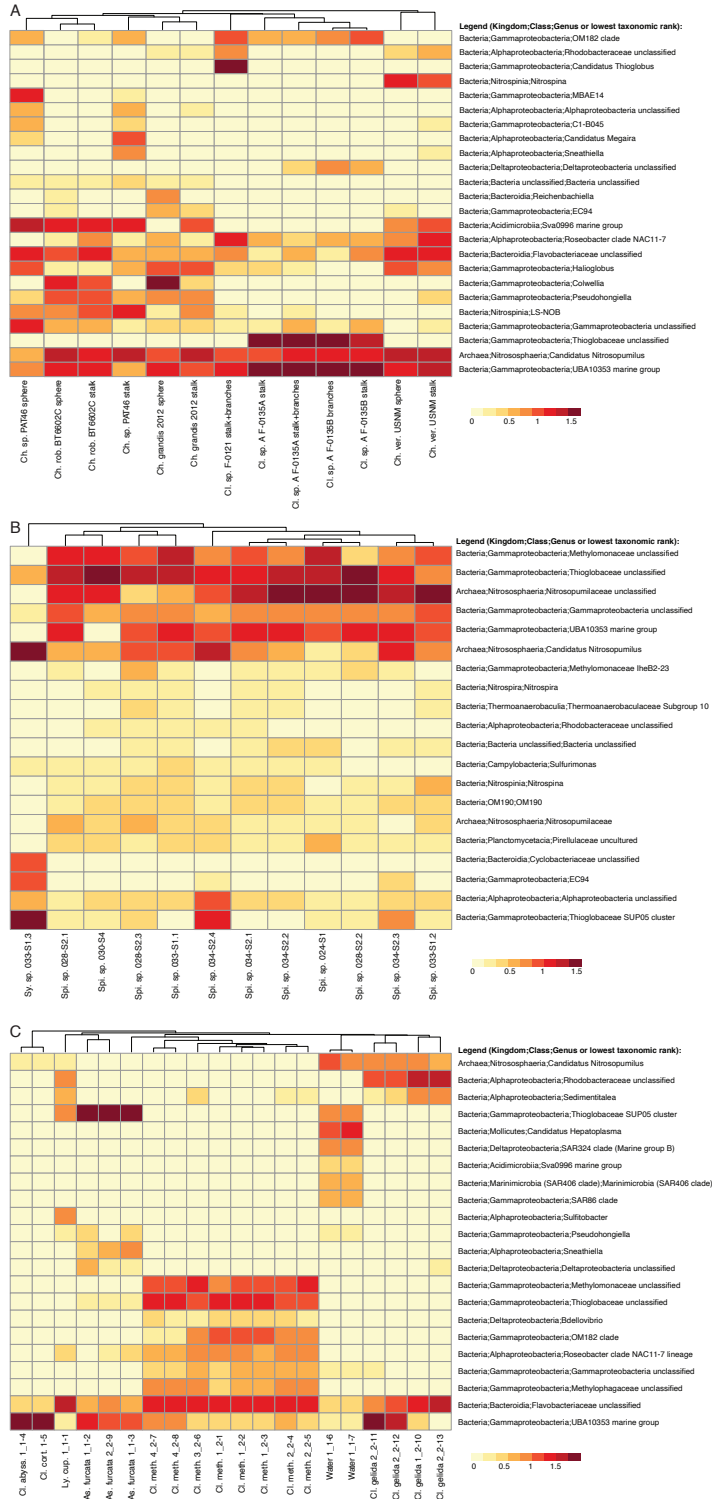
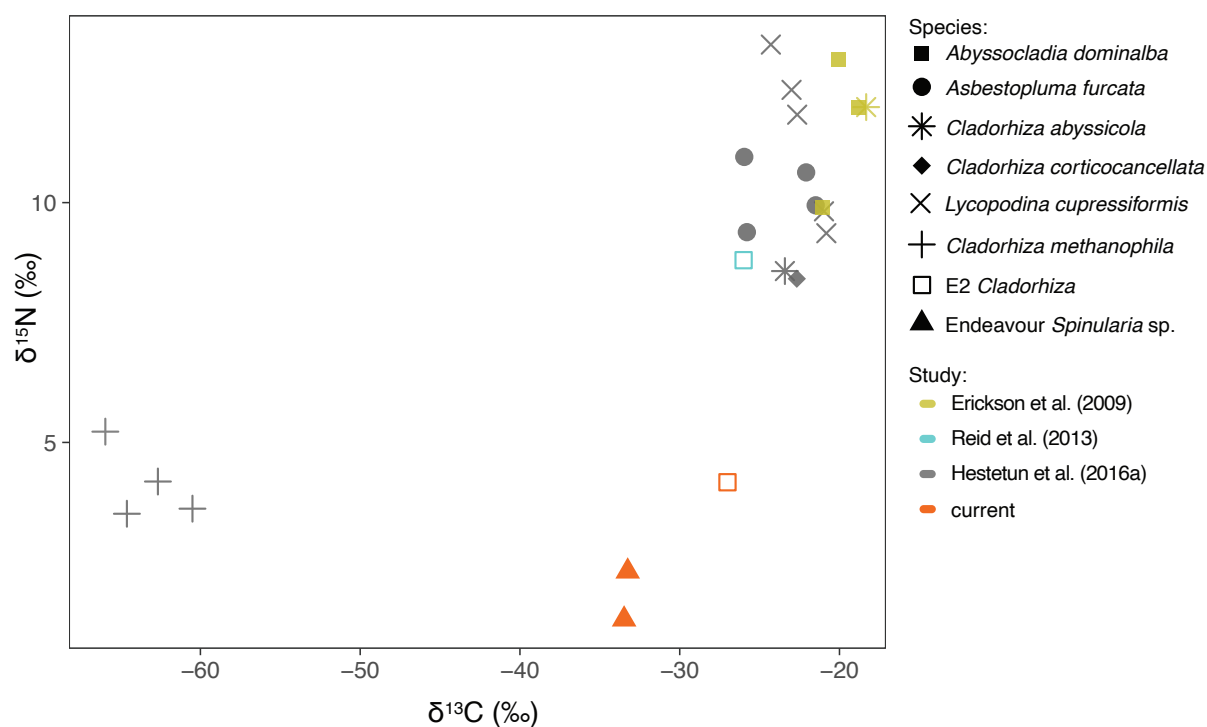


## Supplementary figures to:

Georgieva MN, Taboada S, Riesgo A, Díez-Vives C, De Leo FC, Jeffreys RM, Copley JT, Little CTS, Ríos P, Cristobo J, Hestetun JT and Glover AG (2020) Evidence of vent-adaptation in sponges living at the periphery of hydrothermal vent environments: ecological and evolutionary implications. *Frontiers in Microbiology* 11:1636. doi: 10.3389/fmicb.2020.01636



**Figure S1.** Relative abundances (log10 transformed) of the most common prokaryotes for individual sponge samples at the genus level. Genera with relative abundances lower than 0.5% across the dataset were omitted from the figure. The heatmaps also illustrate similarity (weighted UniFrac distance cladograms) of microbiome composition for each microbiome dataset analysed, **A**, *Cladorhiza-Chondrocladia* (Dataset 1) and **B**, *Spinularia-Sycon* (Dataset 2), while **C**, Cladorhizidae dataset generated by Hestetun et al. (2016) (Dataset 3). Genus and species names are abbreviated as follows: Cl. *Cladorhiza*, Ch. *Chondrocladia*, rob. *robertballardi*, ver. *verticillata*, Ly. cup. *Lycopina cupressiformis*, As. *Asbestopluma*, meth. *methanophila*, abyss. *abyssicola*, cort. *corticocancellata*, Spi. *Spinularia*, Sy. *Sycon*.



**Figure S2.** Carbon and nitrogen isotopic results ( $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ ) for *E2 Cladorhiza* and Endeavour *Spinularia* sp. specimens analysed during the present study in comparison to results for cladorhizid sponges from the previous studies of Erickson et al., (2009), Reid et al. (2013), Hestetun et al. (2016).

## References

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