

Project Name: test

NormalyzerDE (ver 1.19.7)

Report created on: 2024-04-09

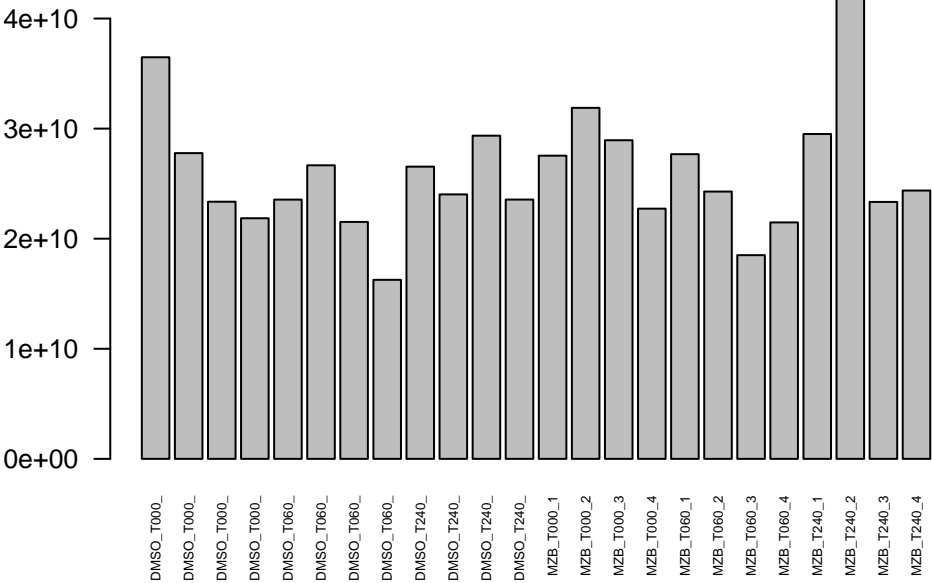
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

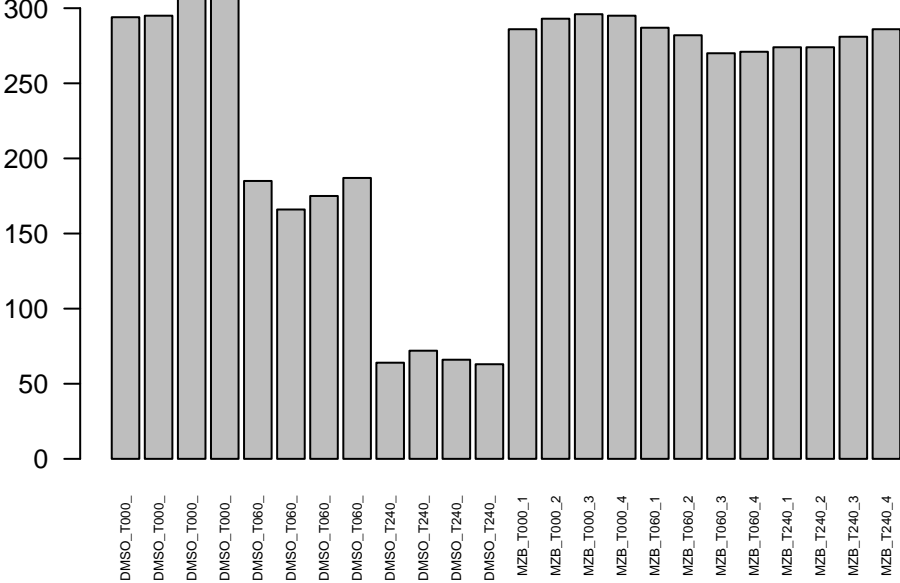
Group nbr.	Design group	Nbr. samples in cond.
1	DMSO_T000	4
2	DMSO_T060	4
3	DMSO_T240	4
4	MZB_T000	4
5	MZB_T060	4
6	MZB_T240	4

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

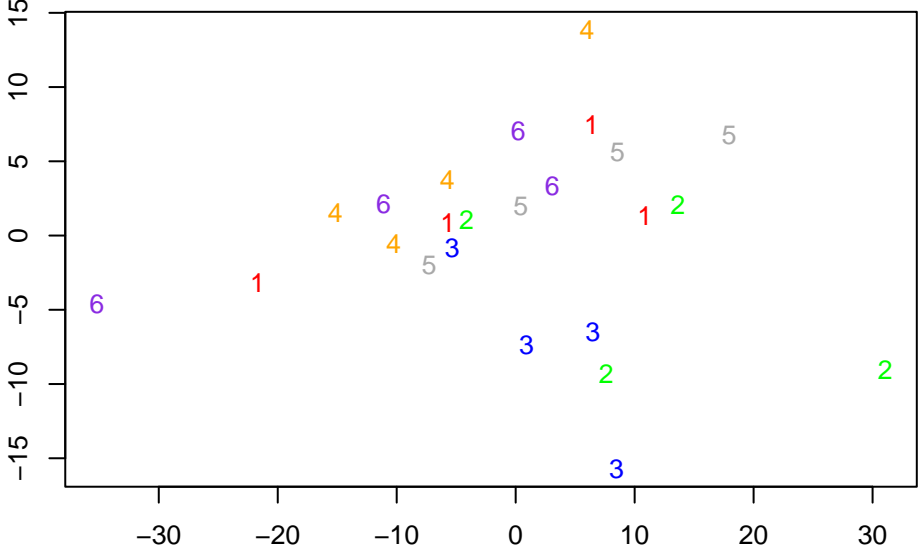
Total intensity

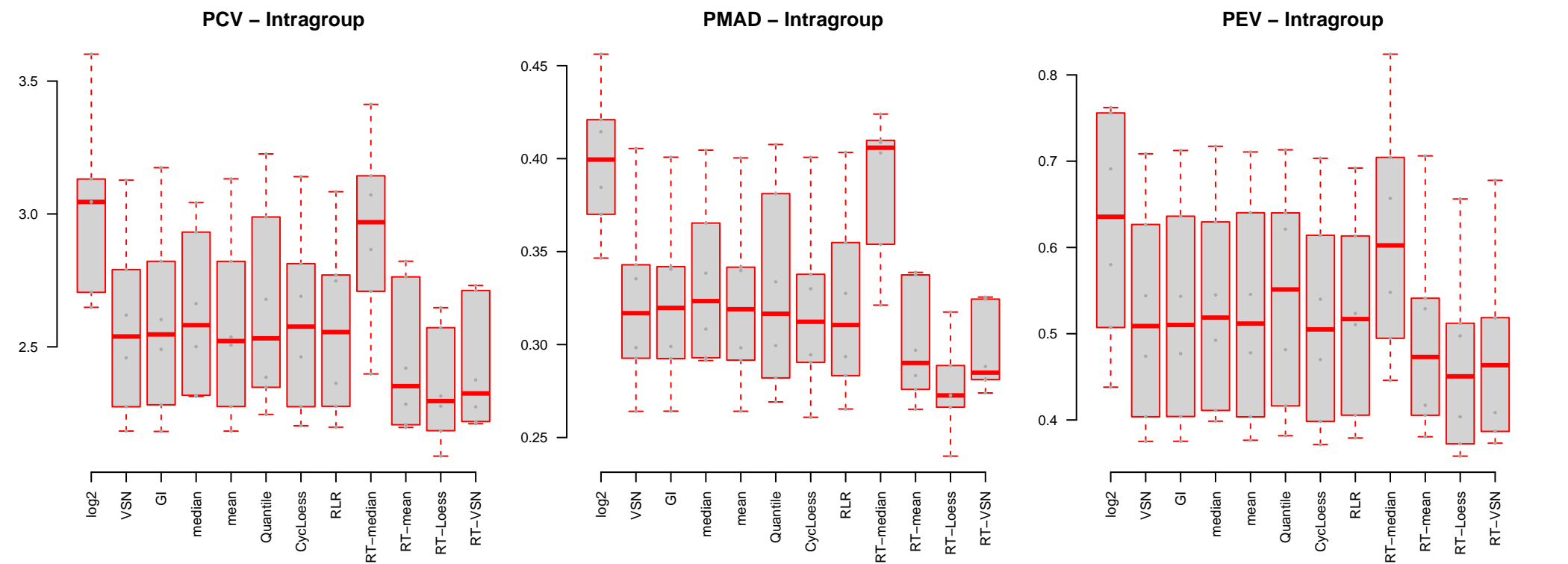


Total missing

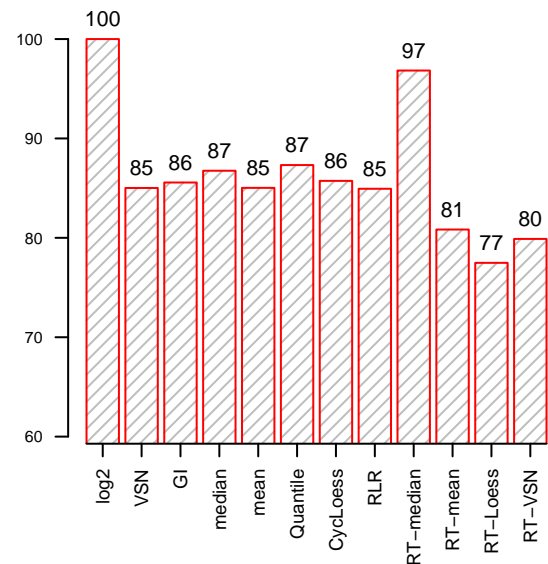


Log2-MDS plot

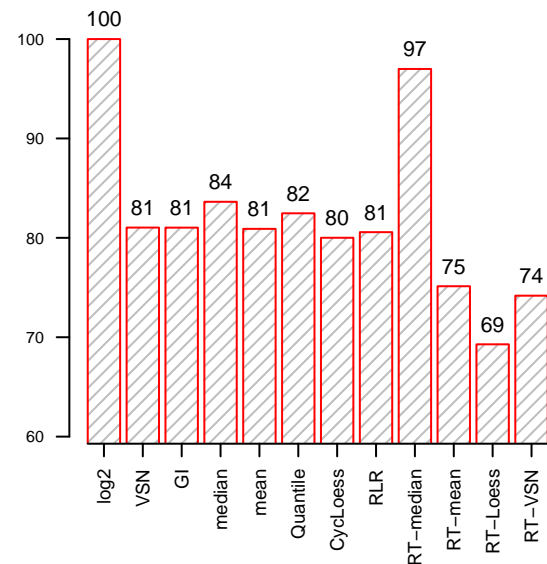




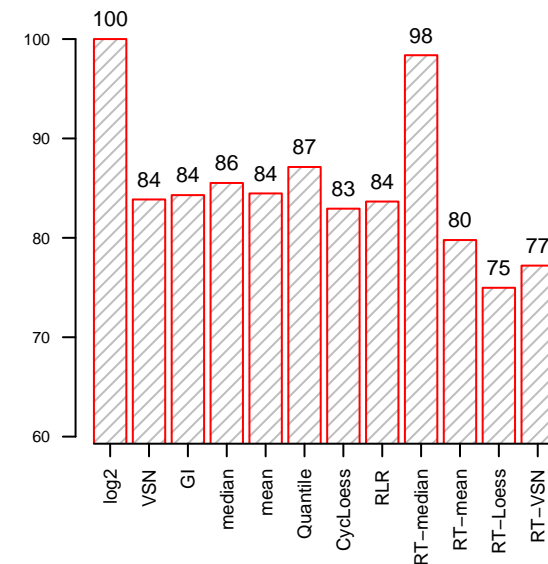
PCV compared to log2



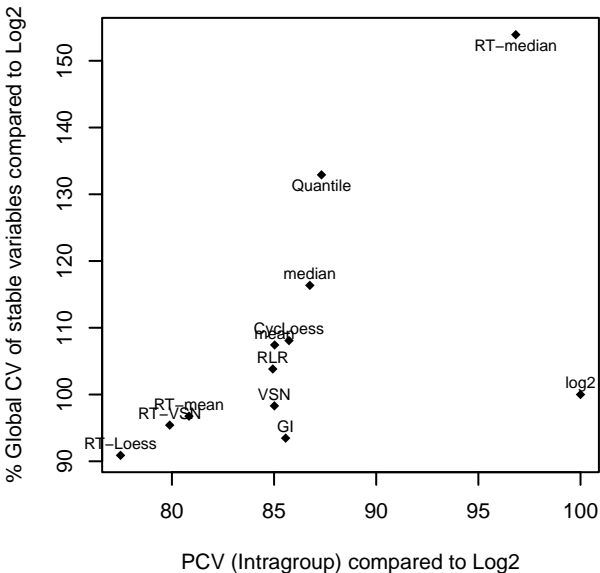
PMAD compared to log2

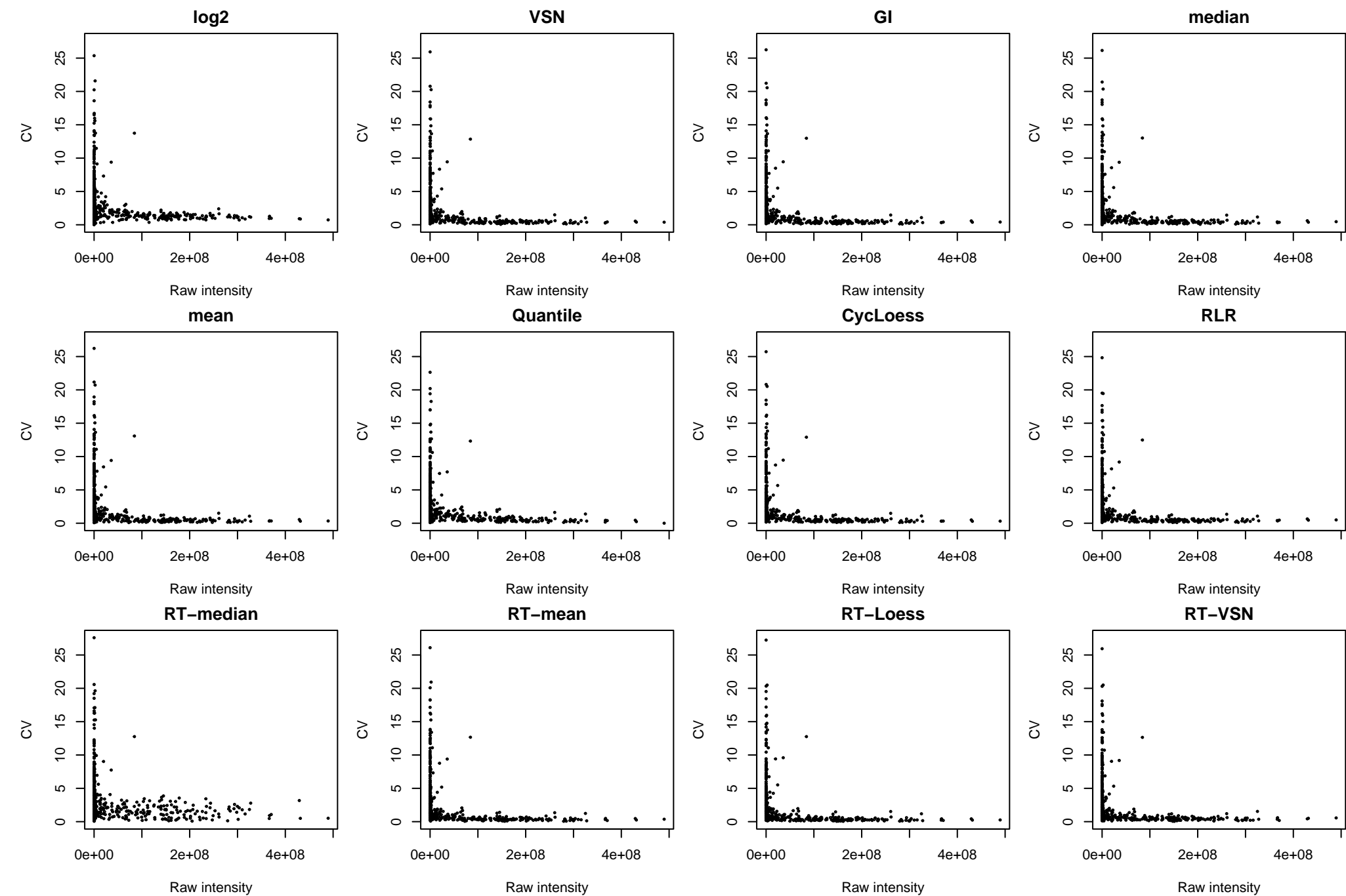


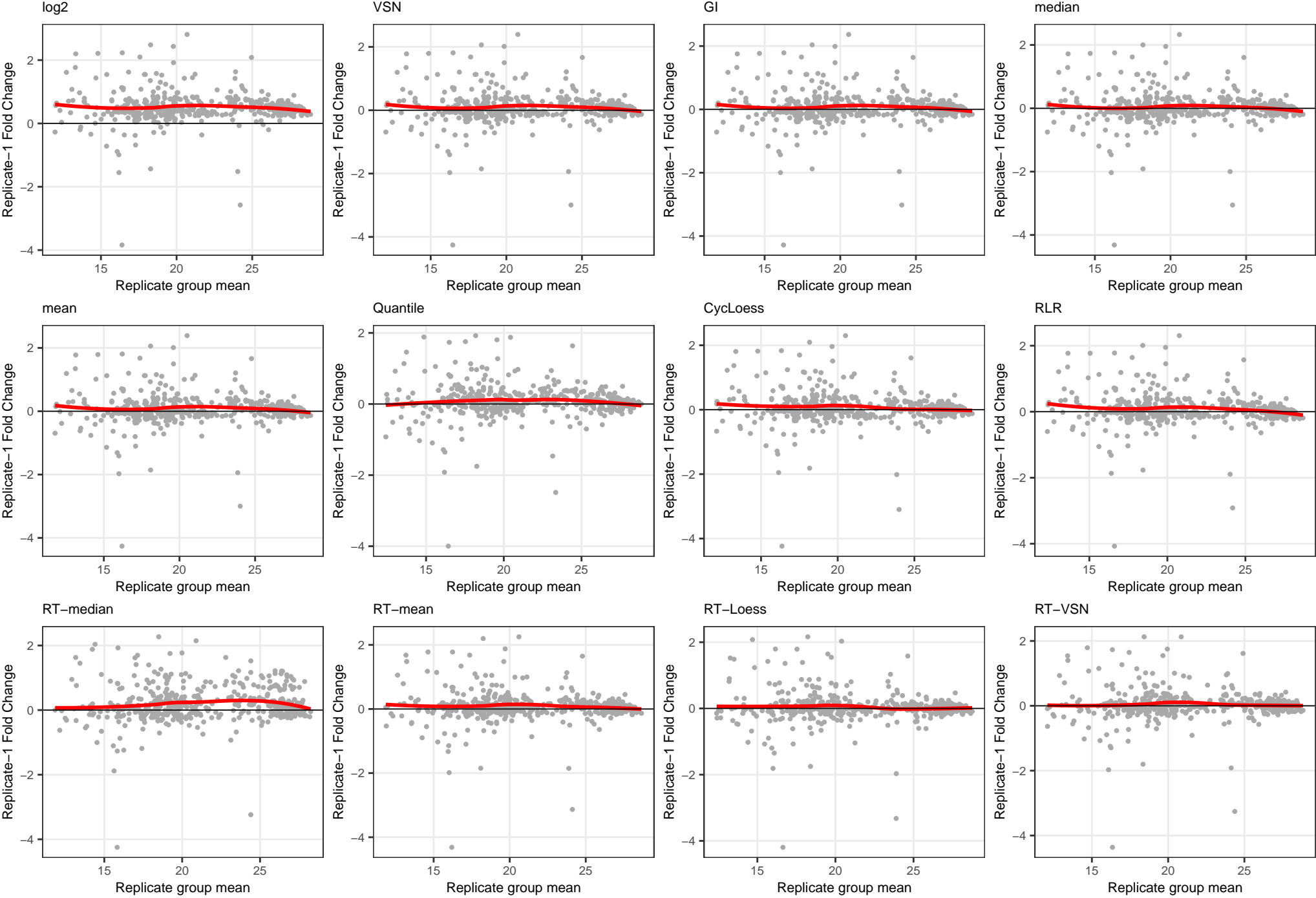
%PEV – compared to log2

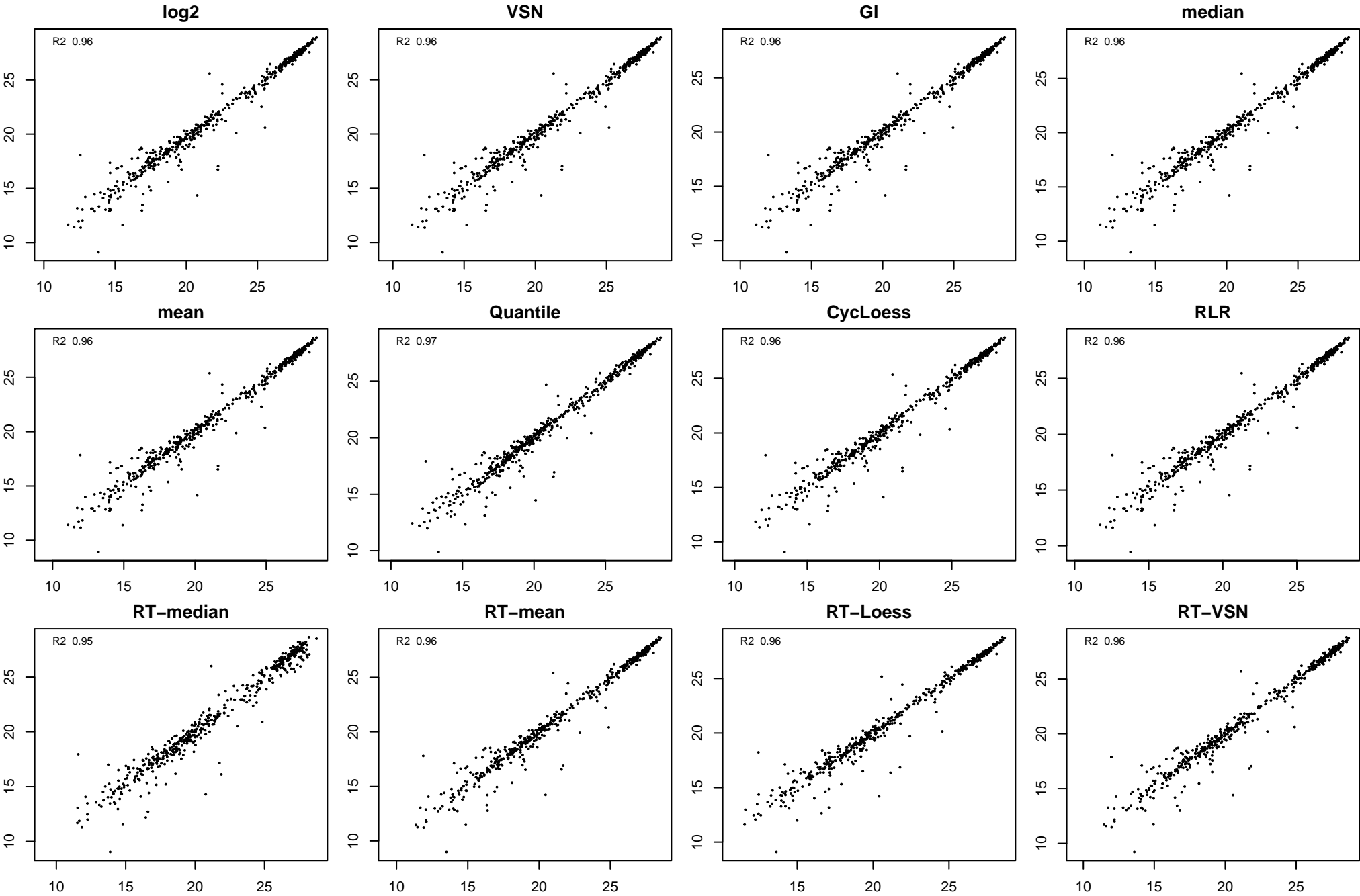


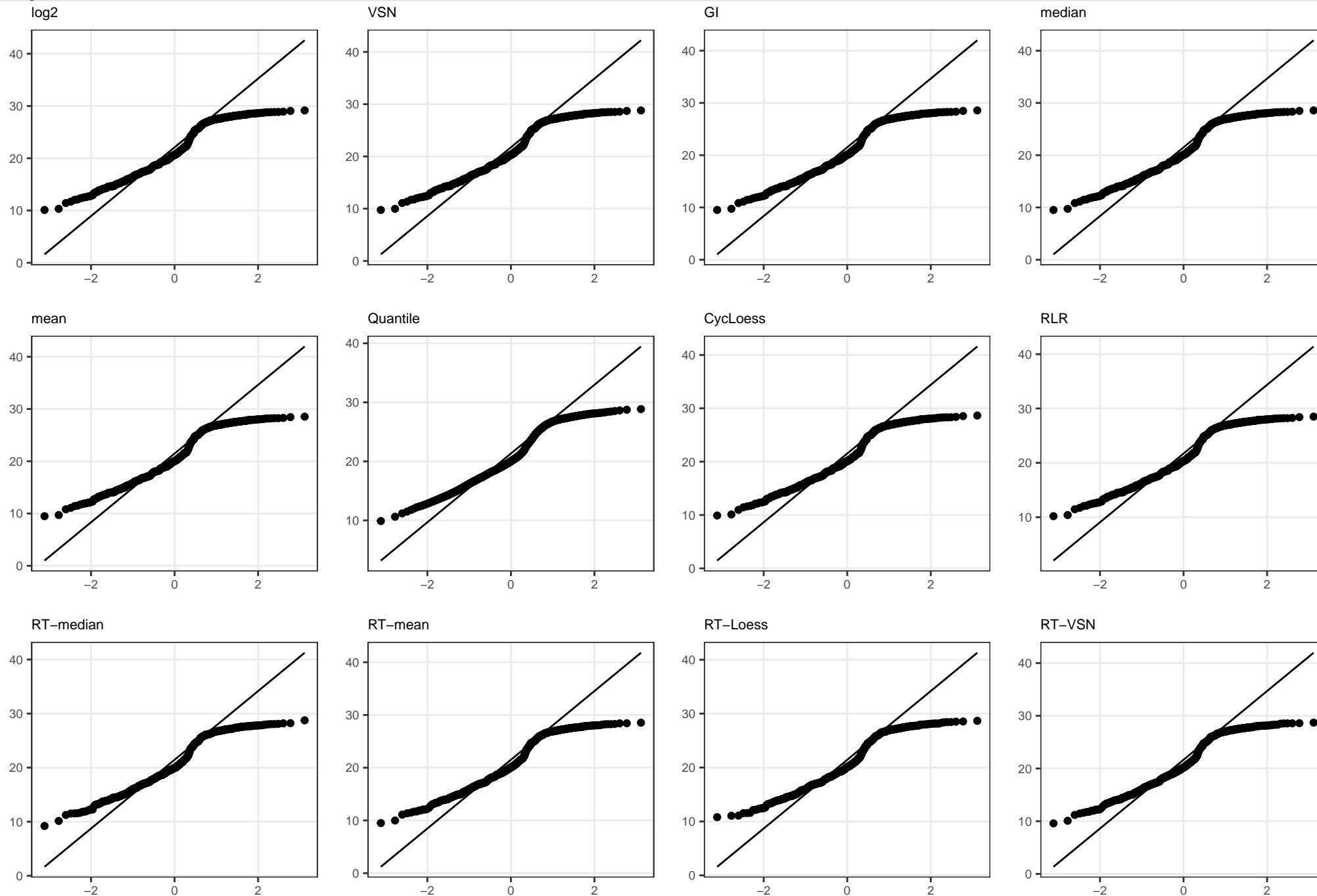
Stable variables plot



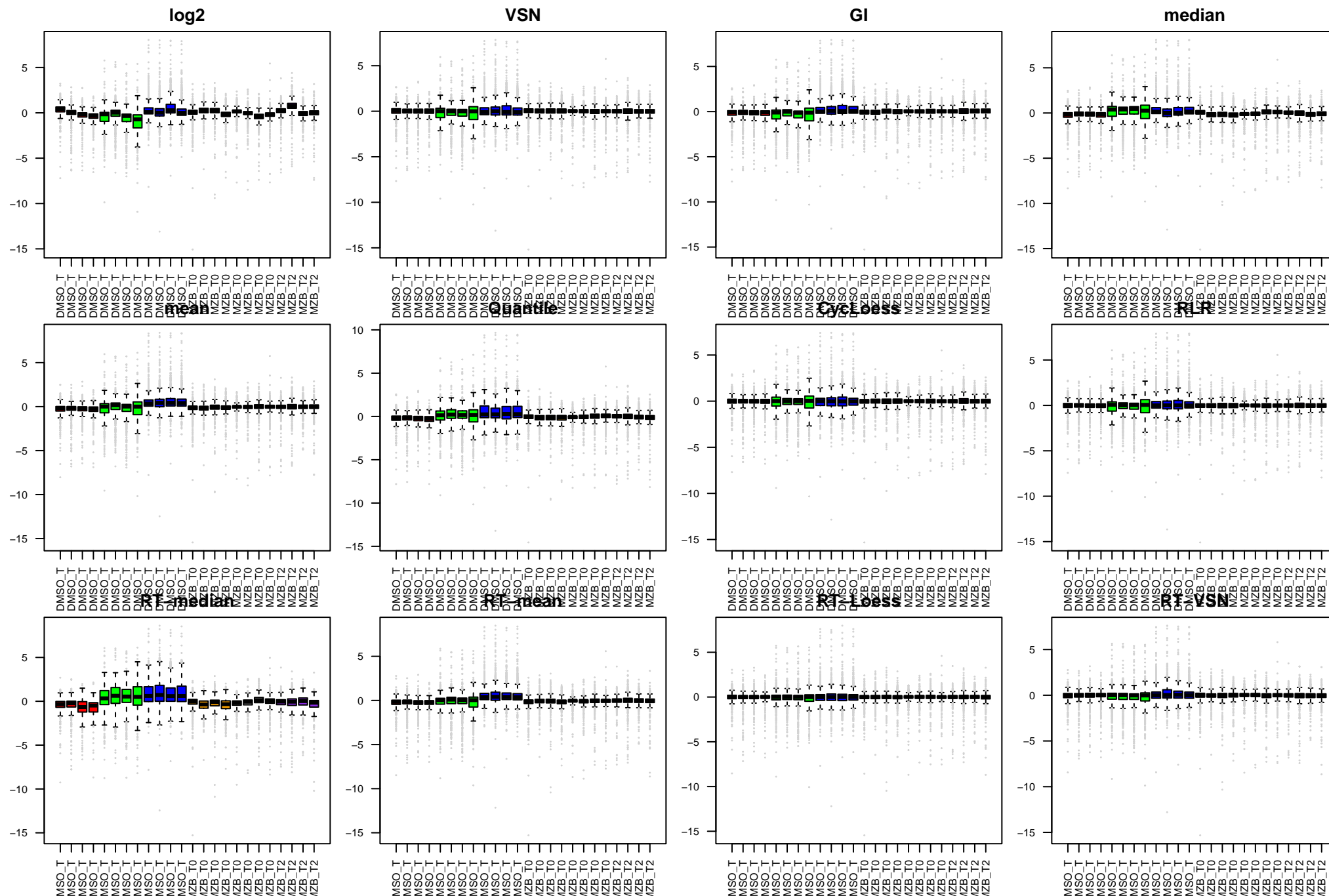




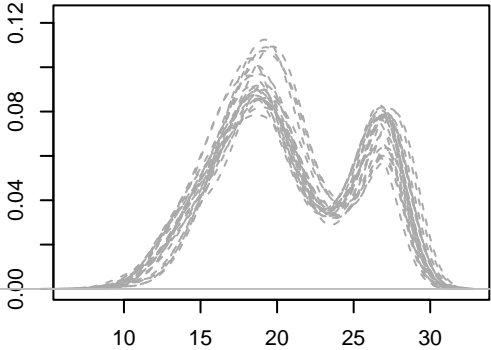




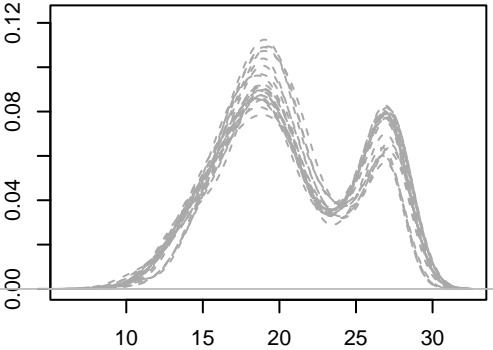




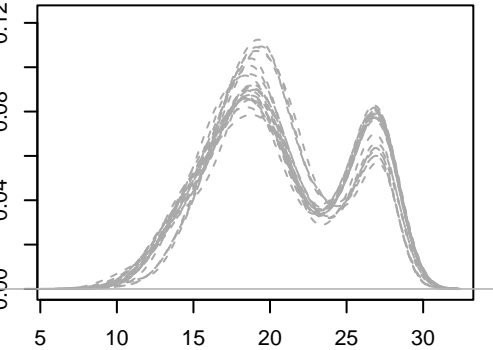
log2



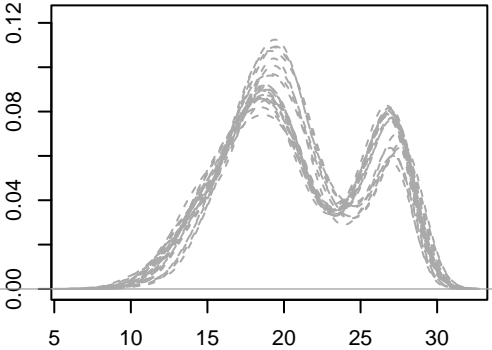
VSN



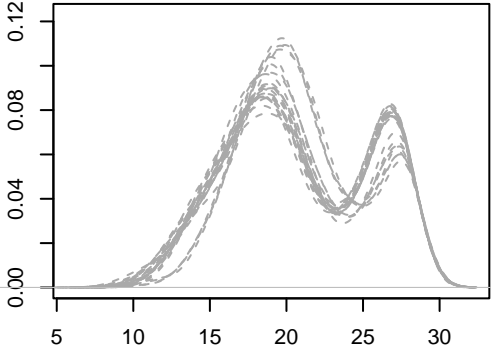
GI



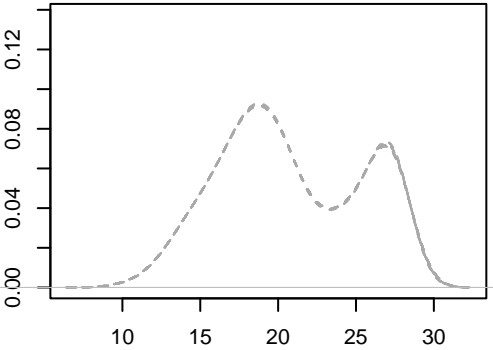
median



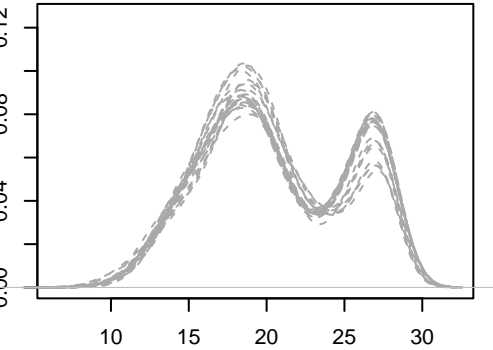
mean



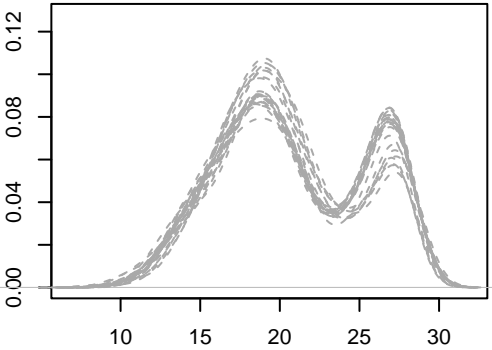
Quantile



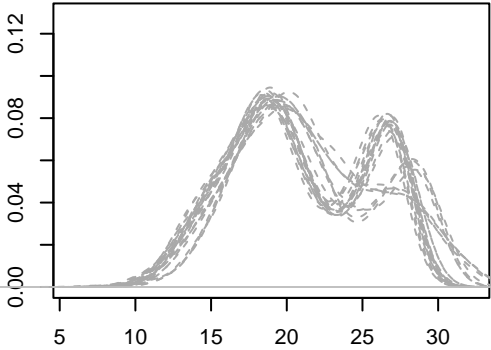
CycLoess



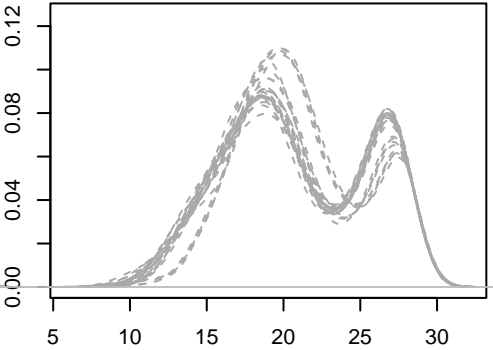
RLR



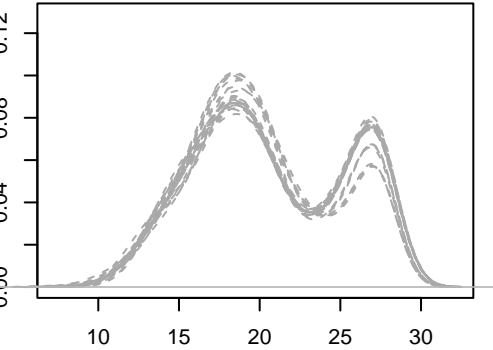
RT-median



RT-mean



RT-Loess



RT-VSN

