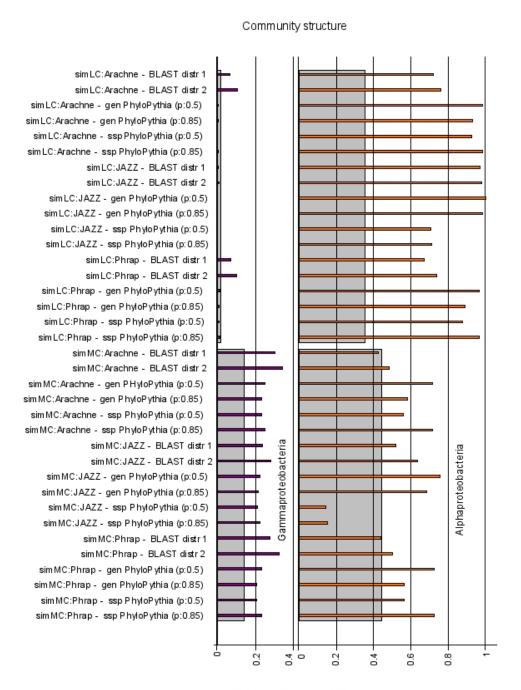
Supplementary Figure 2. Relative abundance of Alpha (right) and Gamma (left) proteobacteria as derived from binning results for the simLC and simMC datasets. The results are based on the assignments of contigs at the rank of Class (or lower taxonomic ranks in the case of PhyloPythia). Grey boxes indicate the relative abundance of the Alpha and Gamma proteobacterial dominant populations in the simulated dataset.



Relative abundance (Binned sequence/ total assembled sequence)