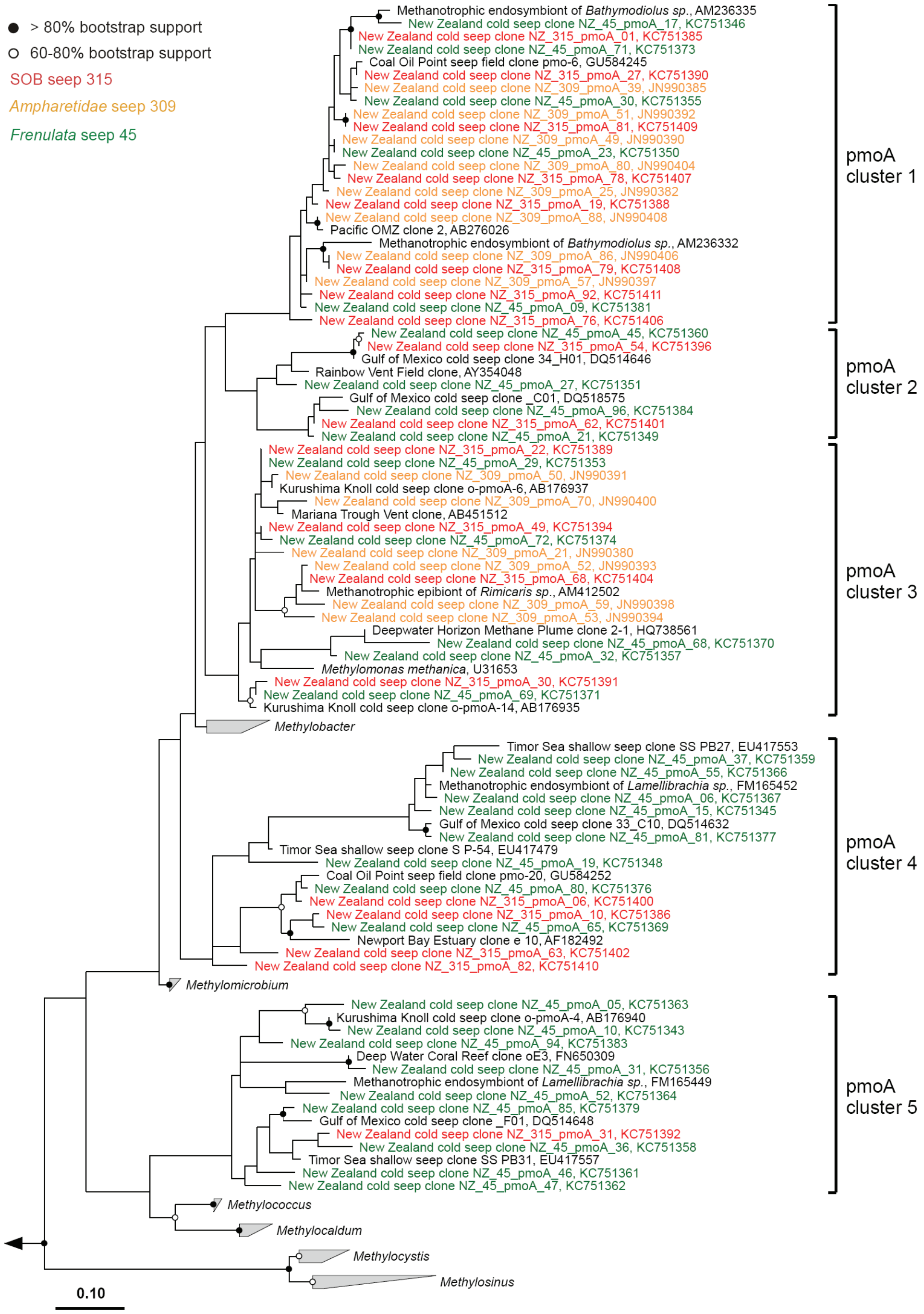

Figure S4: Phylogeny of *pmoA* protein

Phylogeny of the *pmoA* protein at the frenulate site 45, the ampharetid site 309 and the SOB site 315. The tree was calculated using 98 non-redundant, curated amino acid sequences,from the three habitats and 90 reference sequences. We used a maximum likelihood algorithm employing 100 bootstraps and a positional variability filter, excluding the highly variable regions. Bar = 10% estimated sequence divergence.