# Online Supporting Material for Chapter 6

# Functional heterogeneity of *Marinobacter* links lifestyle and evolutionary history

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# Tables

**Table 6.1 –** Isolation Source and Habitat classes of *Marinobacter* genomes. List of all genomes used in the analysis, with phylogenetic clade, habitat class and geographical coordinates of isolation sites.

**Table 6.2 –** List of Algal-associated Marinobacters derived from literature. Shown are the strain names, isolation source, algal host as well as 16S rRNA sequences used to infer ML phylogeny. References include (Al-Wahaib et al., 2016; Amin et al., 2015; Baker et al., 2016; Brennan, 2014; Le Chevanton et al., 2013; Frazier et al., 2007; Green et al., 2004, 2015; Grossart et al., 2004; Jasti et al., 2005; Kuo and Lin, 2013; Ruh et al., 2009; Seibold et al., 2001; Sher et al., 2011; Tapia et al., 2016)

**Table 6.3 –** List of *Marinobacter* type strains.

**Table 6.4 –** Enriched orthologous gene families per phylogenetic clade as identified by Scoary (Brynildsrud et al., 2016).

**Table 6.5 –** Depleted orthologous gene families per phylogenetic clade as identified by Scoary (Brynildsrud et al., 2016).

**Table 6.6 –** Lineage associated orthologous gene families as determined by RandomForest (Liaw and Wiener, 2002), sorted by variable importance.

**Table 6.7 –** Lineage associated orthologous gene families as determined by RandomForest (Liaw and Wiener, 2002), Scoary (Brynildsrud et al., 2016), and Kruskal-Wallis. The list contains those orthologous gene families that were picked up by all three methods.

**Table 6.8 –** Habitat associated gene and domain families as determined by PhyloLM. PhyloLM estimates are given, with Standard Error, p value and FDR-corrected p-values < 0.05. Analysis was run on matrices containing Pfam, CAZY, TCDB and COG.

**Table 6.9** – Genome statistics for genomes used in Chapter 6, as derived from CheckM (Parks et al., 2015)

**Table 6.10** – Distribution of Carbohydrate Active Enzyme domains identified in Marinobacter genomes.

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