

Project Name: PXD001819

NormalyzerDE (ver 1.5.4)

Report created on: 2021-02-01

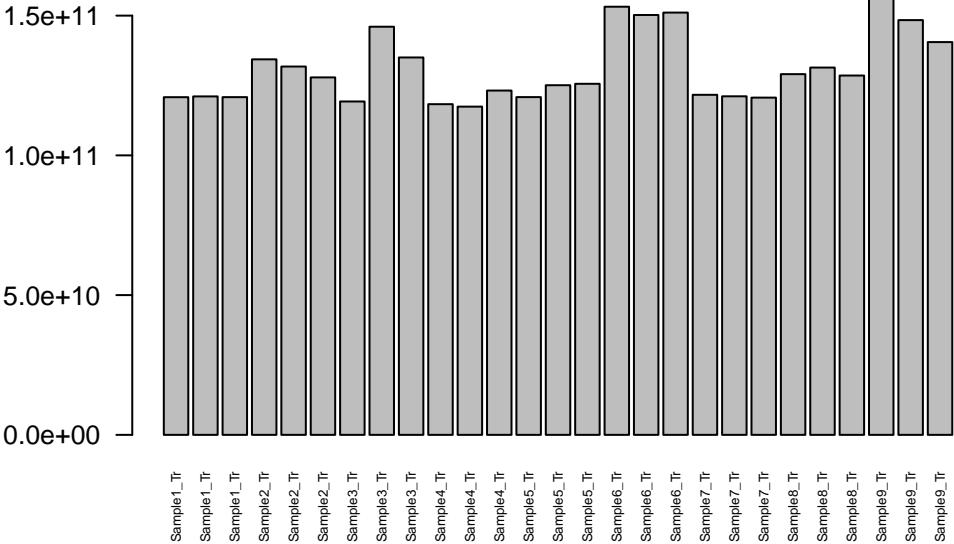
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

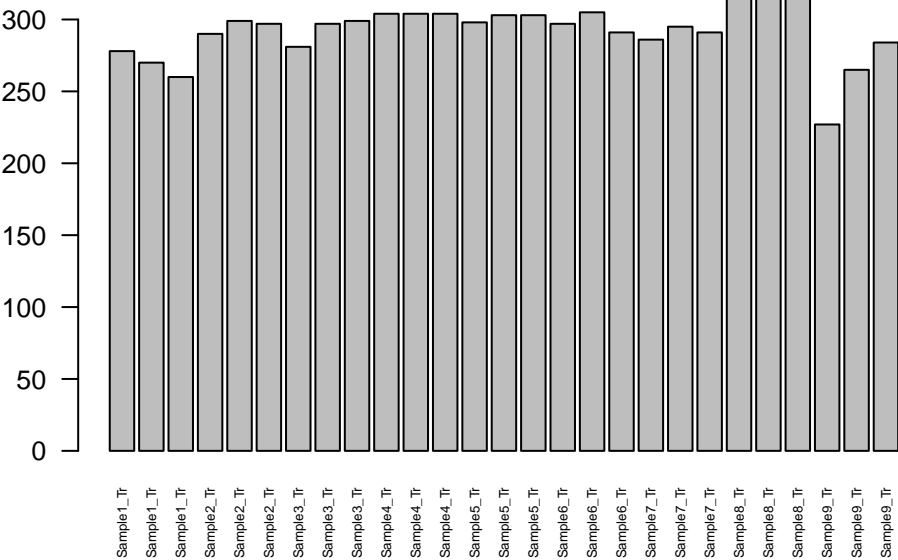
Group nbr.	Design group	Nbr. samples in cond.
1	12500amol	3
2	125amol	3
3	25000amol	3
4	2500amol	3
5	250amol	3
6	50000amol	3
7	5000amol	3
8	500amol	3
9	50amol	3

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

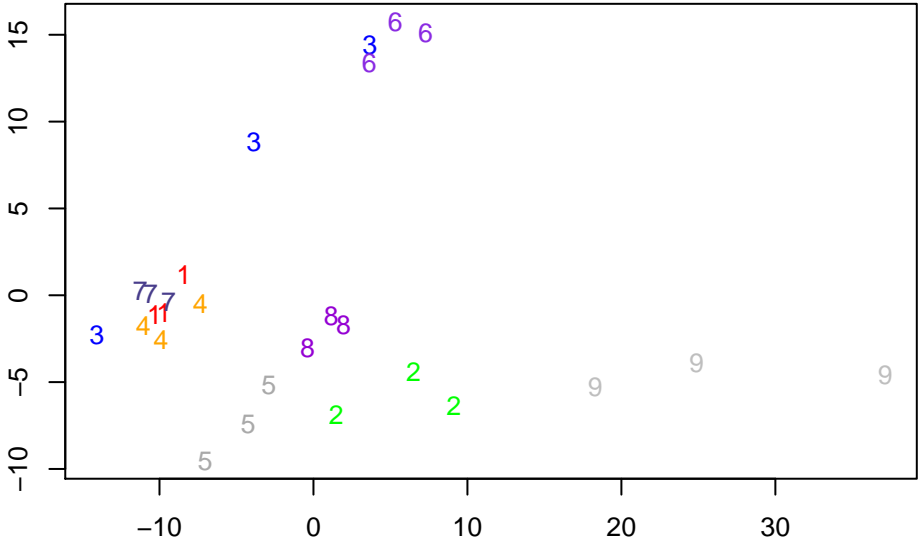
Total intensity

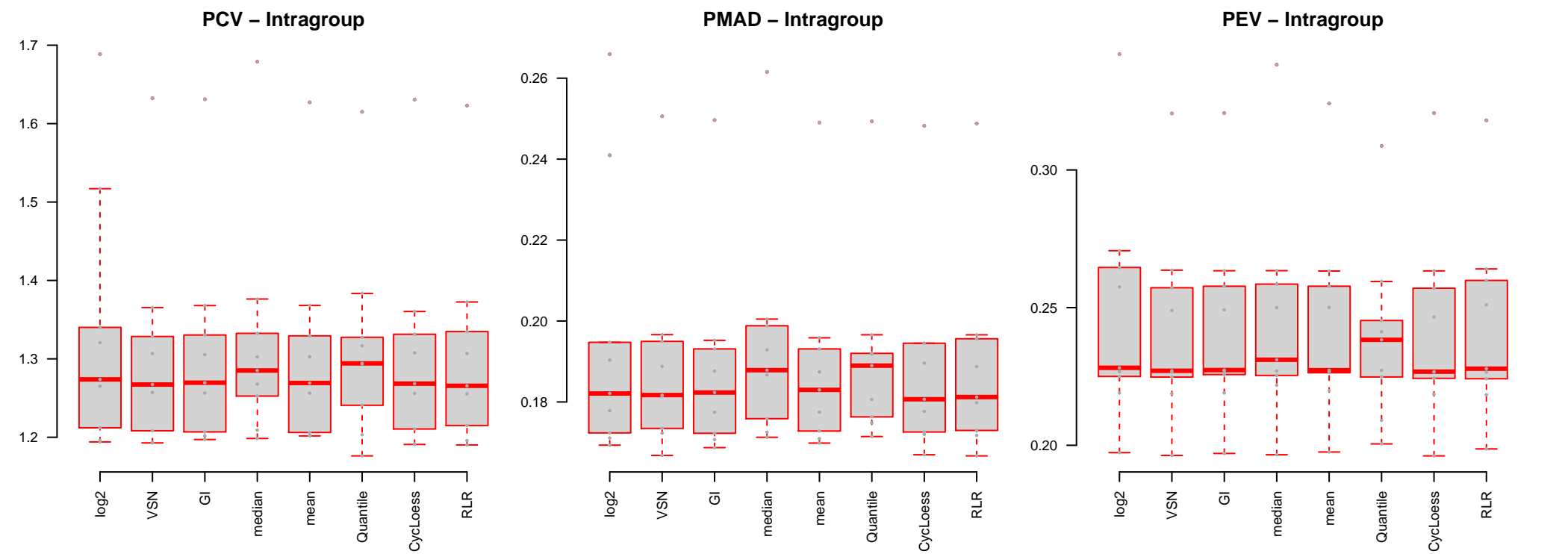


Total missing

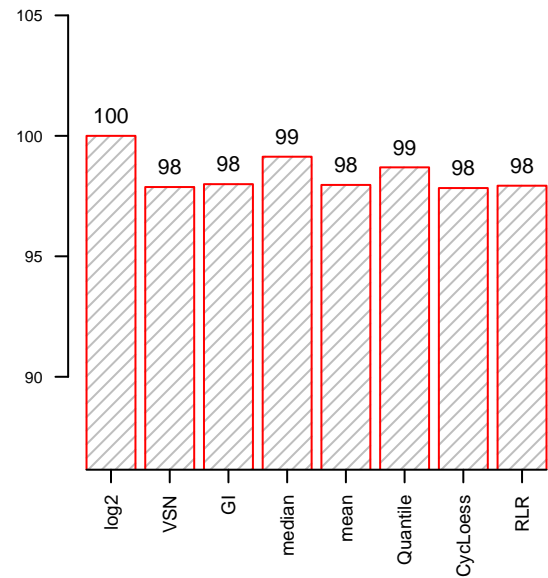


Log2-MDS plot

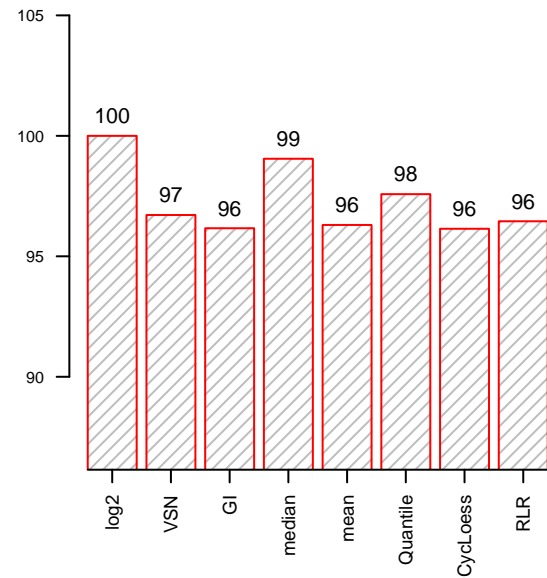




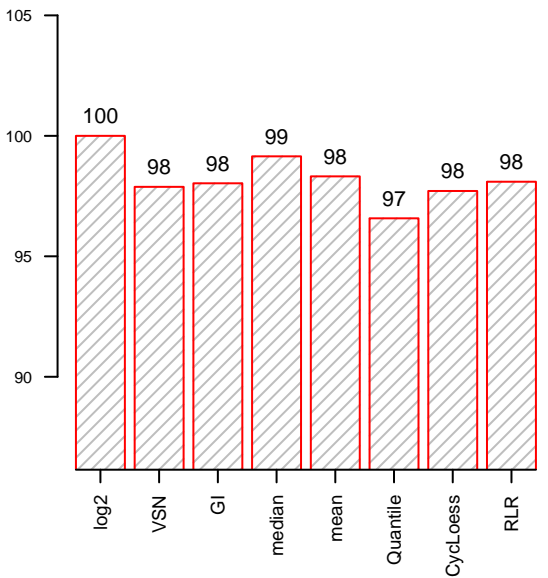
PCV compared to log2



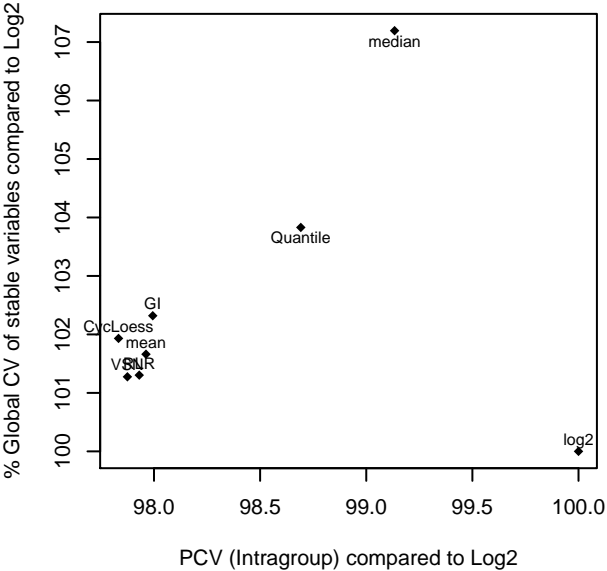
PMAD compared to log2

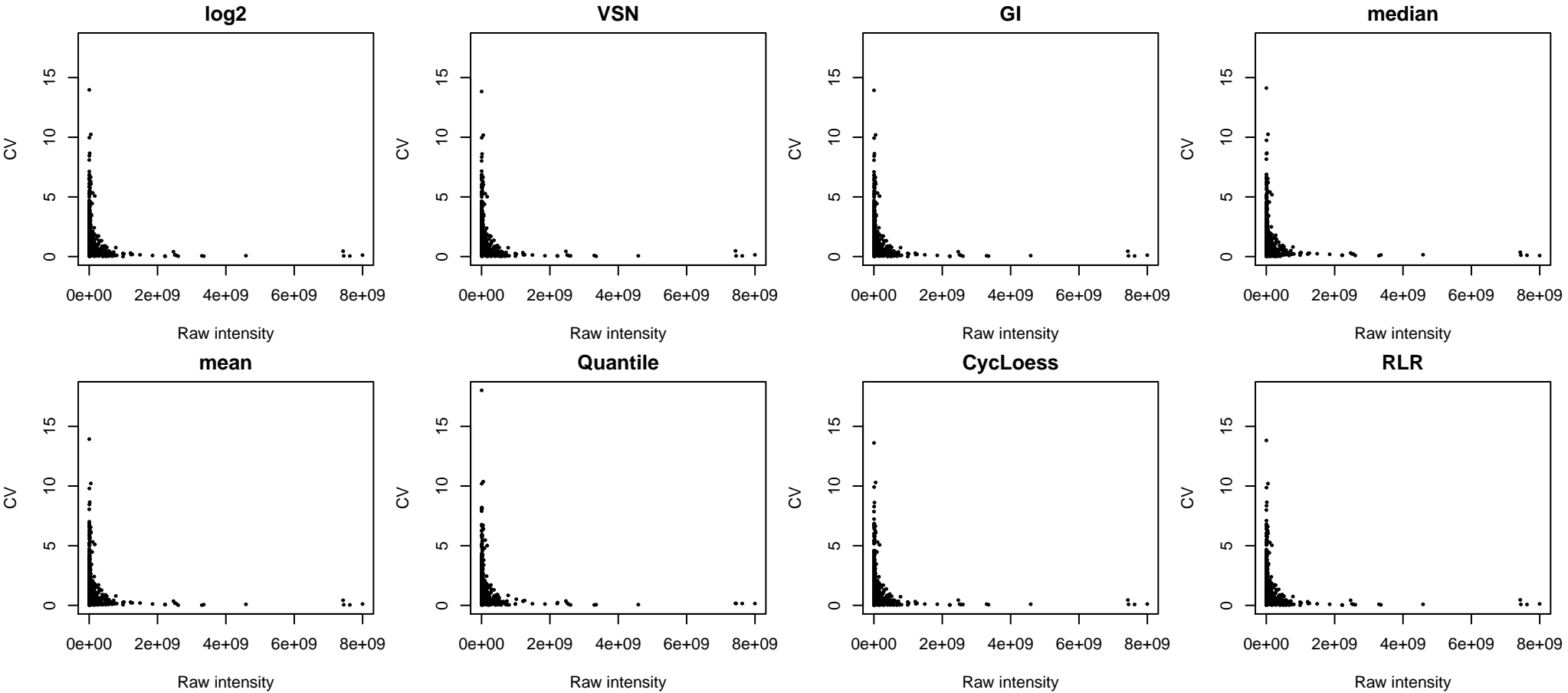


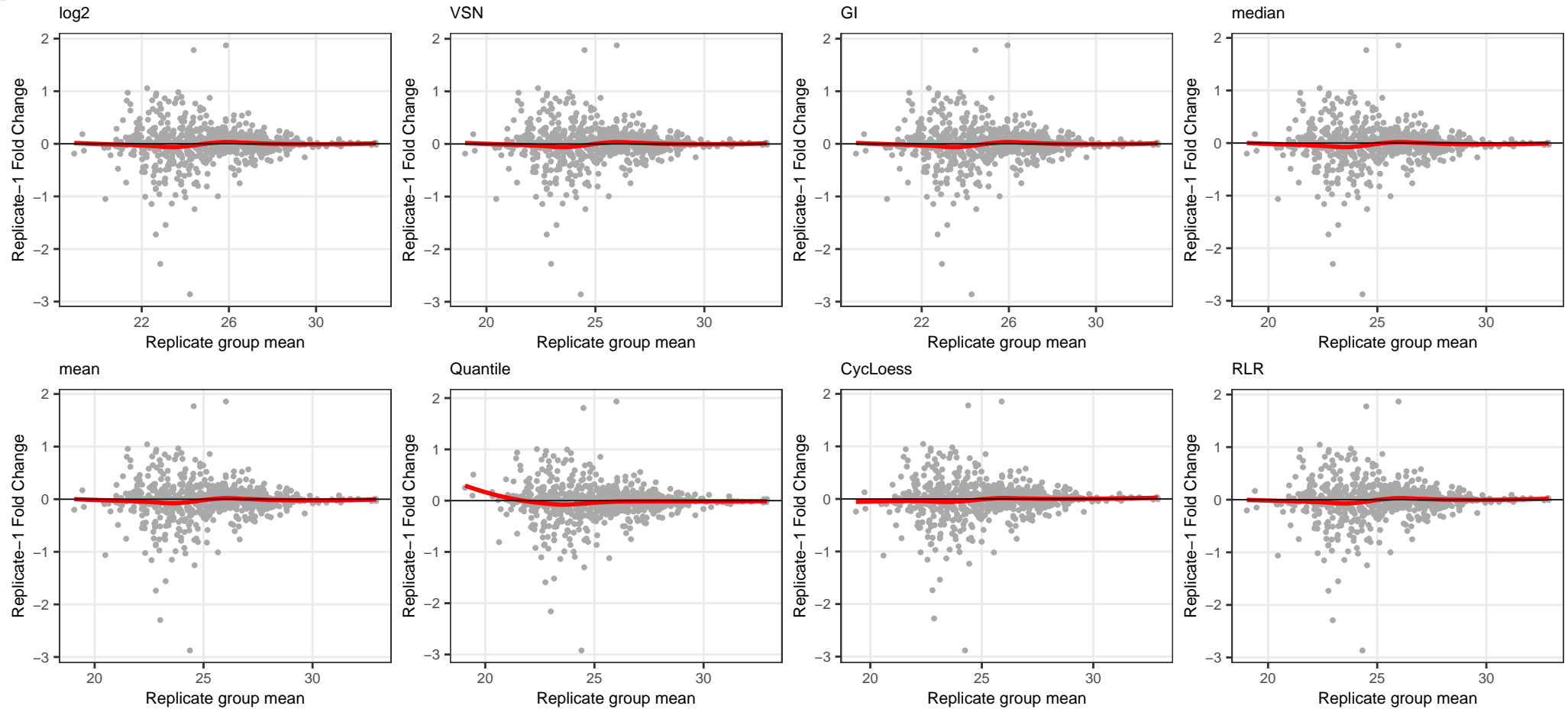
%PEV – compared to log2

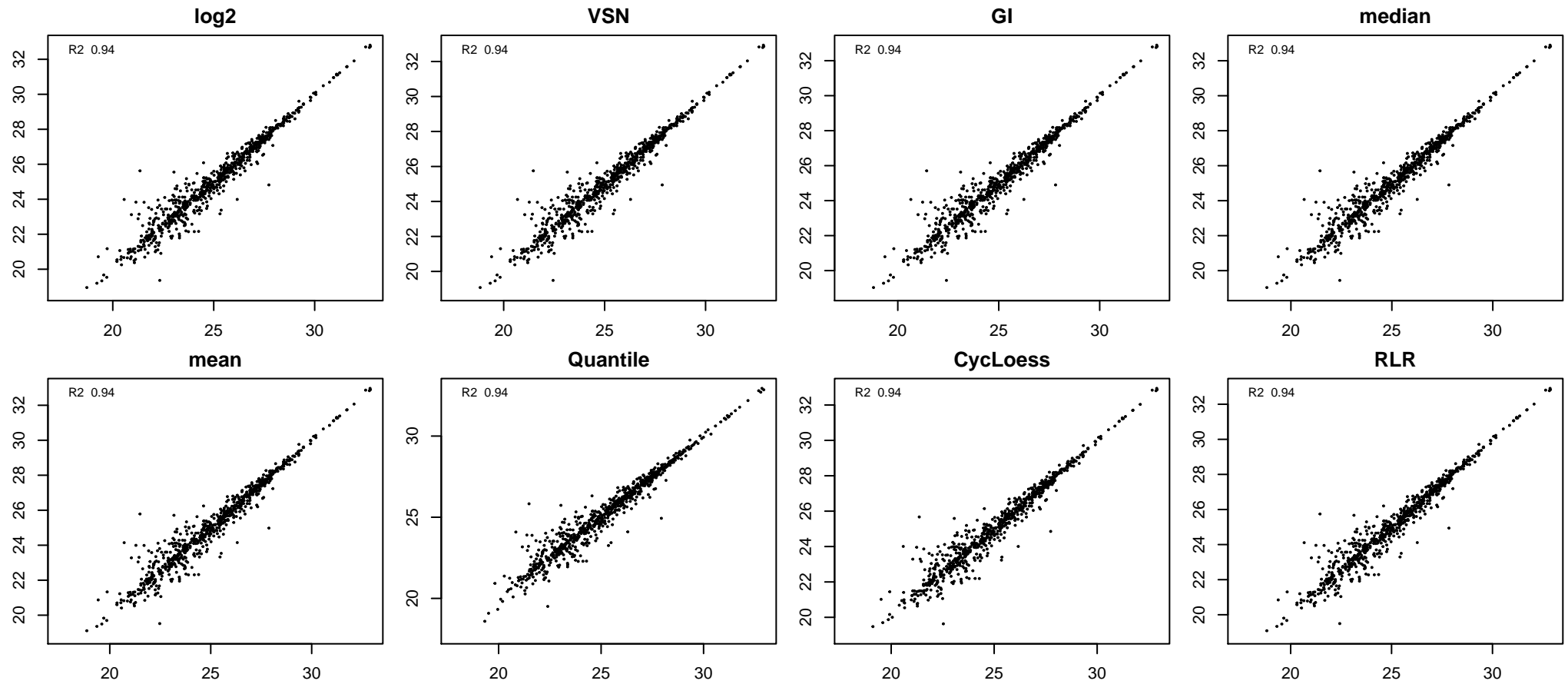


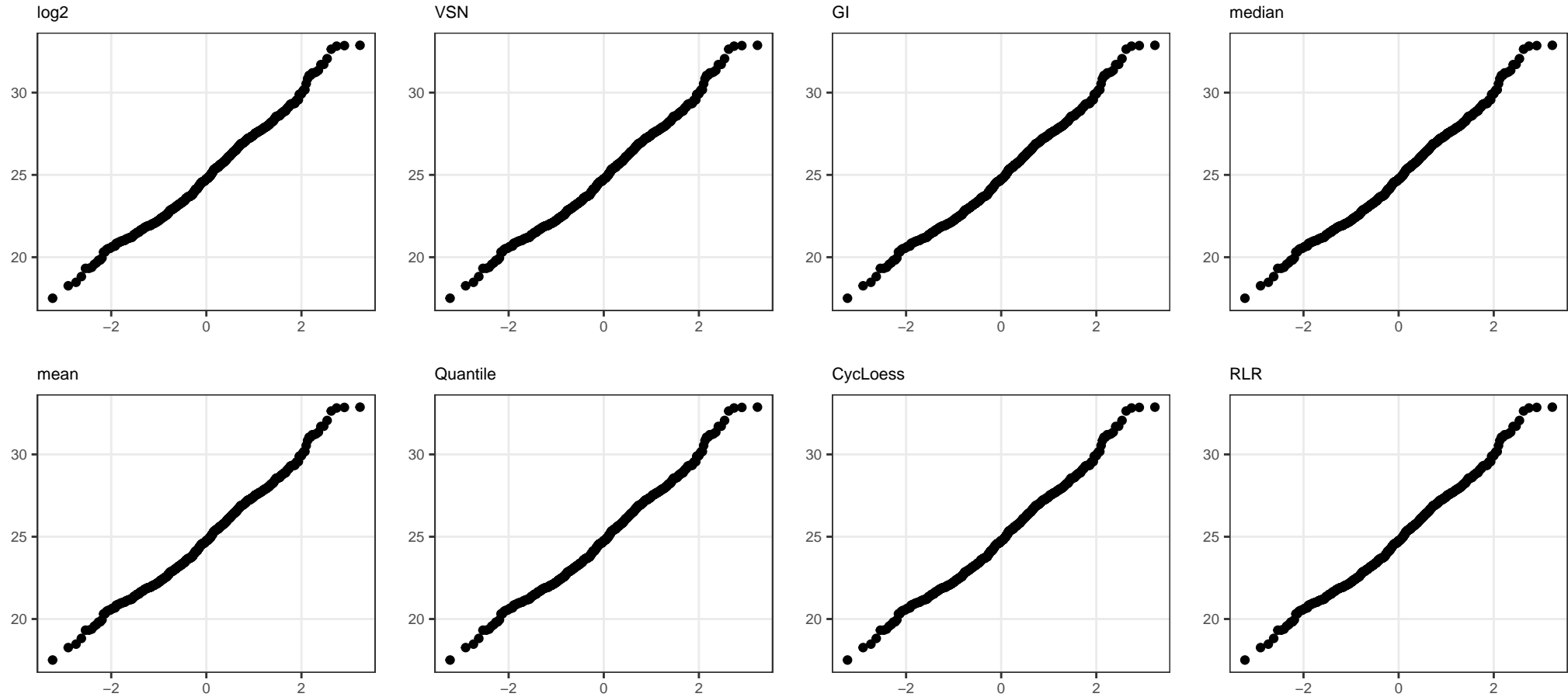
Stable variables plot

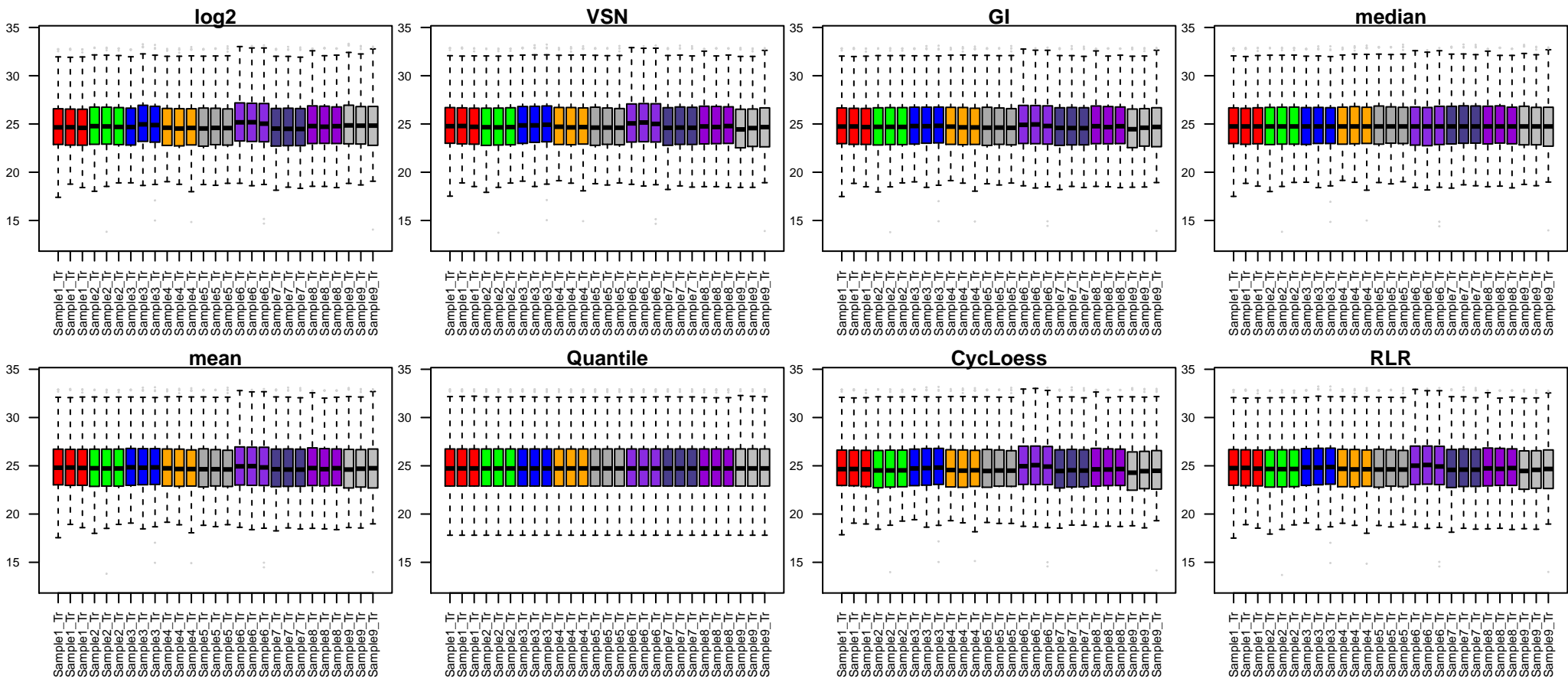


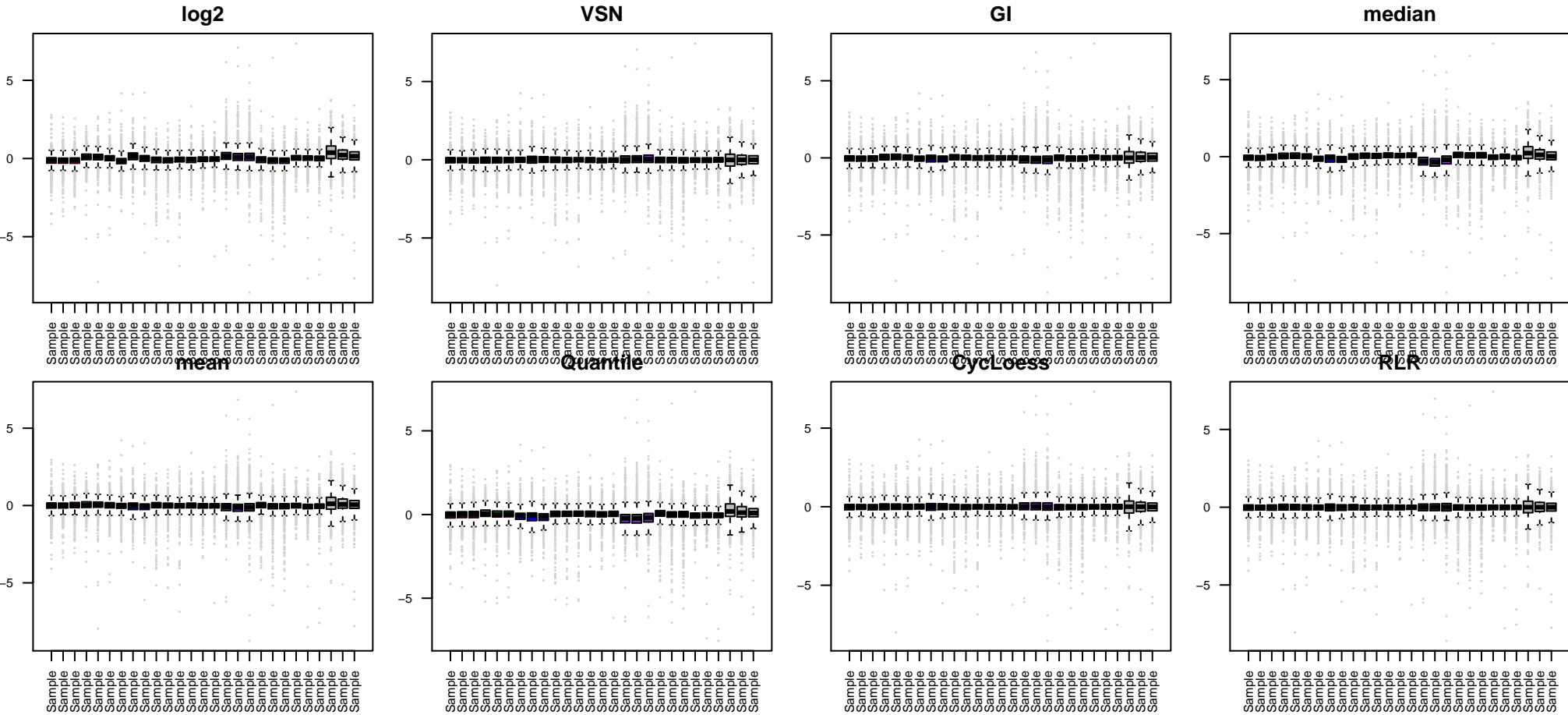










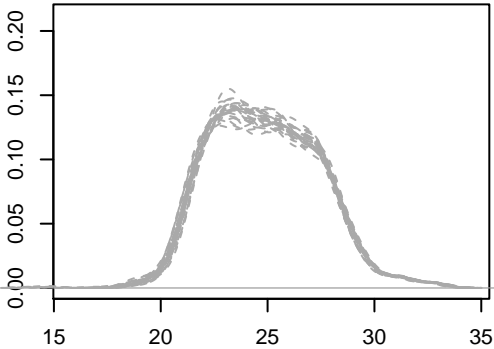
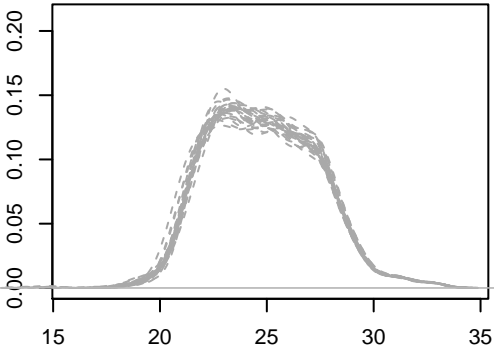
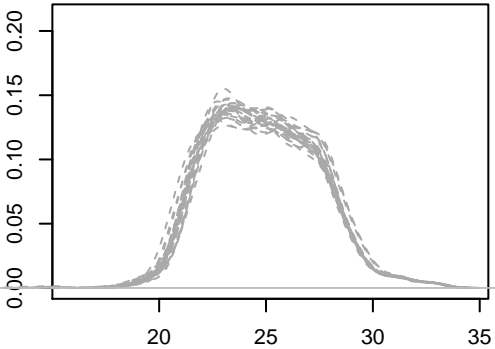
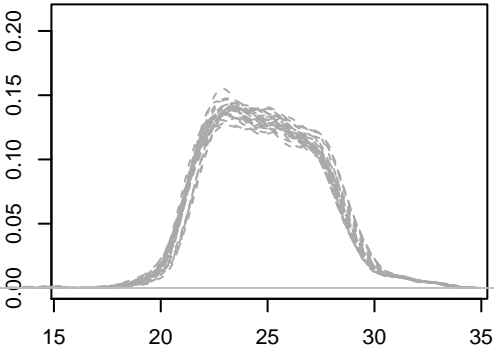


log2

VSN

GI

median

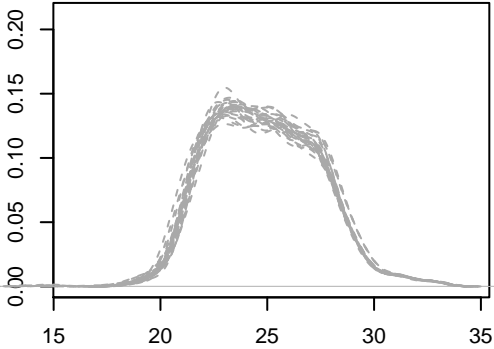
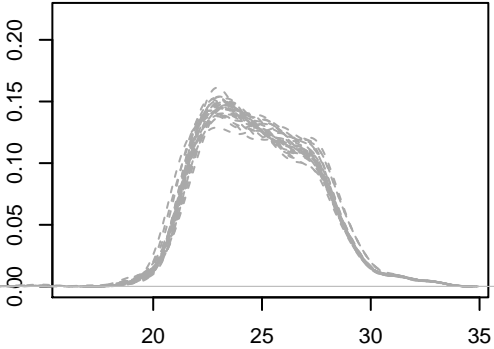
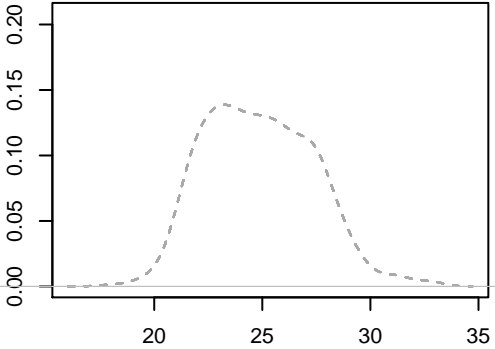
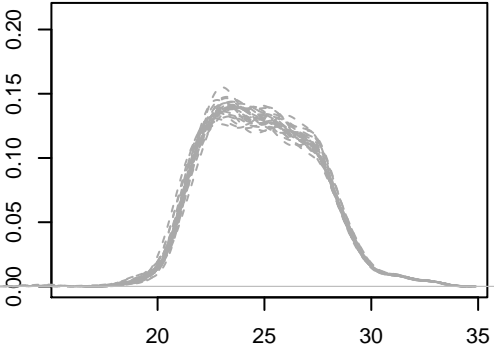


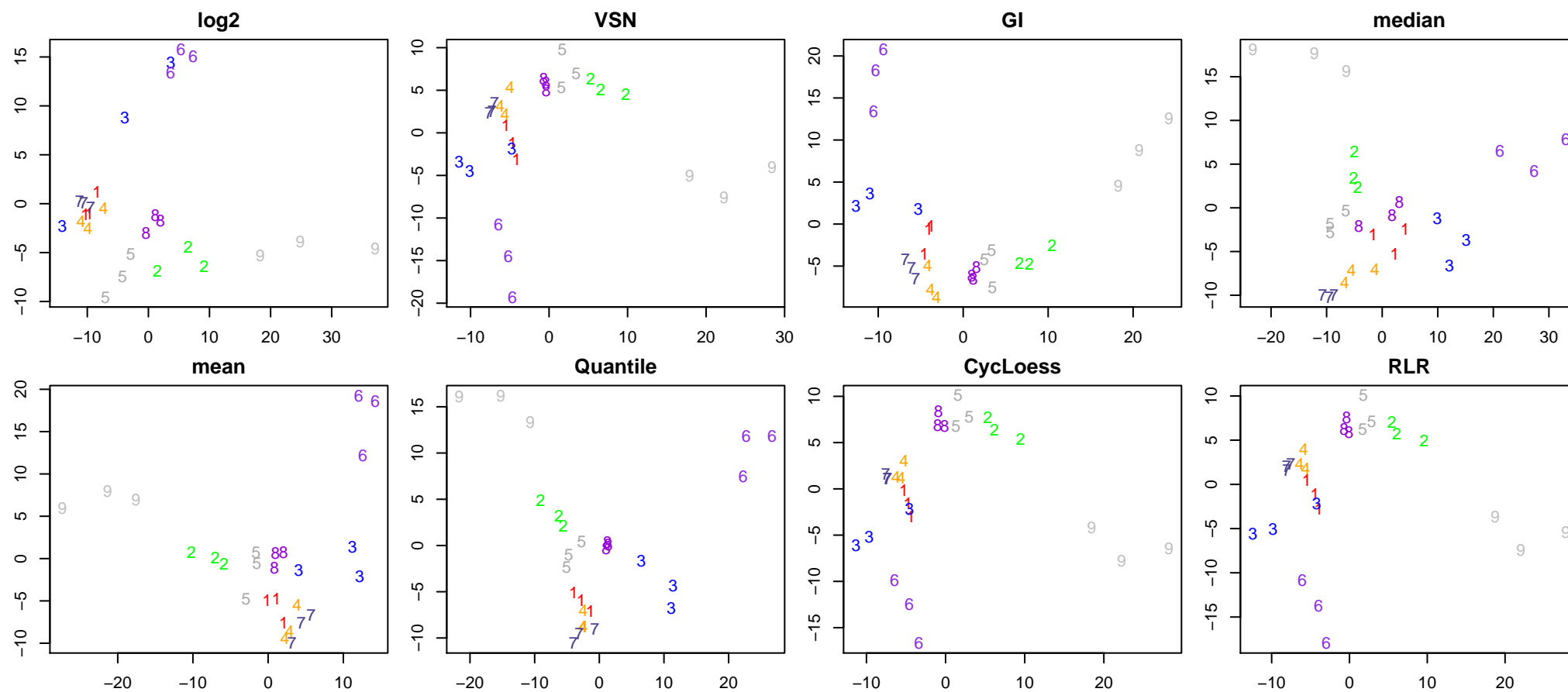
mean

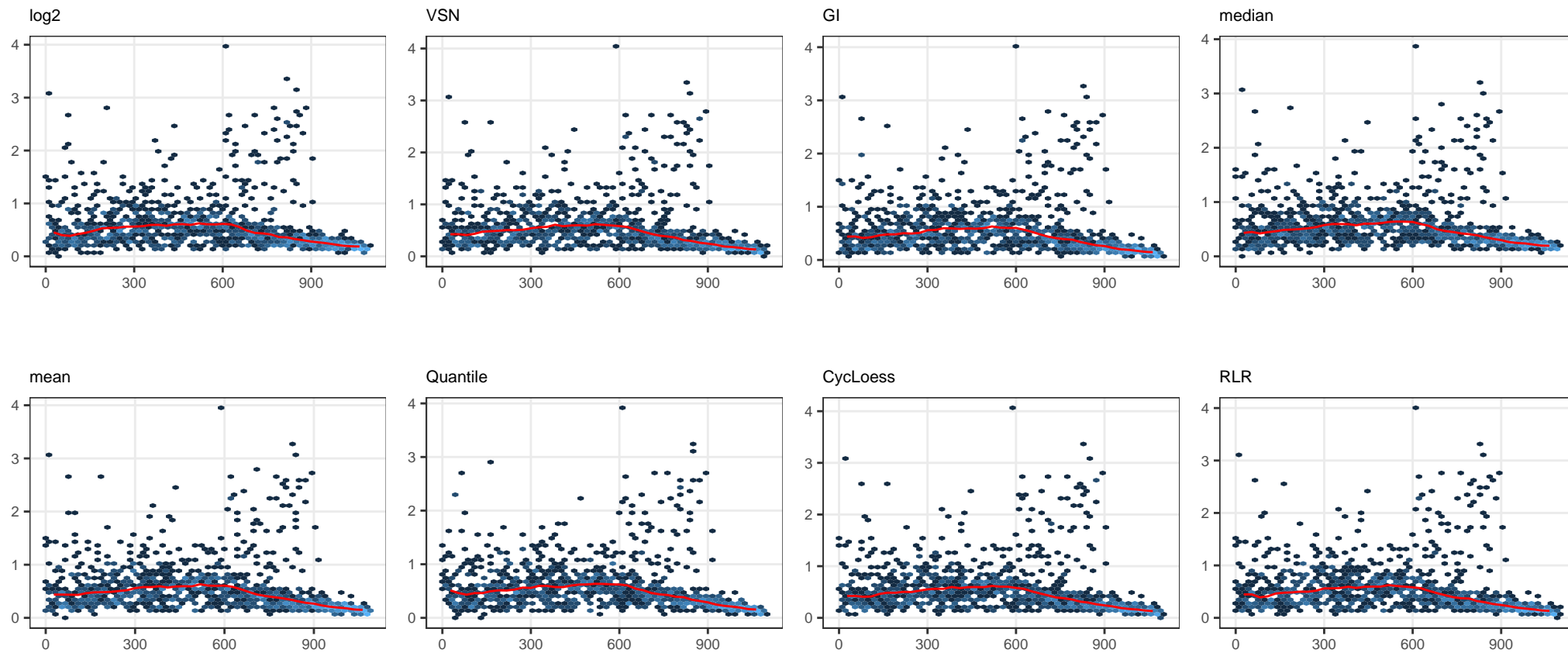
Quantile

CycLoess

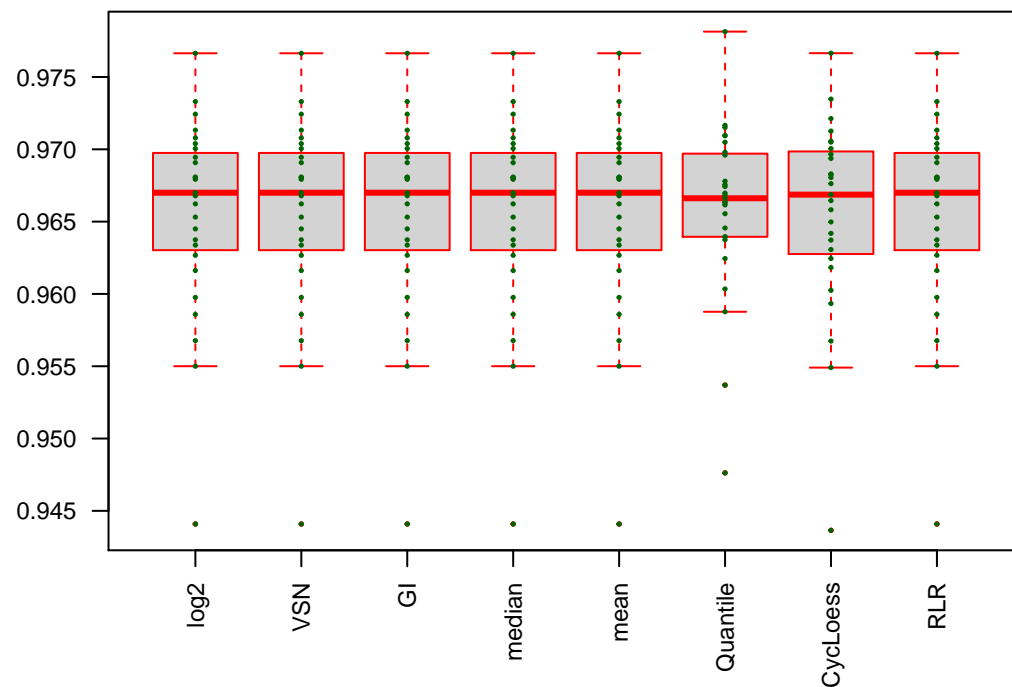
RLR







Pearson correlation – Intragroup



Spearman correlation – Intragroup

