

Project Name: NormalizerPeptides

# NormalizerDE (ver 1.14.0 )

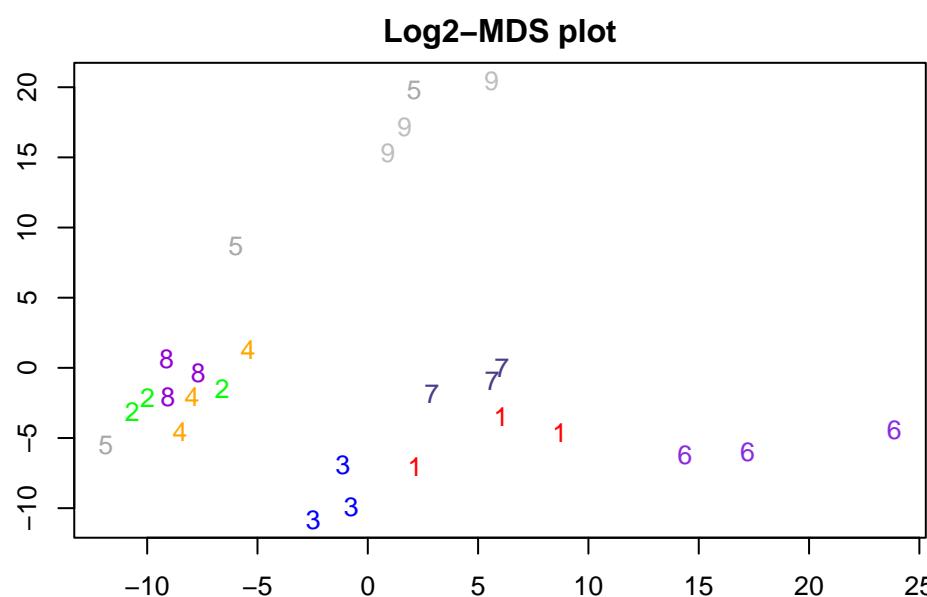
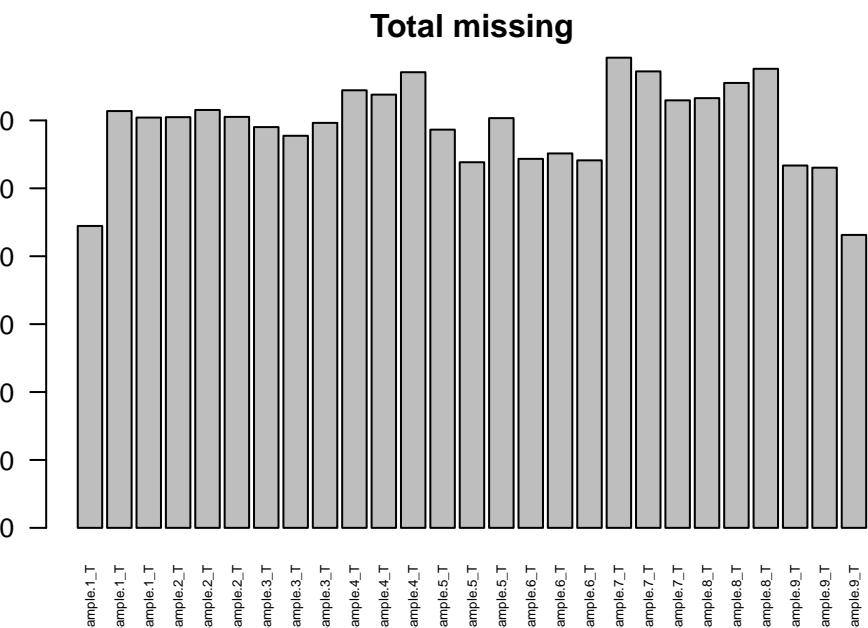
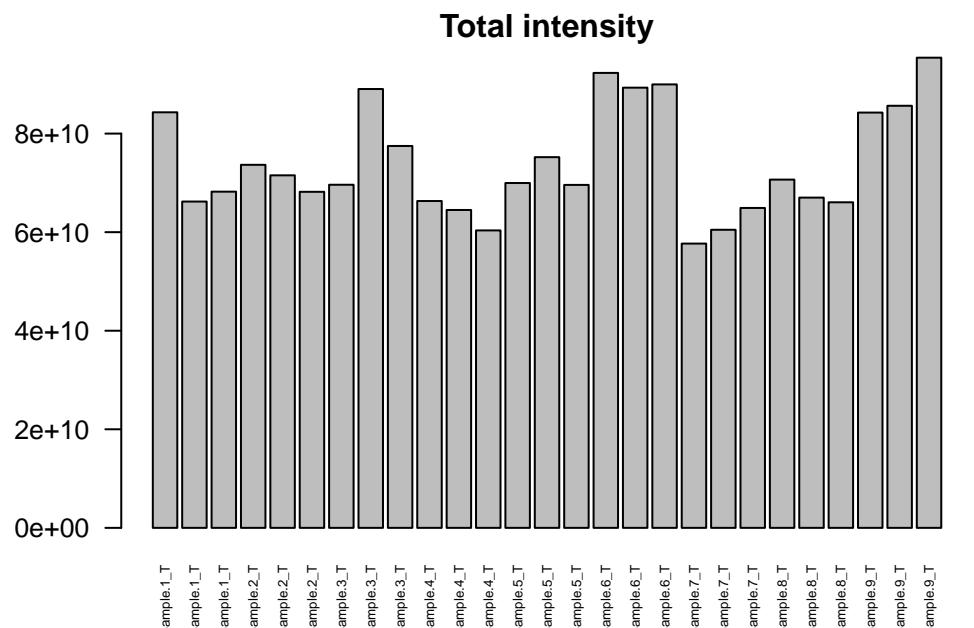
Report created on: 2022-07-12

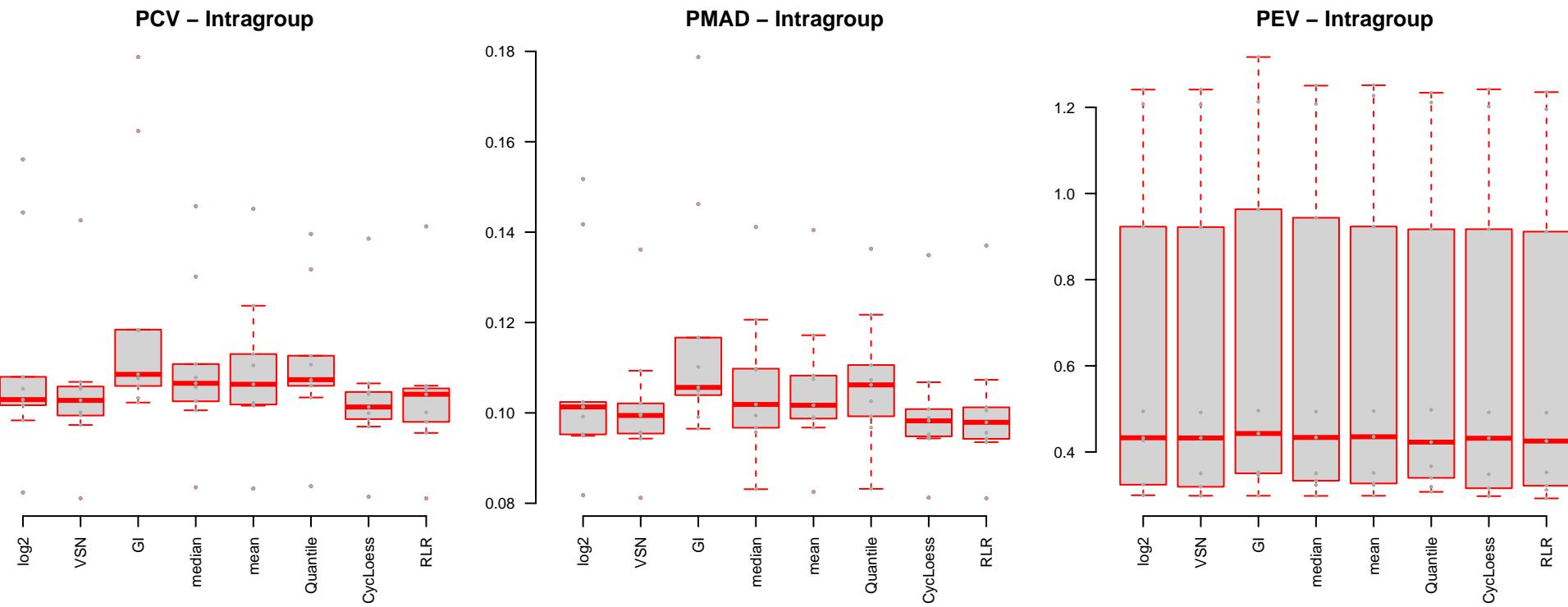
Citation: NormalizerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis  
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

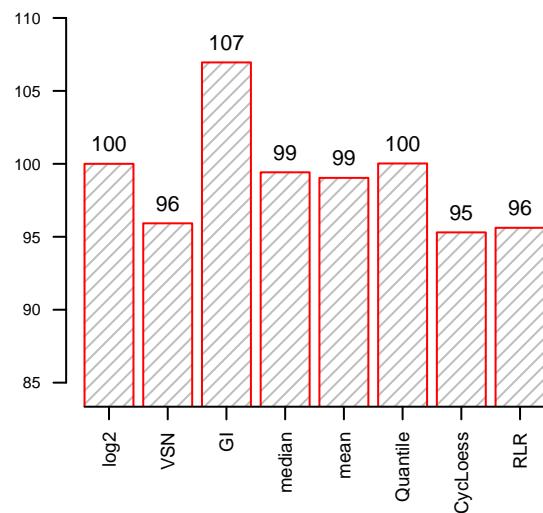
Group nbr.	Design group	Nbr. samples in cond.
1	125.amol	3
2	12500.amol	3
3	250.amol	3
4	2500.amol	3
5	25000.amol	3
6	50.amol	3
7	500.amol	3
8	5000.amol	3
9	50000.amol	3

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

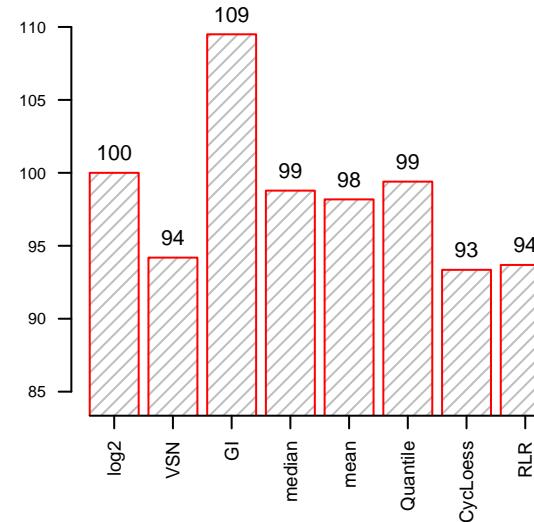




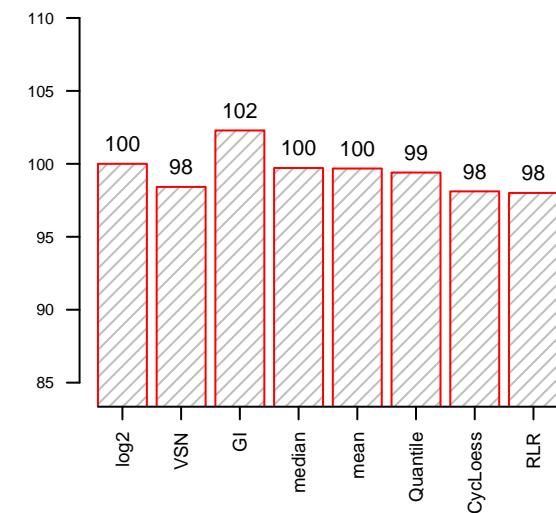
PCV compared to log2



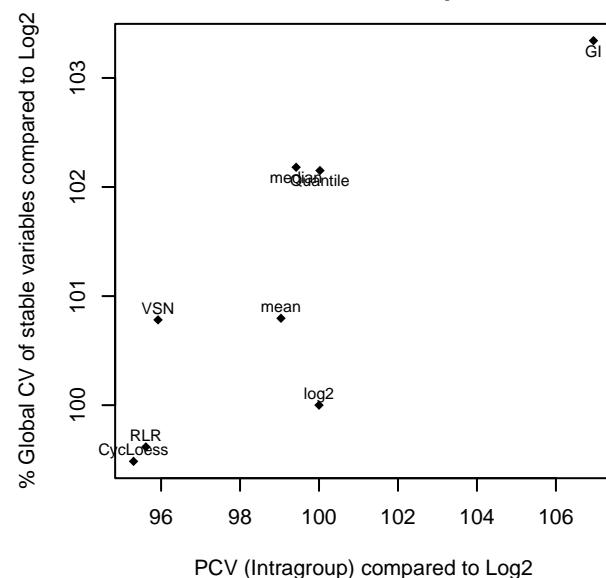
PMAD compared to log2

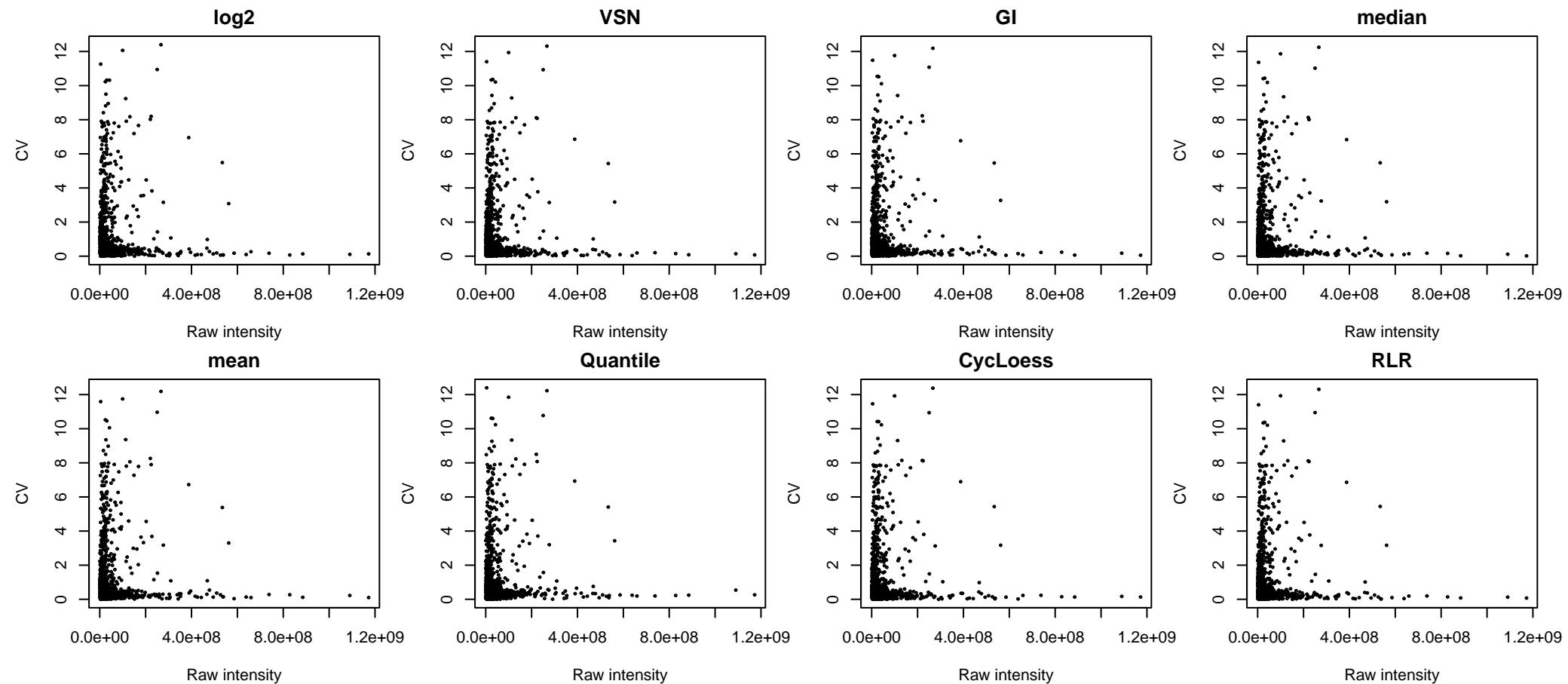


%PEV – compared to log2



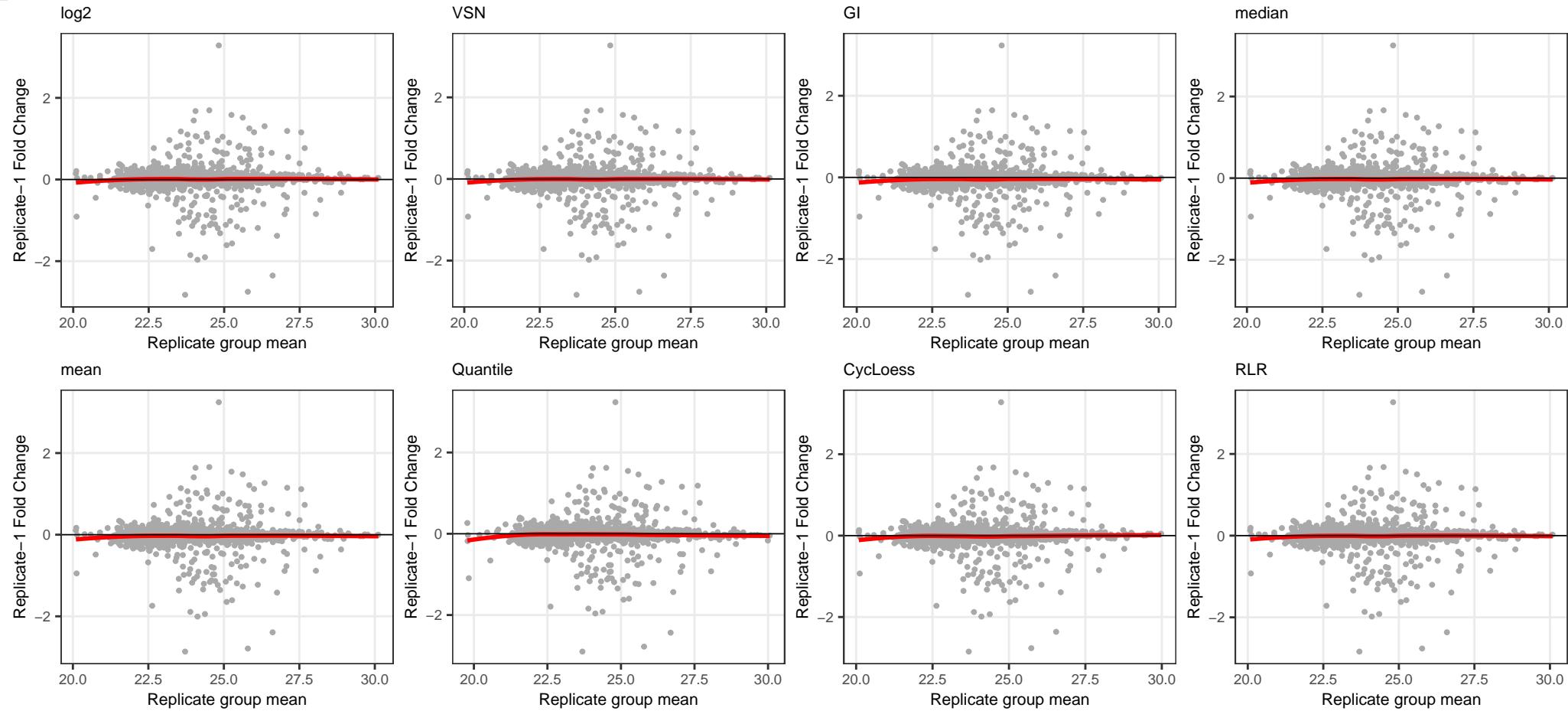
Stable variables plot

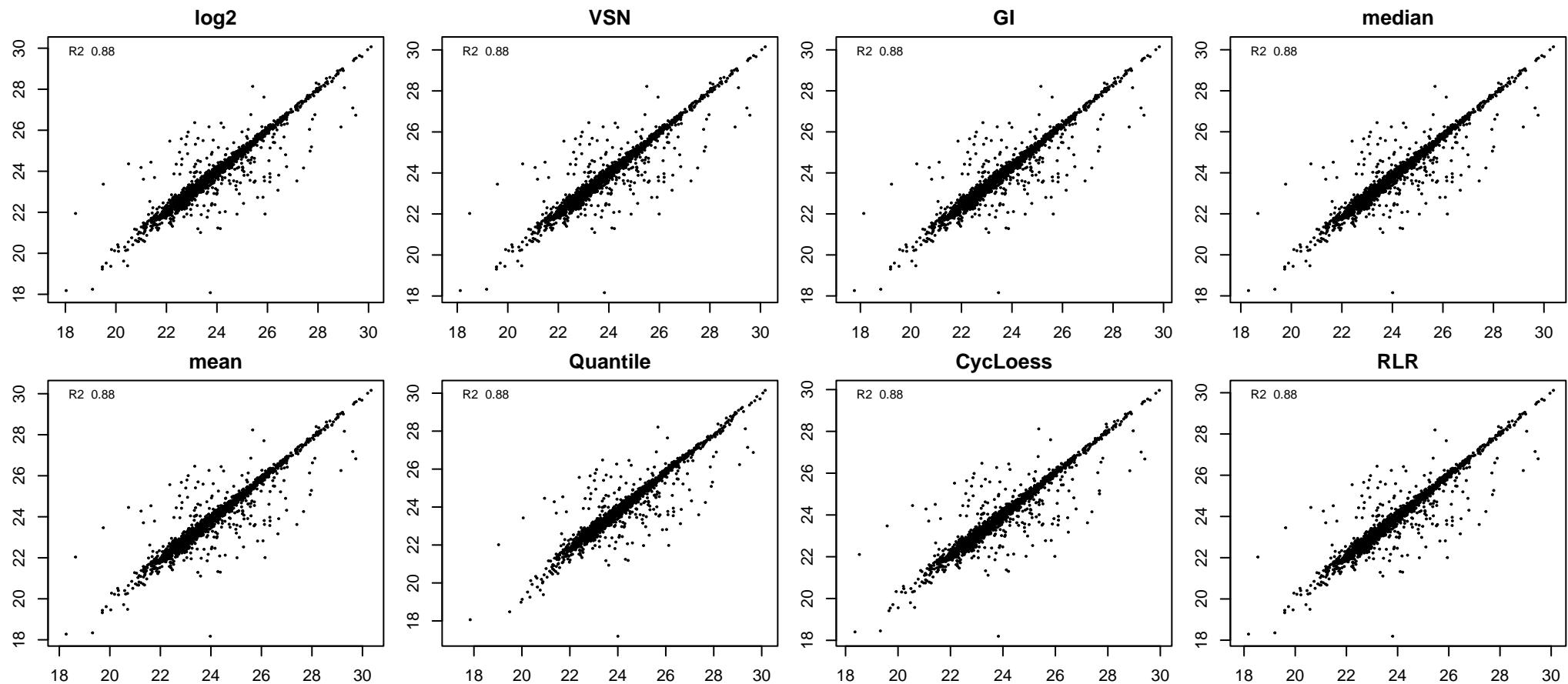




## MA plots

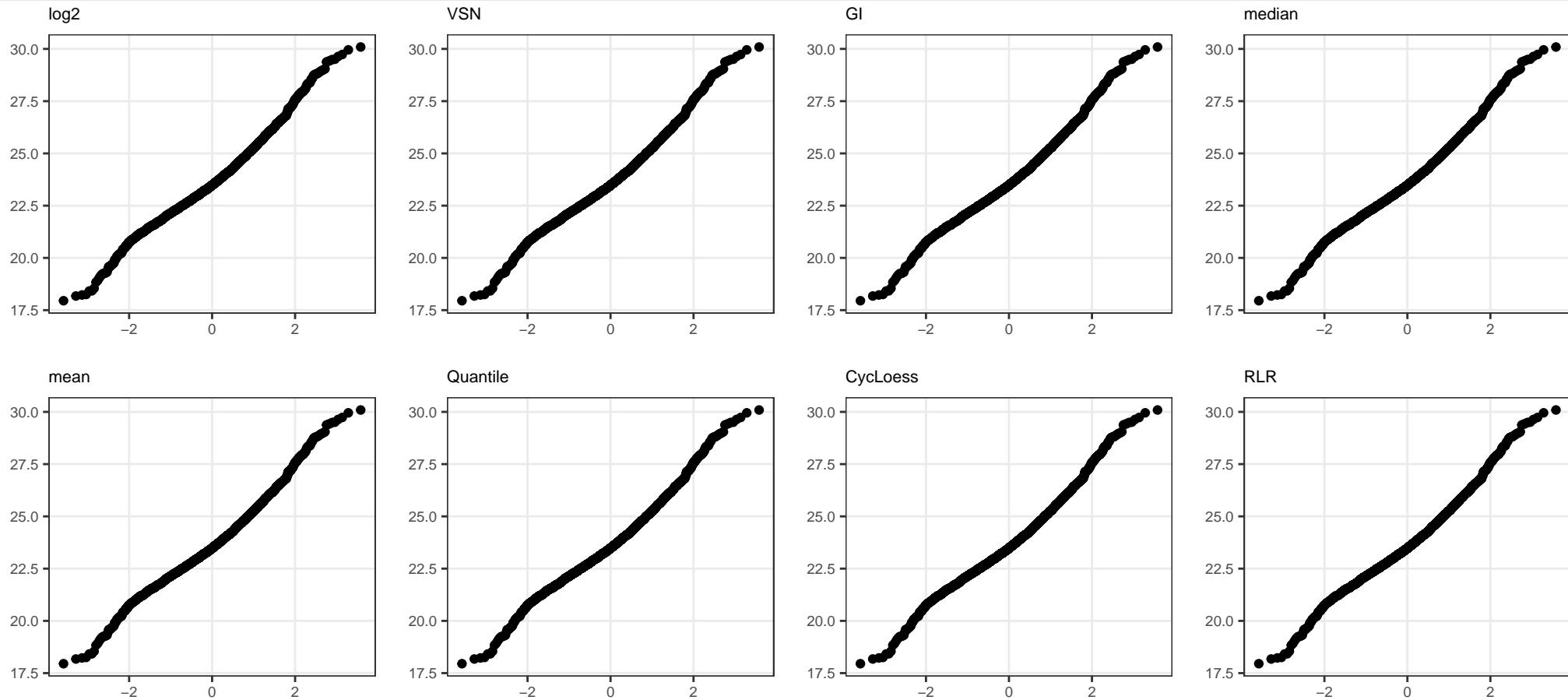
## NormalizerDE Report

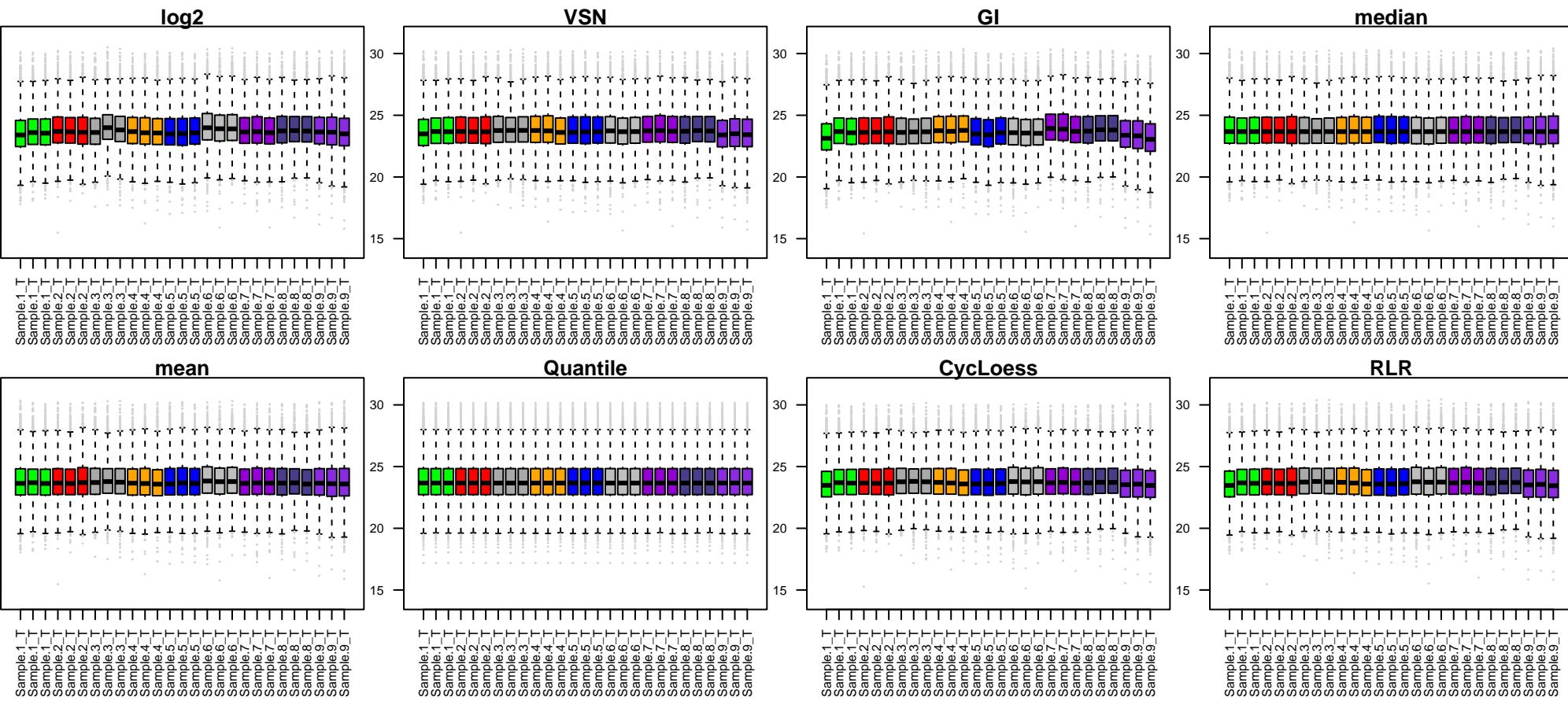




## Q-Q plots

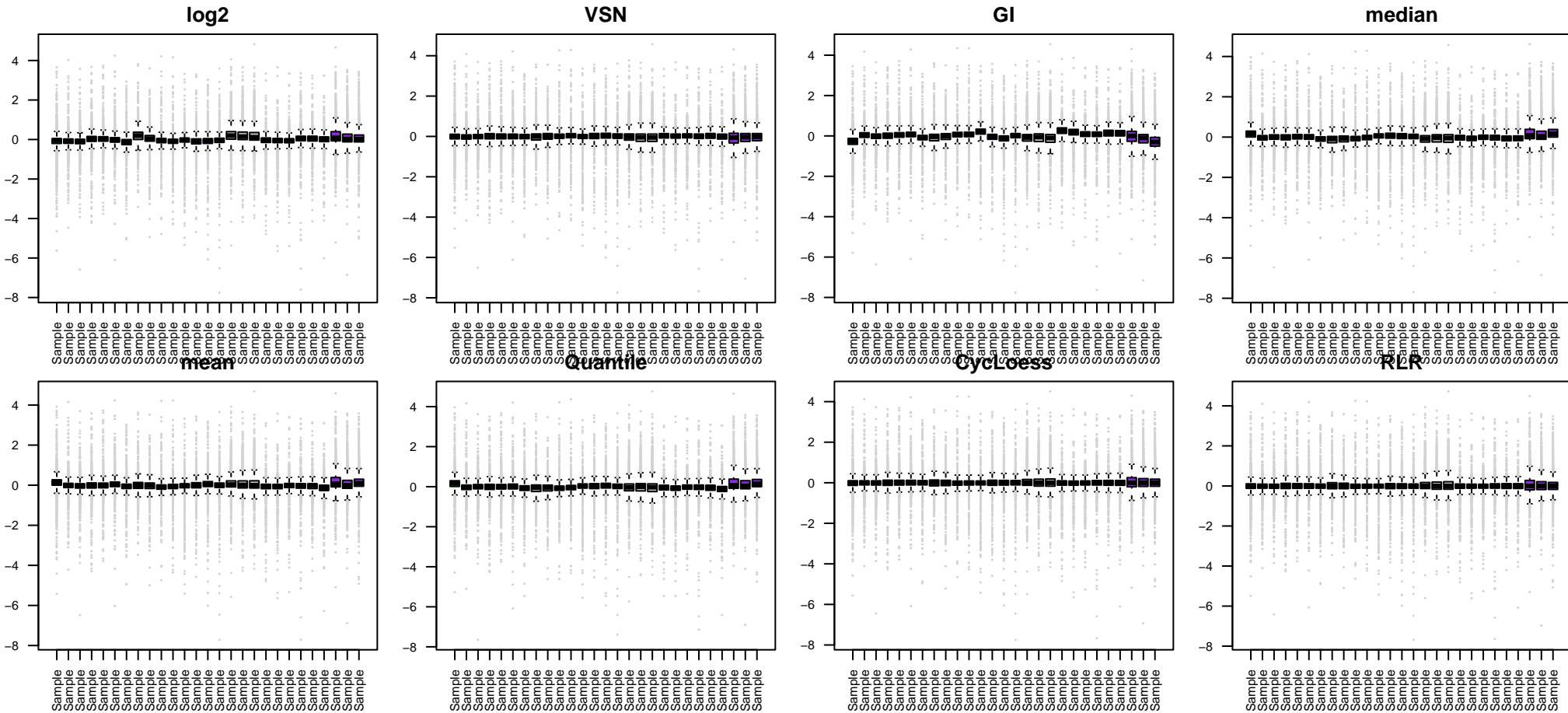
## NormalizerDE Report

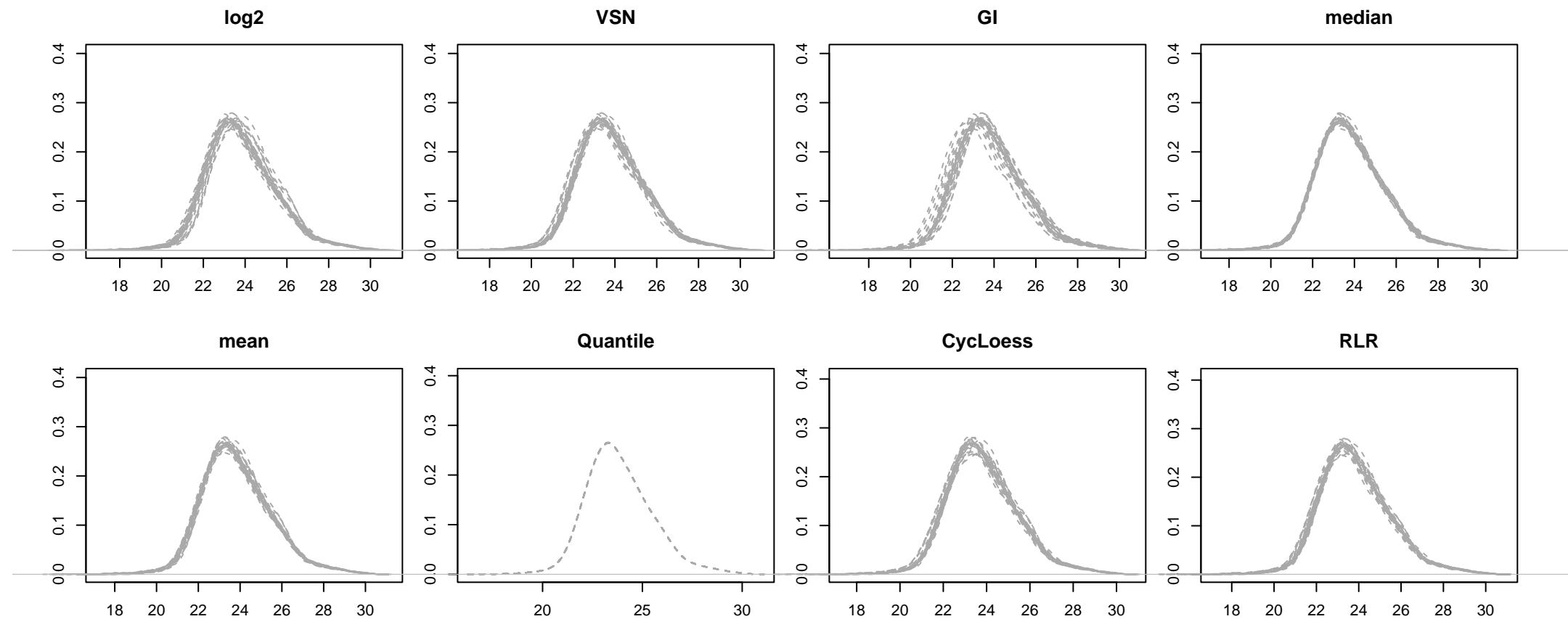


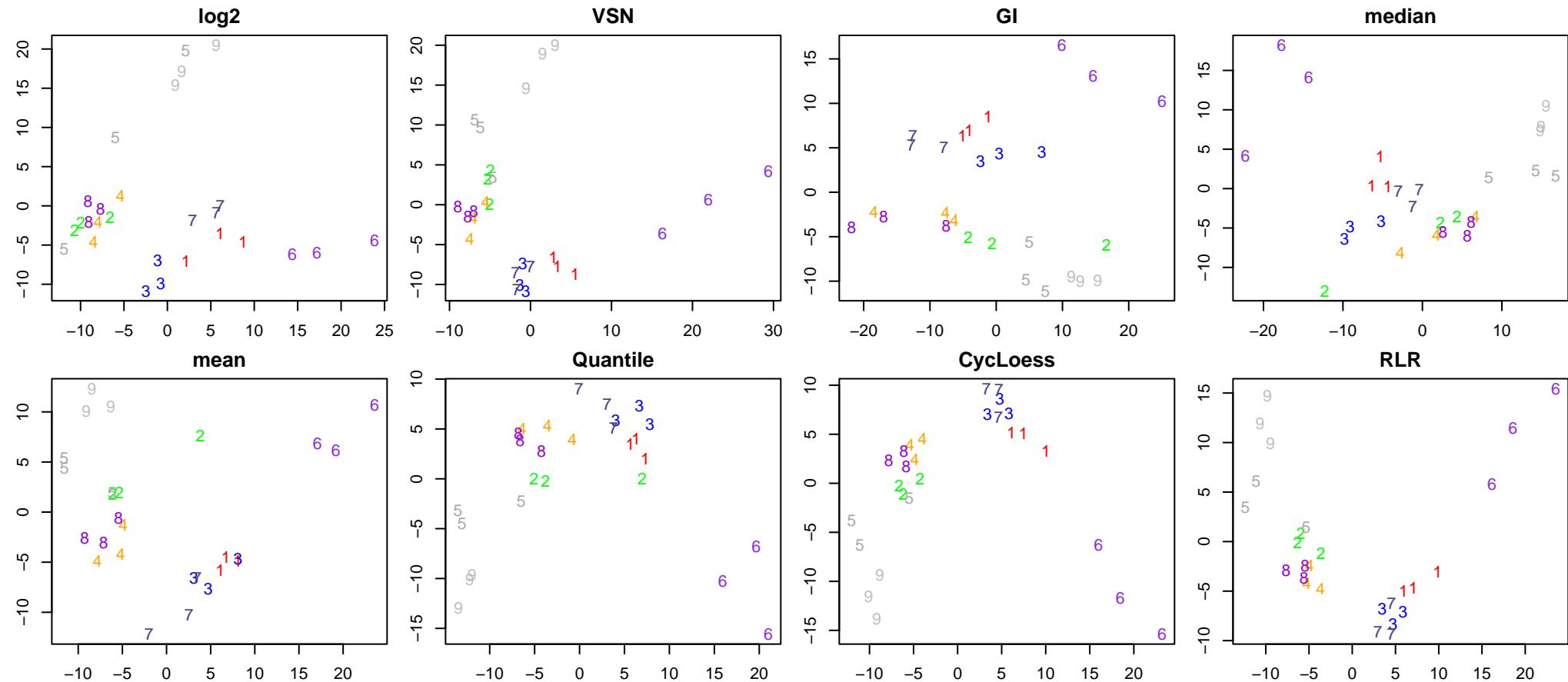


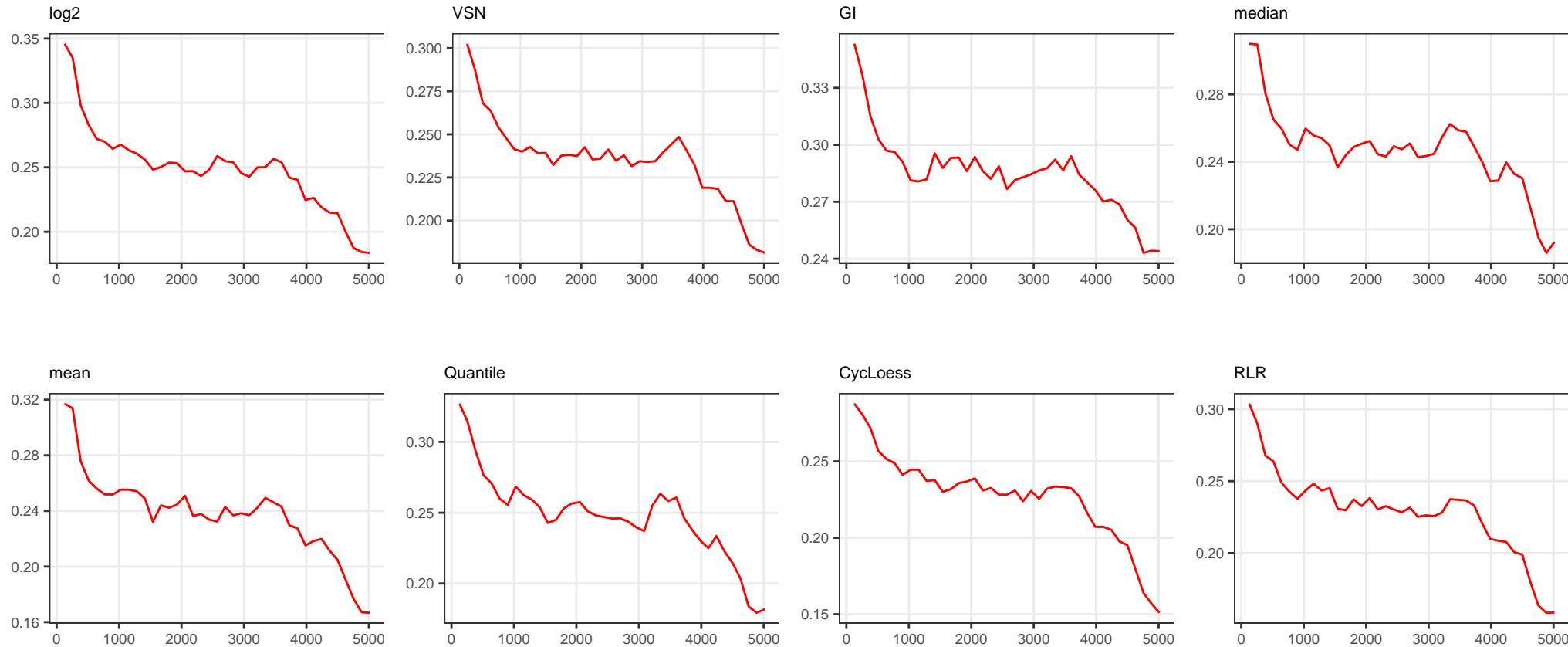
# Relative Log Expression (RLE) plots

NormalizerDE Report

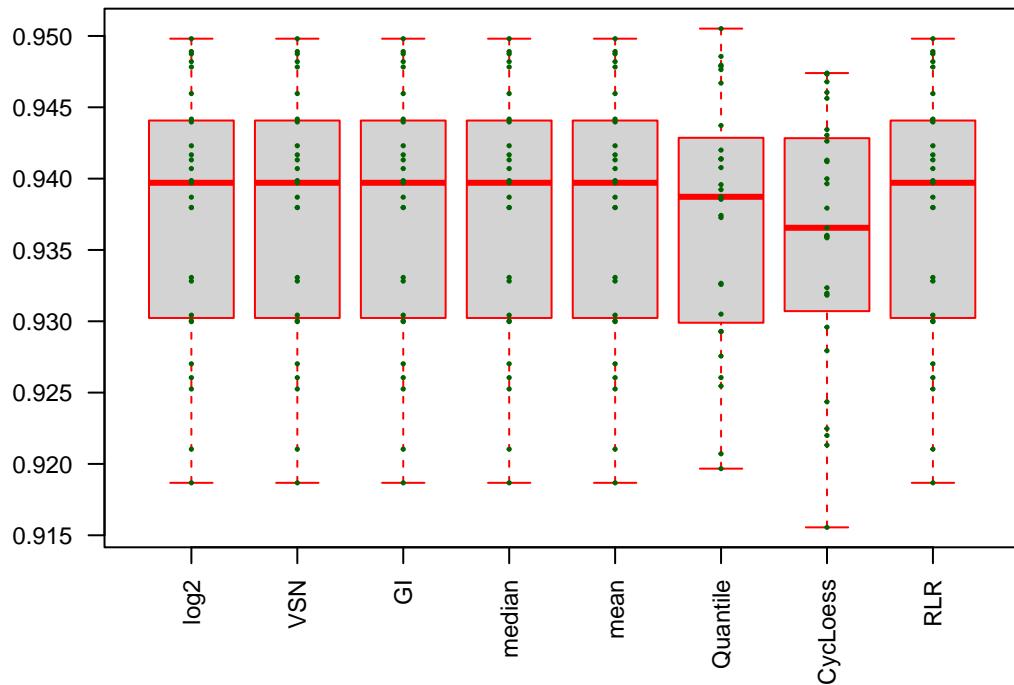




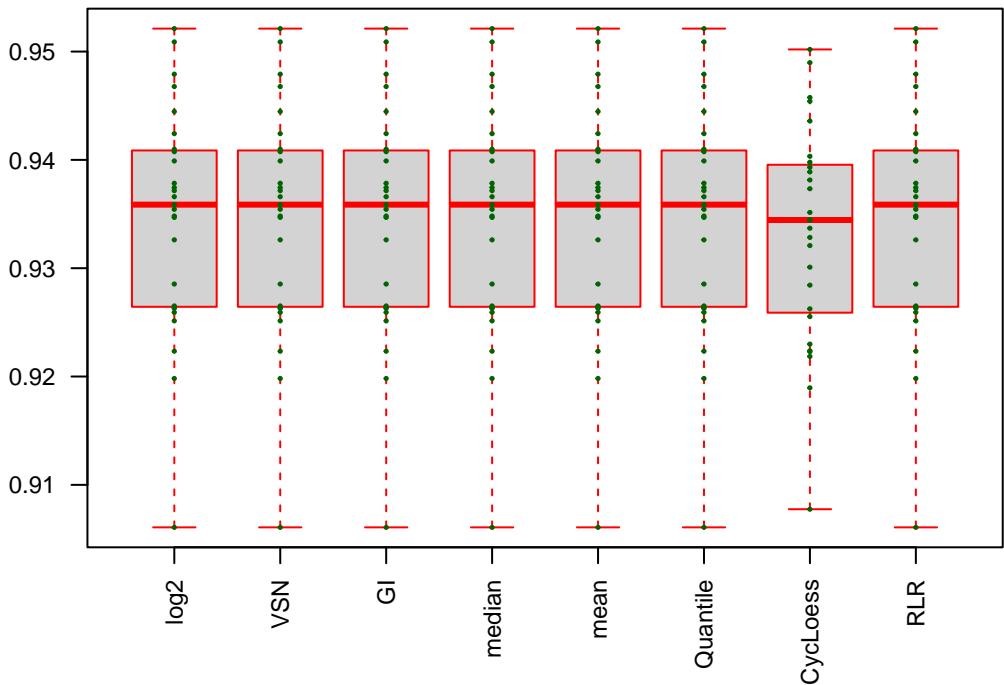




Pearson correlation – Intragroup

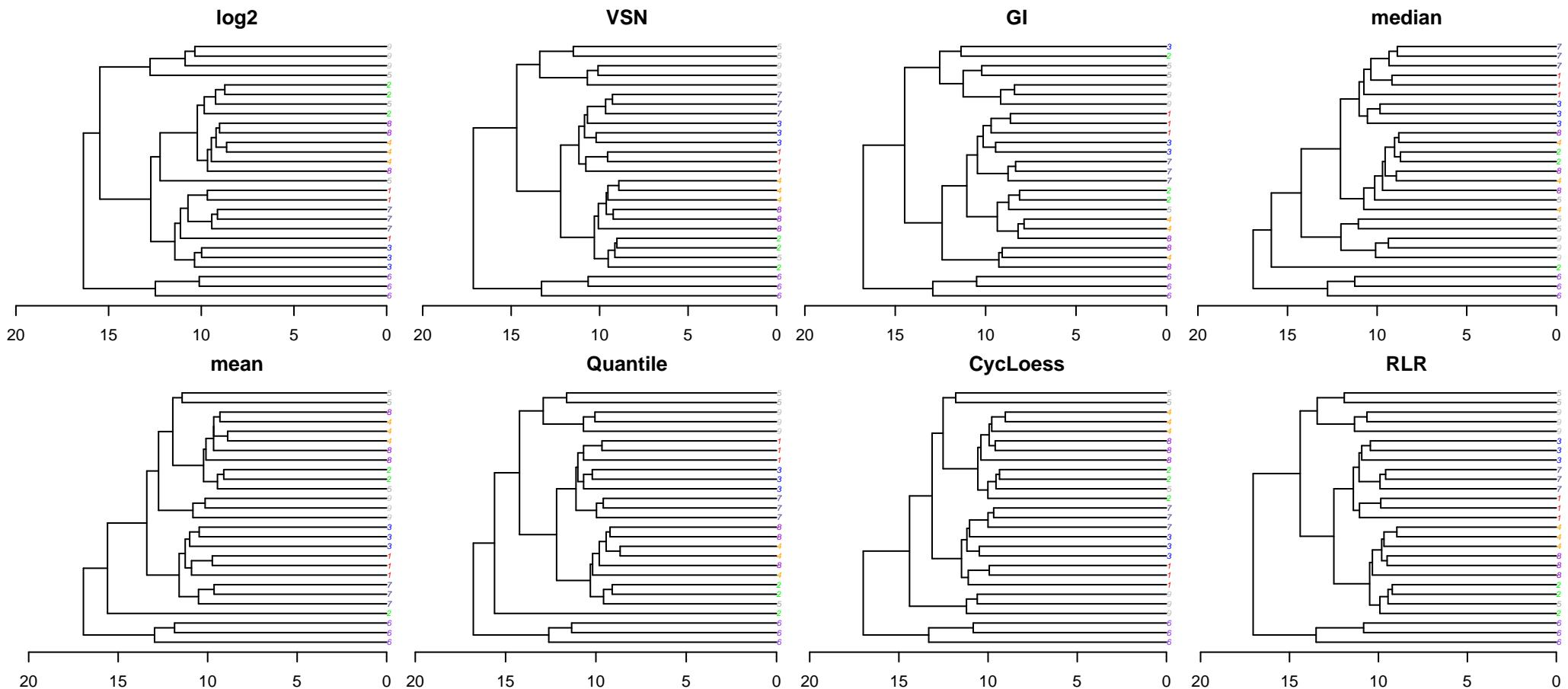


Spearman correlation – Intragroup



# Dendrograms – Built from 379 variables containing non–missing data

NormalizerDE Report



## HistPlots

## NormalizerDE Report

