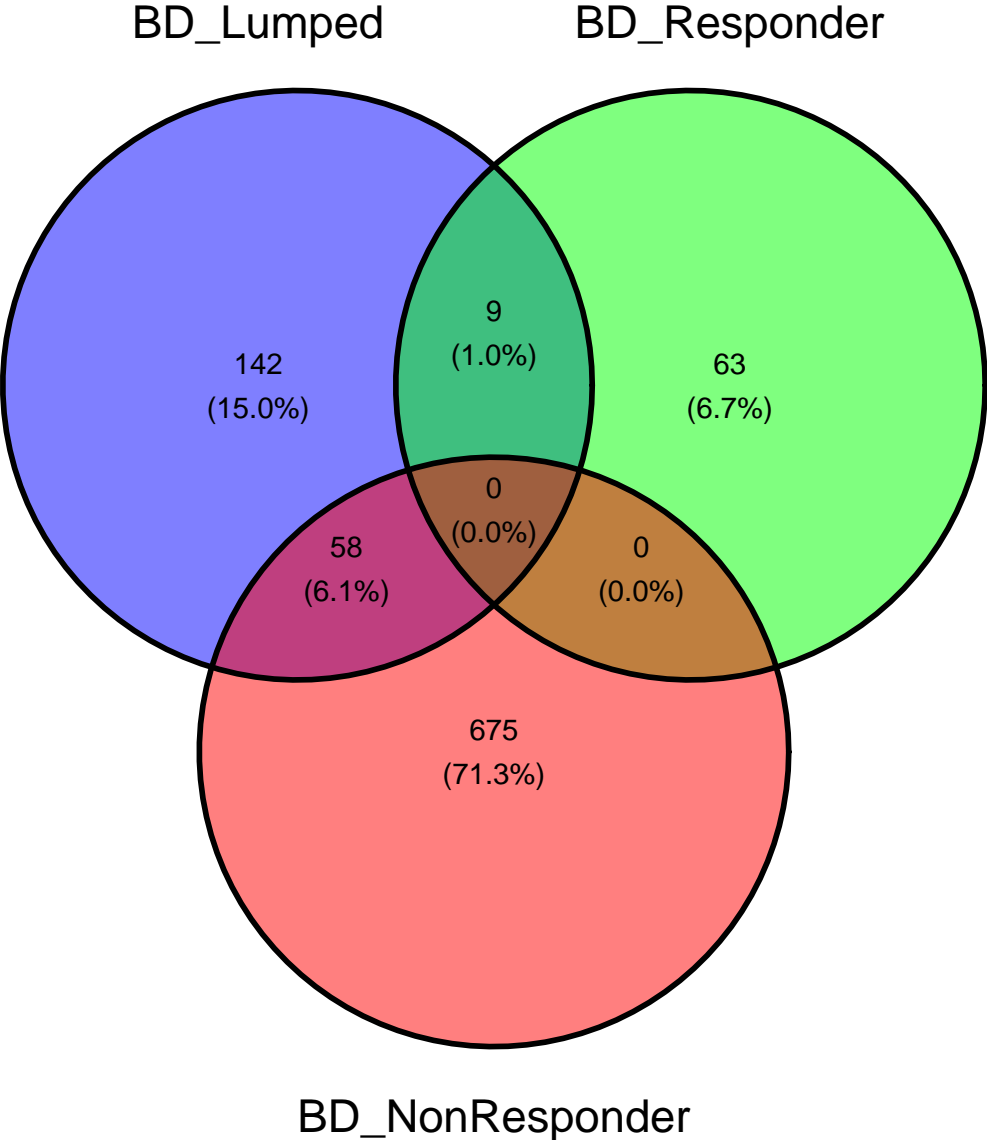
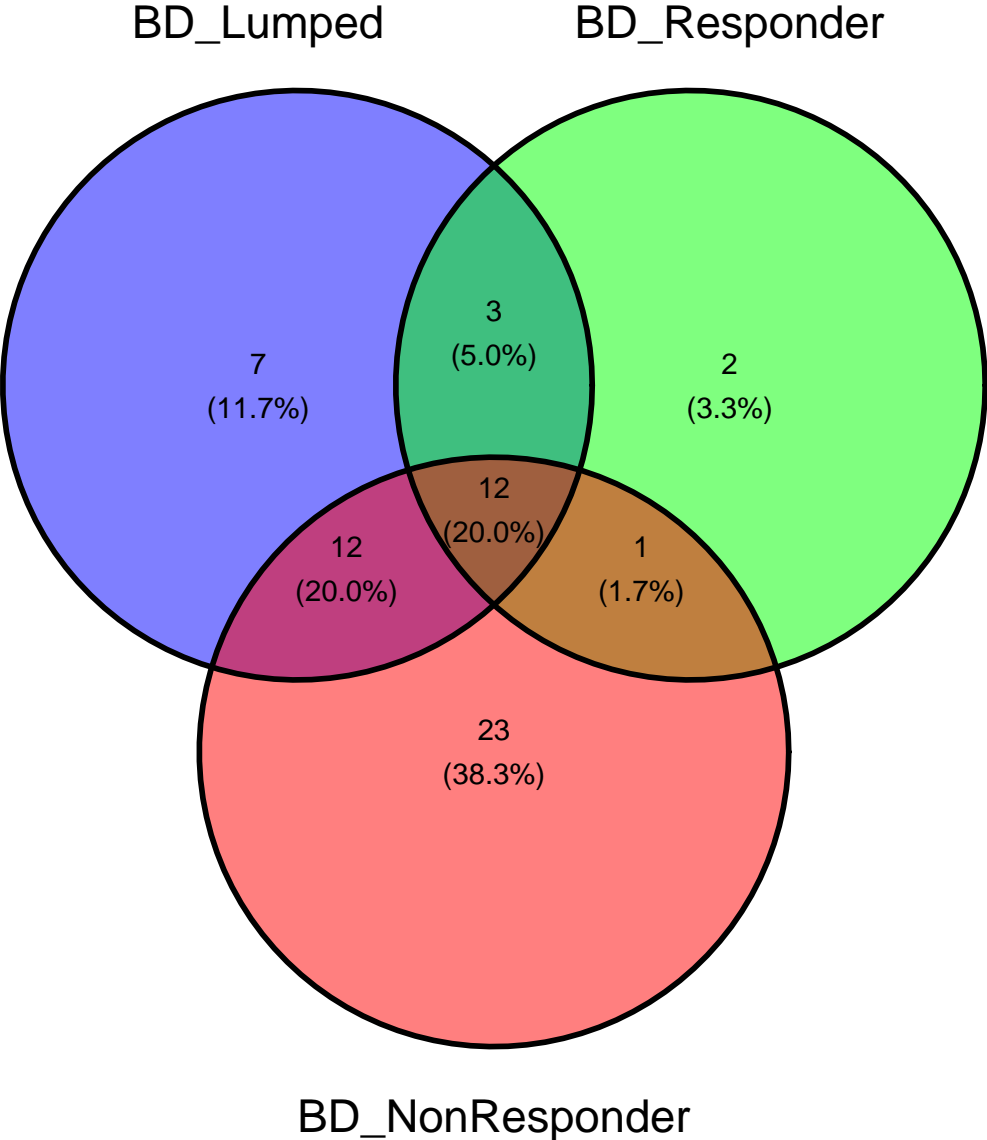


Overlap in rxns disrupted between models

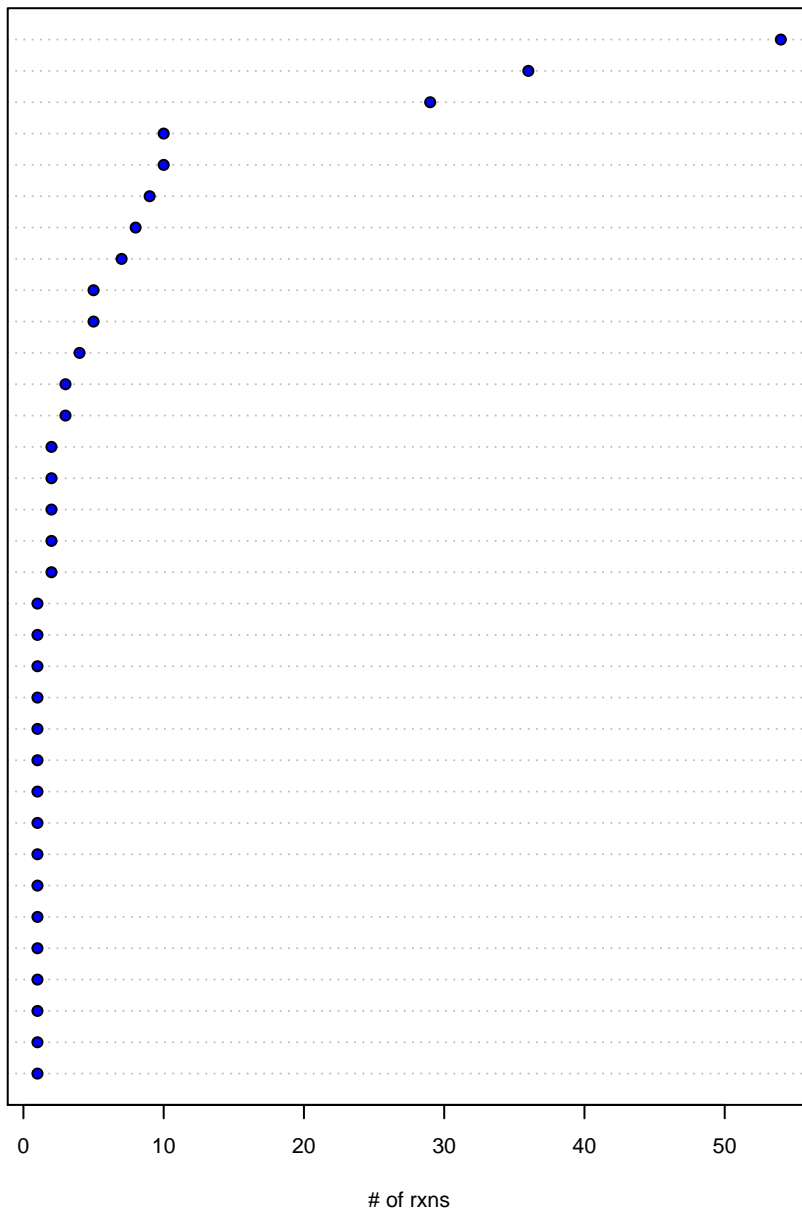


Overlap in subSystems disrupted between models



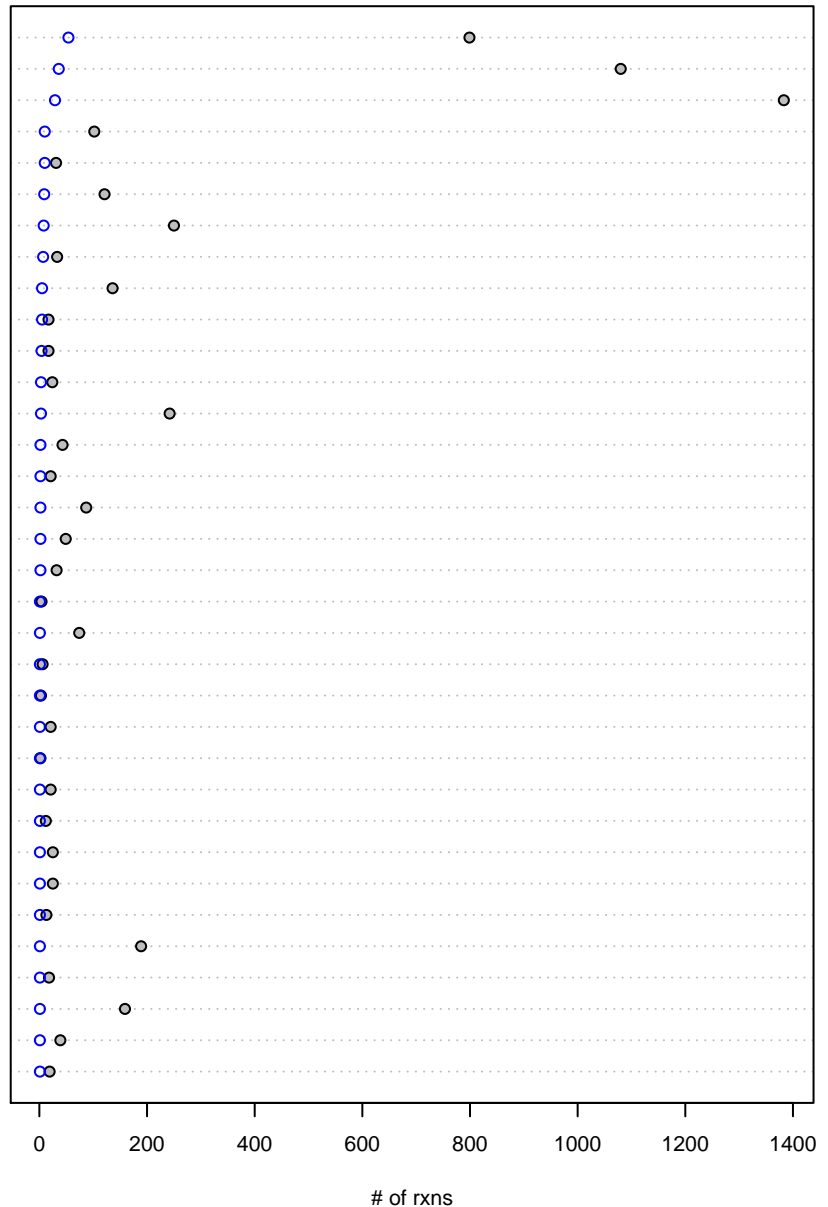
# # of disrupted rxns (n=209, bd\_lumped)

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



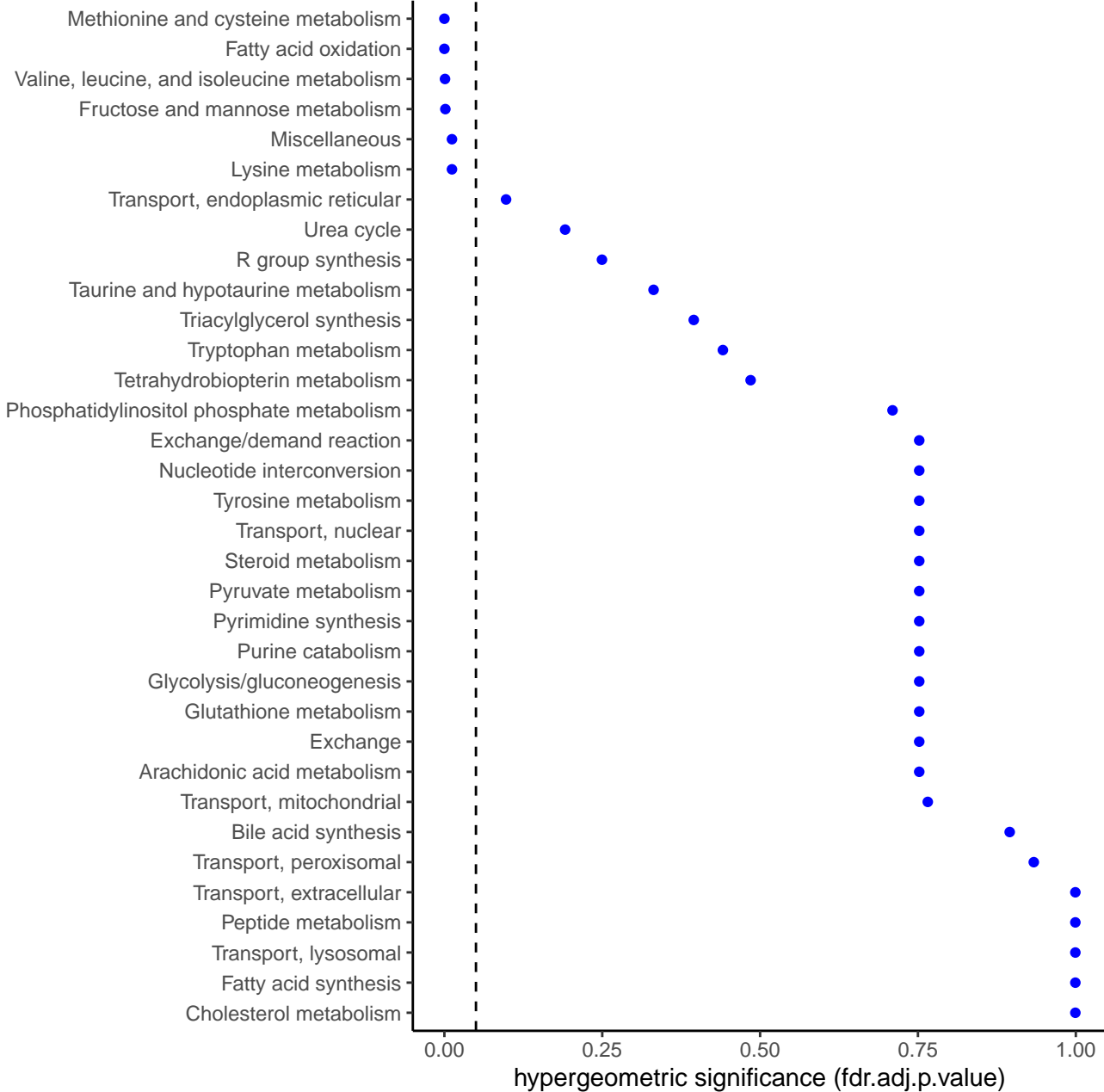
# of disrupted rxns (n=209, bd\_lumped) vs all rxns

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

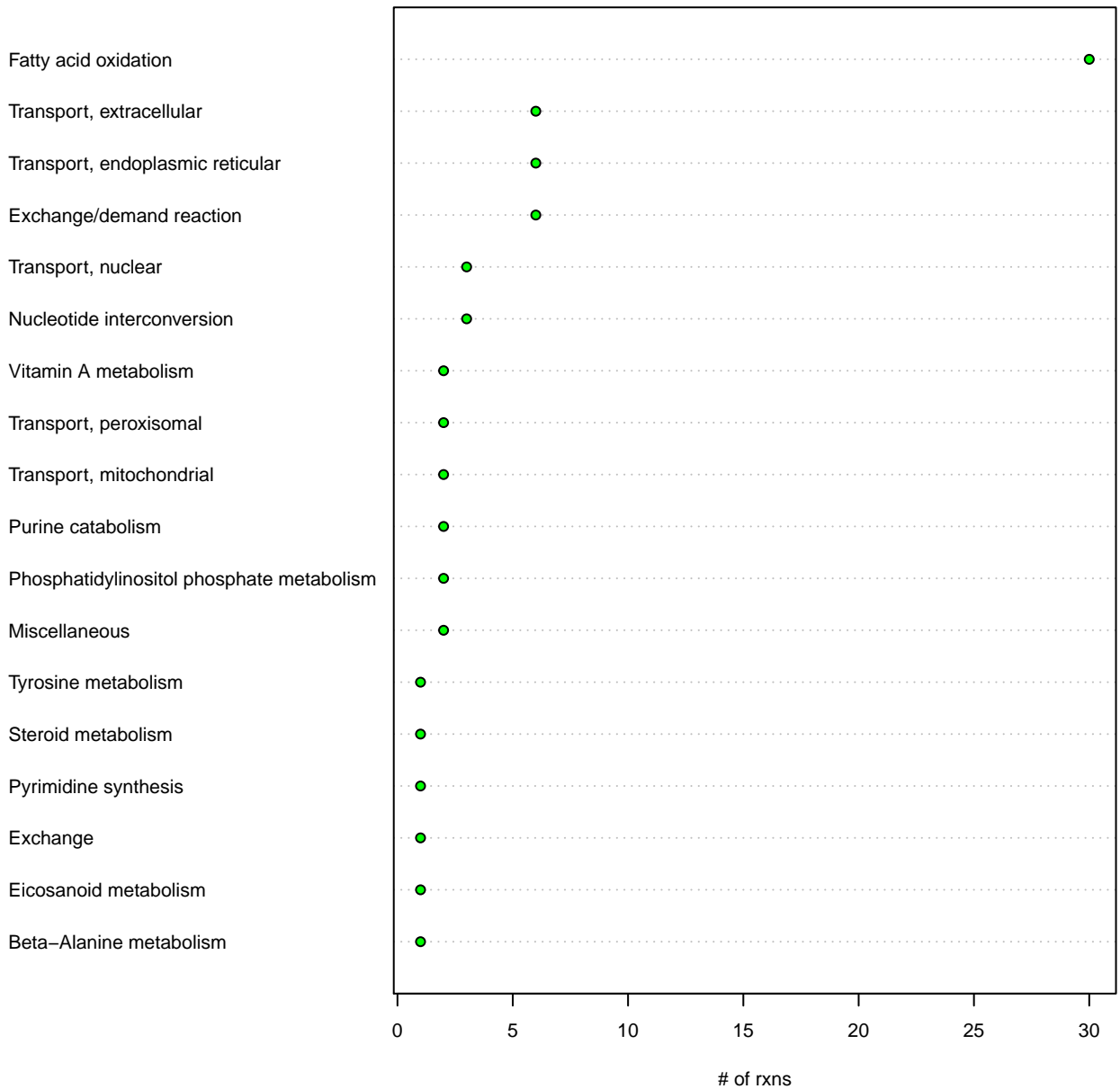


# over-representation analysis, bd\_lumped

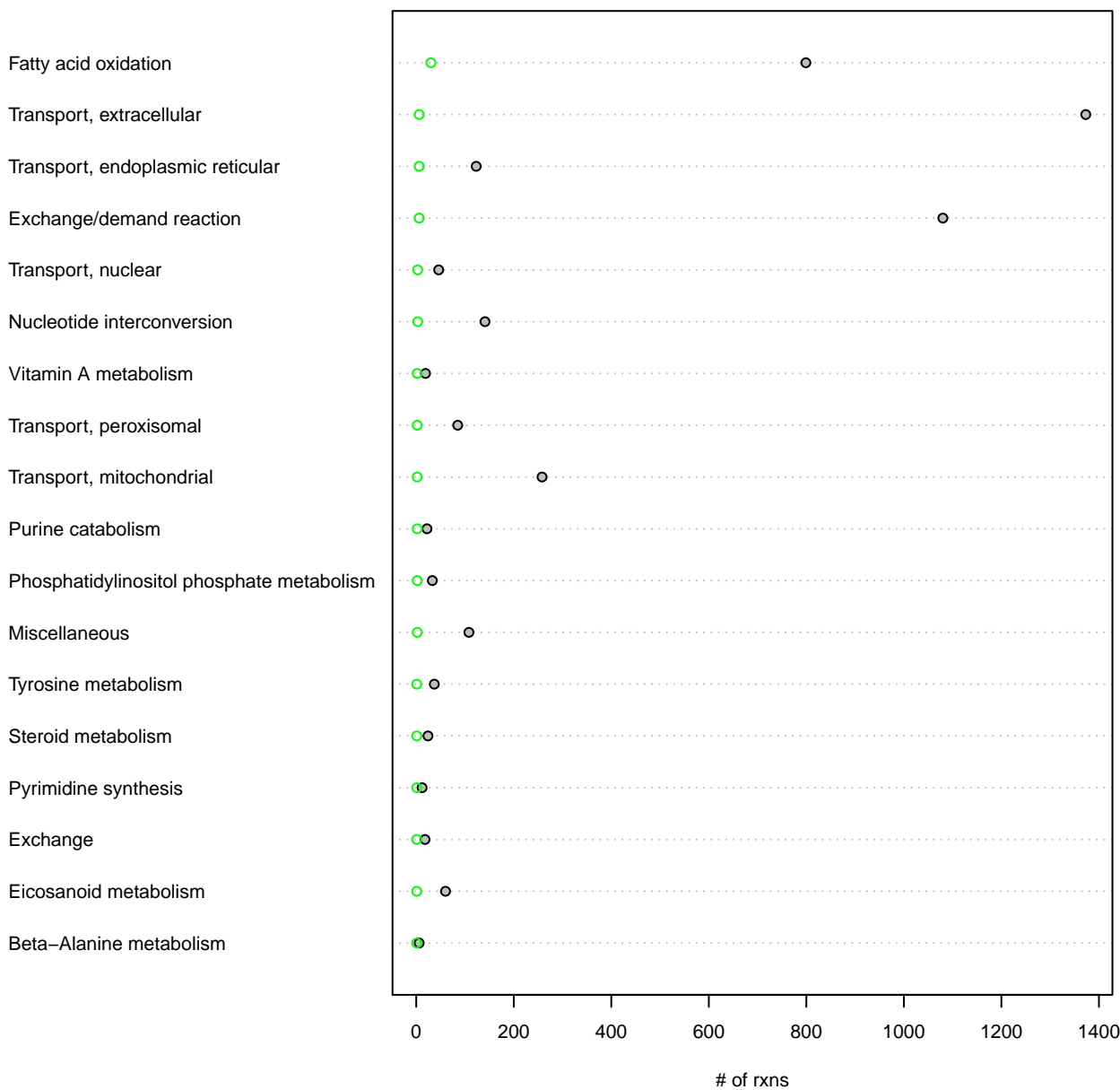
subSystem



# of disrupted rxns (n=72, bd\_responder)

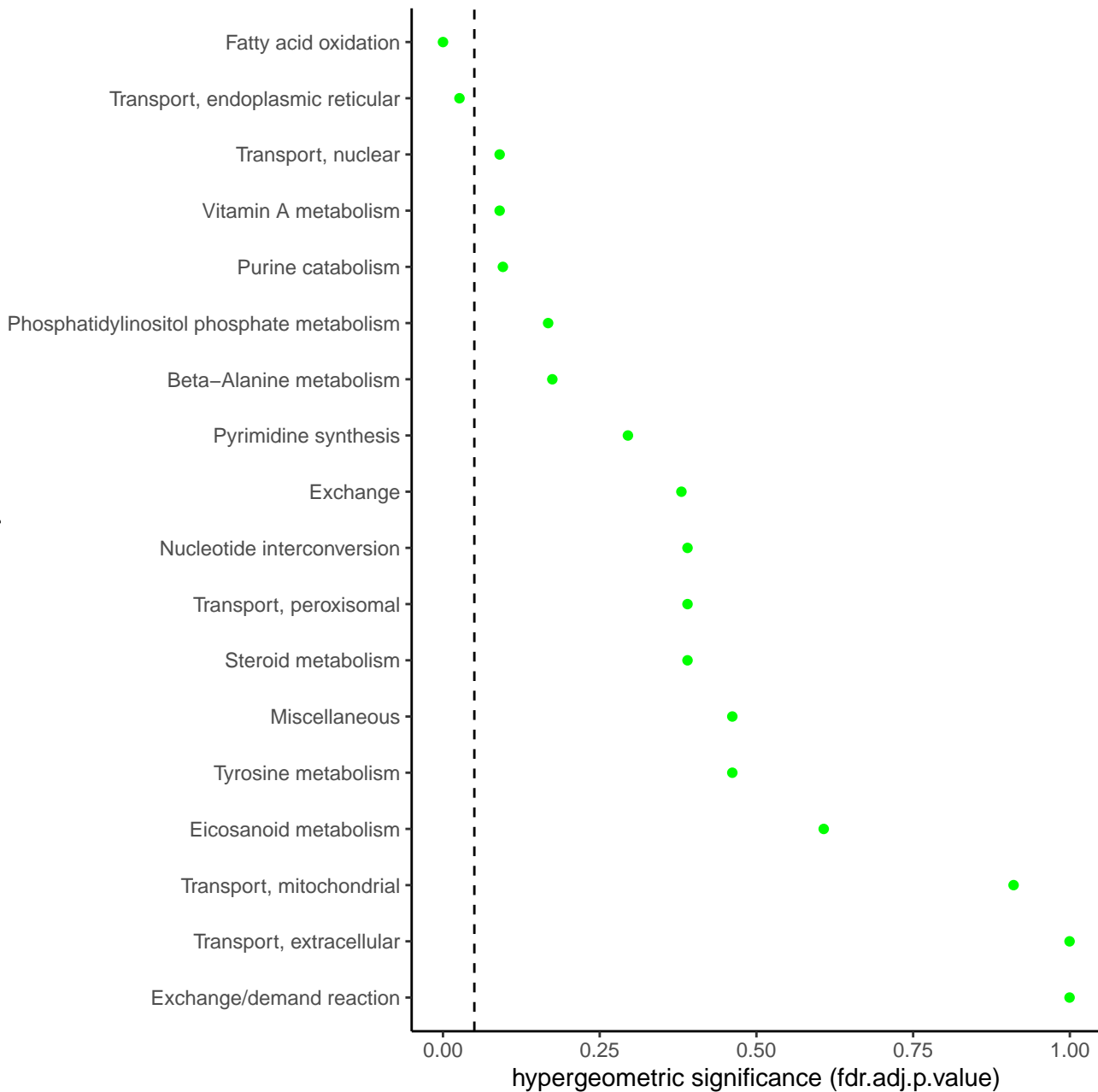


# of disrupted rxns (n=72, bd\_responder) vs all rxns



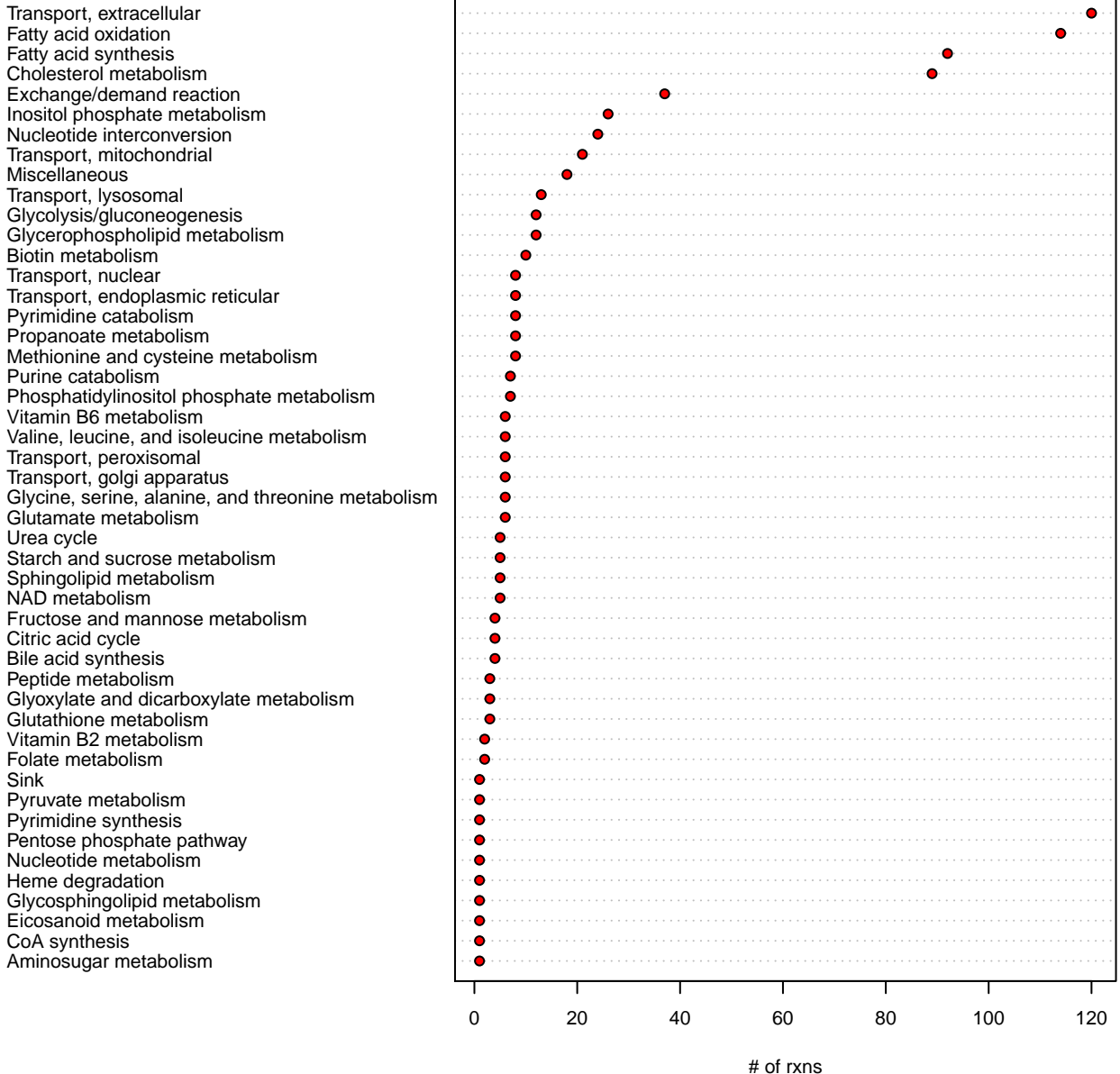
# over-representation analysis, bd\_responder

subSystem

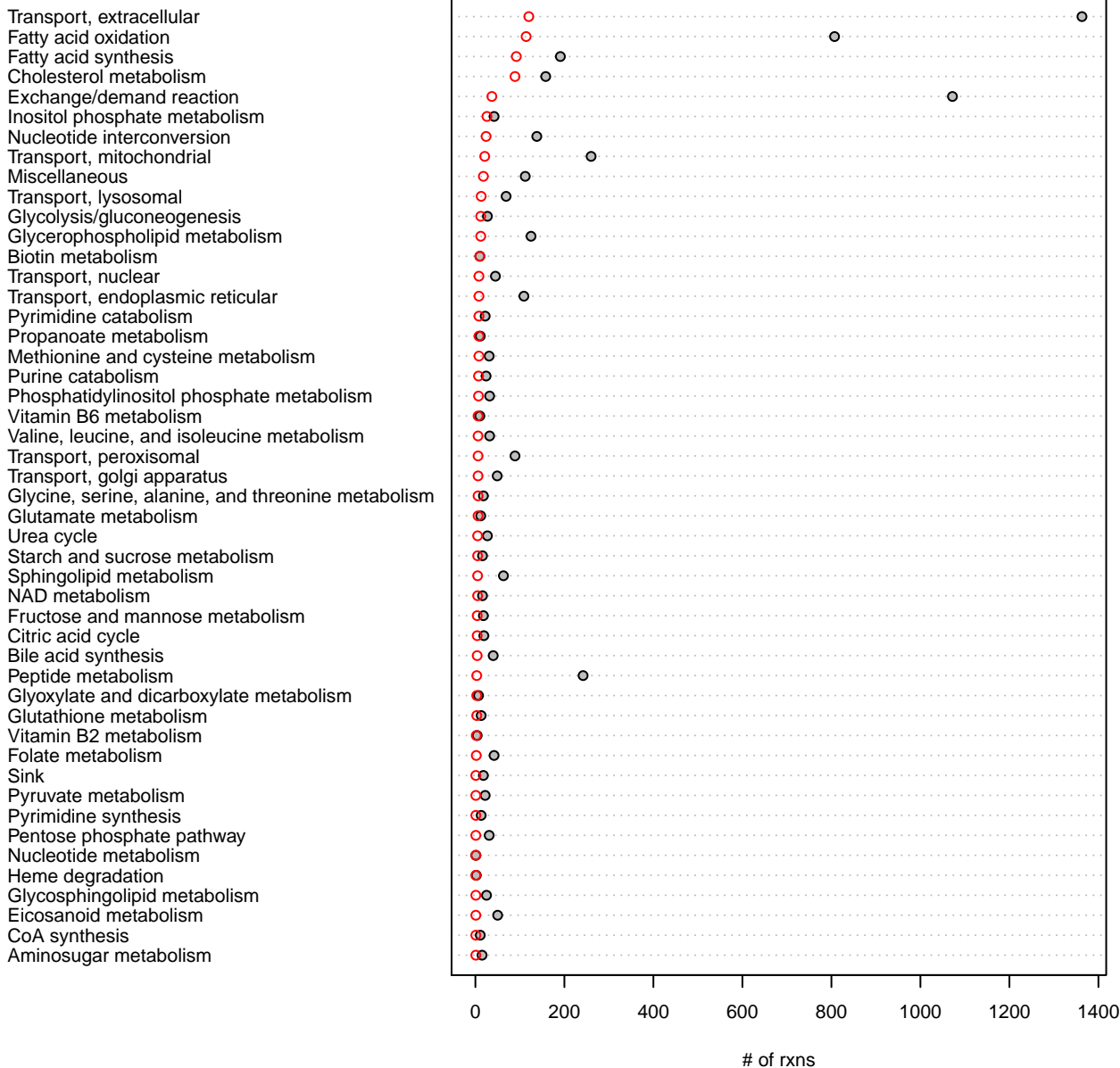




# # of disrupted rxns (n=733, bd\_nonresponder)

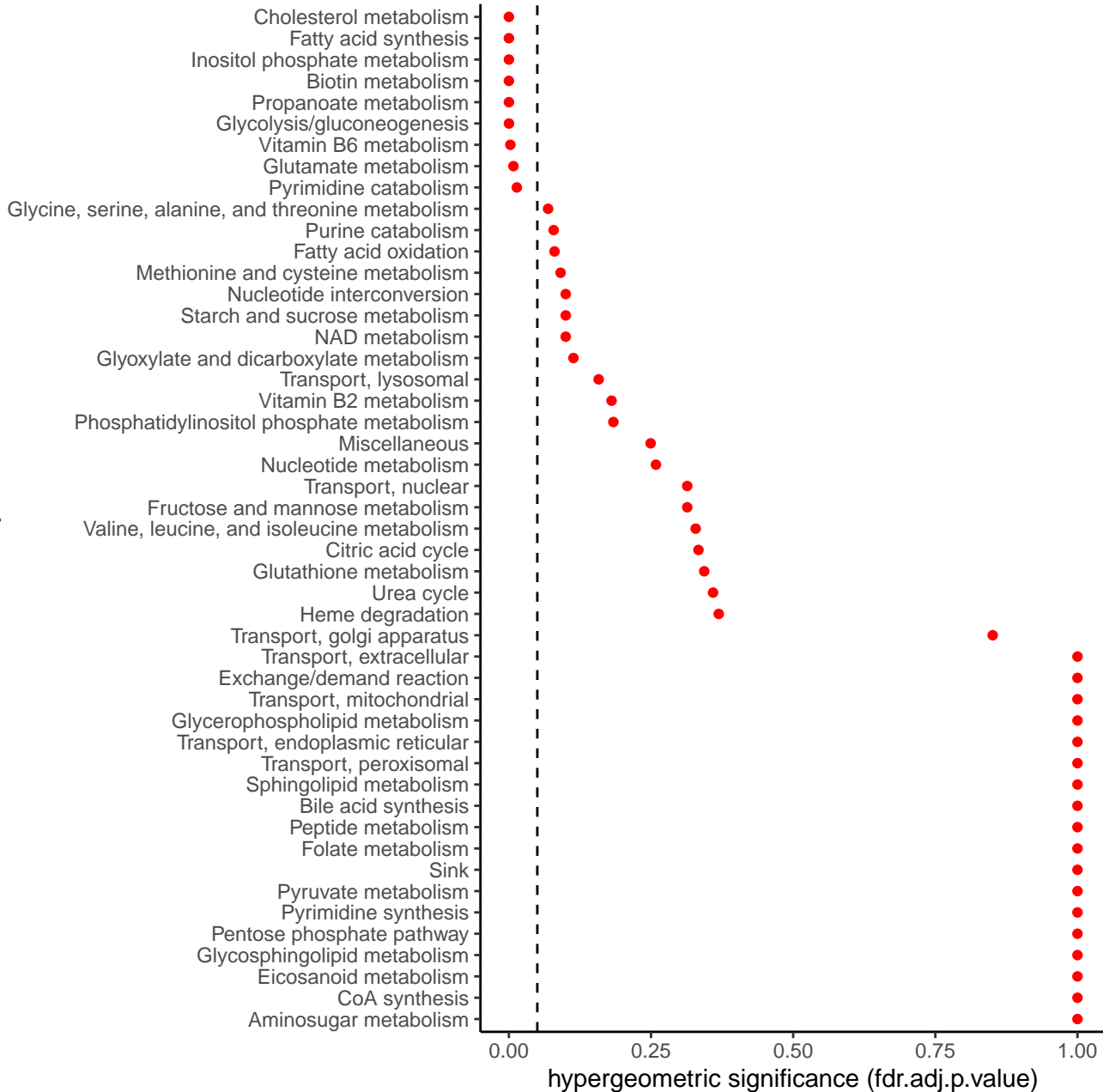


# of disrupted rxns (n=733, bd\_nonresponder) vs all rxns

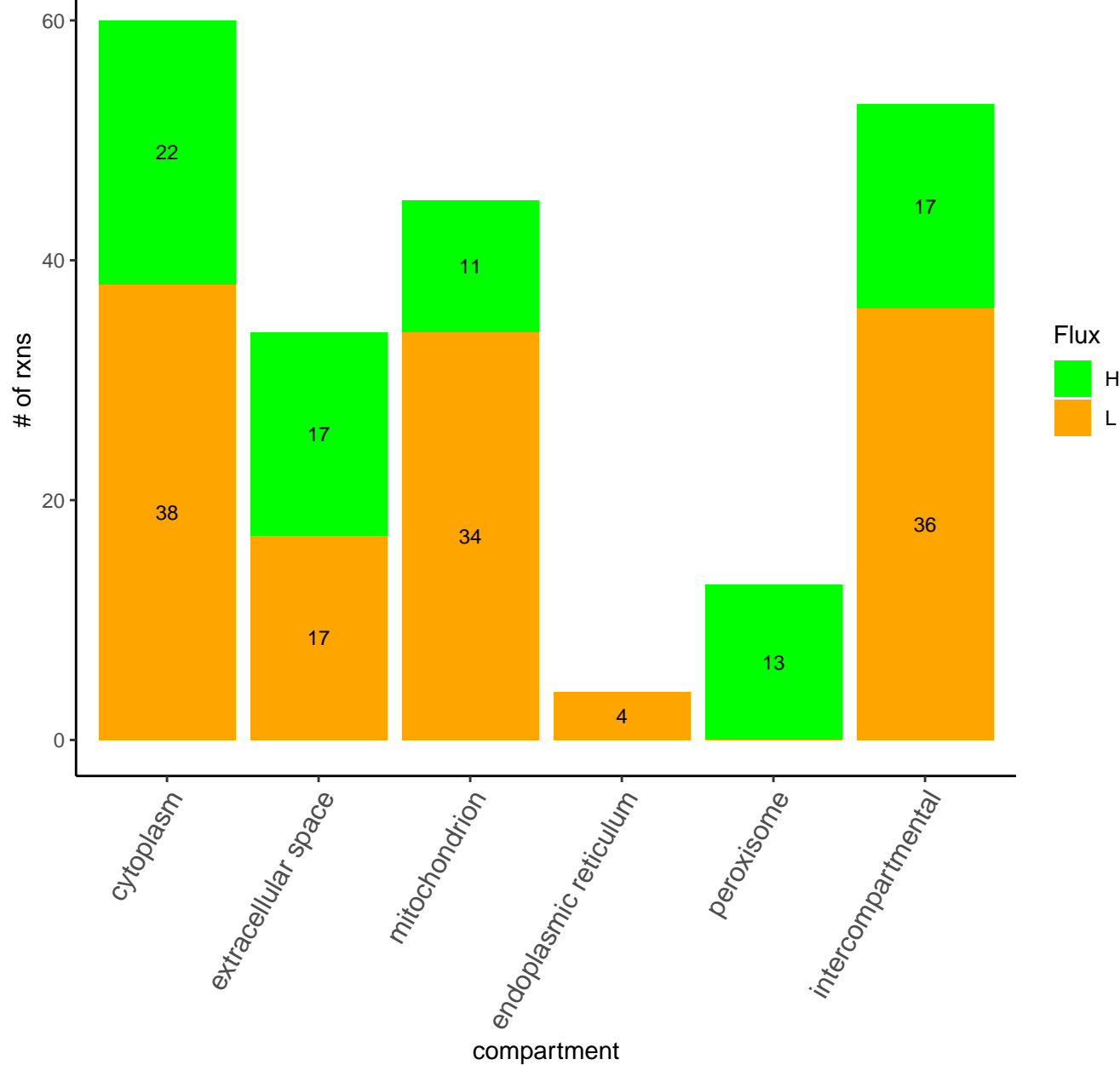


# over-representation analysis, bd\_nonresponder

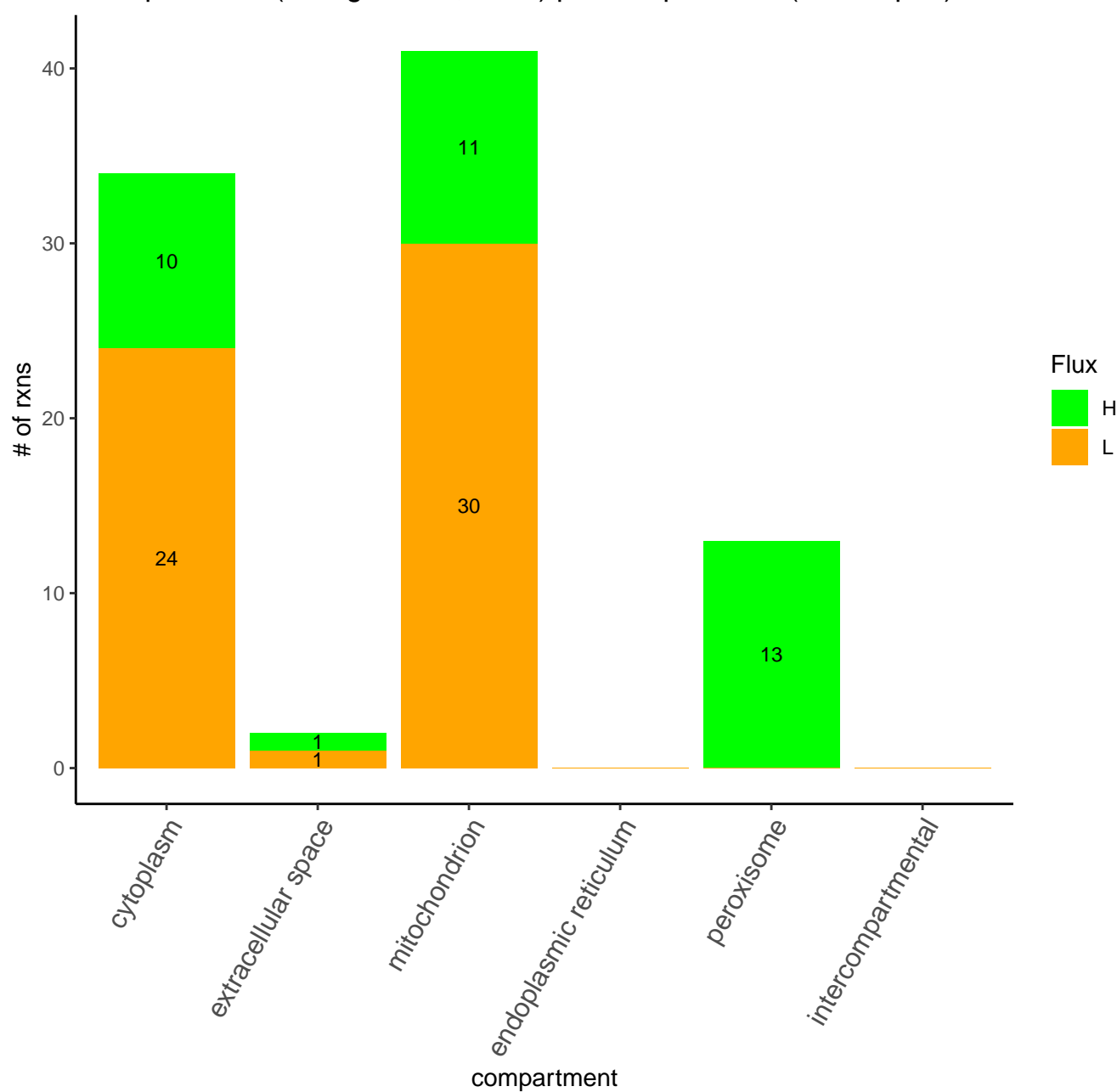
subSystem



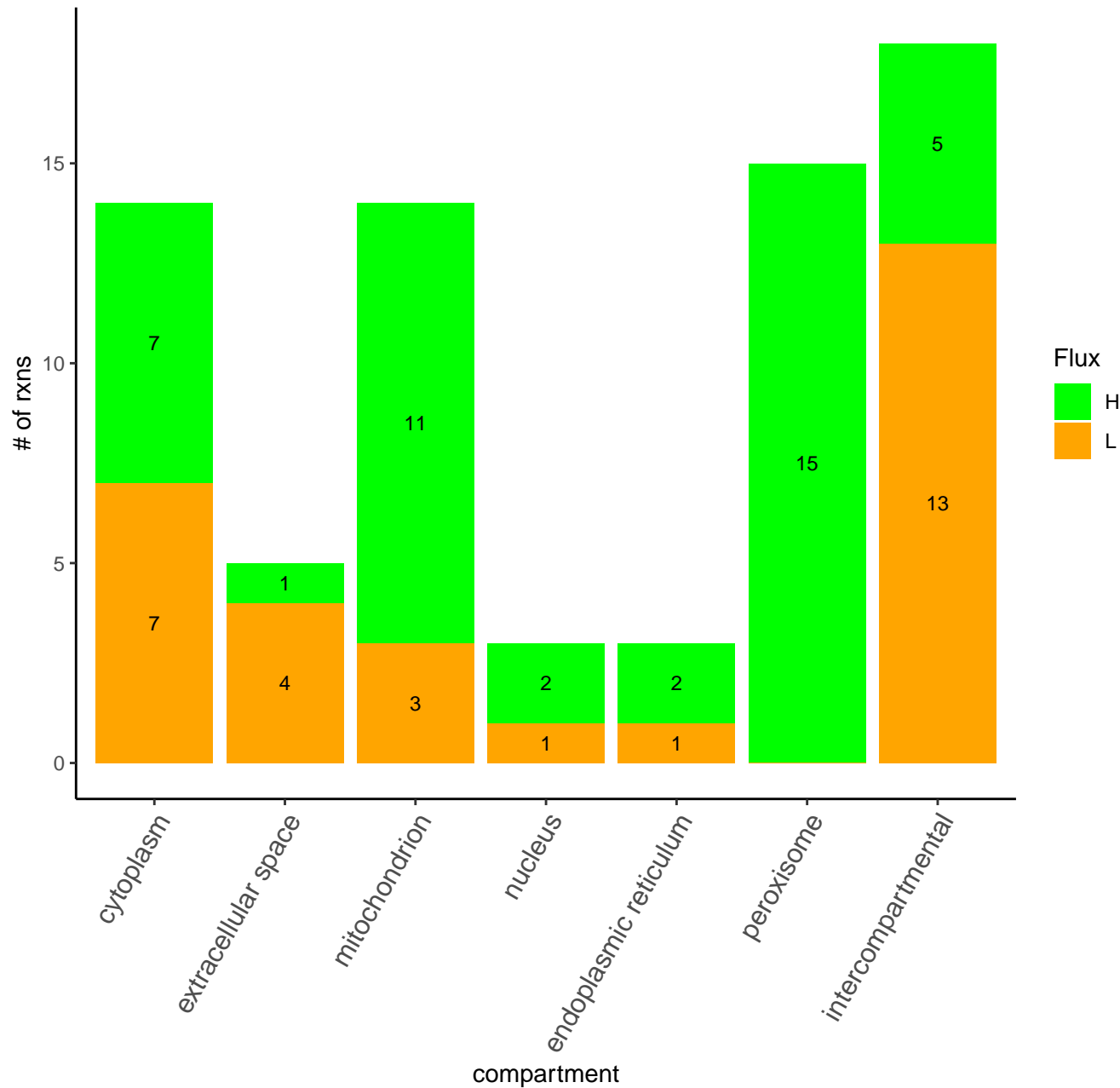
Disrupted rxns (all, n=209) per compartment (bd\_lumped)



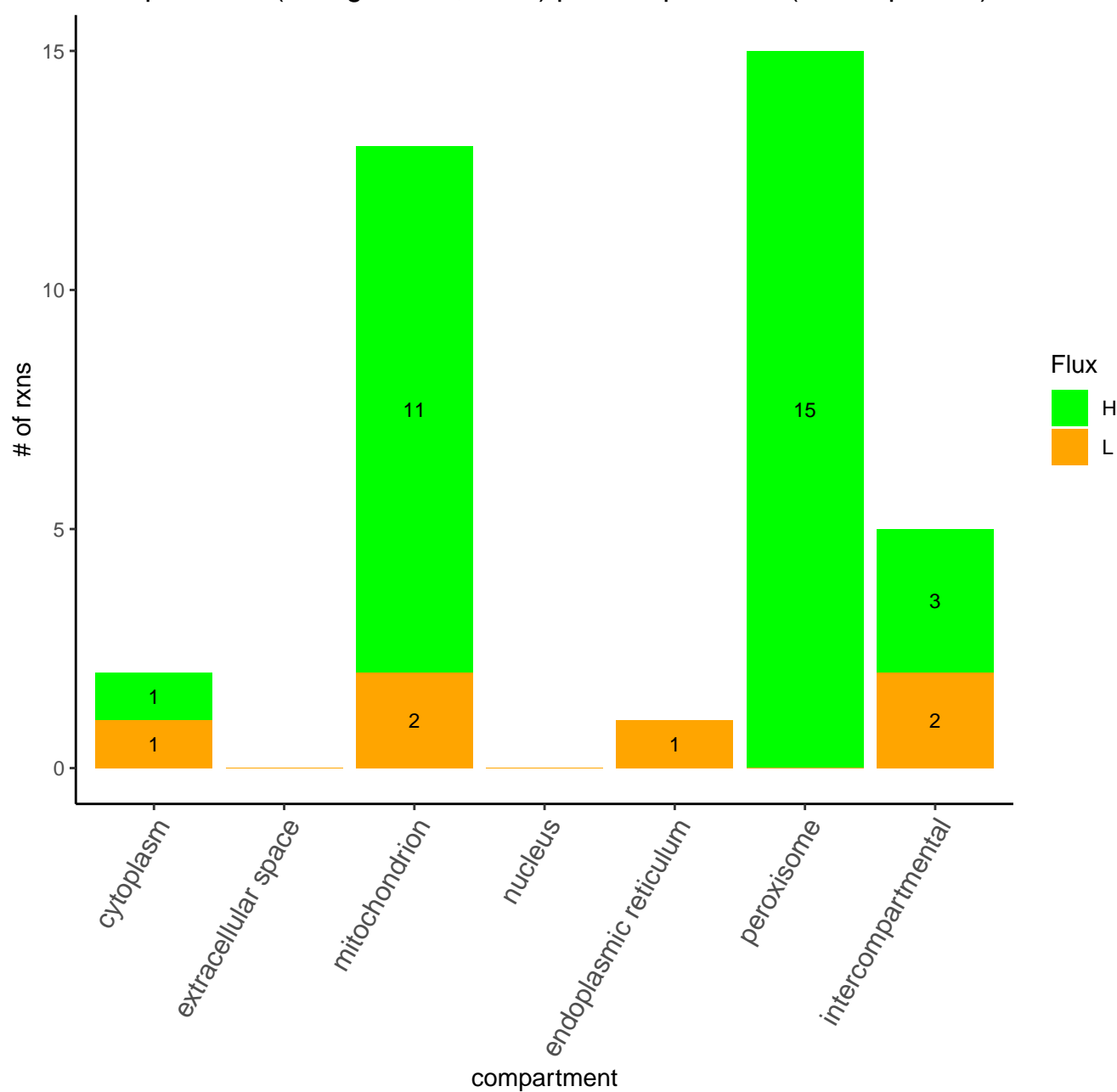
Disrupted rxns (fdr.significant, n=90) per compartment (bd\_lumped)



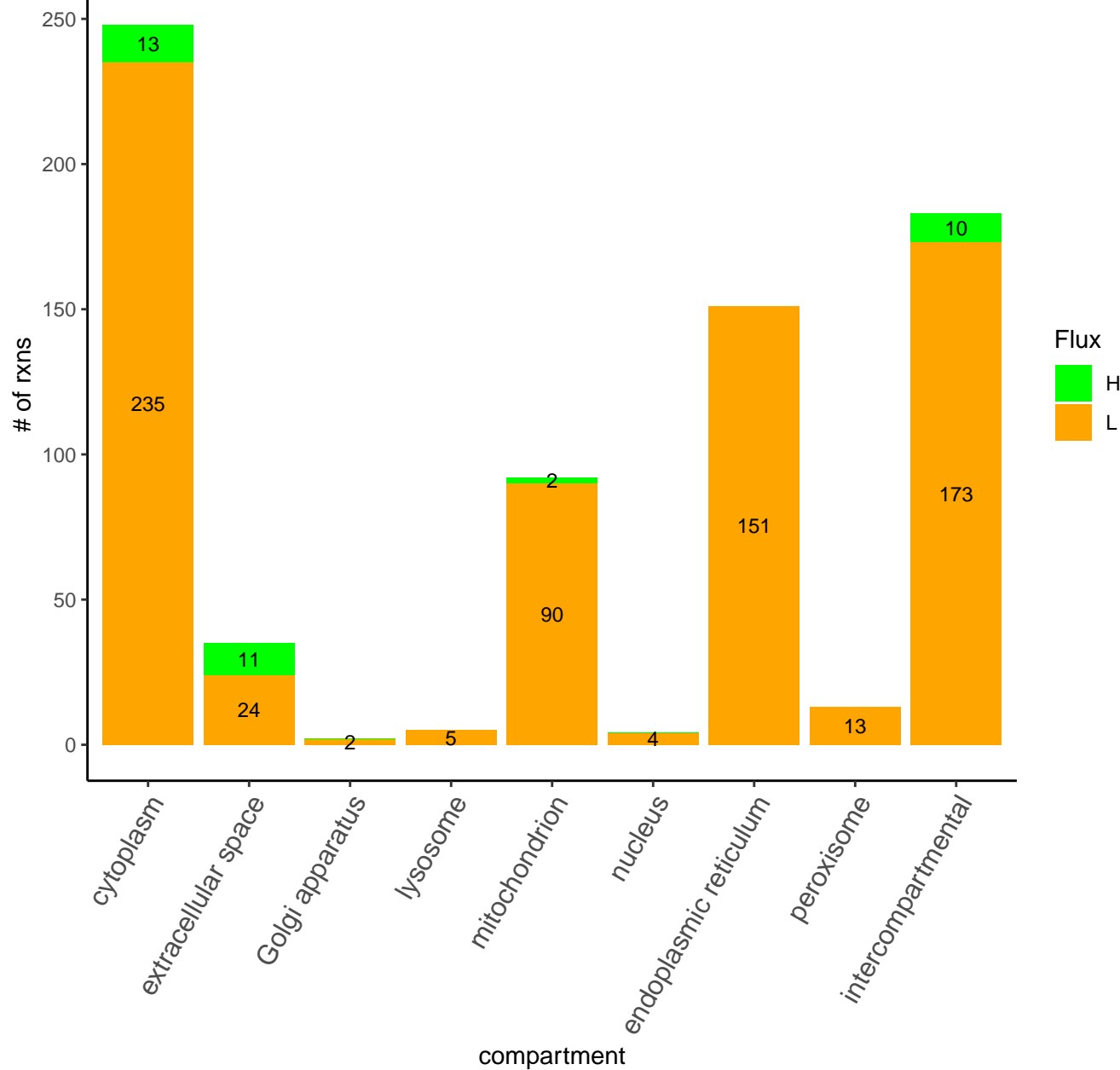
Disrupted rxns (all, n=72) per compartment (bd\_responder)



Disrupted rxns (fdr.significant, n=36) per compartment (bd\_responder)

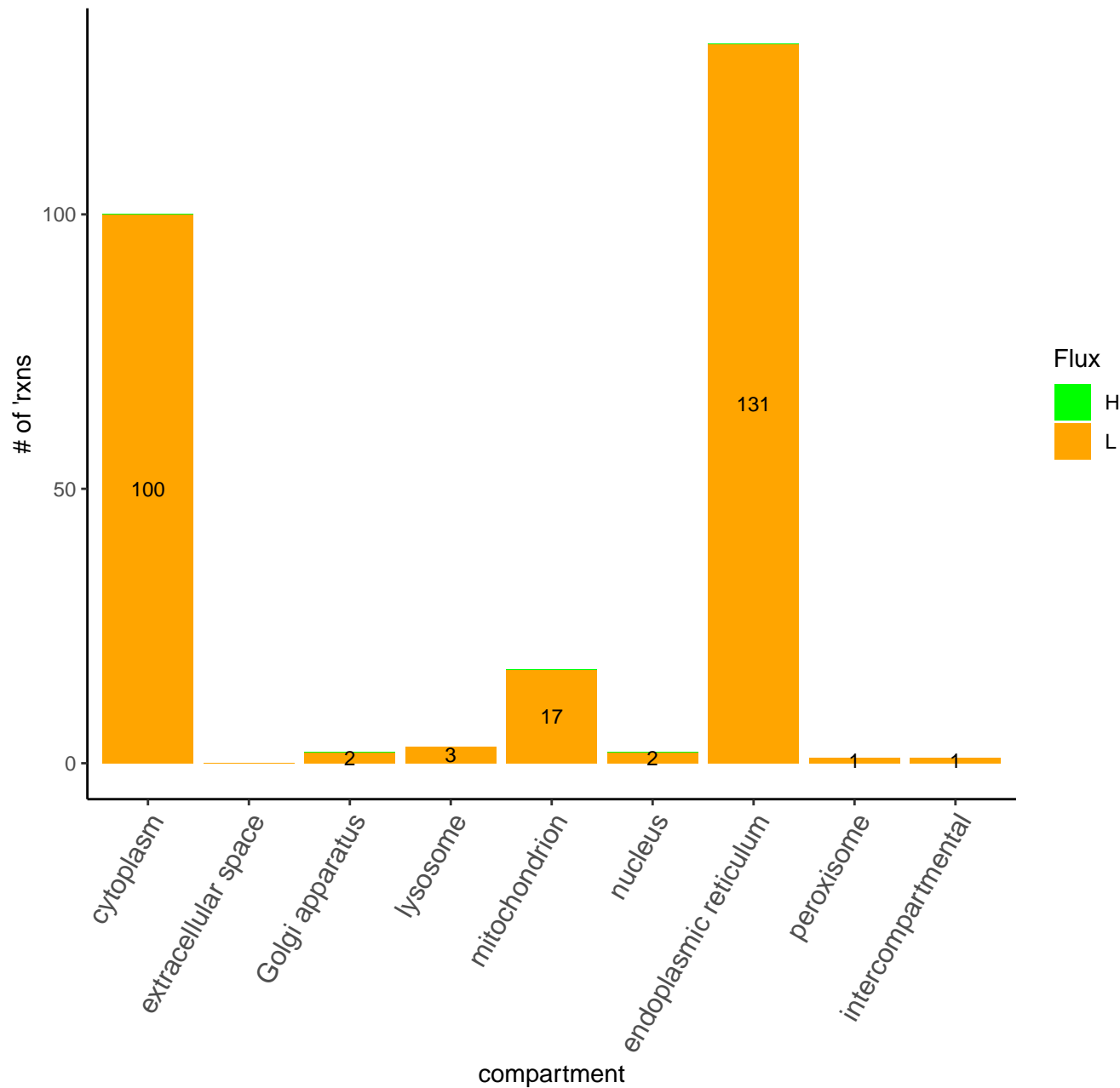


Disrupted rxns (all, n=733) per compartment (bd\_nonresponder)

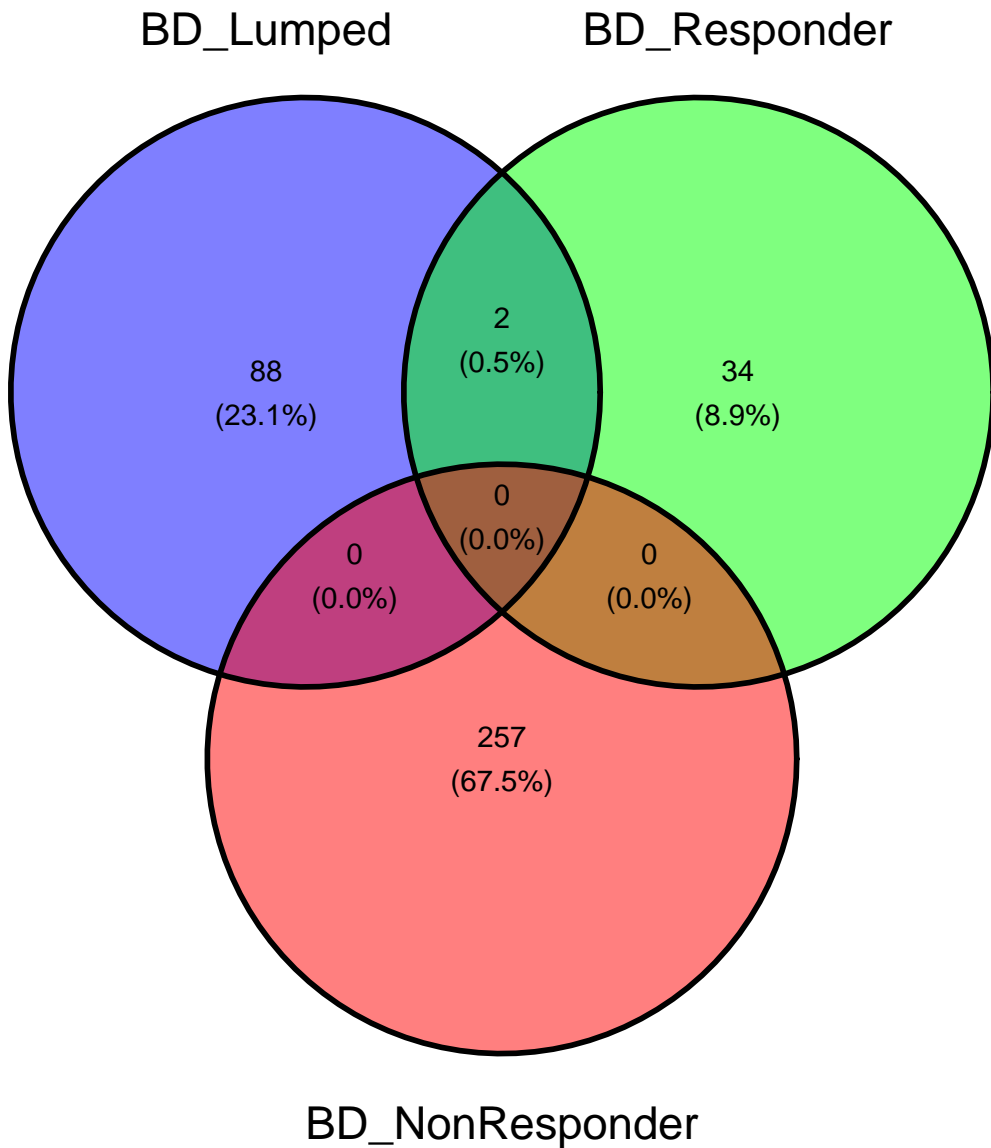




Disrupted rxns (fdr.significant, n=257) per compartment (bd\_nonresponder)



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

