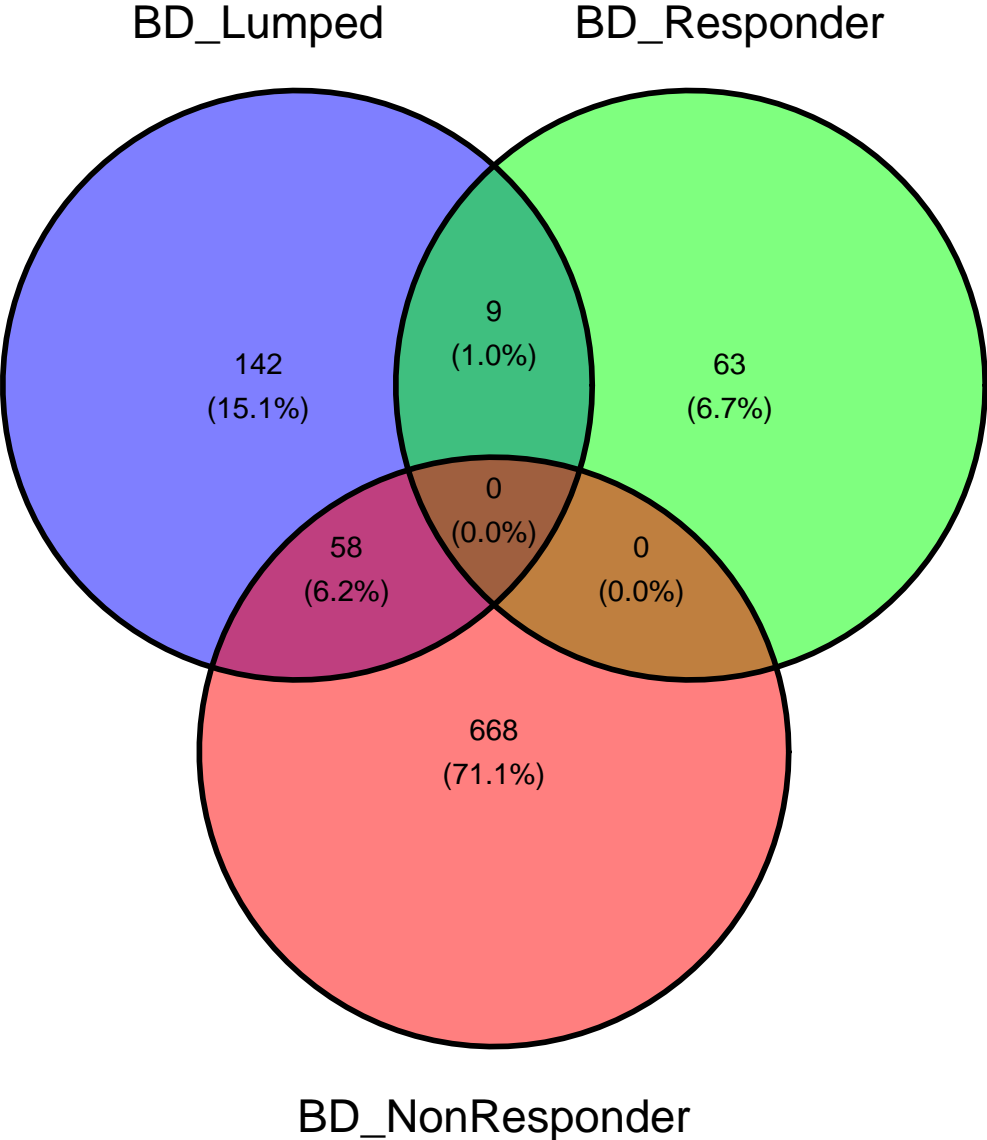
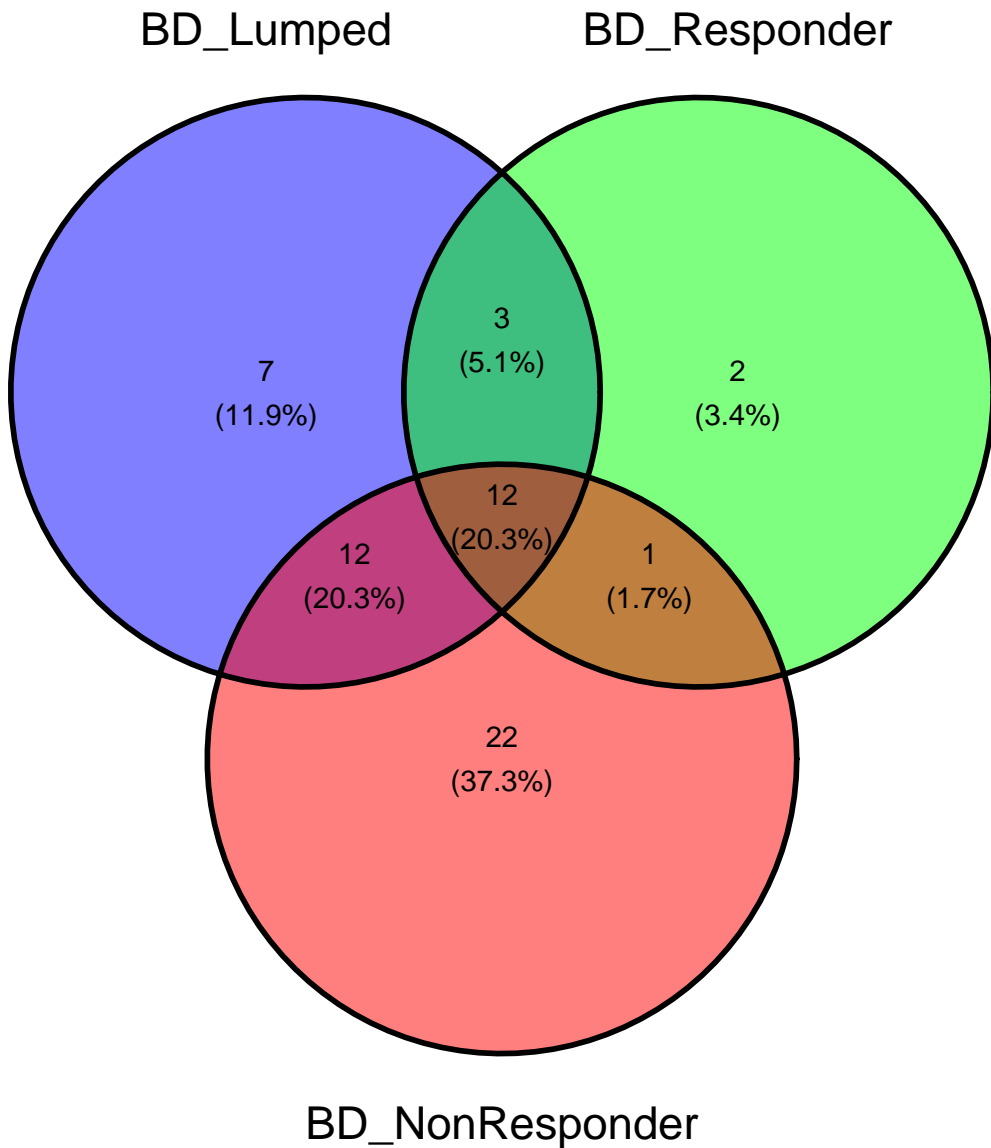


Overlap in rxns disrupted between models

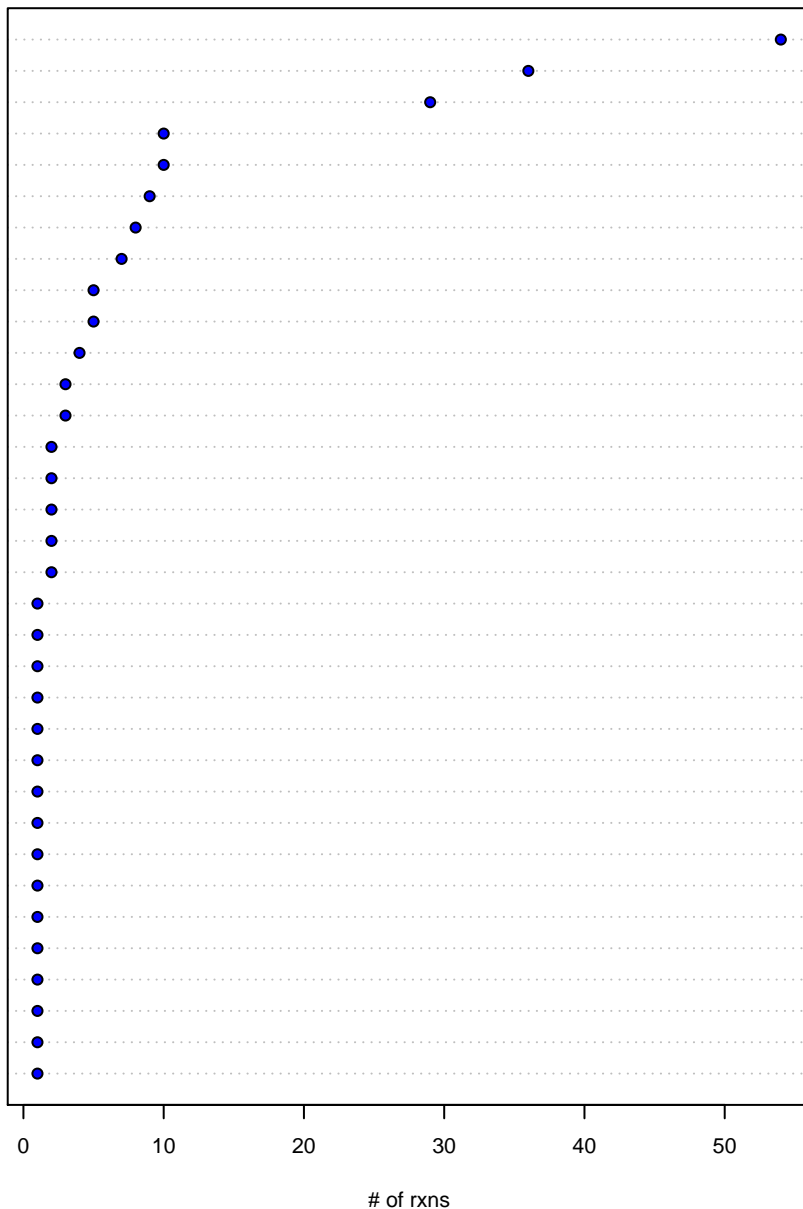


Overlap in subSystems disrupted between models

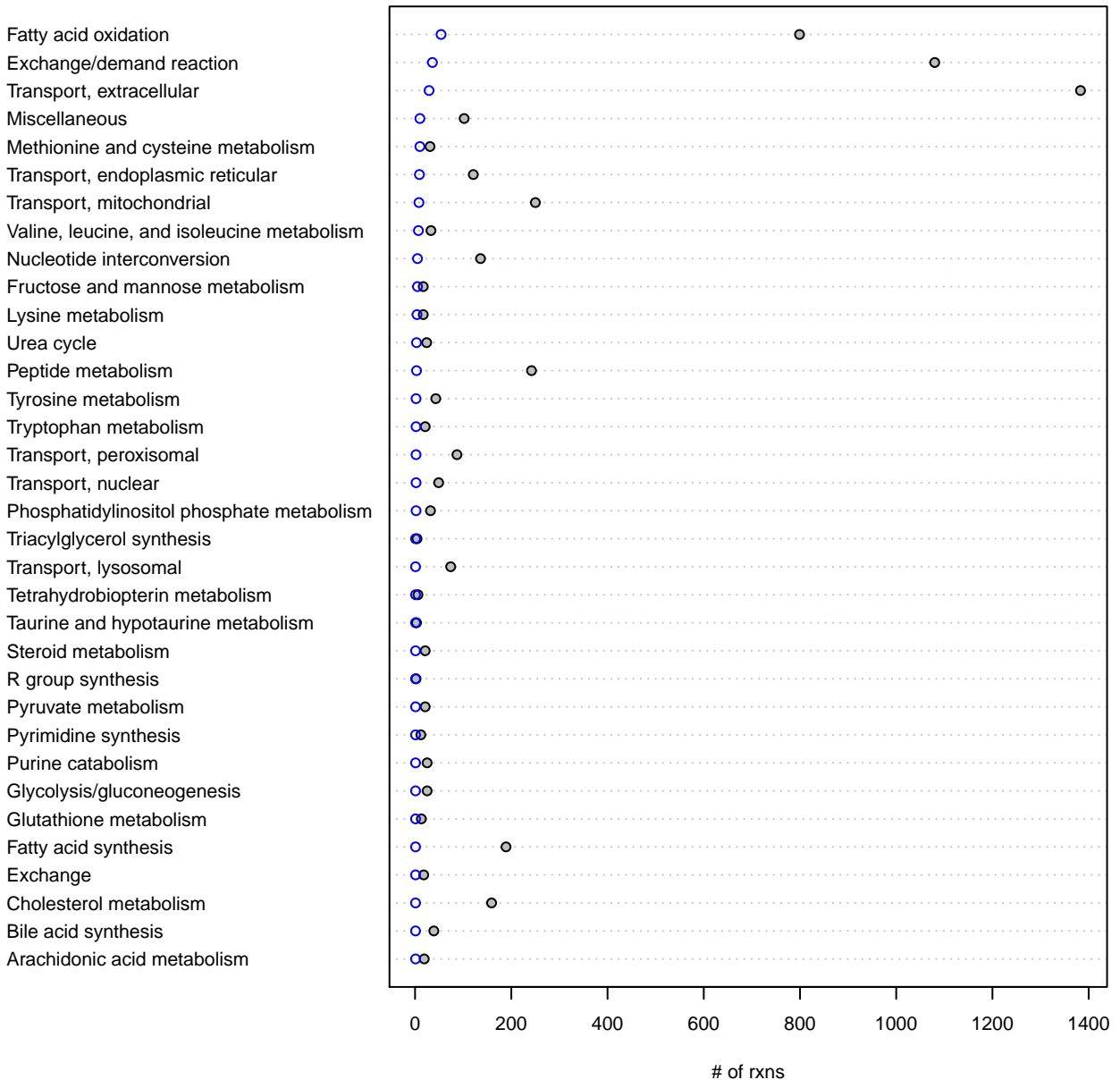


of disrupted rxns (n=209, bd_lumped)

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

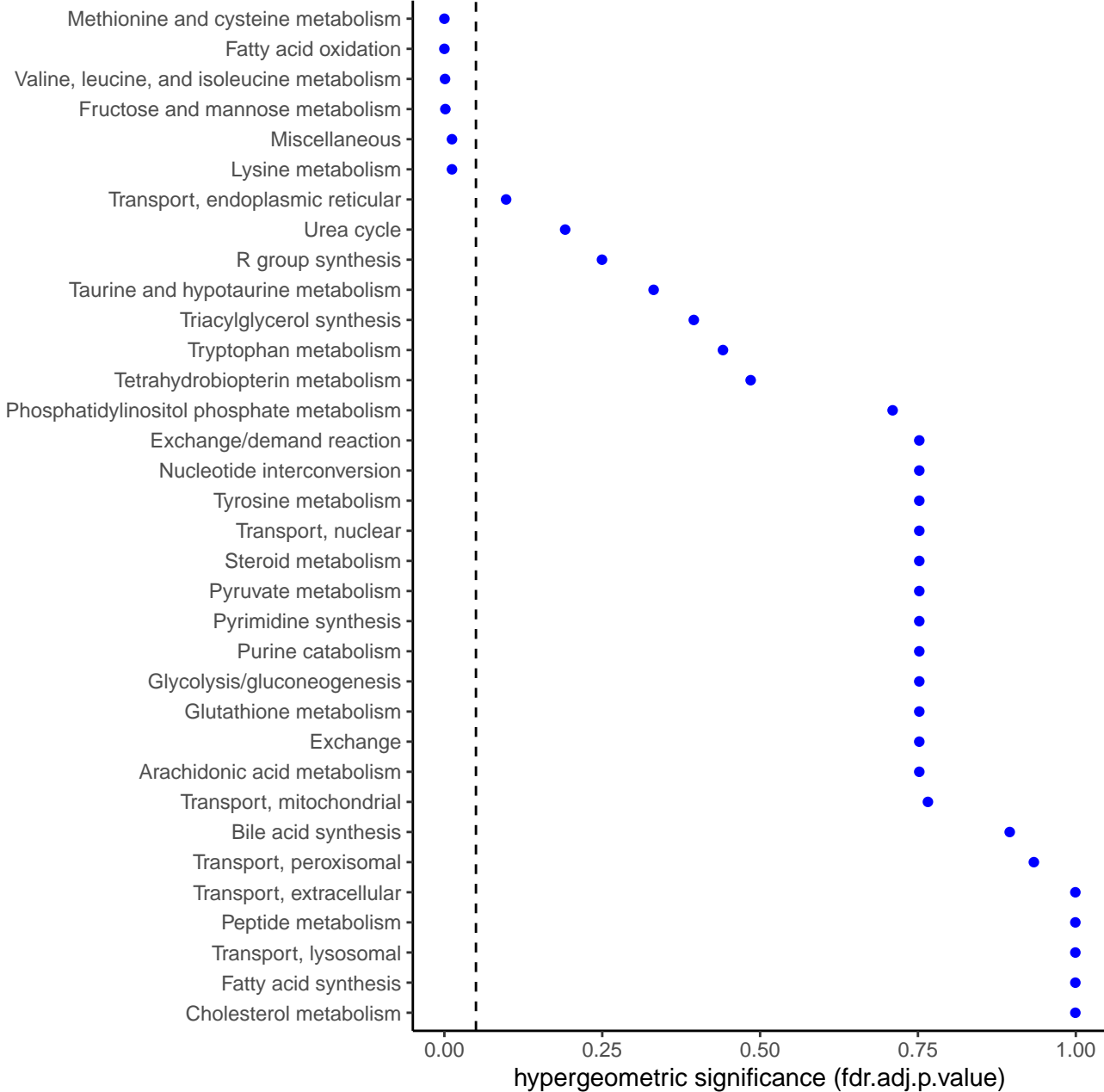


of disrupted rxns (n=209, bd_lumped) vs all rxns

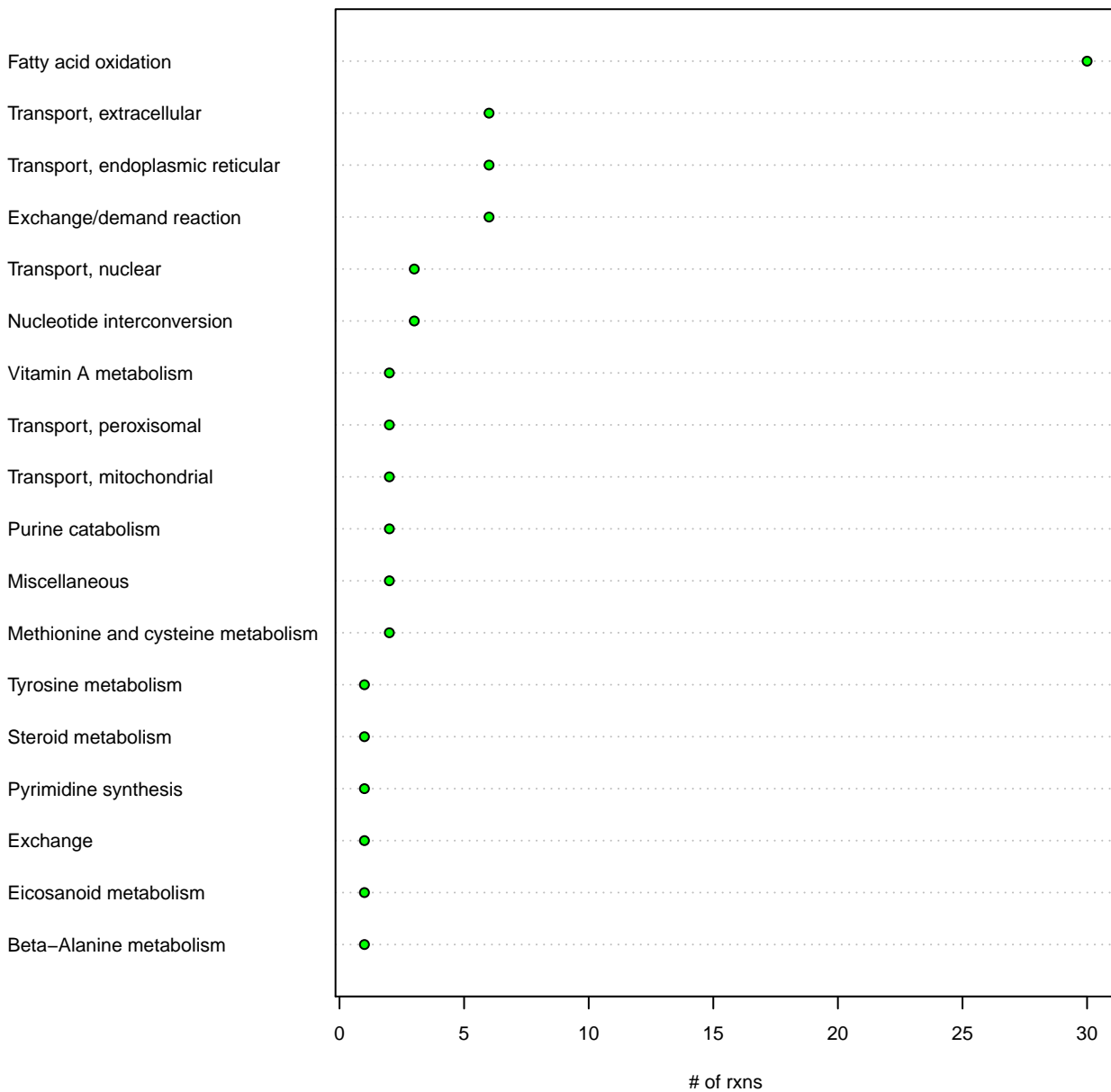


over-representation analysis, bd_lumped

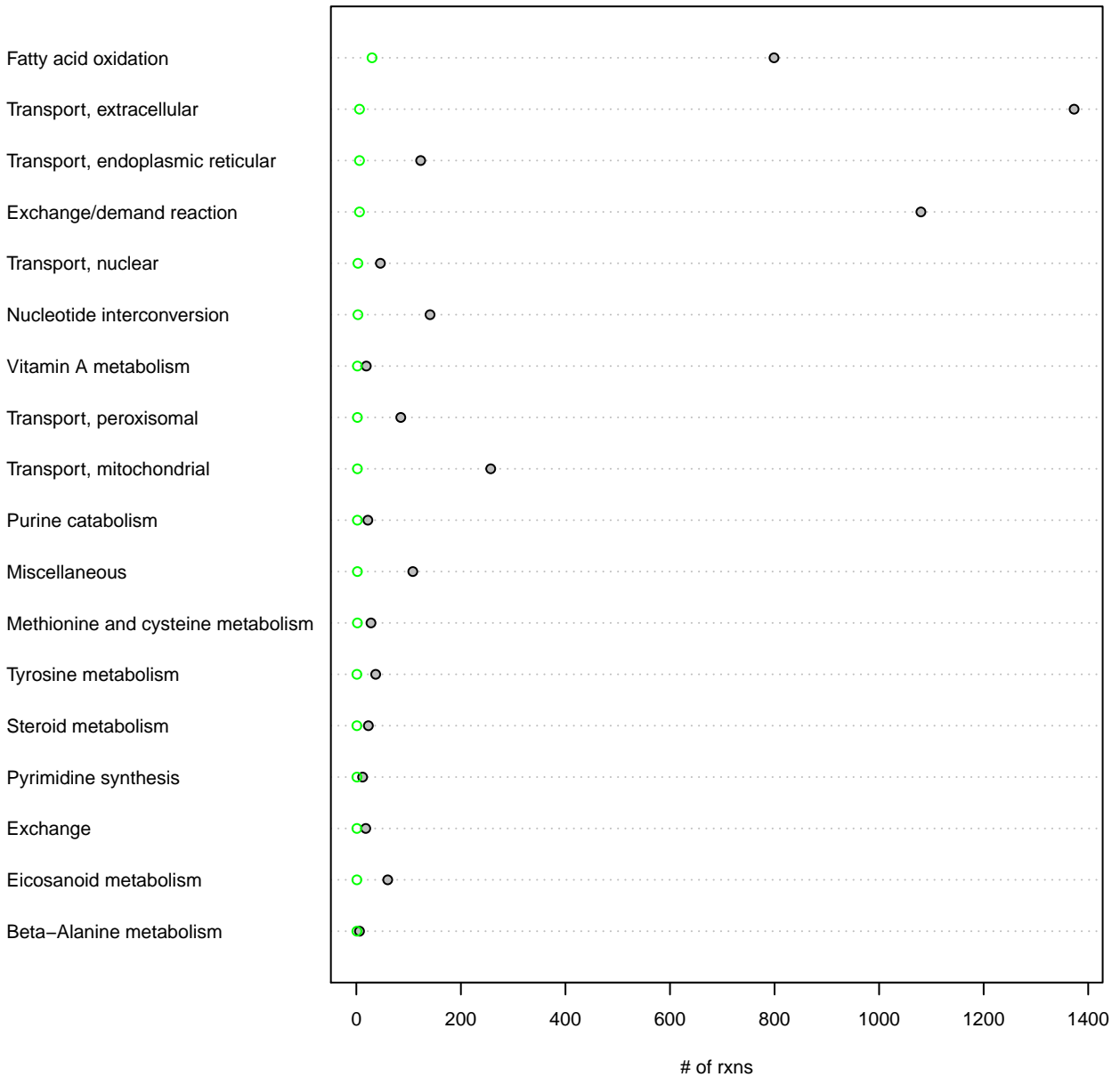
subSystem



of disrupted rxns (n=72, bd_responder)

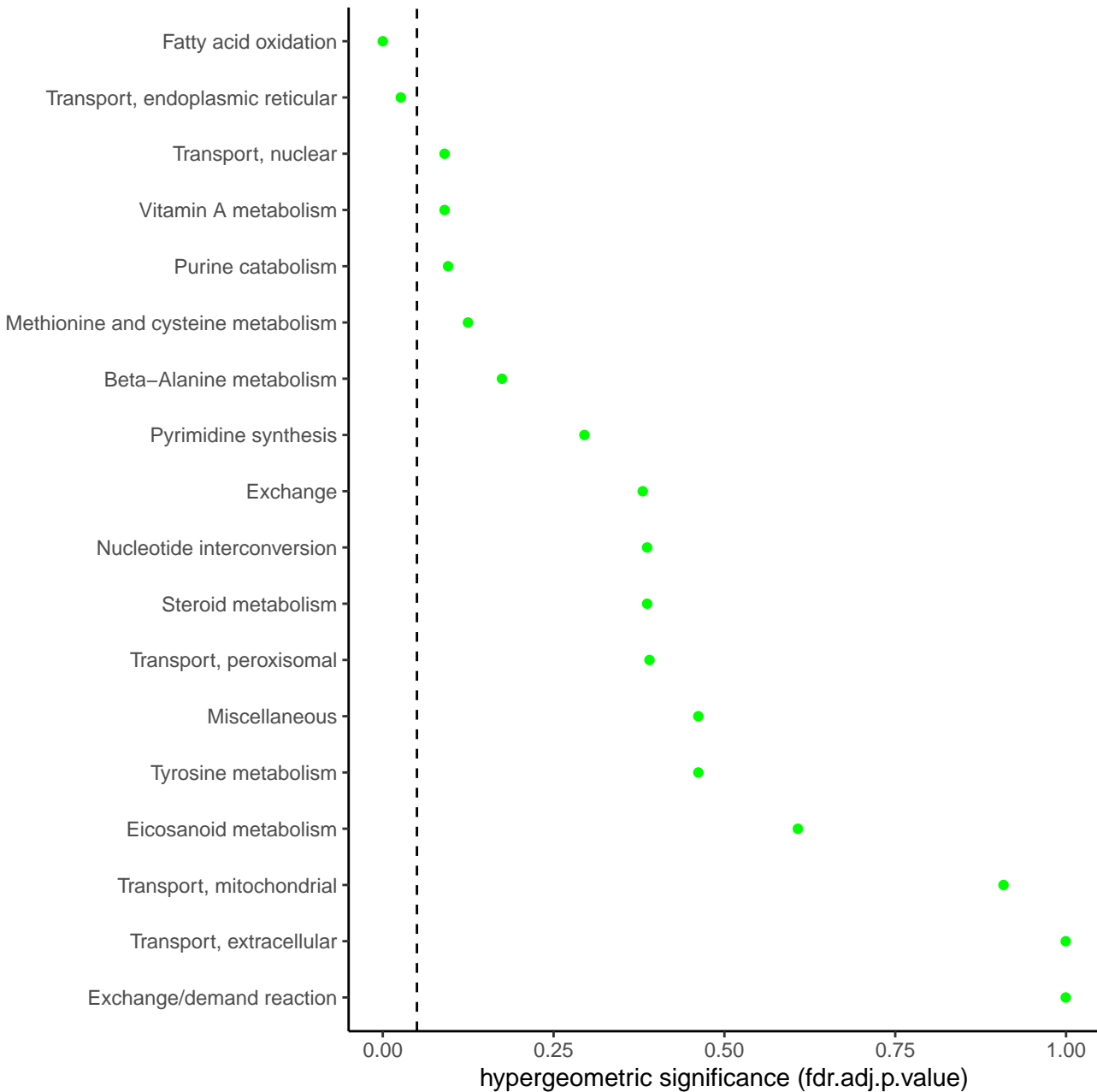


of disrupted rxns (n=72, bd_responder) vs all rxns



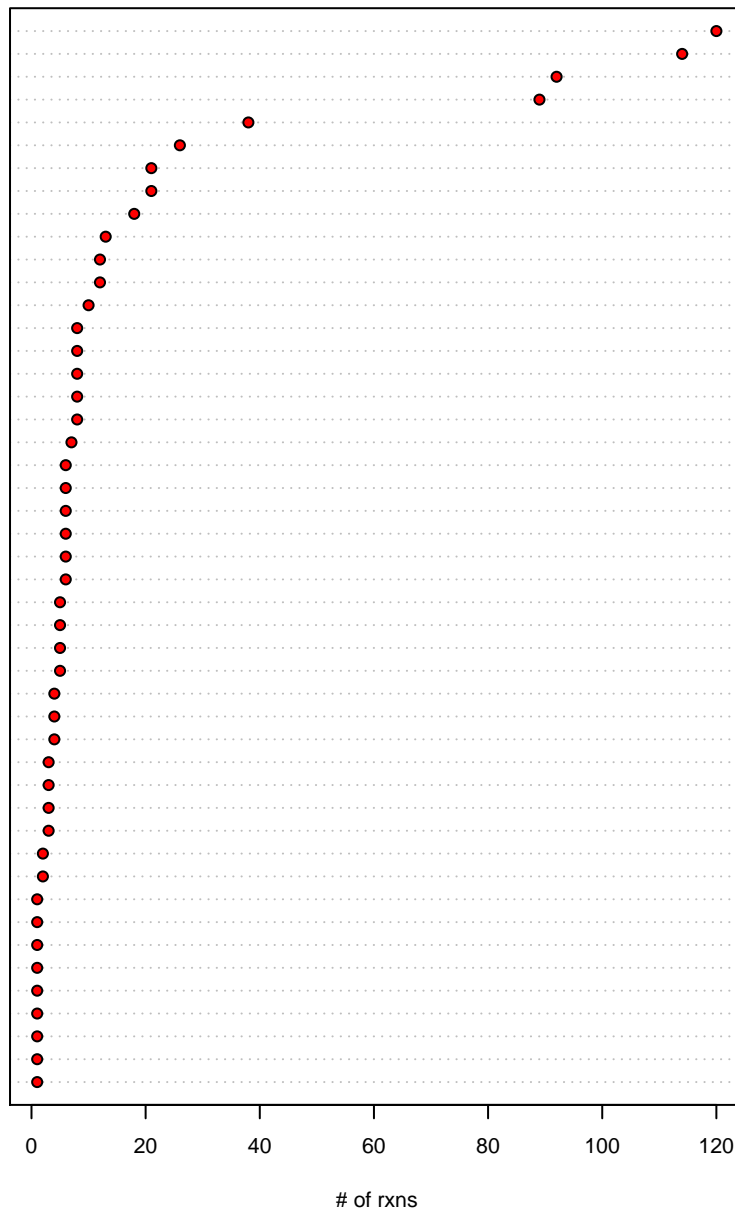
over-representation analysis, bd_responder

subSystem

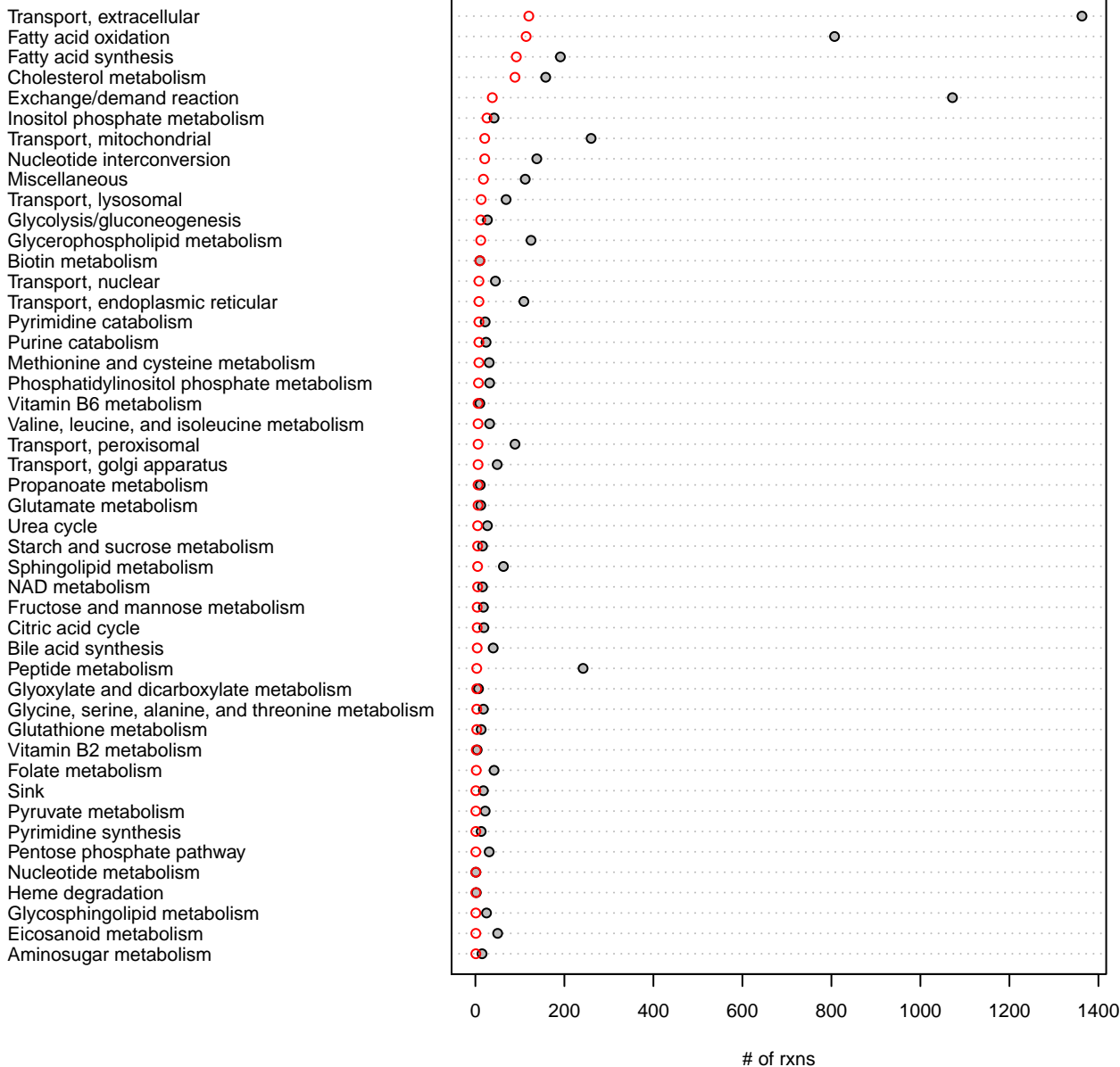


of disrupted rxns (n=726, bd_nonresponder)

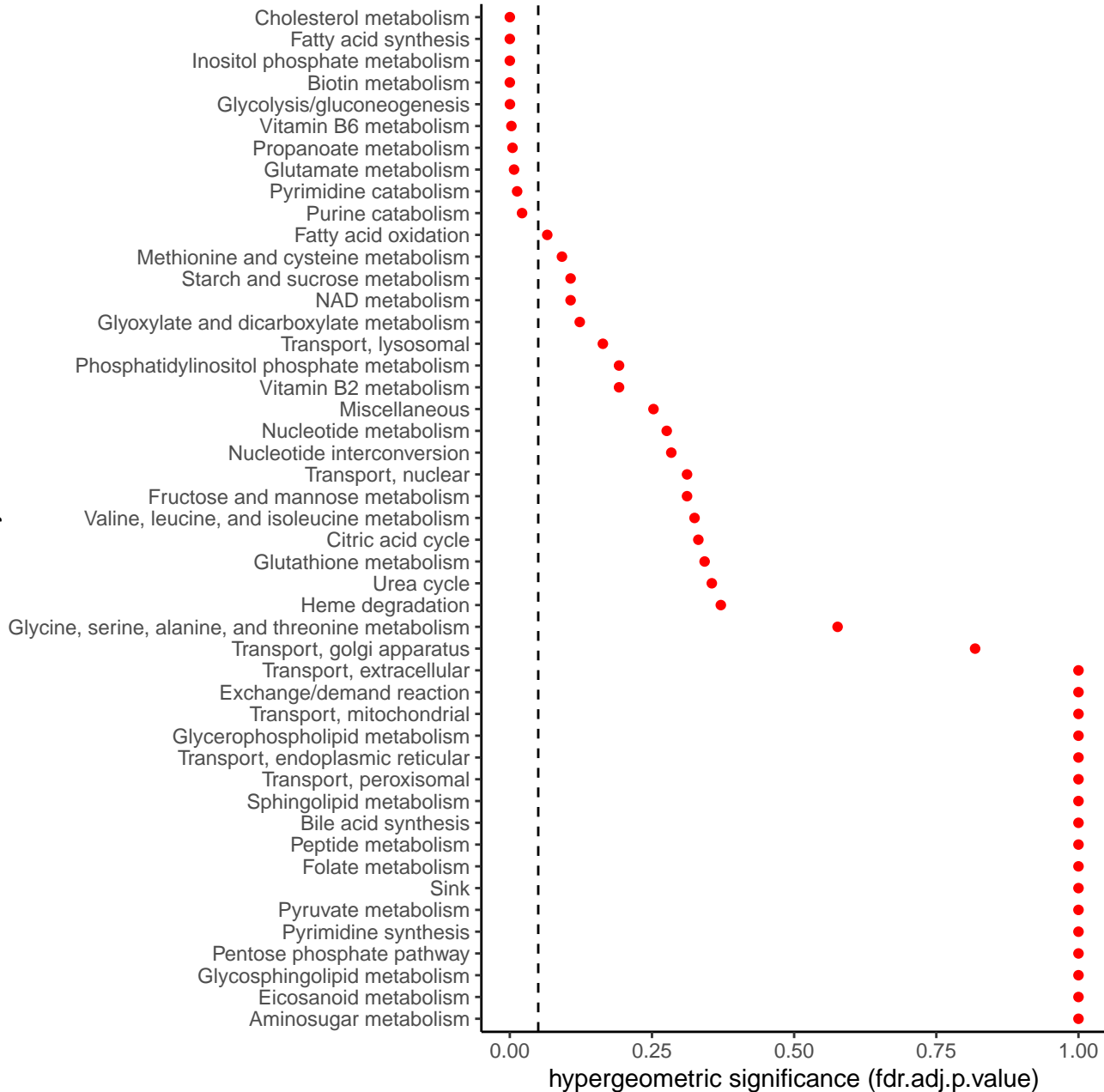
Transport, extracellular
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Exchange/demand reaction
Inositol phosphate metabolism
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Biotin metabolism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



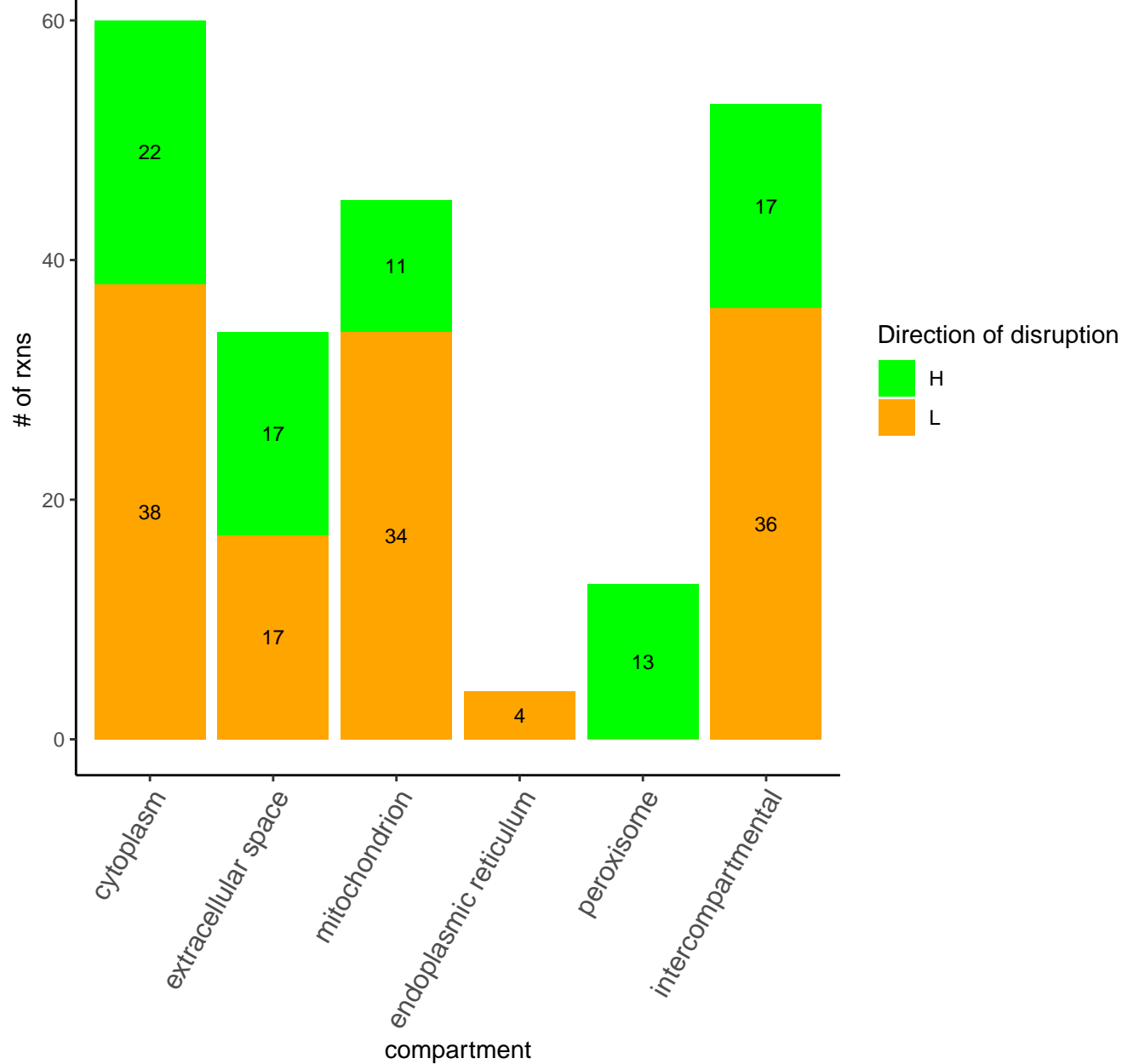
of disrupted rxns (n=726, bd_nonresponder) vs all rxns



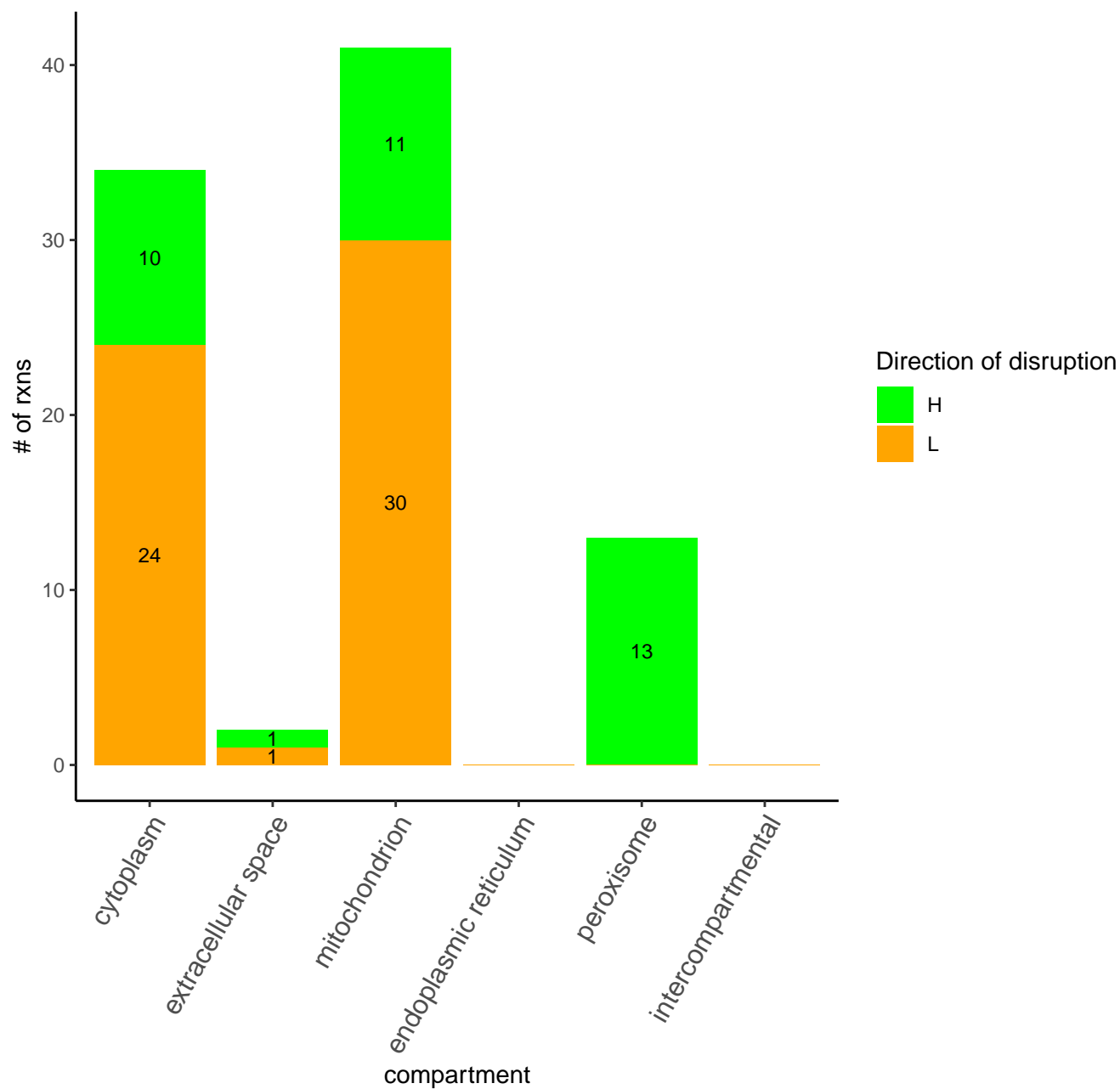
subSystem



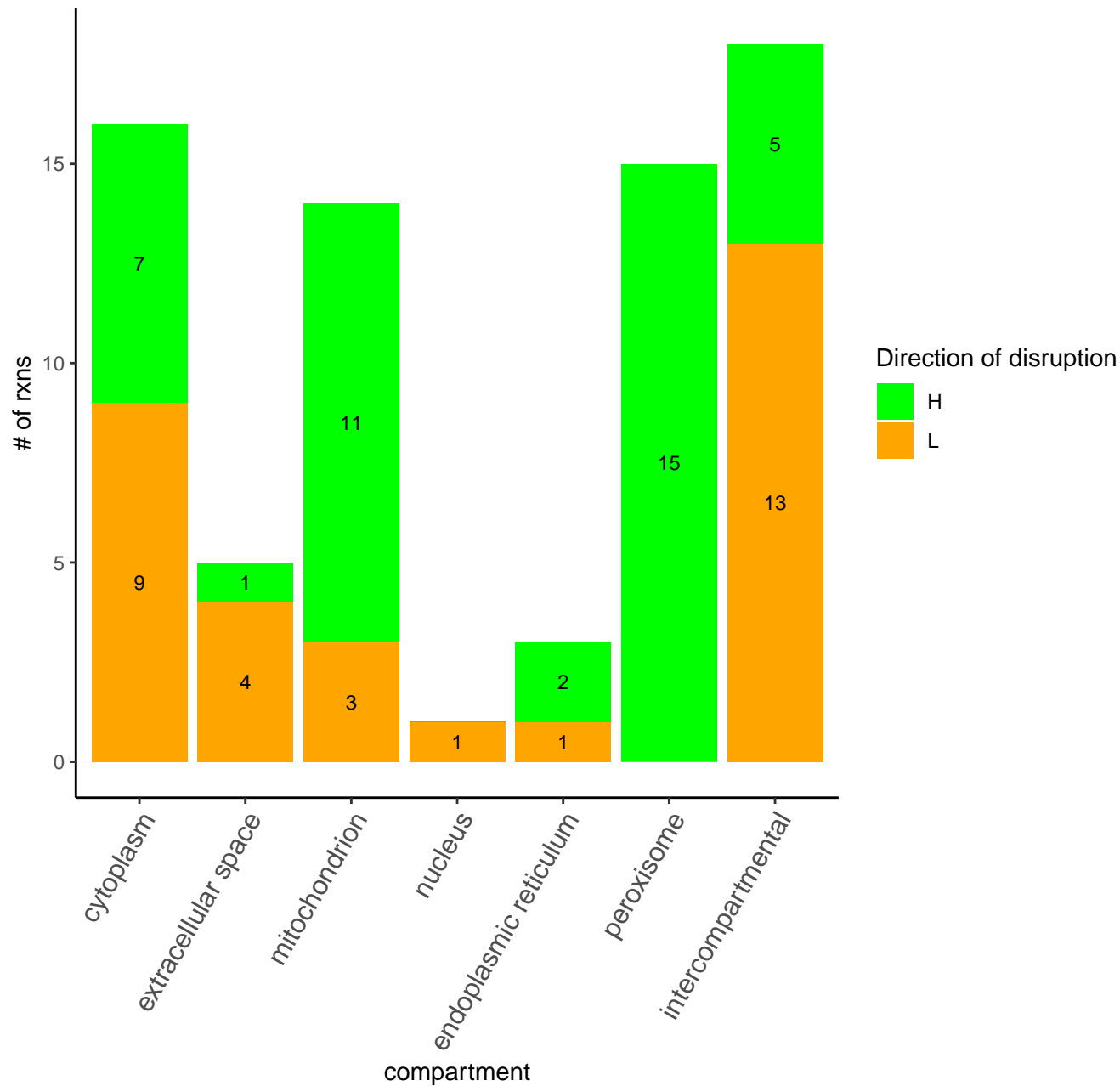
Disrupted rxns (all, n=209) per compartment (bd_lumped)



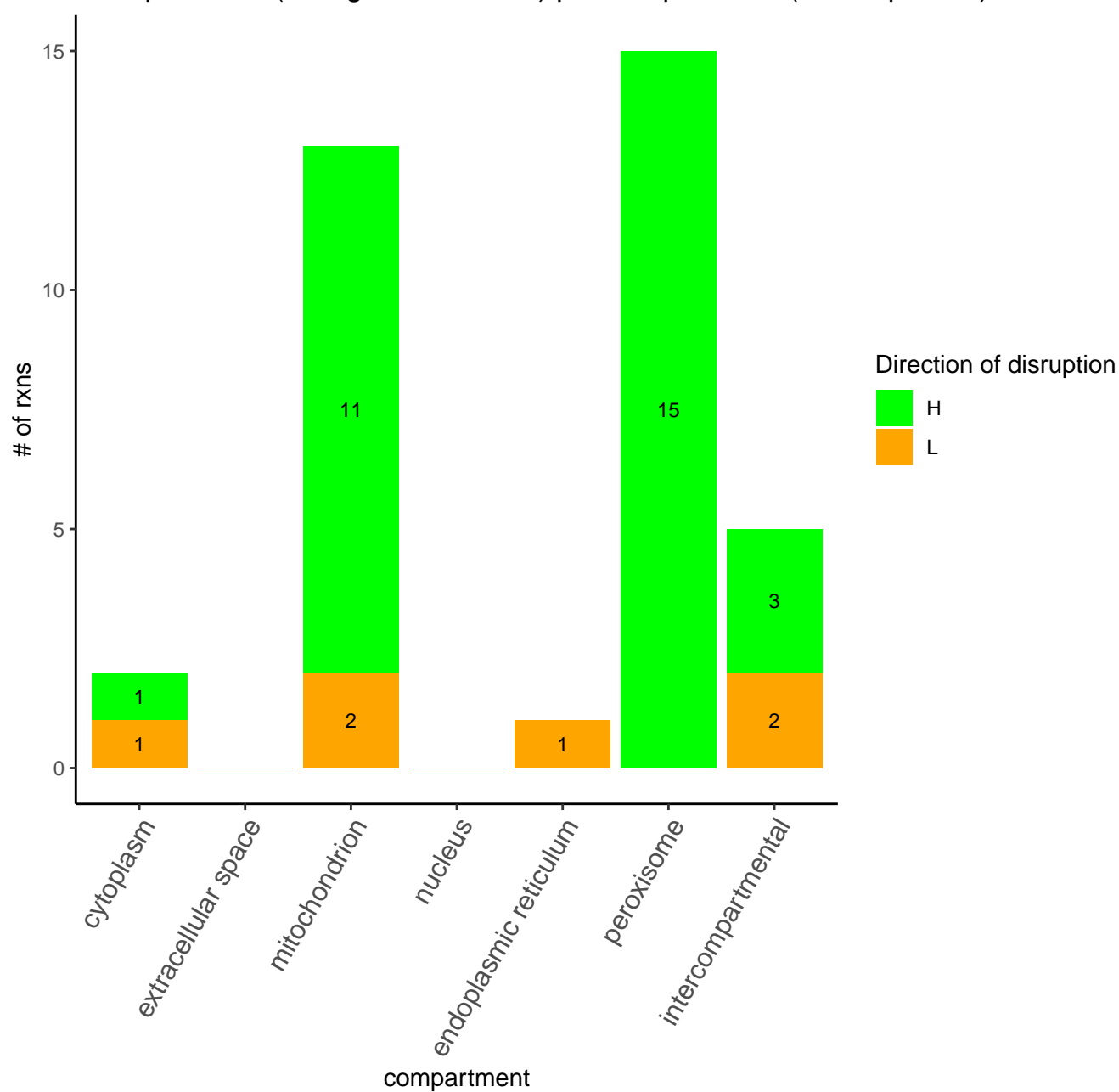
Disrupted rxns (fdr.significant, n=90) per compartment (bd_lumped)



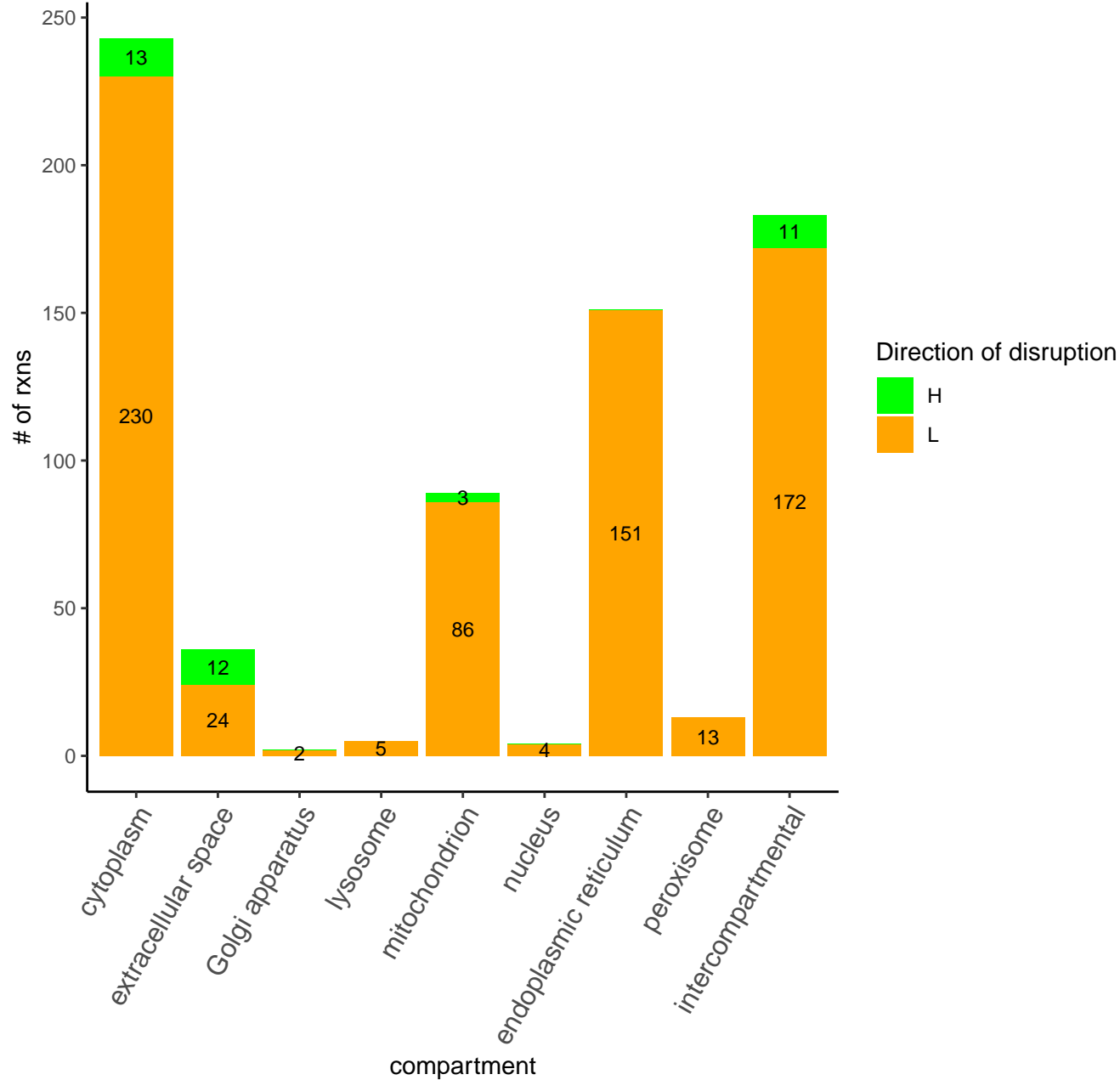
Disrupted rxns (all, n=72) per compartment (bd_responder)



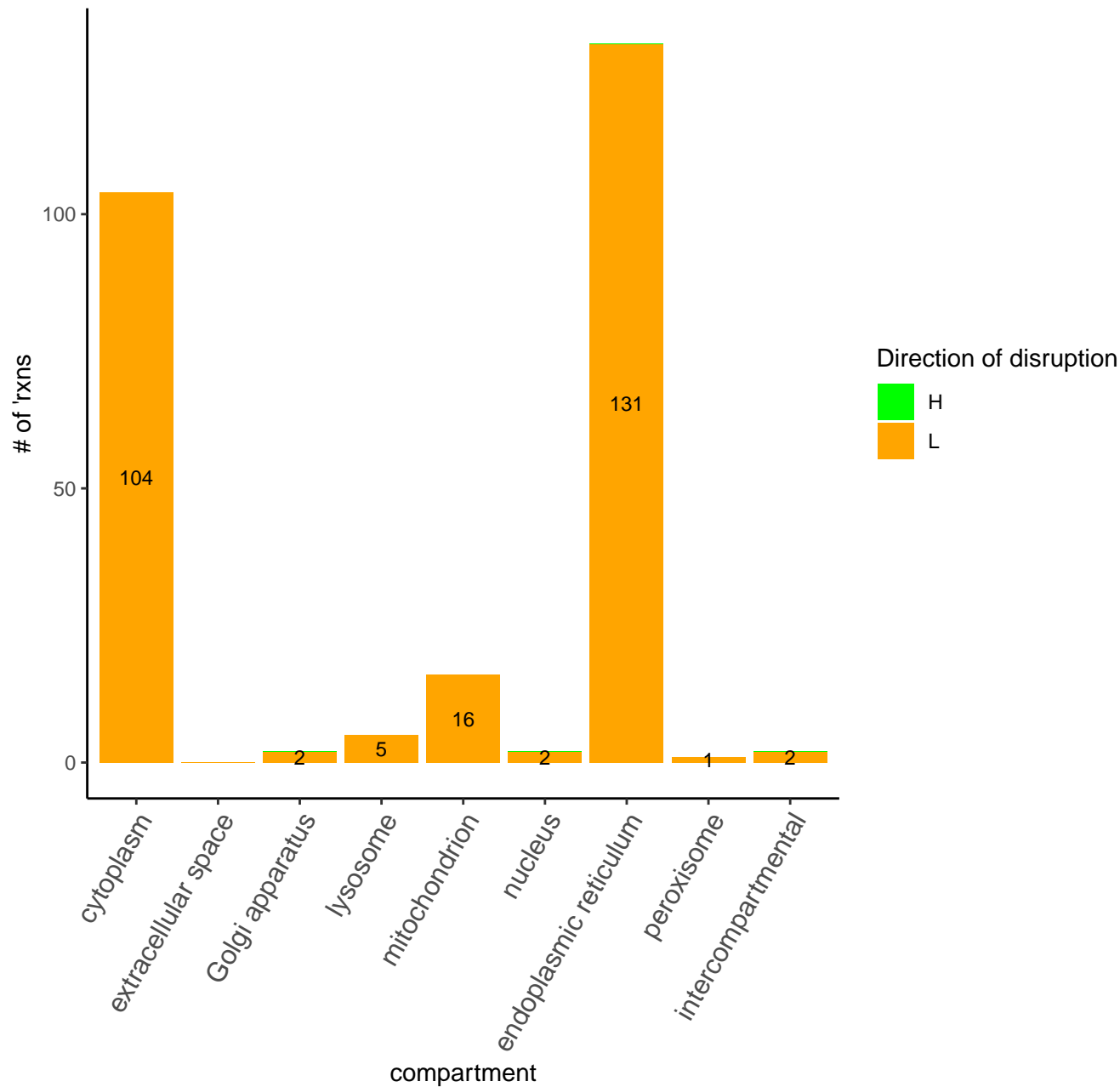
Disrupted rxns (fdr.significant, n=36) per compartment (bd_responder)



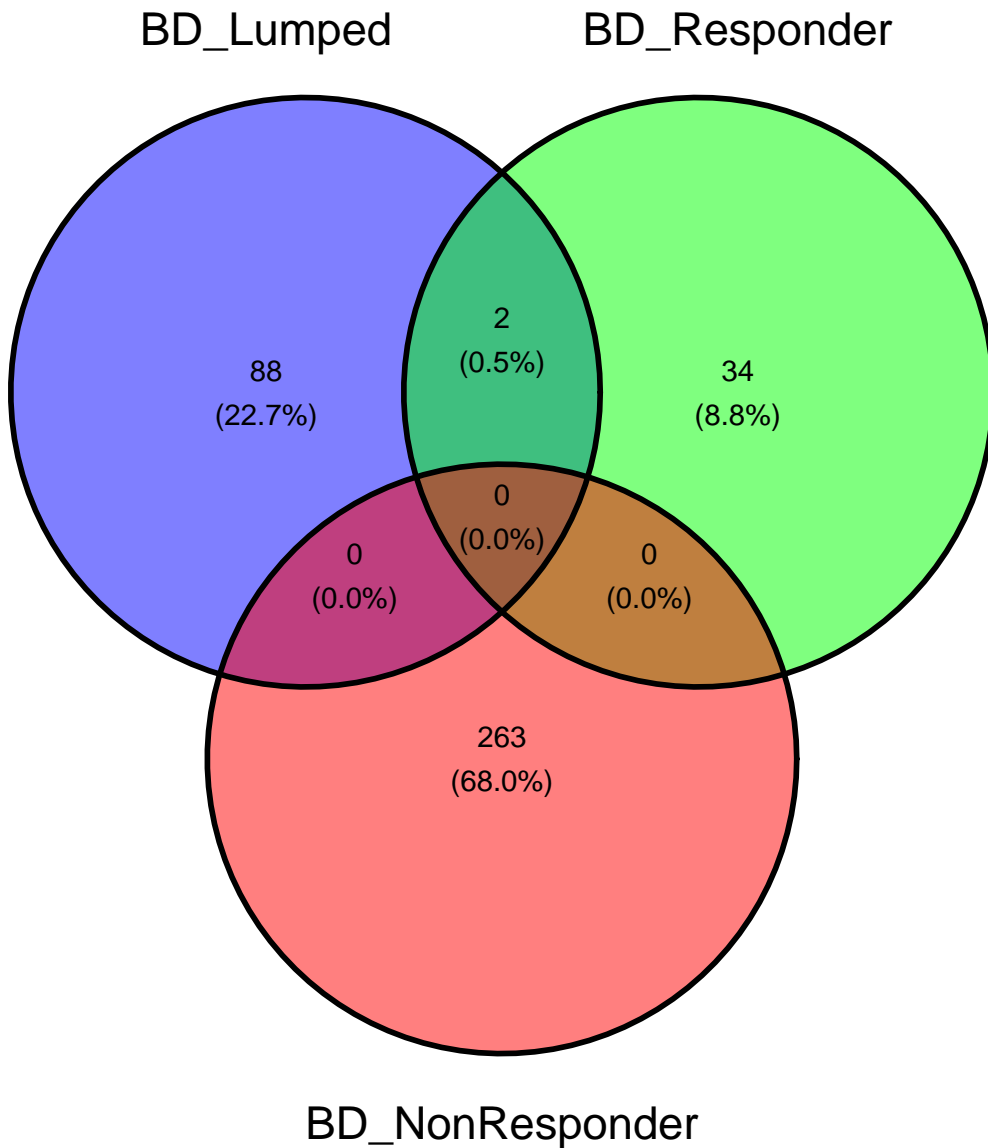
Disrupted rxns (all, n=726) per compartment (bd_nonresponder)



Disrupted rxns (fdr.significant, n=263) per compartment (bd_nonresponder)



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

