

Project Name: proteomics_norm

NormalyzerDE (ver 1.13.2)

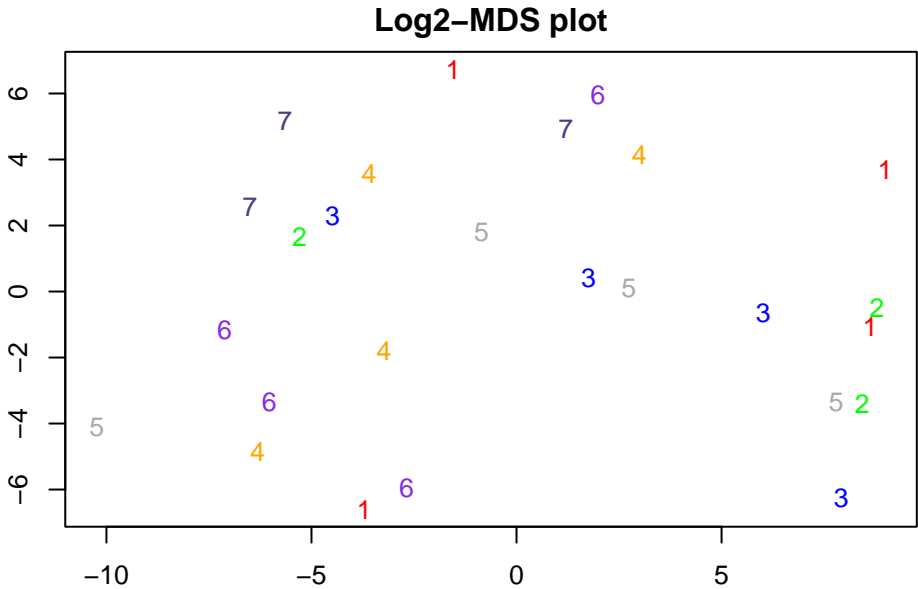
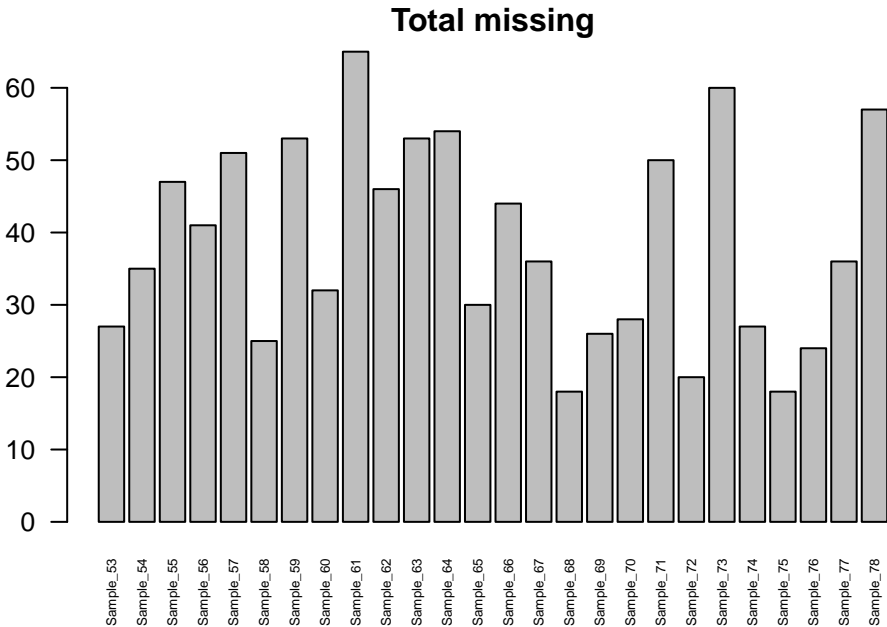
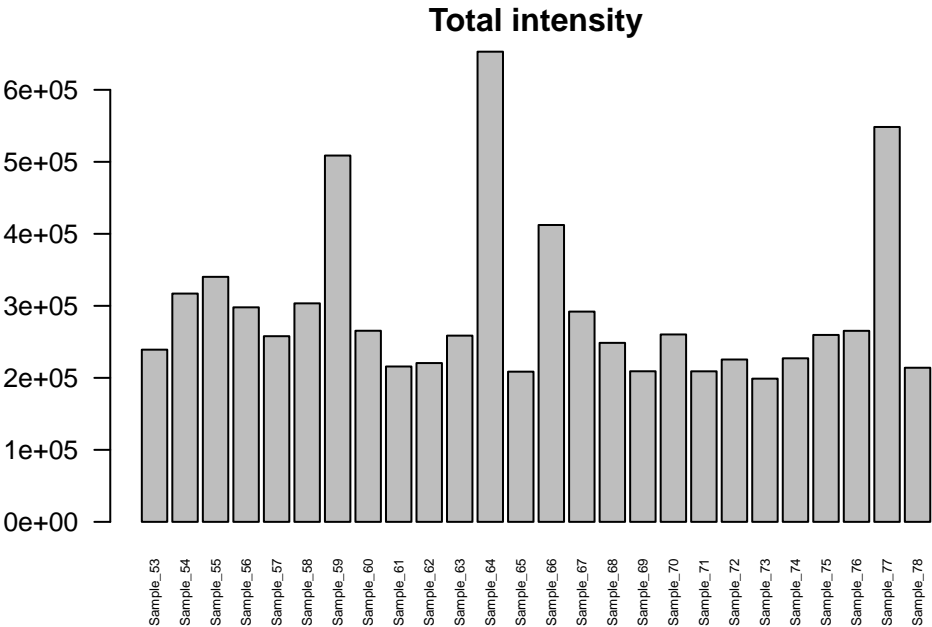
Report created on: 2022-10-03

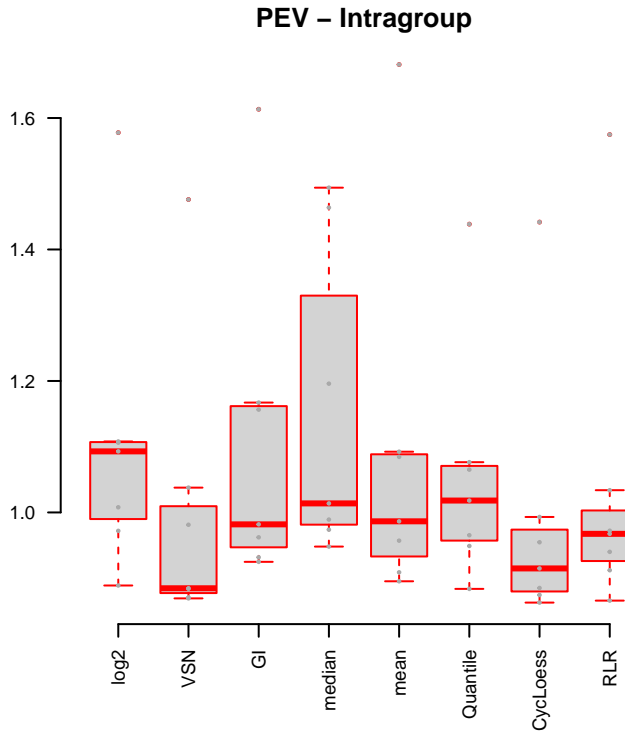
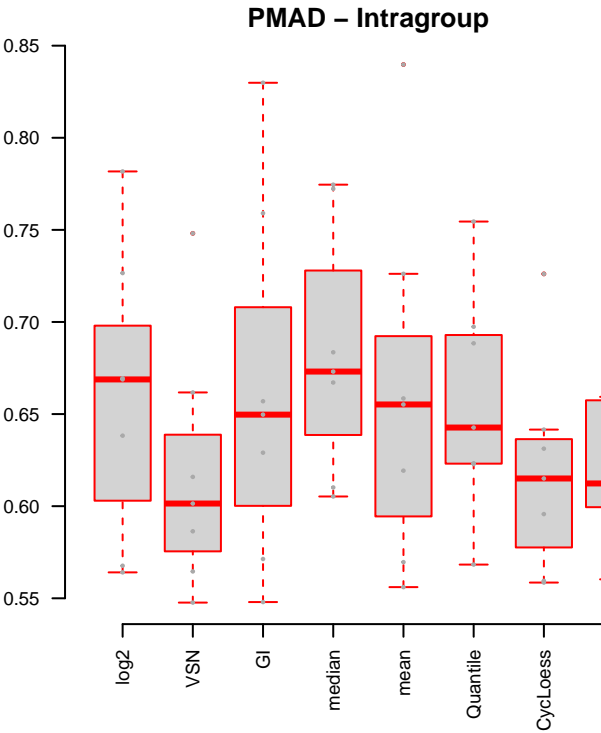
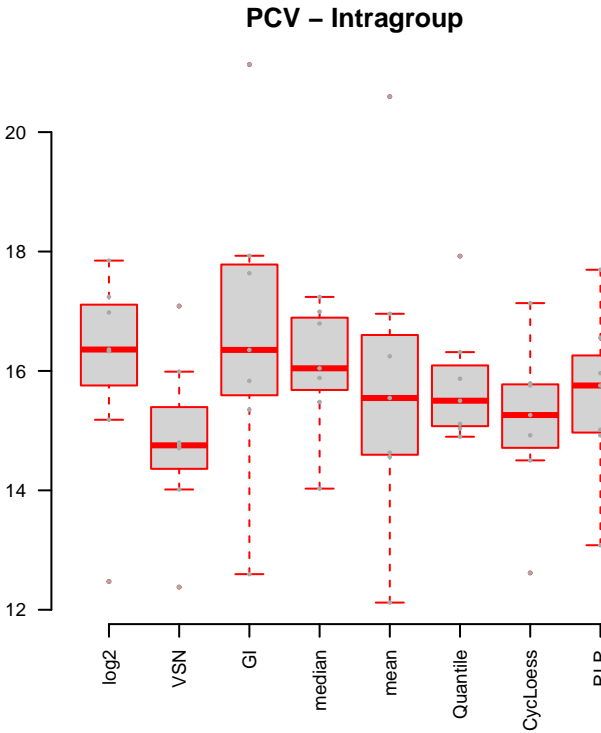
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

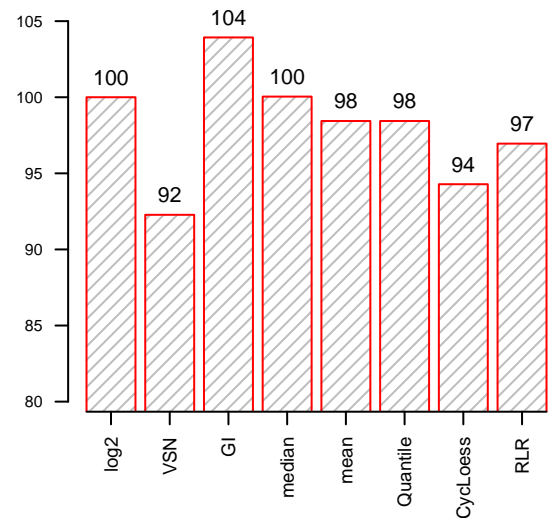
Group nbr.	Design group	Nbr. samples in cond.
1	0	4
2	10	3
3	35	4
4	42	4
5	49	4
6	56	4
7	63	3

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

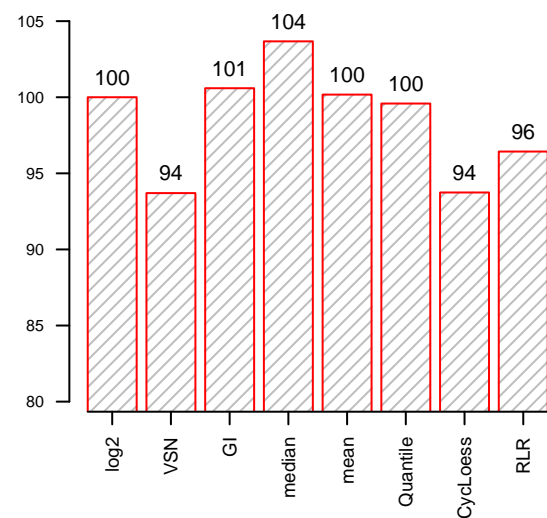




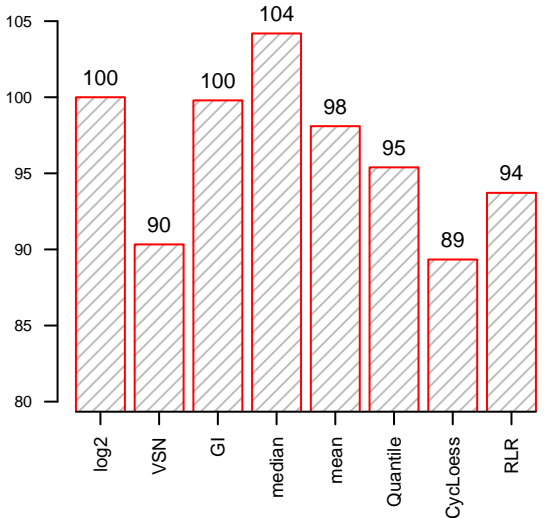
PCV compared to log2



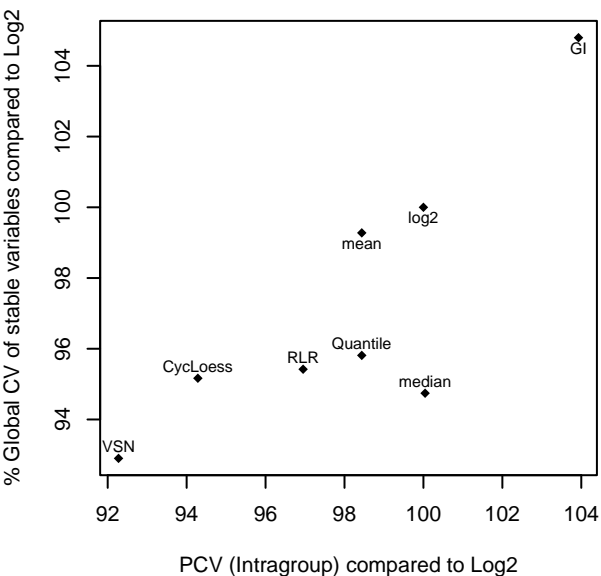
PMAD compared to log2

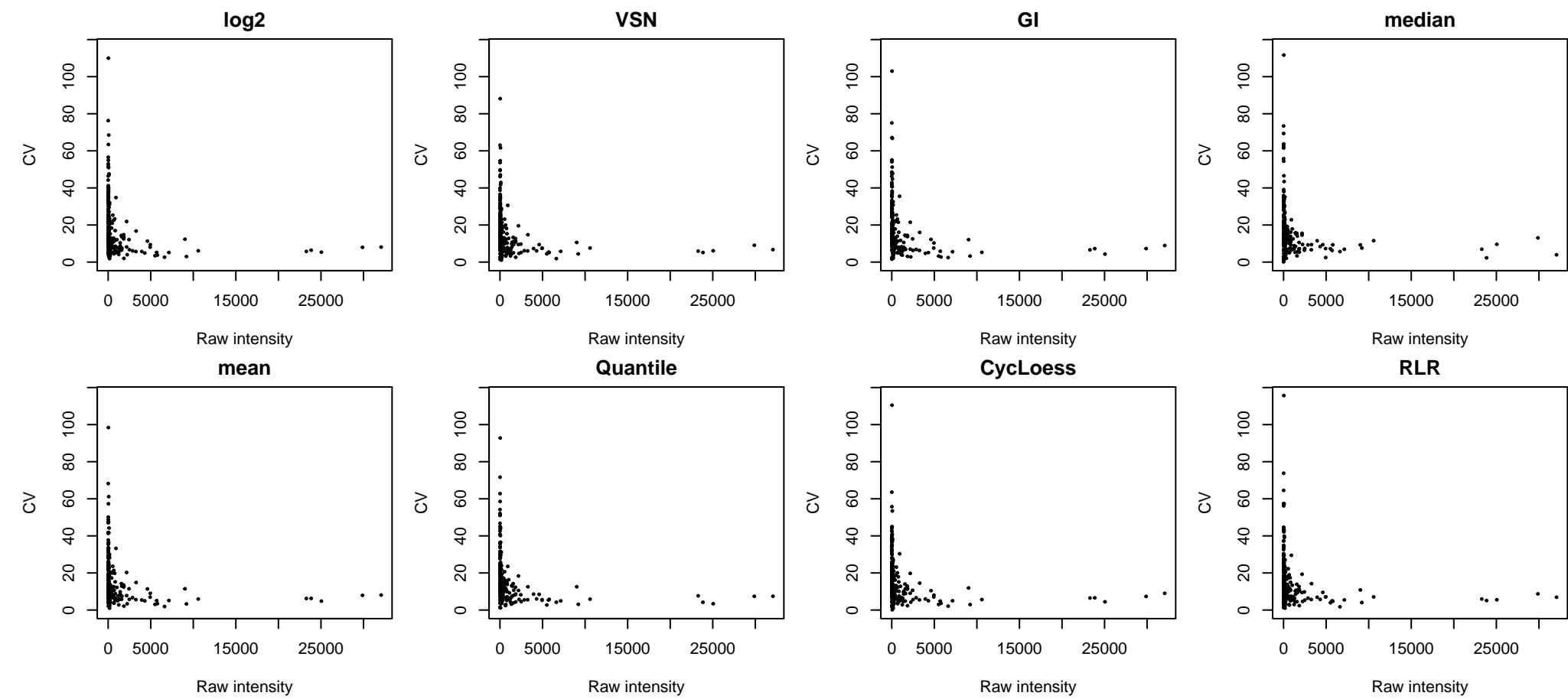


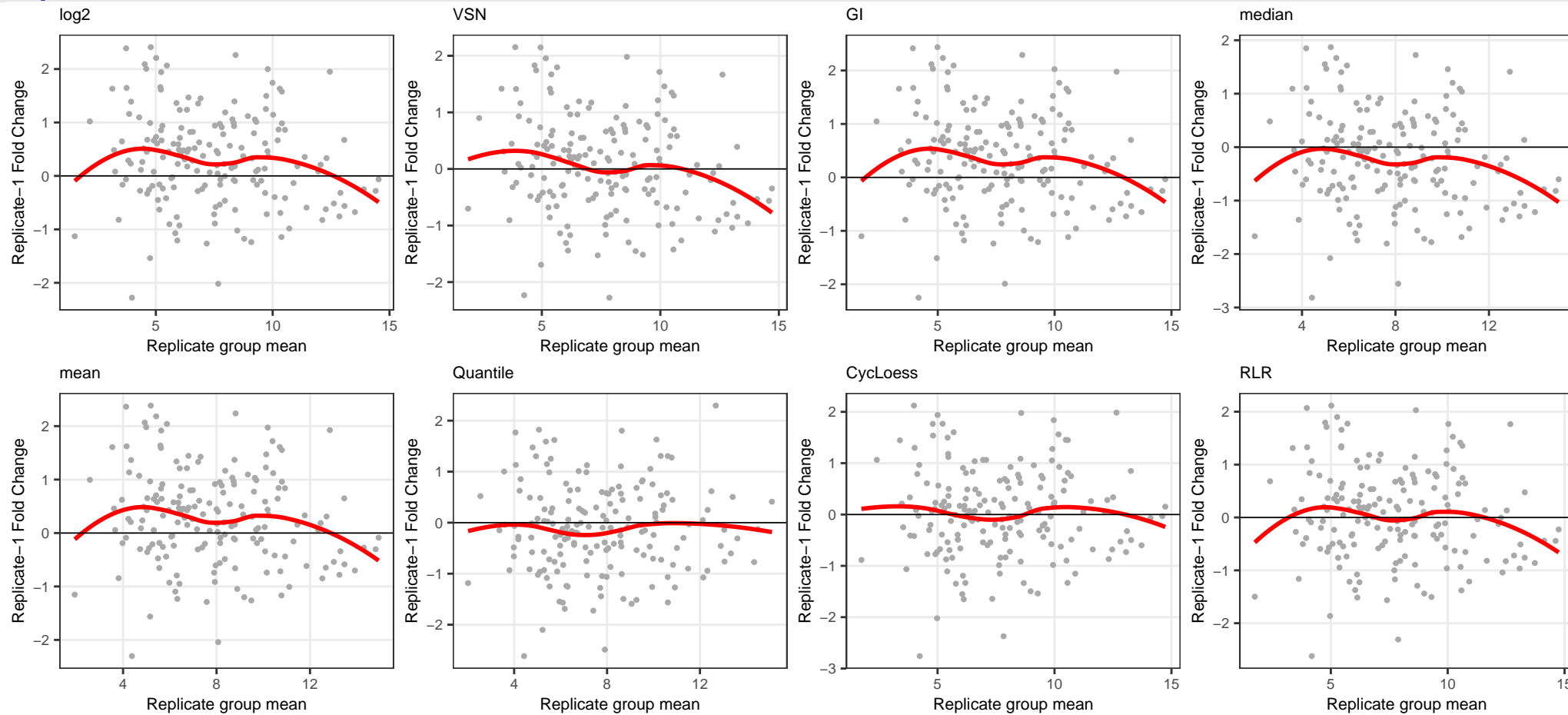
%PEV – compared to log2

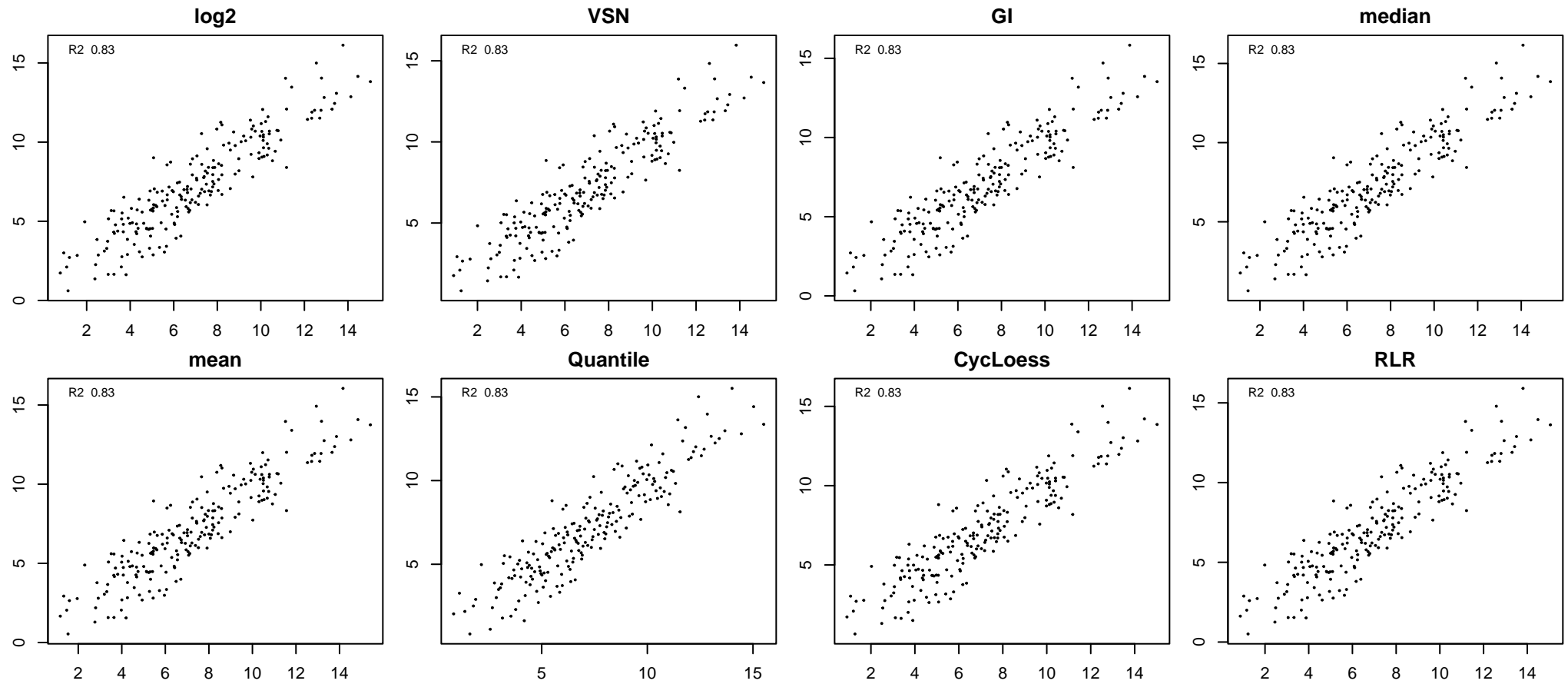


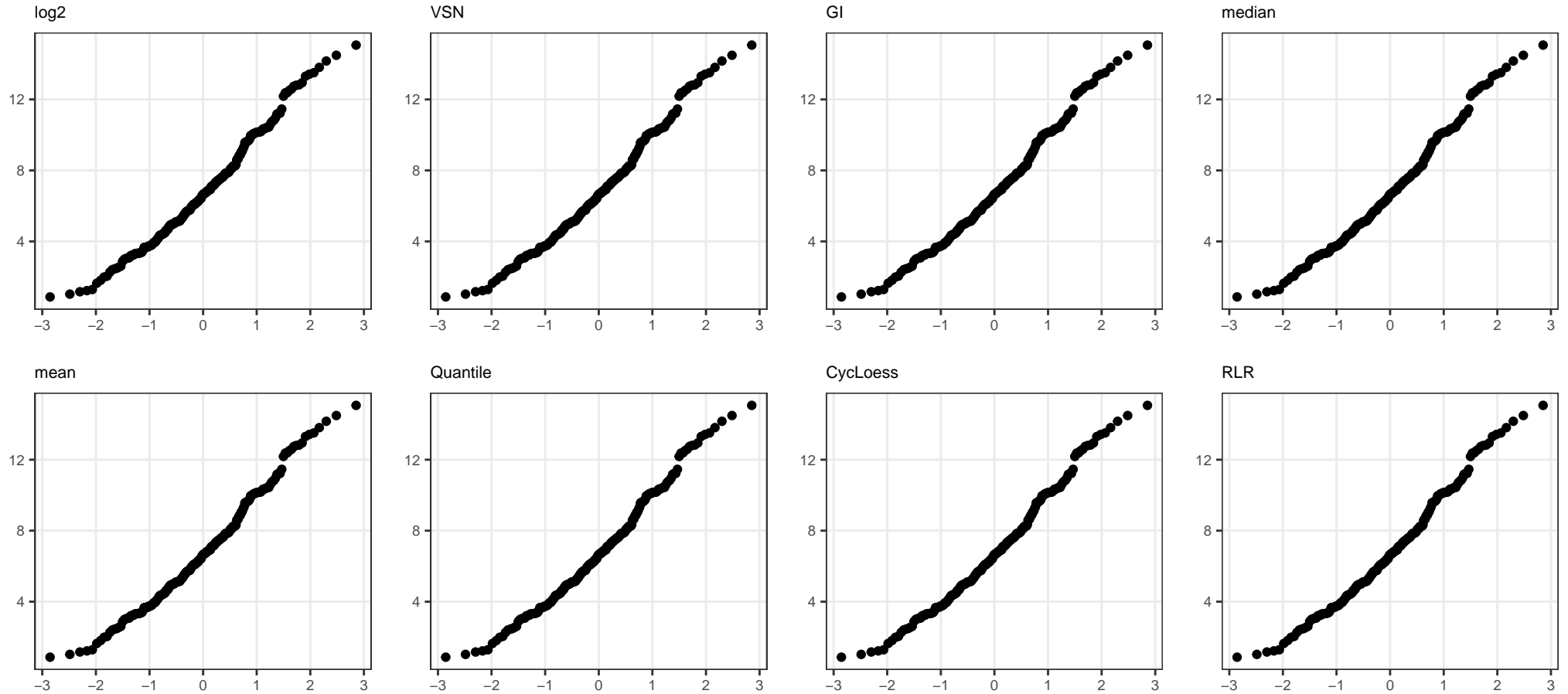
Stable variables plot

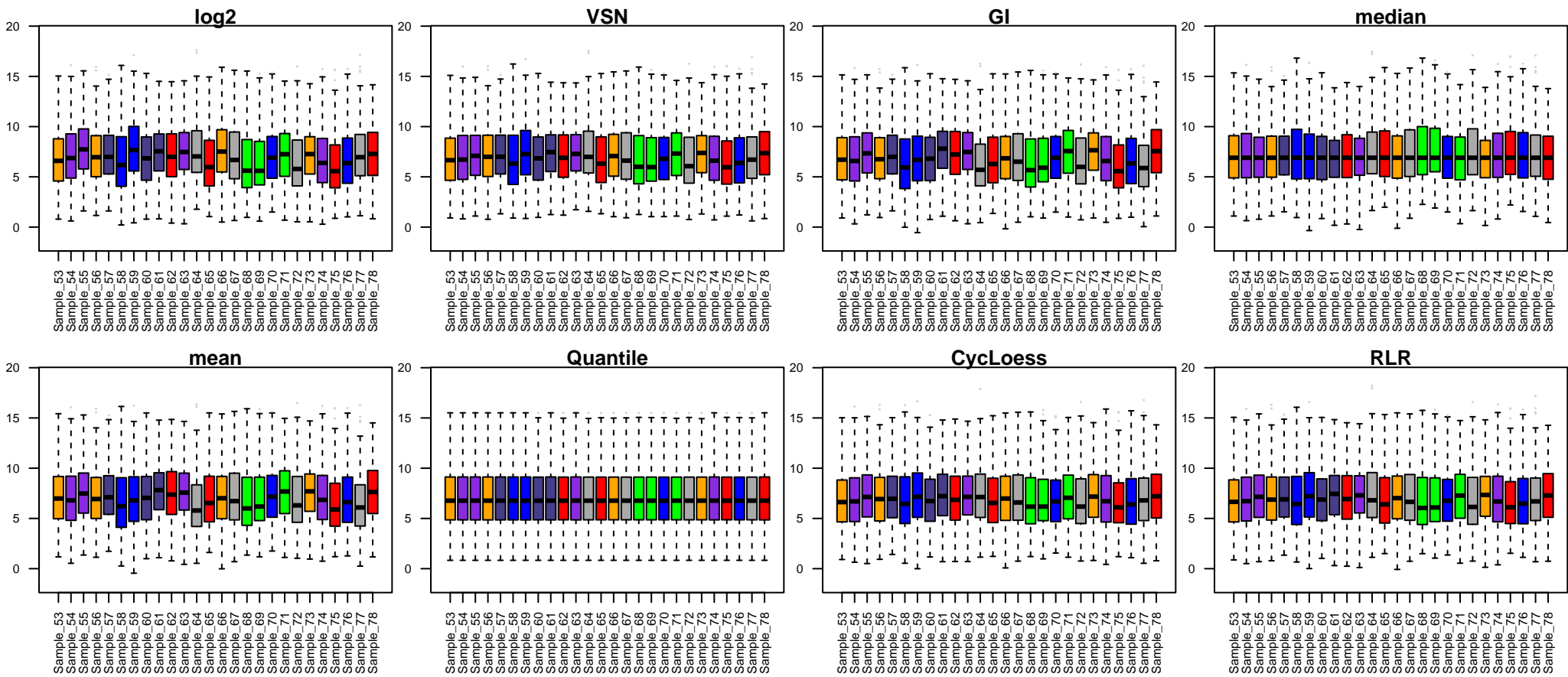


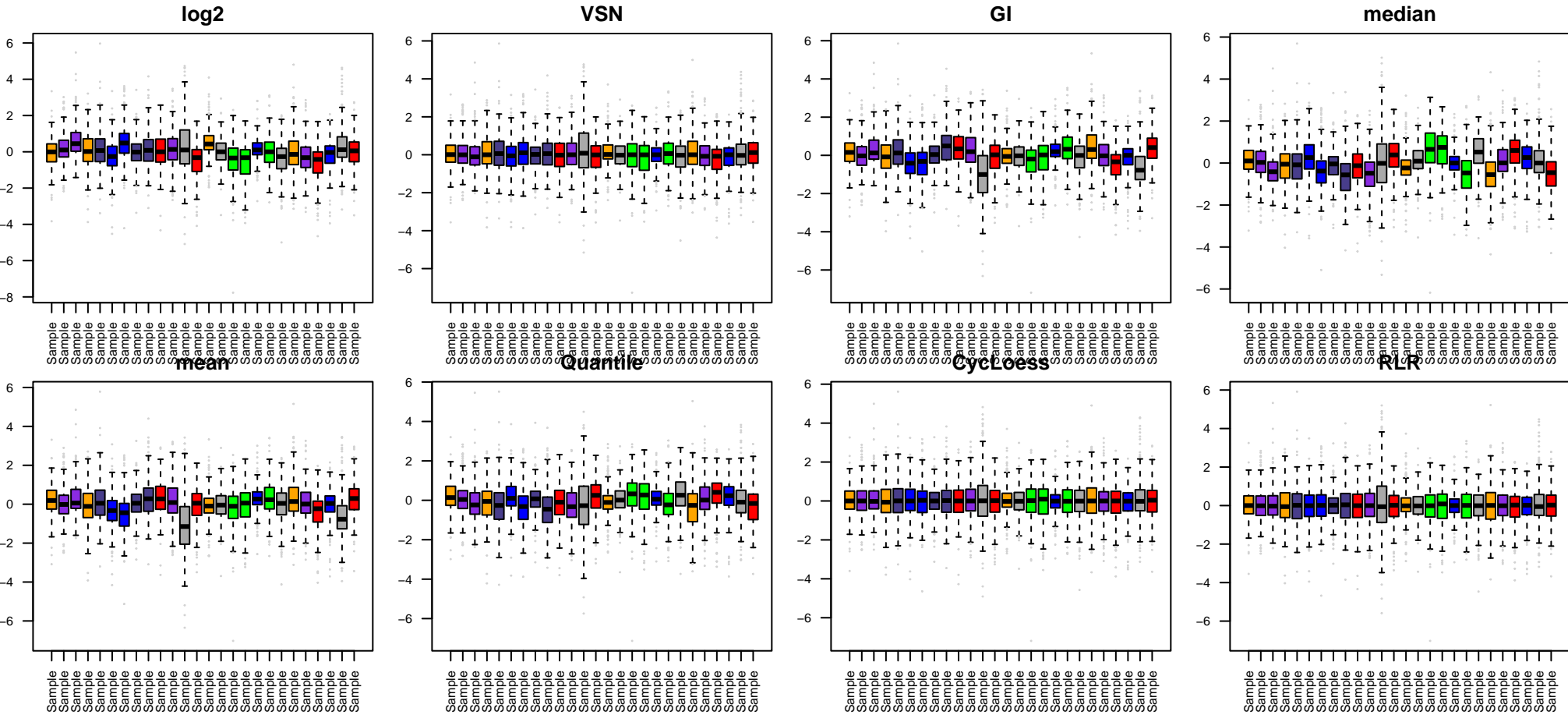










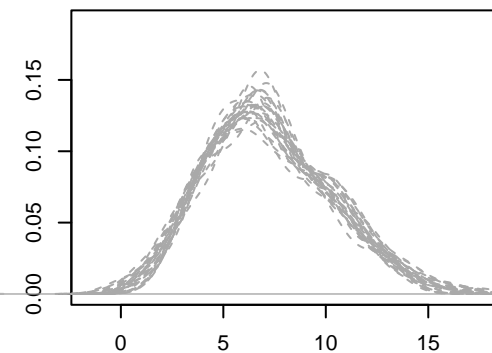
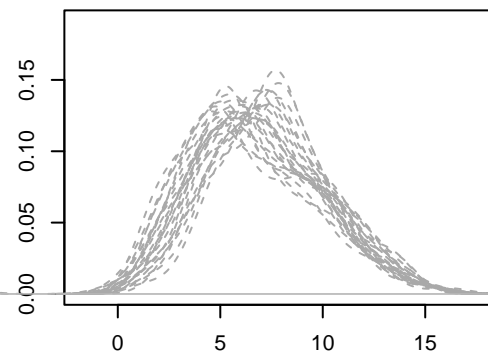
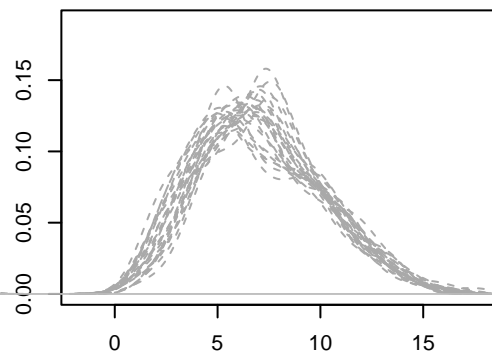
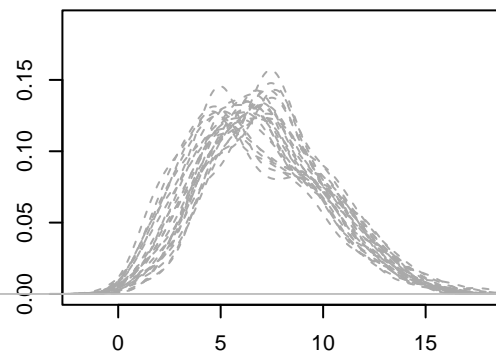


log2

VSN

GI

median



mean

Quantile

CycLoess

RLR

