# 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 5.1 - 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.