

Project Name: LD_normalization

NormalizerDE (ver 1.14.0)

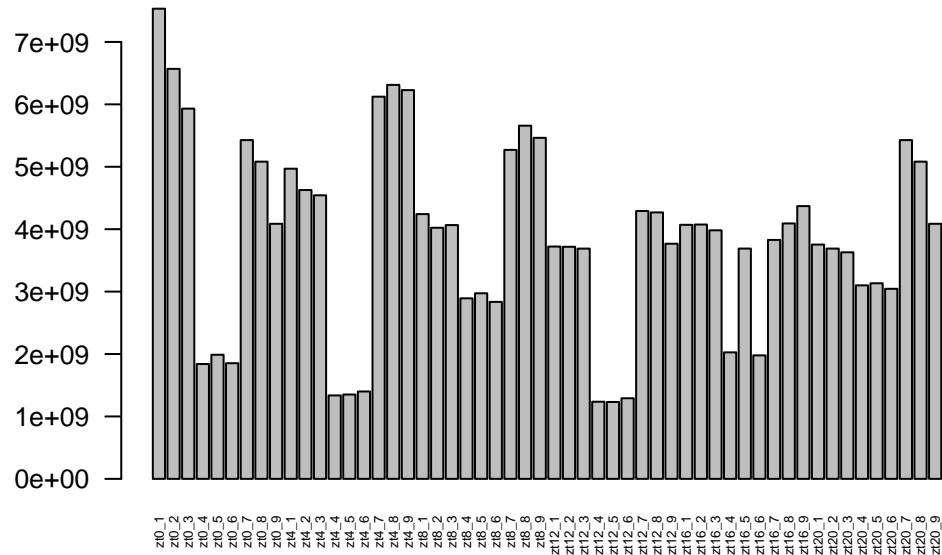
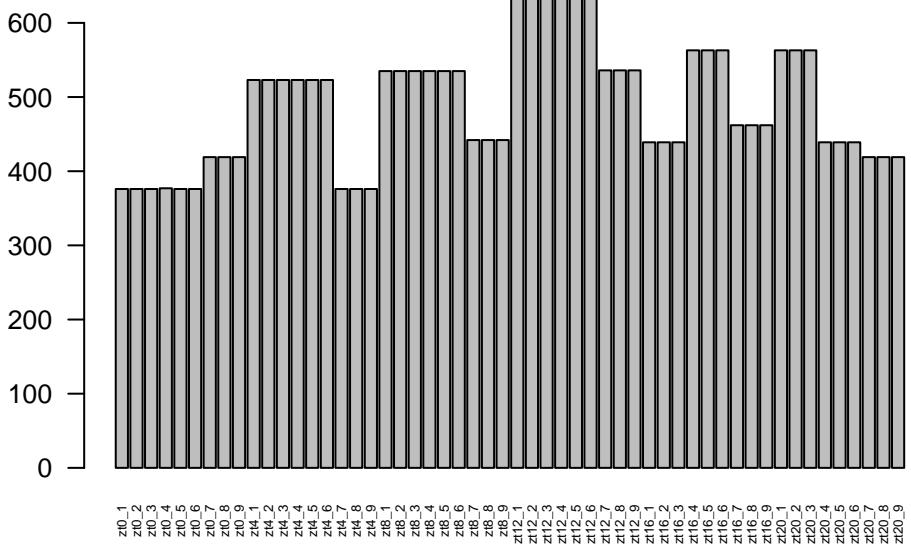
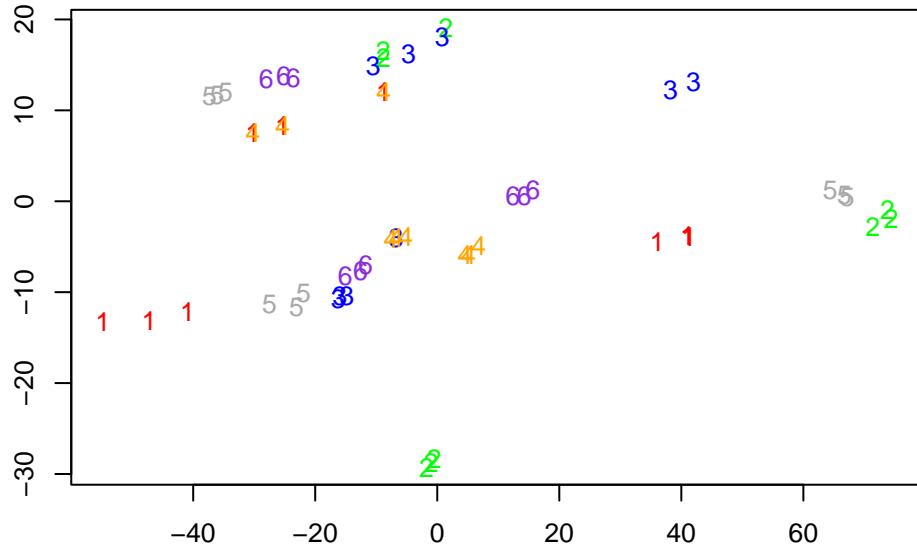
Report created on: 2022-10-20

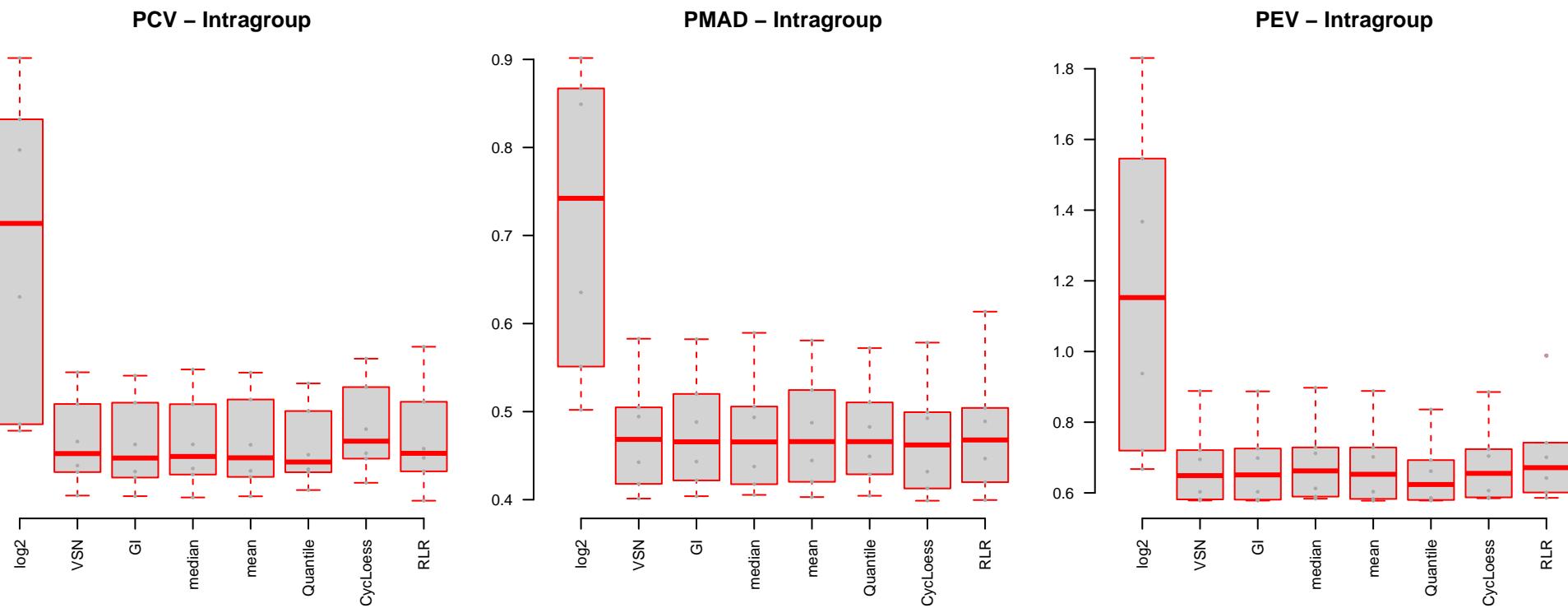
Citation: NormalizerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

Documentation for analyzing this report can be found at <http://quantitativeproteomics.org/normalizer/help.php>

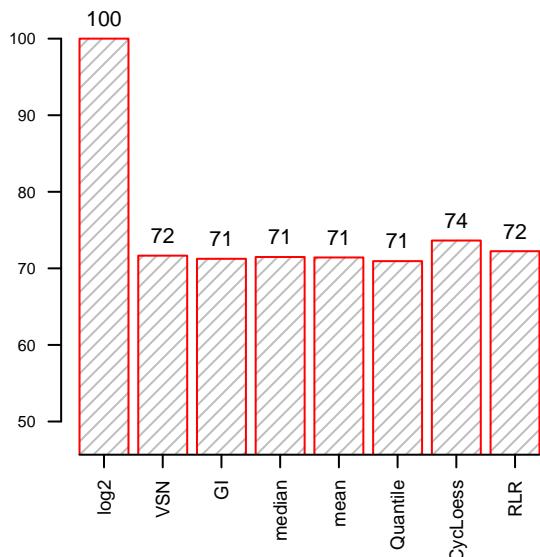
Group nbr.	Design group	Nbr. samples in cond.
1	zt0	9
2	zt12	9
3	zt16	9
4	zt20	9
5	zt4	9
6	zt8	9

Please note that the grouping only impacts evaluation measures and visuals seen in the report, they do not impact the performed normalizations.

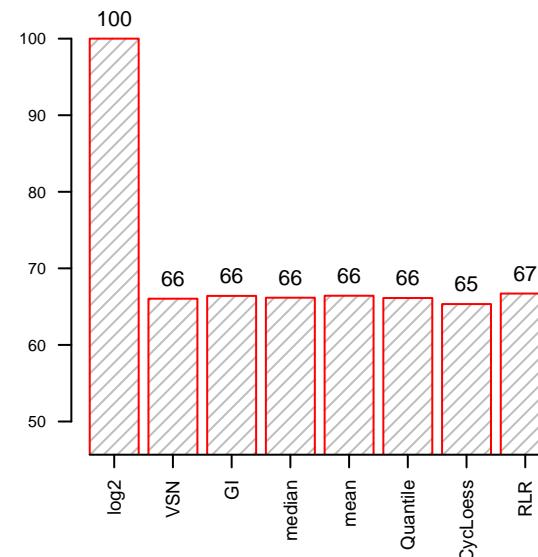
Total intensity**Total missing****Log2-MDS plot**



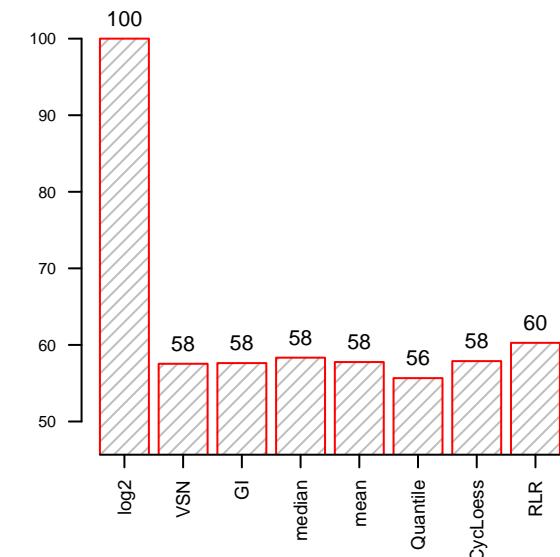
PCV compared to log2



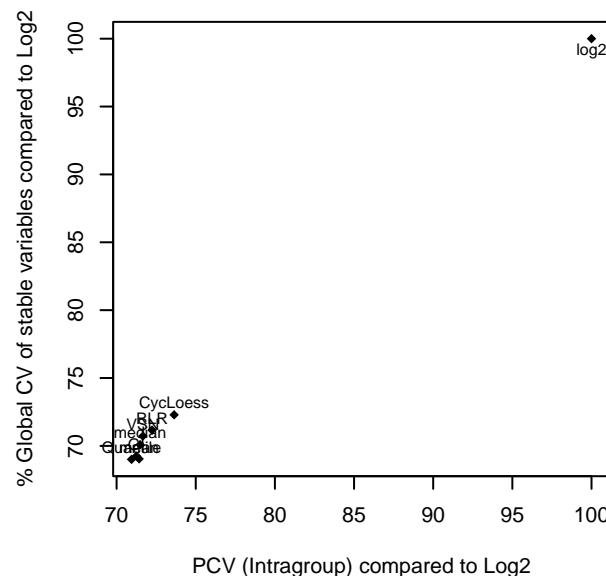
PMAD compared to log2

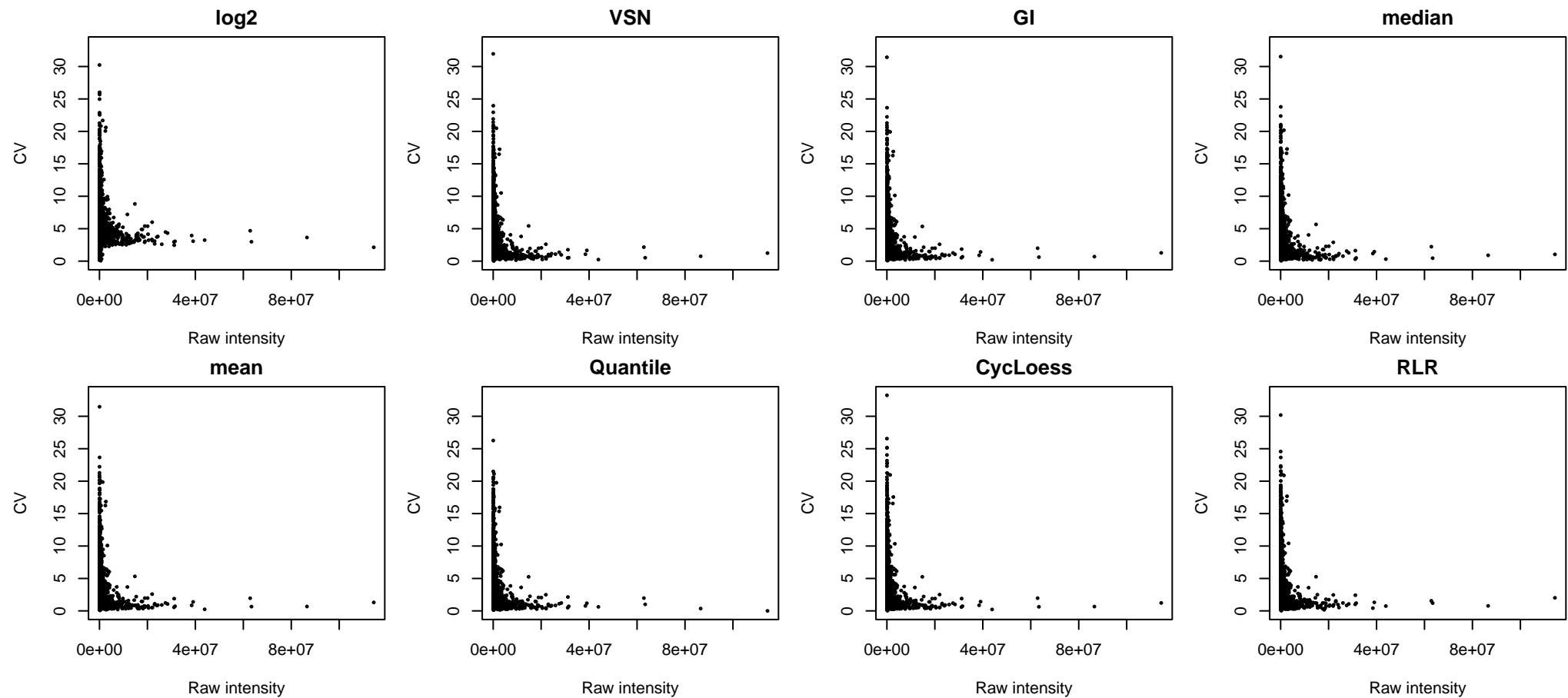


%PEV – compared to log2



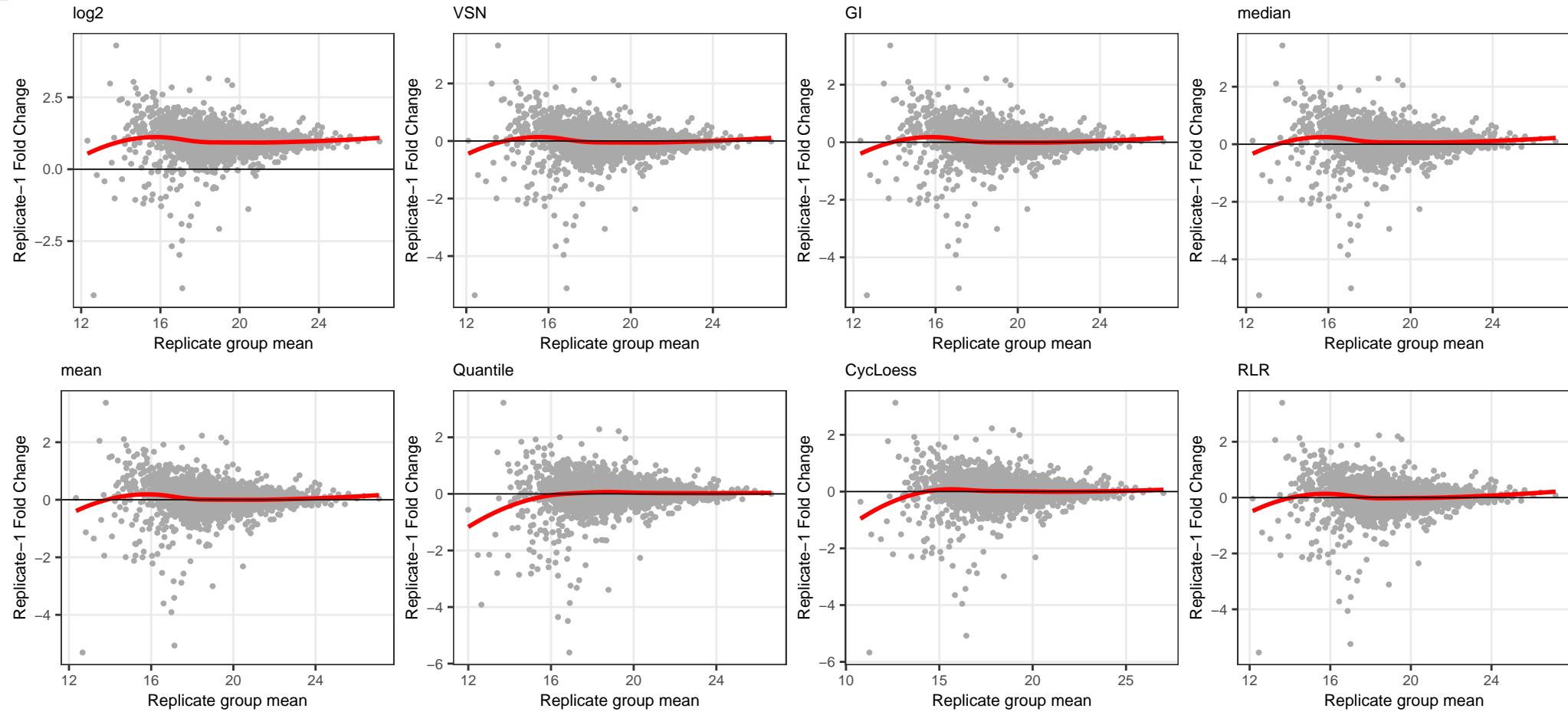
Stable variables plot

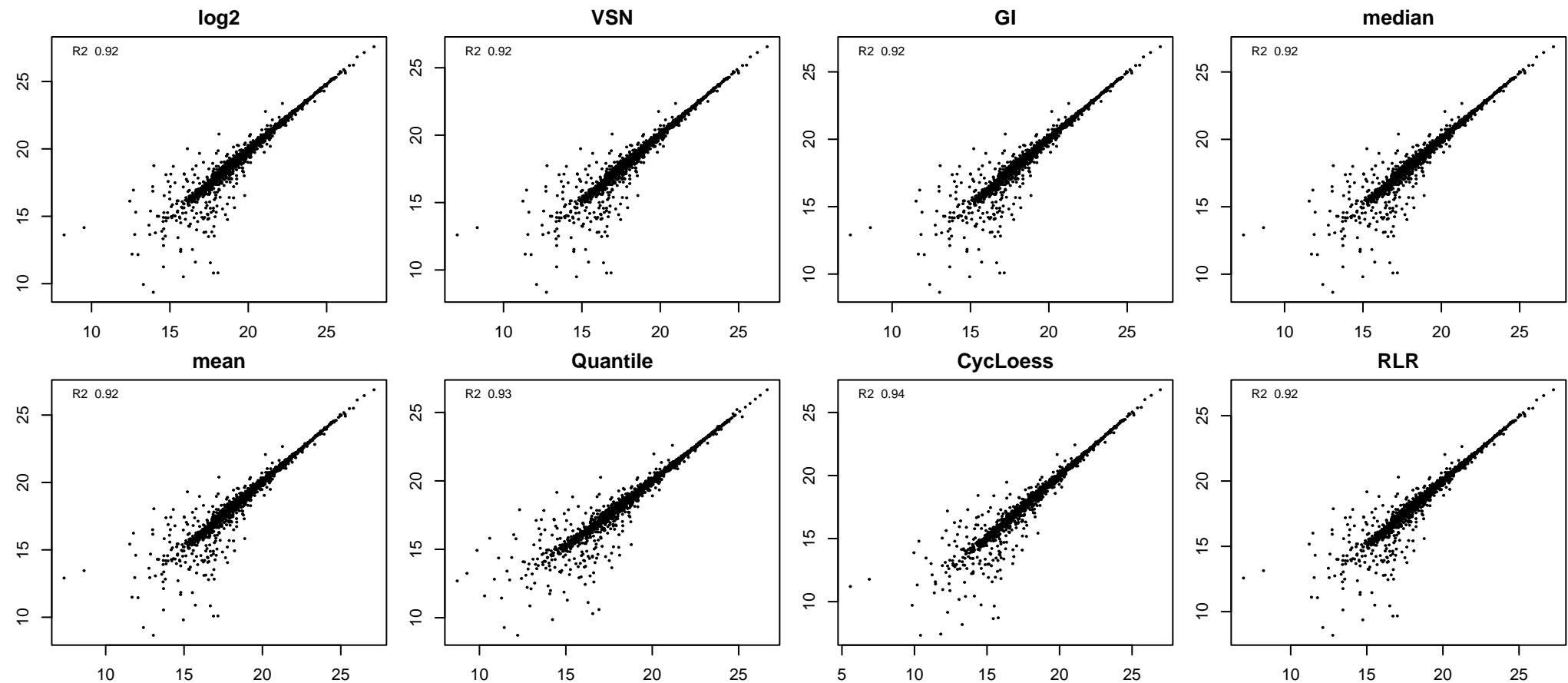




MA plots

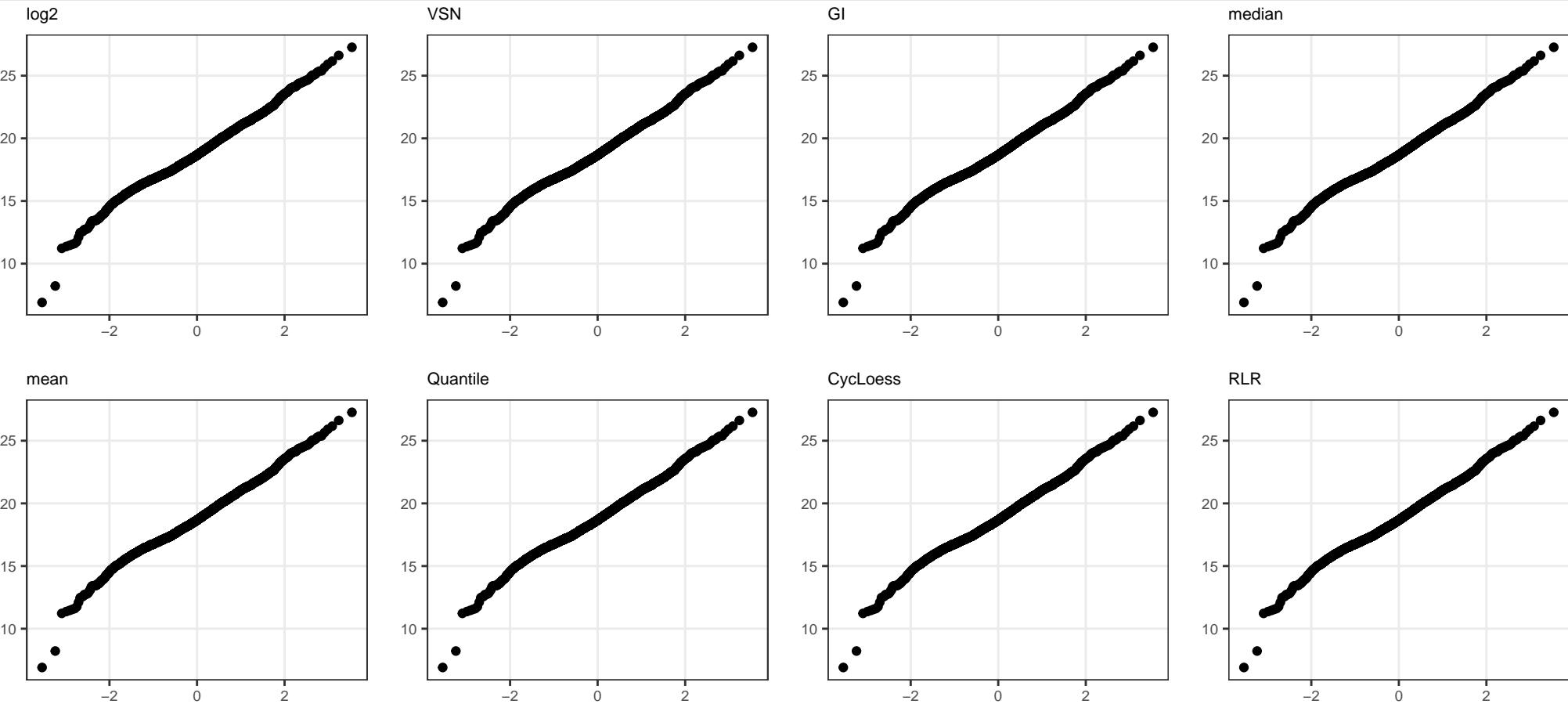
NormalizerDE Report

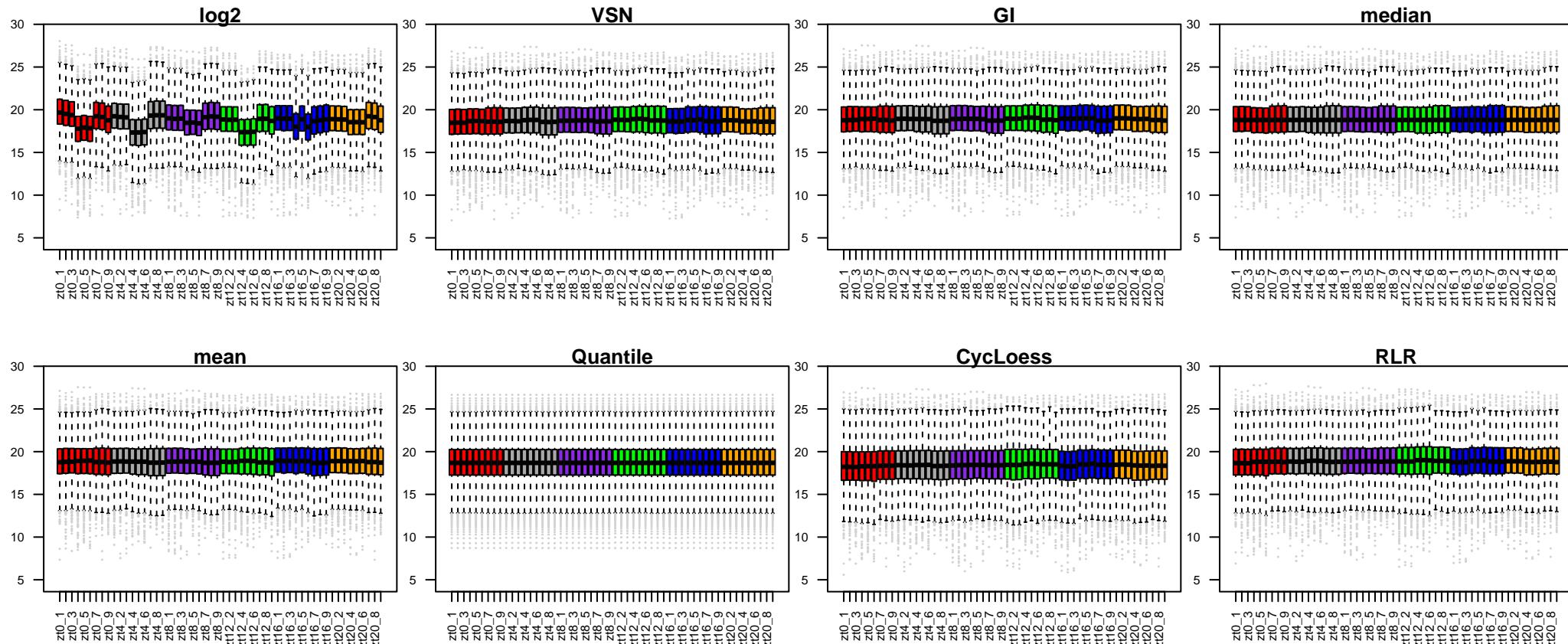


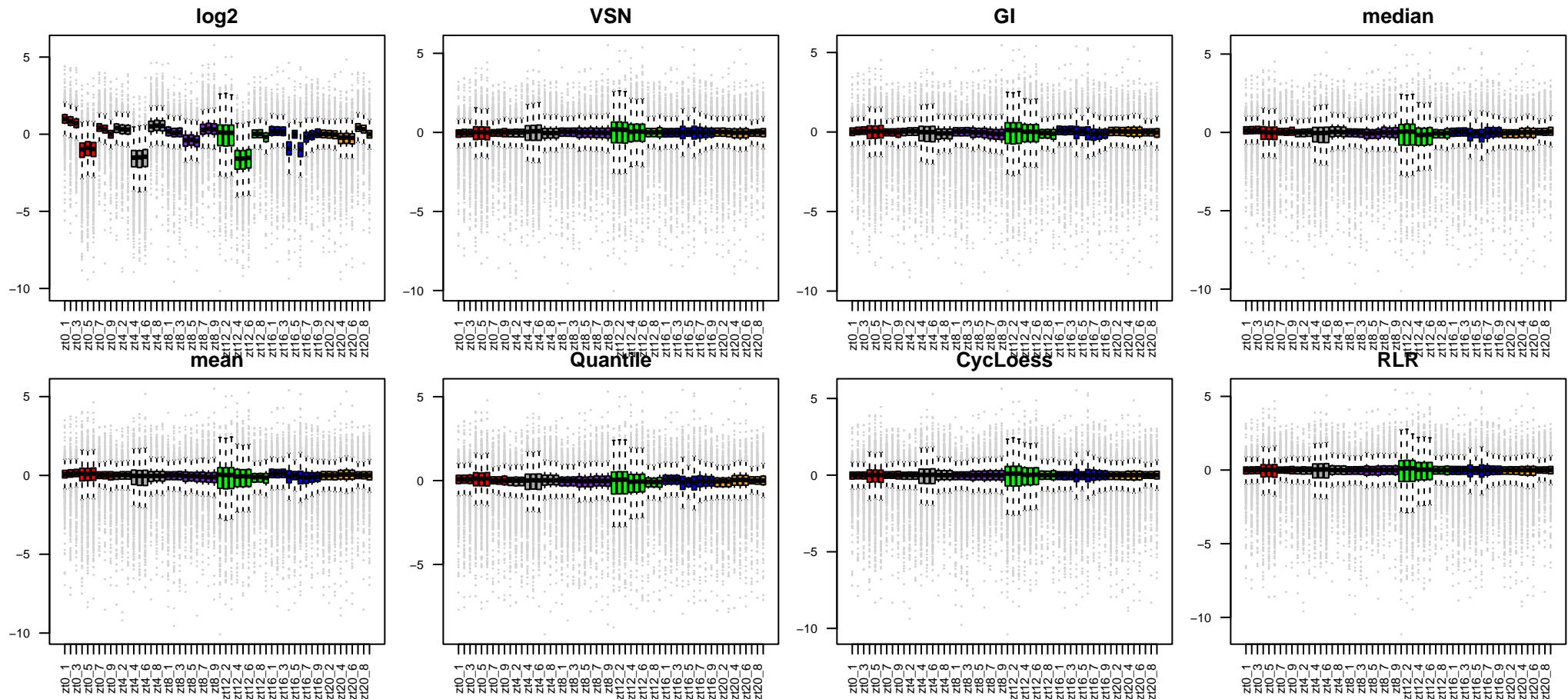


Q-Q plots

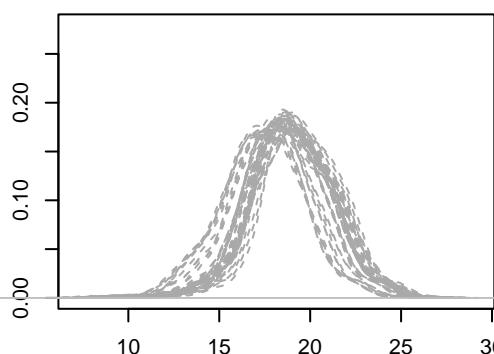
NormalizerDE Report



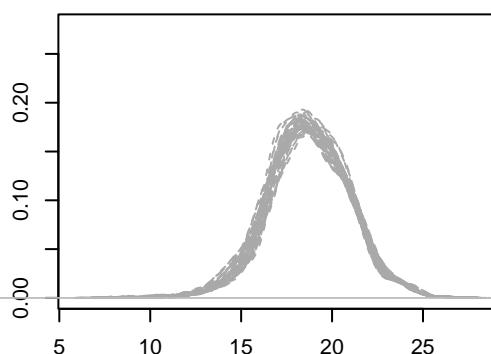




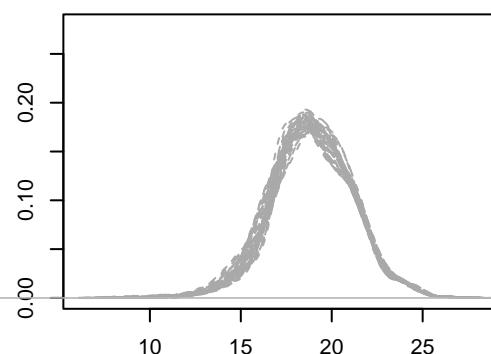
log2



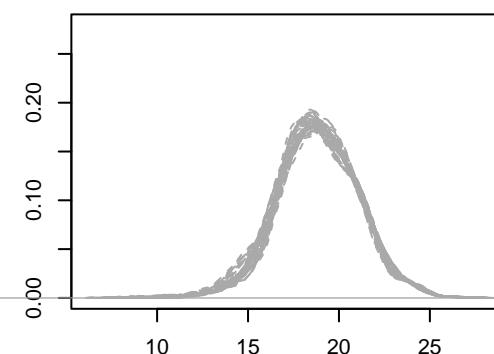
VSN



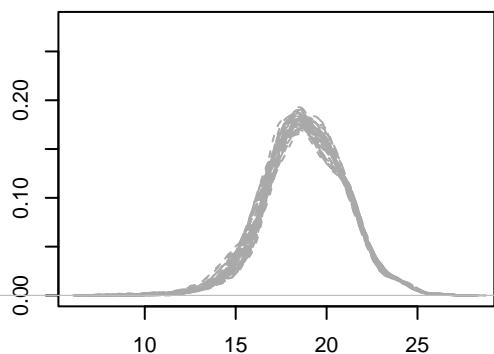
GI



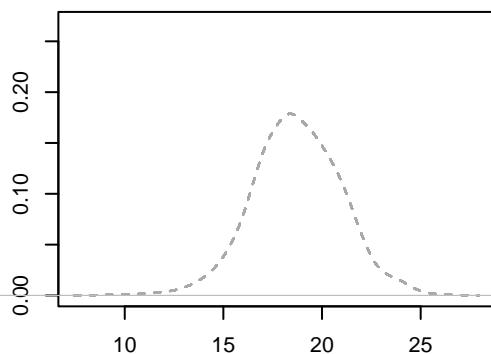
median



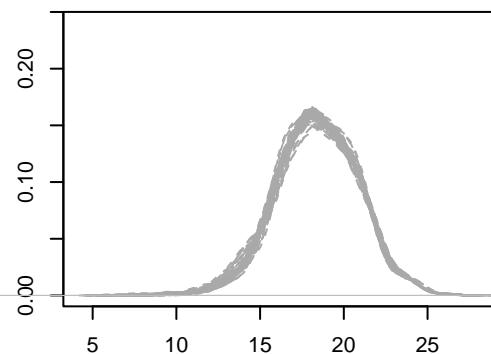
mean



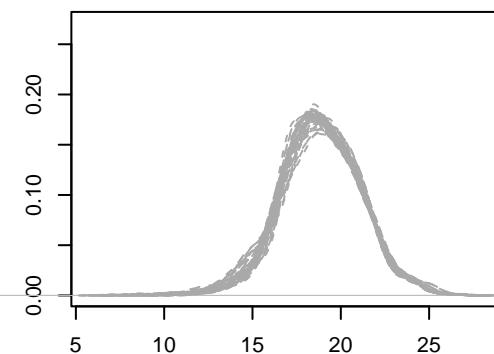
Quantile

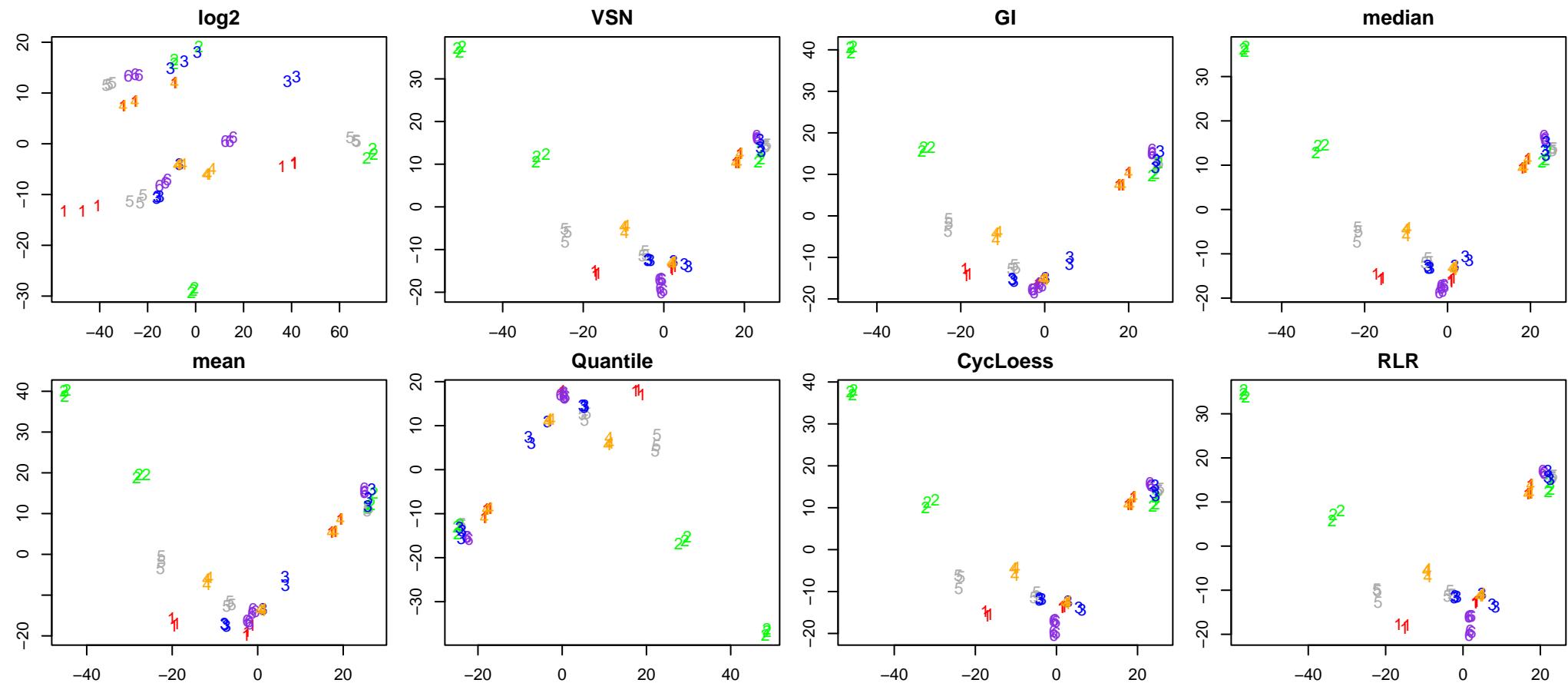


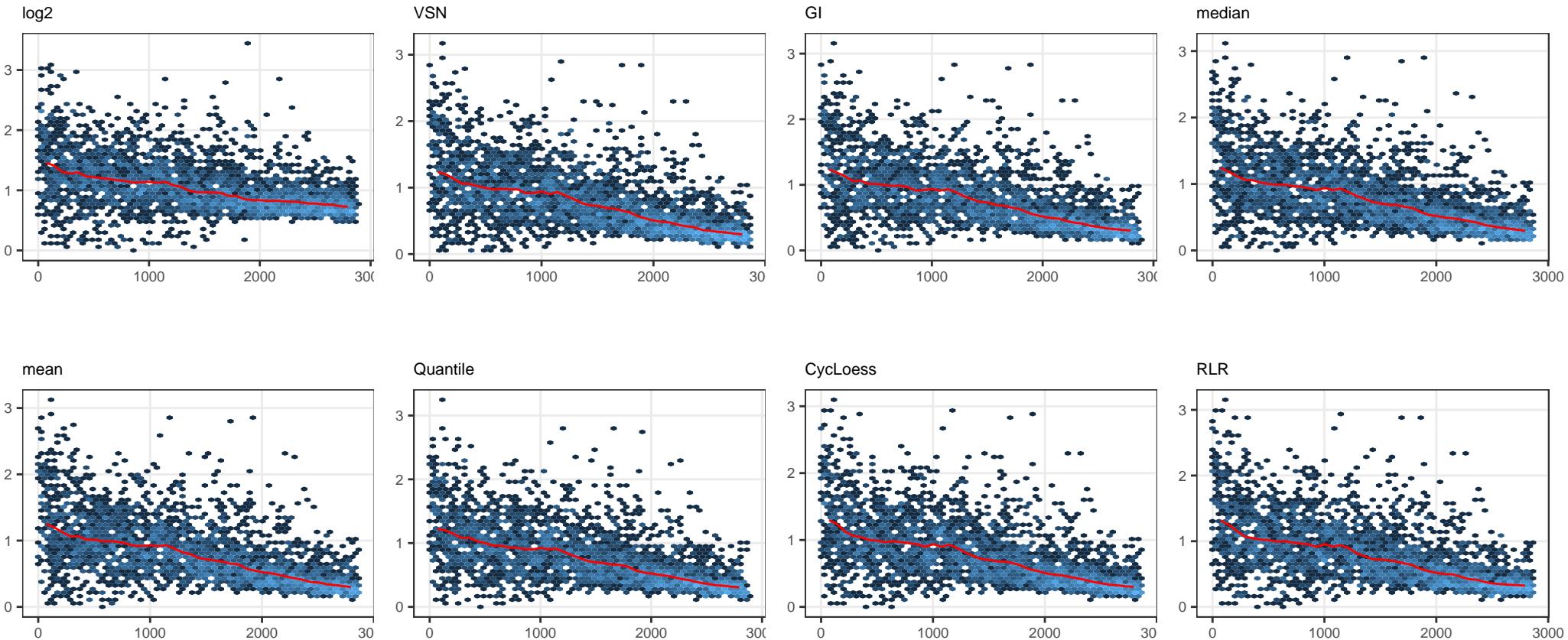
CycLoess



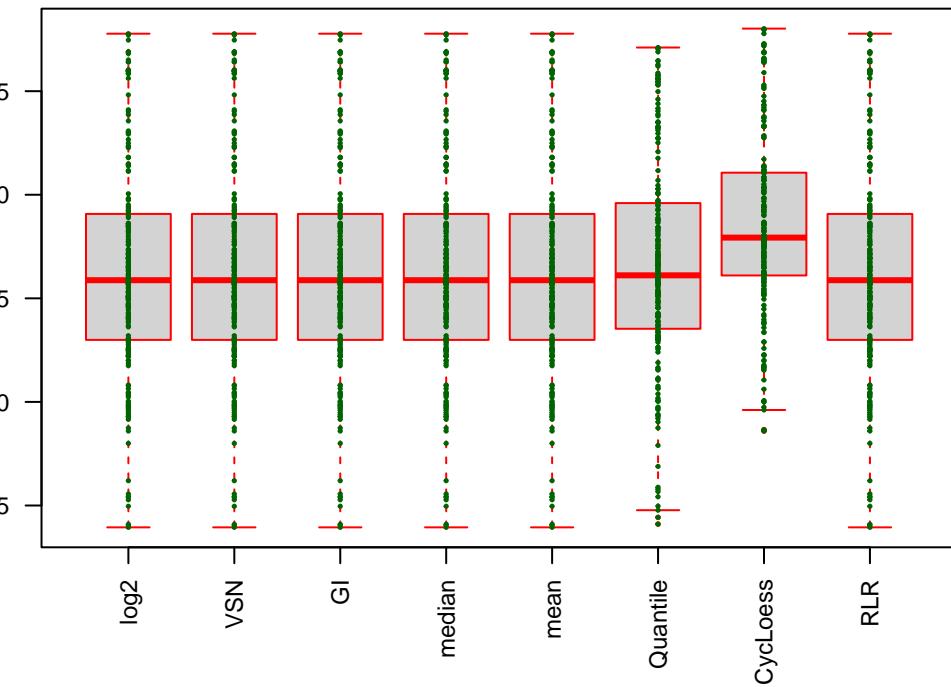
RLR



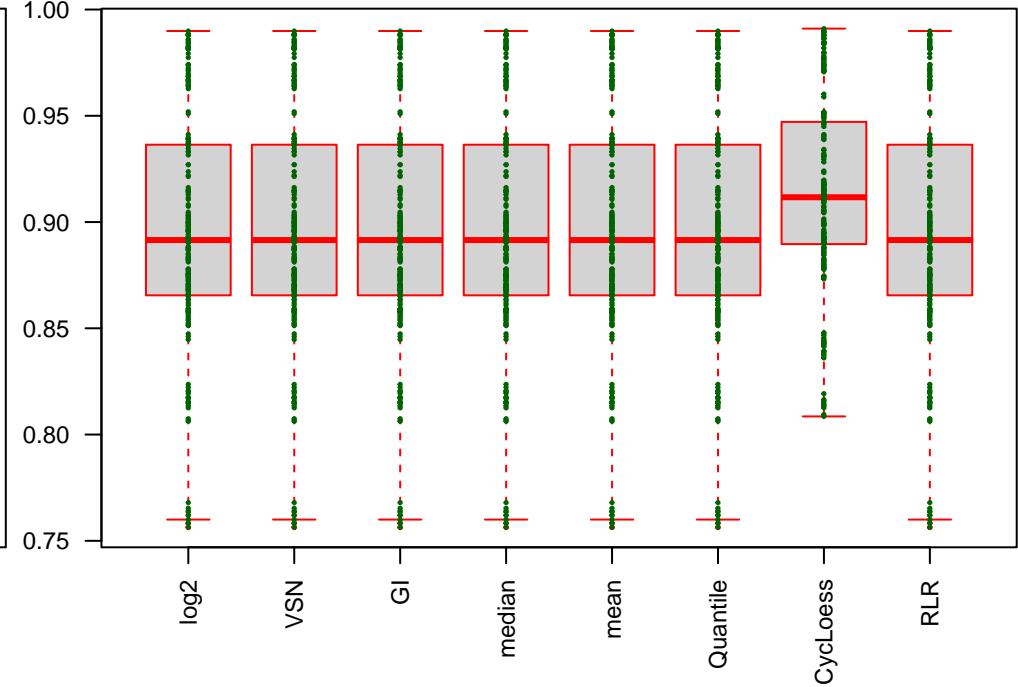




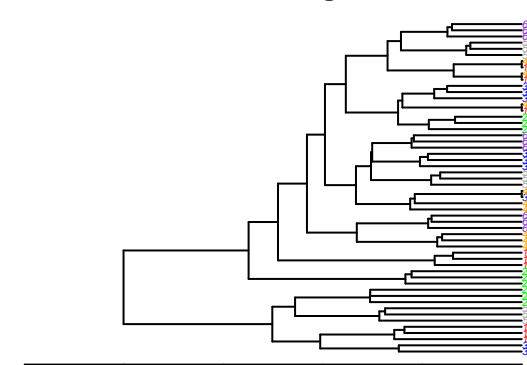
Pearson correlation – Intragroup



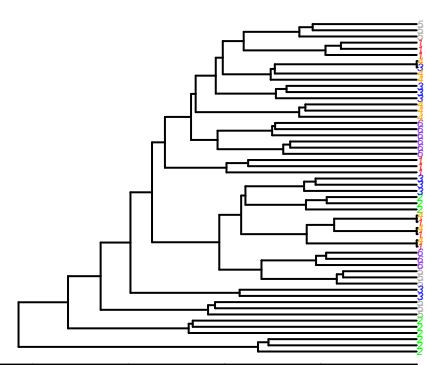
Spearman correlation – Intragroup



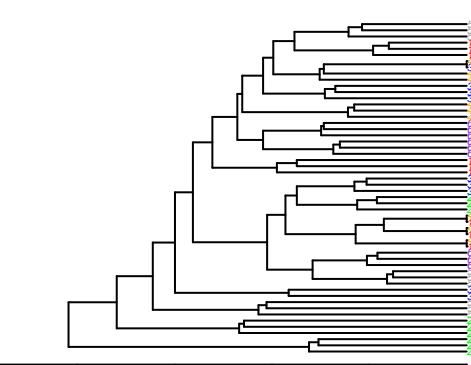
log2



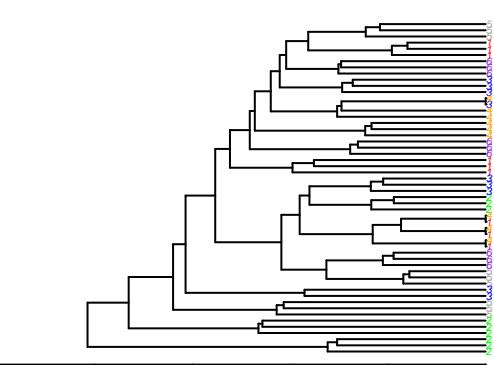
VSN



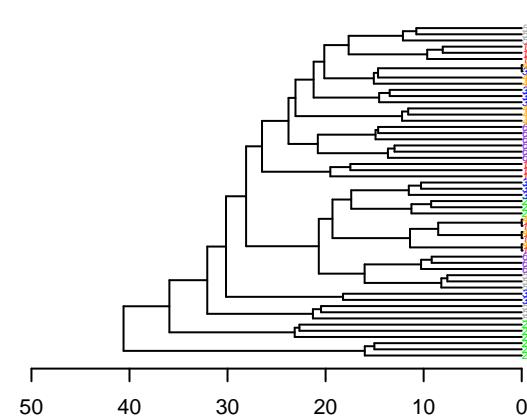
GI



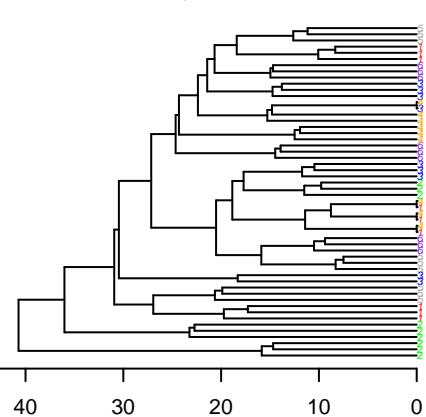
median



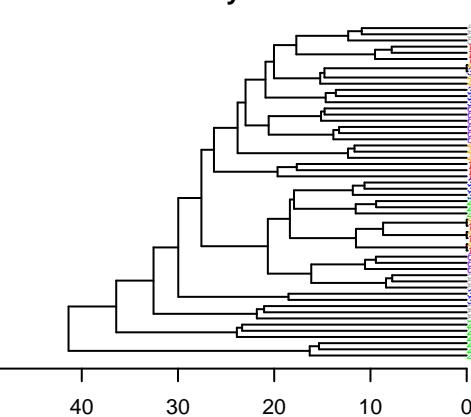
mean



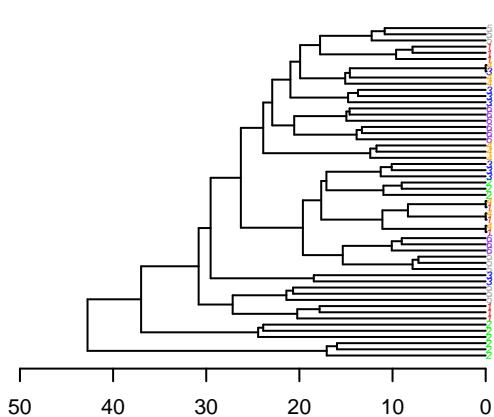
Quantile



CycLoess



RLR



HistPlots

NormalizerDE Report

