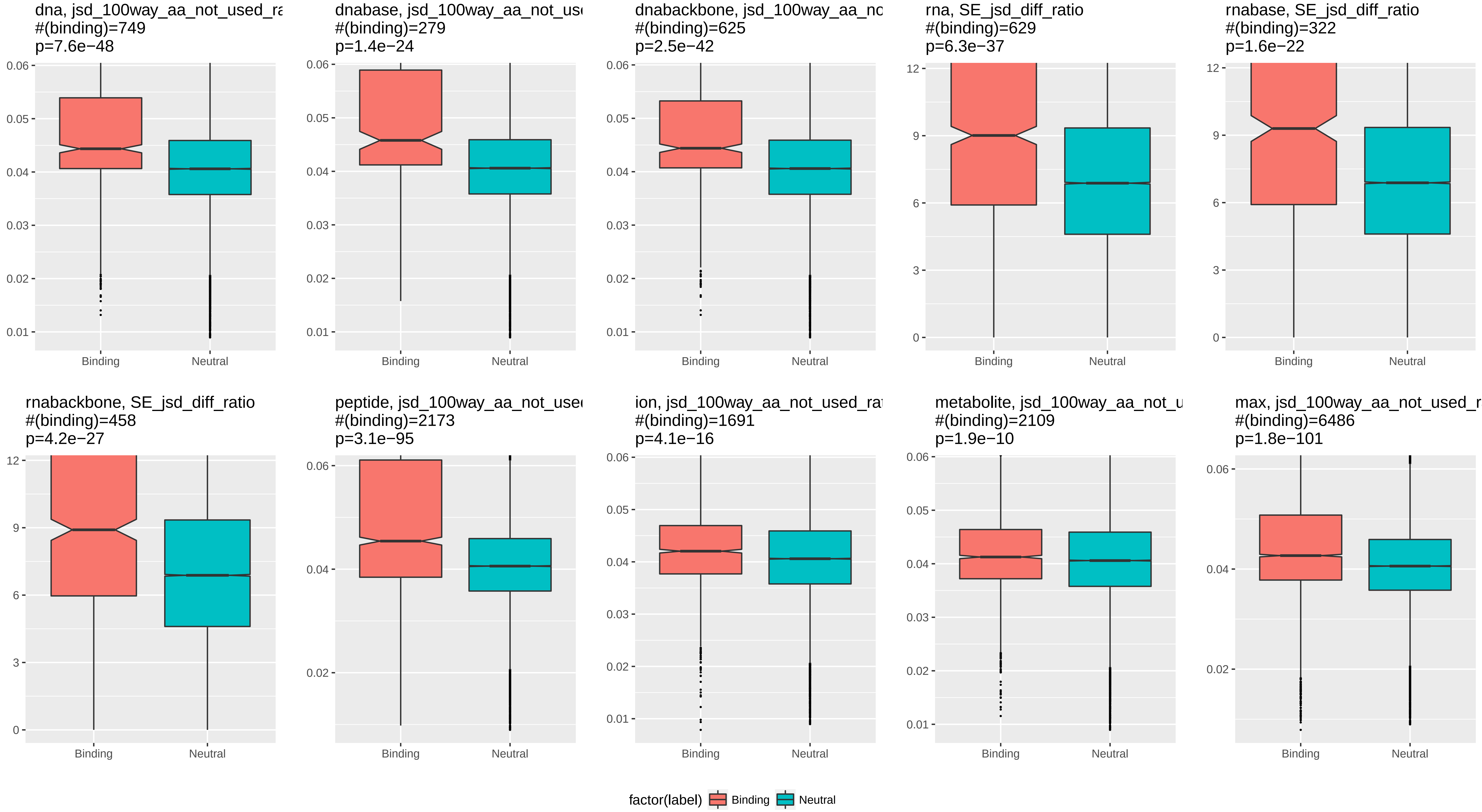
dna, jsd_100way_aa_not_used_ra
#(binding)=749
p=7.6e−48
dnabase, jsd_100way_aa_not_us
#(binding)=279
p=1.4e−24
dnabackbone, jsd_100way_aa_nc
#(binding)=625
p=2.5e−42
rna, SE_jsd_diff_ratio
#(binding)=629
p=6.3e−37
rnabase, SE_jsd_diff_ratio
#(binding)=322
p=1.6e−22
rnabackbone, SE_jsd_diff_ratio
#(binding)=458
p=4.2e−27
peptide, jsd_100way_aa_not_use
#(binding)=2173
p=3.1e−95
ion, jsd_100way_aa_not_used_ra
#(binding)=1691
p=4.1e−16
metabolite, jsd_100way_aa_not_u
#(binding)=2109
p=1.9e−10
max, jsd_100way_aa_not_used_r
#(binding)=6486
p=1.8e−101
0.01
0.02
0.03
0.04
0.05
0.06
0
3
6
9
12
Binding
Neutral
factor(label)
Binding
Neutral