#### Bioinformatic analysis:

16S rRNA amplicon data was processed via our in-house pipeline available on github (<https://github.com/MSMortensen/DF_GMH_pipeline>) using the pipelines default settings. Briefly, raw amplicon sequence data was demultiplexed using cutadapt (v. 4.1) (Martin 2011), denoised using DADA2 (v. 1.22)(Callahan *et al.* 2016) and ASVs classified against rdp\_train\_set\_18 (Cole *et al.* 2014)**.** Further processing were done using Phyloseq (v.1.42.0) (McMurdie and Holmes 2013) running in R (v. 4.2) (R Core Team 2022). Detailed settings included in supplementary file …

References

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