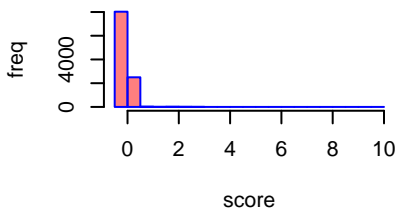
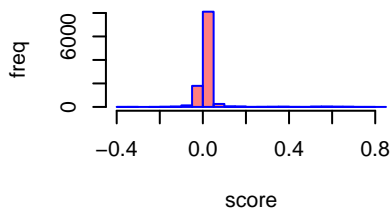
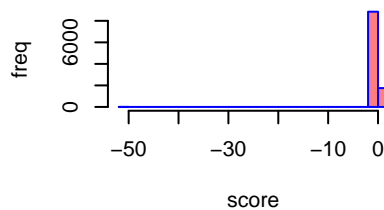
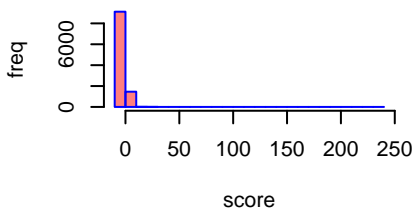
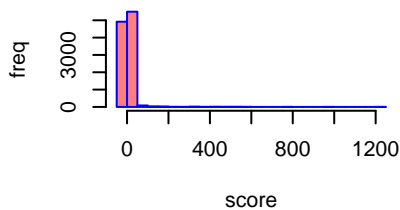
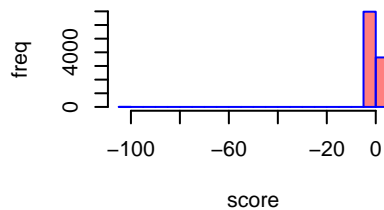
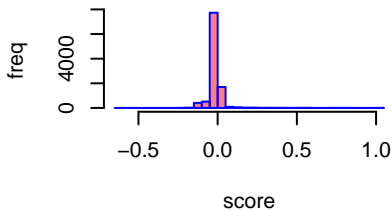
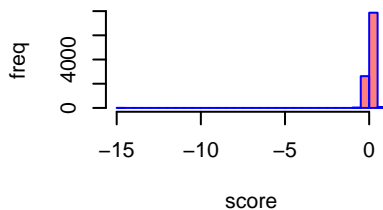
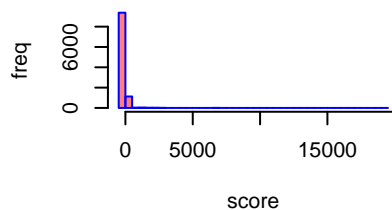
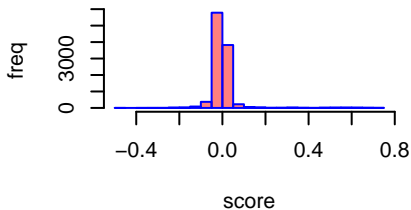
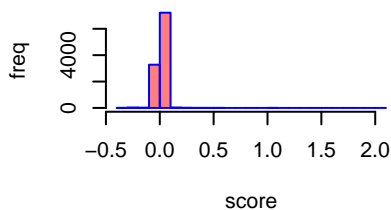
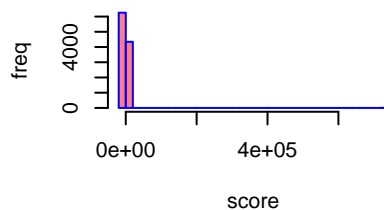
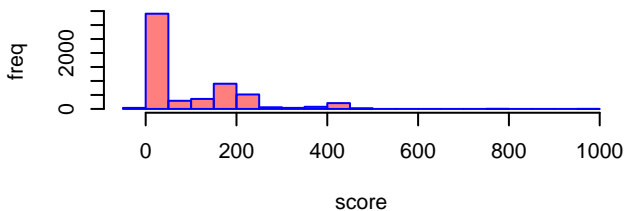
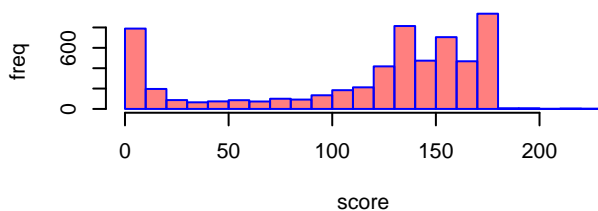
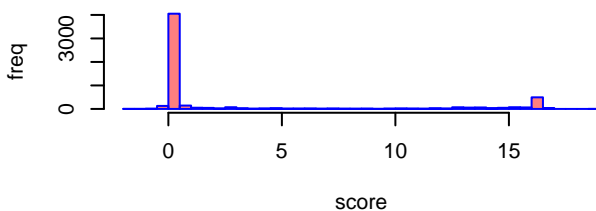
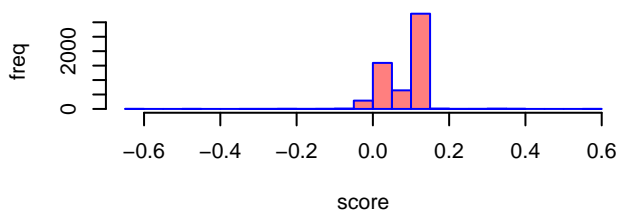
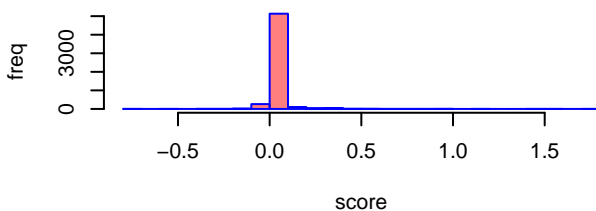
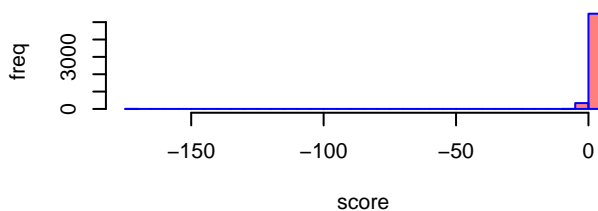
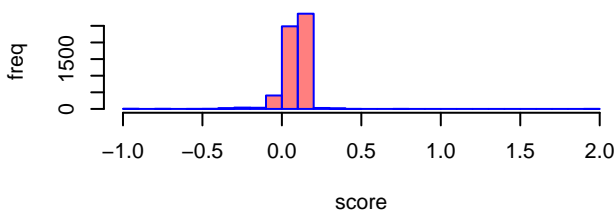
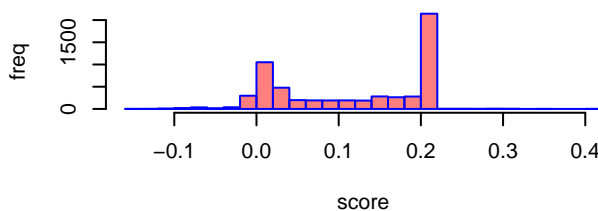
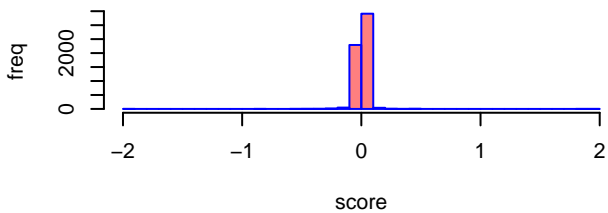


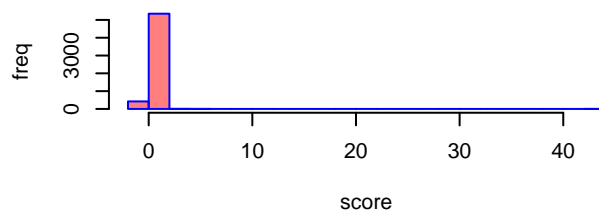
**NHBE****Calu-3****A549****Vero****293T****Caco-2****Swab.Butler****Swab.Lieberman****BALF****SC.Liao****SC.Chua.Basal****SC.Chua.Ciliated**

**Ctrl\_to\_Primary****Primary\_to\_Ctrl****Ctrl\_to\_BD****BD\_to\_Ctrl****Ctrl\_to\_BD\_R****BD\_R\_to\_Ctrl****Ctrl\_to\_BD\_NR****BD\_NR\_to\_Ctrl**

R\_to\_NR



NR\_to\_R



Intersection Size

2000  
1500  
1000  
500  
0

68

100

123

150

172

187

191

198

278

315

370

404

424

666

1926

BD\_NR\_top

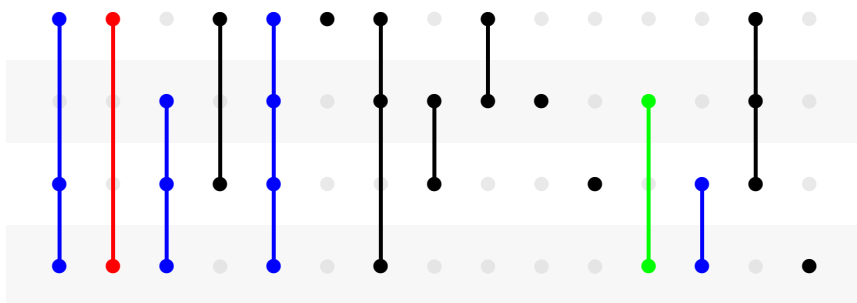
BD\_R\_top

BD\_top

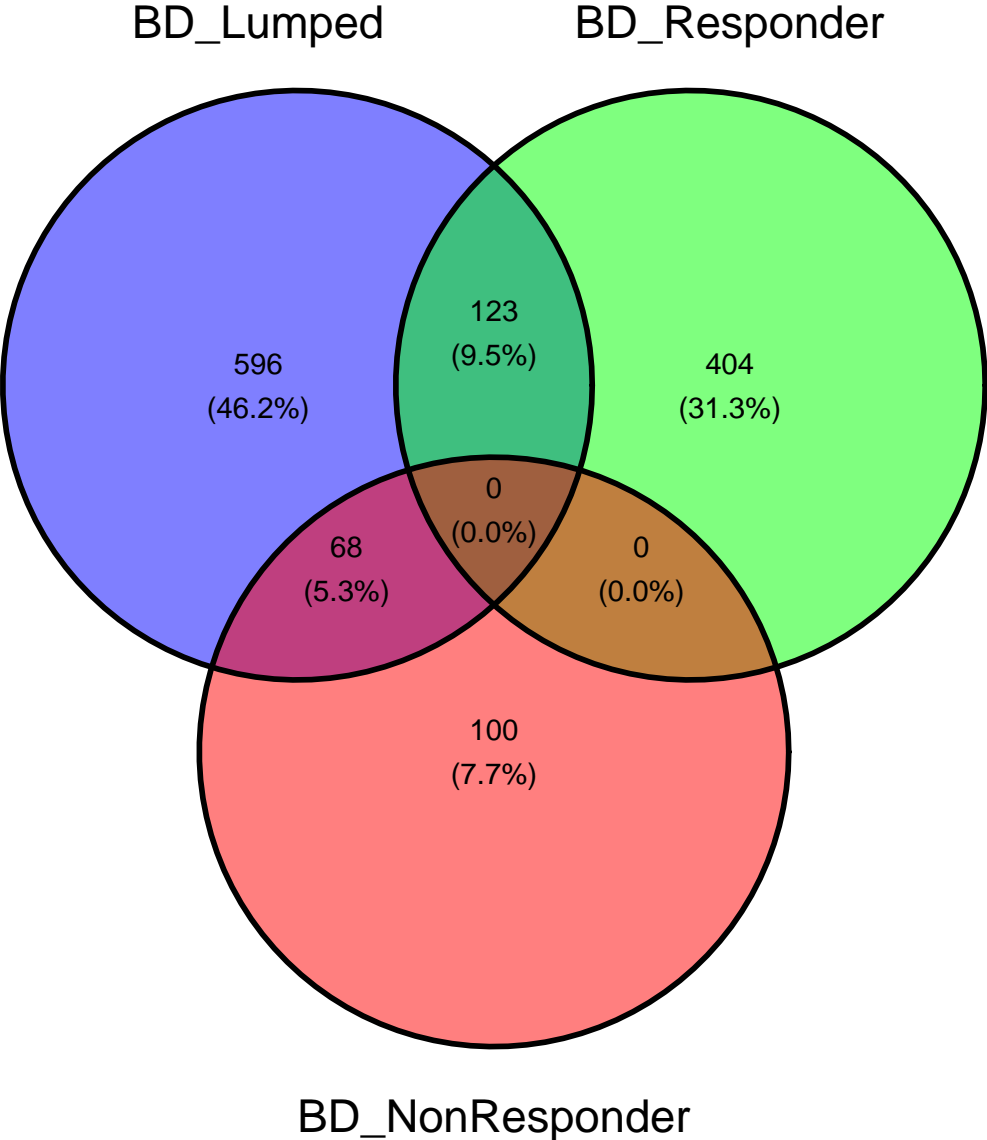
Ctrl\_unchanged

3000 2000 1000 0

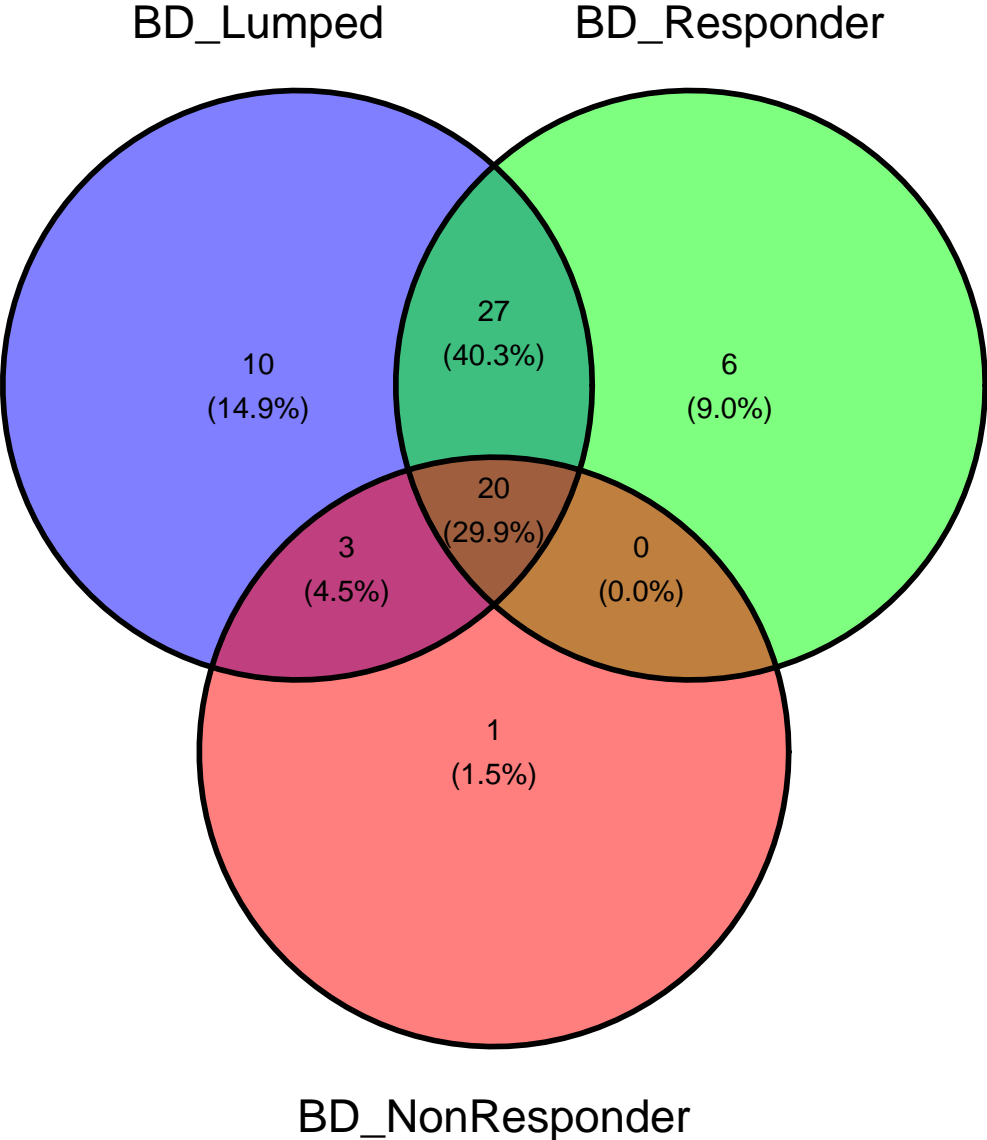
Set Size



Overlap in rxns disrupted between models



Overlap in subSystems disrupted between models

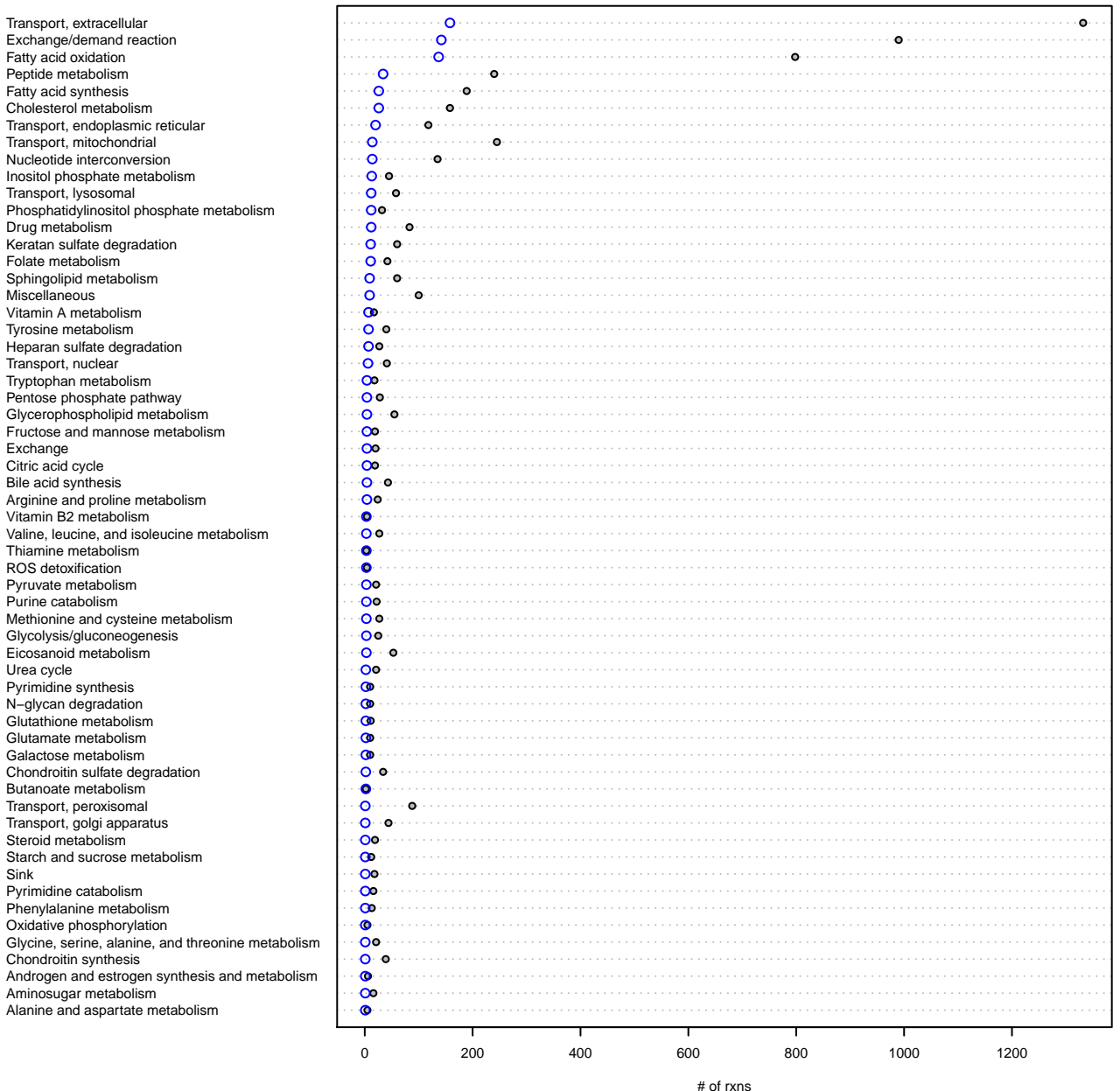


# of mta hits (bd\_lumped)

Transport, extracellular  
Exchange/demand reaction  
Fatty acid oxidation  
Peptide metabolism  
Fatty acid synthesis  
Cholesterol metabolism  
Transport, endoplasmic reticular  
Transport, mitochondrial  
Nucleotide interconversion  
Inositol phosphate metabolism  
Transport, lysosomal  
Phosphatidylinositol phosphate metabolism  
Drug metabolism  
Keratan sulfate degradation  
Folate metabolism  
Sphingolipid metabolism  
Miscellaneous  
Vitamin A metabolism  
Tyrosine metabolism  
Heparan sulfate degradation  
Transport, nuclear  
Tryptophan metabolism  
Pentose phosphate pathway  
Glycerophospholipid metabolism  
Fructose and mannose metabolism  
Exchange  
Citric acid cycle  
Bile acid synthesis  
Arginine and proline metabolism  
Vitamin B2 metabolism  
Valine, leucine, and isoleucine metabolism  
Thiamine metabolism  
ROS detoxification  
Pyruvate metabolism  
Purine catabolism  
Methionine and cysteine metabolism  
Glycolysis/gluconeogenesis  
Eicosanoid metabolism  
Urea cycle  
Pyrimidine synthesis  
N-glycan degradation  
Glutathione metabolism  
Glutamate metabolism  
Galactose metabolism  
Chondroitin sulfate degradation  
Butanoate metabolism  
Transport, peroxisomal  
Transport, golgi apparatus  
Steroid metabolism  
Starch and sucrose metabolism  
Sink  
Pyrimidine catabolism  
Phenylalanine metabolism  
Oxidative phosphorylation  
Glycine, serine, alanine, and threonine metabolism  
Chondroitin synthesis  
Androgen and estrogen synthesis and metabolism  
Aminosugar metabolism  
Alanine and aspartate metabolism



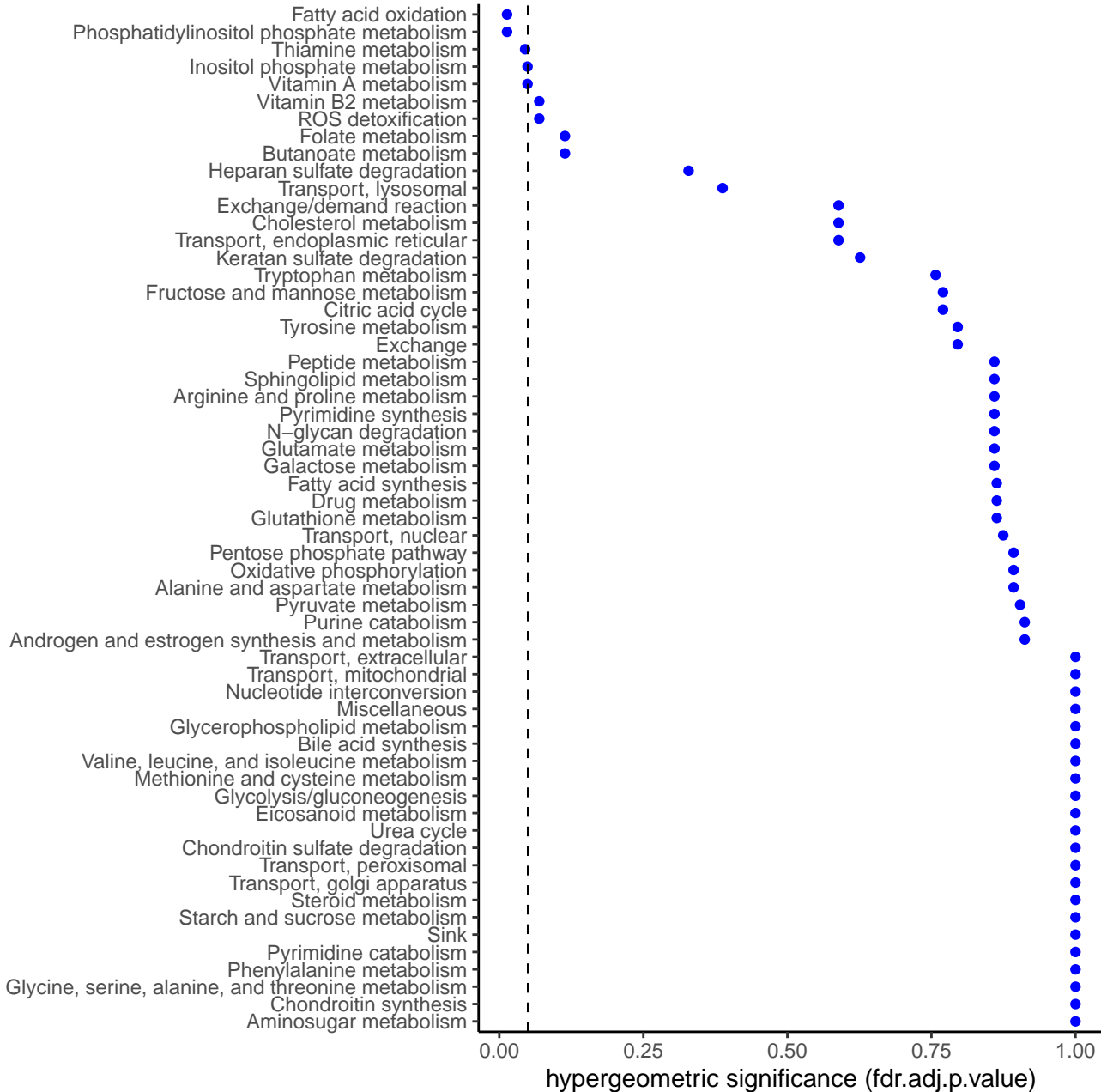
# of mta hits (bd\_lumped) vs all rxns





# over-representation analysis, bd\_lumped

subSystem\_BC



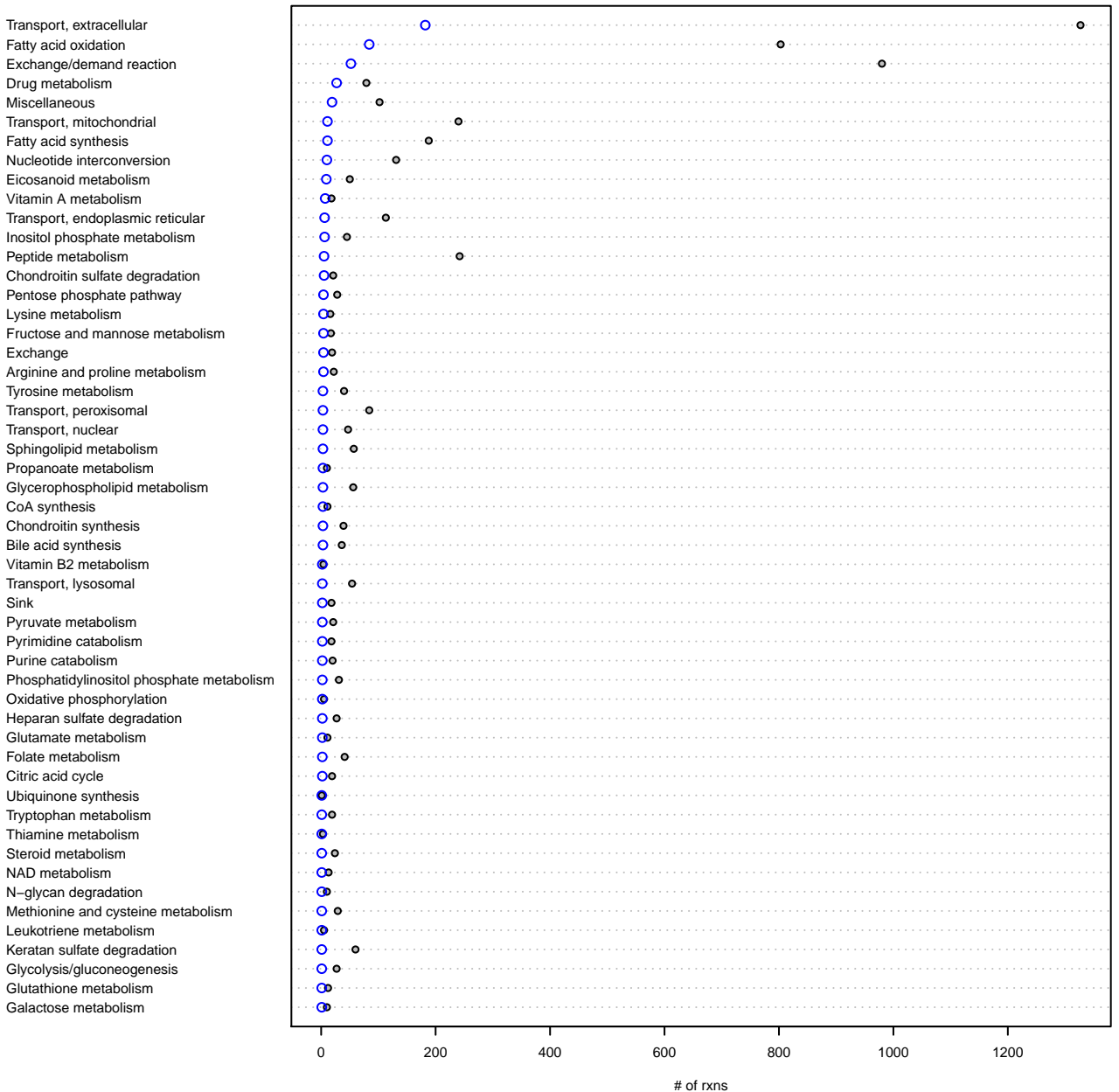
# of mta hits (bd\_responder)

Transport, extracellular  
Fatty acid oxidation  
Exchange/demand reaction  
Drug metabolism  
Miscellaneous  
Transport, mitochondrial  
Fatty acid synthesis  
Nucleotide interconversion  
Eicosanoid metabolism  
Vitamin A metabolism  
Transport, endoplasmic reticular  
Inositol phosphate metabolism  
Peptide metabolism  
Chondroitin sulfate degradation  
Pentose phosphate pathway  
Lysine metabolism  
Fructose and mannose metabolism  
Exchange  
Arginine and proline metabolism  
Tyrosine metabolism  
Transport, peroxisomal  
Transport, nuclear  
Sphingolipid metabolism  
Propanoate metabolism  
Glycerophospholipid metabolism  
CoA synthesis  
Chondroitin synthesis  
Bile acid synthesis  
Vitamin B2 metabolism  
Transport, lysosomal  
Sink  
Pyruvate metabolism  
Pyrimidine catabolism  
Purine catabolism  
Phosphatidylinositol phosphate metabolism  
Oxidative phosphorylation  
Heparan sulfate degradation  
Glutamate metabolism  
Folate metabolism  
Citric acid cycle  
Ubiquinone synthesis  
Tryptophan metabolism  
Thiamine metabolism  
Steroid metabolism  
NAD metabolism  
N-glycan degradation  
Methionine and cysteine metabolism  
Leukotriene metabolism  
Keratan sulfate degradation  
Glycolysis/gluconeogenesis  
Glutathione metabolism  
Galactose metabolism



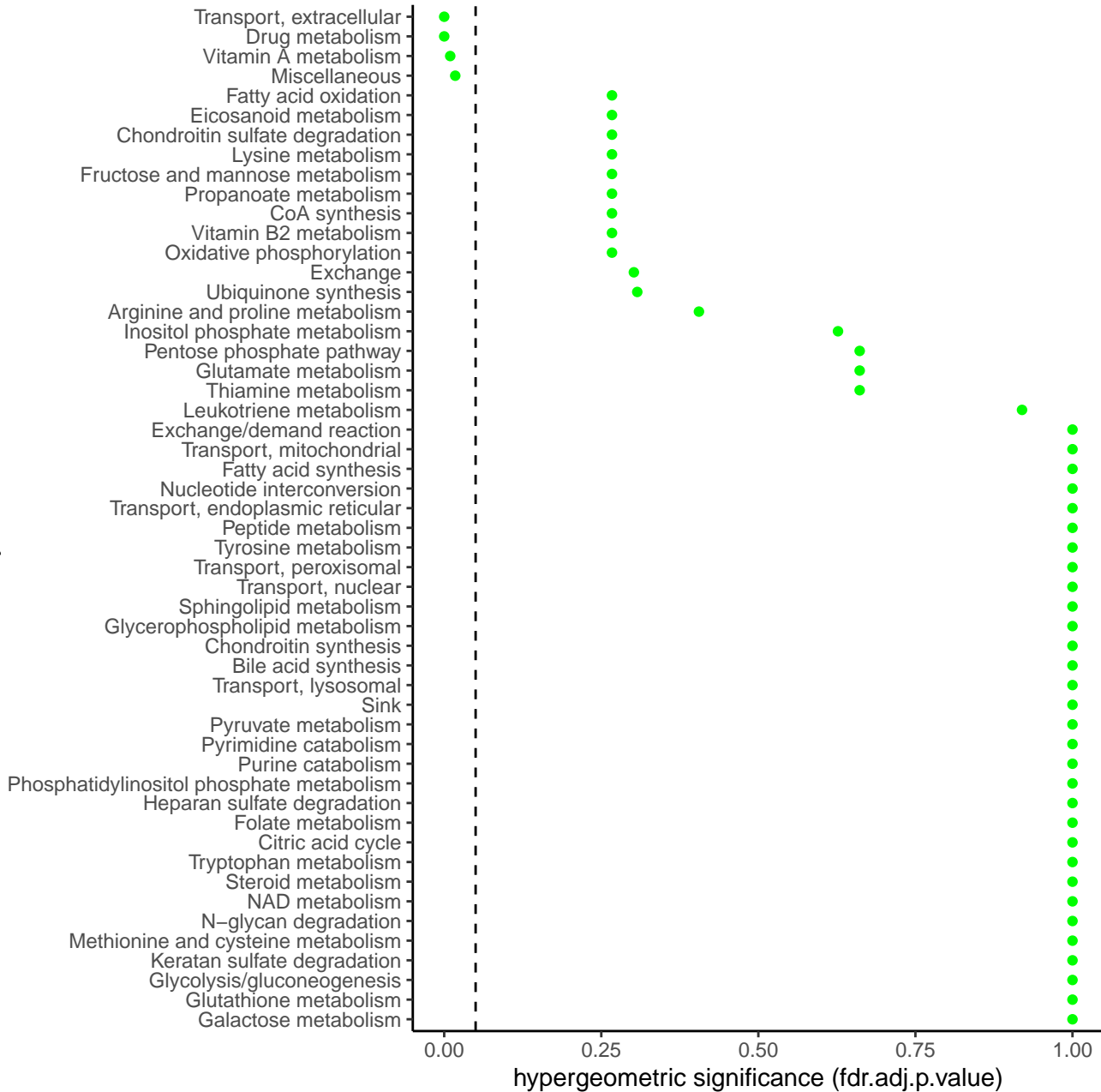
# of rxns

# of mta hits (bd\_responder) vs all rxns

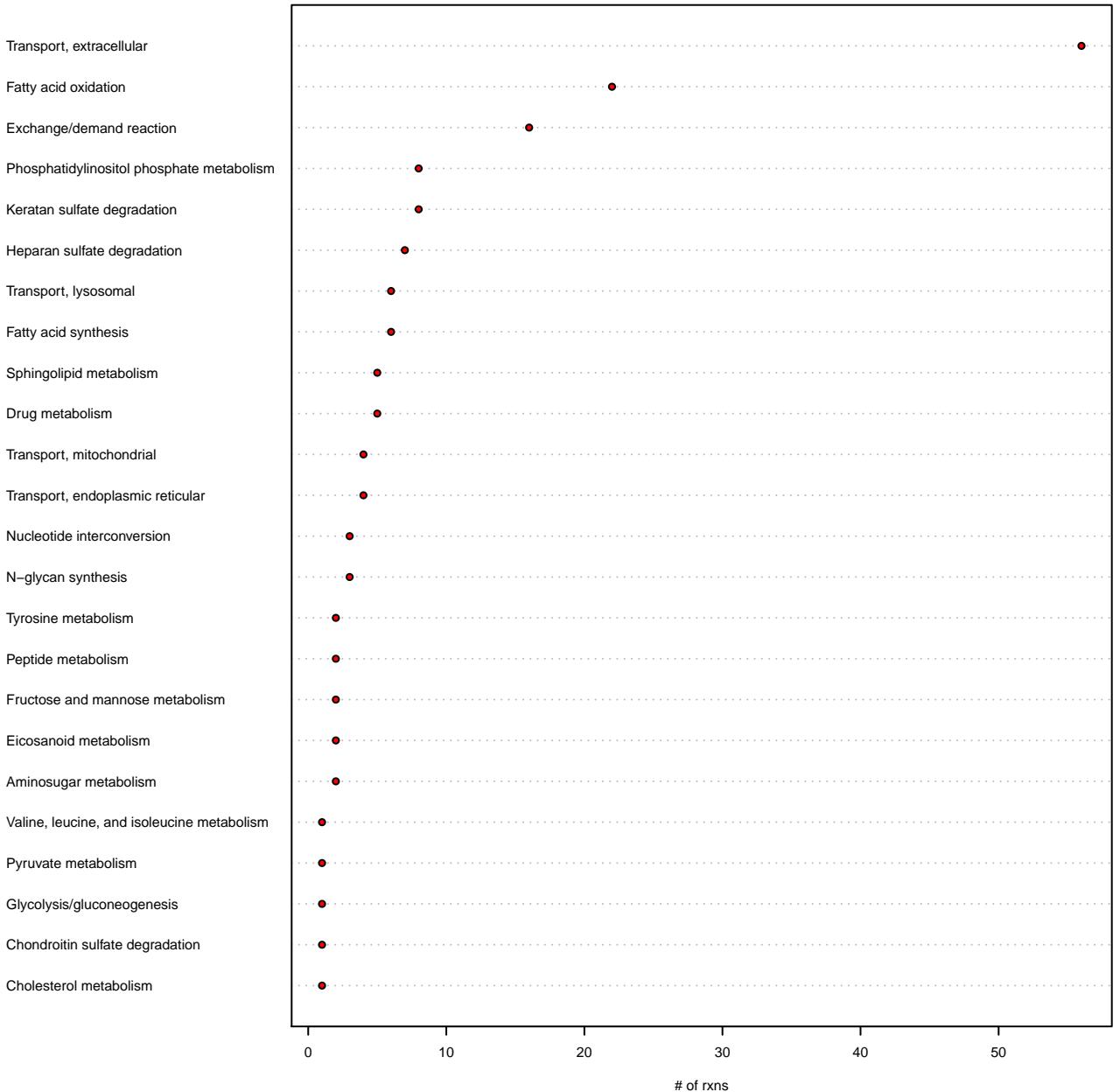


# over-representation analysis, bd\_responder

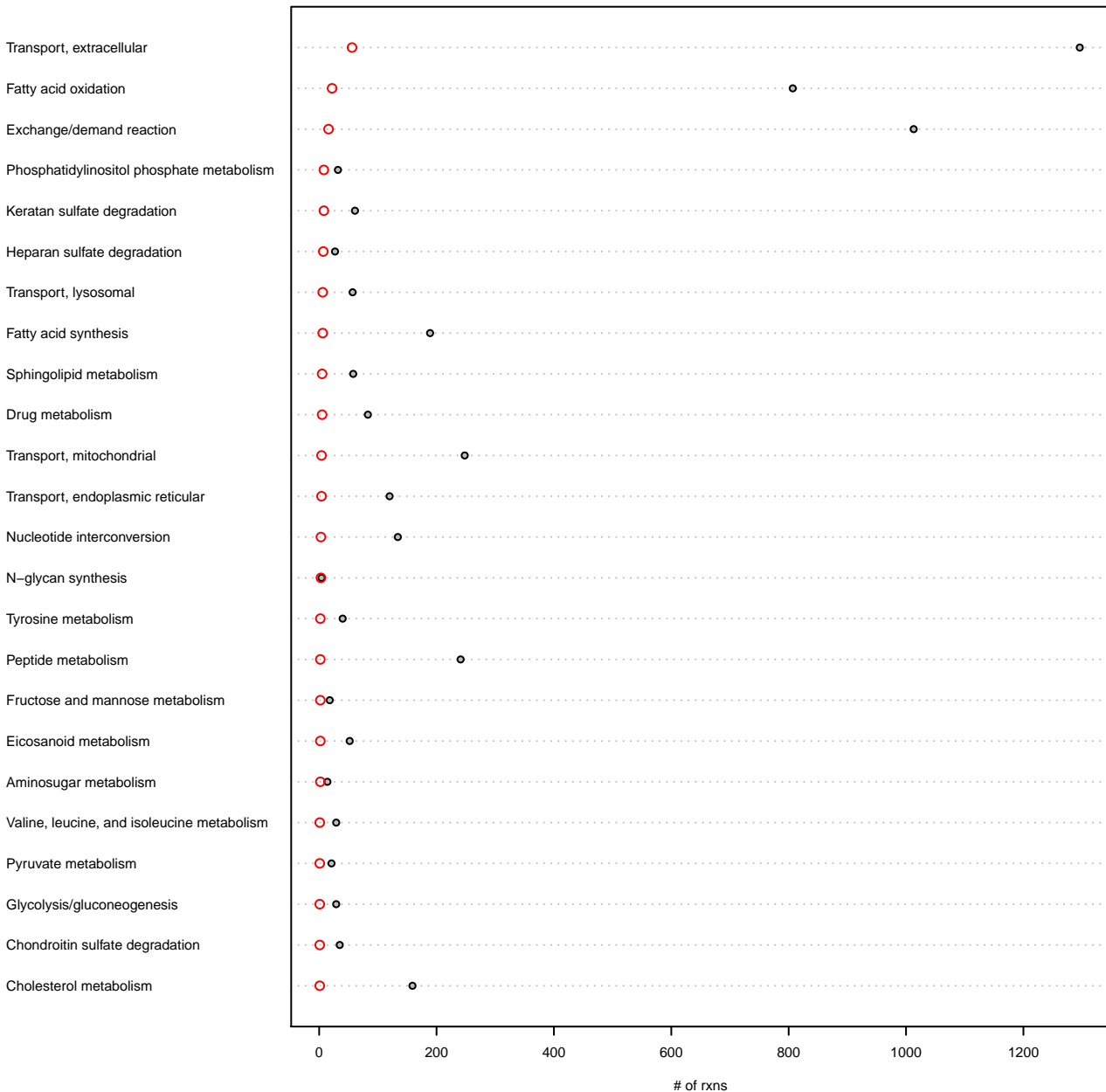
subSystem\_BRC



# of disrupted rxns (bd\_nonresponder)

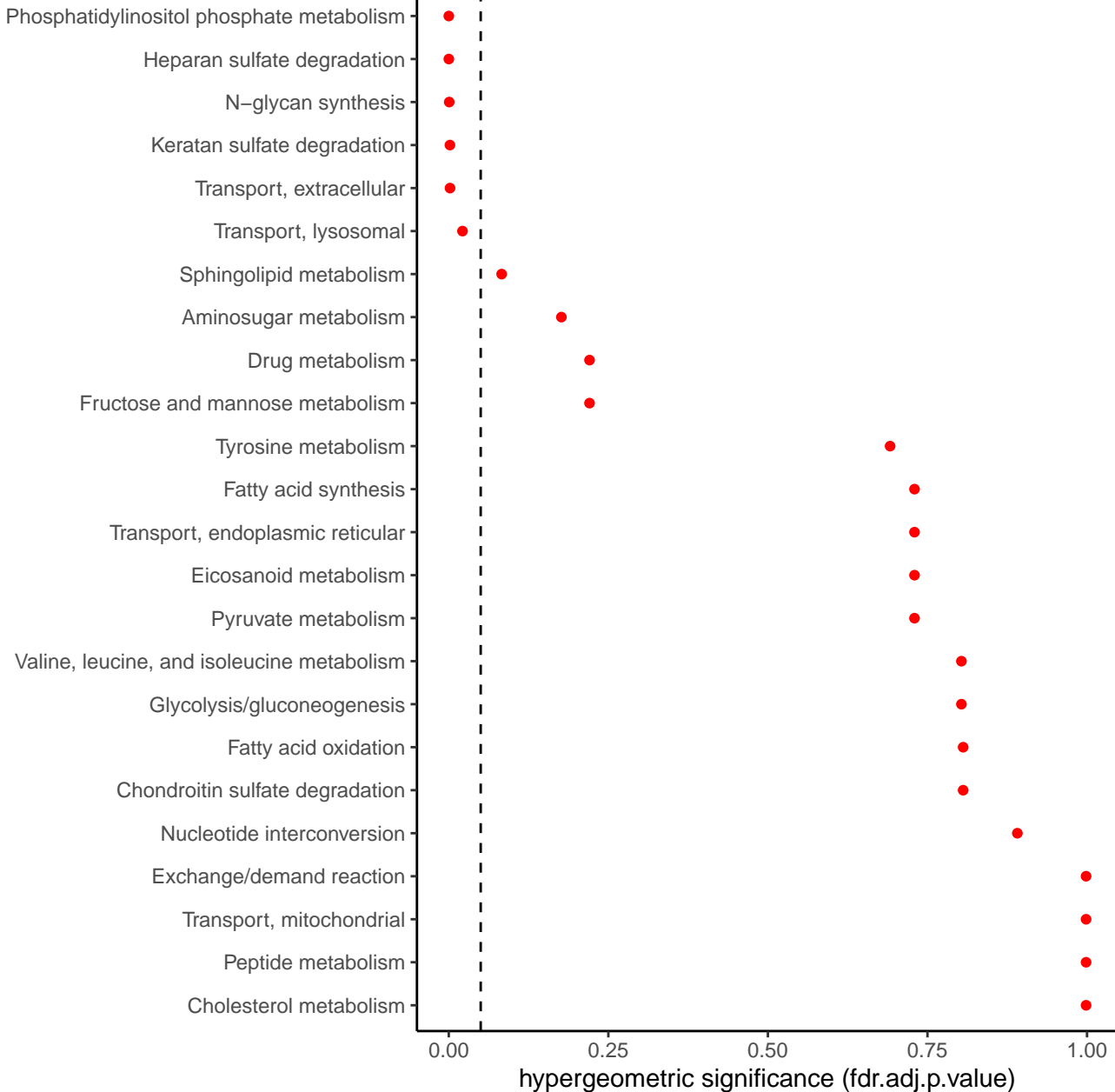


# of disrupted rxns (bd\_nonresponder) vs all rxns

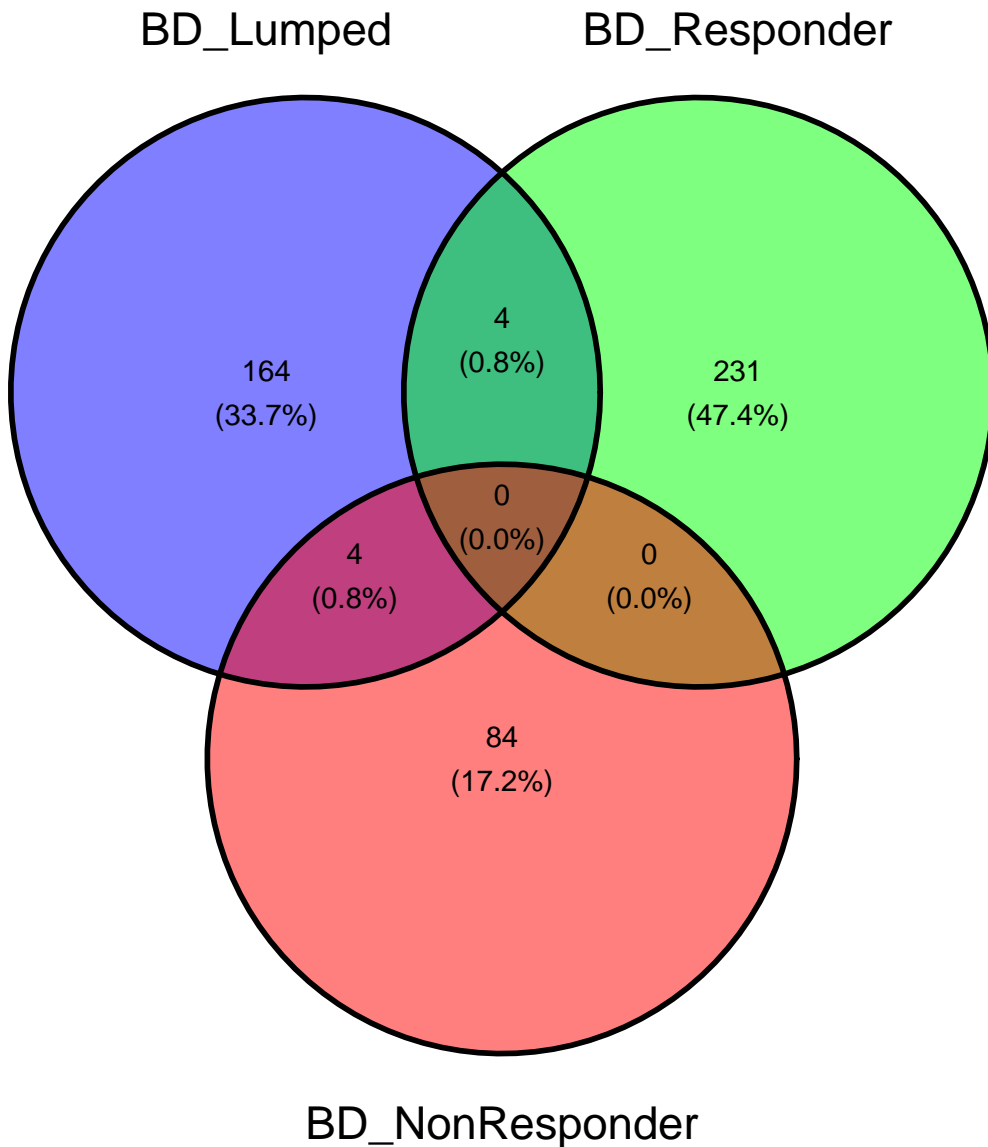


# over-representation analysis, bd\_nonresponder

subSystem\_BNRC



Overlap in rxns (fdr.significant) disrupted between models





Overlap in subSystems (fdr.significant) disrupted between models

