# Online Supporting Material for Chapter 5

# Pangenome and phylogenomic relationship of *Marinobacter* and related *Gammaproteobacteria*: proposal to transfer *Marinobacter* gen. nov. from *Alteromonadales* ord. nov. to *Oceanospirillales* ord. nov. within the new family *Marinobacteraceae* fam. nov.

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# Tables

**Table 5.1 – List of complete genome sequences used in Chapter 5**. Gammaproteobacteria as well as a Alphaproteobacterial outgroup containing *Rhodobacter*, *Roseobacter*, *Rugegeria*, *Dinoroseobacter* and *Pheobacter* strains.

**Table 5.2 - Genome statistics** for genomes used in Chapter 5, as derived from CheckM (Parks et al., 2015).

**Table 5.3 – Phenotypic data derived from IJSEM** (Barberán et al., 2017).

**Table 5.4 - Marinobacter signature orthologs.** Pan-genome was calculated for *Oceanospirilalles* genomes as well as members of the *Marinobacter* genus. Shown are orthologous gene families which are shared among all *Marinobacter* genomes but absent in all *Oceanospirilalles* genomes. Indicated are locus tags from *Marinobacter* *hydrocarbonoclasticus* SP17.

# References

Barberán, A., Caceres Velazquez, H., Jones, S., and Fierer, N. (2017). Hiding in Plain Sight: Mining Bacterial Species Records for Phenotypic Trait Information. *mSphere*. doi:10.1128/msphere.00237-17.

Parks, D. H., Imelfort, M., Skennerton, C. T., Hugenholtz, P., and Tyson, G. W. (2015). CheckM : assessing the quality of microbial genomes recovered from isolates , single cells , and metagenomes. *Genome Res.* 25, 1043–1055. doi:10.1101/gr.186072.114.Freely.