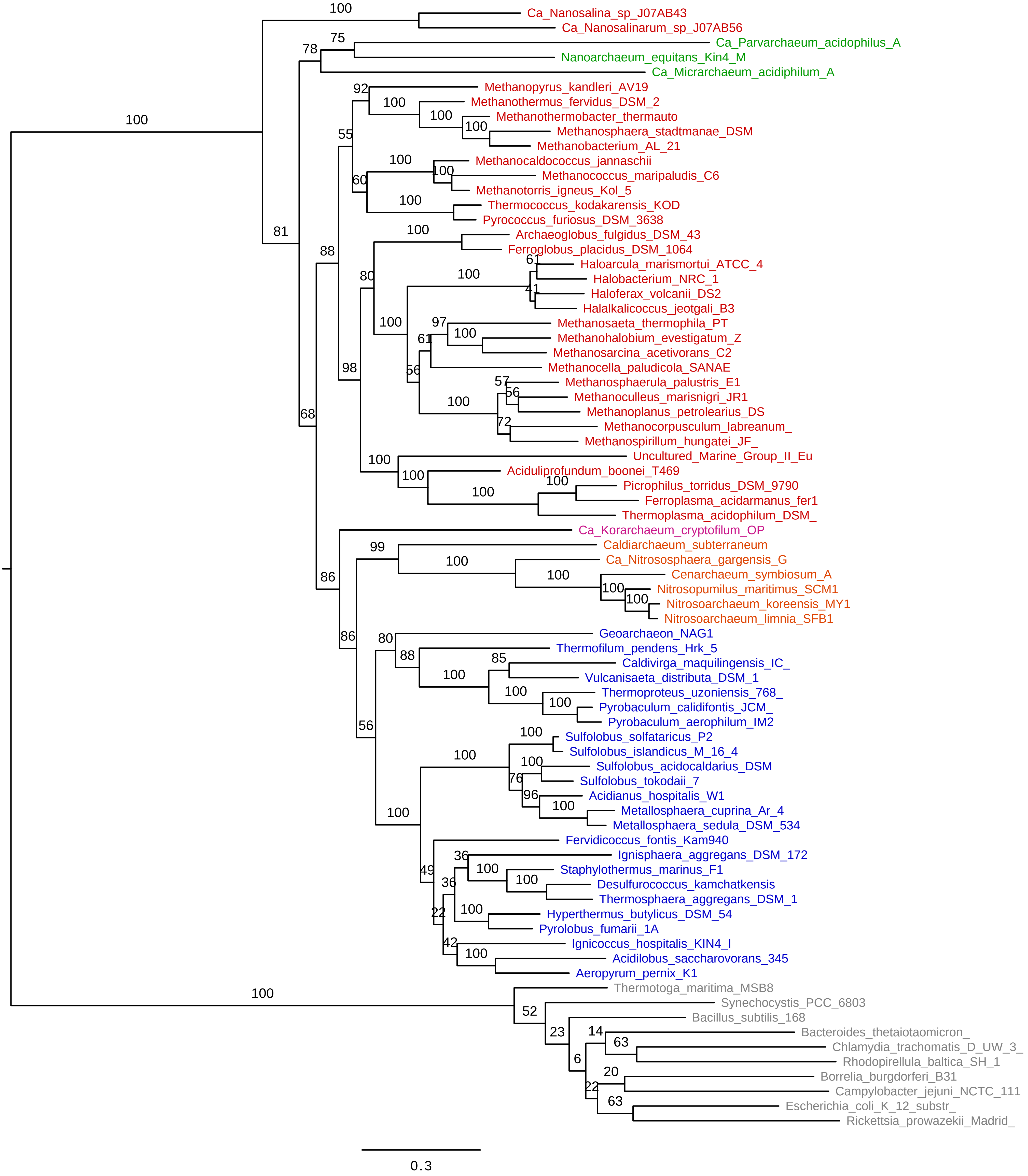


A: ML phylogeny (RAxML, CAT LG) of 33 r-proteins

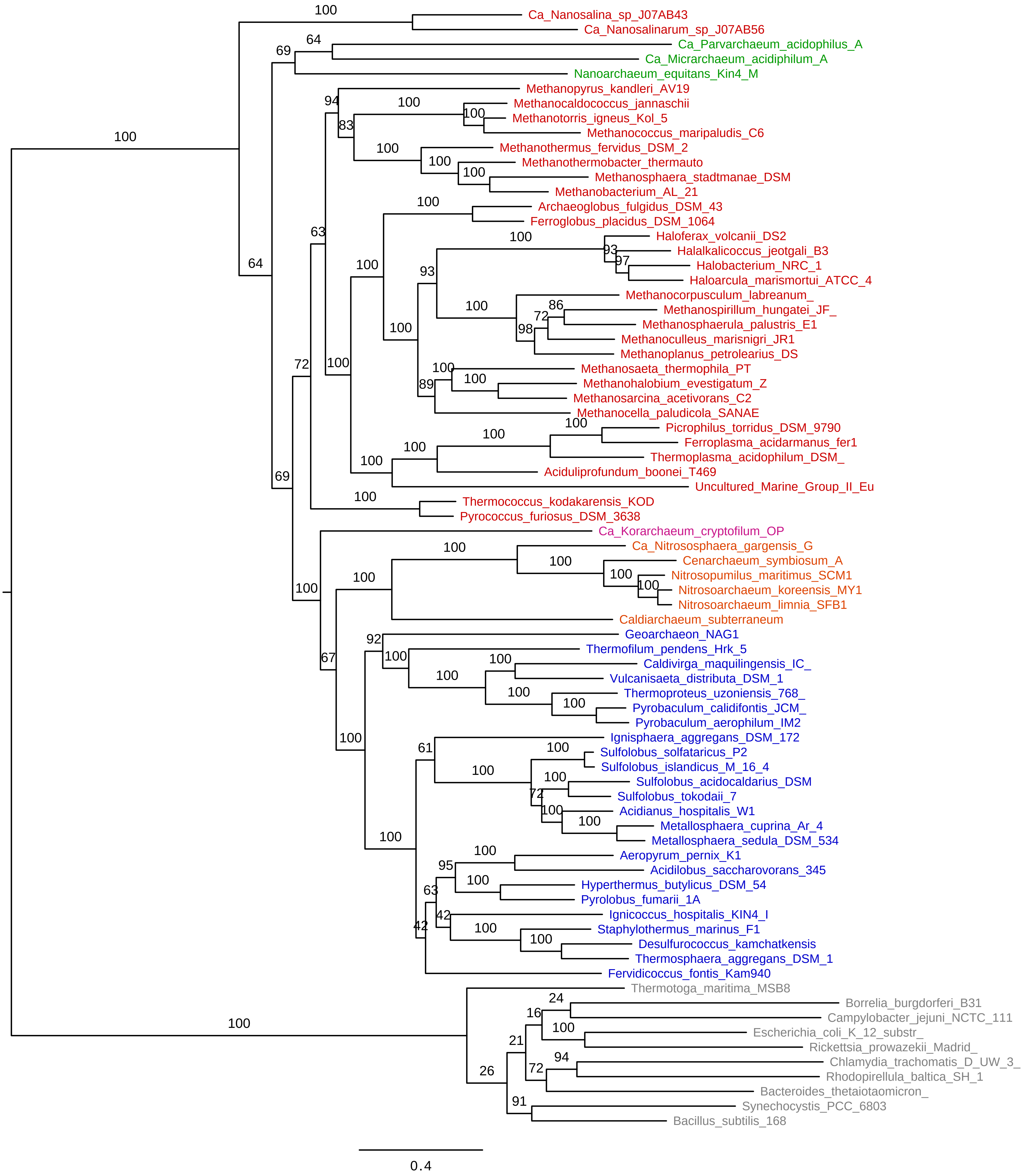


B: ML phylogeny (RAxML, CAT LG) of the 50% most biased sites of 33 r-proteins

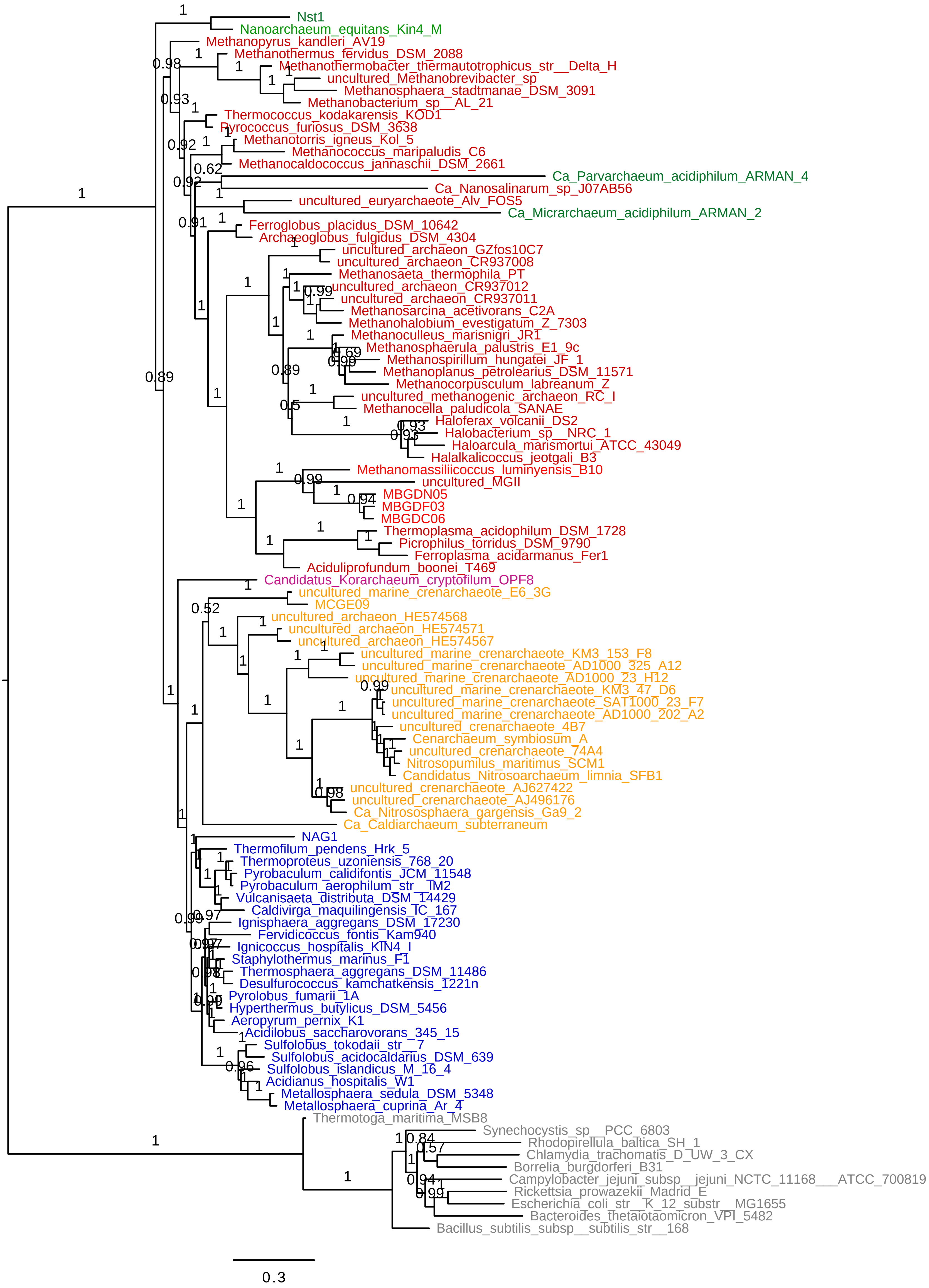


C: ML phylogeny (RAxML, CAT LG) of the 50% least biased sites of 33 r-proteins

D: ML phylogeny (RAxML, CAT LG) of 25 non-r-proteins



E: ML phylogeny (RAxML, CAT LG) of 57 conserved proteins



F: Bayesian phylogeny (phylobayes, CAT-Poisson) of 16S/23S rRNA