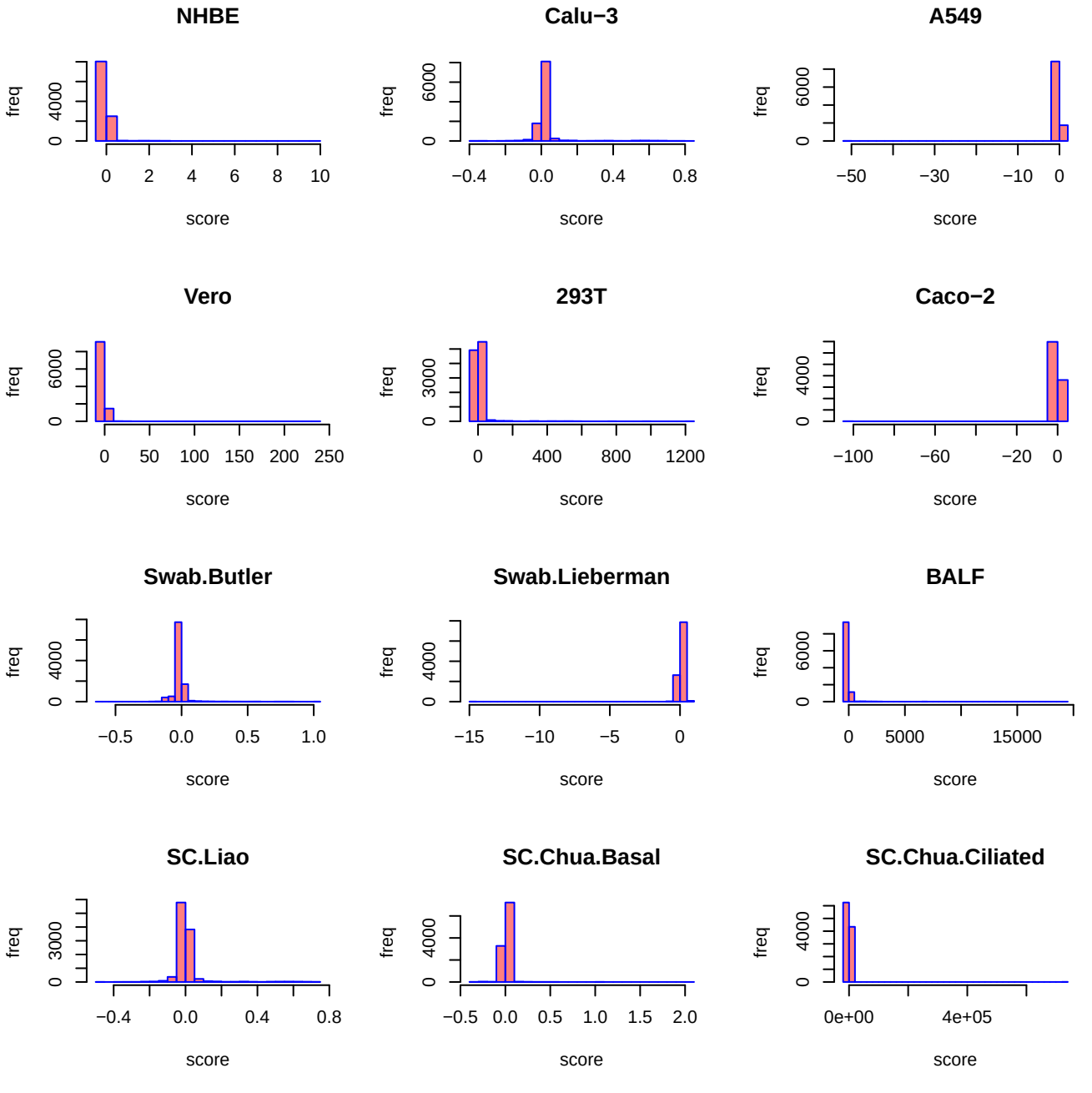
NHBE
freq
0
4000
0
2
4
6
8
10
score
Calu−3
freq
0
6000
−0.4
0.0
0.4
0.8
score
A549
freq
0
6000
−50
−30
−10
0
score
Vero
freq
0
6000
0
50
100
150
200
250
score
293T
freq
0
3000
0
400
800
1200
score
Caco−2
freq
0
4000
−100
−60
−20
0
score
Swab.Butler
freq
0
4000
−0.5
0.0
0.5
1.0
score
Swab.Lieberman
freq
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
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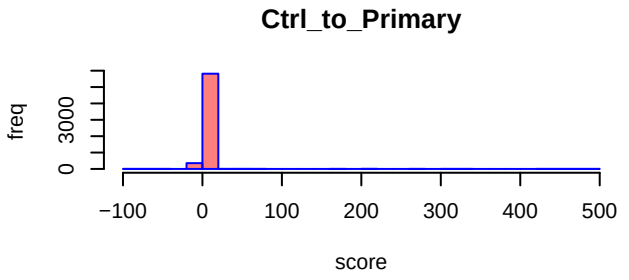
0e+00
4e+05
score


Ctrl_to_Primary
freq
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3000
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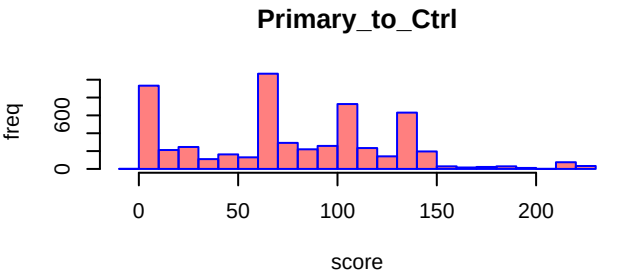
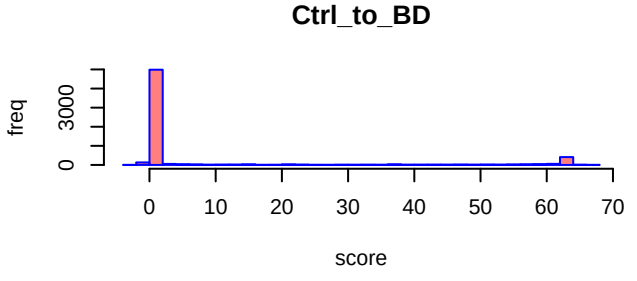
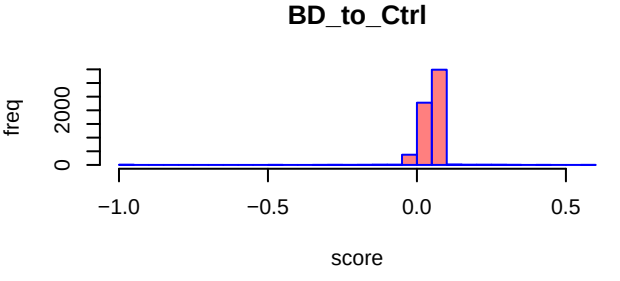
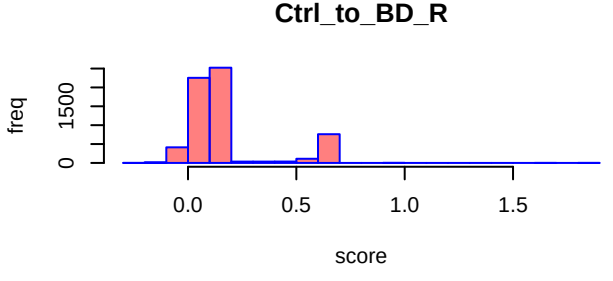
0
100
200
300
400
500
score


Primary_to_Ctrl
freq
0
600
0
50
100
150
200
score


Ctrl_to_BD
freq
0
3000
0
10
20
30
40
50
60
70
score


BD_to_Ctrl
freq
0
2000
−1.0
−0.5
0.0
0.5
score


Ctrl_to_BD_R
freq
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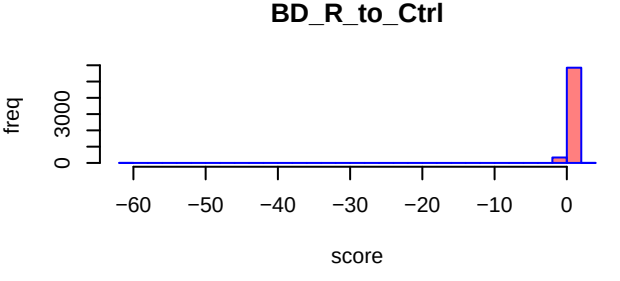
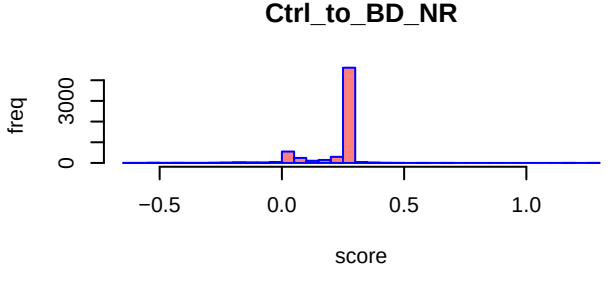
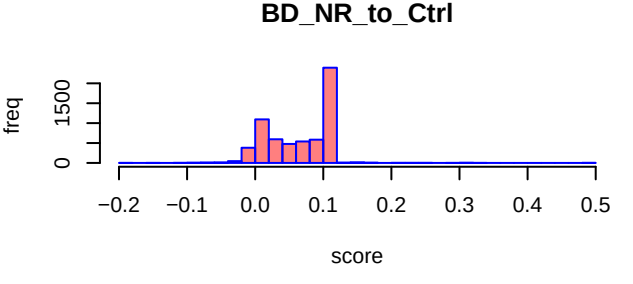
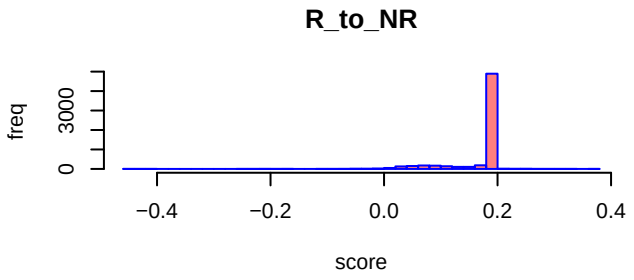
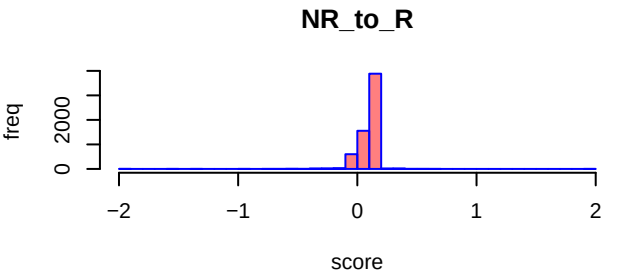
1500
0.0
0.5
1.0
1.5
score

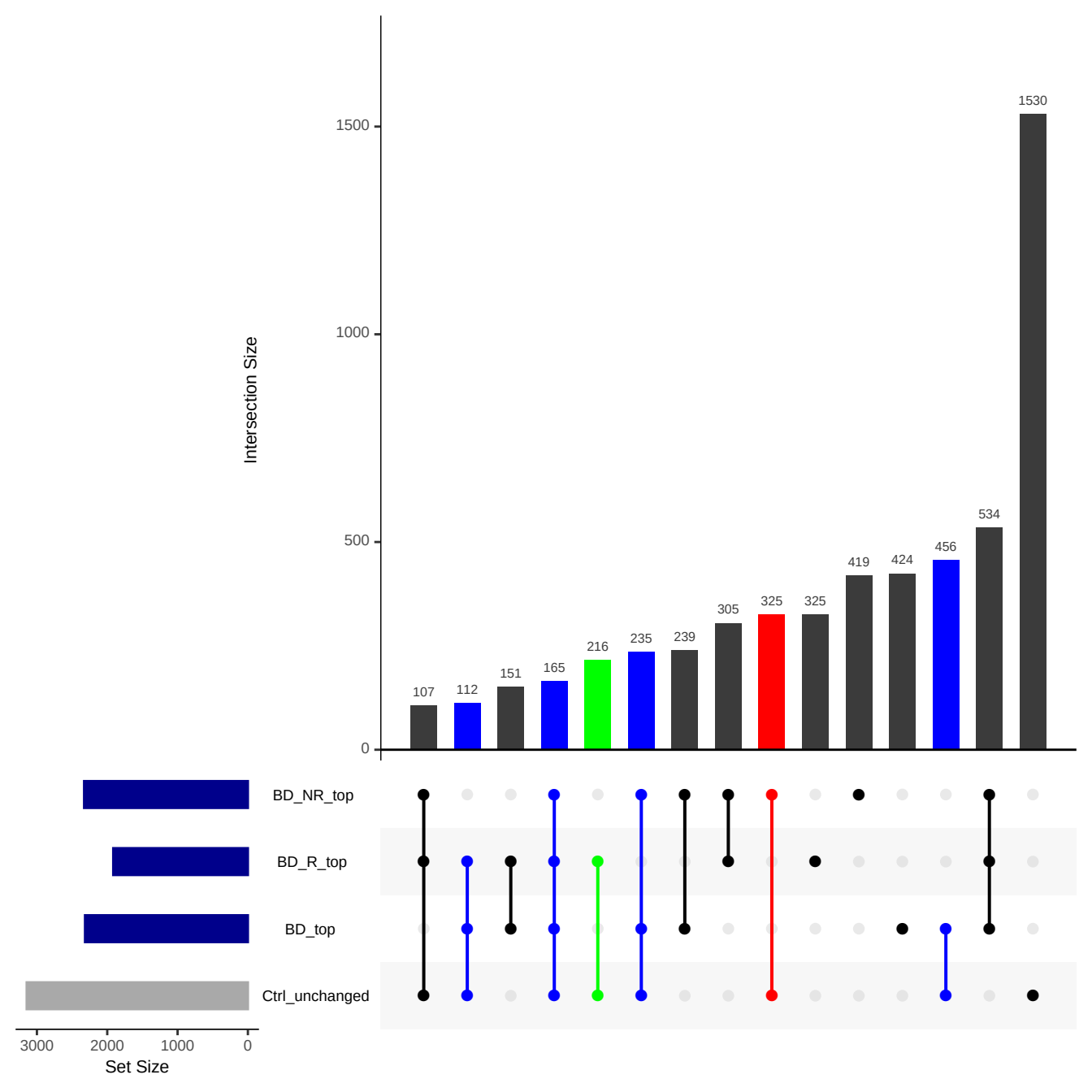

BD_R_to_Ctrl
freq
0
3000
−60
−50
−40
−30
−20
−10
0
score


Ctrl_to_BD_NR
freq
0
3000
−0.5
0.0
0.5
1.0
score

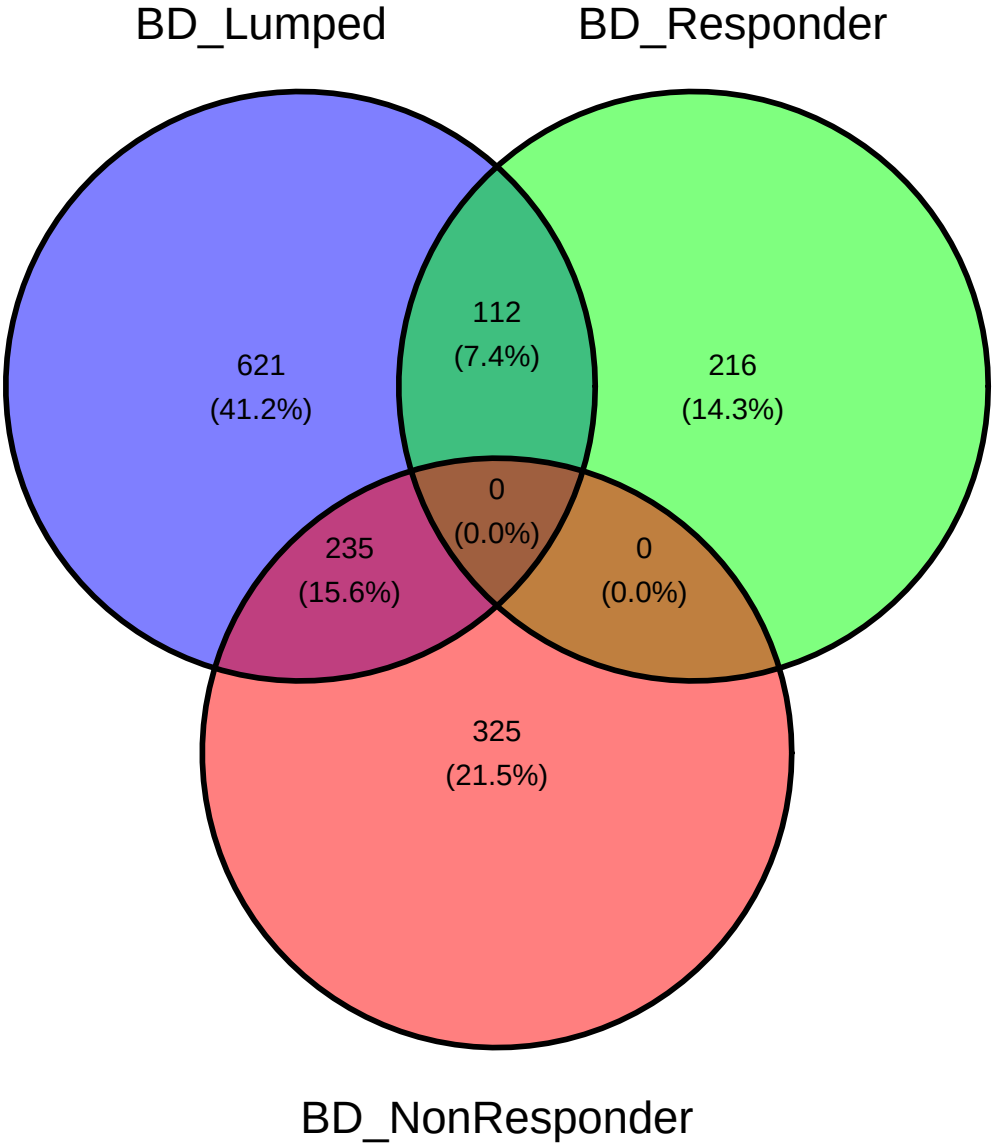

BD_NR_to_Ctrl
freq
0
1500
−0.2
−0.1
0.0
0.1
0.2
0.3
0.4
0.5
score


R_to_NR
freq
0
3000
−0.4
−0.2
0.0
0.2
0.4
score

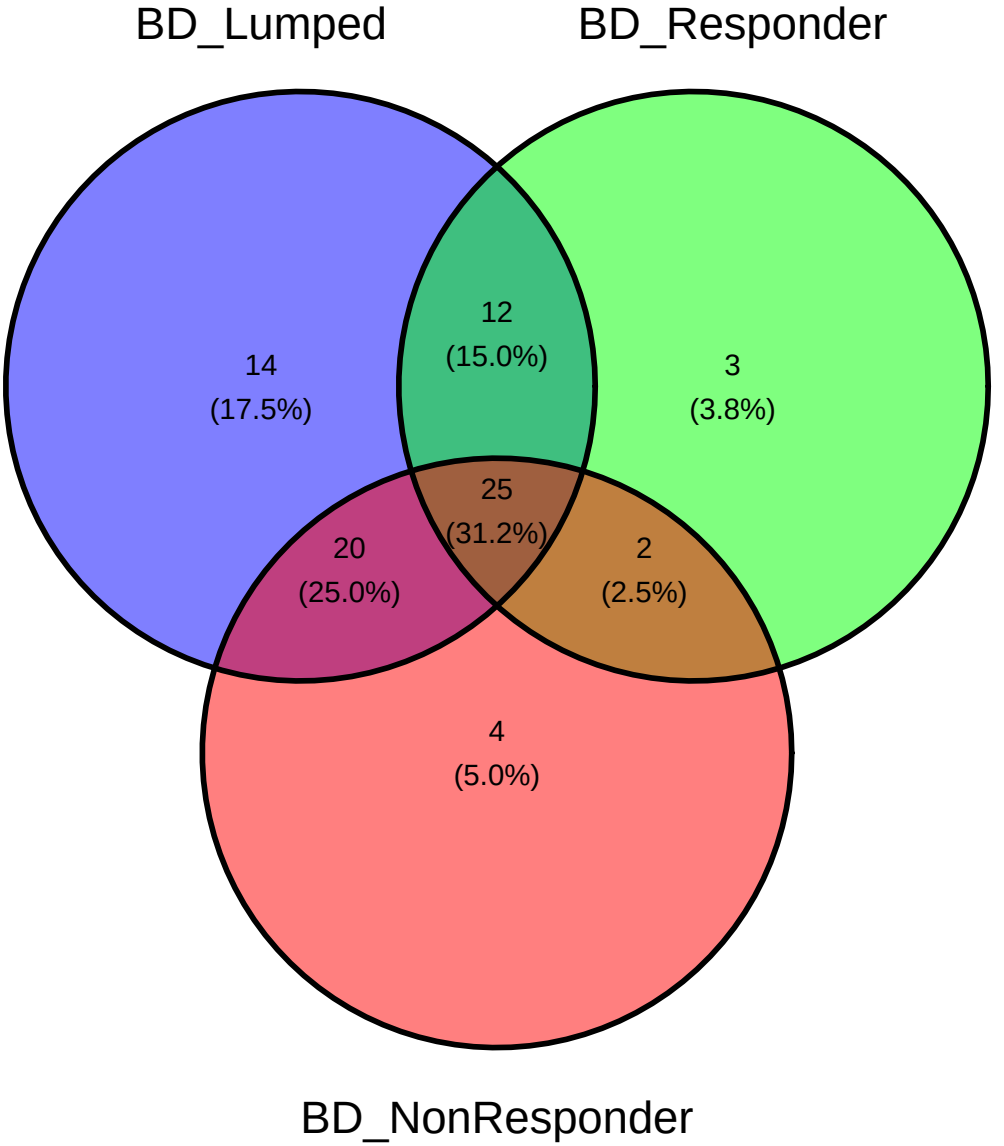

NR_to_R
freq
0
2000
−2
−1
0
1
2
score

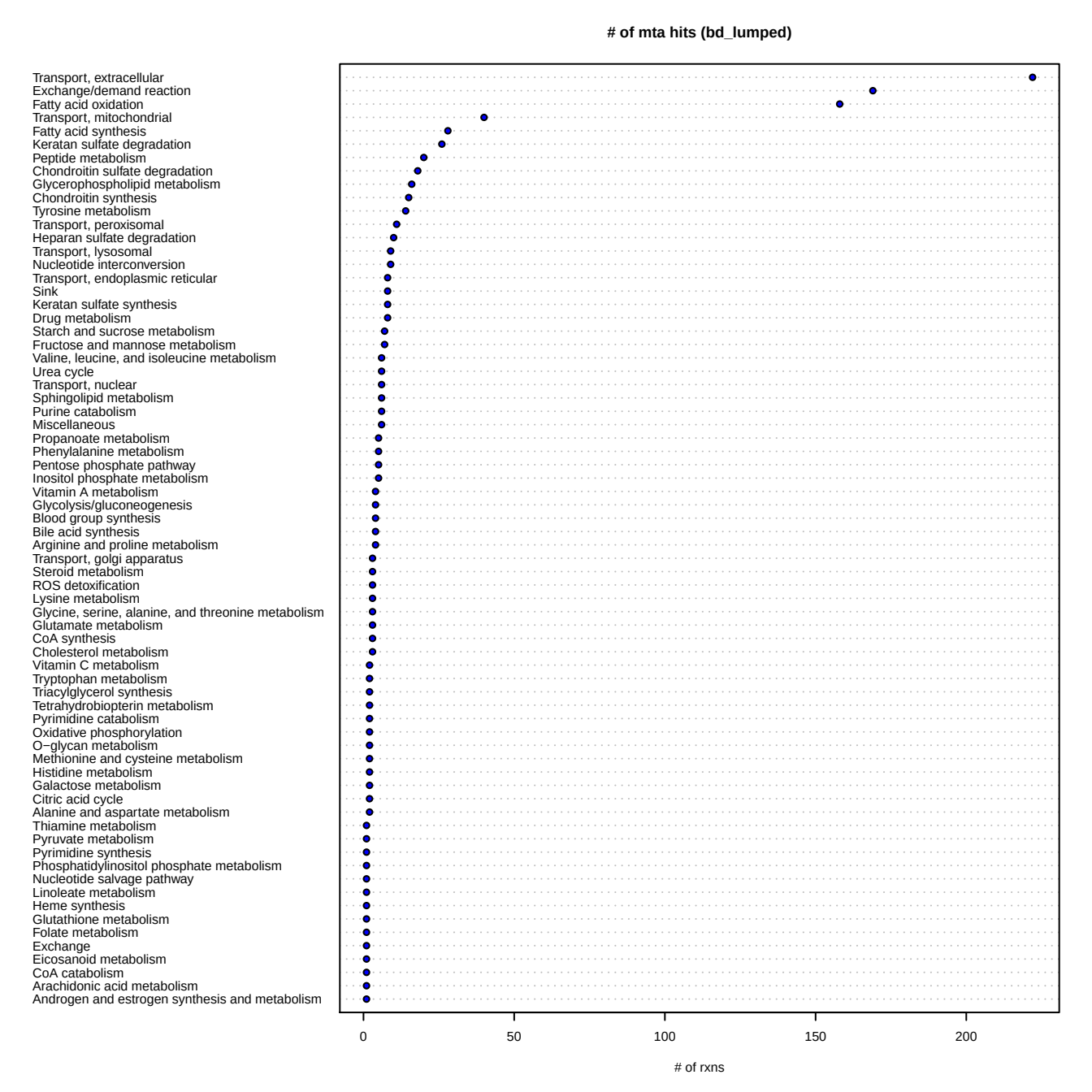

Intersection Size
1500
1000
500
0
1530
534
456
424
419
325
325
305
239
235
216
165
151
112
107
BD_NR_top
BD_R_top
BD_top
Ctrl_unchanged
3000
2000
1000
0
Set Size

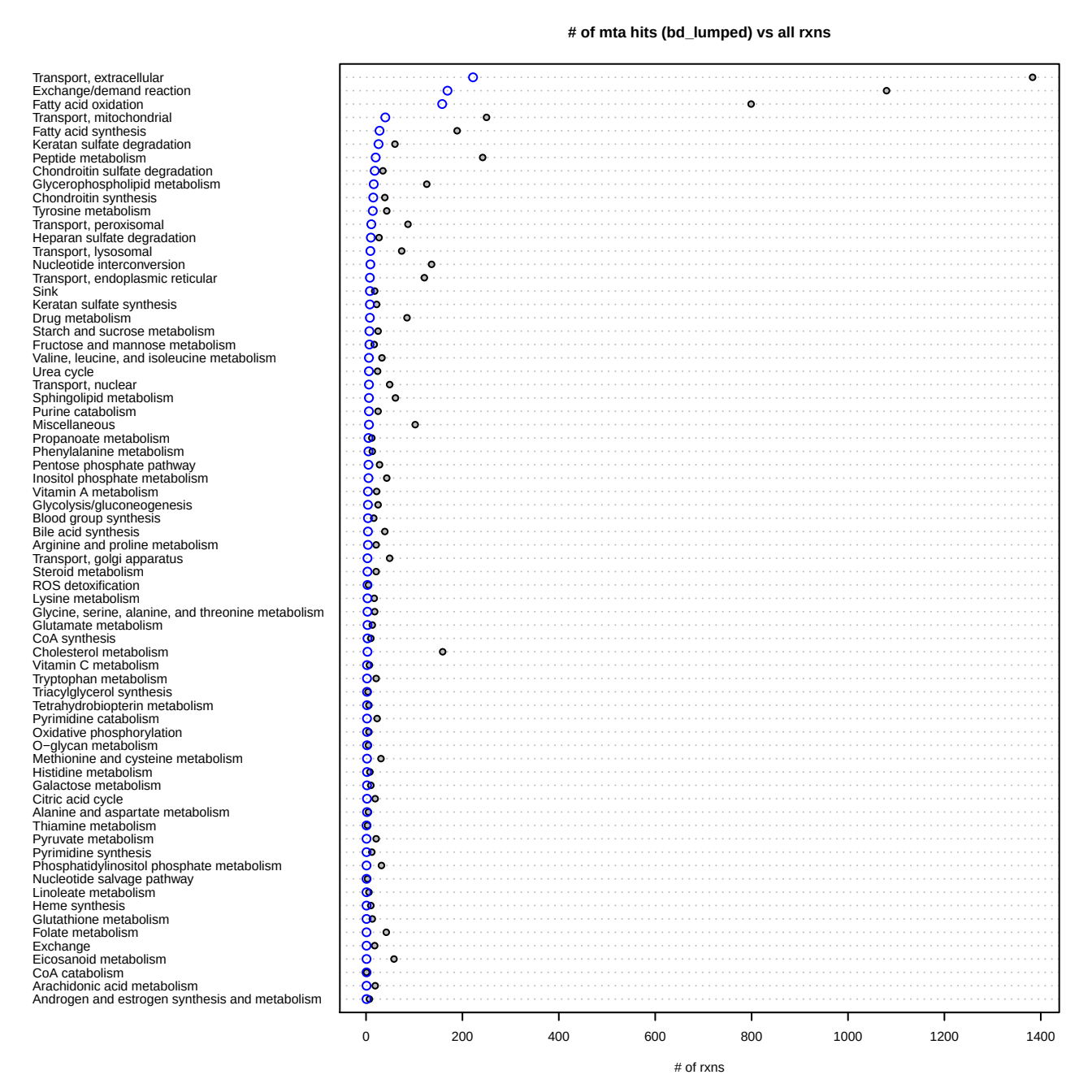
Overlap in rxns disrupted between models

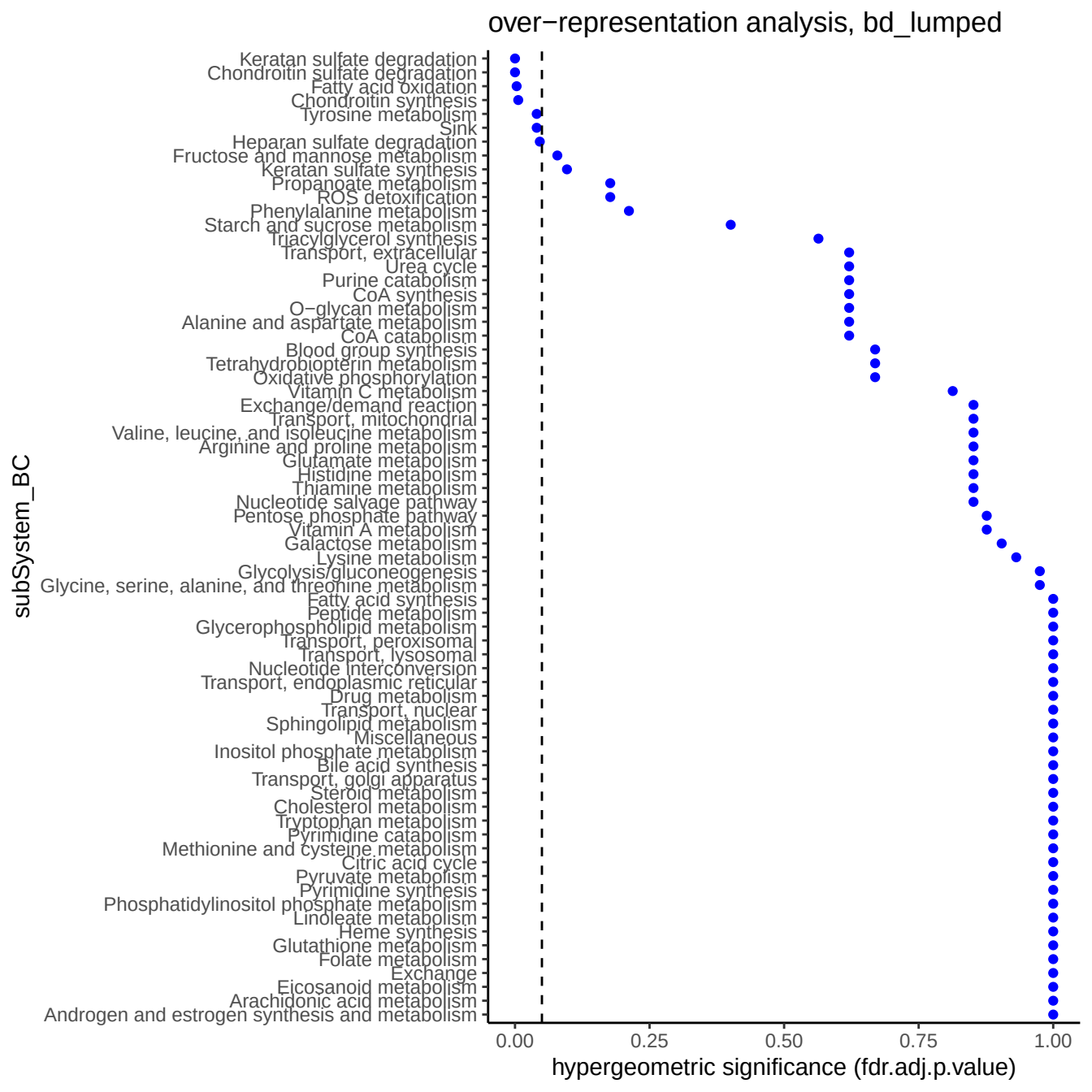


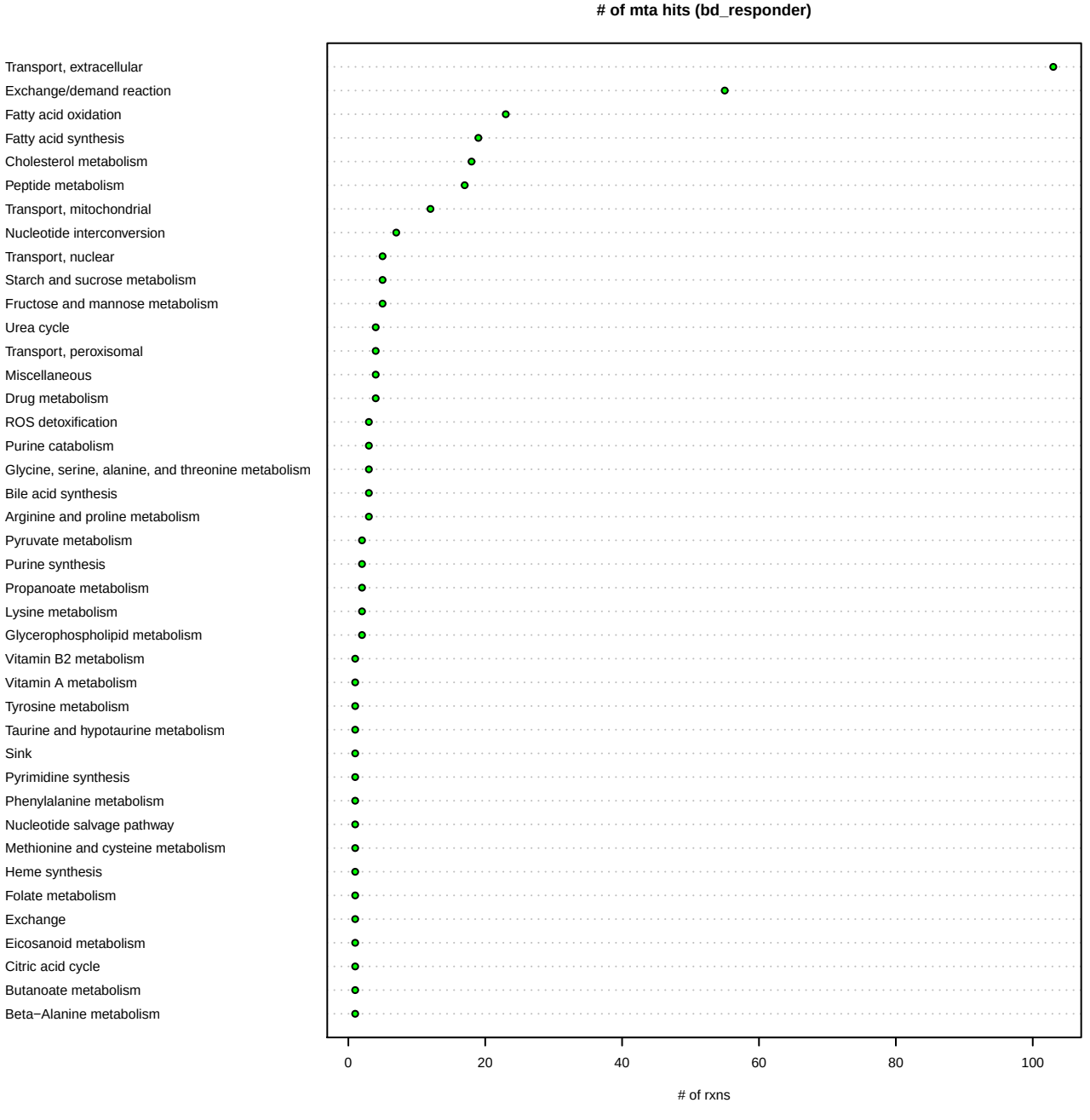
Overlap in subSystems disrupted between models

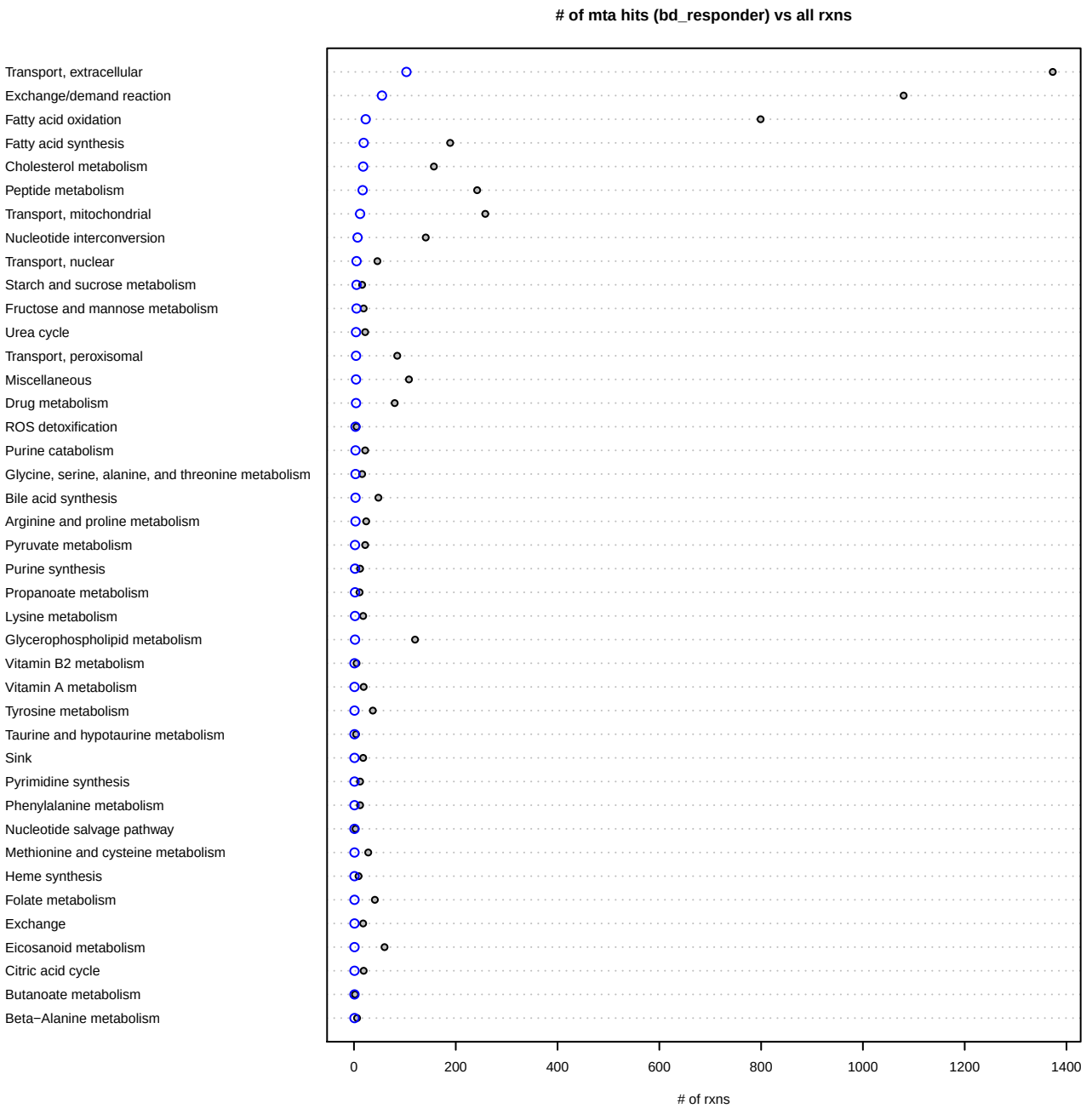


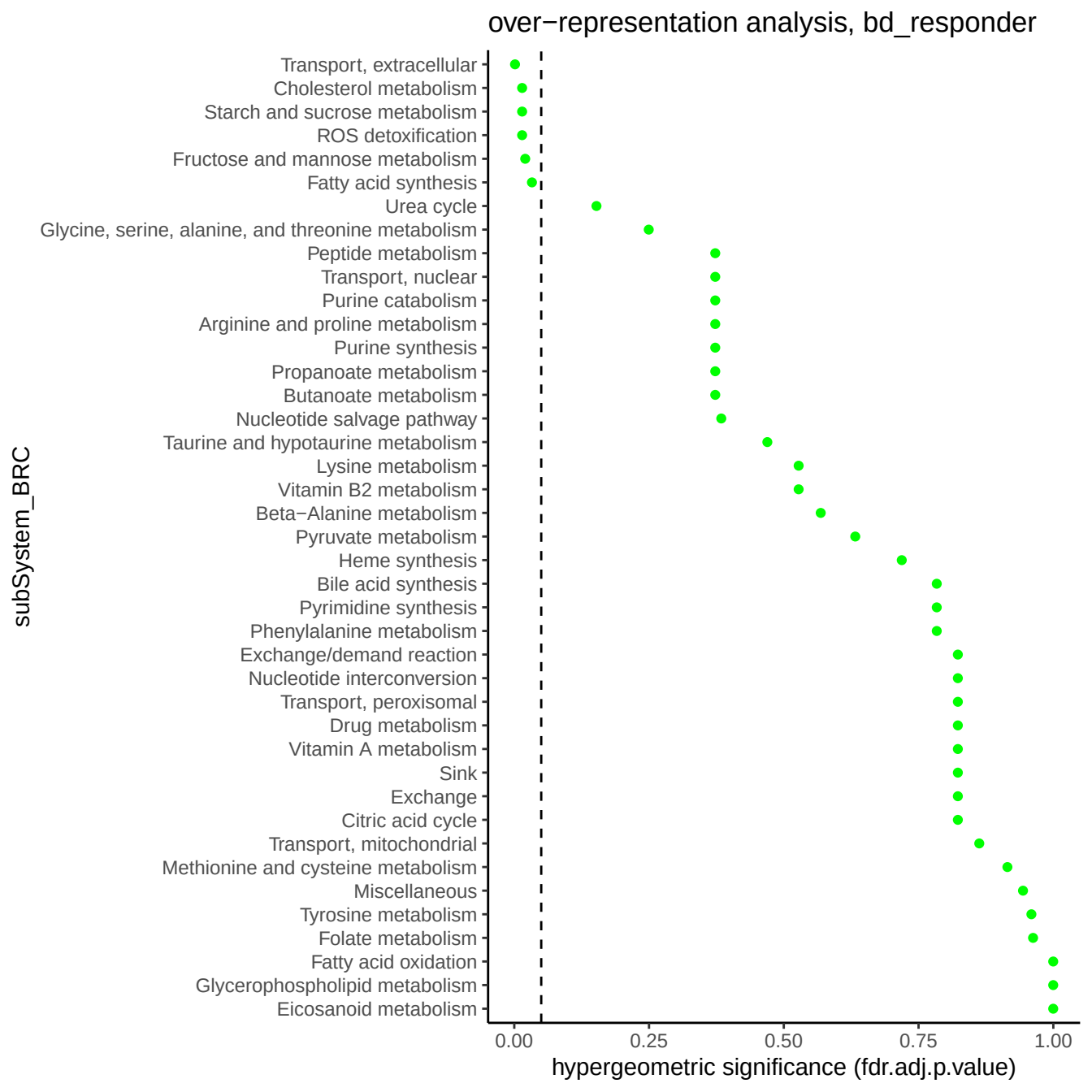

# of mta hits (bd_lumped)
Transport, extracellular
Exchange/demand reaction
Fatty acid oxidation
Transport, mitochondrial
Fatty acid synthesis
Keratan sulfate degradation
Peptide metabolism
Chondroitin sulfate degradation
Glycerophospholipid metabolism
Chondroitin synthesis
Tyrosine metabolism
Transport, peroxisomal
Heparan sulfate degradation
Transport, lysosomal
Nucleotide interconversion
Transport, endoplasmic reticular
Sink
Keratan sulfate synthesis
Drug metabolism
Starch and sucrose metabolism
Fructose and mannose metabolism
Valine, leucine, and isoleucine metabolism
Urea cycle
Transport, nuclear
Sphingolipid metabolism
Purine catabolism
Miscellaneous
Propanoate metabolism
Phenylalanine metabolism
Pentose phosphate pathway
Inositol phosphate metabolism
Vitamin A metabolism
Glycolysis/gluconeogenesis
Blood group synthesis
Bile acid synthesis
Arginine and proline metabolism
Transport, golgi apparatus
Steroid metabolism
ROS detoxification
Lysine metabolism
Glycine, serine, alanine, and threonine metabolism
Glutamate metabolism
CoA synthesis
Cholesterol metabolism
Vitamin C metabolism
Tryptophan metabolism
Triacylglycerol synthesis
Tetrahydrobiopterin metabolism
Pyrimidine catabolism
Oxidative phosphorylation
O−glycan metabolism
Methionine and cysteine metabolism
Histidine metabolism
Galactose metabolism
Citric acid cycle
Alanine and aspartate metabolism
Thiamine metabolism
Pyruvate metabolism
Pyrimidine synthesis
Phosphatidylinositol phosphate metabolism
Nucleotide salvage pathway
Linoleate metabolism
Heme synthesis
Glutathione metabolism
Folate metabolism
Exchange
Eicosanoid metabolism
CoA catabolism
Arachidonic acid metabolism
Androgen and estrogen synthesis and metabolism
0
50
100
150
200
# of rxns

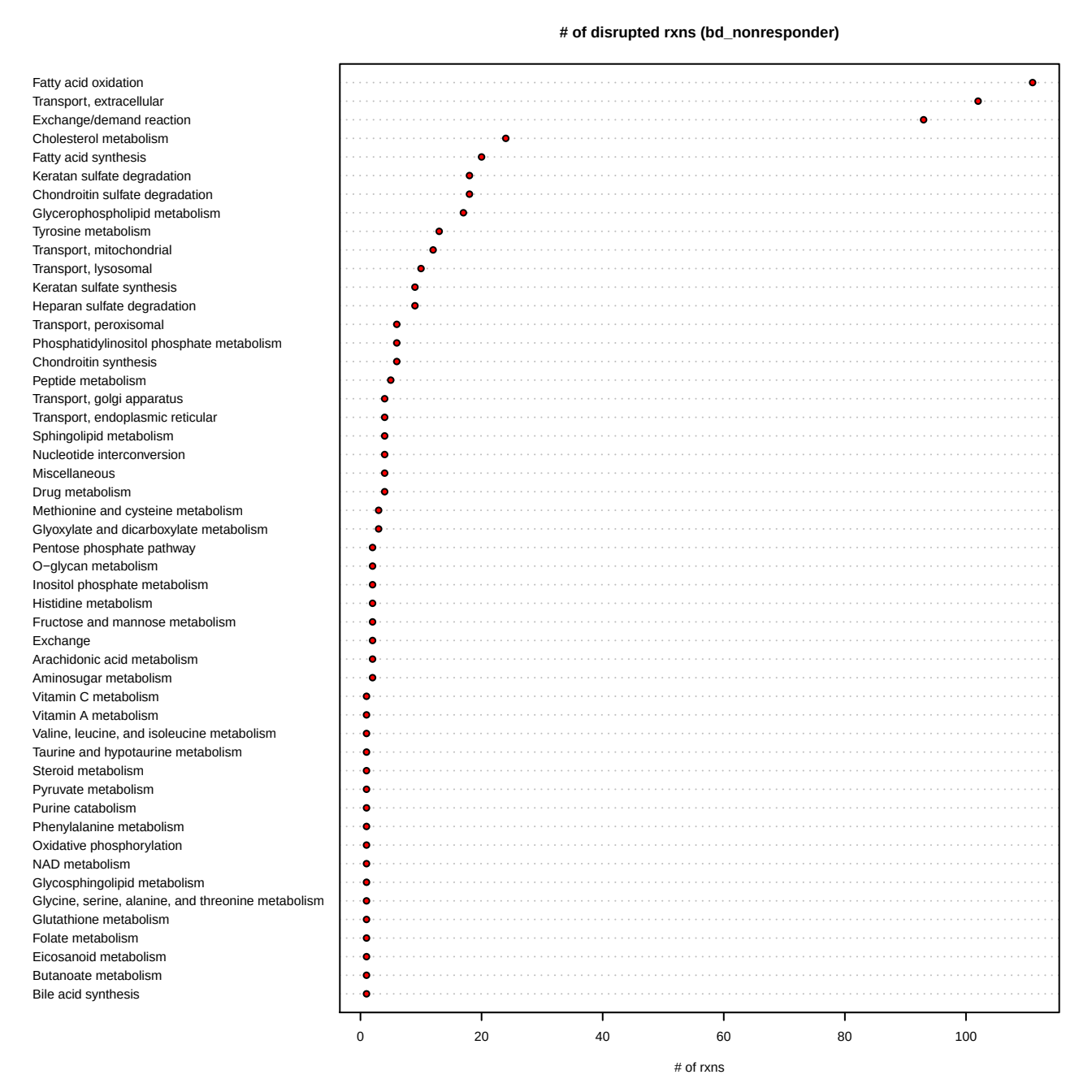

# of mta hits (bd_lumped) vs all rxns
Transport, extracellular
Exchange/demand reaction
Fatty acid oxidation
Transport, mitochondrial
Fatty acid synthesis
Keratan sulfate degradation
Peptide metabolism
Chondroitin sulfate degradation
Glycerophospholipid metabolism
Chondroitin synthesis
Tyrosine metabolism
Transport, peroxisomal
Heparan sulfate degradation
Transport, lysosomal
Nucleotide interconversion
Transport, endoplasmic reticular
Sink
Keratan sulfate synthesis
Drug metabolism
Starch and sucrose metabolism
Fructose and mannose metabolism
Valine, leucine, and isoleucine metabolism
Urea cycle
Transport, nuclear
Sphingolipid metabolism
Purine catabolism
Miscellaneous
Propanoate metabolism
Phenylalanine metabolism
Pentose phosphate pathway
Inositol phosphate metabolism
Vitamin A metabolism
Glycolysis/gluconeogenesis
Blood group synthesis
Bile acid synthesis
Arginine and proline metabolism
Transport, golgi apparatus
Steroid metabolism
ROS detoxification
Lysine metabolism
Glycine, serine, alanine, and threonine metabolism
Glutamate metabolism
CoA synthesis
Cholesterol metabolism
Vitamin C metabolism
Tryptophan metabolism
Triacylglycerol synthesis
Tetrahydrobiopterin metabolism
Pyrimidine catabolism
Oxidative phosphorylation
O−glycan metabolism
Methionine and cysteine metabolism
Histidine metabolism
Galactose metabolism
Citric acid cycle
Alanine and aspartate metabolism
Thiamine metabolism
Pyruvate metabolism
Pyrimidine synthesis
Phosphatidylinositol phosphate metabolism
Nucleotide salvage pathway
Linoleate metabolism
Heme synthesis
Glutathione metabolism
Folate metabolism
Exchange
Eicosanoid metabolism
CoA catabolism
Arachidonic acid metabolism
Androgen and estrogen synthesis and metabolism
0
200
400
600
800
1000
1200
1400
# of rxns

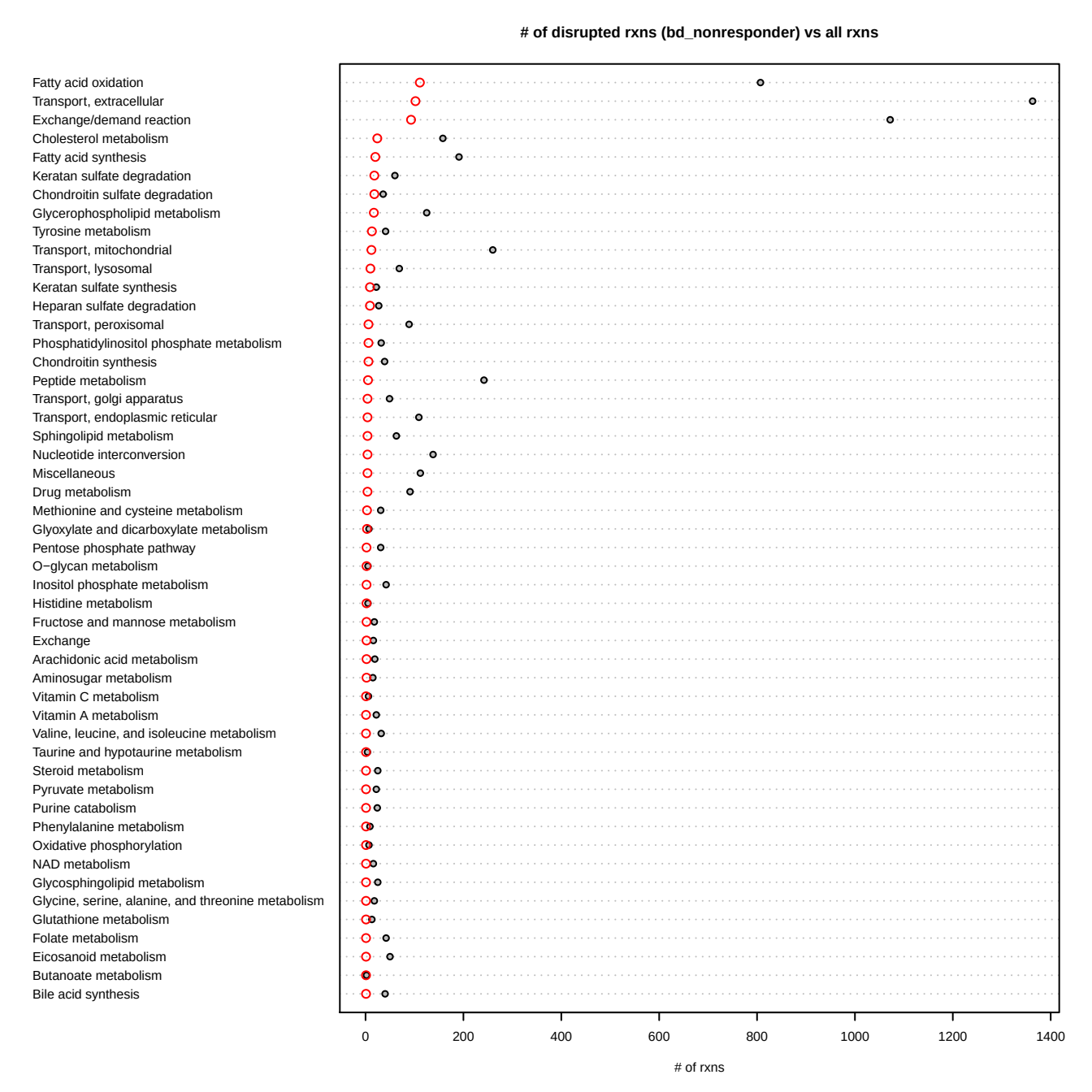

over−representation analysis, bd_lumped
subSystem_BC
Keratan sulfate degradation
Chondroitin sulfate degradation
Fatty acid oxidation
Chondroitin synthesis
Tyrosine metabolism
Sink
Heparan sulfate degradation
Fructose and mannose metabolism
Keratan sulfate synthesis
Propanoate metabolism
ROS detoxification
Phenylalanine metabolism
Starch and sucrose metabolism
Triacylglycerol synthesis
Transport, extracellular
Urea cycle
Purine catabolism
CoA synthesis
O−glycan metabolism
Alanine and aspartate metabolism
CoA catabolism
Blood group synthesis
Tetrahydrobiopterin metabolism
Oxidative phosphorylation
Vitamin C metabolism
Exchange/demand reaction
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Arginine and proline metabolism
Glutamate metabolism
Histidine metabolism
Thiamine metabolism
Nucleotide salvage pathway
Pentose phosphate pathway
Vitamin A metabolism
Galactose metabolism
Lysine metabolism
Glycolysis/gluconeogenesis
Glycine, serine, alanine, and threonine metabolism
Fatty acid synthesis
Peptide metabolism
Glycerophospholipid metabolism
Transport, peroxisomal
Transport, lysosomal
Nucleotide interconversion
Transport, endoplasmic reticular
Drug metabolism
Transport, nuclear
Sphingolipid metabolism
Miscellaneous
Inositol phosphate metabolism
Bile acid synthesis
Transport, golgi apparatus
Steroid metabolism
Cholesterol metabolism
Tryptophan metabolism
Pyrimidine catabolism
Methionine and cysteine metabolism
Citric acid cycle
Pyruvate metabolism
Pyrimidine synthesis
Phosphatidylinositol phosphate metabolism
Linoleate metabolism
Heme synthesis
Glutathione metabolism
Folate metabolism
Exchange
Eicosanoid metabolism
Arachidonic acid metabolism
Androgen and estrogen synthesis and metabolism
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

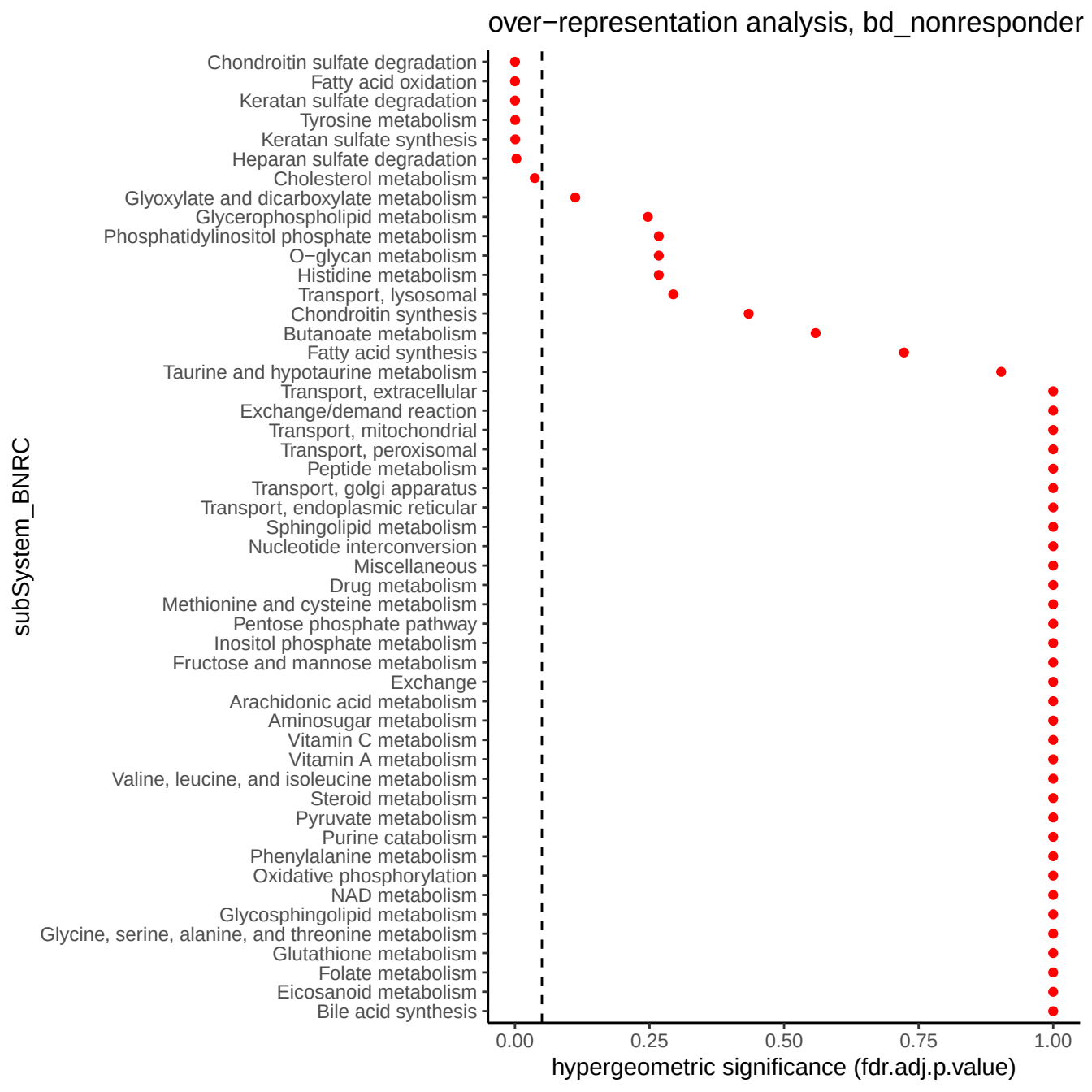

# of mta hits (bd_responder)
Transport, extracellular
Exchange/demand reaction
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Peptide metabolism
Transport, mitochondrial
Nucleotide interconversion
Transport, nuclear
Starch and sucrose metabolism
Fructose and mannose metabolism
Urea cycle
Transport, peroxisomal
Miscellaneous
Drug metabolism
ROS detoxification
Purine catabolism
Glycine, serine, alanine, and threonine metabolism
Bile acid synthesis
Arginine and proline metabolism
Pyruvate metabolism
Purine synthesis
Propanoate metabolism
Lysine metabolism
Glycerophospholipid metabolism
Vitamin B2 metabolism
Vitamin A metabolism
Tyrosine metabolism
Taurine and hypotaurine metabolism
Sink
Pyrimidine synthesis
Phenylalanine metabolism
Nucleotide salvage pathway
Methionine and cysteine metabolism
Heme synthesis
Folate metabolism
Exchange
Eicosanoid metabolism
Citric acid cycle
Butanoate metabolism
Beta−Alanine metabolism
0
20
40
60
80
100
# of rxns


# of mta hits (bd_responder) vs all rxns
Transport, extracellular
Exchange/demand reaction
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Peptide metabolism
Transport, mitochondrial
Nucleotide interconversion
Transport, nuclear
Starch and sucrose metabolism
Fructose and mannose metabolism
Urea cycle
Transport, peroxisomal
Miscellaneous
Drug metabolism
ROS detoxification
Purine catabolism
Glycine, serine, alanine, and threonine metabolism
Bile acid synthesis
Arginine and proline metabolism
Pyruvate metabolism
Purine synthesis
Propanoate metabolism
Lysine metabolism
Glycerophospholipid metabolism
Vitamin B2 metabolism
Vitamin A metabolism
Tyrosine metabolism
Taurine and hypotaurine metabolism
Sink
Pyrimidine synthesis
Phenylalanine metabolism
Nucleotide salvage pathway
Methionine and cysteine metabolism
Heme synthesis
Folate metabolism
Exchange
Eicosanoid metabolism
Citric acid cycle
Butanoate metabolism
Beta−Alanine metabolism
0
200
400
600
800
1000
1200
1400
# of rxns

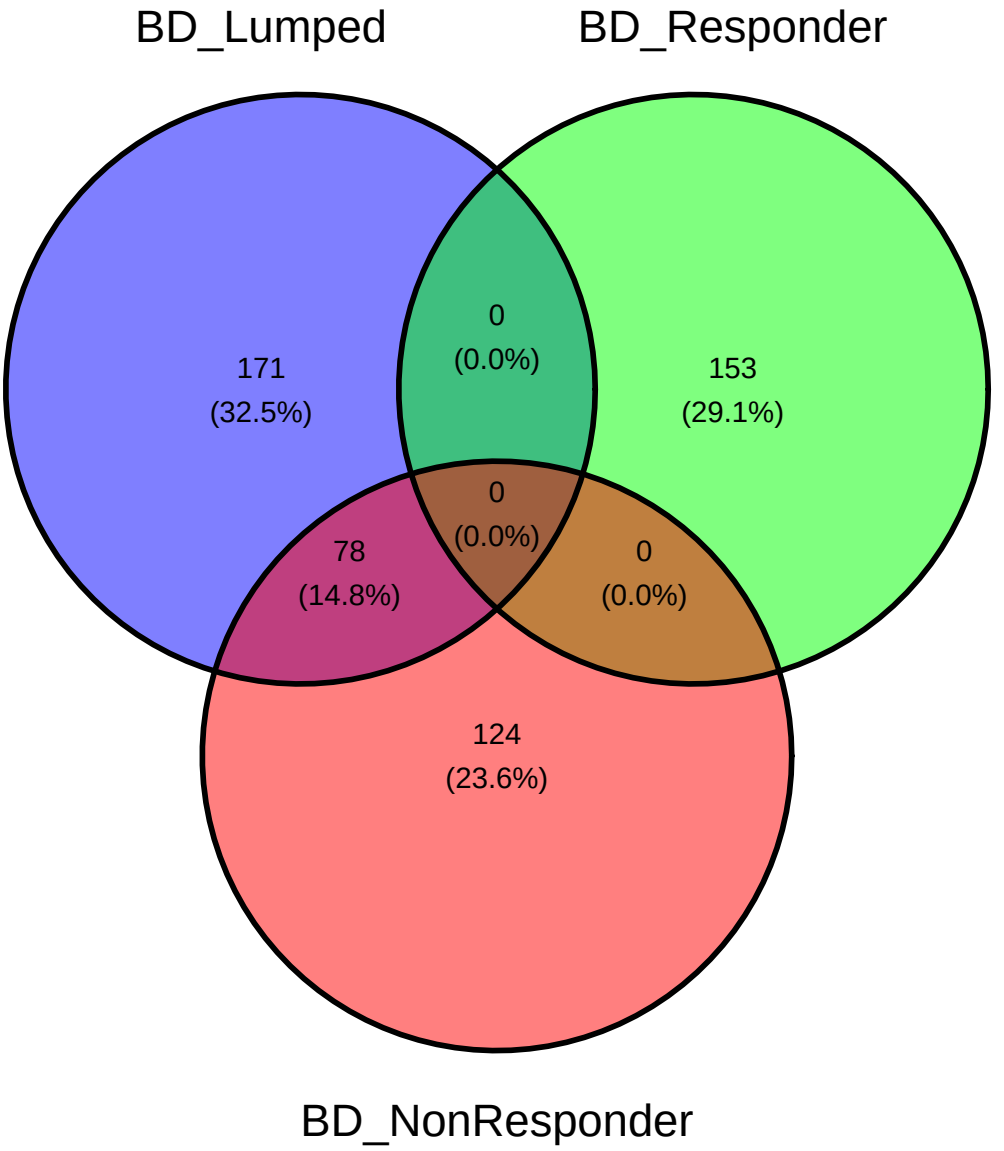

over−representation analysis, bd_responder
subSystem_BRC
Transport, extracellular
Cholesterol metabolism
Starch and sucrose metabolism
ROS detoxification
Fructose and mannose metabolism
Fatty acid synthesis
Urea cycle
Glycine, serine, alanine, and threonine metabolism
Peptide metabolism
Transport, nuclear
Purine catabolism
Arginine and proline metabolism
Purine synthesis
Propanoate metabolism
Butanoate metabolism
Nucleotide salvage pathway
Taurine and hypotaurine metabolism
Lysine metabolism
Vitamin B2 metabolism
Beta−Alanine metabolism
Pyruvate metabolism
Heme synthesis
Bile acid synthesis
Pyrimidine synthesis
Phenylalanine metabolism
Exchange/demand reaction
Nucleotide interconversion
Transport, peroxisomal
Drug metabolism
Vitamin A metabolism
Sink
Exchange
Citric acid cycle
Transport, mitochondrial
Methionine and cysteine metabolism
Miscellaneous
Tyrosine metabolism
Folate metabolism
Fatty acid oxidation
Glycerophospholipid metabolism
Eicosanoid metabolism
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)


# of disrupted rxns (bd_nonresponder)
Fatty acid oxidation
Transport, extracellular
Exchange/demand reaction
Cholesterol metabolism
Fatty acid synthesis
Keratan sulfate degradation
Chondroitin sulfate degradation
Glycerophospholipid metabolism
Tyrosine metabolism
Transport, mitochondrial
Transport, lysosomal
Keratan sulfate synthesis
Heparan sulfate degradation
Transport, peroxisomal
Phosphatidylinositol phosphate metabolism
Chondroitin synthesis
Peptide metabolism
Transport, golgi apparatus
Transport, endoplasmic reticular
Sphingolipid metabolism
Nucleotide interconversion
Miscellaneous
Drug metabolism
Methionine and cysteine metabolism
Glyoxylate and dicarboxylate metabolism
Pentose phosphate pathway
O−glycan metabolism
Inositol phosphate metabolism
Histidine metabolism
Fructose and mannose metabolism
Exchange
Arachidonic acid metabolism
Aminosugar metabolism
Vitamin C metabolism
Vitamin A metabolism
Valine, leucine, and isoleucine metabolism
Taurine and hypotaurine metabolism
Steroid metabolism
Pyruvate metabolism
Purine catabolism
Phenylalanine metabolism
Oxidative phosphorylation
NAD metabolism
Glycosphingolipid metabolism
Glycine, serine, alanine, and threonine metabolism
Glutathione metabolism
Folate metabolism
Eicosanoid metabolism
Butanoate metabolism
Bile acid synthesis
0
20
40
60
80
100
# of rxns


# of disrupted rxns (bd_nonresponder) vs all rxns
Fatty acid oxidation
Transport, extracellular
Exchange/demand reaction
Cholesterol metabolism
Fatty acid synthesis
Keratan sulfate degradation
Chondroitin sulfate degradation
Glycerophospholipid metabolism
Tyrosine metabolism
Transport, mitochondrial
Transport, lysosomal
Keratan sulfate synthesis
Heparan sulfate degradation
Transport, peroxisomal
Phosphatidylinositol phosphate metabolism
Chondroitin synthesis
Peptide metabolism
Transport, golgi apparatus
Transport, endoplasmic reticular
Sphingolipid metabolism
Nucleotide interconversion
Miscellaneous
Drug metabolism
Methionine and cysteine metabolism
Glyoxylate and dicarboxylate metabolism
Pentose phosphate pathway
O−glycan metabolism
Inositol phosphate metabolism
Histidine metabolism
Fructose and mannose metabolism
Exchange
Arachidonic acid metabolism
Aminosugar metabolism
Vitamin C metabolism
Vitamin A metabolism
Valine, leucine, and isoleucine metabolism
Taurine and hypotaurine metabolism
Steroid metabolism
Pyruvate metabolism
Purine catabolism
Phenylalanine metabolism
Oxidative phosphorylation
NAD metabolism
Glycosphingolipid metabolism
Glycine, serine, alanine, and threonine metabolism
Glutathione metabolism
Folate metabolism
Eicosanoid metabolism
Butanoate metabolism
Bile acid synthesis
0
200
400
600
800
1000
1200
1400
# of rxns


over−representation analysis, bd_nonresponder
subSystem_BNRC
Chondroitin sulfate degradation
Fatty acid oxidation
Keratan sulfate degradation
Tyrosine metabolism
Keratan sulfate synthesis
Heparan sulfate degradation
Cholesterol metabolism
Glyoxylate and dicarboxylate metabolism
Glycerophospholipid metabolism
Phosphatidylinositol phosphate metabolism
O−glycan metabolism
Histidine metabolism
Transport, lysosomal
Chondroitin synthesis
Butanoate metabolism
Fatty acid synthesis
Taurine and hypotaurine metabolism
Transport, extracellular
Exchange/demand reaction
Transport, mitochondrial
Transport, peroxisomal
Peptide metabolism
Transport, golgi apparatus
Transport, endoplasmic reticular
Sphingolipid metabolism
Nucleotide interconversion
Miscellaneous
Drug metabolism
Methionine and cysteine metabolism
Pentose phosphate pathway
Inositol phosphate metabolism
Fructose and mannose metabolism
Exchange
Arachidonic acid metabolism
Aminosugar metabolism
Vitamin C metabolism
Vitamin A metabolism
Valine, leucine, and isoleucine metabolism
Steroid metabolism
Pyruvate metabolism
Purine catabolism
Phenylalanine metabolism
Oxidative phosphorylation
NAD metabolism
Glycosphingolipid metabolism
Glycine, serine, alanine, and threonine metabolism
Glutathione metabolism
Folate metabolism
Eicosanoid metabolism
Bile acid synthesis
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