Project Name: Prot_spermine

NormalyzerDE (ver 1.14.0)

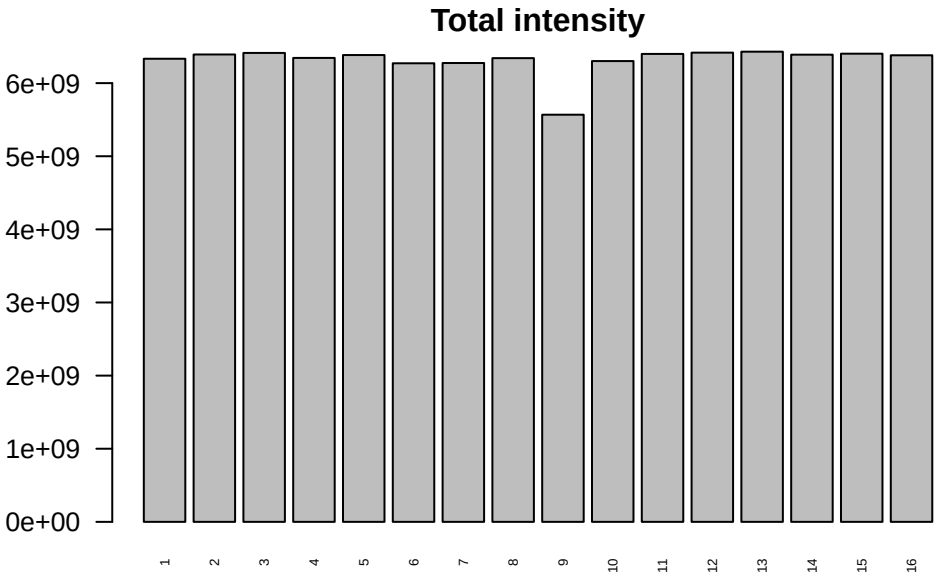
Report created on: 2023−02−20

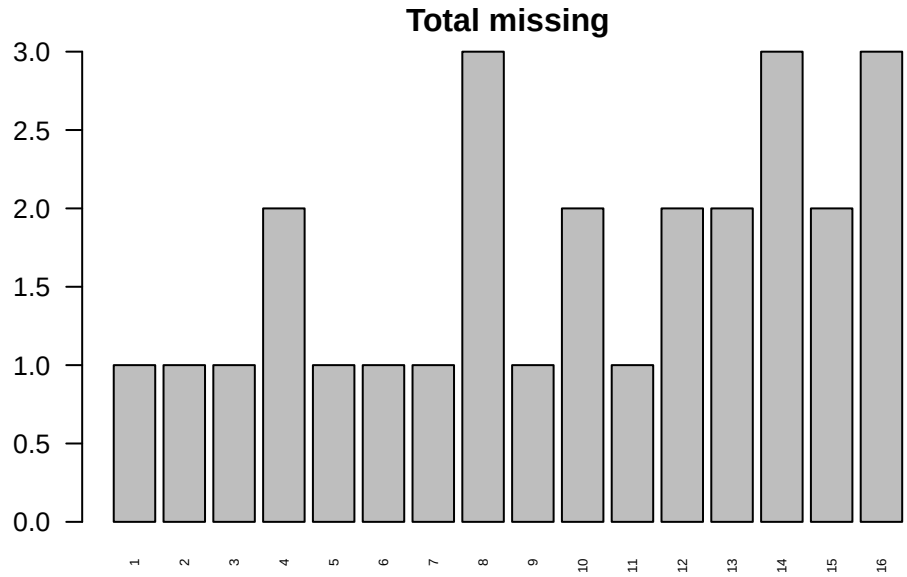
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High−Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

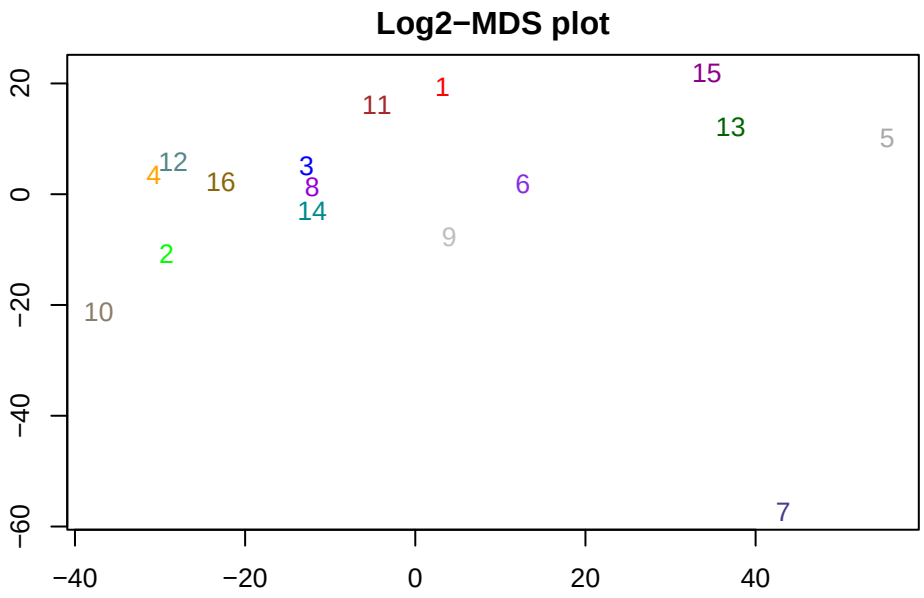
Documentation for analyzing this report can be found at http://quantitativeproteomics.org/normalyzer/help.php

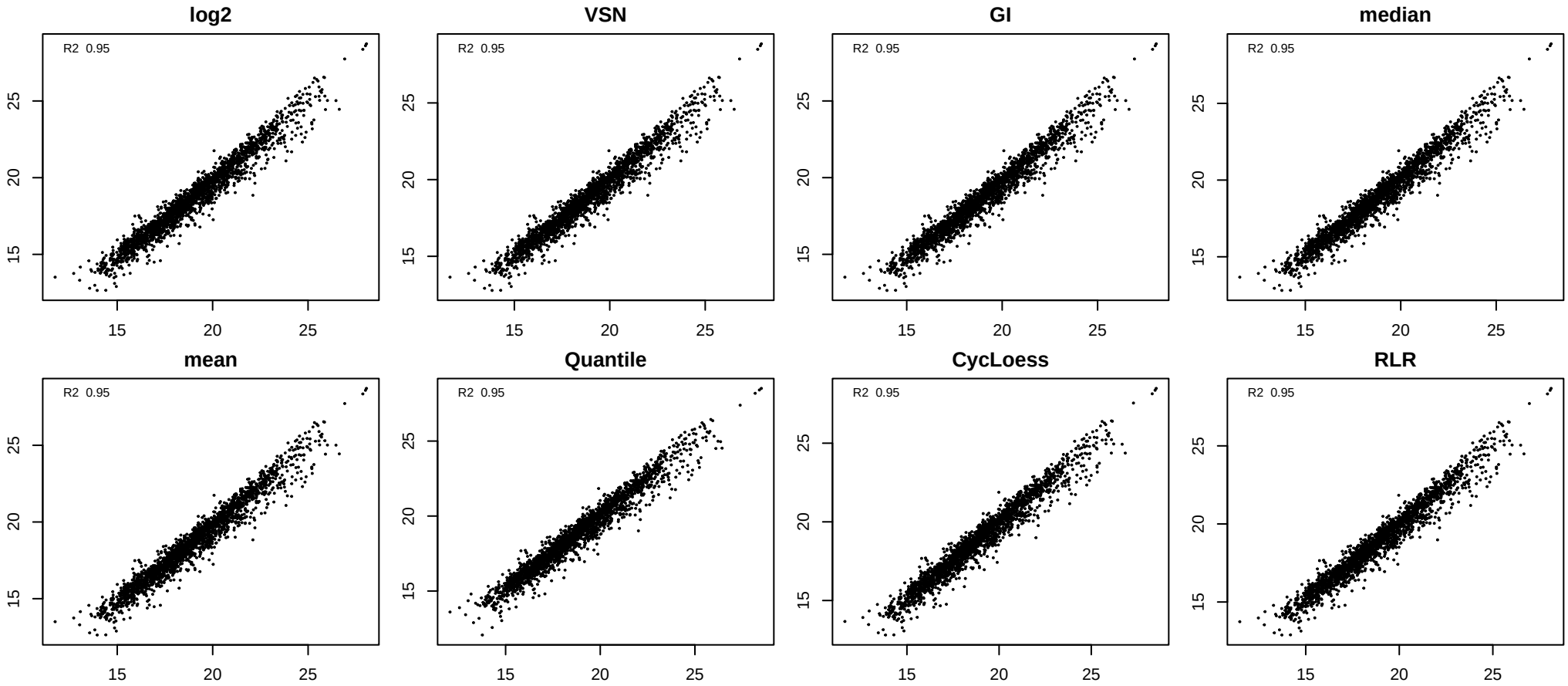
Group nbr.	Design group	Nbr. samples in cond.
1	Both_D1	1
2	Both_D2	1
3	Both_D3	1
4	Both_D4	1
5	Control_D1	1
6	Control_D2	1
7	Control_D3	1
8	Control_D4	1
9	Spermidine_D1	1
10	Spermidine_D2	1
11	Spermidine_D3	1
12	Spermidine_D4	1
13	Spermine_D1	1
14	Spermine_D2	1
15	Spermine_D3	1
16	Spermine_D4	1

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

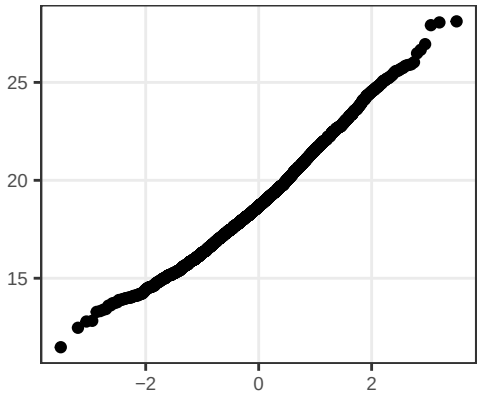

Total intensity
6e+09
5e+09
4e+09
3e+09
2e+09
1e+09
0e+00
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16


Total missing
3.0
2.5
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16

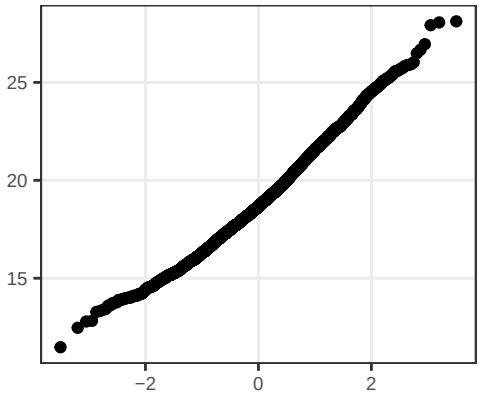

Log2−MDS plot
20
0
−20
−40
−60
−40
−20
0
20
40
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16


log2
R2 0.95
VSN
R2 0.95
GI
R2 0.95
median
R2 0.95
mean
R2 0.95
Quantile
R2 0.95
CycLoess
R2 0.95
RLR
R2 0.95
15
20
25

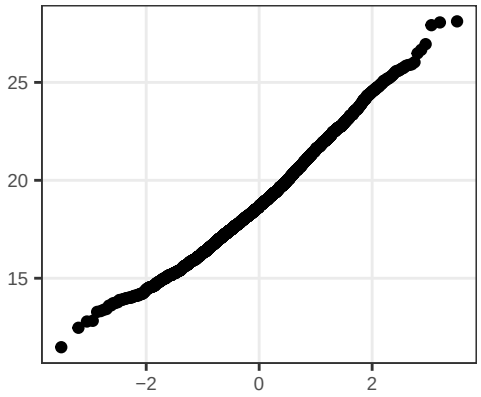
log2



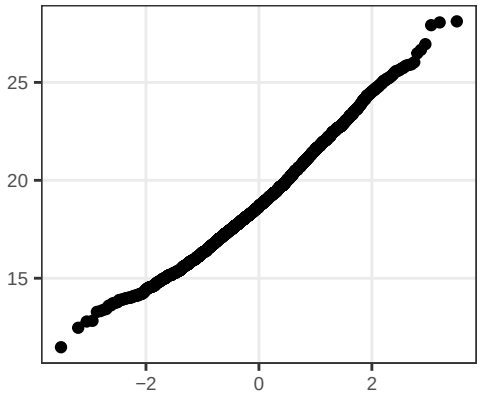
VSN



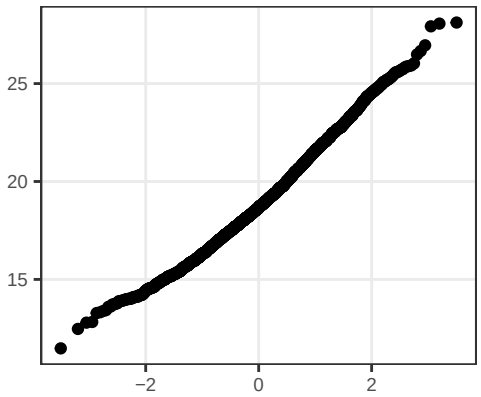
GI



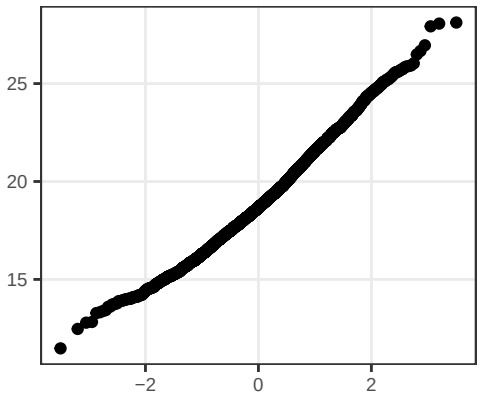
median



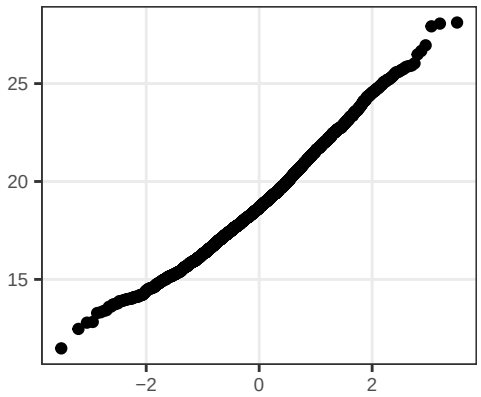
mean



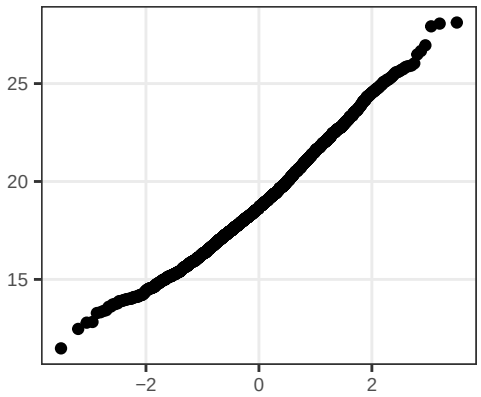
Quantile

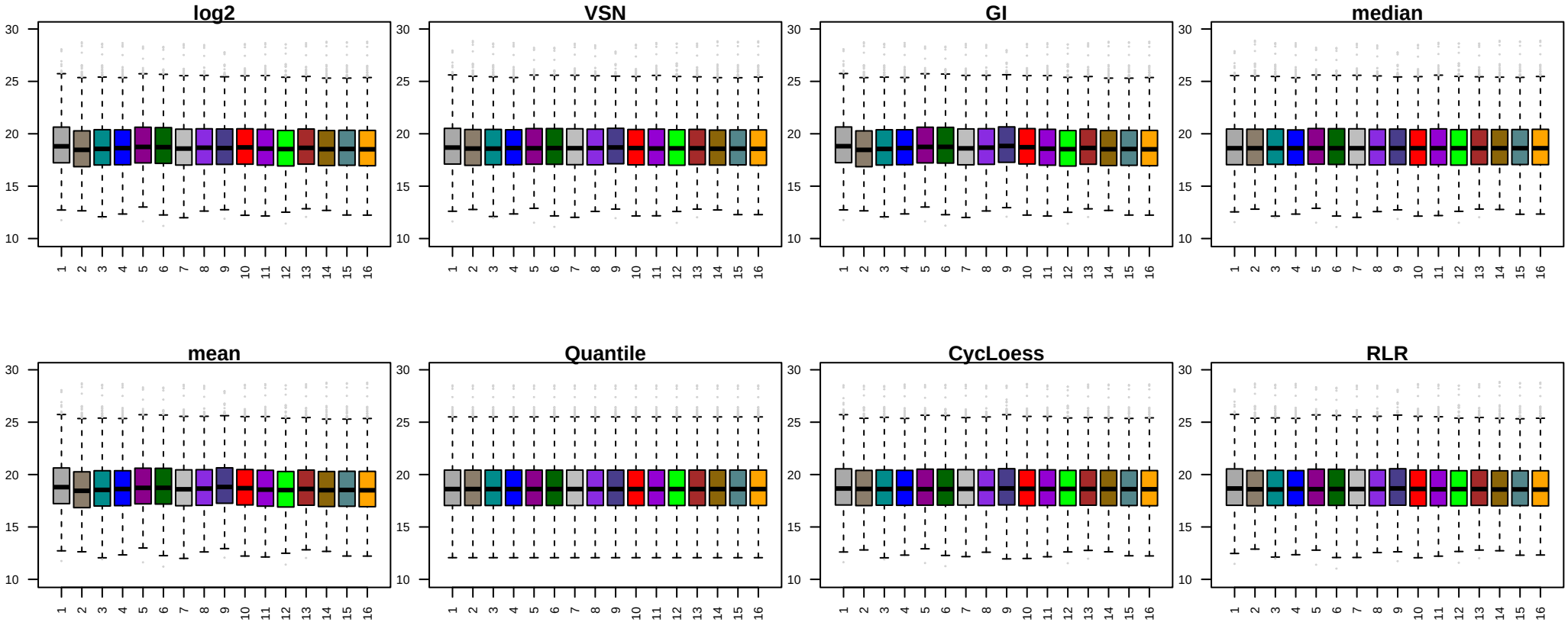


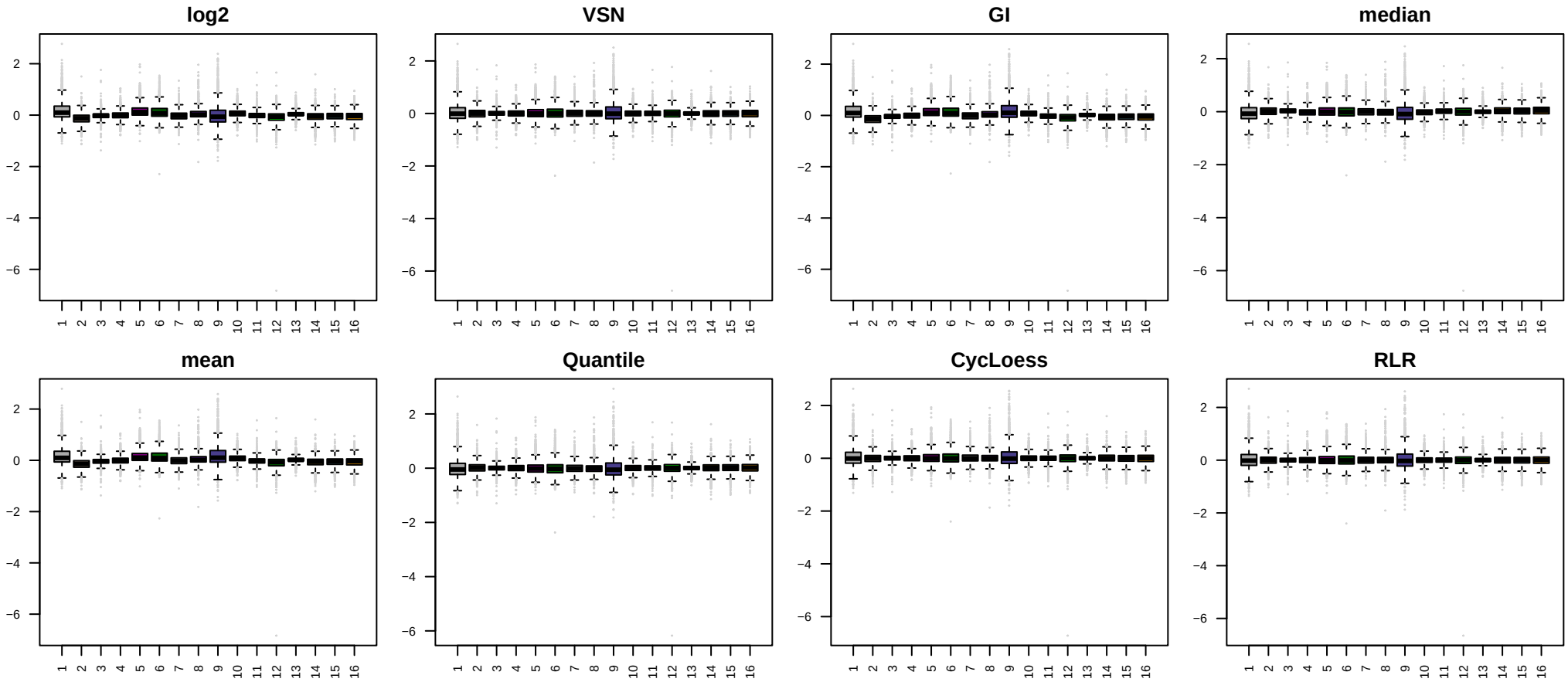
CycLoess

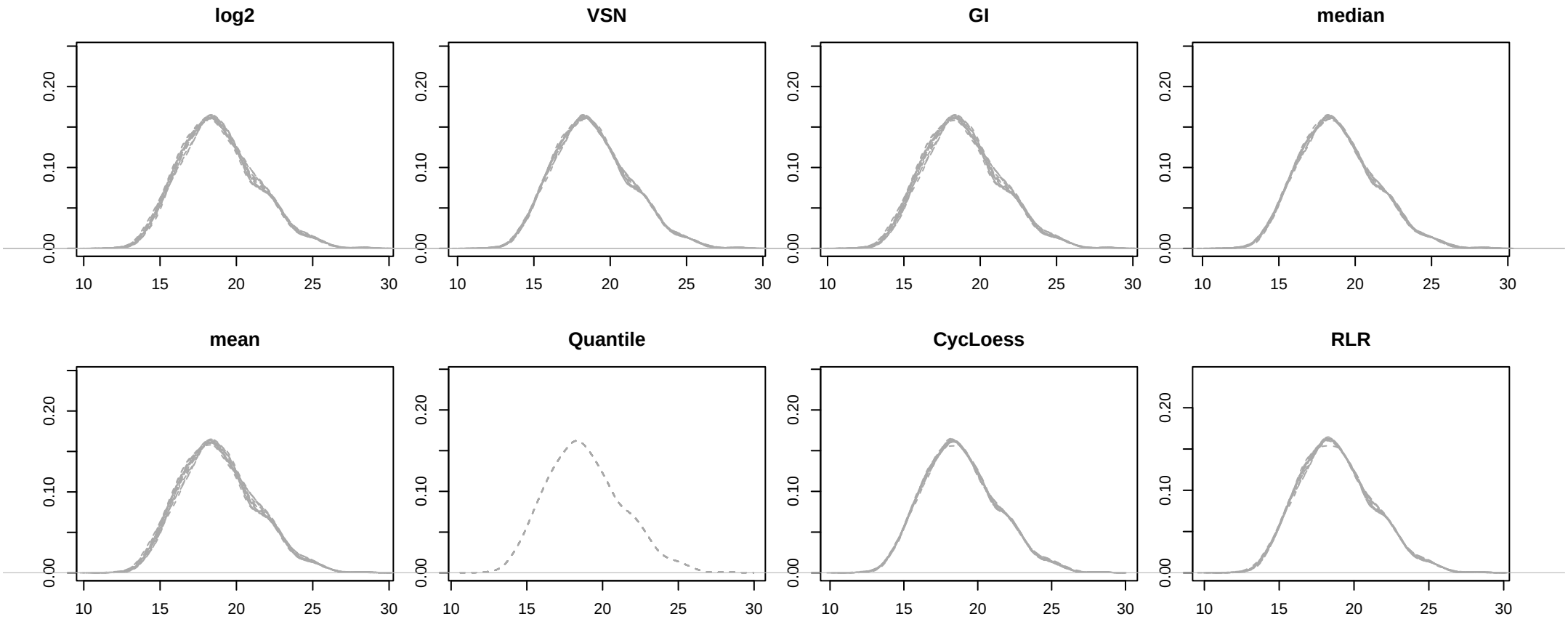


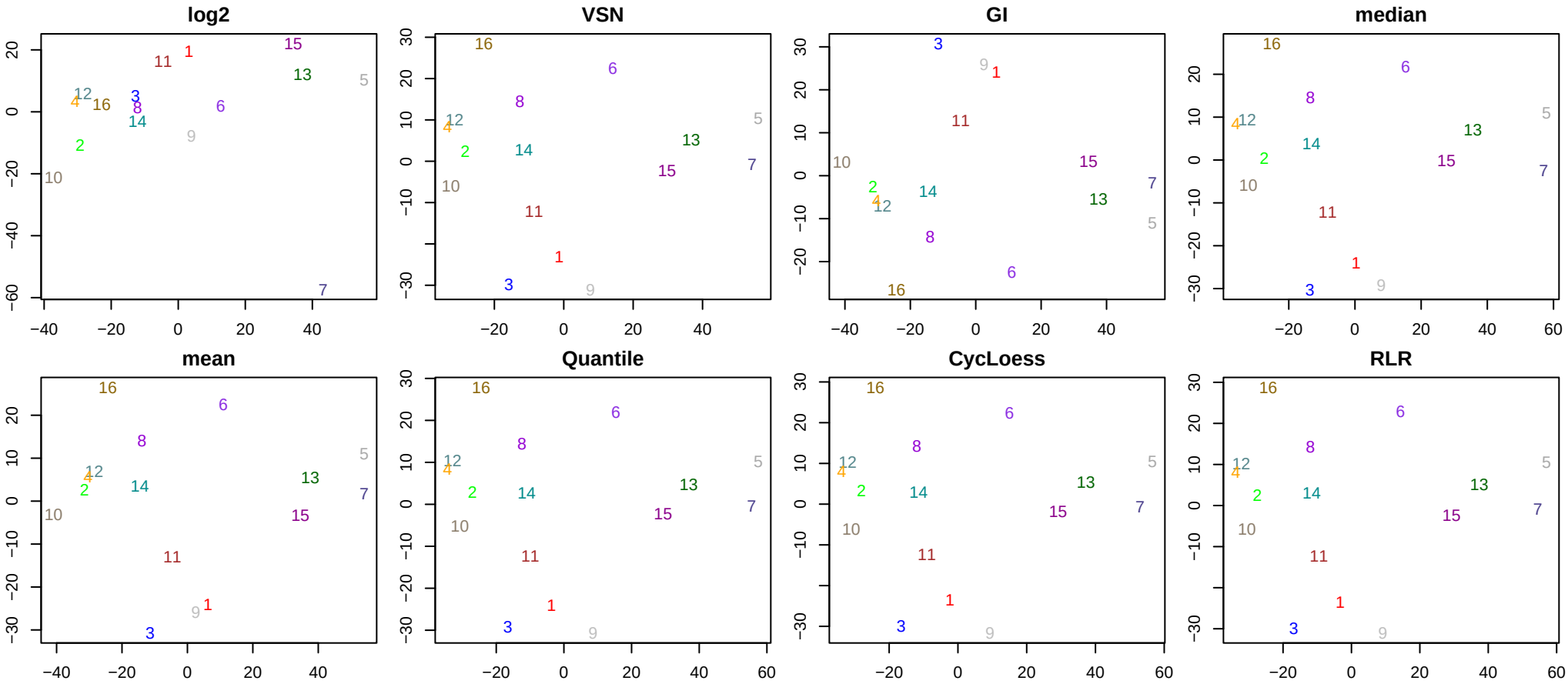
RLR

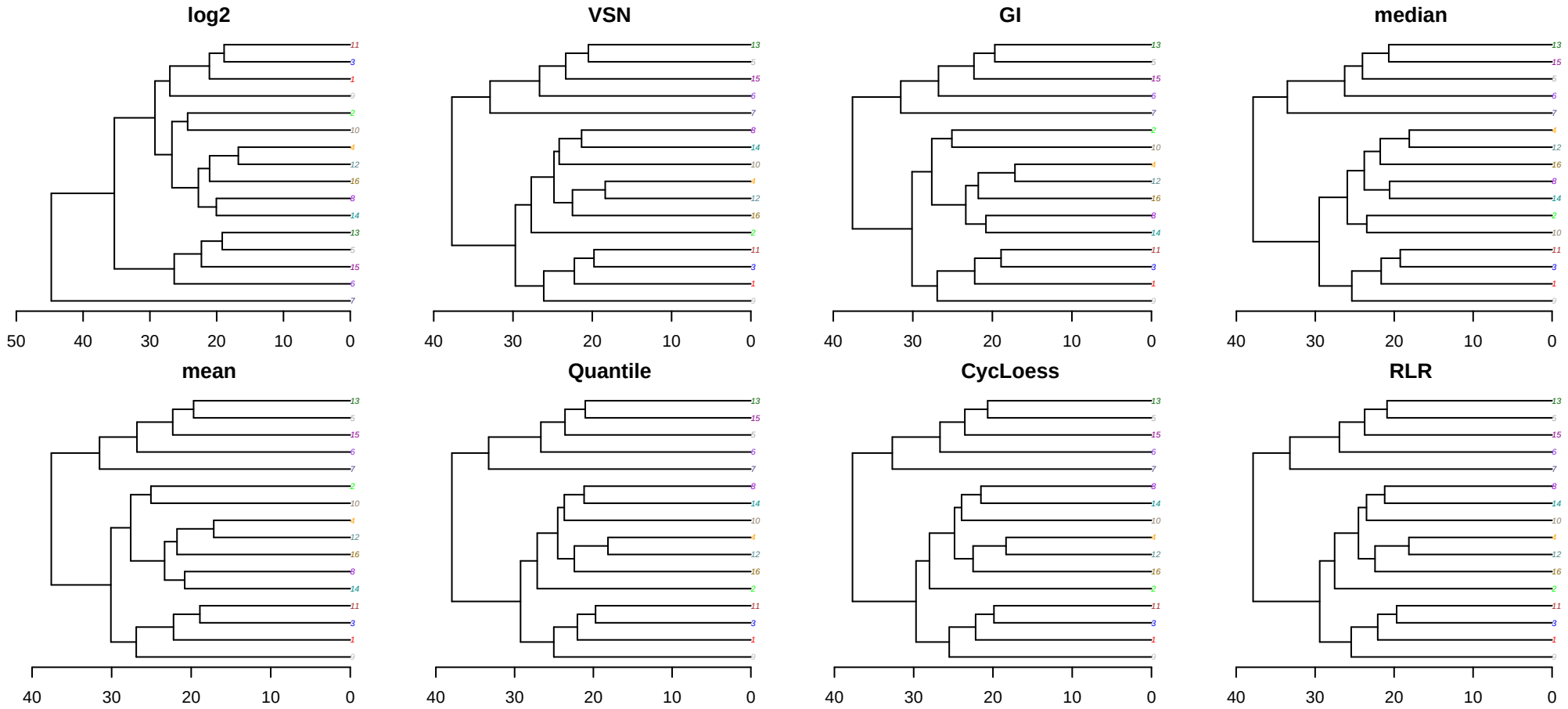



log2
VSN
GI
median
mean
Quantile
CycLoess
RLR


log2
VSN
GI
median
mean
Quantile
CycLoess
RLR


log2
VSN
GI
median
mean
Quantile
CycLoess
RLR
0.00
0.10
0.20
10
15
20
25
30


log2
VSN
GI
median
mean
Quantile
CycLoess
RLR


log2
VSN
GI
median
mean
Quantile
CycLoess
RLR