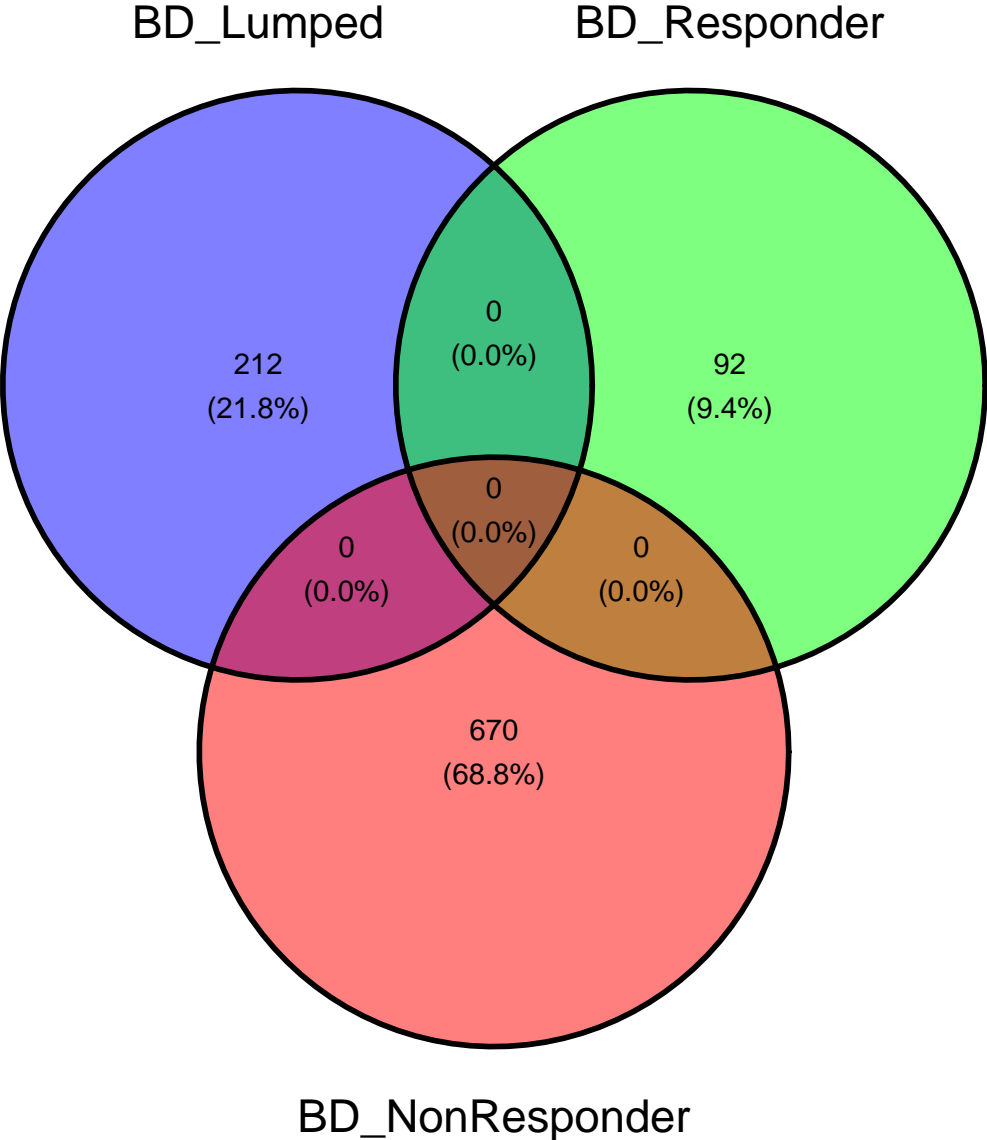
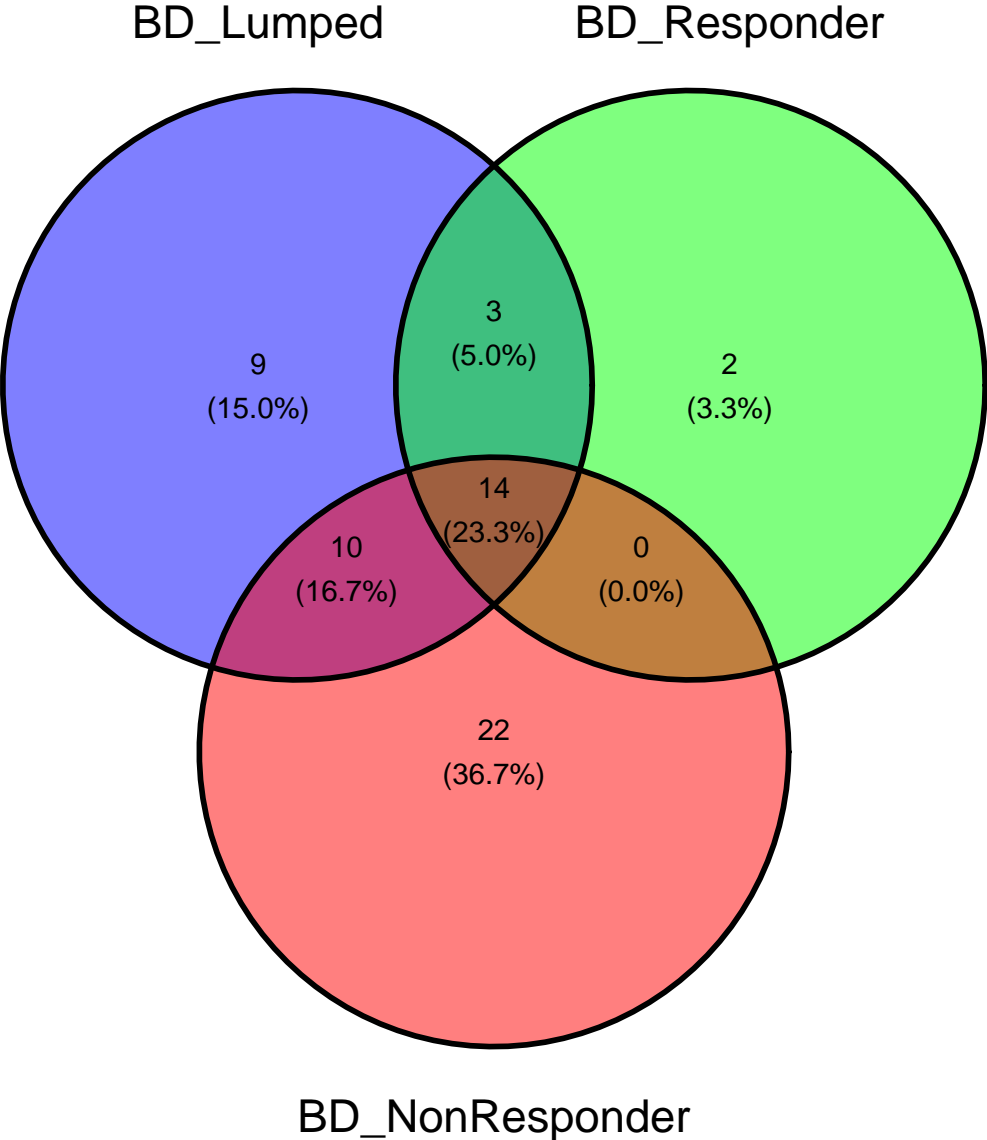


Overlap in rxns disrupted between models

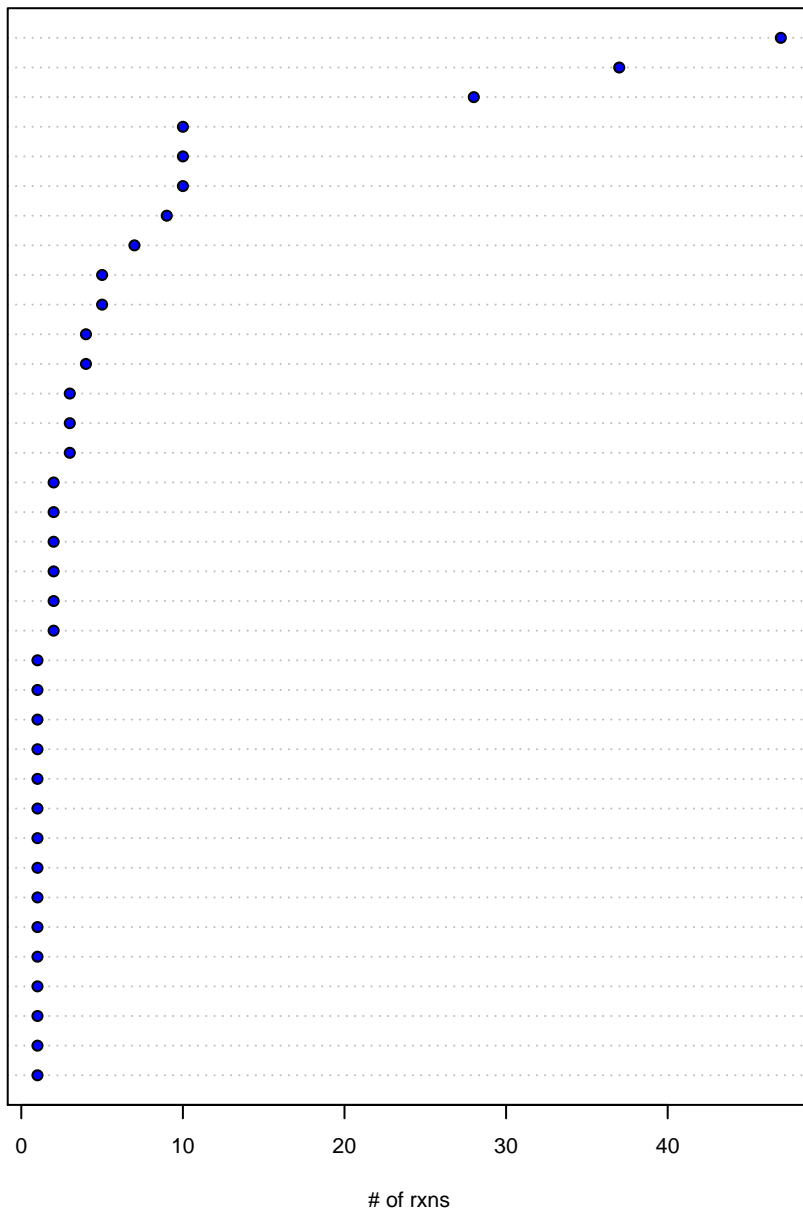


Overlap in subSystems disrupted between models



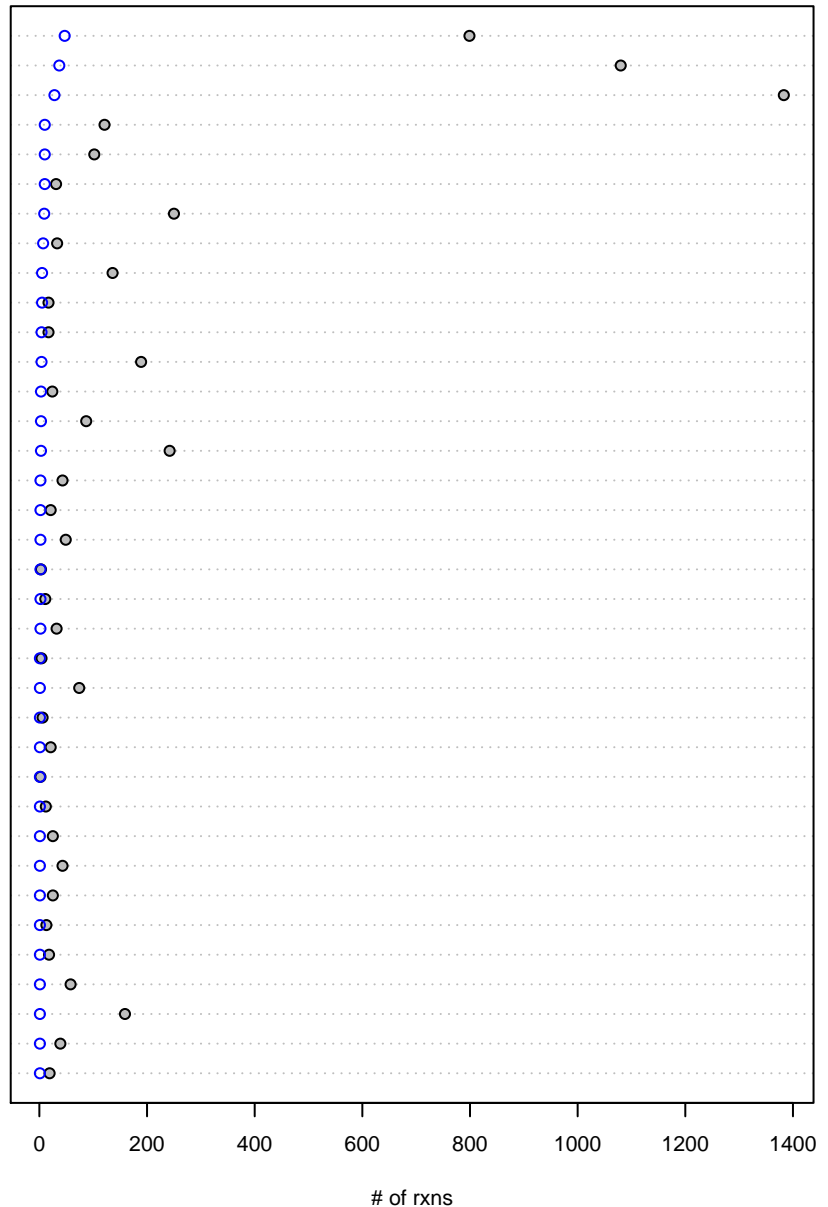
of disrupted rxns (n=212, bd_lumped)

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



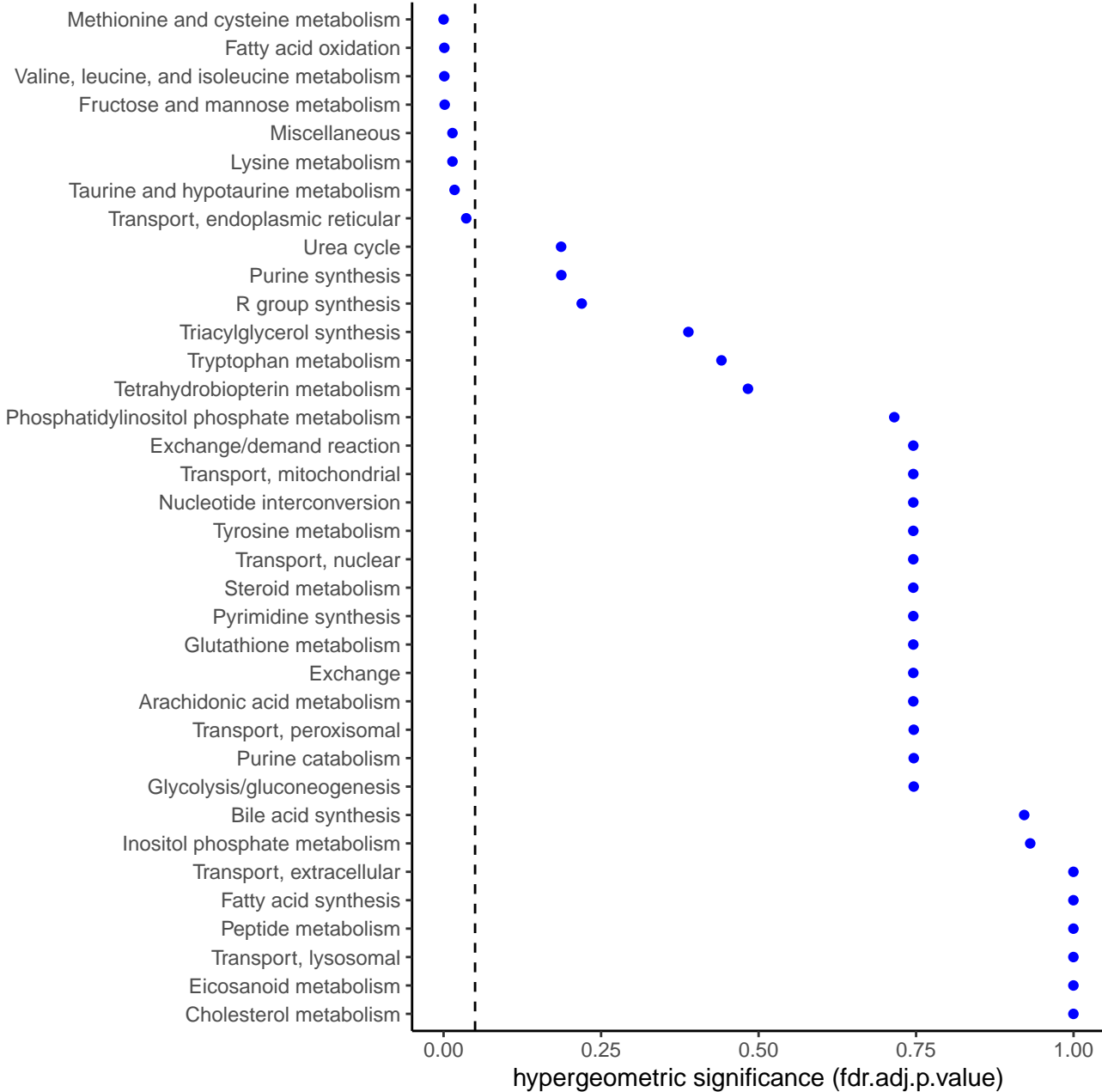
of disrupted rxns (n=212, bd_lumped) vs all rxns

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

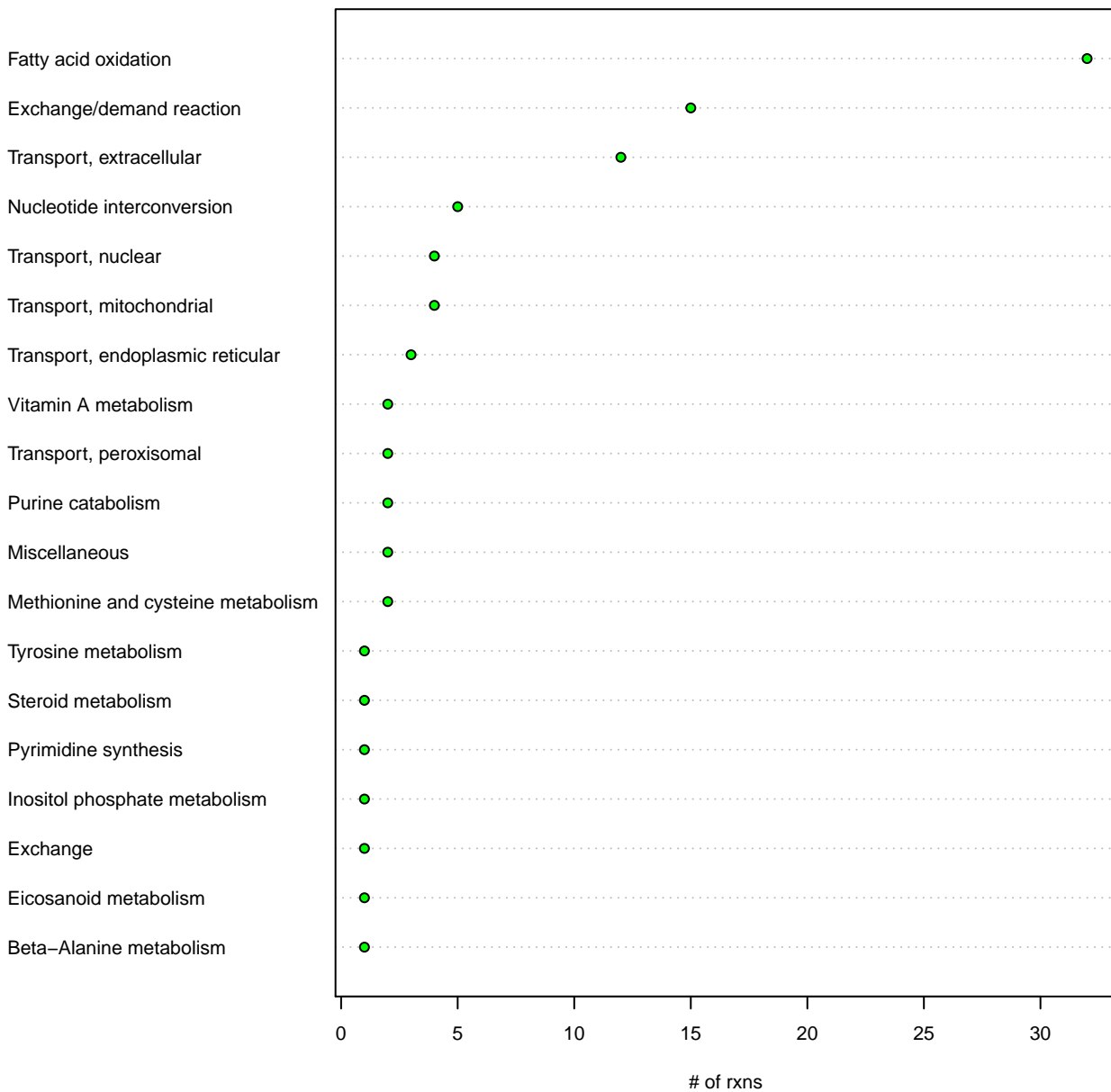


over-representation analysis, bd_lumped

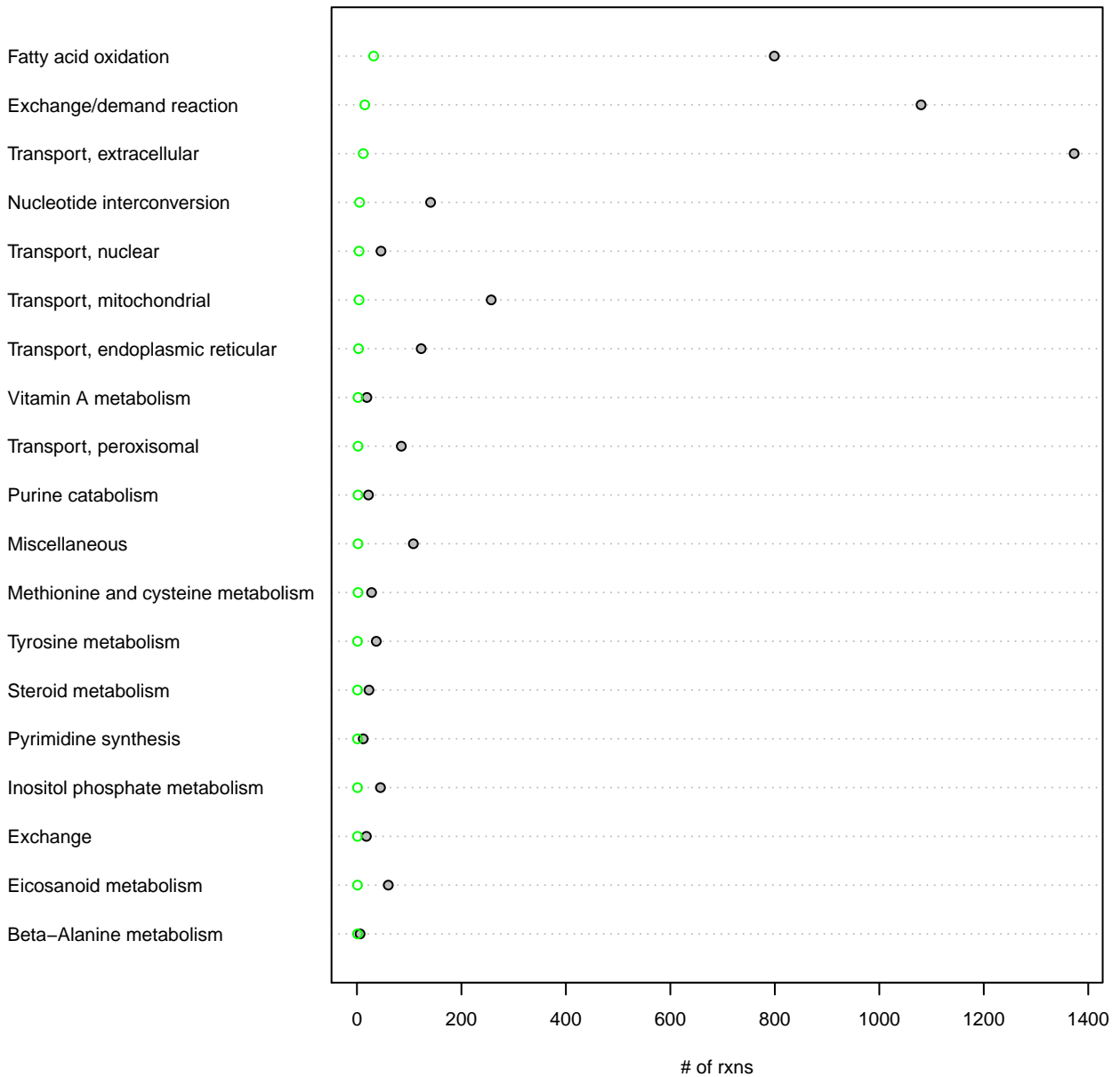
subSystem



of disrupted rxns (n=92, bd_responder)

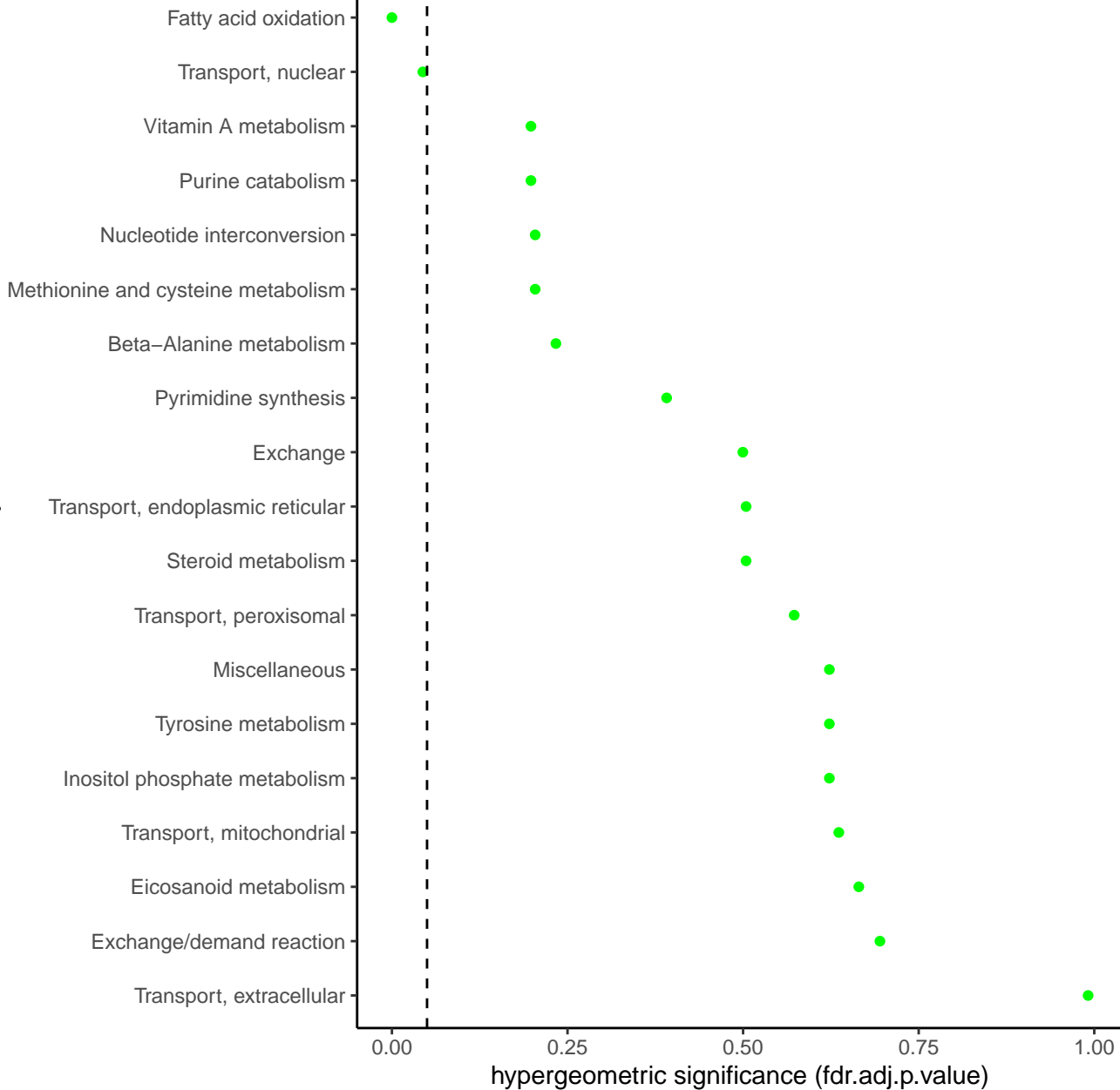


of disrupted rxns (n=92, bd_responder) vs all rxns

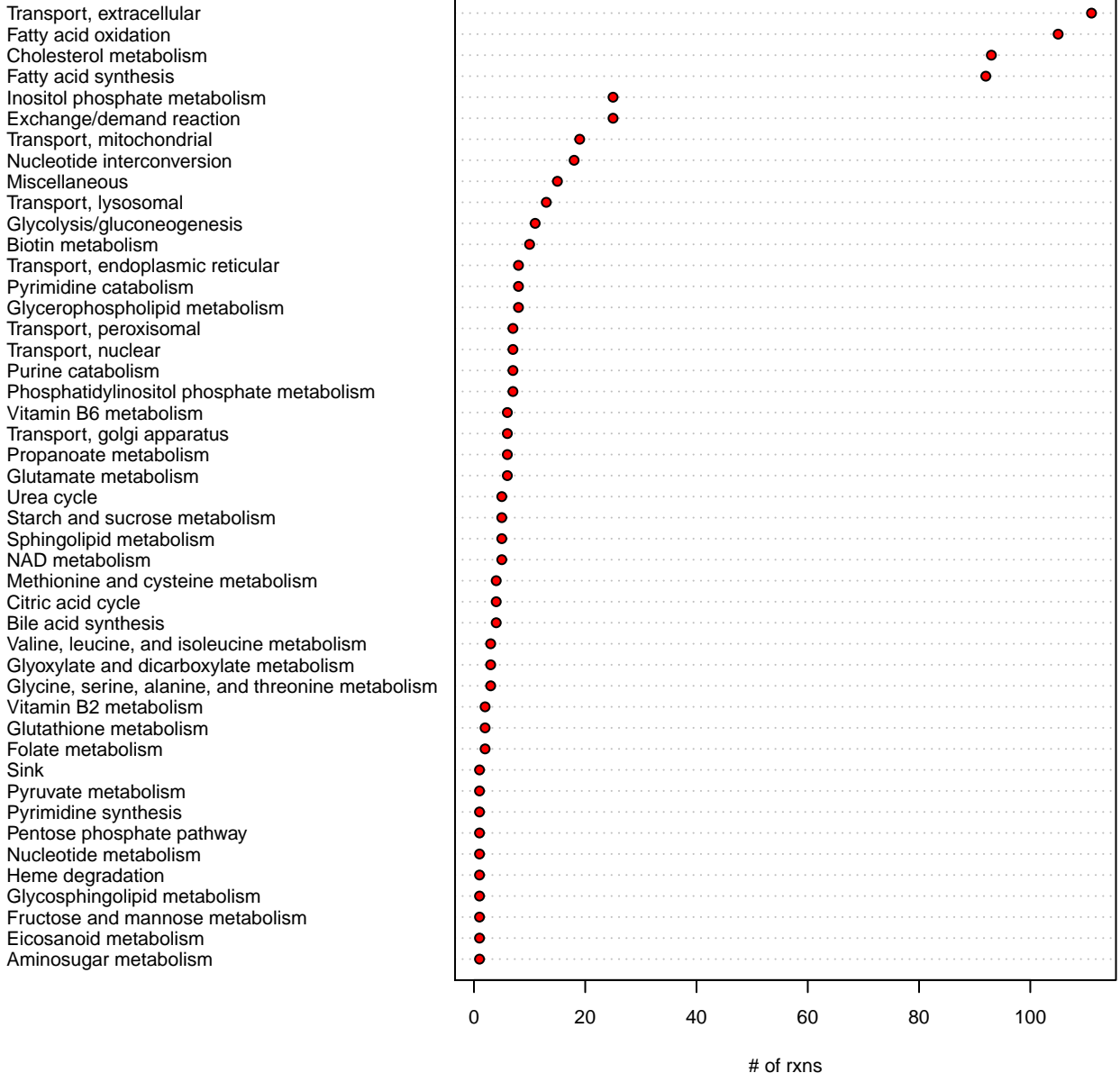


over-representation analysis, bd_responder

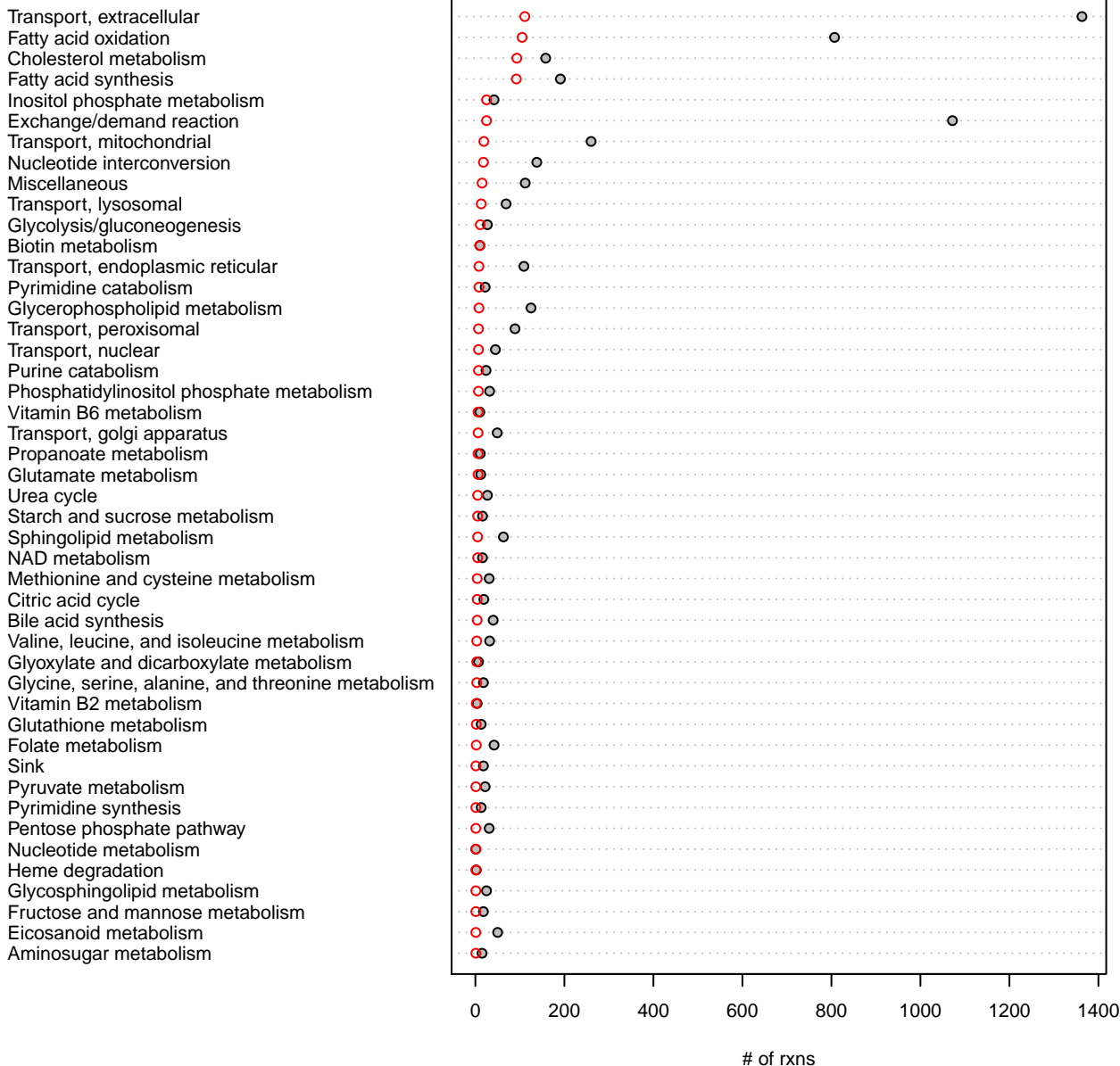
subSystem



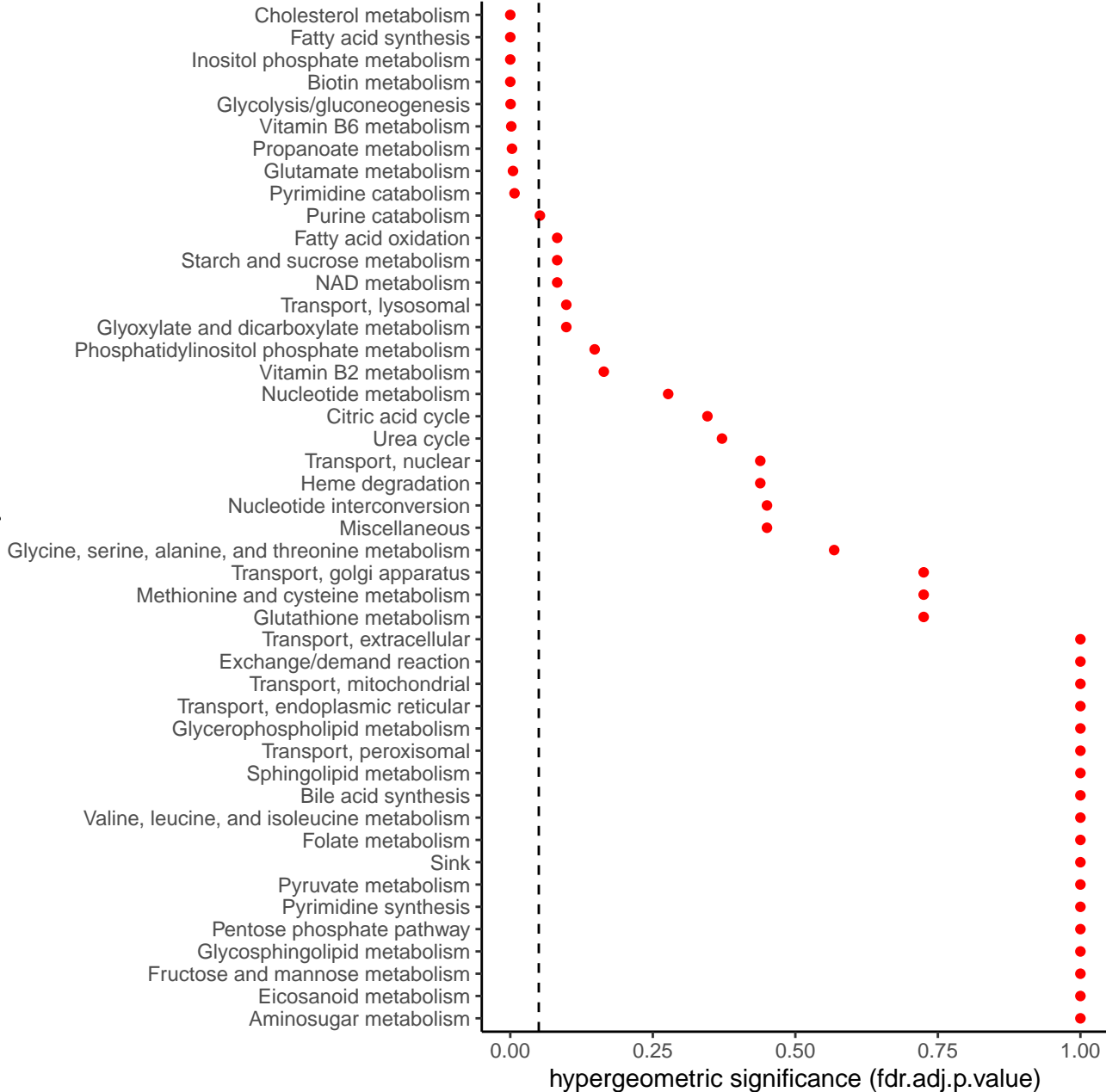
of disrupted rxns (n=670, bd_nonresponder)



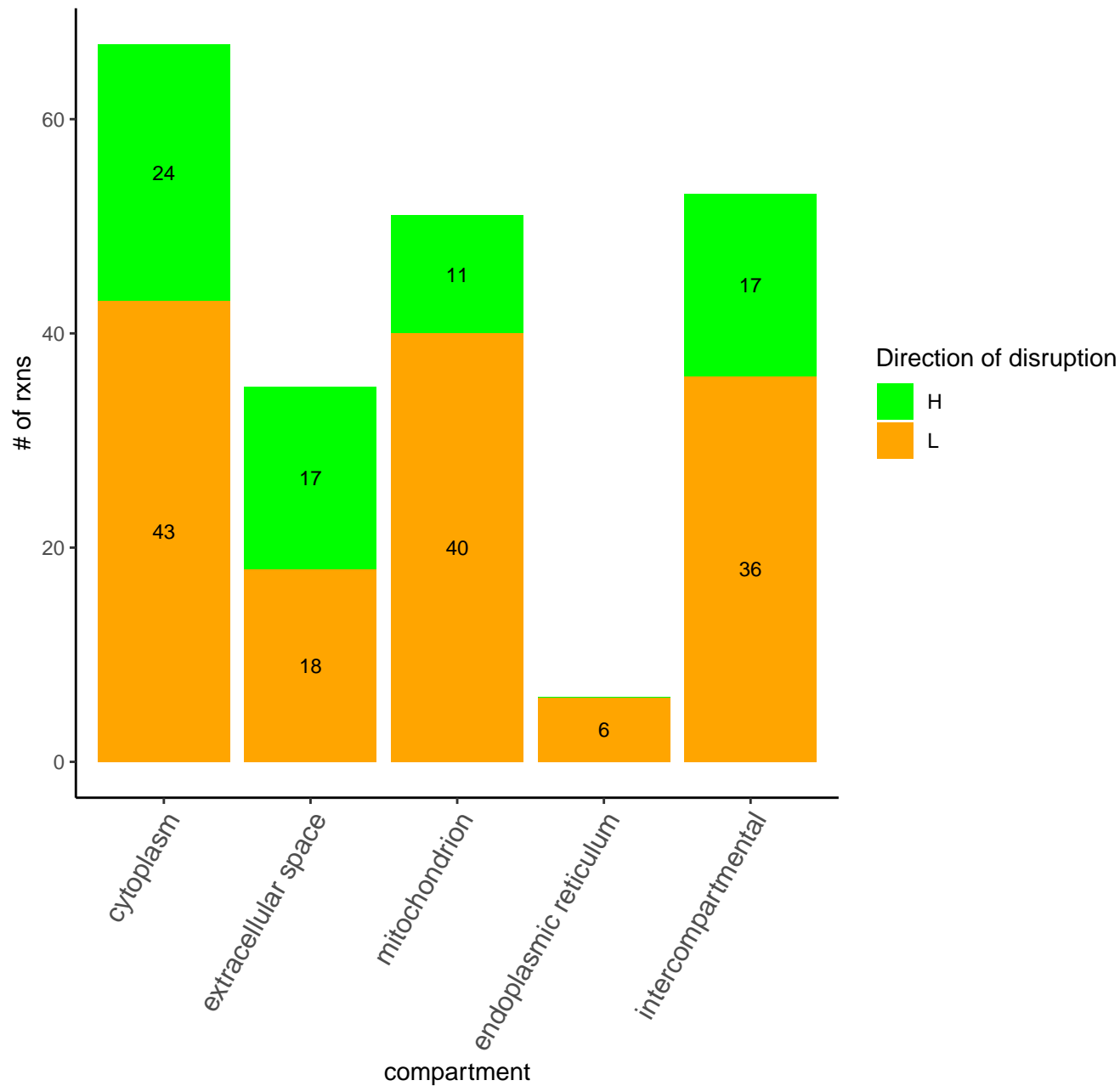
of disrupted rxns (n=670, bd_nonresponder) vs all rxns



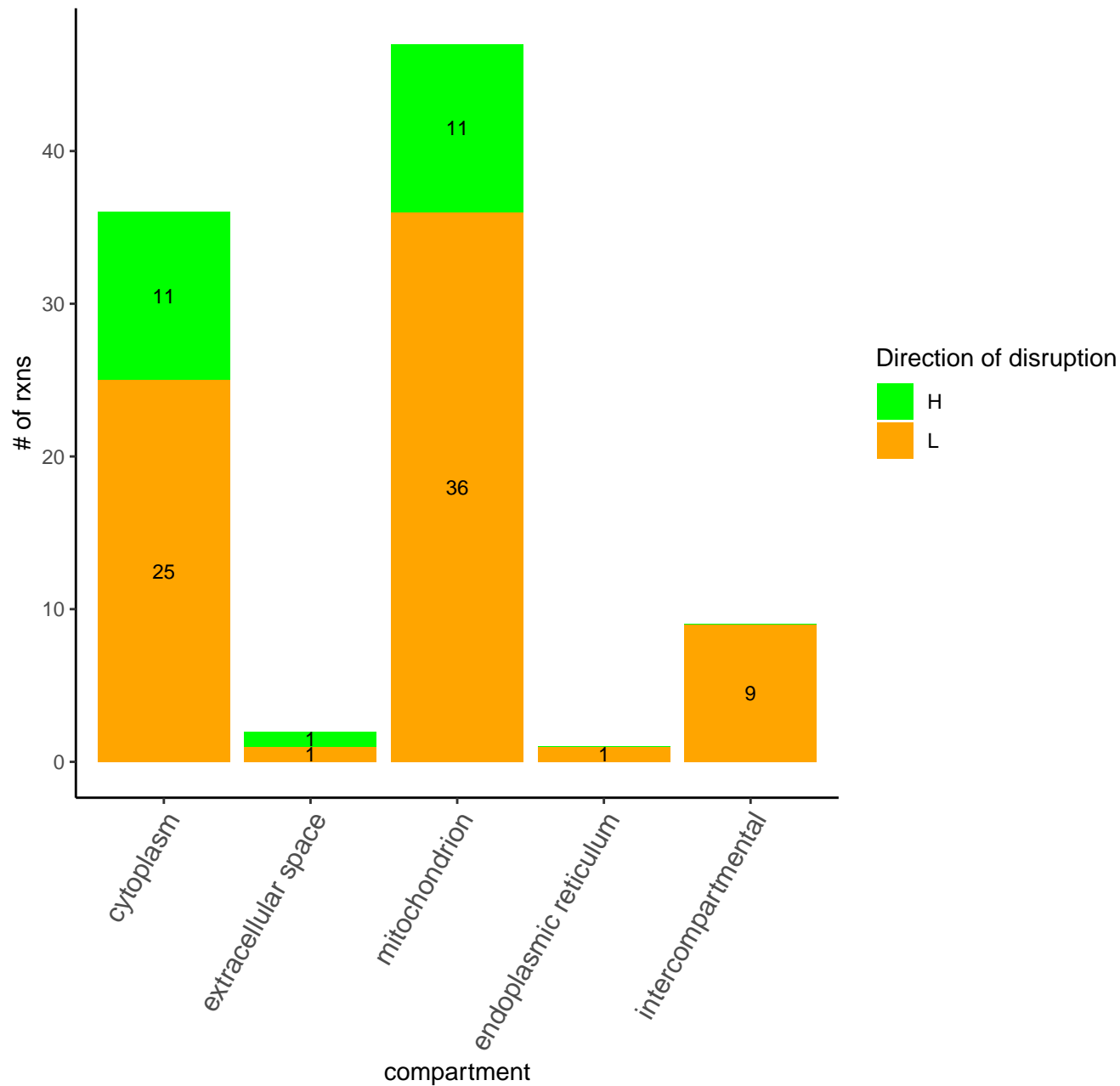
subSystem



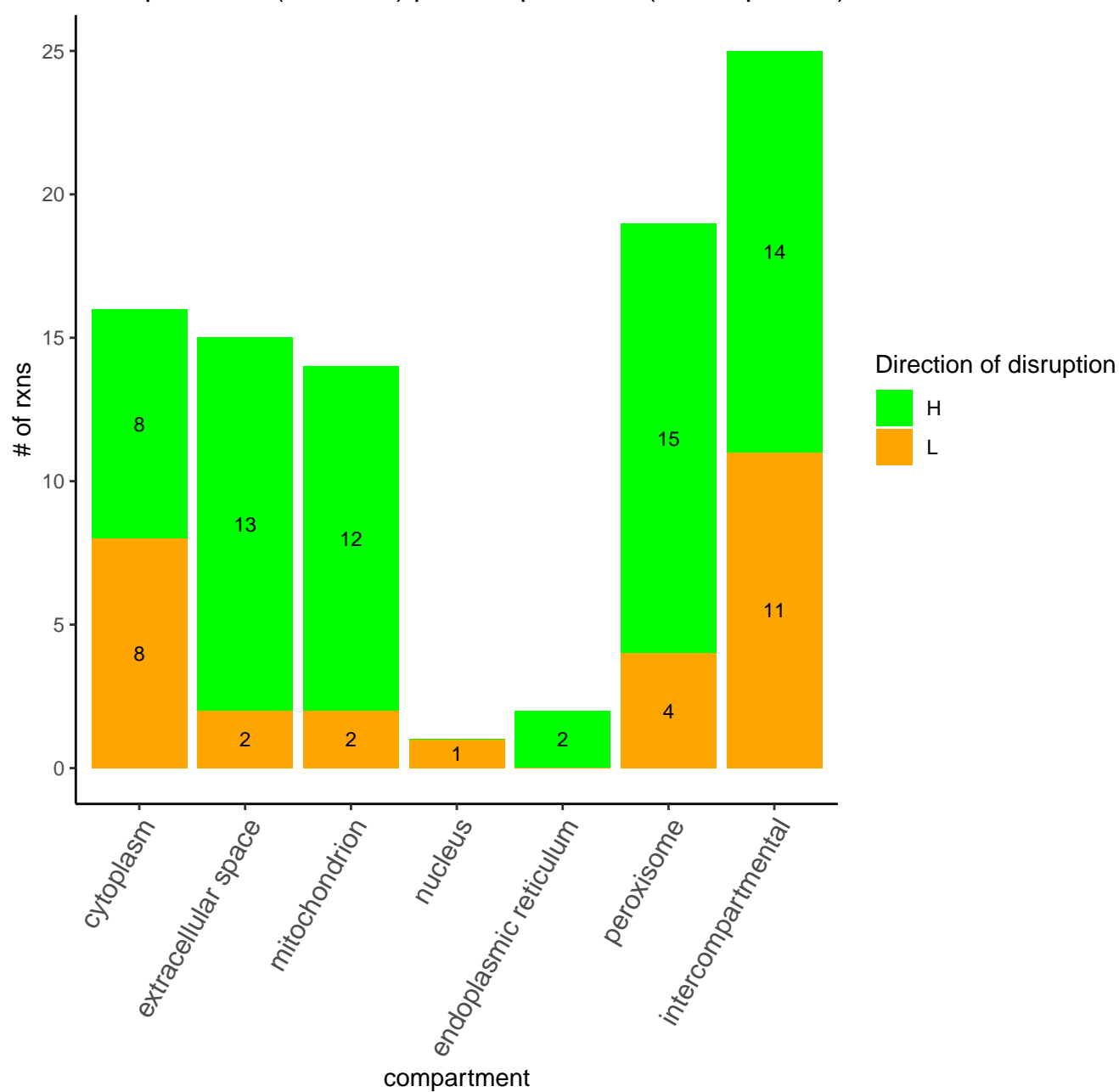
Disrupted rxns (all, n=212) per compartment (bd_lumped)



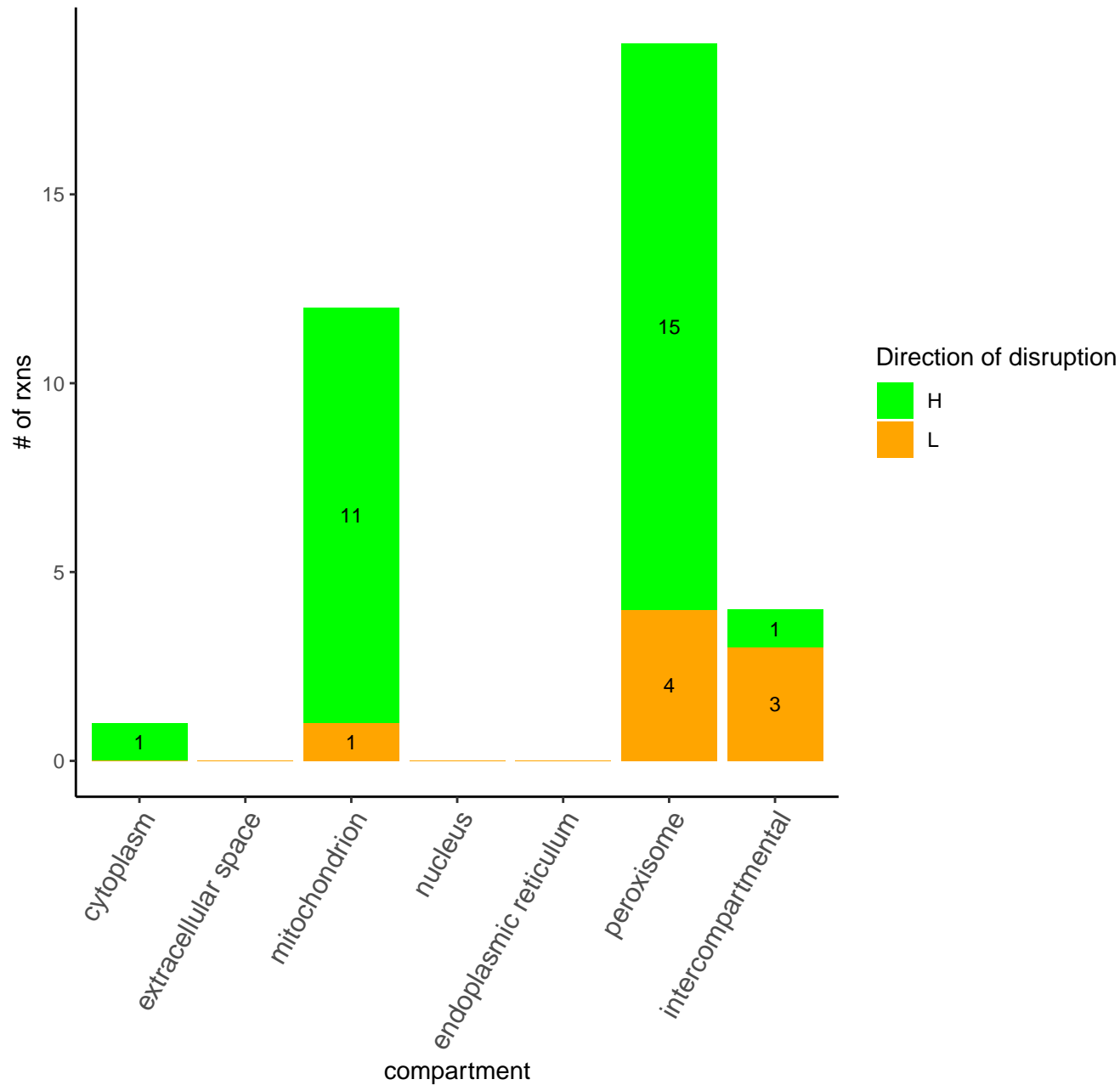
Disrupted rxns (fdr.significant, n=95) per compartment (bd_lumped)



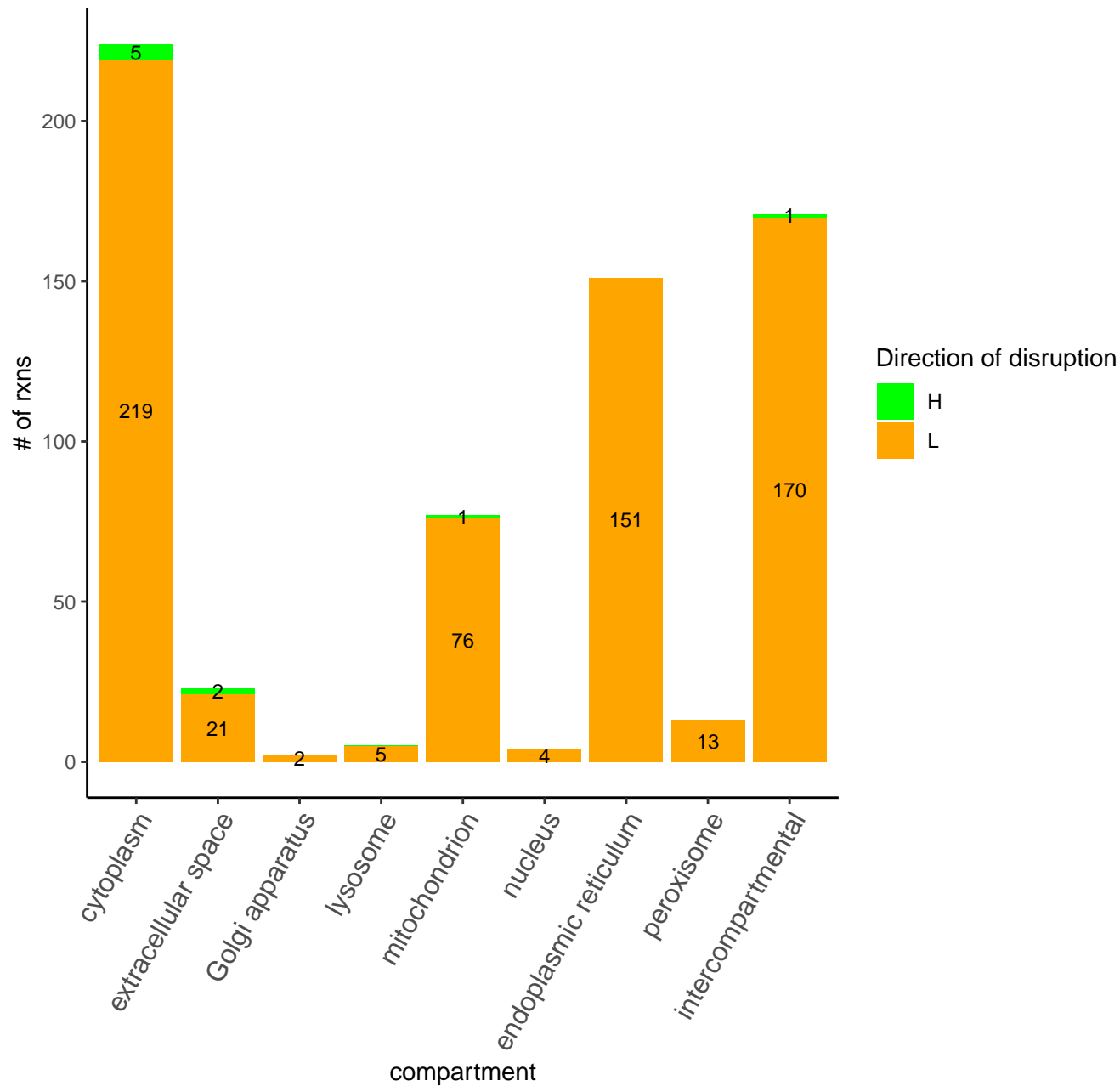
Disrupted rxns (all, n=92) per compartment (bd_responder)



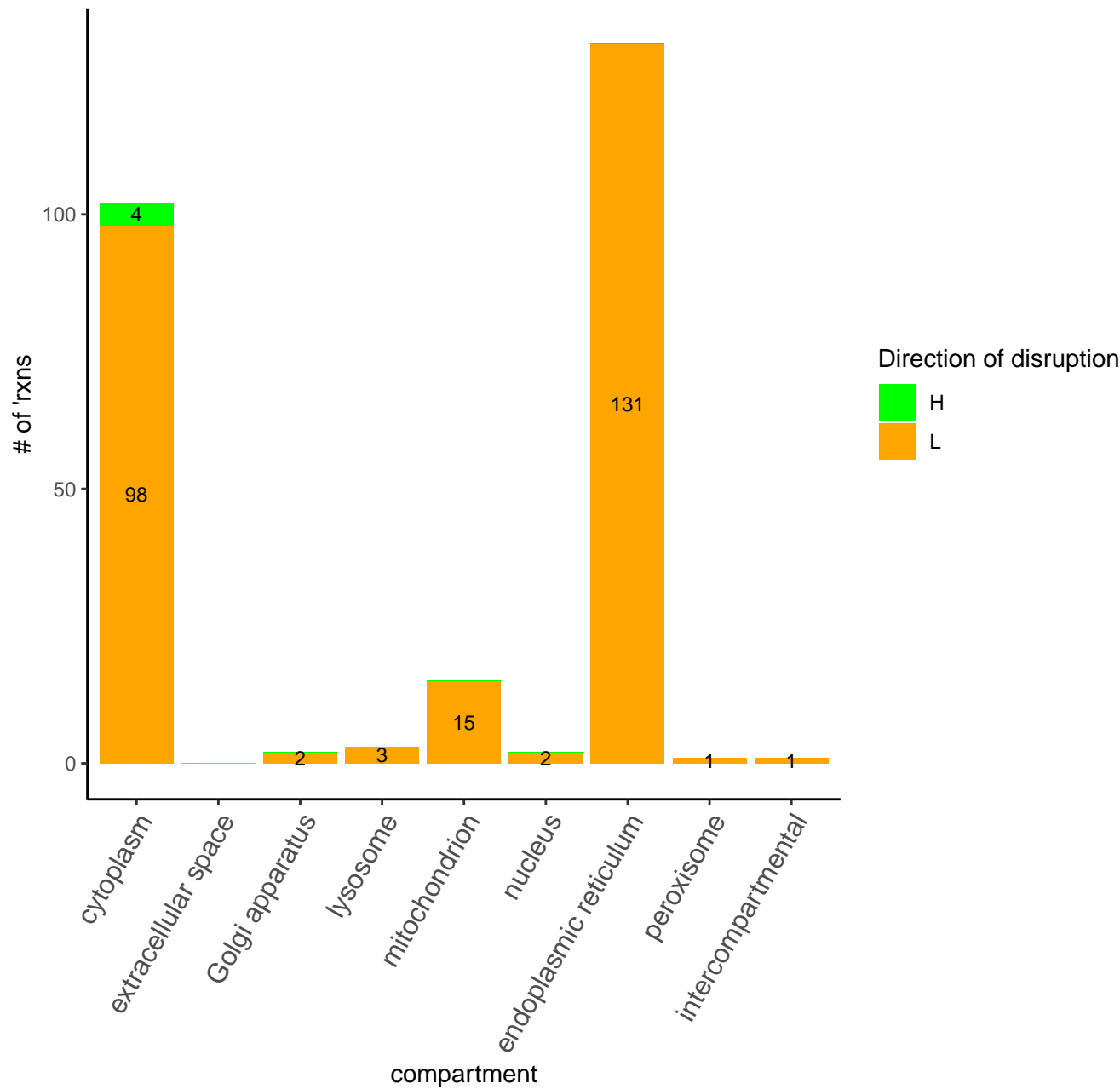
Disrupted rxns (fdr.significant, n=36) per compartment (bd_responder)



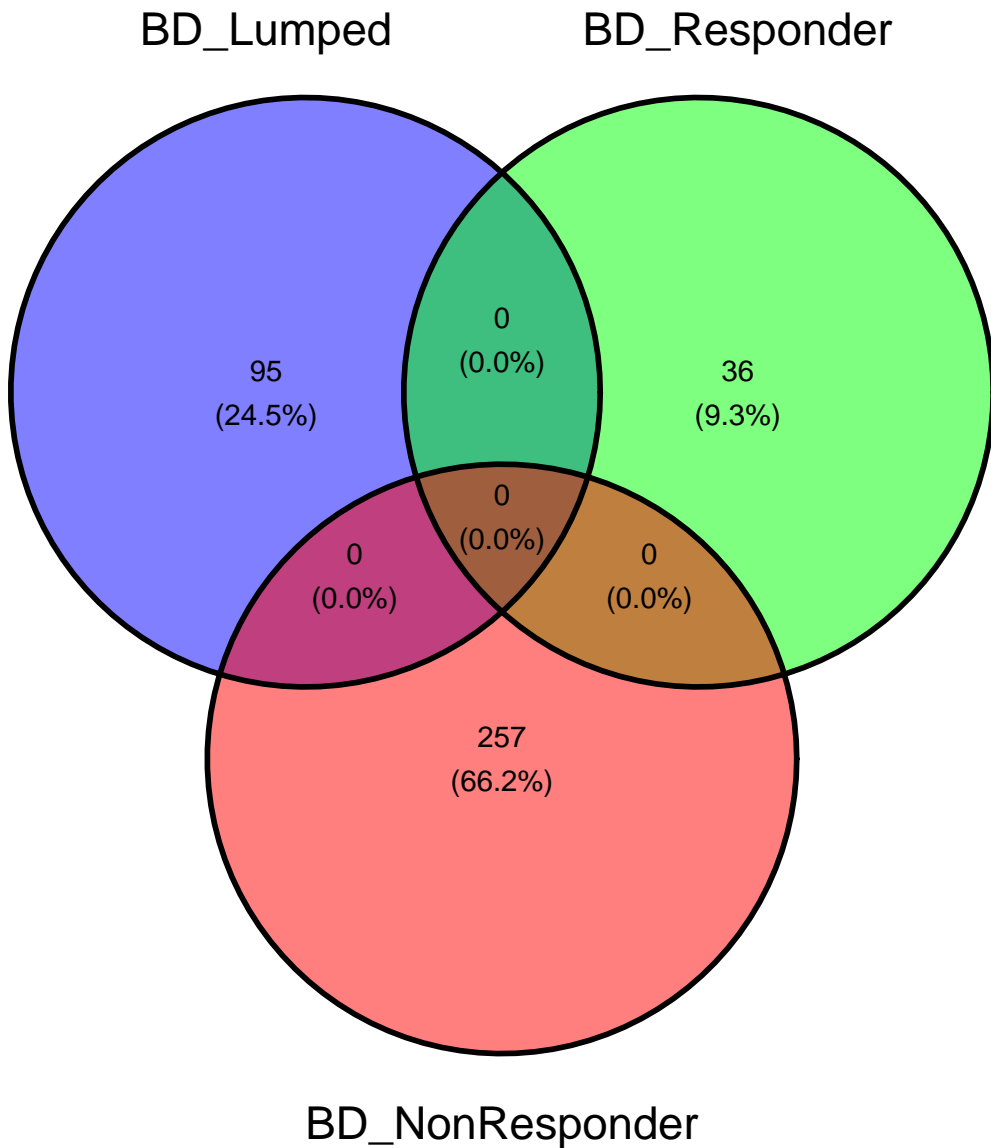
Disrupted rxns (all, n=670) per compartment (bd_nonresponder)



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

