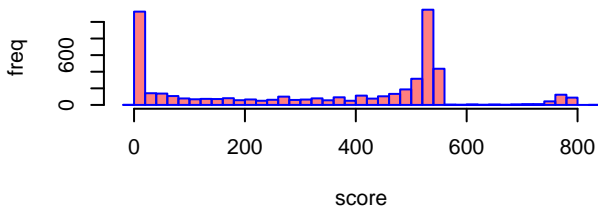
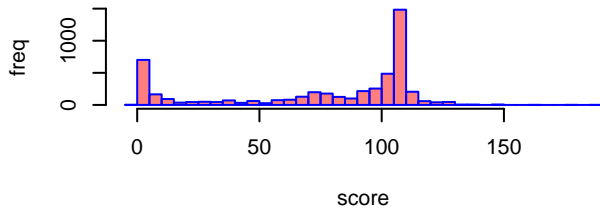


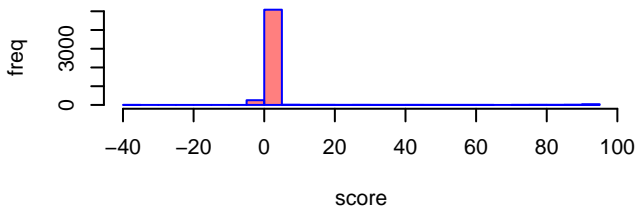
**Ctrl\_to\_Primary**



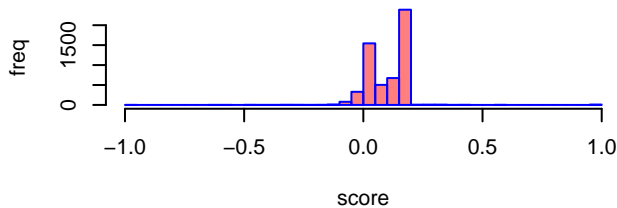
**Primary\_to\_Ctrl**



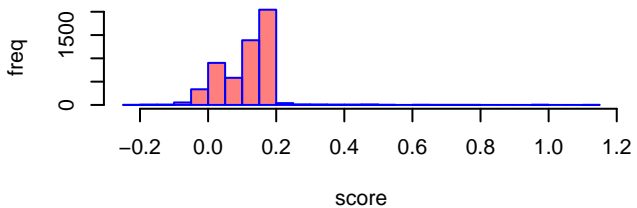
**Ctrl\_to\_BD**



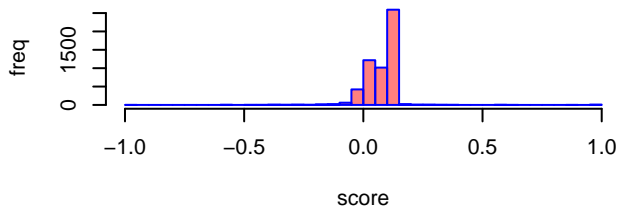
**BD\_to\_Ctrl**



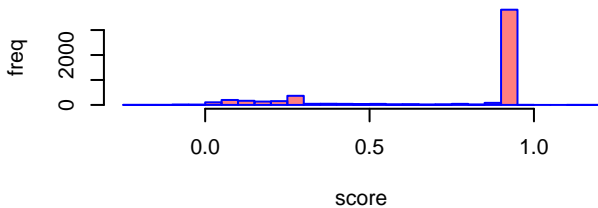
**Ctrl\_to\_BD\_R**



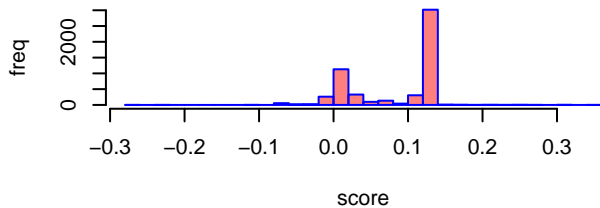
**BD\_R\_to\_Ctrl**



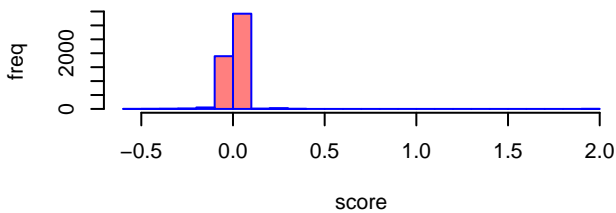
**Ctrl\_to\_BD\_NR**



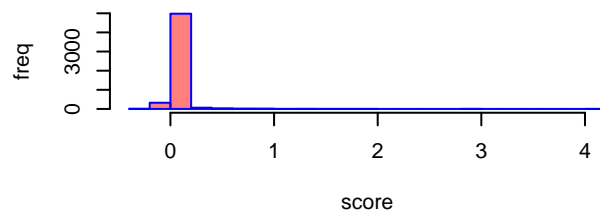
**BD\_NR\_to\_Ctrl**



**R\_to\_NR**

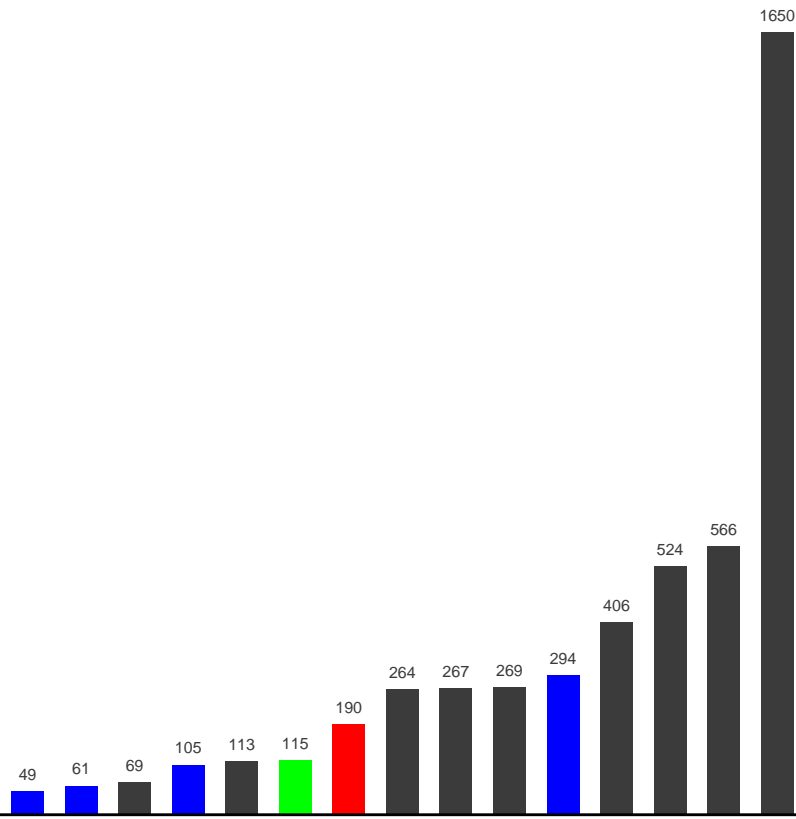


**NR\_to\_R**



Intersection Size

1500  
1000  
500  
0

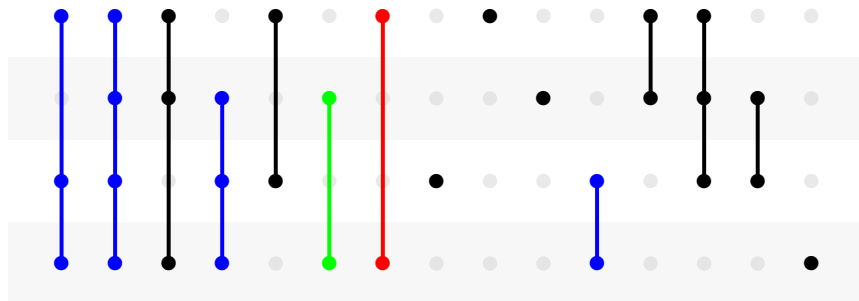


BD\_NR\_top

BD\_R\_top

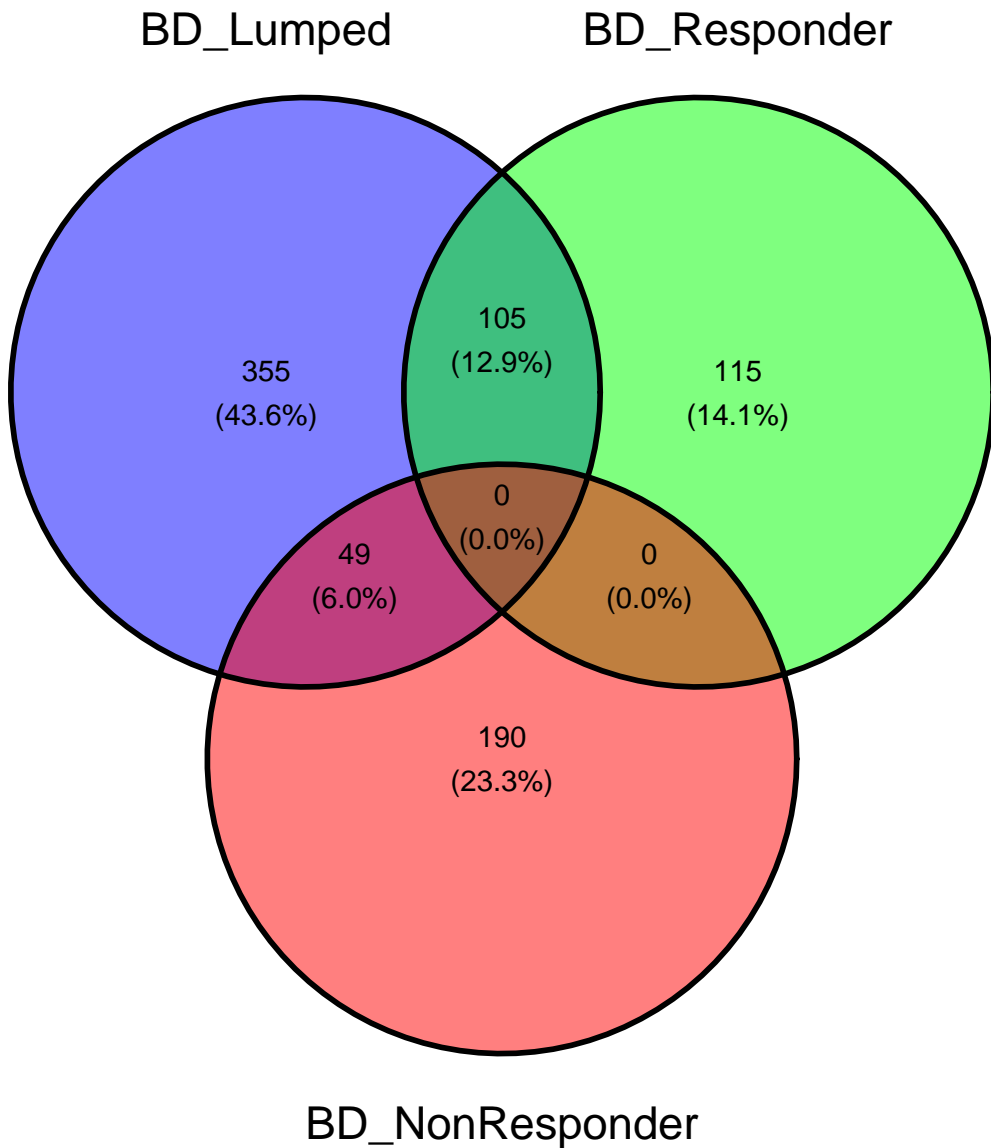
BD\_top

Ctrl\_unchanged

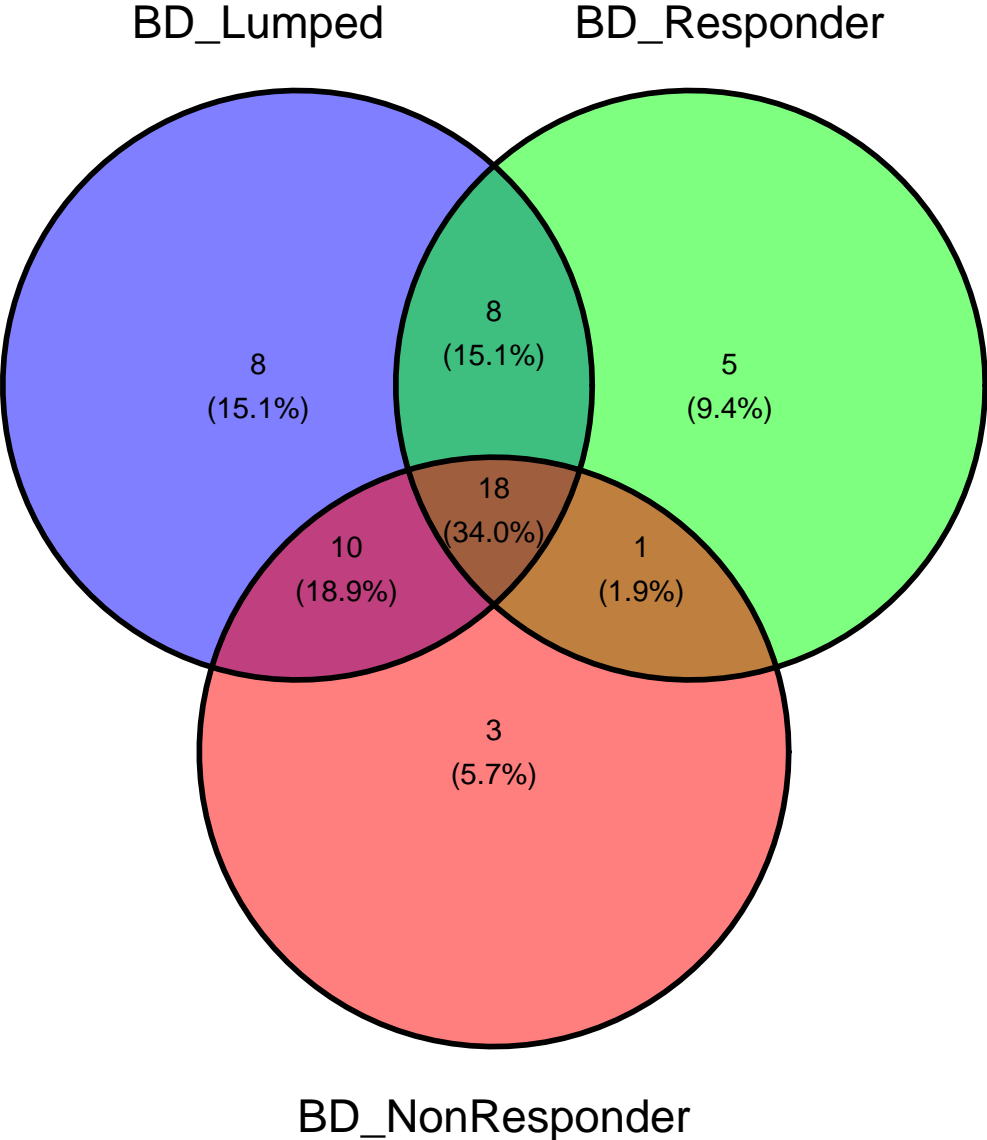


2500 2000 1500 1000 500 0  
Set Size

# Overlap in rxns disrupted between models



Overlap in subSystems disrupted between models

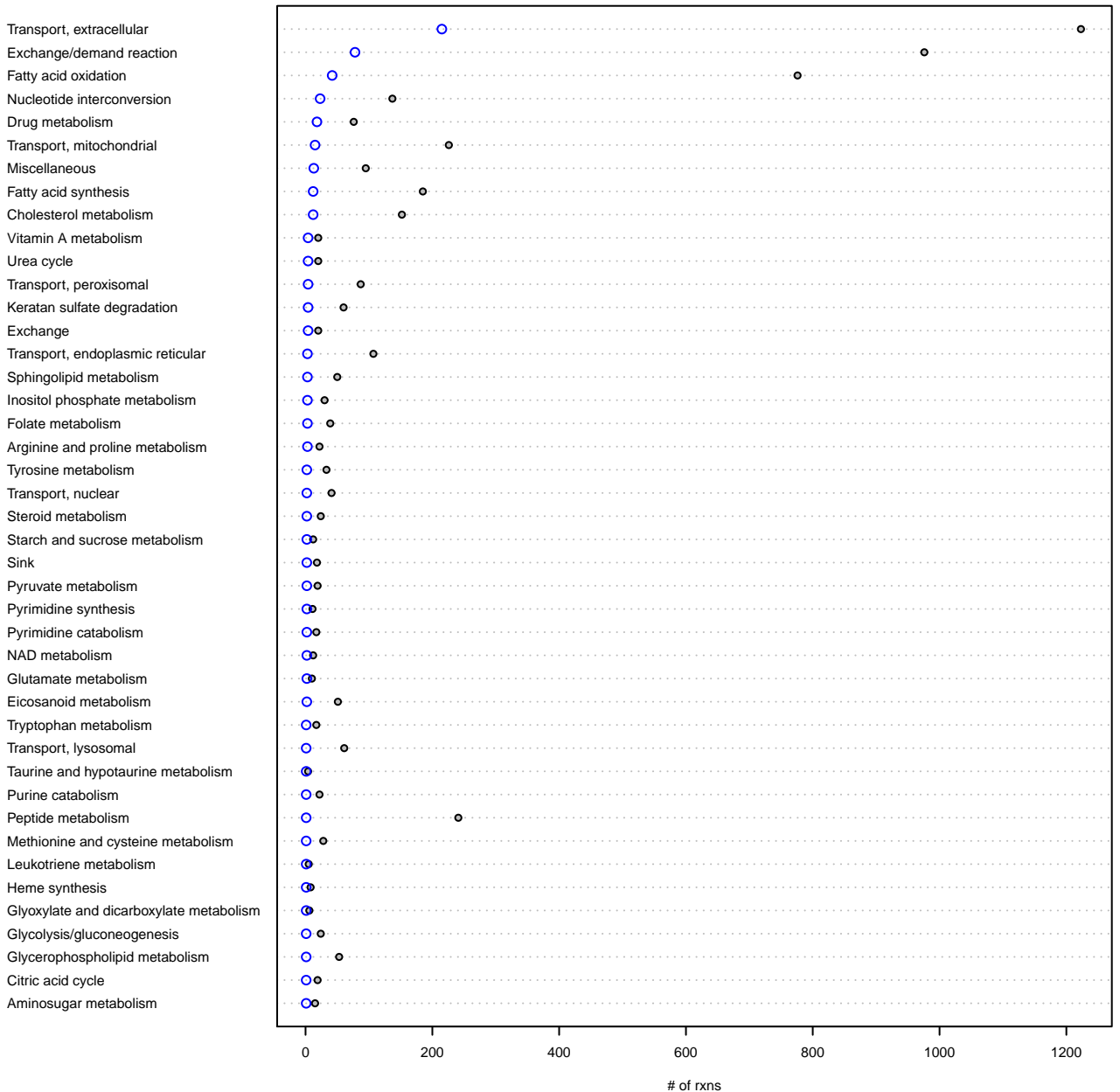


# of mta hits (bd\_lumped)

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

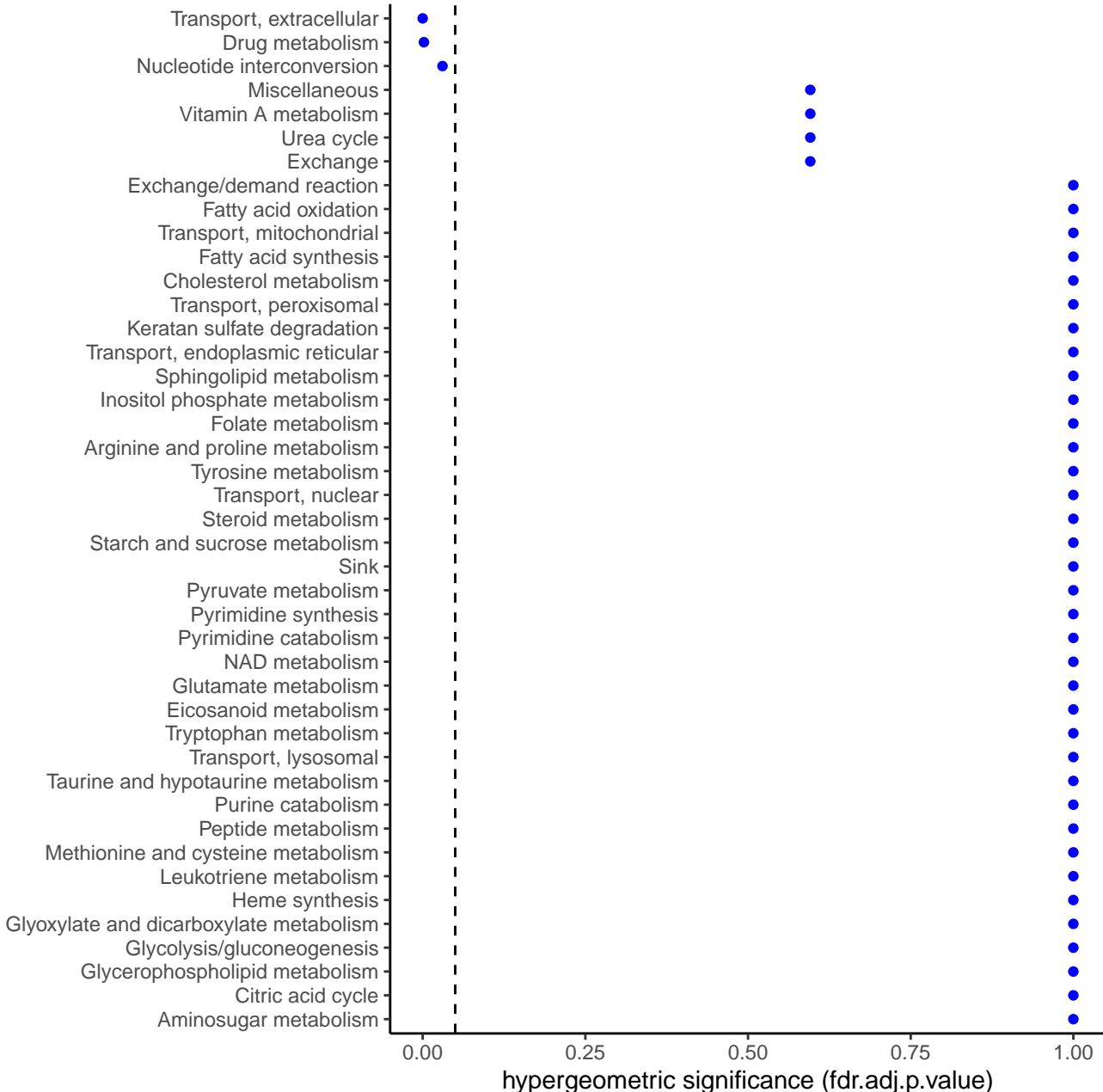


# of mta hits (bd\_lumped) vs all rxns



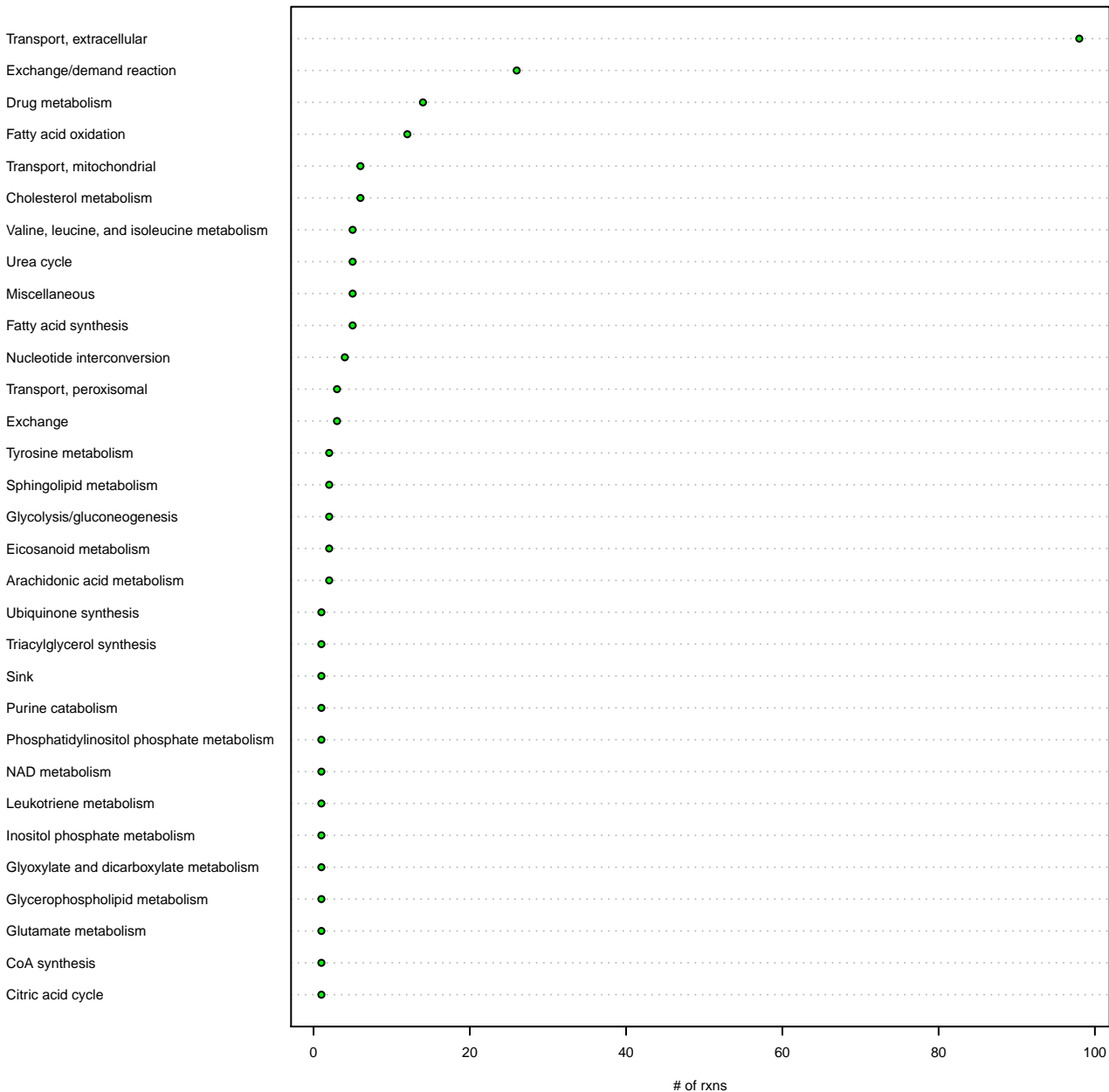
# over-representation analysis, bd\_lumped

subSystem\_BC

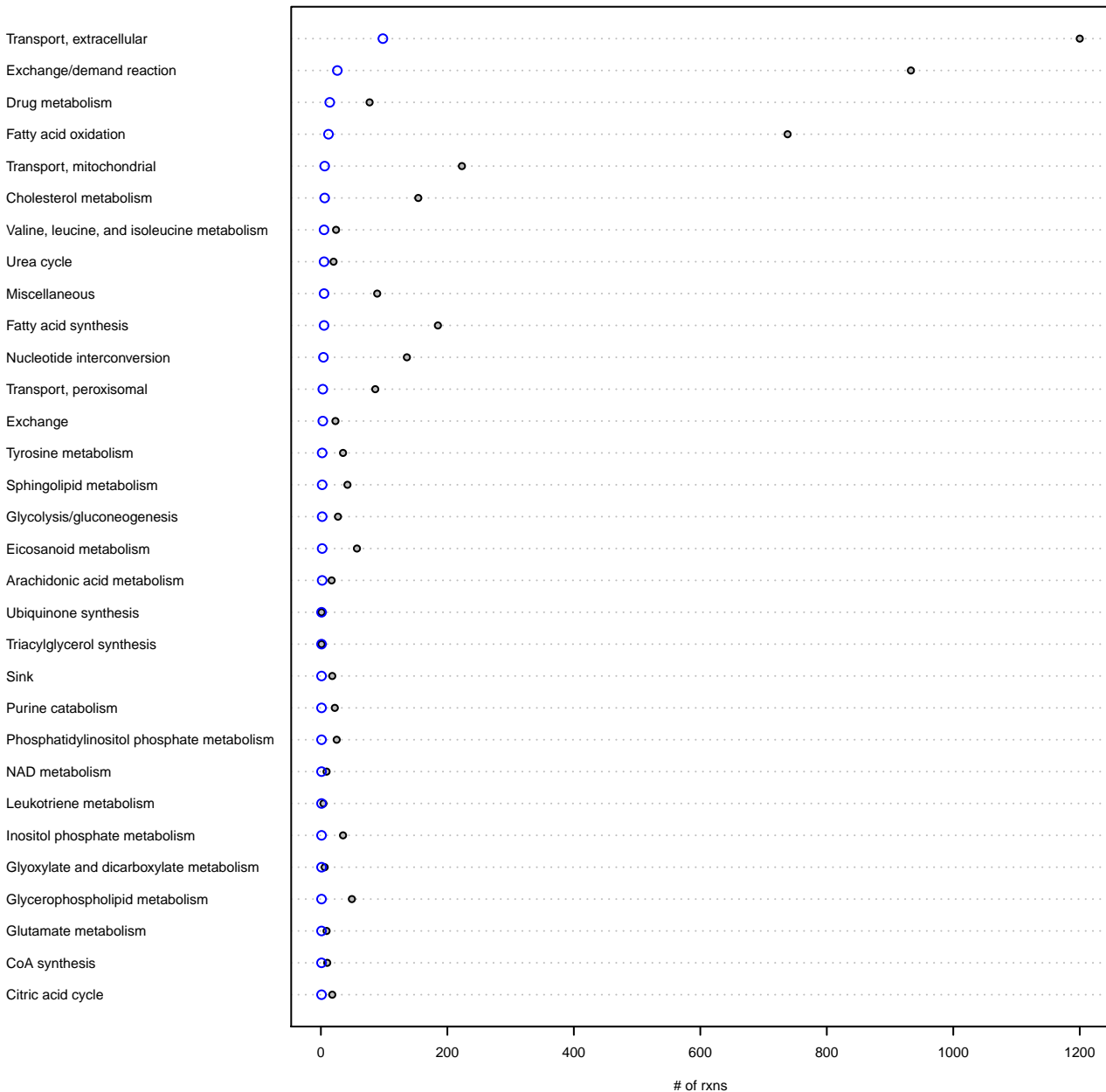




# of mta hits (bd\_responder)

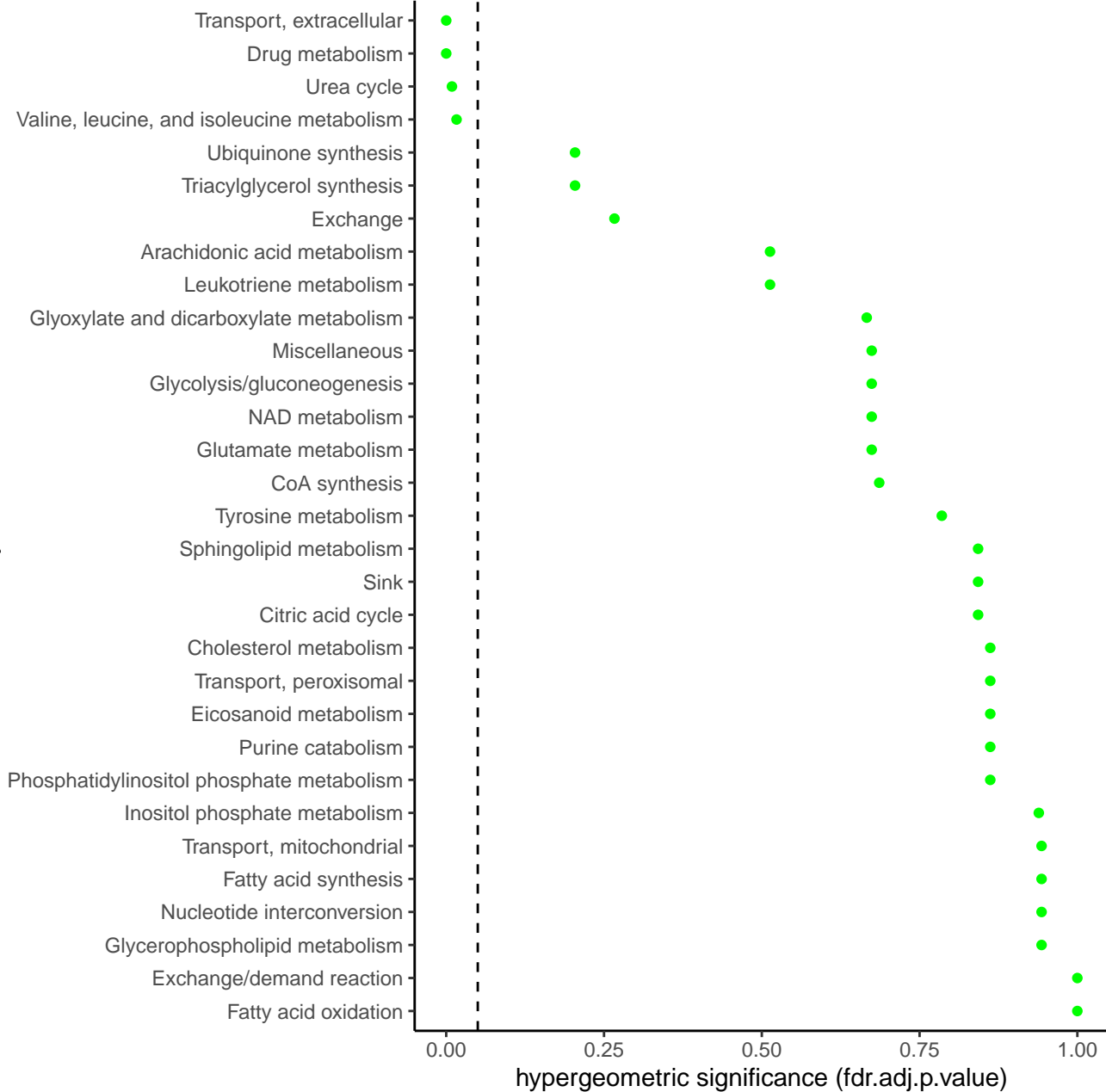


# of mta hits (bd\_responder) vs all rxns

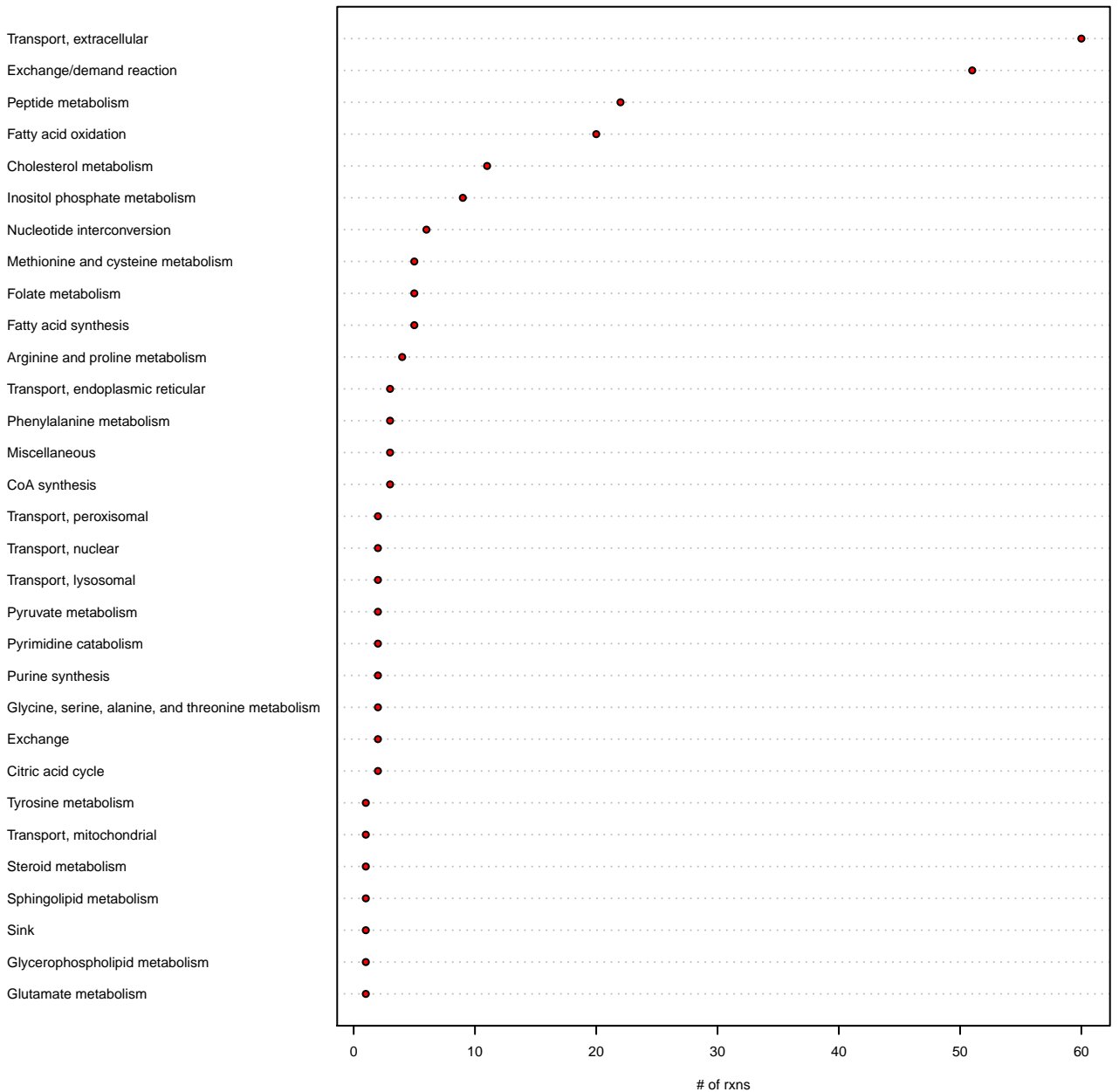


# over-representation analysis, bd\_responder

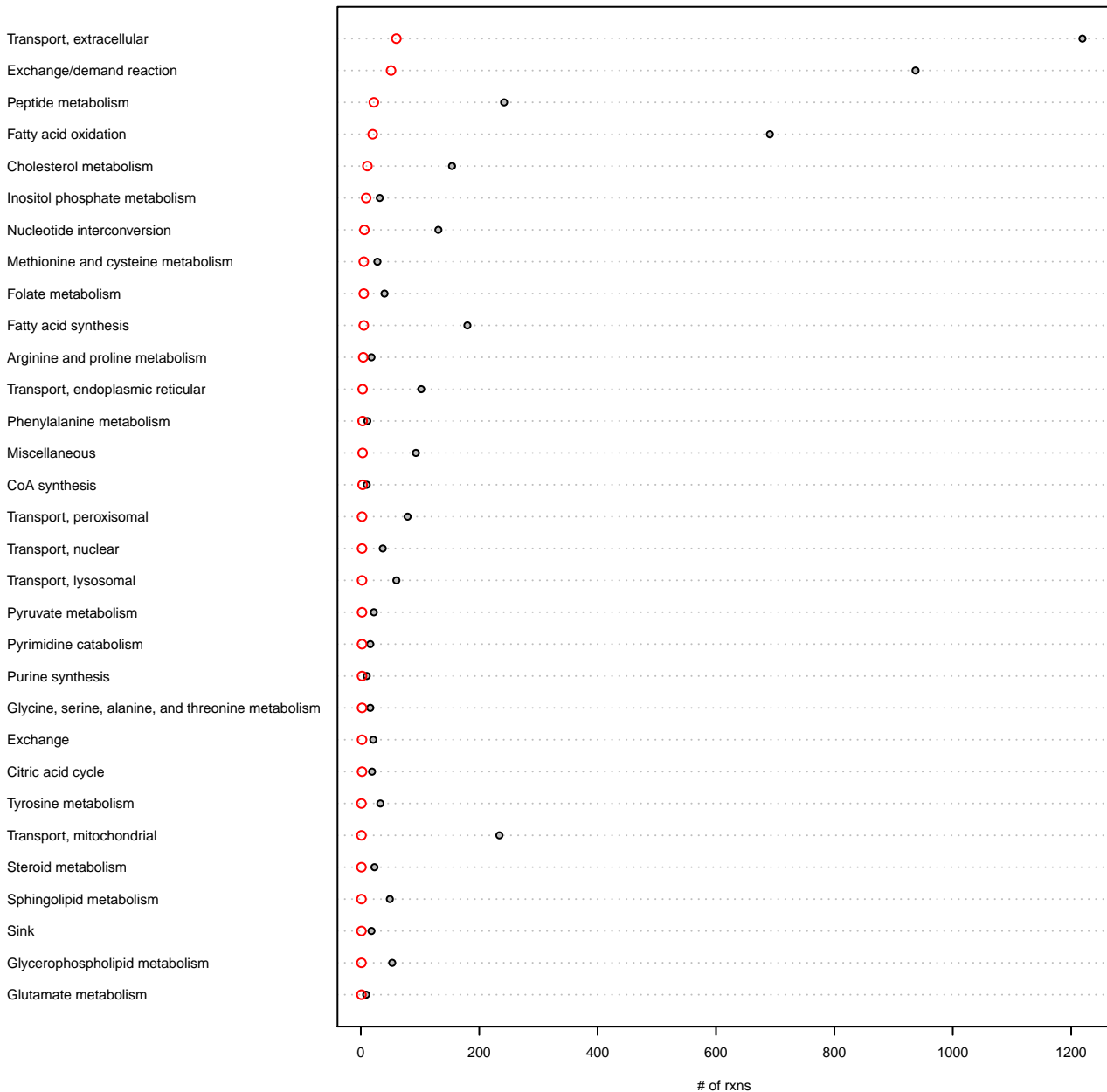
subSystem\_BRC



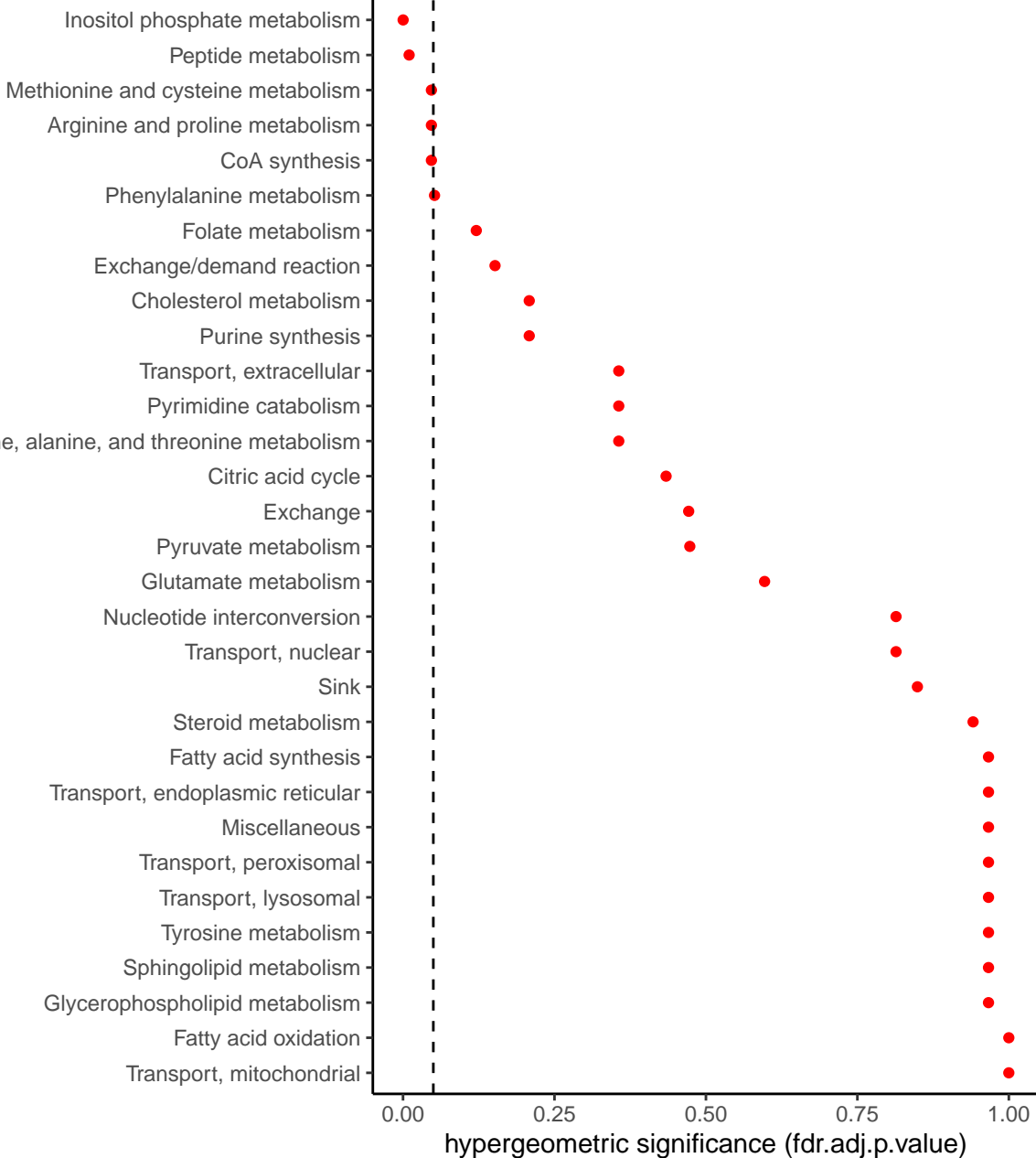
# of disrupted rxns (bd\_nonresponder)



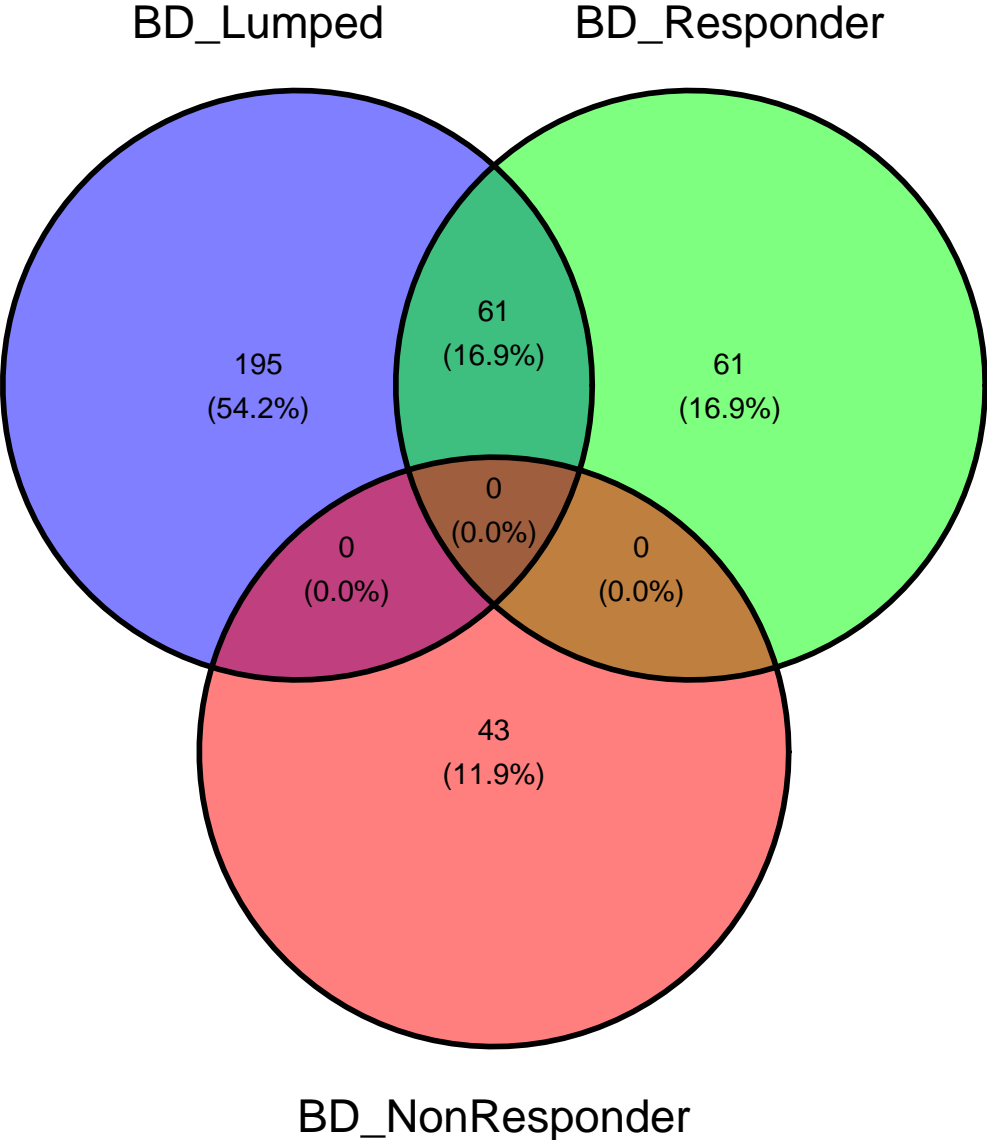
# of disrupted rxns (bd\_nonresponder) vs all rxns



subSystem\_BNRC



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

