

Project Name: con\_sp.hsa.canonical.isoforms\_junc.exons\_protein\_groups

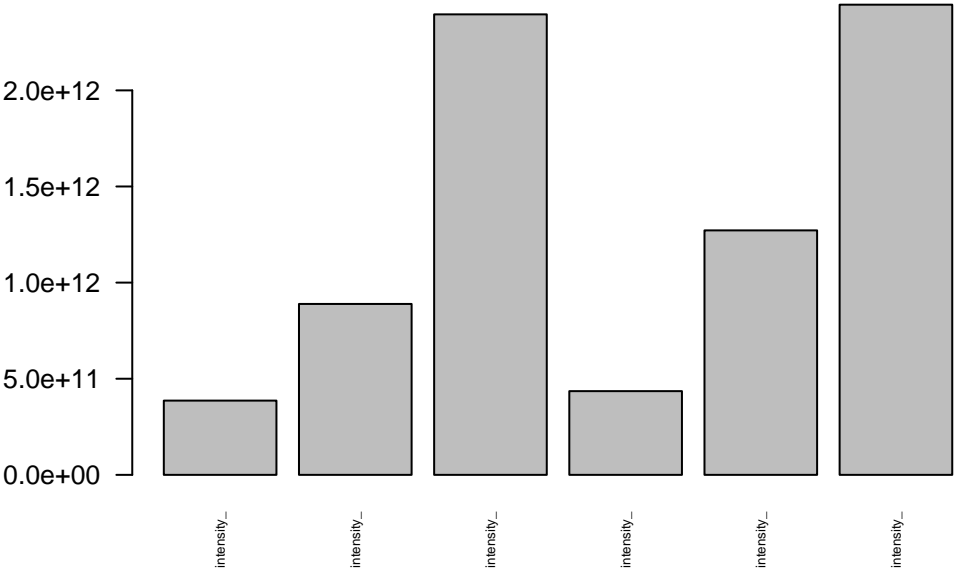
# Normalyzer (ver 1.4.0 )

Report created on: 2020-05-08

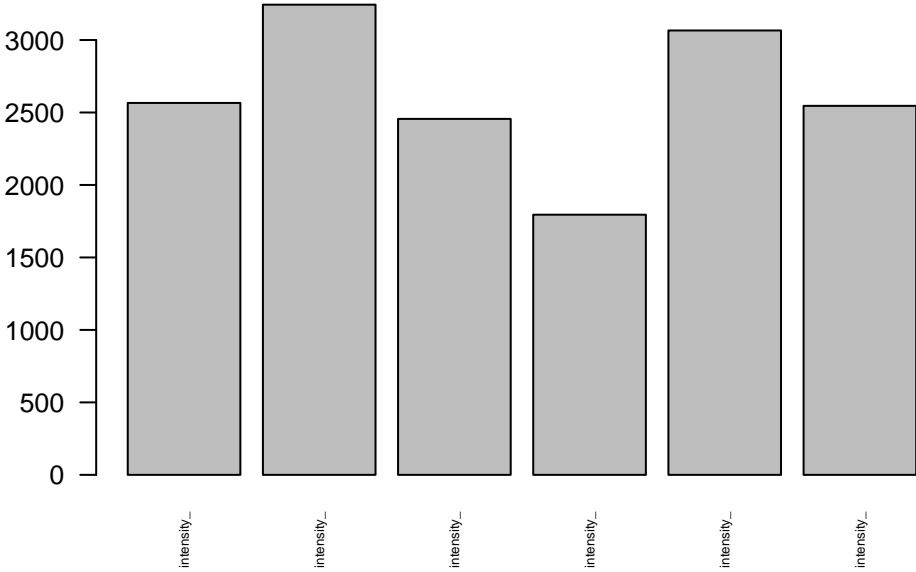
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis  
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

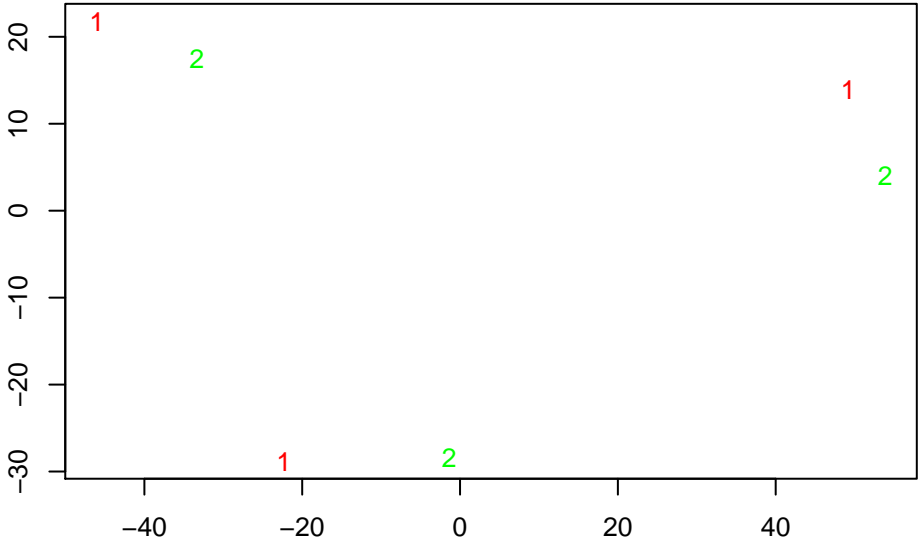
Total intensity

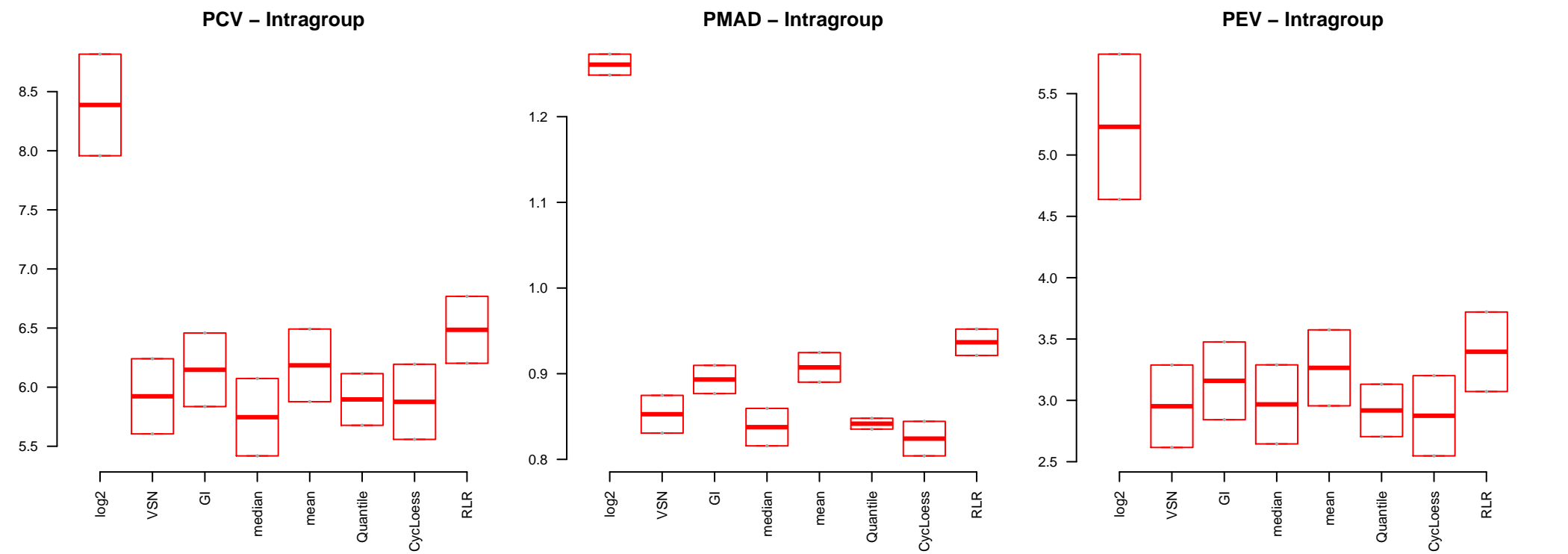


Total missing

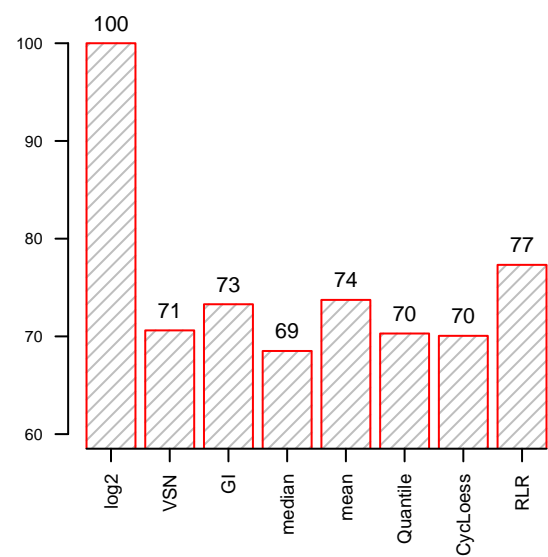


Log2-MDS plot

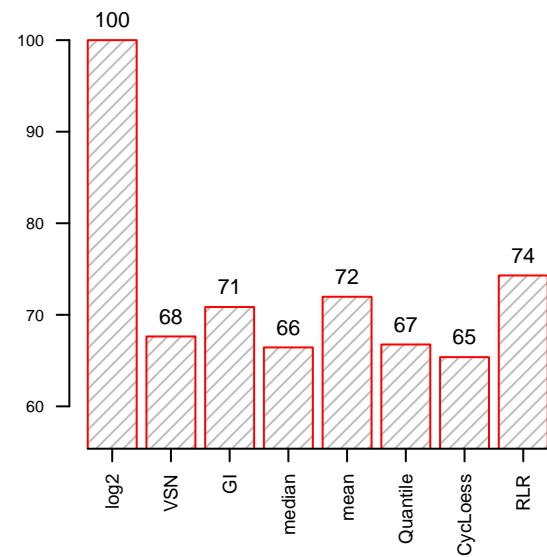




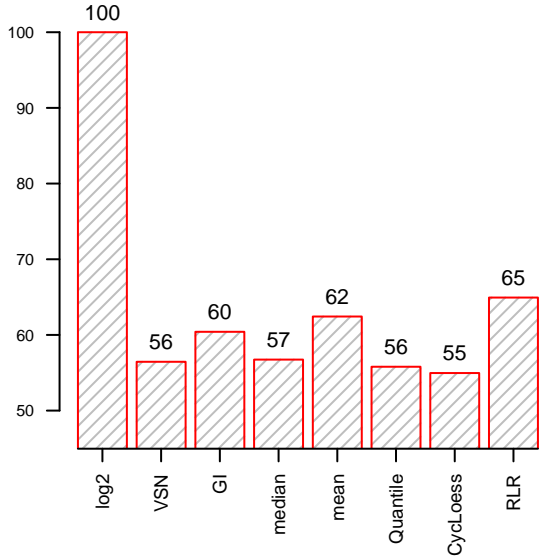
PCV compared to log2



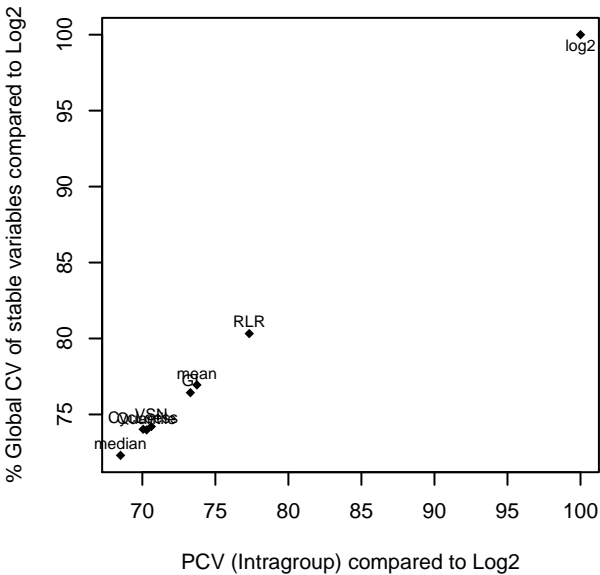
PMAD compared to log2

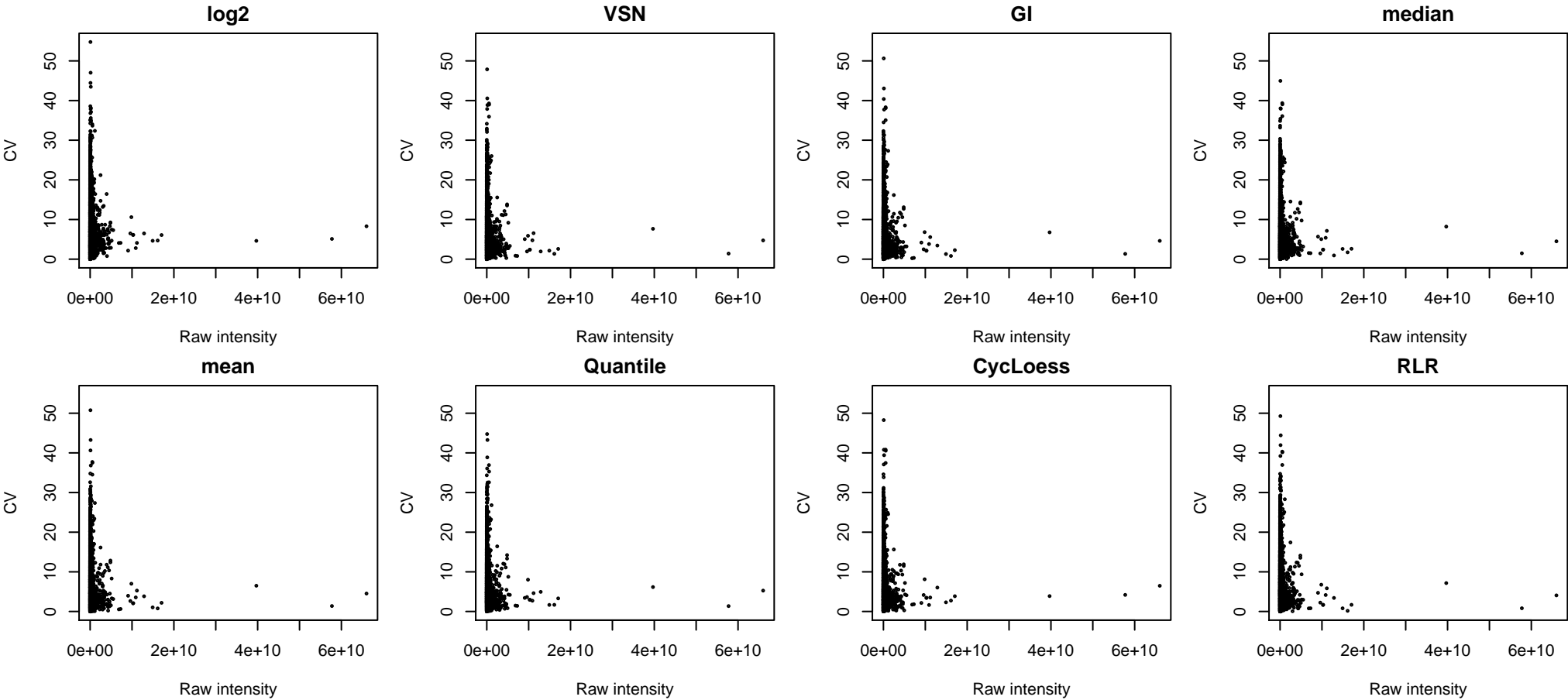


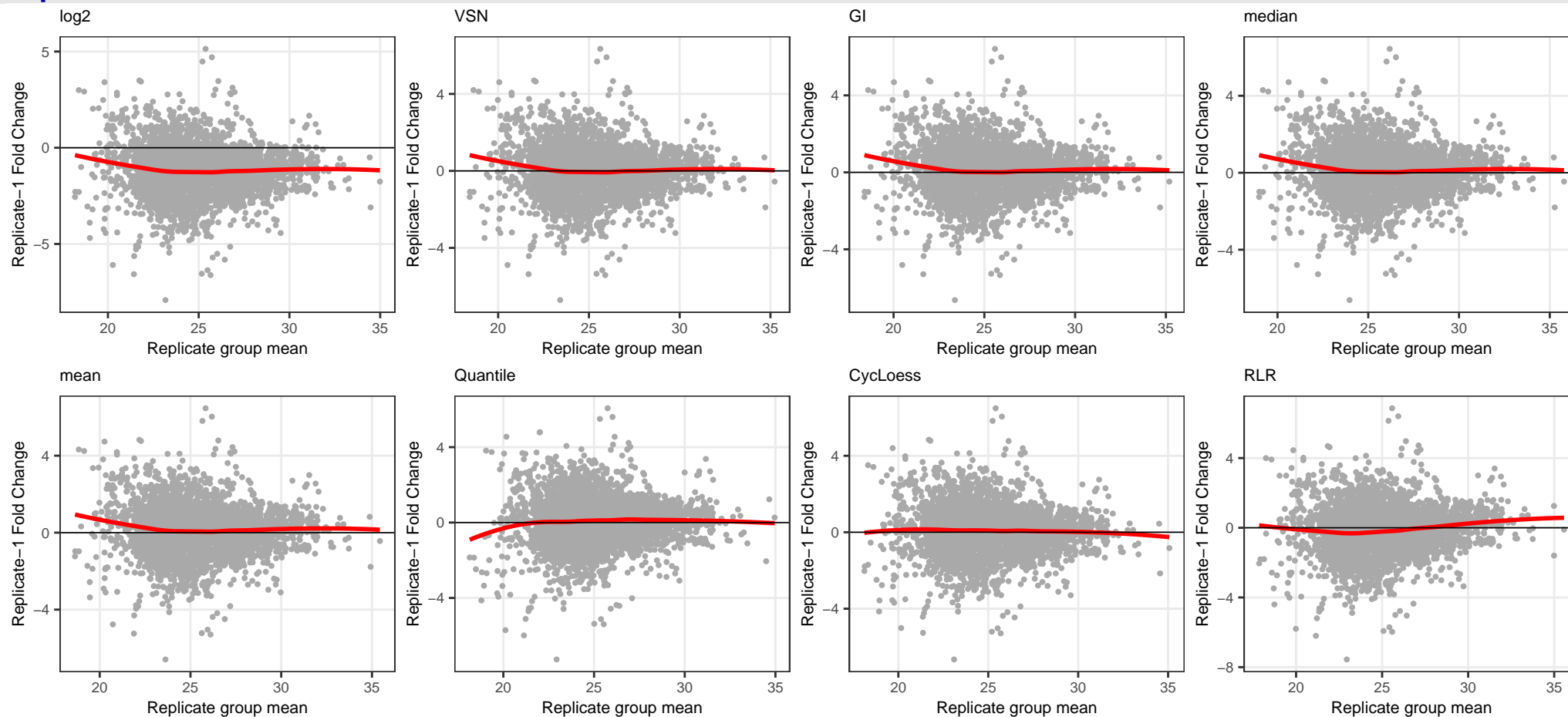
%PEV – compared to log2

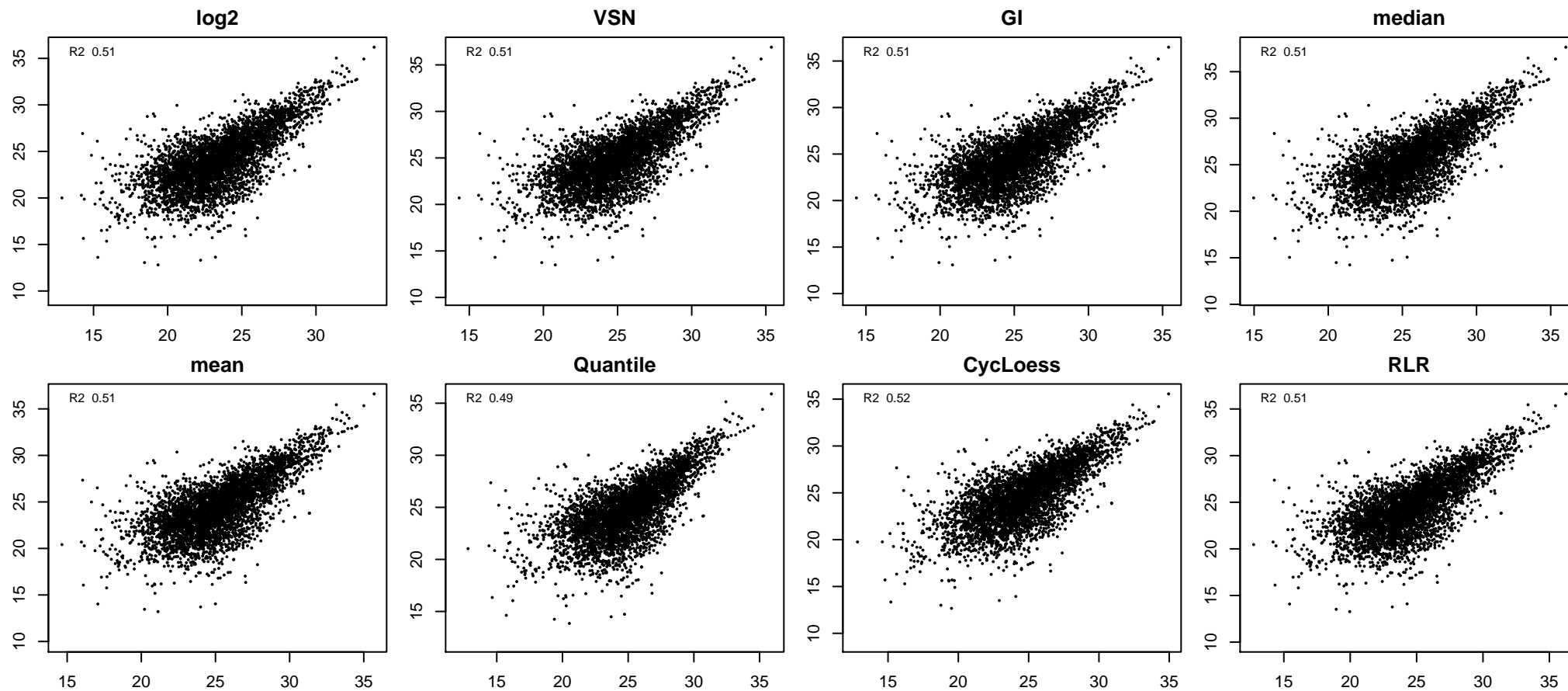


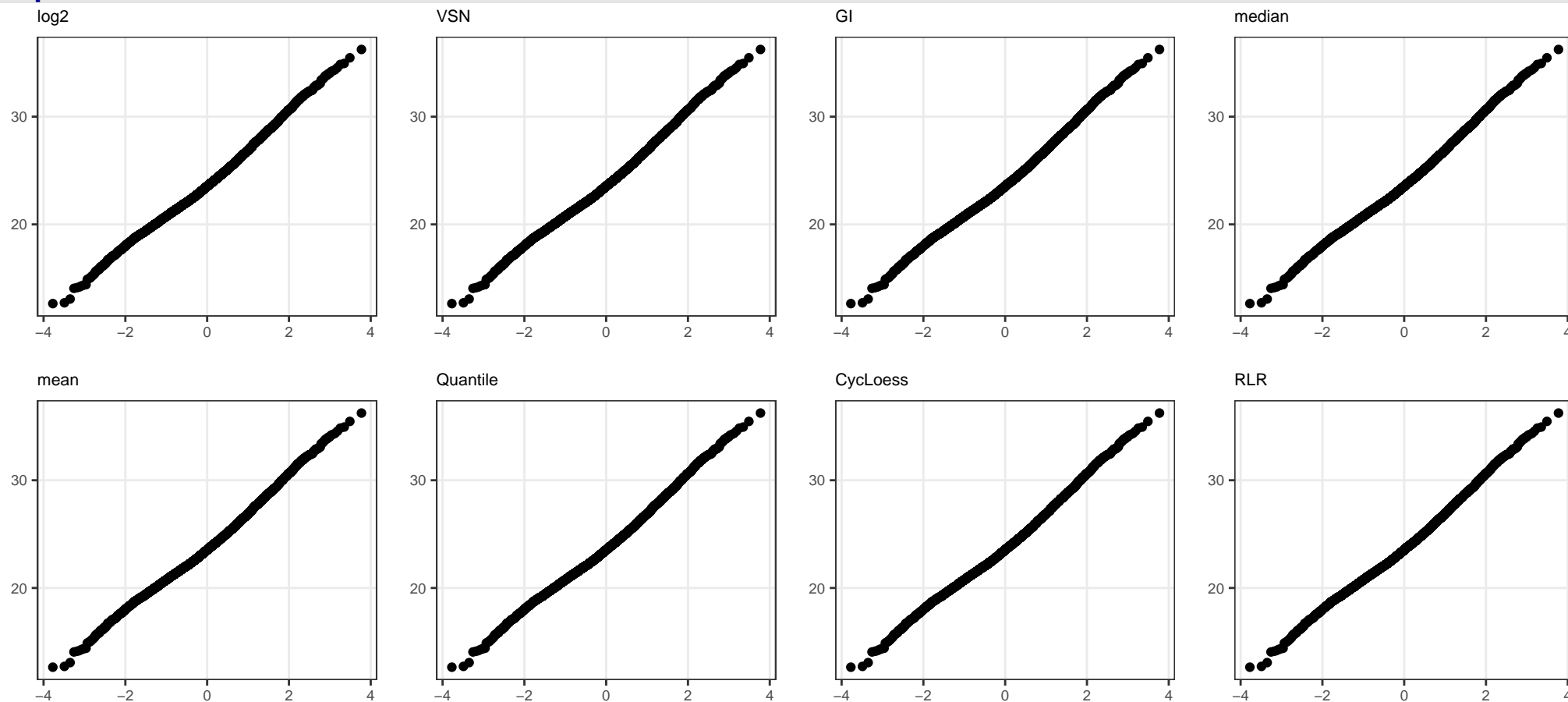
Stable variables plot



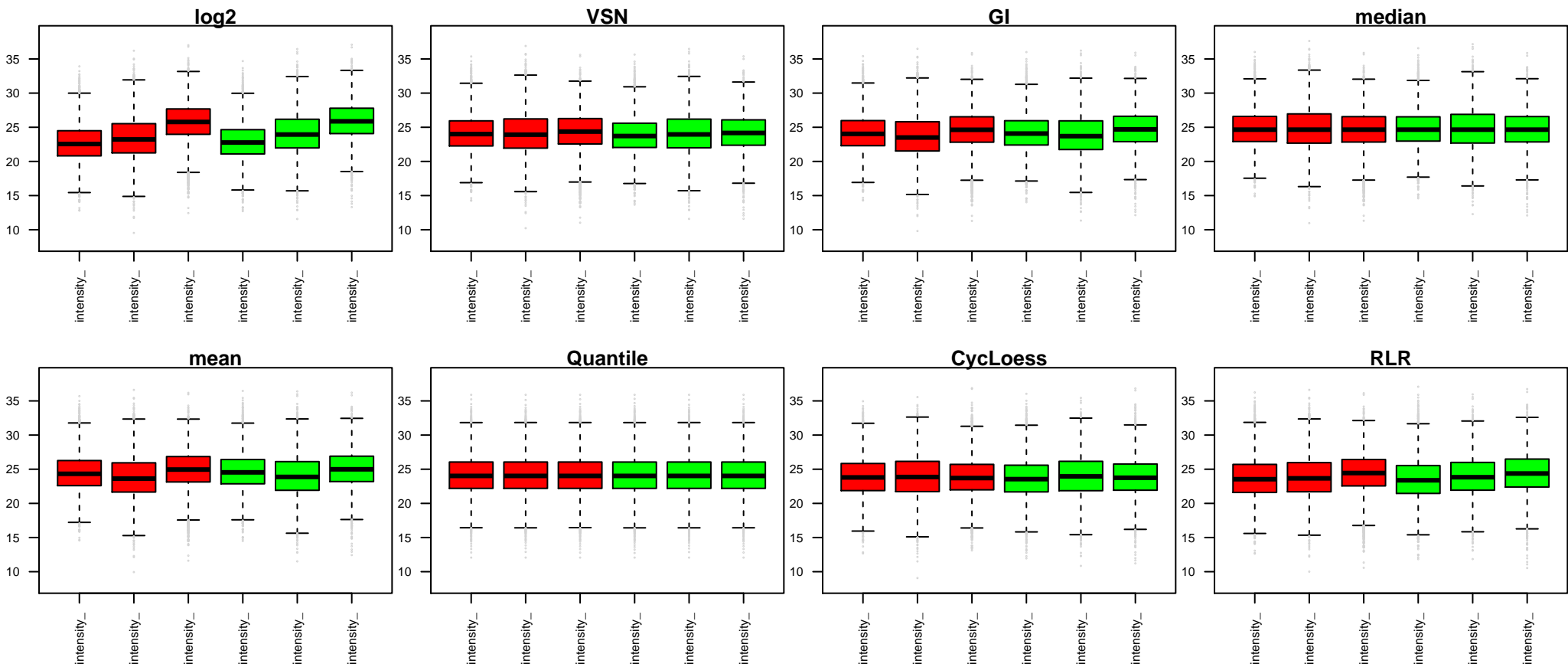


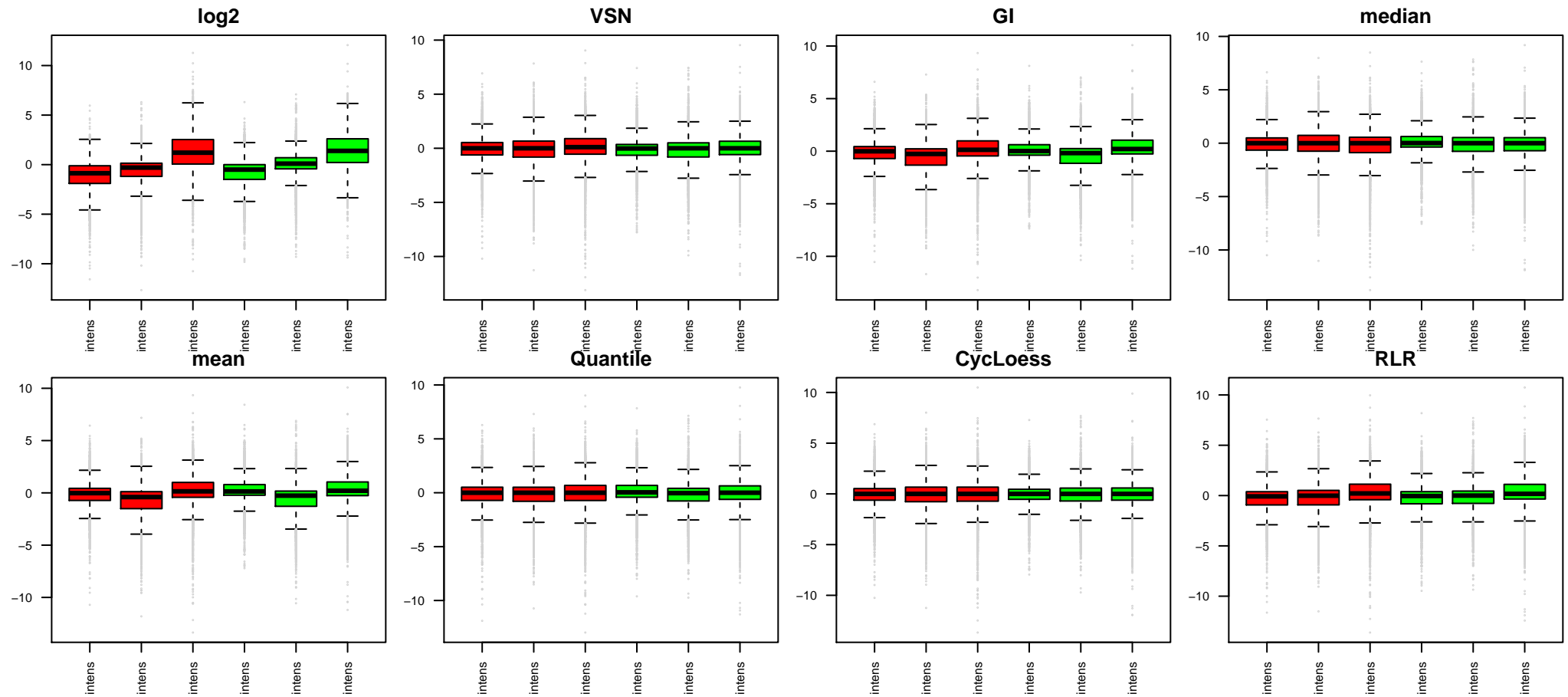




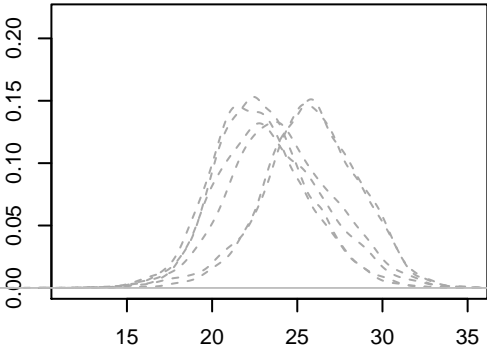




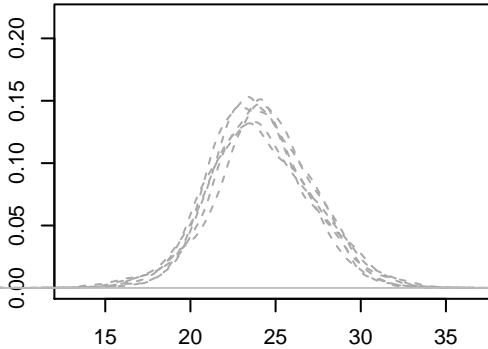




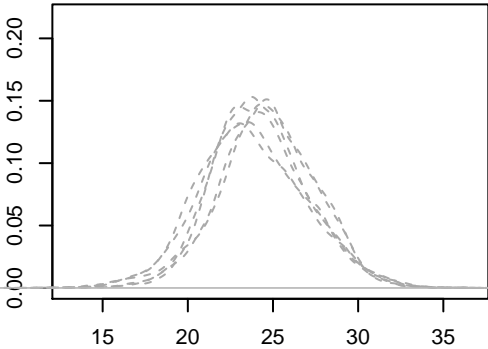
log2



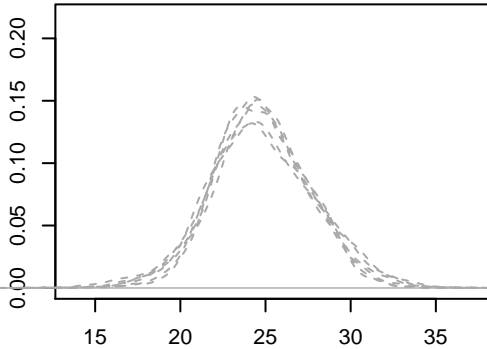
VSN



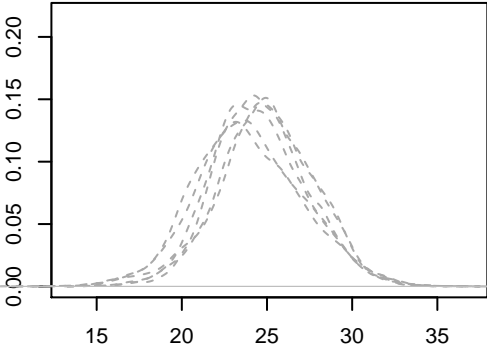
GI



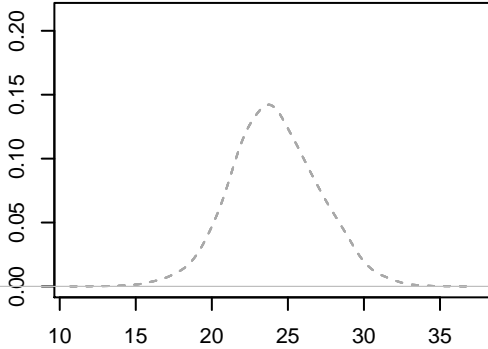
median



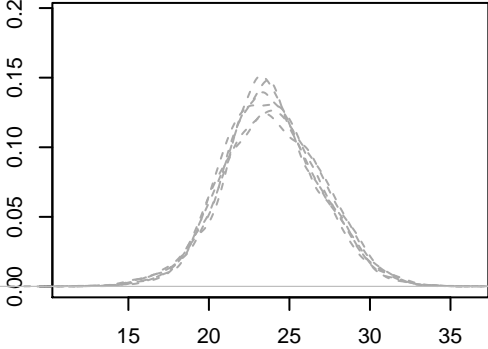
mean



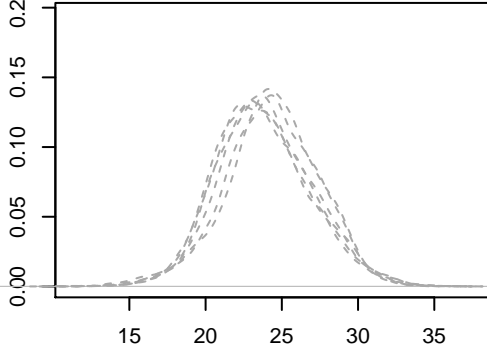
Quantile

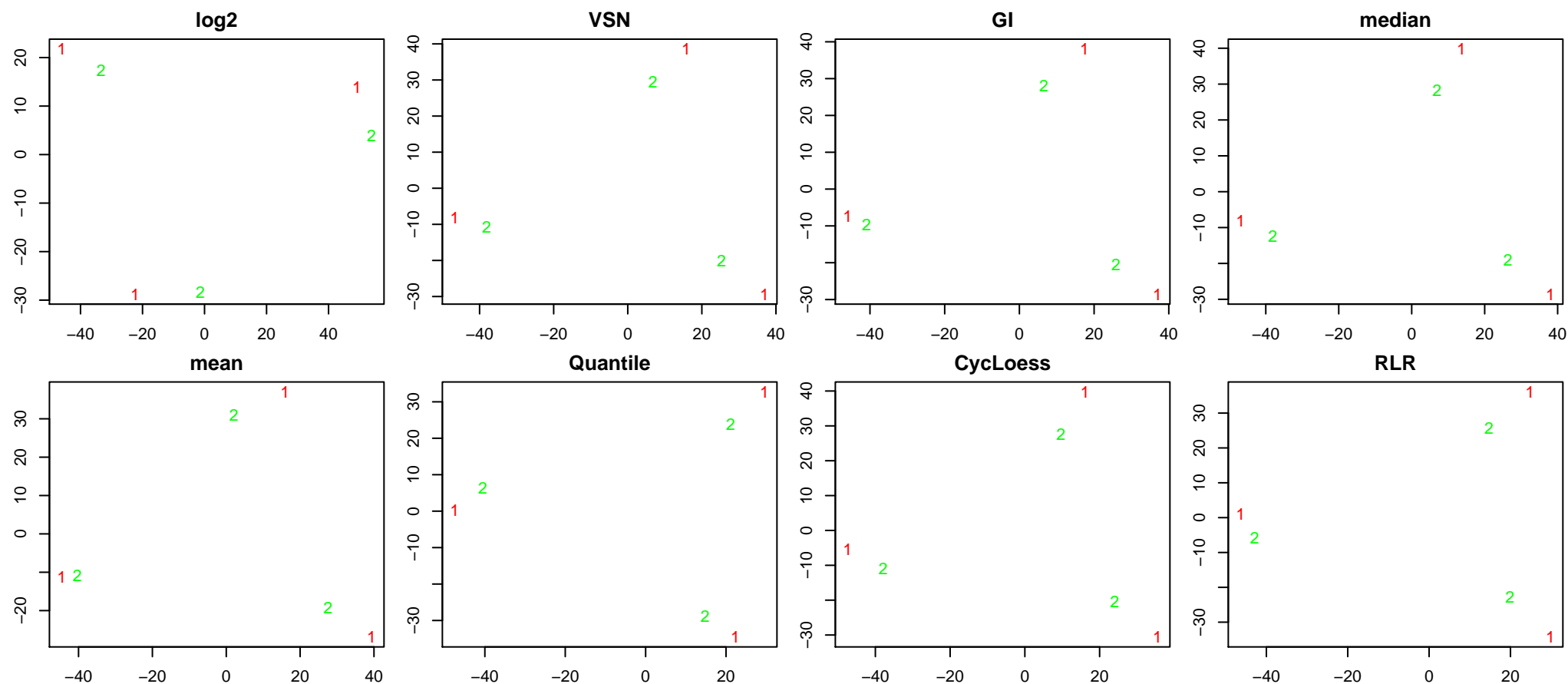


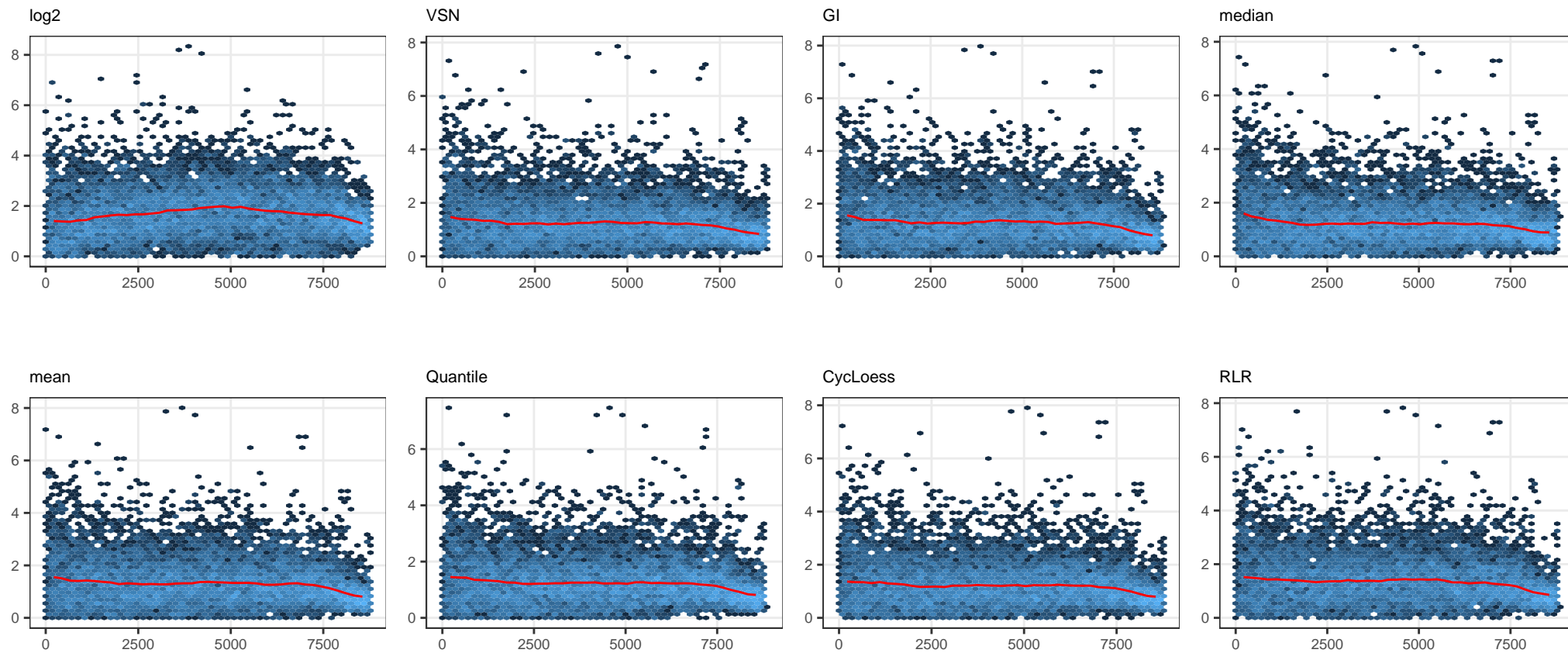
CycLoess



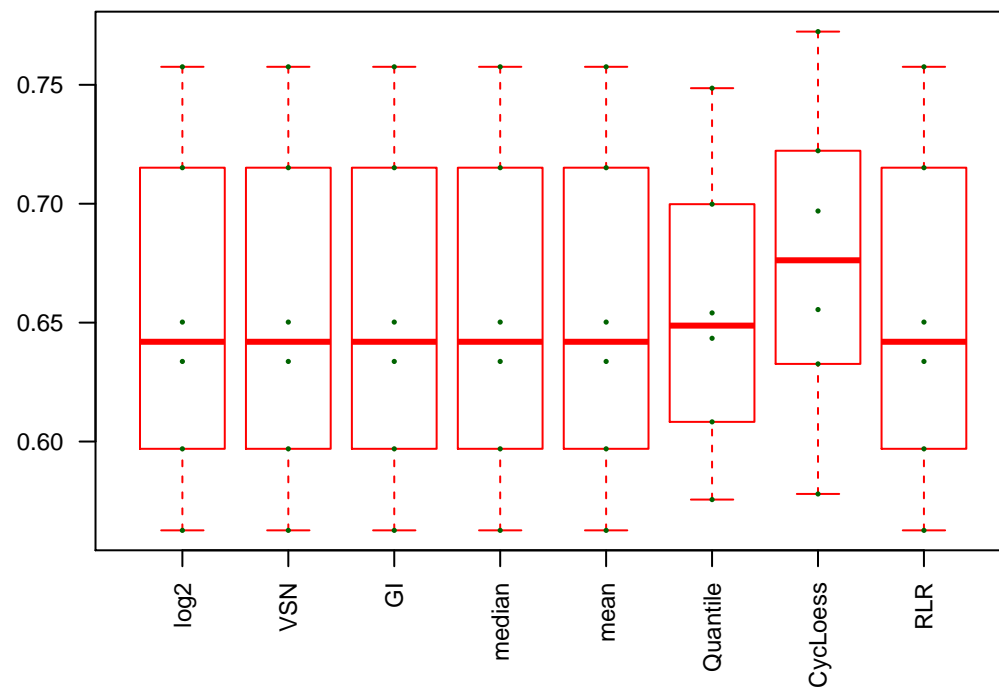
RLR







Pearson correlation – Intragroup



Spearman correlation – Intragroup

