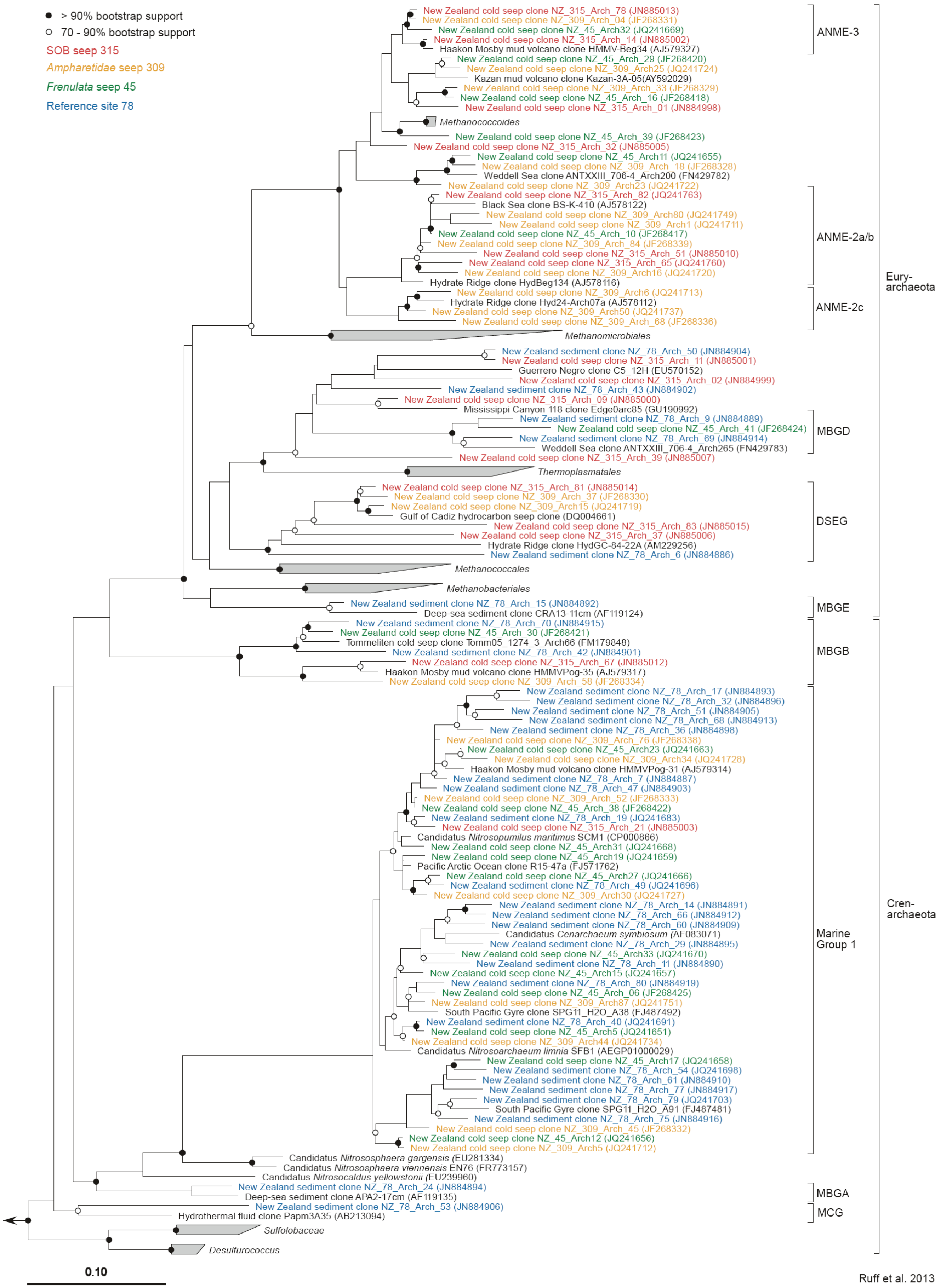

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Figure S2: Phylogeny of archaeal 16S rRNA

16S rRNA based phylogenetic tree showing archaeal sequences detected at the Hikurangi margin together with selected reference sequences of the domain *Archaea*. The tree is based on the RAxML algorithm as implemented in ARB. Full-length sequences were obtained from the ampharetid site 309 (yellow) and the frenulate site 45 (green). Partial sequences were retrieved from the SOB site 315 (red) and the reference site 78 (blue). Bar = 10% estimated sequence divergence.