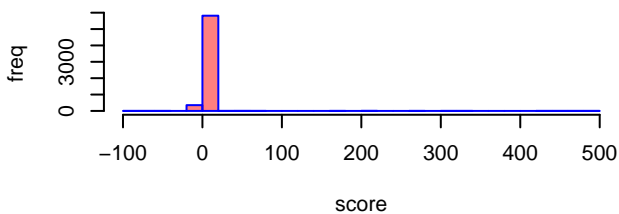
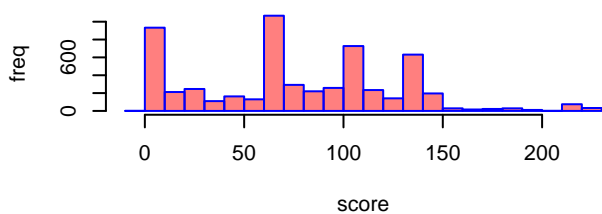


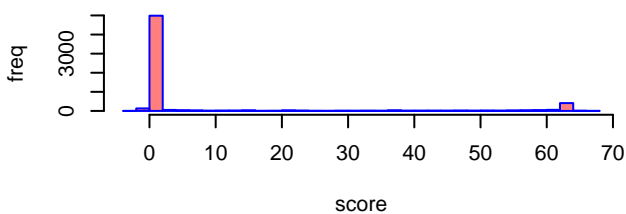
Ctrl_to_Primary



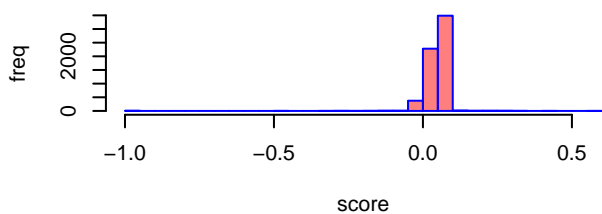
Primary_to_Ctrl



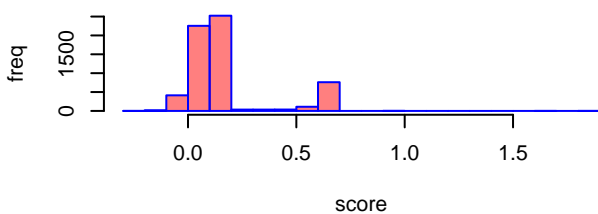
Ctrl_to_BD



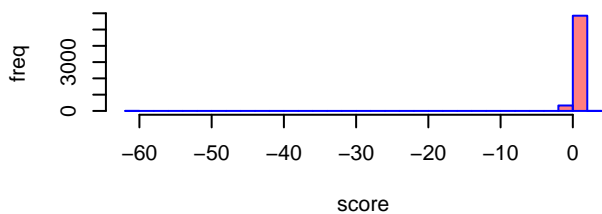
BD_to_Ctrl



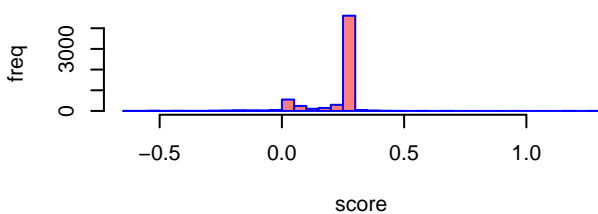
Ctrl_to_BD_R



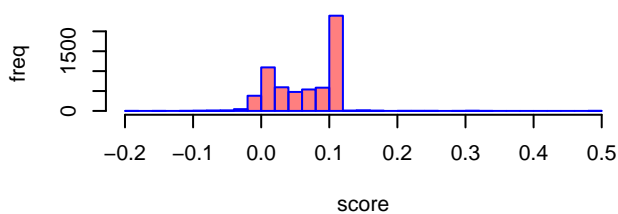
BD_R_to_Ctrl



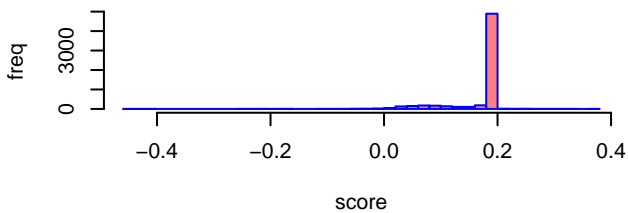
Ctrl_to_BD_NR



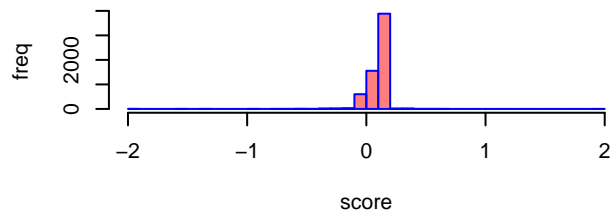
BD_NR_to_Ctrl



R_to_NR



NR_to_R



Intersection Size

1500

1000

500

0

107

112

151

165

216

235

239

305

325

325

419

424

456

534

1530

BD_NR_top

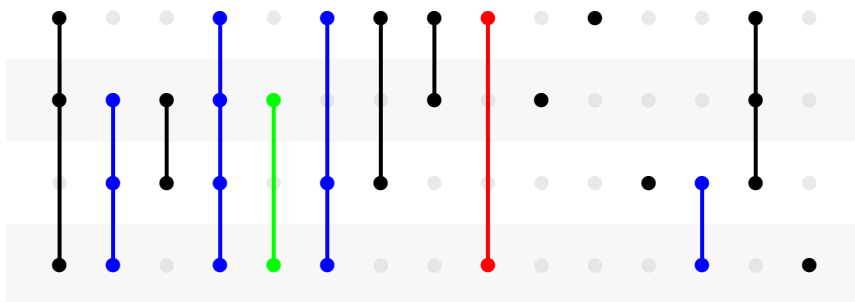
BD_R_top

BD_top

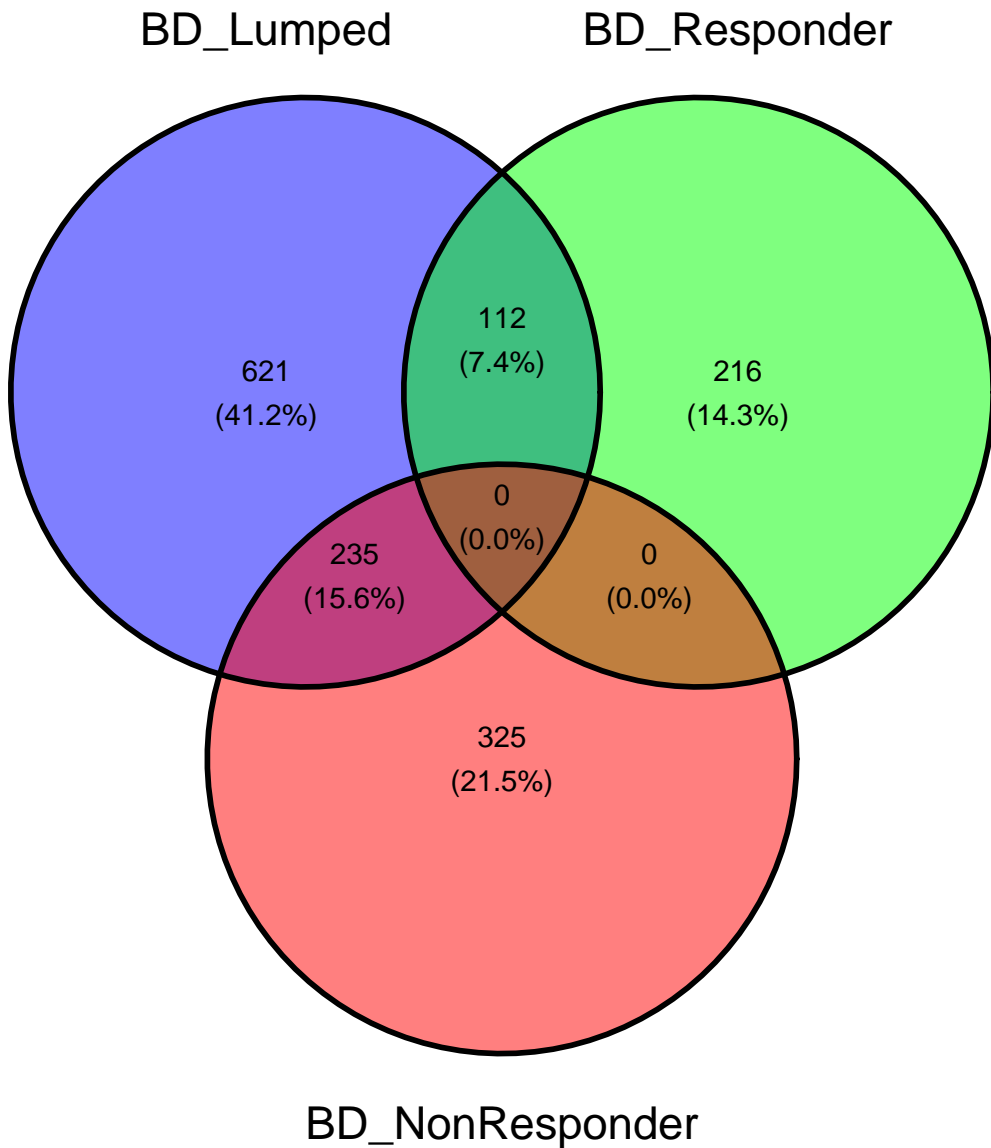
Ctrl_unchanged

3000 2000 1000 0

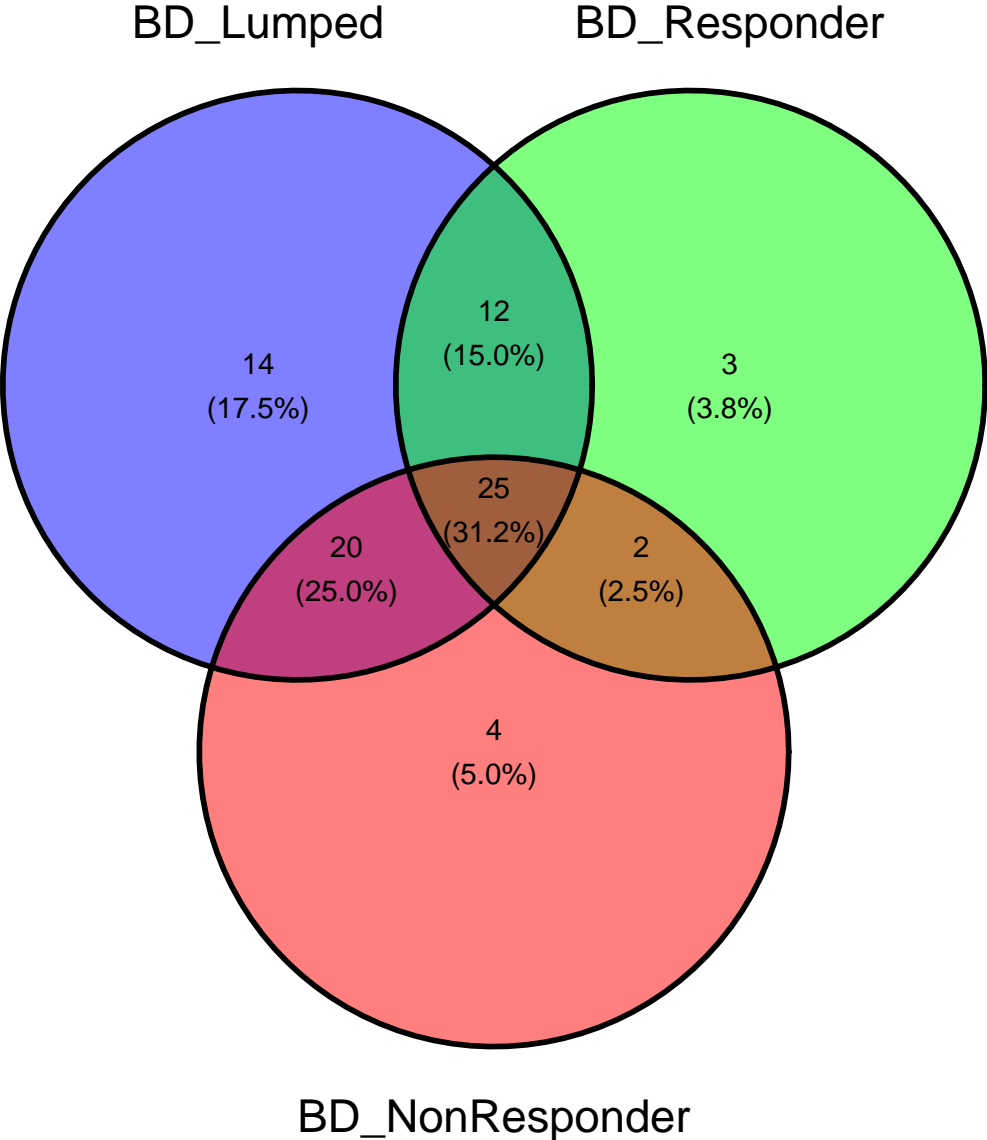
Set Size



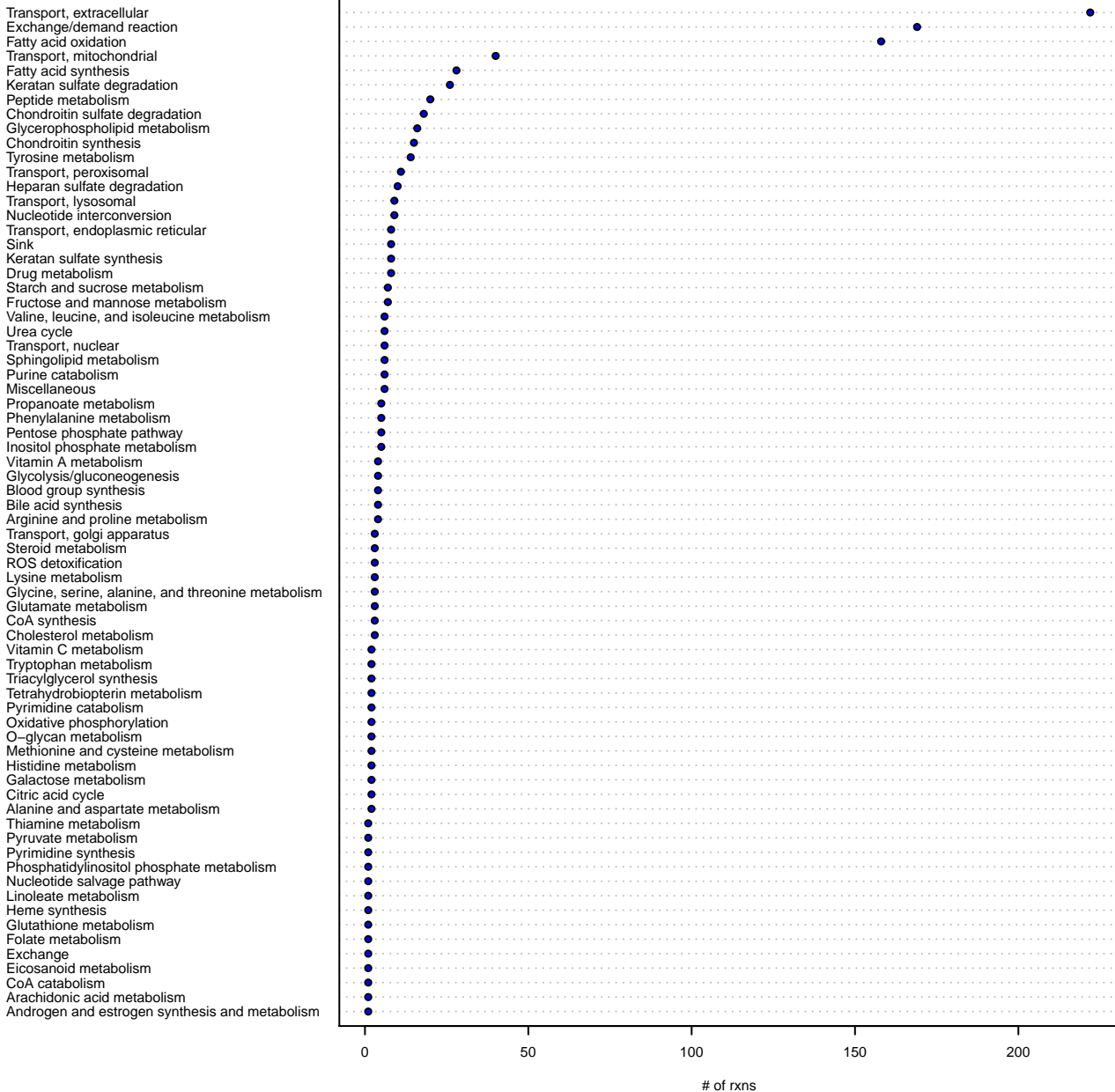
Overlap in rxns disrupted between models



Overlap in subSystems disrupted between models

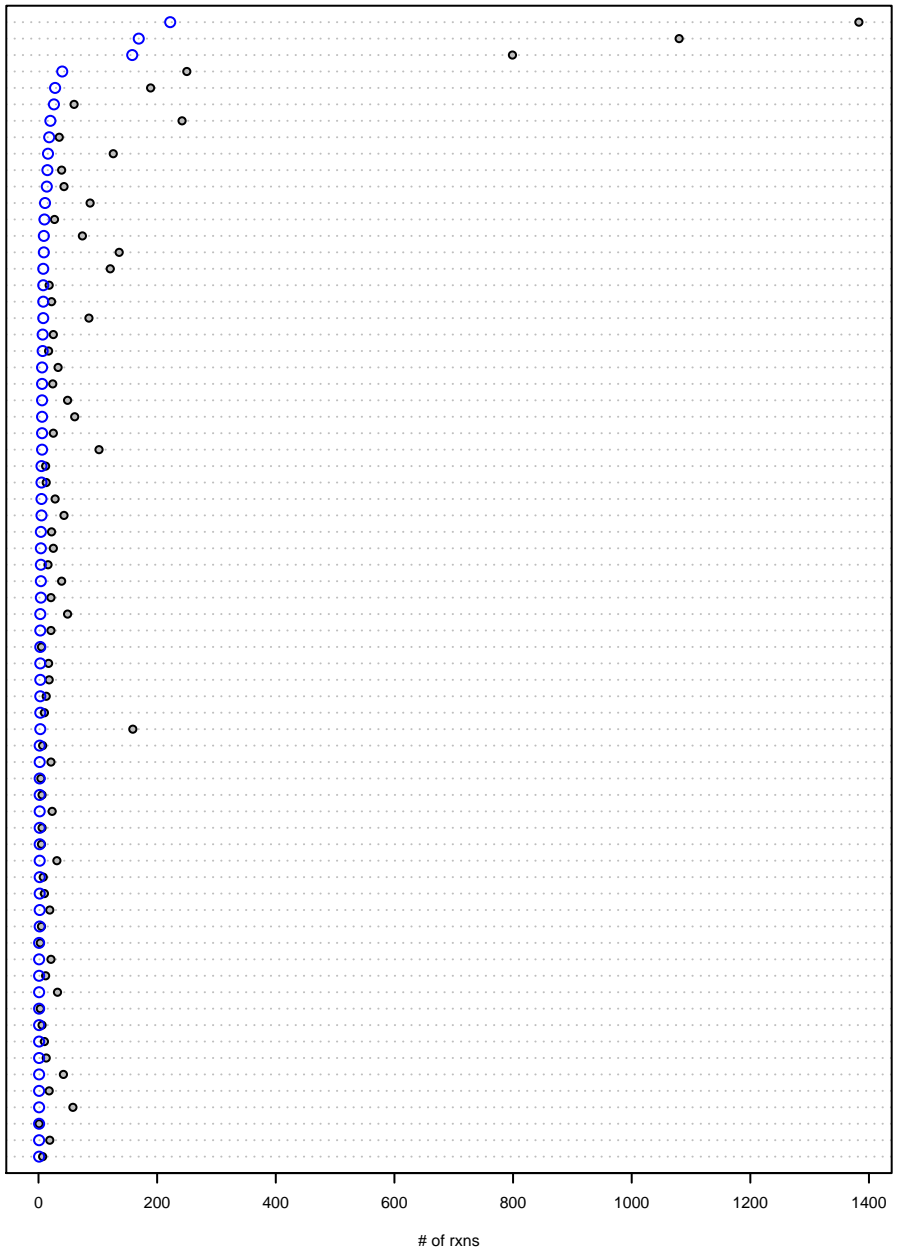


of mta hits (bd_lumped)



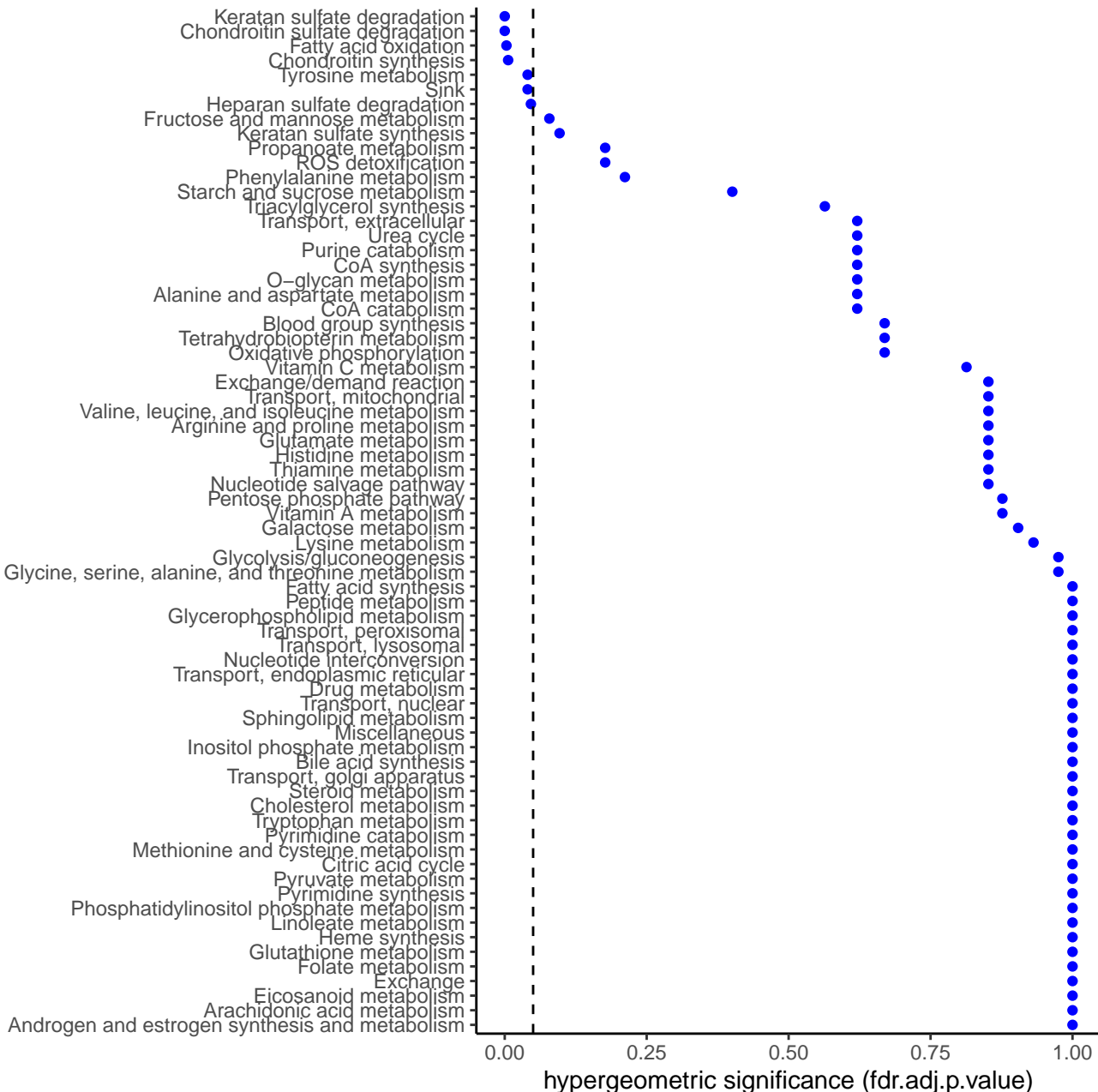
of mta hits (bd_lumped) vs all rxns

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

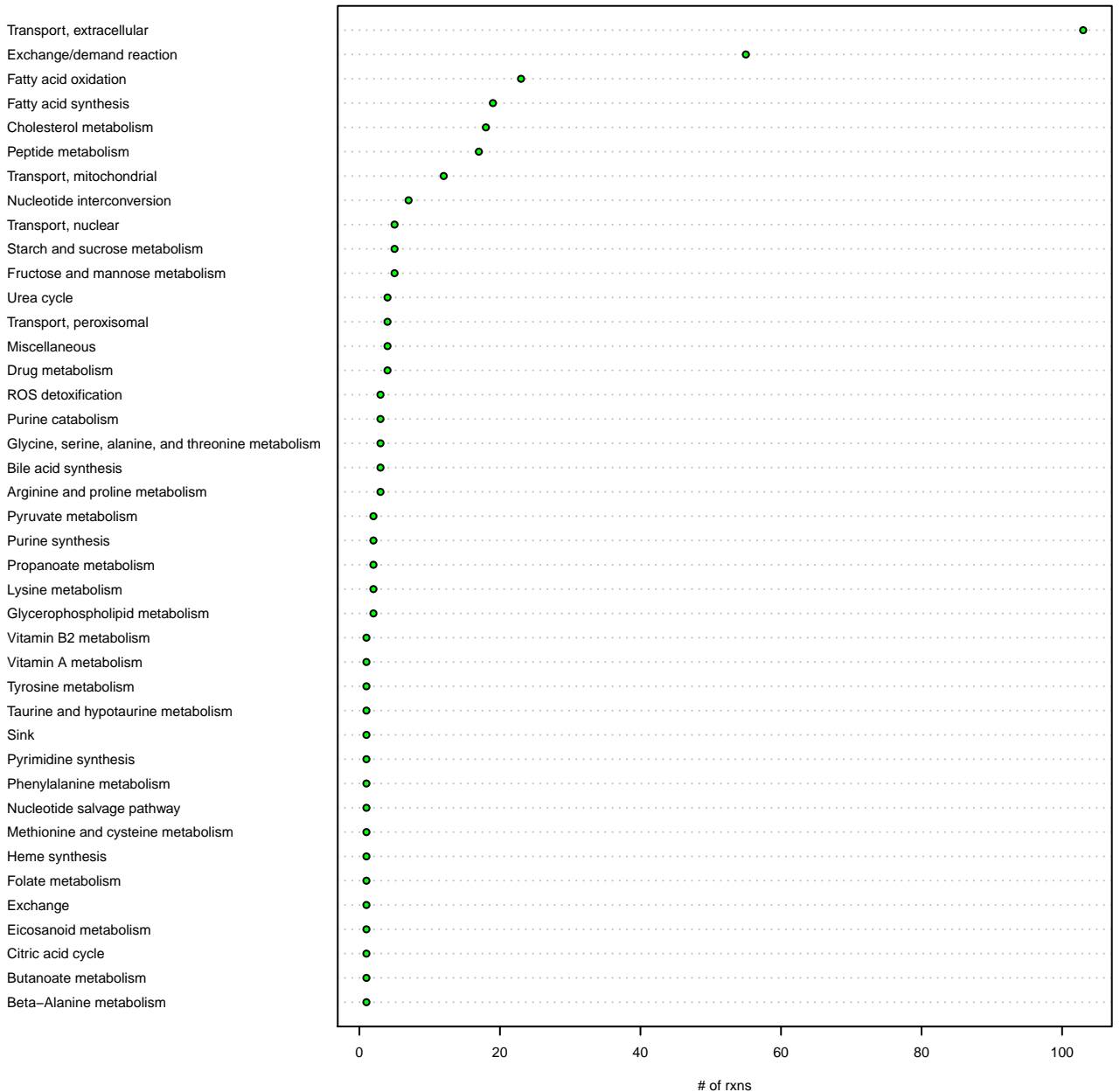


over-representation analysis, bd_lumped

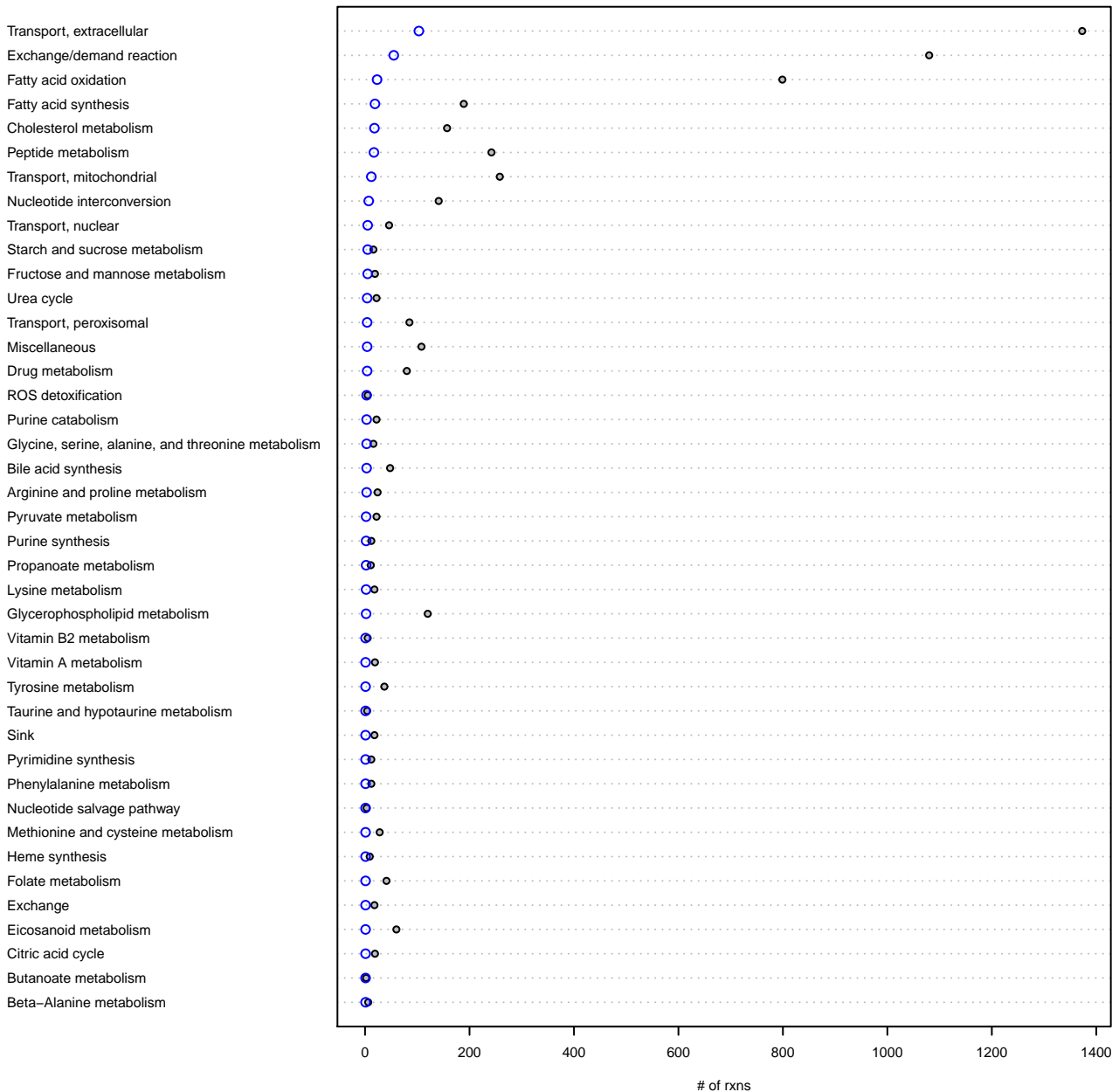
subSystem_BC



of mta hits (bd_responder)

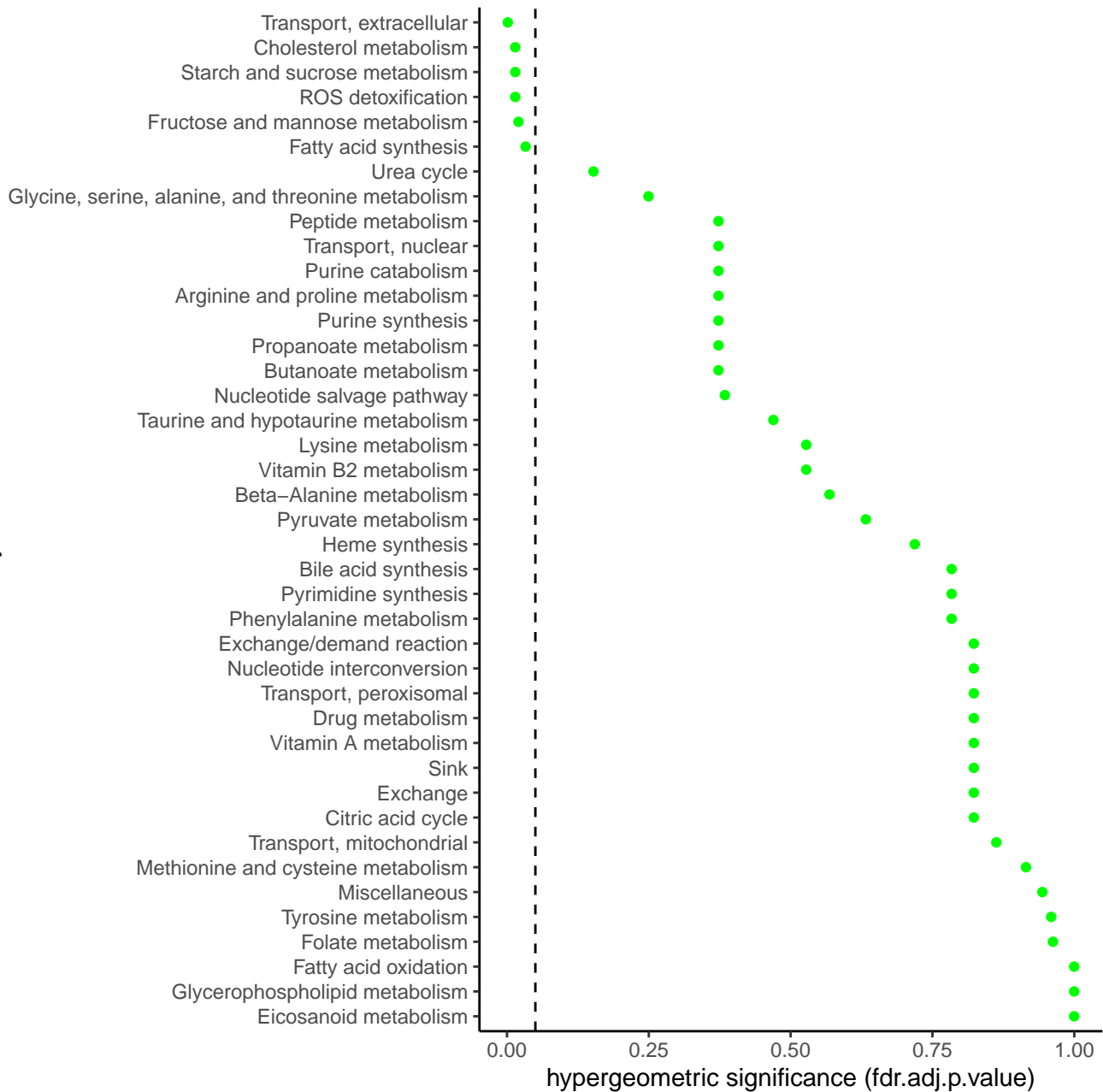


of mta hits (bd_responder) vs all rxns



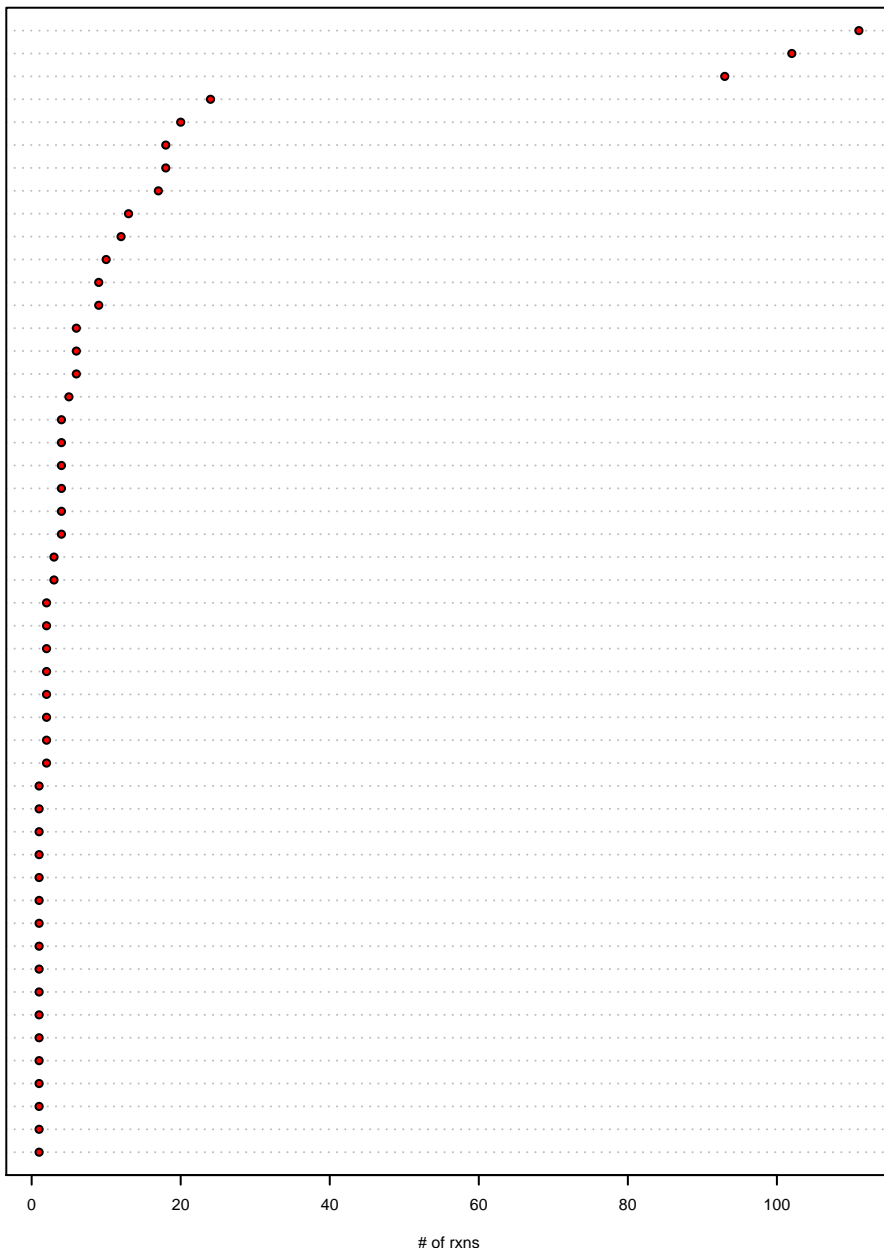
over-representation analysis, bd_responder

subSystem_BRC

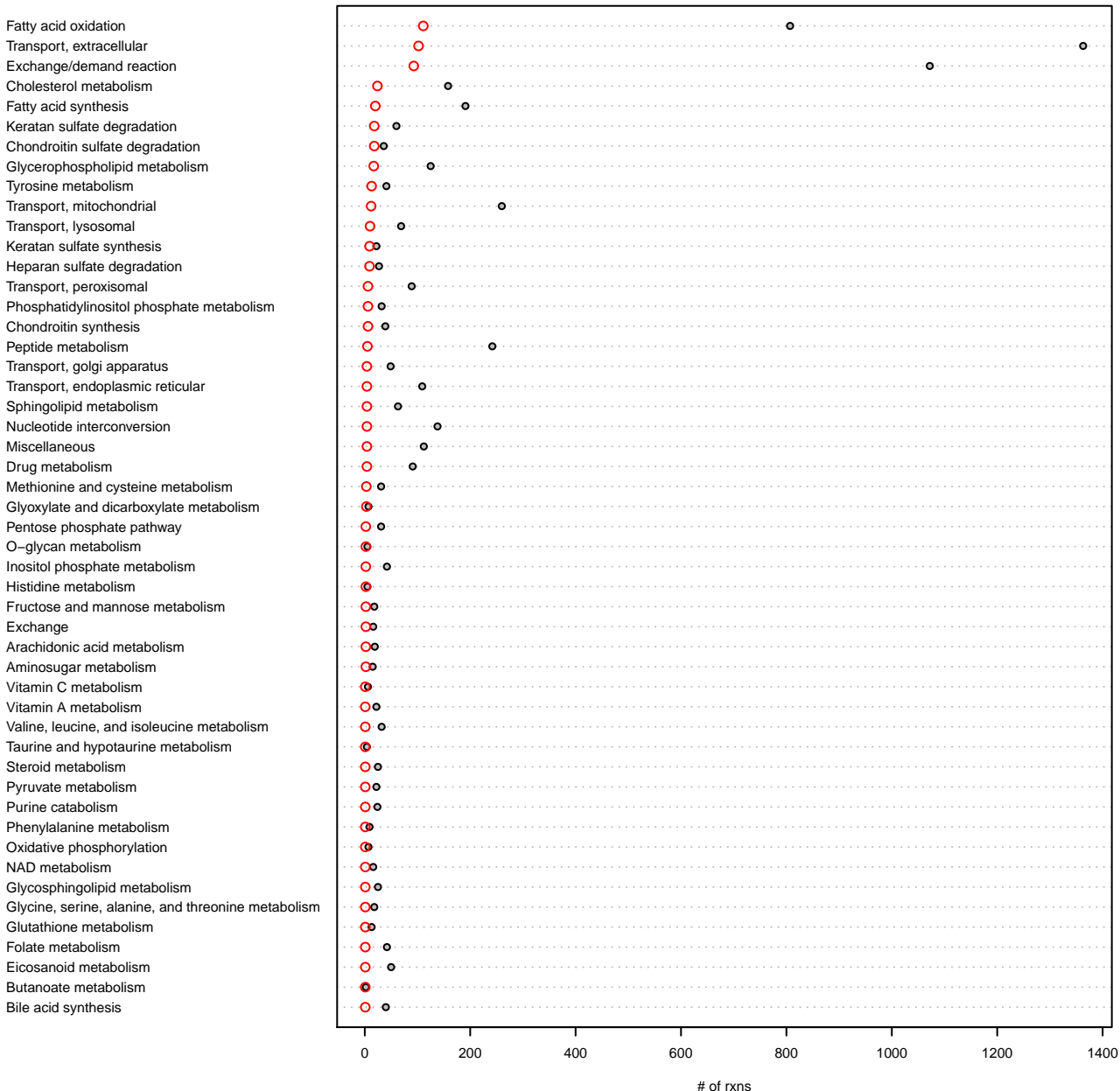


of disrupted rxns (bd_nonresponder)

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

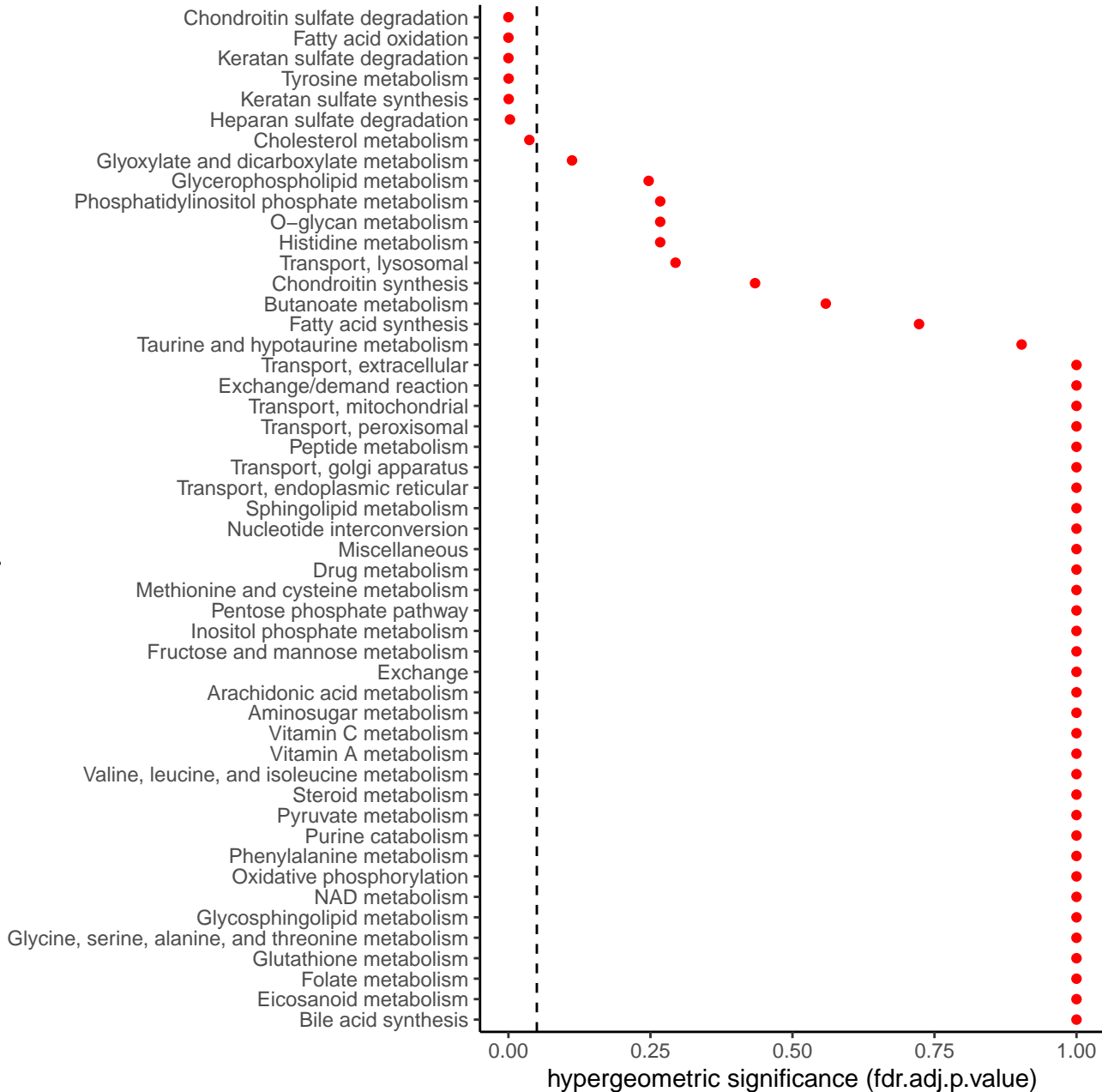


of disrupted rxns (bd_nonresponder) vs all rxns

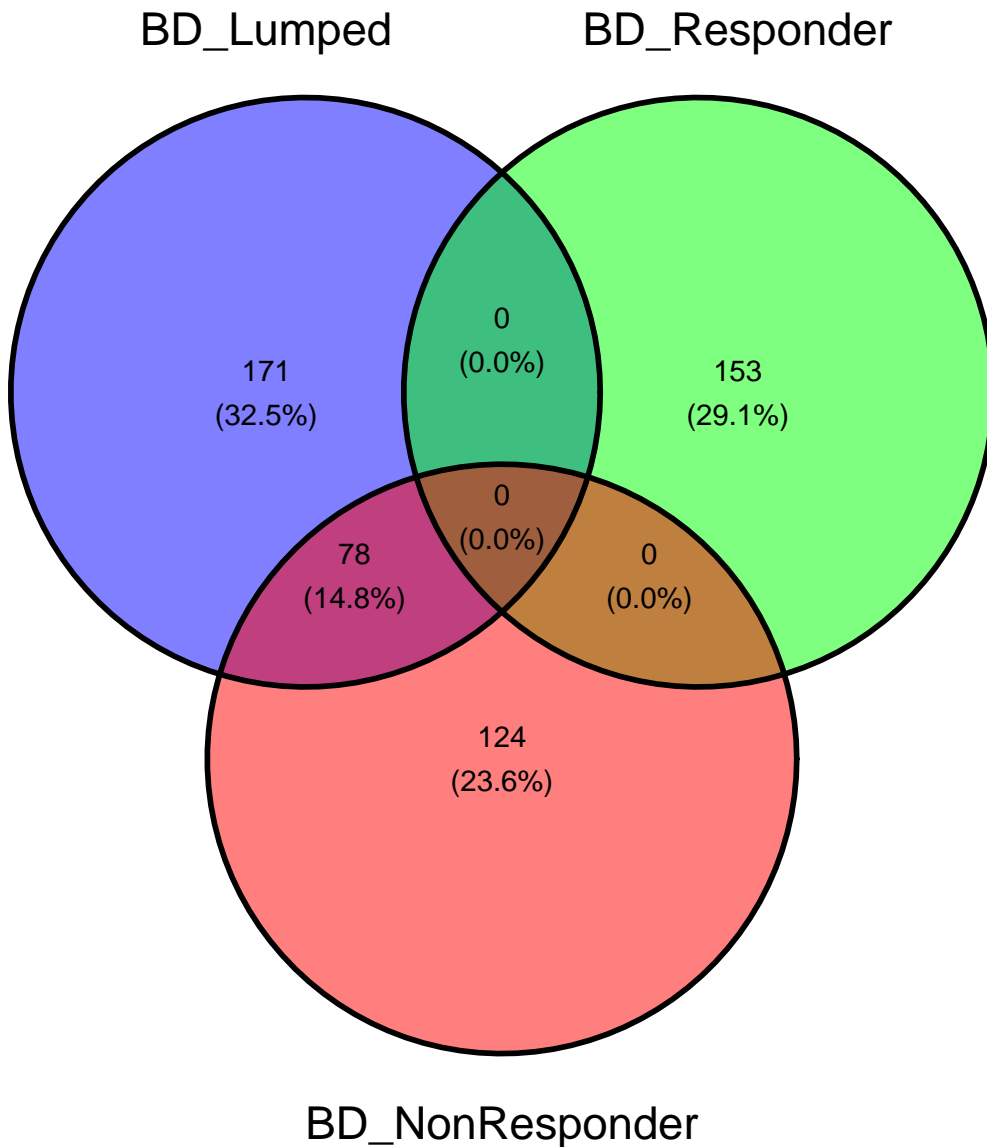


over-representation analysis, bd_nonresponder

subSystem_BNRC



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

