

- > 90% bootstrap support
 - 70 - 90% bootstrap support
- SOB seep 315
Ampharetidae seep 309
Frenulata seep 45
Reference site 78

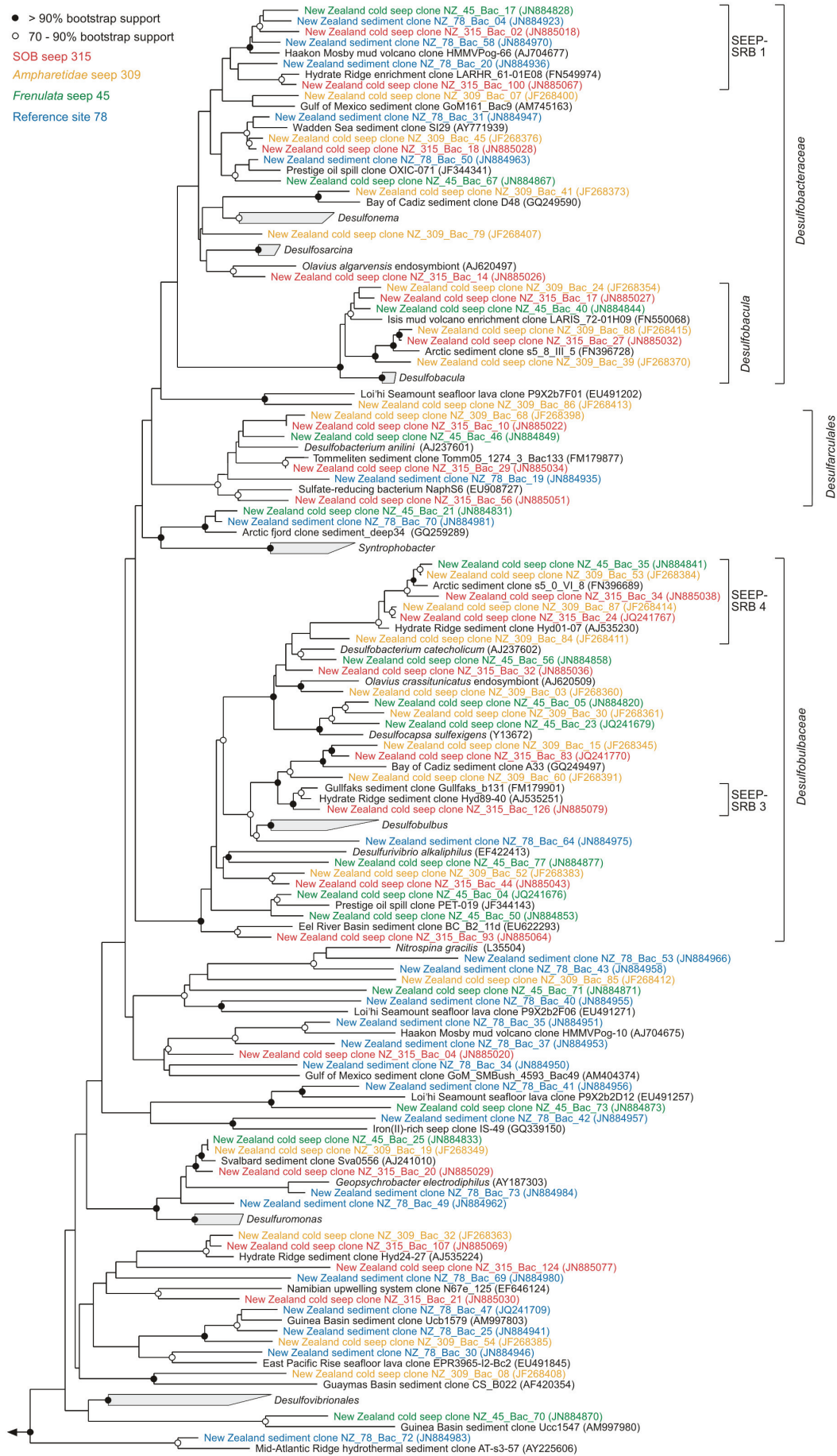


Figure S3: Phylogeny of deltaproteobacterial 16S rRNA

16S rRNA based phylogenetic tree showing sequences of *Deltaproteobacteria* detected at the Hikurangi margin and selected reference sequences of that bacterial class. 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.