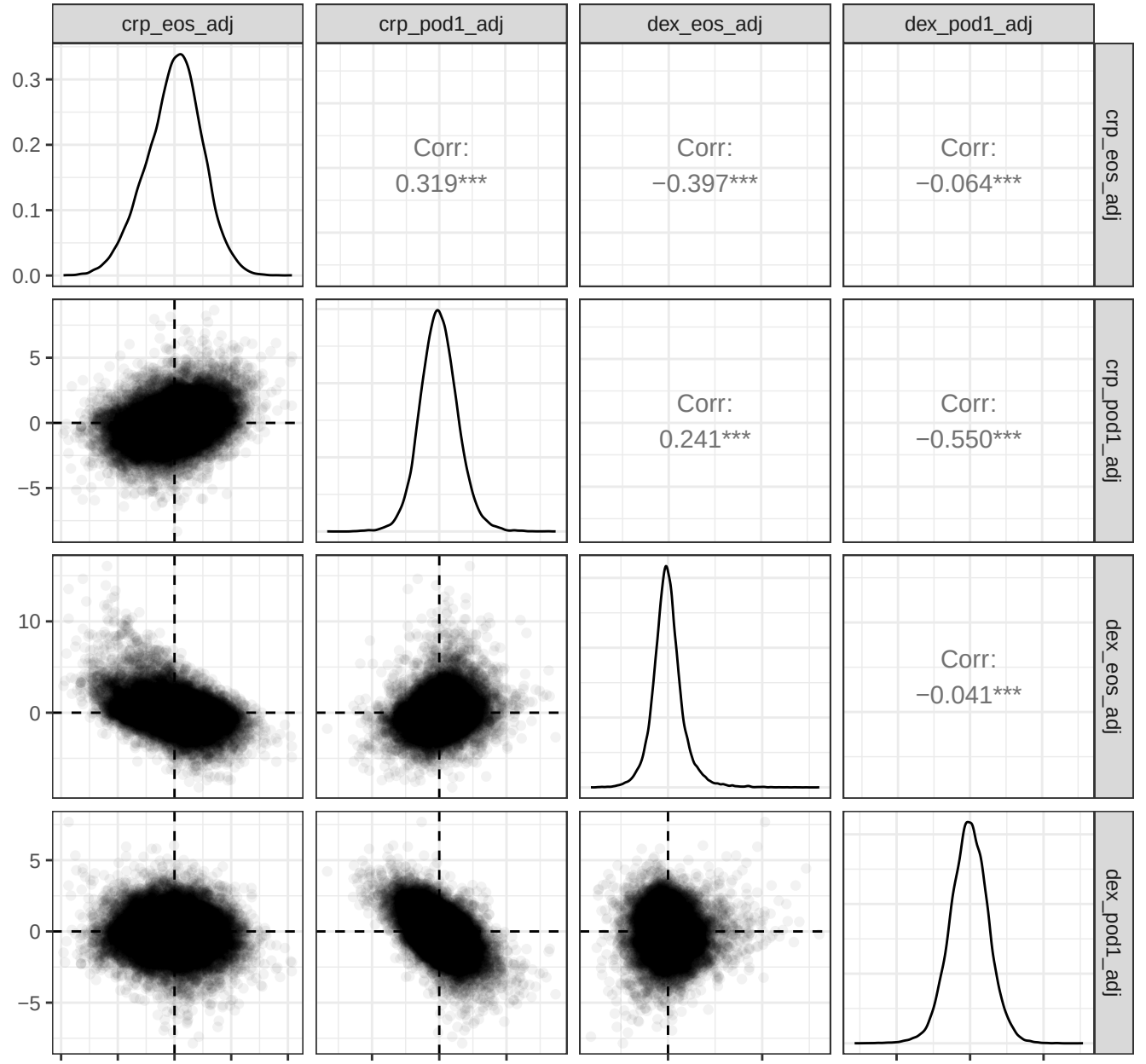
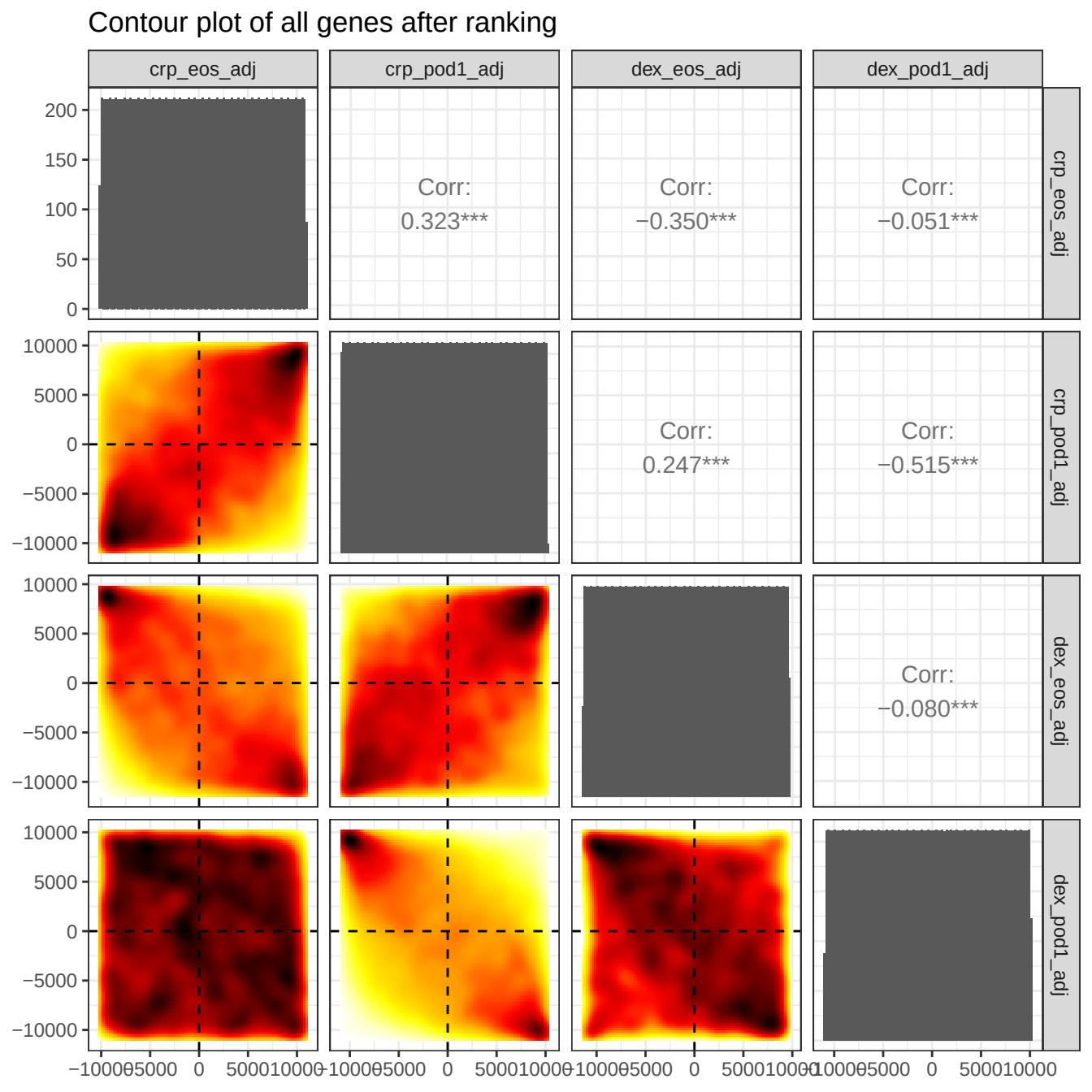
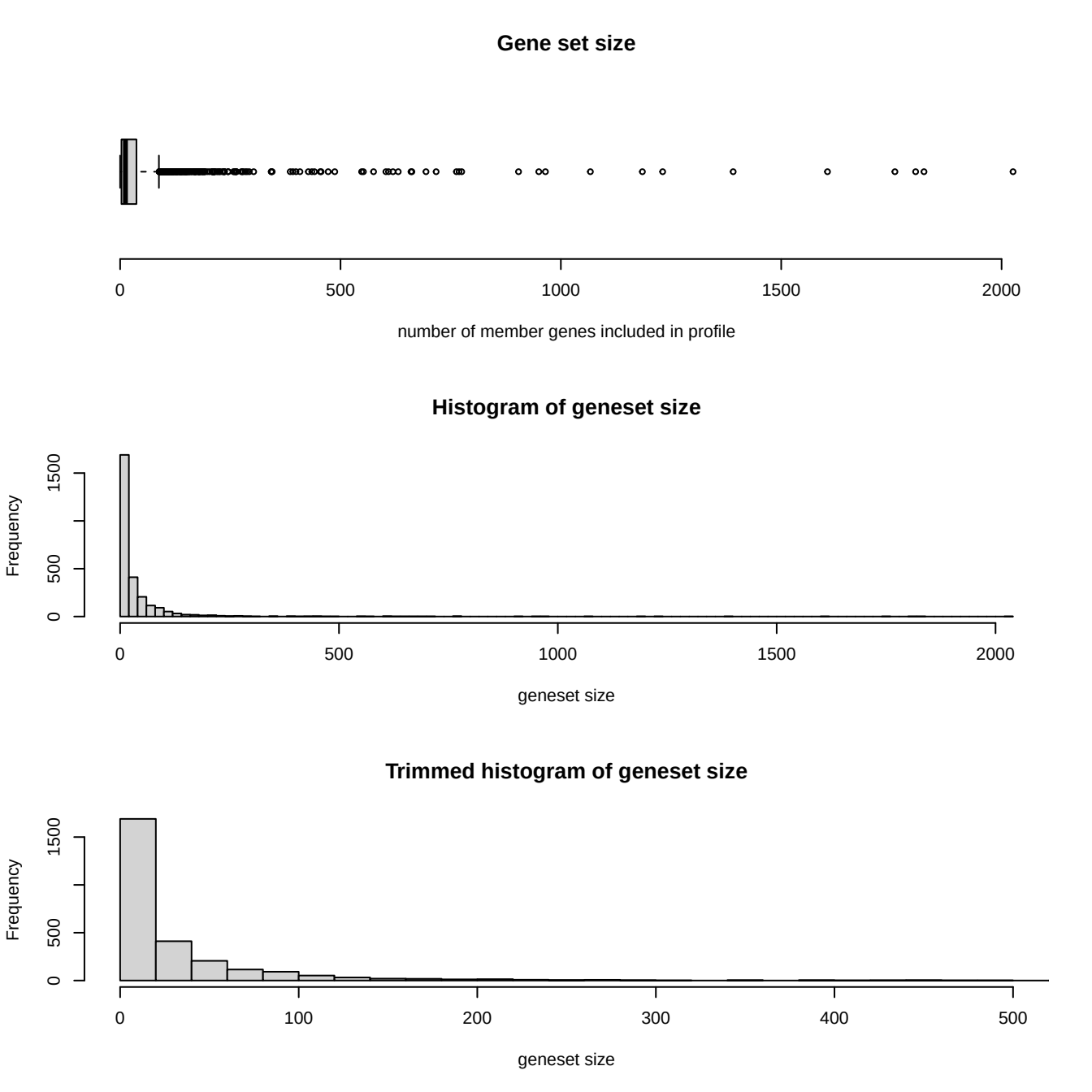
Scatterplot of all genes

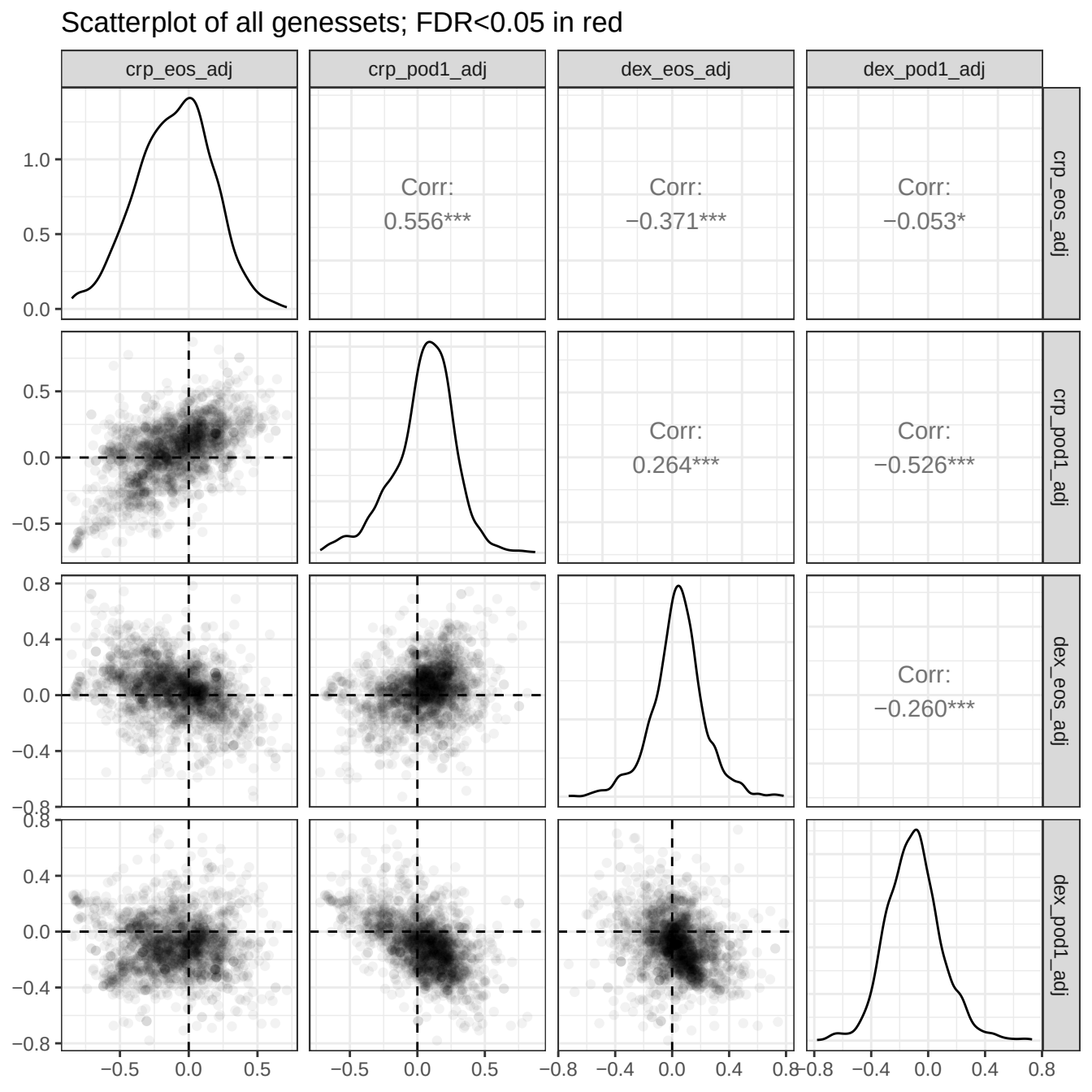


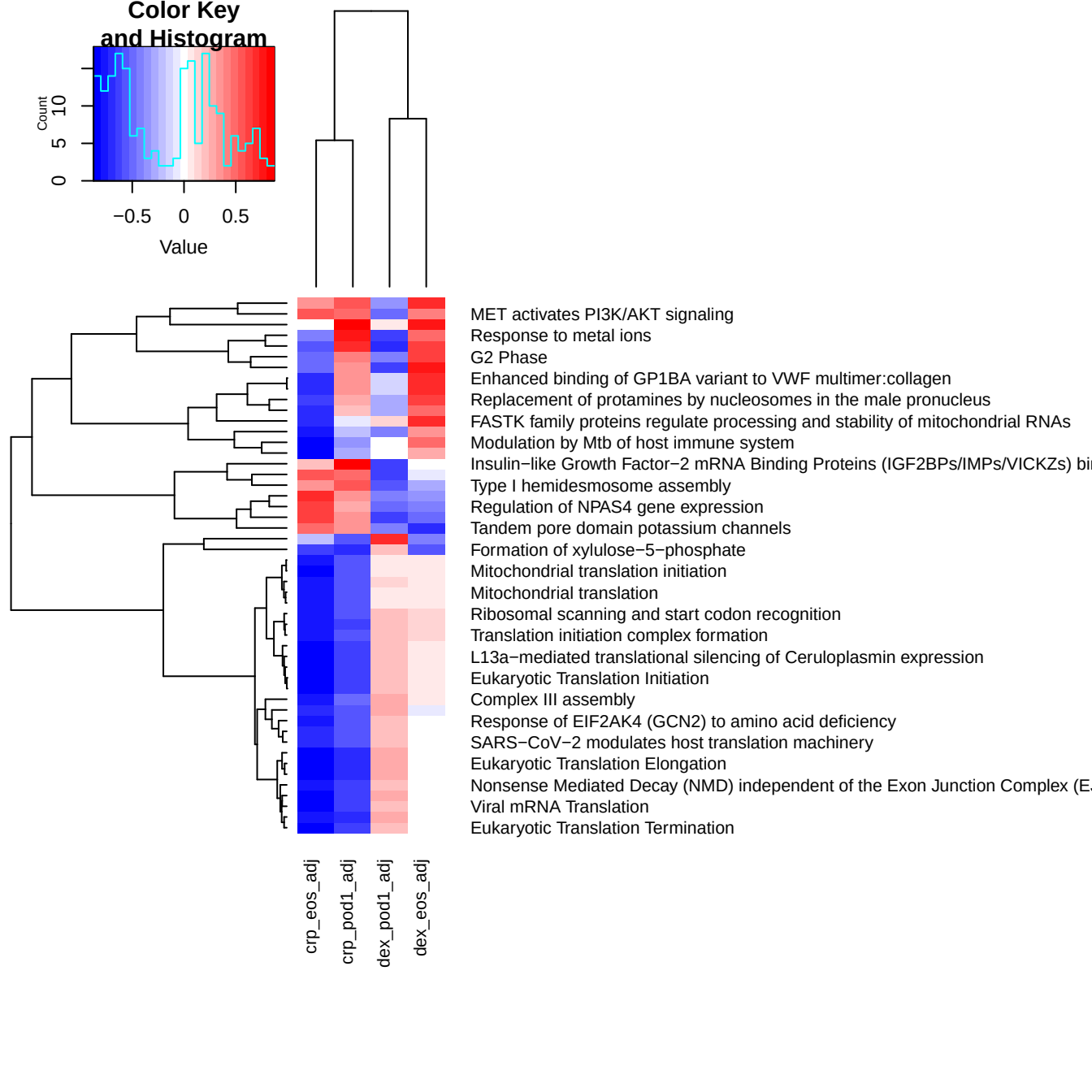

Contour plot of all genes after ranking
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.323***
Corr:
−0.350***
Corr:
−0.051***
Corr:
0.247***
Corr:
−0.515***
Corr:
−0.080***
200
150
100
50
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

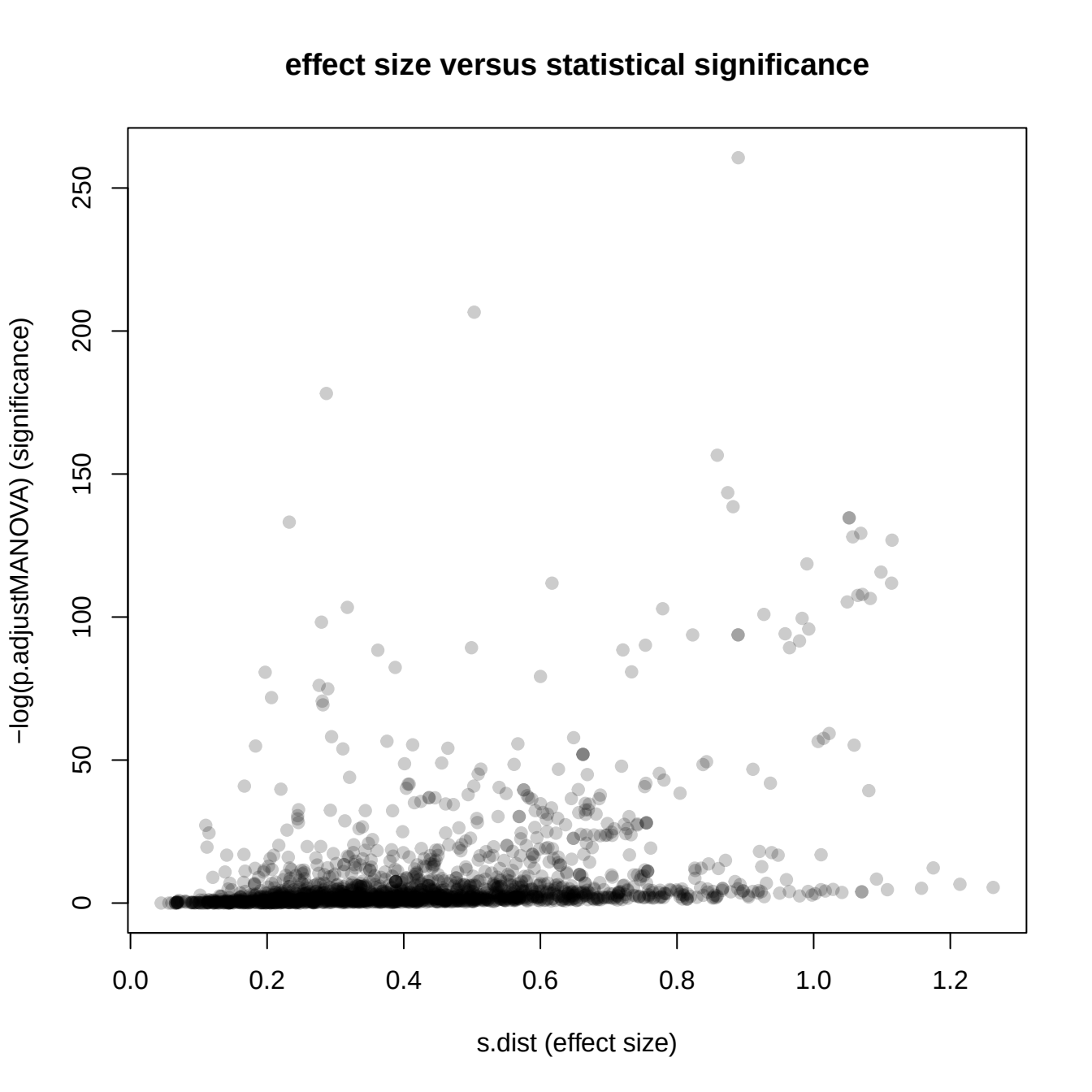
	crp_eos_adj	crp_pod1_adj	dex_eos_adj	dex_pod1_adj	Number of genes in each sector
1	−1	−1	−1	−1	1206
2	1	−1	−1	−1	1111
3	−1	0	−1	−1	1
4	−1	1	−1	−1	728
5	1	1	−1	−1	2526
6	−1	−1	1	−1	1169
7	1	−1	1	−1	298
8	−1	1	1	−1	2000
9	1	1	1	−1	1930
10	1	1	−1	0	1
11	−1	−1	−1	1	2167
12	0	−1	−1	1	1
13	1	−1	−1	1	2317
14	−1	1	−1	1	215
15	1	1	−1	1	1122
16	−1	−1	0	1	1
17	−1	−1	1	1	1915
18	1	−1	1	1	687
19	−1	1	1	1	758
20	1	1	1	1	976

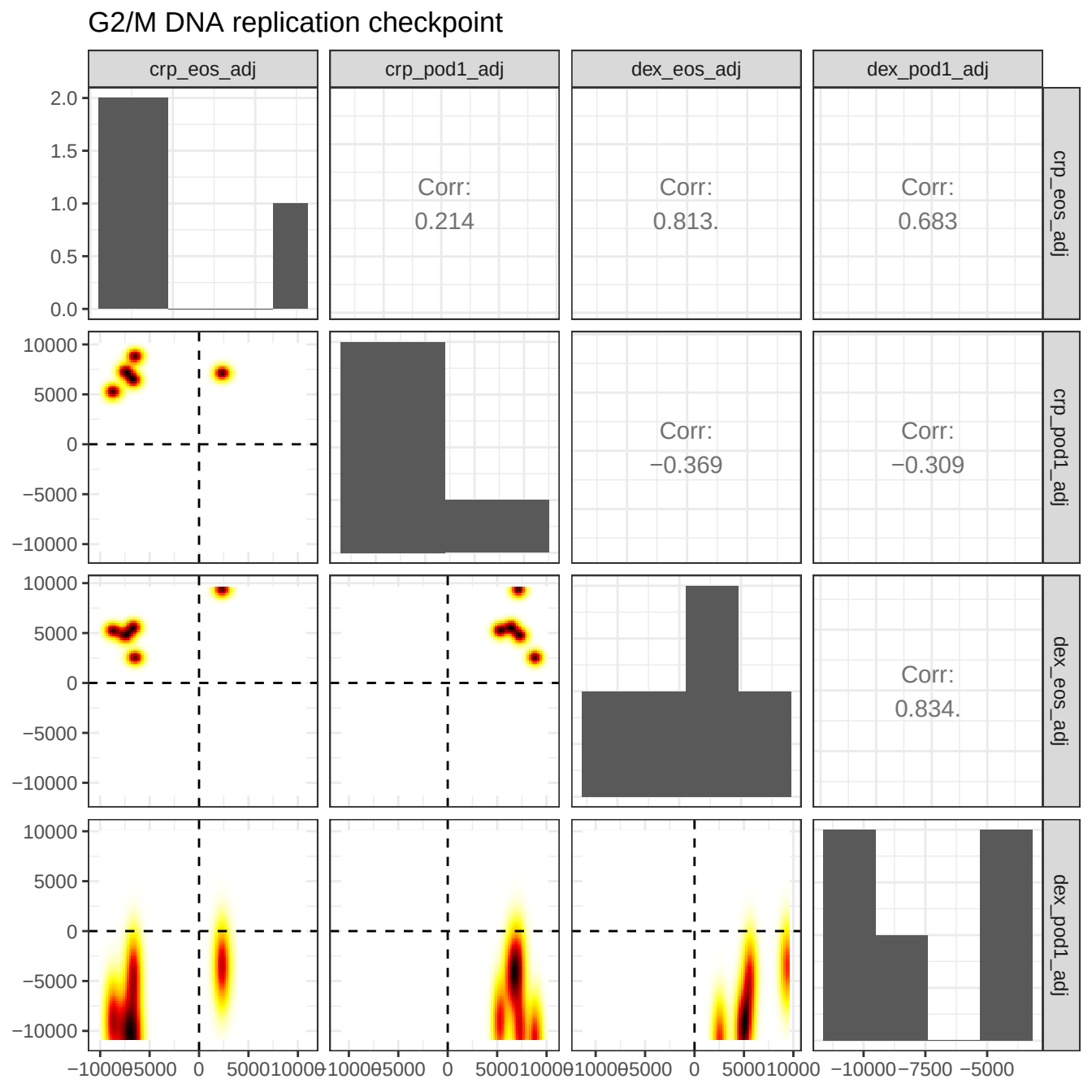

Gene set size
0
500
1000
1500
2000
number of member genes included in profile
Histogram of geneset size
Frequency
0
500
1500
0
500
1000
1500
2000
geneset size
Trimmed histogram of geneset size
Frequency
0
500
1500
0
100
200
300
400
500
geneset size

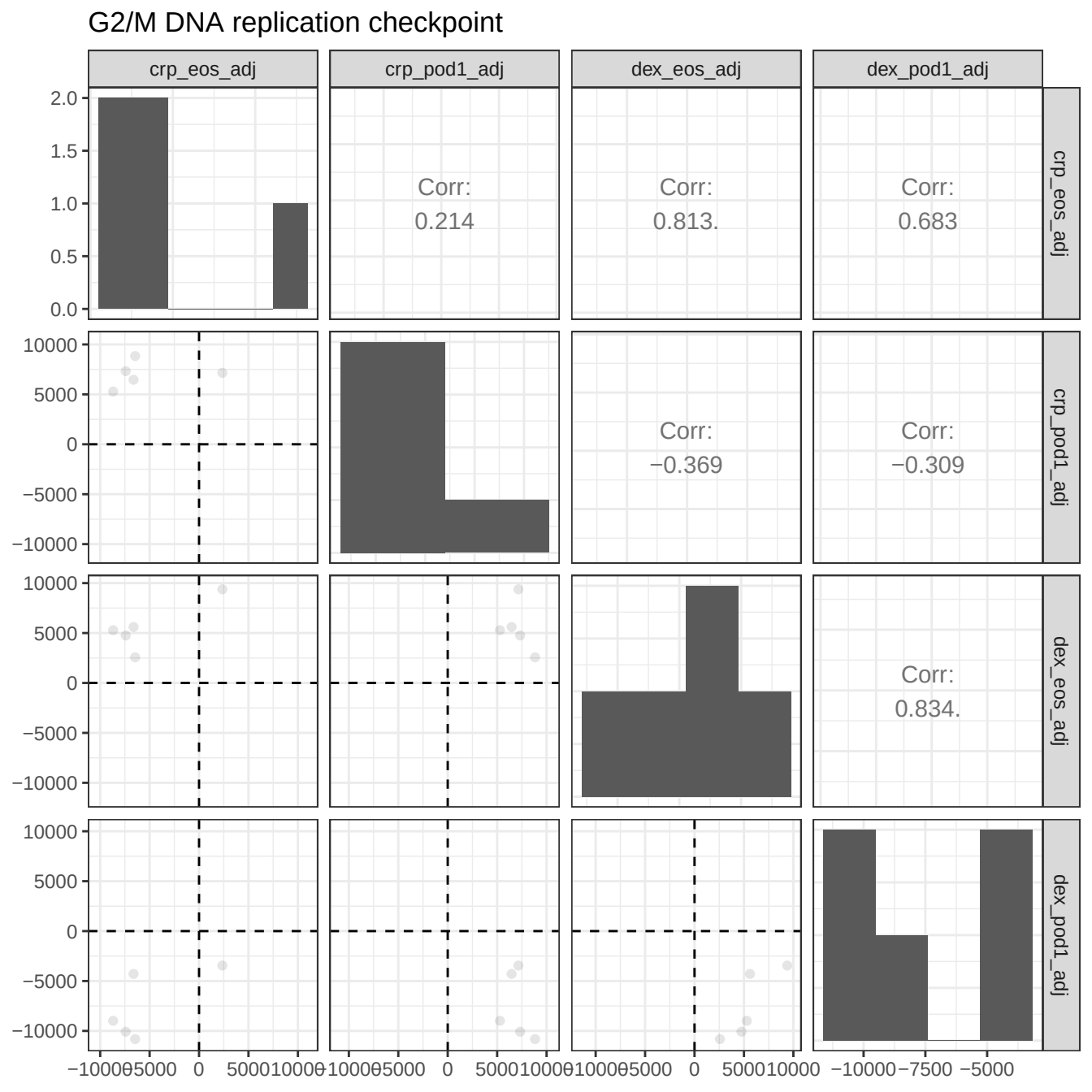
	s.crp_eos_adj	s.crp_pod1_adj	s.dex_eos_adj	s.dex_pod1_adj	Number of gene sets in each sector
1	−1	−1	−1	−1	68
2	1	−1	−1	−1	1
3	−1	1	−1	−1	23
4	1	1	−1	−1	61
5	−1	−1	1	−1	97
6	−1	1	1	−1	297
7	1	1	1	−1	56
8	−1	−1	−1	1	51
9	1	−1	−1	1	7
10	−1	1	−1	1	3
11	1	1	−1	1	9
12	−1	−1	1	1	84
13	−1	1	1	1	7
14	1	1	1	1	6

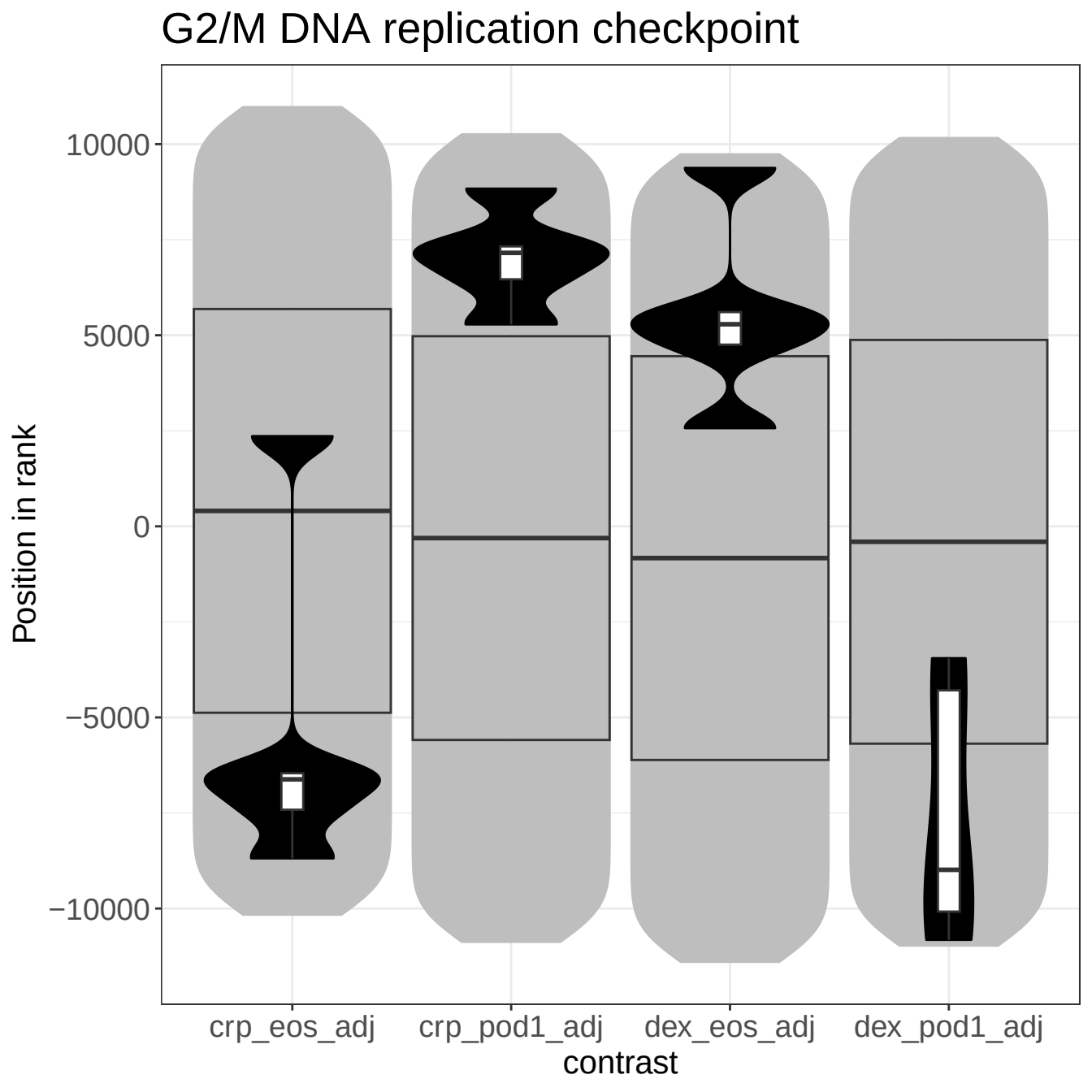

Scatterplot of all genessets; FDR<0.05 in red
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.556***
Corr:
−0.371***
Corr:
−0.053*
Corr:
0.264***
Corr:
−0.526***
Corr:
−0.260***

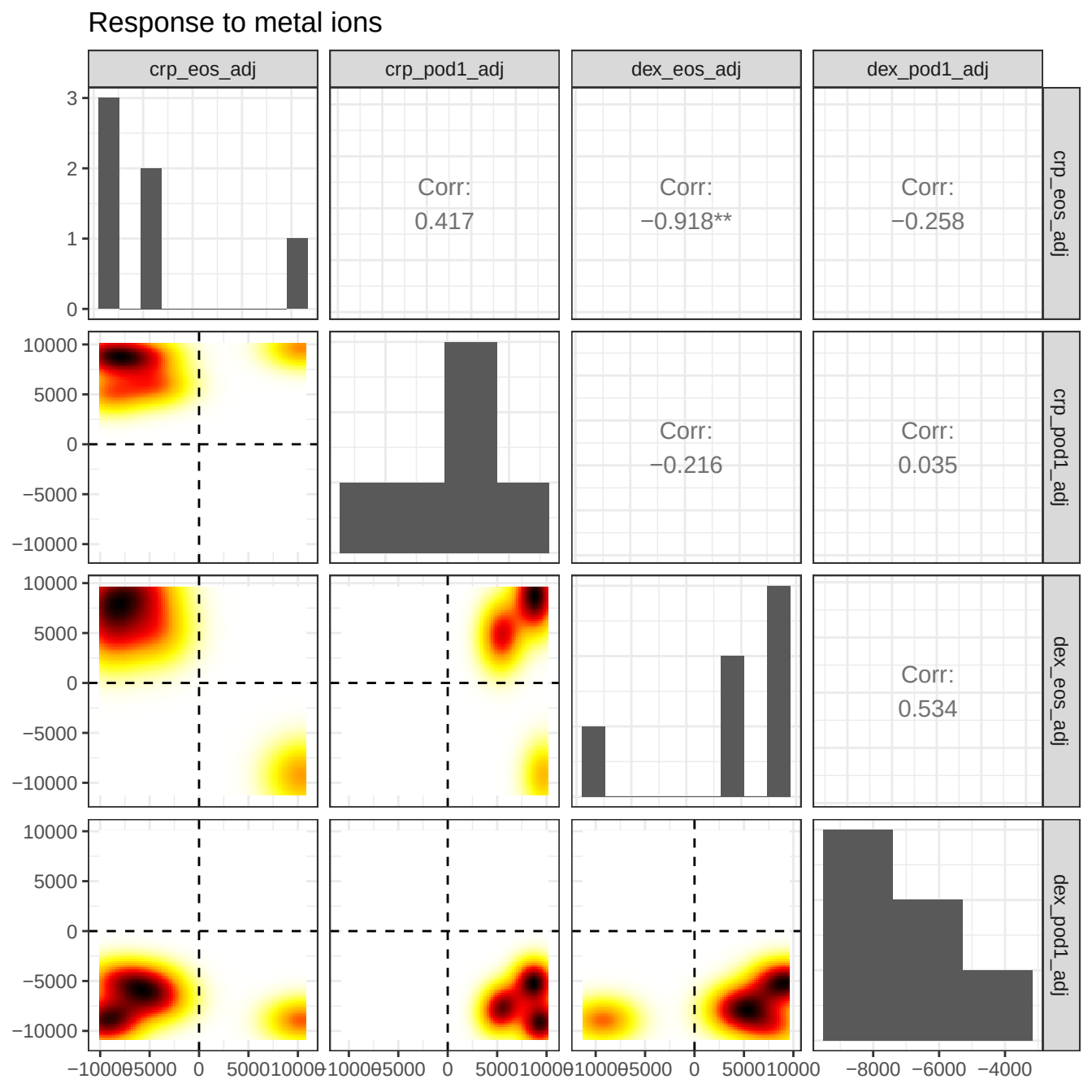

Color Key and Histogram
Count
0
5
10
−0.5
0
0.5
Value
MET activates PI3K/AKT signaling
Response to metal ions
G2 Phase
Enhanced binding of GP1BA variant to VWF multimer:collagen
Replacement of protamines by nucleosomes in the male pronucleus
FASTK family proteins regulate processing and stability of mitochondrial RNAs
Modulation by Mtb of host immune system
Insulin−like Growth Factor−2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bi
Type I hemidesmosome assembly
Regulation of NPAS4 gene expression
Tandem pore domain potassium channels
Formation of xylulose−5−phosphate
Mitochondrial translation initiation
Mitochondrial translation
Ribosomal scanning and start codon recognition
Translation initiation complex formation
L13a−mediated translational silencing of Ceruloplasmin expression
Eukaryotic Translation Initiation
Complex III assembly
Response of EIF2AK4 (GCN2) to amino acid deficiency
SARS−CoV−2 modulates host translation machinery
Eukaryotic Translation Elongation
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (E
Viral mRNA Translation
Eukaryotic Translation Termination
crp_eos_adj
crp_pod1_adj
dex_pod1_adj
dex_eos_adj

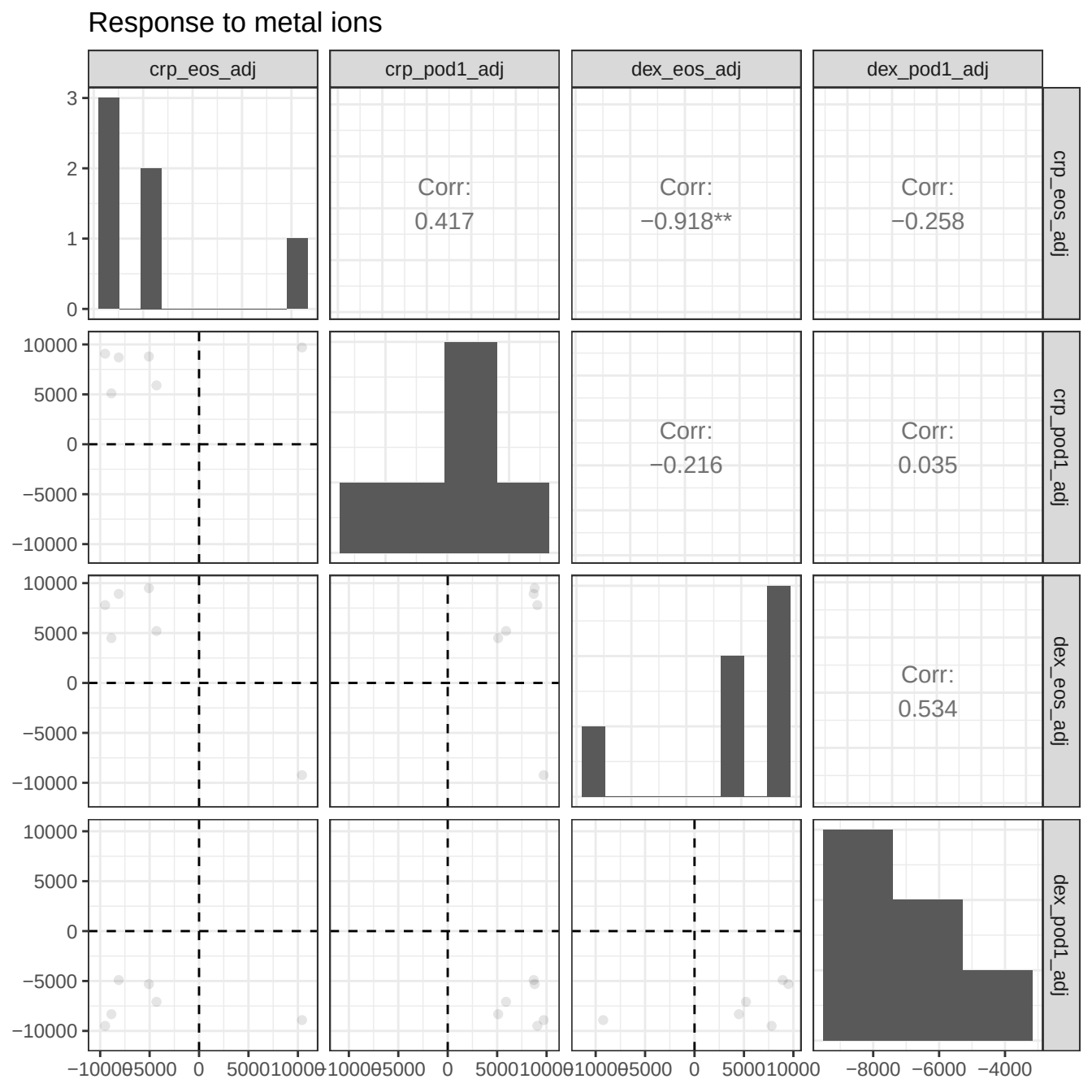

effect size versus statistical significance
−log(p.adjustMANOVA) (significance)
0
50
100
150
200
250
0.0
0.2
0.4
0.6
0.8
1.0
1.2
s.dist (effect size)

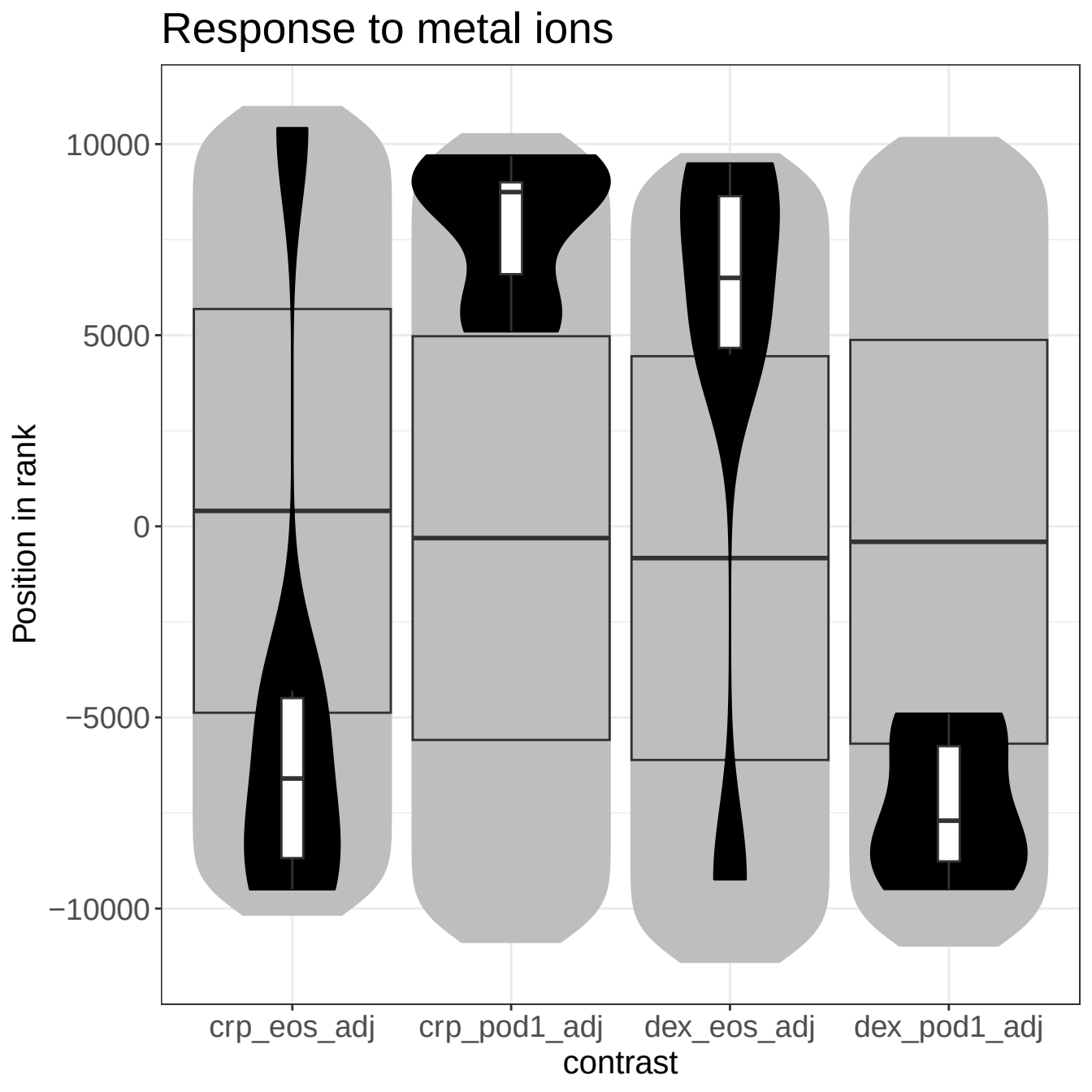

G2/M DNA replication checkpoint
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.214
Corr:
0.813.
Corr:
0.683
Corr:
−0.369
Corr:
−0.309
Corr:
0.834.
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−10000
−7500
−5000

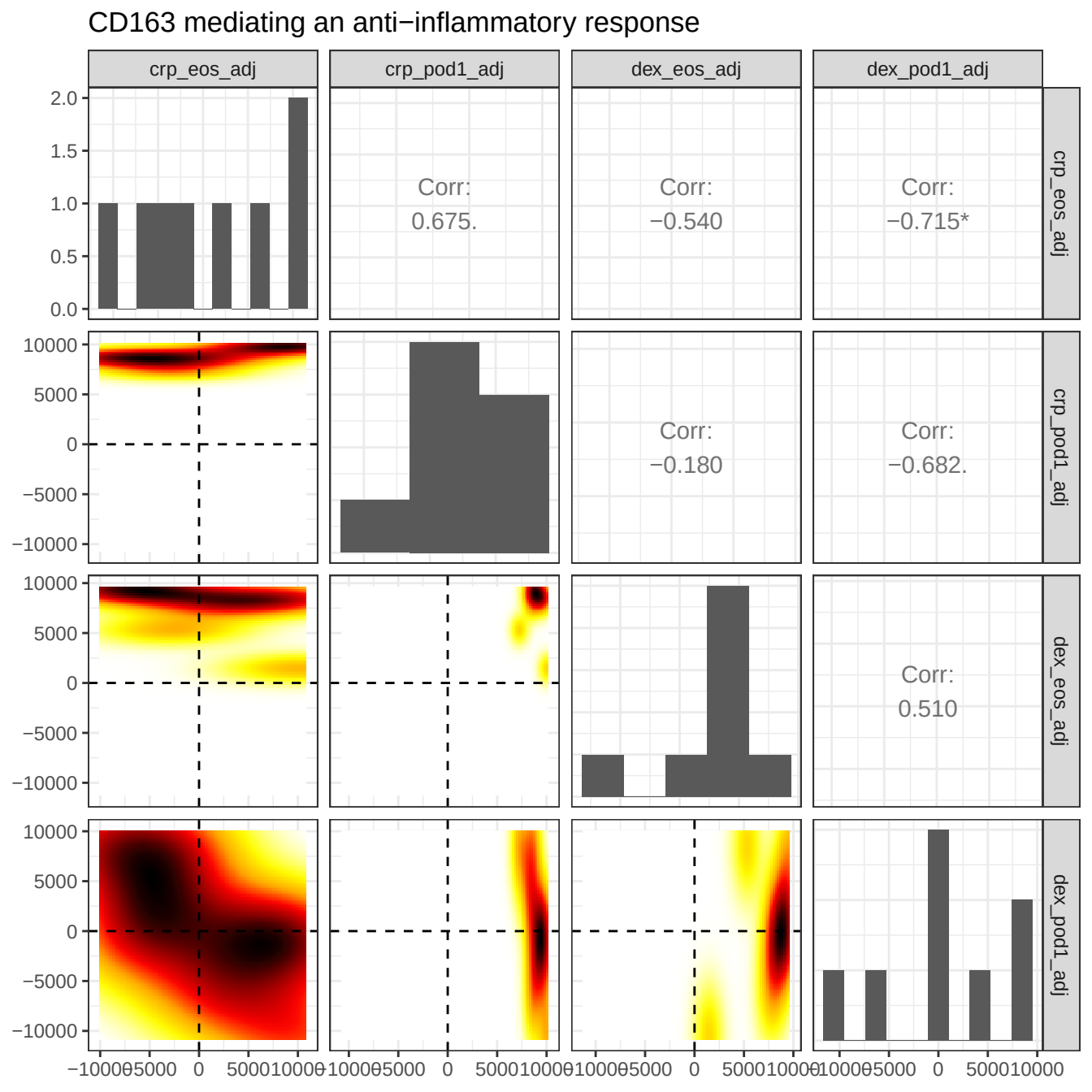

G2/M DNA replication checkpoint
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.214
Corr:
0.813.
Corr:
0.683
Corr:
−0.369
Corr:
−0.309
Corr:
0.834.
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000−5000 0 5000 10000
−10000−7500 −5000

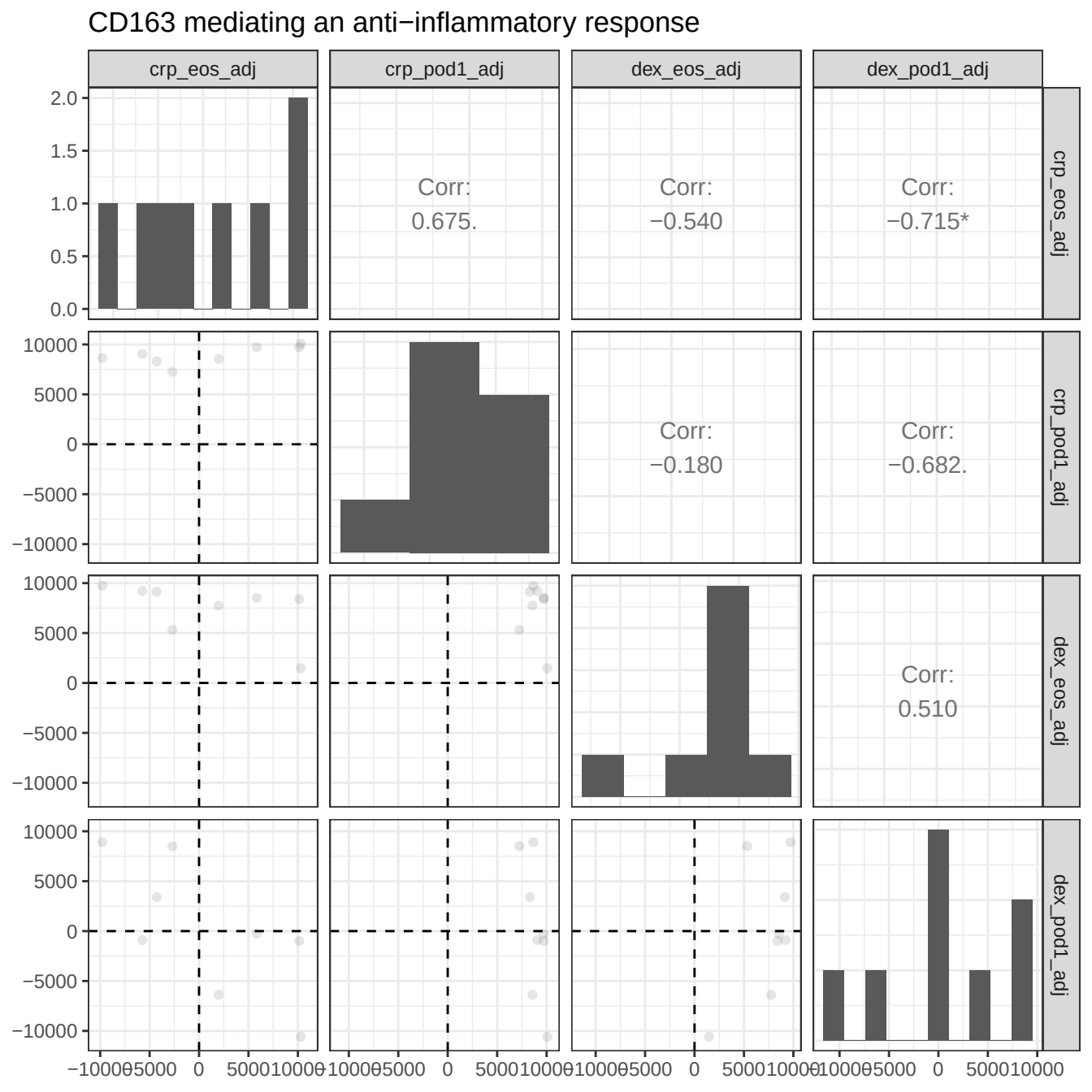

G2/M DNA replication checkpoint
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

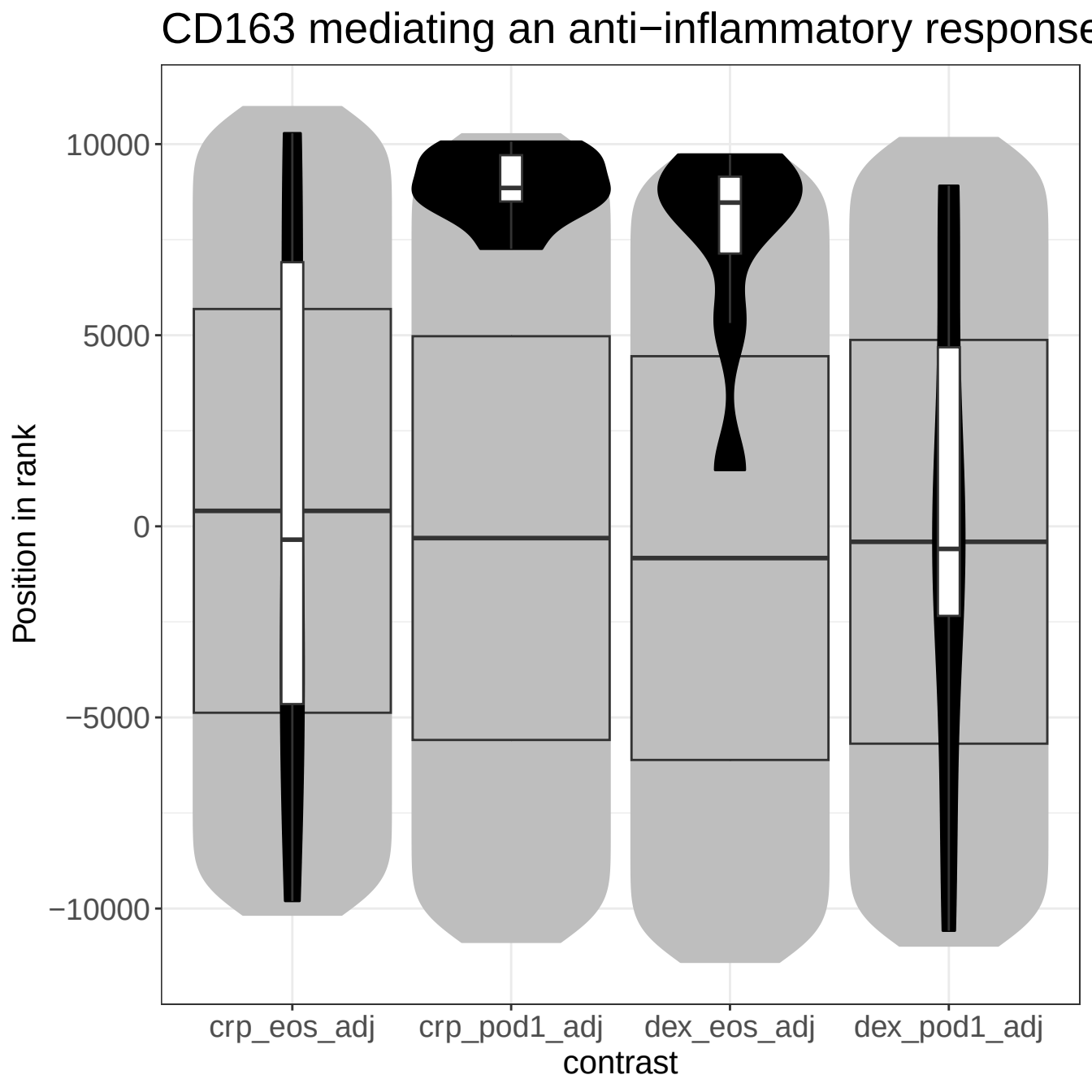

Response to metal ions
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.417
Corr:
−0.918**
Corr:
−0.258
Corr:
−0.216
Corr:
0.035
Corr:
0.534
−8000
−6000
−4000

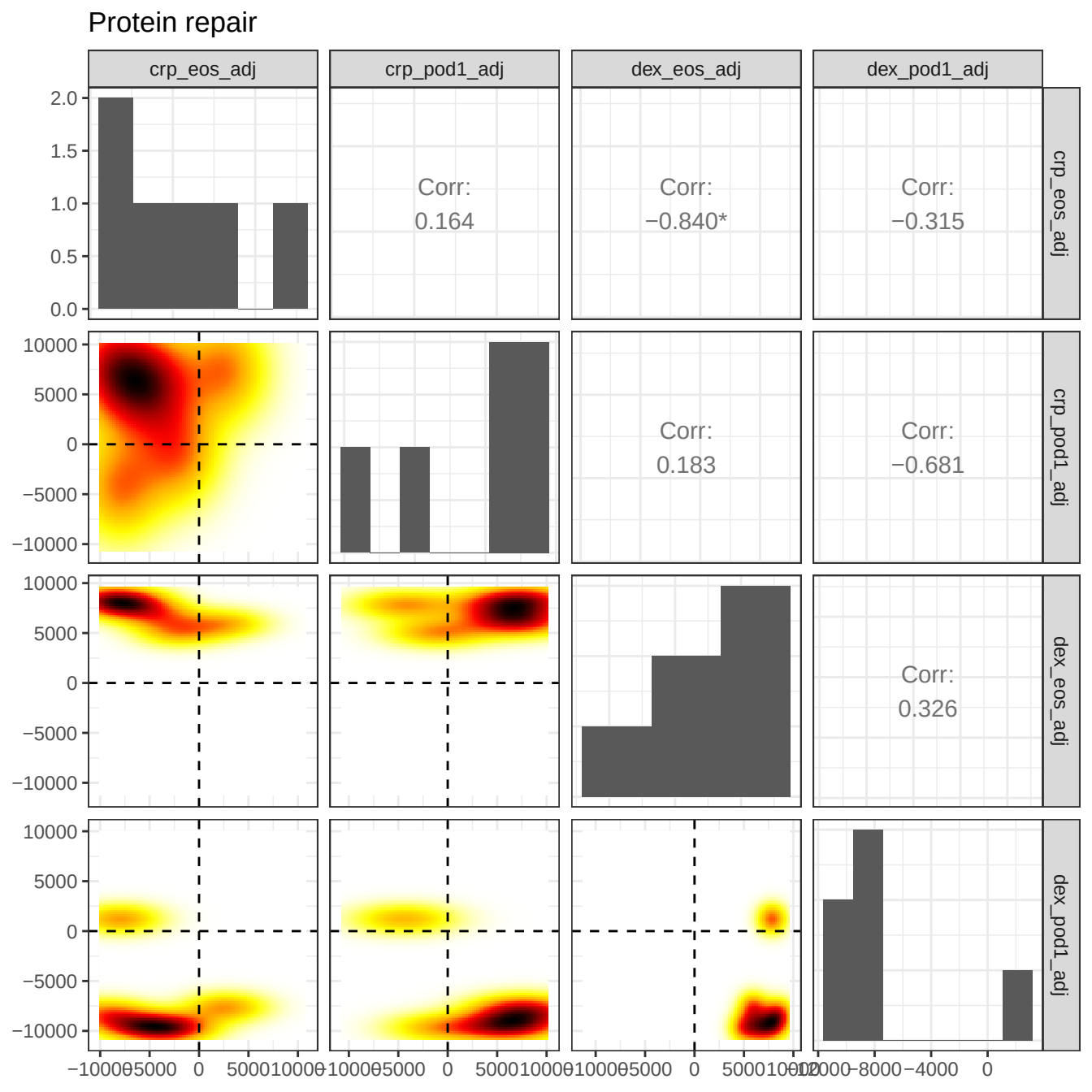

Response to metal ions
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.417
Corr:
−0.918**
Corr:
−0.258
Corr:
−0.216
Corr:
0.035
Corr:
0.534
3
2
1
0
10000
5000
0
−5000
−10000
−8000
−6000
−4000

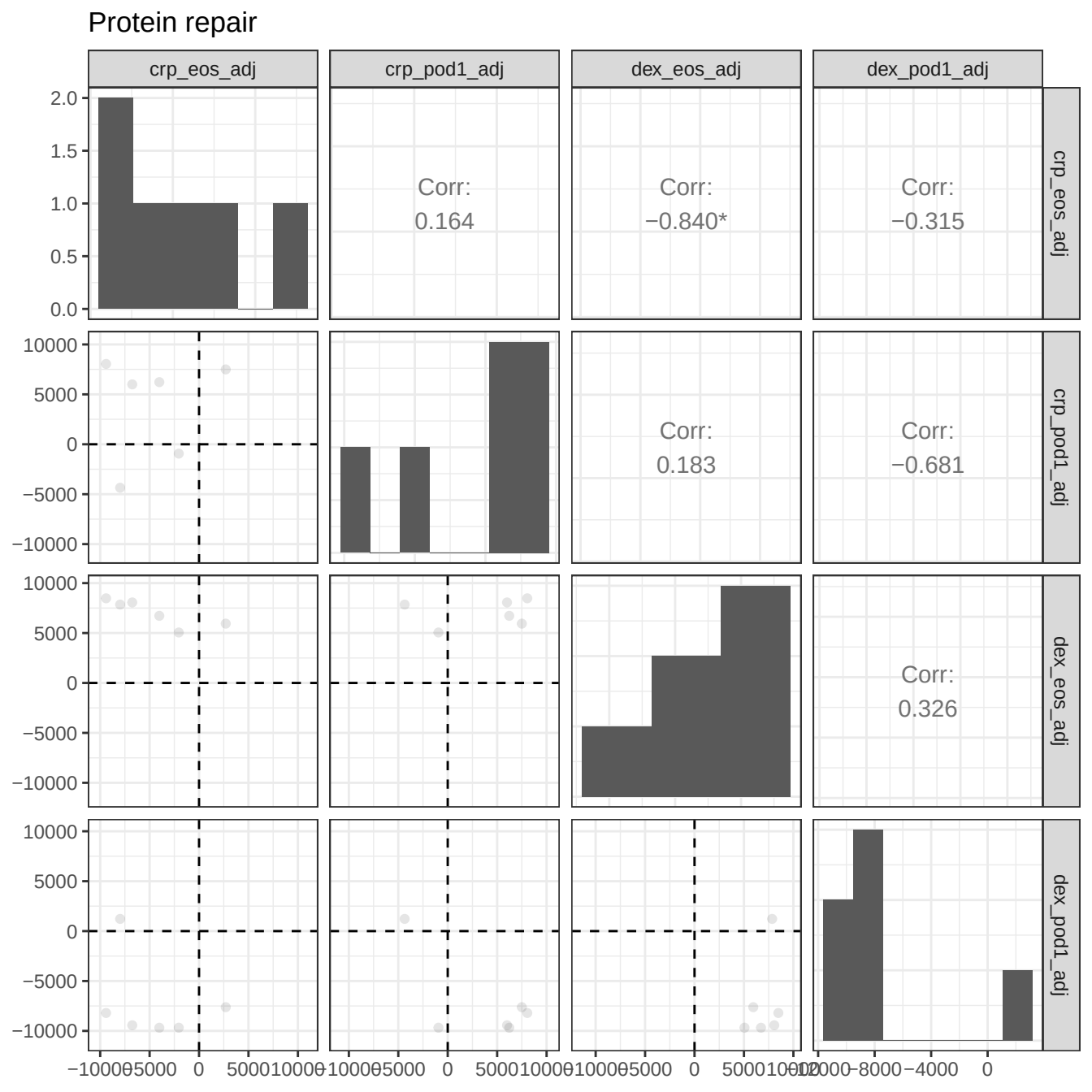

Response to metal ions
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

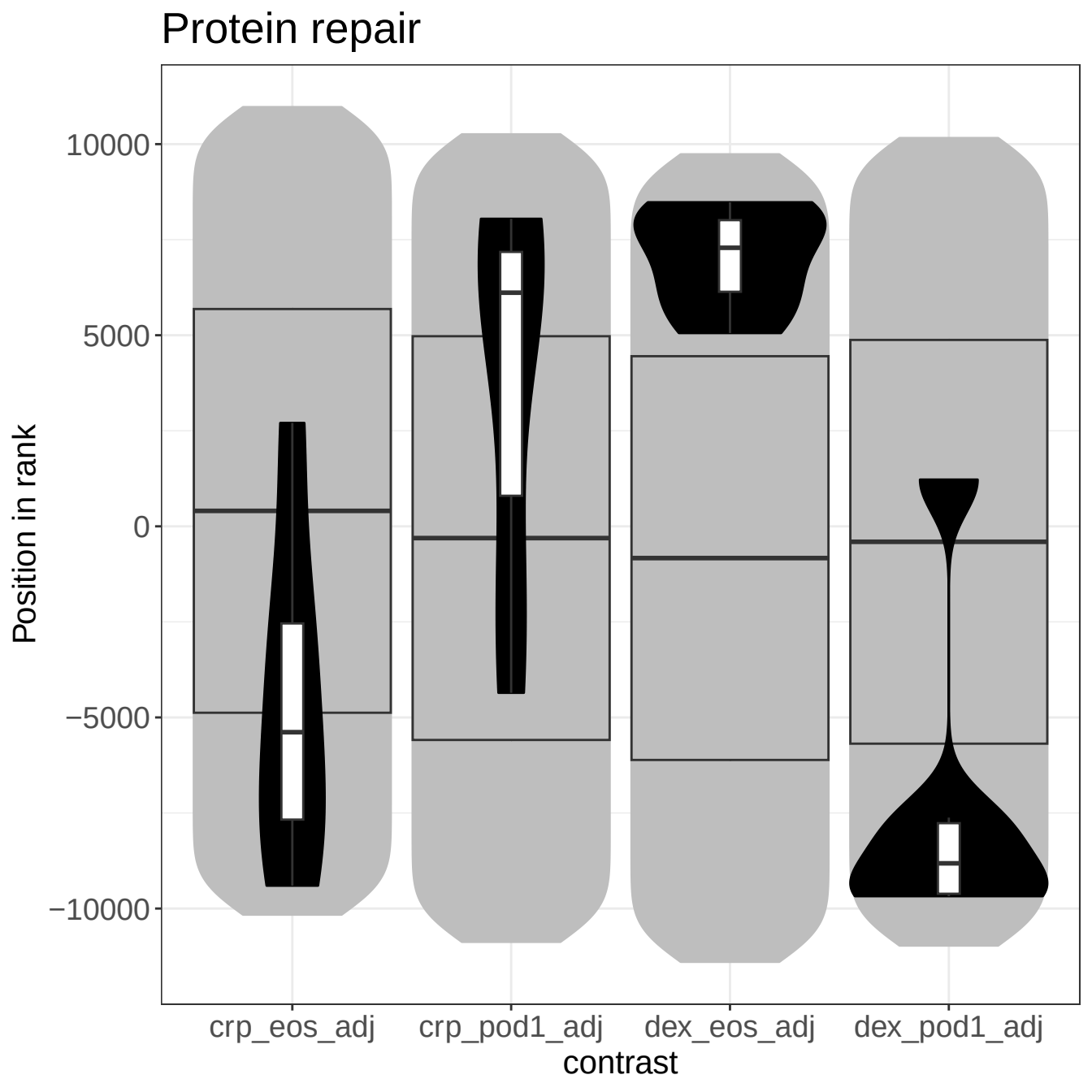

CD163 mediating an anti−inflammatory response
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.675.
Corr:
−0.540
Corr:
−0.715*
Corr:
−0.180
Corr:
−0.682.
Corr:
0.510
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

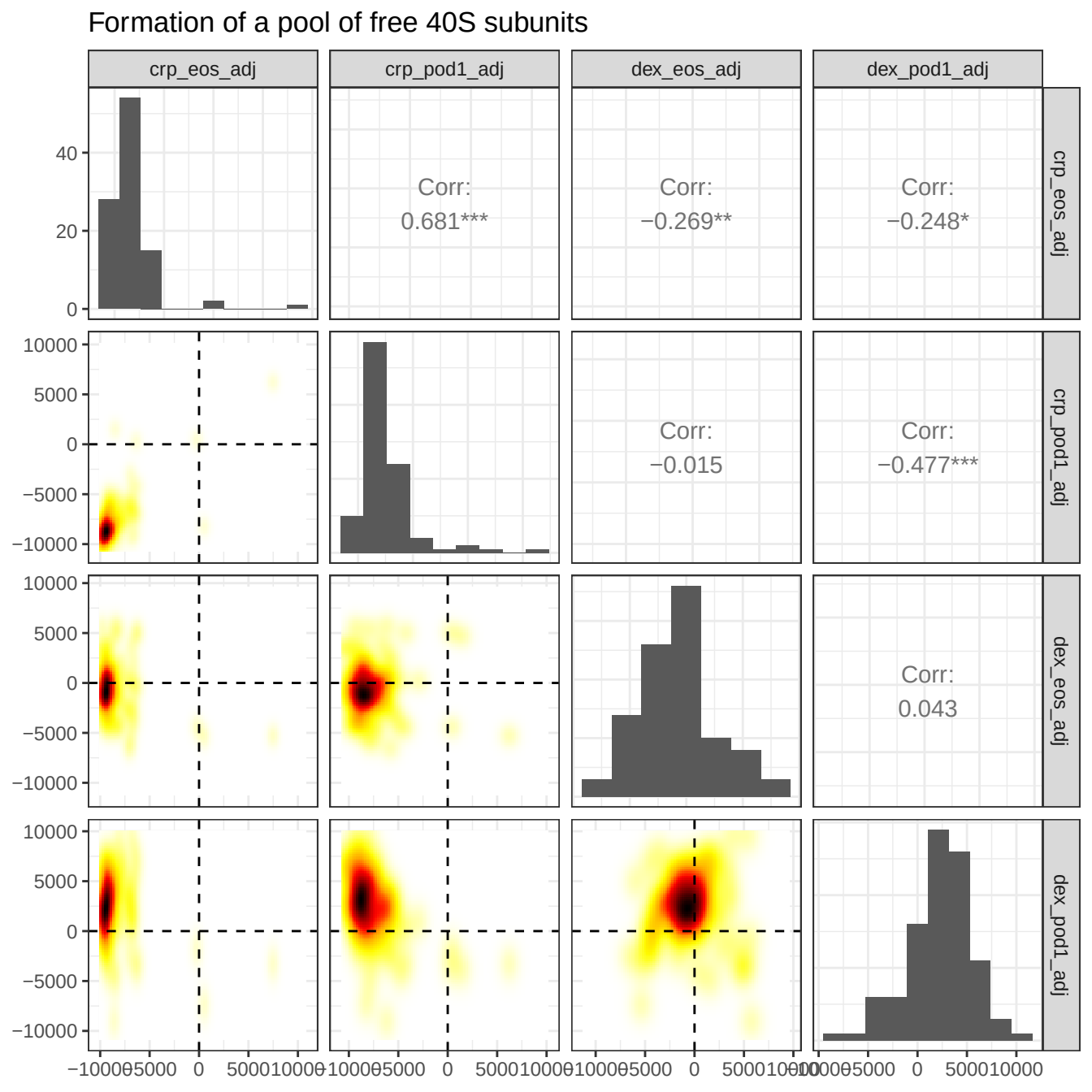

CD163 mediating an anti−inflammatory response
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.675.
Corr:
−0.540
Corr:
−0.715*
Corr:
−0.180
Corr:
−0.682.
Corr:
0.510
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000

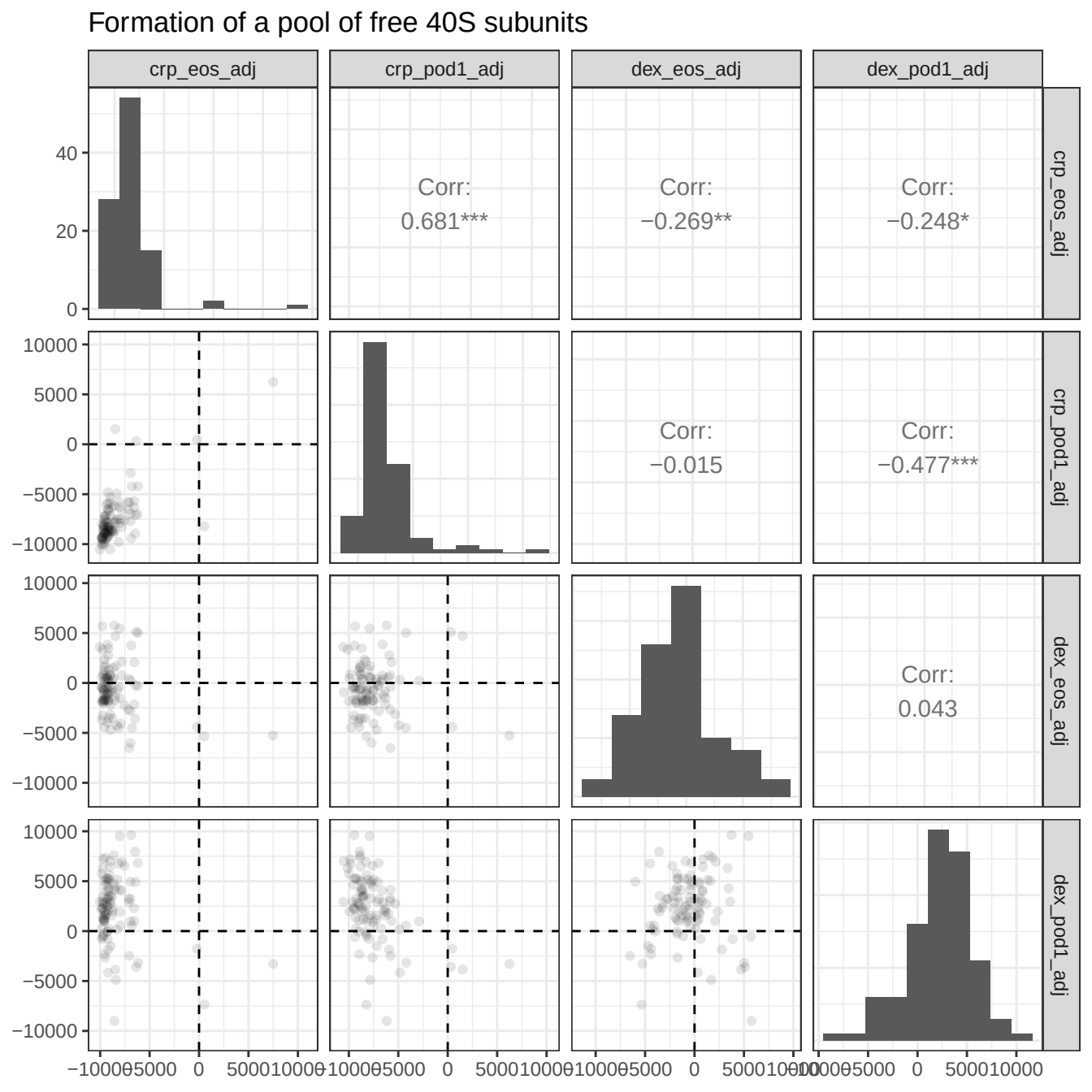

CD163 mediating an anti−inflammatory response
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

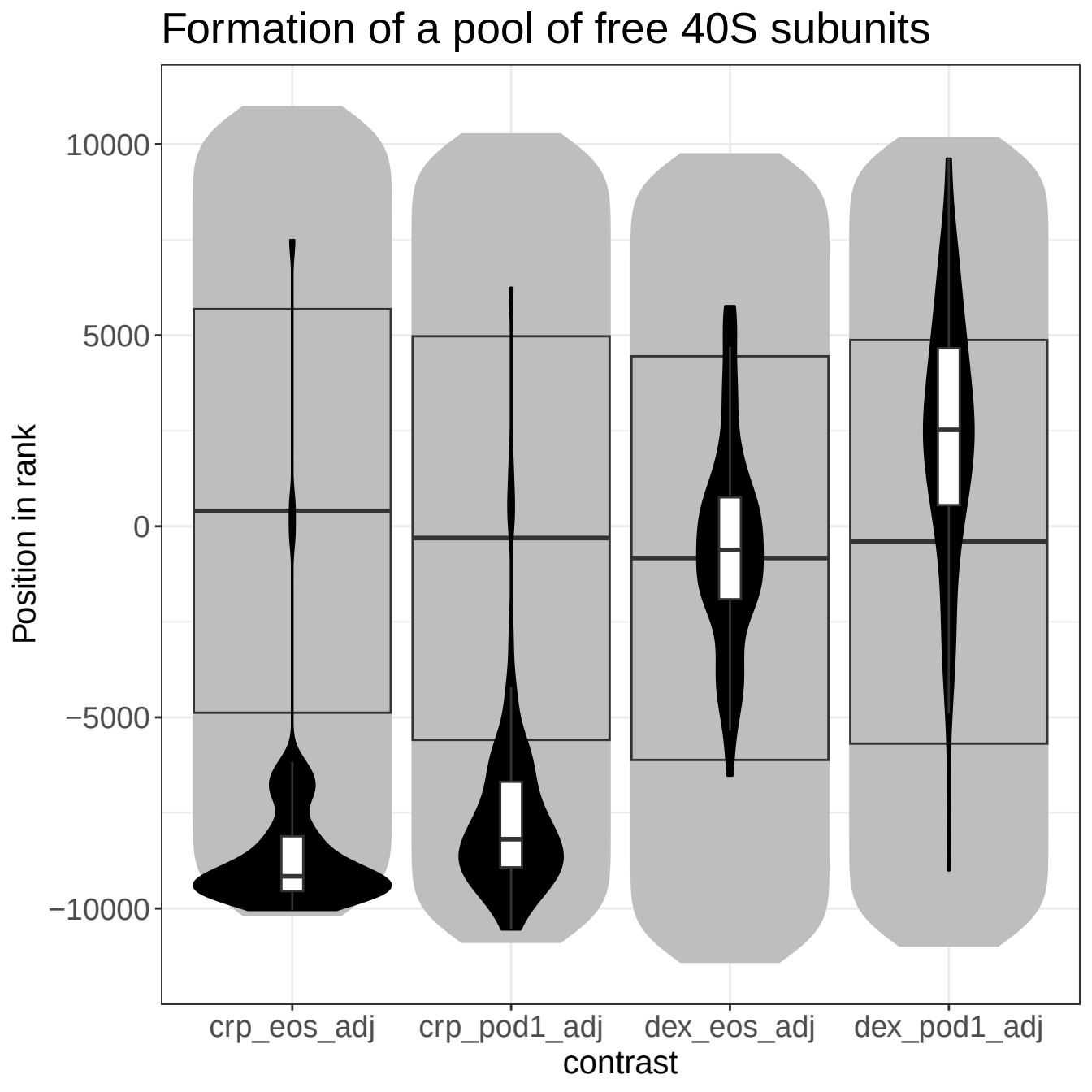

Protein repair
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.164
Corr:
−0.840*
Corr:
−0.315
Corr:
0.183
Corr:
−0.681
Corr:
0.326
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−12000
−8000
−4000
0

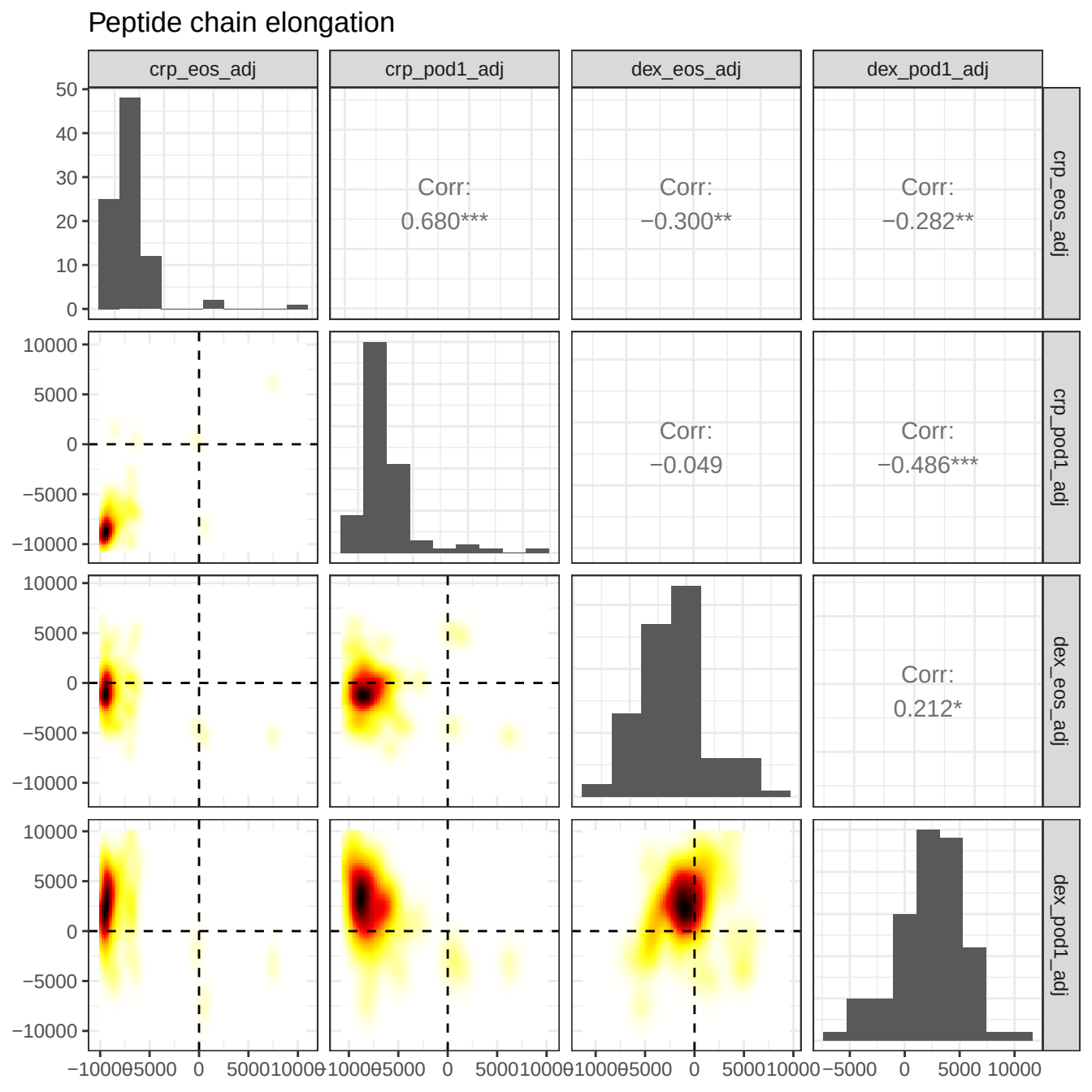

Protein repair
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.164
Corr:
−0.840*
Corr:
−0.315
Corr:
0.183
Corr:
−0.681
Corr:
0.326

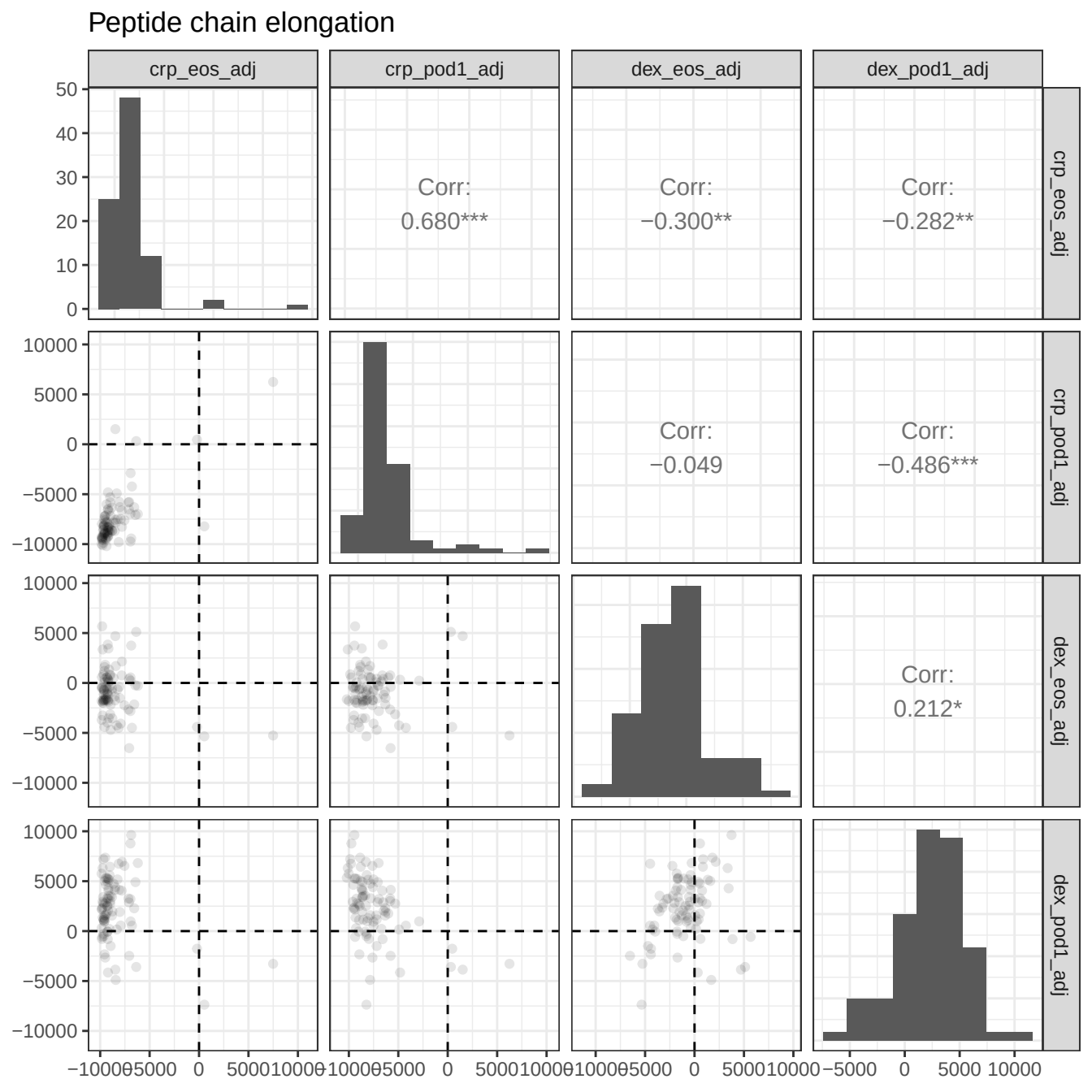

Protein repair
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

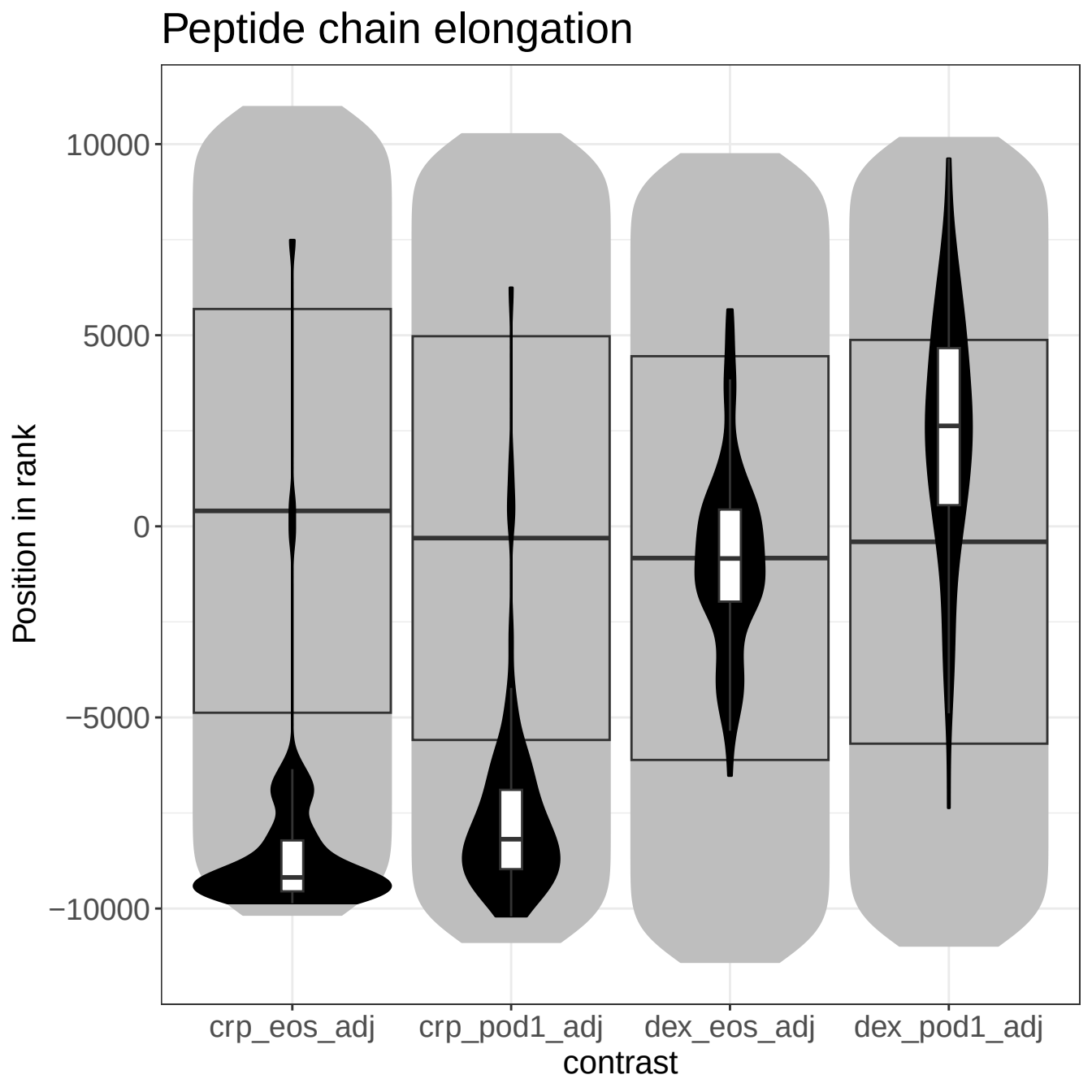

Formation of a pool of free 40S subunits
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.681***
Corr:
−0.269**
Corr:
−0.248*
Corr:
−0.015
Corr:
−0.477***
Corr:
0.043
40
20
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

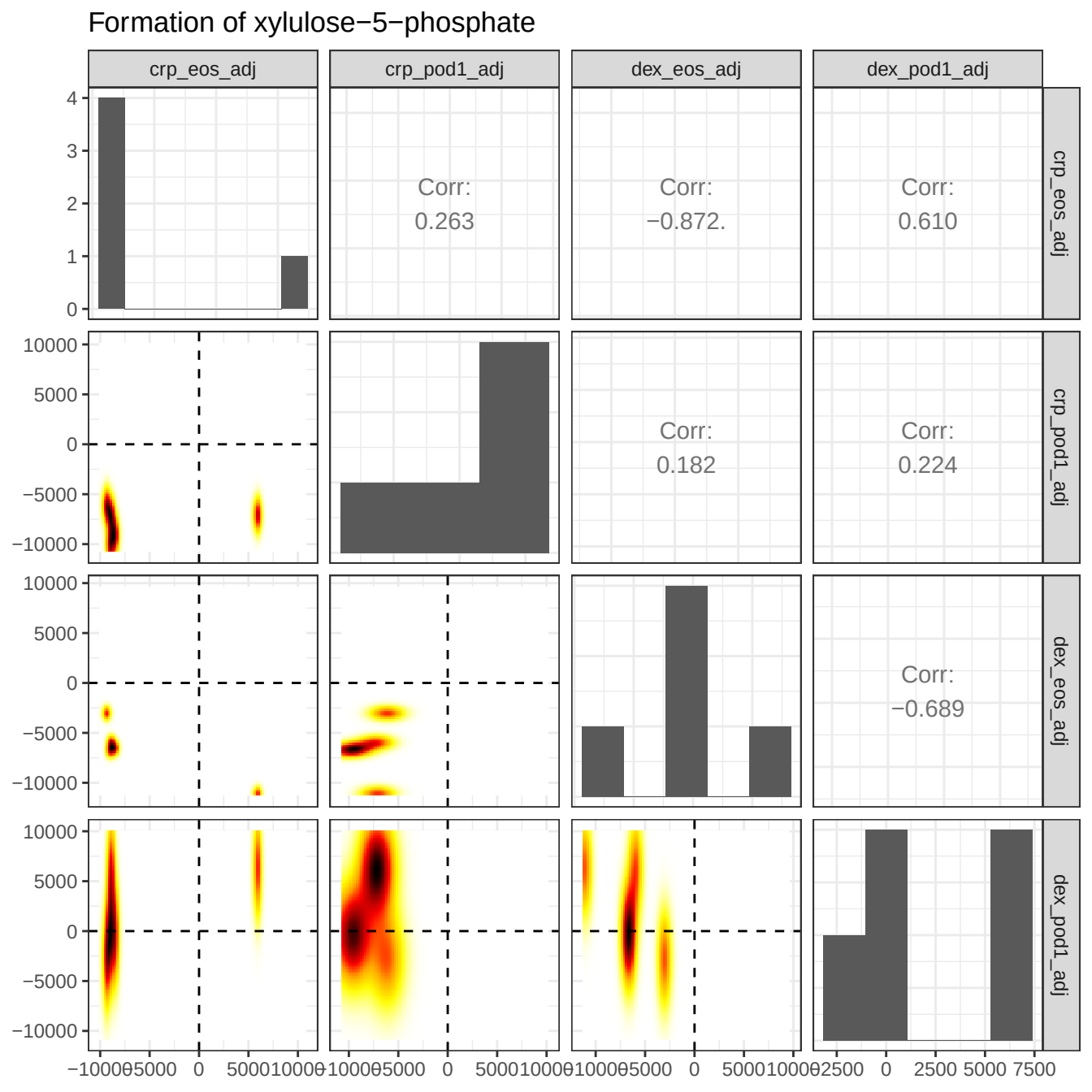

Formation of a pool of free 40S subunits
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.681***
Corr:
−0.269**
Corr:
−0.248*
Corr:
−0.015
Corr:
−0.477***
Corr:
0.043
40
20
0
10000
5000
0
−5000
−10000

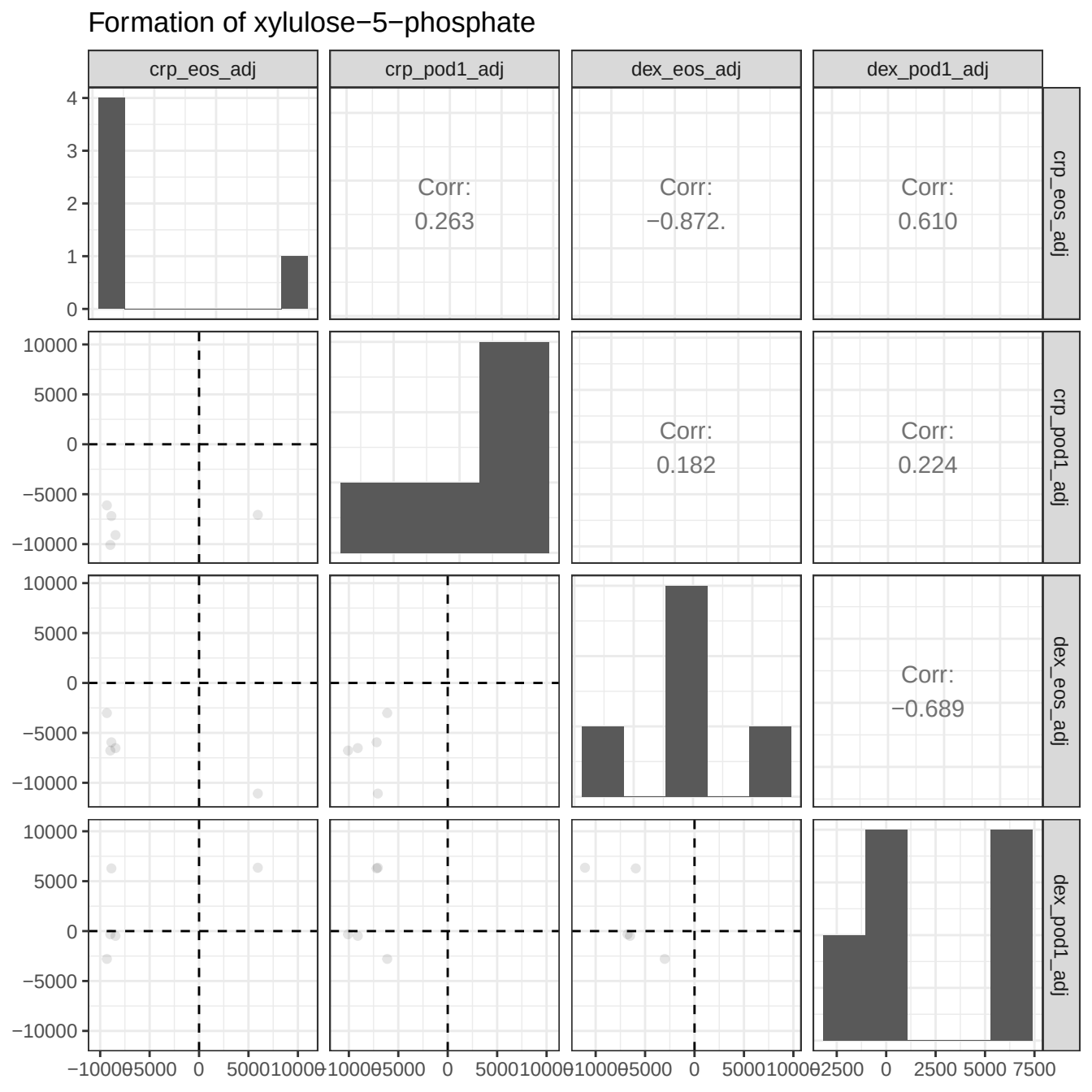

Formation of a pool of free 40S subunits
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

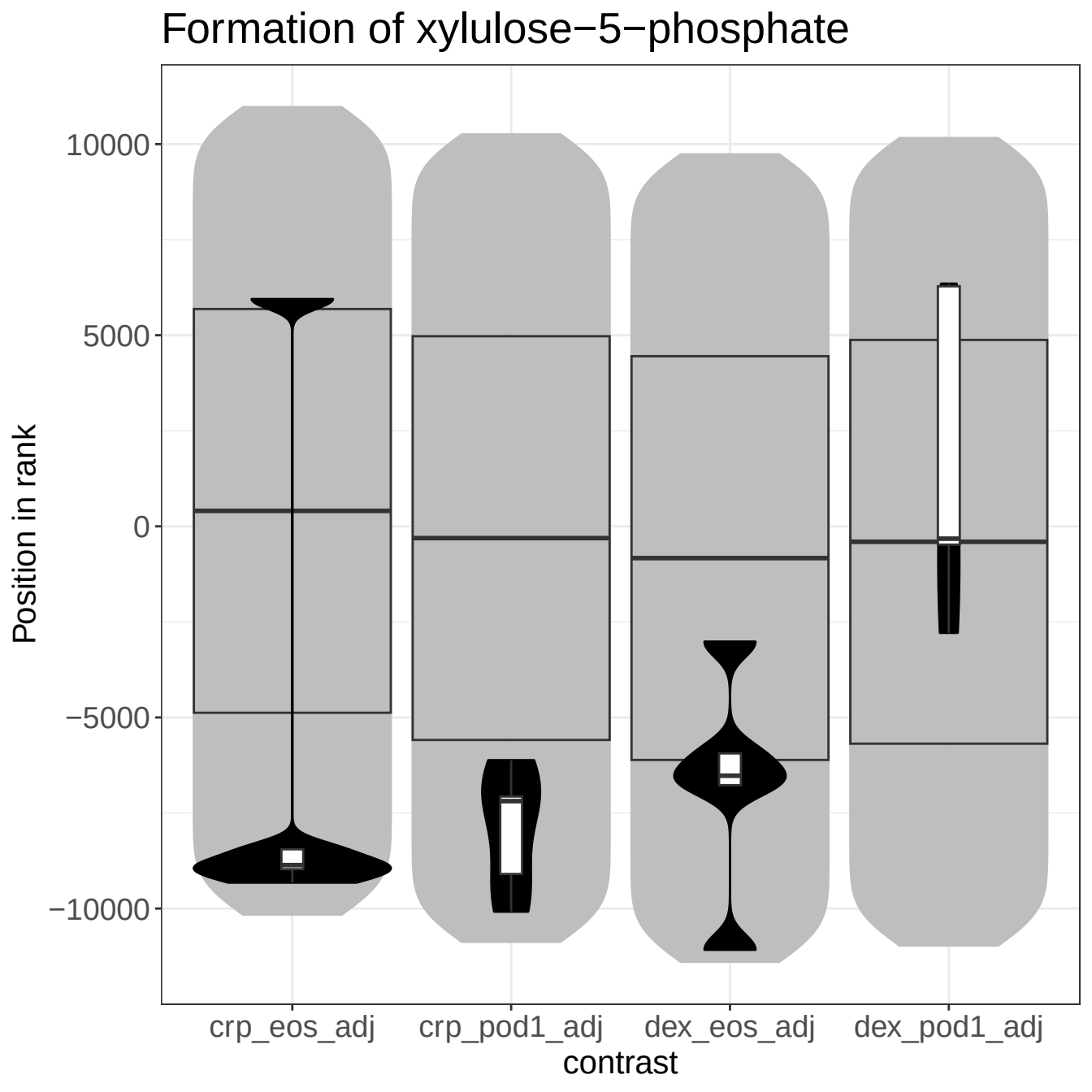

Peptide chain elongation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.680***
Corr:
−0.300**
Corr:
−0.282**
Corr:
−0.049
Corr:
−0.486***
Corr:
0.212*
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000 −5000 0 5000 10000
−5000 0 5000 10000

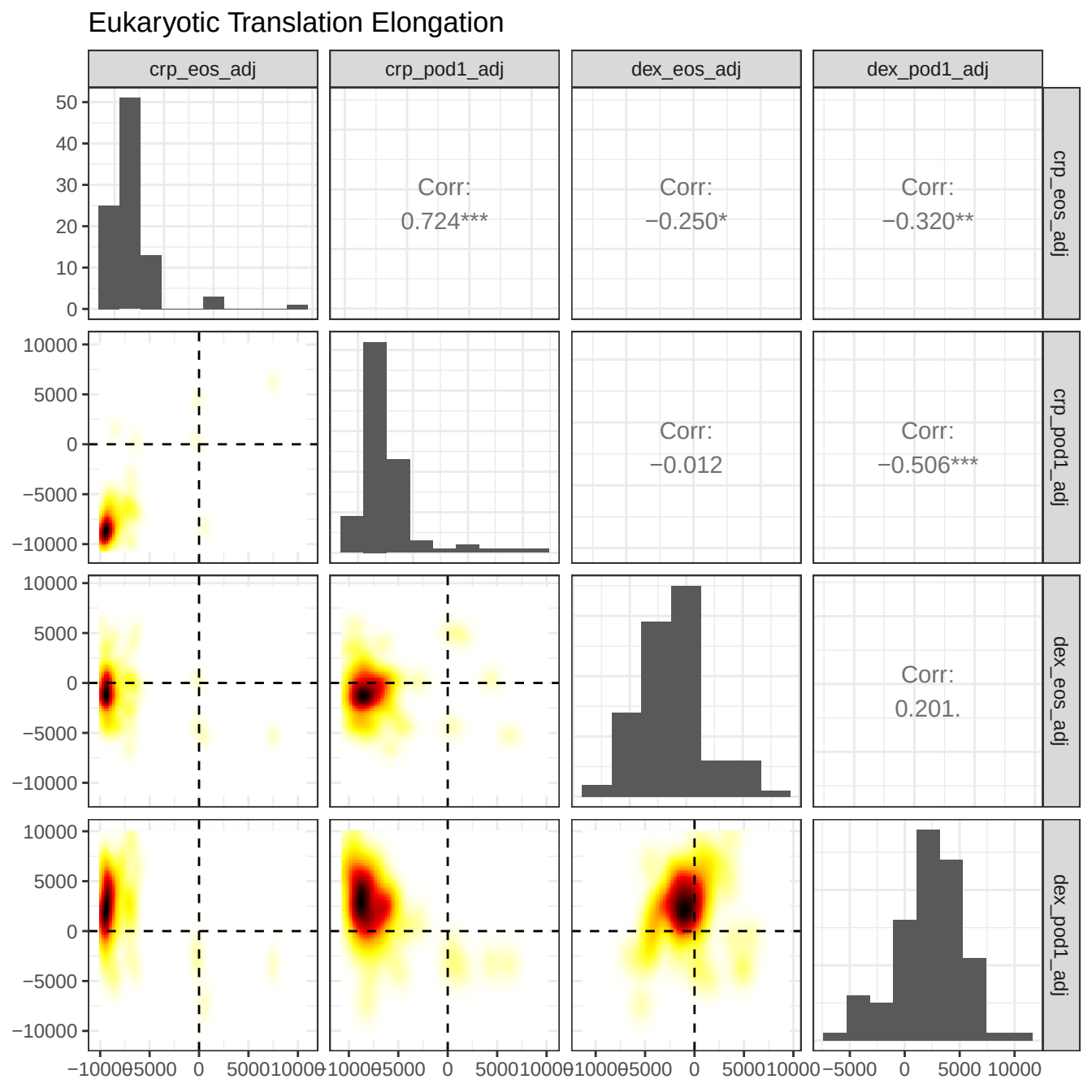

Peptide chain elongation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.680***
Corr:
−0.300**
Corr:
−0.282**
Corr:
−0.049
Corr:
−0.486***
Corr:
0.212*

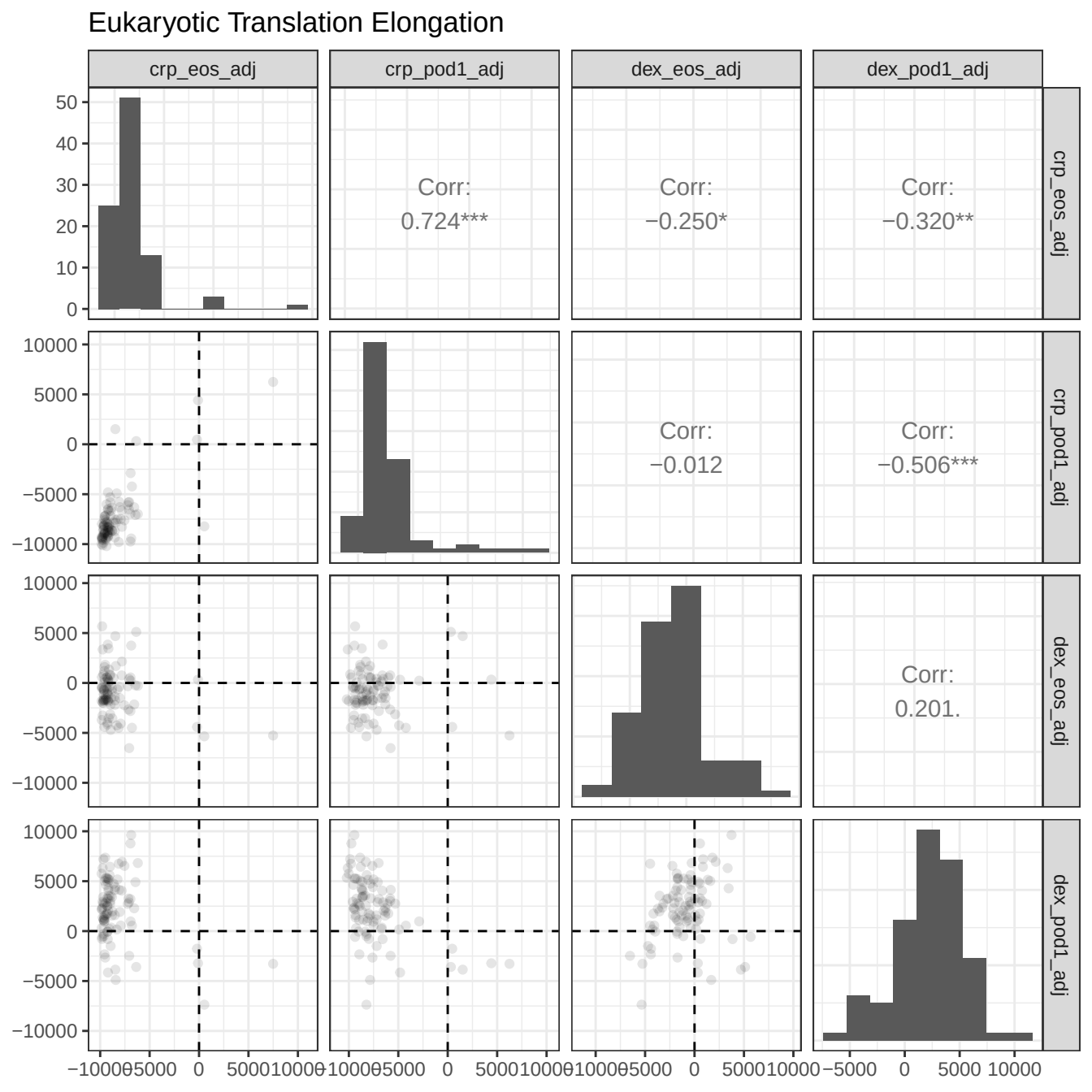

Peptide chain elongation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

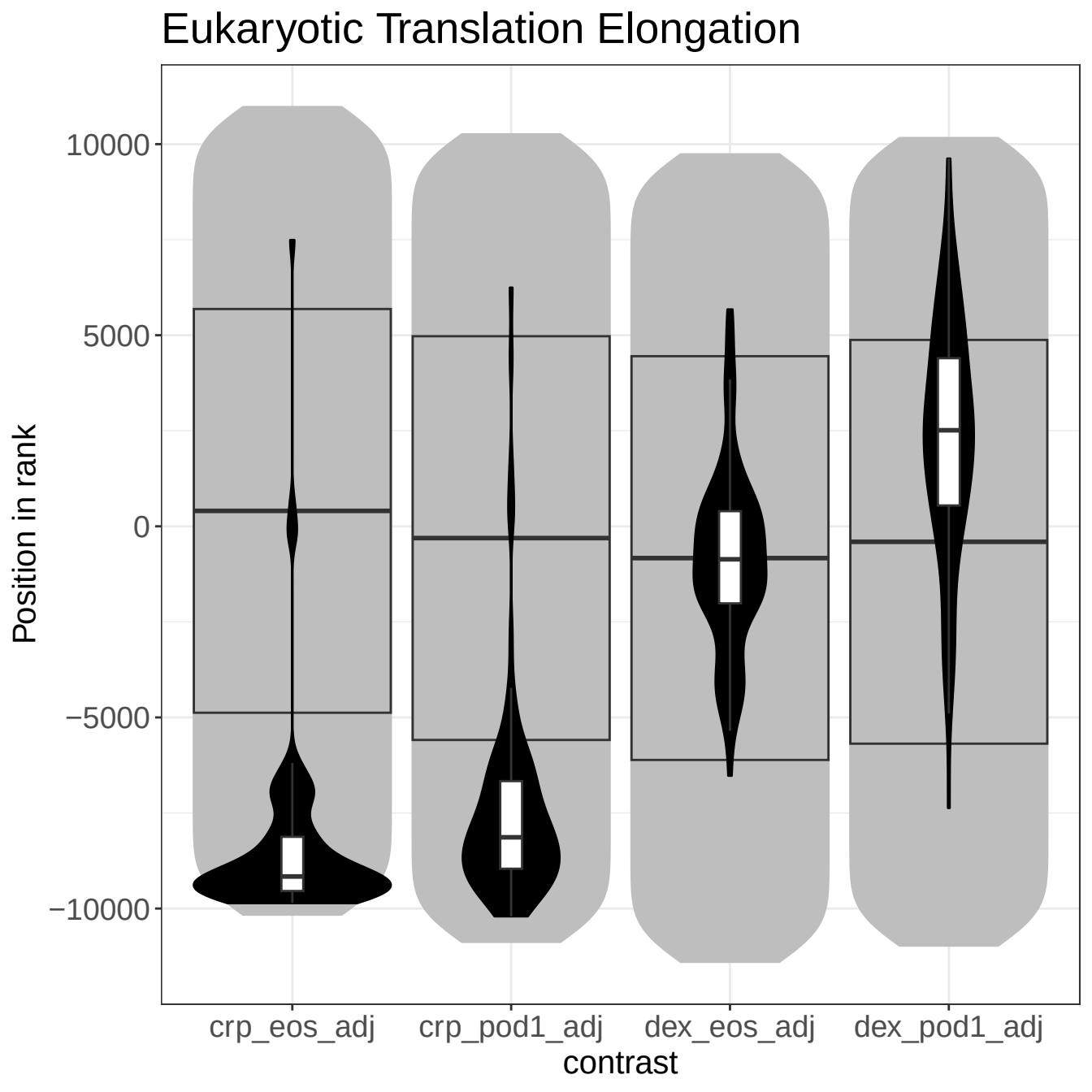

Formation of xylulose−5−phosphate
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.263
Corr:
−0.872.
Corr:
0.610
Corr:
0.182
Corr:
0.224
Corr:
−0.689
4
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−2500
0
2500
5000
7500

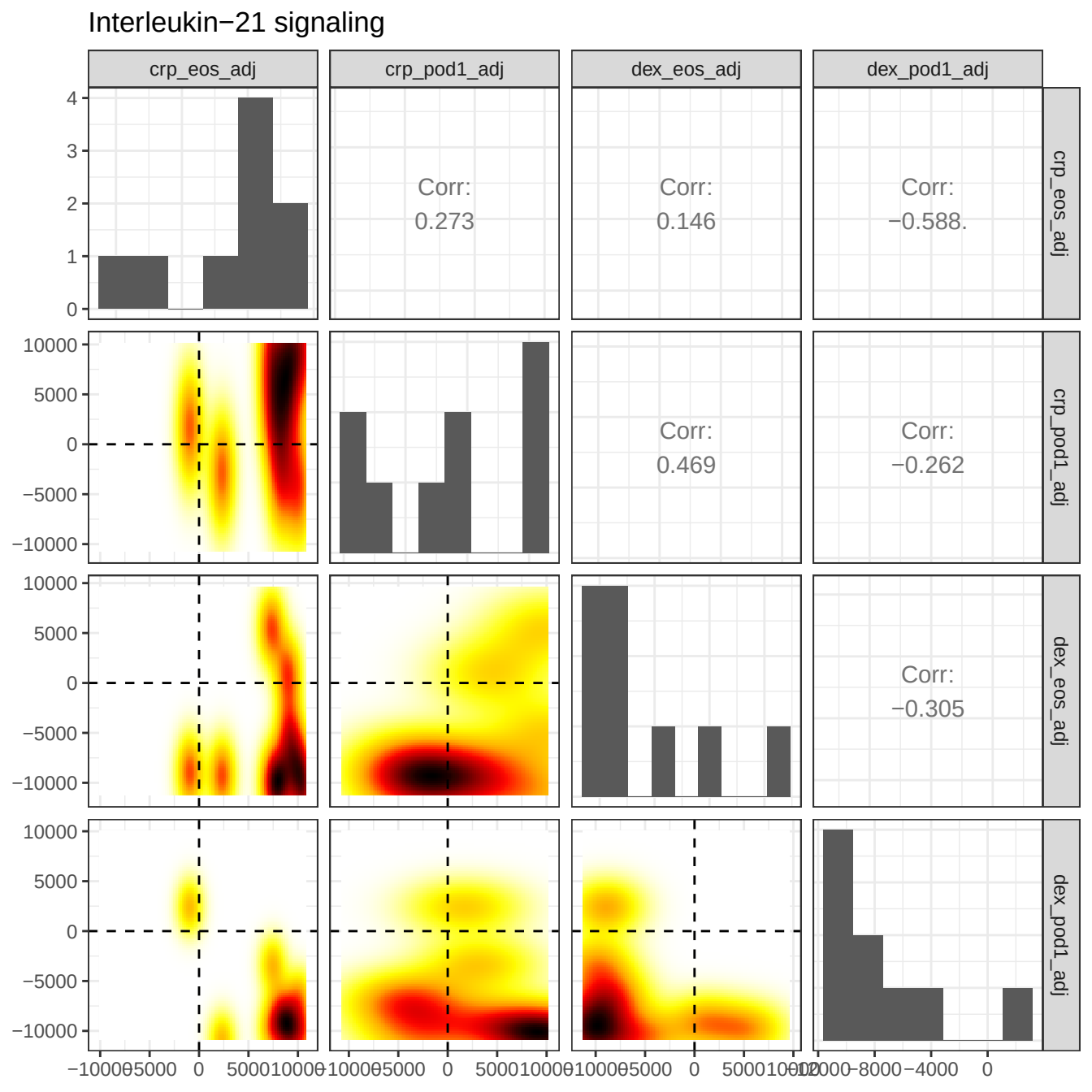

Formation of xylulose−5−phosphate
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.263
Corr:
−0.872.
Corr:
0.610
Corr:
0.182
Corr:
0.224
Corr:
−0.689
4
3
2
1
0
10000
5000
0
−5000
−10000
−10000 −5000 0 5000 10000
−2500 0 2500 5000 7500

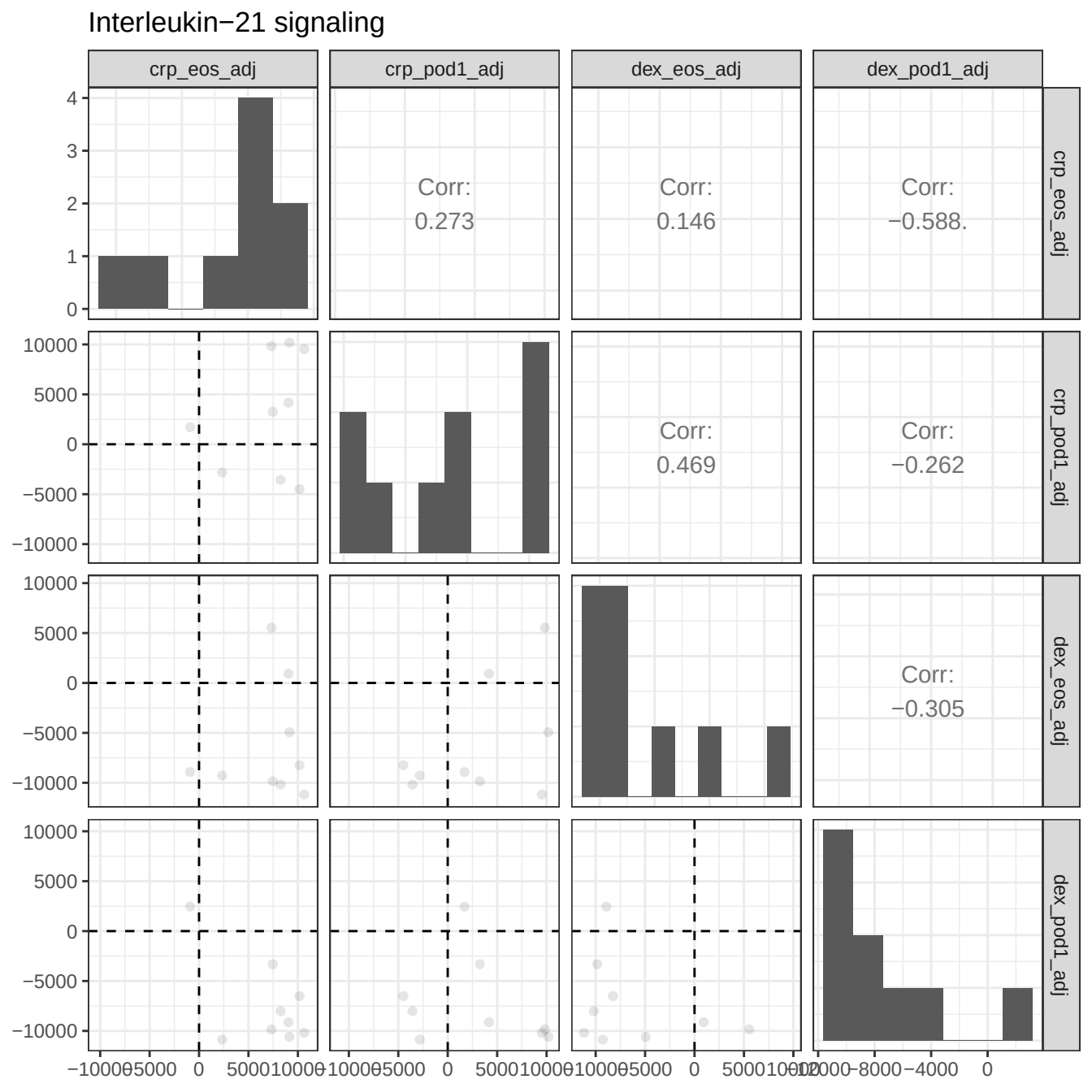

Formation of xylulose−5−phosphate
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

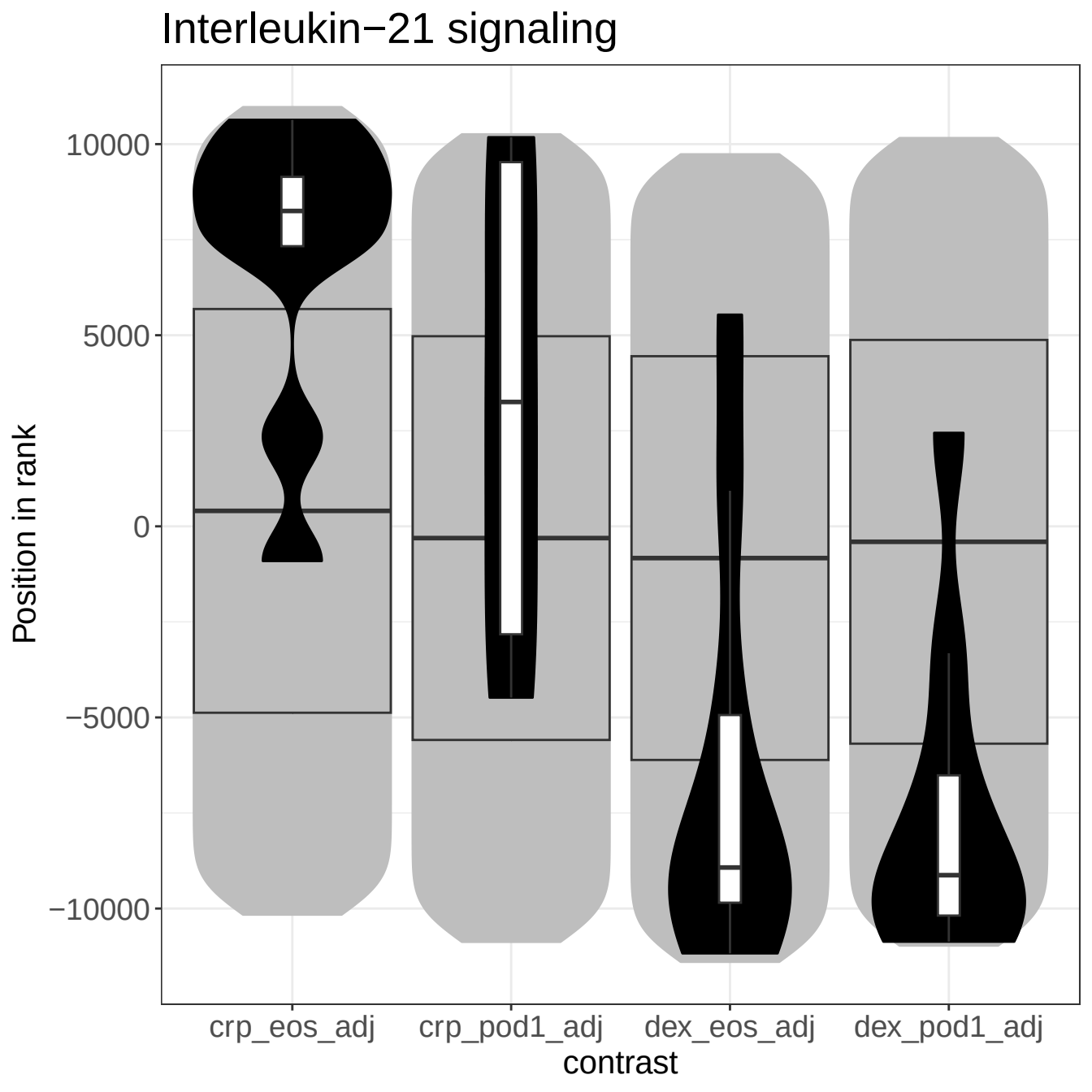

Eukaryotic Translation Elongation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.724***
Corr:
−0.250*
Corr:
−0.320**
Corr:
−0.012
Corr:
−0.506***
Corr:
0.201.
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000 −5000 0 5000 10000
−5000 0 5000 10000

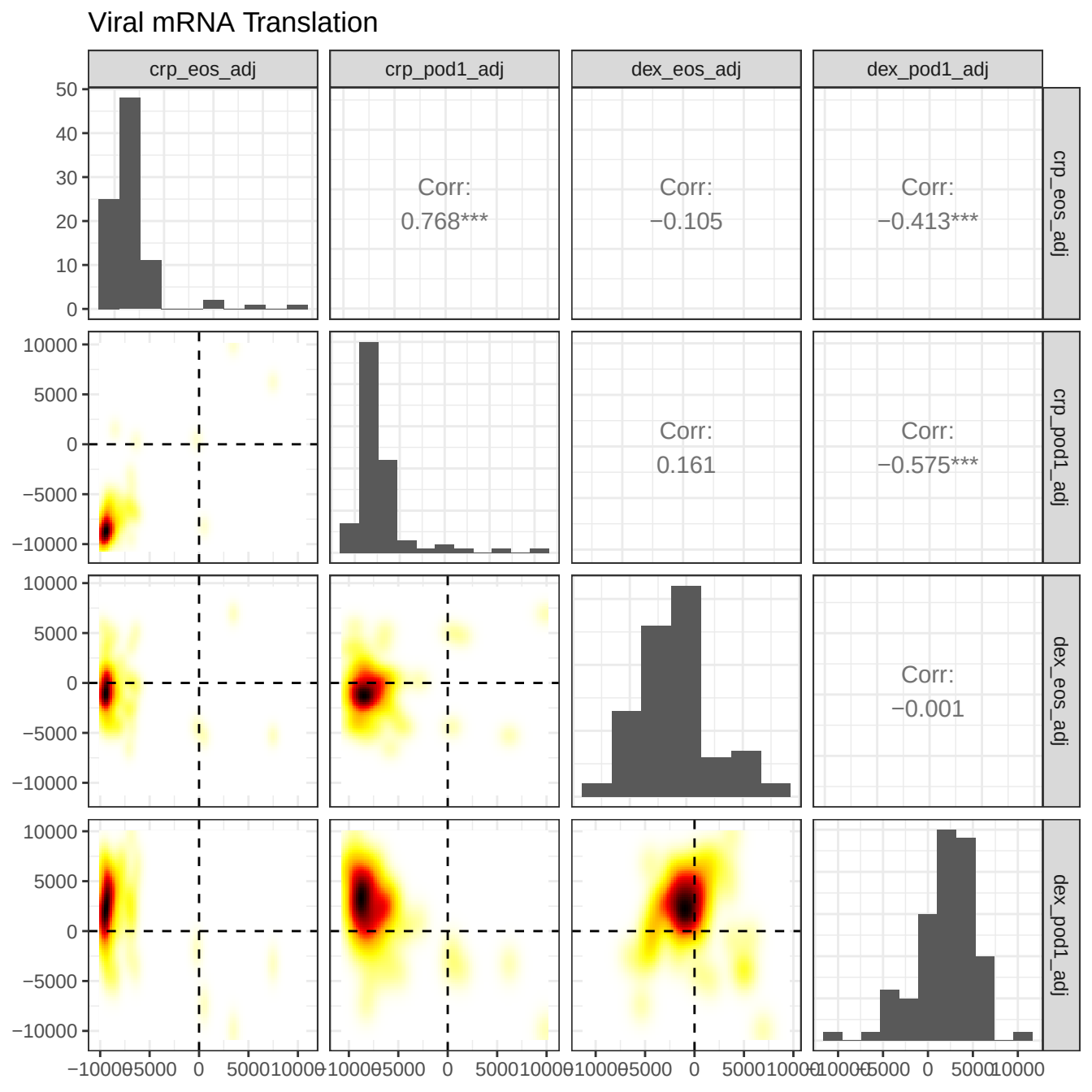

Eukaryotic Translation Elongation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.724***
Corr:
−0.250*
Corr:
−0.320**
Corr:
−0.012
Corr:
−0.506***
Corr:
0.201.

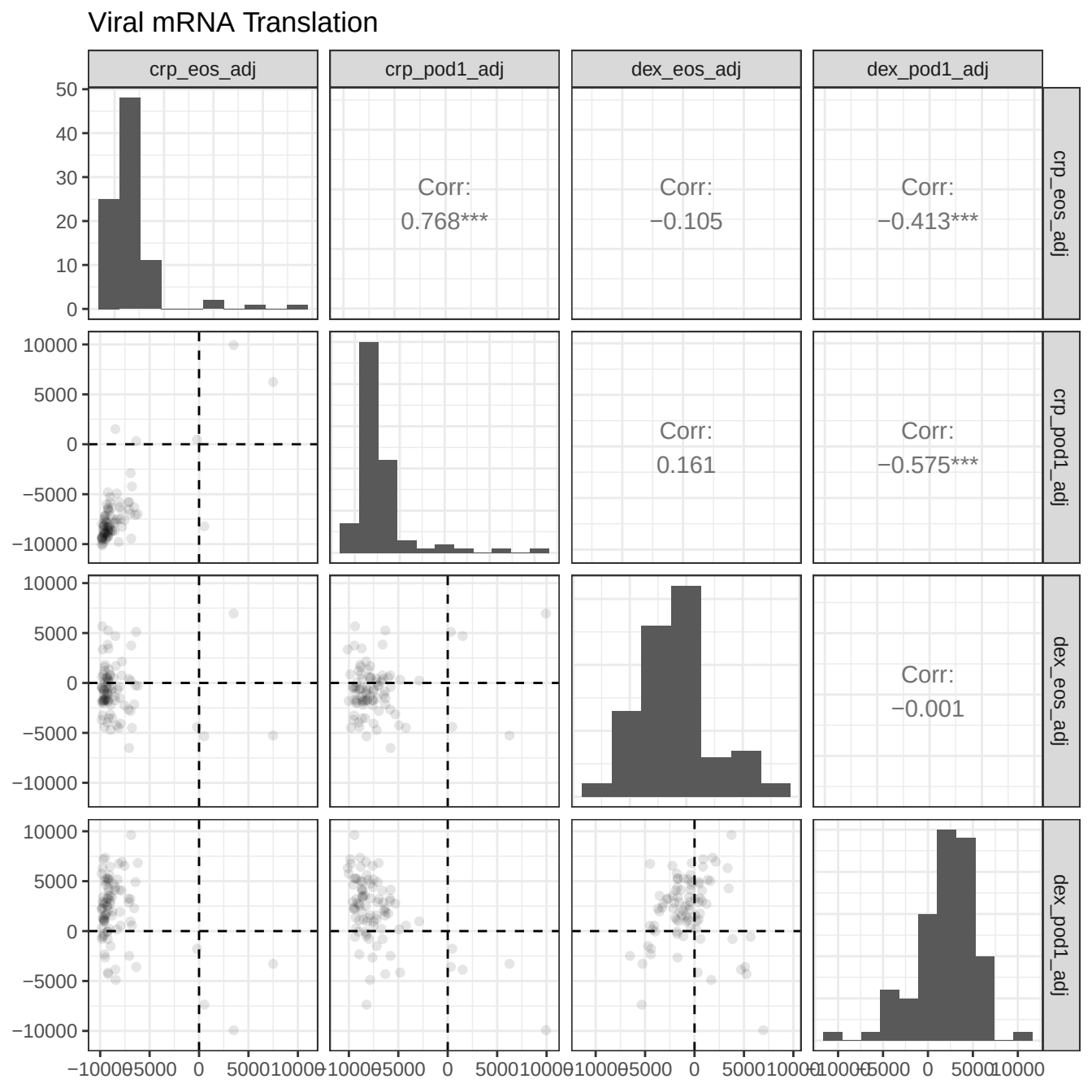

Eukaryotic Translation Elongation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

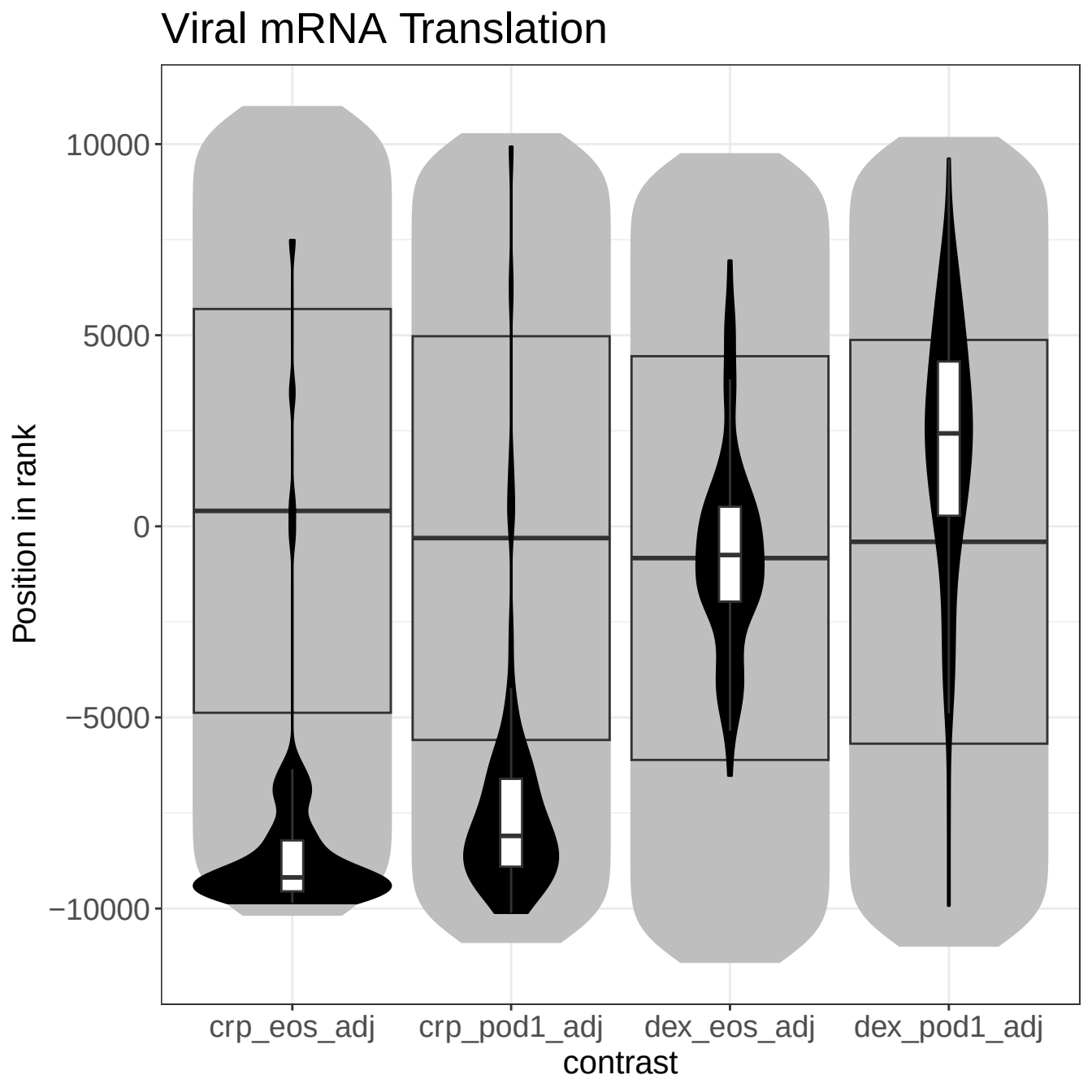

Interleukin−21 signaling
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.273
Corr:
0.146
Corr:
−0.588.
Corr:
0.469
Corr:
−0.262
Corr:
−0.305
4
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−12000
−8000
−4000
0

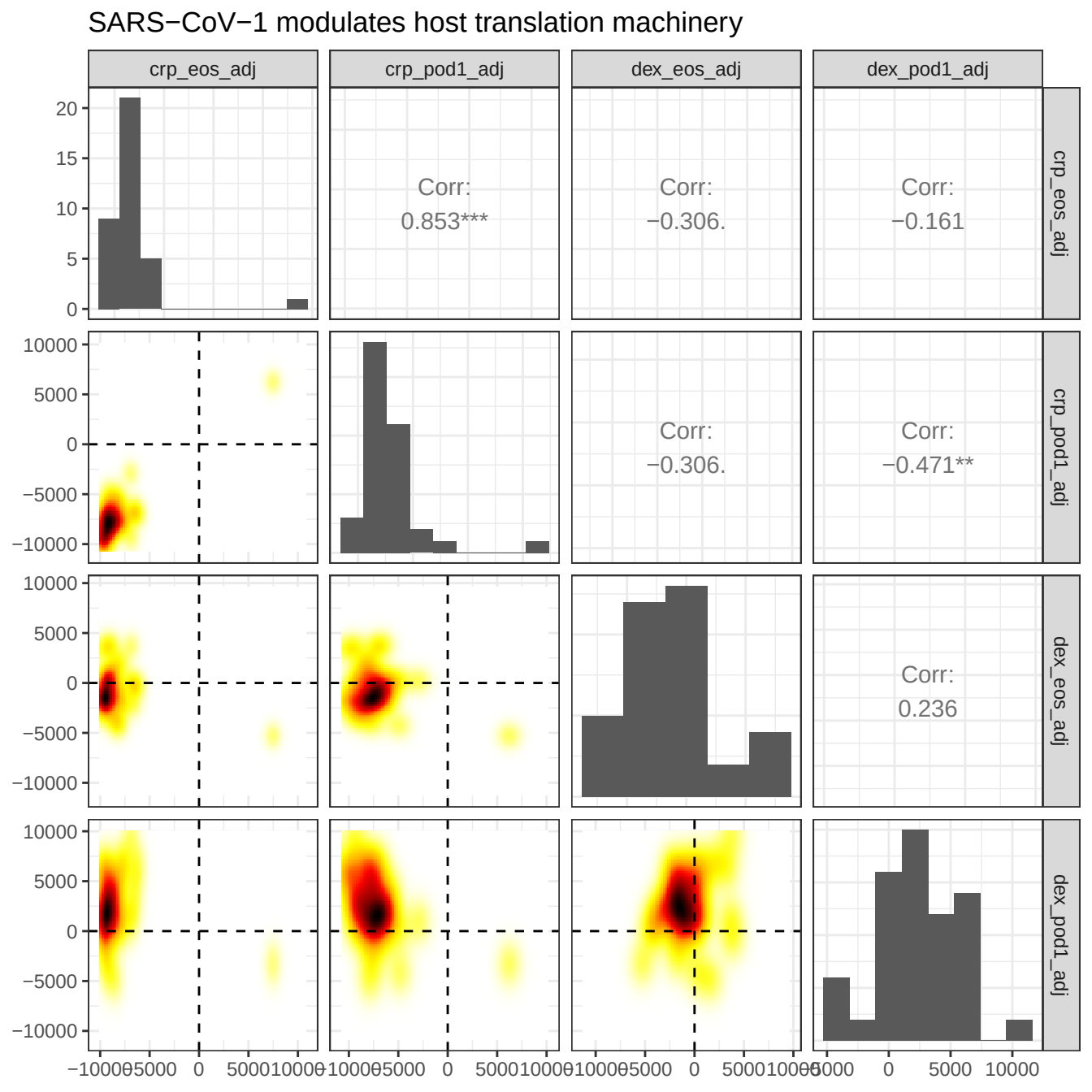

Interleukin−21 signaling
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.273
Corr:
0.146
Corr:
−0.588.
Corr:
0.469
Corr:
−0.262
Corr:
−0.305
4
3
2
1
0
10000
5000
0
−5000
−10000
−8000
−4000

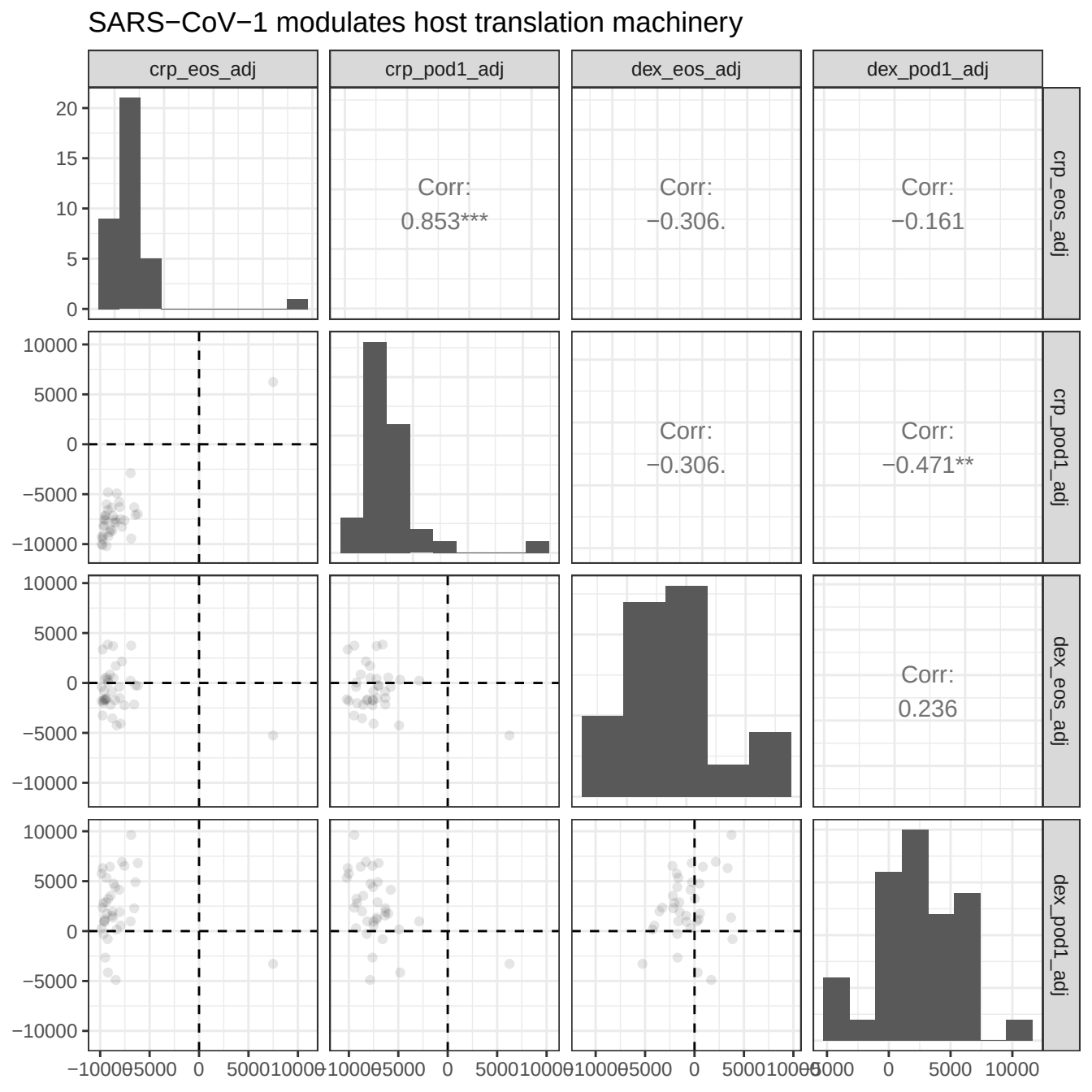

Interleukin−21 signaling
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

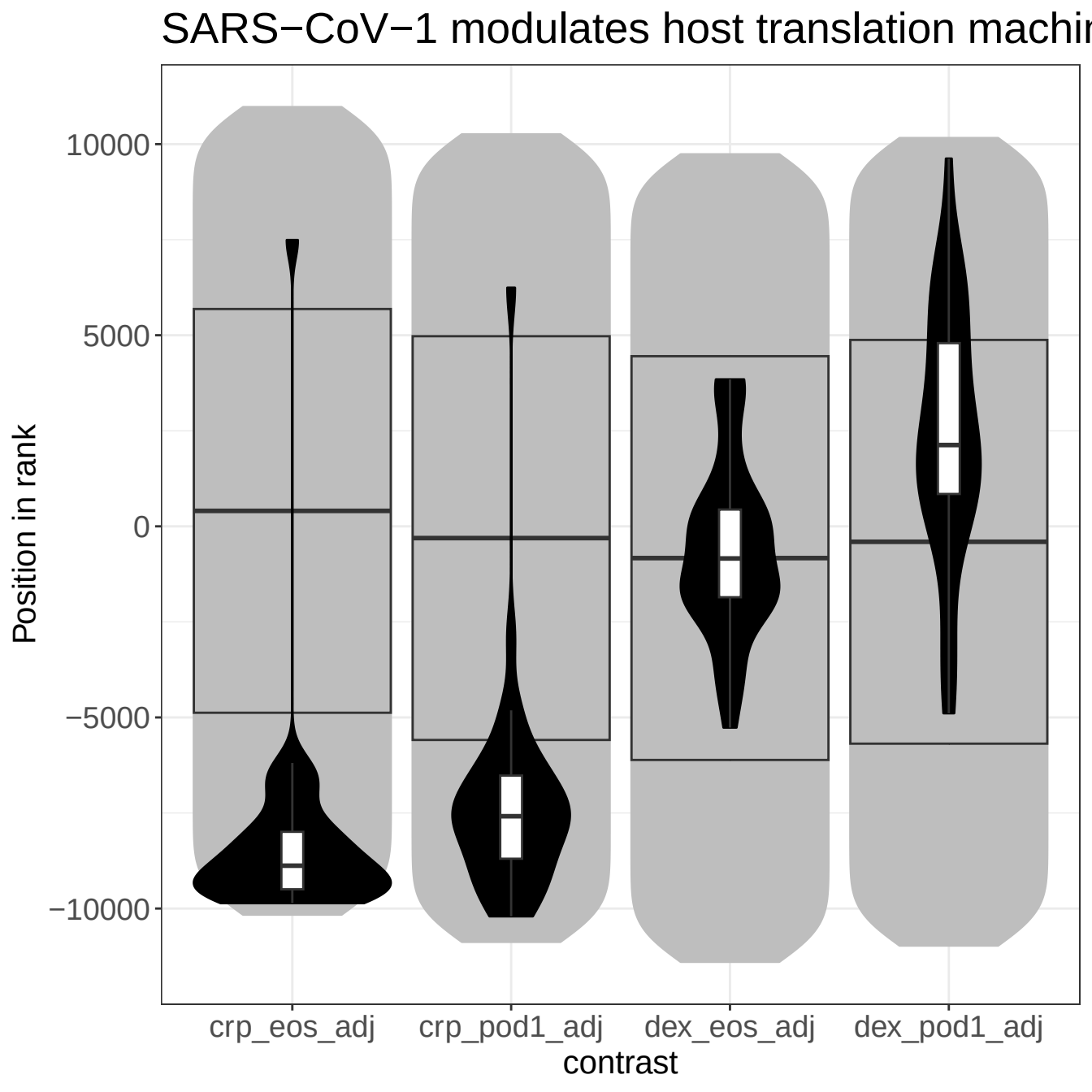

Viral mRNA Translation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.768***
Corr:
−0.105
Corr:
−0.413***
Corr:
0.161
Corr:
−0.575***
Corr:
−0.001
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

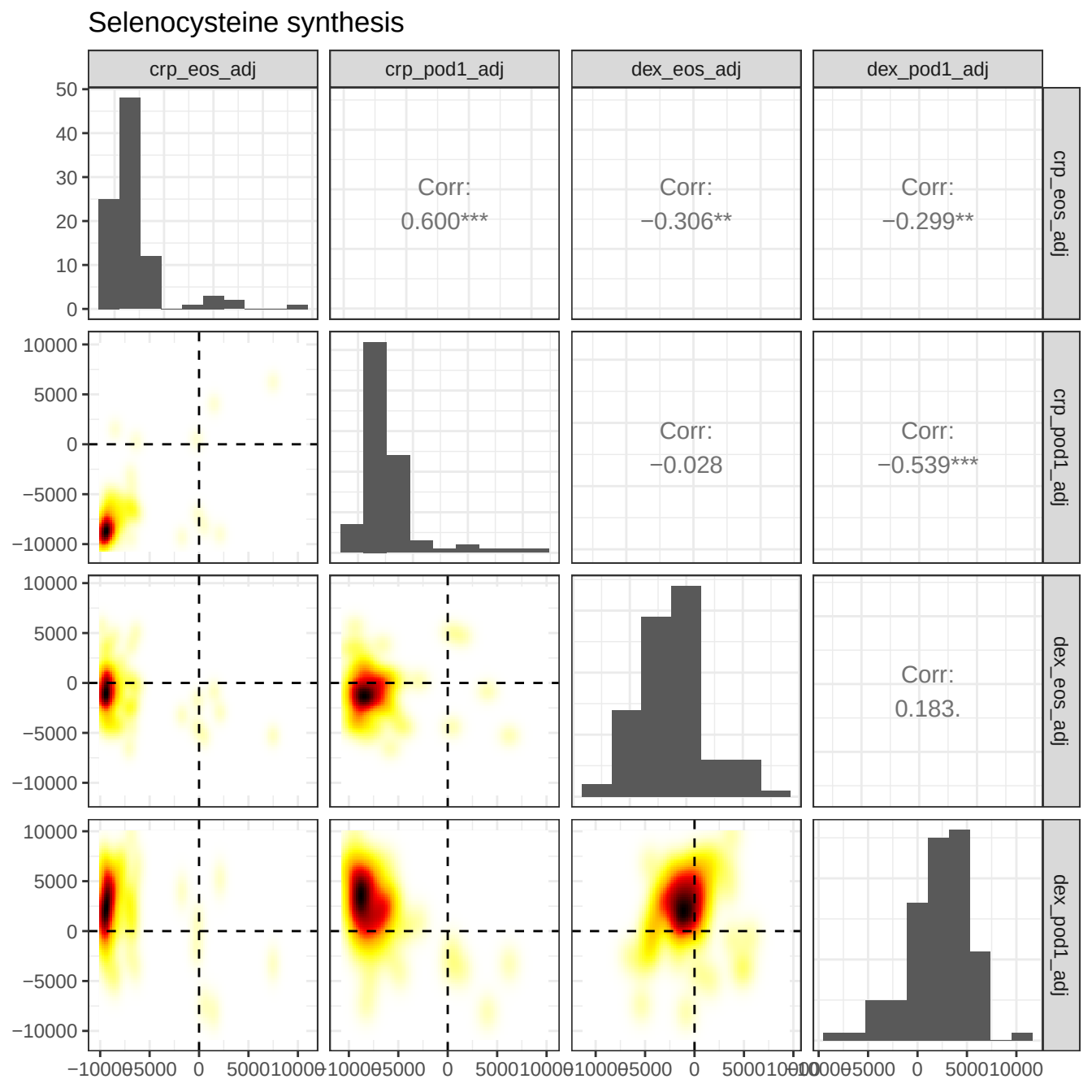

Viral mRNA Translation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.768***
Corr:
−0.105
Corr:
−0.413***
Corr:
0.161
Corr:
−0.575***
Corr:
−0.001
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

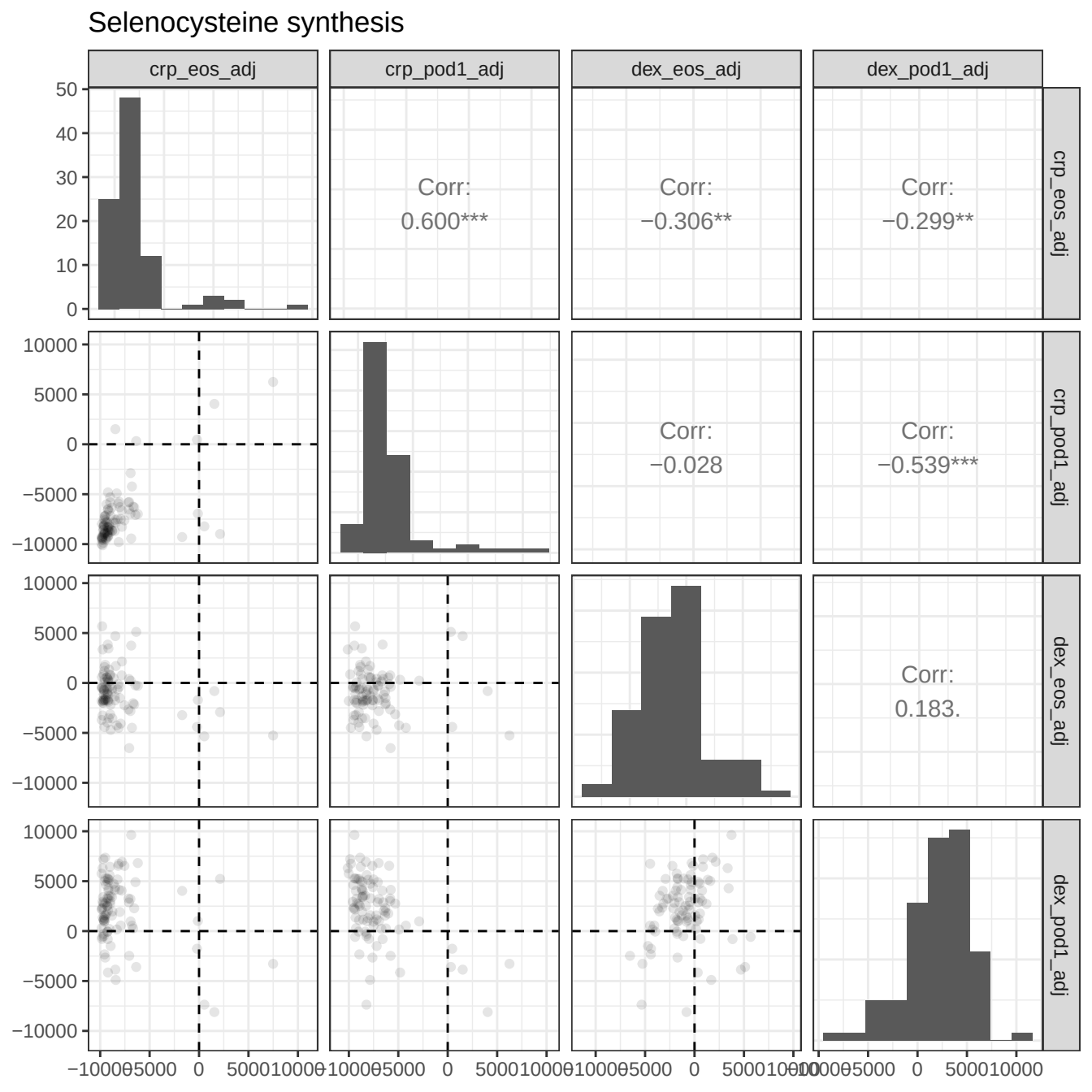

Viral mRNA Translation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

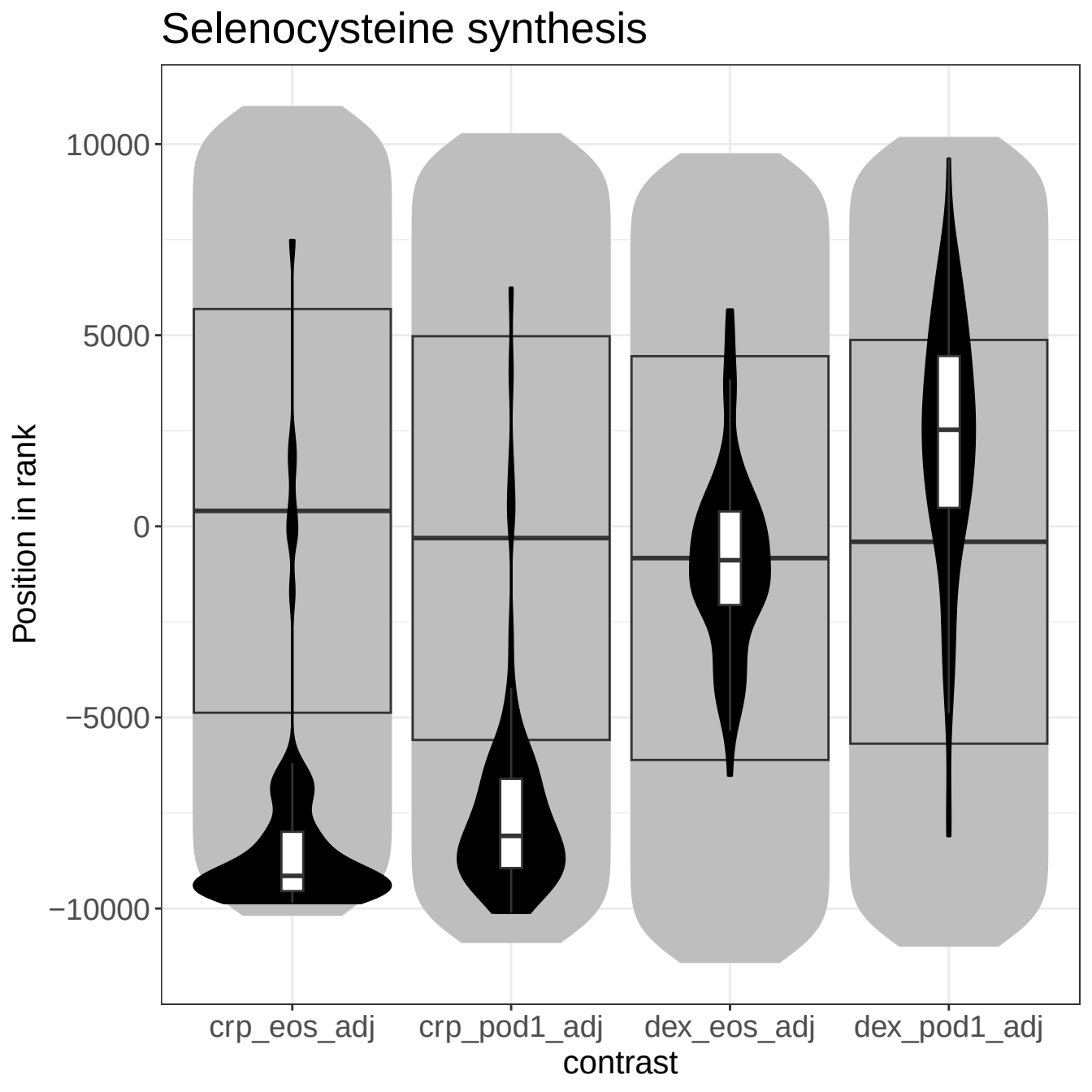

SARS−CoV−1 modulates host translation machinery
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.853***
Corr:
−0.306.
Corr:
−0.161
Corr:
−0.306.
Corr:
−0.471**
Corr:
0.236
20
15
10
5
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000


SARS−CoV−1 modulates host translation machinery
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.853***
Corr:
−0.306.
Corr:
−0.161
Corr:
−0.306.
Corr:
−0.471**
Corr:
0.236
20
15
10
5
0
10000
5000
0
−5000
−10000

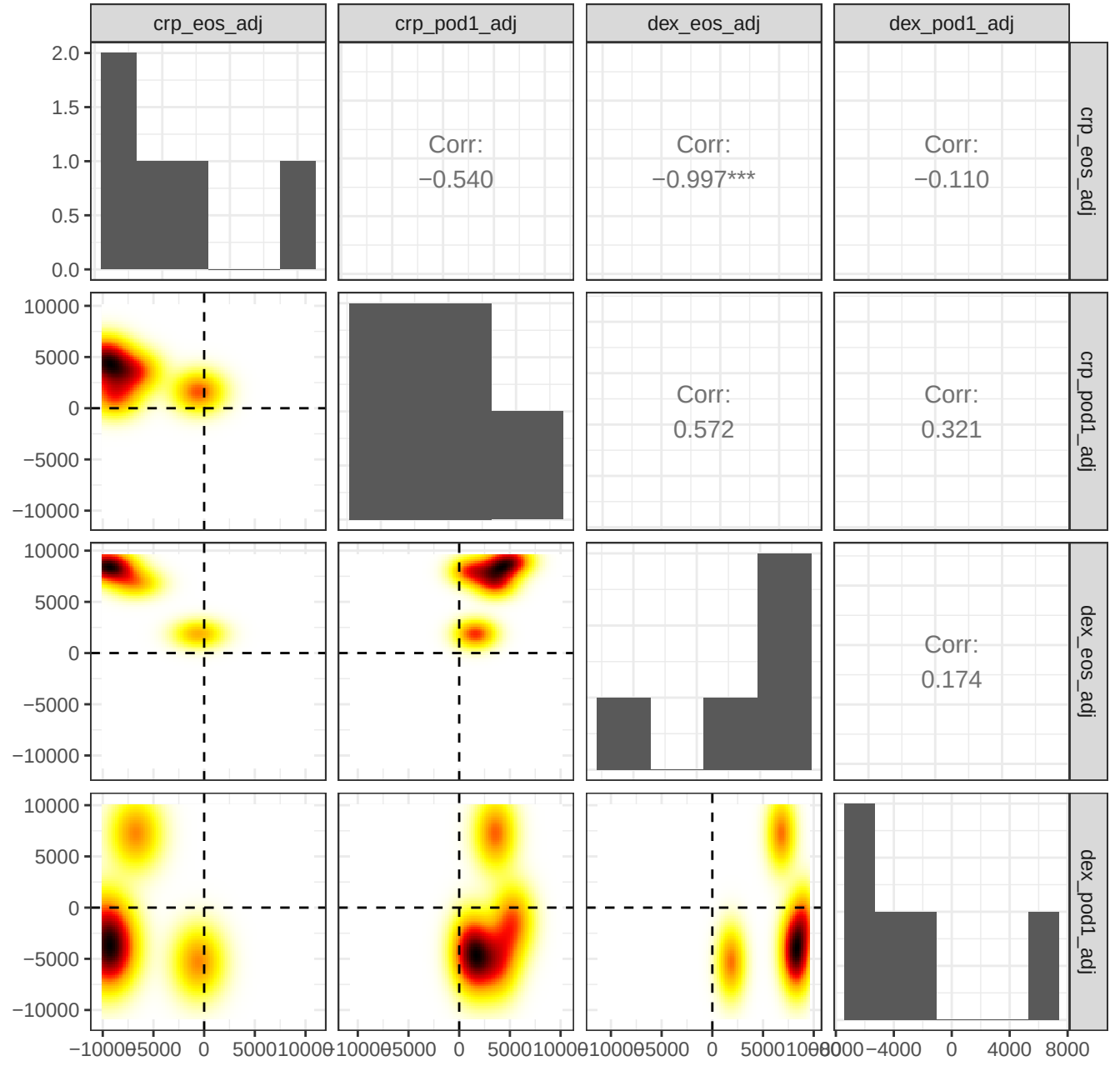

SARS−CoV−1 modulates host translation machin
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

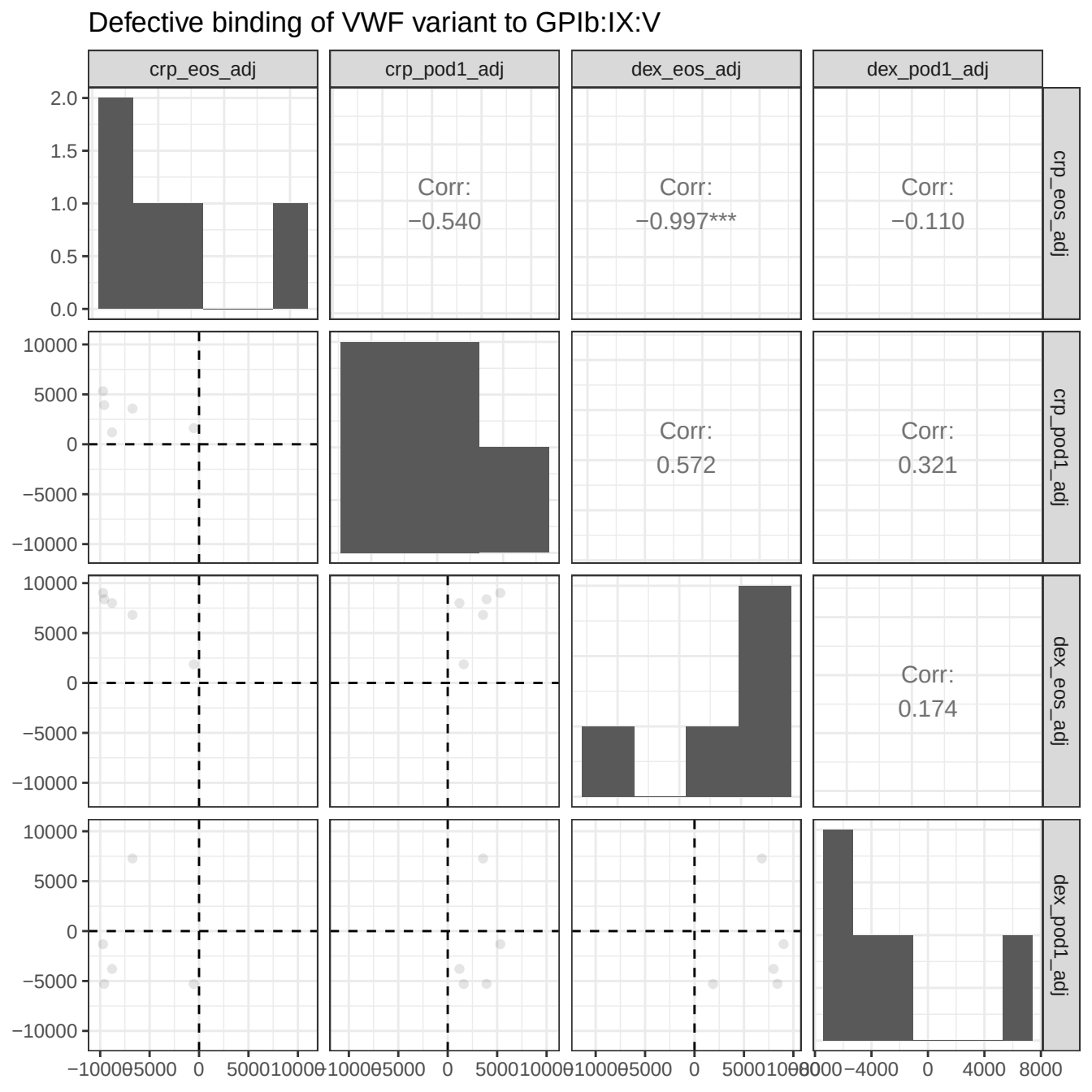

Selenocysteine synthesis
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.600***
Corr:
−0.306**
Corr:
−0.299**
Corr:
−0.028
Corr:
−0.539***
Corr:
0.183.
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

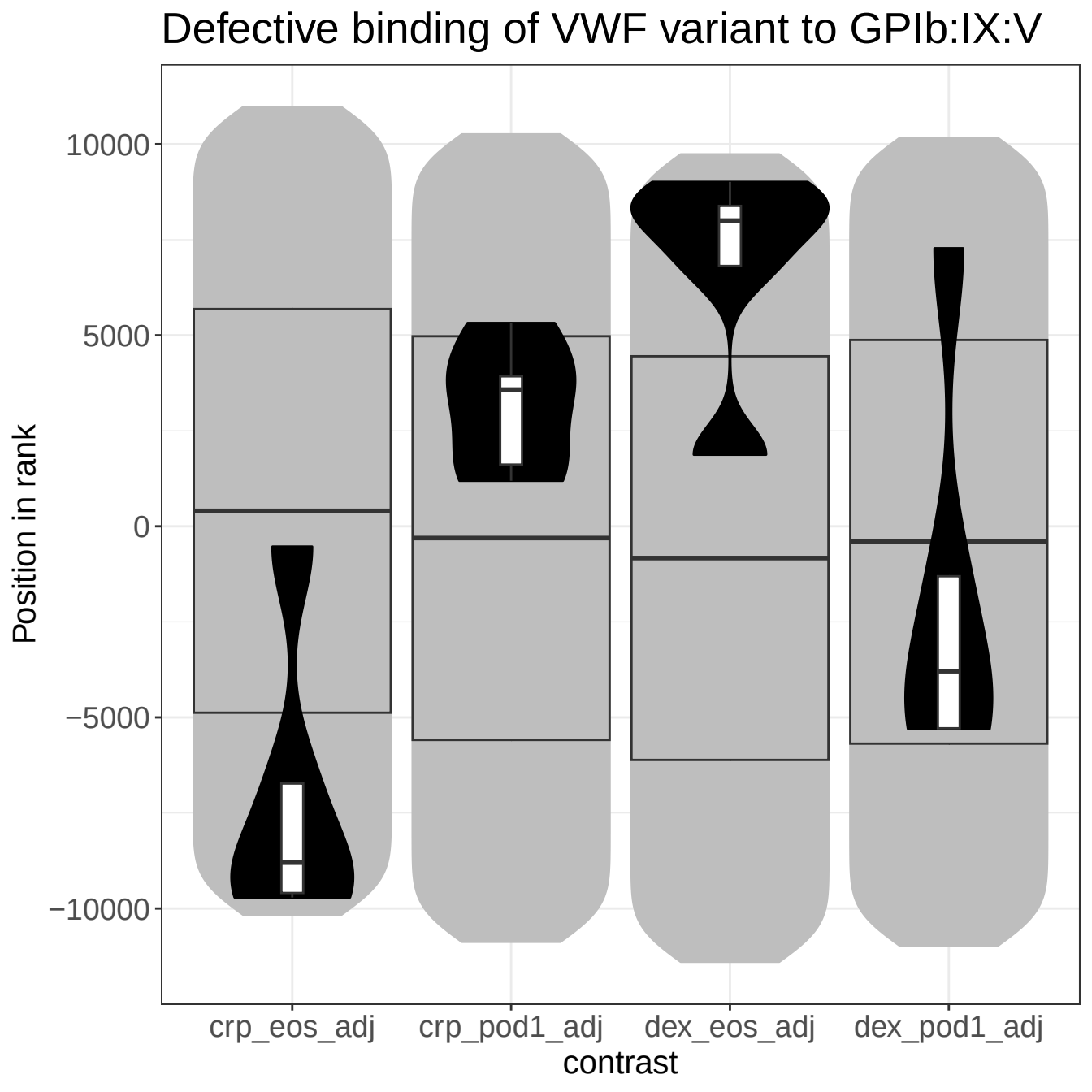

Selenocysteine synthesis
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.600***
Corr:
−0.306**
Corr:
−0.299**
Corr:
−0.028
Corr:
−0.539***
Corr:
0.183.

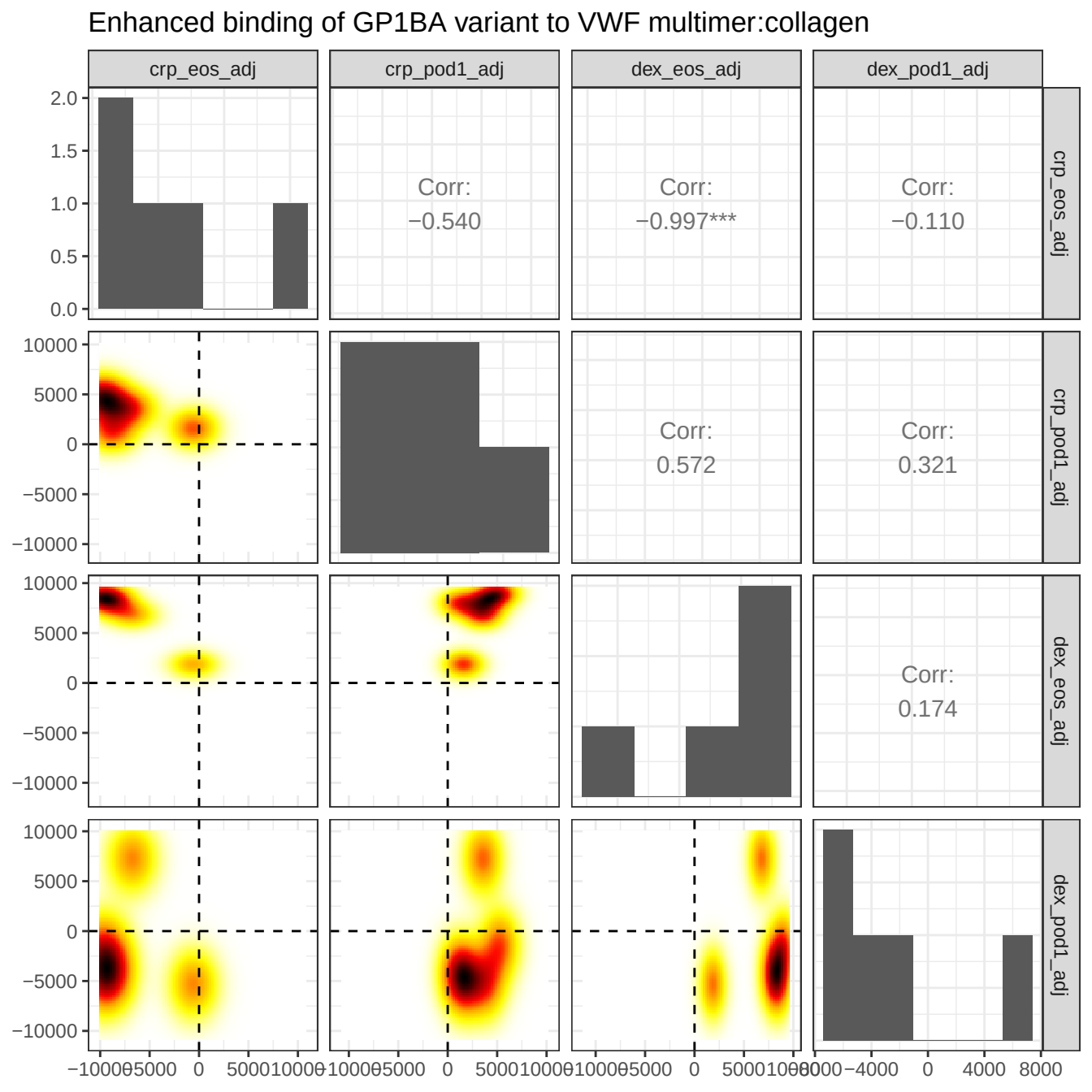

Selenocysteine synthesis
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

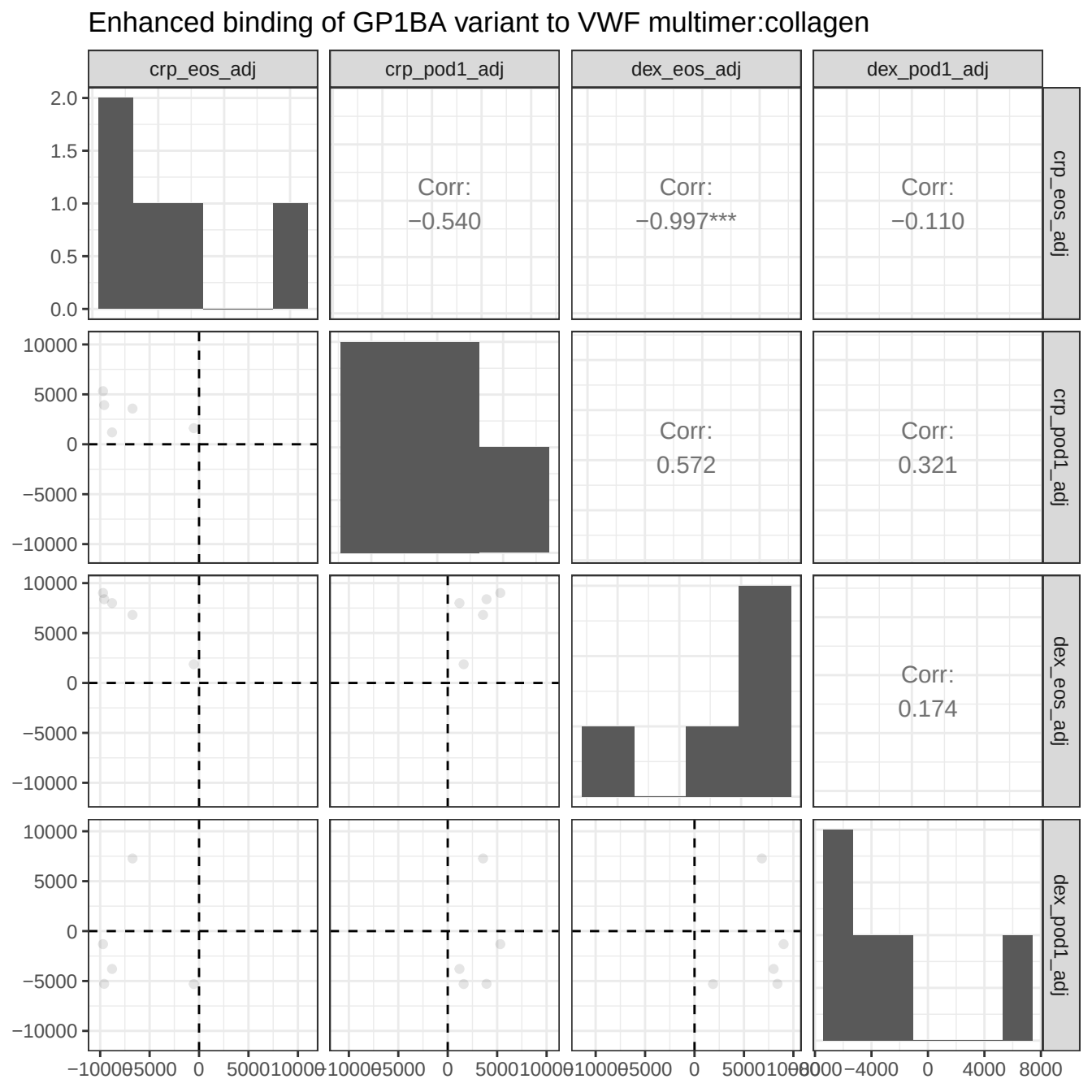
Defective binding of VWF variant to GPIb:IX:V

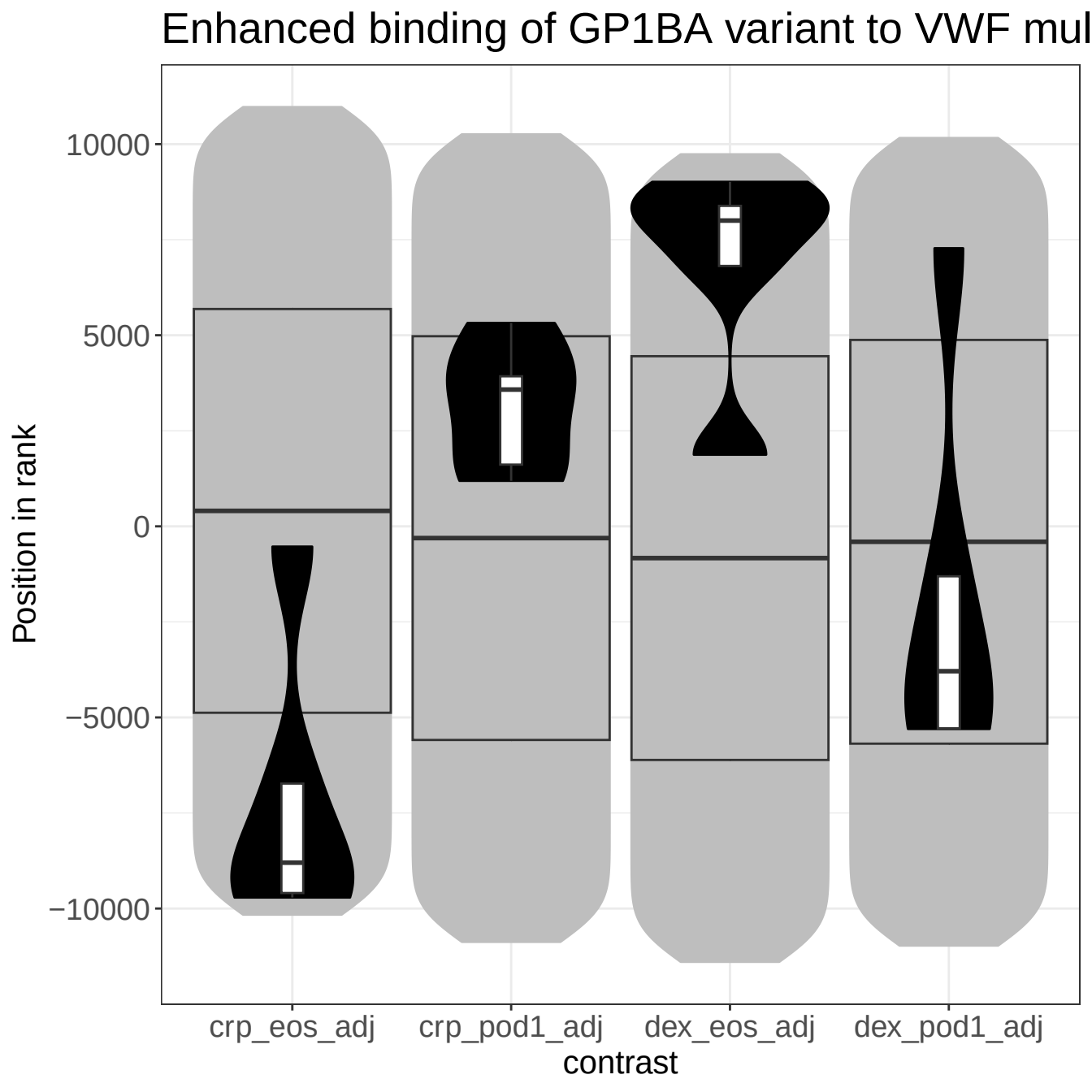


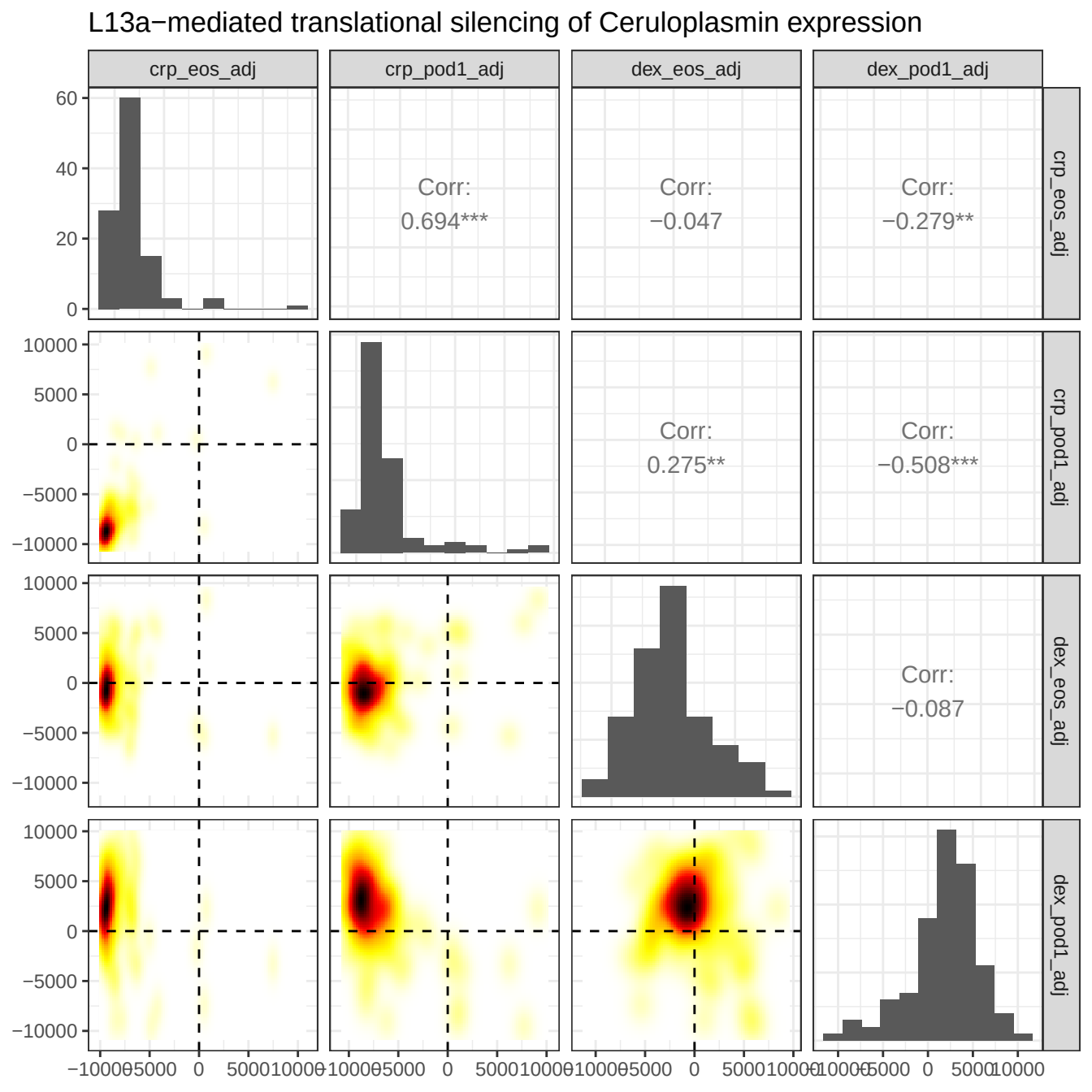

Defective binding of VWF variant to GPIb:IX:V
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.540
Corr:
−0.997***
Corr:
−0.110
Corr:
0.572
Corr:
0.321
Corr:
0.174
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−4000
4000
8000

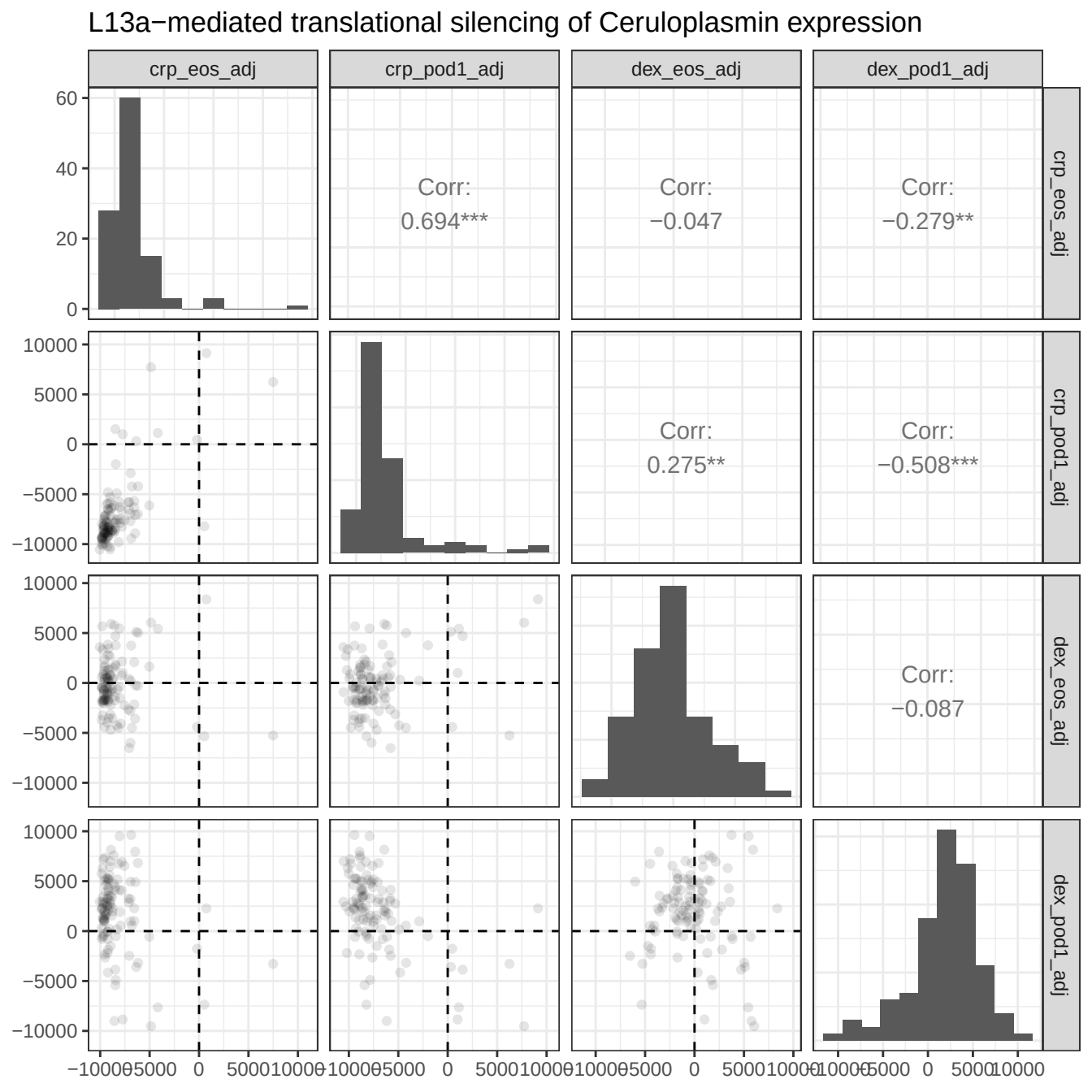

Defective binding of VWF variant to GPIb:IX:V
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

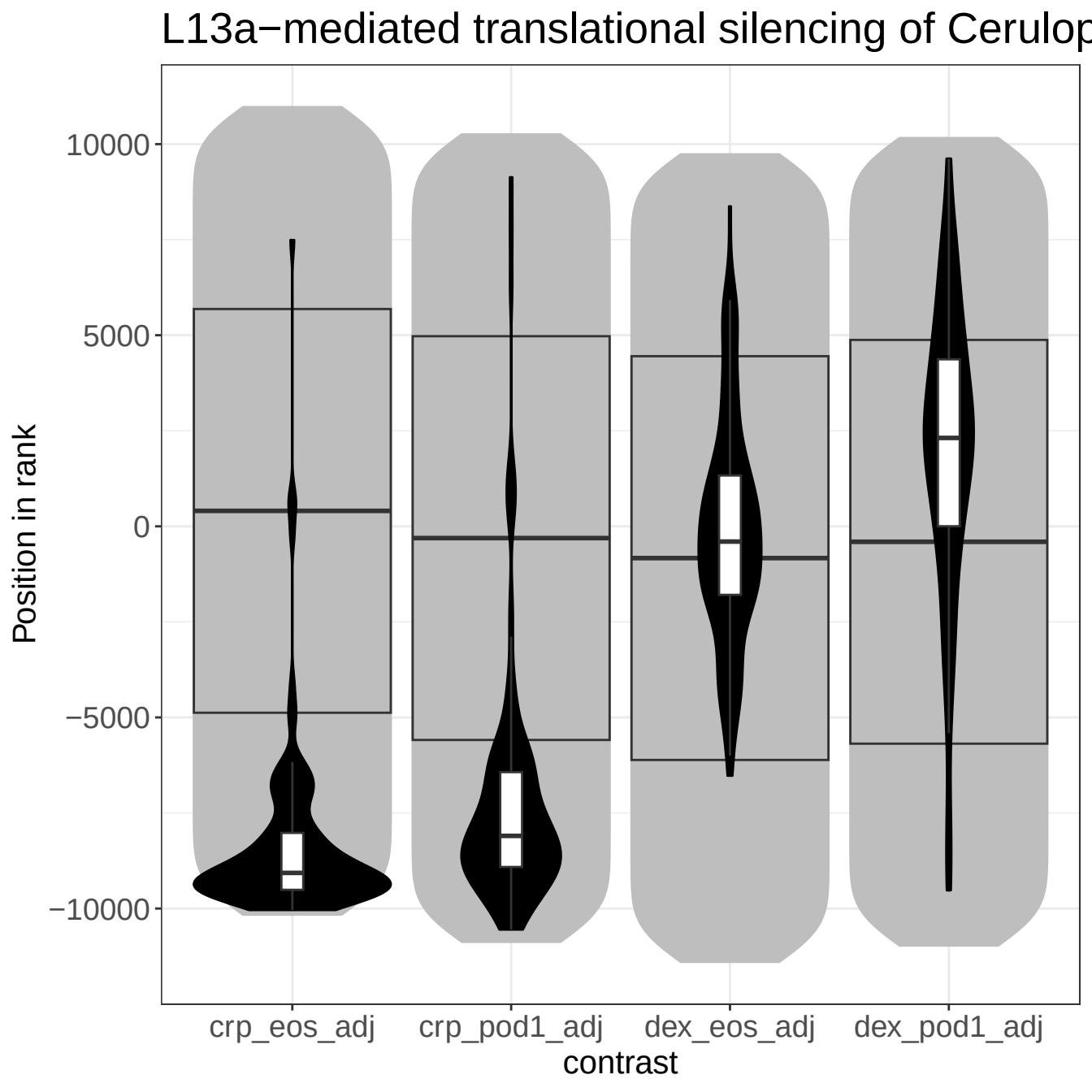

Enhanced binding of GP1BA variant to VWF multimer:collagen
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.540
Corr:
−0.997***
Corr:
−0.110
Corr:
0.572
Corr:
0.321
Corr:
0.174
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−8000
−4000
0
4000
8000

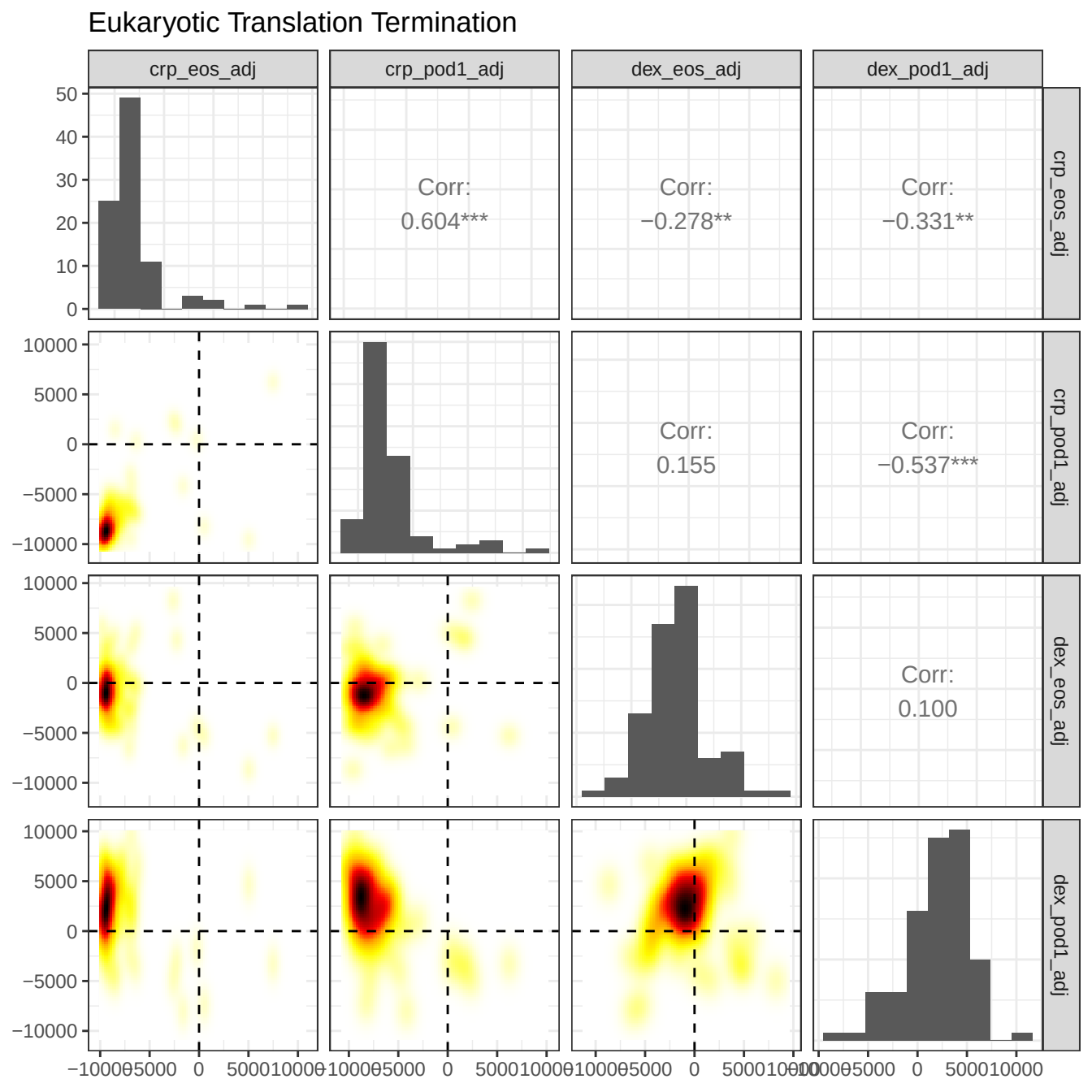

Enhanced binding of GP1BA variant to VWF multimer:collagen
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.540
Corr:
−0.997***
Corr:
−0.110
Corr:
0.572
Corr:
0.321
Corr:
0.174
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−4000
0
4000
8000

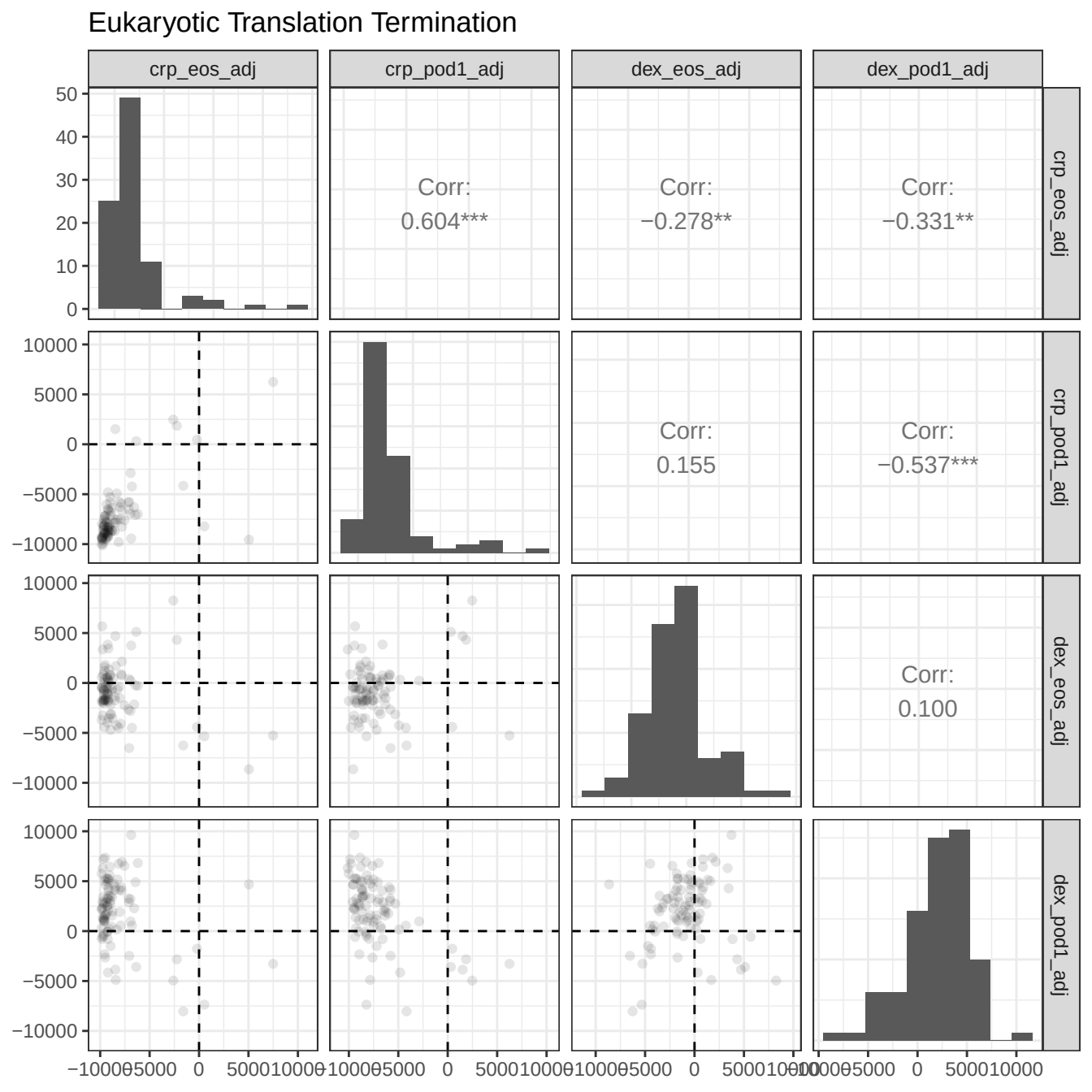

Enhanced binding of GP1BA variant to VWF mul
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

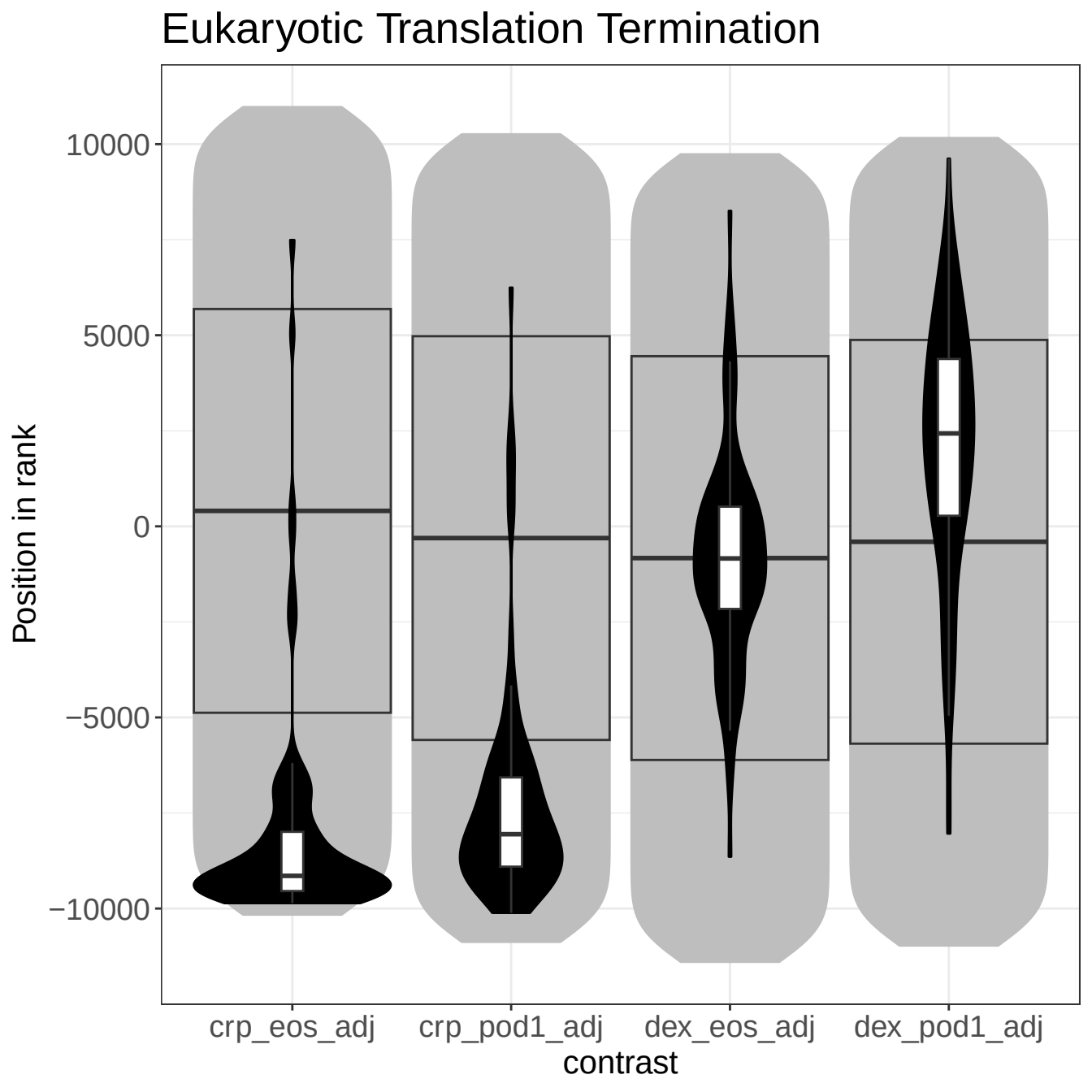

L13a−mediated translational silencing of Ceruloplasmin expression
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.694***
Corr:
−0.047
Corr:
−0.279**
Corr:
0.275**
Corr:
−0.508***
Corr:
−0.087
60
40
20
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000


L13a−mediated translational silencing of Ceruloplasmin expression
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.694***
Corr:
−0.047
Corr:
−0.279**
Corr:
0.275**
Corr:
−0.508***
Corr:
−0.087
60
40
20
0
10000
5000
0
−5000
−10000

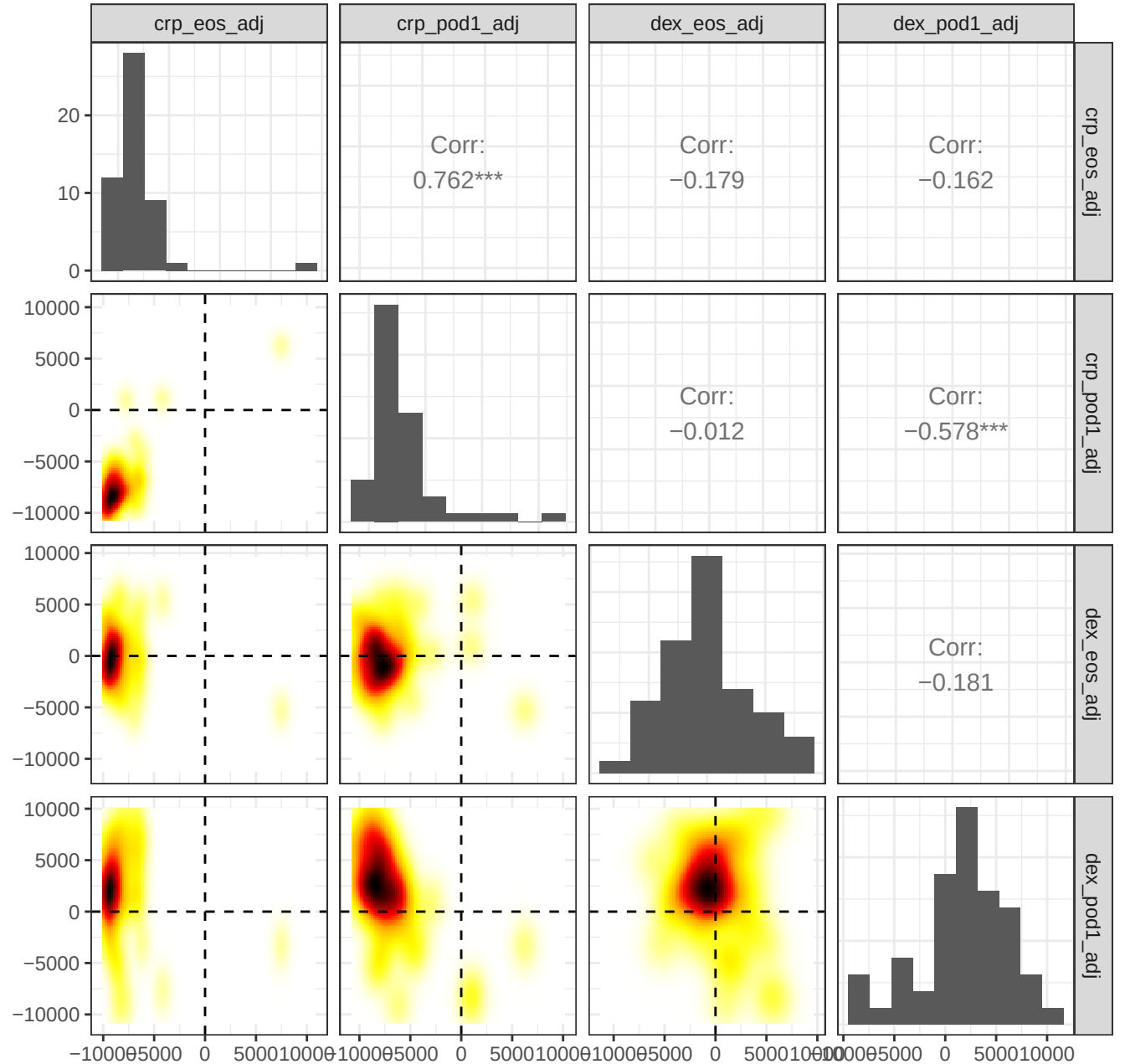

L13a−mediated translational silencing of Cerulop
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast


Eukaryotic Translation Termination
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.604***
Corr:
−0.278**
Corr:
−0.331**
Corr:
0.155
Corr:
−0.537***
Corr:
0.100
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

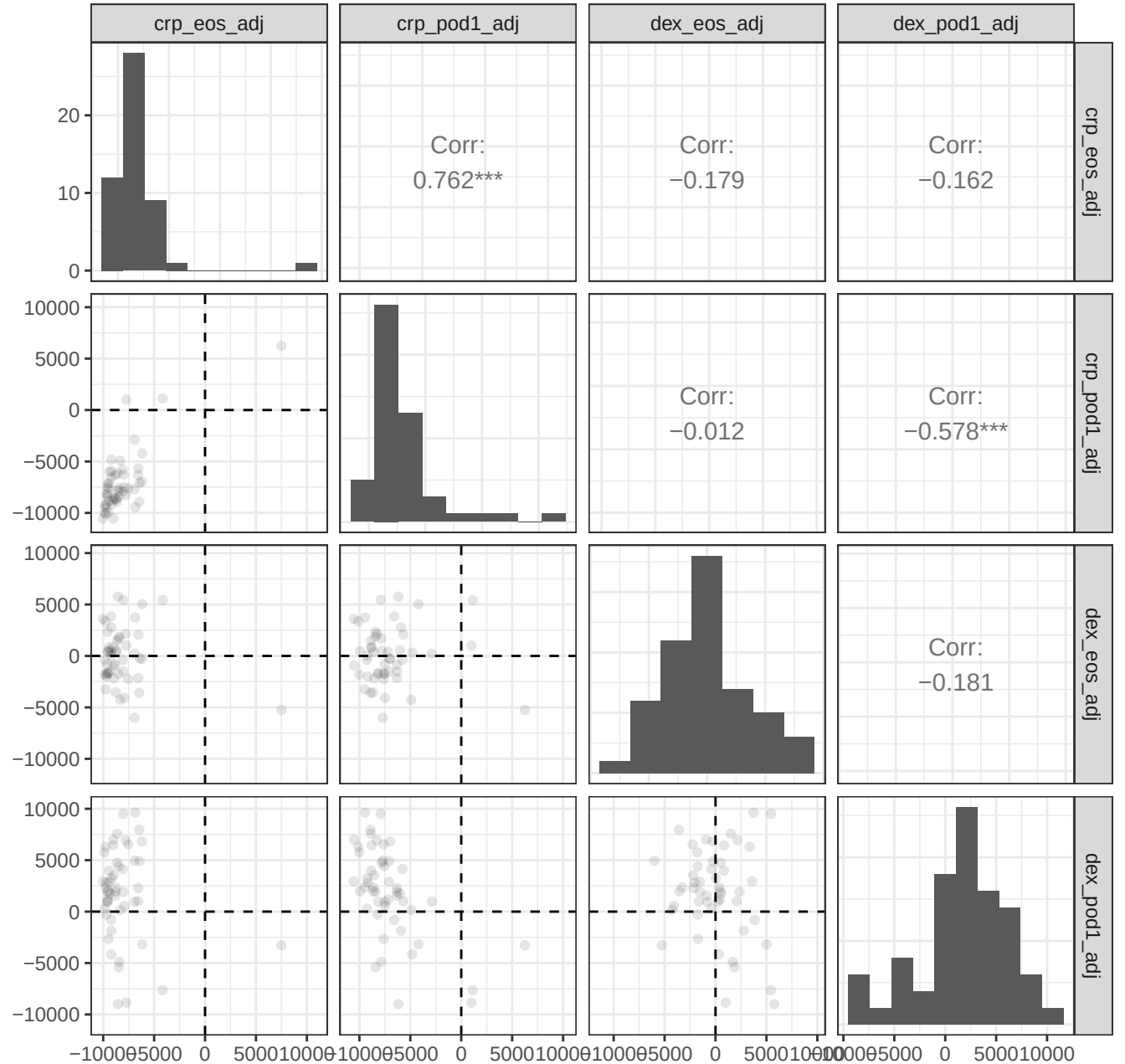

Eukaryotic Translation Termination
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.604***
Corr:
−0.278**
Corr:
−0.331**
Corr:
0.155
Corr:
−0.537***
Corr:
0.100

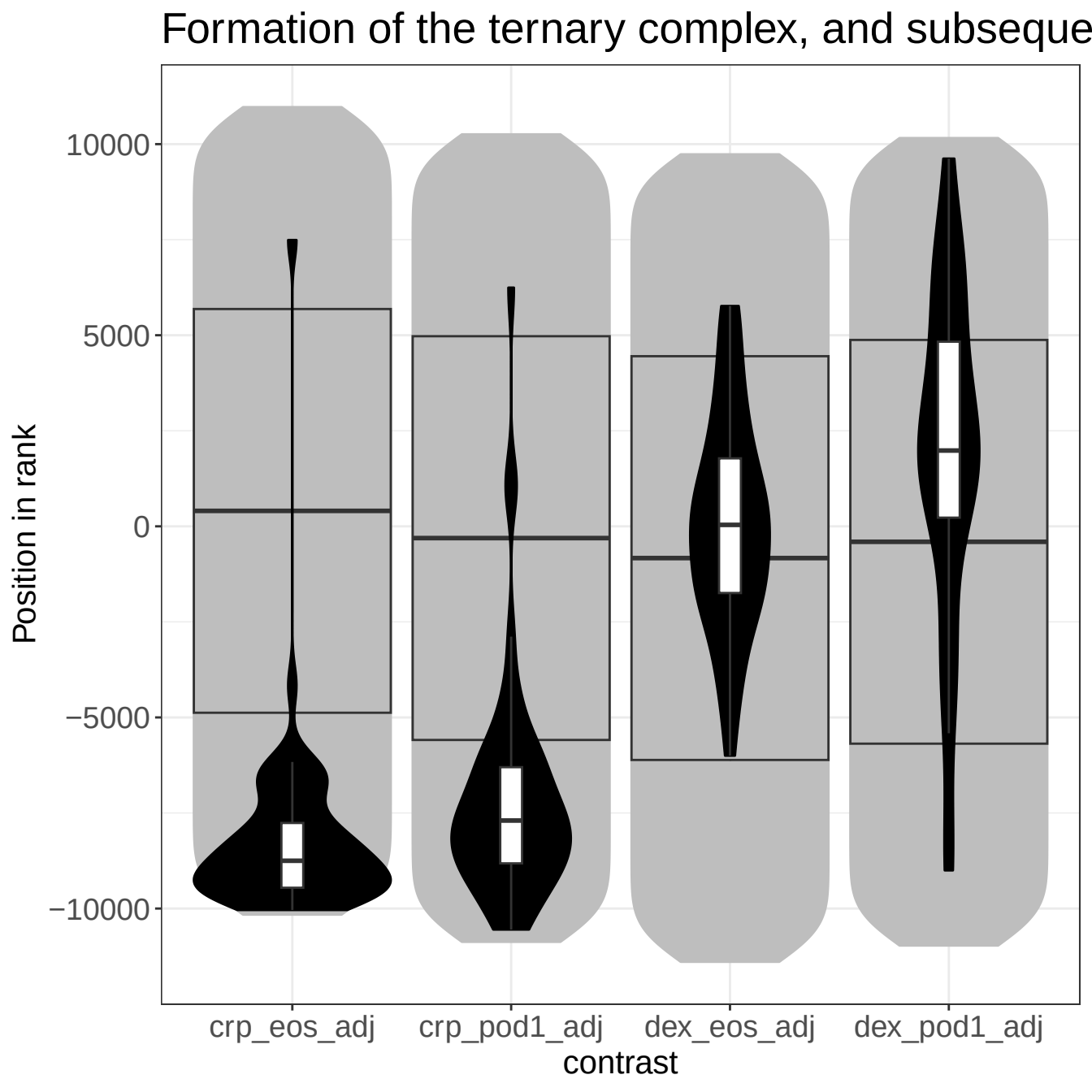

Eukaryotic Translation Termination
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

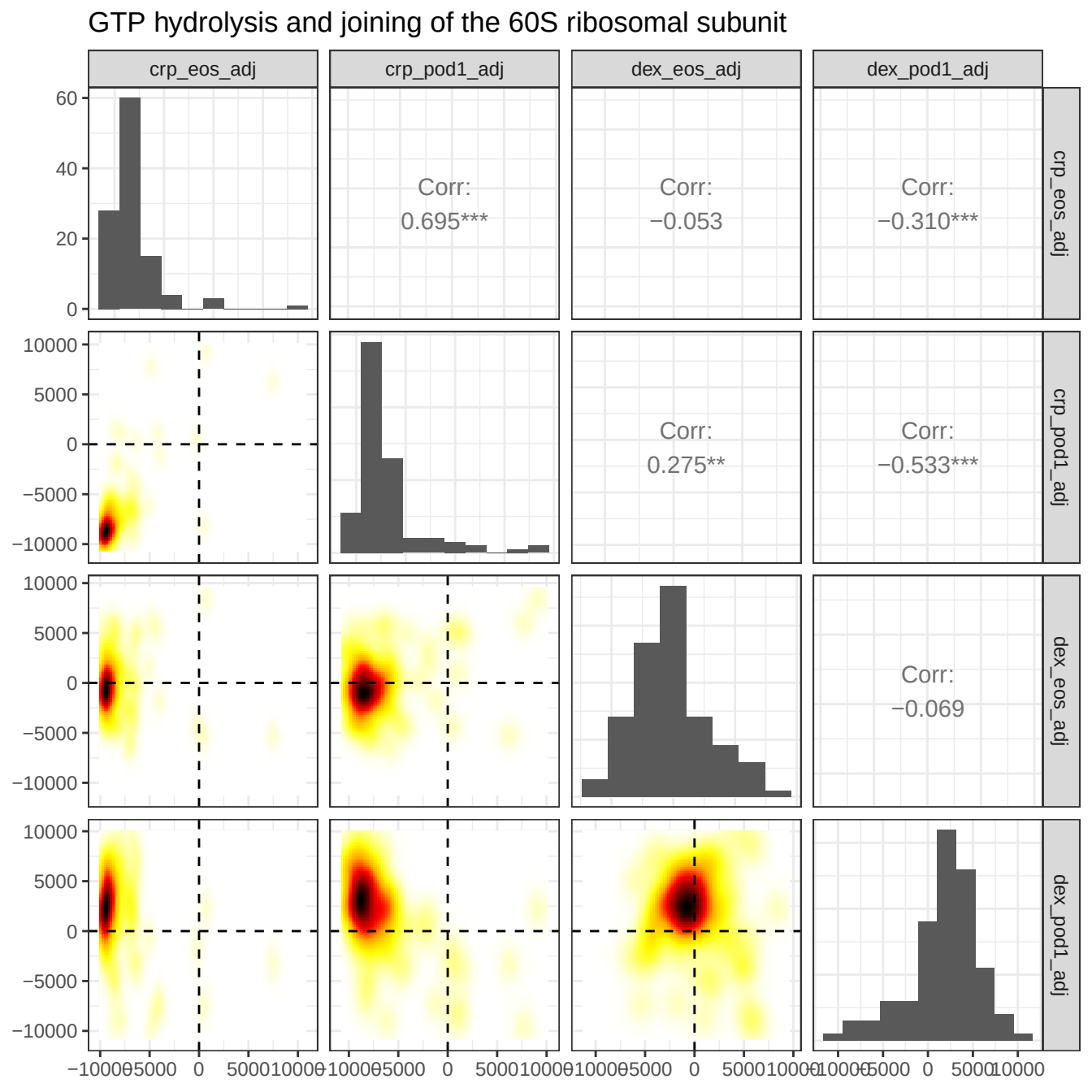
Formation of the ternary complex, and subsequently, the 43S complex

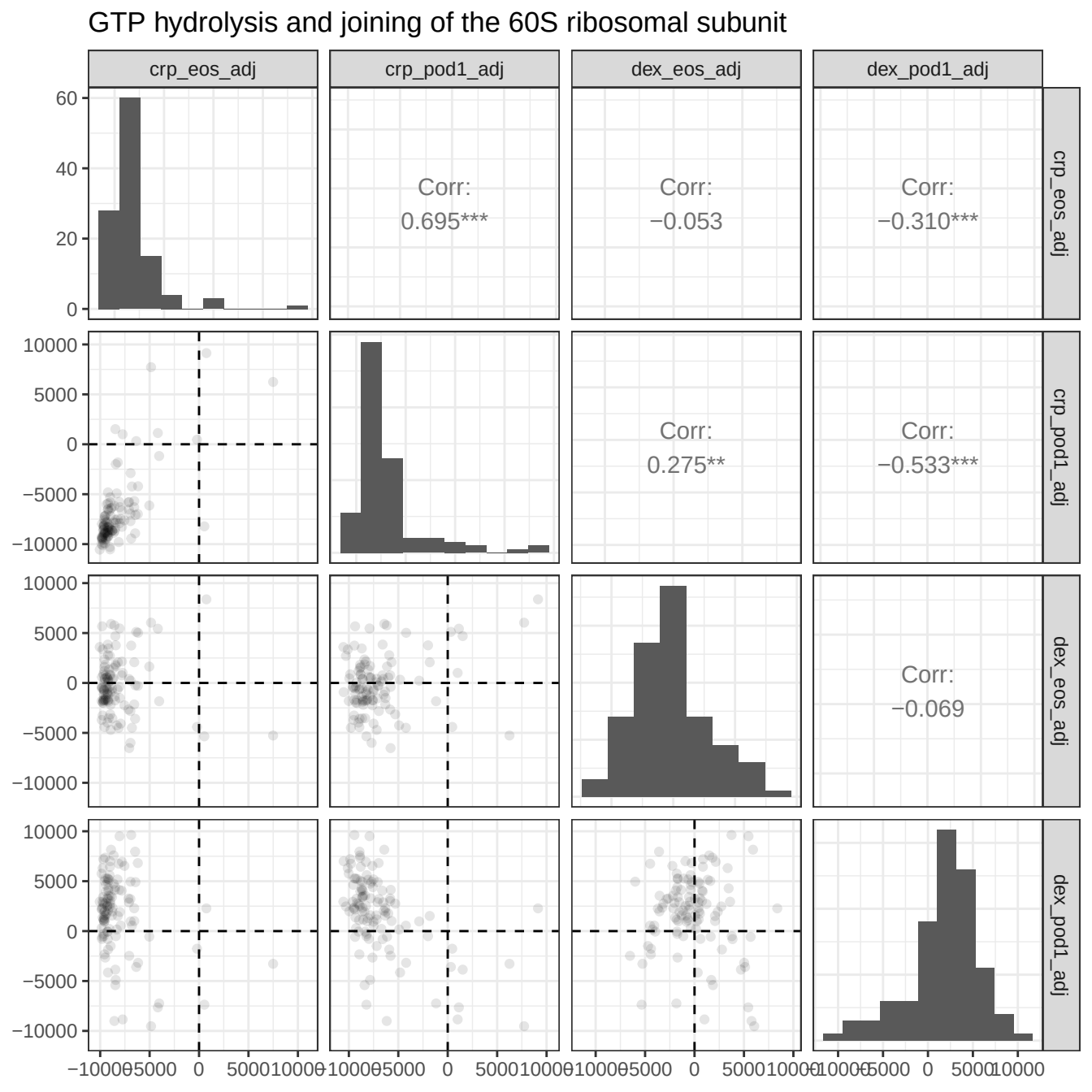


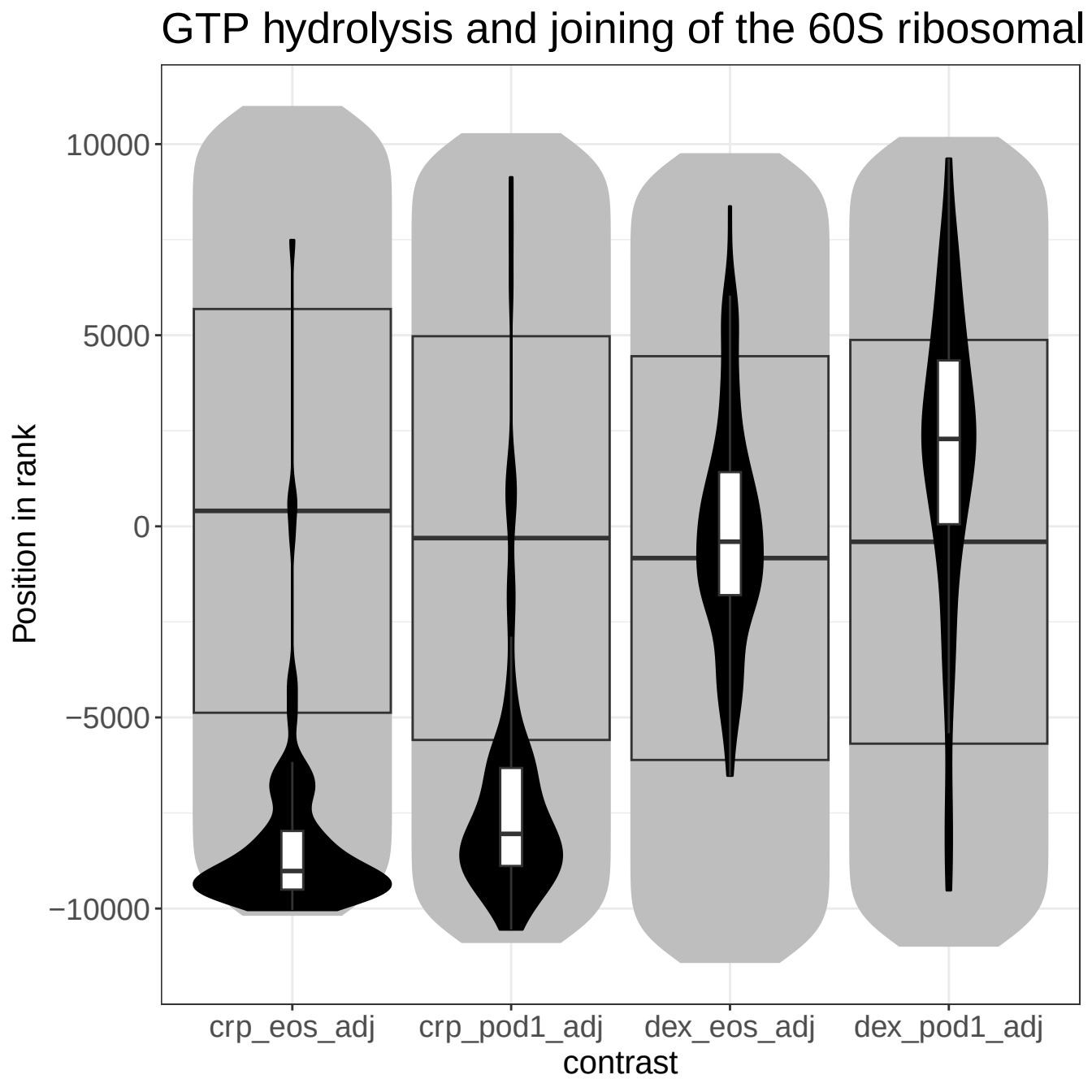
Formation of the ternary complex, and subsequently, the 43S complex

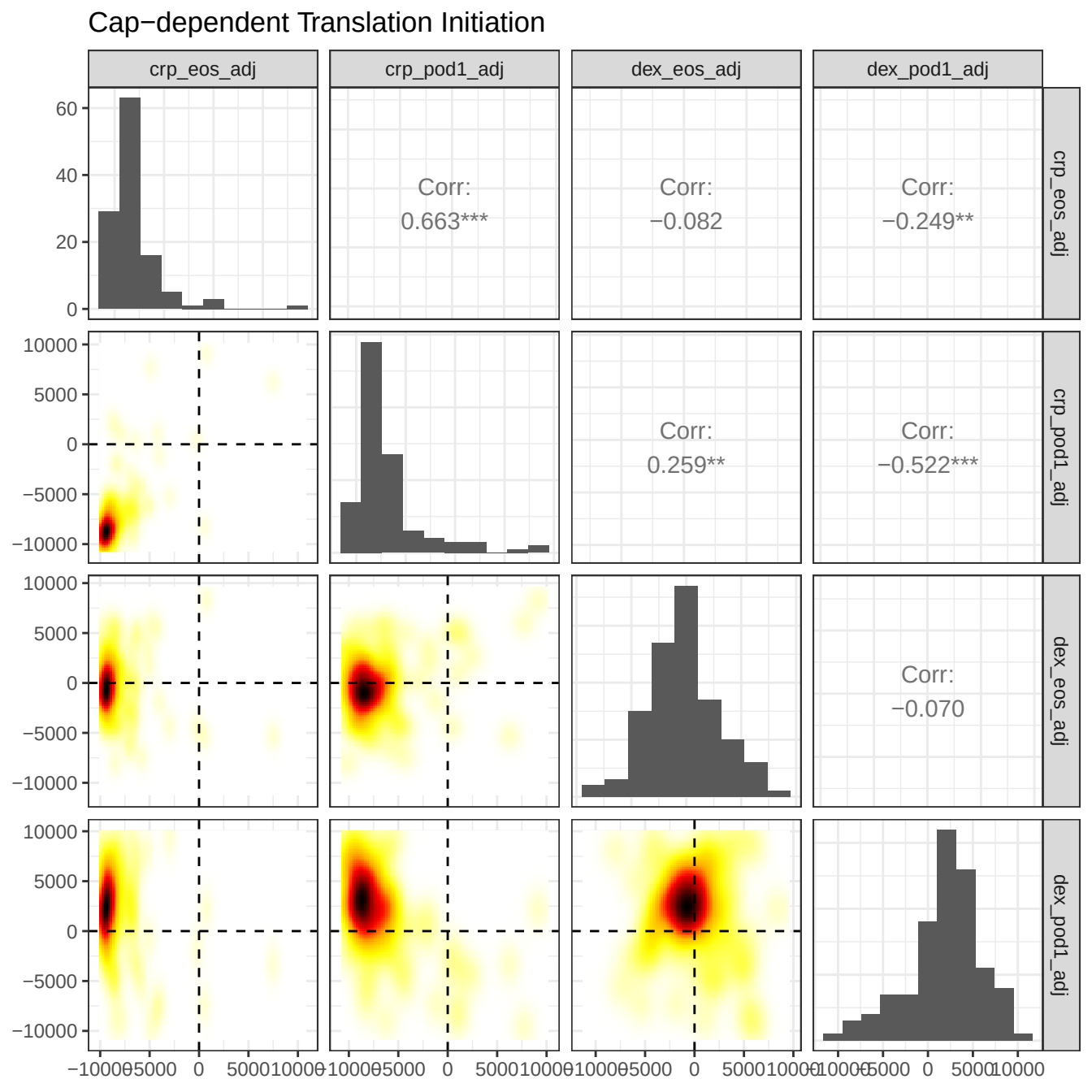


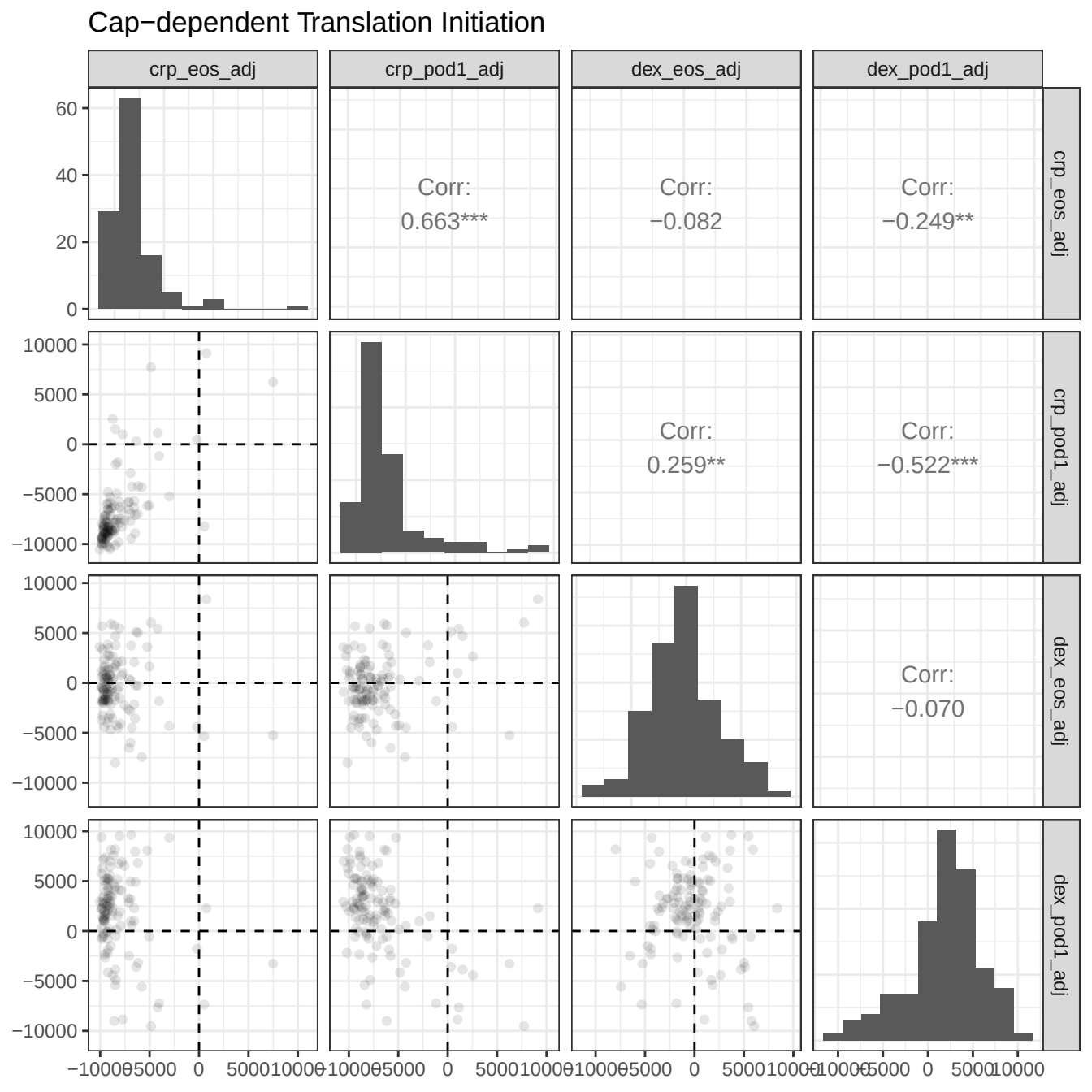

Formation of the ternary complex, and subseque
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

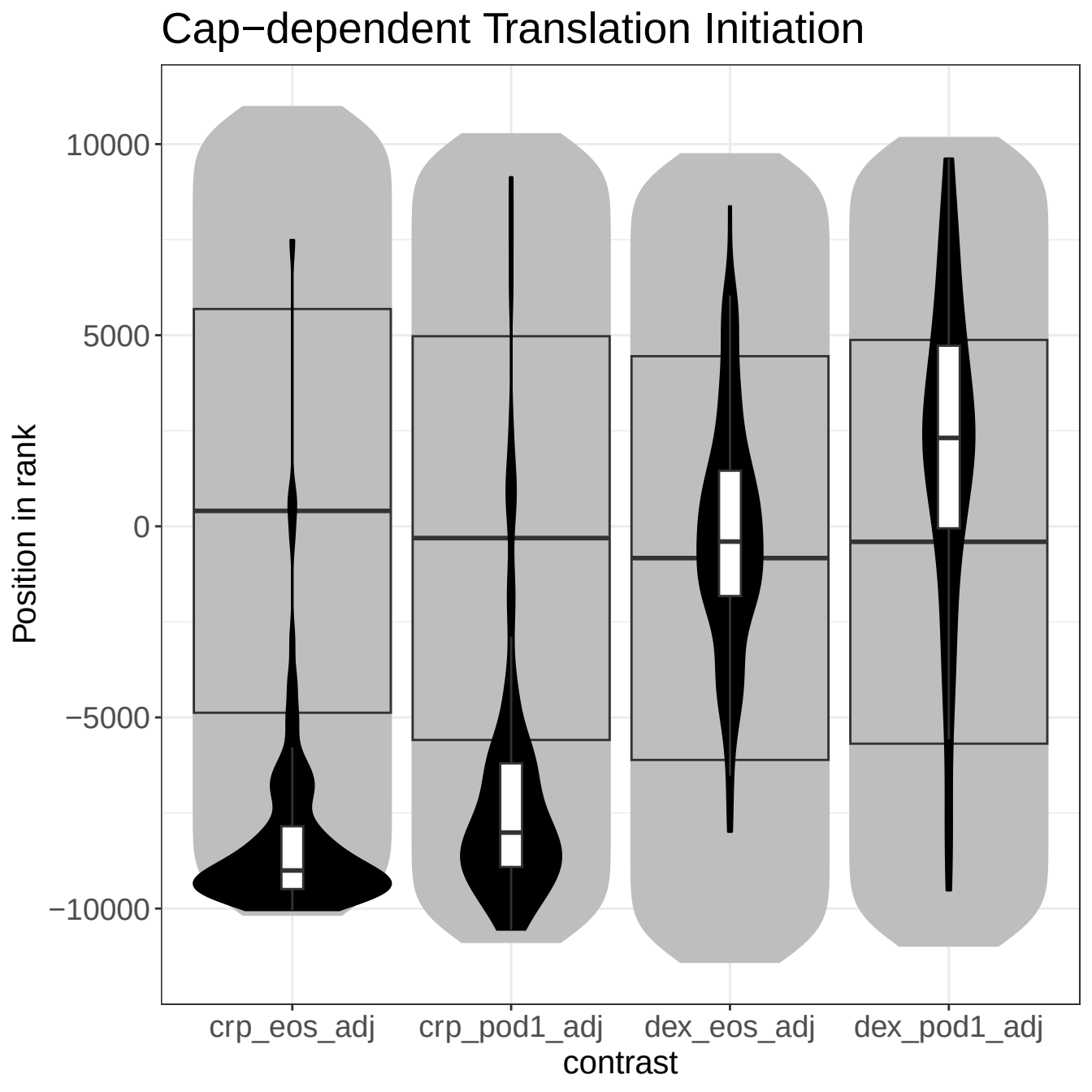

GTP hydrolysis and joining of the 60S ribosomal subunit
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.695***
Corr:
−0.053
Corr:
−0.310***
Corr:
0.275**
Corr:
−0.533***
Corr:
−0.069
60
40
20
0
10000
5000
0
−5000
−10000

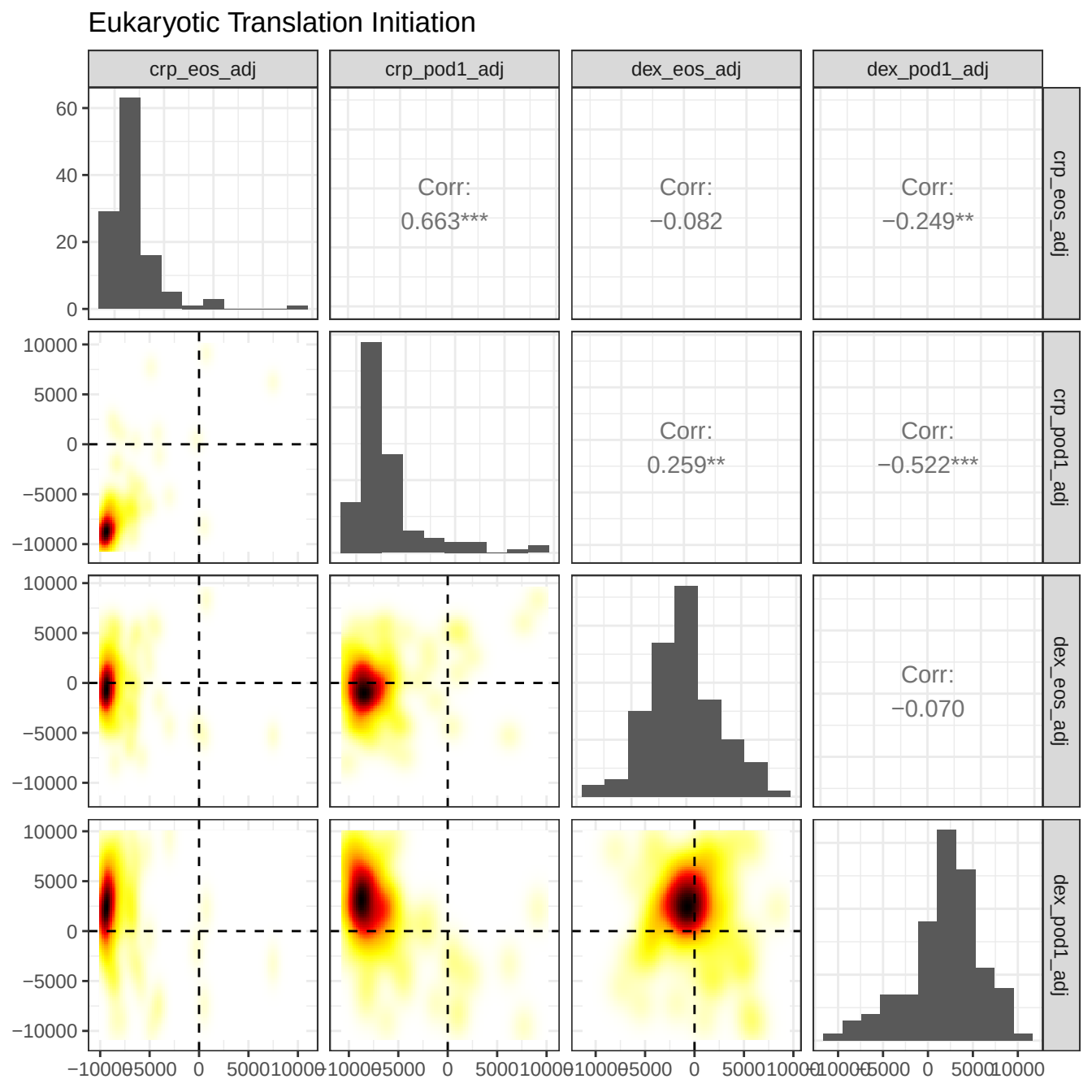

GTP hydrolysis and joining of the 60S ribosomal subunit
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.695***
Corr:
−0.053
Corr:
−0.310***
Corr:
0.275**
Corr:
−0.533***
Corr:
−0.069
60
40
20
0
10000
5000
0
−5000
−10000

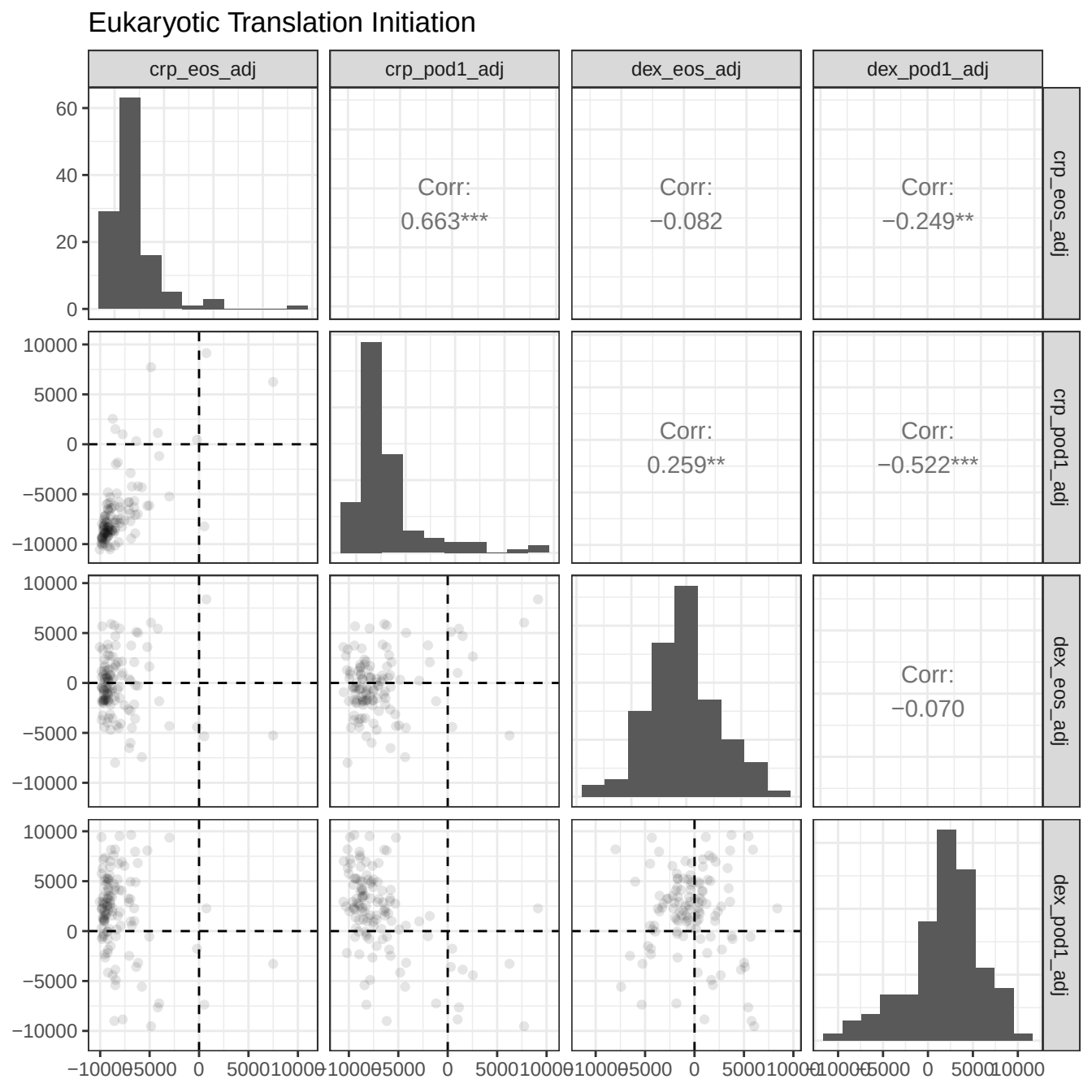

GTP hydrolysis and joining of the 60S ribosomal
Position in rank
10000
5000
0
−5000
−10000
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

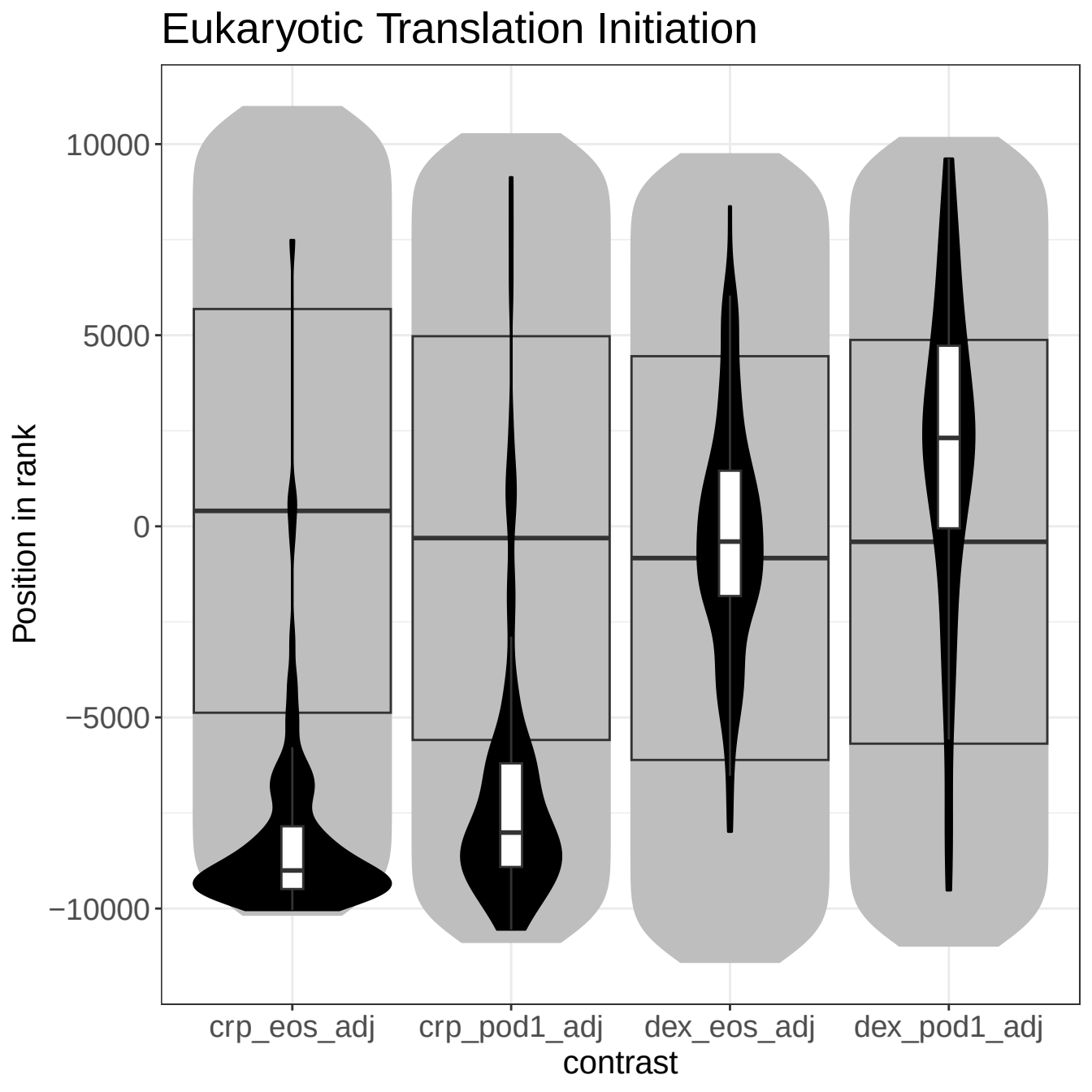

Cap−dependent Translation Initiation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.663***
Corr:
−0.082
Corr:
−0.249**
Corr:
0.259**
Corr:
−0.522***
Corr:
−0.070
60
40
20
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

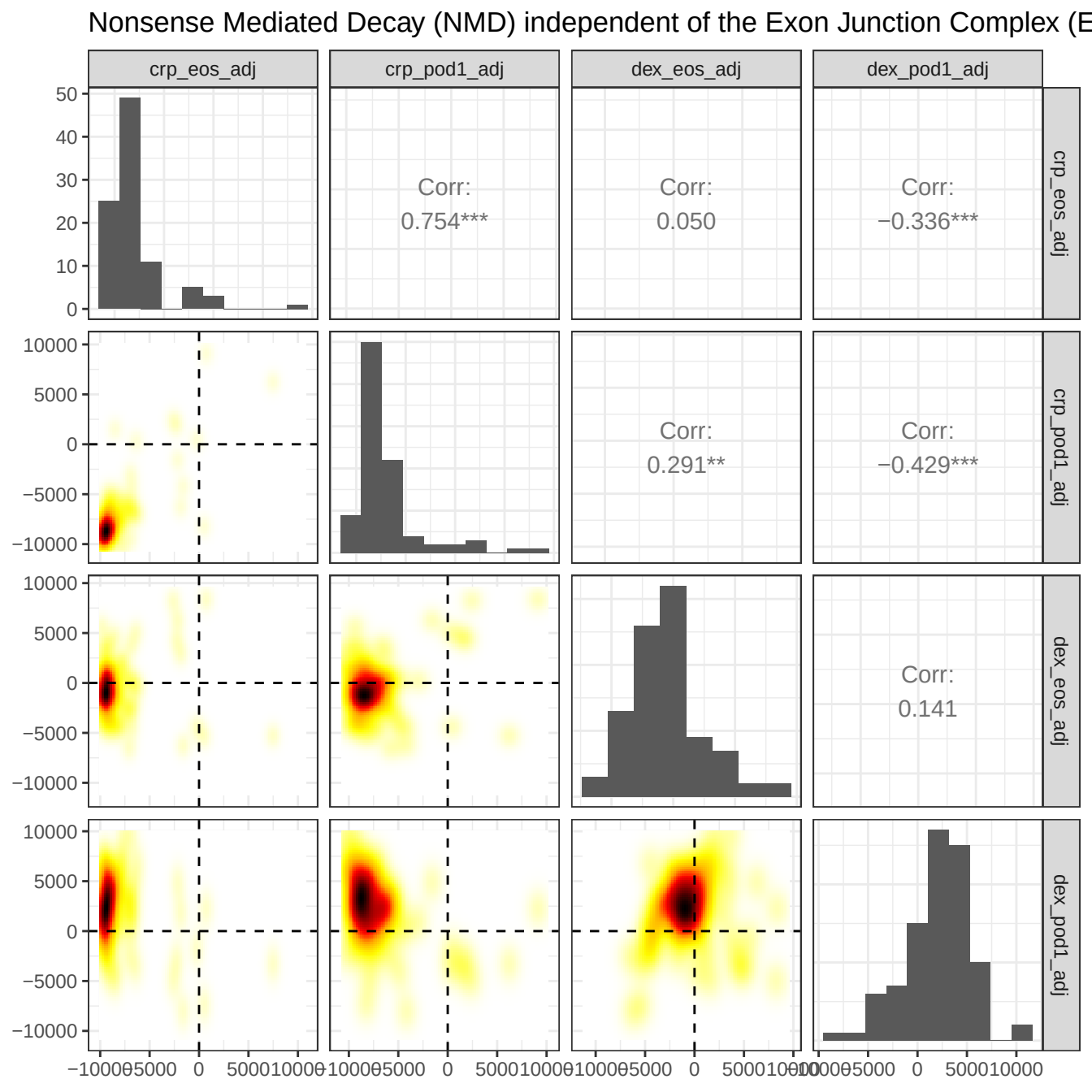

Cap−dependent Translation Initiation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.663***
Corr:
−0.082
Corr:
−0.249**
Corr:
0.259**
Corr:
−0.522***
Corr:
−0.070
60
40
20
0
10000
5000
0
−5000
−10000

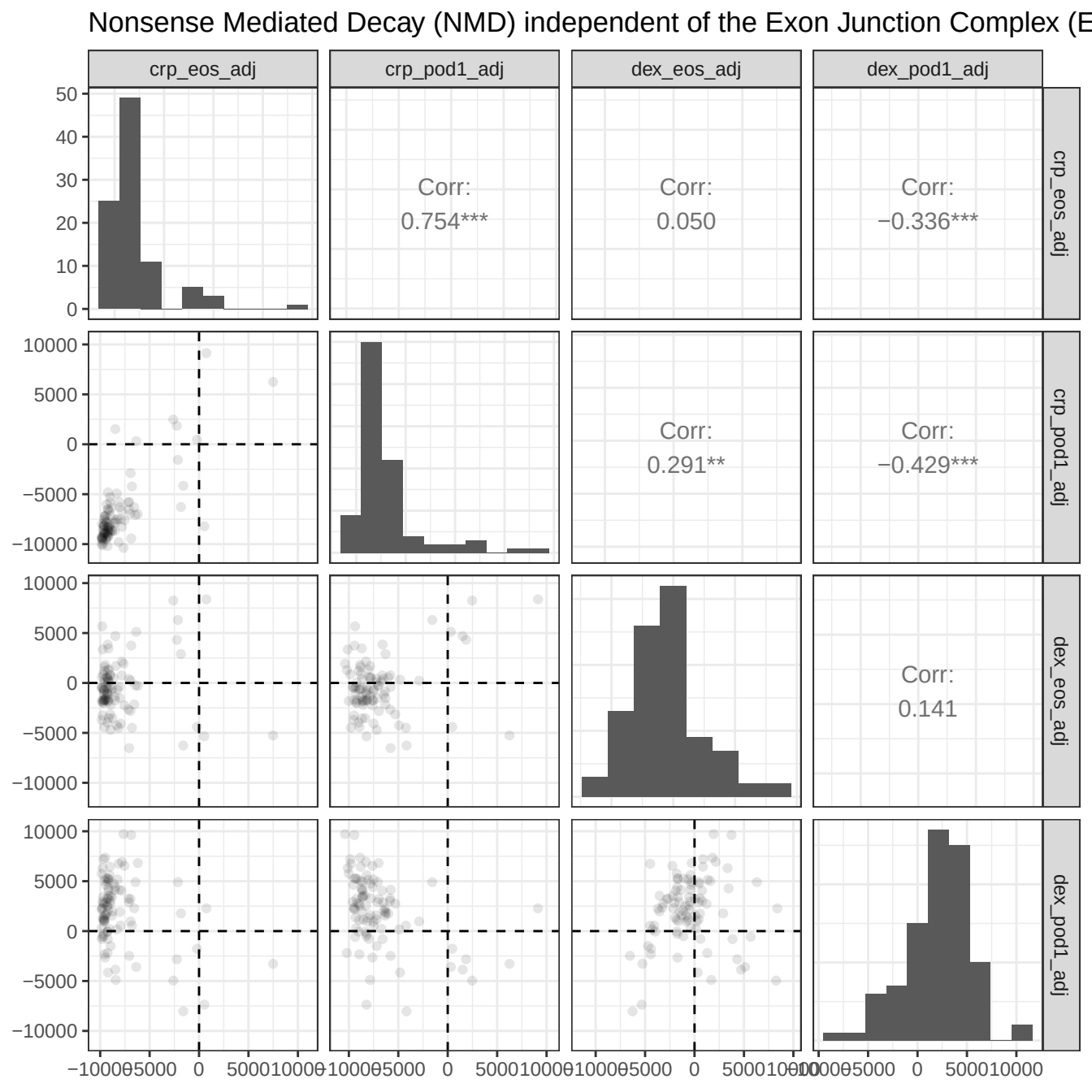

Cap−dependent Translation Initiation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

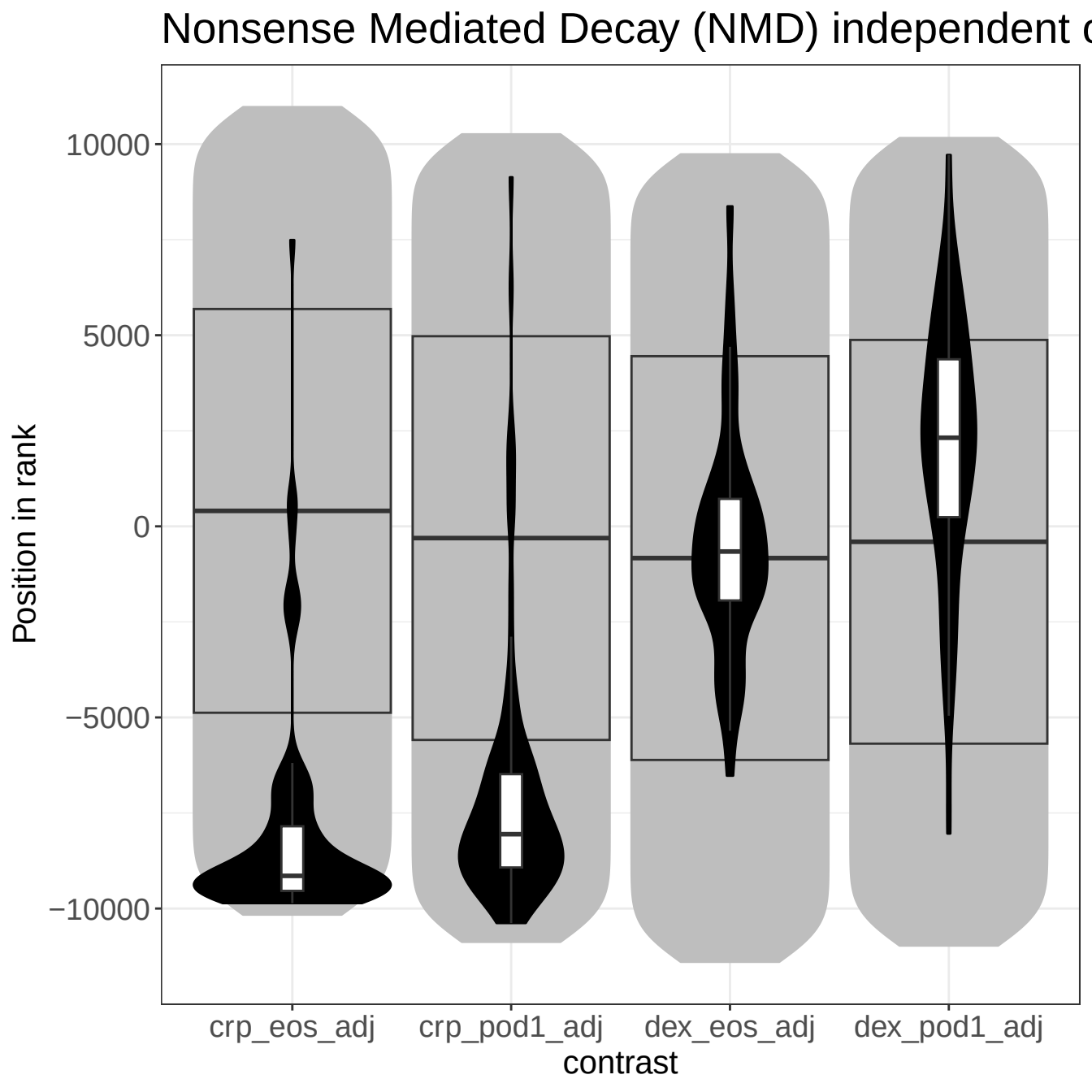

Eukaryotic Translation Initiation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.663***
Corr:
−0.082
Corr:
−0.249**
Corr:
0.259**
Corr:
−0.522***
Corr:
−0.070
60
40
20
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

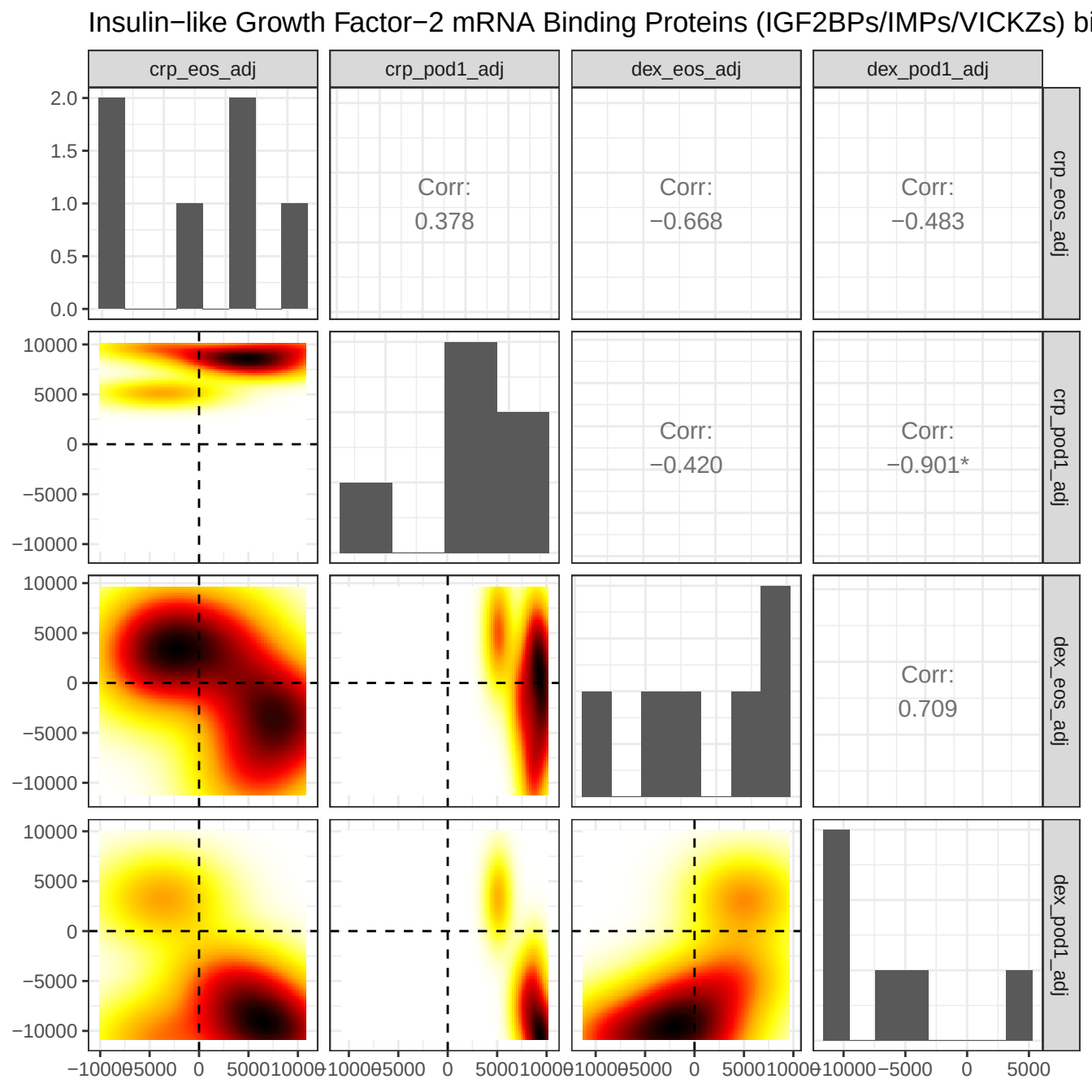

Eukaryotic Translation Initiation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.663***
Corr:
−0.082
Corr:
−0.249**
Corr:
0.259**
Corr:
−0.522***
Corr:
−0.070
60
40
20
0
10000
5000
0
−5000
−10000

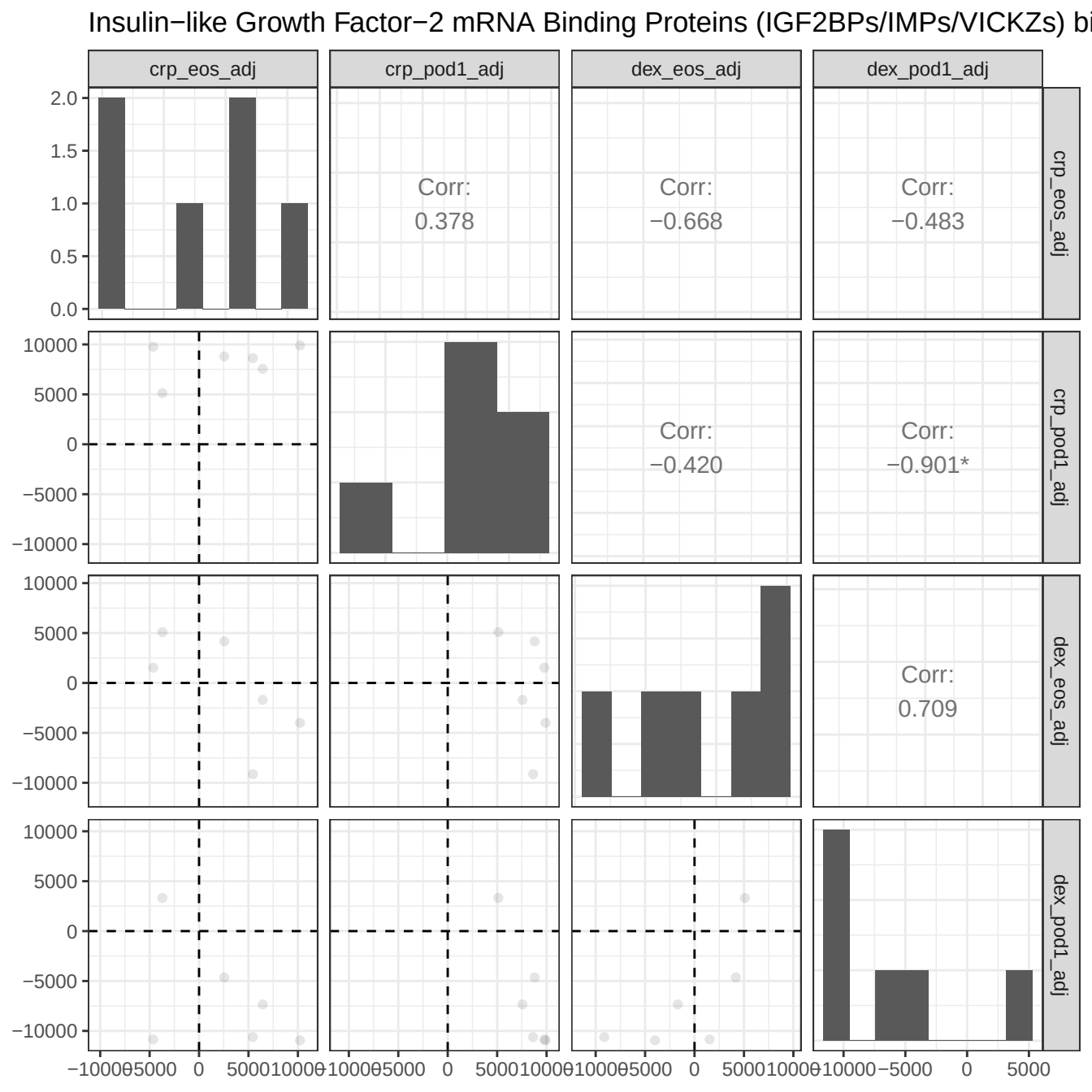

Eukaryotic Translation Initiation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

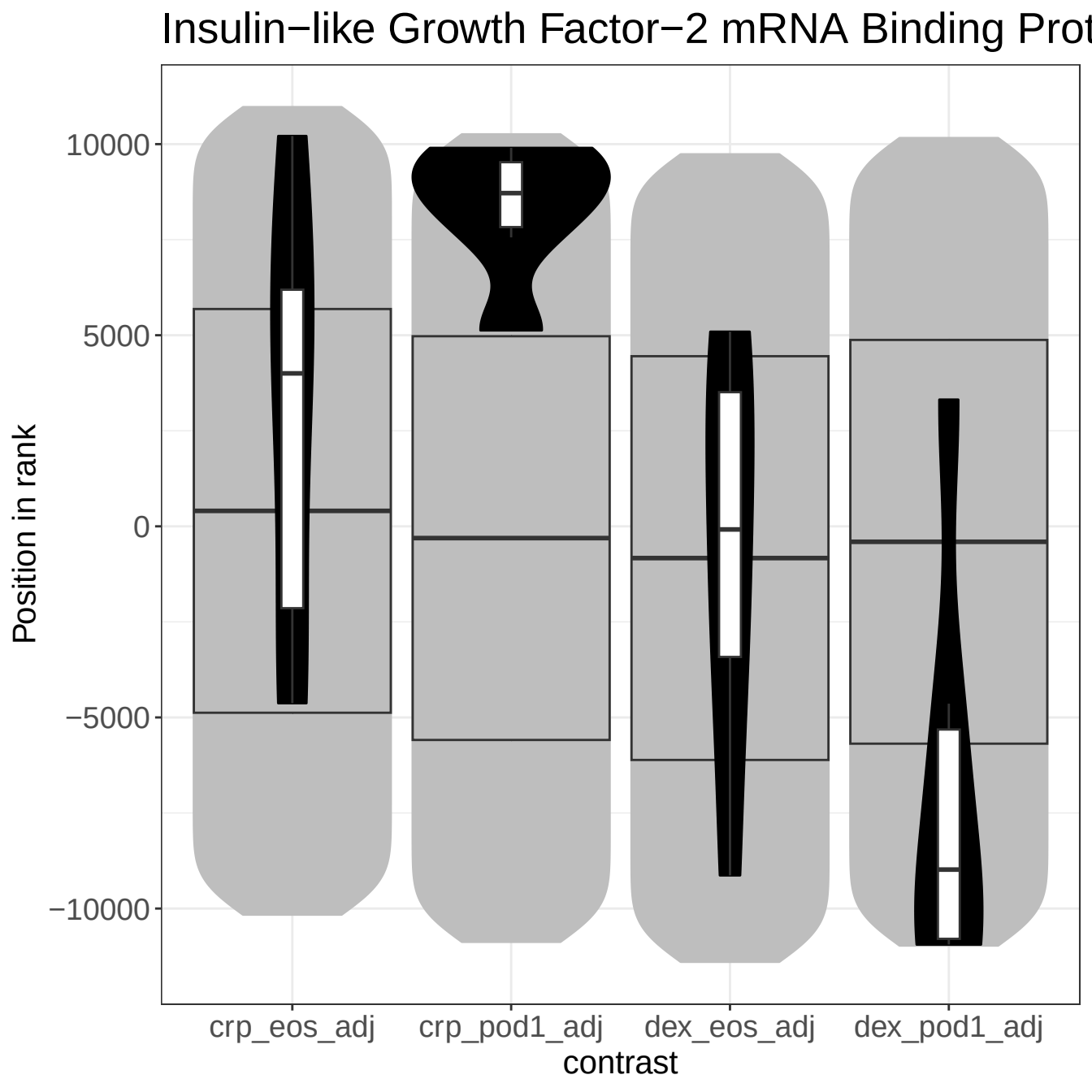

Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (E
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.754***
Corr:
0.050
Corr:
−0.336***
Corr:
0.291**
Corr:
−0.429***
Corr:
0.141
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

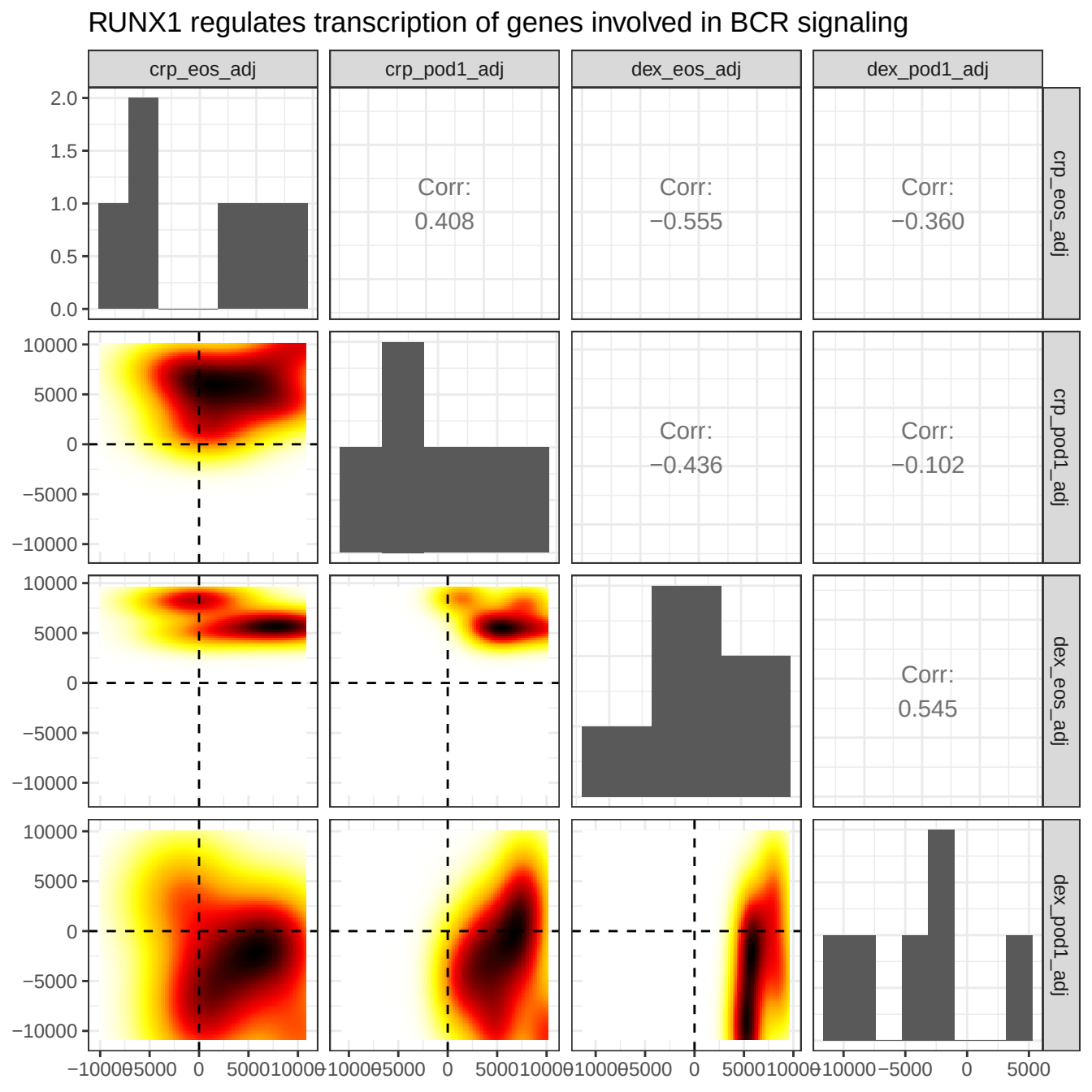

Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (E
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.754***
Corr:
0.050
Corr:
−0.336***
Corr:
0.291**
Corr:
−0.429***
Corr:
0.141
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

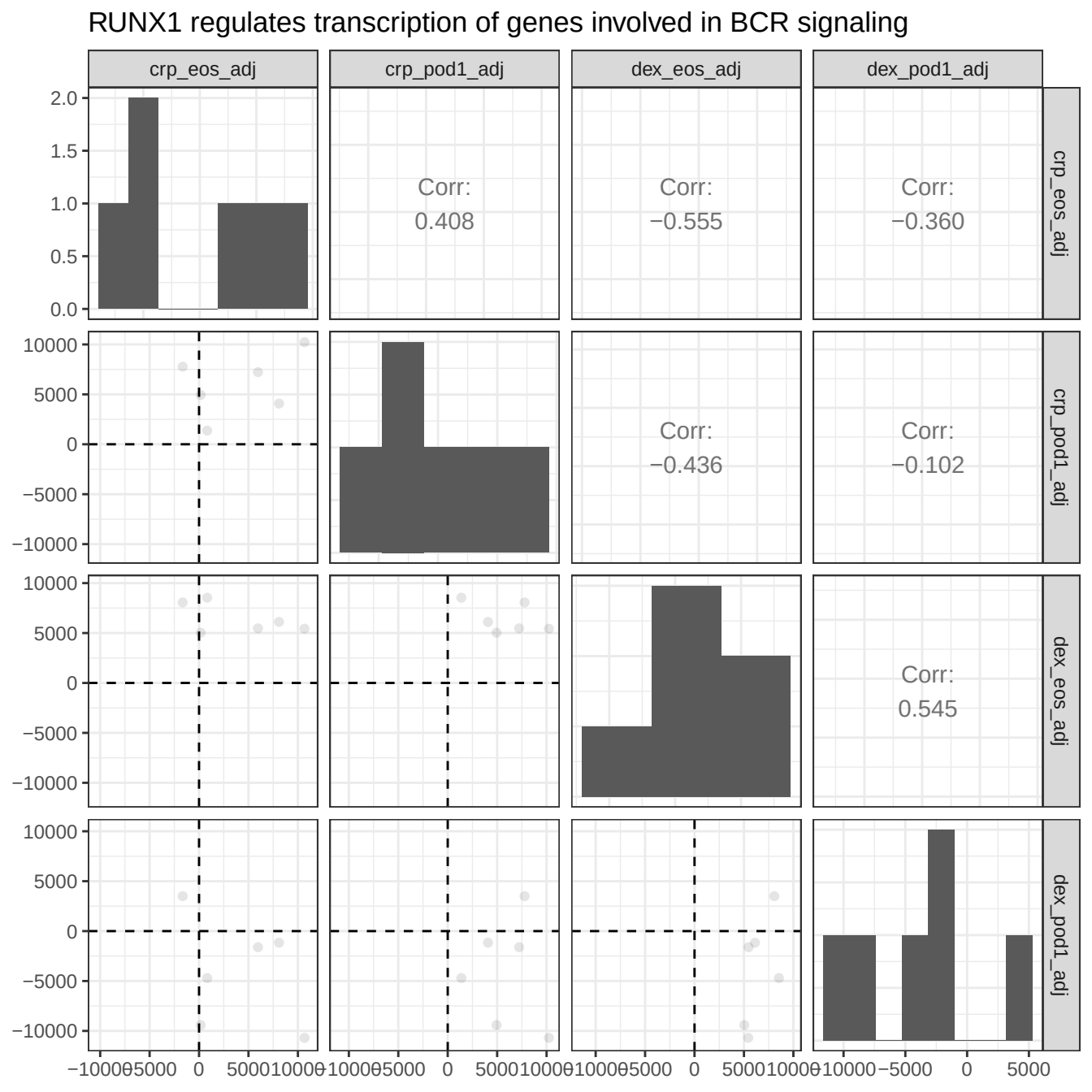

Nonsense Mediated Decay (NMD) independent
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

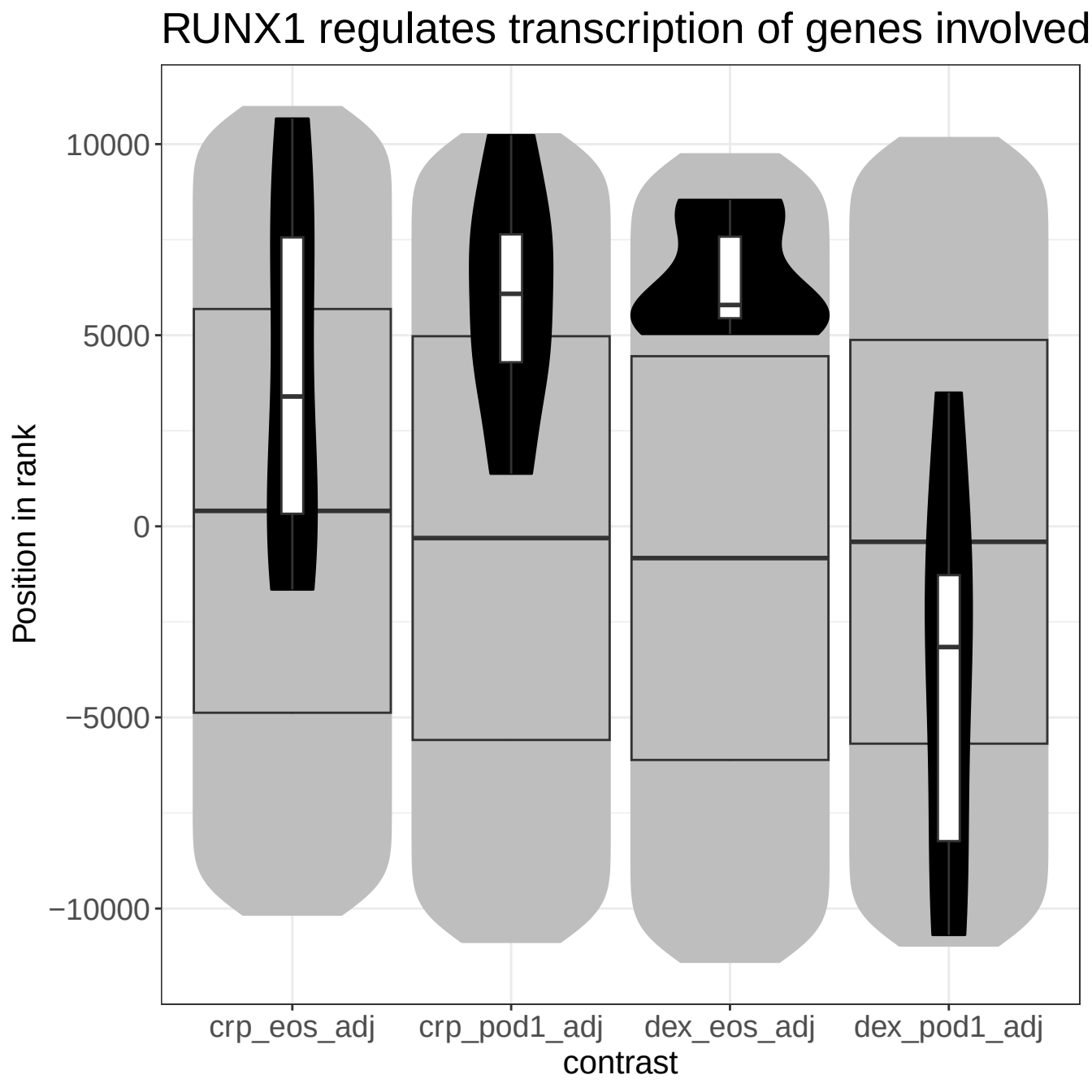

Insulin−like Growth Factor−2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bi
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.378
Corr:
−0.668
Corr:
−0.483
Corr:
−0.420
Corr:
−0.901*
Corr:
0.709
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

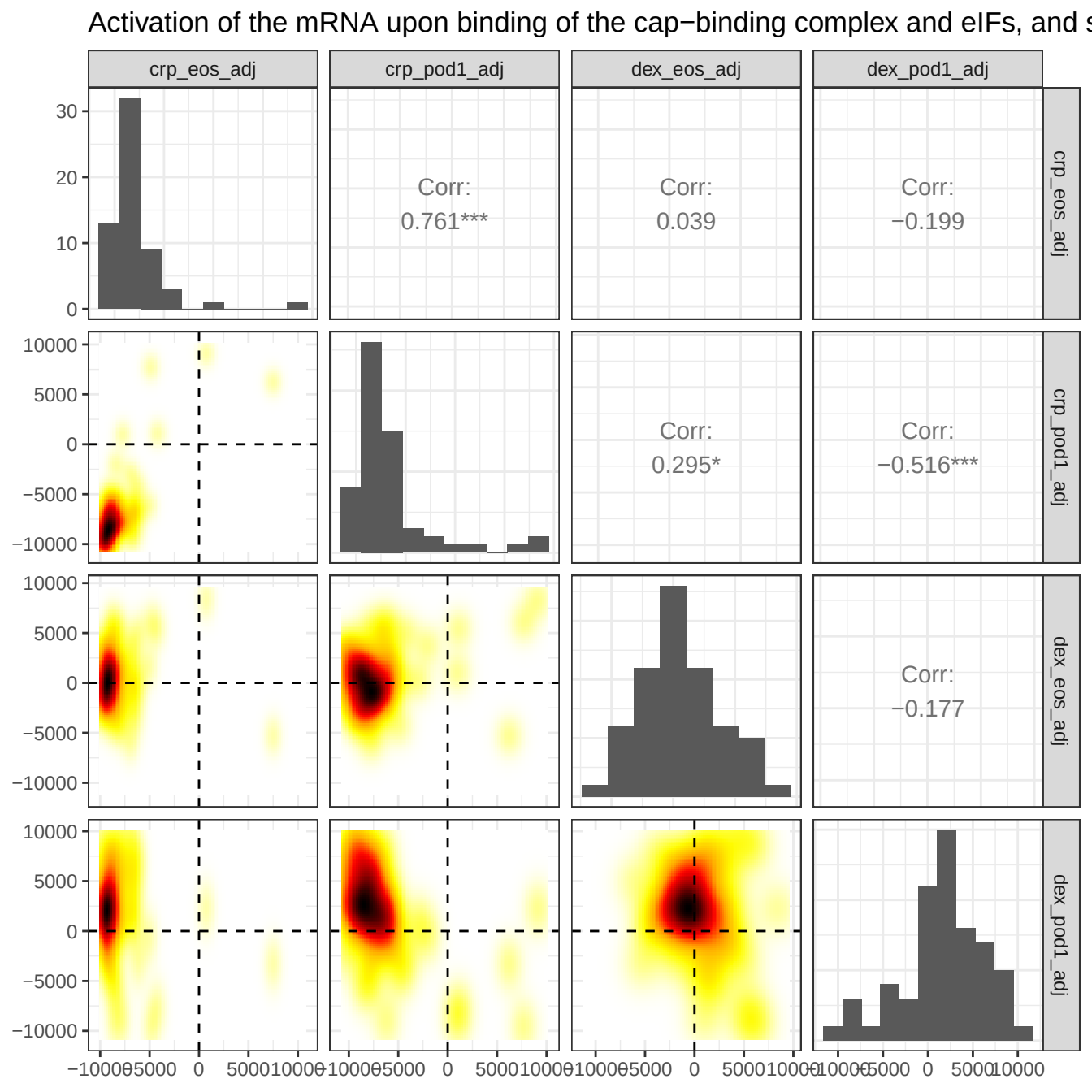

Insulin−like Growth Factor−2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bi
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.378
Corr:
−0.668
Corr:
−0.483
Corr:
−0.420
Corr:
−0.901*
Corr:
0.709
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000

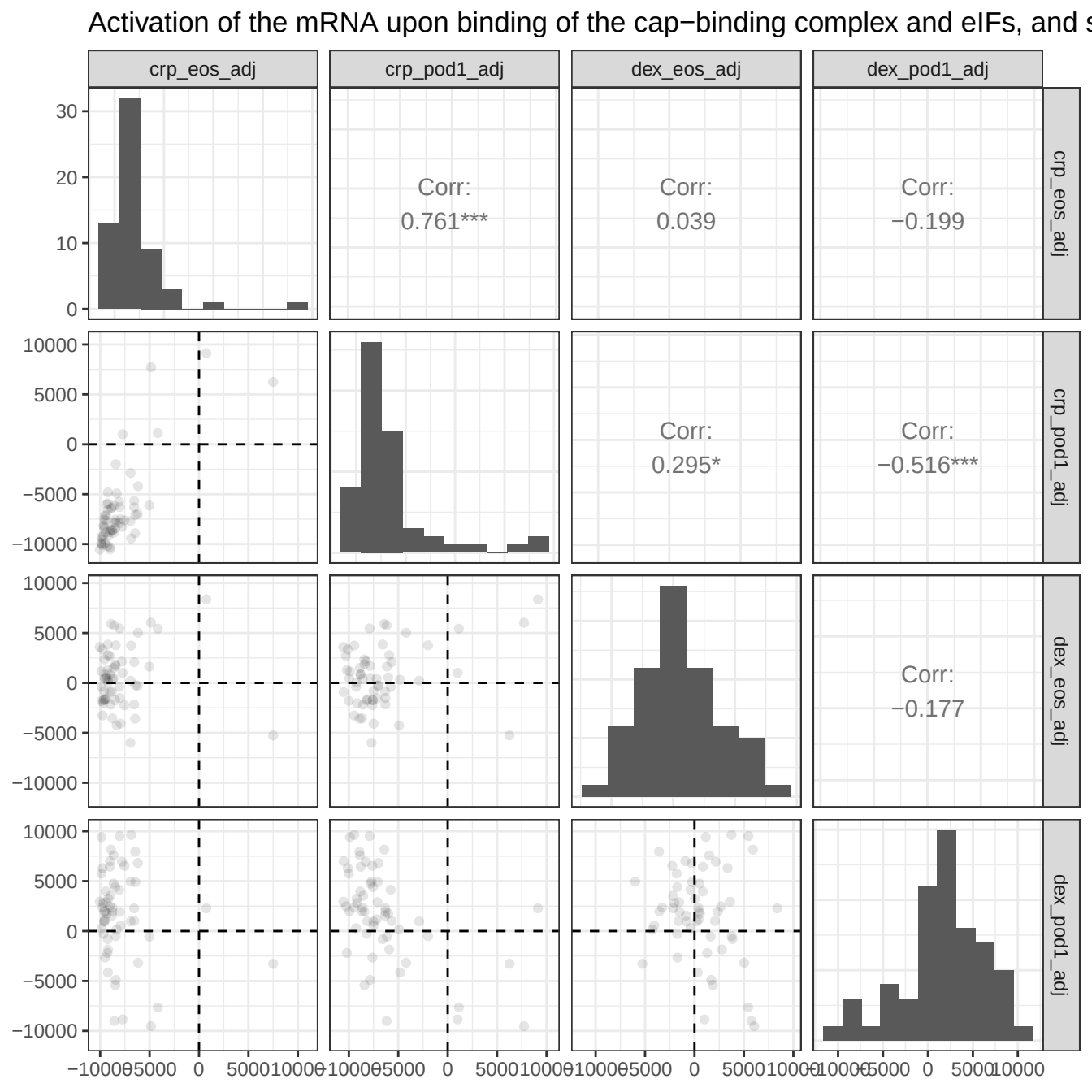

Insulin−like Growth Factor−2 mRNA Binding Prot
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

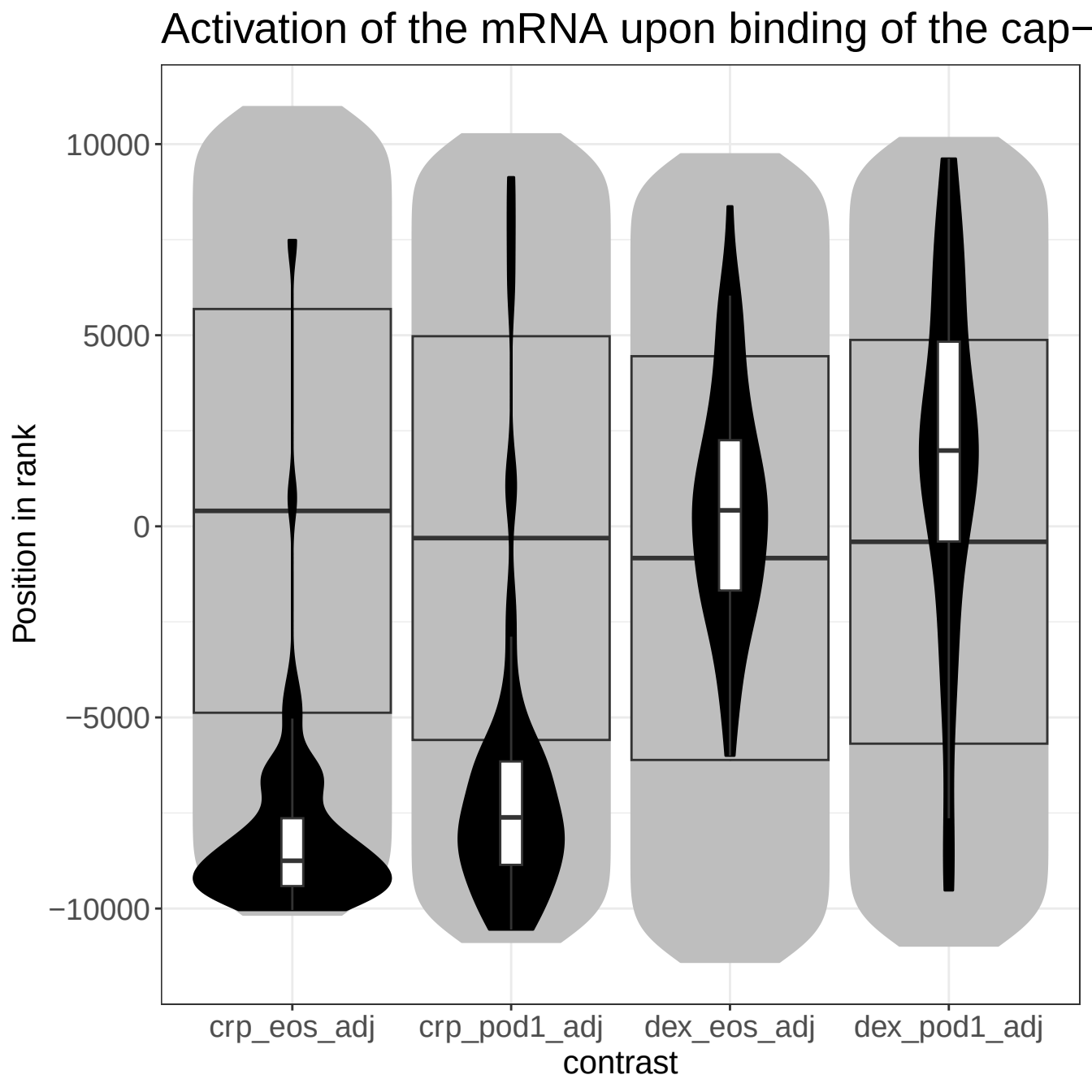

RUNX1 regulates transcription of genes involved in BCR signaling
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.408
Corr:
−0.555
Corr:
−0.360
Corr:
−0.436
Corr:
−0.102
Corr:
0.545
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

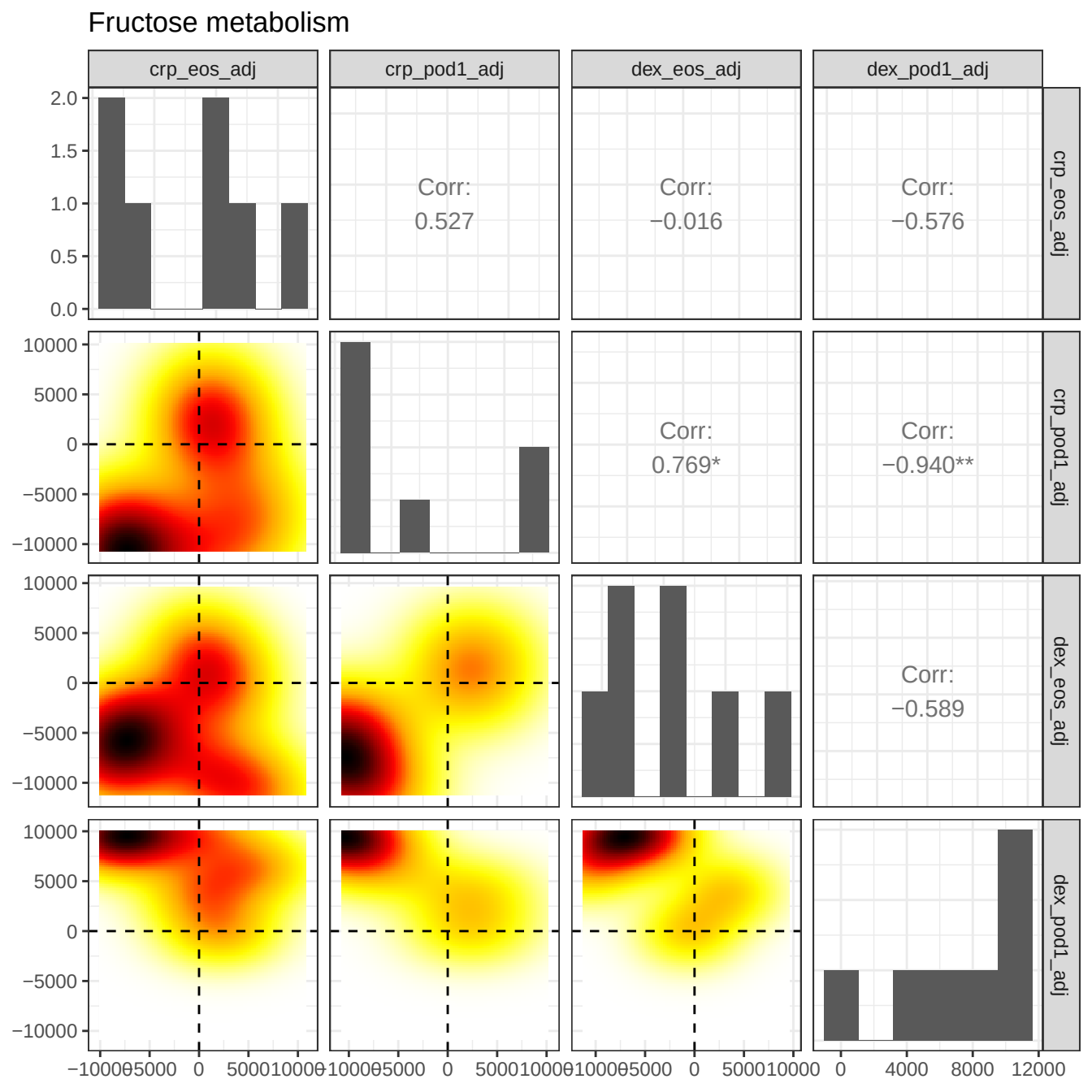

RUNX1 regulates transcription of genes involved in BCR signaling
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.408
Corr:
−0.555
Corr:
−0.360
Corr:
−0.436
Corr:
−0.102
Corr:
0.545

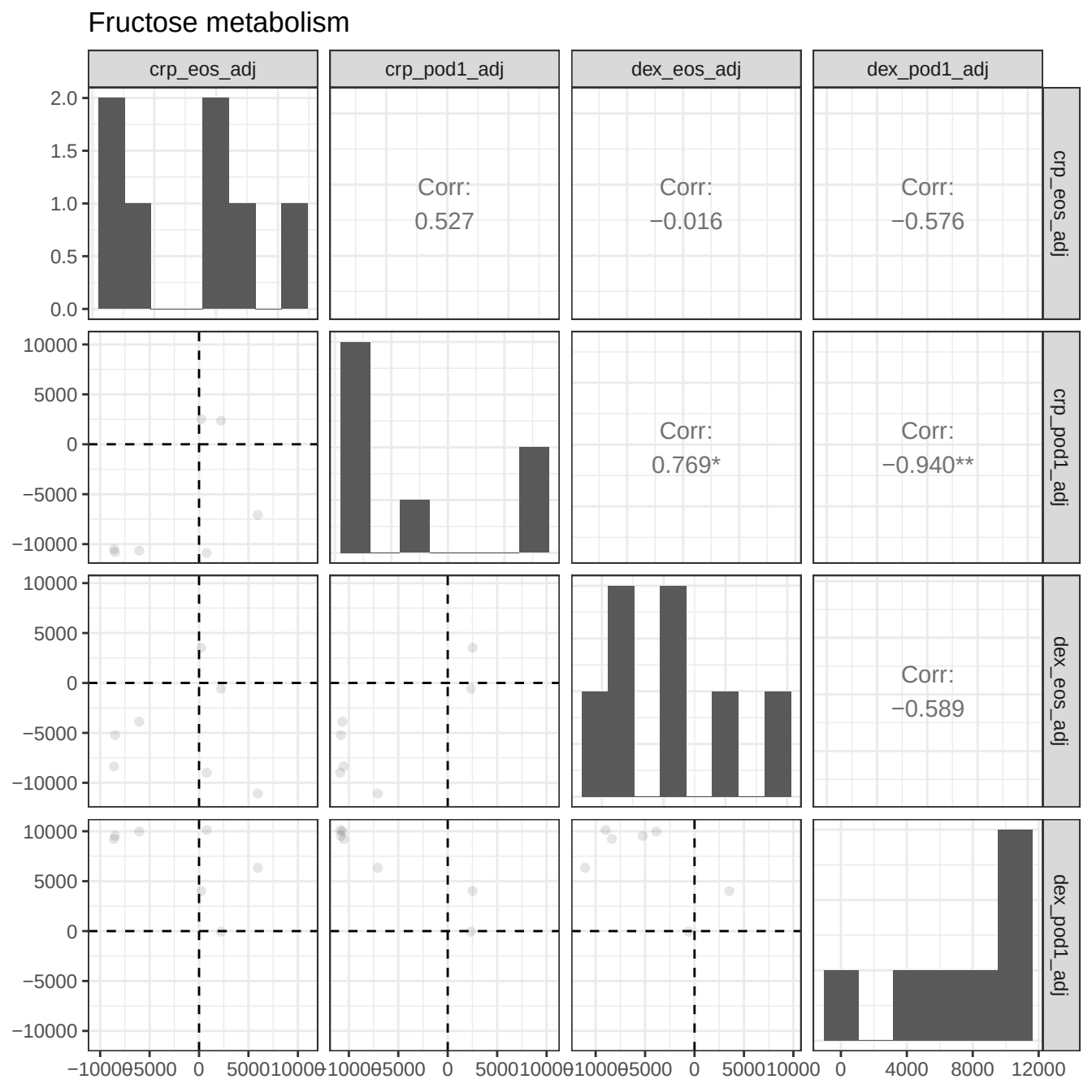

RUNX1 regulates transcription of genes involved
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

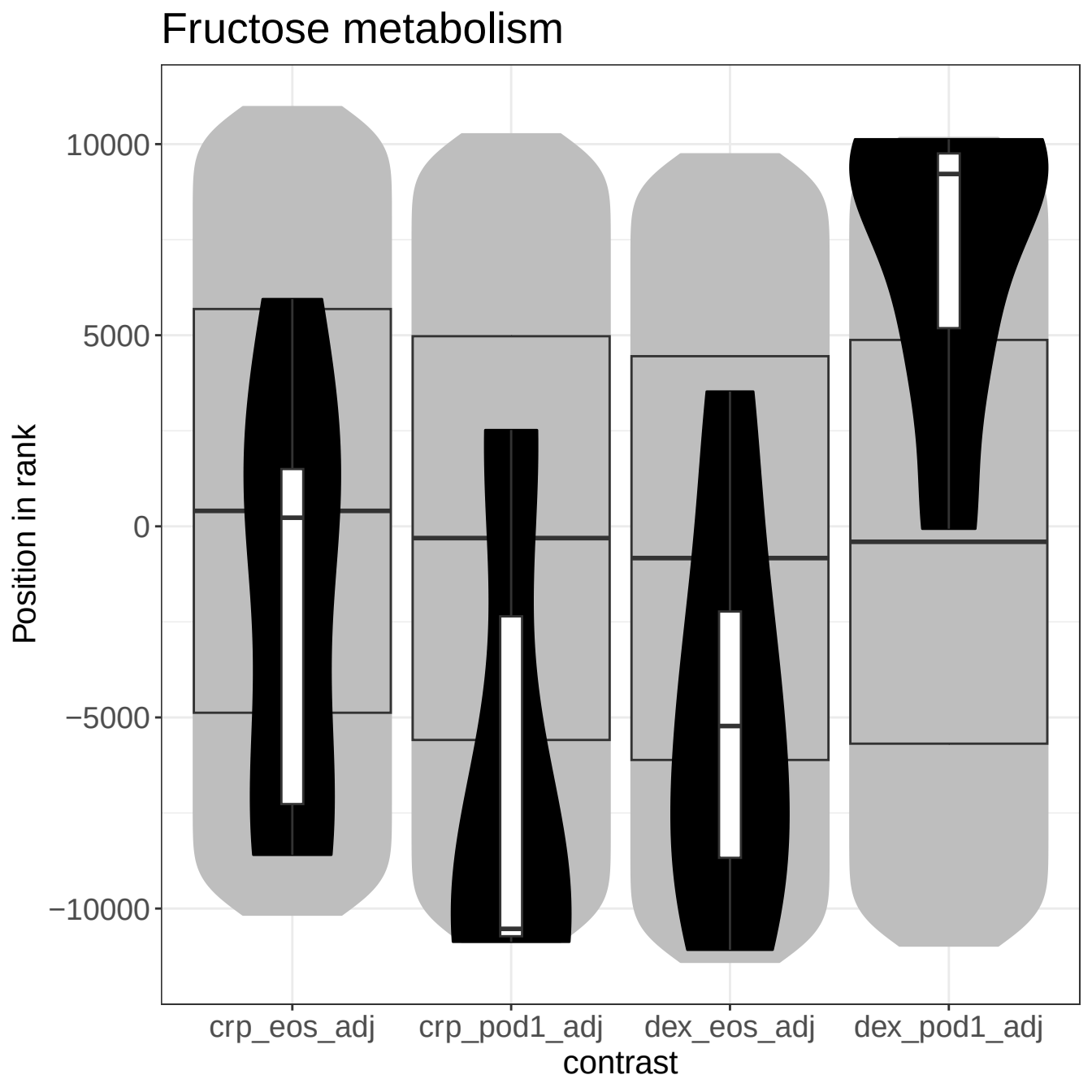

Activation of the mRNA upon binding of the cap−binding complex and eIFs, and s
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.761***
Corr:
0.039
Corr:
−0.199
Corr:
0.295*
Corr:
−0.516***
Corr:
−0.177
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

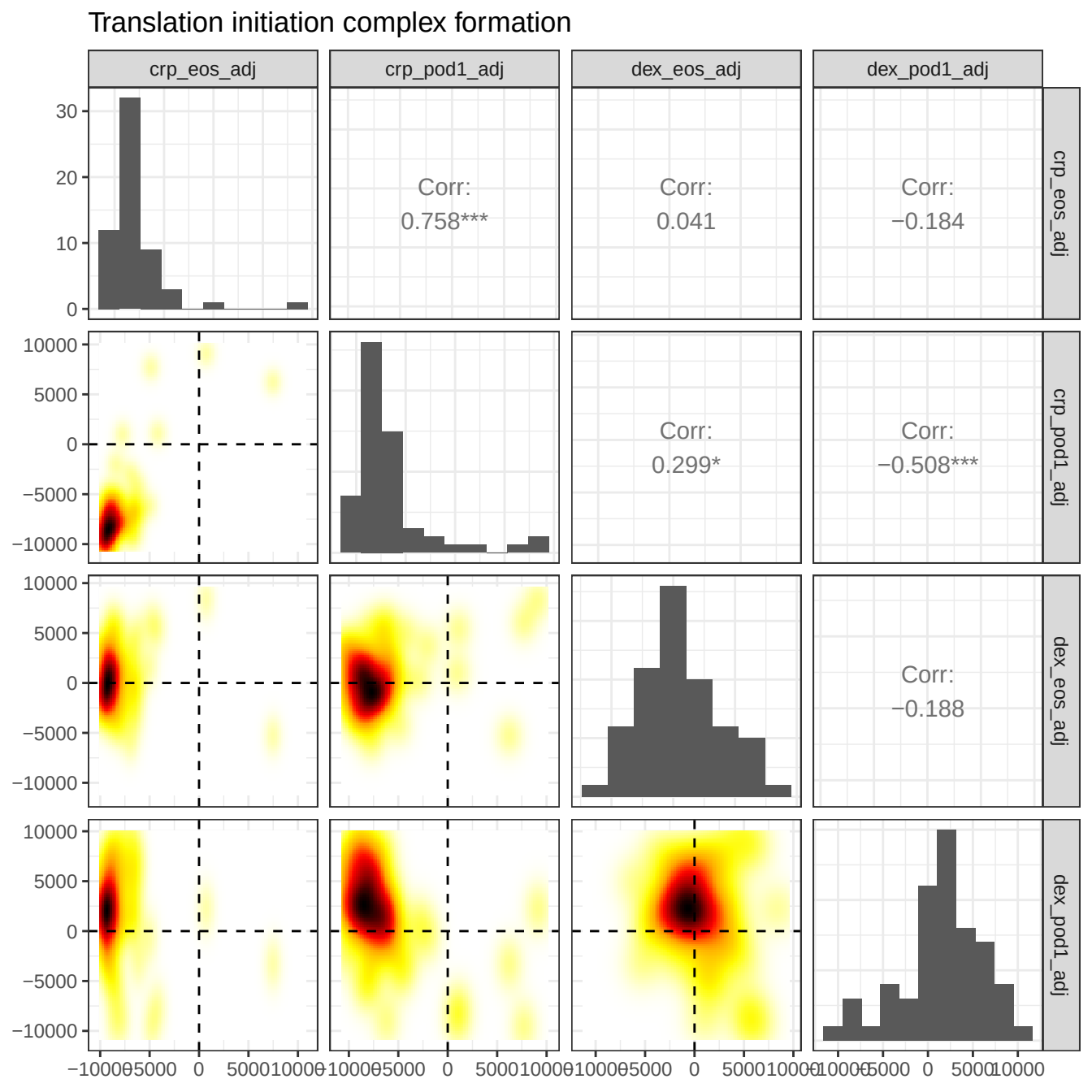

Activation of the mRNA upon binding of the cap−binding complex and eIFs, and s
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.761***
Corr:
0.039
Corr:
−0.199
Corr:
0.295*
Corr:
−0.516***
Corr:
−0.177
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

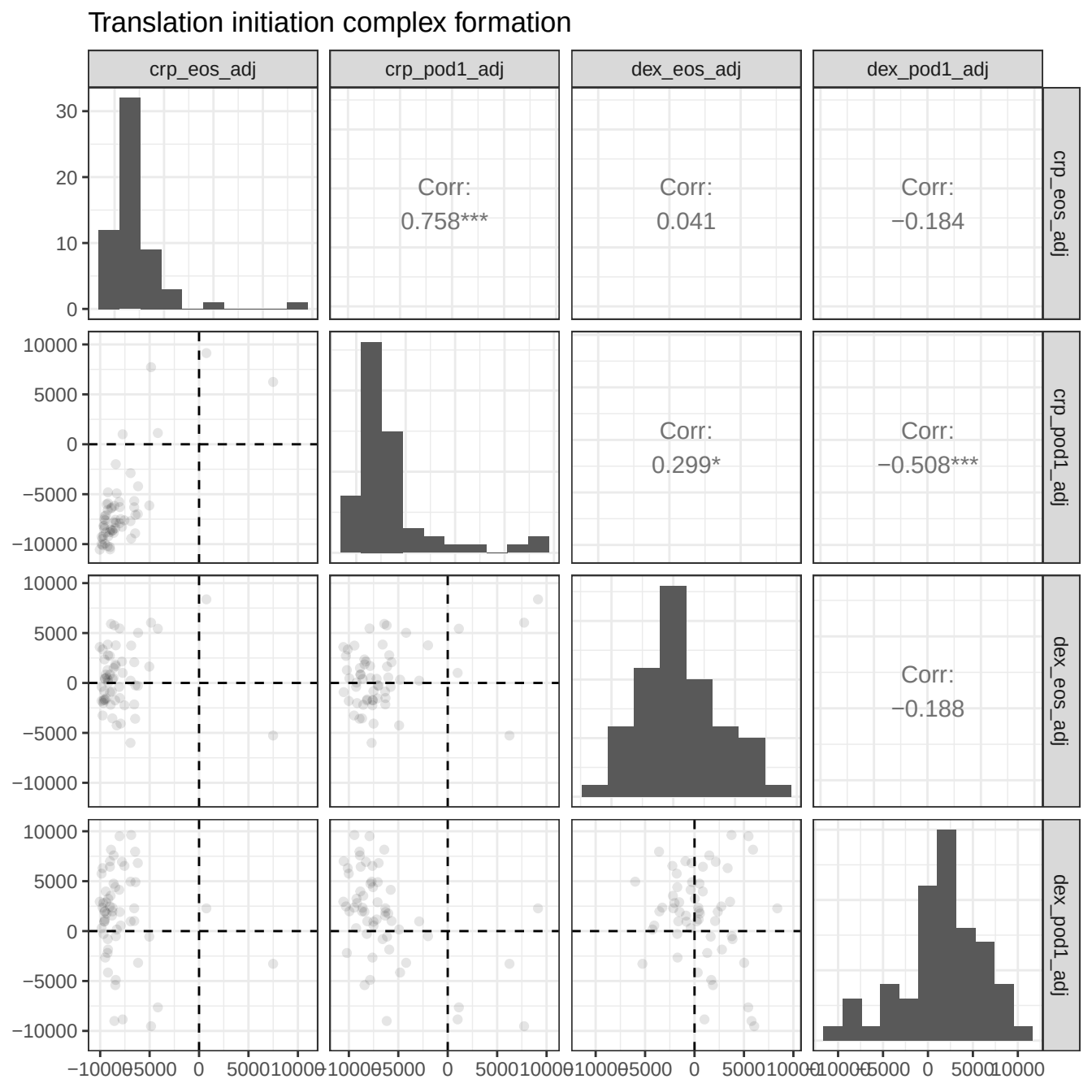

Activation of the mRNA upon binding of the cap−
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

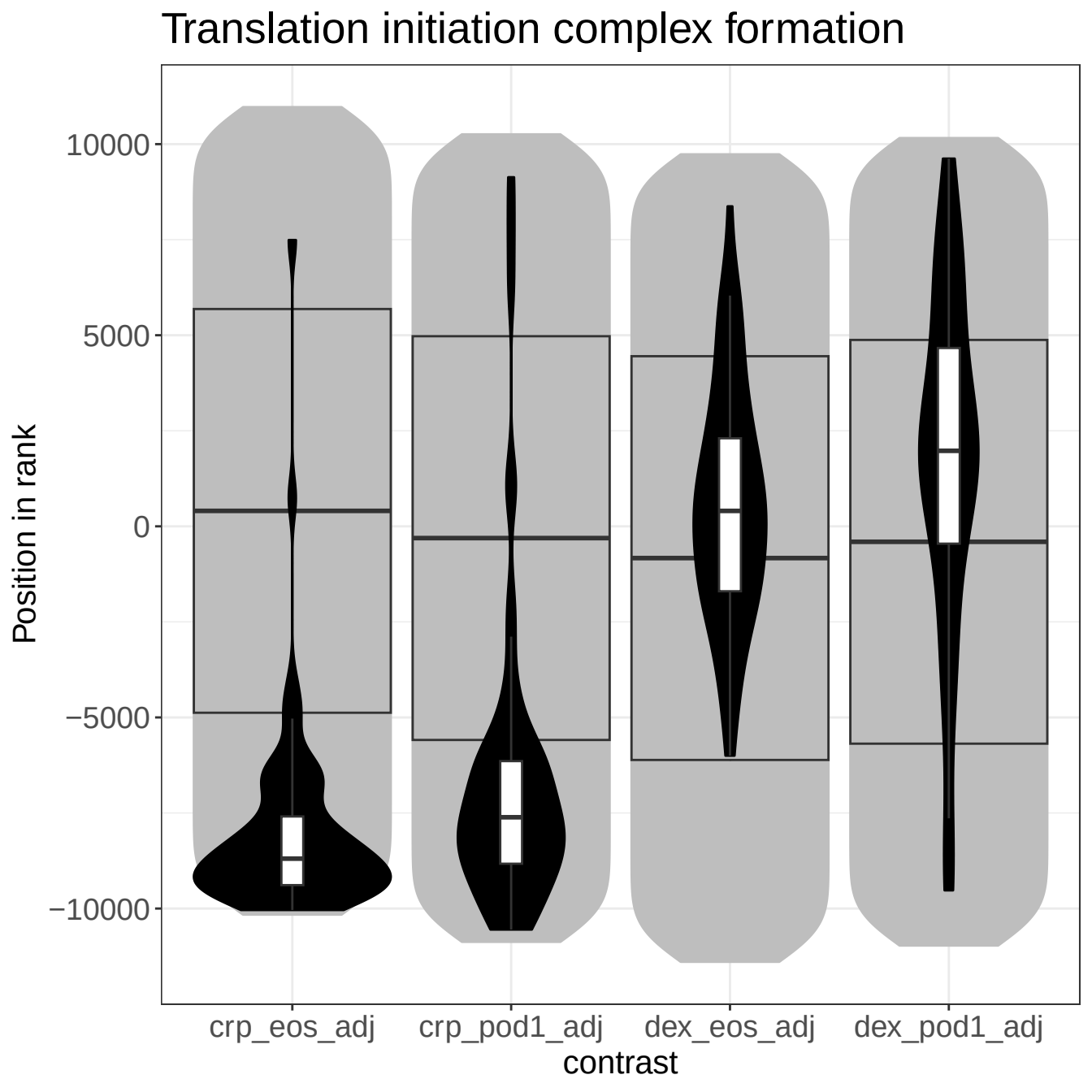

Fructose metabolism
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.527
Corr:
−0.016
Corr:
−0.576
Corr:
0.769*
Corr:
−0.940**
Corr:
−0.589
2.0
1.5
1.0
0.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
0
4000
8000
12000


Fructose metabolism
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.527
Corr:
−0.016
Corr:
−0.576
Corr:
0.769*
Corr:
−0.940**
Corr:
−0.589

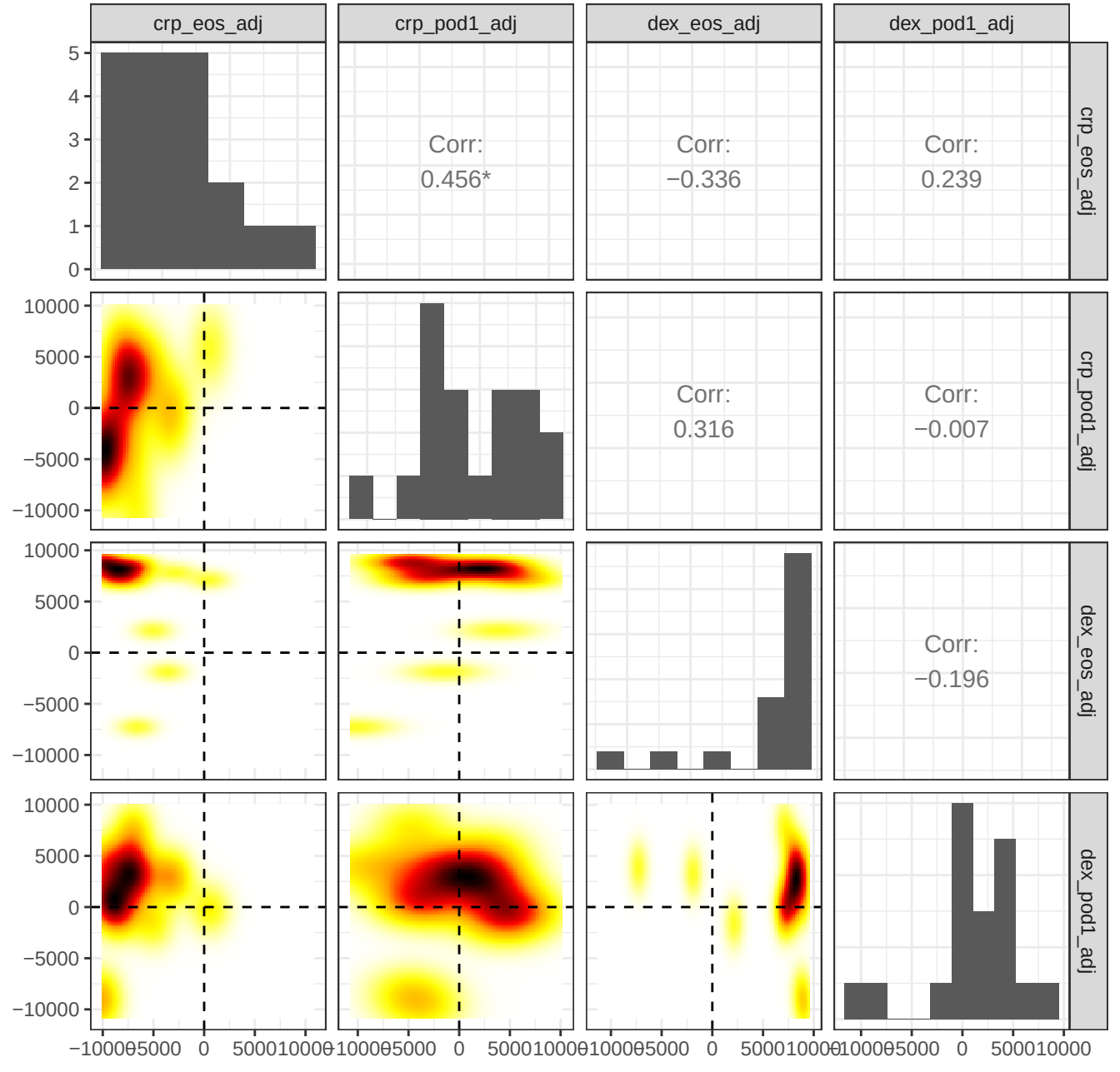

Fructose metabolism
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

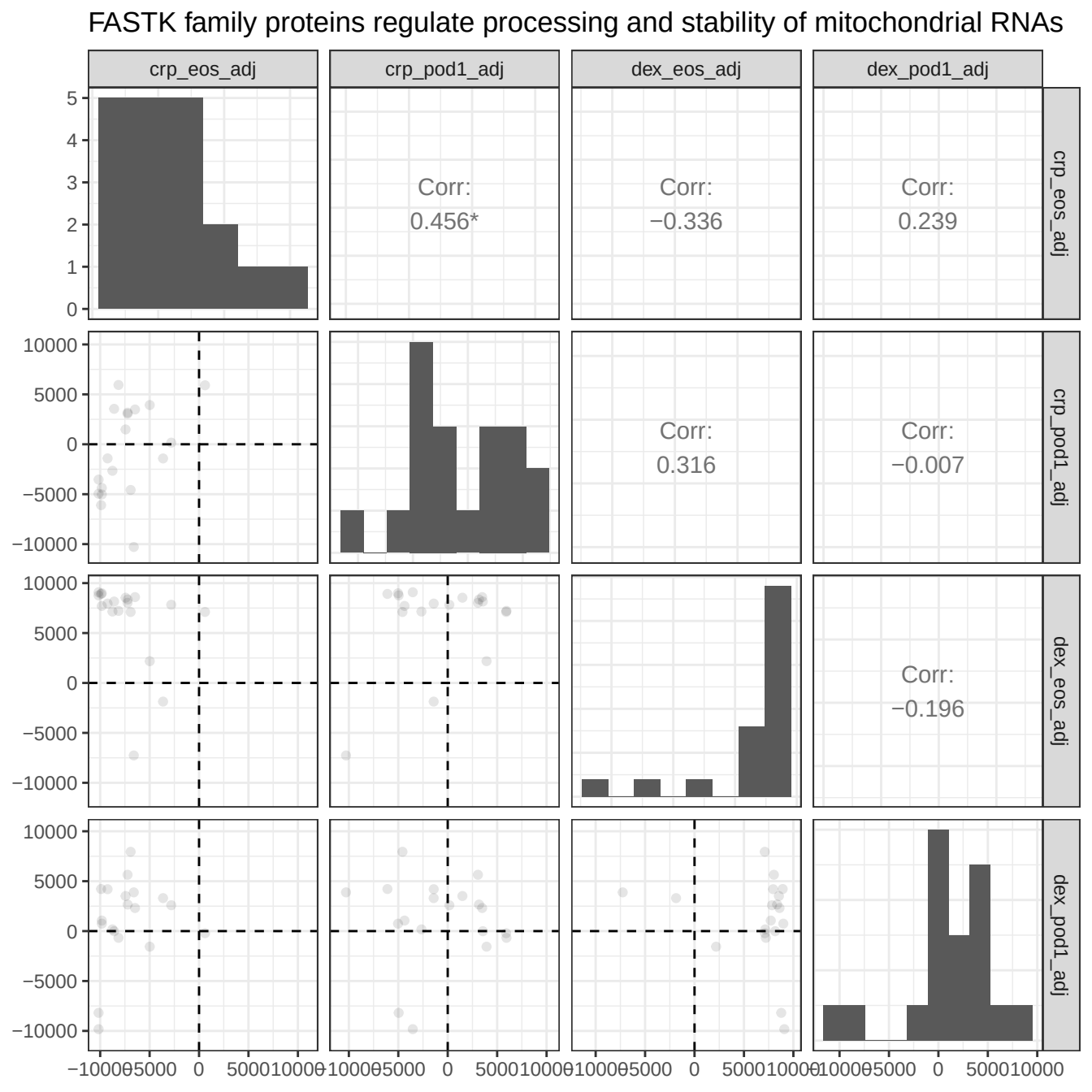

Translation initiation complex formation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.758***
Corr:
0.041
Corr:
−0.184
Corr:
0.299*
Corr:
−0.508***
Corr:
−0.188
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

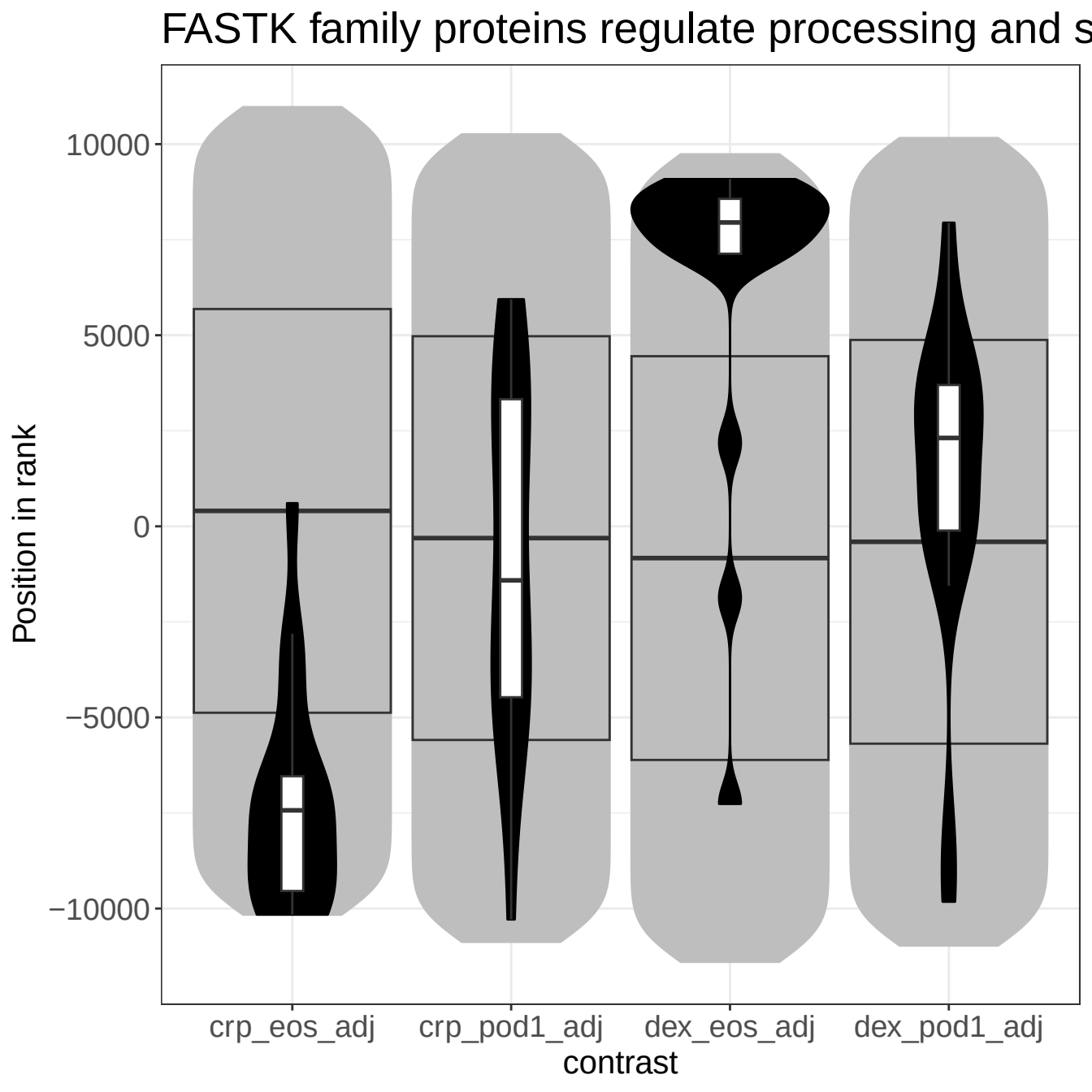

Translation initiation complex formation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.758***
Corr:
0.041
Corr:
−0.184
Corr:
0.299*
Corr:
−0.508***
Corr:
−0.188
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

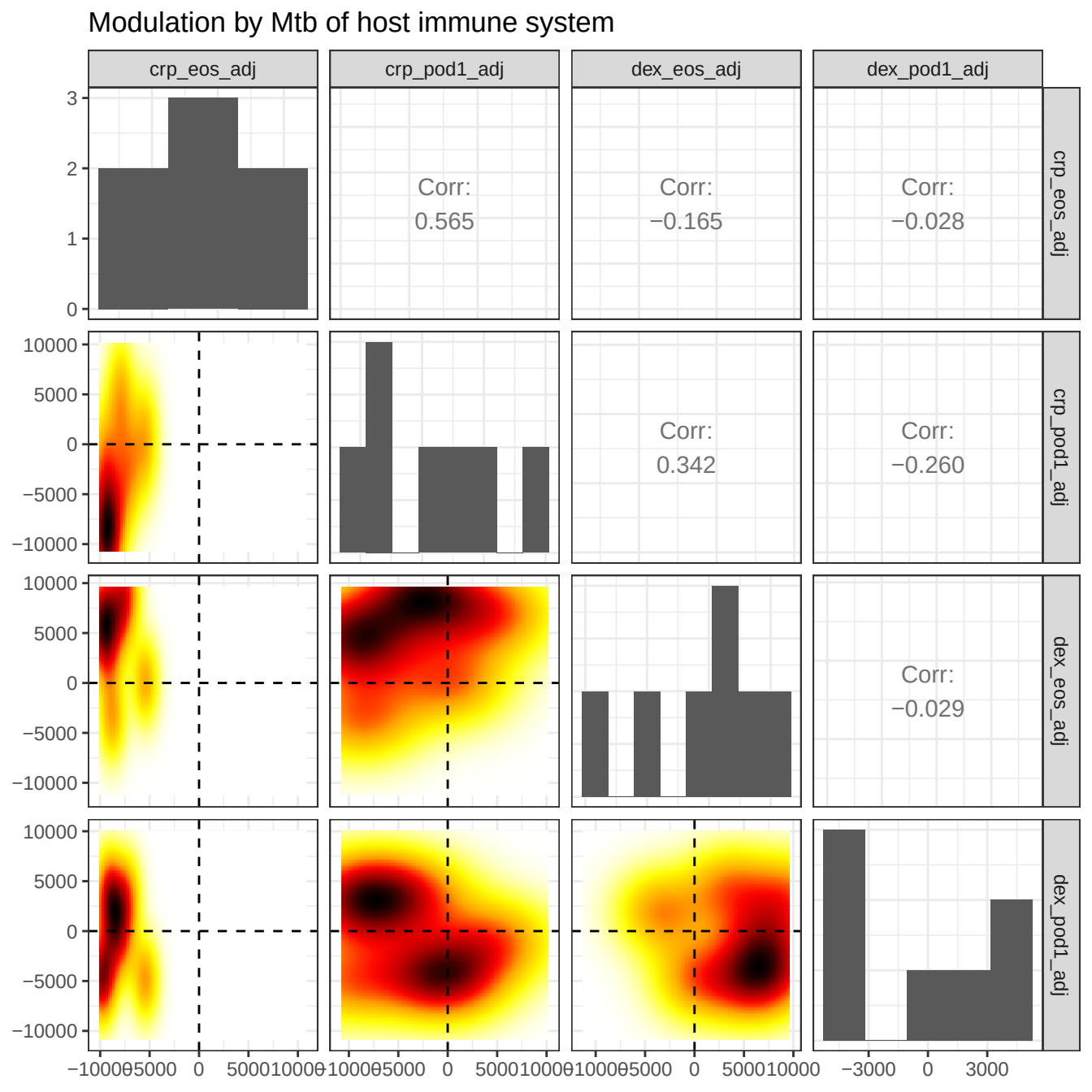

Translation initiation complex formation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

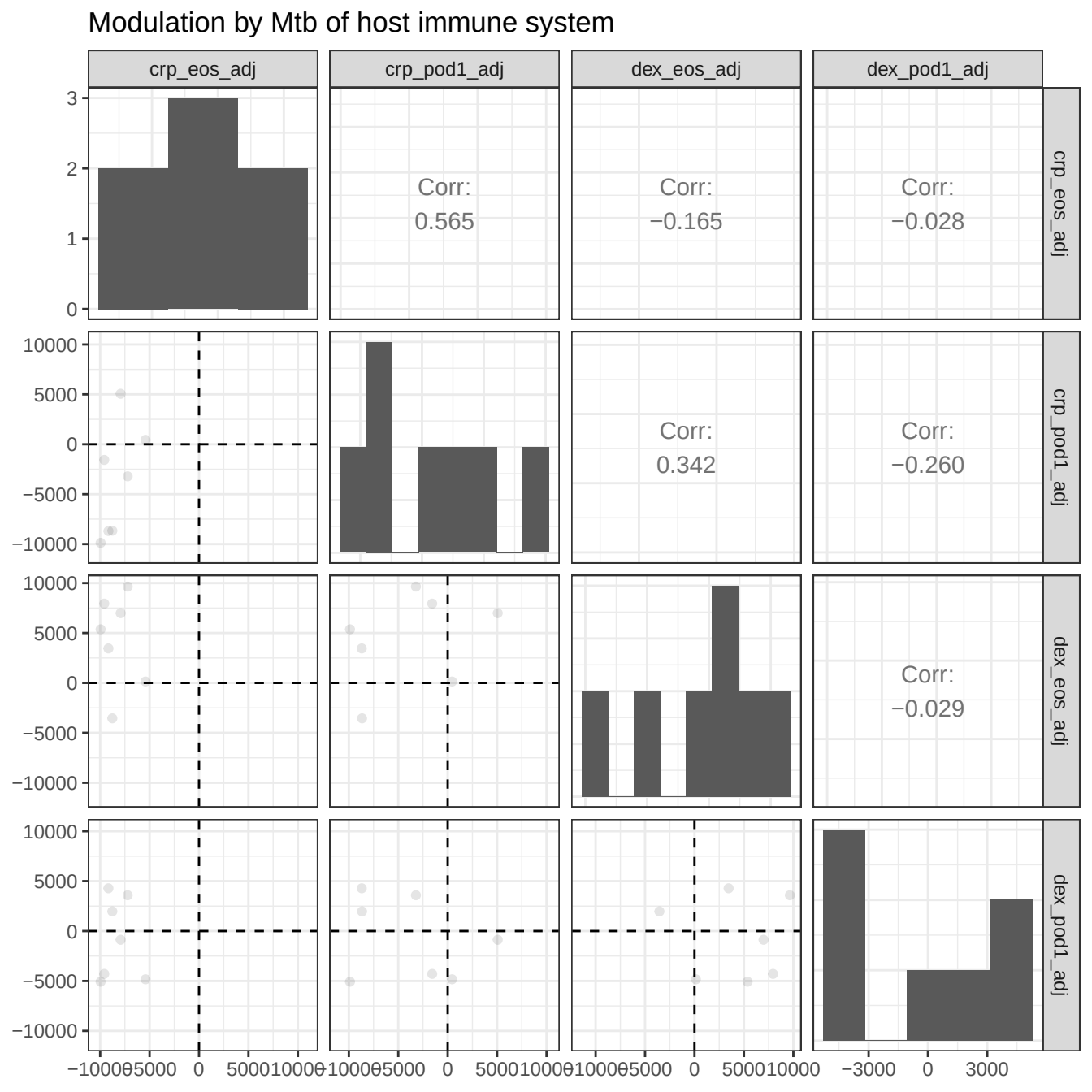
FASTK family proteins regulate processing and stability of mitochondrial RNAs

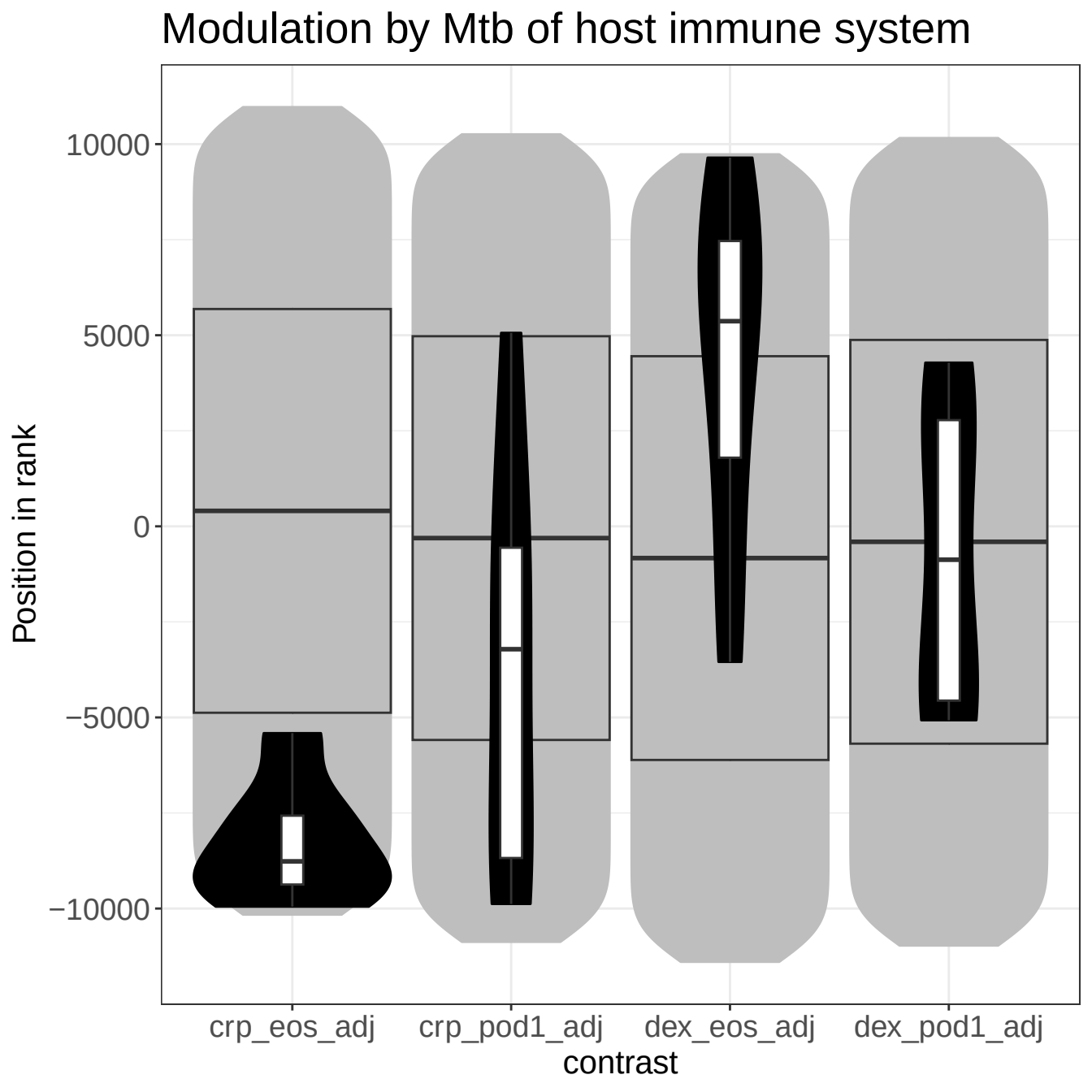


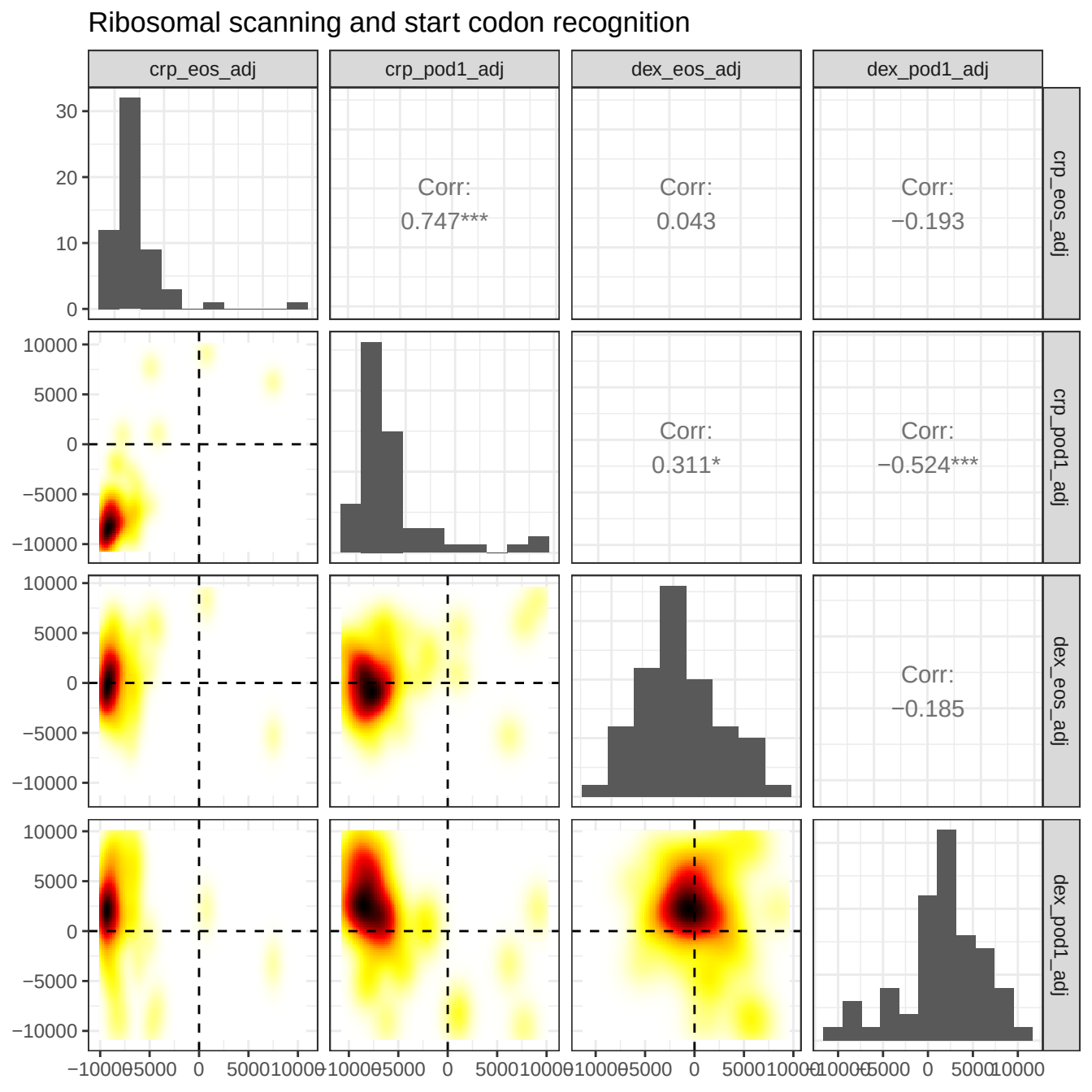

FASTK family proteins regulate processing and stability of mitochondrial RNAs
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.456*
Corr:
−0.336
Corr:
0.239
Corr:
0.316
Corr:
−0.007
Corr:
−0.196
5
4
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

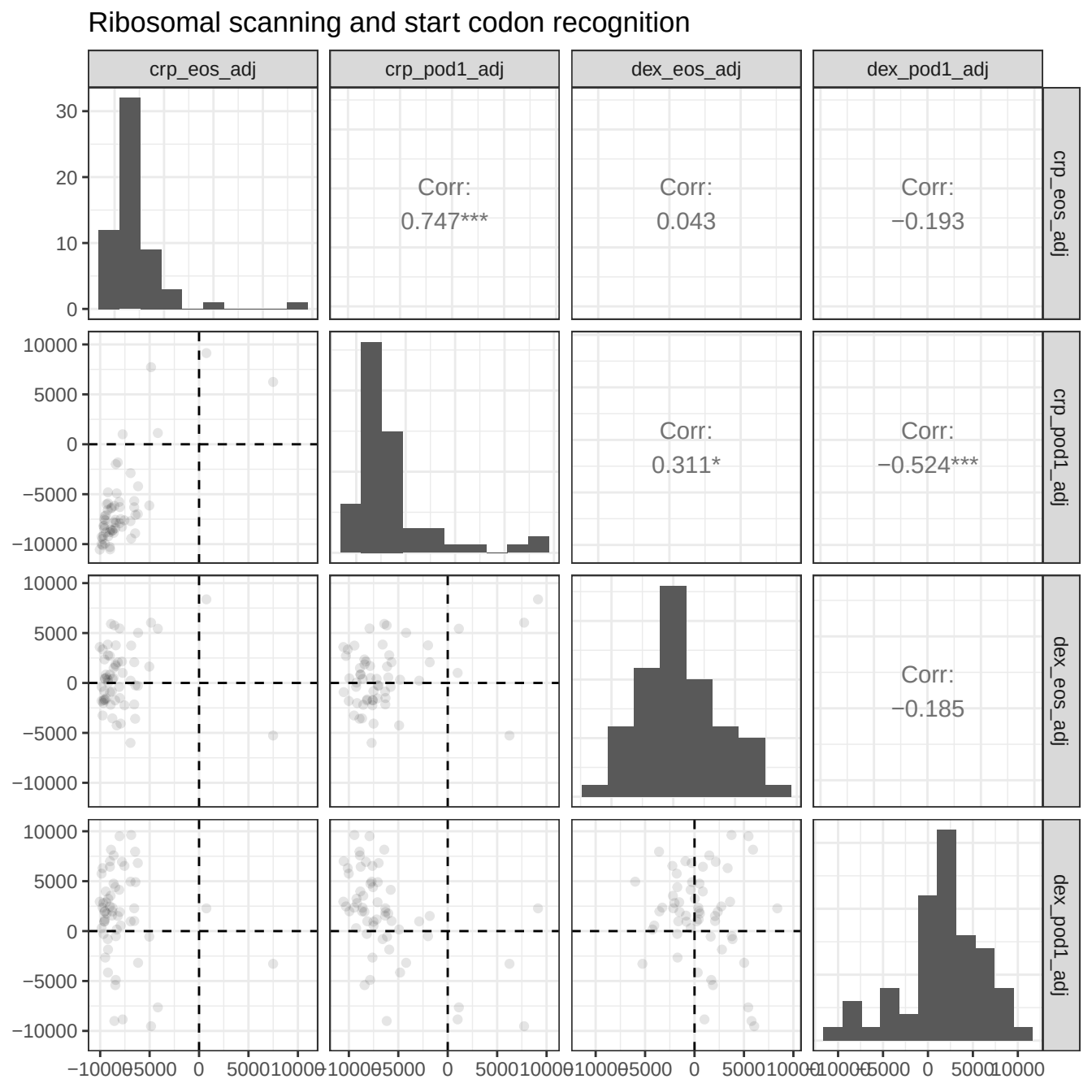

FASTK family proteins regulate processing and s
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

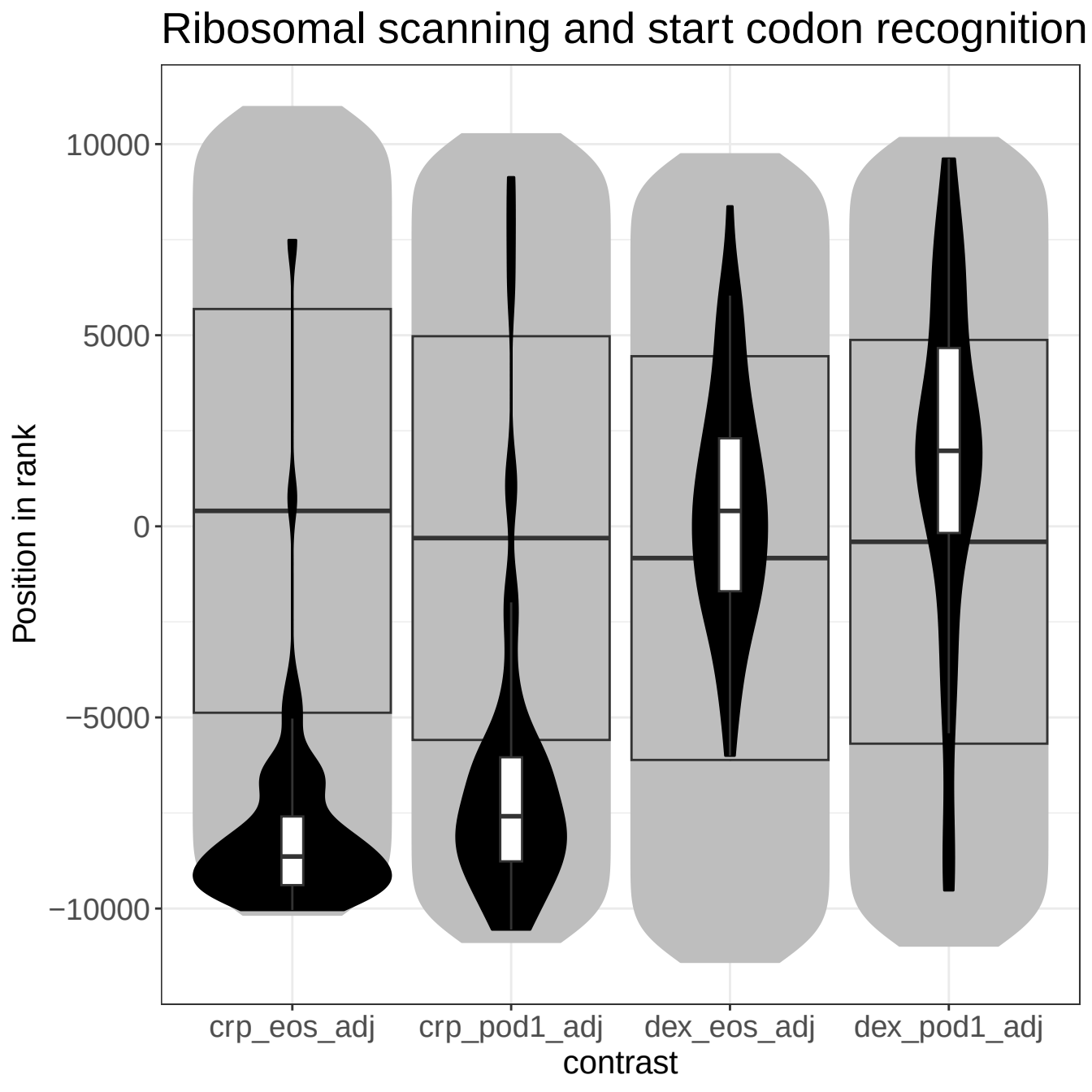

Modulation by Mtb of host immune system
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.565
Corr:
−0.165
Corr:
−0.028
Corr:
0.342
Corr:
−0.260
Corr:
−0.029
3
2
1
0
10000
5000
0
−5000
−10000
−3000
3000


Modulation by Mtb of host immune system
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.565
Corr:
−0.165
Corr:
−0.028
Corr:
0.342
Corr:
−0.260
Corr:
−0.029
3
2
1
0
10000
5000
0
−5000
−10000
−3000
0
3000

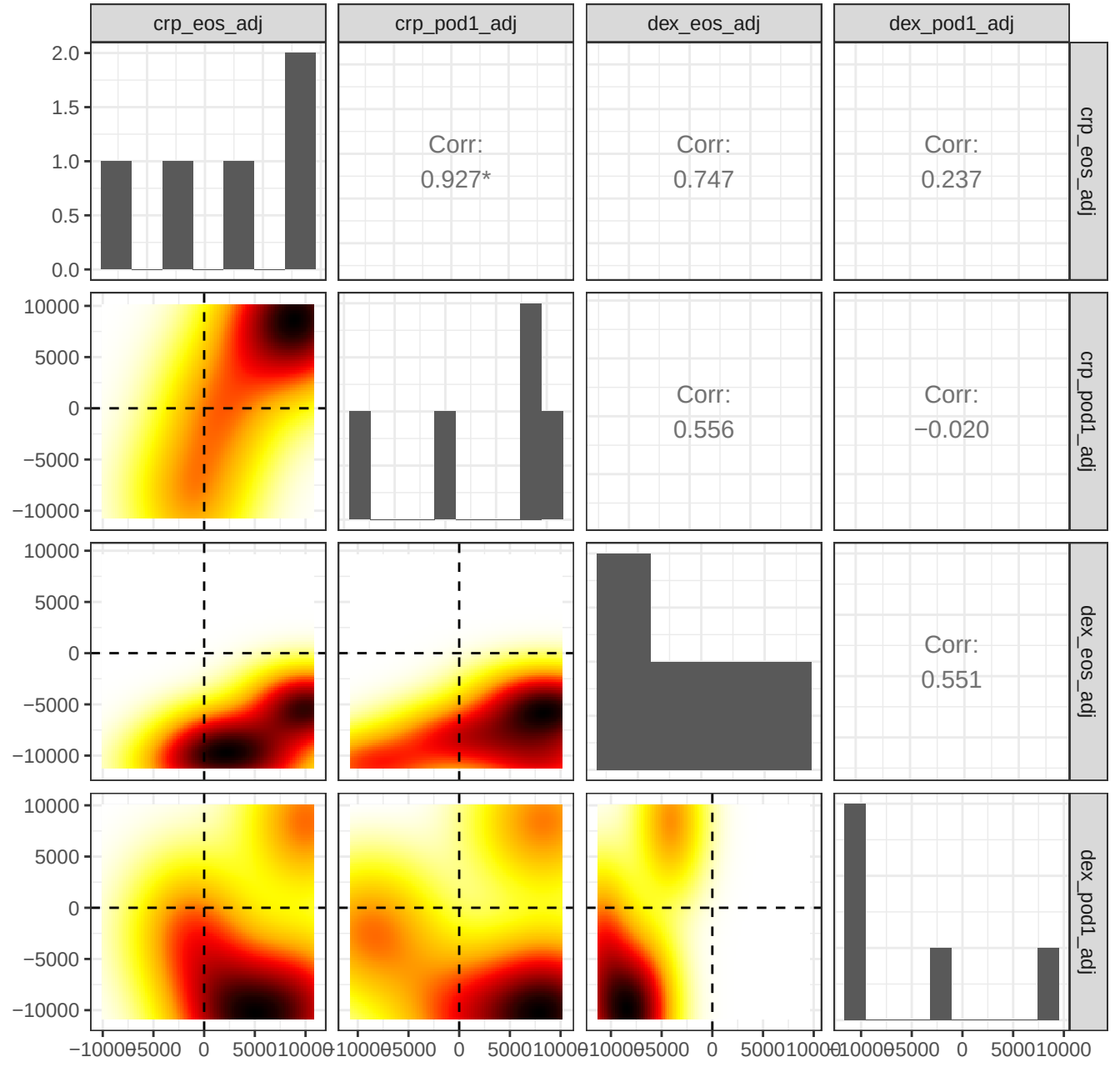

Modulation by Mtb of host immune system
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast


Ribosomal scanning and start codon recognition
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.747***
Corr:
0.043
Corr:
−0.193
Corr:
0.311*
Corr:
−0.524***
Corr:
−0.185
30
20
10
0
10000
5000
0
−5000
−10000

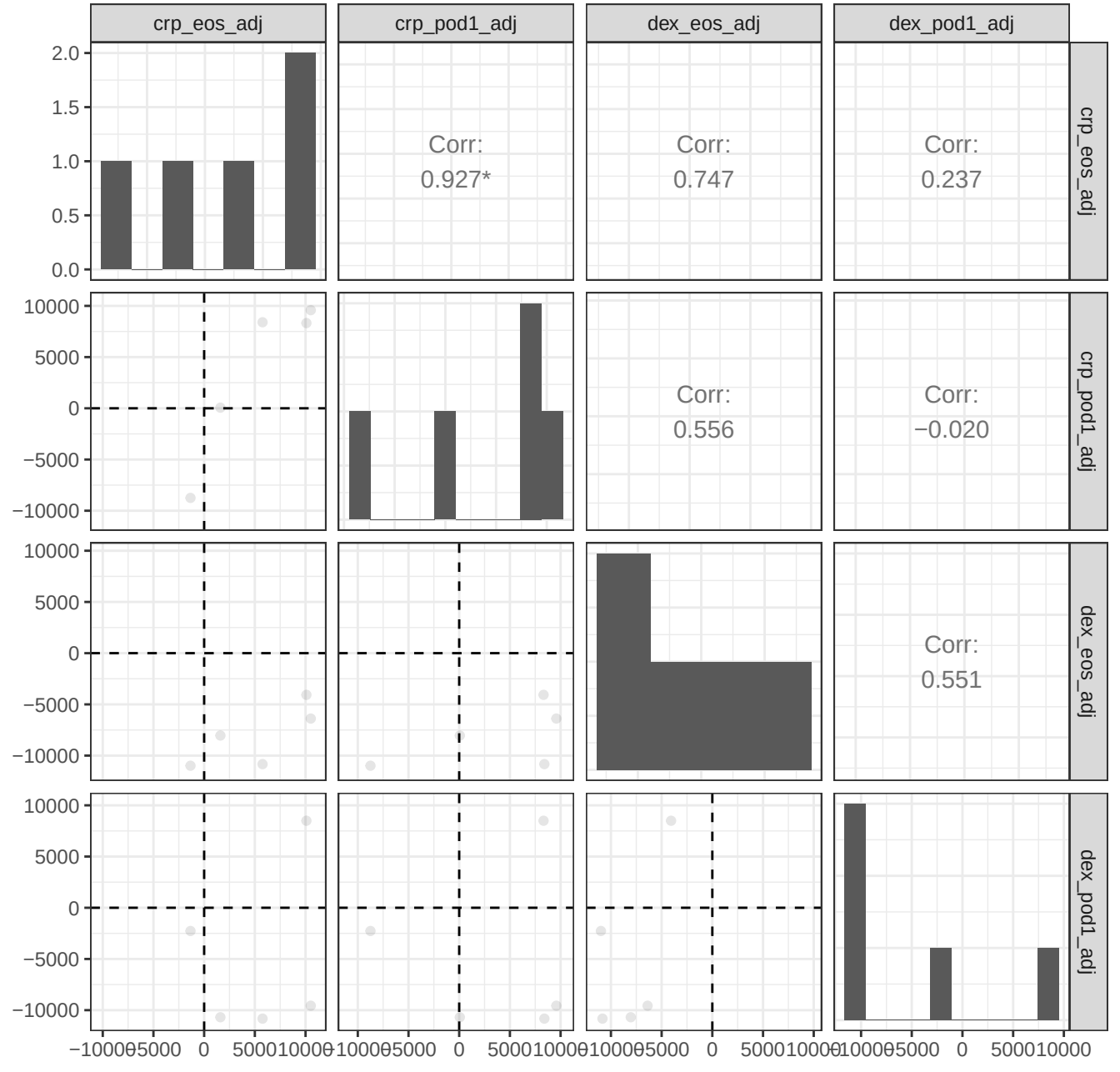

Ribosomal scanning and start codon recognition
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.747***
Corr:
0.043
Corr:
−0.193
Corr:
0.311*
Corr:
−0.524***
Corr:
−0.185
30
20
10
0
10000
5000
0
−5000
−10000

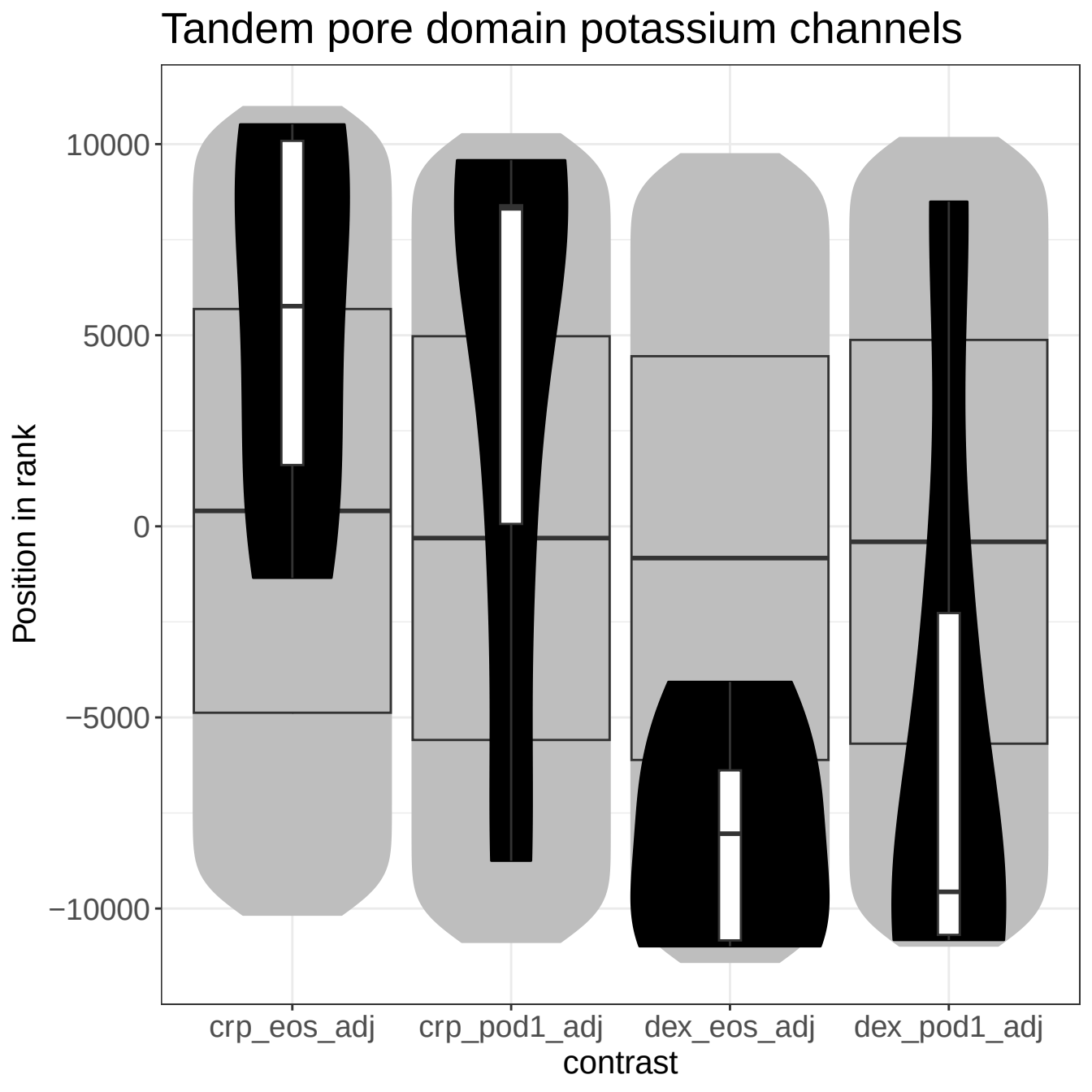

Ribosomal scanning and start codon recognition
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

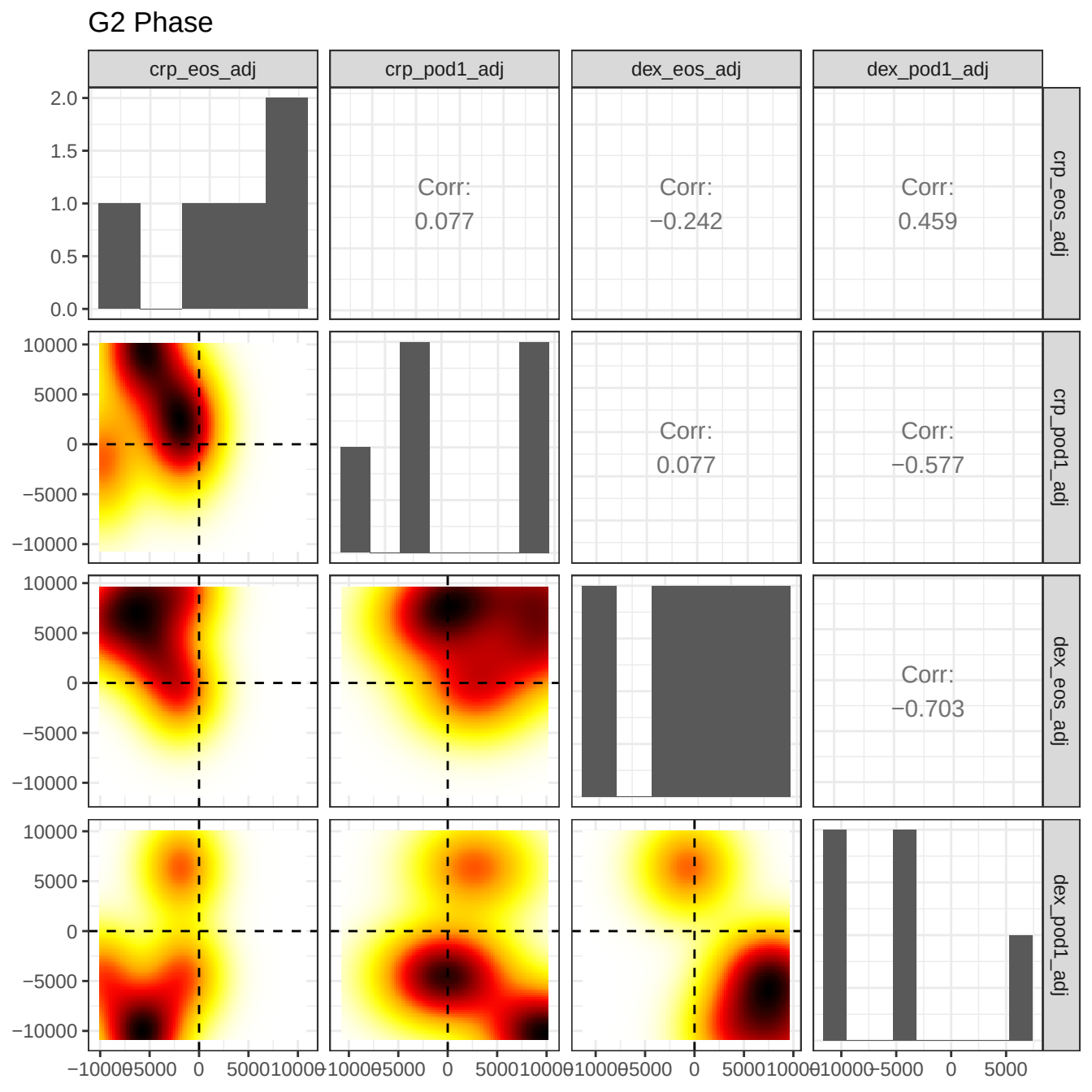
Tandem pore domain potassium channels

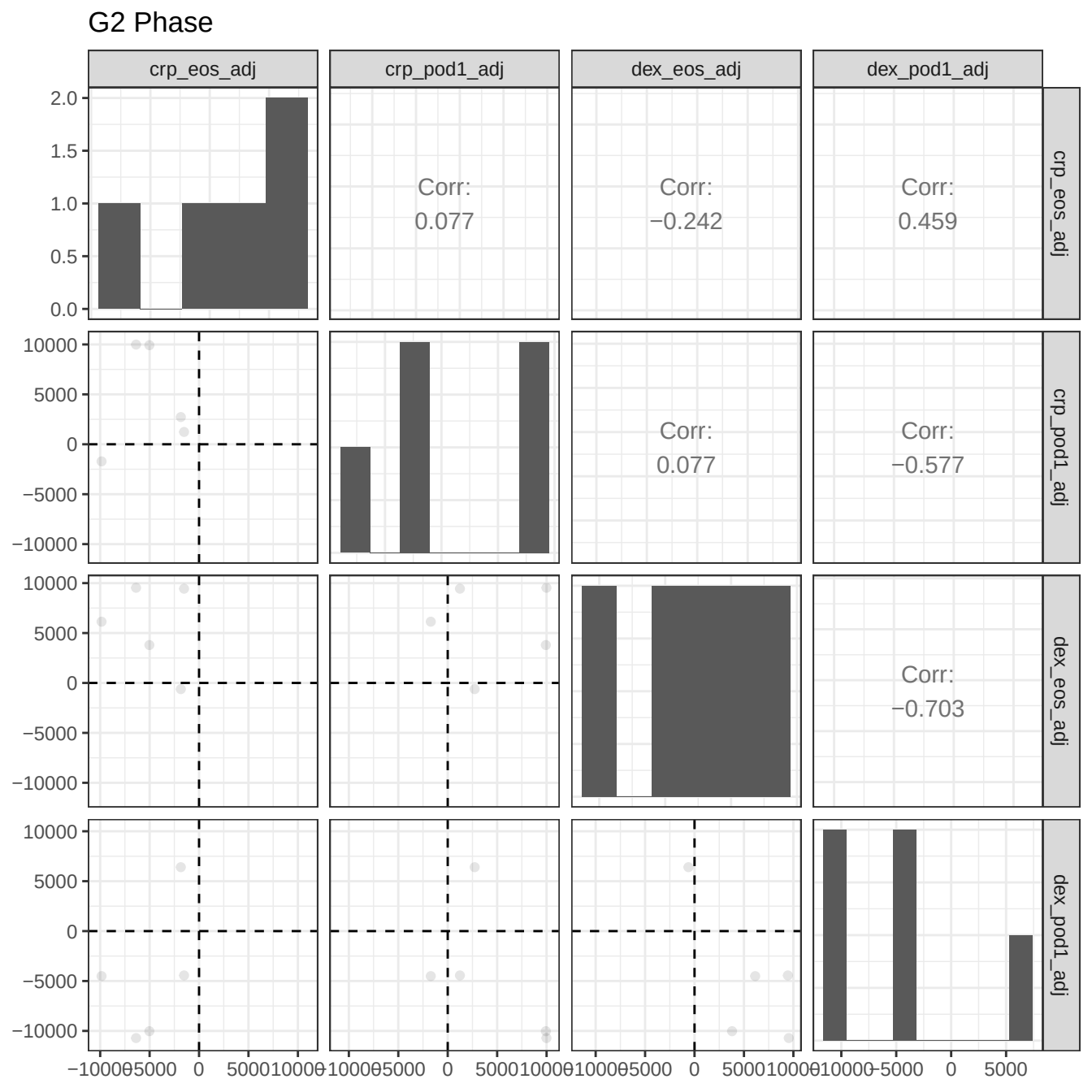


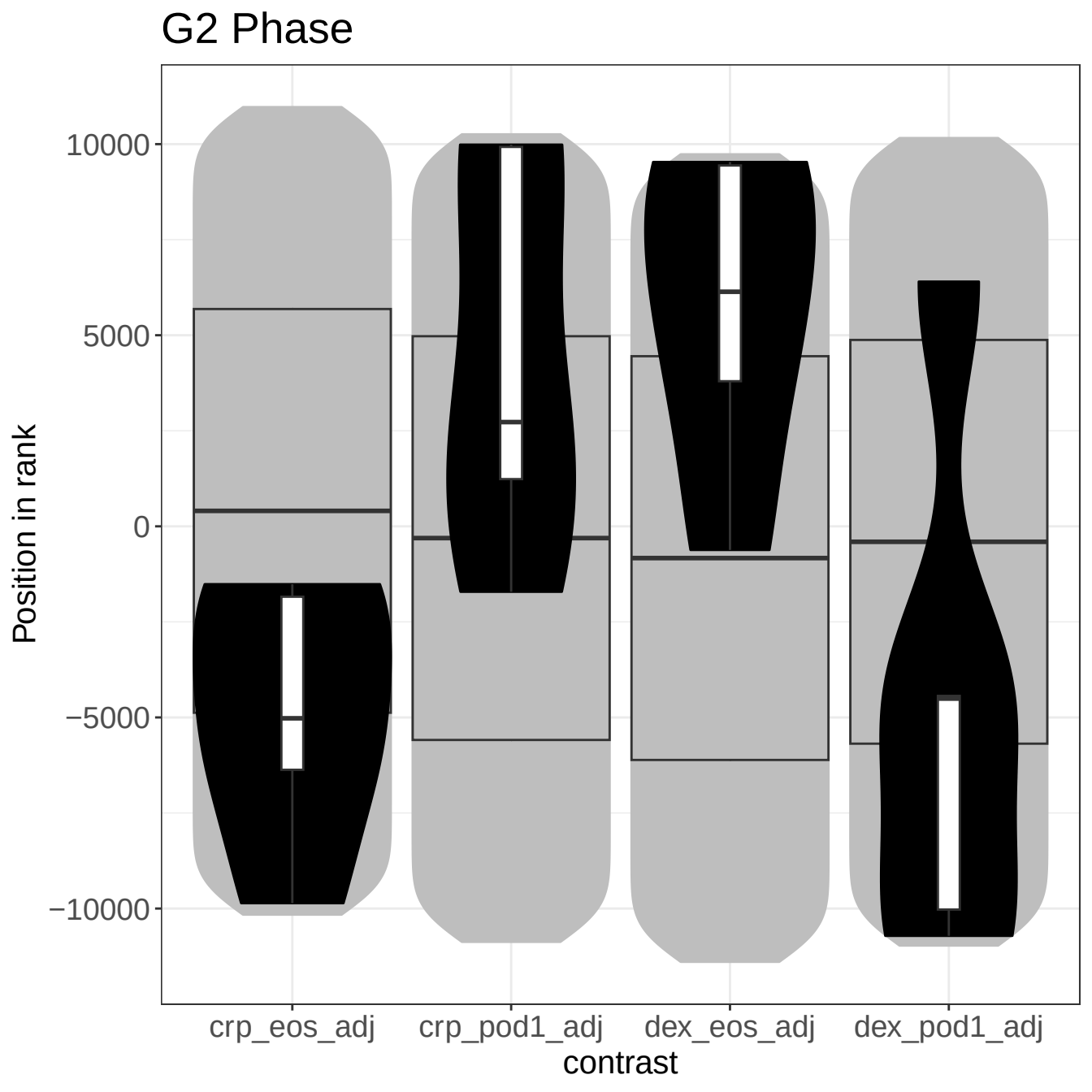
Tandem pore domain potassium channels

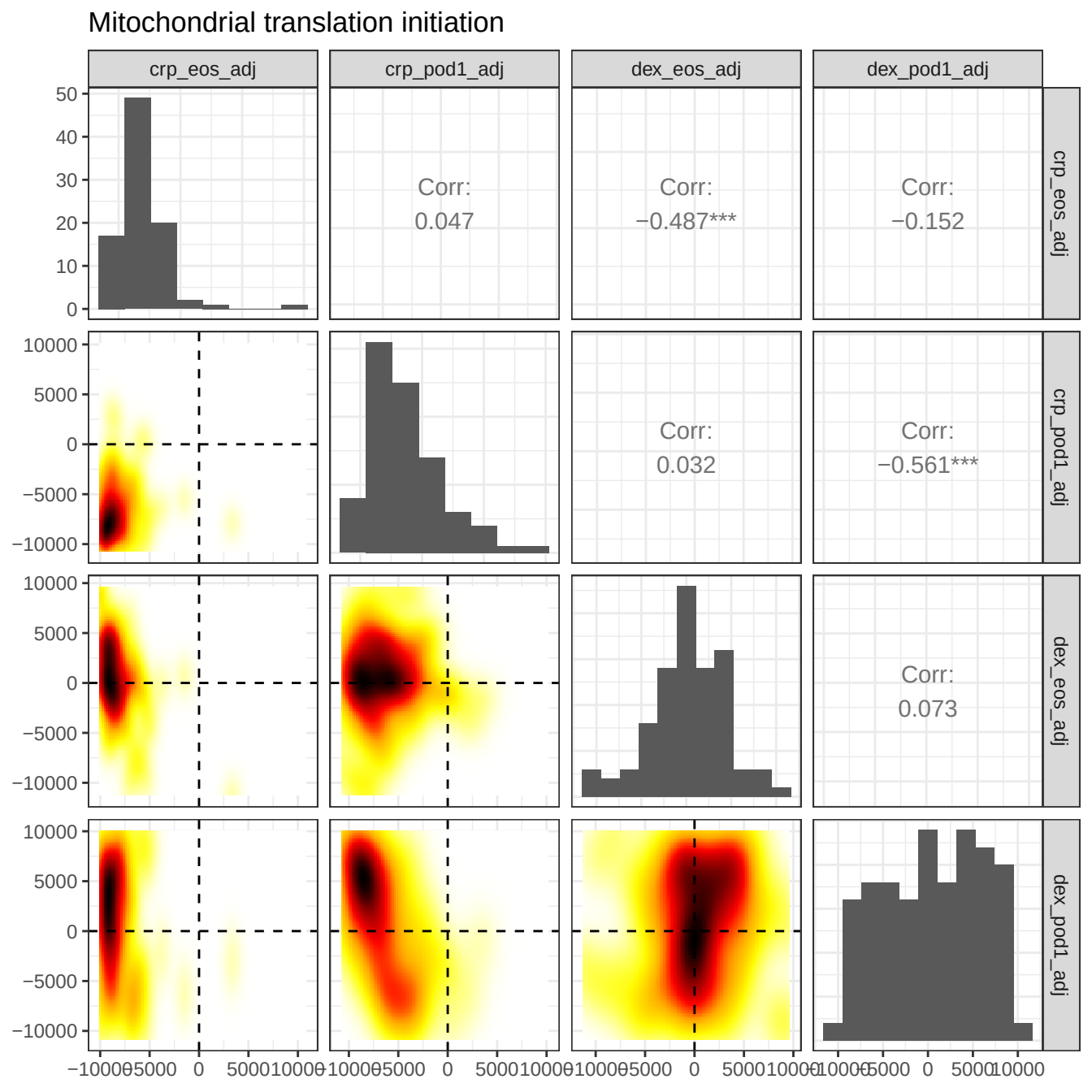


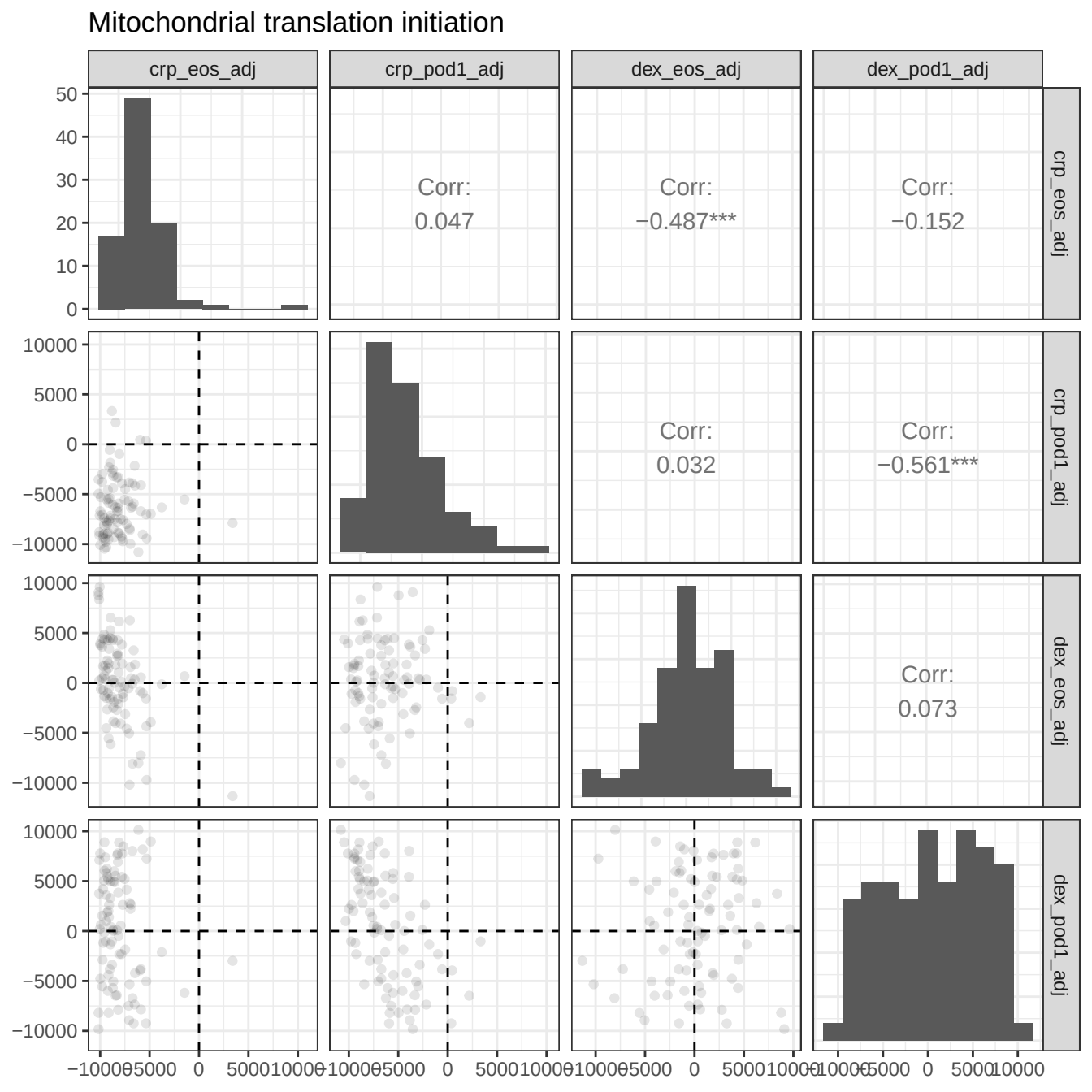

Tandem pore domain potassium channels
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

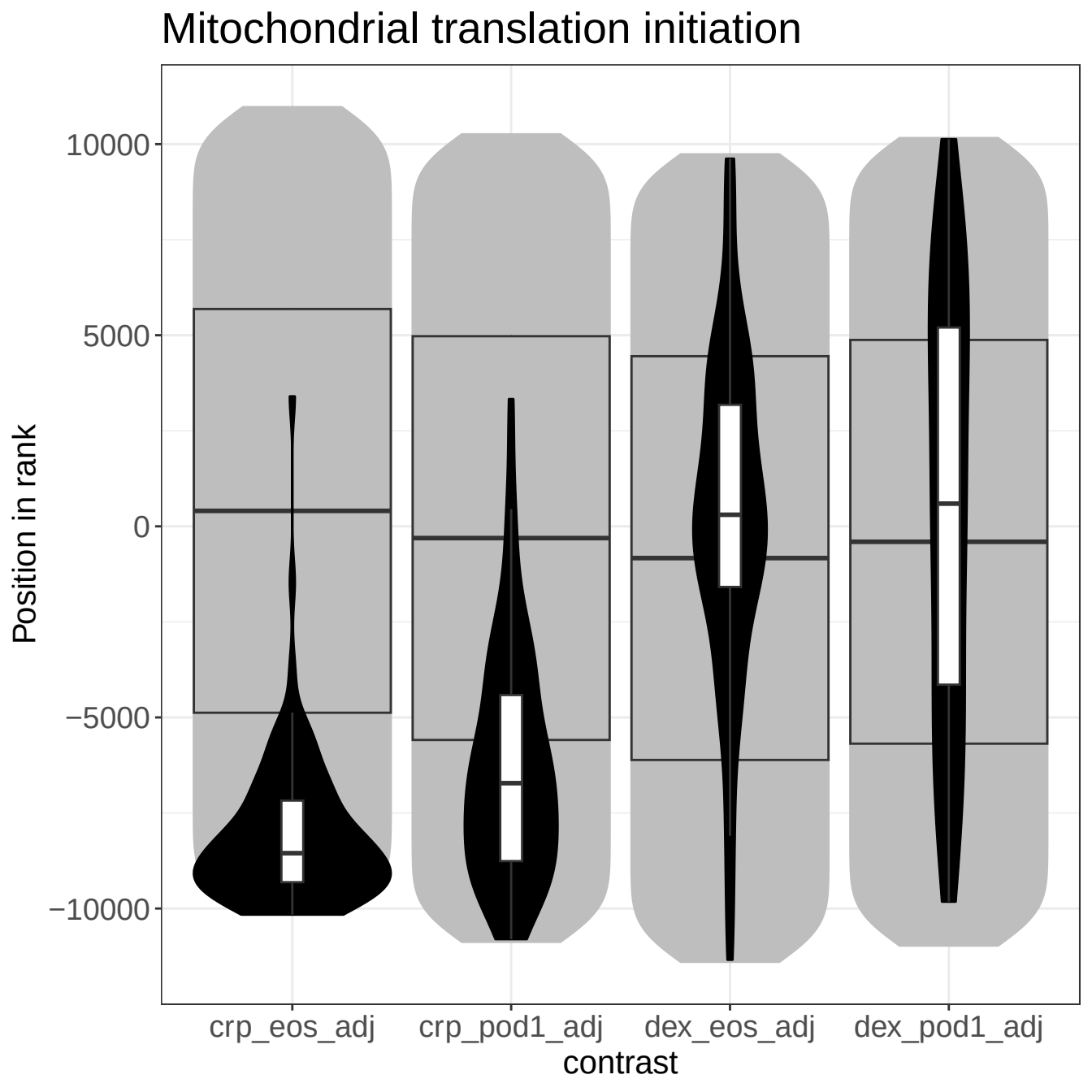

G2 Phase
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.077
Corr:
−0.242
Corr:
0.459
Corr:
0.077
Corr:
−0.577
Corr:
−0.703


G2 Phase
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.077
Corr:
−0.242
Corr:
0.459
Corr:
0.077
Corr:
−0.577
Corr:
−0.703

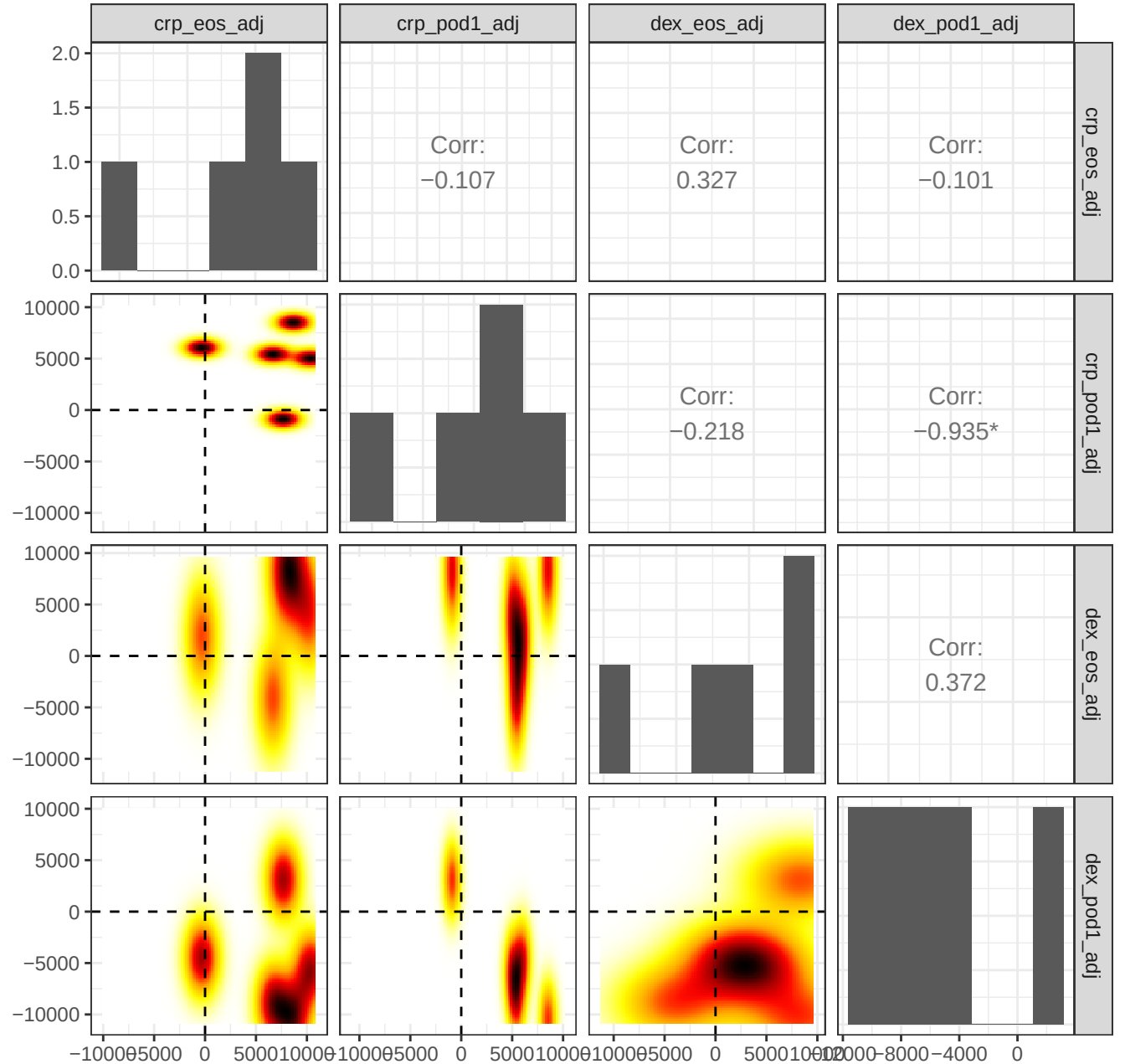

G2 Phase
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast


Mitochondrial translation initiation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.047
Corr:
−0.487***
Corr:
−0.152
Corr:
0.032
Corr:
−0.561***
Corr:
0.073
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

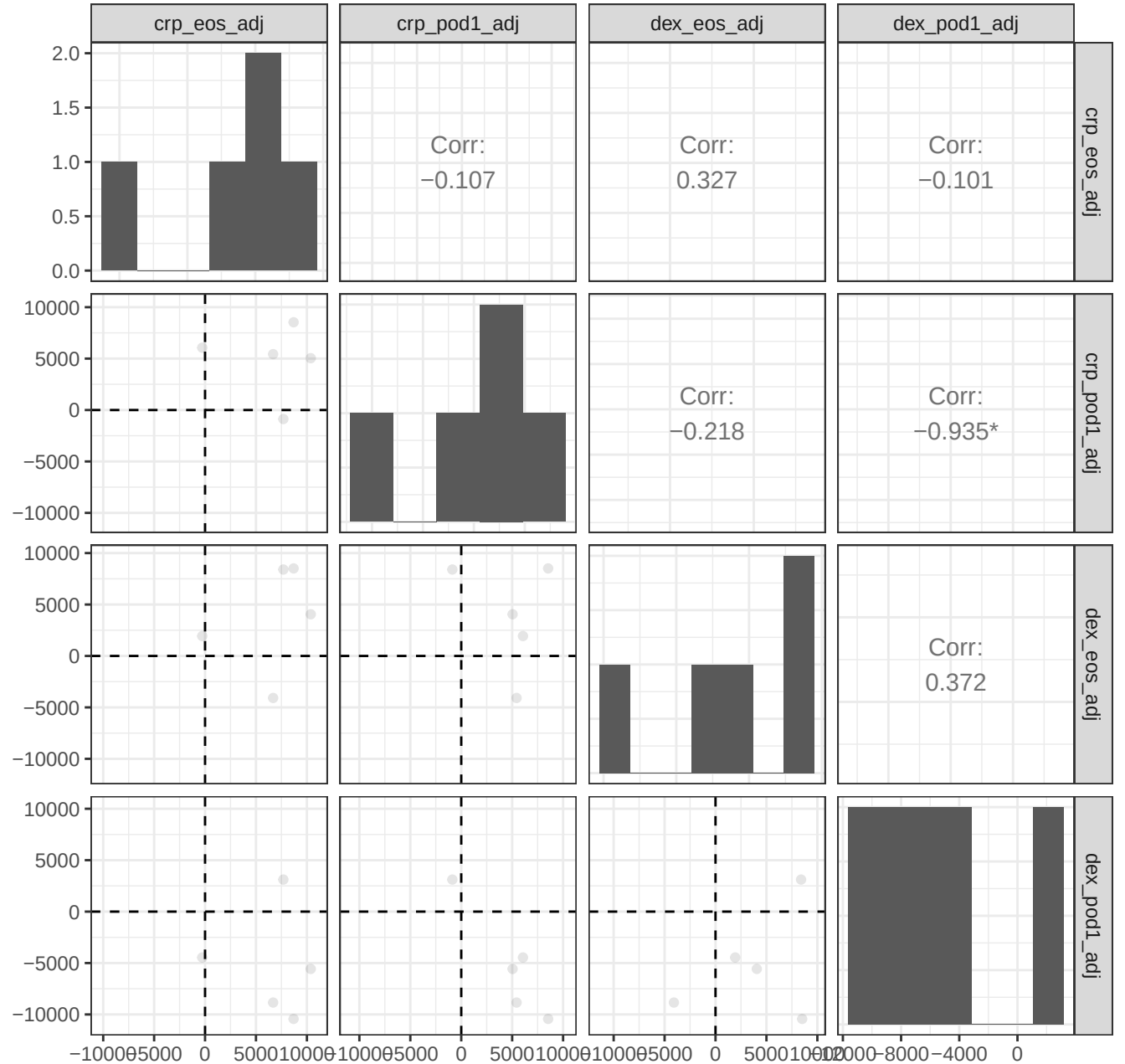

Mitochondrial translation initiation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.047
Corr:
−0.487***
Corr:
−0.152
Corr:
0.032
Corr:
−0.561***
Corr:
0.073
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

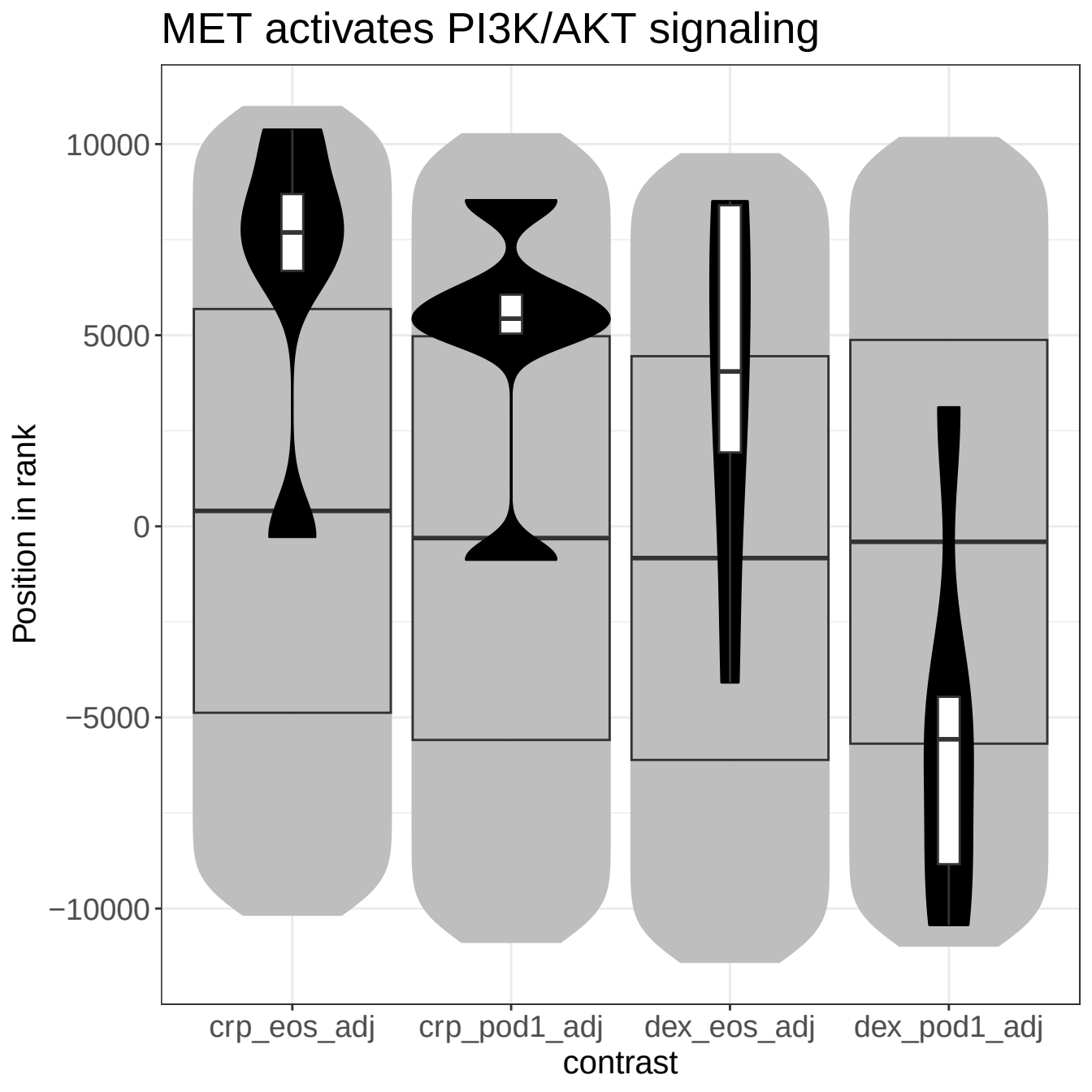

Mitochondrial translation initiation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

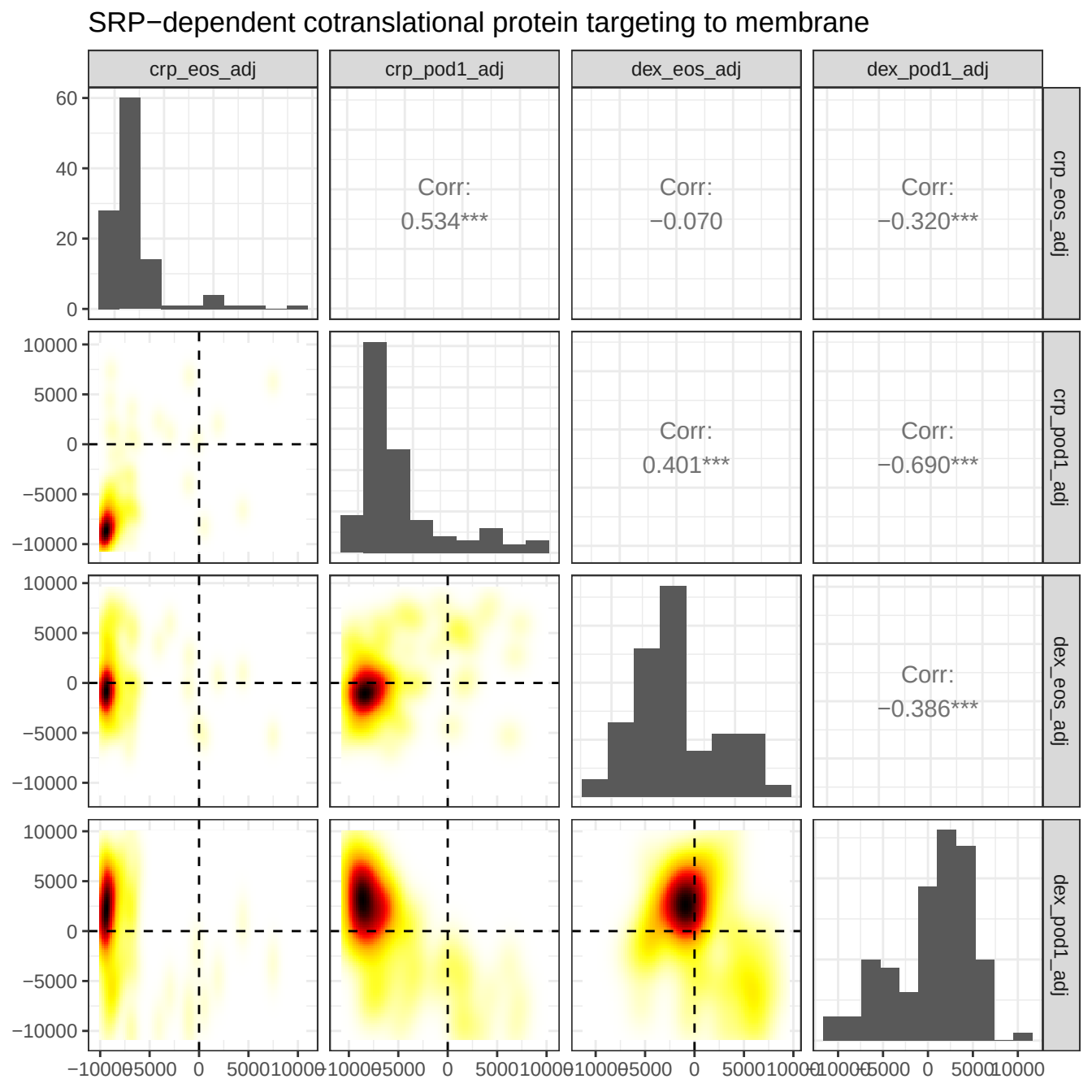
MET activates PI3K/AKT signaling

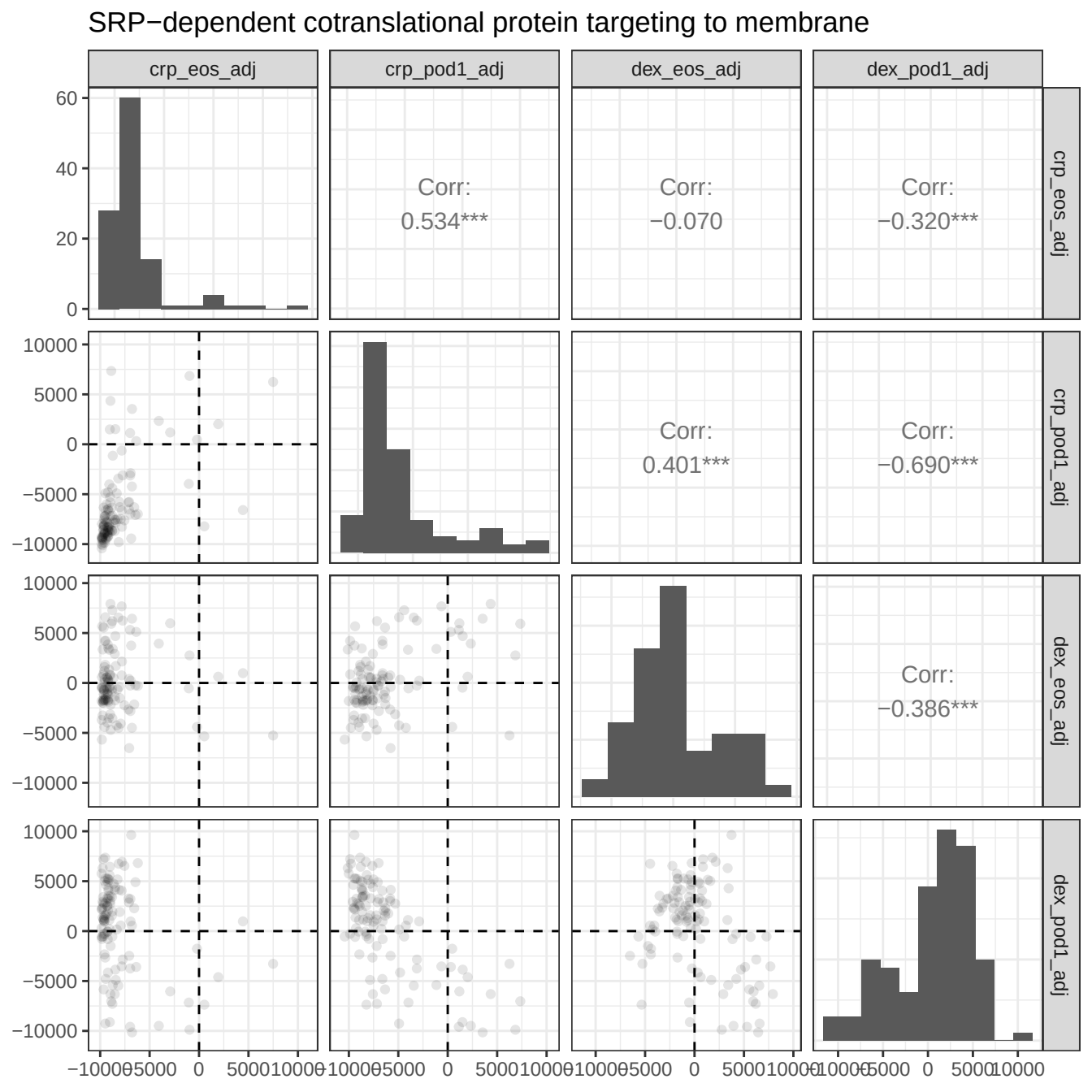


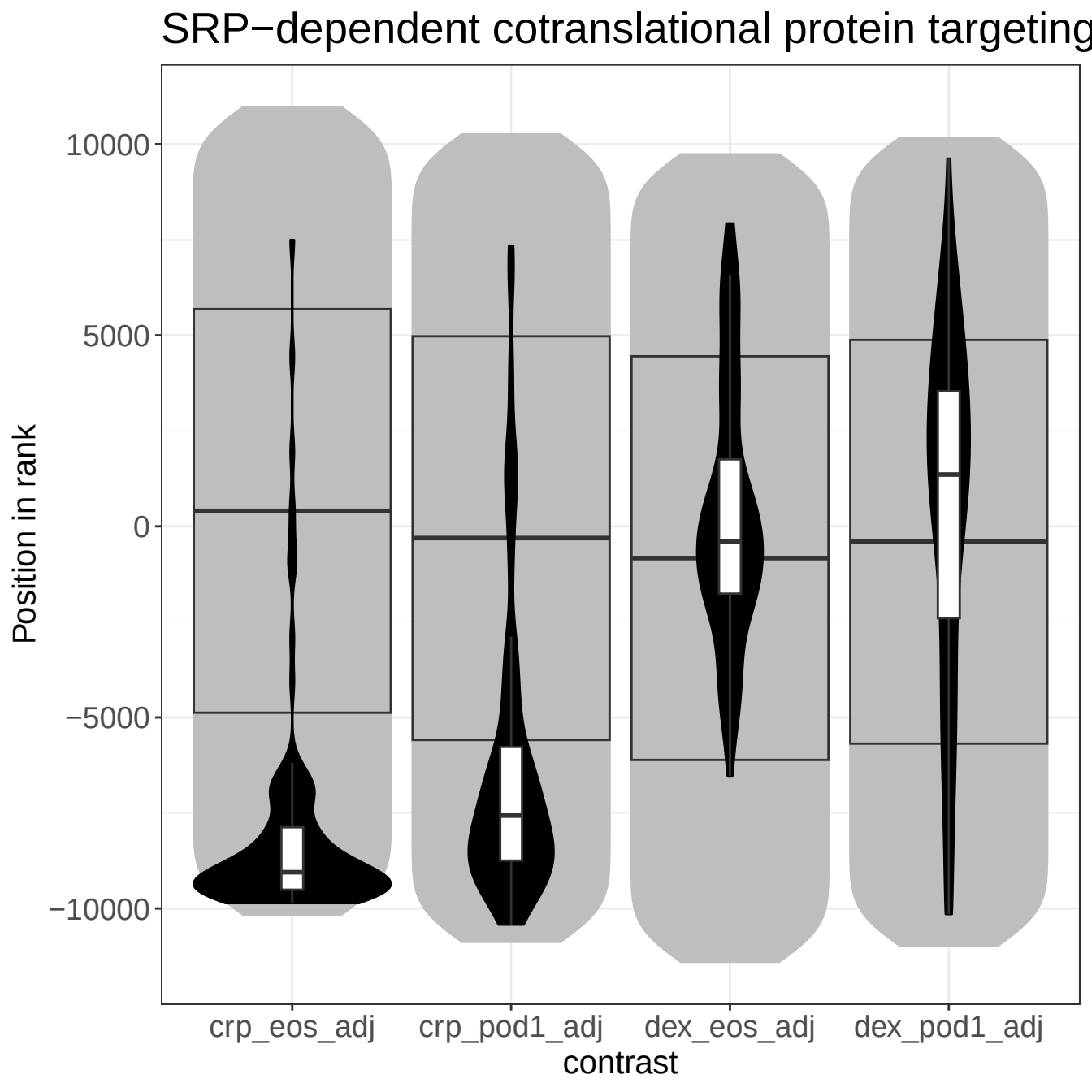
MET activates PI3K/AKT signaling

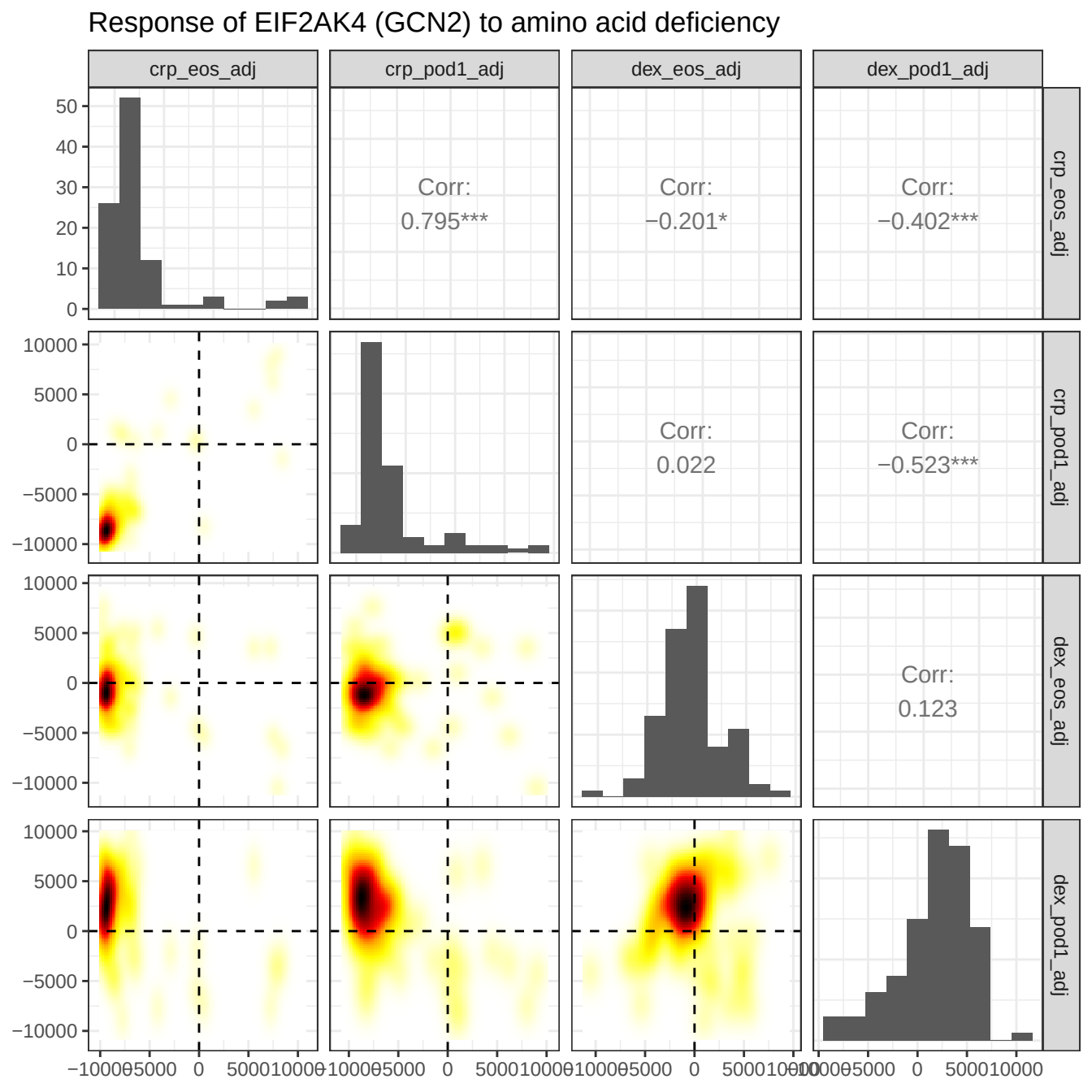


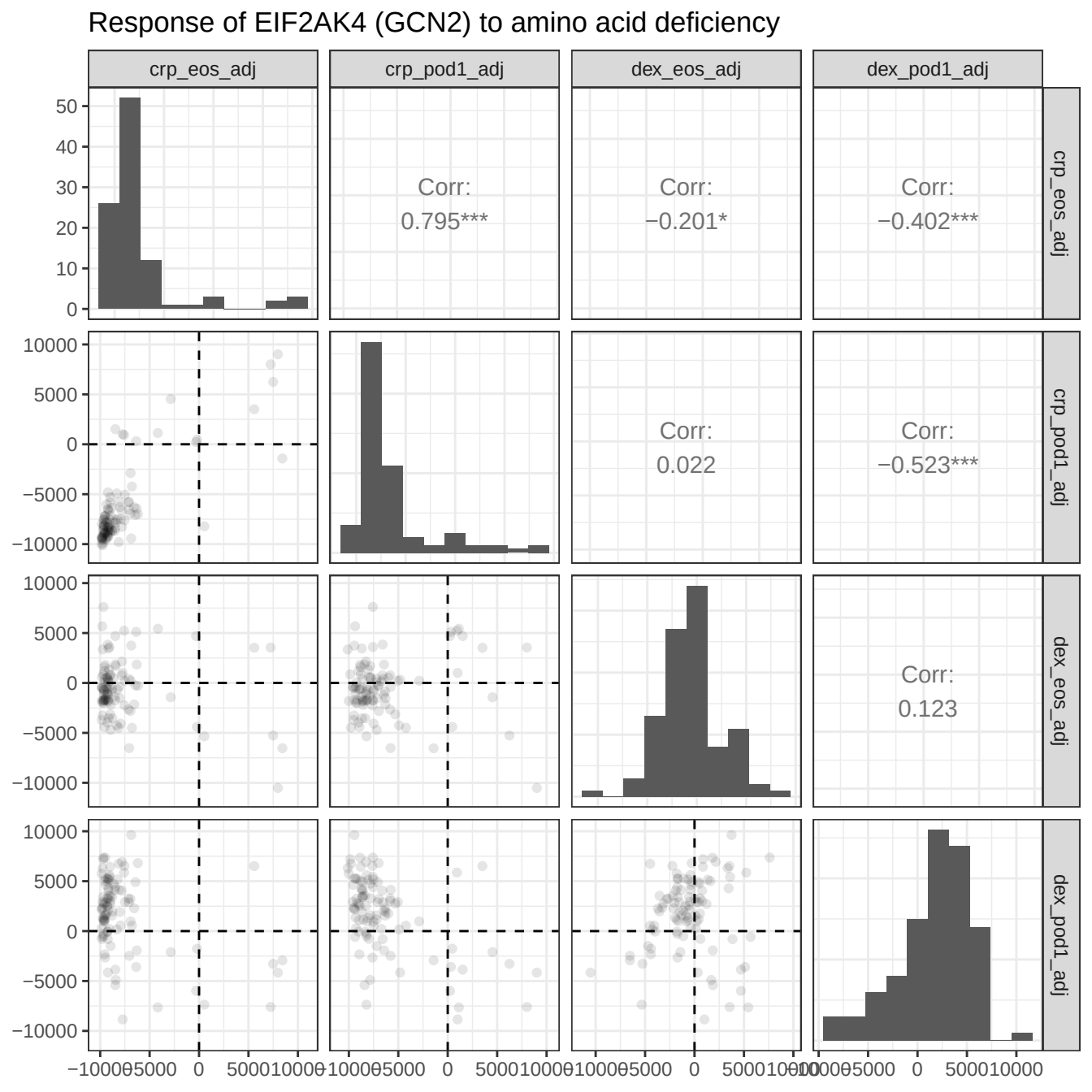

MET activates PI3K/AKT signaling
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

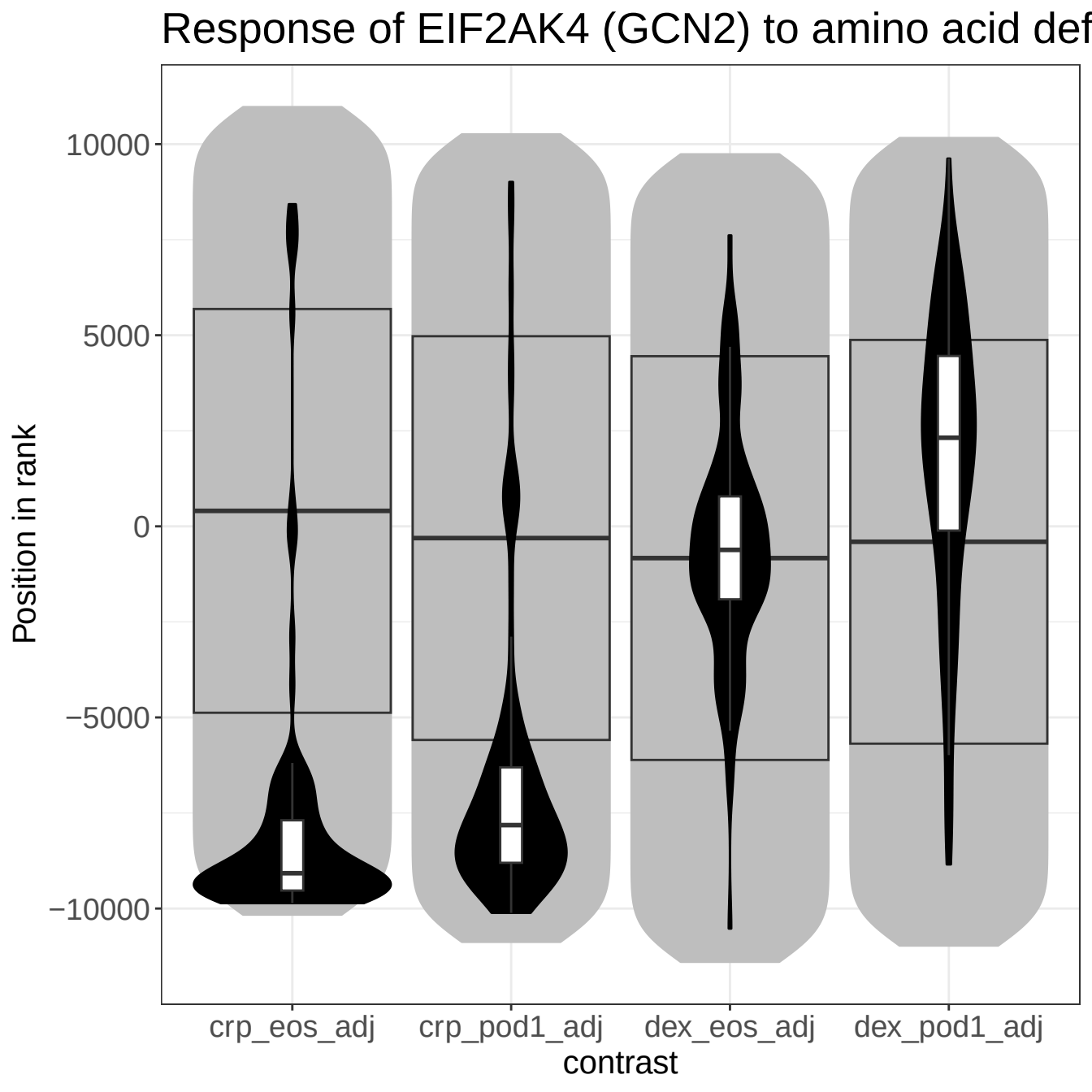

SRP−dependent cotranslational protein targeting to membrane
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.534***
Corr:
−0.070
Corr:
−0.320***
Corr:
0.401***
Corr:
−0.690***
Corr:
−0.386***
60
40
20
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

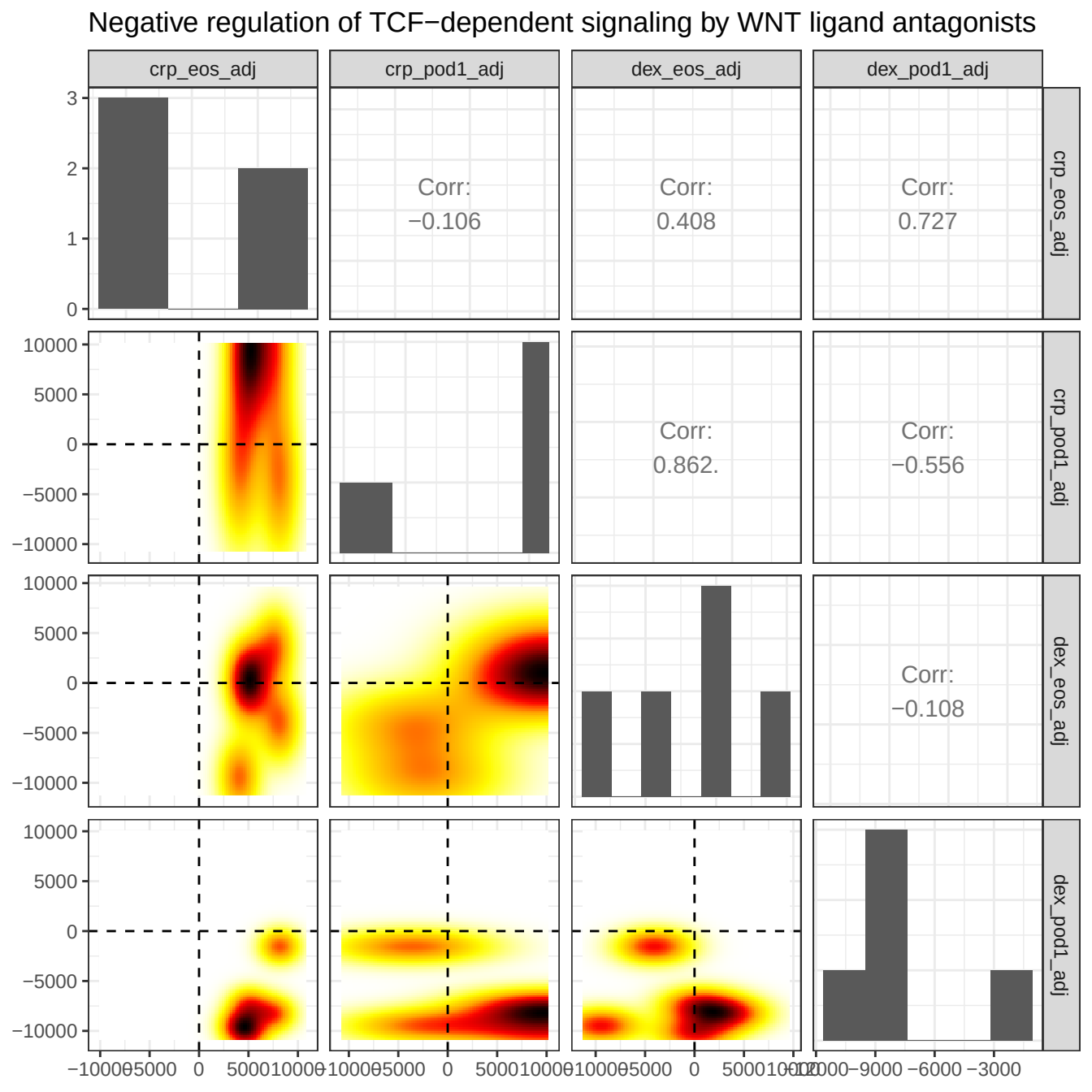

SRP−dependent cotranslational protein targeting to membrane
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.534***
Corr:
−0.070
Corr:
−0.320***
Corr:
0.401***
Corr:
−0.690***
Corr:
−0.386***
60
40
20
0
10000
5000
0
−5000
−10000

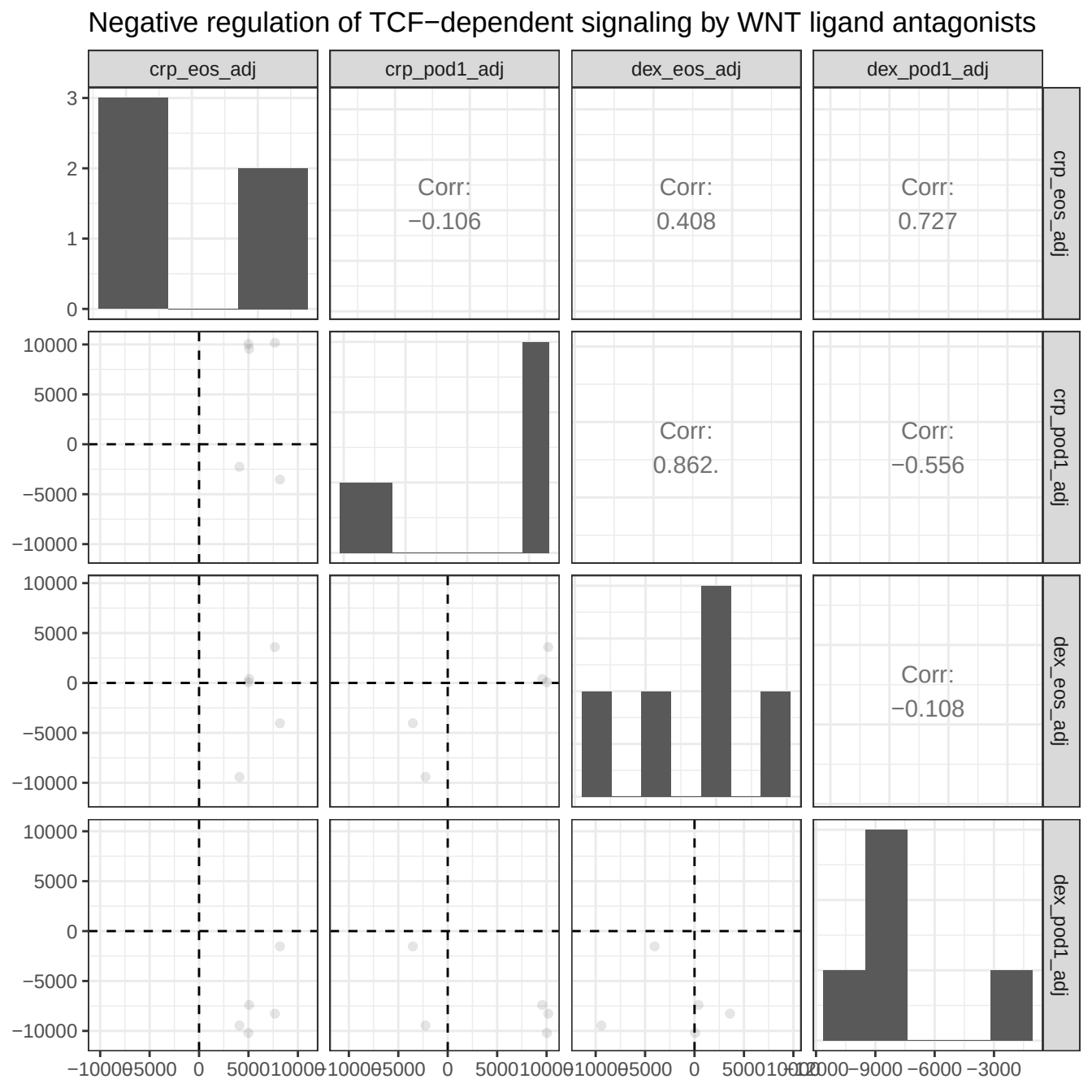

SRP−dependent cotranslational protein targeting
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

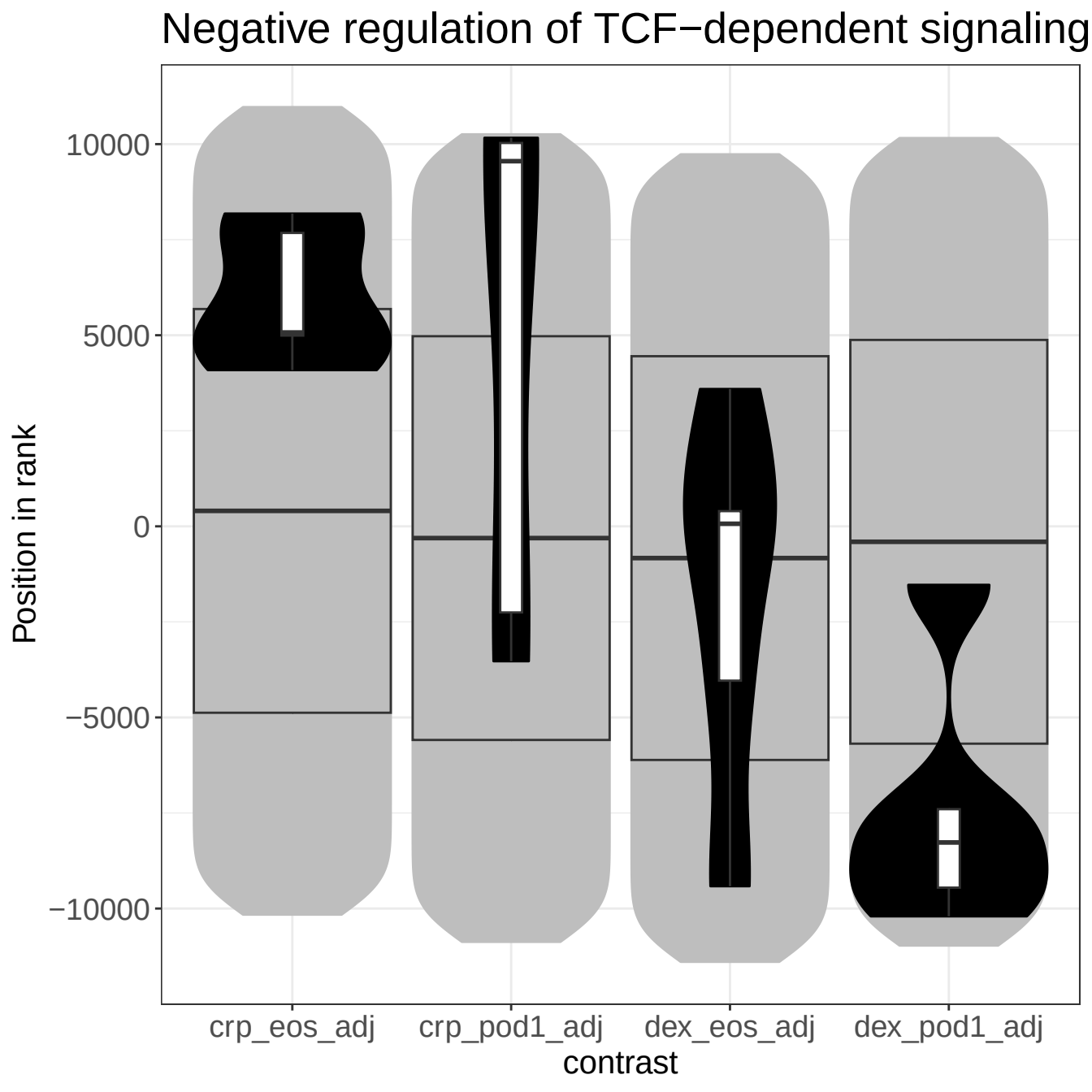

Response of EIF2AK4 (GCN2) to amino acid deficiency
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.795***
Corr:
−0.201*
Corr:
−0.402***
Corr:
0.022
Corr:
−0.523***
Corr:
0.123
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

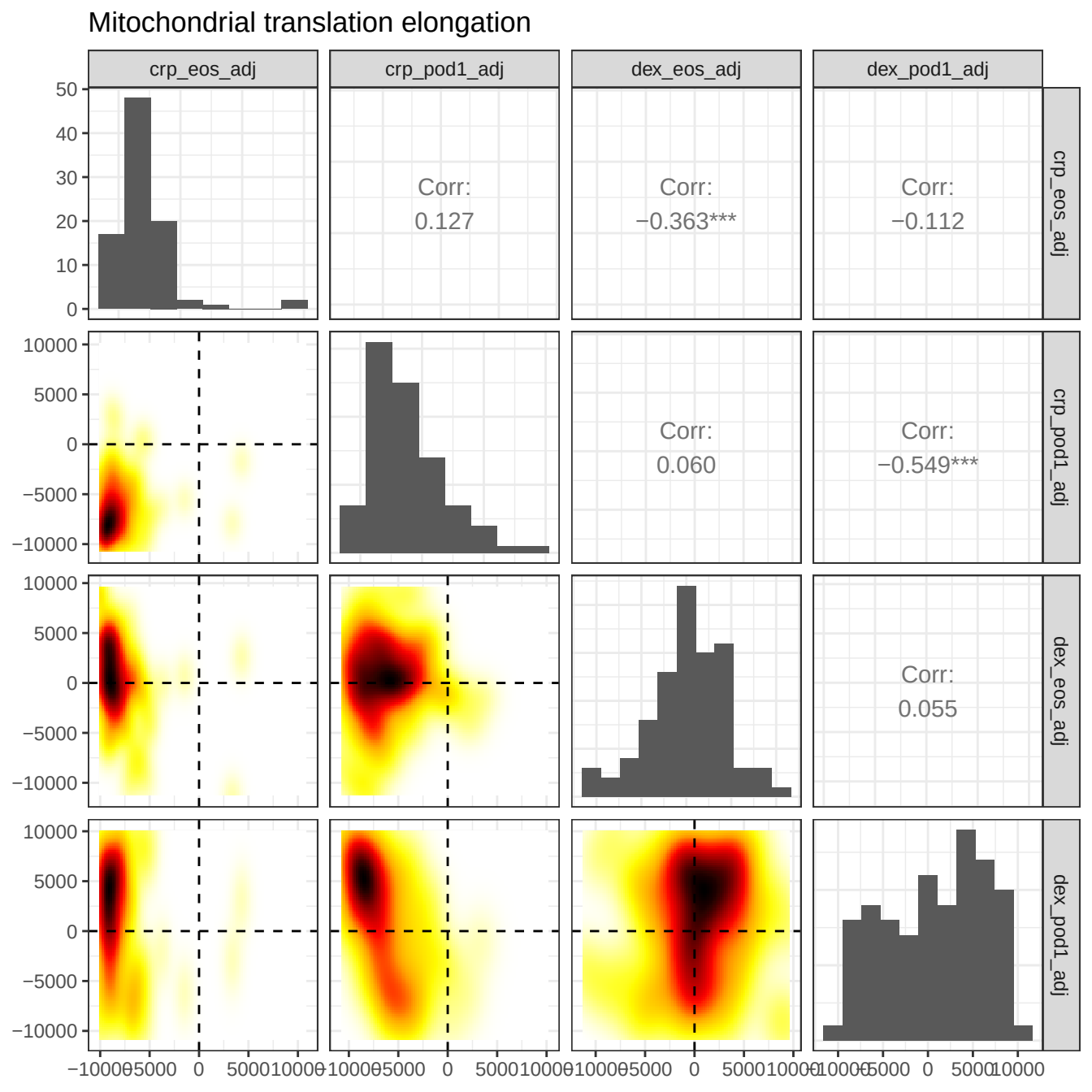

Response of EIF2AK4 (GCN2) to amino acid deficiency
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.795***
Corr:
−0.201*
Corr:
−0.402***
Corr:
0.022
Corr:
−0.523***
Corr:
0.123
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

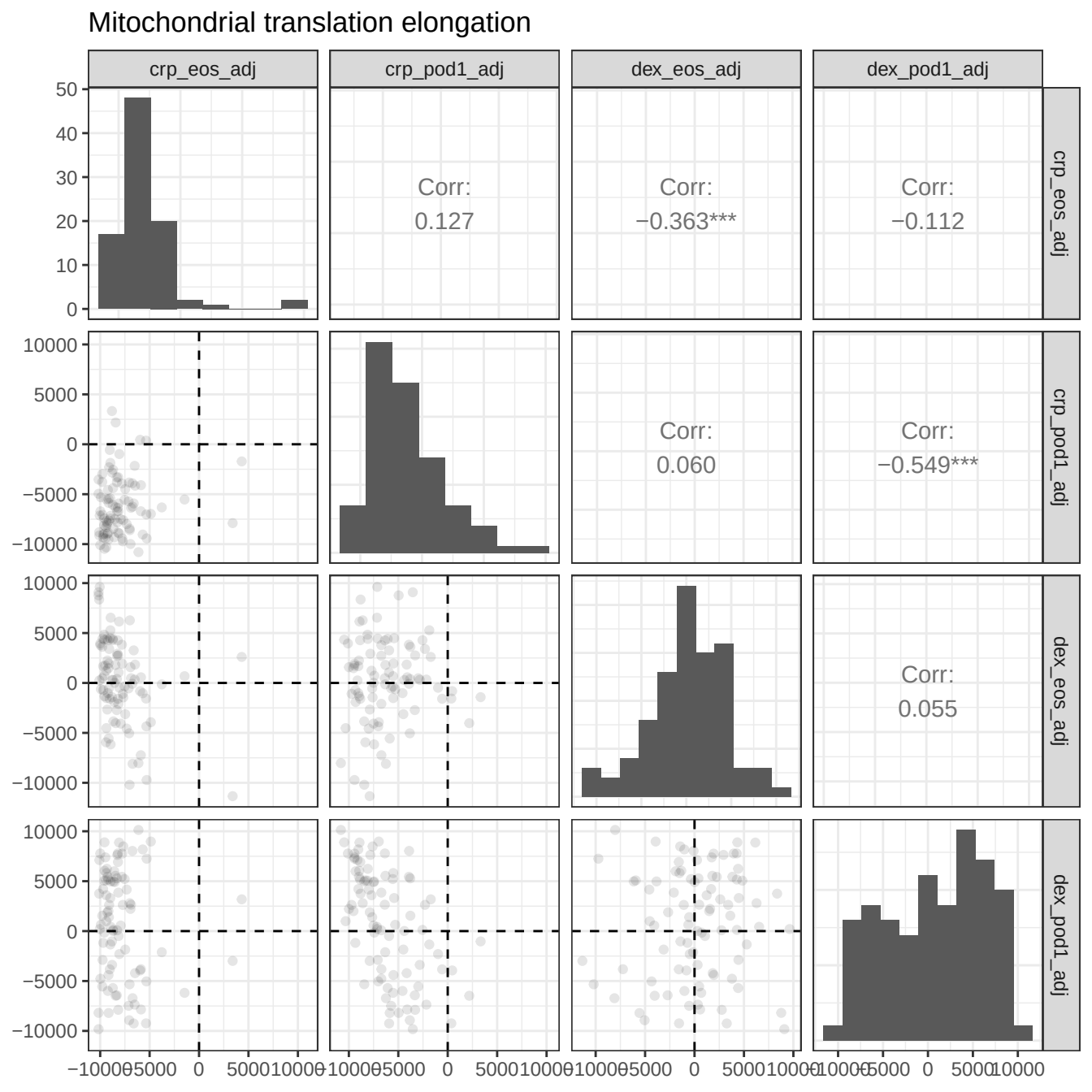

Response of EIF2AK4 (GCN2) to amino acid def
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

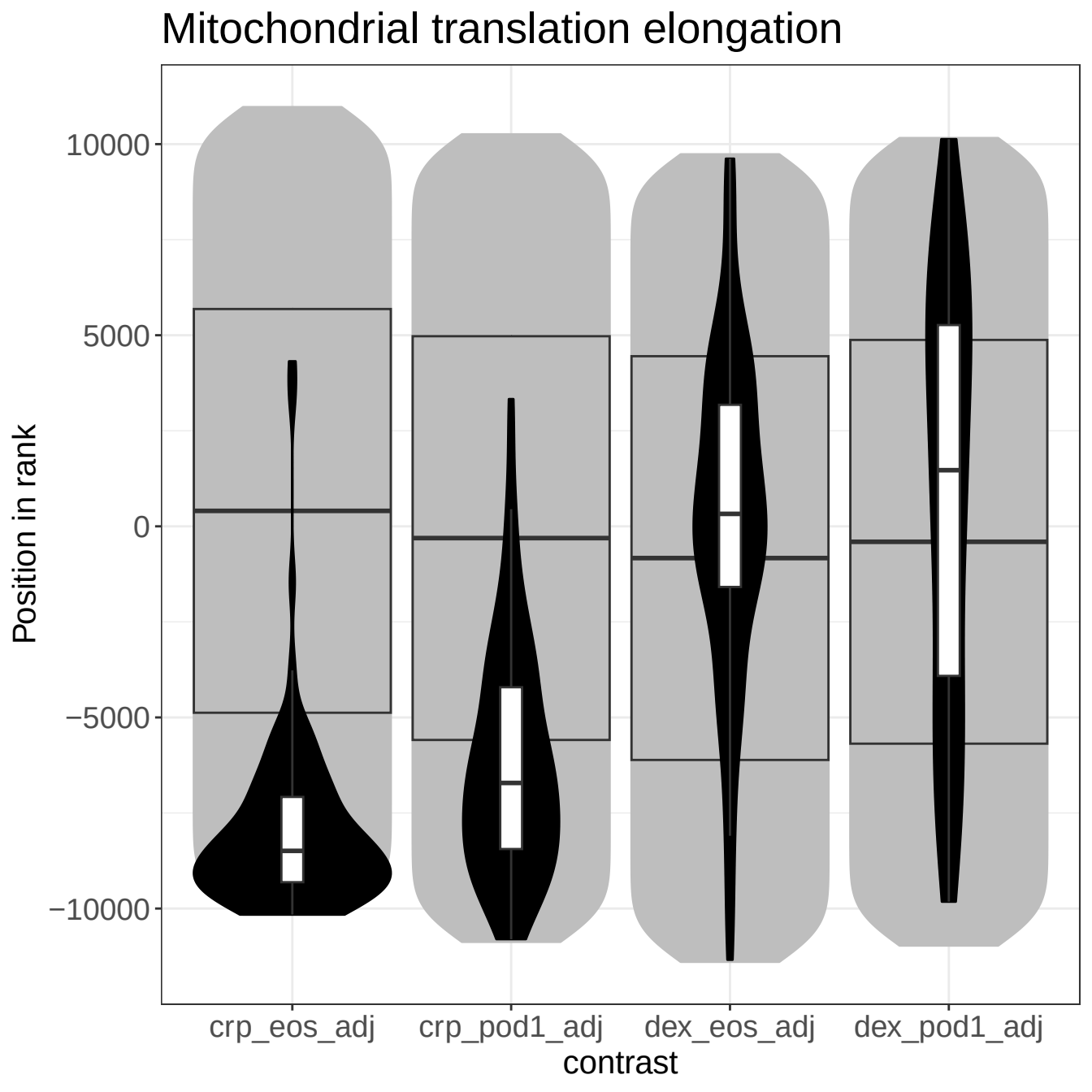

Negative regulation of TCF−dependent signaling by WNT ligand antagonists
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.106
Corr:
0.408
Corr:
0.727
Corr:
0.862.
Corr:
−0.556
Corr:
−0.108
3
2
1
0
10000
5000
0
−5000
−10000
−10000−5000 0 5000 10000
−12000 −9000 −6000 −3000

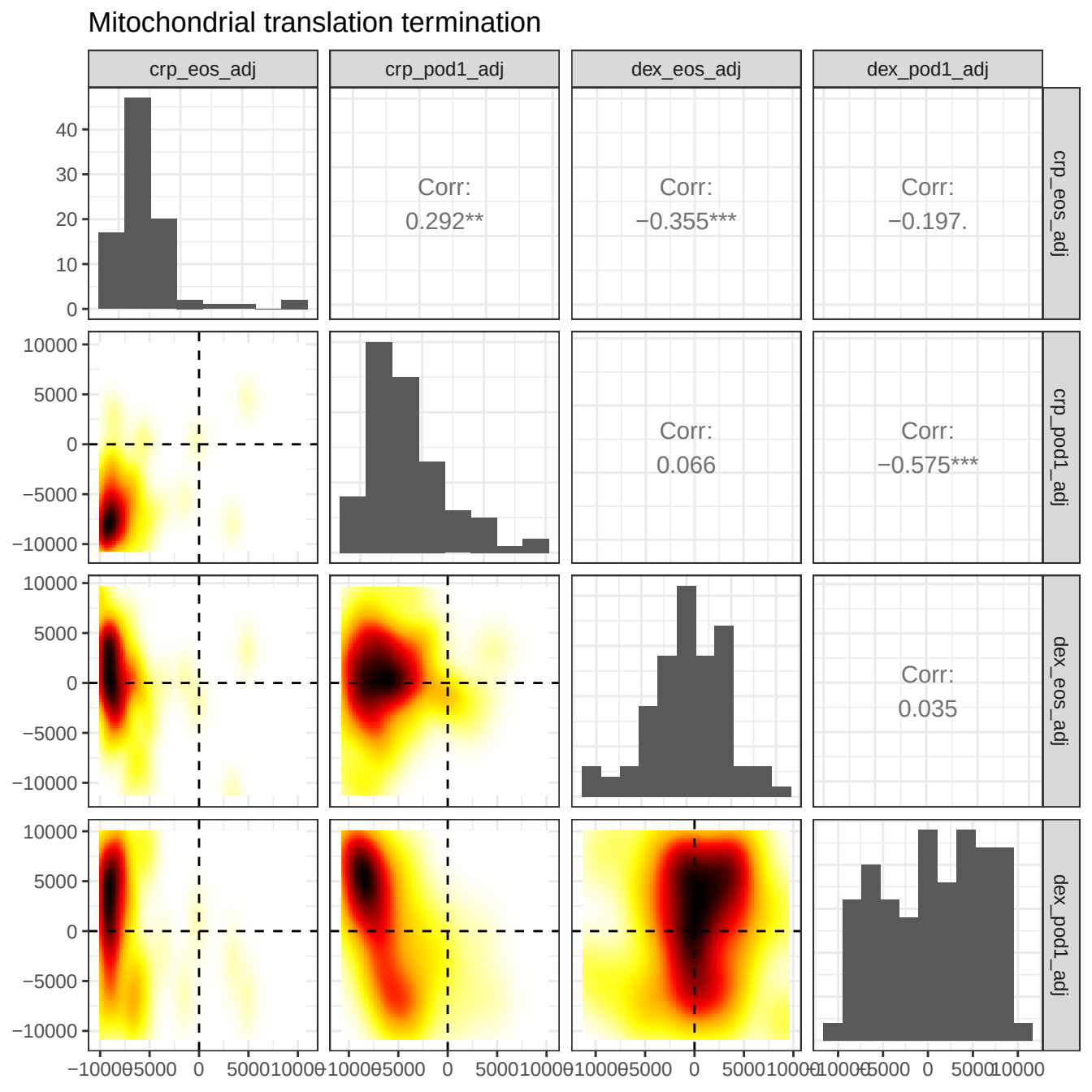

Negative regulation of TCF−dependent signaling by WNT ligand antagonists
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.106
Corr:
0.408
Corr:
0.727
Corr:
0.862.
Corr:
−0.556
Corr:
−0.108
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−12000
−9000
−6000
−3000

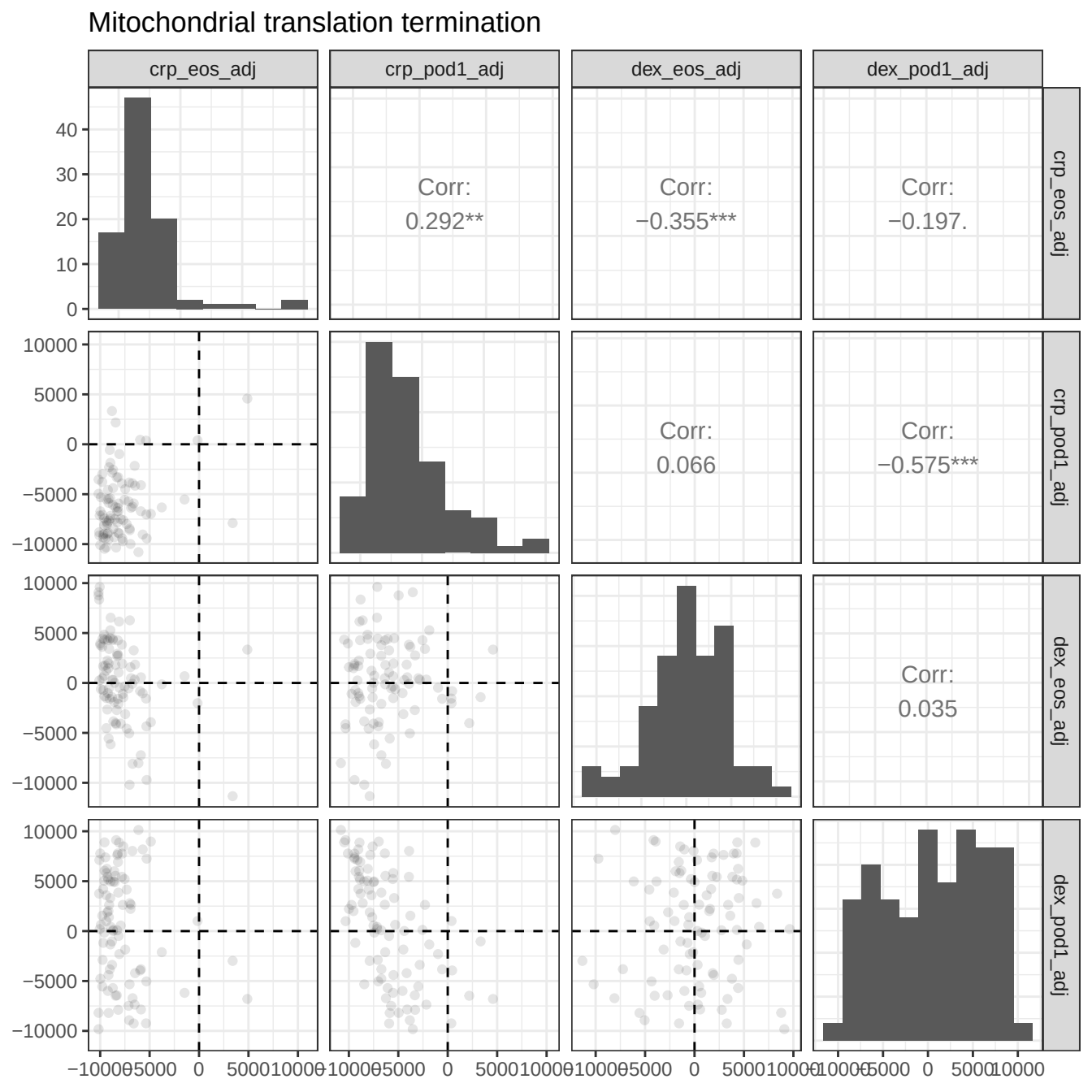

Negative regulation of TCF−dependent signaling
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

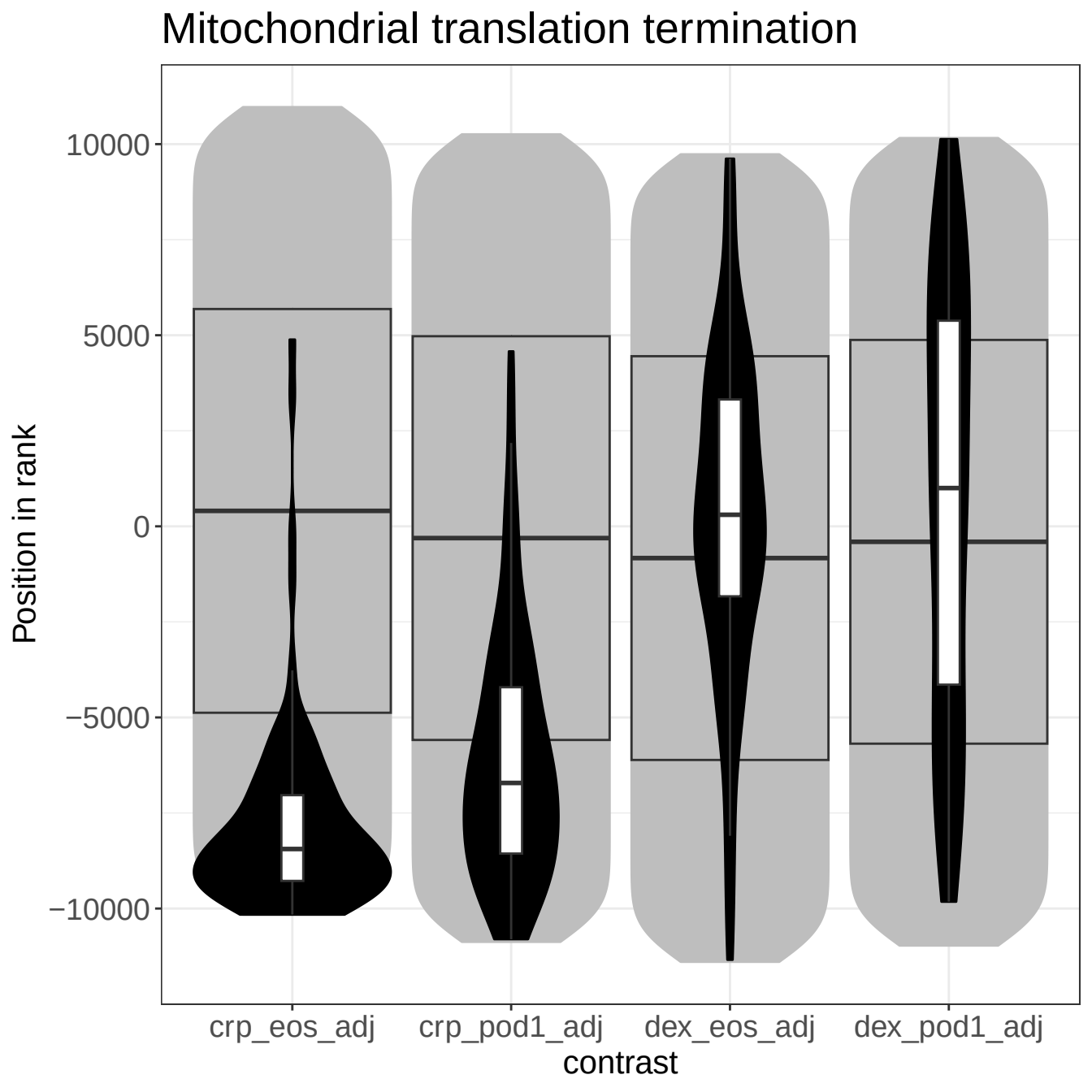

Mitochondrial translation elongation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.127
Corr:
−0.363***
Corr:
−0.112
Corr:
0.060
Corr:
−0.549***
Corr:
0.055
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

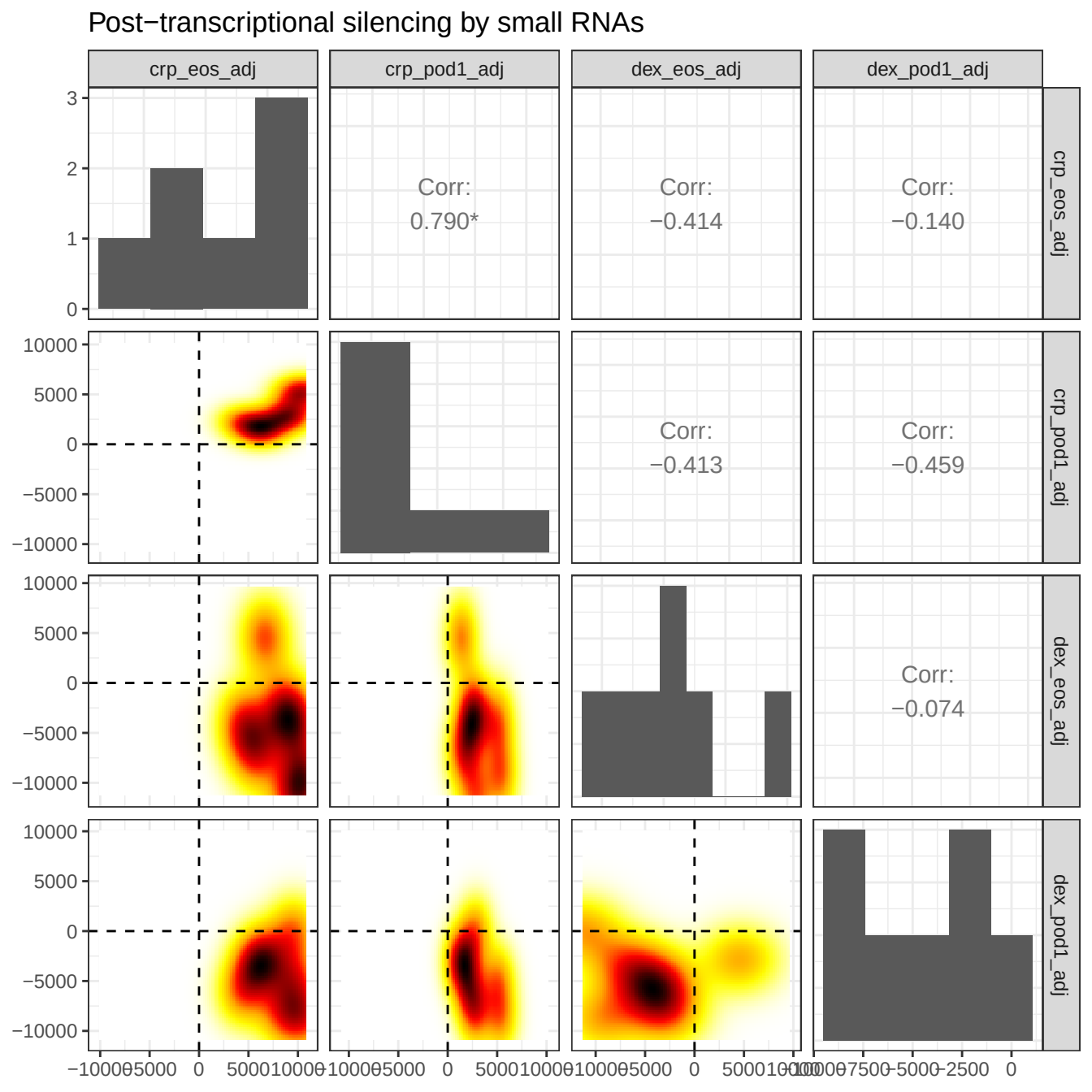

Mitochondrial translation elongation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.127
Corr:
−0.363***
Corr:
−0.112
Corr:
0.060
Corr:
−0.549***
Corr:
0.055
50
40
30
20
10
0
10000
5000
0
−5000
−10000

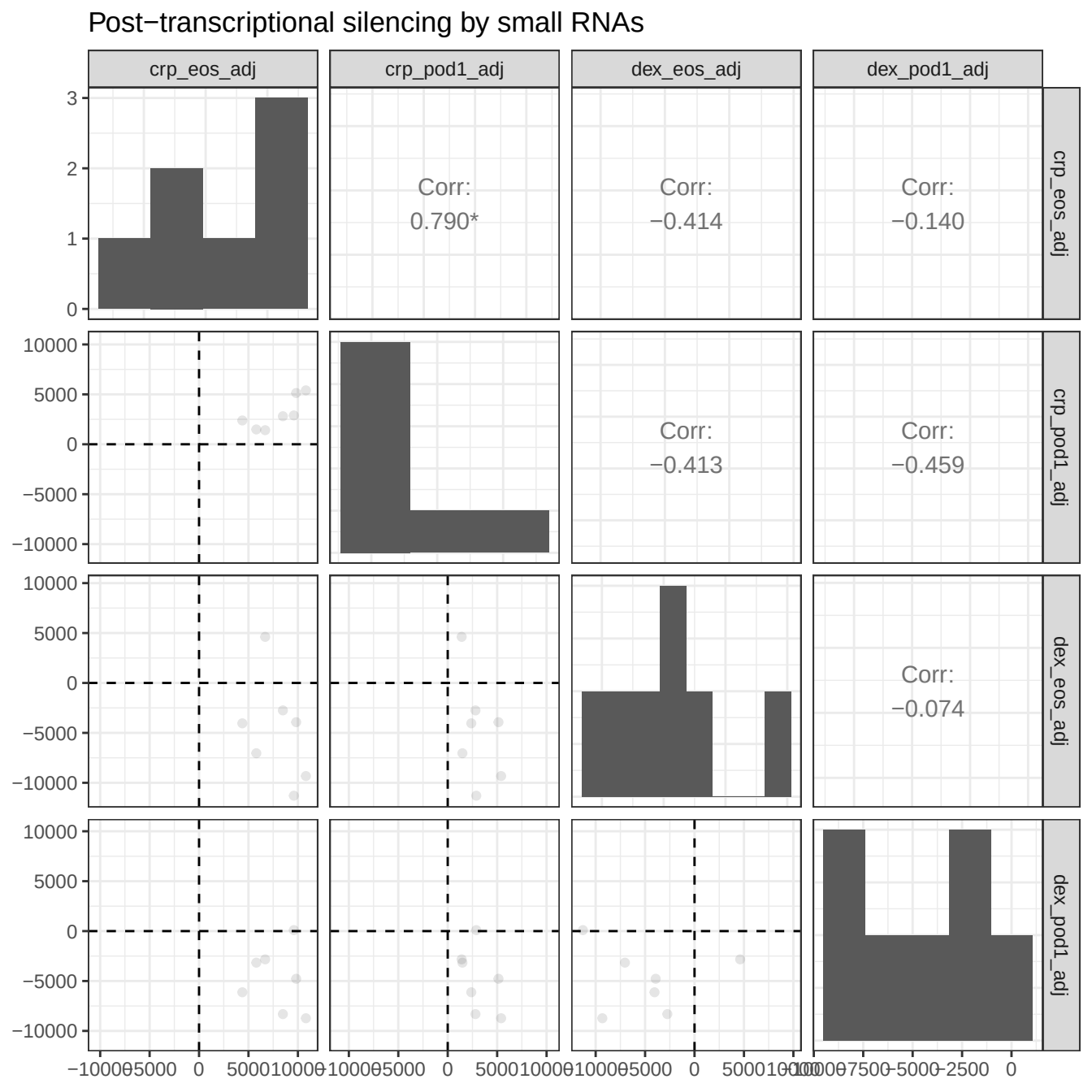

Mitochondrial translation elongation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

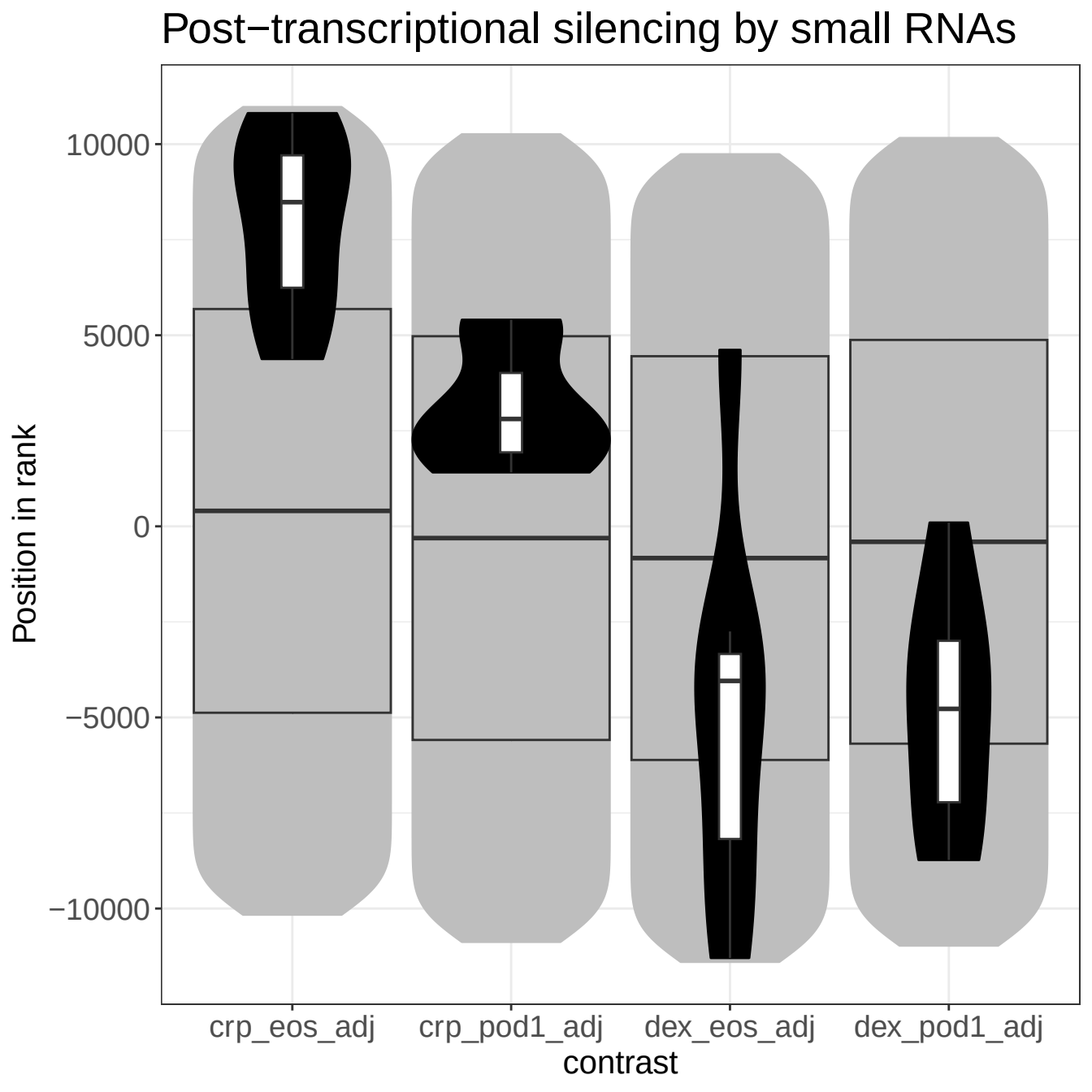

Mitochondrial translation termination
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.292**
Corr:
−0.355***
Corr:
−0.197.
Corr:
0.066
Corr:
−0.575***
Corr:
0.035
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

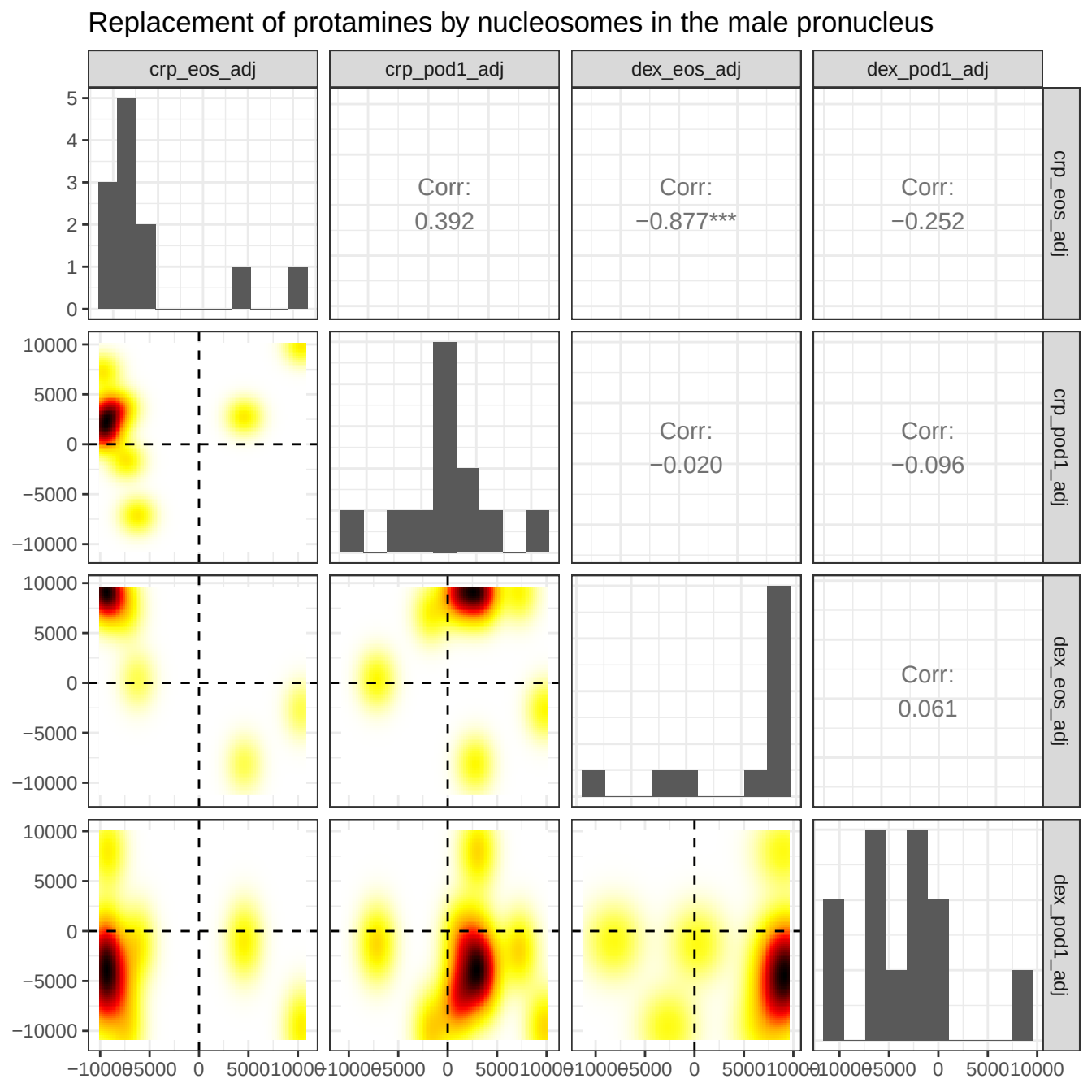

Mitochondrial translation termination
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.292**
Corr:
−0.355***
Corr:
−0.197.
Corr:
0.066
Corr:
−0.575***
Corr:
0.035
40
30
20
10
0
10000
5000
0
−5000
−10000

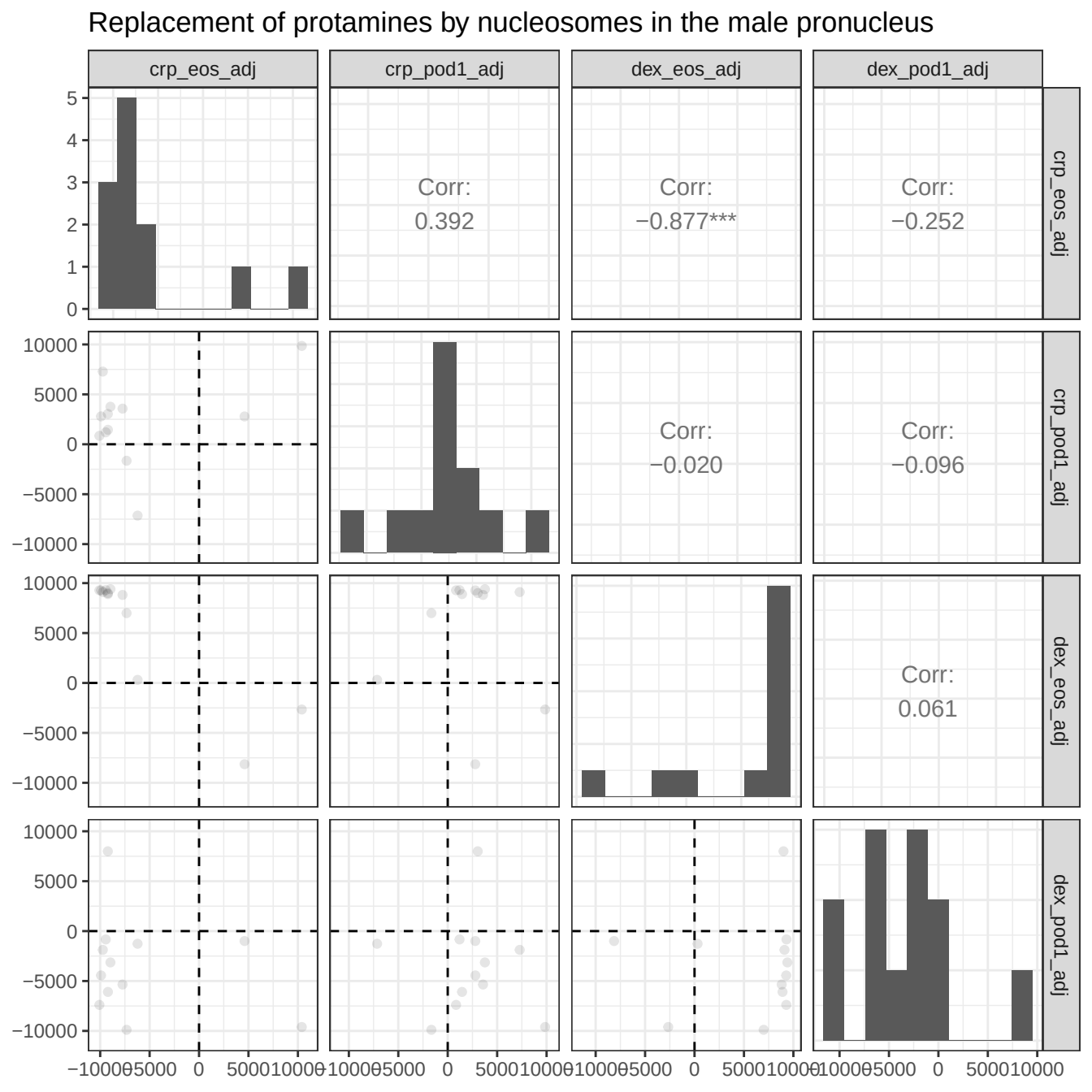

Mitochondrial translation termination
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

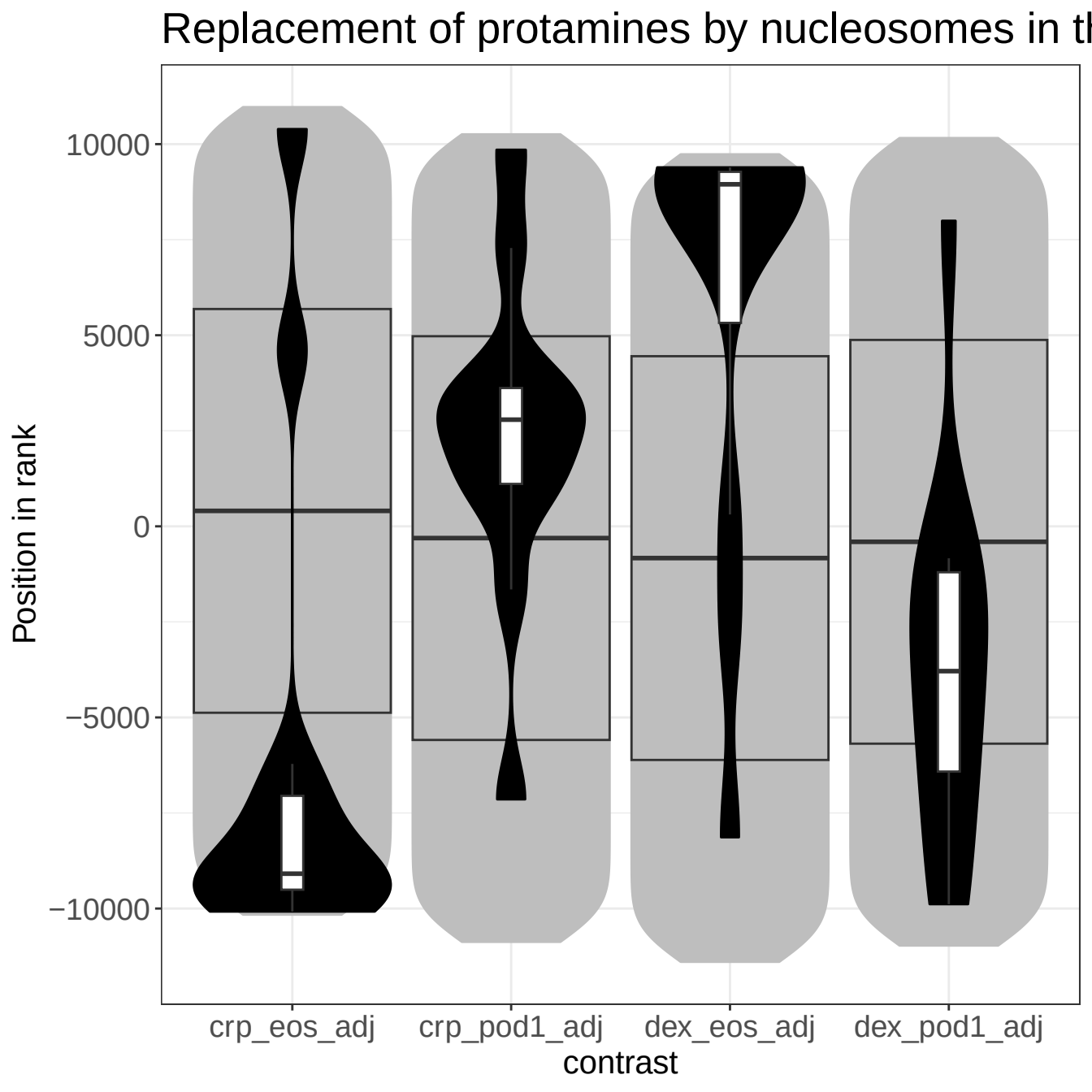

Post−transcriptional silencing by small RNAs
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.790*
Corr:
−0.414
Corr:
−0.140
Corr:
−0.413
Corr:
−0.459
Corr:
−0.074
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−10000
−7500
−5000
−2500
0

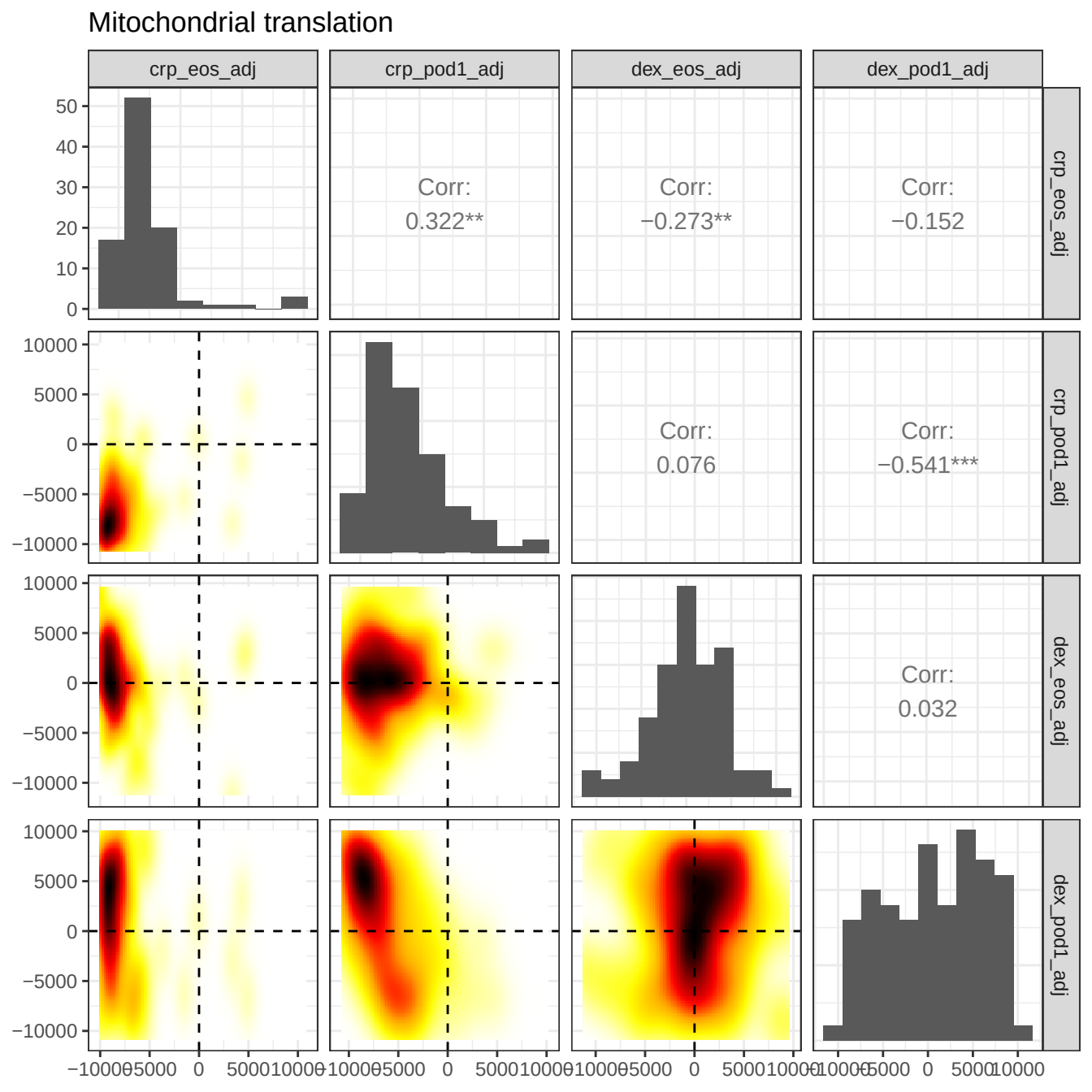

Post−transcriptional silencing by small RNAs
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.790*
Corr:
−0.414
Corr:
−0.140
Corr:
−0.413
Corr:
−0.459
Corr:
−0.074

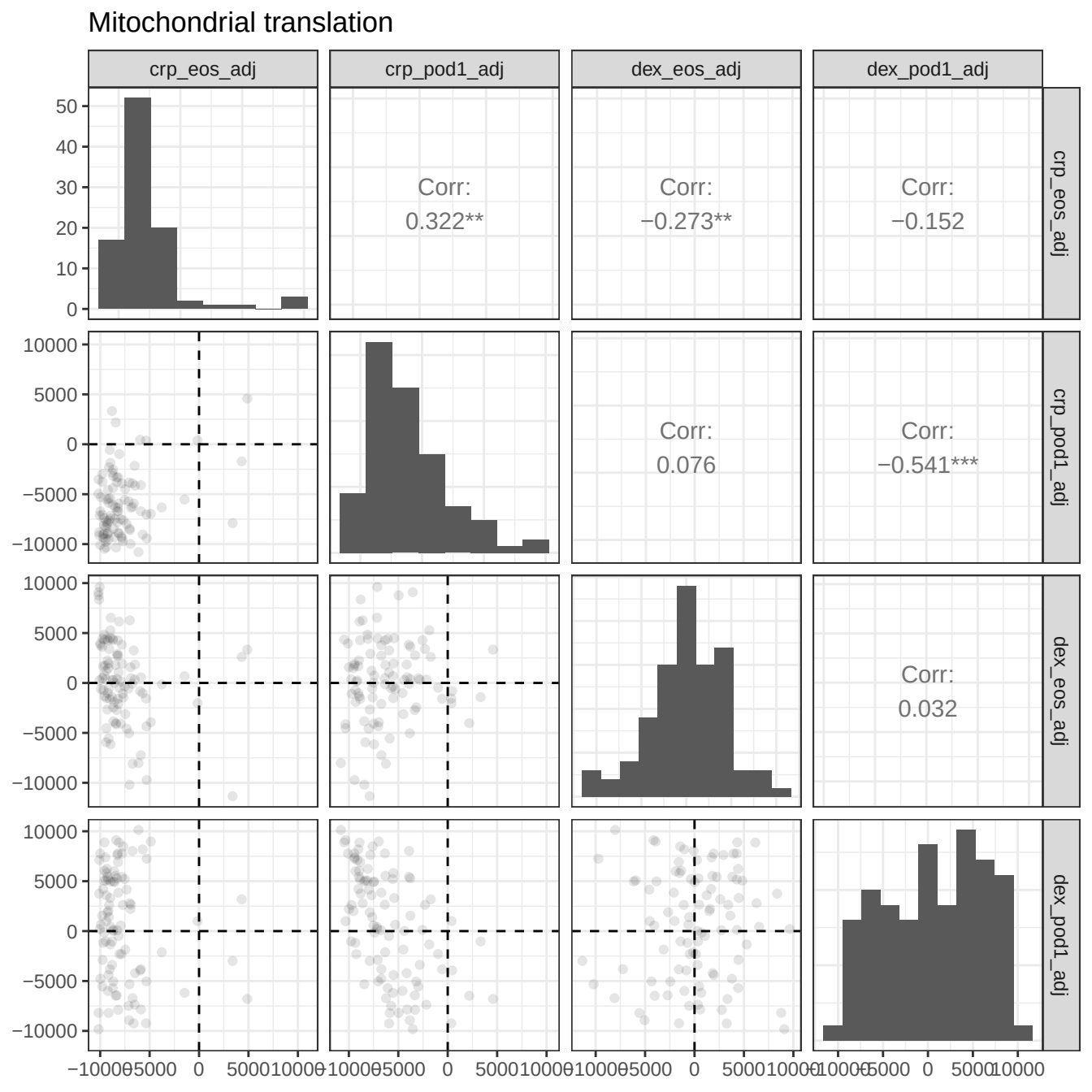

Post−transcriptional silencing by small RNAs
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

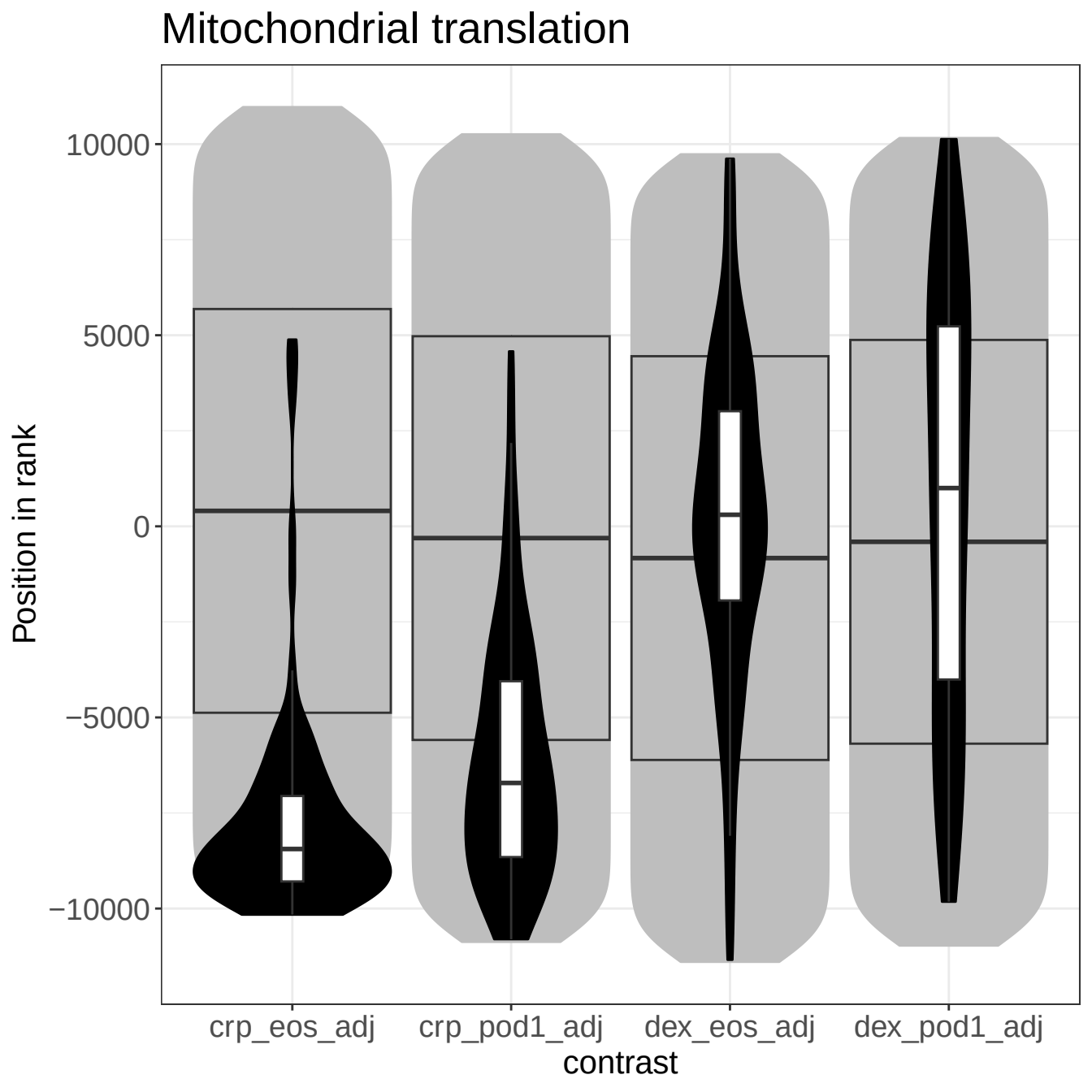

Replacement of protamines by nucleosomes in the male pronucleus
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.392
Corr:
−0.877***
Corr:
−0.252
Corr:
−0.020
Corr:
−0.096
Corr:
0.061
0
1
2
3
4
5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000


Replacement of protamines by nucleosomes in the male pronucleus
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.392
Corr:
−0.877***
Corr:
−0.252
Corr:
−0.020
Corr:
−0.096
Corr:
0.061
0
1
2
3
4
5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

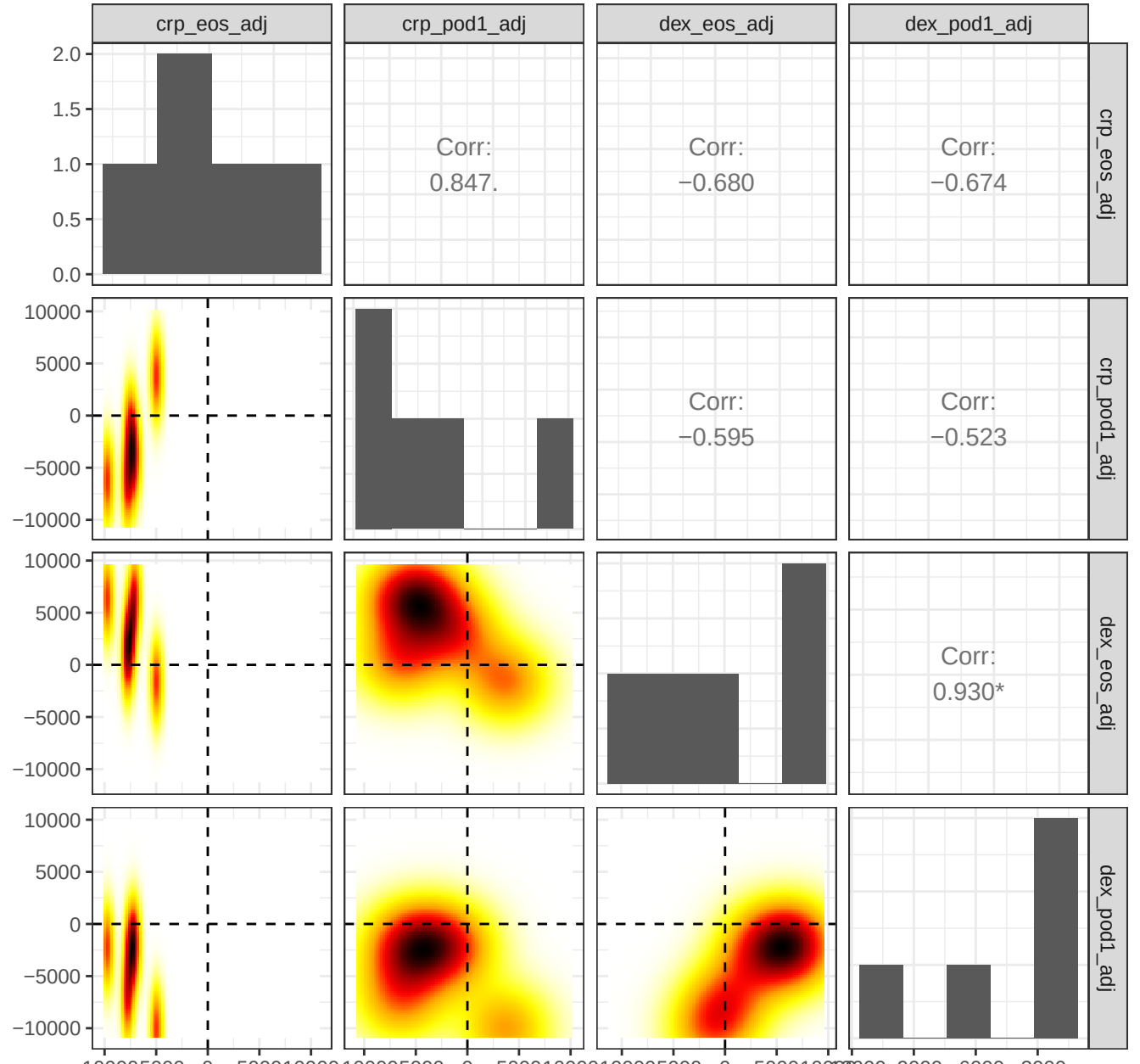

Replacement of protamines by nucleosomes in th
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

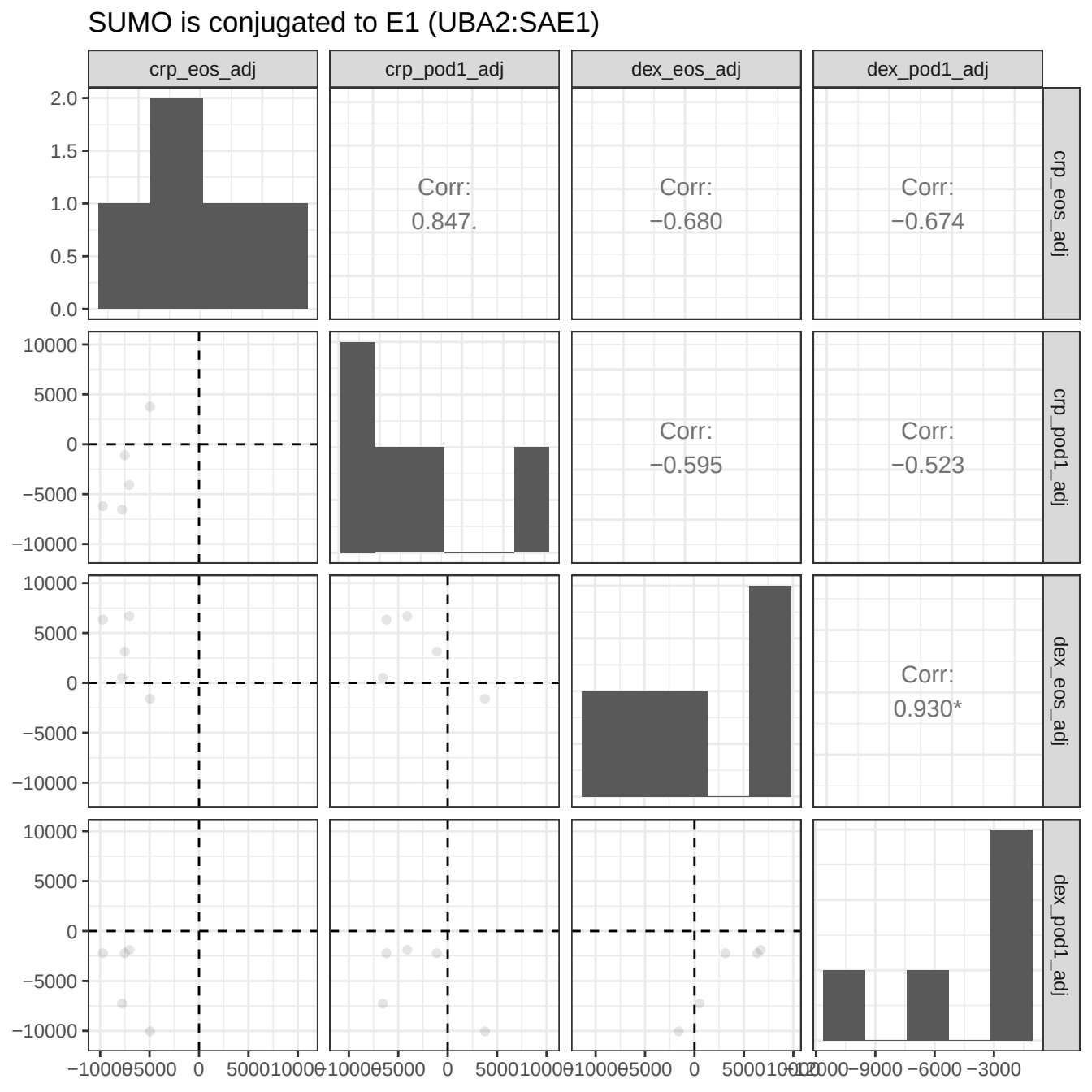

Mitochondrial translation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.322**
Corr:
−0.273**
Corr:
−0.152
Corr:
0.076
Corr:
−0.541***
Corr:
0.032
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

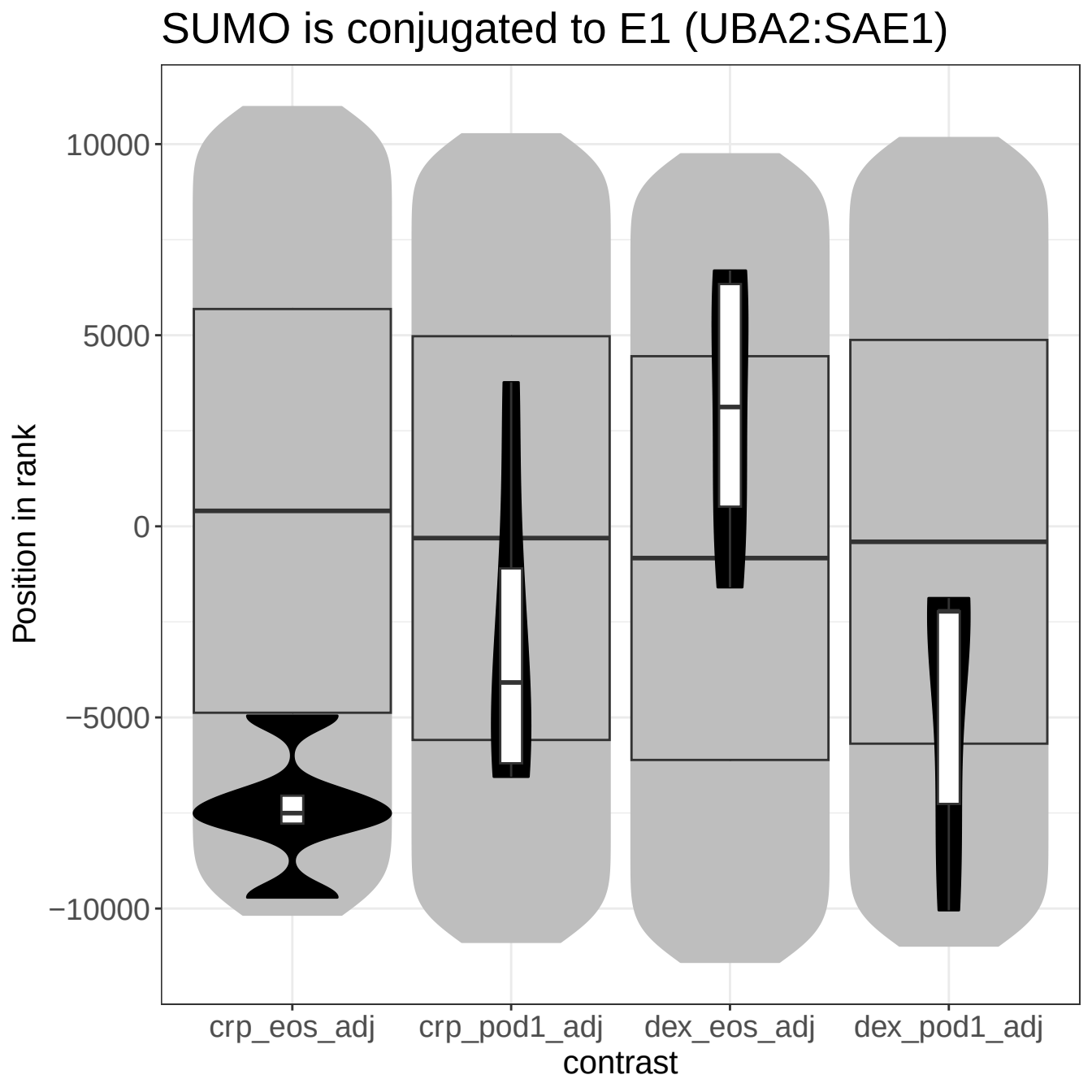

Mitochondrial translation
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.322**
Corr:
−0.273**
Corr:
−0.152
Corr:
0.076
Corr:
−0.541***
Corr:
0.032
50
40
30
20
10
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

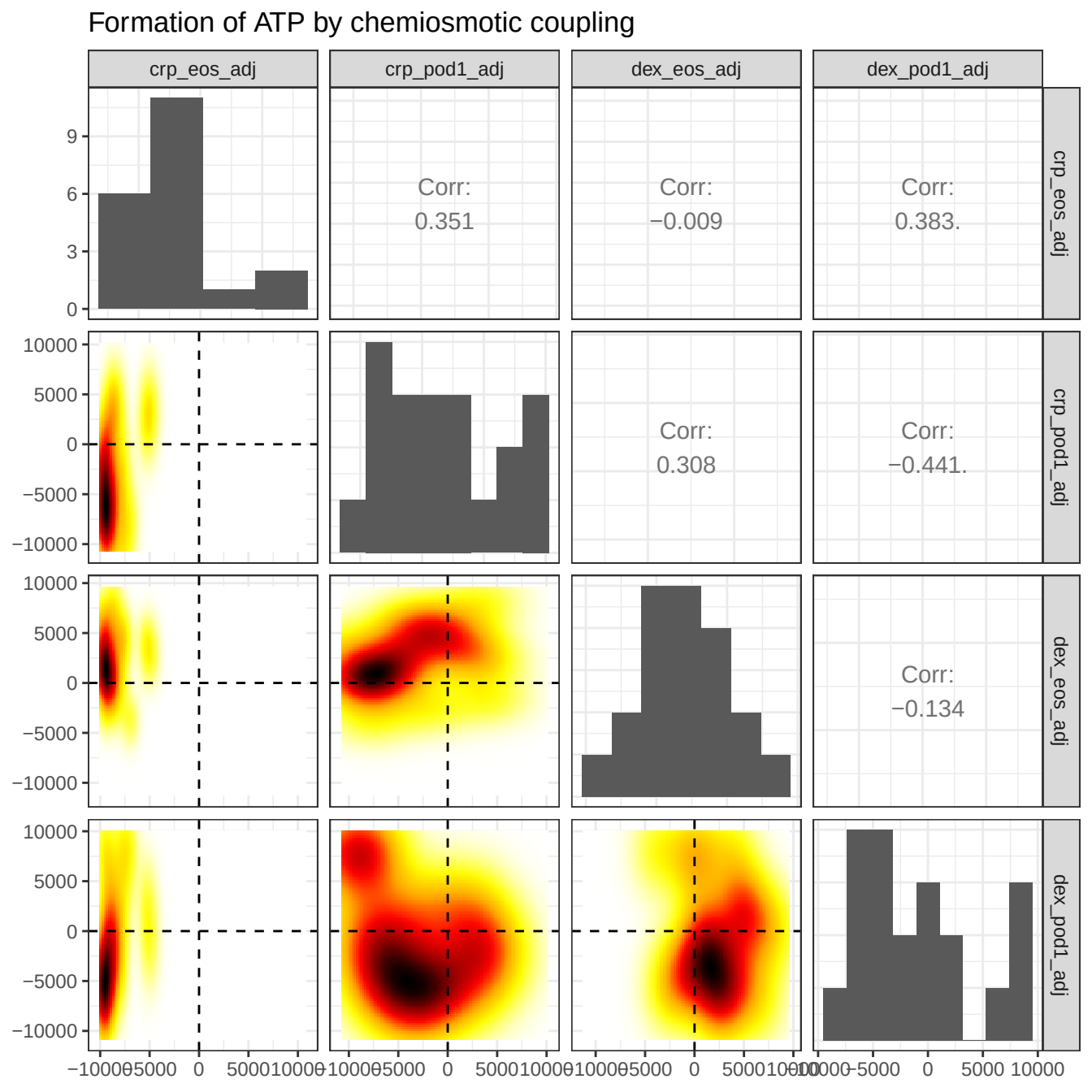

Mitochondrial translation
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

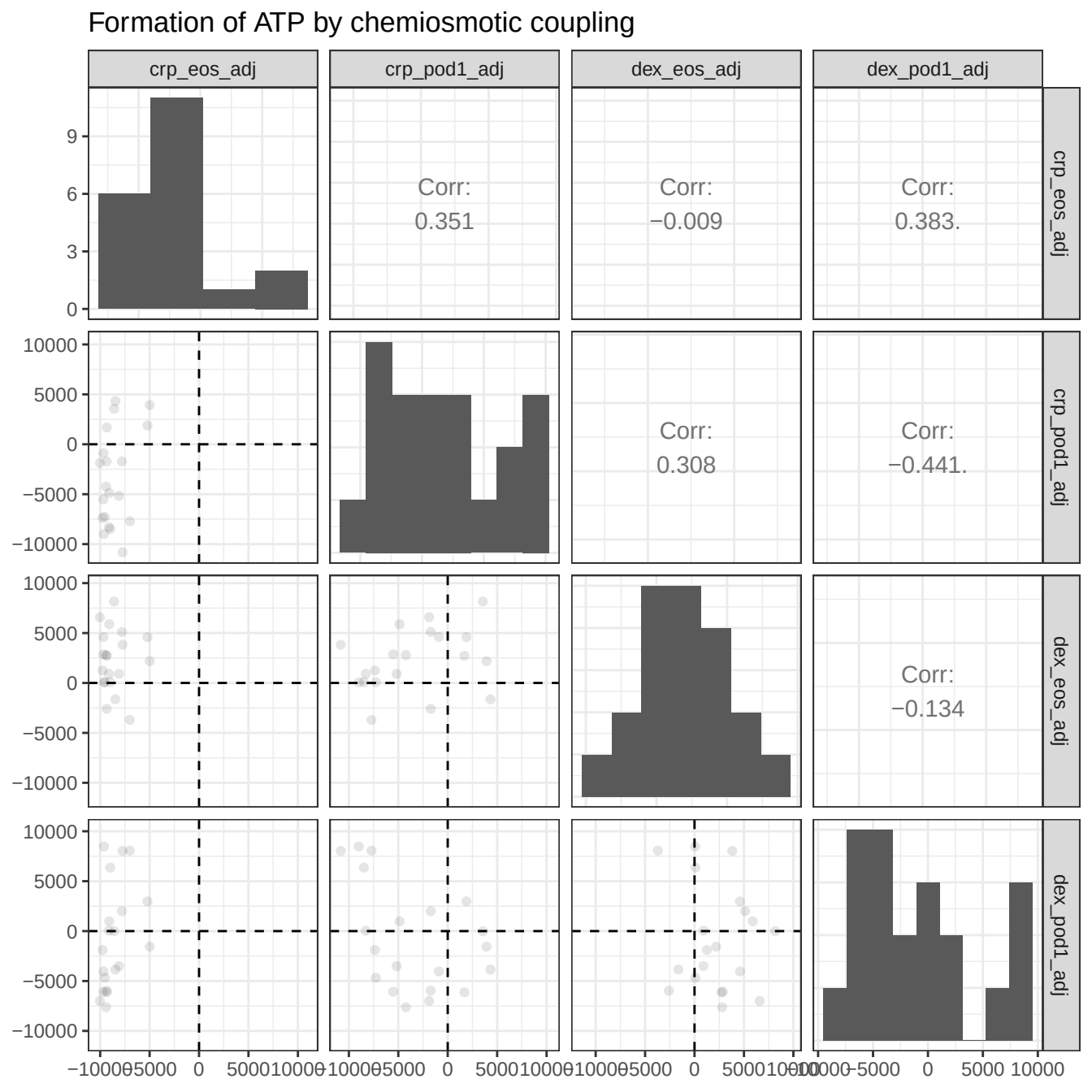
SUMO is conjugated to E1 (UBA2:SAE1)

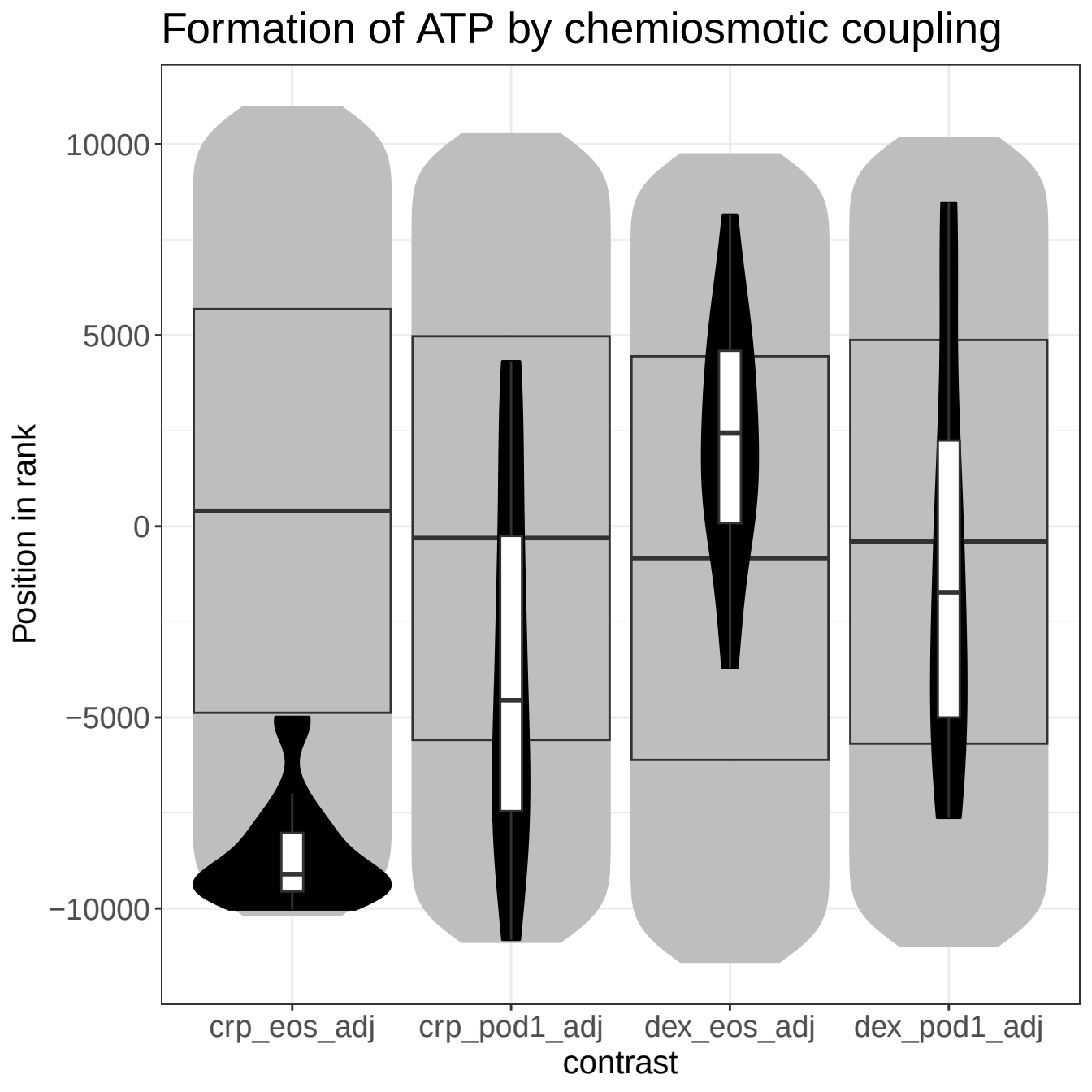


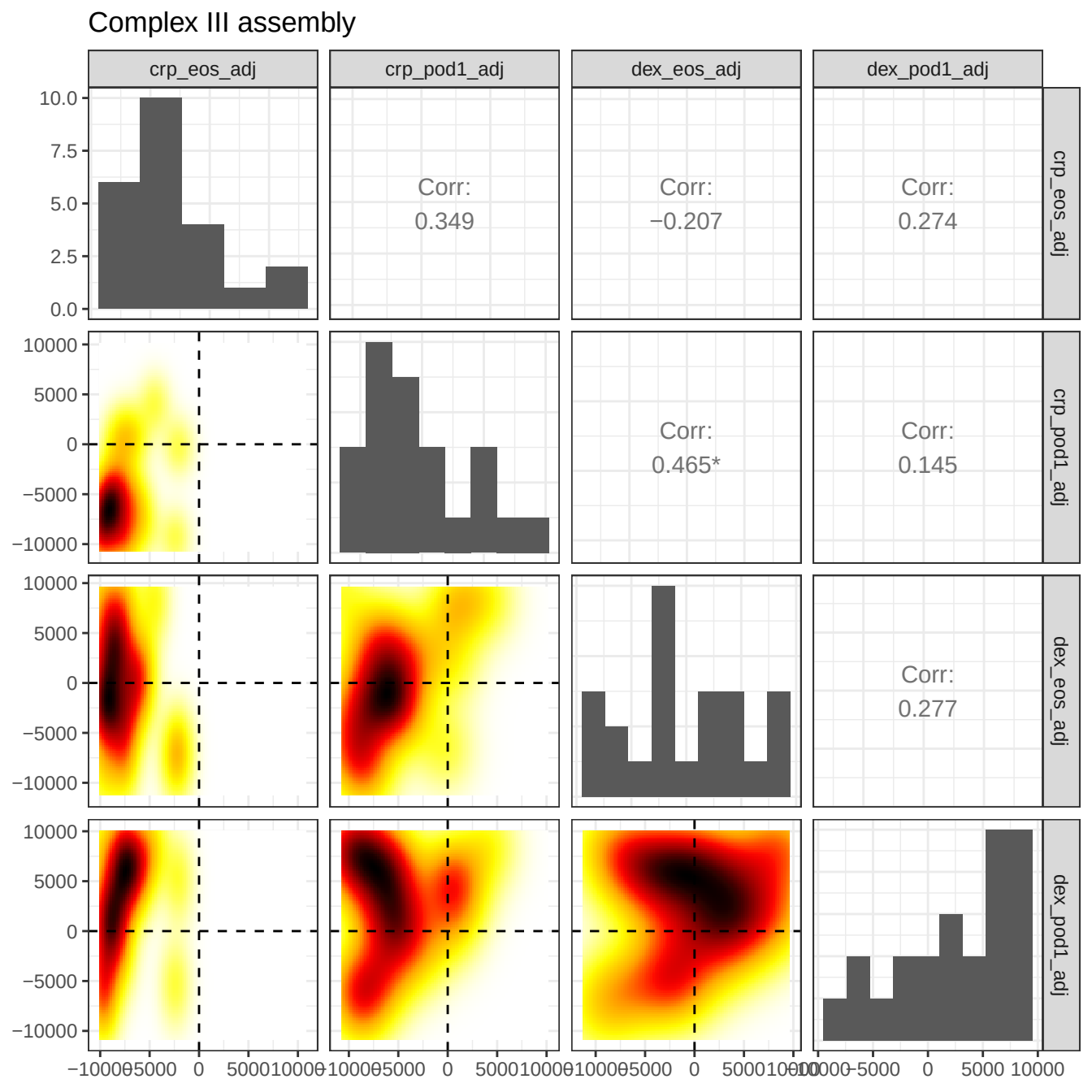

SUMO is conjugated to E1 (UBA2:SAE1)
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.847.
Corr:
−0.680
Corr:
−0.674
Corr:
−0.595
Corr:
−0.523
Corr:
0.930*

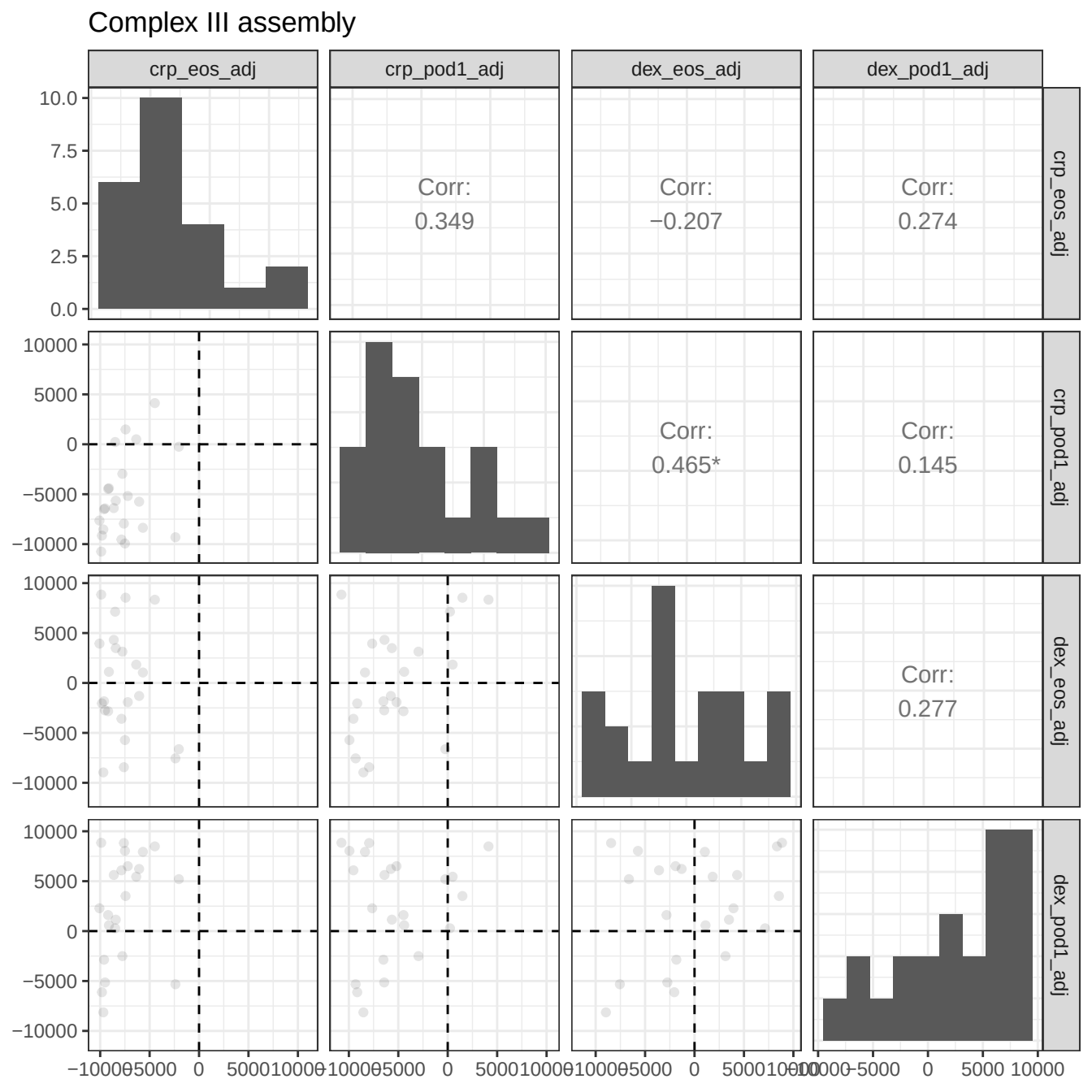

SUMO is conjugated to E1 (UBA2:SAE1)
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

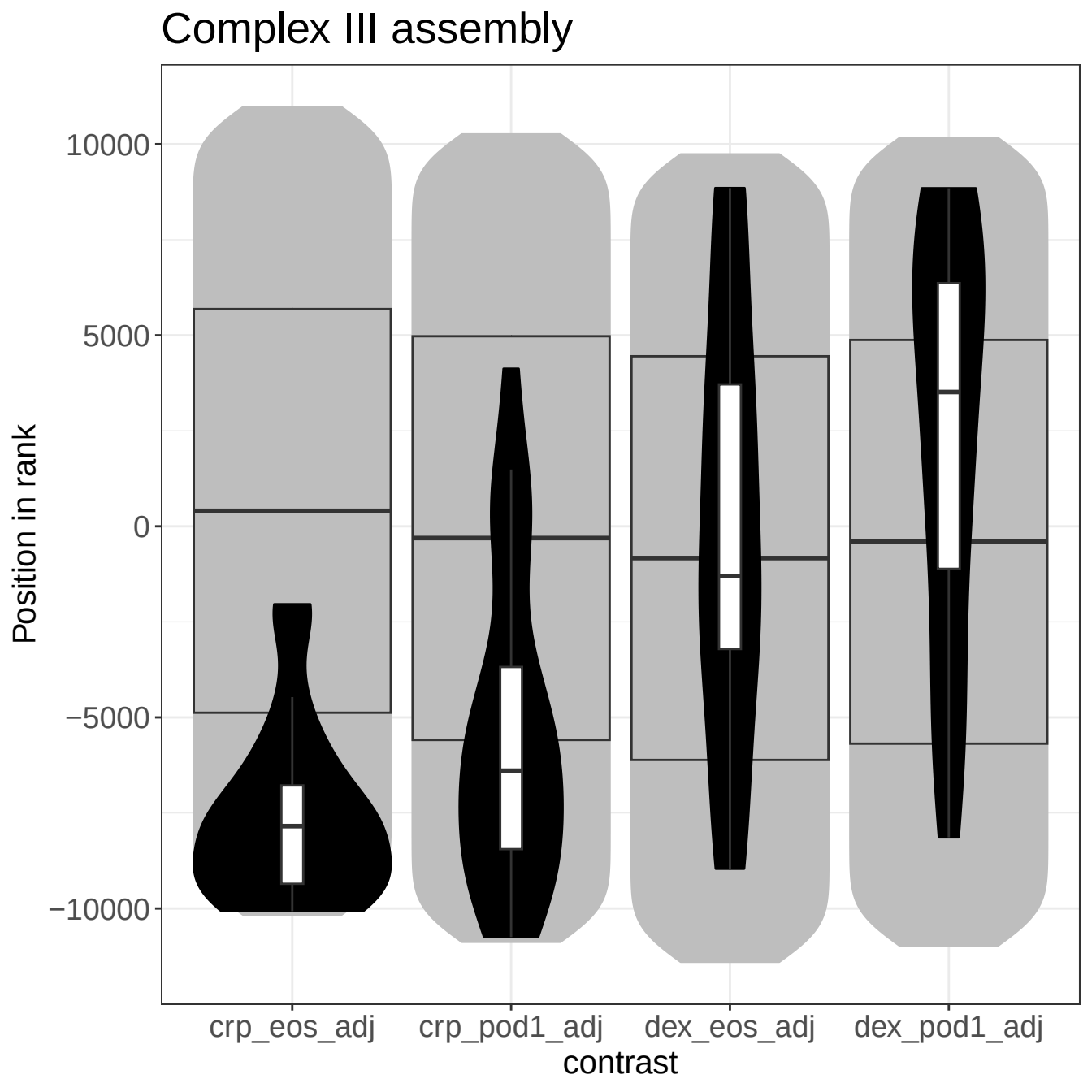

Formation of ATP by chemiosmotic coupling
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.351
Corr:
−0.009
Corr:
0.383.
Corr:
0.308
Corr:
−0.441.
Corr:
−0.134
9
6
3
0
10000
5000
0
−5000
−10000
−10000 −5000 0 5000 10000

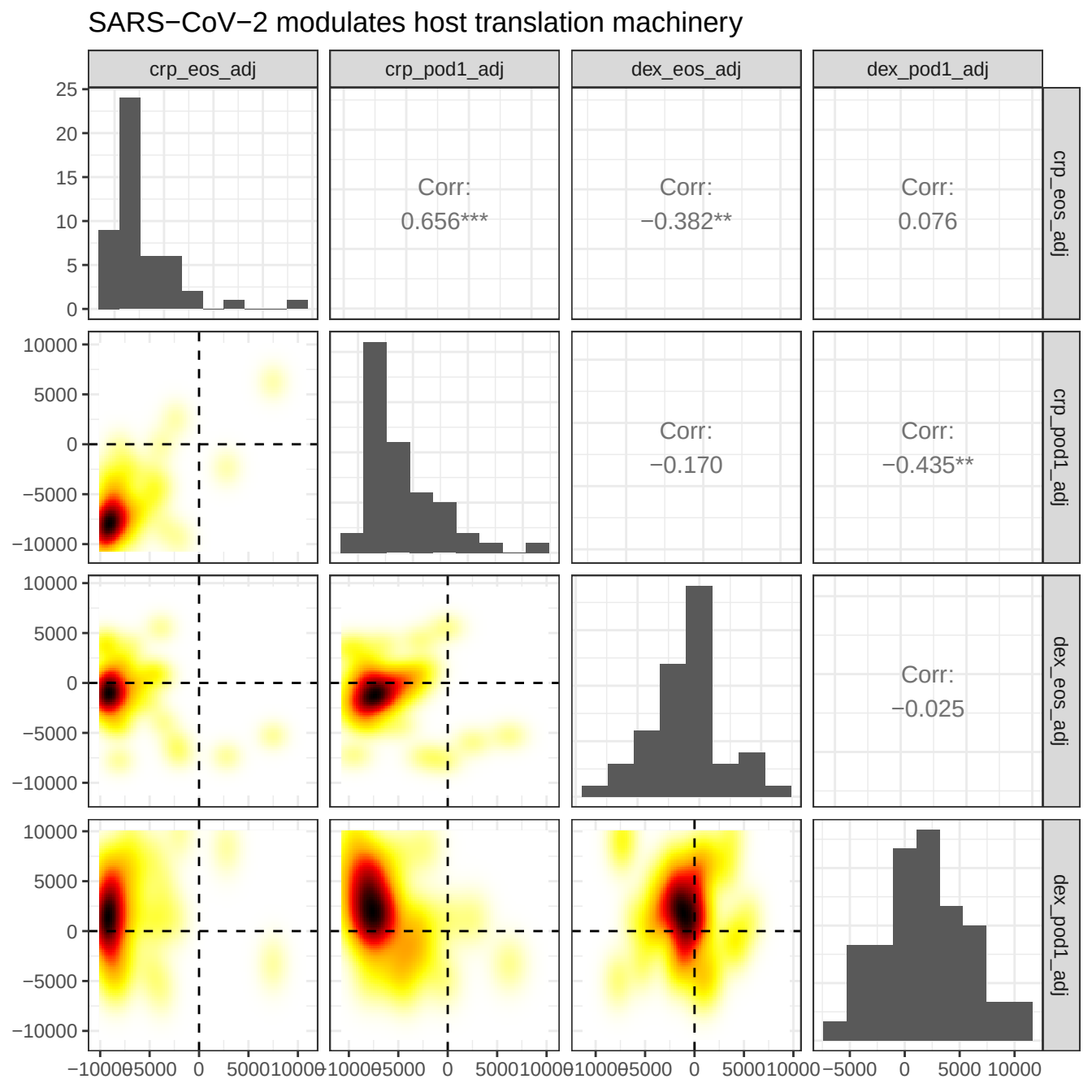

Formation of ATP by chemiosmotic coupling
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.351
Corr:
−0.009
Corr:
0.383.
Corr:
0.308
Corr:
−0.441.
Corr:
−0.134
9
6
3
0
10000
5000
0
−5000
−10000

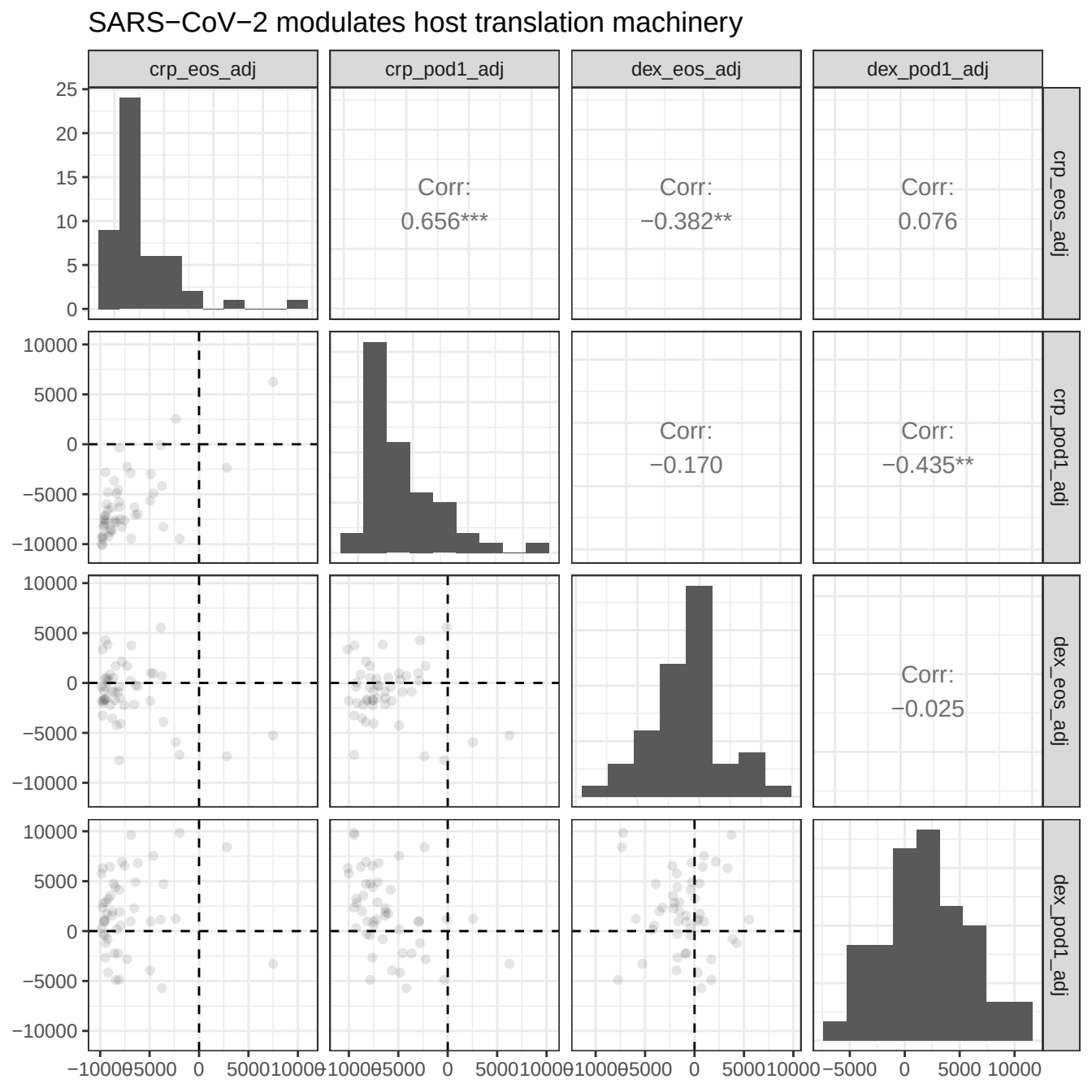

Formation of ATP by chemiosmotic coupling
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

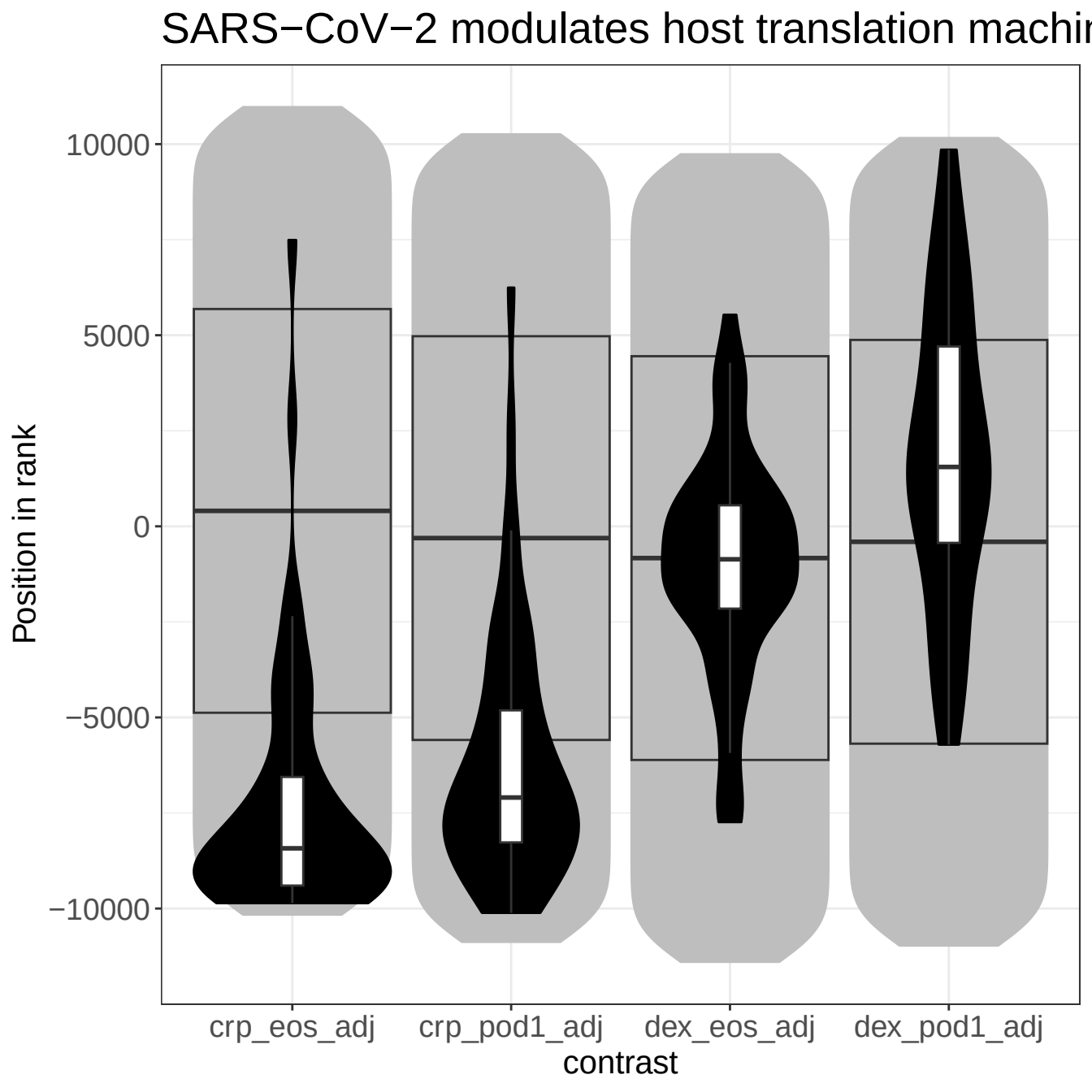

Complex III assembly
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.349
Corr:
−0.207
Corr:
0.274
Corr:
0.465*
Corr:
0.145
Corr:
0.277
10.0
7.5
5.0
2.5
0.0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

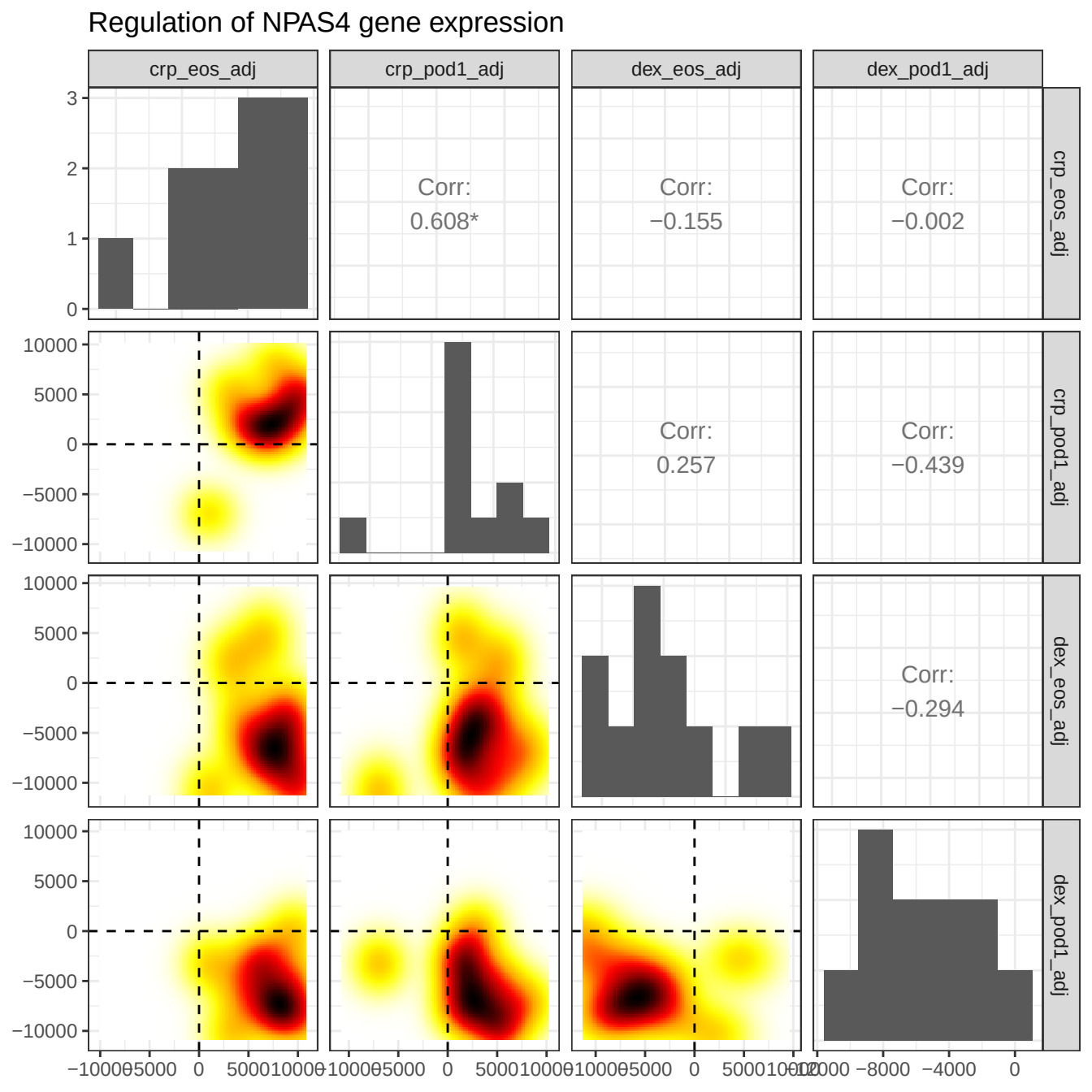

Complex III assembly
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.349
Corr:
−0.207
Corr:
0.274
Corr:
0.465*
Corr:
0.145
Corr:
0.277
10.0
7.5
5.0
2.5
0.0
10000
5000
0
−5000
−10000

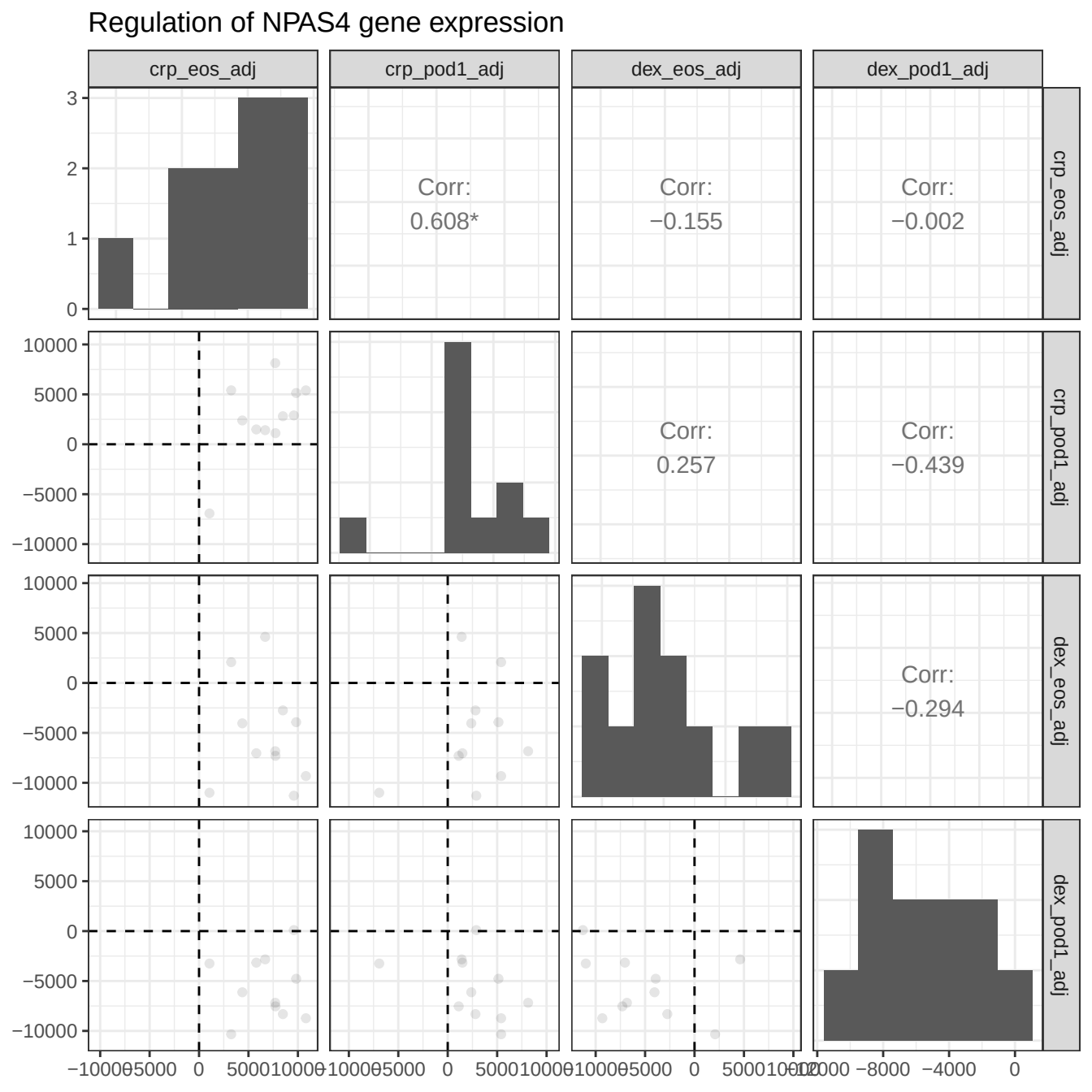

Complex III assembly
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

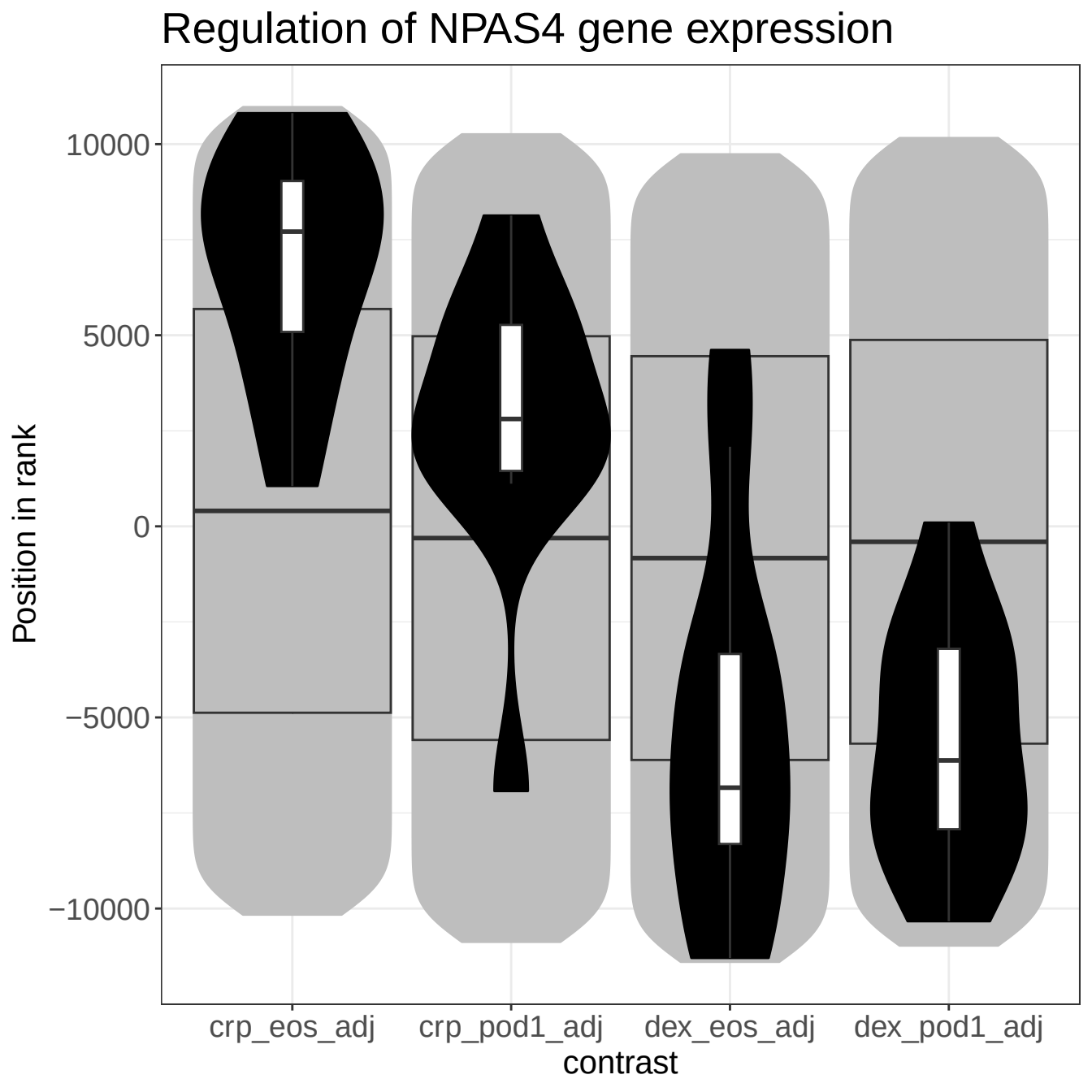

SARS−CoV−2 modulates host translation machinery
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.656***
Corr:
−0.382**
Corr:
0.076
Corr:
−0.170
Corr:
−0.435**
Corr:
−0.025

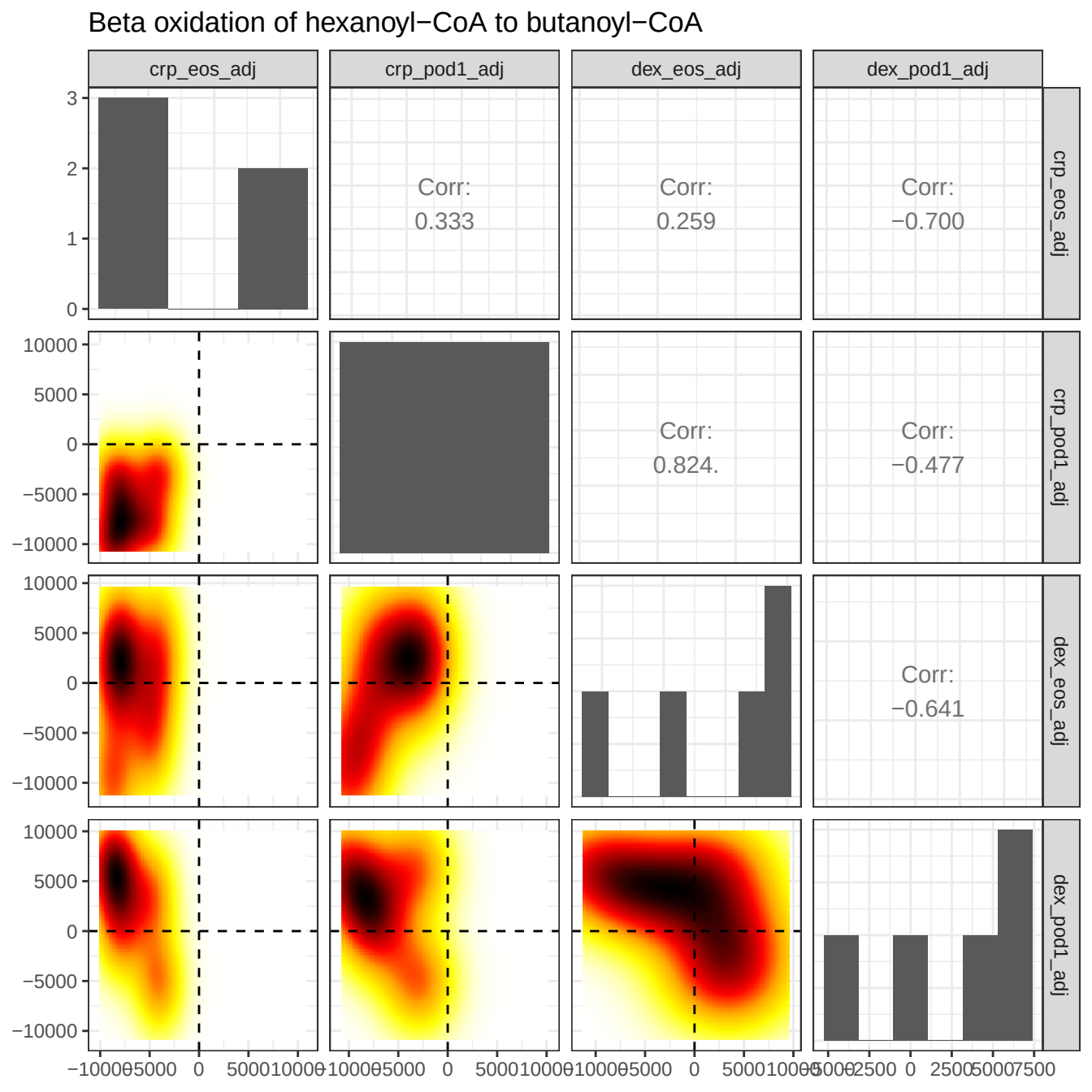

SARS−CoV−2 modulates host translation machinery
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.656***
Corr:
−0.382**
Corr:
0.076
Corr:
−0.170
Corr:
−0.435**
Corr:
−0.025

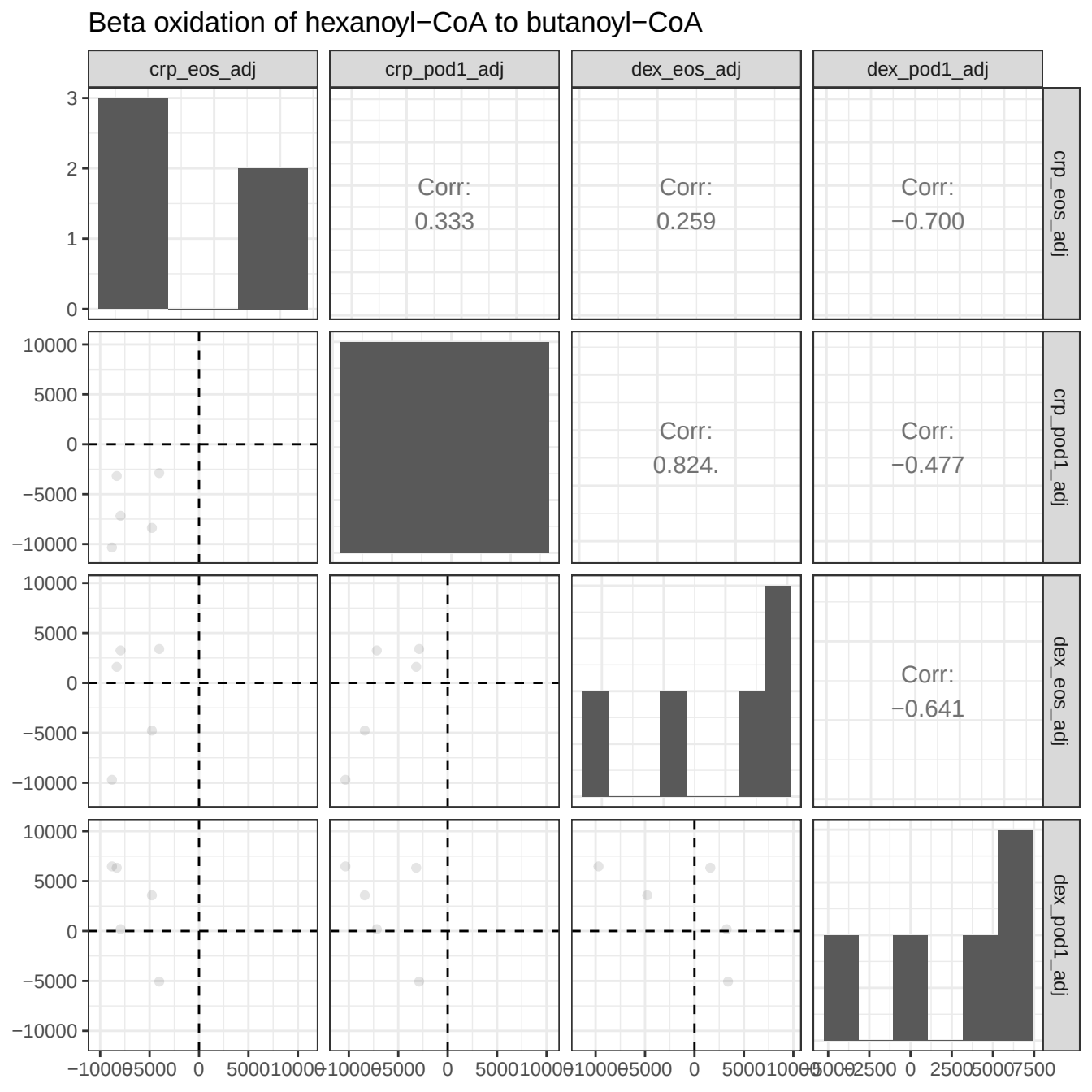

SARS−CoV−2 modulates host translation machin
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

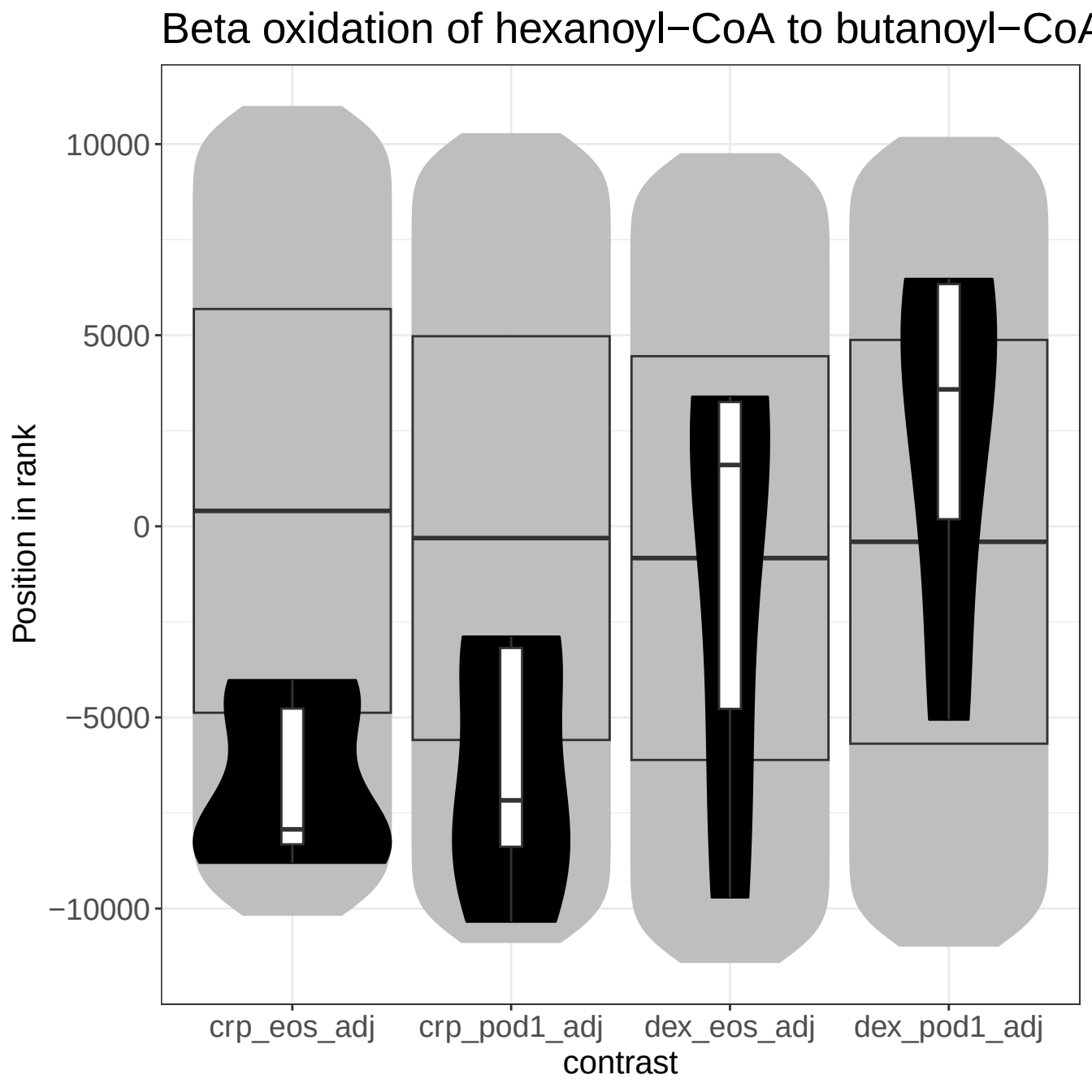

Regulation of NPAS4 gene expression
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.608*
Corr:
−0.155
Corr:
−0.002
Corr:
0.257
Corr:
−0.439
Corr:
−0.294
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−8000
−4000

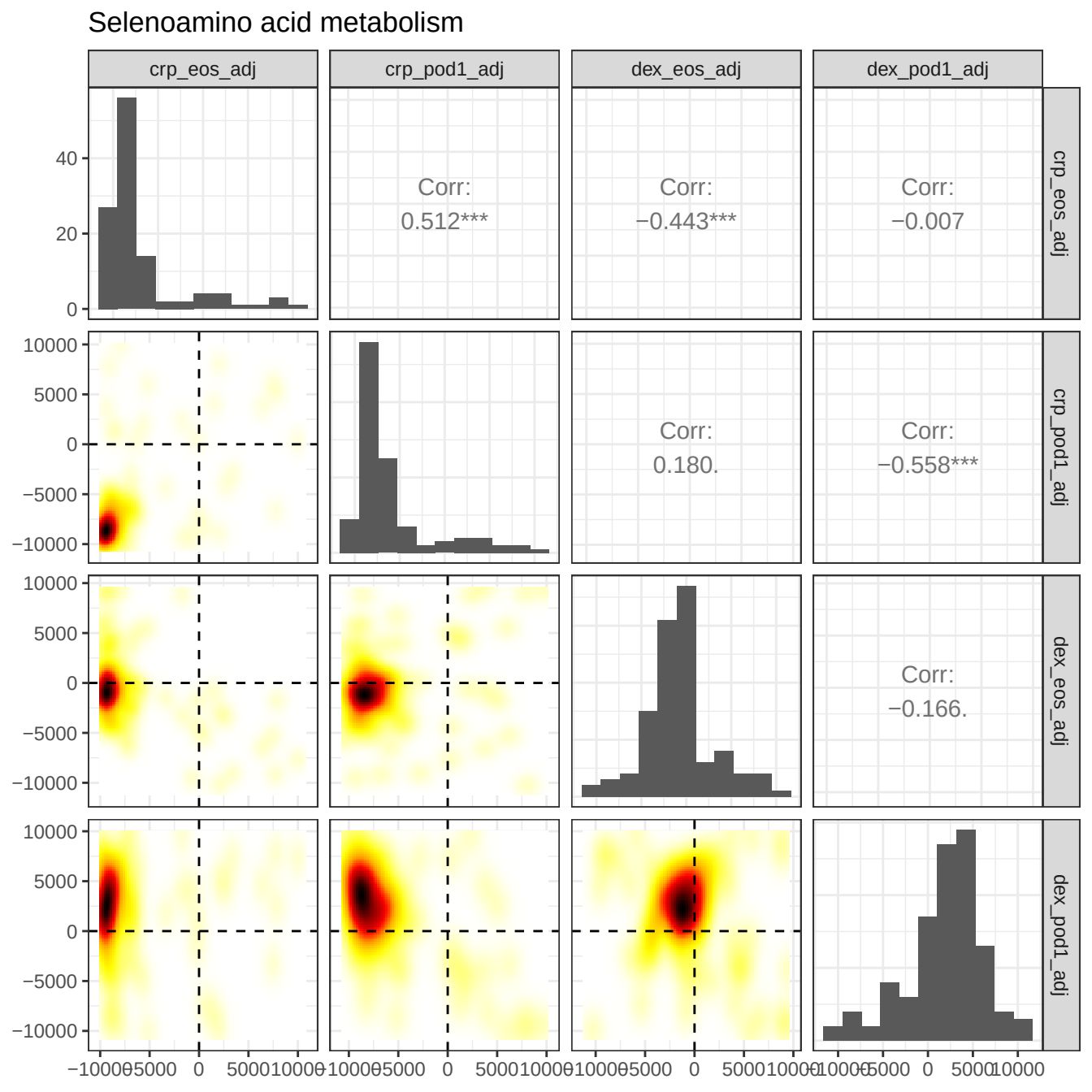

Regulation of NPAS4 gene expression
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.608*
Corr:
−0.155
Corr:
−0.002
Corr:
0.257
Corr:
−0.439
Corr:
−0.294
3
2
1
0
10000
5000
0
−5000
−10000
−8000
−4000

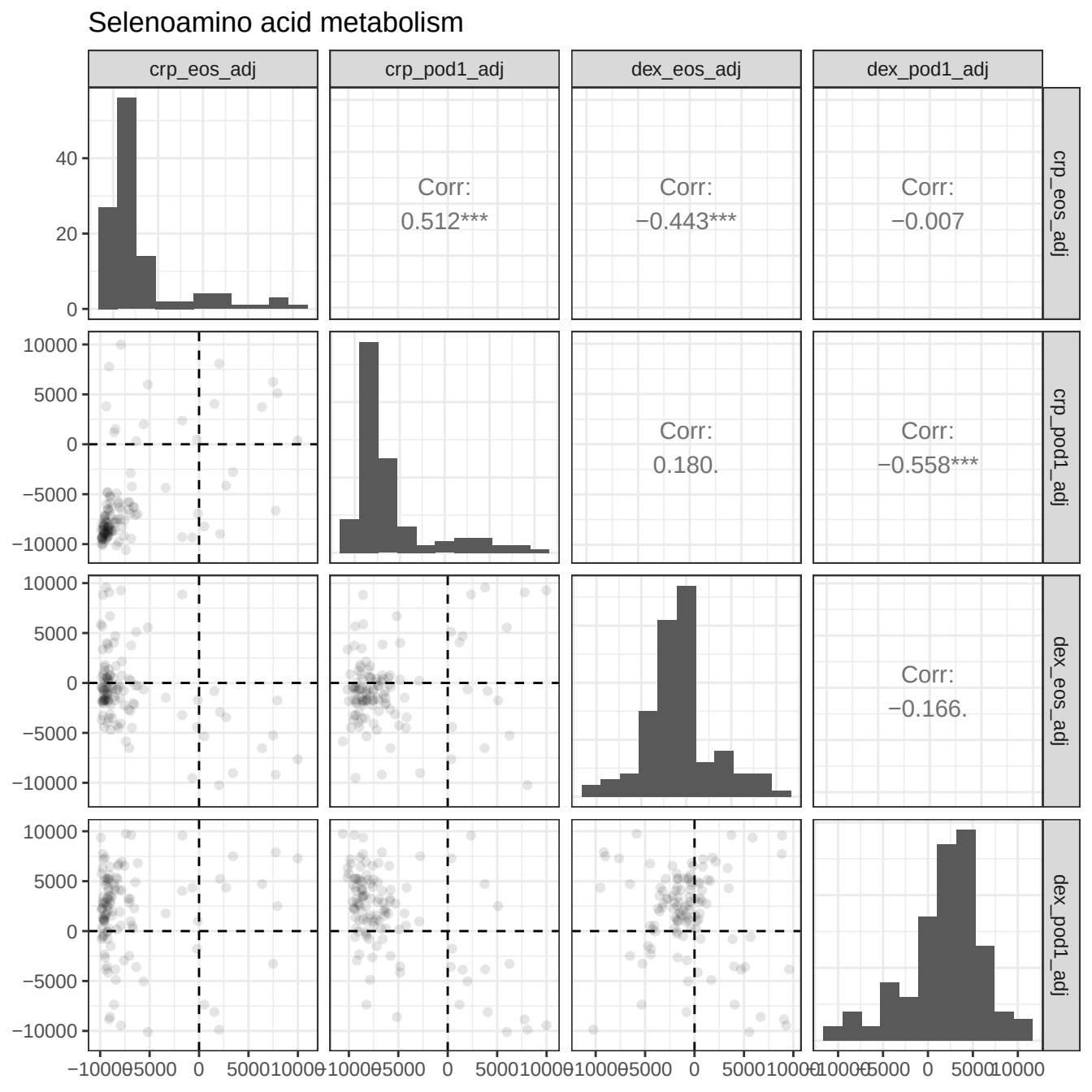

Regulation of NPAS4 gene expression
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast

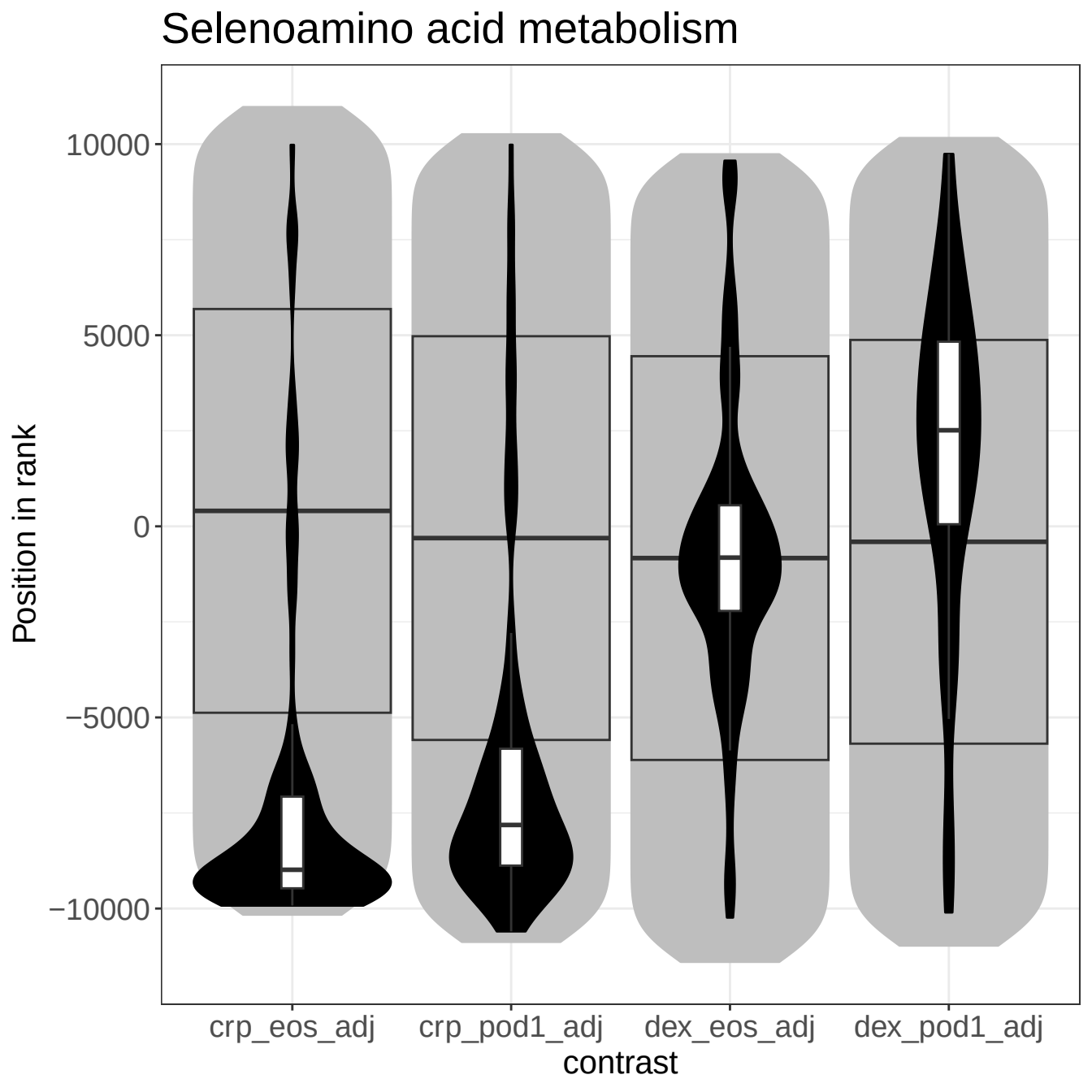

Beta oxidation of hexanoyl−CoA to butanoyl−CoA
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.333
Corr:
0.259
Corr:
−0.700
Corr:
0.824.
Corr:
−0.477
Corr:
−0.641
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−5000
−2500
0
2500
5000
7500

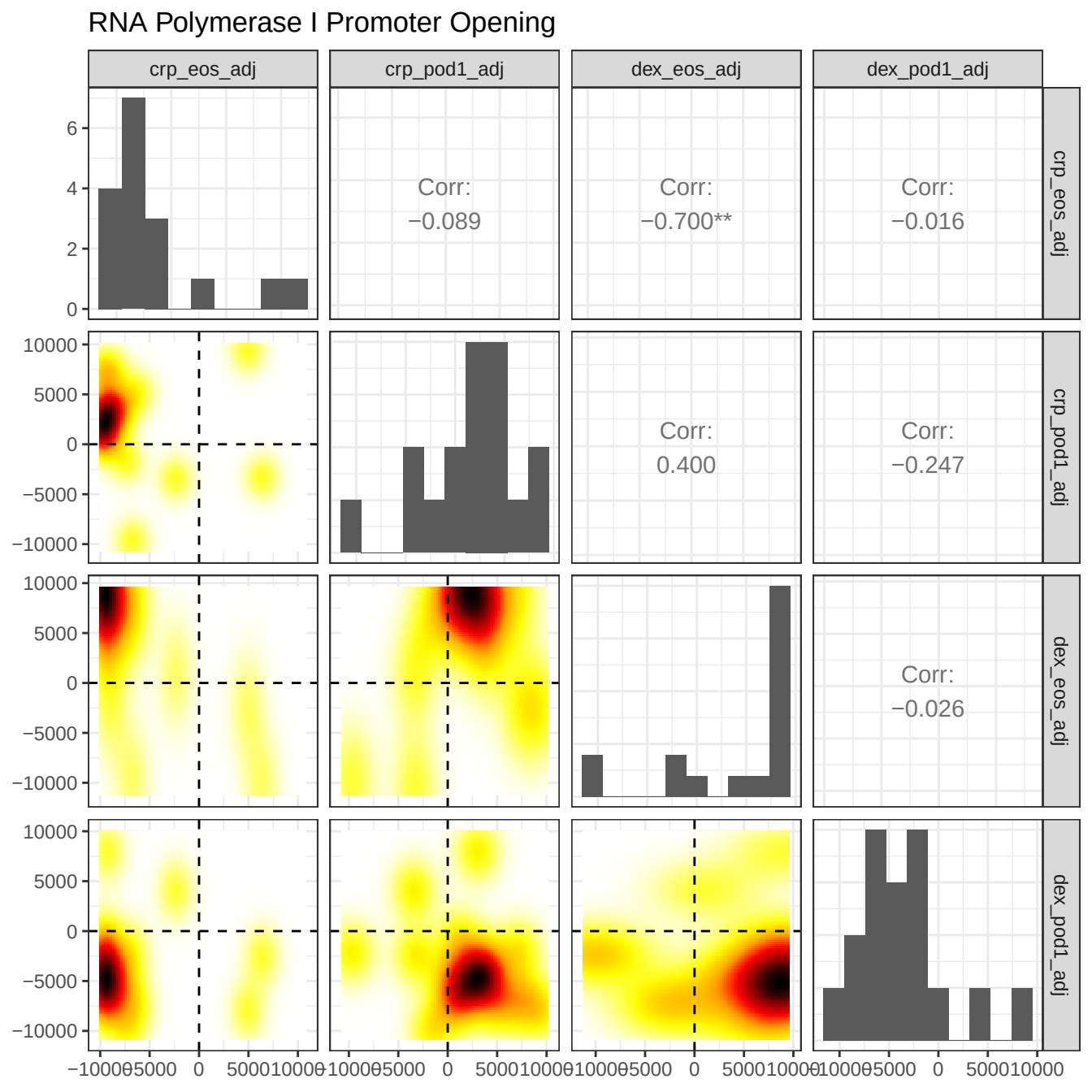

Beta oxidation of hexanoyl−CoA to butanoyl−CoA
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.333
Corr:
0.259
Corr:
−0.700
Corr:
0.824.
Corr:
−0.477
Corr:
−0.641
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−5000
−2500
0
2500
5000
7500

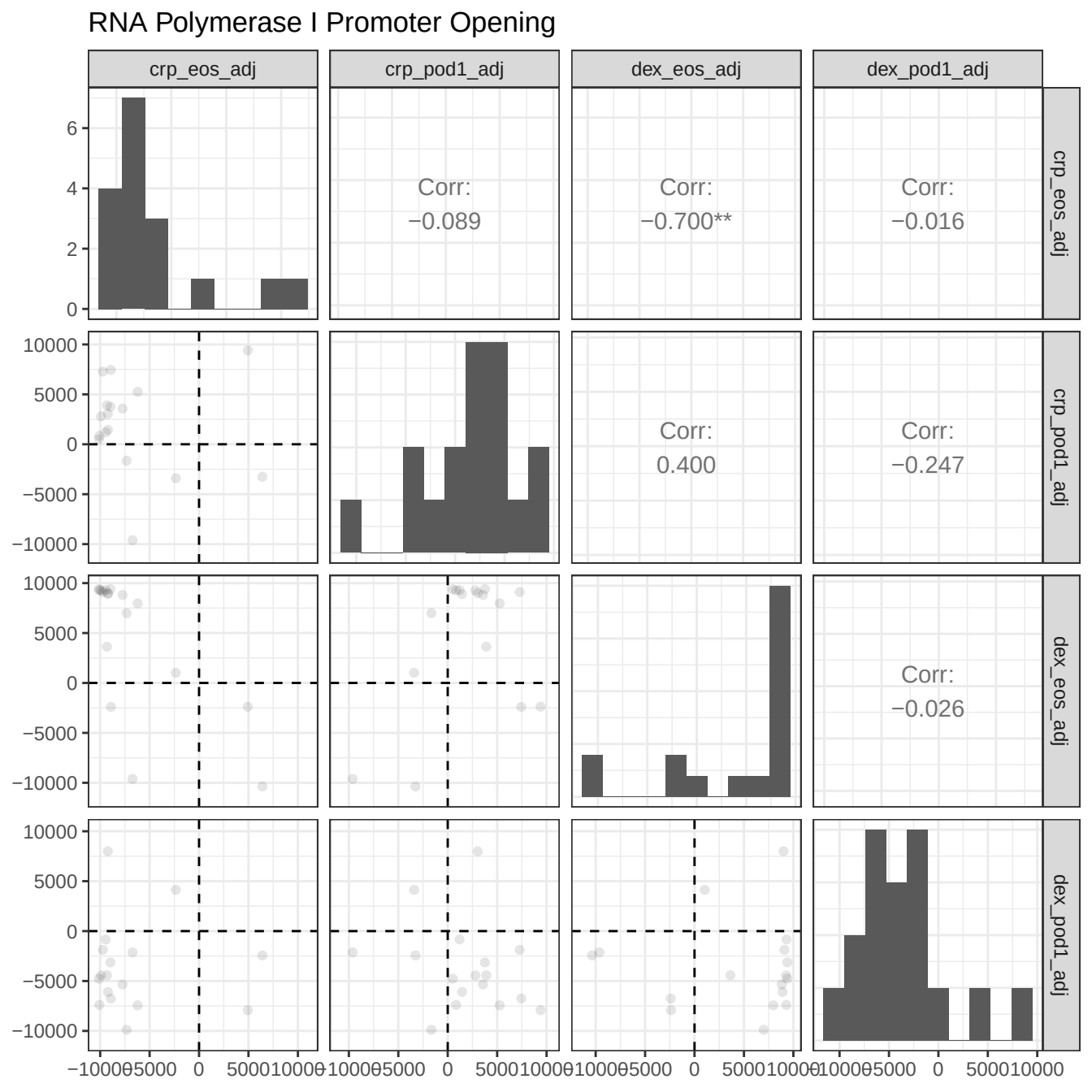

Beta oxidation of hexanoyl−CoA to butanoyl−CoA
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast


Selenoamino acid metabolism
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.512***
Corr:
−0.443***
Corr:
−0.007
Corr:
0.180.
Corr:
−0.558***
Corr:
−0.166.
40
20
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000


Selenoamino acid metabolism
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.512***
Corr:
−0.443***
Corr:
−0.007
Corr:
0.180.
Corr:
−0.558***
Corr:
−0.166.
40
20
0
10000
5000
0
−5000
−10000


Selenoamino acid metabolism
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast


RNA Polymerase I Promoter Opening
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.089
Corr:
−0.700**
Corr:
−0.016
Corr:
0.400
Corr:
−0.247
Corr:
−0.026
0
2
4
6
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000


RNA Polymerase I Promoter Opening
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
−0.089
Corr:
−0.700**
Corr:
−0.016
Corr:
0.400
Corr:
−0.247
Corr:
−0.026
6
4
2
0
10000
5000
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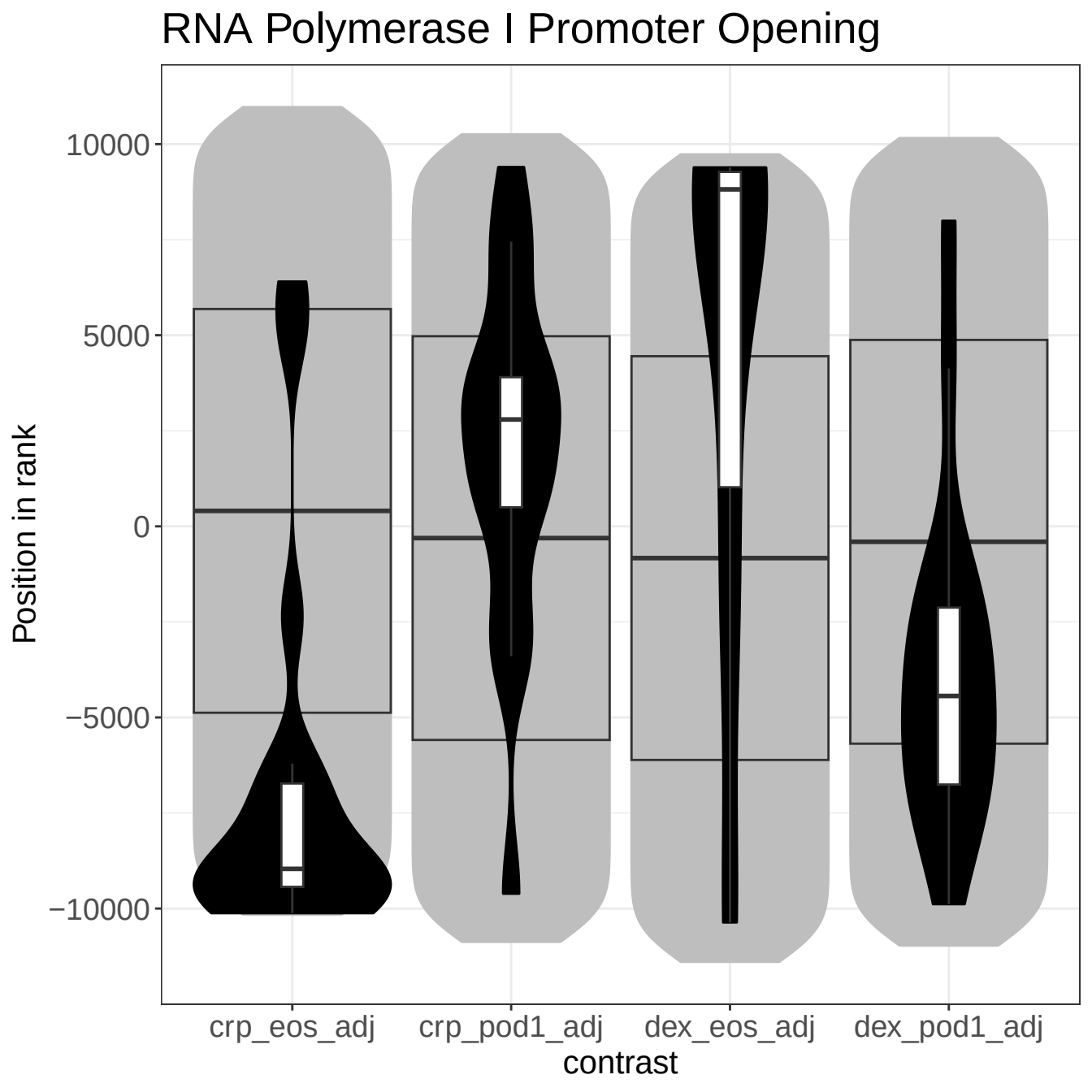
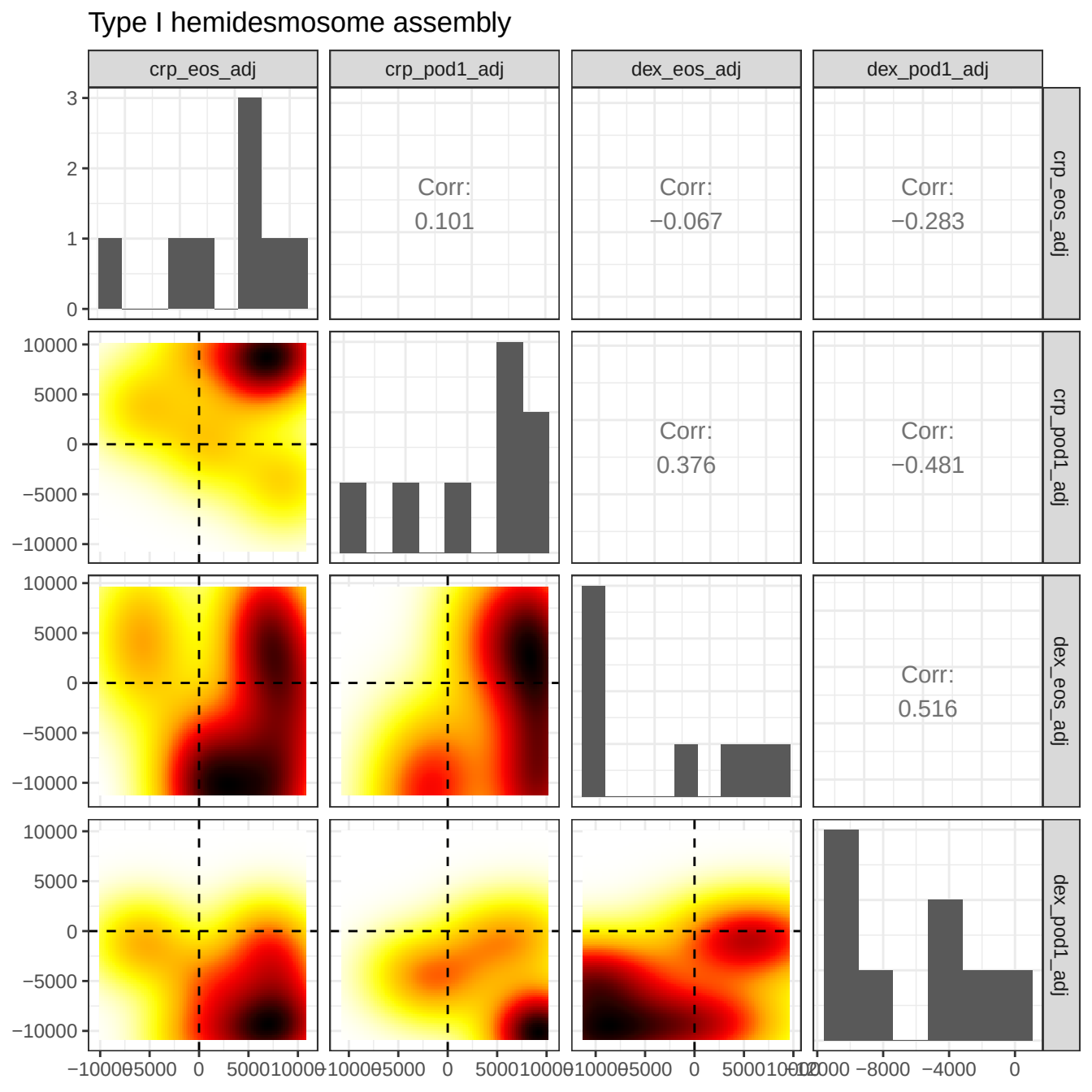
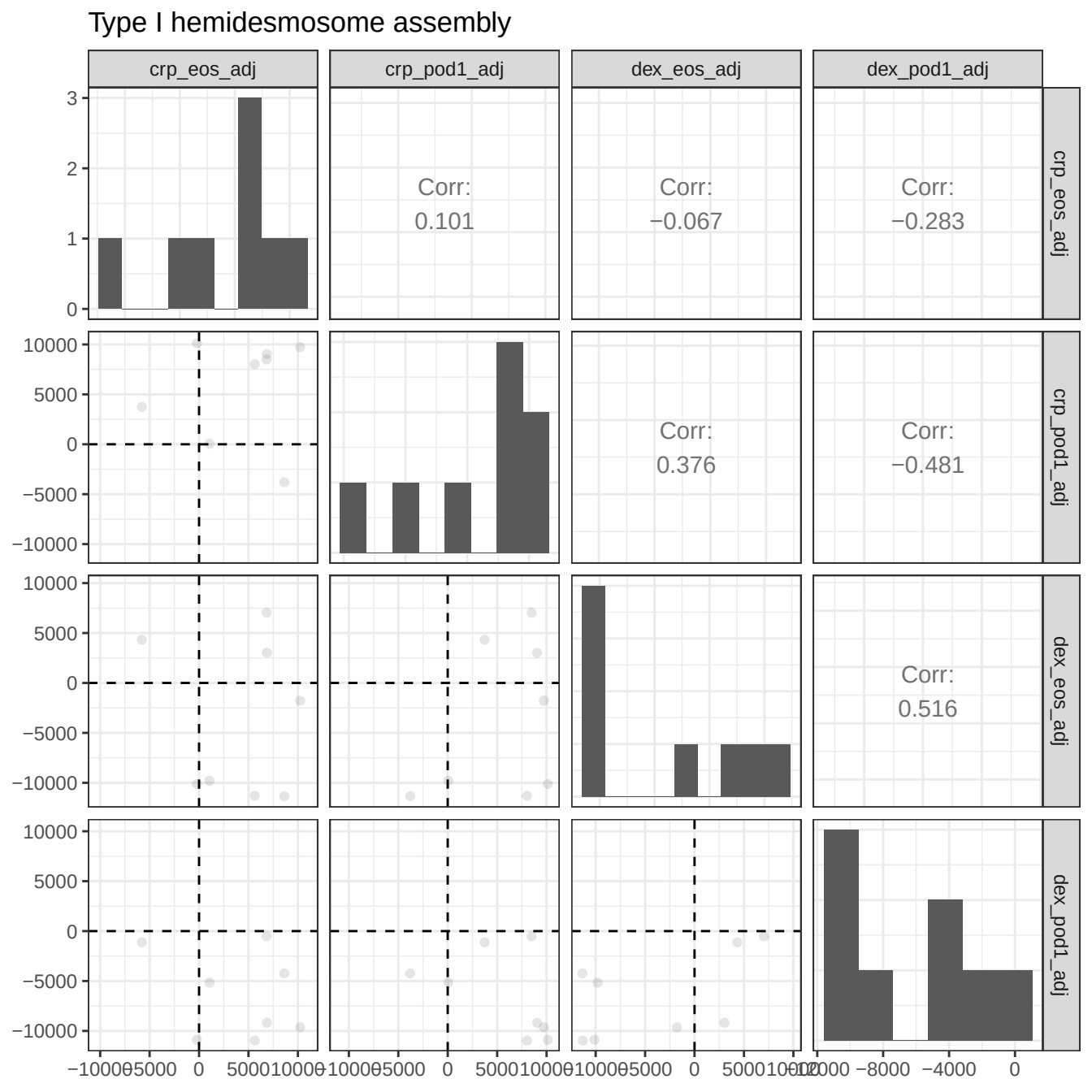
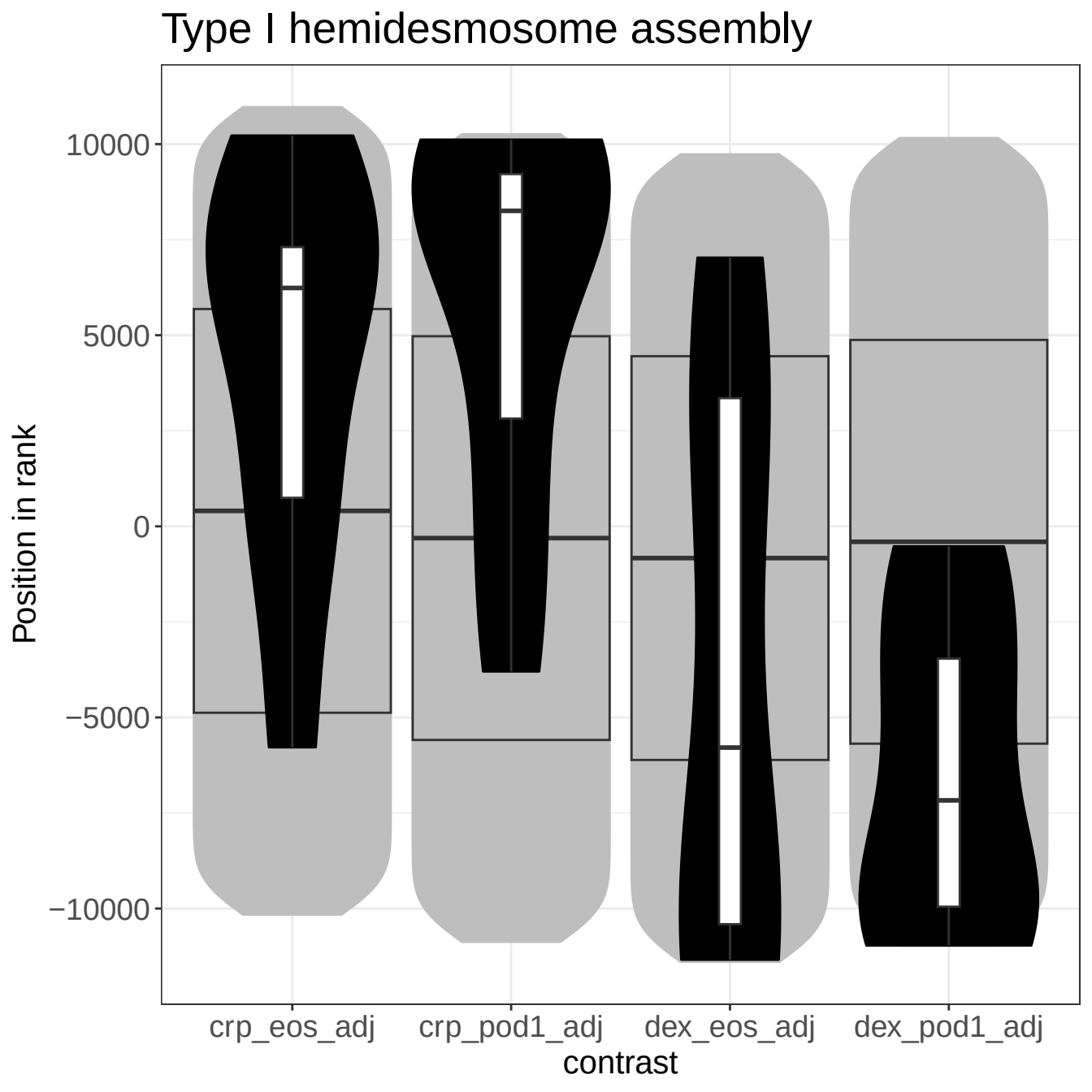
−5000
−10000
−10000
−5000
0
5000
10000


RNA Polymerase I Promoter Opening
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast


Type I hemidesmosome assembly
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.101
Corr:
−0.067
Corr:
−0.283
Corr:
0.376
Corr:
−0.481
Corr:
0.516
3
2
1
0
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
−12000
−8000
−4000
0


Type I hemidesmosome assembly
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
Corr:
0.101
Corr:
−0.067
Corr:
−0.283
Corr:
0.376
Corr:
−0.481
Corr:
0.516
3
2
1
0
10000
5000
0
−5000
−10000
−8000
−4000


Type I hemidesmosome assembly
10000
5000
0
−5000
−10000
Position in rank
crp_eos_adj
crp_pod1_adj
dex_eos_adj
dex_pod1_adj
contrast