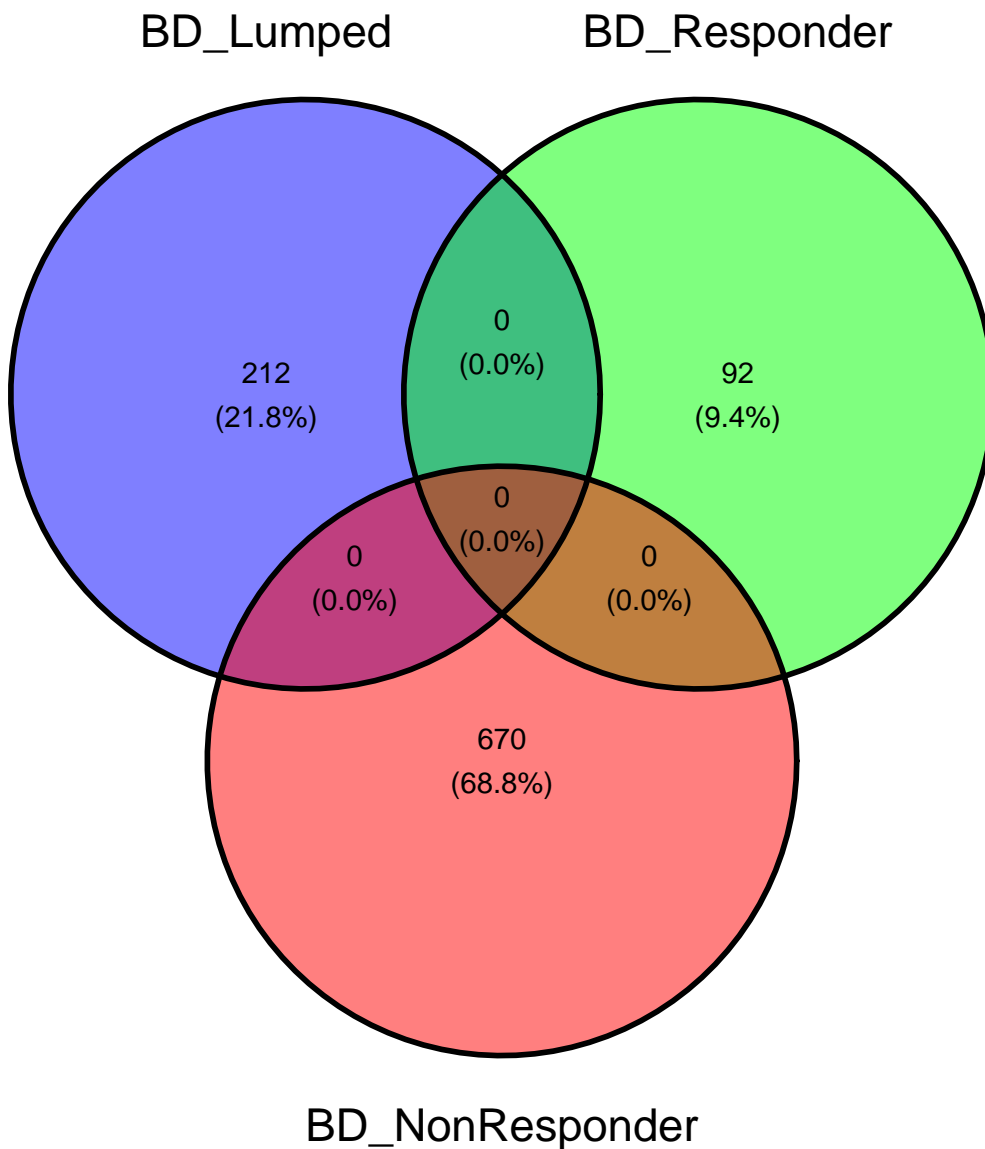
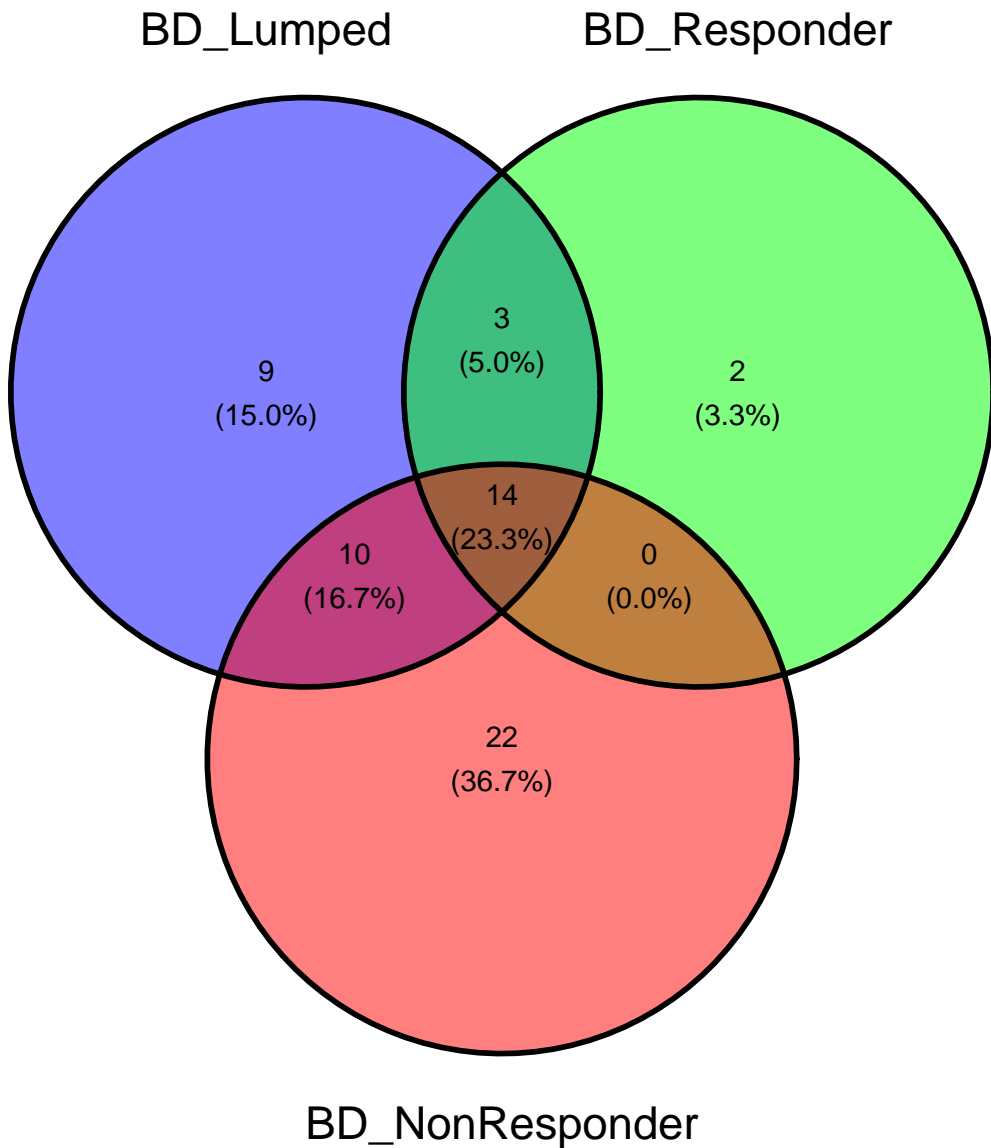


Overlap in rxns disrupted between models

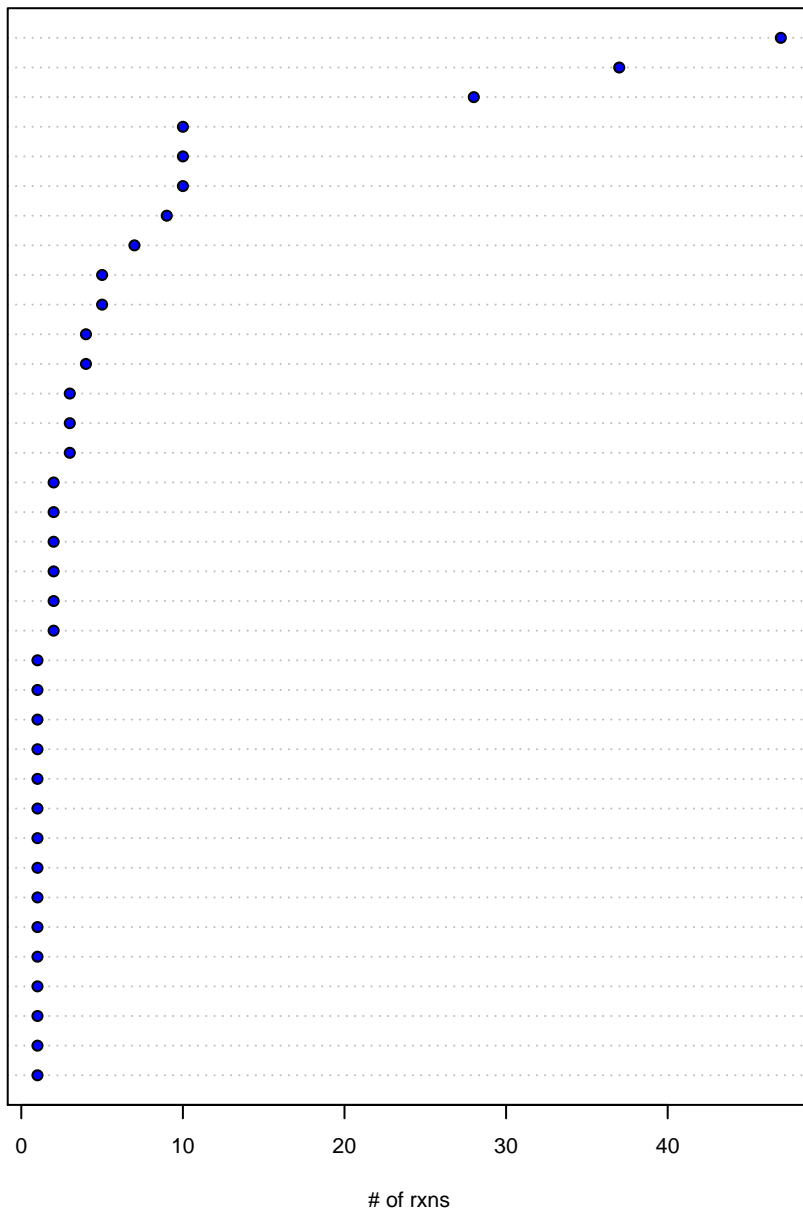


Overlap in subSystems disrupted between models



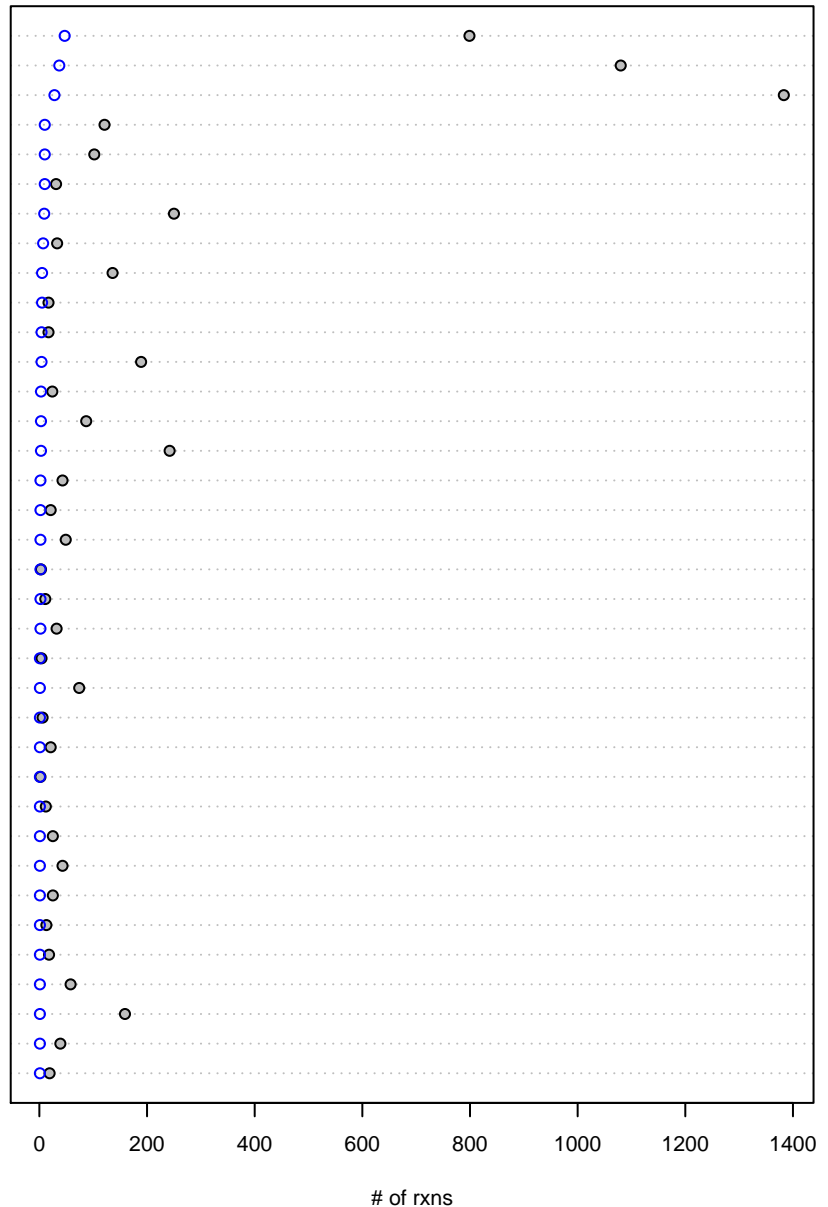
of disrupted rxns (n=212, bd_lumped)

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Transport, endoplasmic reticular
Miscellaneous
Methionine and cysteine metabolism
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose metabolism
Lysine metabolism
Fatty acid synthesis
Urea cycle
Transport, peroxisomal
Peptide metabolism
Tyrosine metabolism
Tryptophan metabolism
Transport, nuclear
Taurine and hypotaurine metabolism
Purine synthesis
Phosphatidylinositol phosphate metabolism
Triacylglycerol synthesis
Transport, lysosomal
Tetrahydrobiopterin metabolism
Steroid metabolism
R group synthesis
Pyrimidine synthesis
Purine catabolism
Inositol phosphate metabolism
Glycolysis/gluconeogenesis
Glutathione metabolism
Exchange
Eicosanoid metabolism
Cholesterol metabolism
Bile acid synthesis
Arachidonic acid metabolism



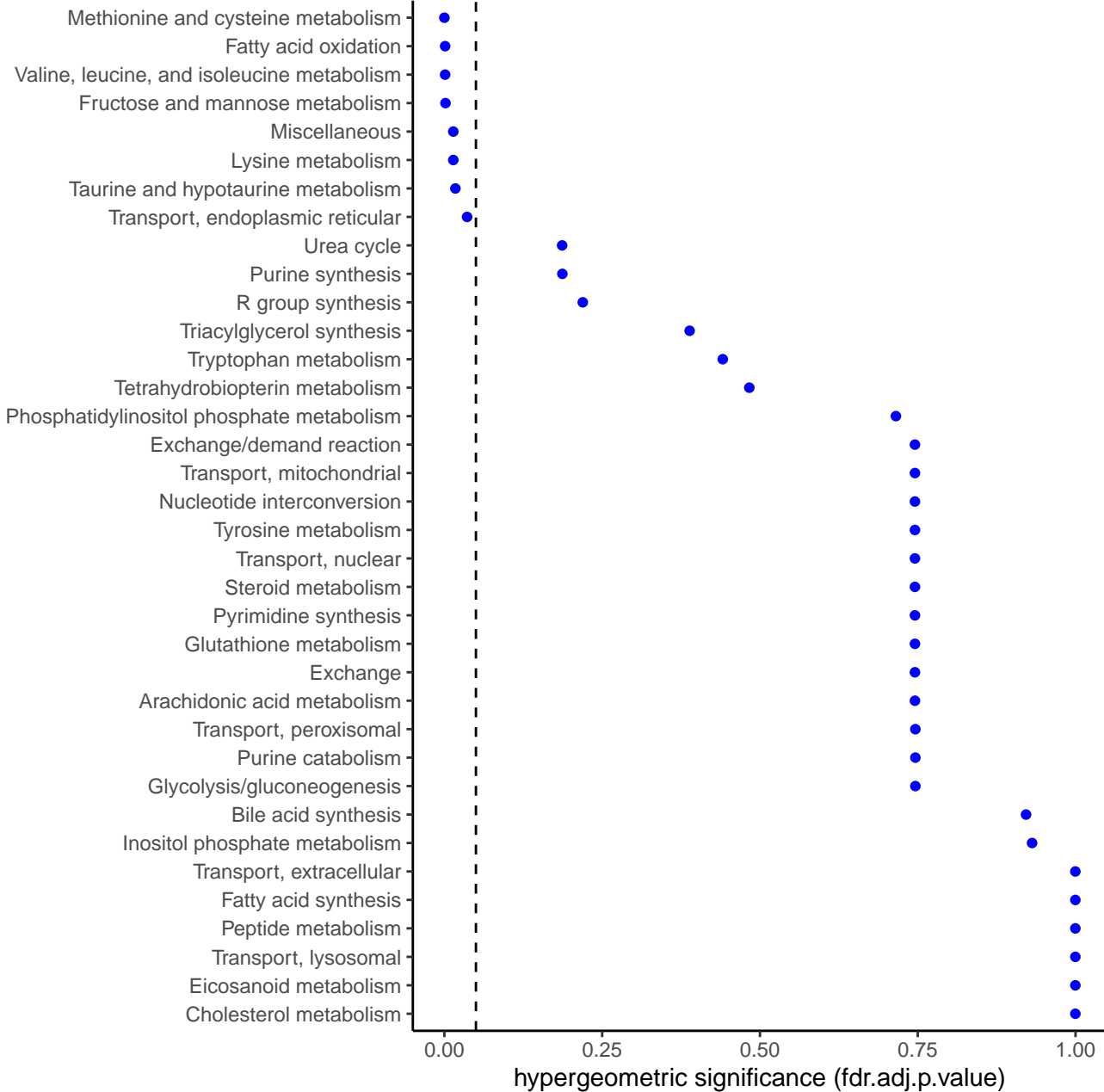
of disrupted rxns (n=212, bd_lumped) vs all rxns

Fatty acid oxidation
 Exchange/demand reaction
 Transport, extracellular
 Transport, endoplasmic reticular
 Miscellaneous
 Methionine and cysteine metabolism
 Transport, mitochondrial
 Valine, leucine, and isoleucine metabolism
 Nucleotide interconversion
 Fructose and mannose metabolism
 Lysine metabolism
 Fatty acid synthesis
 Urea cycle
 Transport, peroxisomal
 Peptide metabolism
 Tyrosine metabolism
 Tryptophan metabolism
 Transport, nuclear
 Taurine and hypotaurine metabolism
 Purine synthesis
 Phosphatidylinositol phosphate metabolism
 Triacylglycerol synthesis
 Transport, lysosomal
 Tetrahydrobiopterin metabolism
 Steroid metabolism
 R group synthesis
 Pyrimidine synthesis
 Purine catabolism
 Inositol phosphate metabolism
 Glycolysis/gluconeogenesis
 Glutathione metabolism
 Exchange
 Eicosanoid metabolism
 Cholesterol metabolism
 Bile acid synthesis
 Arachidonic acid metabolism

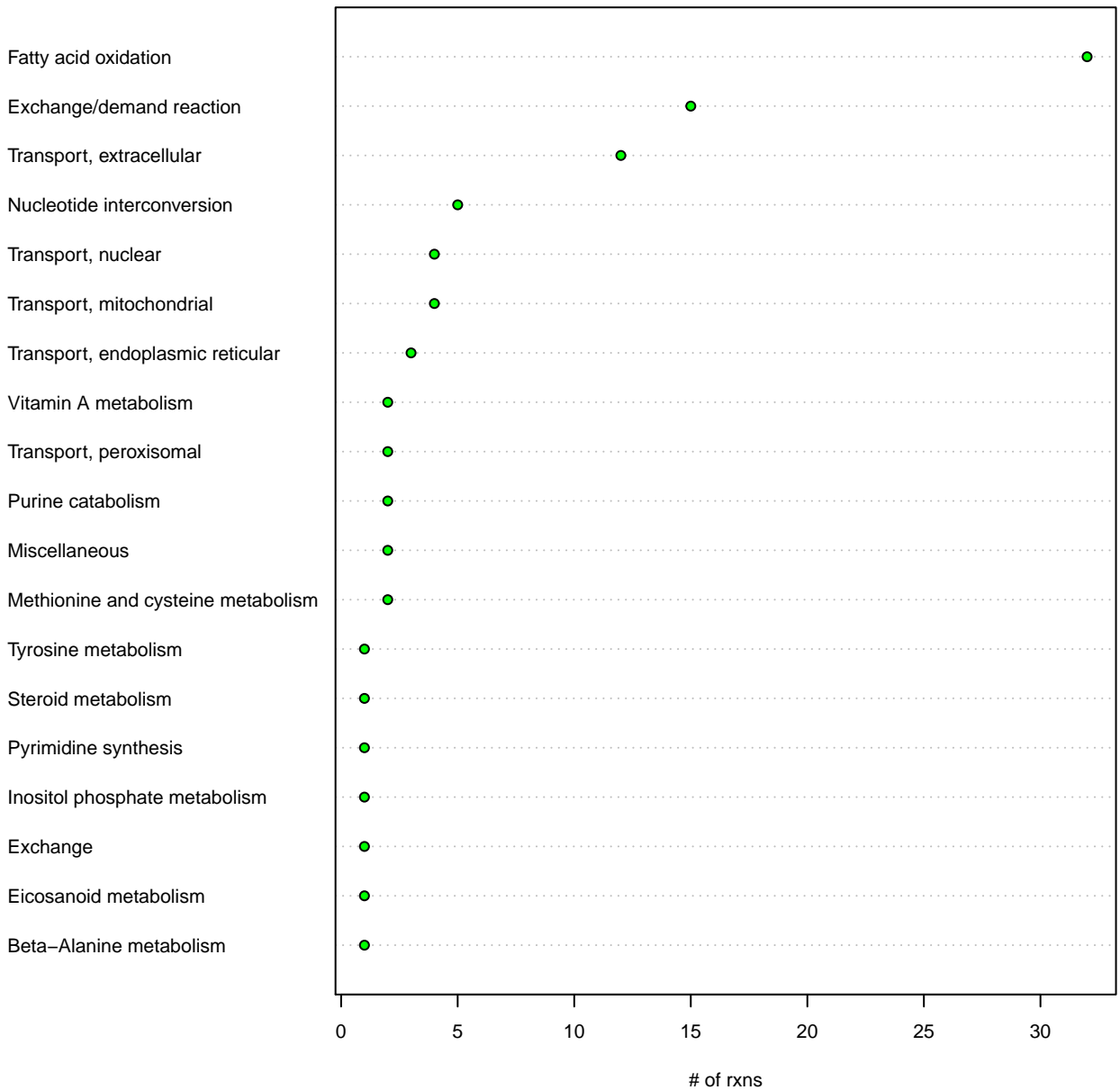


over-representation analysis, bd_lumped

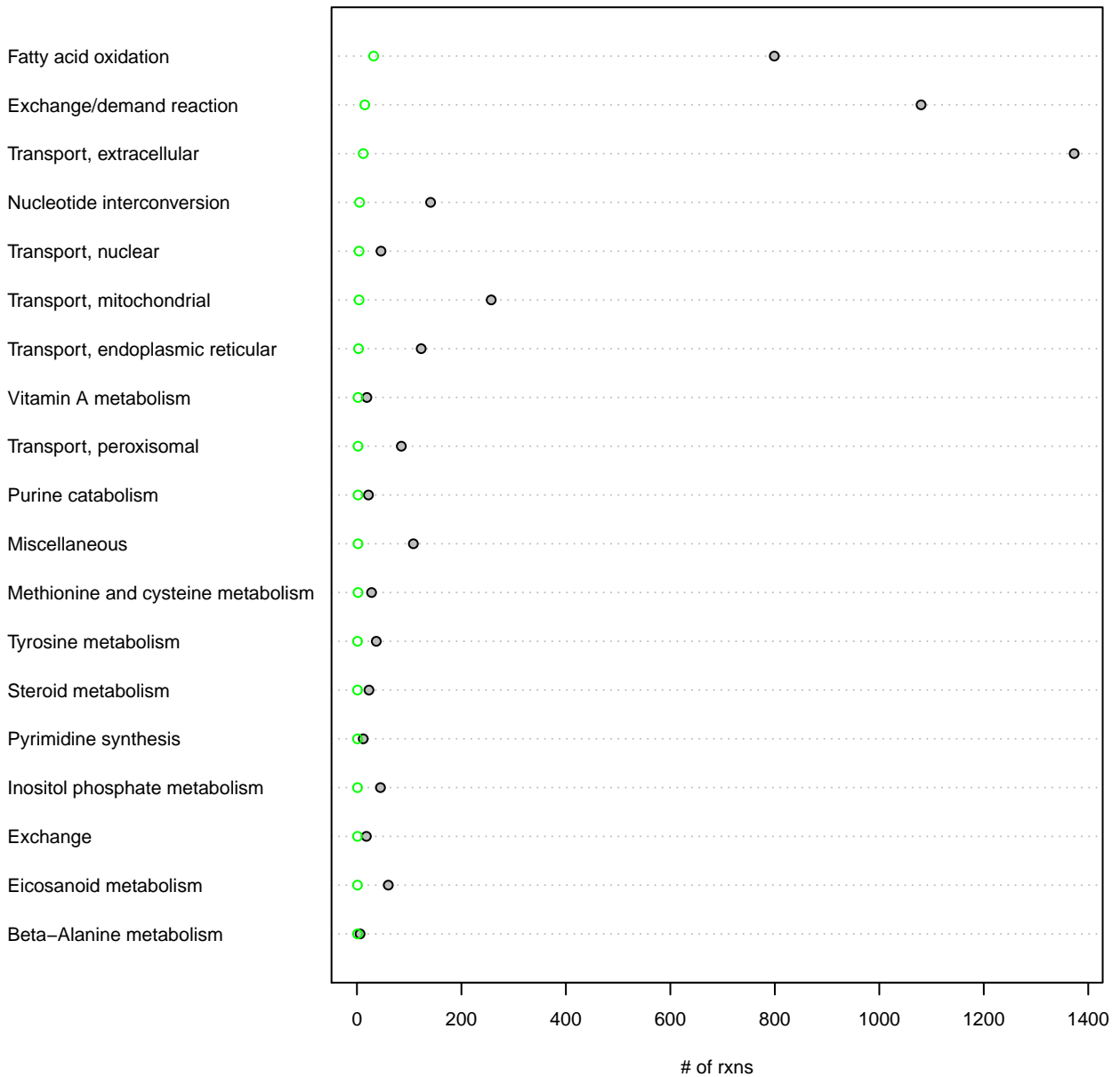
subSystem



of disrupted rxns (n=92, bd_responder)

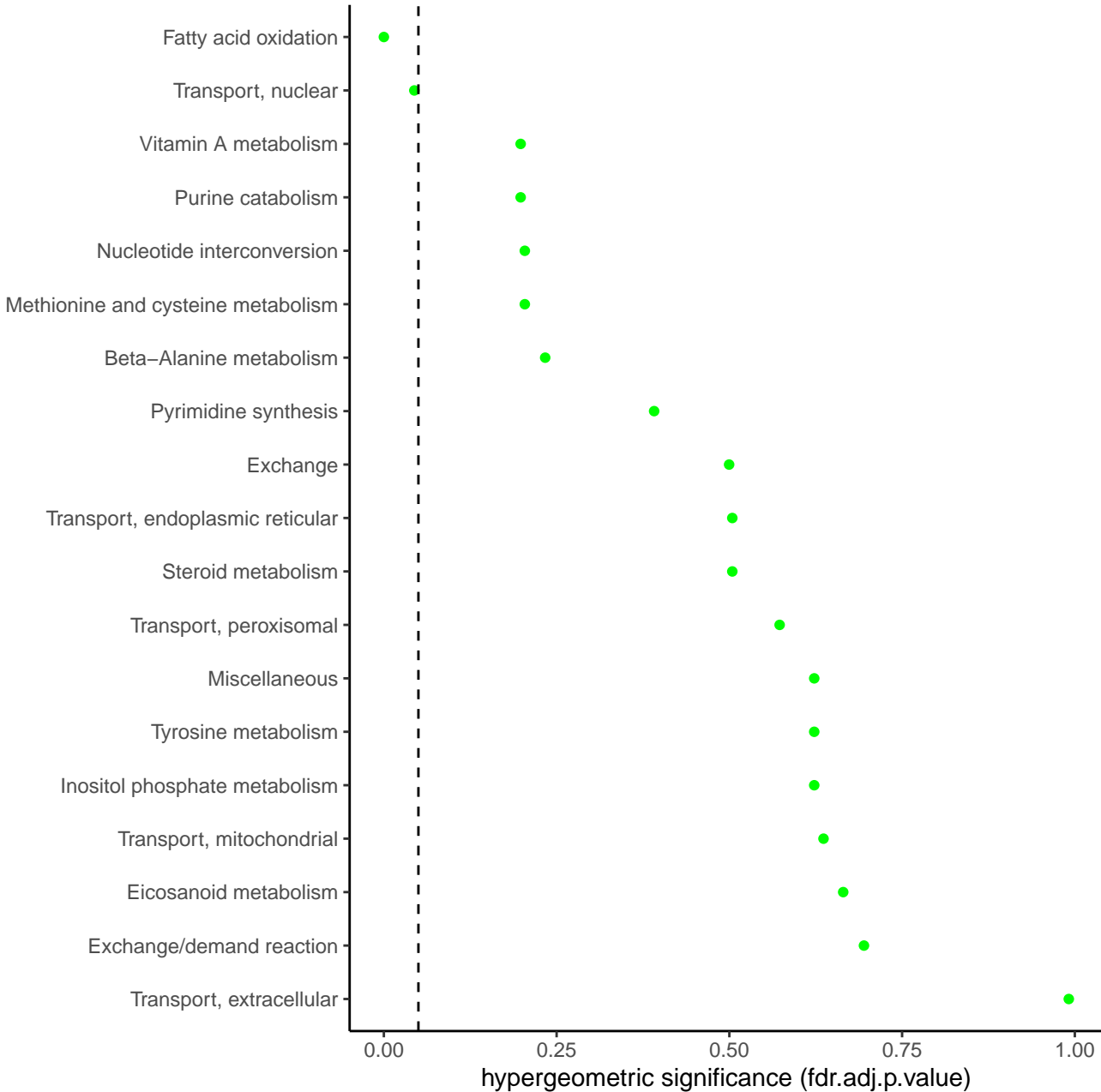


of disrupted rxns (n=92, bd_responder) vs all rxns



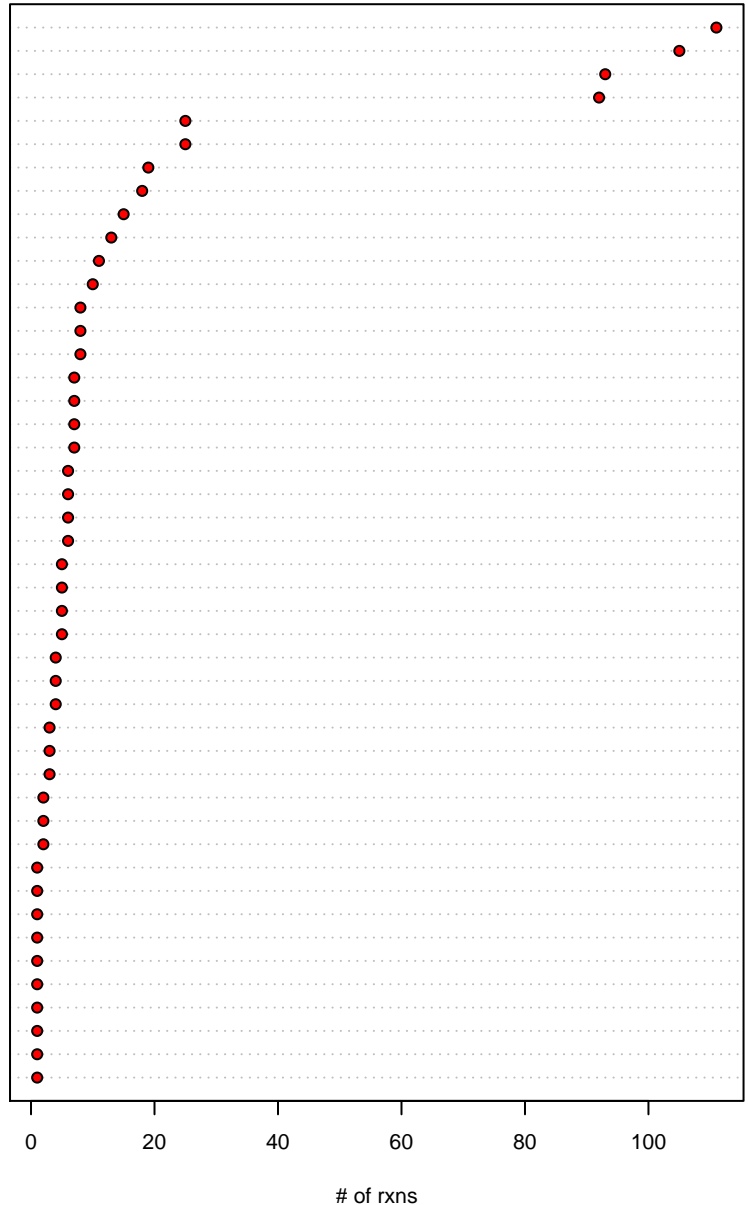
over-representation analysis, bd_responder

subSystem



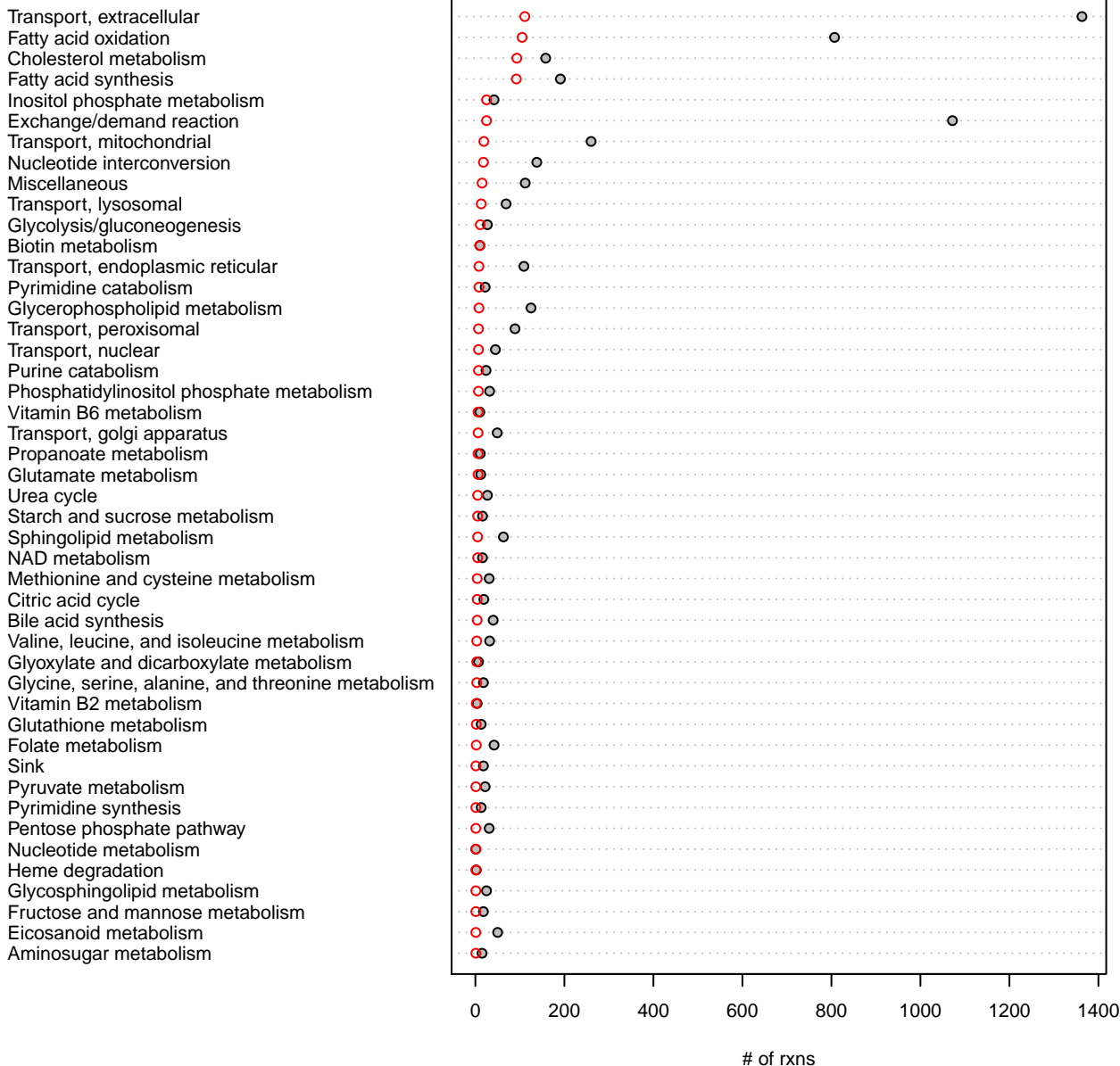
of disrupted rxns (n=670, bd_nonresponder)

Transport, extracellular
Fatty acid oxidation
Cholesterol metabolism
Fatty acid synthesis
Inositol phosphate metabolism
Exchange/demand reaction
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Biotin metabolism
Transport, endoplasmic reticular
Pyrimidine catabolism
Glycerophospholipid metabolism
Transport, peroxisomal
Transport, nuclear
Purine catabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Transport, golgi apparatus
Propanoate metabolism
Glutamate metabolism
Urea cycle
Starch and sucrose metabolism
Sphingolipid metabolism
NAD metabolism
Methionine and cysteine metabolism
Citric acid cycle
Bile acid synthesis
Valine, leucine, and isoleucine metabolism
Glyoxylate and dicarboxylate metabolism
Glycine, serine, alanine, and threonine metabolism
Vitamin B2 metabolism
Glutathione metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Fructose and mannose metabolism
Eicosanoid metabolism
Aminosugar metabolism

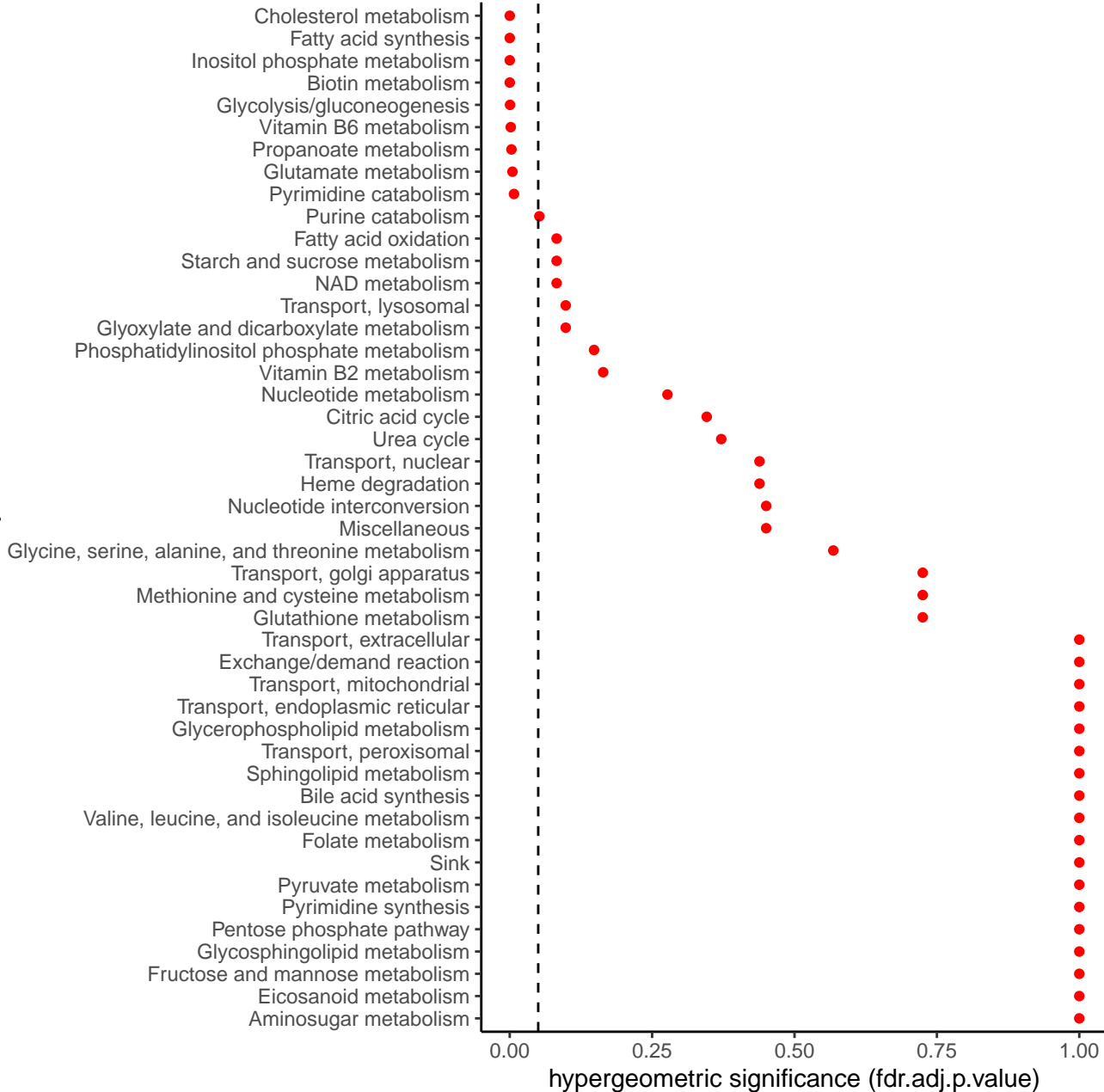


of rxns

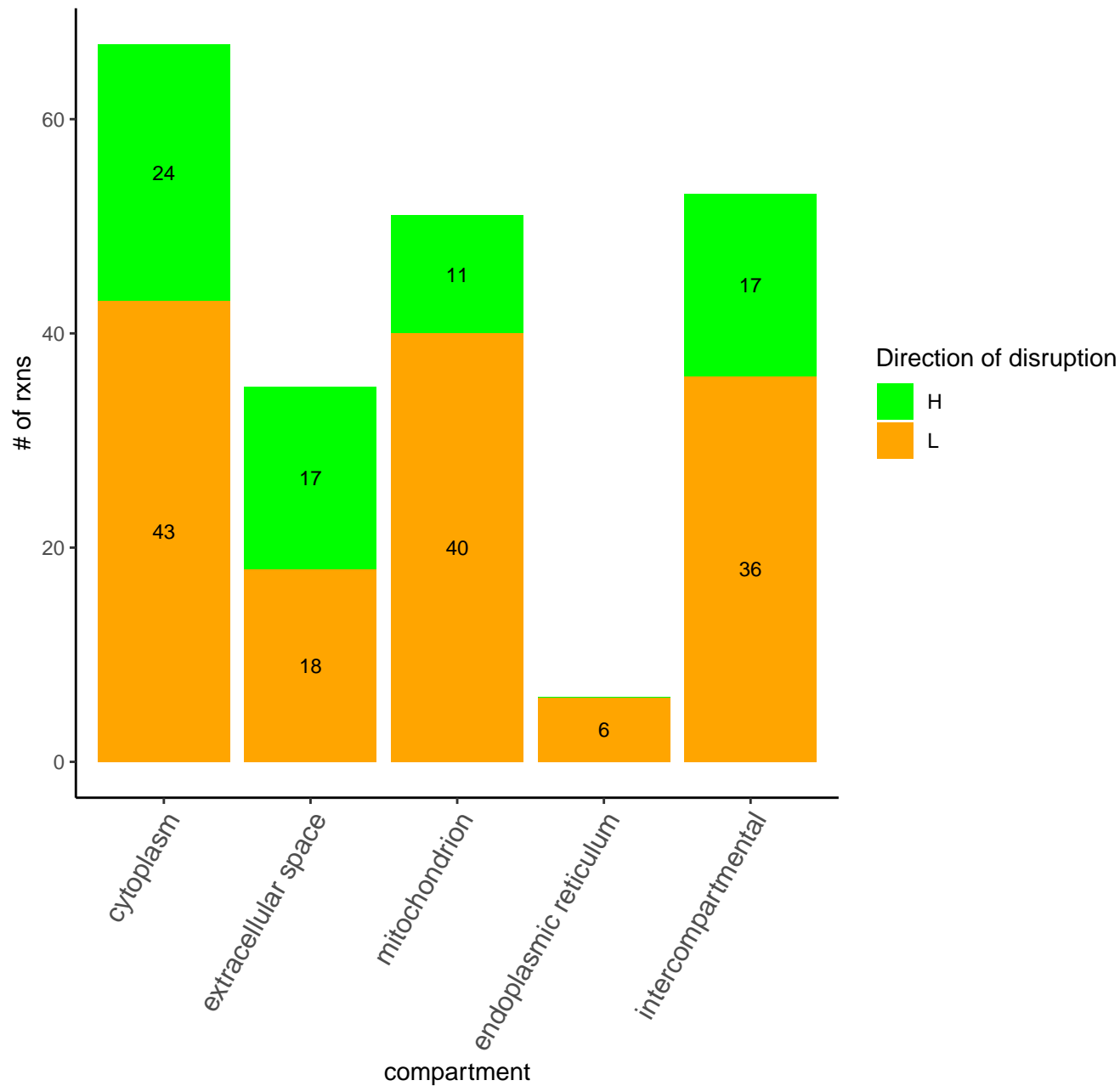
of disrupted rxns (n=670, bd_nonresponder) vs all rxns



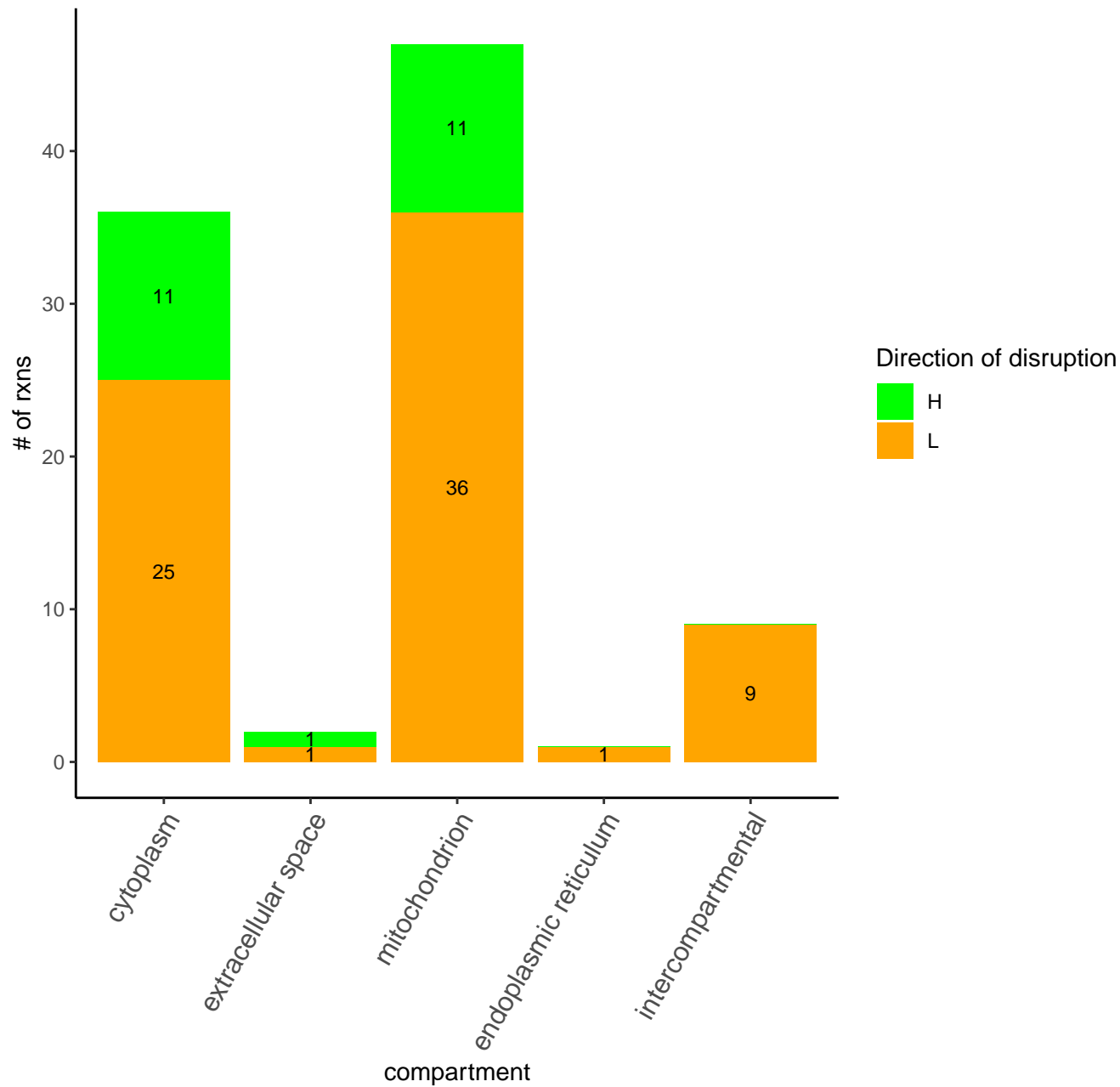
subSystem



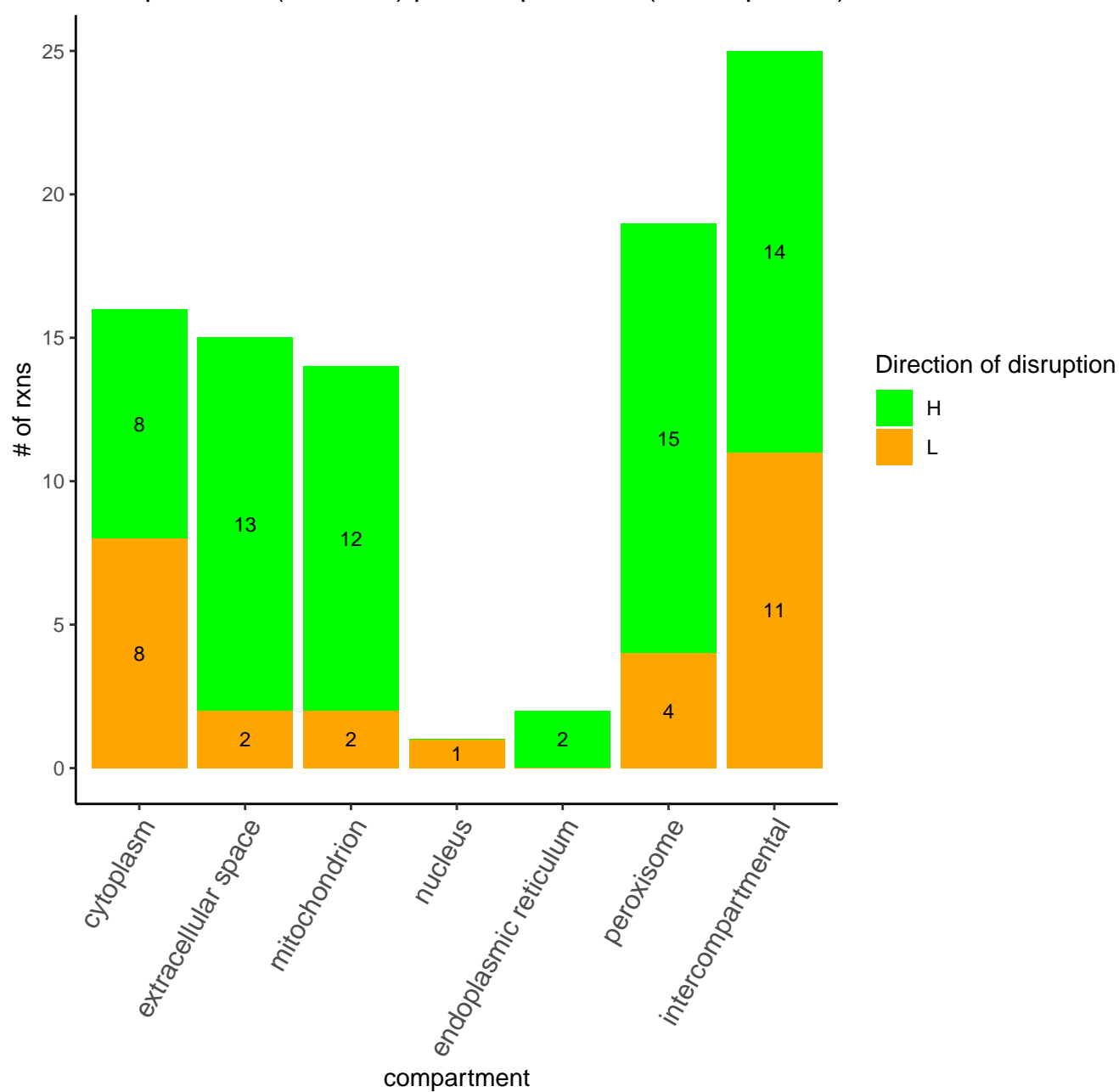
Disrupted rxns (all, n=212) per compartment (bd_lumped)



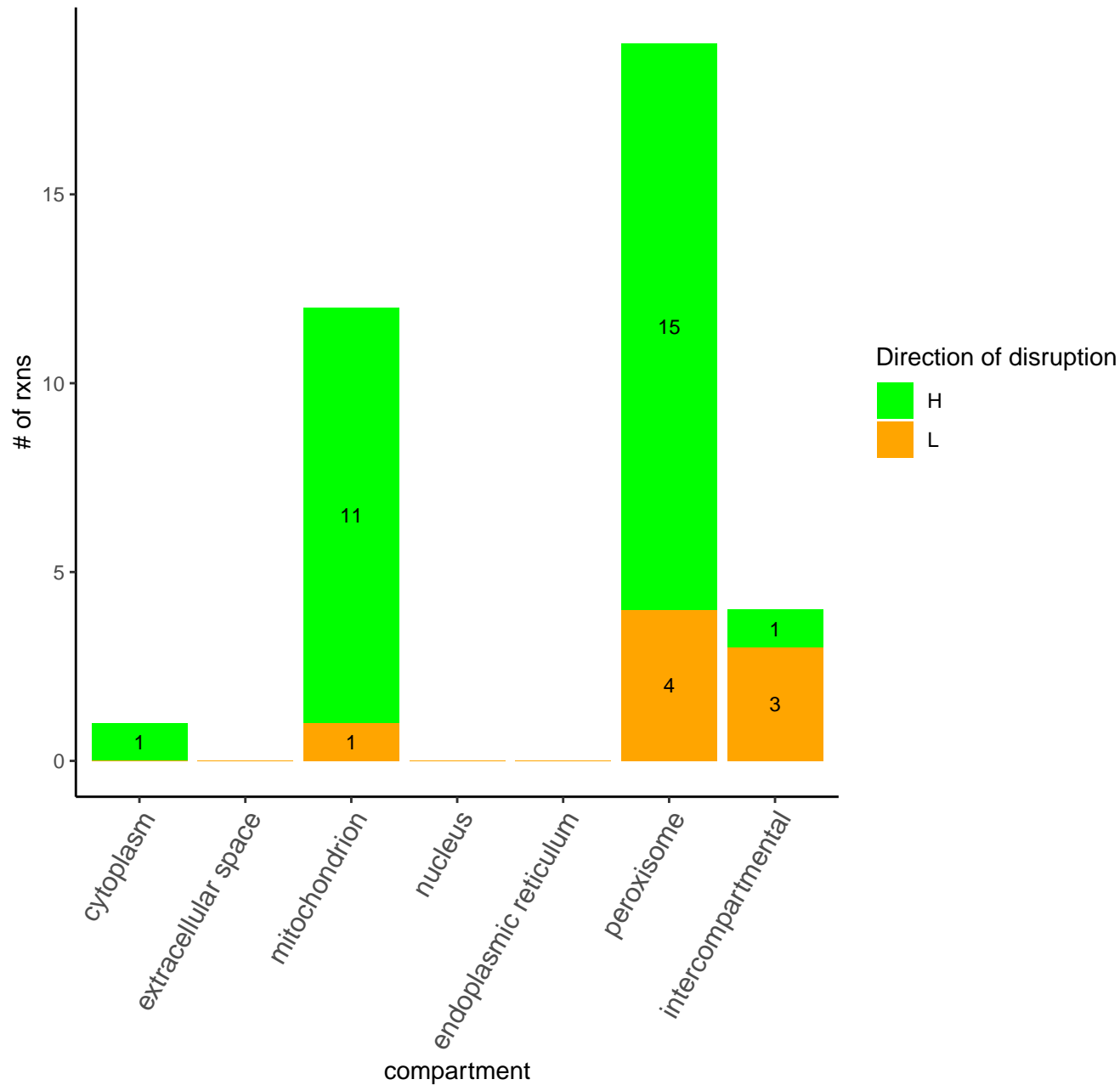
Disrupted rxns (fdr.significant, n=95) per compartment (bd_lumped)



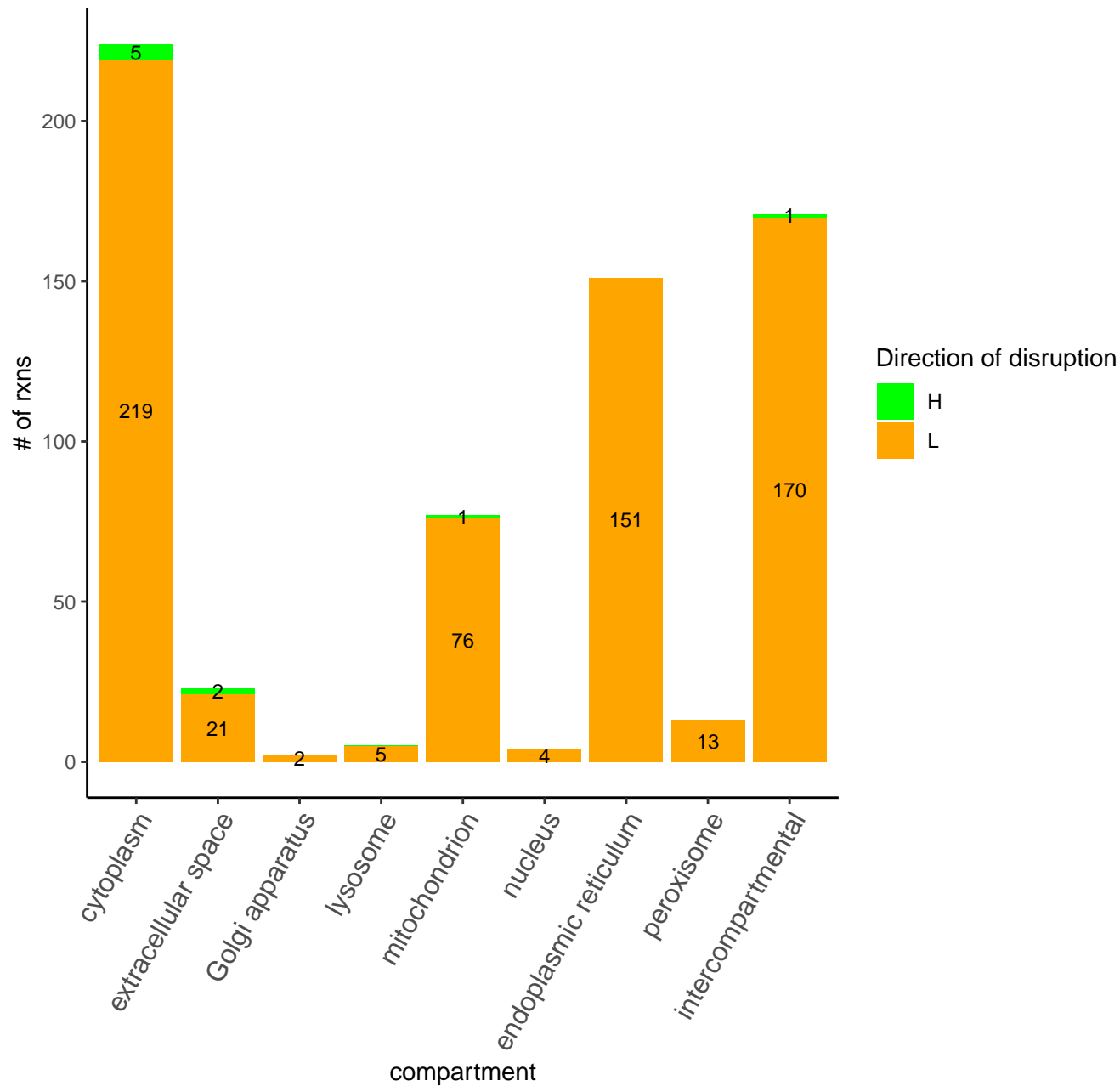
Disrupted rxns (all, n=92) per compartment (bd_responder)



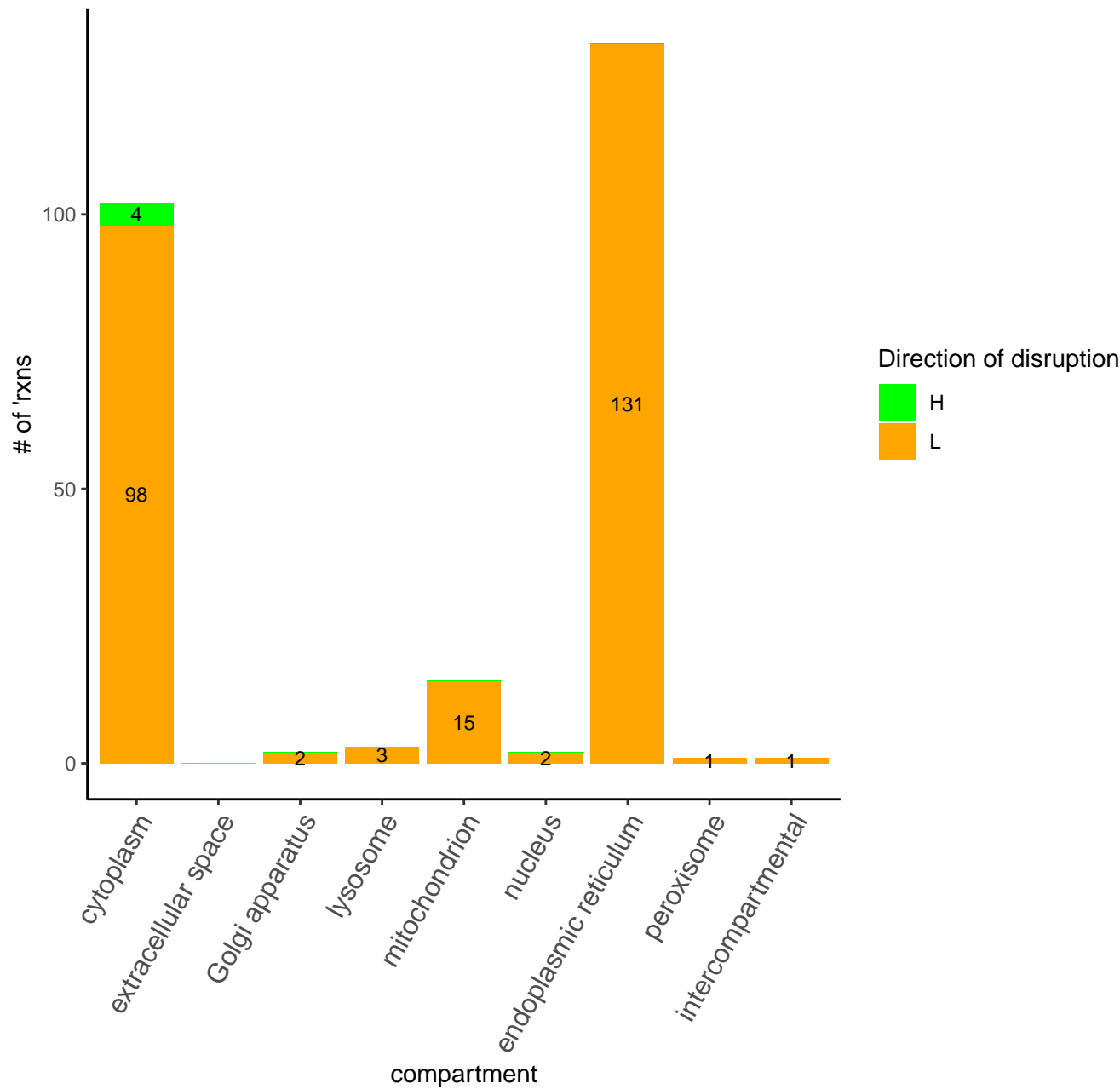
Disrupted rxns (fdr.significant, n=36) per compartment (bd_responder)



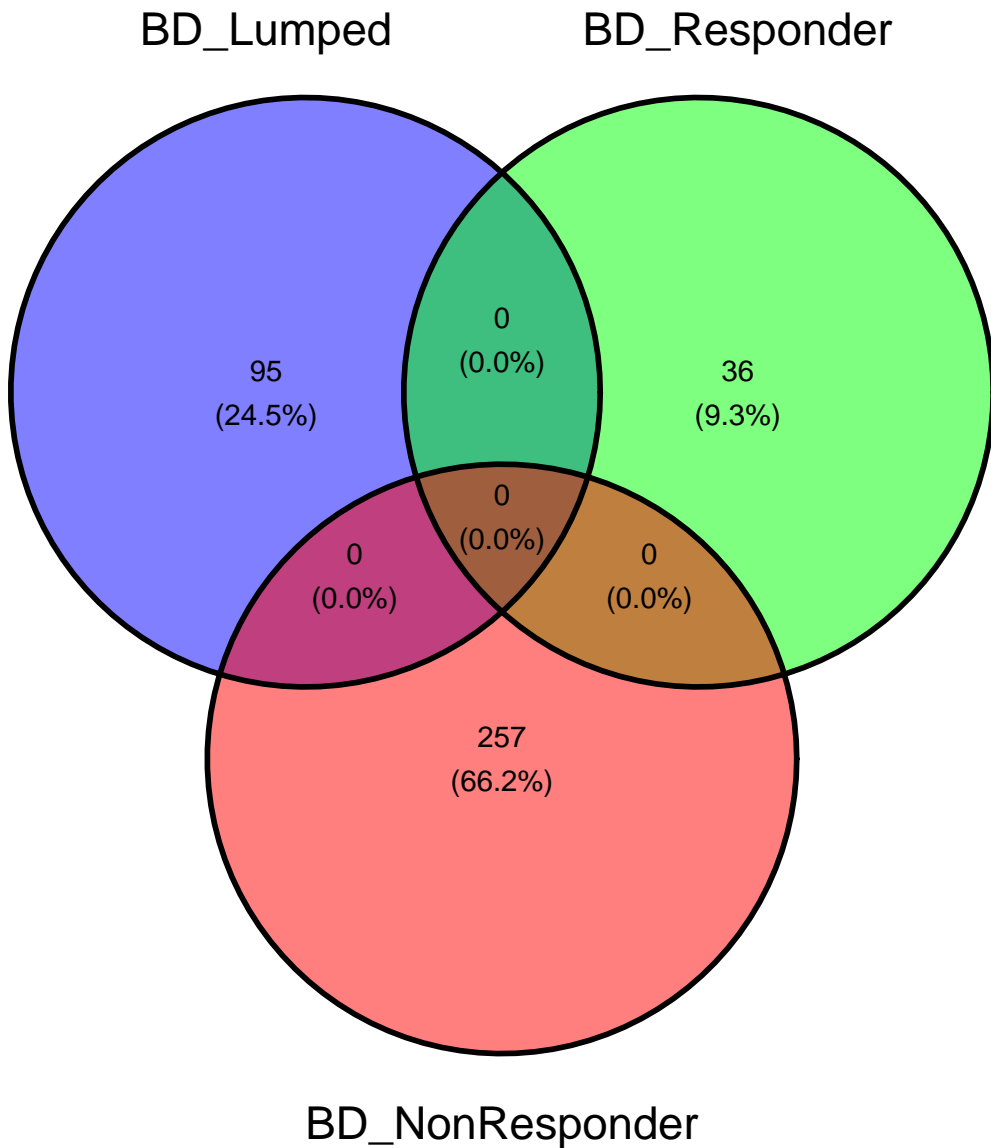
Disrupted rxns (all, n=670) per compartment (bd_nonresponder)



Disrupted rxns (fdr.significant, n=257) per compartment (bd_nonresponder)



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

