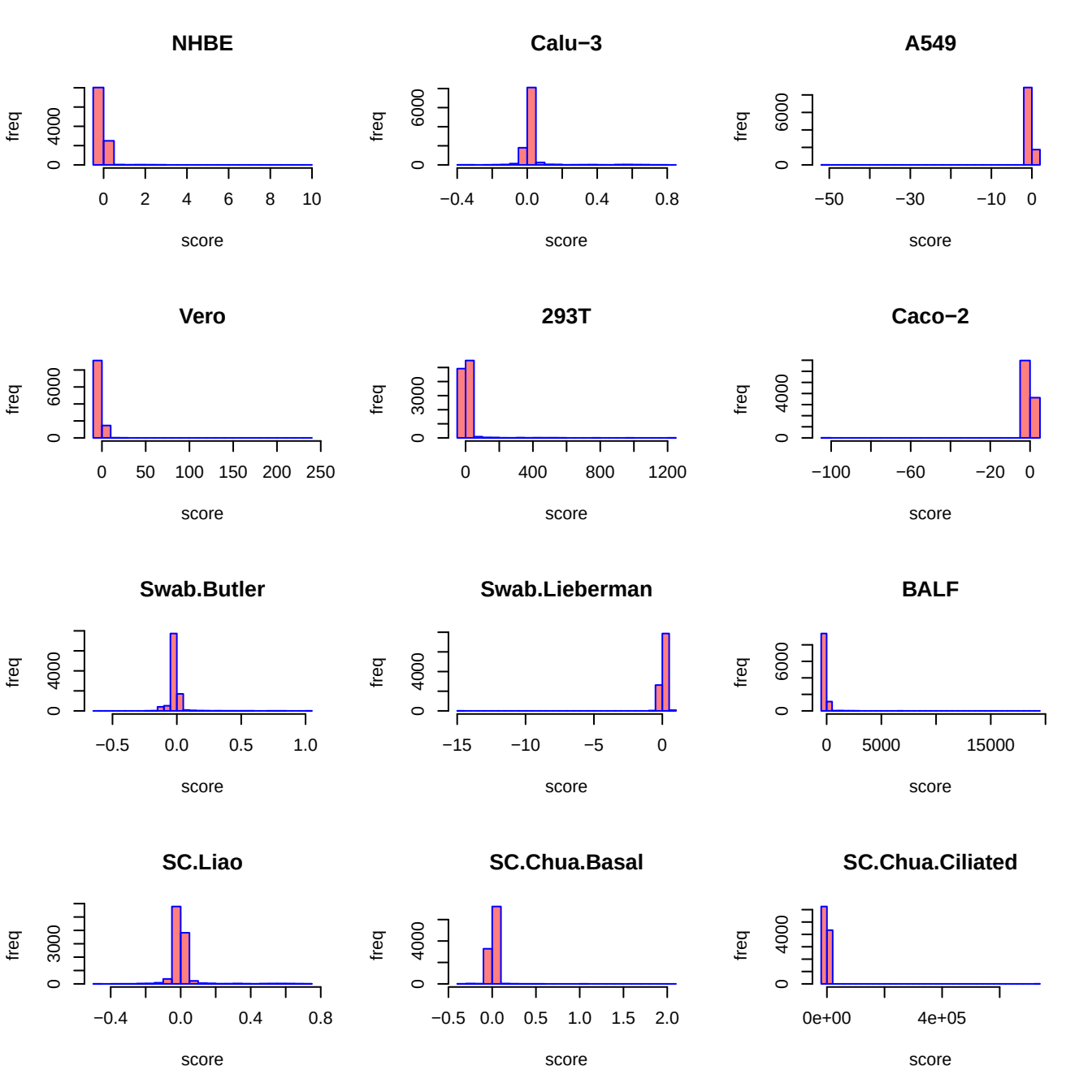
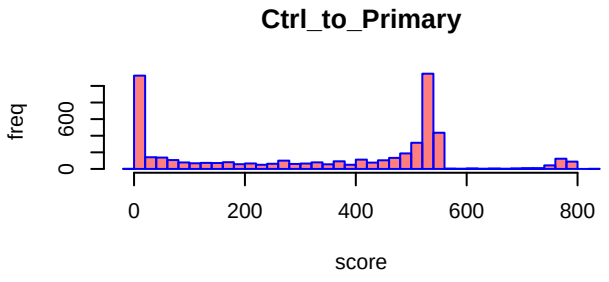
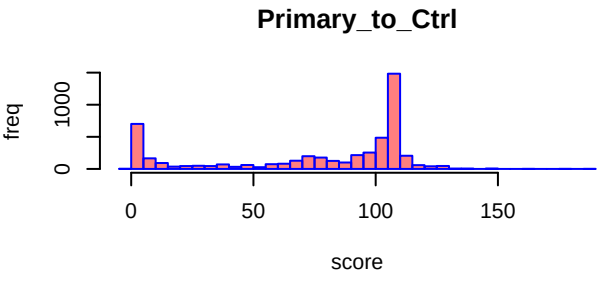
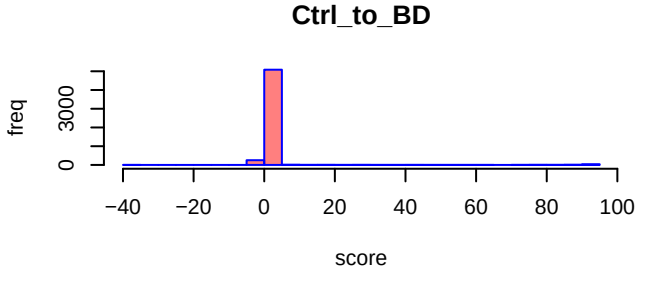

NHBE
freq
0
4000
0
2
4
6
8
10
score
Calu−3
freq
0
6000
−0.4
0.0
0.4
0.8
score
A549
freq
0
6000
−50
−30
−10
0
score
Vero
freq
0
6000
0
50
100
150
200
250
score
293T
freq
0
3000
0
400
800
1200
score
Caco−2
freq
0
4000
−100
−60
−20
0
score
Swab.Butler
freq
0
4000
−0.5
0.0
0.5
1.0
score
Swab.Lieberman
freq
0
4000
−15
−10
−5
0
score
BALF
freq
0
6000
0
5000
15000
score
SC.Liao
freq
0
3000
−0.4
0.0
0.4
0.8
score
SC.Chua.Basal
freq
0
4000
−0.5
0.0
0.5
1.0
1.5
2.0
score
SC.Chua.Ciliated
freq
0
4000
0e+00
4e+05
score


Ctrl_to_Primary
freq
0
600
0
200
400
600
800
score


Primary_to_Ctrl
freq
0
1000
0
50
100
150
score


Ctrl_to_BD
freq
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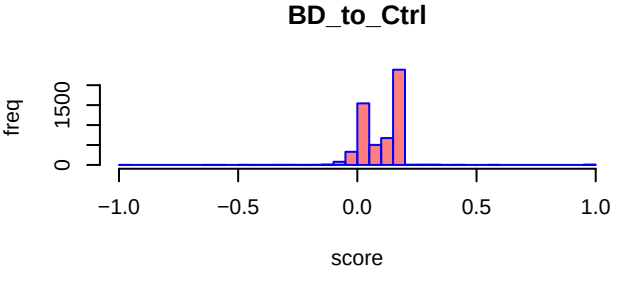
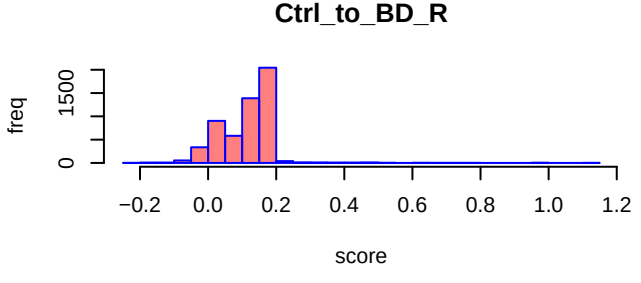
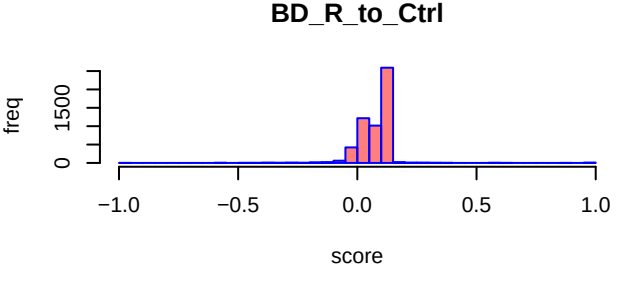
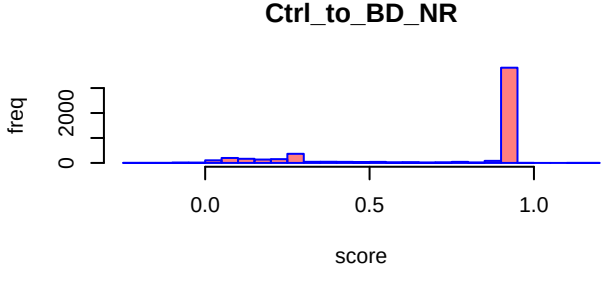
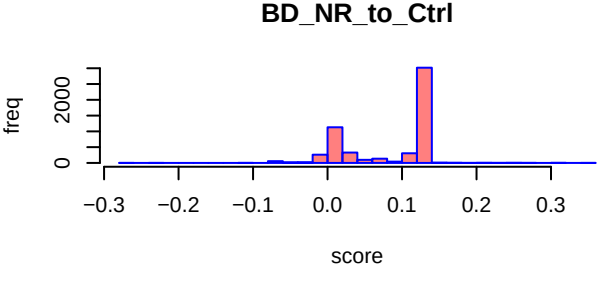
3000
−40
−20
0
20
40
60
80
100
score

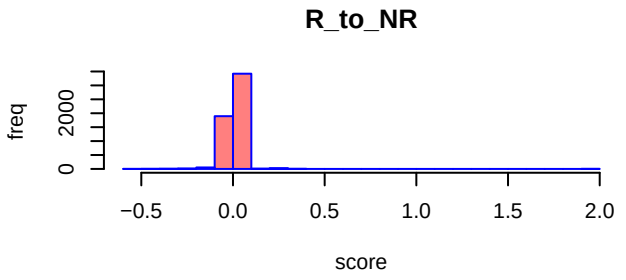

BD_to_Ctrl
freq
0
1500
−1.0
−0.5
0.0
0.5
1.0
score

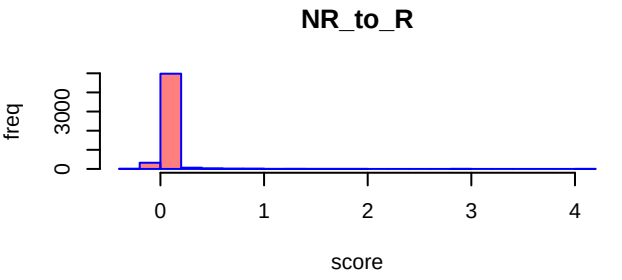

Ctrl_to_BD_R
freq
0
1500
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
1.2
score

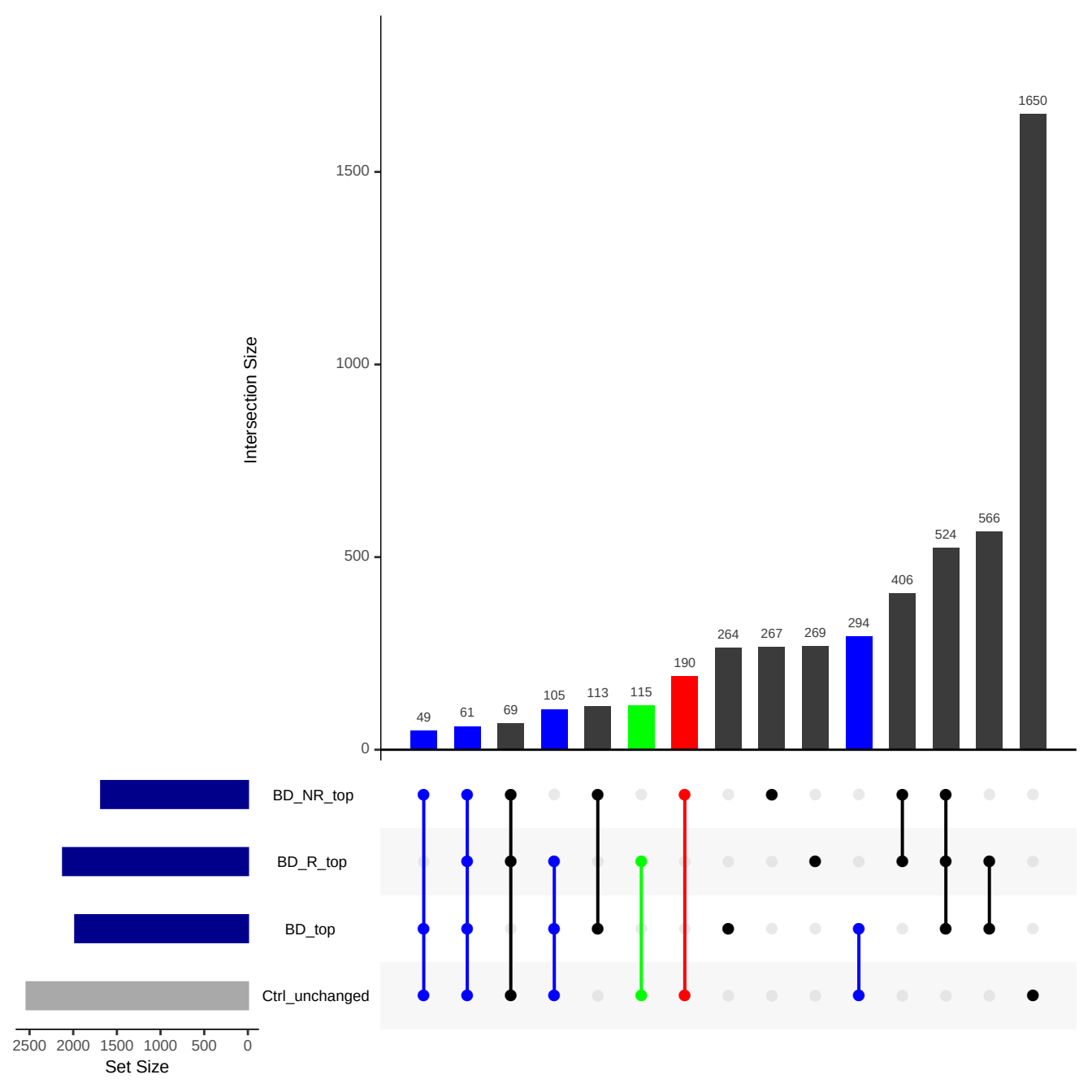

BD_R_to_Ctrl
freq
0
1500
−1.0
−0.5
0.0
0.5
1.0
score


Ctrl_to_BD_NR
freq
0
2000
0.0
0.5
1.0
score

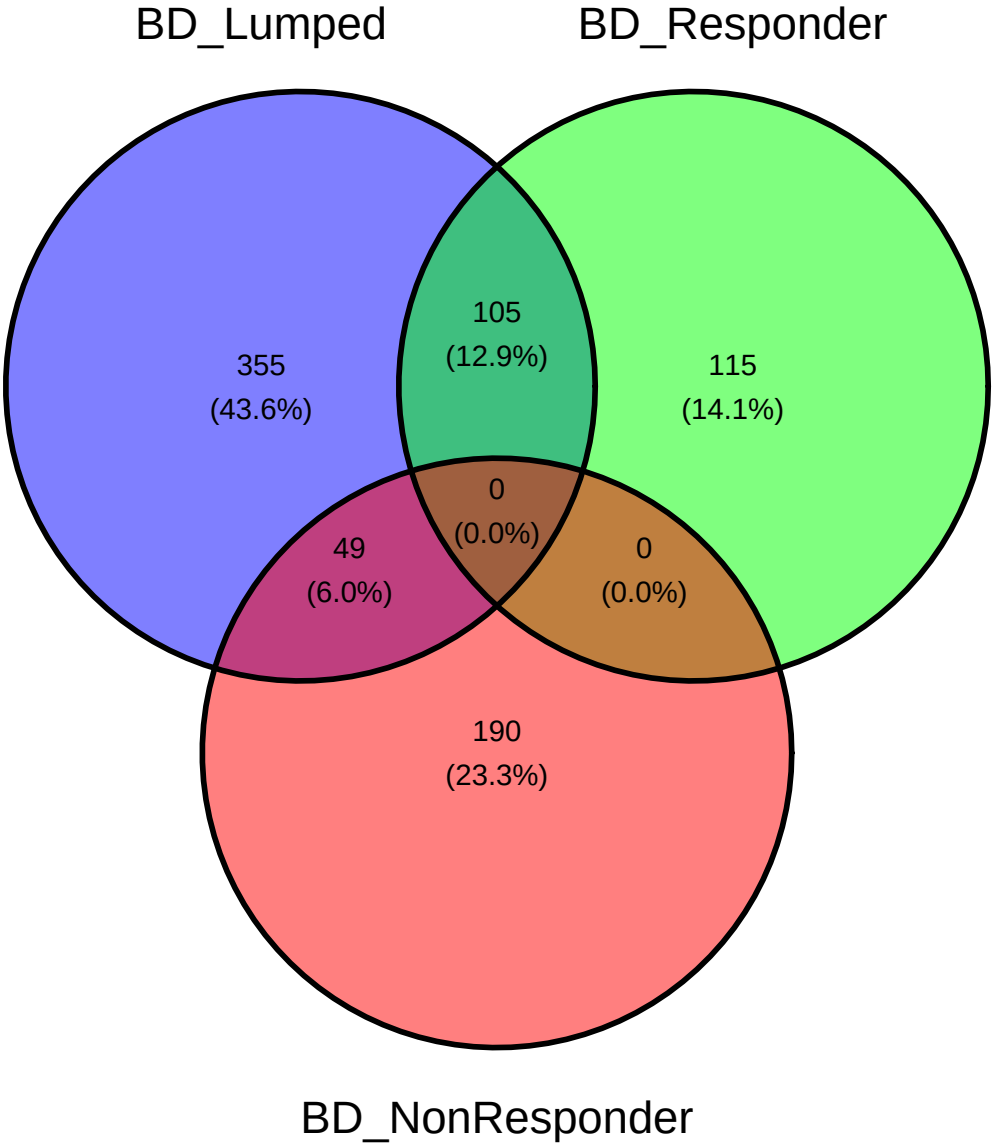

BD_NR_to_Ctrl
freq
0
2000
−0.3
−0.2
−0.1
0.0
0.1
0.2
0.3
score


R_to_NR
freq
0
2000
−0.5
0.0
0.5
1.0
1.5
2.0
score

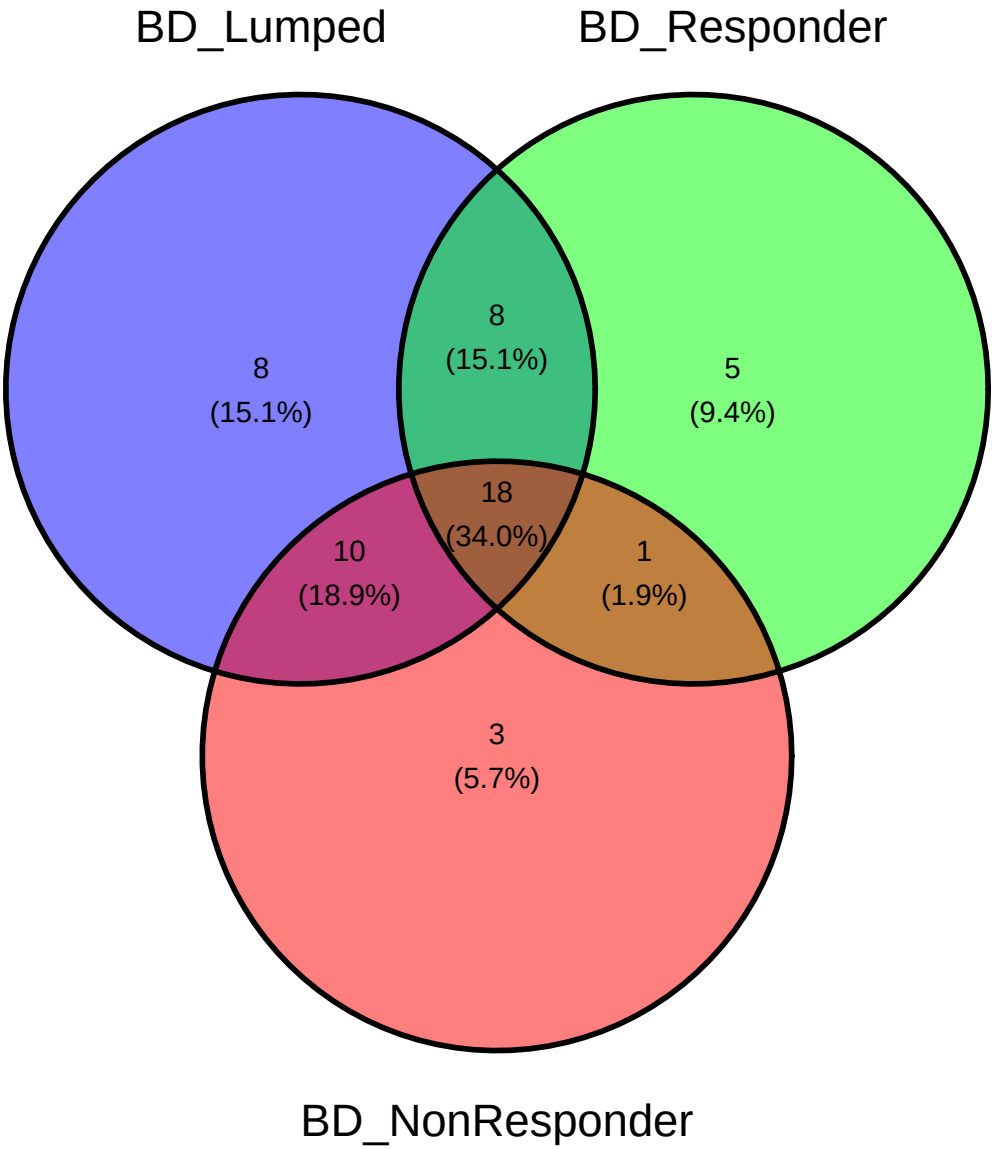

NR_to_R
freq
0
3000
0
1
2
3
4
score

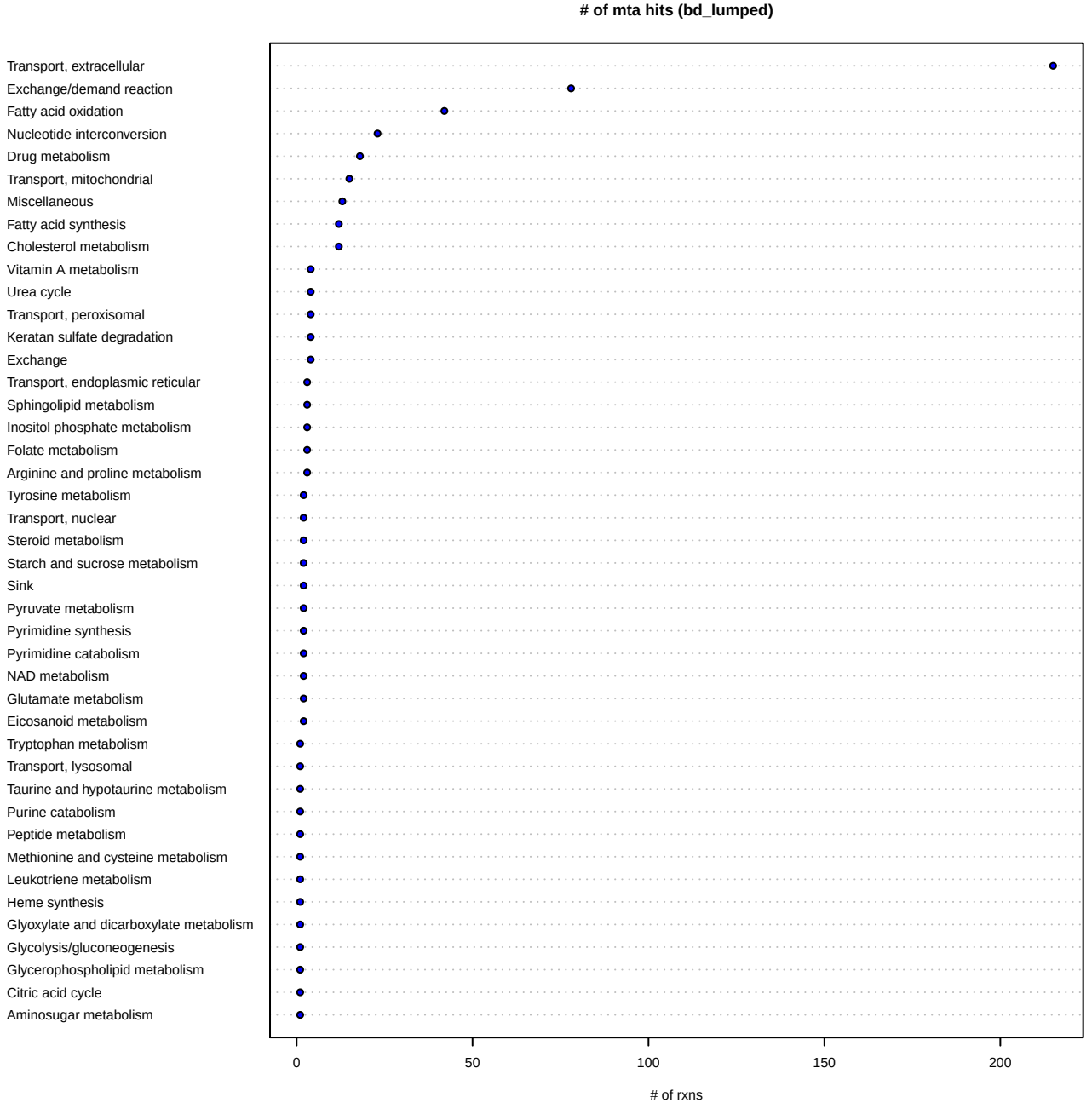

Intersection Size
1500
1000
500
0
49
61
69
105
113
115
190
264
267
269
294
406
524
566
1650
BD_NR_top
BD_R_top
BD_top
Ctrl_unchanged
2500
2000
1500
1000
500
0
Set Size

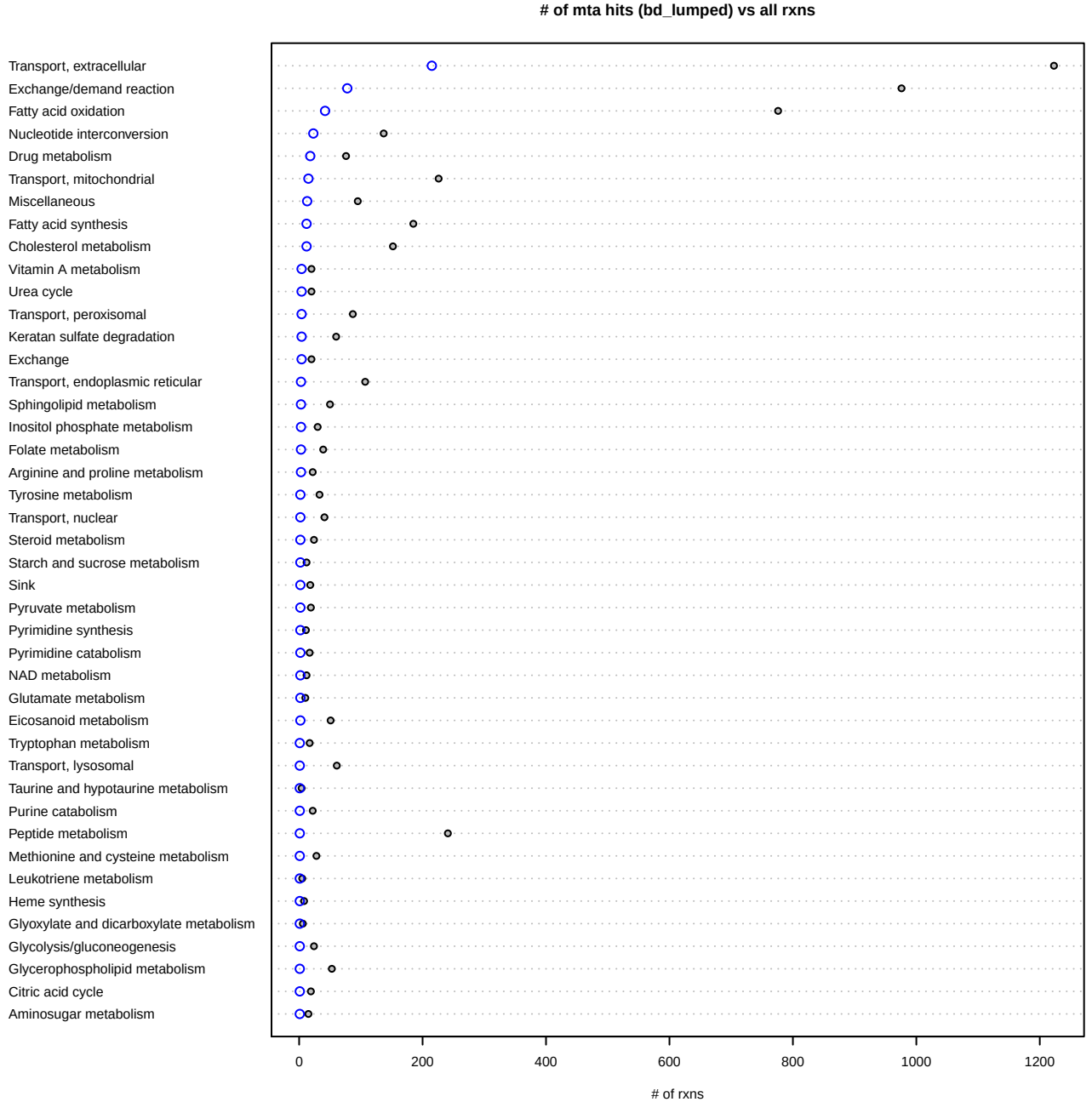
Overlap in rxns disrupted between models

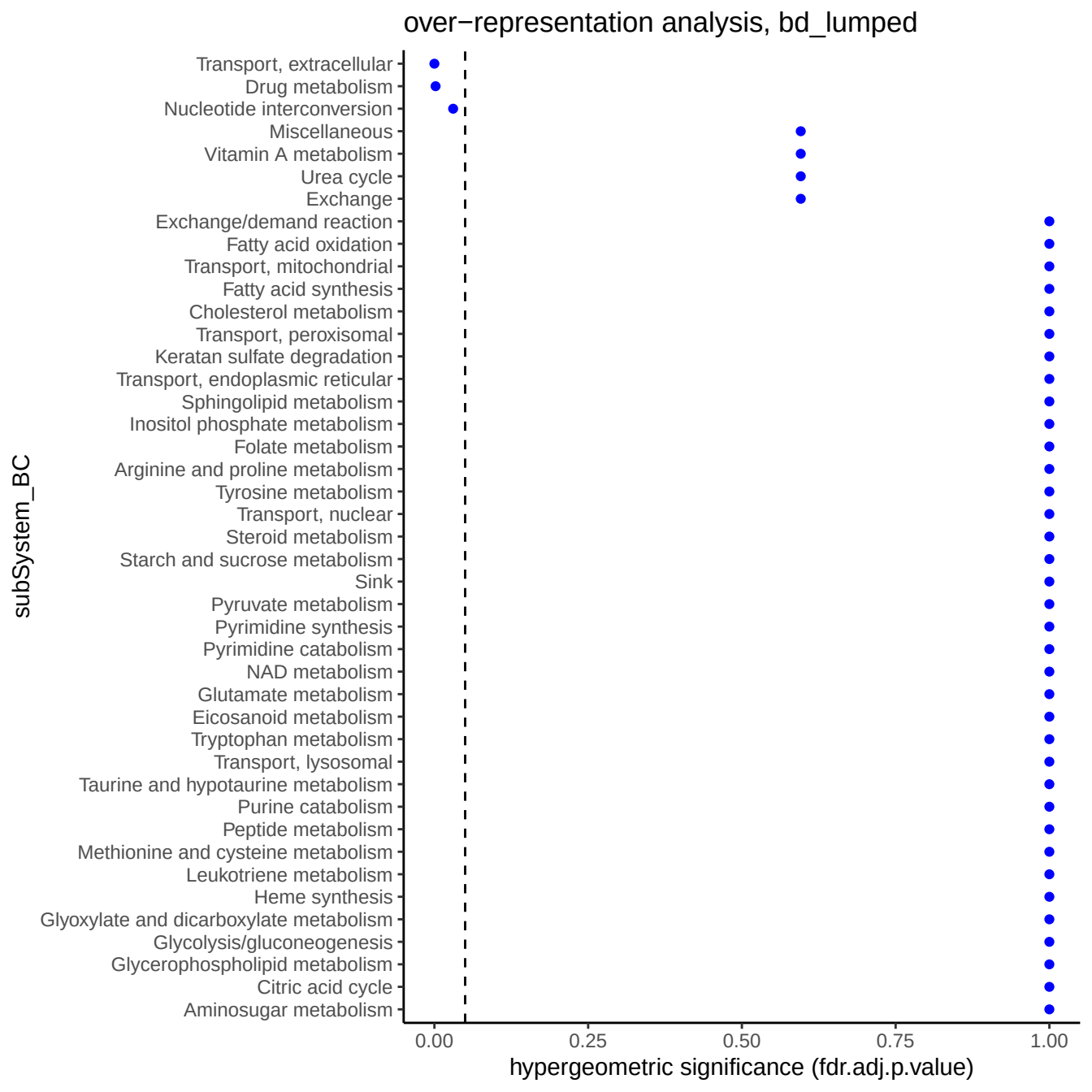


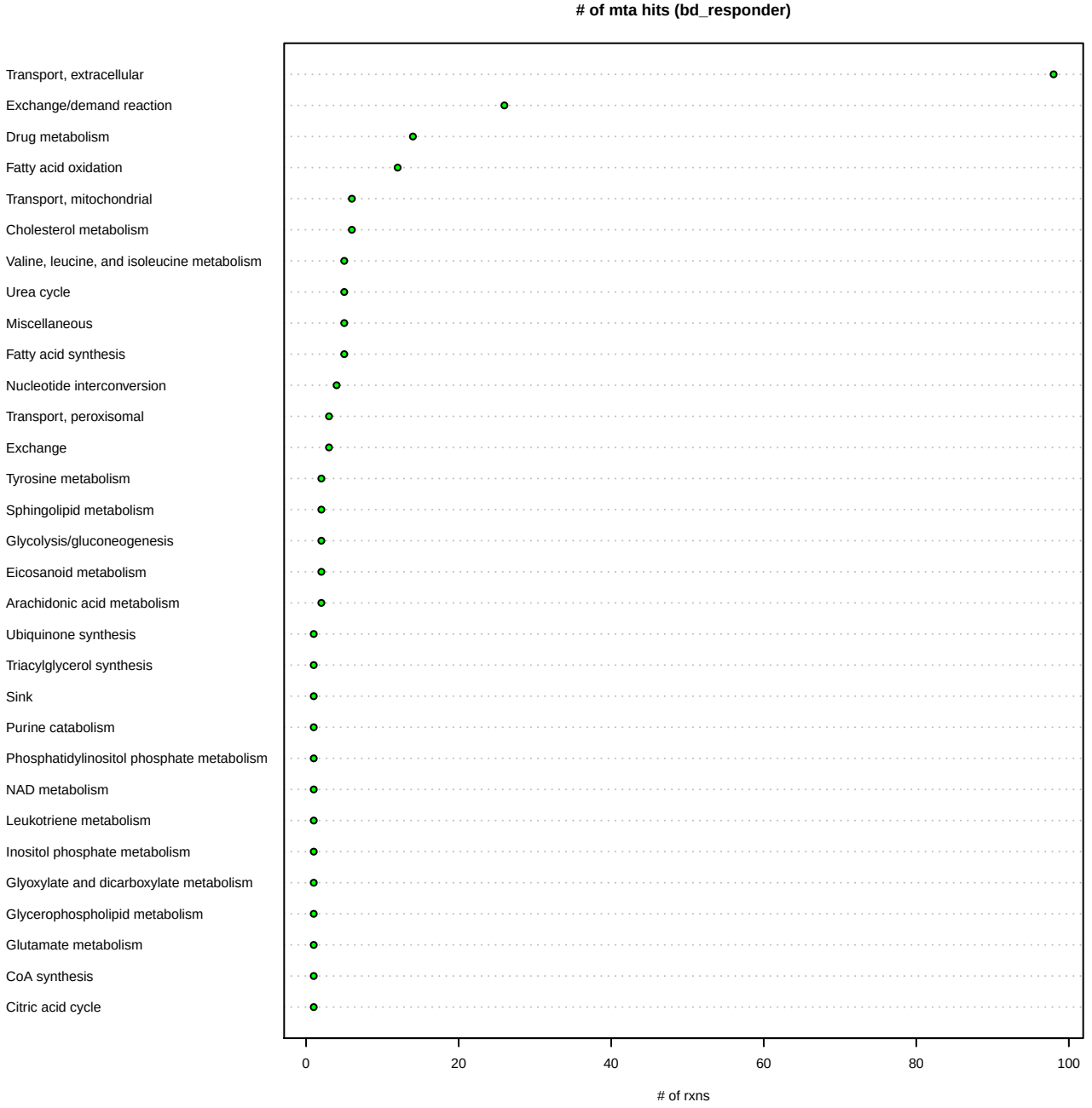
Overlap in subSystems disrupted between models

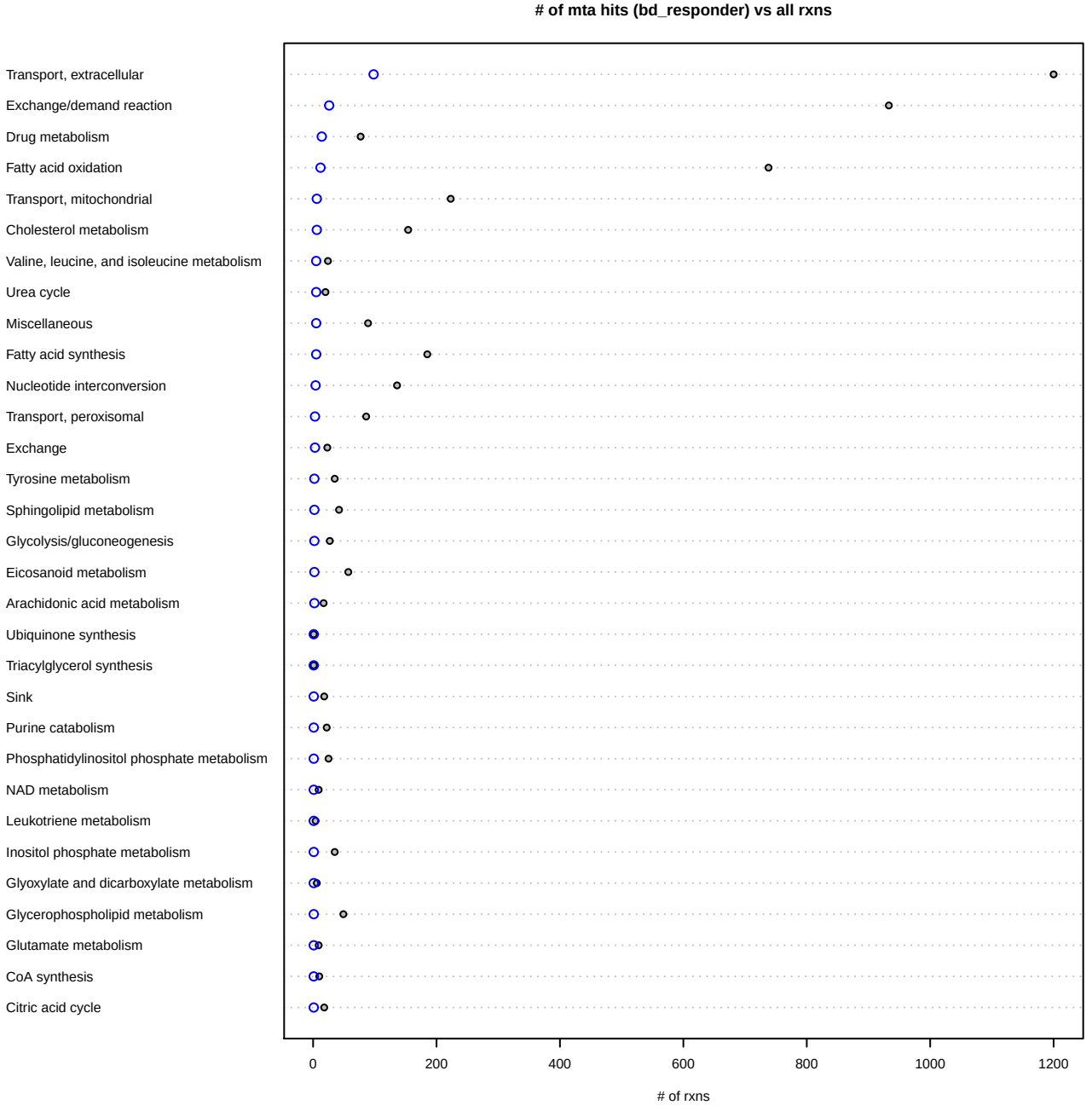


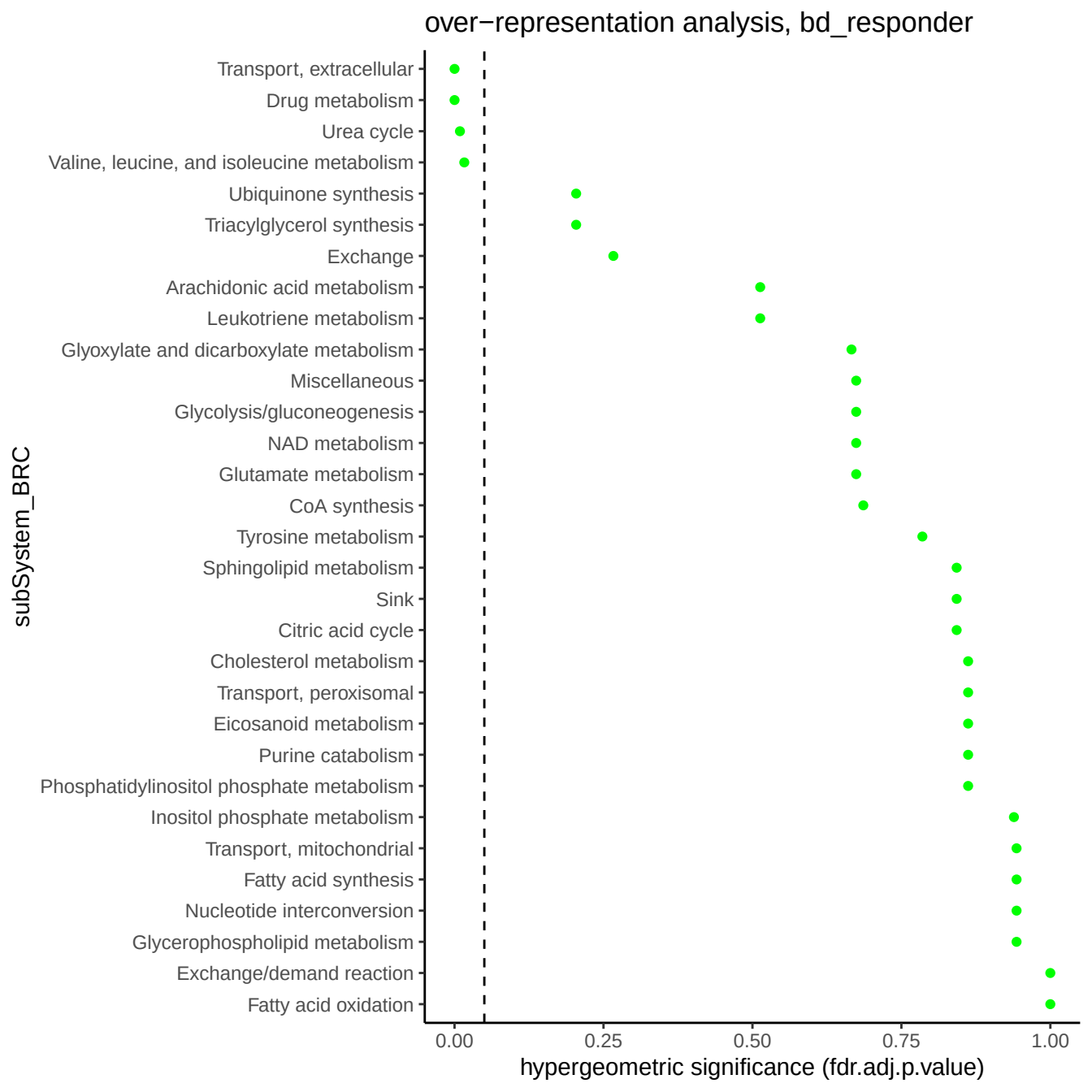

# of mta hits (bd_lumped)
Transport, extracellular
Exchange/demand reaction
Fatty acid oxidation
Nucleotide interconversion
Drug metabolism
Transport, mitochondrial
Miscellaneous
Fatty acid synthesis
Cholesterol metabolism
Vitamin A metabolism
Urea cycle
Transport, peroxisomal
Keratan sulfate degradation
Exchange
Transport, endoplasmic reticular
Sphingolipid metabolism
Inositol phosphate metabolism
Folate metabolism
Arginine and proline metabolism
Tyrosine metabolism
Transport, nuclear
Steroid metabolism
Starch and sucrose metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pyrimidine catabolism
NAD metabolism
Glutamate metabolism
Eicosanoid metabolism
Tryptophan metabolism
Transport, lysosomal
Taurine and hypotaurine metabolism
Purine catabolism
Peptide metabolism
Methionine and cysteine metabolism
Leukotriene metabolism
Heme synthesis
Glyoxylate and dicarboxylate metabolism
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Citric acid cycle
Aminosugar metabolism
0
50
100
150
200
# of rxns

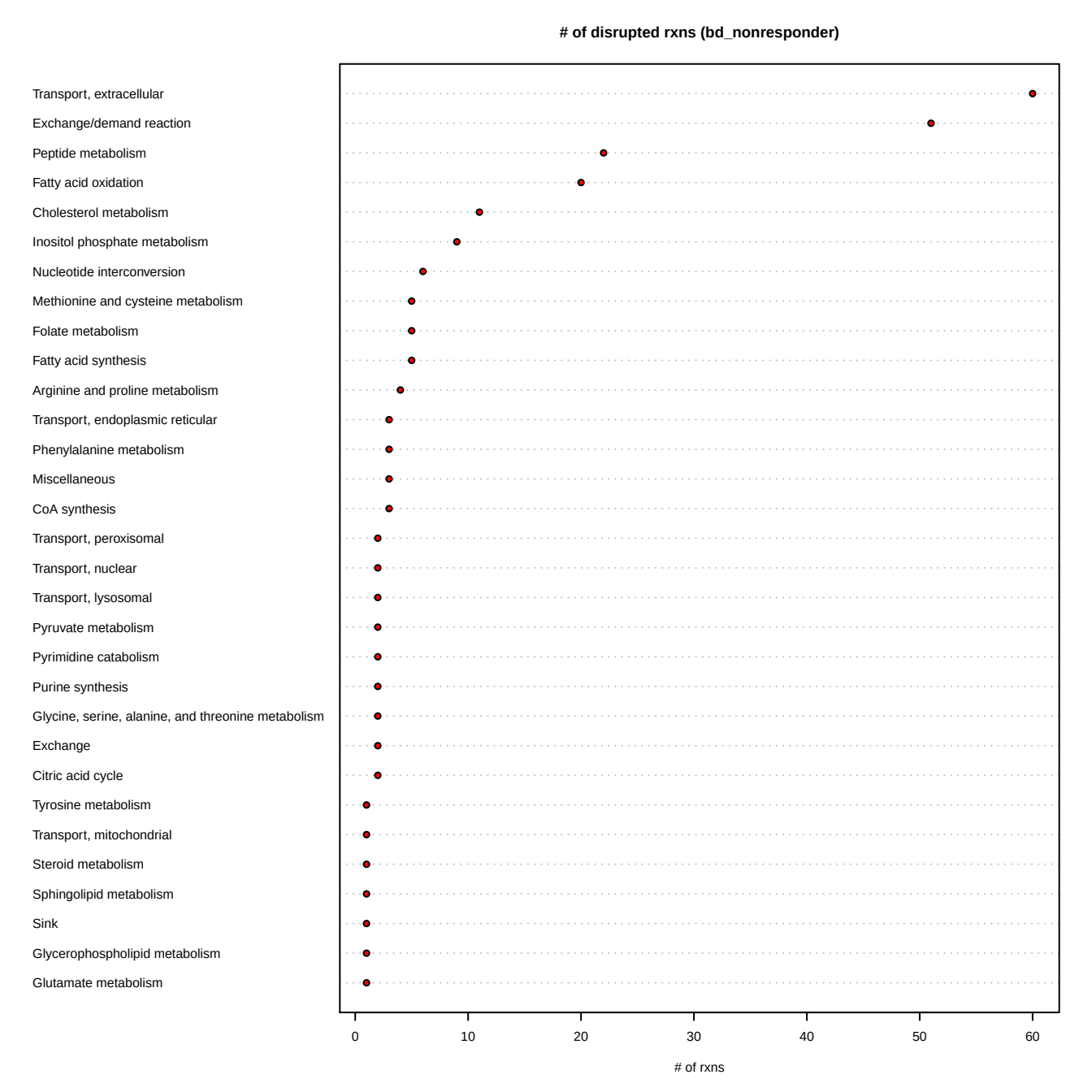

# of mta hits (bd_lumped) vs all rxns
Transport, extracellular
Exchange/demand reaction
Fatty acid oxidation
Nucleotide interconversion
Drug metabolism
Transport, mitochondrial
Miscellaneous
Fatty acid synthesis
Cholesterol metabolism
Vitamin A metabolism
Urea cycle
Transport, peroxisomal
Keratan sulfate degradation
Exchange
Transport, endoplasmic reticular
Sphingolipid metabolism
Inositol phosphate metabolism
Folate metabolism
Arginine and proline metabolism
Tyrosine metabolism
Transport, nuclear
Steroid metabolism
Starch and sucrose metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pyrimidine catabolism
NAD metabolism
Glutamate metabolism
Eicosanoid metabolism
Tryptophan metabolism
Transport, lysosomal
Taurine and hypotaurine metabolism
Purine catabolism
Peptide metabolism
Methionine and cysteine metabolism
Leukotriene metabolism
Heme synthesis
Glyoxylate and dicarboxylate metabolism
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Citric acid cycle
Aminosugar metabolism
0
200
400
600
800
1000
1200
# of rxns

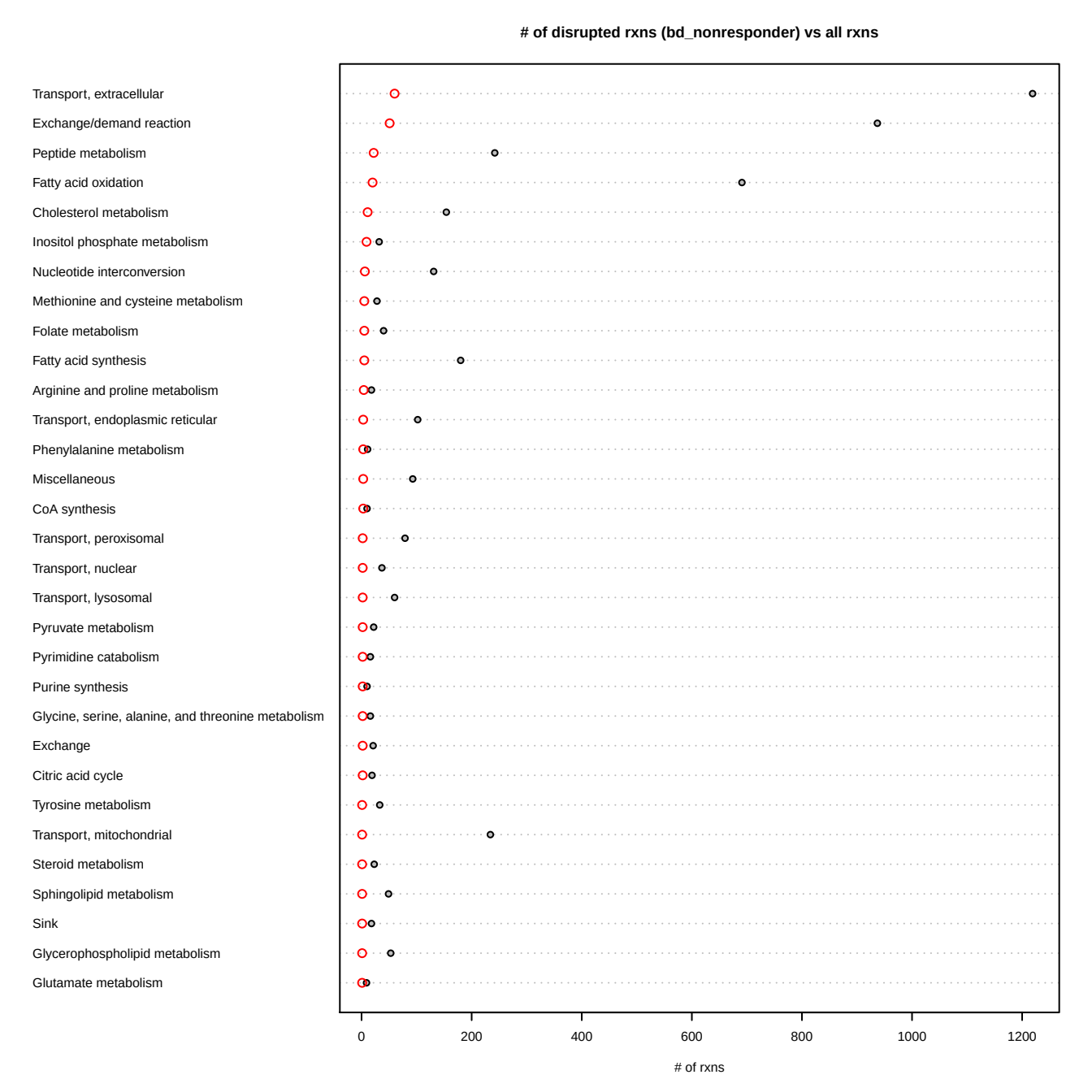

over−representation analysis, bd_lumped
Transport, extracellular
Drug metabolism
Nucleotide interconversion
Miscellaneous
Vitamin A metabolism
Urea cycle
Exchange
Exchange/demand reaction
Fatty acid oxidation
Transport, mitochondrial
Fatty acid synthesis
Cholesterol metabolism
Transport, peroxisomal
Keratan sulfate degradation
Transport, endoplasmic reticular
Sphingolipid metabolism
Inositol phosphate metabolism
Folate metabolism
Arginine and proline metabolism
Tyrosine metabolism
Transport, nuclear
Steroid metabolism
Starch and sucrose metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pyrimidine catabolism
NAD metabolism
Glutamate metabolism
Eicosanoid metabolism
Tryptophan metabolism
Transport, lysosomal
Taurine and hypotaurine metabolism
Purine catabolism
Peptide metabolism
Methionine and cysteine metabolism
Leukotriene metabolism
Heme synthesis
Glyoxylate and dicarboxylate metabolism
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Citric acid cycle
Aminosugar metabolism
subSystem_BC
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

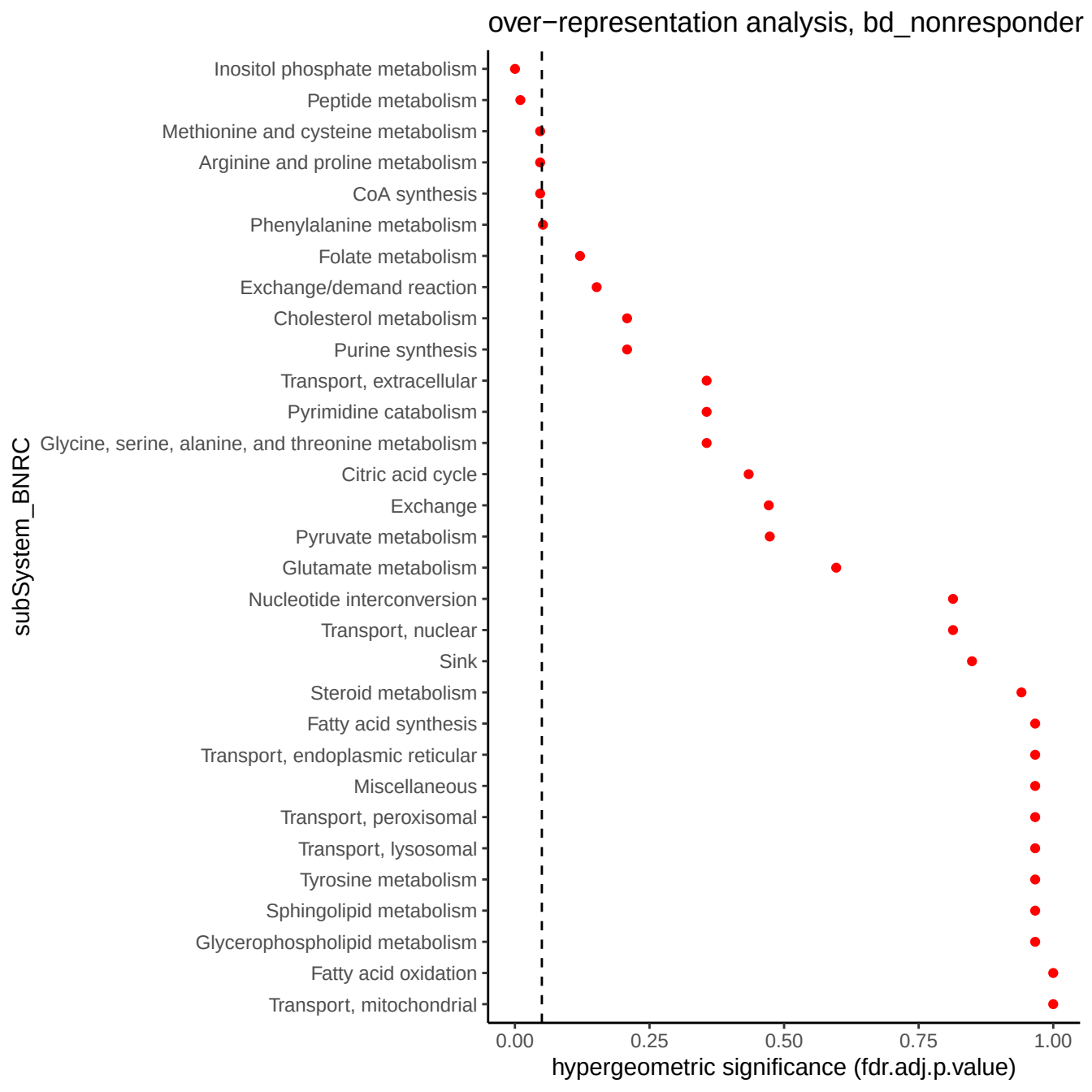

# of mta hits (bd_responder)
Transport, extracellular
Exchange/demand reaction
Drug metabolism
Fatty acid oxidation
Transport, mitochondrial
Cholesterol metabolism
Valine, leucine, and isoleucine metabolism
Urea cycle
Miscellaneous
Fatty acid synthesis
Nucleotide interconversion
Transport, peroxisomal
Exchange
Tyrosine metabolism
Sphingolipid metabolism
Glycolysis/gluconeogenesis
Eicosanoid metabolism
Arachidonic acid metabolism
Ubiquinone synthesis
Triacylglycerol synthesis
Sink
Purine catabolism
Phosphatidylinositol phosphate metabolism
NAD metabolism
Leukotriene metabolism
Inositol phosphate metabolism
Glyoxylate and dicarboxylate metabolism
Glycerophospholipid metabolism
Glutamate metabolism
CoA synthesis
Citric acid cycle
0
20
40
60
80
100
# of rxns


# of mta hits (bd_responder) vs all rxns
Transport, extracellular
Exchange/demand reaction
Drug metabolism
Fatty acid oxidation
Transport, mitochondrial
Cholesterol metabolism
Valine, leucine, and isoleucine metabolism
Urea cycle
Miscellaneous
Fatty acid synthesis
Nucleotide interconversion
Transport, peroxisomal
Exchange
Tyrosine metabolism
Sphingolipid metabolism
Glycolysis/gluconeogenesis
Eicosanoid metabolism
Arachidonic acid metabolism
Ubiquinone synthesis
Triacylglycerol synthesis
Sink
Purine catabolism
Phosphatidylinositol phosphate metabolism
NAD metabolism
Leukotriene metabolism
Inositol phosphate metabolism
Glyoxylate and dicarboxylate metabolism
Glycerophospholipid metabolism
Glutamate metabolism
CoA synthesis
Citric acid cycle
0
200
400
600
800
1000
1200
# of rxns

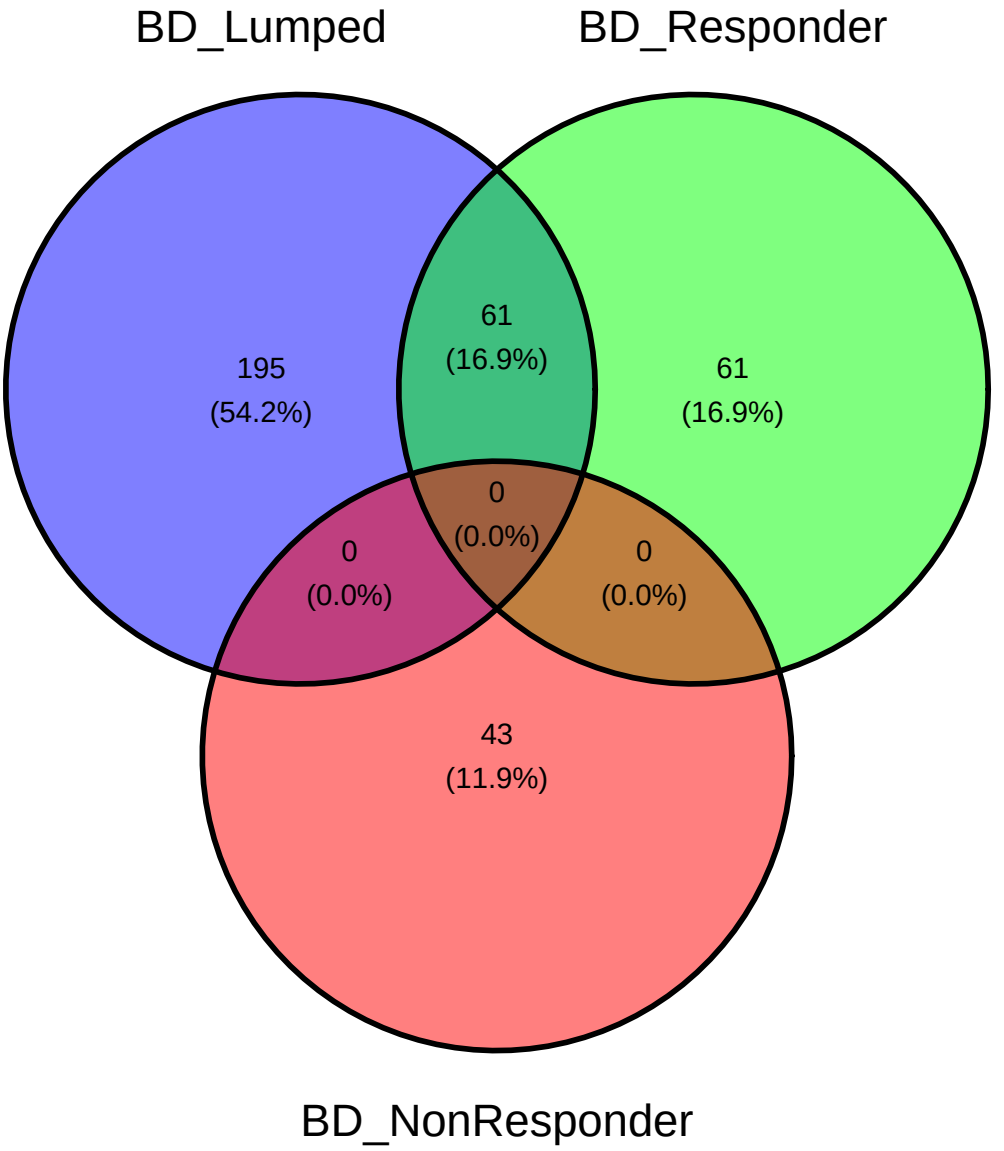
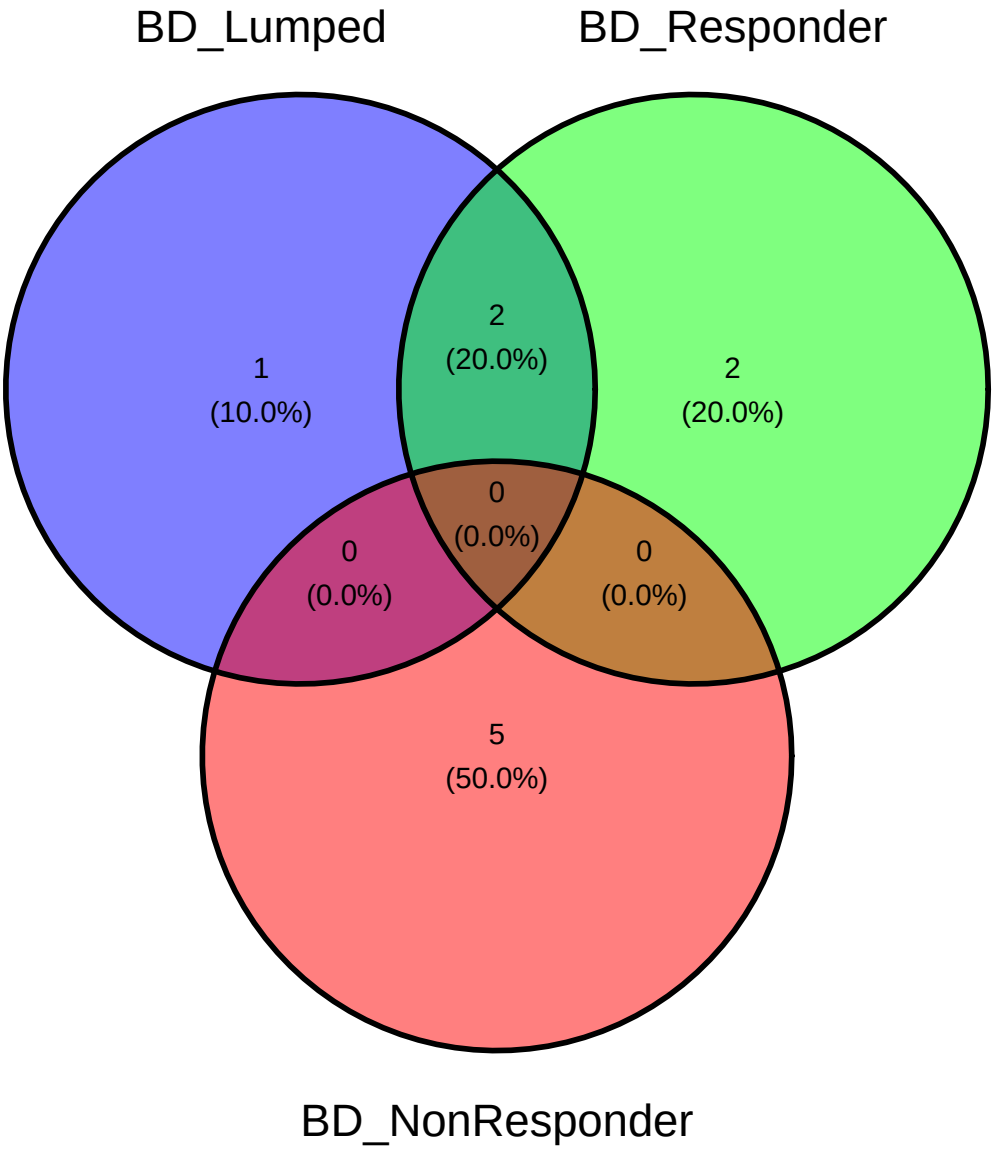

over−representation analysis, bd_responder
Transport, extracellular
Drug metabolism
Urea cycle
Valine, leucine, and isoleucine metabolism
Ubiquinone synthesis
Triacylglycerol synthesis
Exchange
Arachidonic acid metabolism
Leukotriene metabolism
Glyoxylate and dicarboxylate metabolism
Miscellaneous
Glycolysis/gluconeogenesis
NAD metabolism
Glutamate metabolism
CoA synthesis
Tyrosine metabolism
Sphingolipid metabolism
Sink
Citric acid cycle
Cholesterol metabolism
Transport, peroxisomal
Eicosanoid metabolism
Purine catabolism
Phosphatidylinositol phosphate metabolism
Inositol phosphate metabolism
Transport, mitochondrial
Fatty acid synthesis
Nucleotide interconversion
Glycerophospholipid metabolism
Exchange/demand reaction
Fatty acid oxidation
subSystem_BRC
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)


# of disrupted rxns (bd_nonresponder)
Transport, extracellular
Exchange/demand reaction
Peptide metabolism
Fatty acid oxidation
Cholesterol metabolism
Inositol phosphate metabolism
Nucleotide interconversion
Methionine and cysteine metabolism
Folate metabolism
Fatty acid synthesis
Arginine and proline metabolism
Transport, endoplasmic reticular
Phenylalanine metabolism
Miscellaneous
CoA synthesis
Transport, peroxisomal
Transport, nuclear
Transport, lysosomal
Pyruvate metabolism
Pyrimidine catabolism
Purine synthesis
Glycine, serine, alanine, and threonine metabolism
Exchange
Citric acid cycle
Tyrosine metabolism
Transport, mitochondrial
Steroid metabolism
Sphingolipid metabolism
Sink
Glycerophospholipid metabolism
Glutamate metabolism
0
10
20
30
40
50
60
# of rxns


# of disrupted rxns (bd_nonresponder) vs all rxns
Transport, extracellular
Exchange/demand reaction
Peptide metabolism
Fatty acid oxidation
Cholesterol metabolism
Inositol phosphate metabolism
Nucleotide interconversion
Methionine and cysteine metabolism
Folate metabolism
Fatty acid synthesis
Arginine and proline metabolism
Transport, endoplasmic reticular
Phenylalanine metabolism
Miscellaneous
CoA synthesis
Transport, peroxisomal
Transport, nuclear
Transport, lysosomal
Pyruvate metabolism
Pyrimidine catabolism
Purine synthesis
Glycine, serine, alanine, and threonine metabolism
Exchange
Citric acid cycle
Tyrosine metabolism
Transport, mitochondrial
Steroid metabolism
Sphingolipid metabolism
Sink
Glycerophospholipid metabolism
Glutamate metabolism
0
200
400
600
800
1000
1200
# of rxns


over−representation analysis, bd_nonresponder
Inositol phosphate metabolism
Peptide metabolism
Methionine and cysteine metabolism
Arginine and proline metabolism
CoA synthesis
Phenylalanine metabolism
Folate metabolism
Exchange/demand reaction
Cholesterol metabolism
Purine synthesis
Transport, extracellular
Pyrimidine catabolism
Glycine, serine, alanine, and threonine metabolism
Citric acid cycle
Exchange
Pyruvate metabolism
Glutamate metabolism
Nucleotide interconversion
Transport, nuclear
Sink
Steroid metabolism
Fatty acid synthesis
Transport, endoplasmic reticular
Miscellaneous
Transport, peroxisomal
Transport, lysosomal
Tyrosine metabolism
Sphingolipid metabolism
Glycerophospholipid metabolism
Fatty acid oxidation
Transport, mitochondrial
subSystem_BNRC
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

Overlp in rxns (fdr.significant) disrupted between models



Overlp in subSystems (fdr.significant) disrupted between models