Biogeosciences Discuss.,
doi:10.5194/bg-2015-564-AC2, 2016

Biogeosciences
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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

Received and published: 6 June 2016

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Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2015-564, 2016.

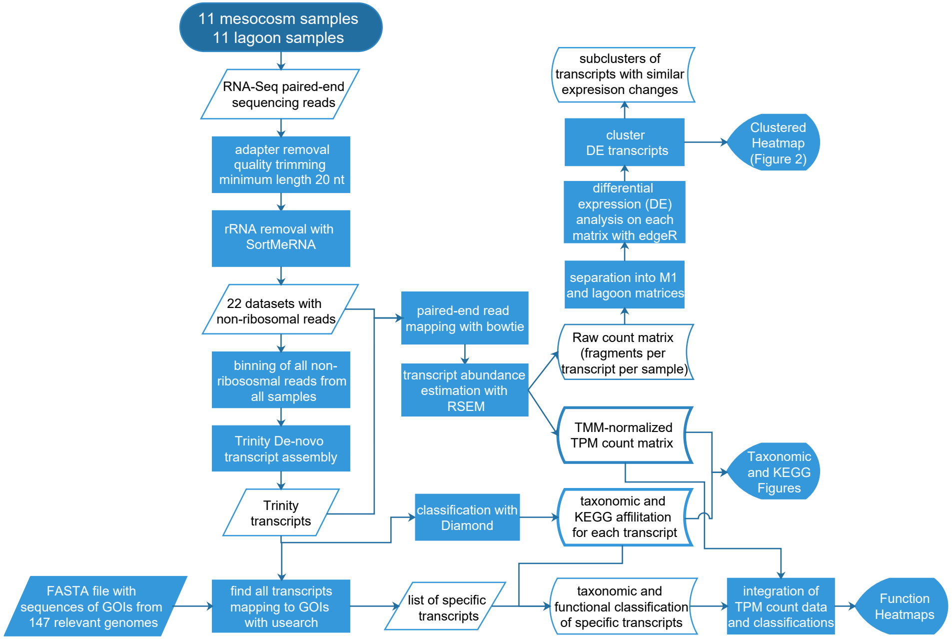

Fig. 1. Flowchart describing the major steps in the bioinformatics workflow. Pre-processing of RNA-Seq reads was done separately for each dataset, leading to 22 datasets of non-ribosomal paired-end reads.

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Discussion paper

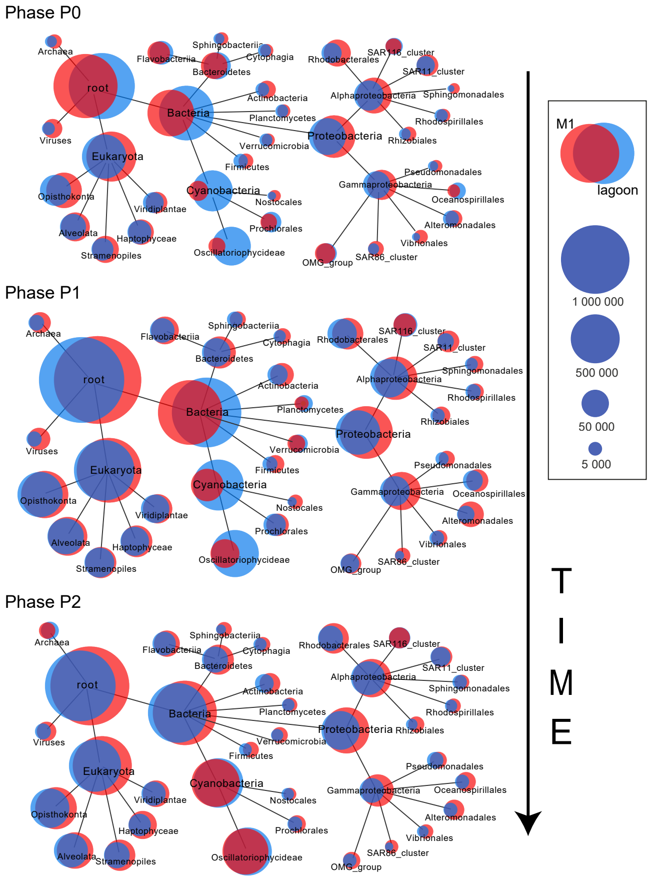

Fig. 2. Figure 4. Comparison of the taxonomic affiliation of mRNA transcripts from M1 and the lagoon in the three chronological phases P0, P1, and P2, visualized with CoVennTree (Lott et al., 2015).

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