

Project Name: unit_test_run_norm

NormalyzerDE (ver 1.5.3)

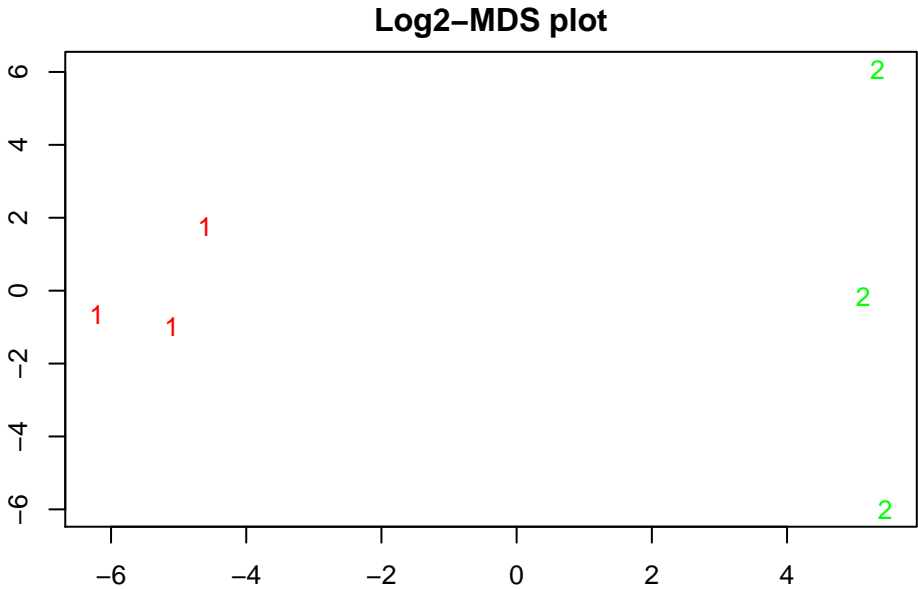
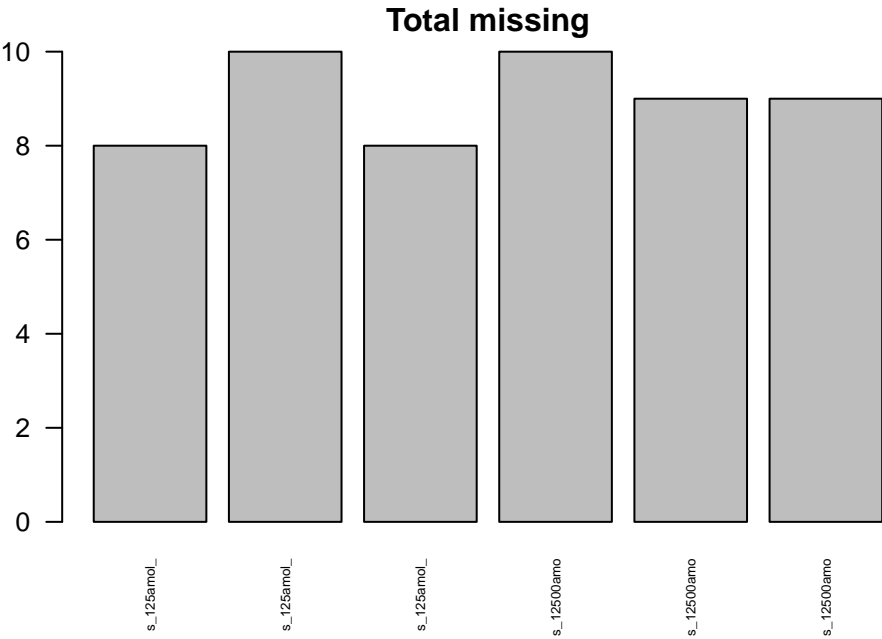
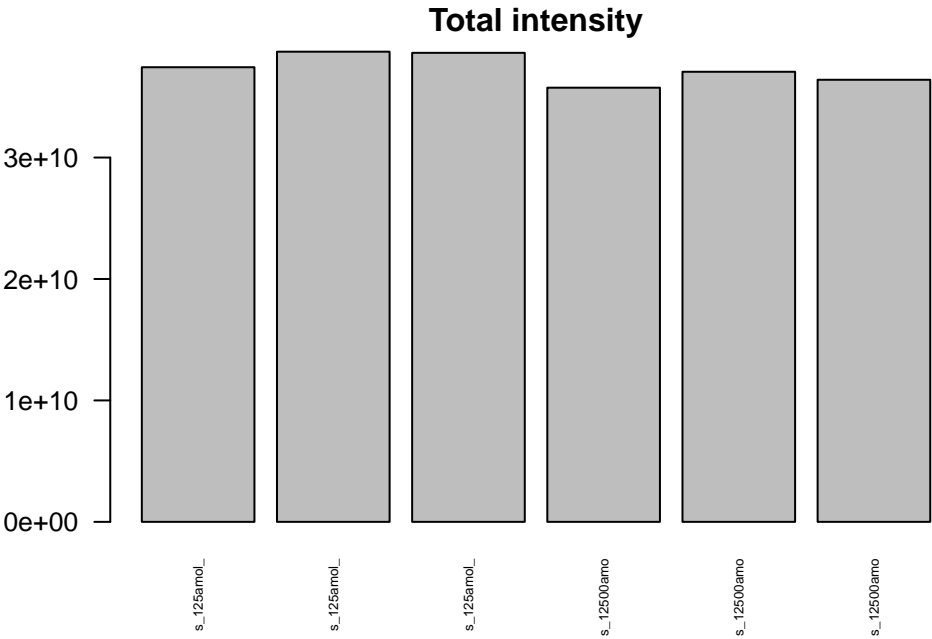
Report created on: 2020-06-08

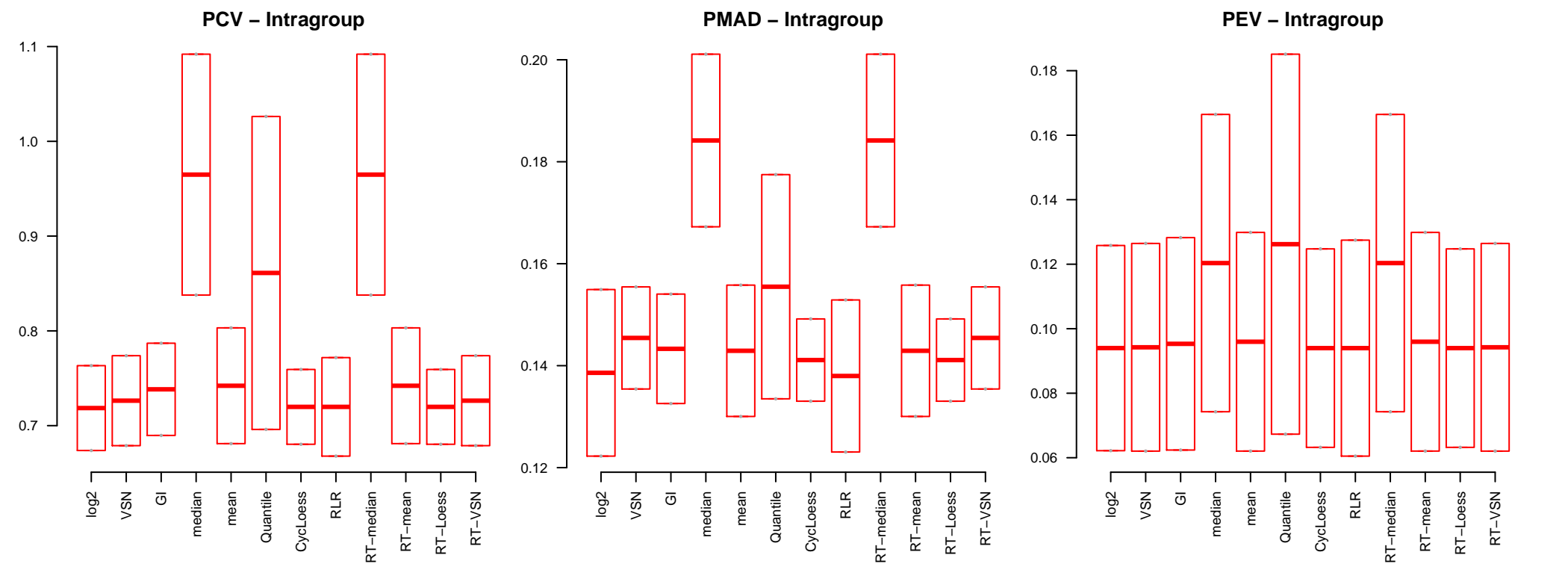
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

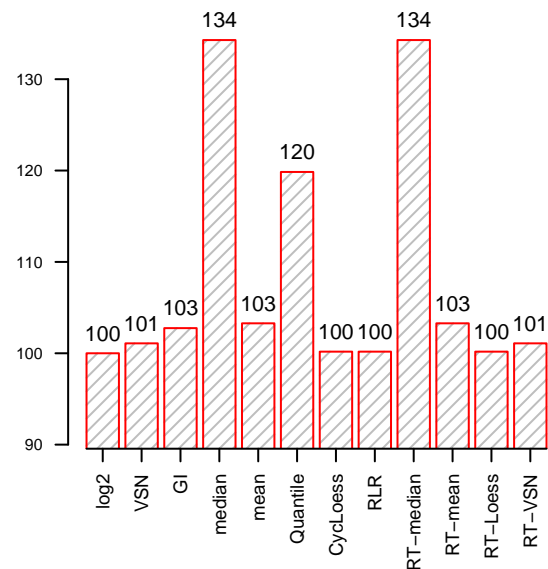
Group nbr.	Design group	Nbr. samples in cond.
1	4	3
2	5	3

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

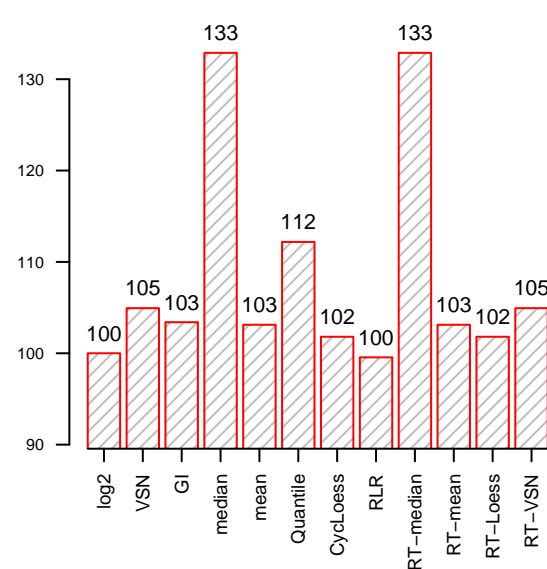




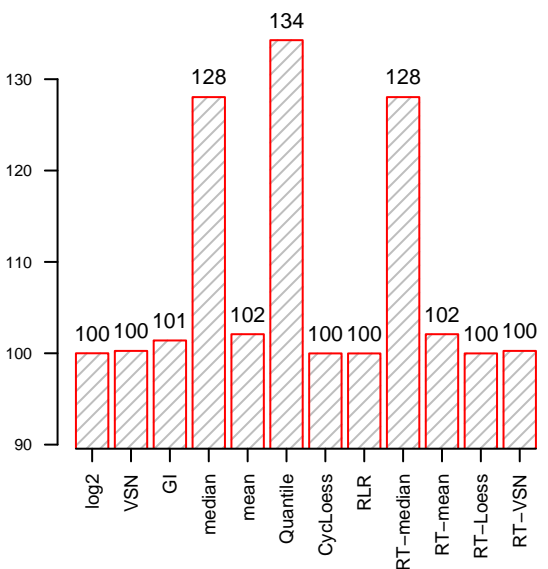
PCV compared to log2



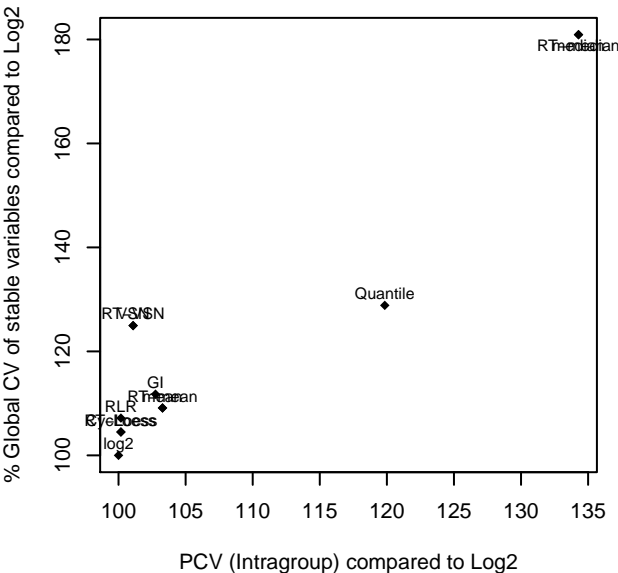
PMAD compared to log2

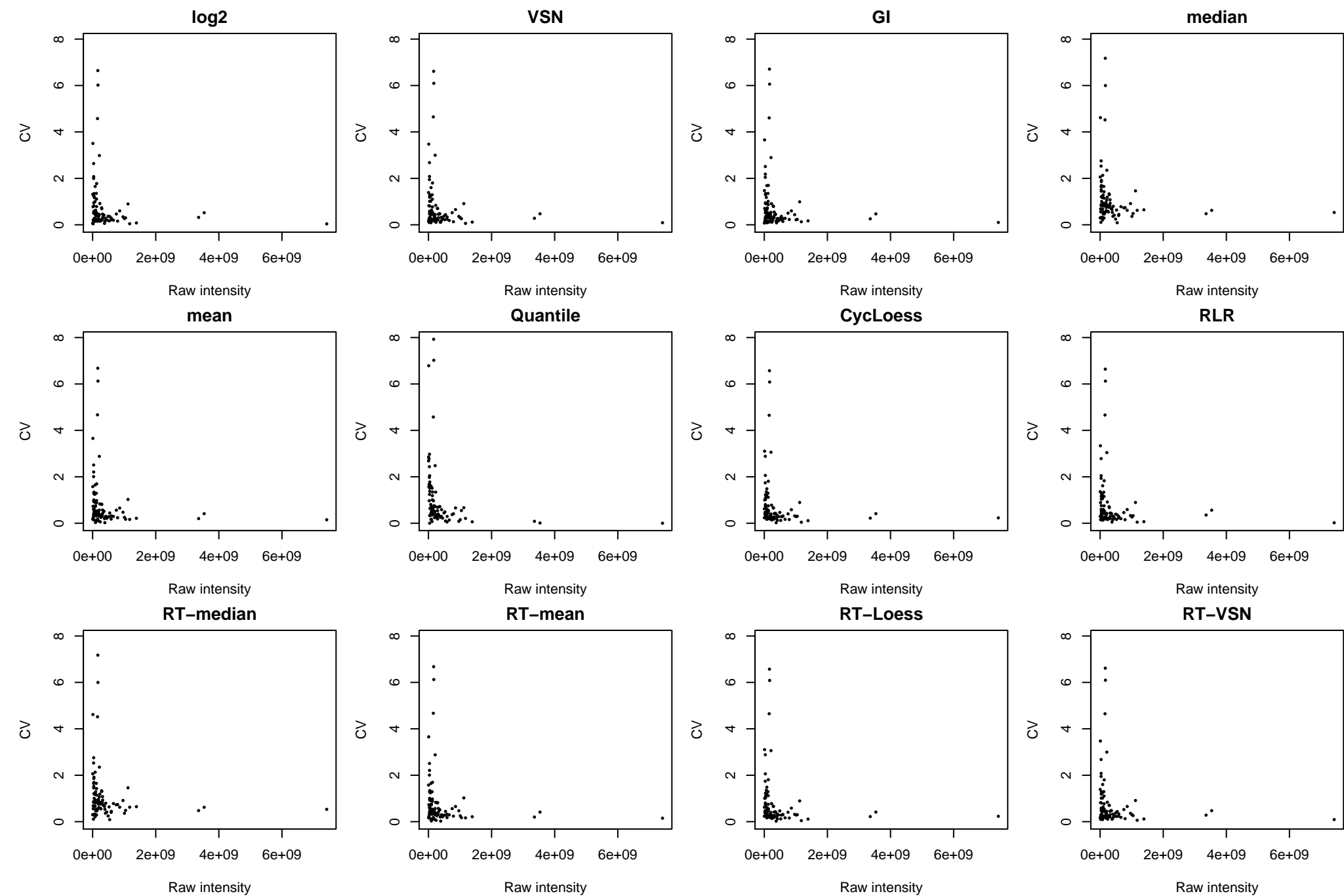


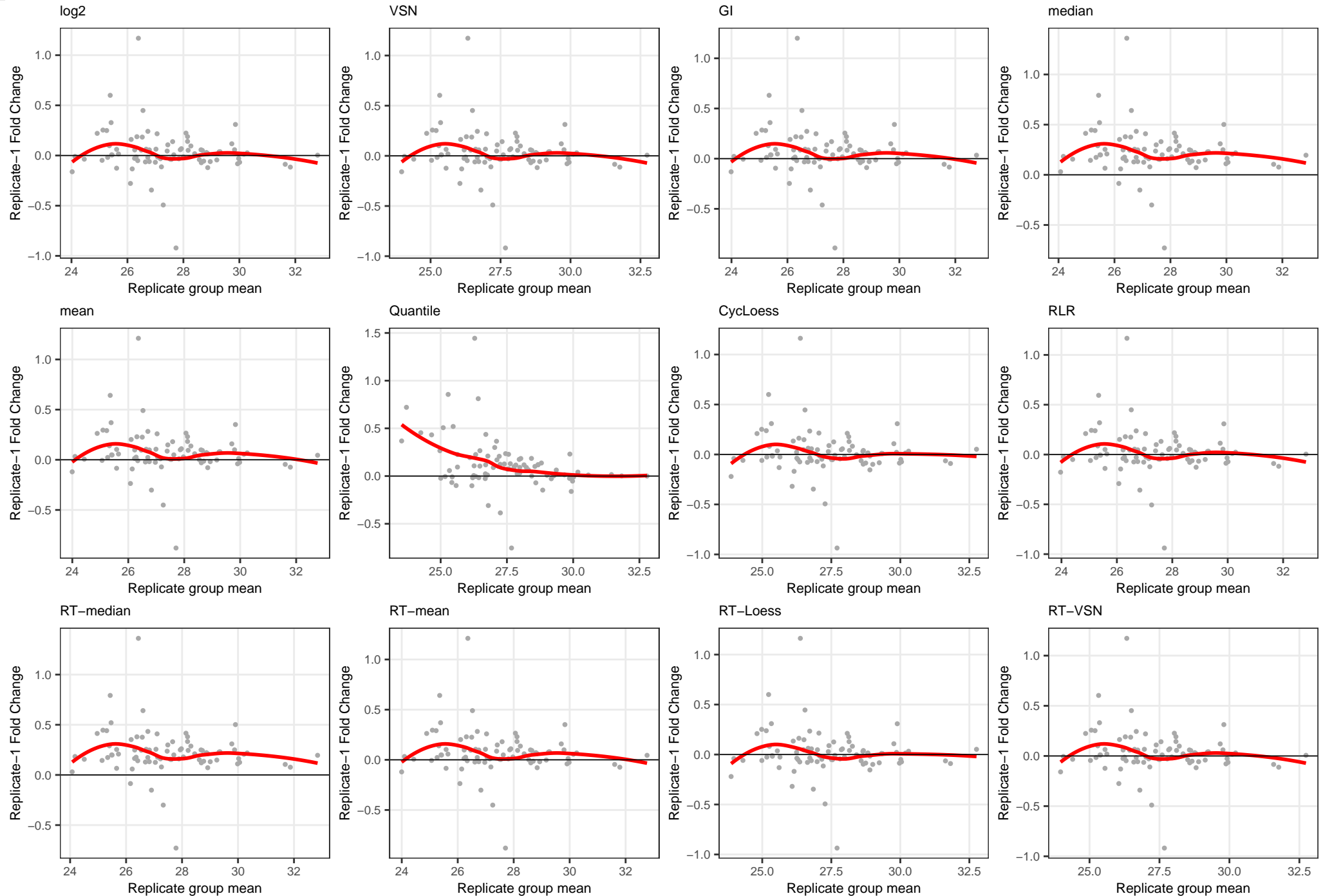
%PEV – compared to log2

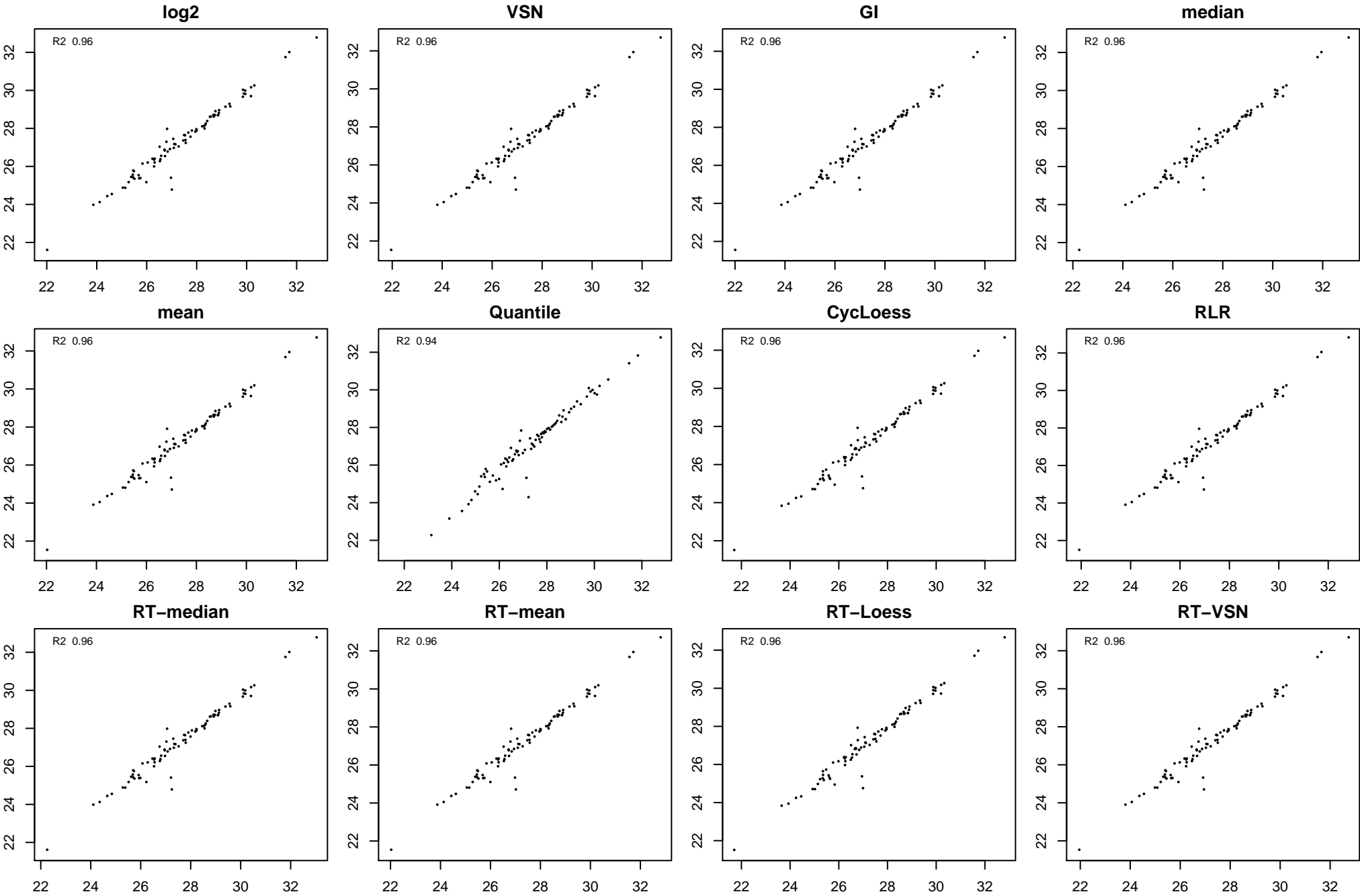


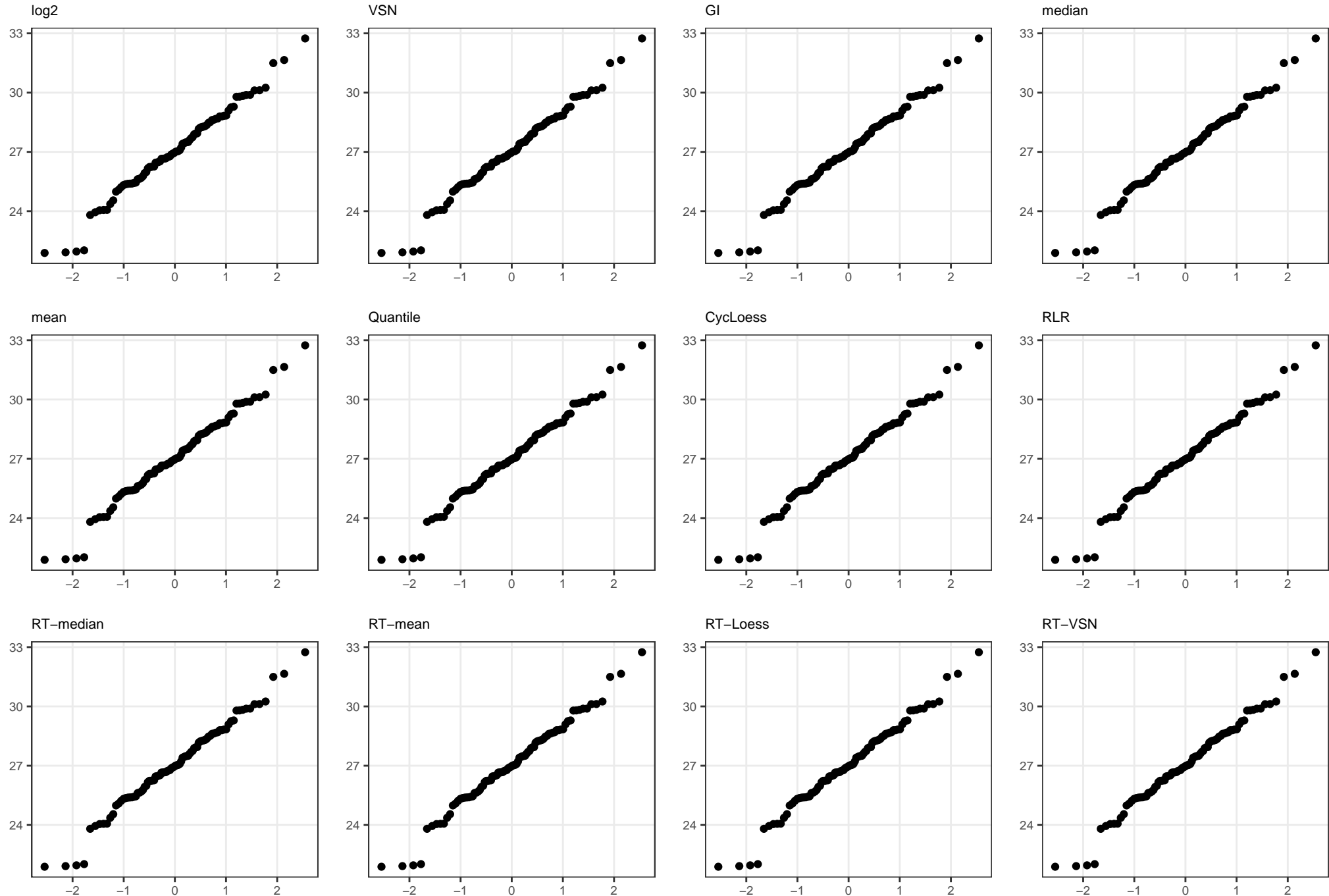
Stable variables plot

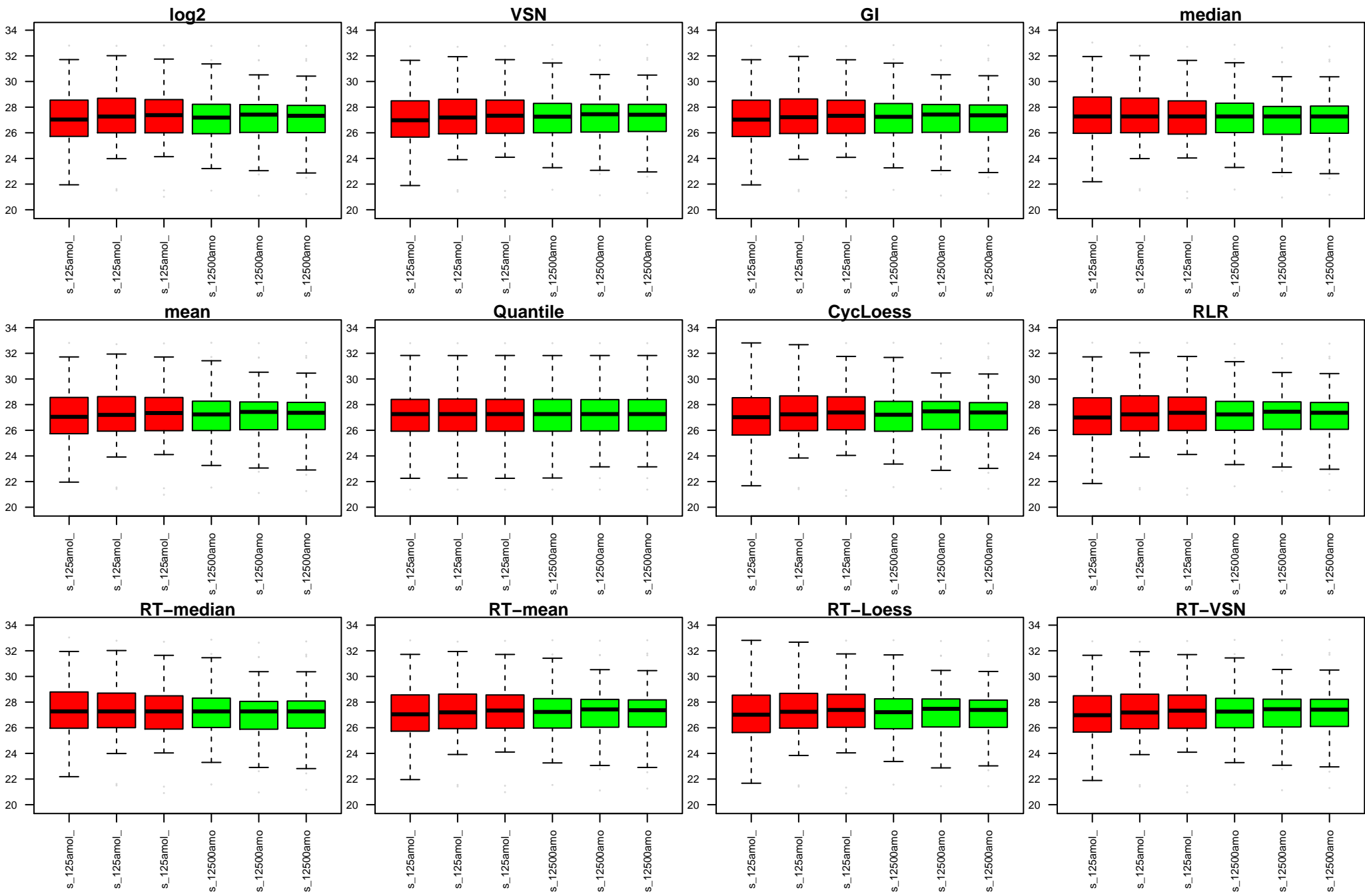


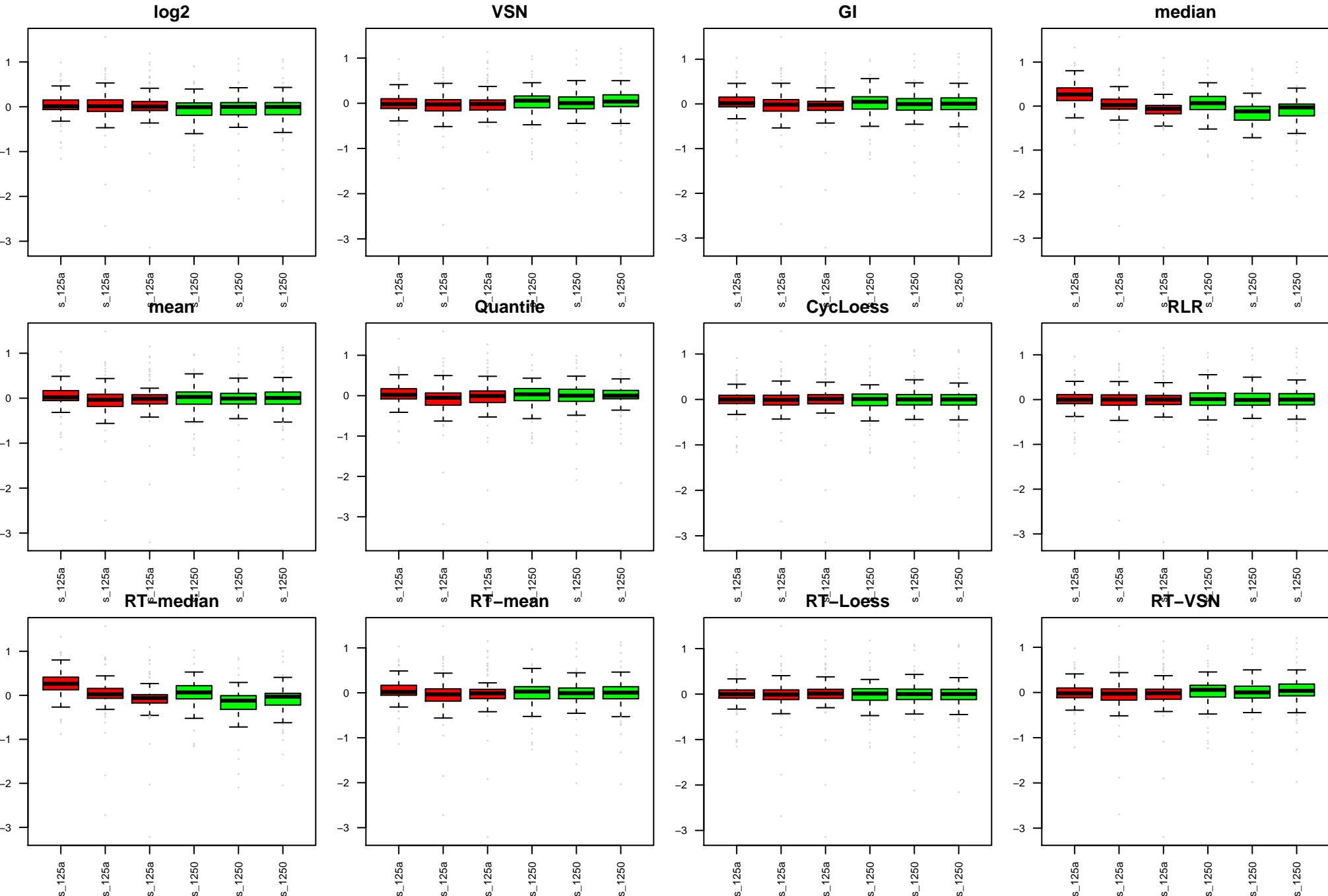




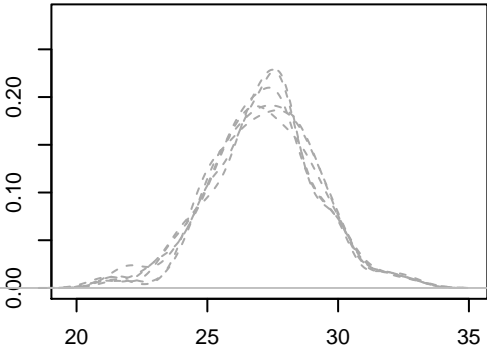




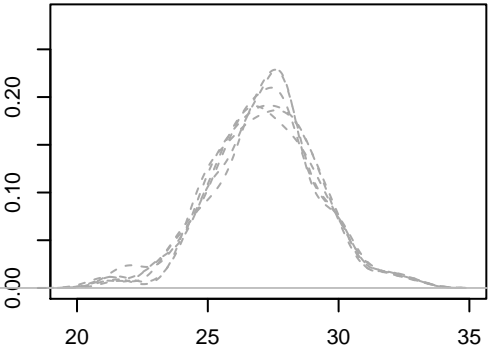




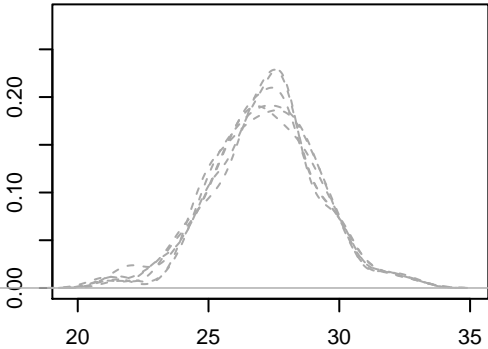
log2



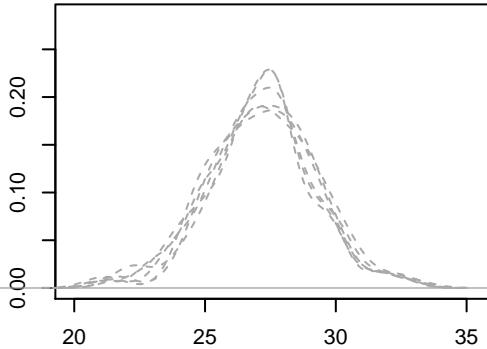
VSN



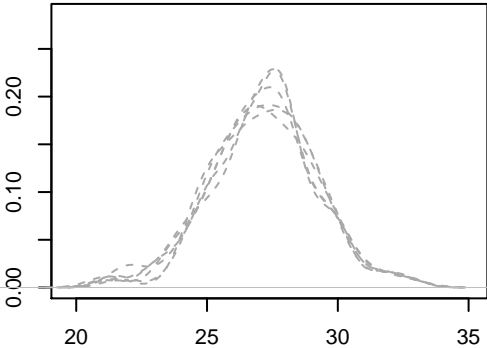
GI



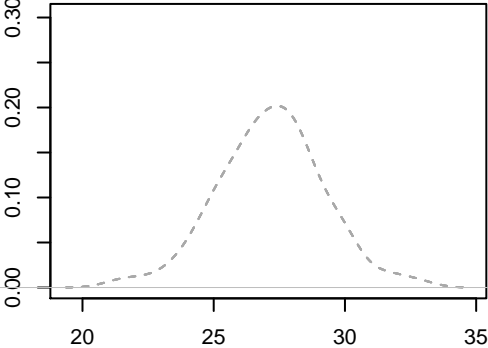
median



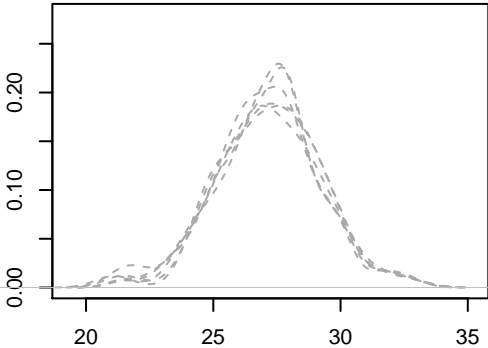
mean



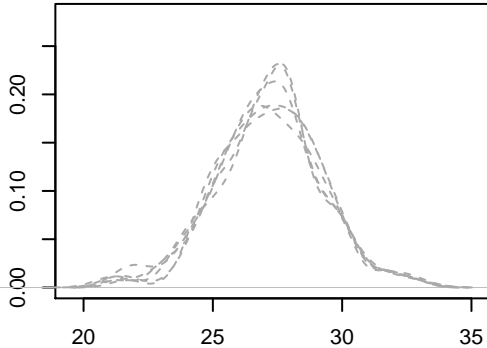
Quantile



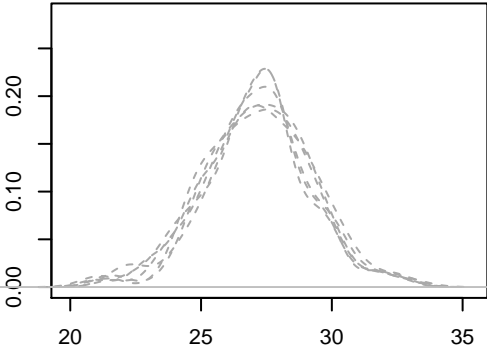
CycLoess



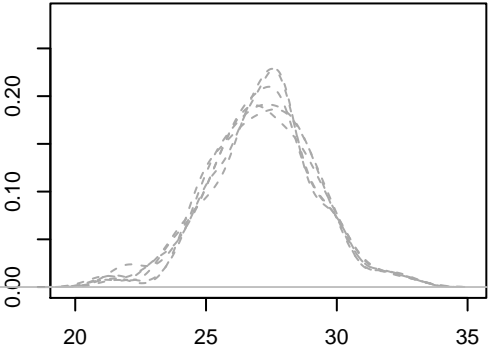
RLR



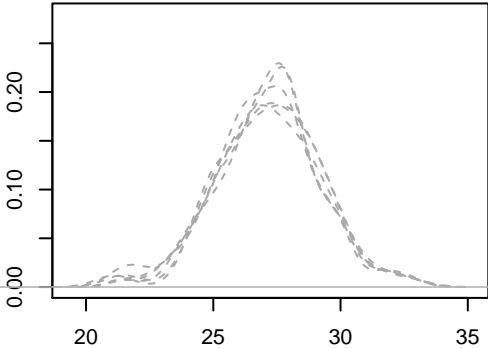
RT-median



RT-mean



RT-Loess



RT-VSN

