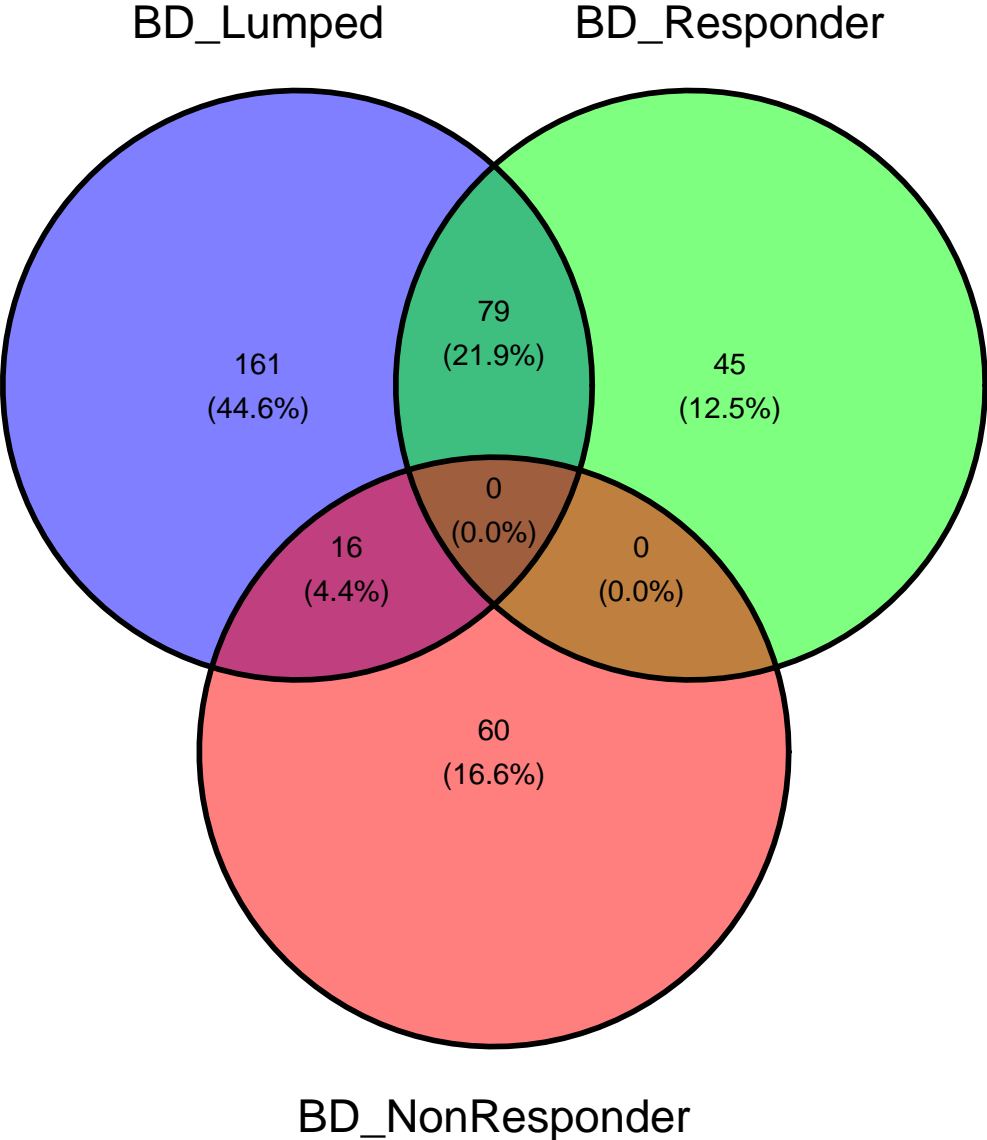
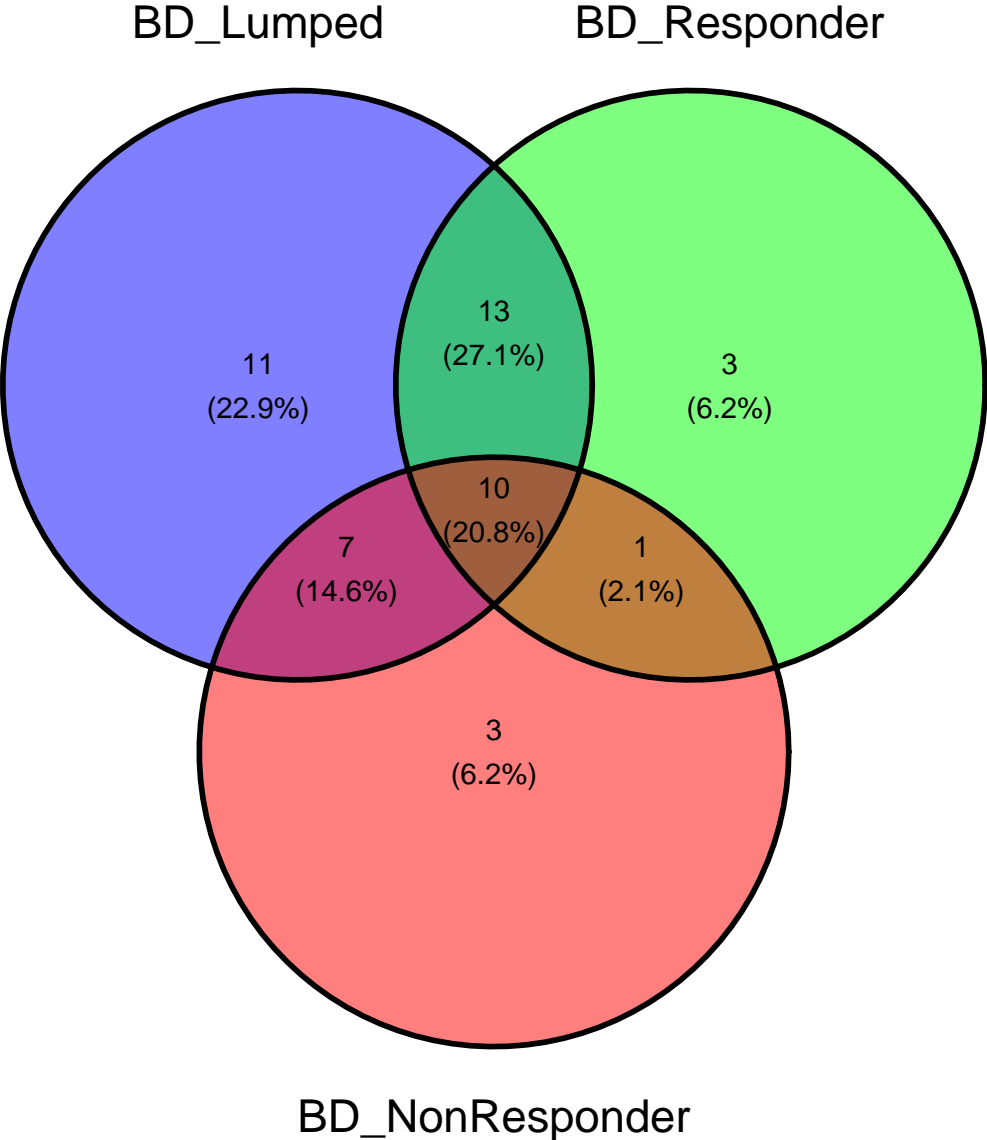


Overlap in rxns disrupted between models

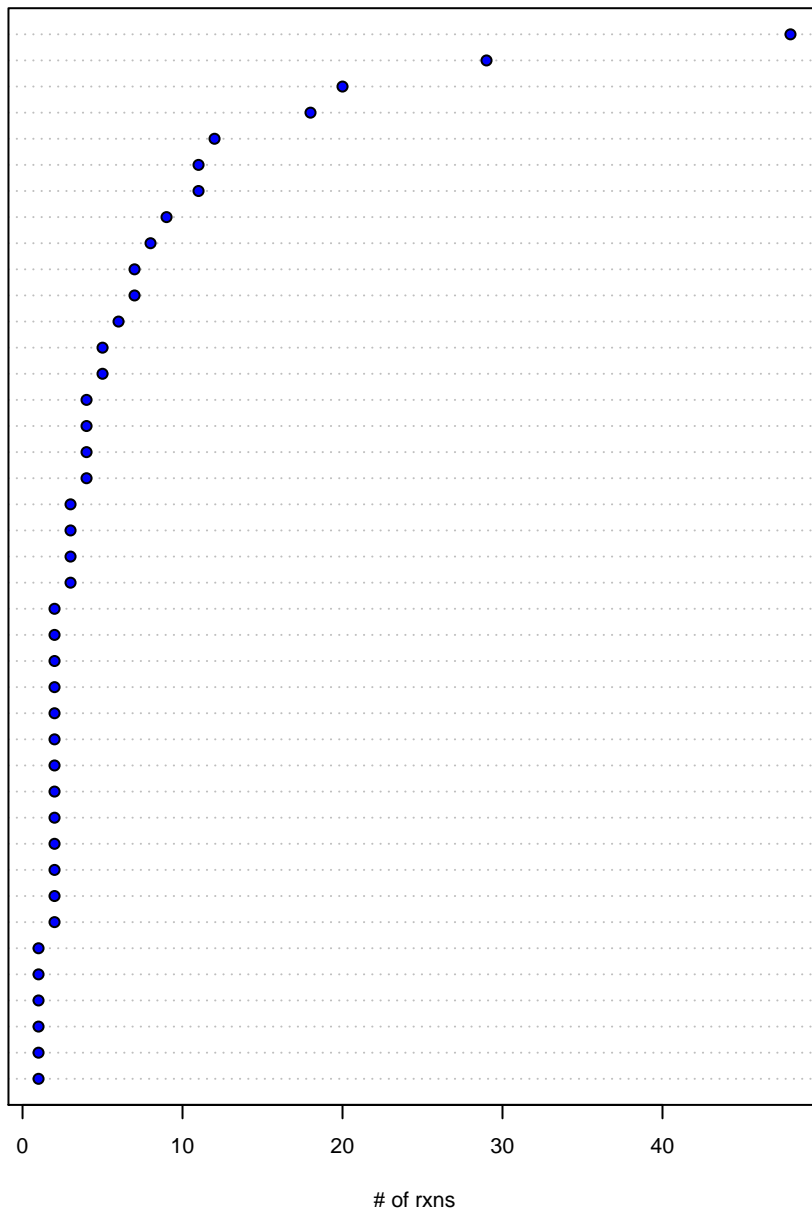


Overlap in subSystems disrupted between models

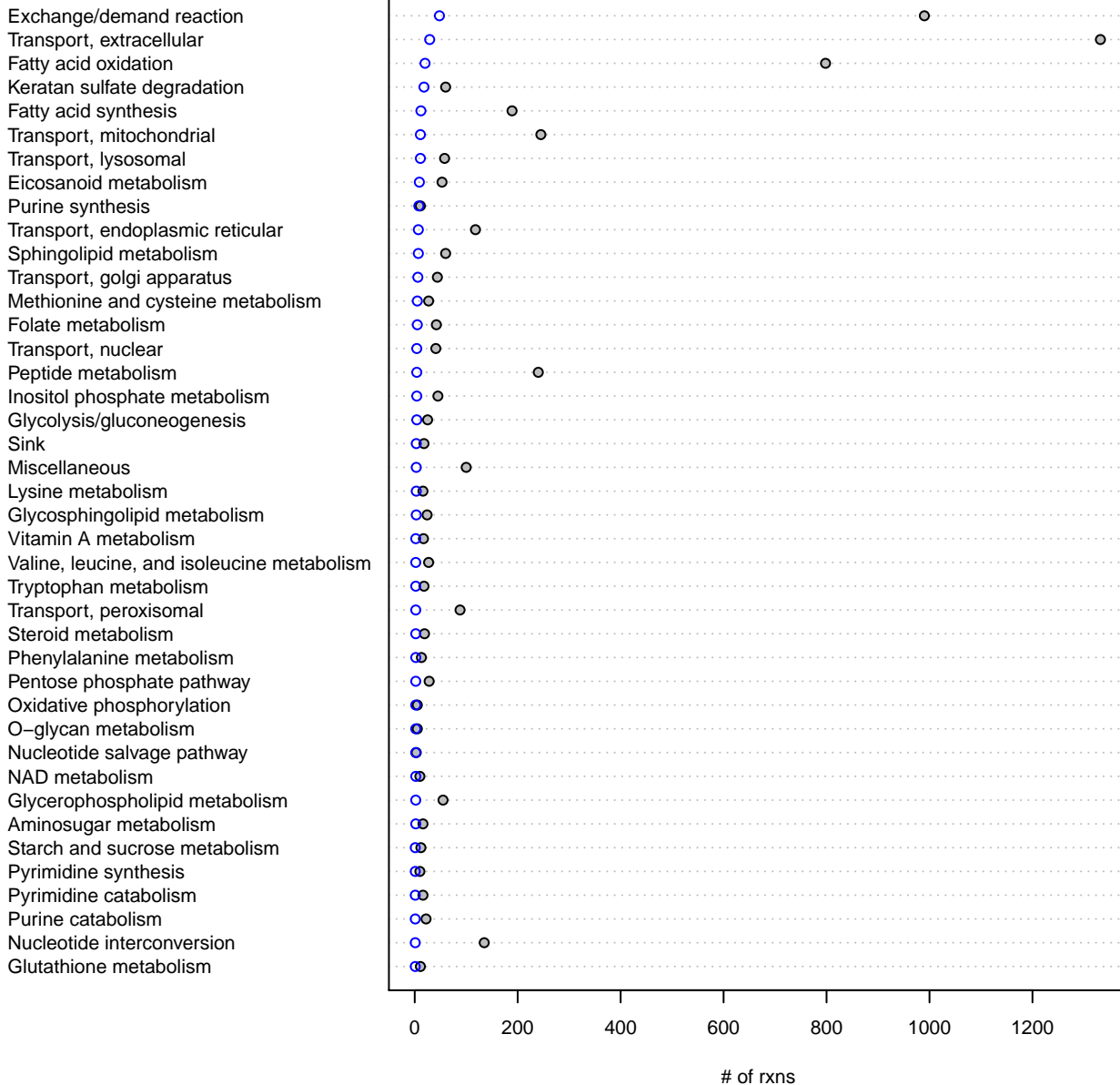


# # of disrupted rxns (n=256, bd\_lumped)

Exchange/demand reaction  
Transport, extracellular  
Fatty acid oxidation  
Keratan sulfate degradation  
Fatty acid synthesis  
Transport, mitochondrial  
Transport, lysosomal  
Eicosanoid metabolism  
Purine synthesis  
Transport, endoplasmic reticular  
Sphingolipid metabolism  
Transport, golgi apparatus  
Methionine and cysteine metabolism  
Folate metabolism  
Transport, nuclear  
Peptide metabolism  
Inositol phosphate metabolism  
Glycolysis/gluconeogenesis  
Sink  
Miscellaneous  
Lysine metabolism  
Glycosphingolipid metabolism  
Vitamin A metabolism  
Valine, leucine, and isoleucine metabolism  
Tryptophan metabolism  
Transport, peroxisomal  
Steroid metabolism  
Phenylalanine metabolism  
Pentose phosphate pathway  
Oxidative phosphorylation  
O-glycan metabolism  
Nucleotide salvage pathway  
NAD metabolism  
Glycerophospholipid metabolism  
Aminosugar metabolism  
Starch and sucrose metabolism  
Pyrimidine synthesis  
Pyrimidine catabolism  
Purine catabolism  
Nucleotide interconversion  
Glutathione metabolism

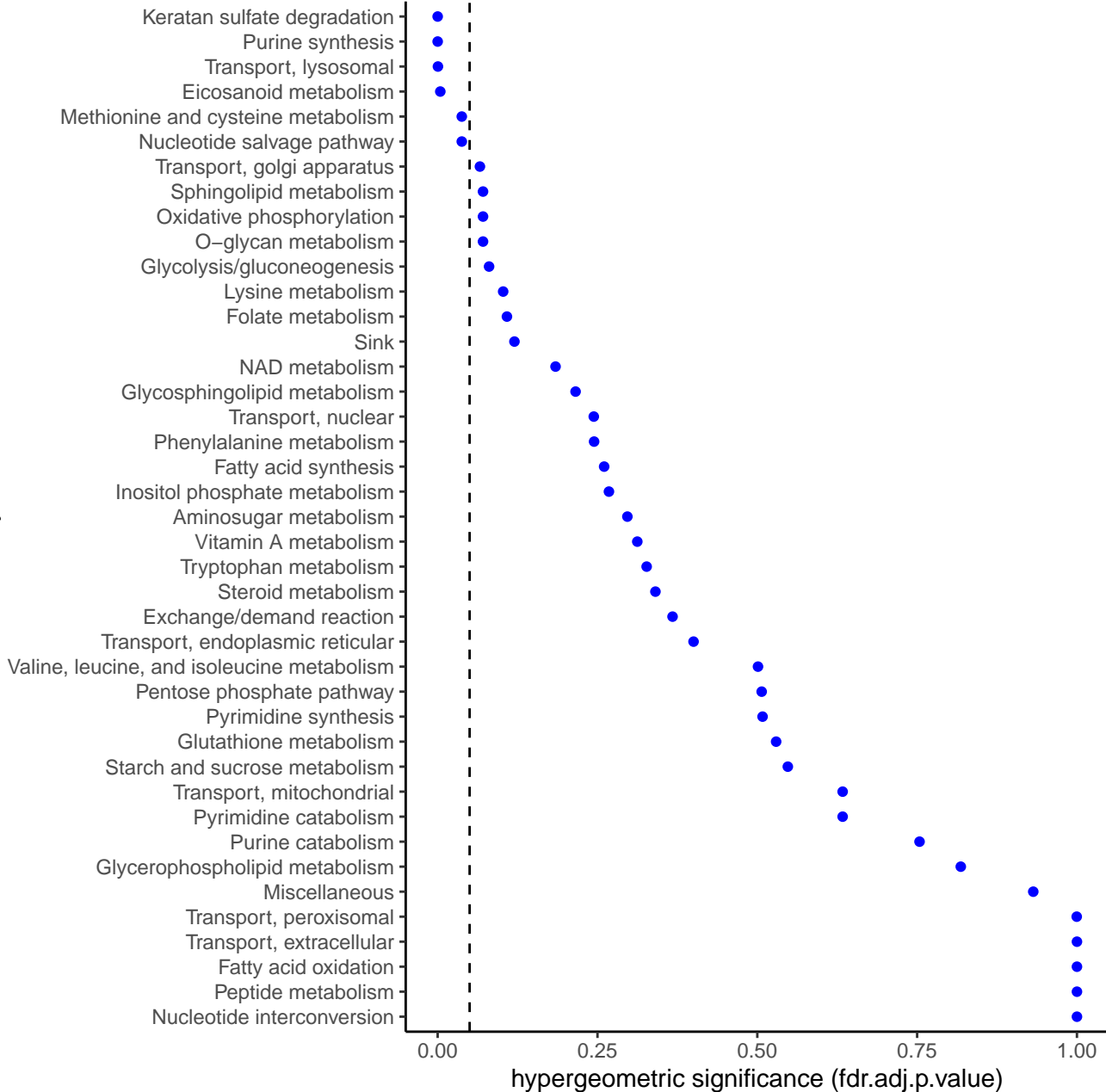


# # of disrupted rxns (n=256, bd\_lumped) vs all rxns

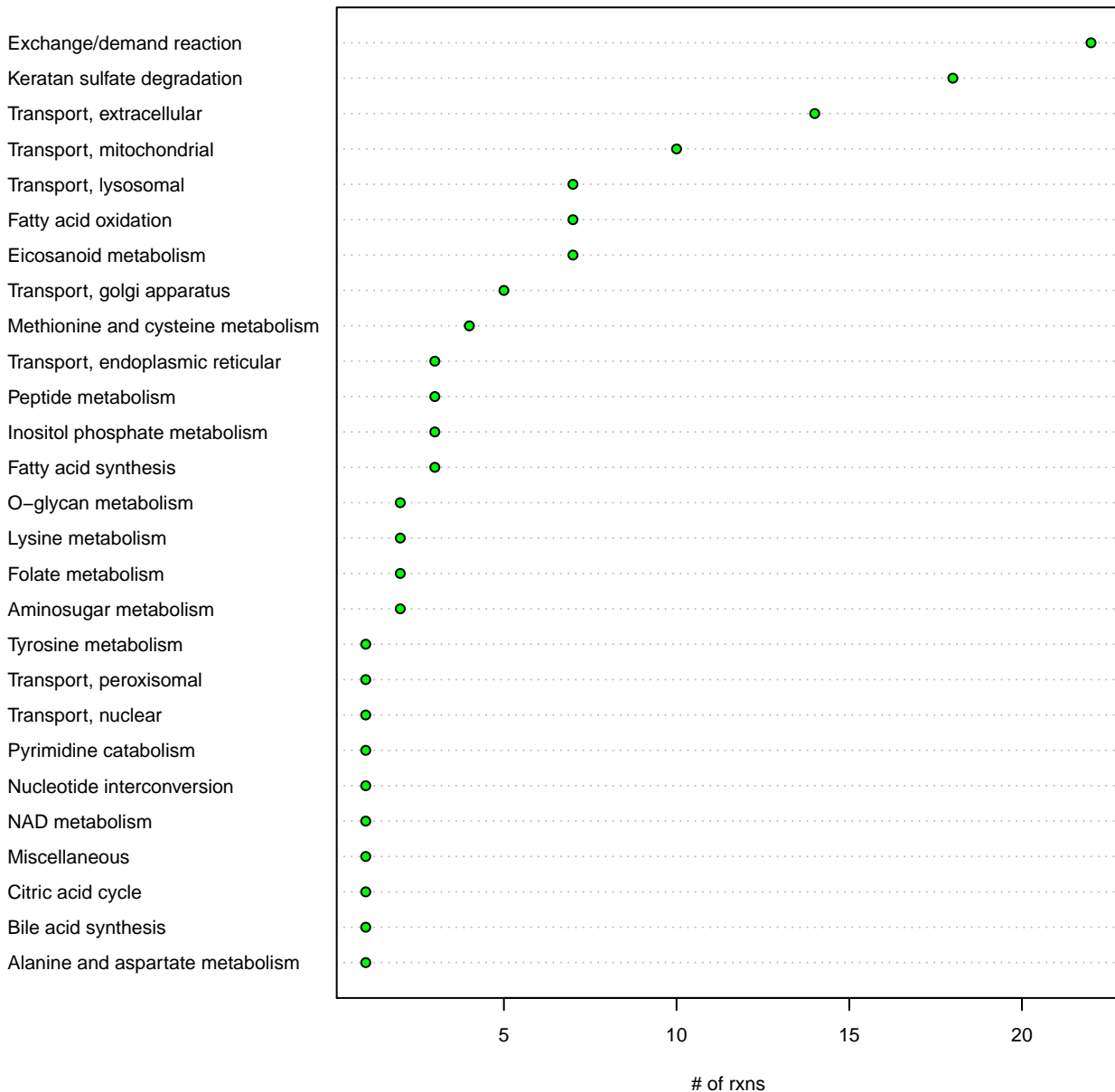


# over-representation analysis, bd\_lumped

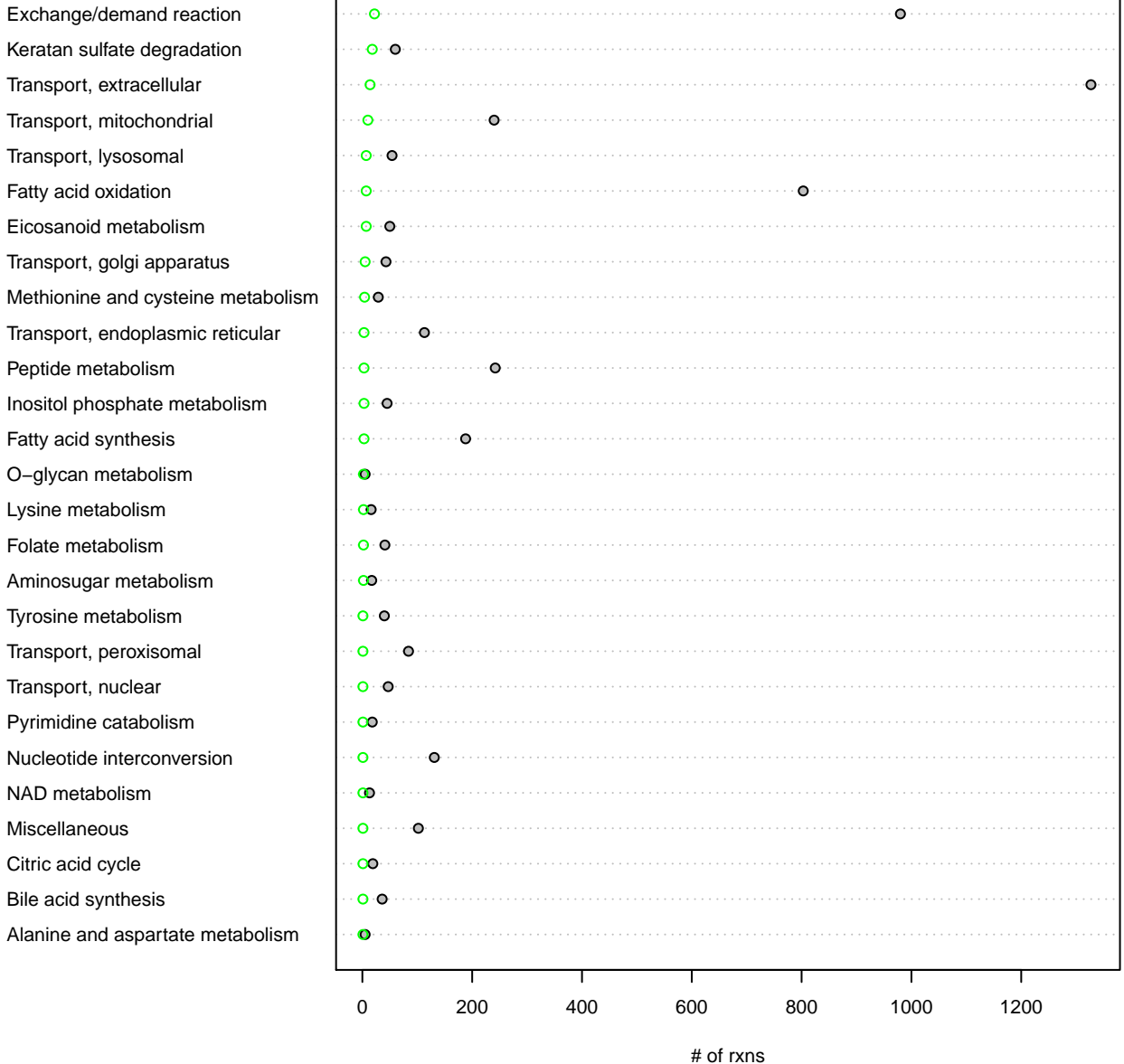
subSystem



# of disrupted rxns (n=124, bd\_responder)

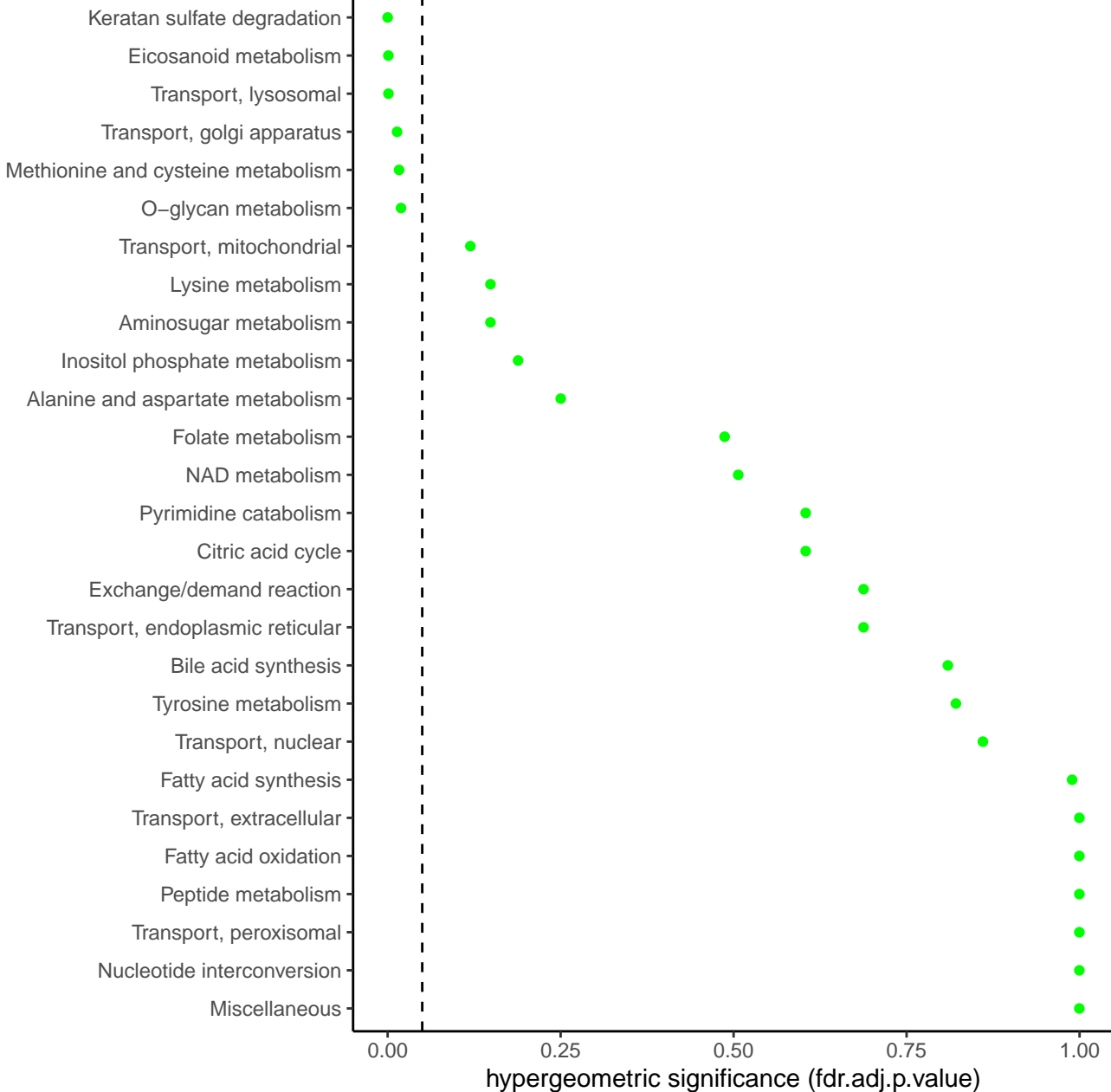


# of disrupted rxns (n=124, bd\_responder) vs all rxns



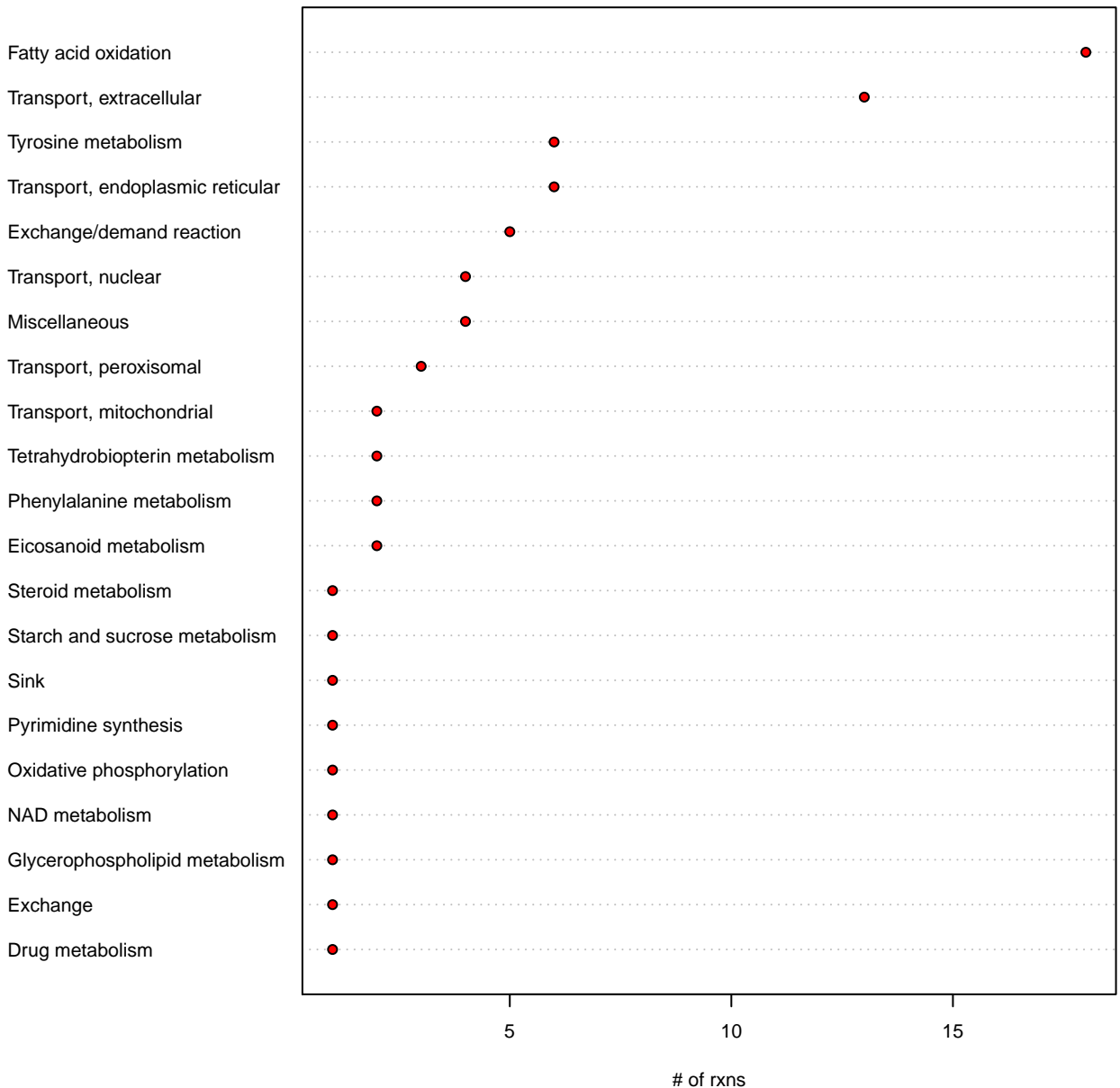
# over-representation analysis, bd\_responder

subSystem

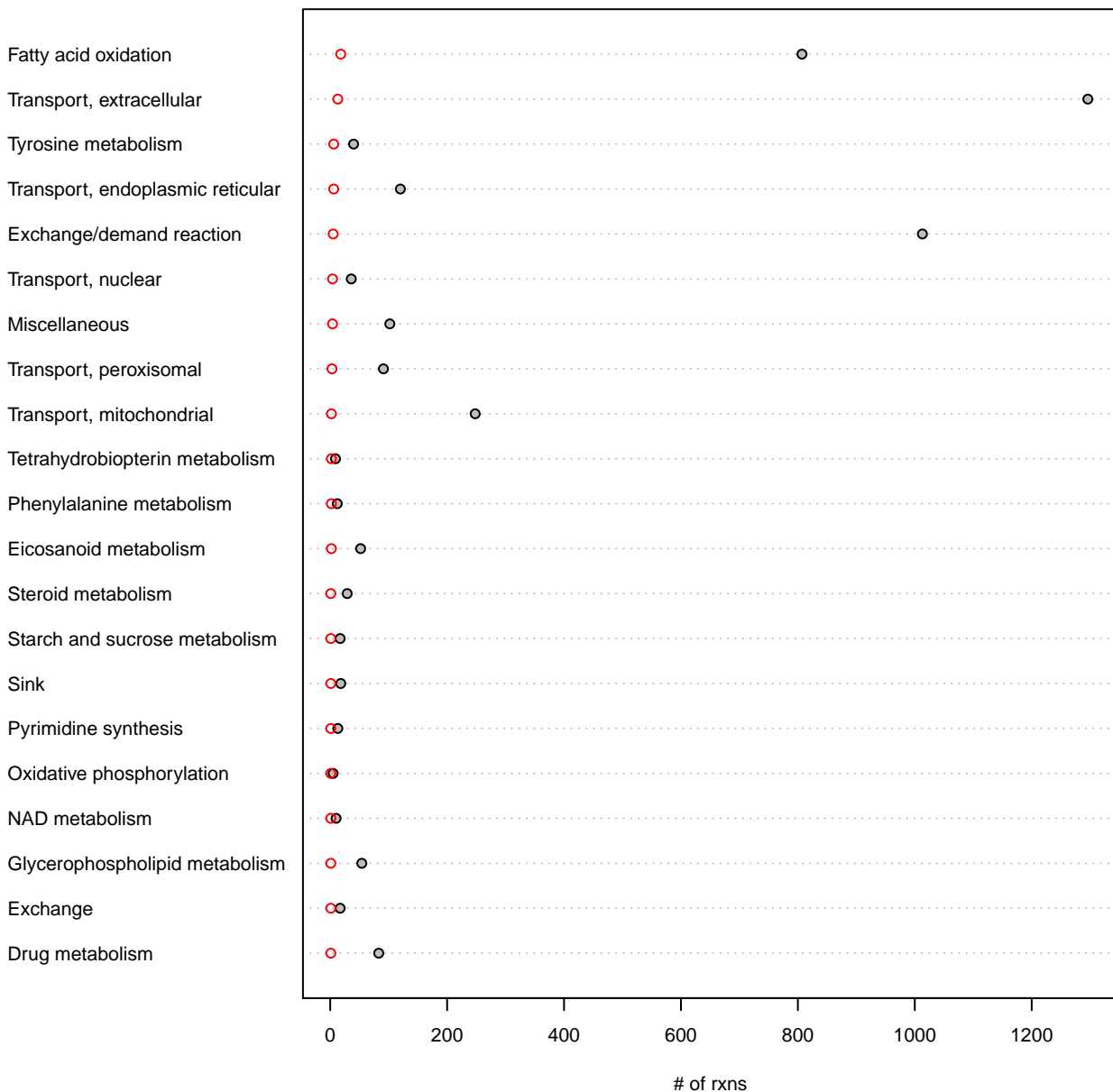




# of disrupted rxns (n=76, bd\_nonresponder)

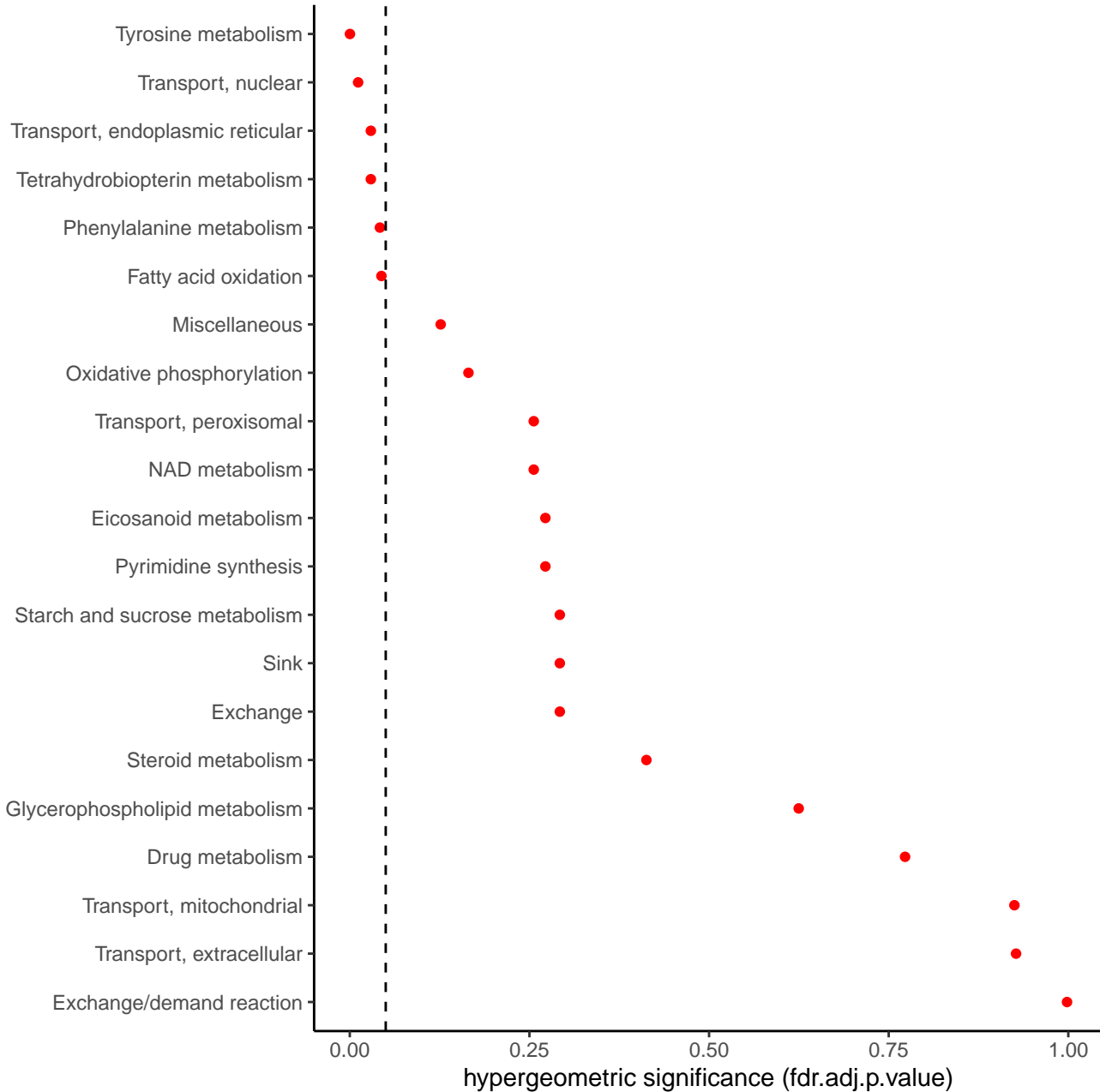


# of disrupted rxns (n=76, bd\_nonresponder) vs all rxns

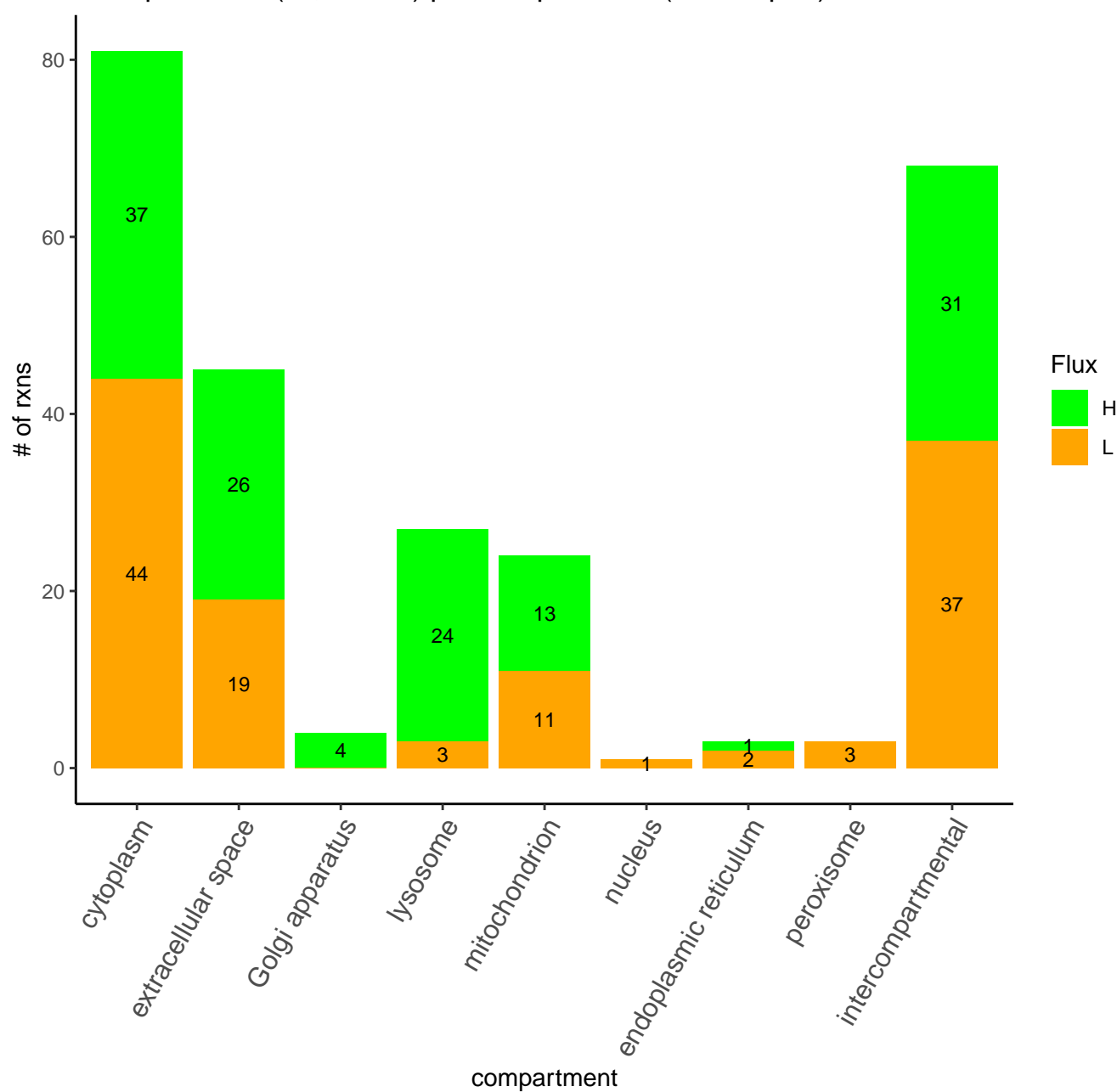


# over-representation analysis, bd\_nonresponder

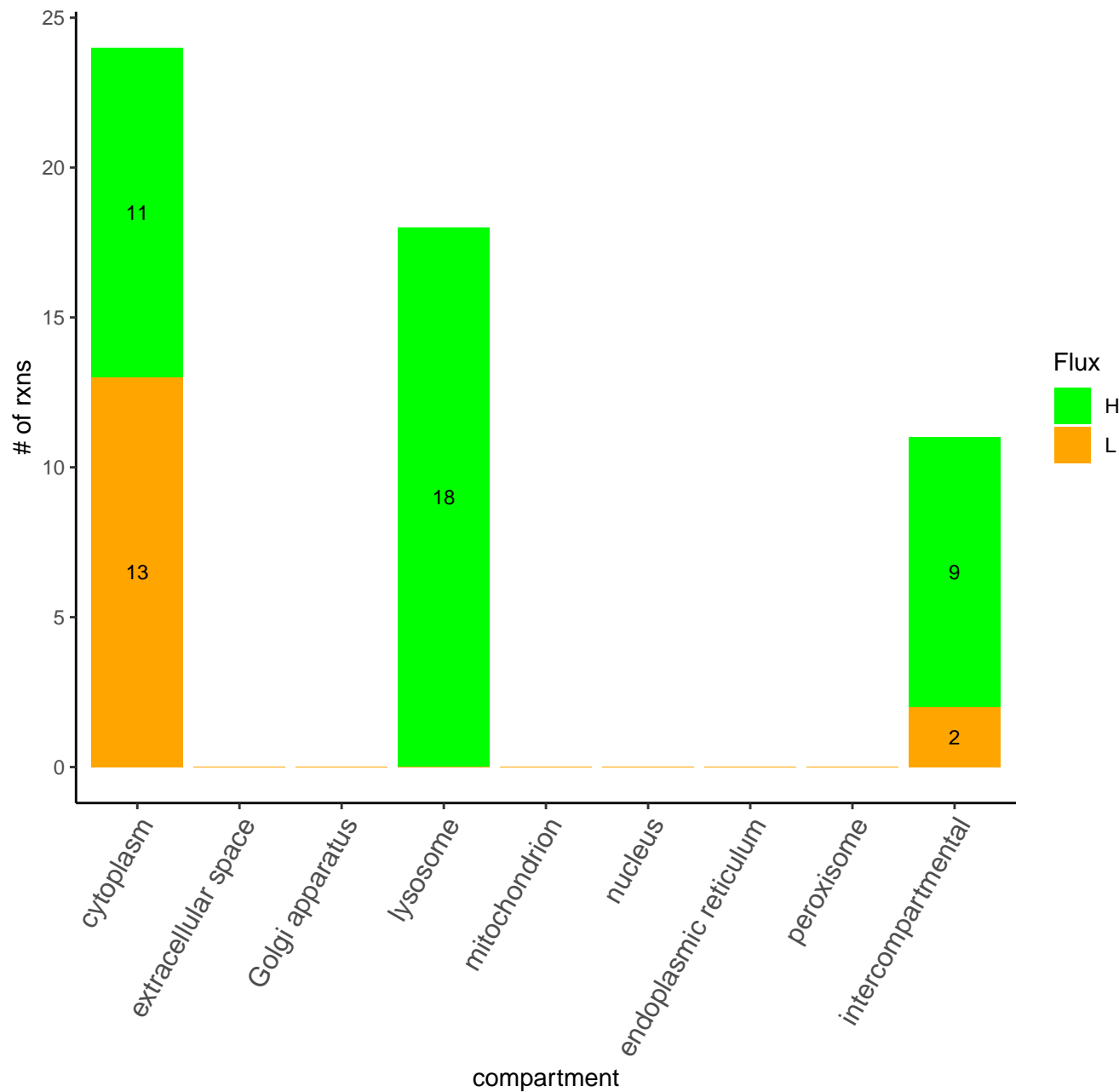
subSystem



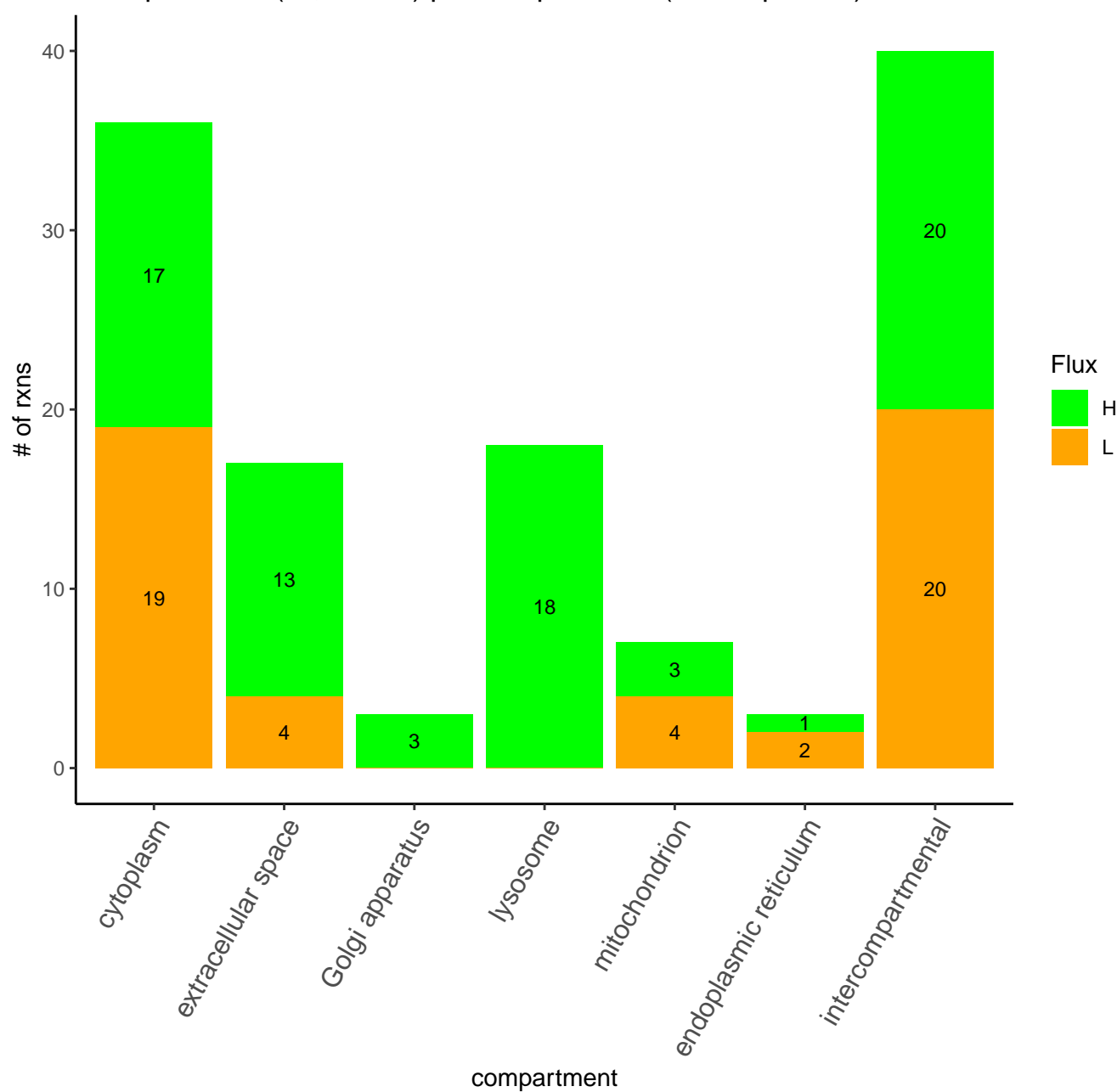
Disrupted rxns (all, n=256) per compartment (bd\_lumped)



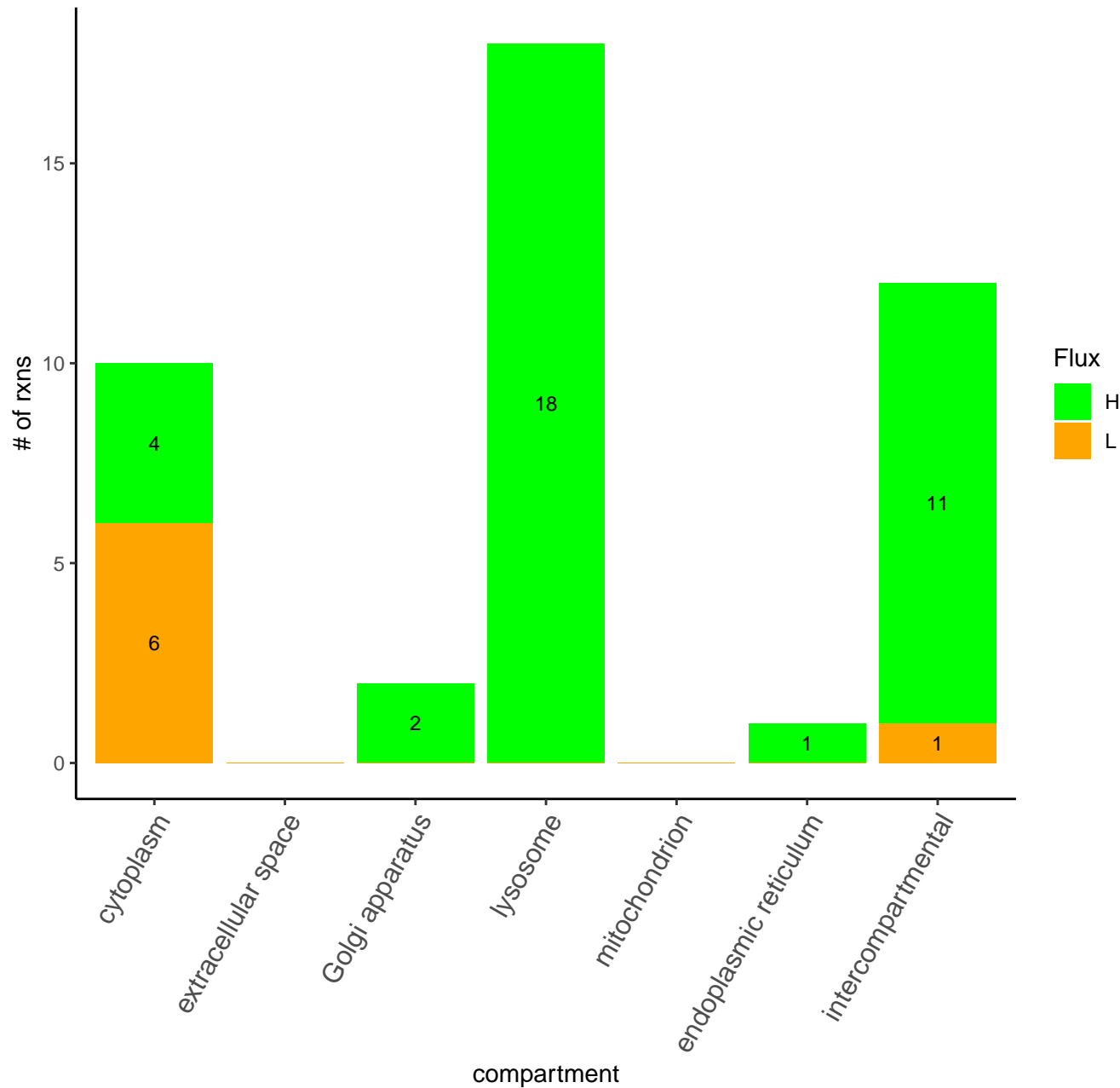
Disrupted rxns (fdr.significant, n=53) per compartment (bd\_lumped)



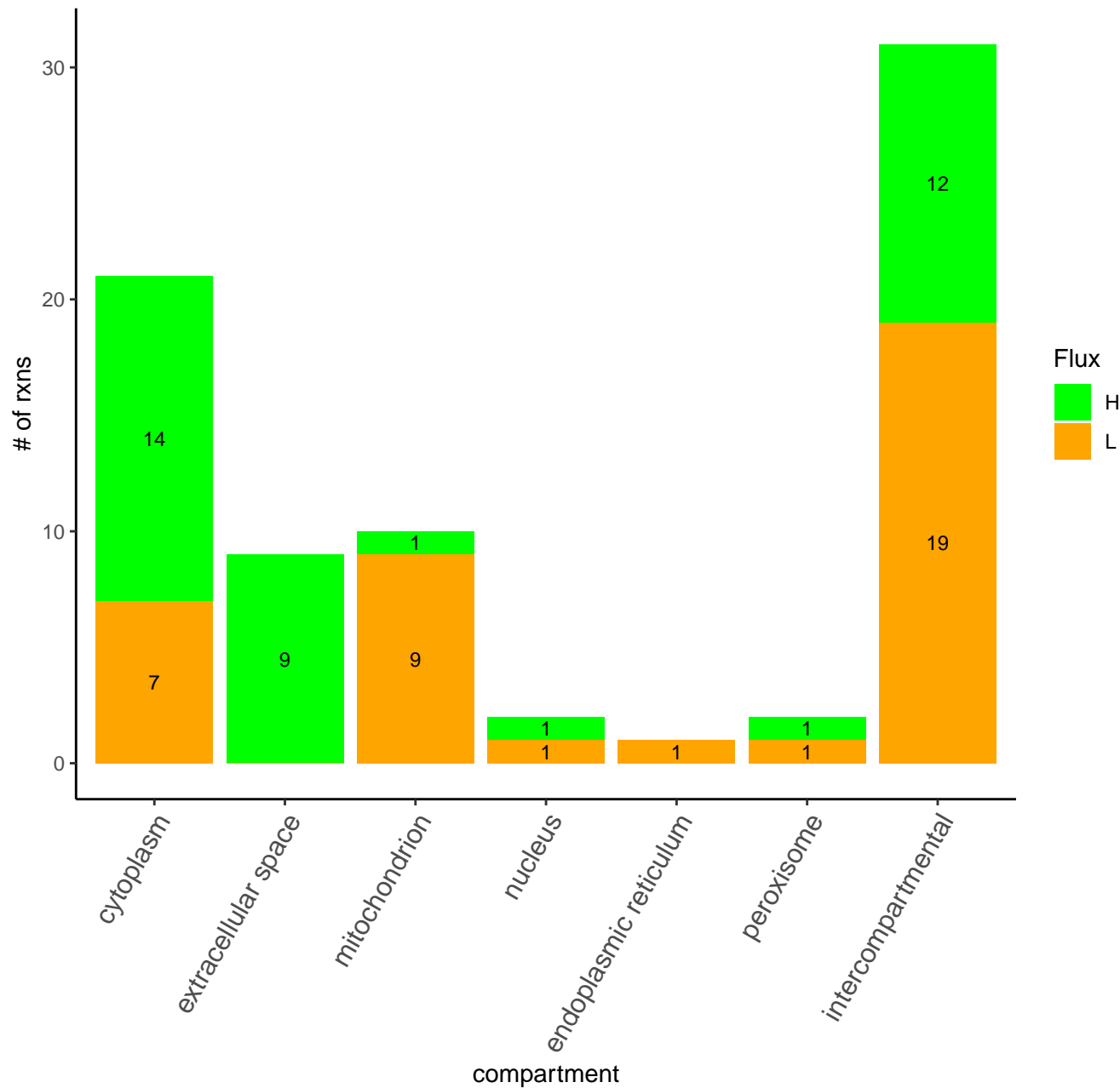
Disrupted rxns (all, n=124) per compartment (bd\_responder)



Disrupted rxns (fdr.significant, n=43) per compartment (bd\_responder)

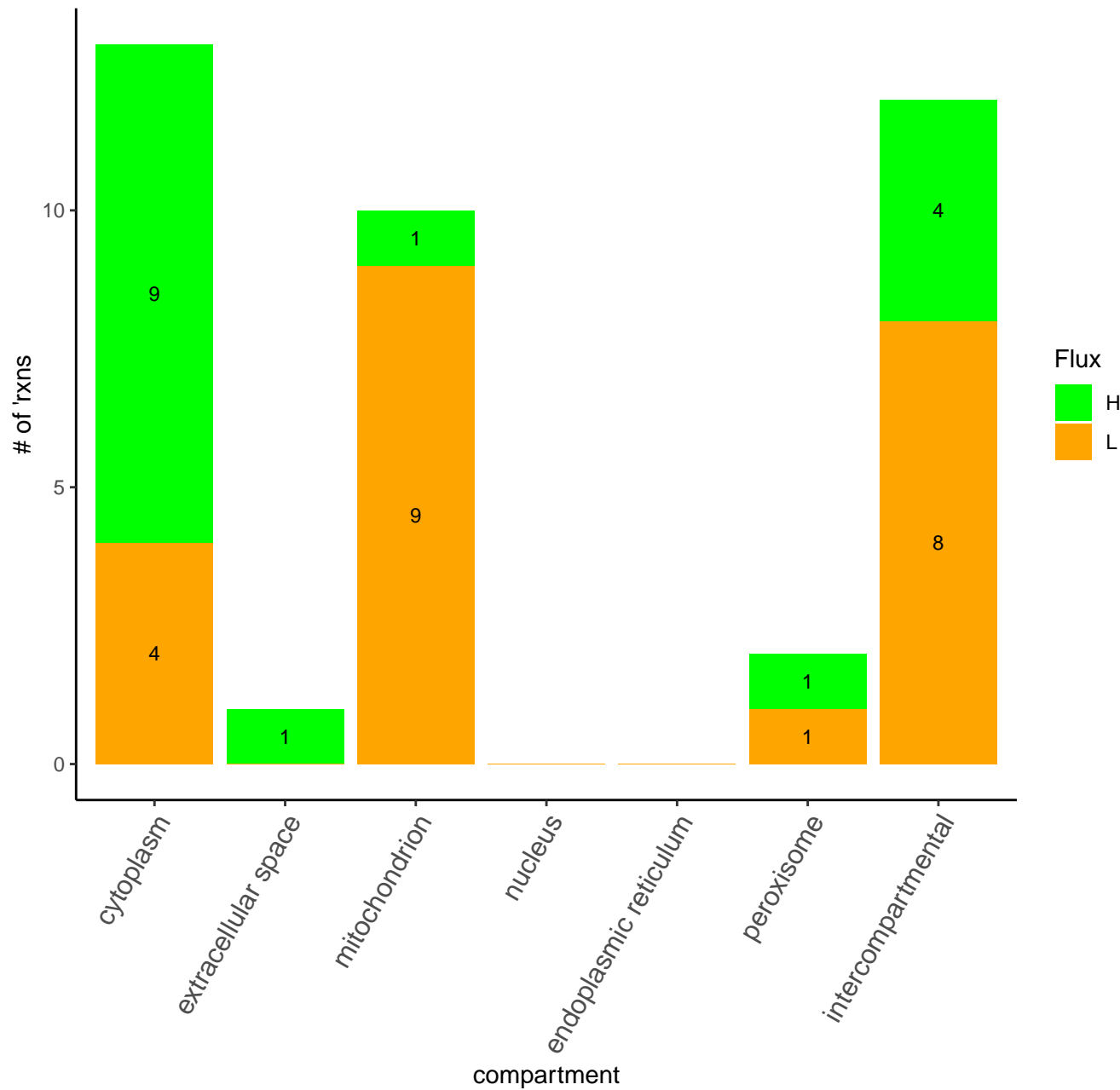


Disrupted rxns (all, n=76) per compartment (bd\_nonresponder)

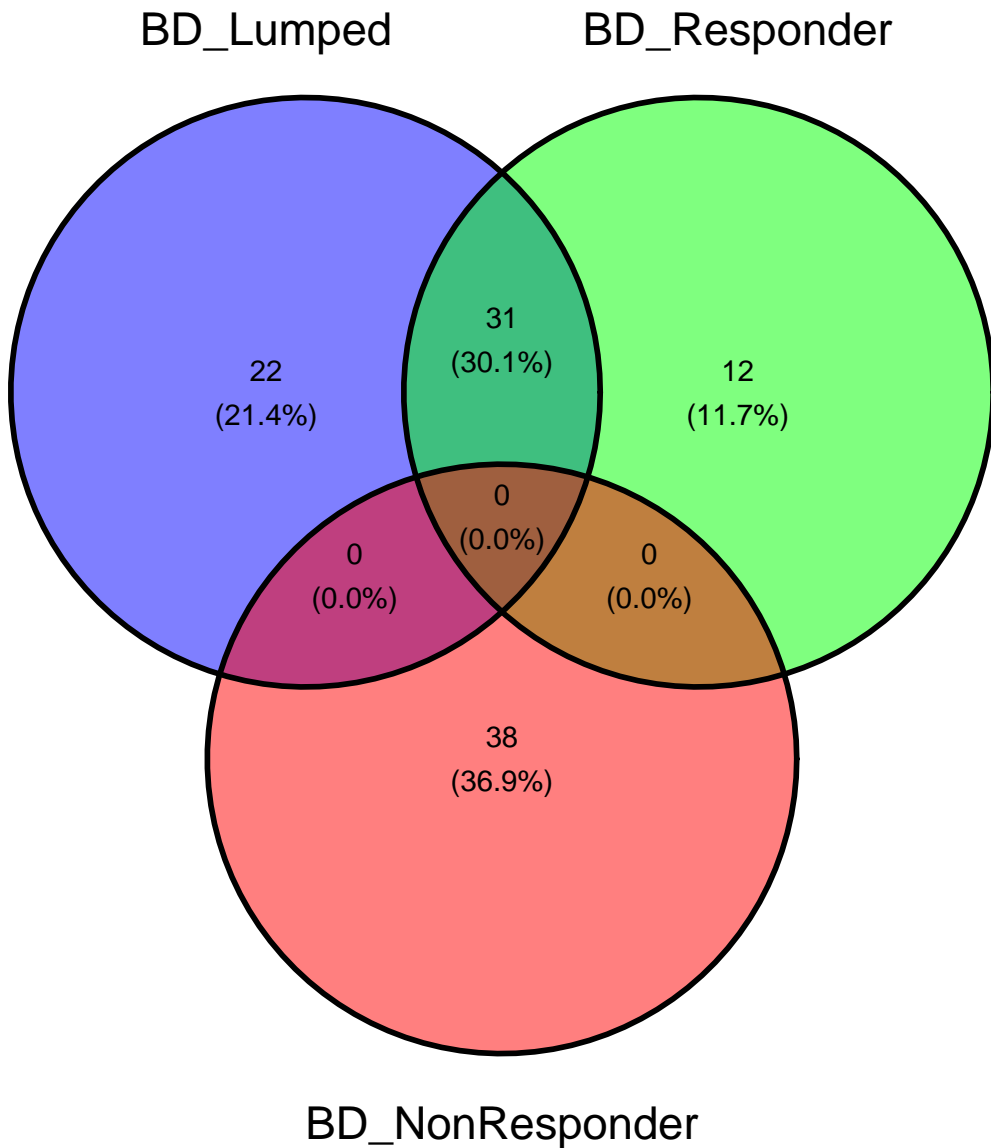




Disrupted rxns (fdr.significant, n=38) per compartment (bd\_nonresponder)



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

