

Project Name: con_sp.canonical.isoforms_PC_protein_groups

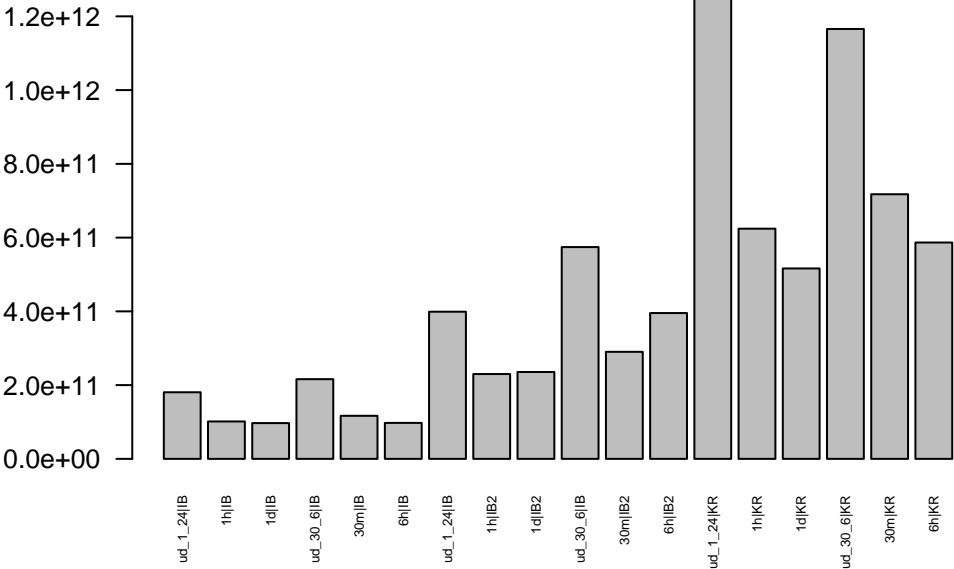
Normalyzer (ver 1.4.0)

Report created on: 2020-05-05

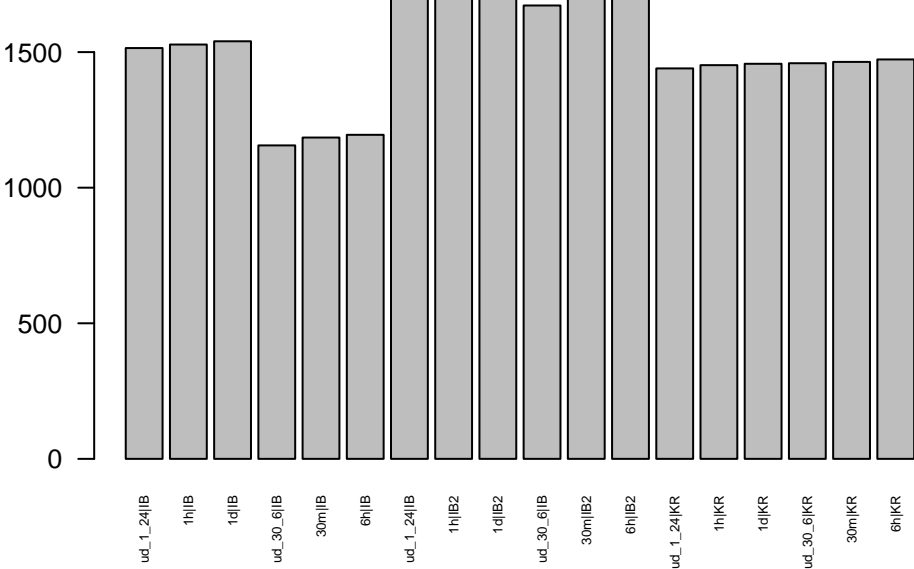
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

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

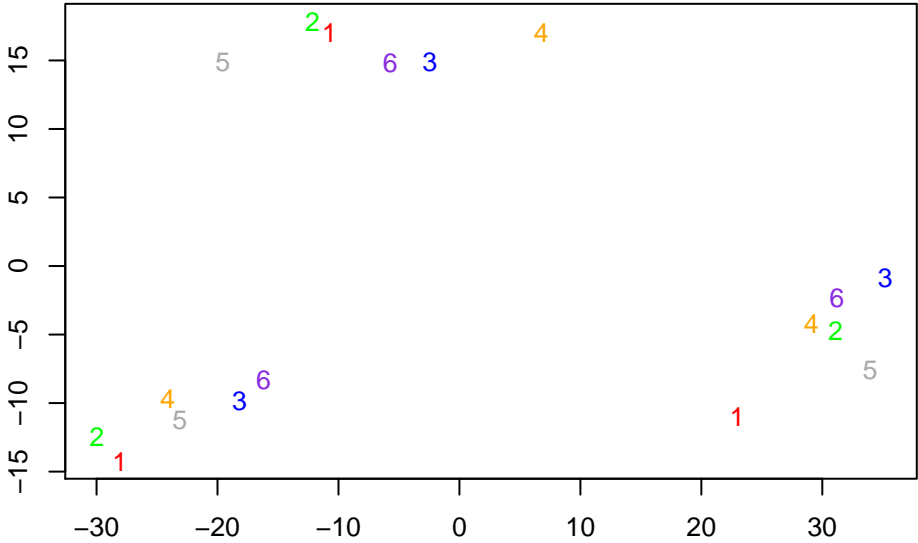
Total intensity

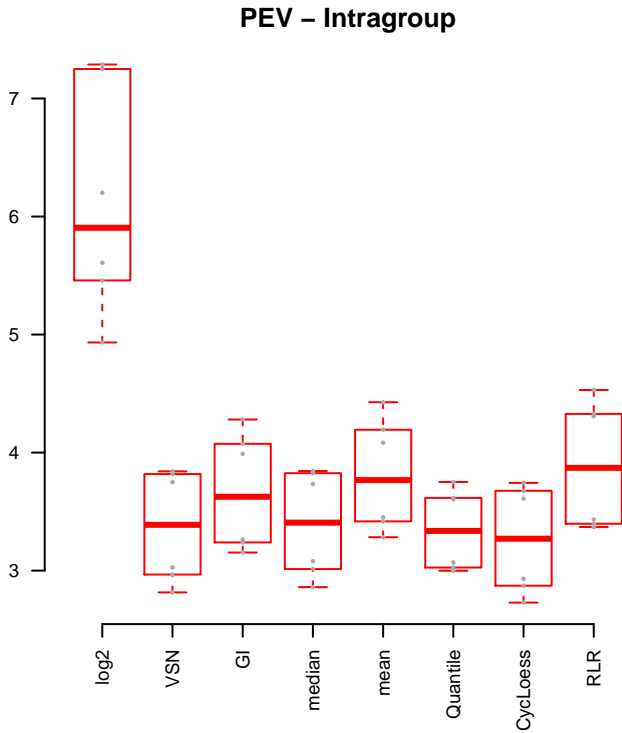
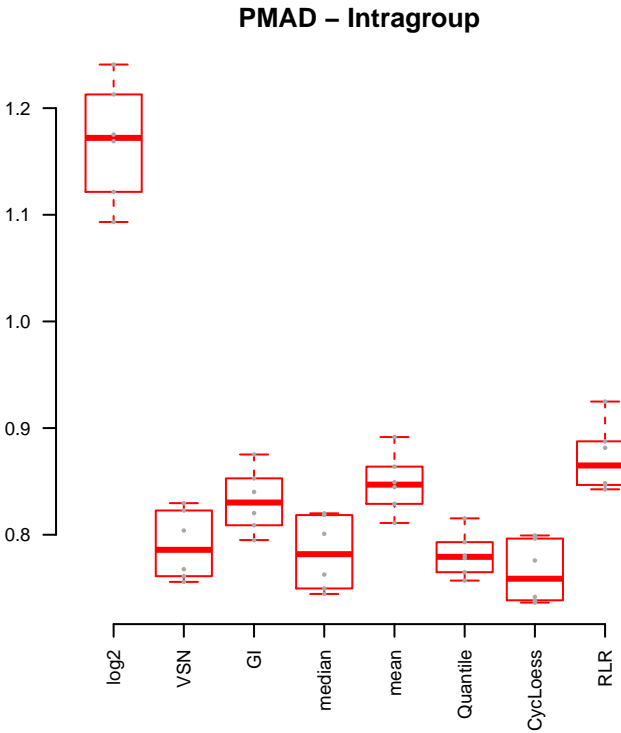
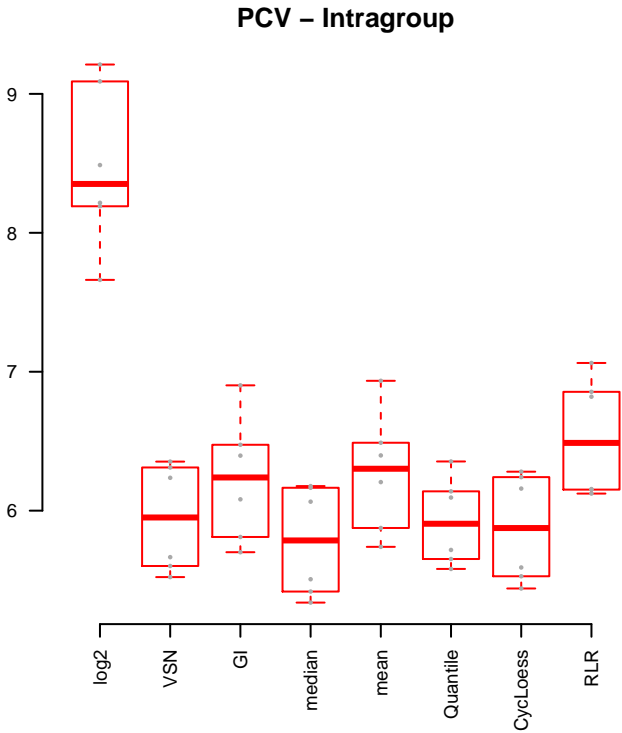


Total missing

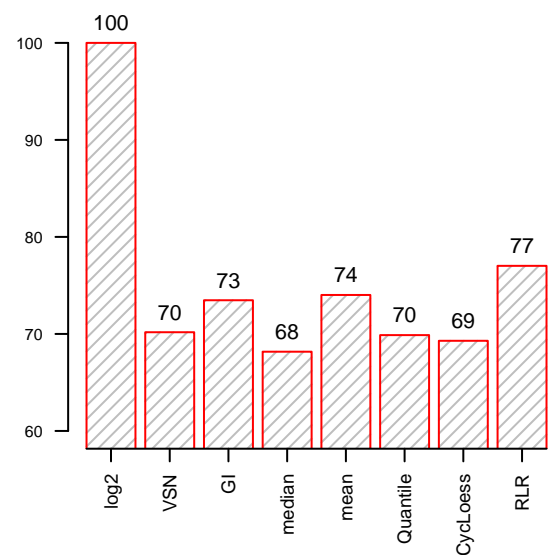


Log2-MDS plot

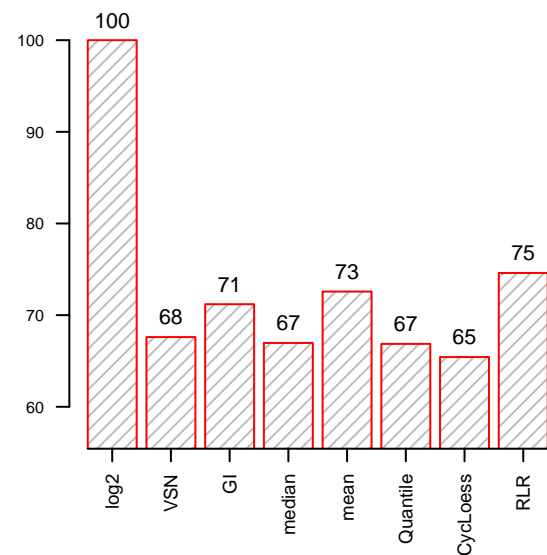




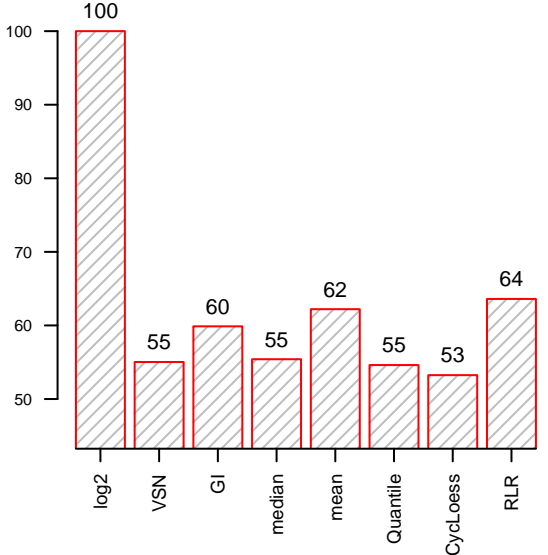
PCV compared to log2



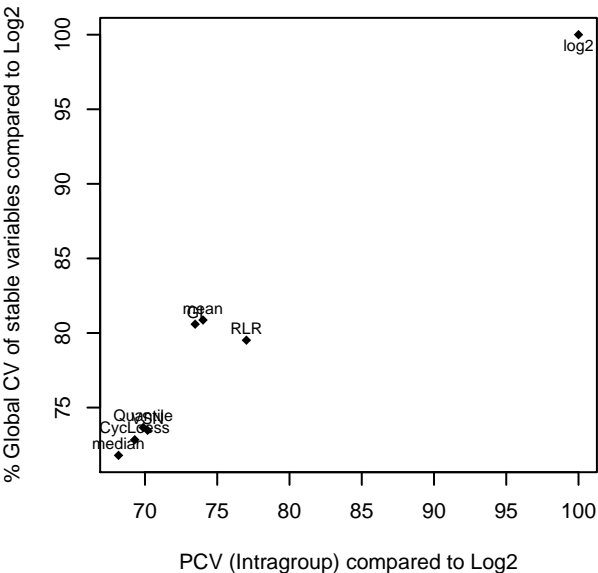
PMAD compared to log2

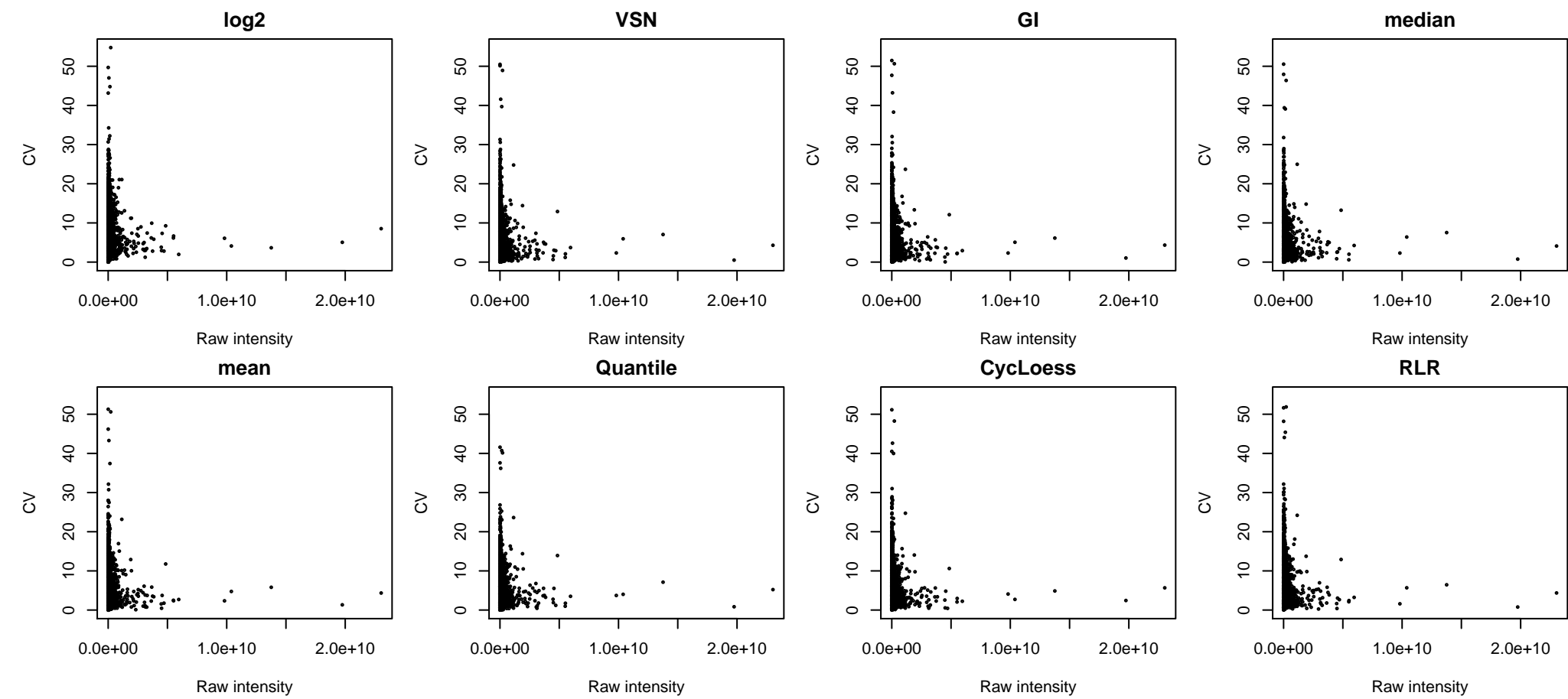


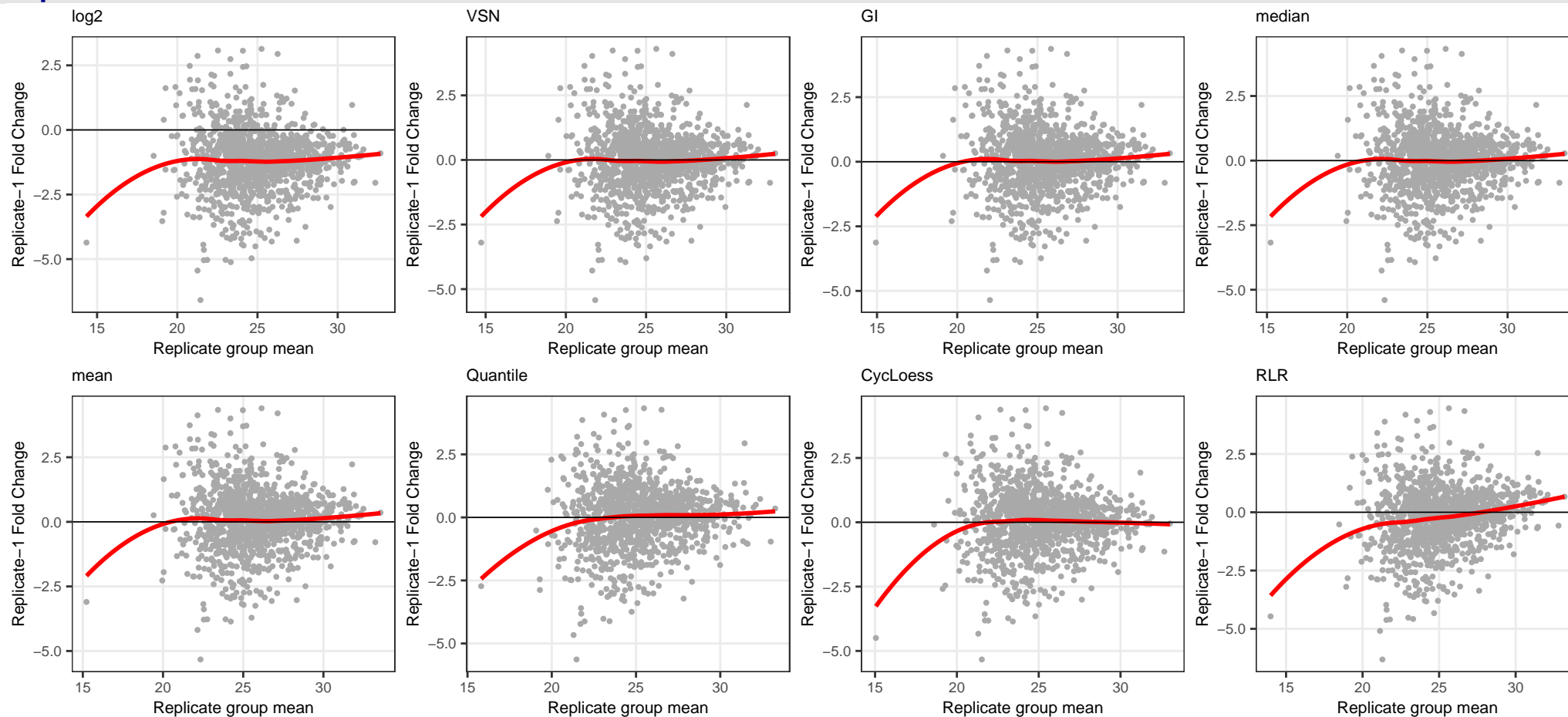
%PEV – compared to log2

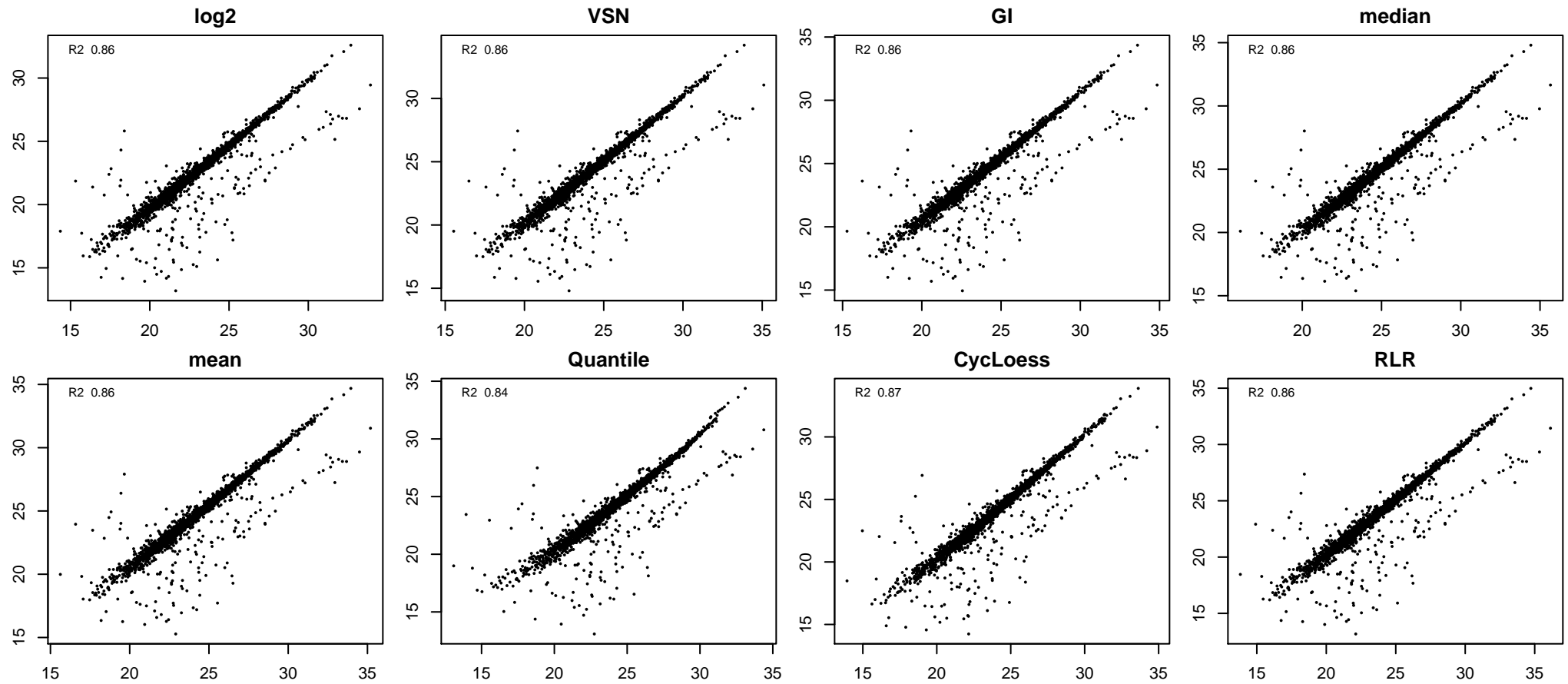


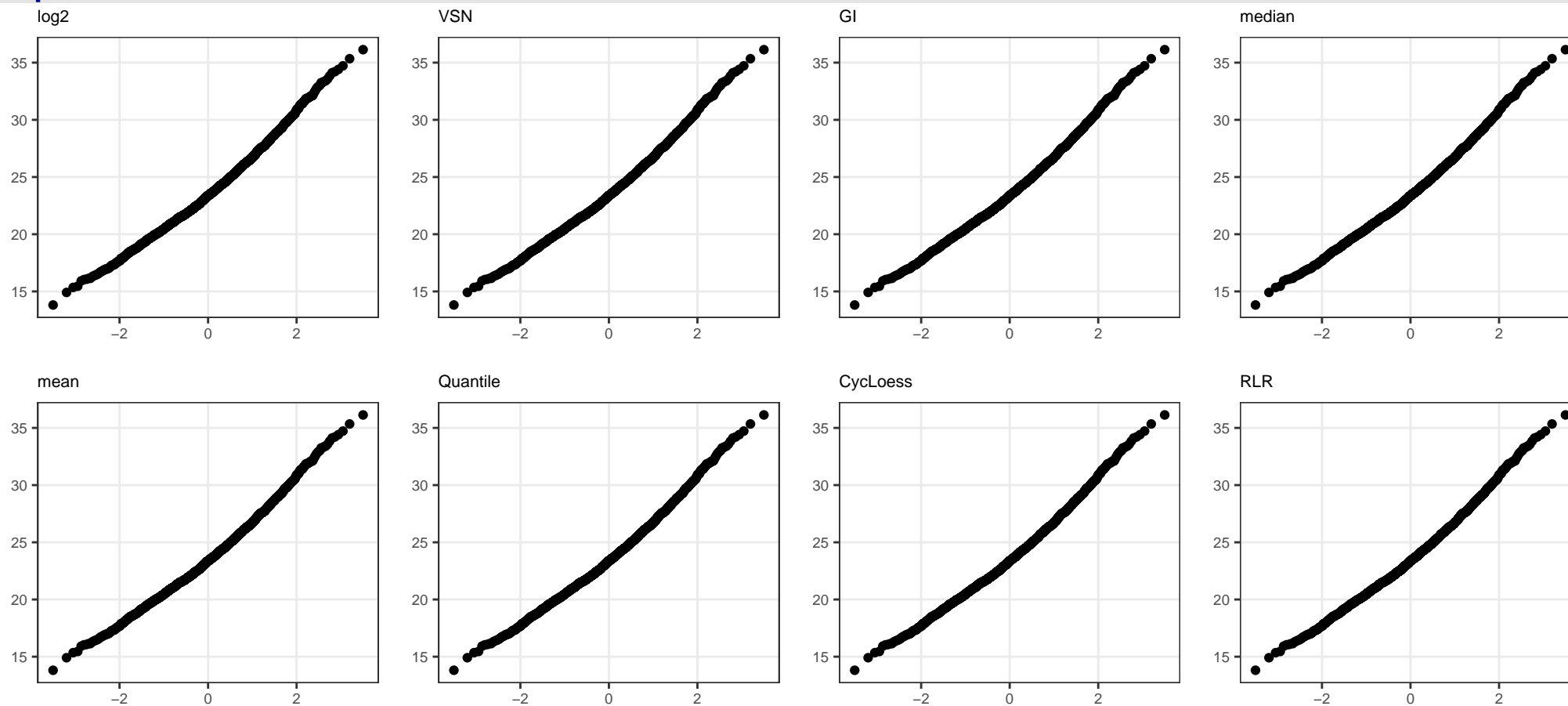
Stable variables plot

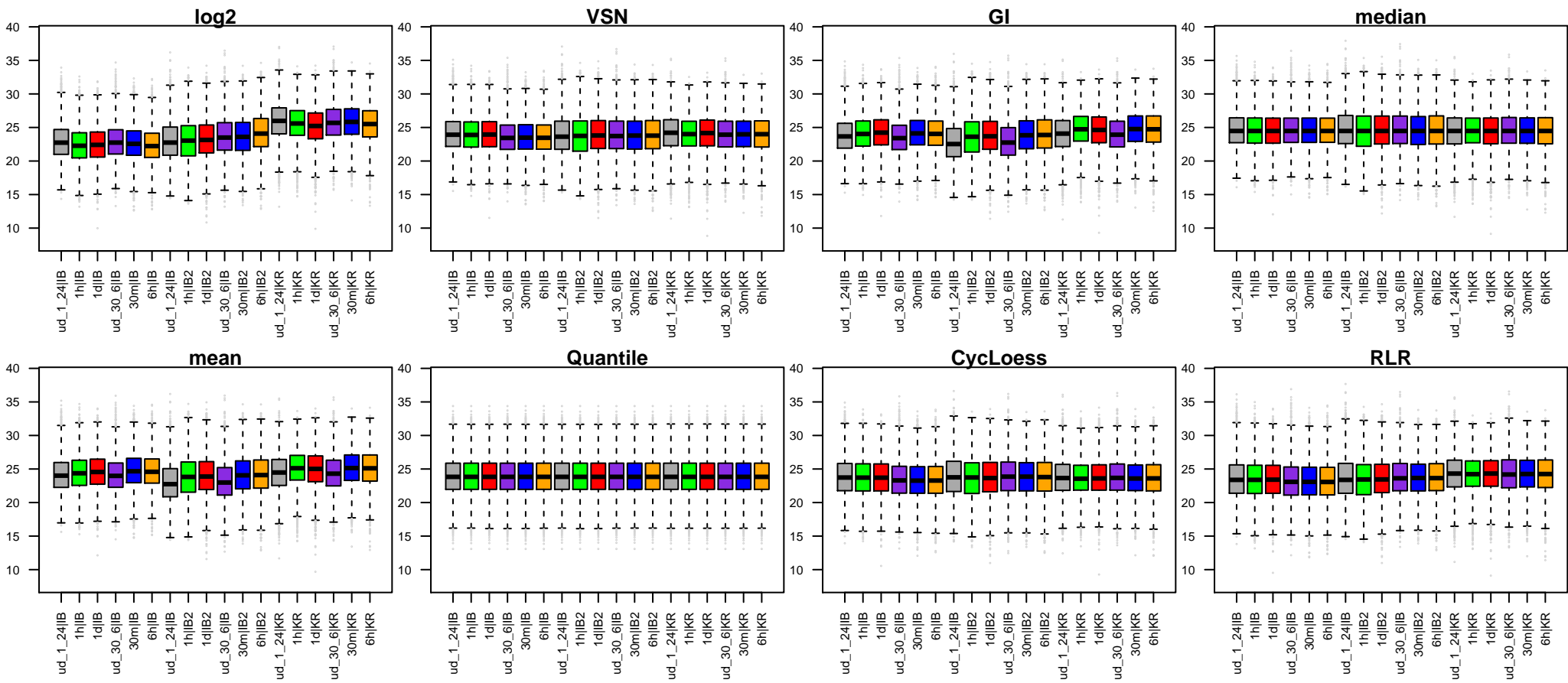


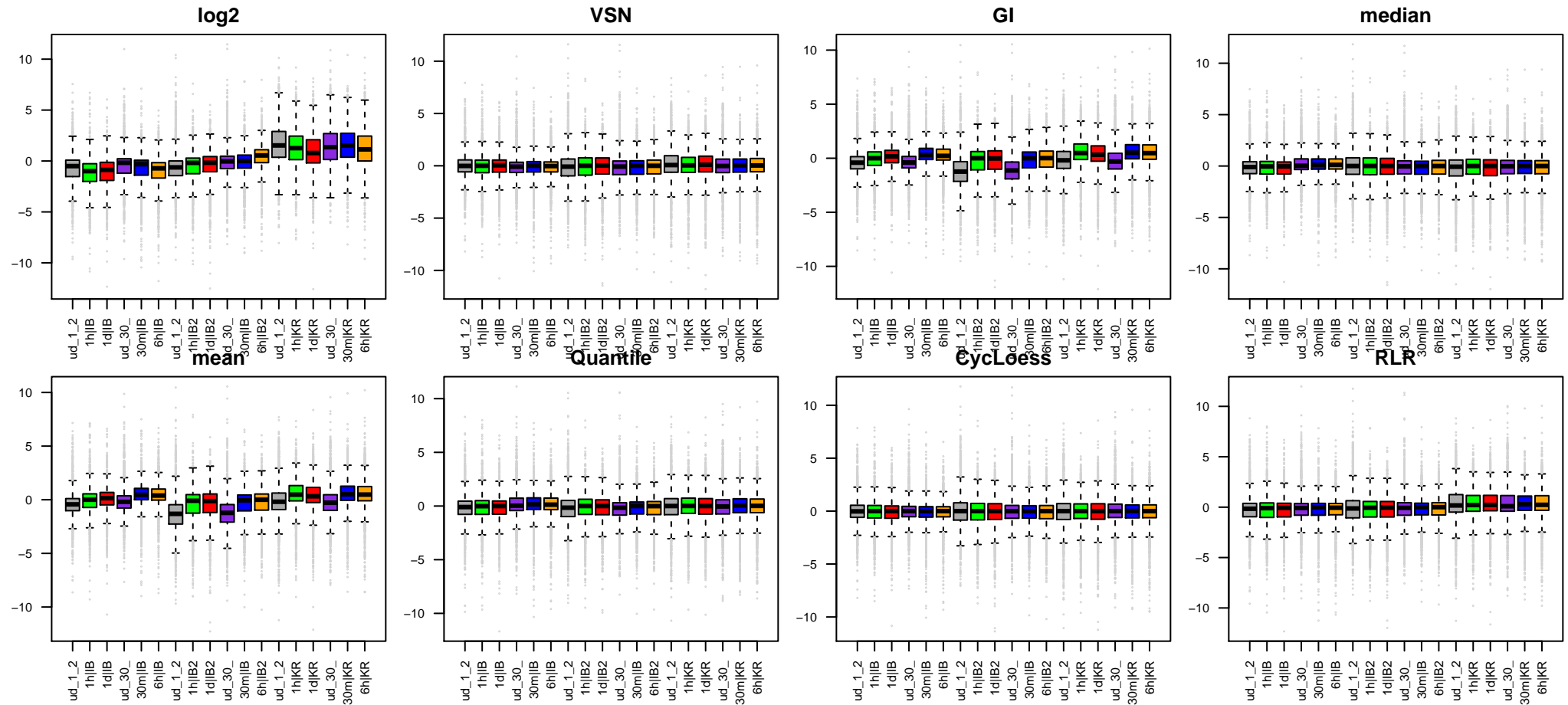










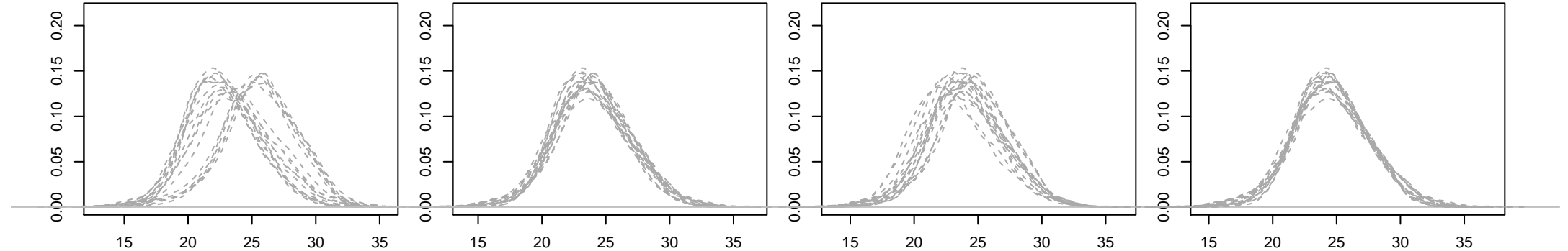


log2

VSN

GI

median

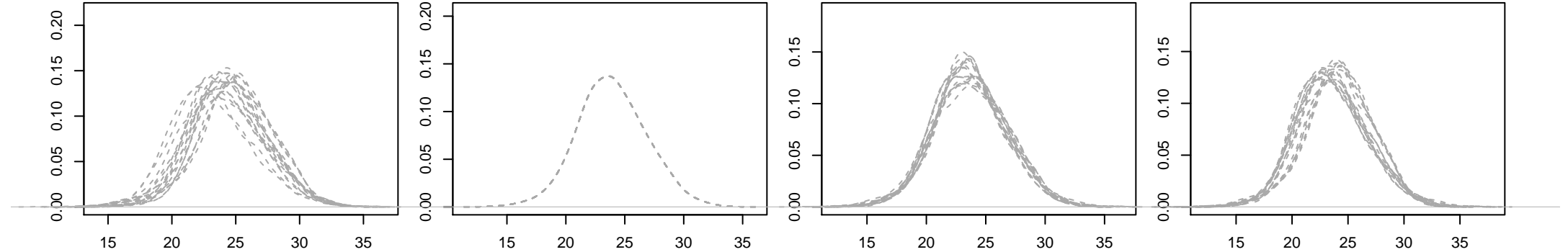


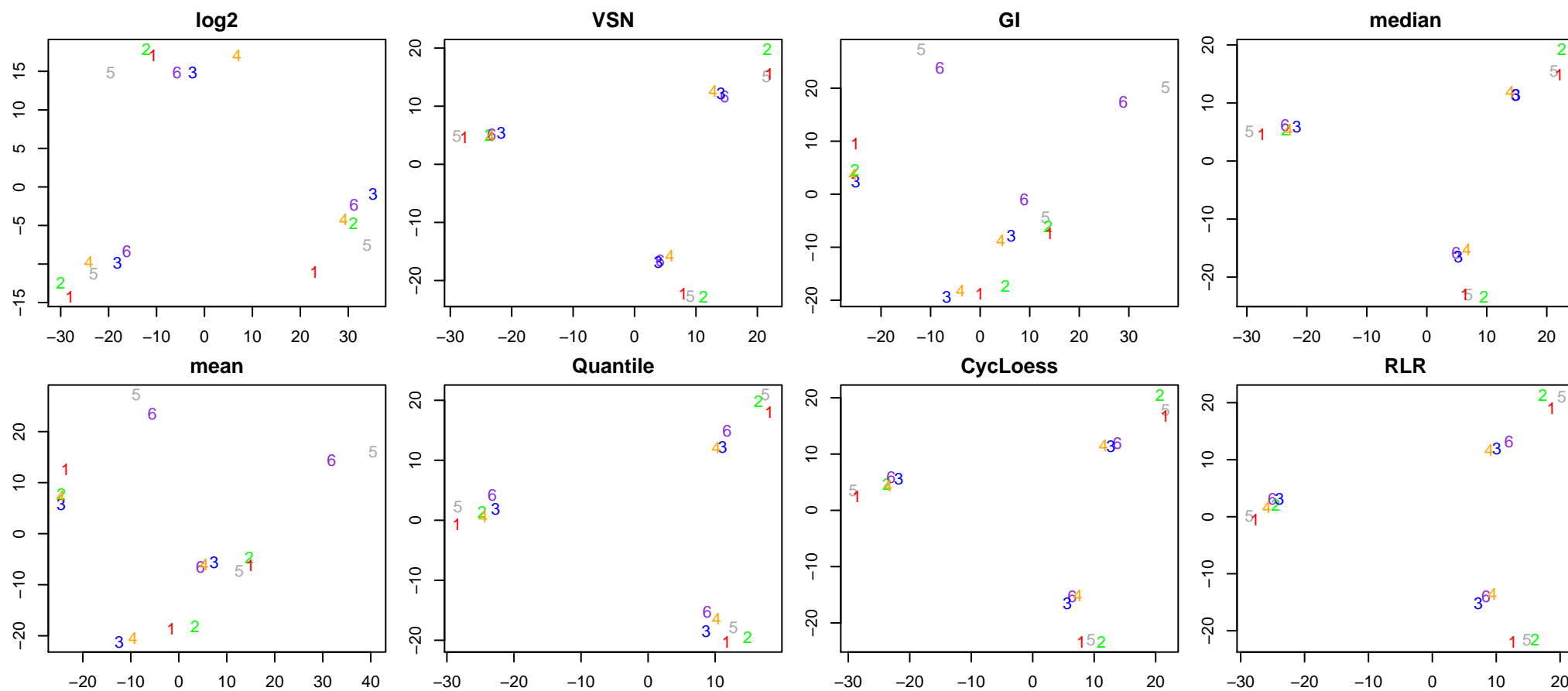
mean

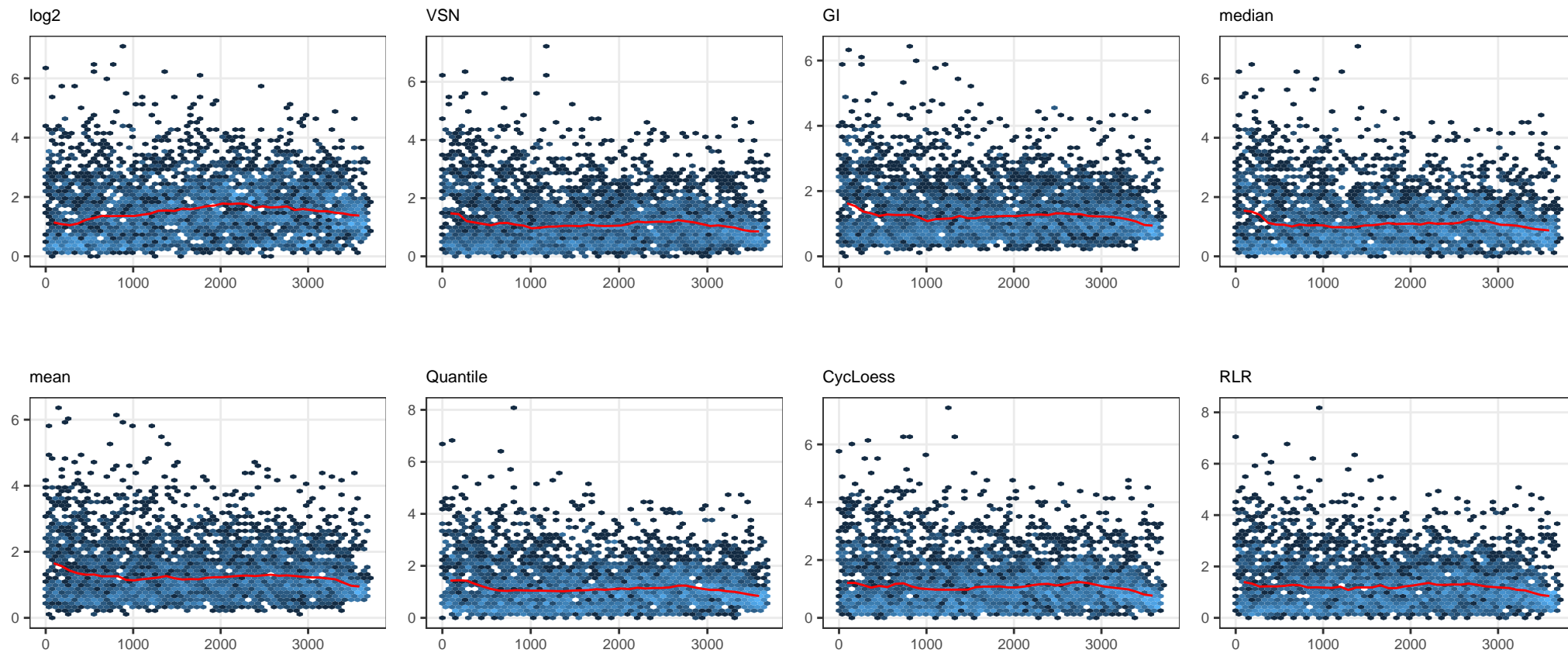
Quantile

CycLoess

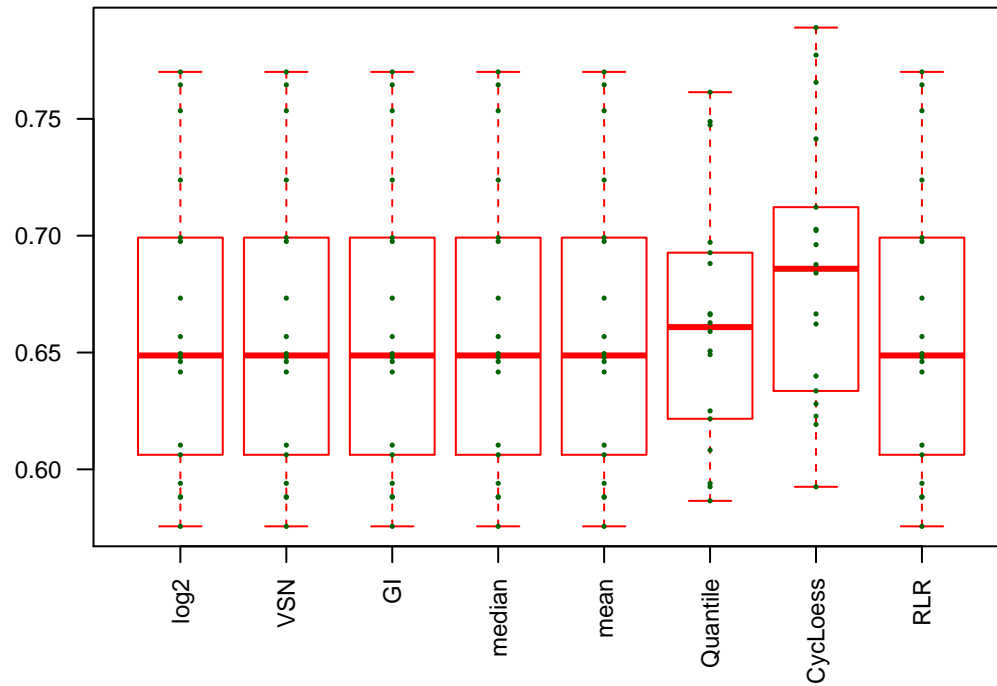
RLR







Pearson correlation – Intragroup



Spearman correlation – Intragroup

