

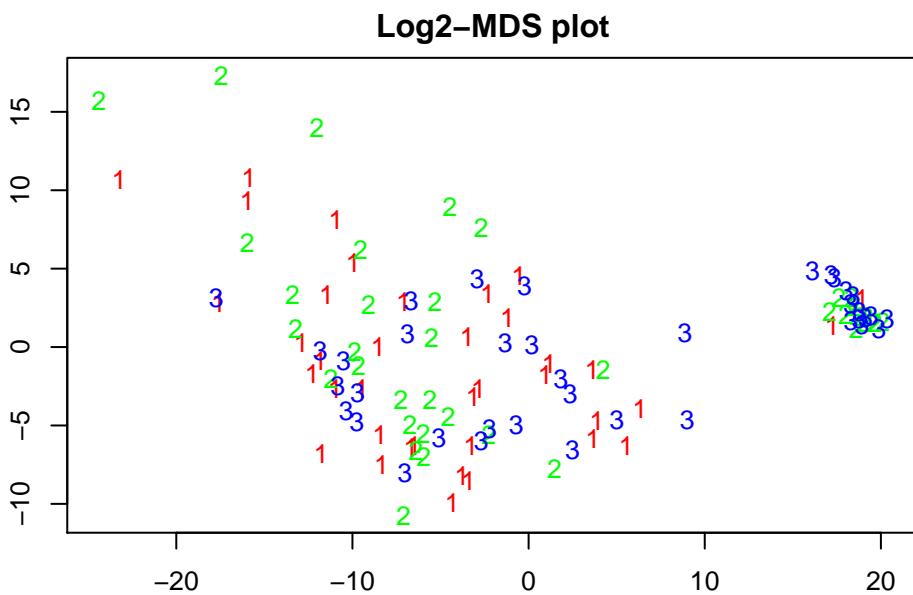
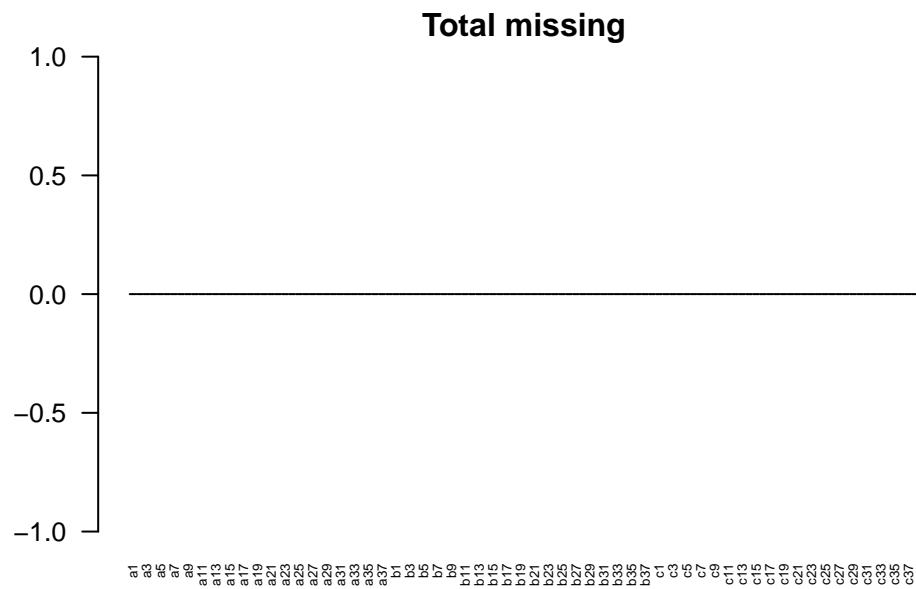
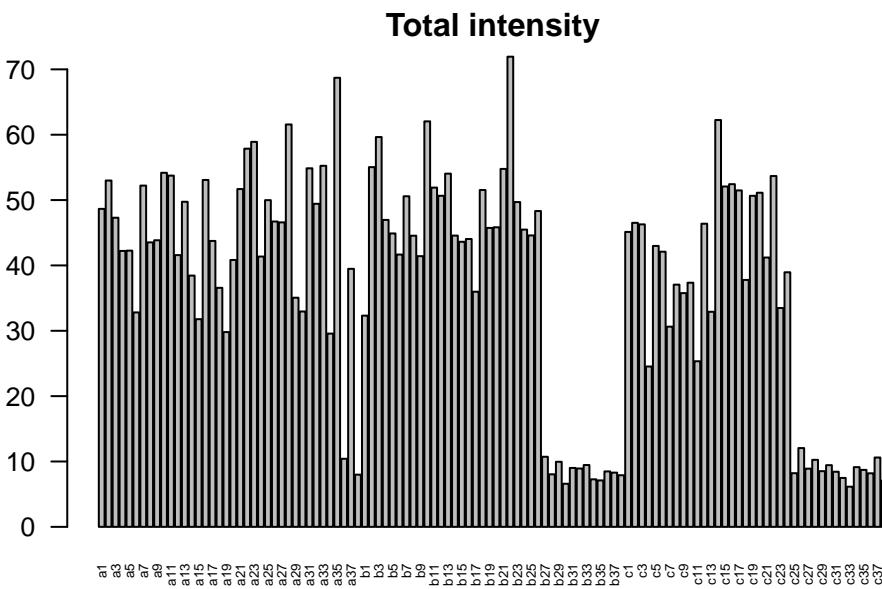
Project Name: proteome\_norm2

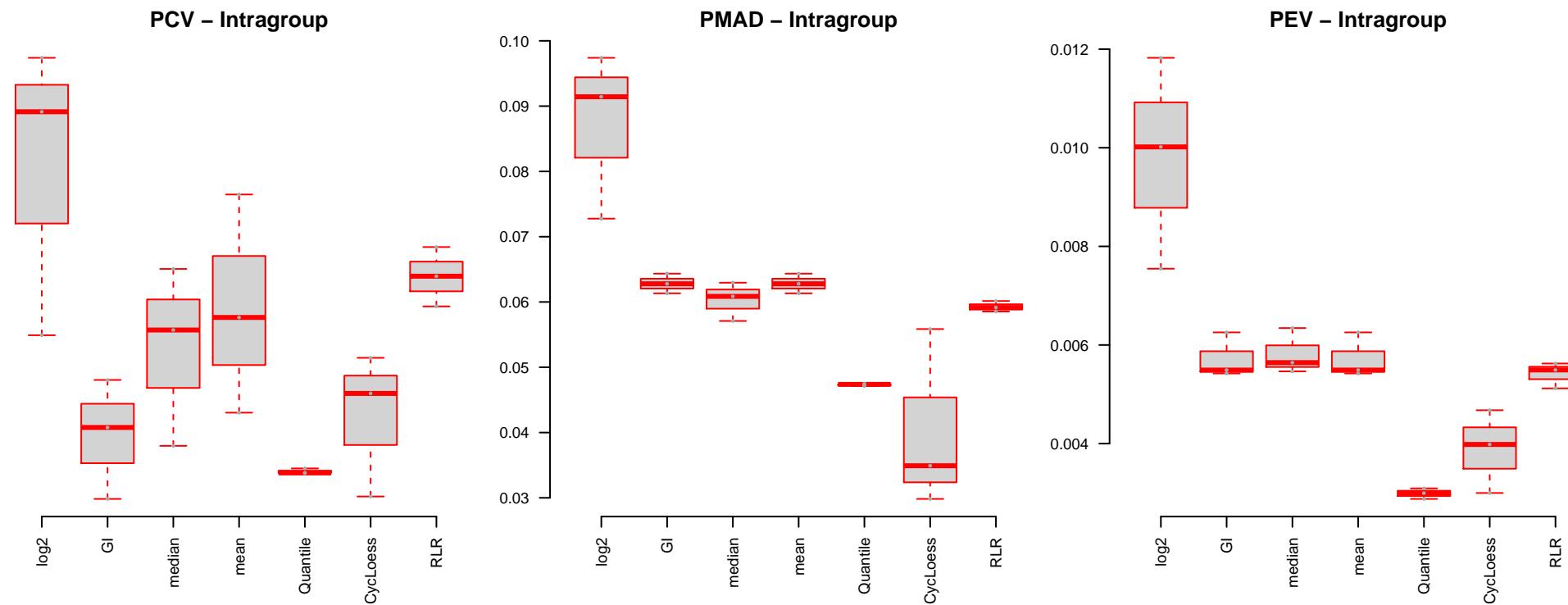
# Normalizer (ver 1.8.0 )

Report created on: 2020-12-24

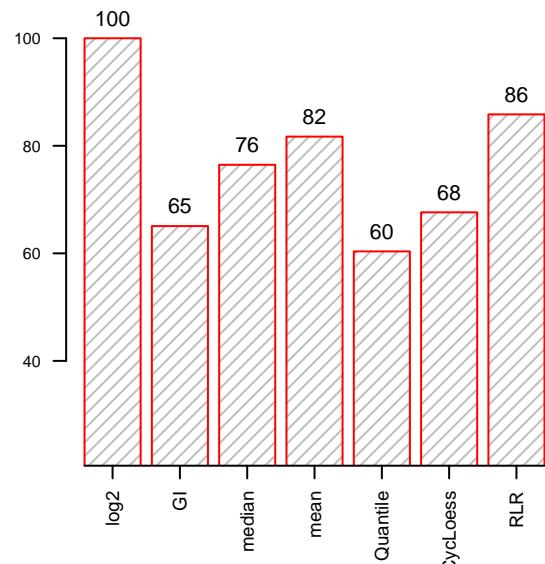
Citation: NormalizerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis  
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

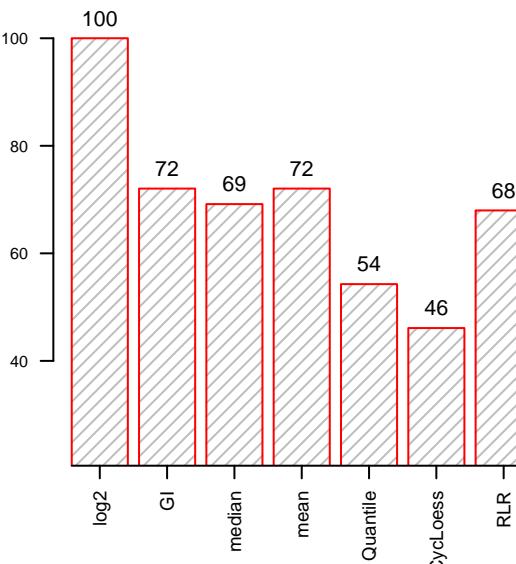




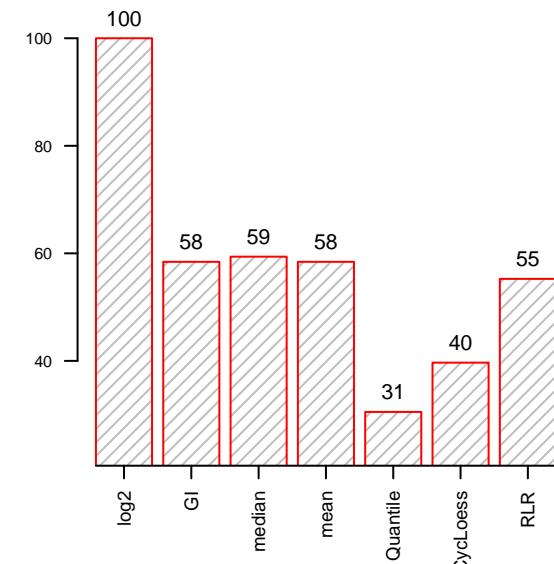
PCV compared to log2



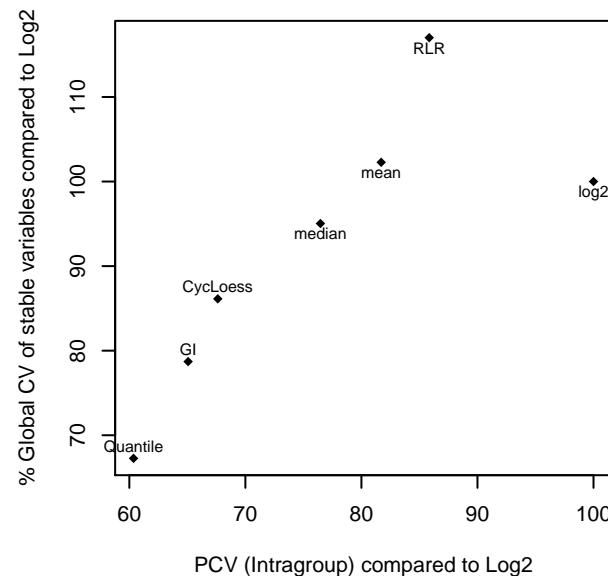
PMAD compared to log2

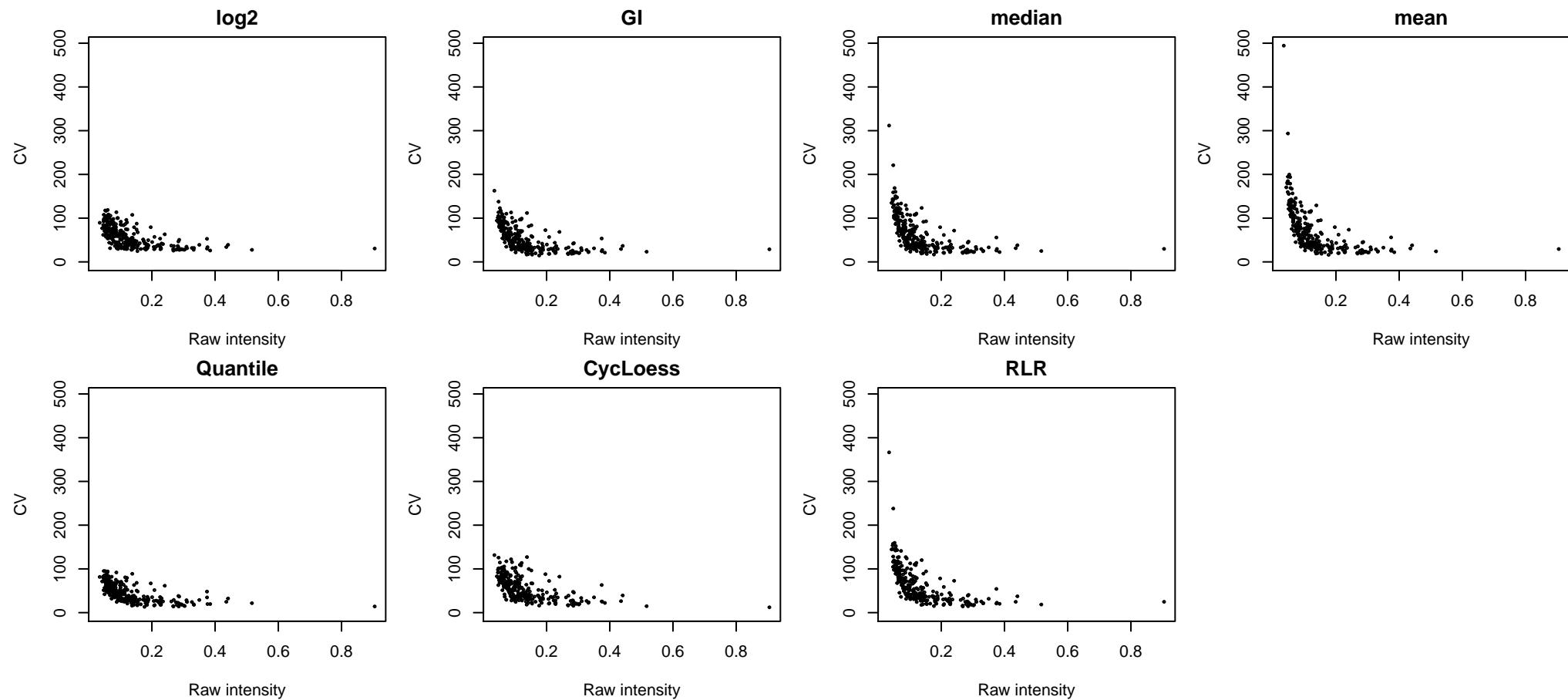


%PEV – compared to log2



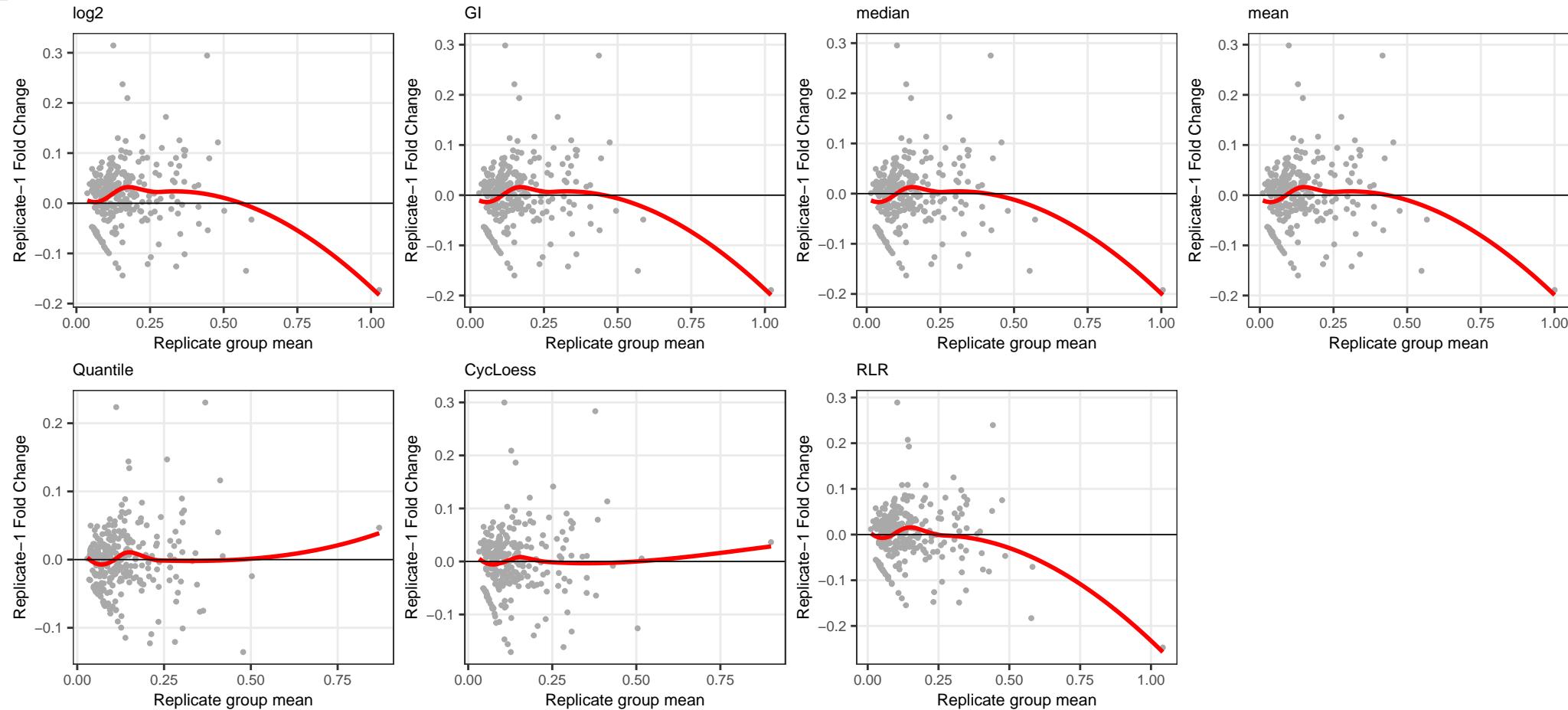
Stable variables plot

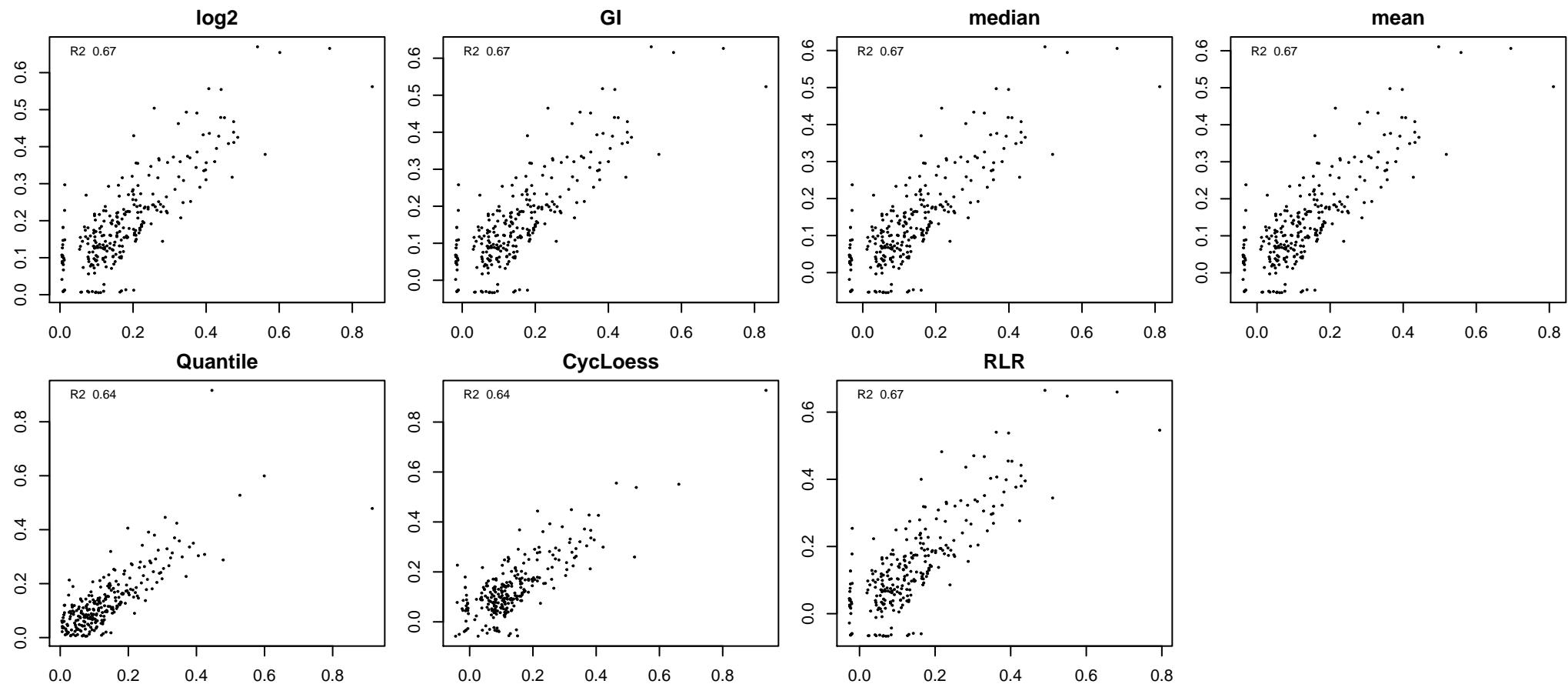




## MA plots

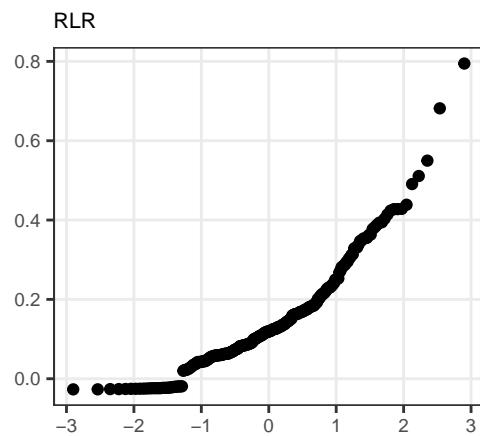
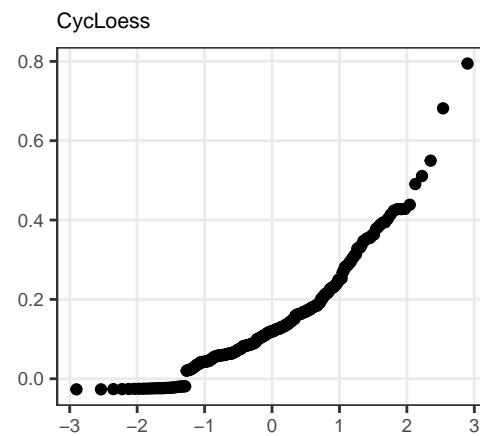
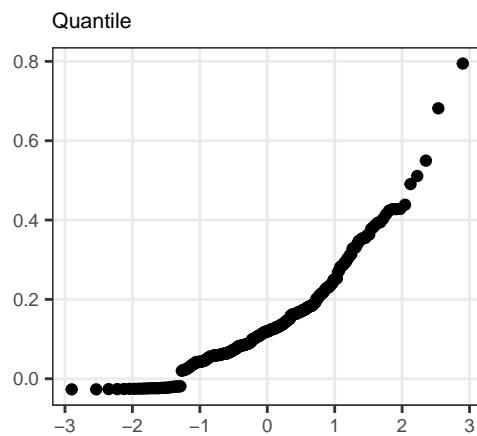
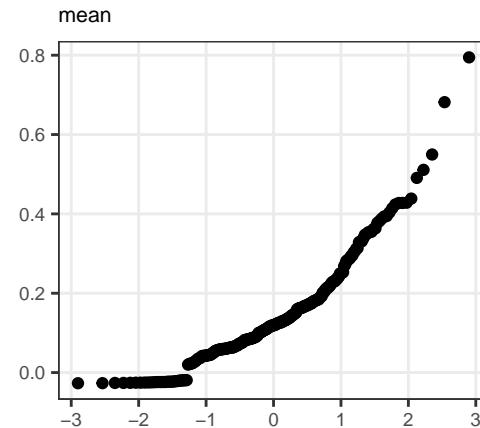
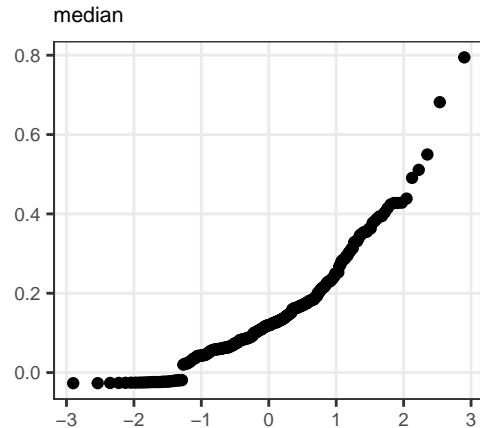
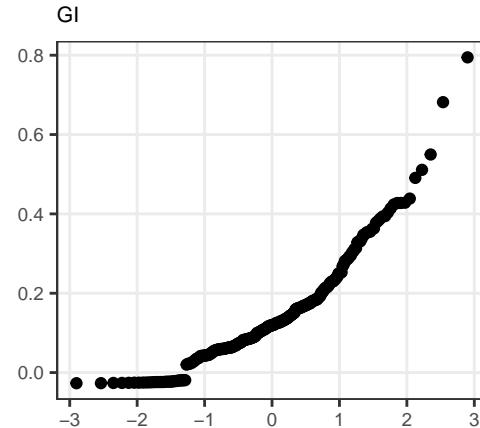
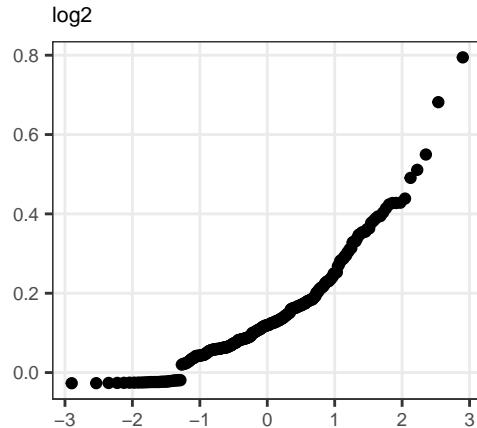
## NormalizerDE Report

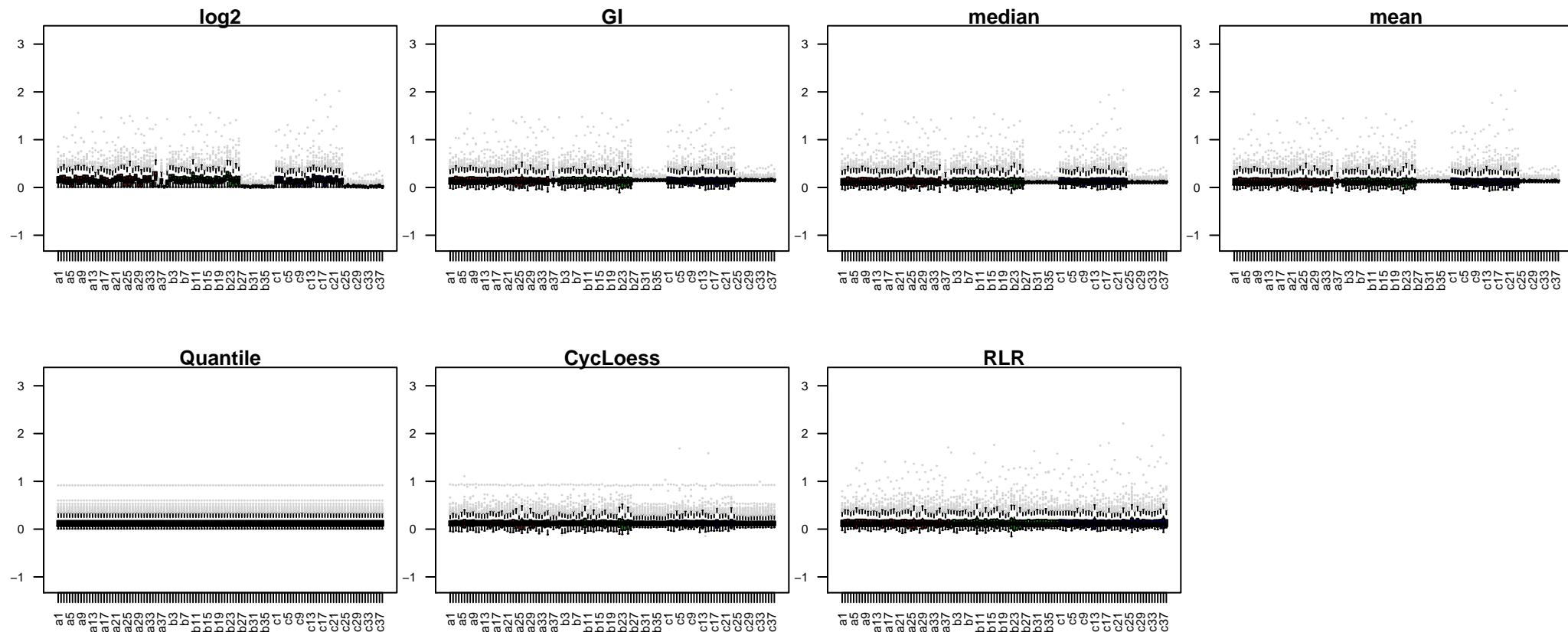


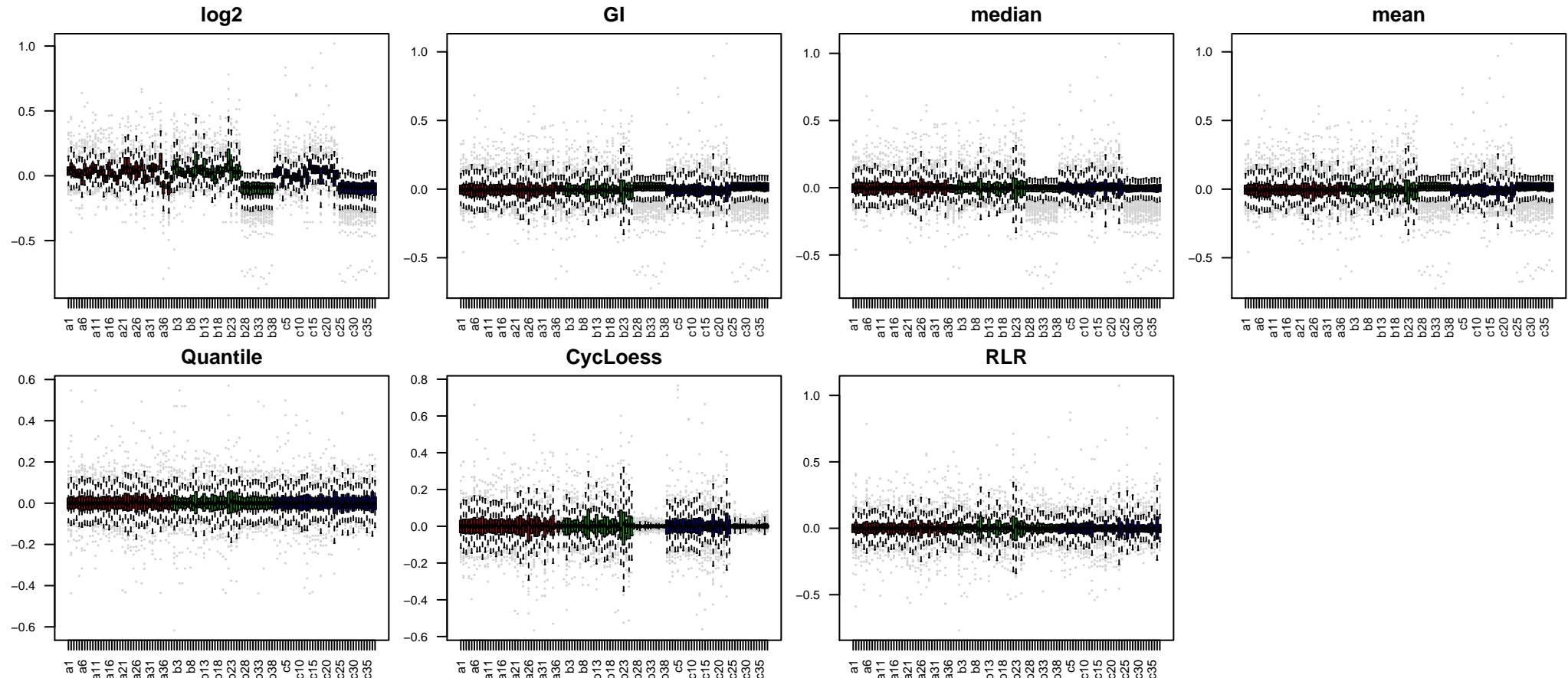


## Q-Q plots

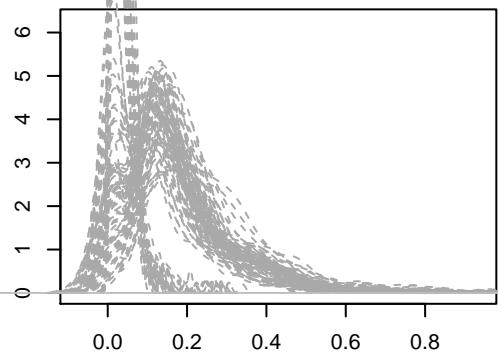
## NormalizerDE Report



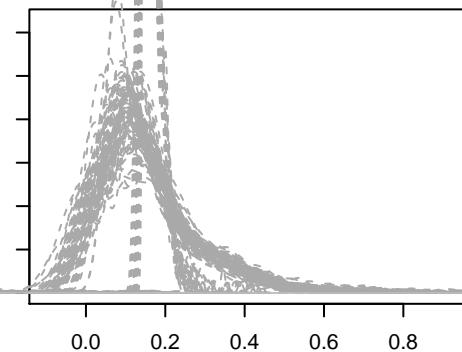




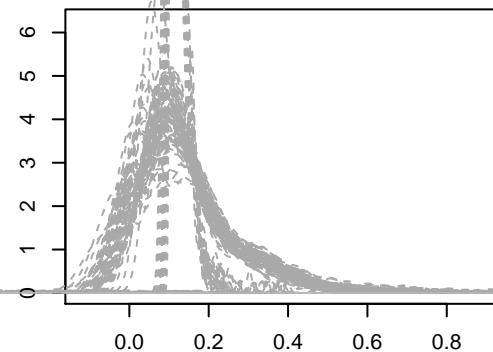
log2



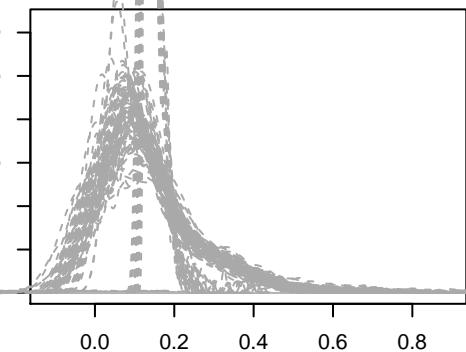
GI



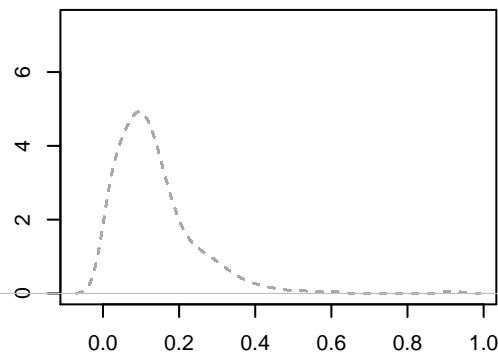
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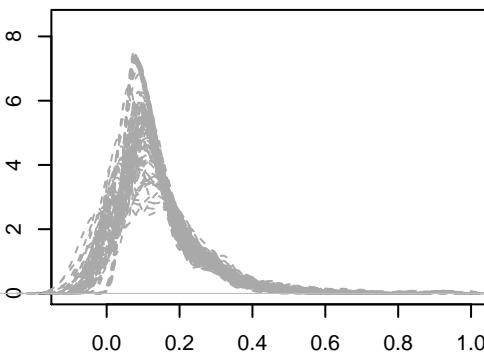
mean



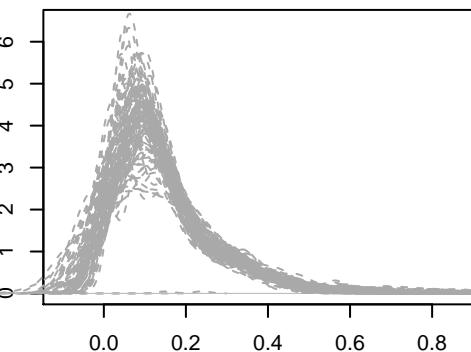
Quantile

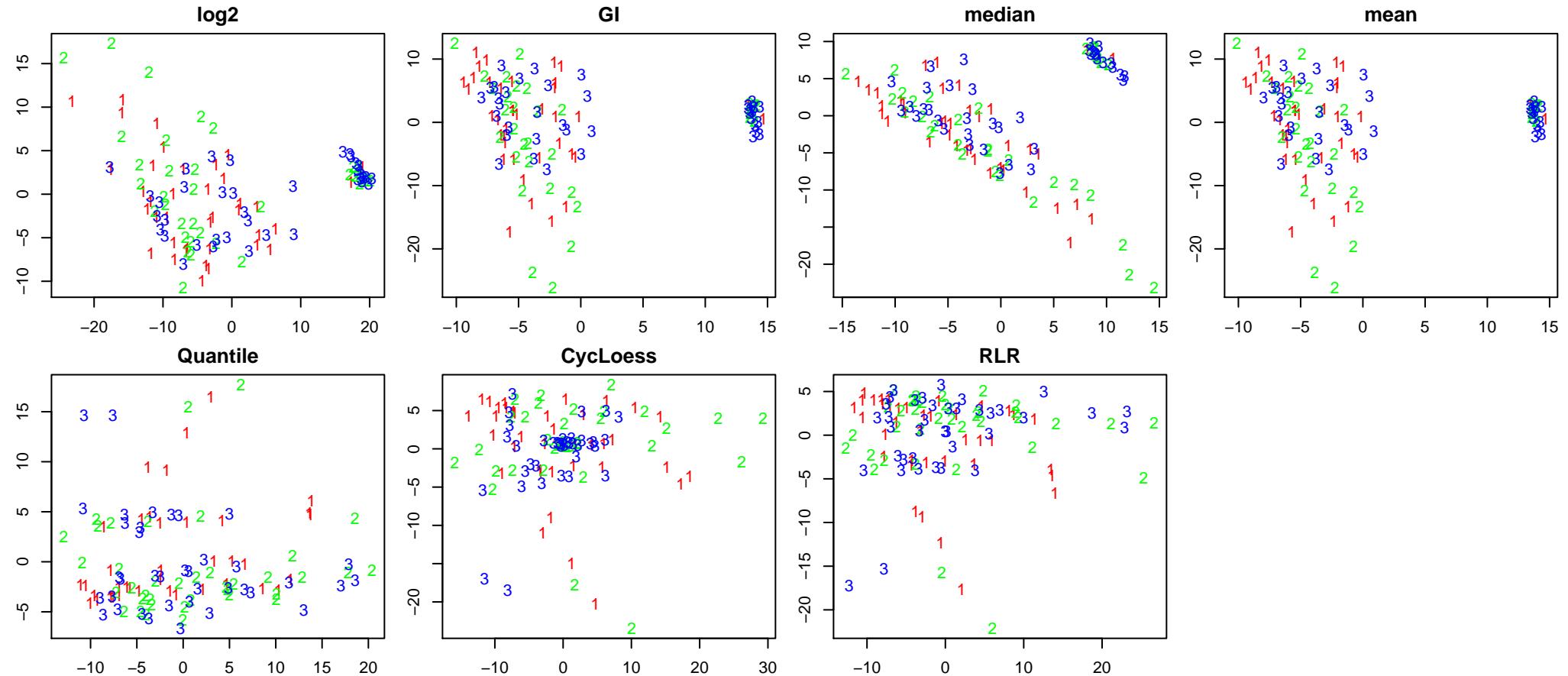


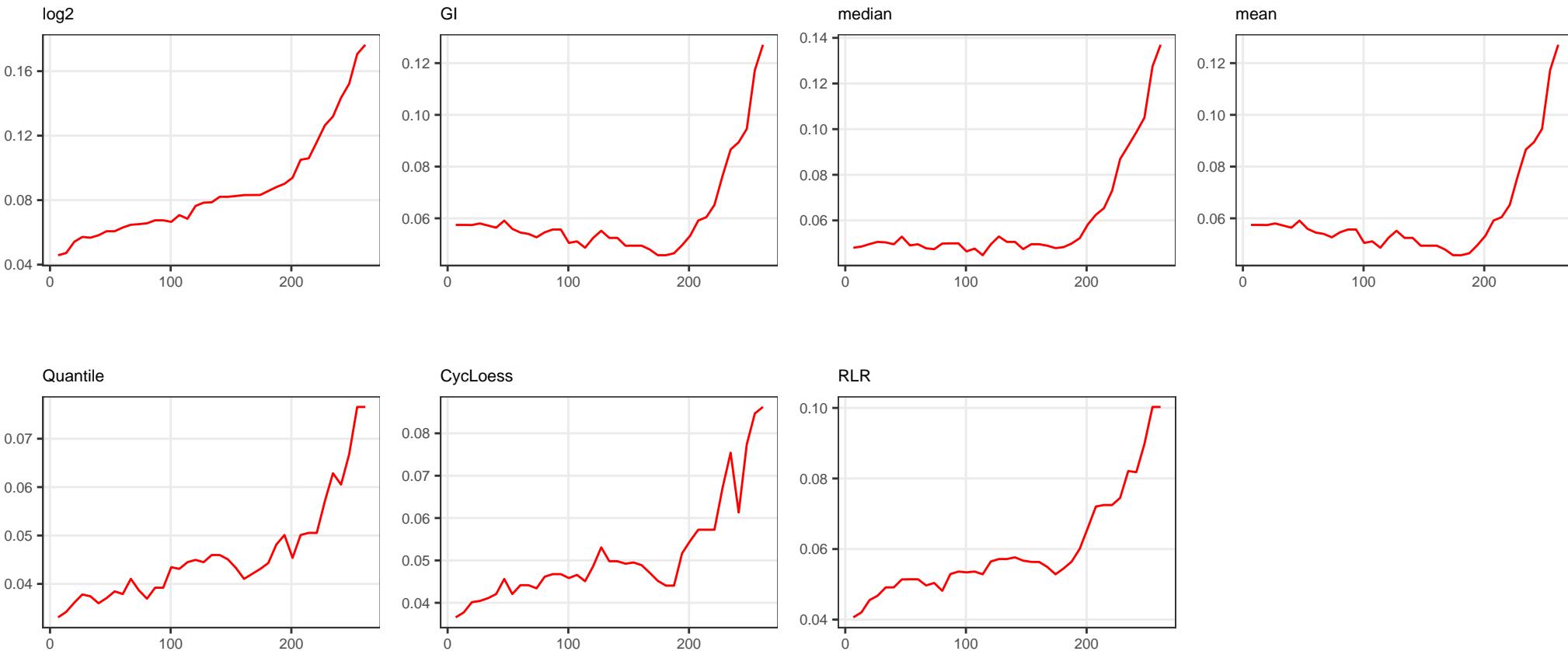
CycLoess



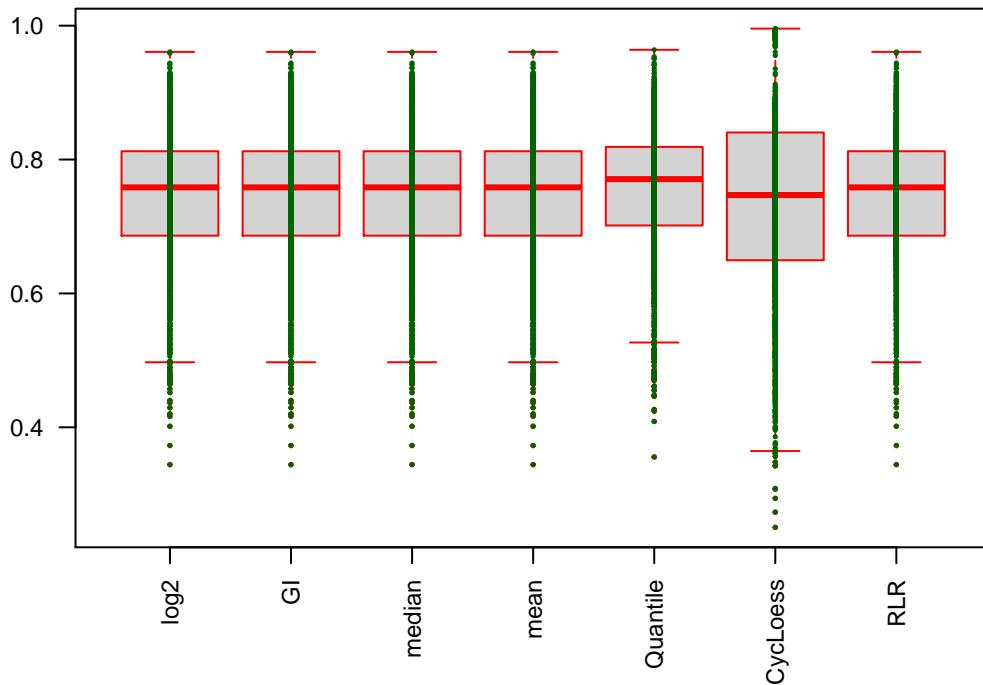
RLR







Pearson correlation – Intragroup



Spearman correlation – Intragroup

