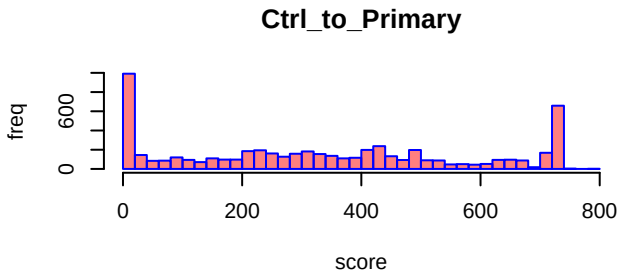
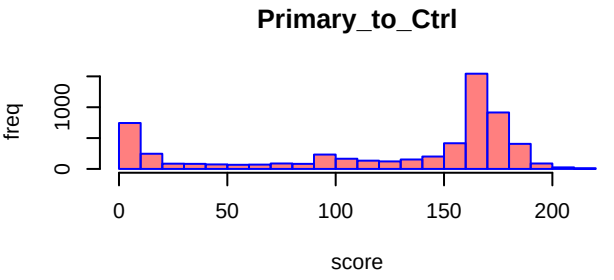
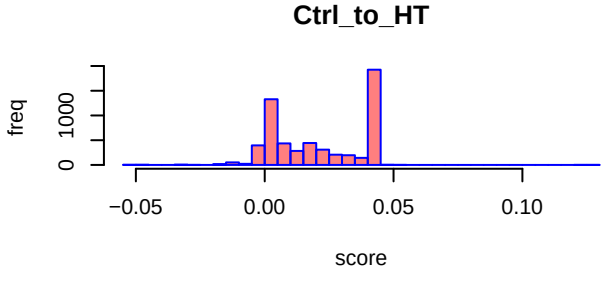
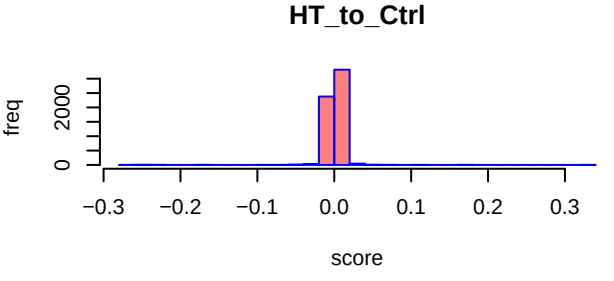
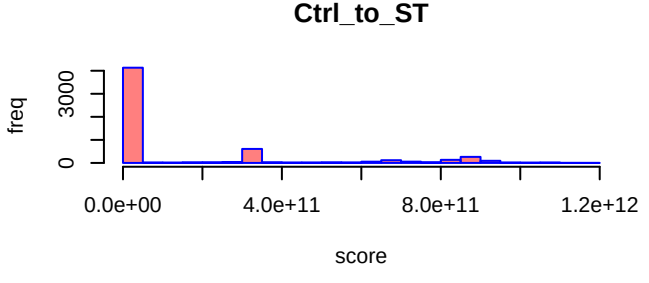
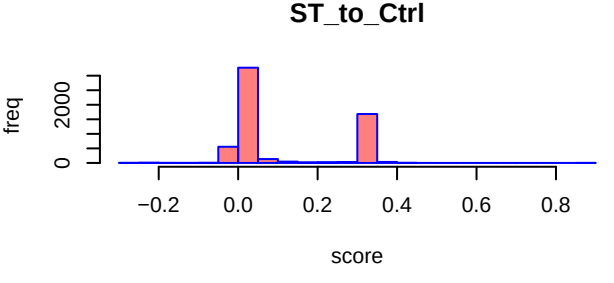

Ctrl_to_Primary
freq
0
600
0
200
400
600
800
score

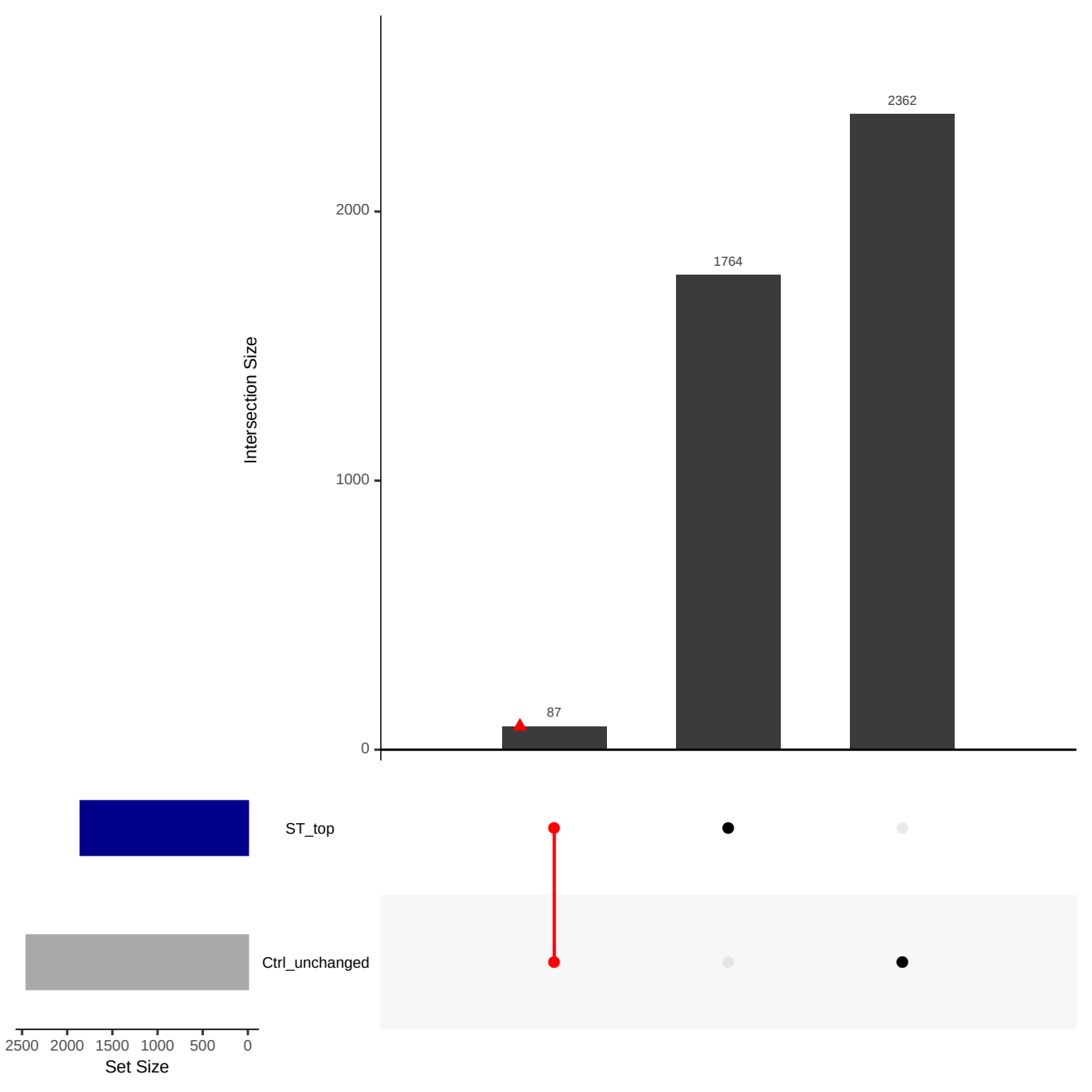

Primary_to_Ctrl
freq
0
1000
0
50
100
150
200
score

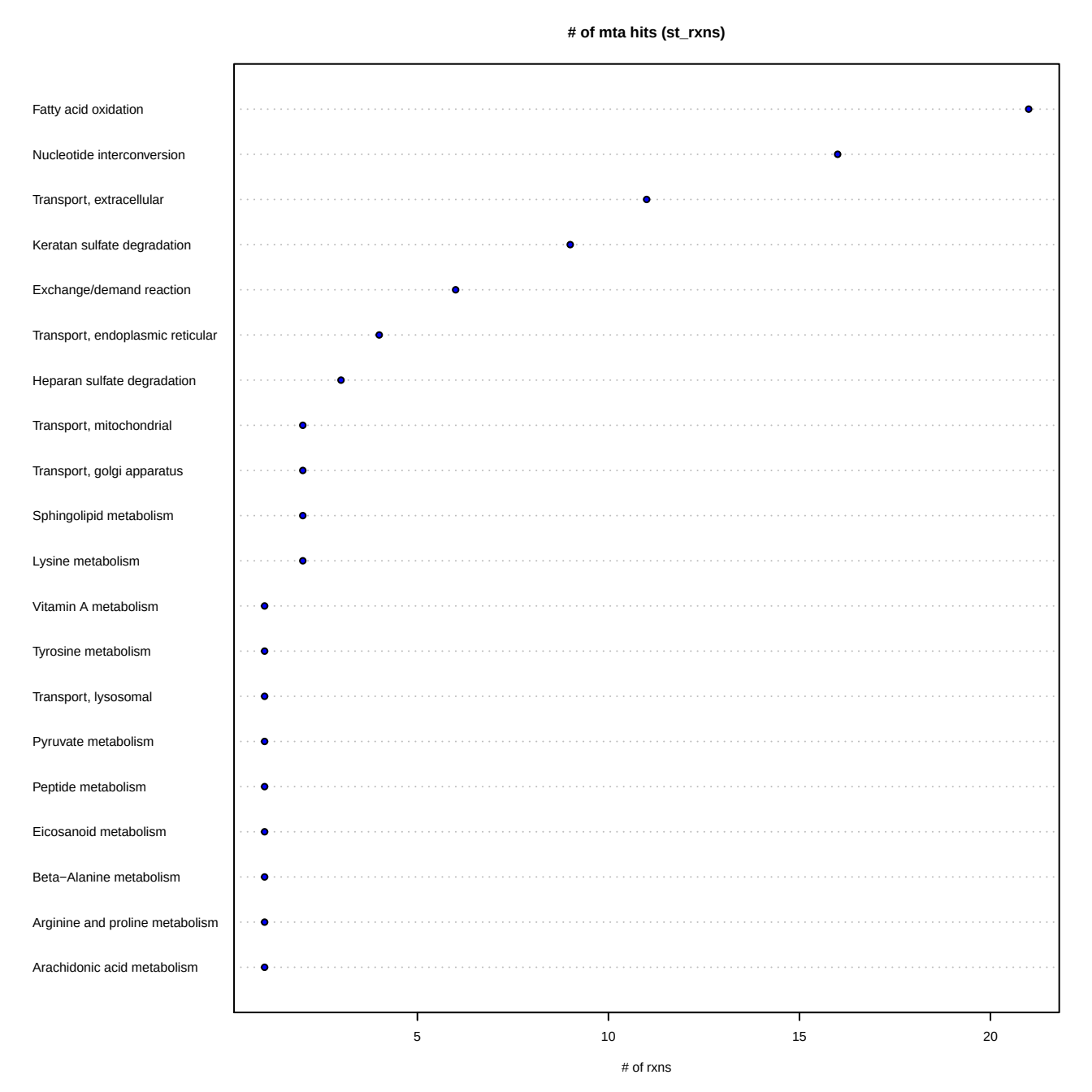

Ctrl_to_HT
freq
0
1000
−0.05
0.00
0.05
0.10
score

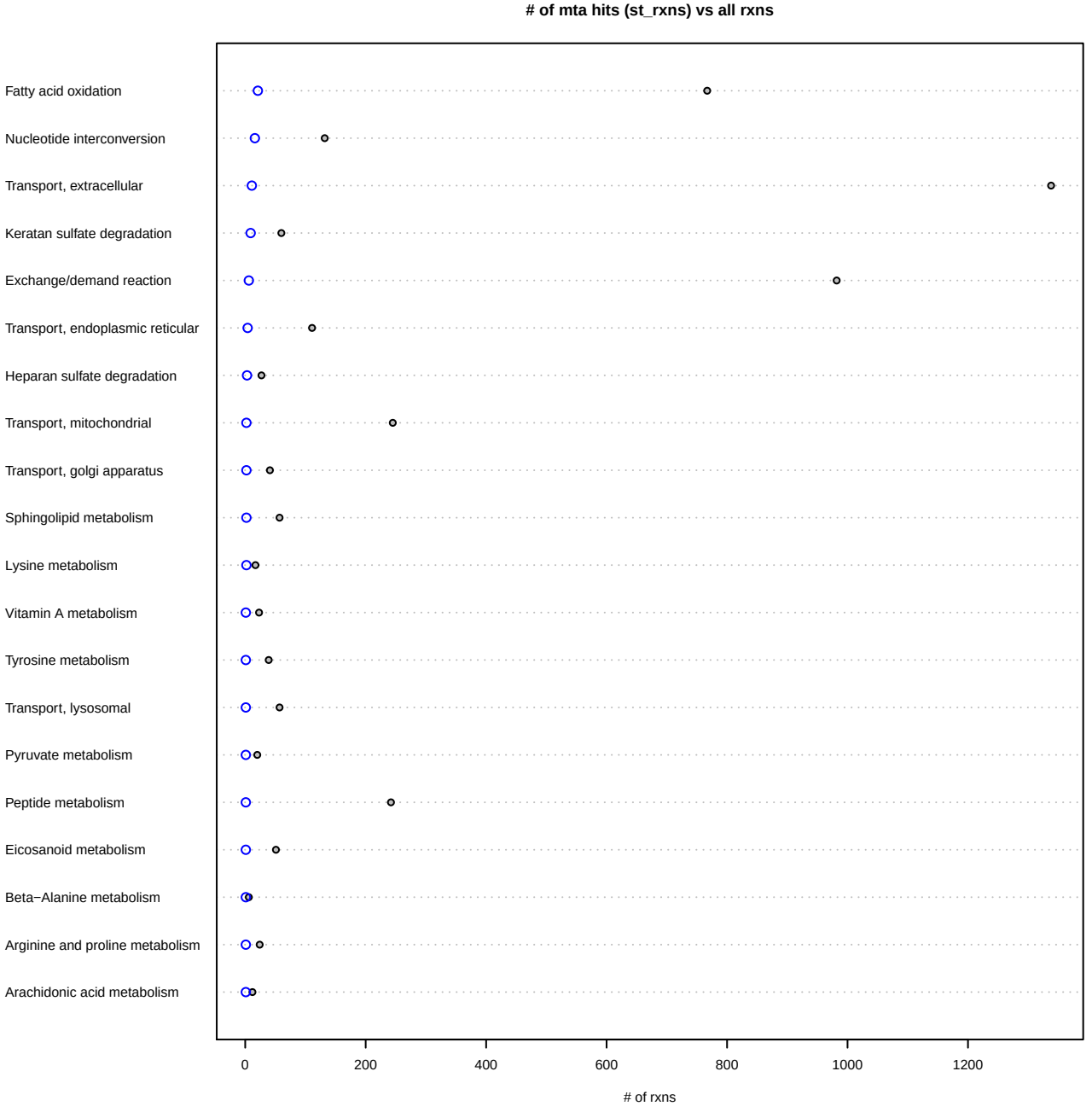

HT_to_Ctrl
freq
0
2000
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3
score

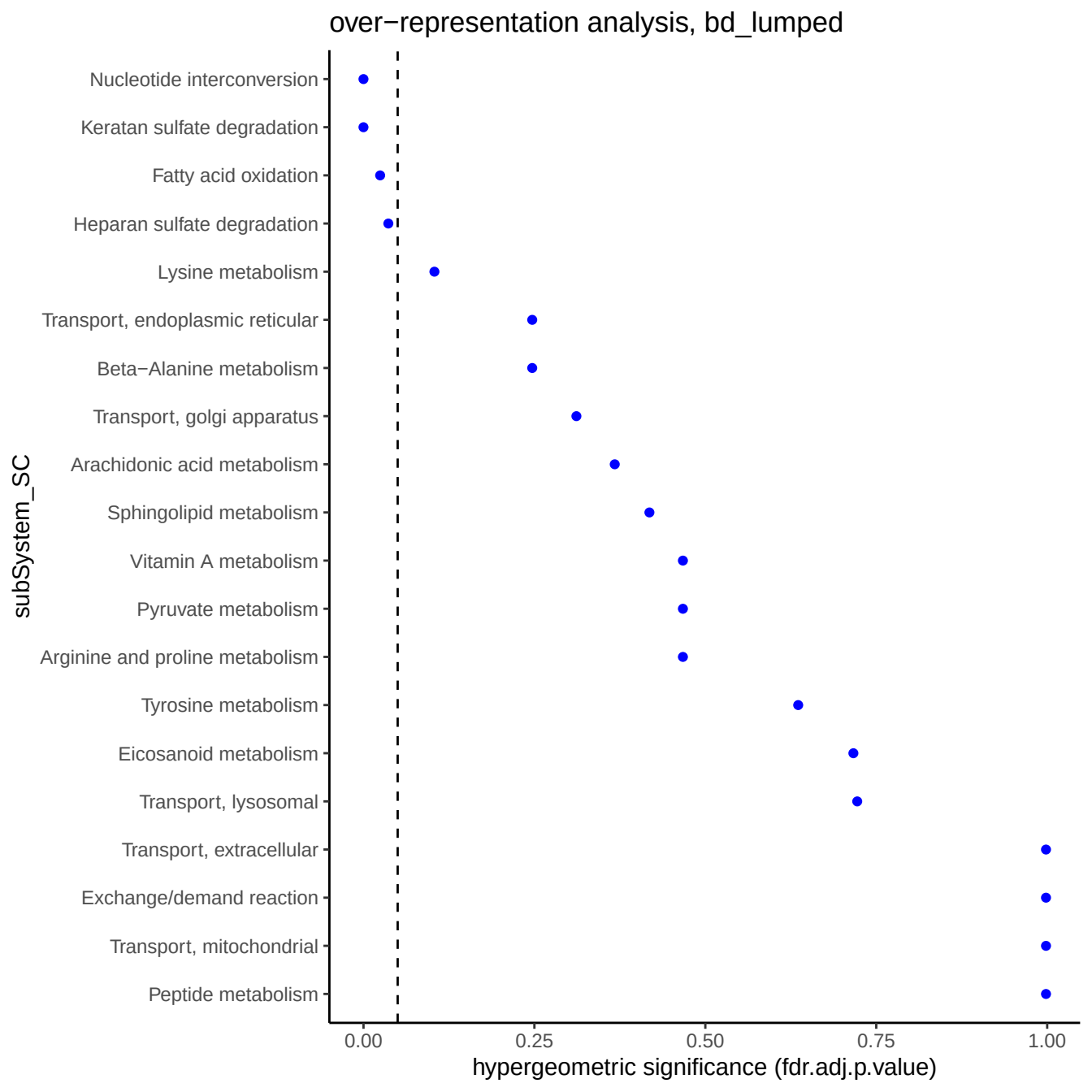

Ctrl_to_ST
freq
0
3000
0.0e+00
4.0e+11
8.0e+11
1.2e+12
score


ST_to_Ctrl
freq
0
2000
−0.2
0.0
0.2
0.4
0.6
0.8
score


Intersection Size
2000
1000
0
2362
1764
87
ST_top
Ctrl_unchanged
2500 2000 1500 1000 500 0
Set Size


# of mta hits (st_rxns)
Fatty acid oxidation
Nucleotide interconversion
Transport, extracellular
Keratan sulfate degradation
Exchange/demand reaction
Transport, endoplasmic reticular
Heparan sulfate degradation
Transport, mitochondrial
Transport, golgi apparatus
Sphingolipid metabolism
Lysine metabolism
Vitamin A metabolism
Tyrosine metabolism
Transport, lysosomal
Pyruvate metabolism
Peptide metabolism
Eicosanoid metabolism
Beta−Alanine metabolism
Arginine and proline metabolism
Arachidonic acid metabolism
5
10
15
20
# of rxns


# of mta hits (st_rxns) vs all rxns
Fatty acid oxidation
Nucleotide interconversion
Transport, extracellular
Keratan sulfate degradation
Exchange/demand reaction
Transport, endoplasmic reticular
Heparan sulfate degradation
Transport, mitochondrial
Transport, golgi apparatus
Sphingolipid metabolism
Lysine metabolism
Vitamin A metabolism
Tyrosine metabolism
Transport, lysosomal
Pyruvate metabolism
Peptide metabolism
Eicosanoid metabolism
Beta−Alanine metabolism
Arginine and proline metabolism
Arachidonic acid metabolism
0
200
400
600
800
1000
1200
# of rxns


over−representation analysis, bd_lumped
Nucleotide interconversion
Keratan sulfate degradation
Fatty acid oxidation
Heparan sulfate degradation
Lysine metabolism
Transport, endoplasmic reticular
Beta−Alanine metabolism
Transport, golgi apparatus
Arachidonic acid metabolism
Sphingolipid metabolism
Vitamin A metabolism
Pyruvate metabolism
Arginine and proline metabolism
Tyrosine metabolism
Eicosanoid metabolism
Transport, lysosomal
Transport, extracellular
Exchange/demand reaction
Transport, mitochondrial
Peptide metabolism
subSystem_SC
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)