

Project Name: NormalyzerProteins

NormalyzerDE (ver 1.14.0)

Report created on: 2022-07-12

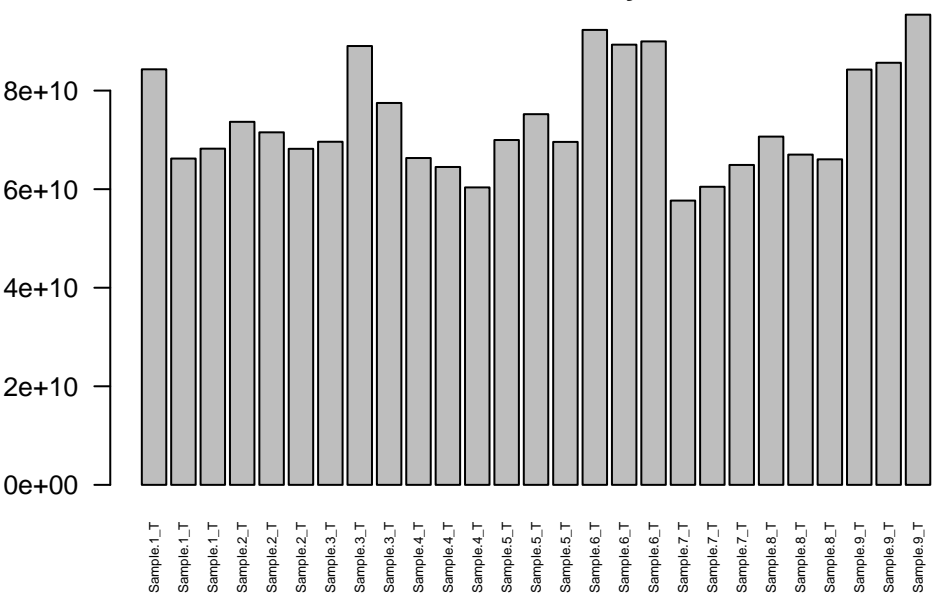
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

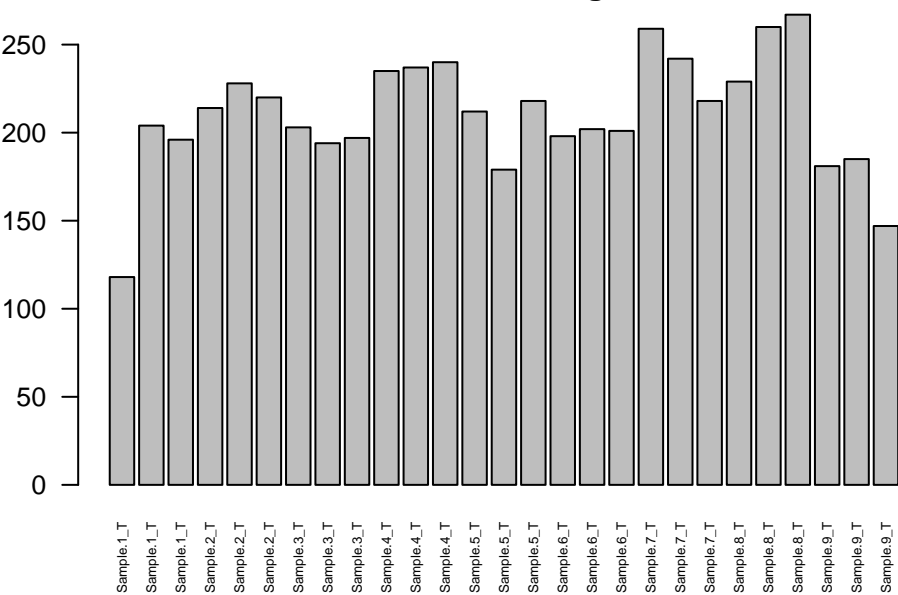
Group nbr.	Design group	Nbr. samples in cond.
1	125.amol	3
2	12500.amol	3
3	250.amol	3
4	2500.amol	3
5	25000.amol	3
6	50.amol	3
7	500.amol	3
8	5000.amol	3
9	50000.amol	3

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

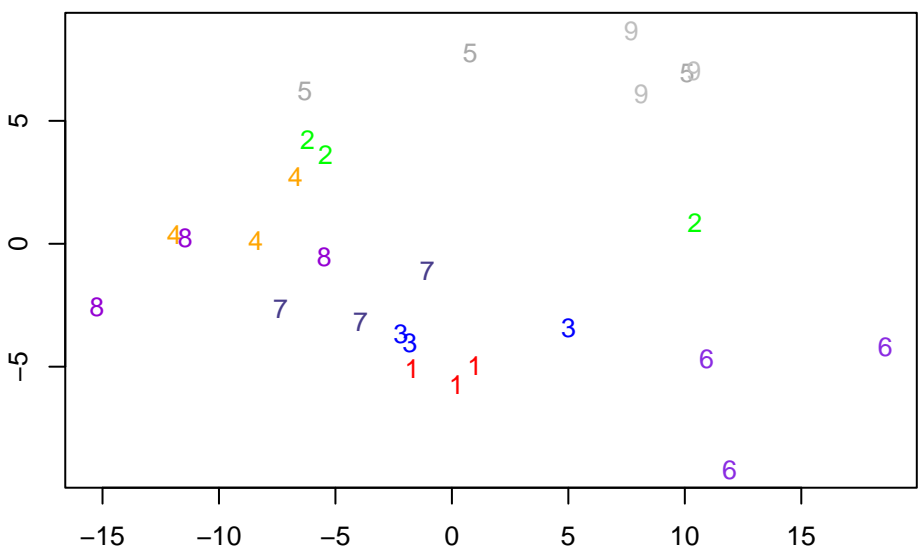
Total intensity

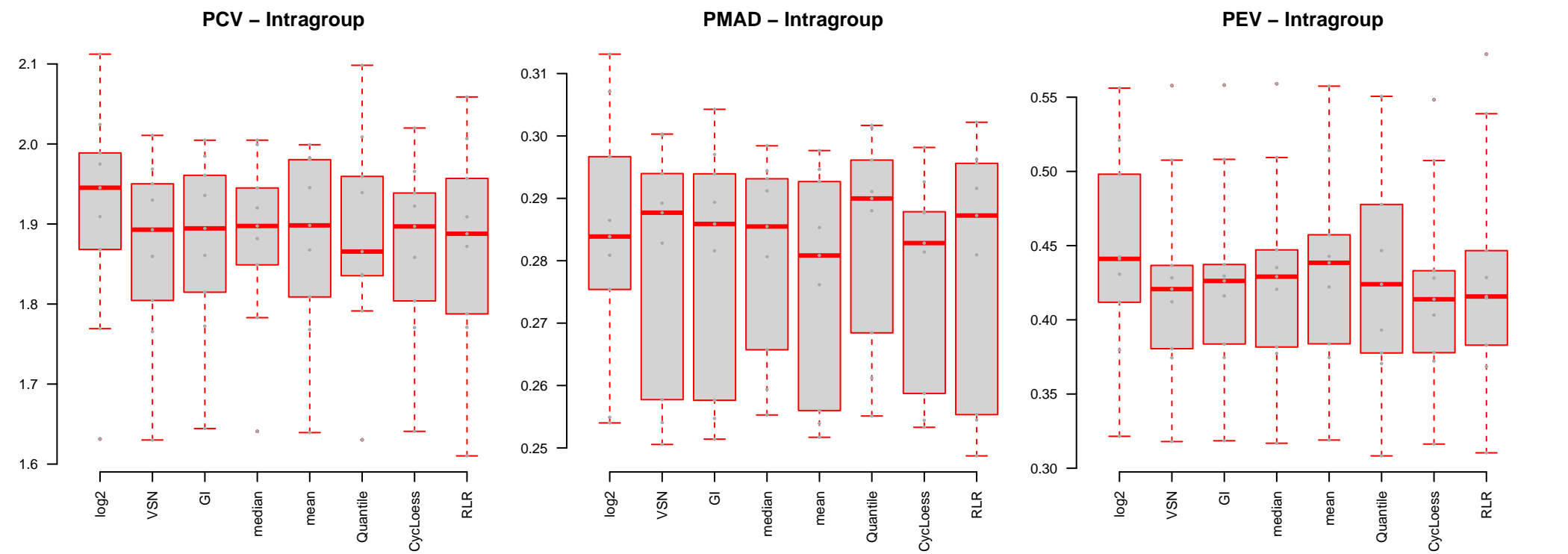


Total missing

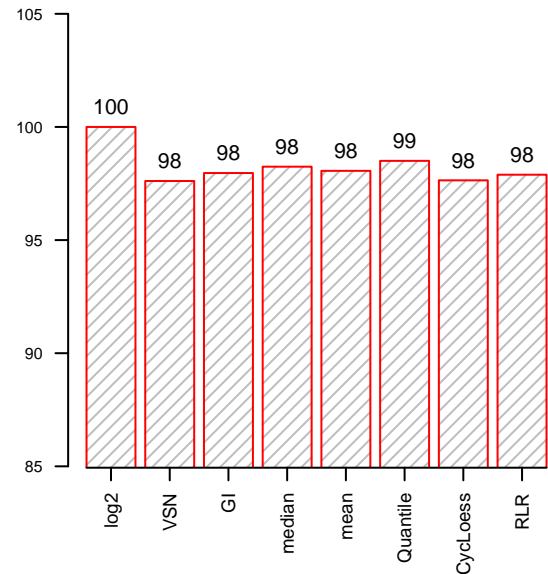


Log2-MDS plot

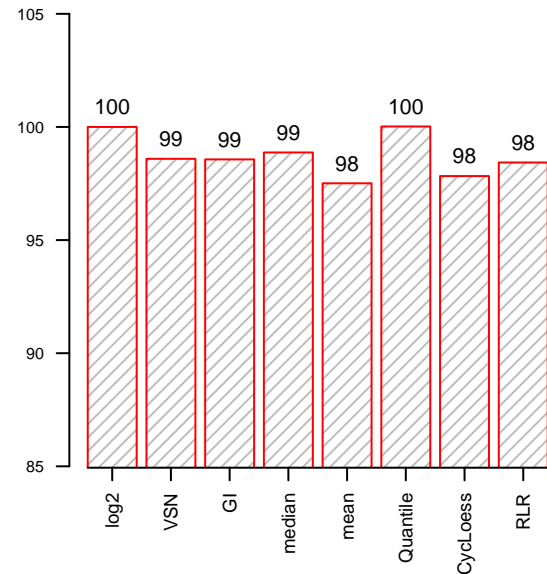




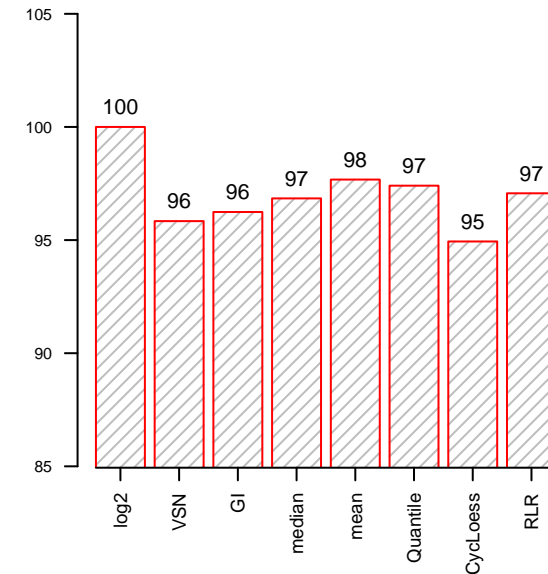
PCV compared to log2



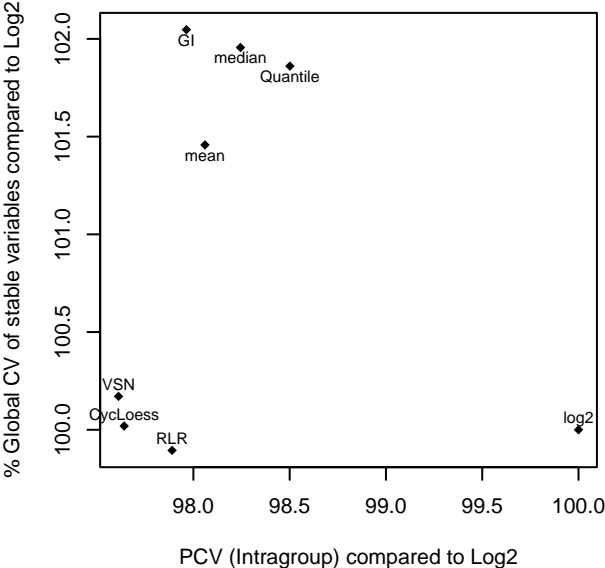
PMAD compared to log2

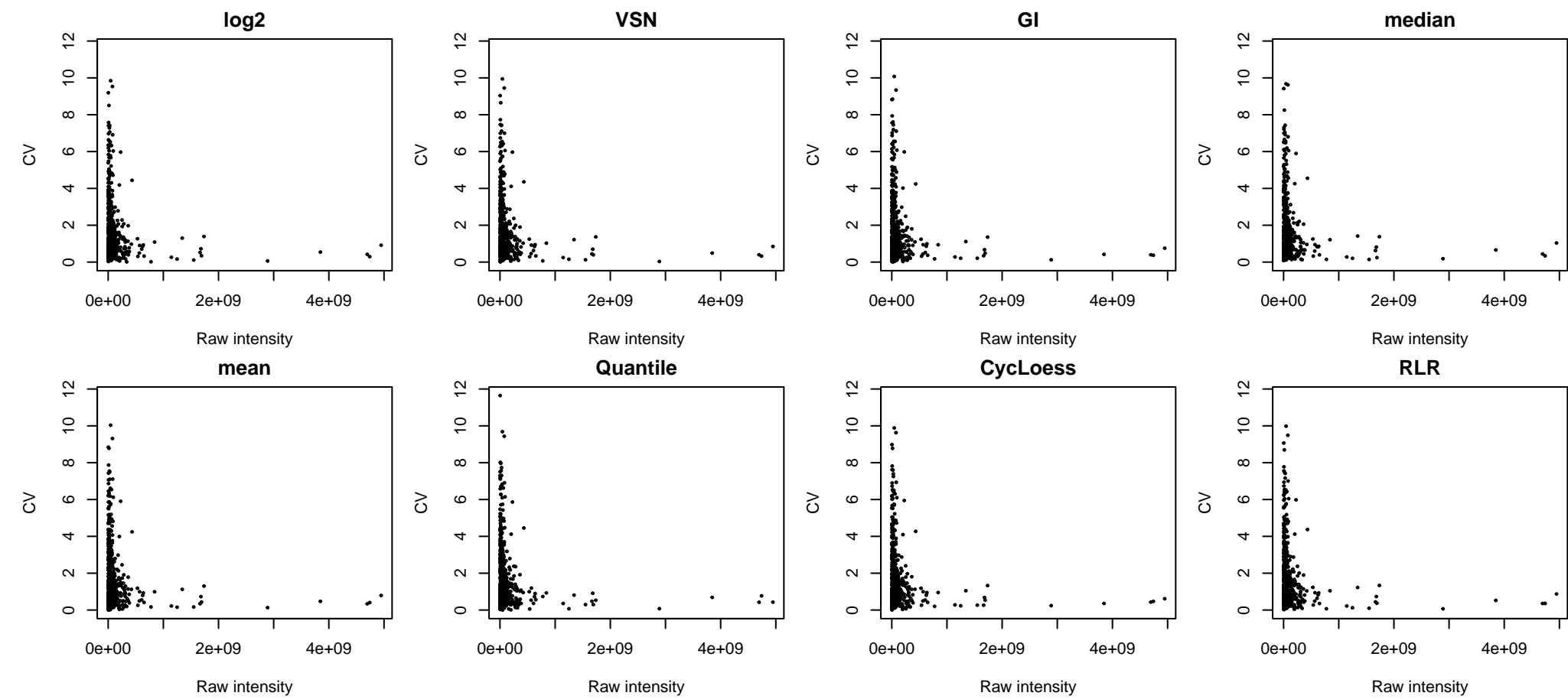


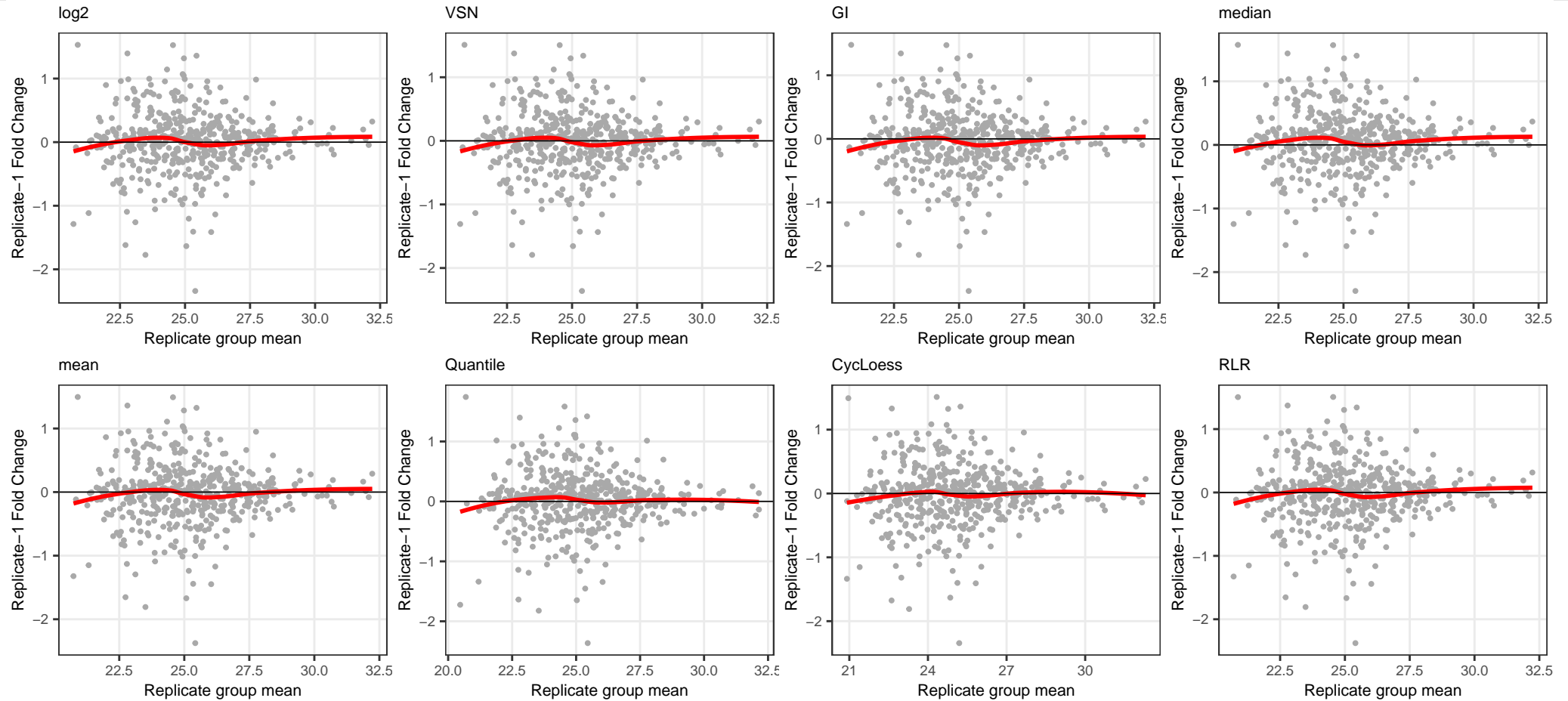
%PEV – compared to log2

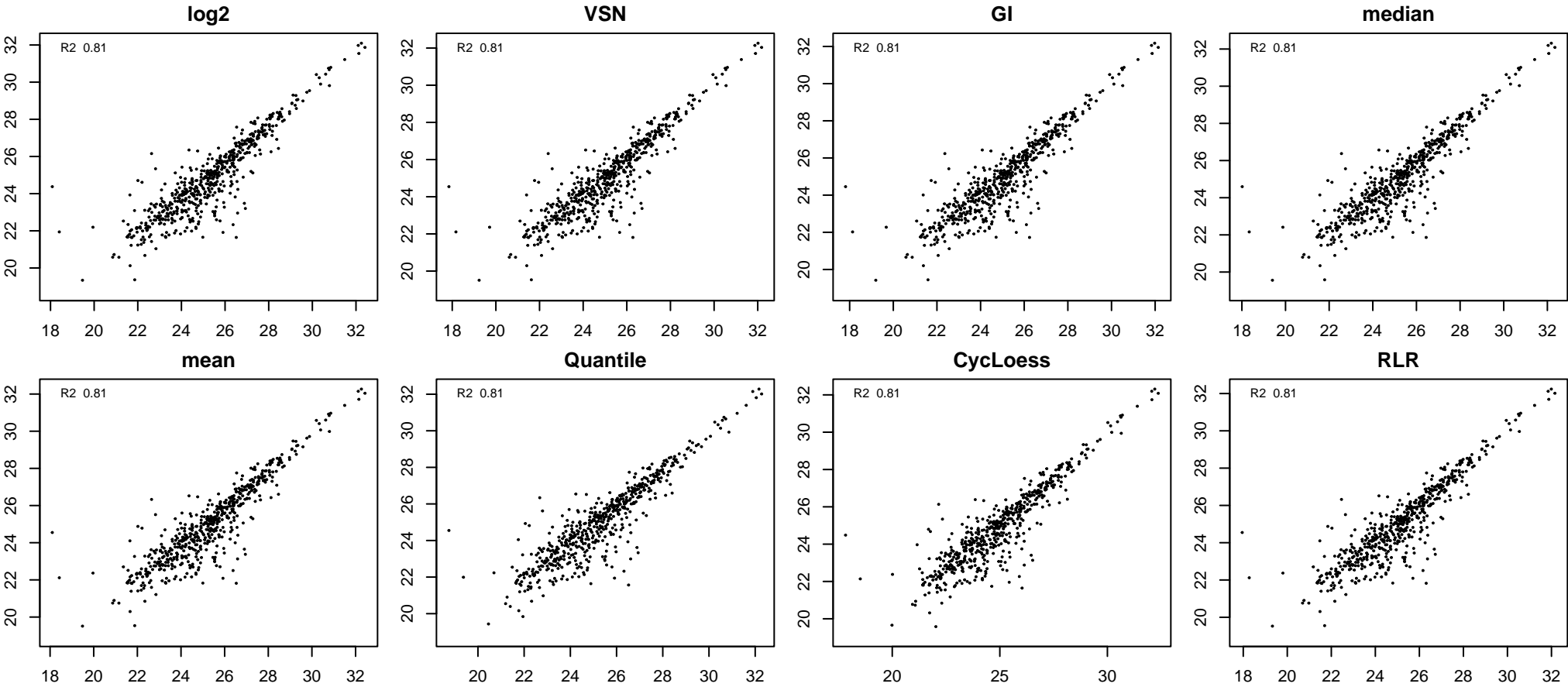


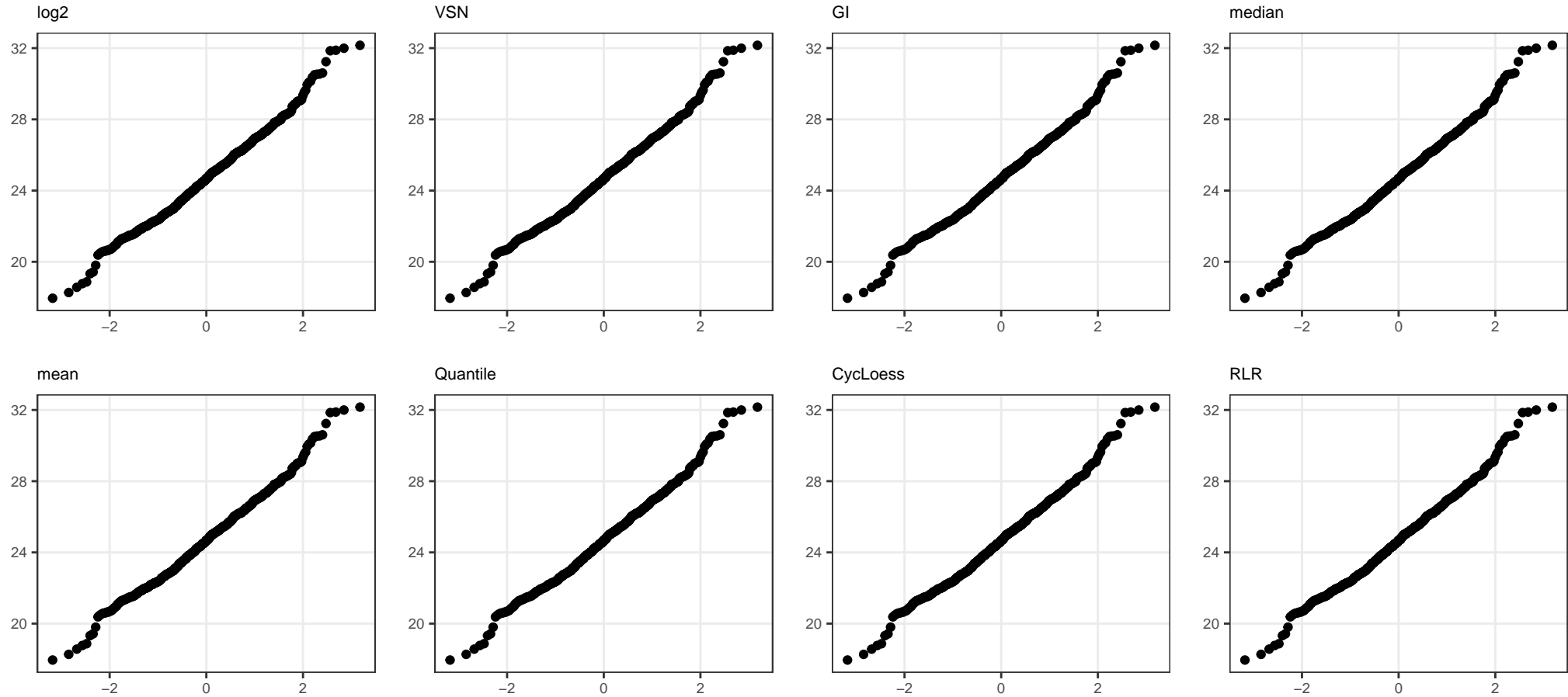
Stable variables plot

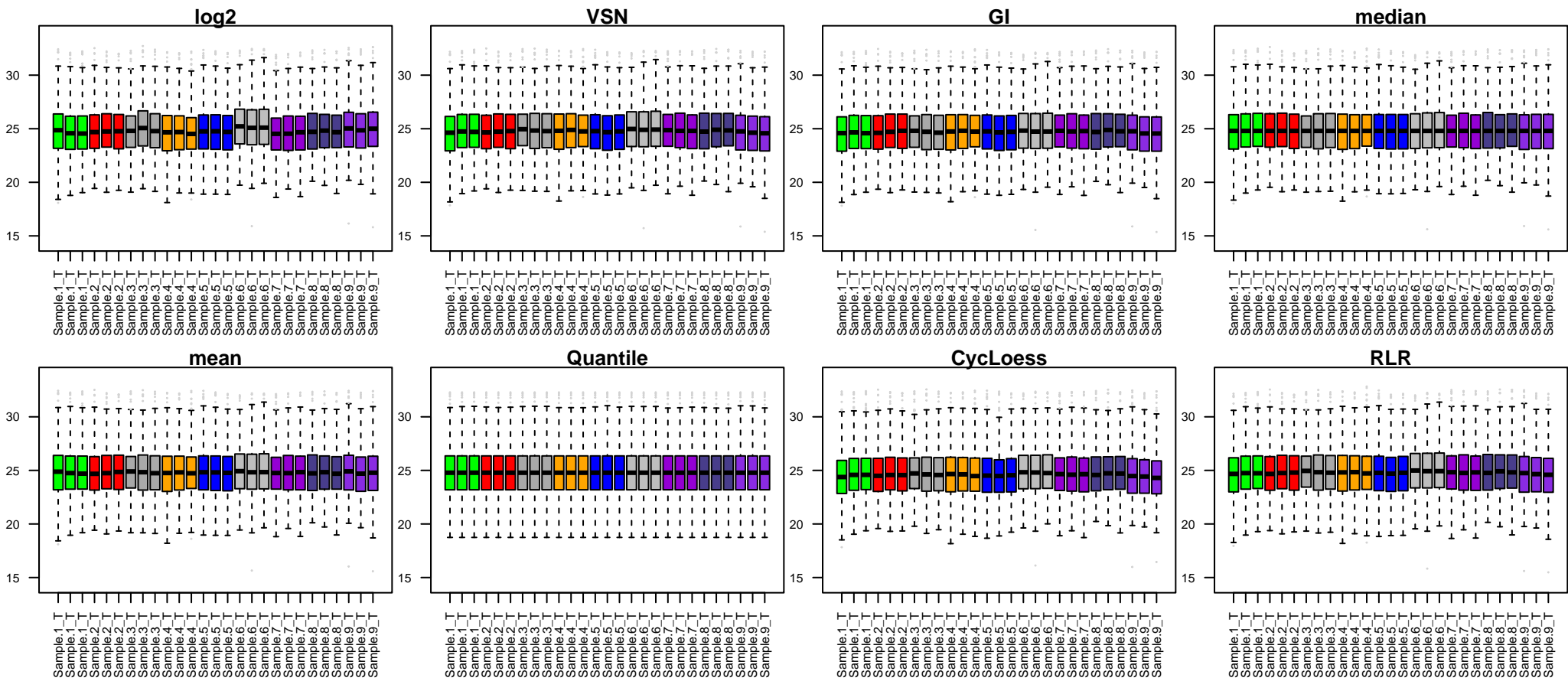


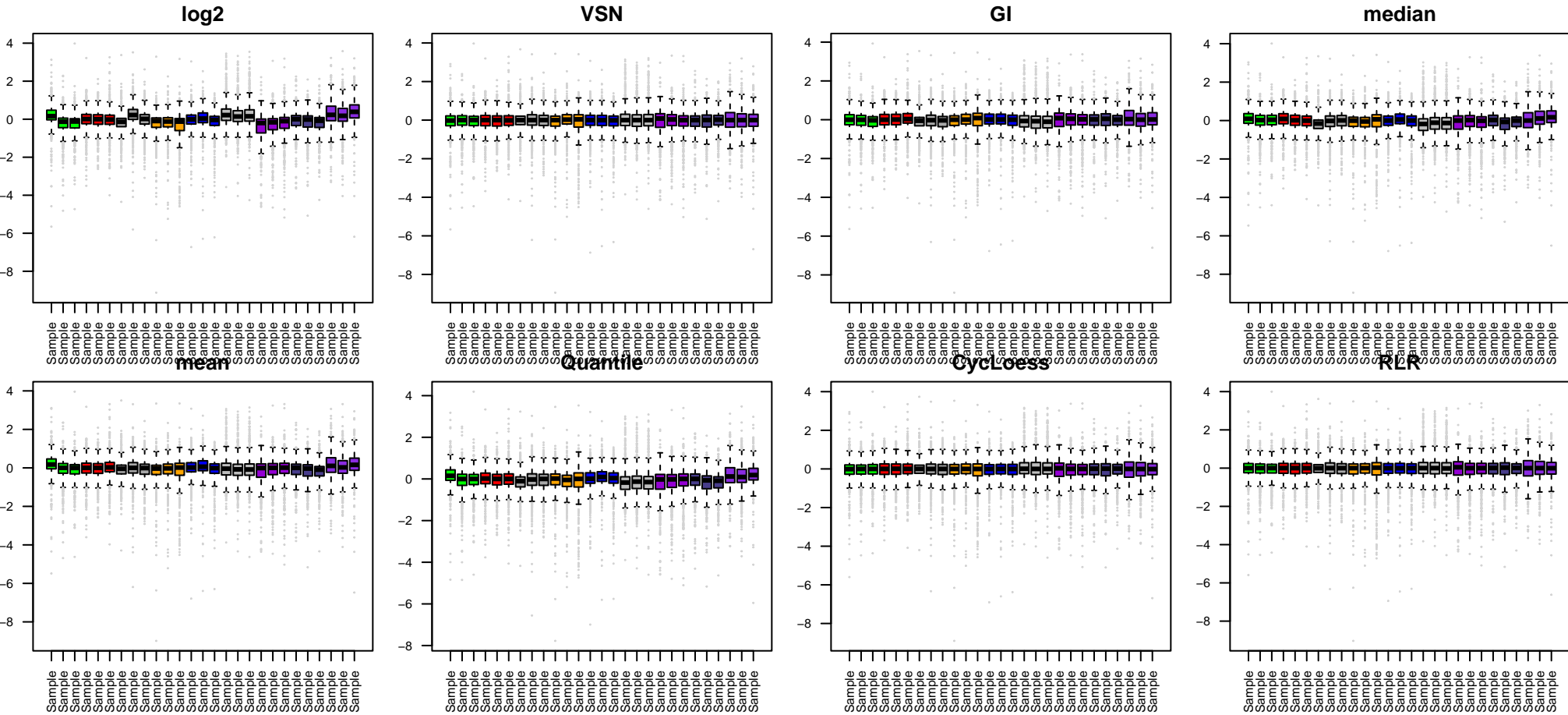




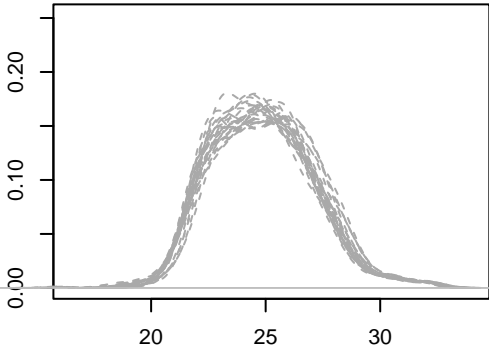




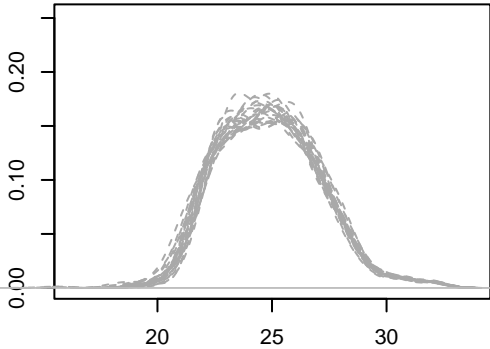




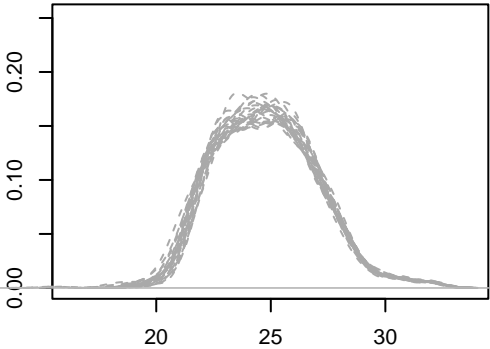
log2



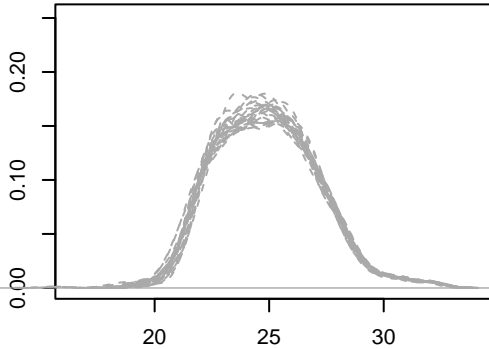
VSN



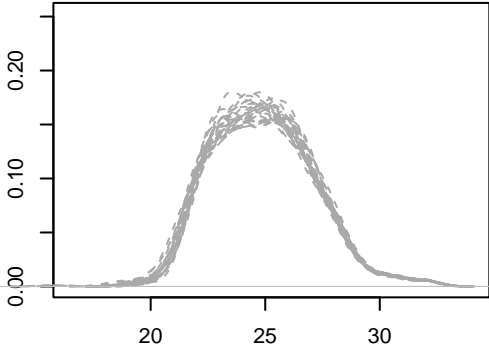
GI



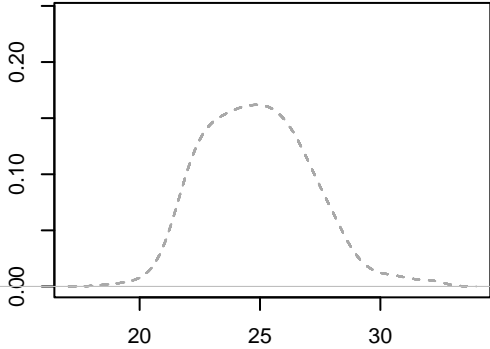
median



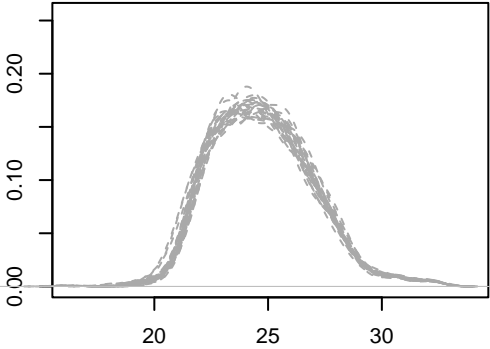
mean



Quantile



CycLoess



RLR

