Interactive comment on "Global analysis of gene expression dynamics within the marine microbial community during the VAHINE mesocosm experiment in the South West Pacific" *by* Ulrike Pfreundt et al.

Ulrike Pfreundt et al.

wolfgang.hess@biologie.uni-freiburg.de

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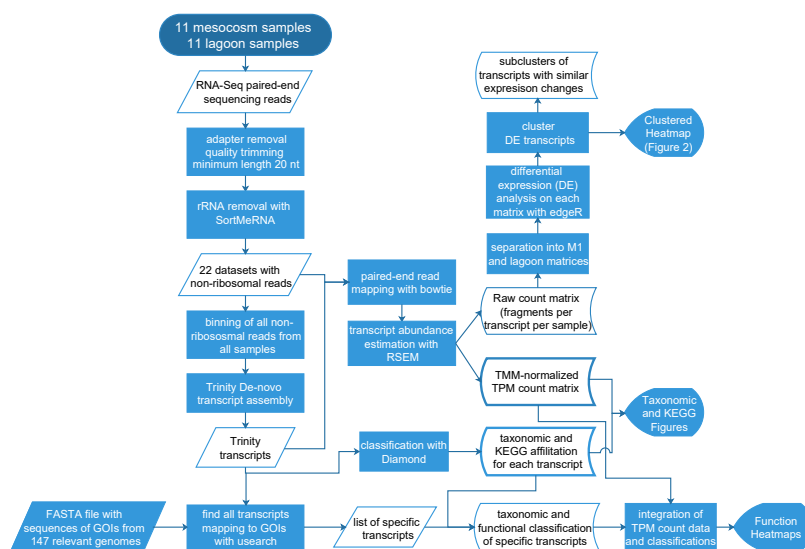
Fig. 1. Flowchart describing the major steps in the bioinformatics workflow. Pre-processing of RNA-Seq reads was done separately for each dataset, leading to 22 datasets of non-ribosomal paired-end reads.
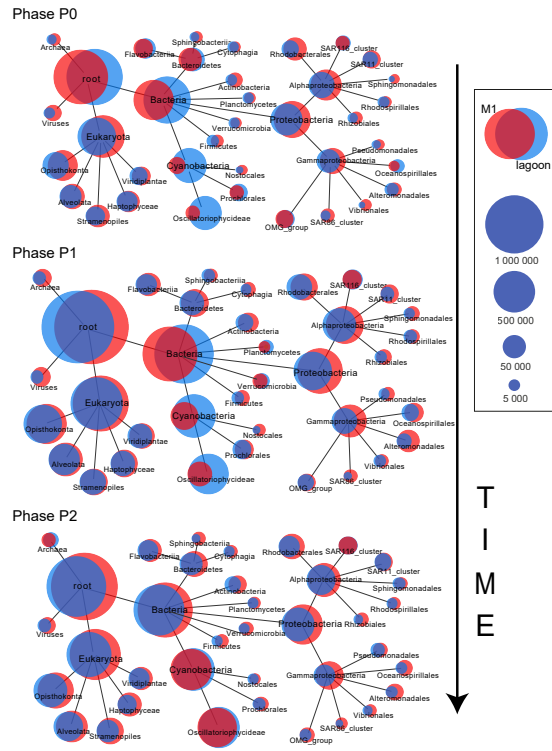
Fig. 2. Figure 4. Comparison of the taxonomic affiliation of mRNA transcripts from M1 and the lagoon in the three chronological phases P0, P1, and P2, visualized with CoVennTree (Lott et al., 2015).