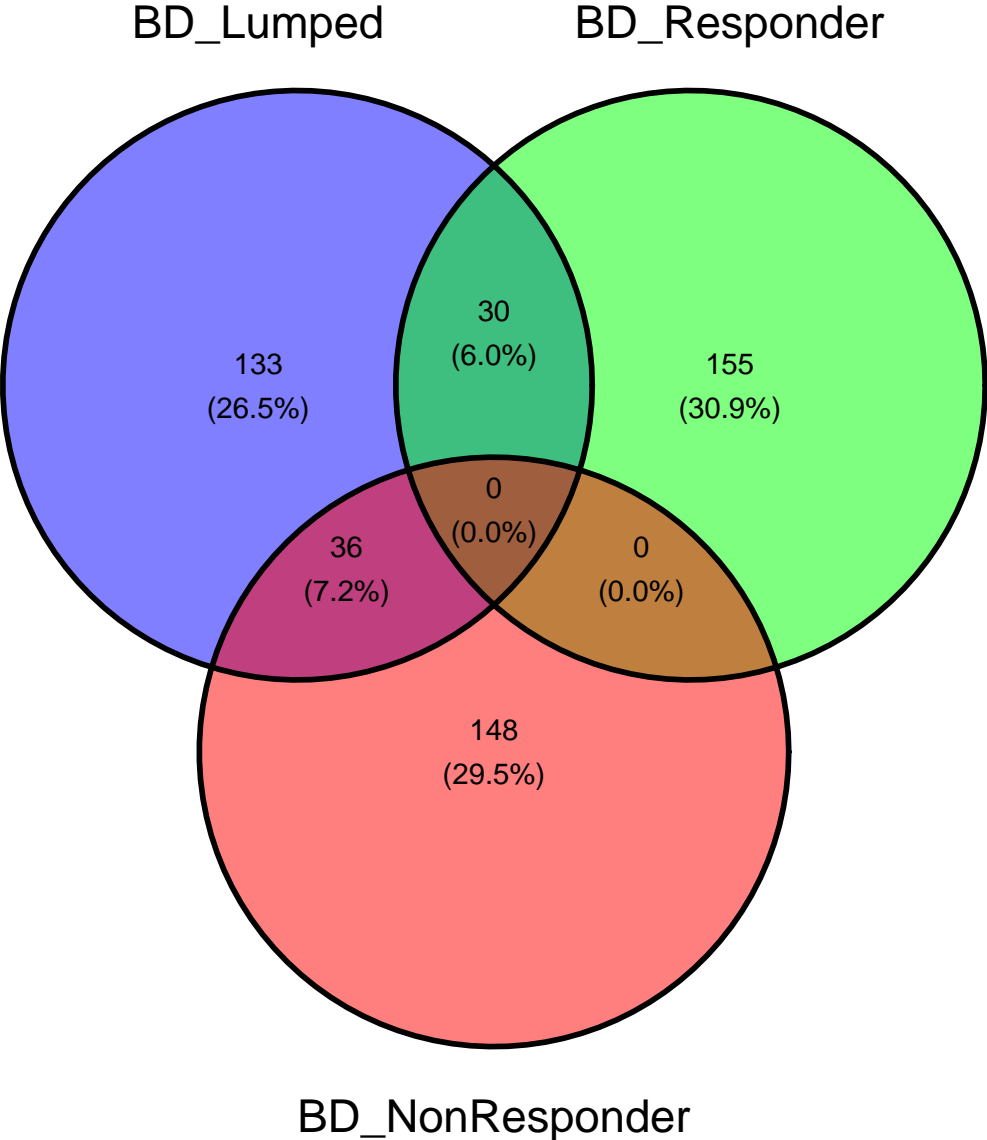
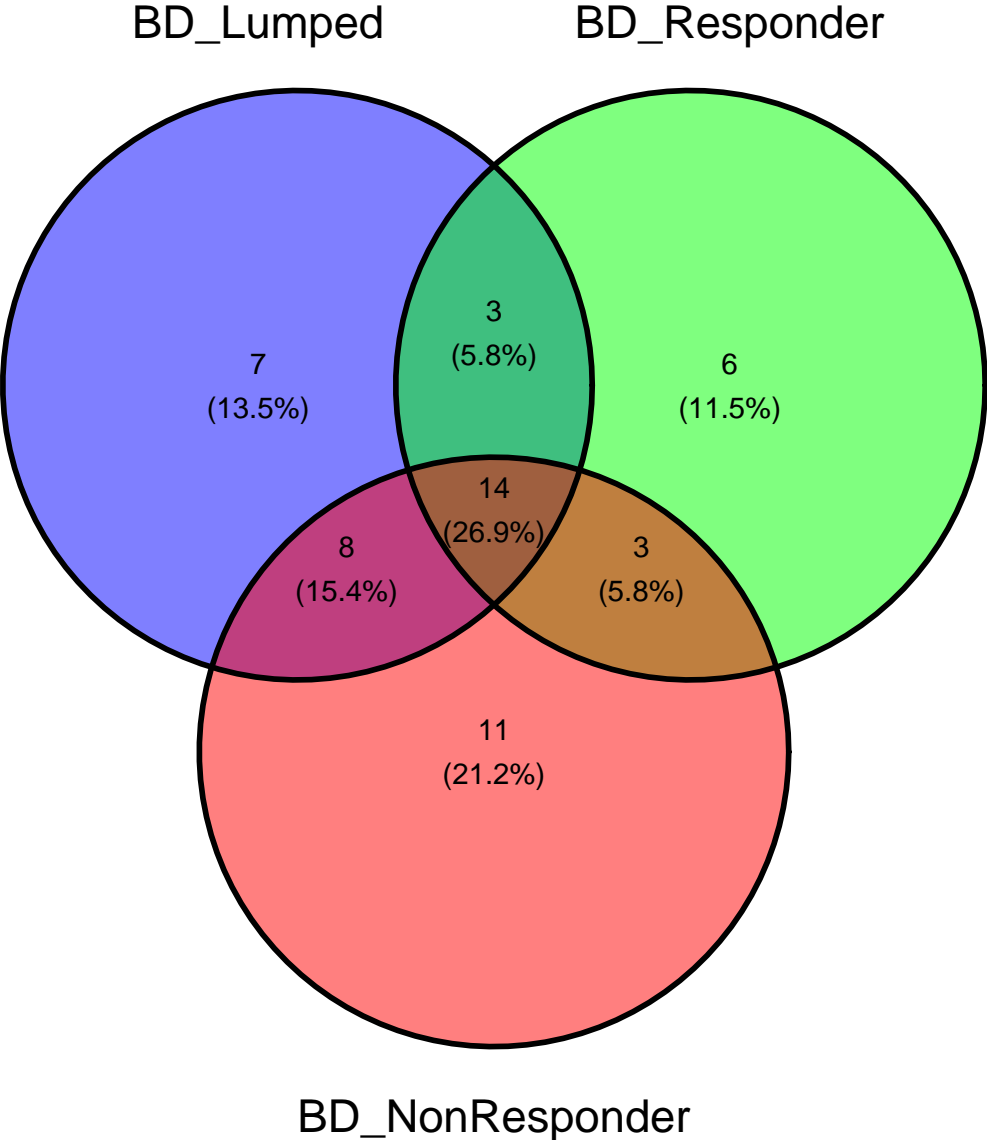


Overlap in rxns disrupted between models

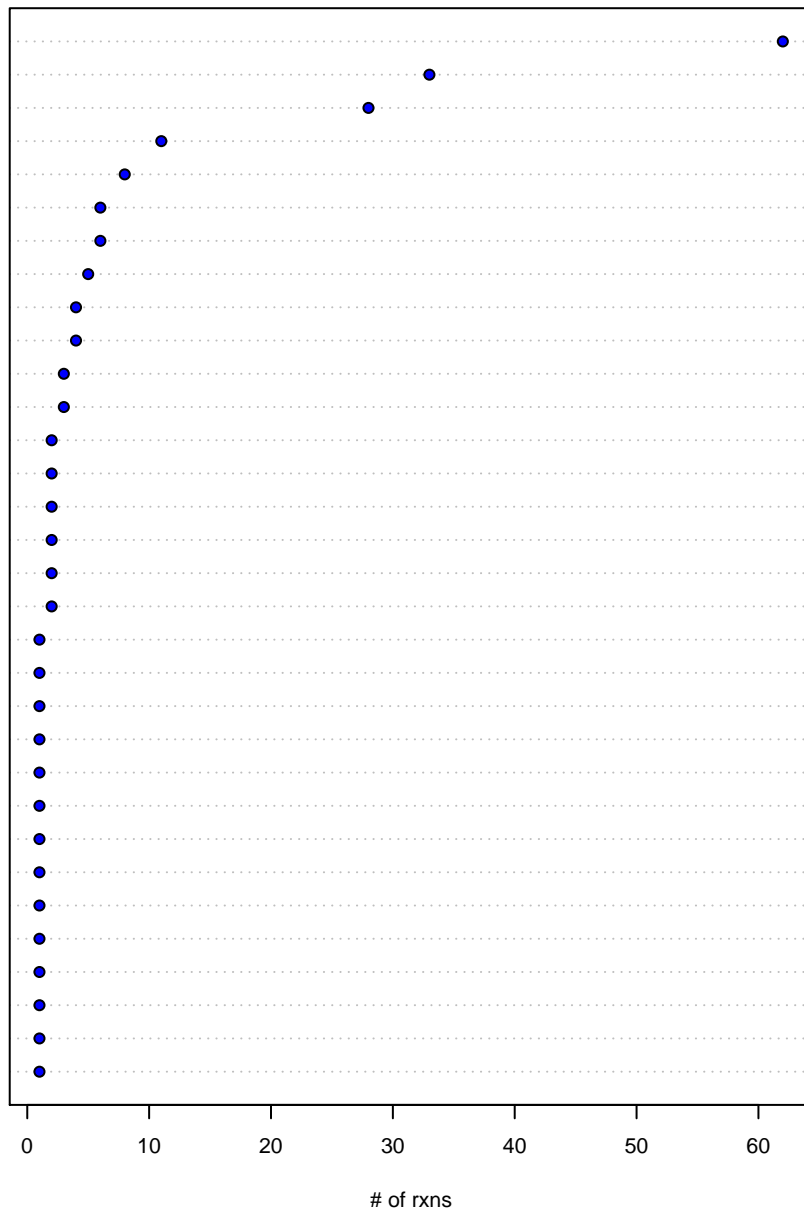


Overlap in subSystems disrupted between models

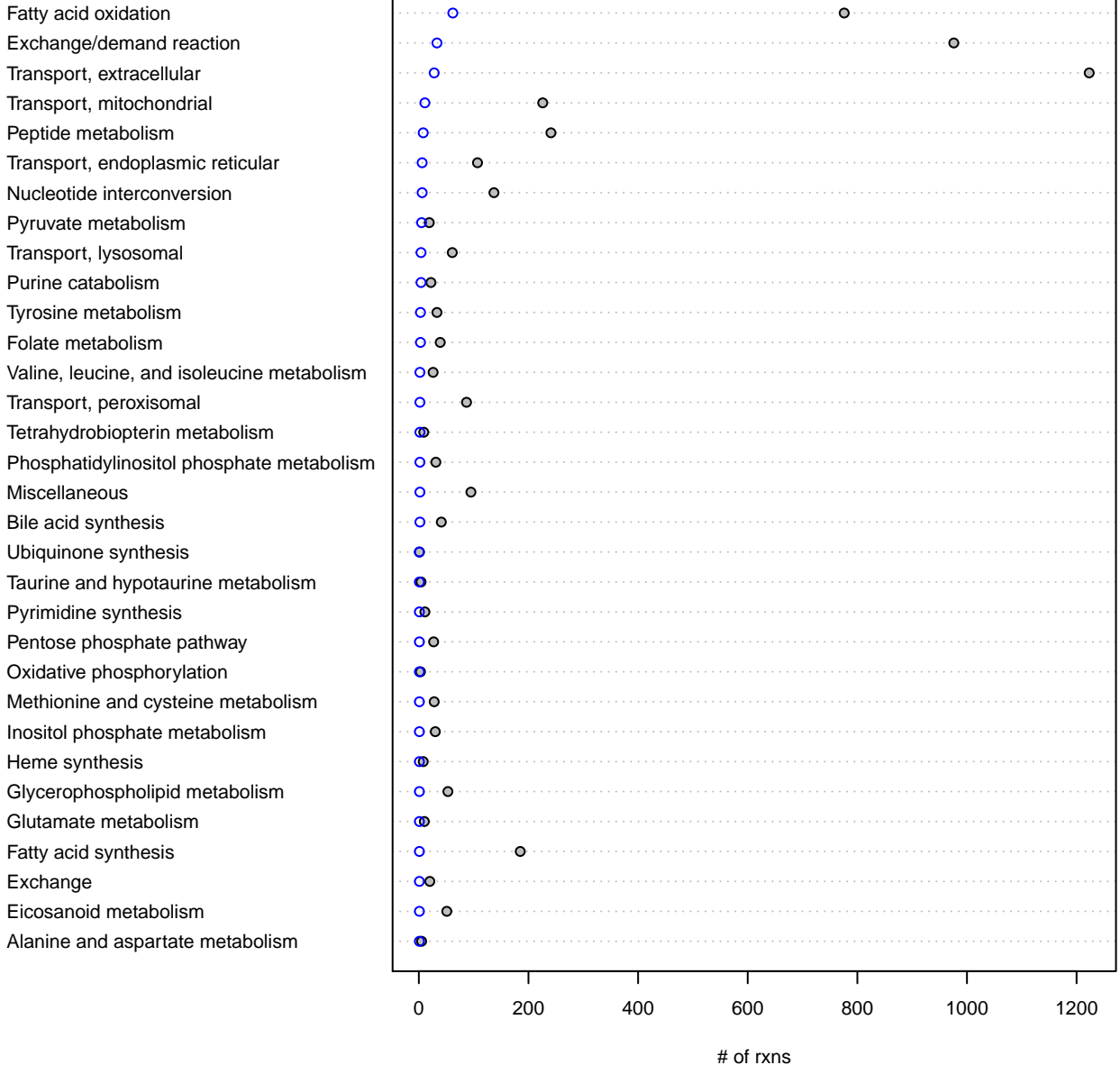


# # of disrupted rxns (n=199, bd\_lumped)

Fatty acid oxidation  
Exchange/demand reaction  
Transport, extracellular  
Transport, mitochondrial  
Peptide metabolism  
Transport, endoplasmic reticular  
Nucleotide interconversion  
Pyruvate metabolism  
Transport, lysosomal  
Purine catabolism  
Tyrosine metabolism  
Folate metabolism  
Valine, leucine, and isoleucine metabolism  
Transport, peroxisomal  
Tetrahydrobiopterin metabolism  
Phosphatidylinositol phosphate metabolism  
Miscellaneous  
Bile acid synthesis  
Ubiquinone synthesis  
Taurine and hypotaurine metabolism  
Pyrimidine synthesis  
Pentose phosphate pathway  
Oxidative phosphorylation  
Methionine and cysteine metabolism  
Inositol phosphate metabolism  
Heme synthesis  
Glycerophospholipid metabolism  
Glutamate metabolism  
Fatty acid synthesis  
Exchange  
Eicosanoid metabolism  
Alanine and aspartate metabolism

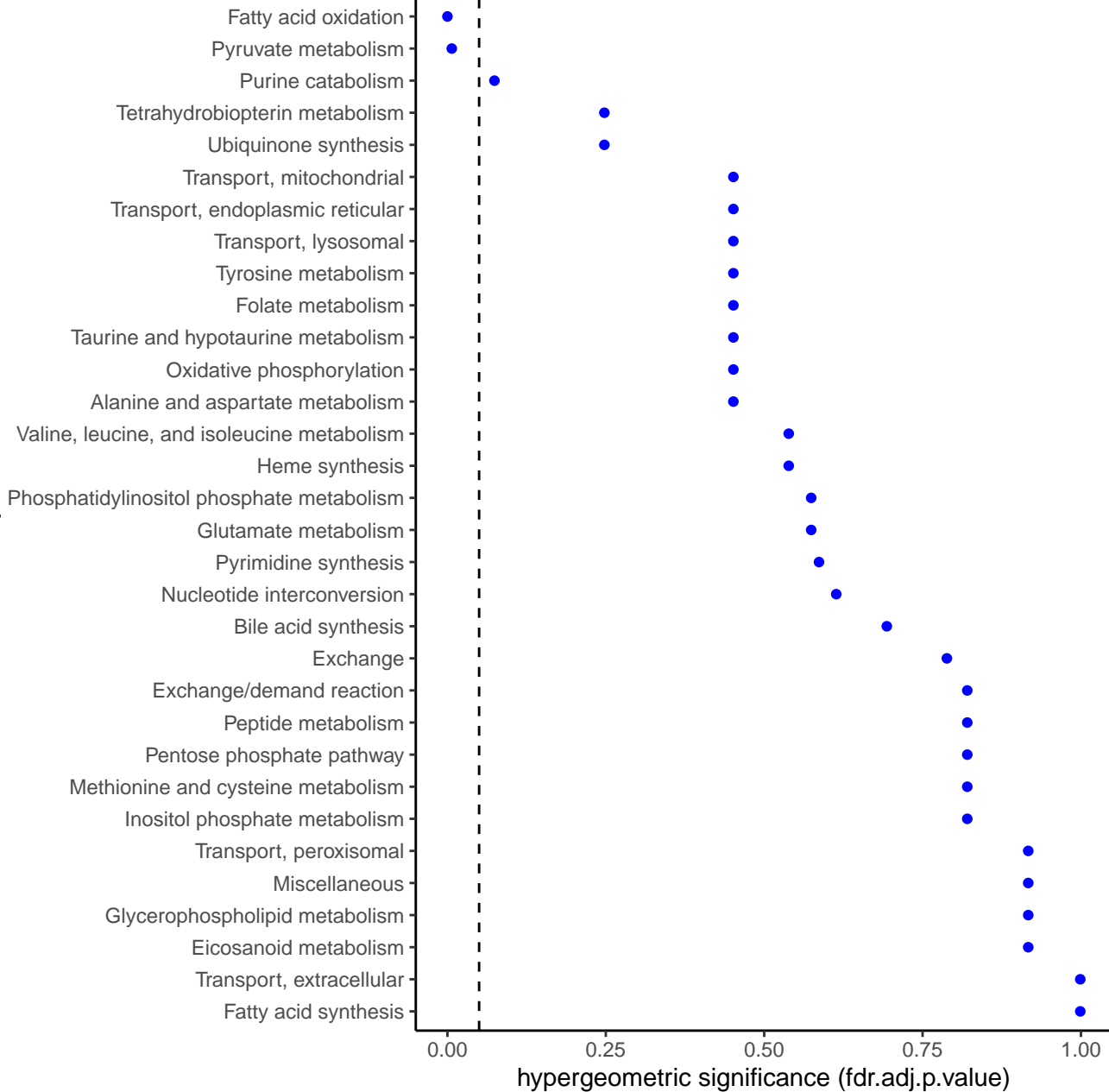


# of disrupted rxns (n=199, bd\_lumped) vs all rxns

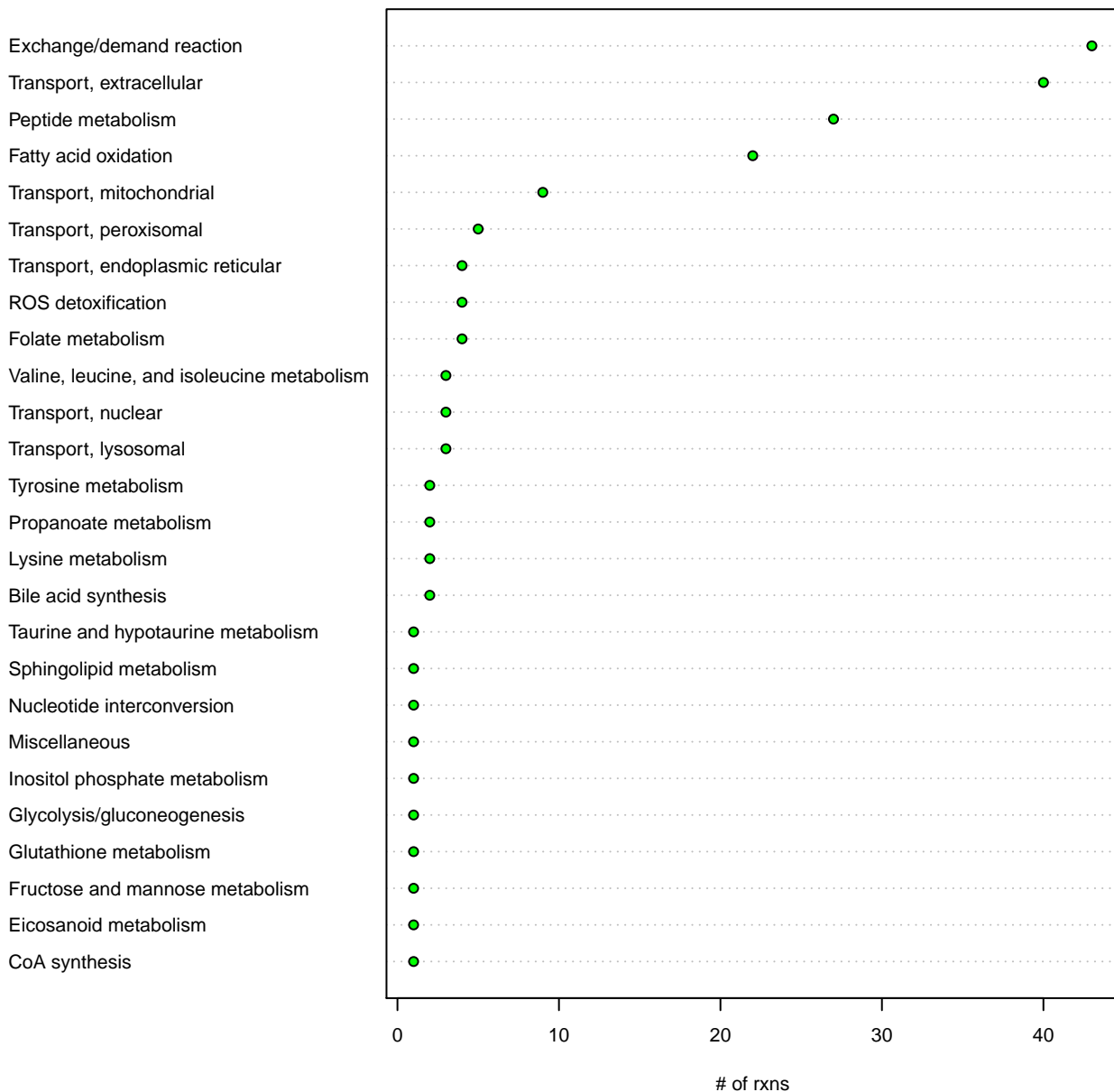


# over-representation analysis, bd\_lumped

subSystem



# of disrupted rxns (n=185, bd\_responder)



# of disrupted rxns (n=185, bd\_responder) vs all rxns

Exchange/demand reaction

Transport, extracellular

Peptide metabolism

Fatty acid oxidation

Transport, mitochondrial

Transport, peroxisomal

Transport, endoplasmic reticular

ROS detoxification

Folate metabolism

Valine, leucine, and isoleucine metabolism

Transport, nuclear

Transport, lysosomal

Tyrosine metabolism

Propanoate metabolism

Lysine metabolism

Bile acid synthesis

Taurine and hypotaurine metabolism

Sphingolipid metabolism

Nucleotide interconversion

Miscellaneous

Inositol phosphate metabolism

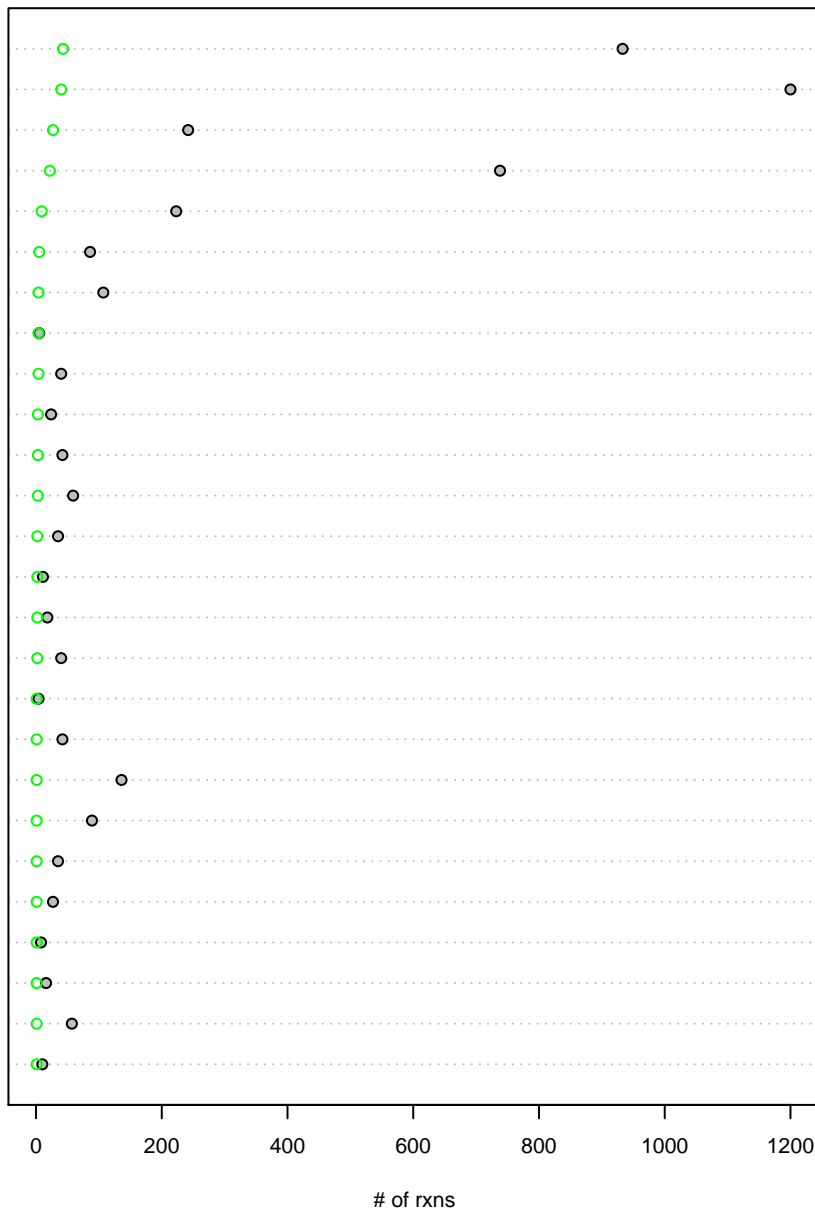
Glycolysis/gluconeogenesis

Glutathione metabolism

Fructose and mannose metabolism

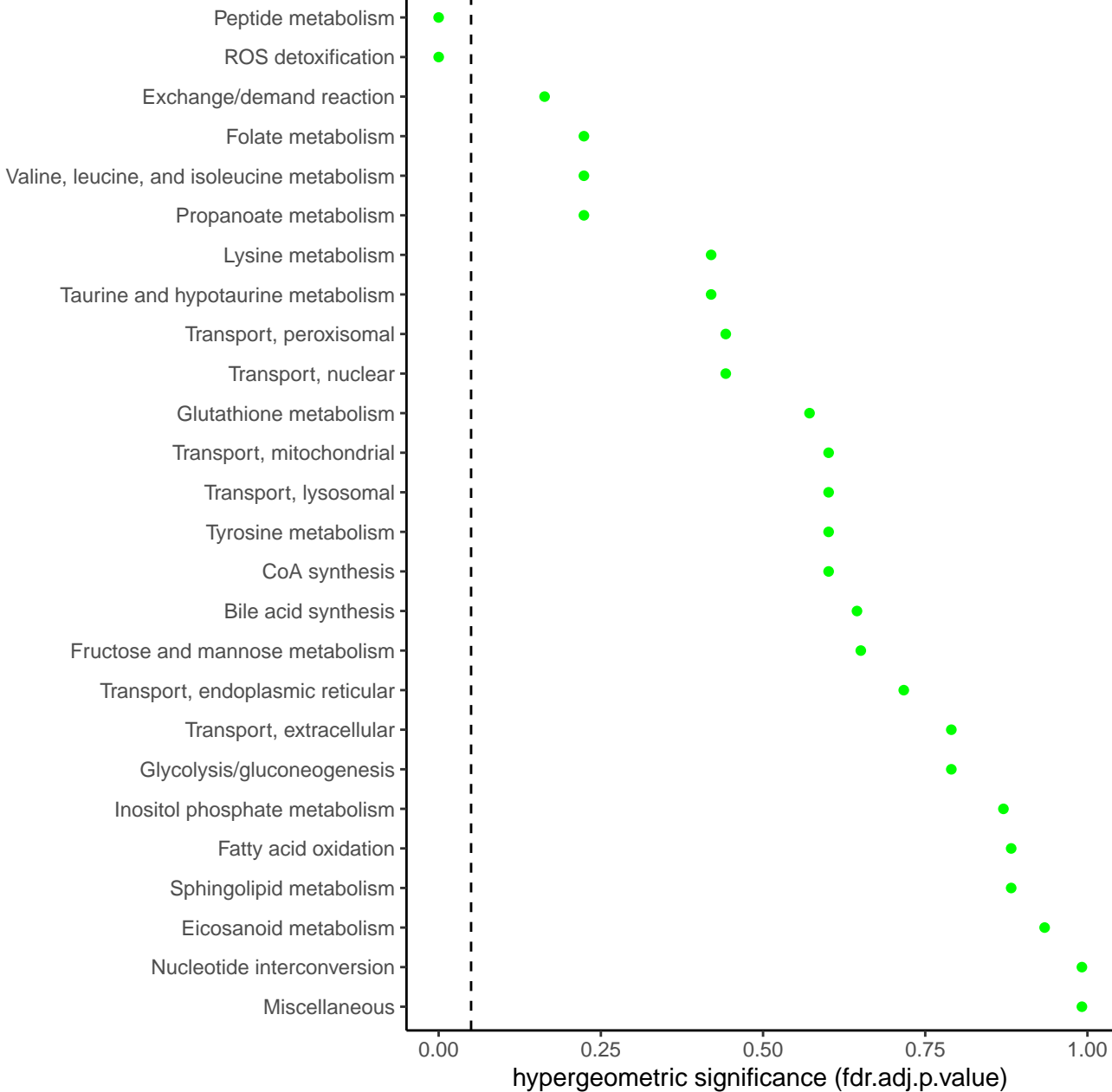
Eicosanoid metabolism

CoA synthesis



# over-representation analysis, bd\_responder

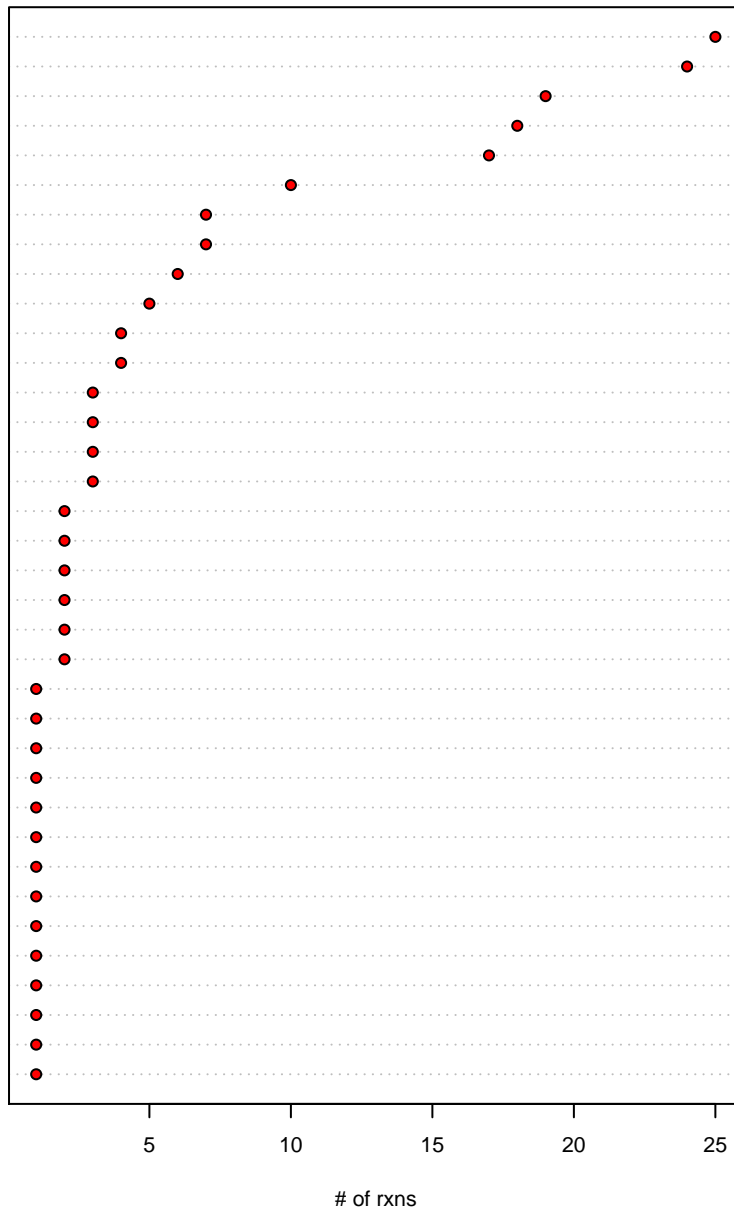
subSystem



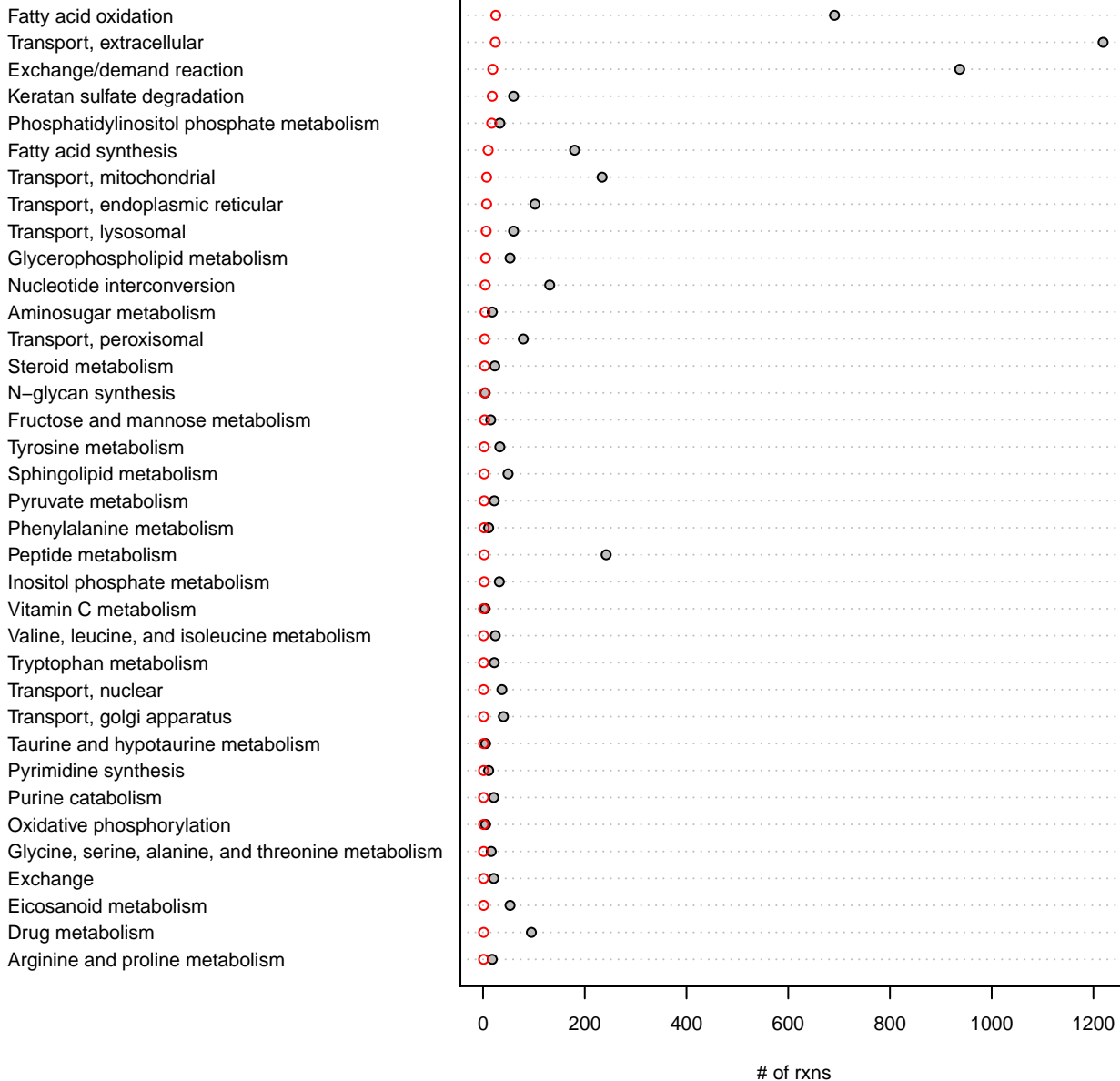


# # of disrupted rxns (n=184, bd\_nonresponder)

Fatty acid oxidation  
Transport, extracellular  
Exchange/demand reaction  
Keratan sulfate degradation  
Phosphatidylinositol phosphate metabolism  
Fatty acid synthesis  
Transport, mitochondrial  
Transport, endoplasmic reticular  
Transport, lysosomal  
Glycerophospholipid metabolism  
Nucleotide interconversion  
Aminosugar metabolism  
Transport, peroxisomal  
Steroid metabolism  
N-glycan synthesis  
Fructose and mannose metabolism  
Tyrosine metabolism  
Sphingolipid metabolism  
Pyruvate metabolism  
Phenylalanine metabolism  
Peptide metabolism  
Inositol phosphate metabolism  
Vitamin C metabolism  
Valine, leucine, and isoleucine metabolism  
Tryptophan metabolism  
Transport, nuclear  
Transport, golgi apparatus  
Taurine and hypotaurine metabolism  
Pyrimidine synthesis  
Purine catabolism  
Oxidative phosphorylation  
Glycine, serine, alanine, and threonine metabolism  
Exchange  
Eicosanoid metabolism  
Drug metabolism  
Arginine and proline metabolism

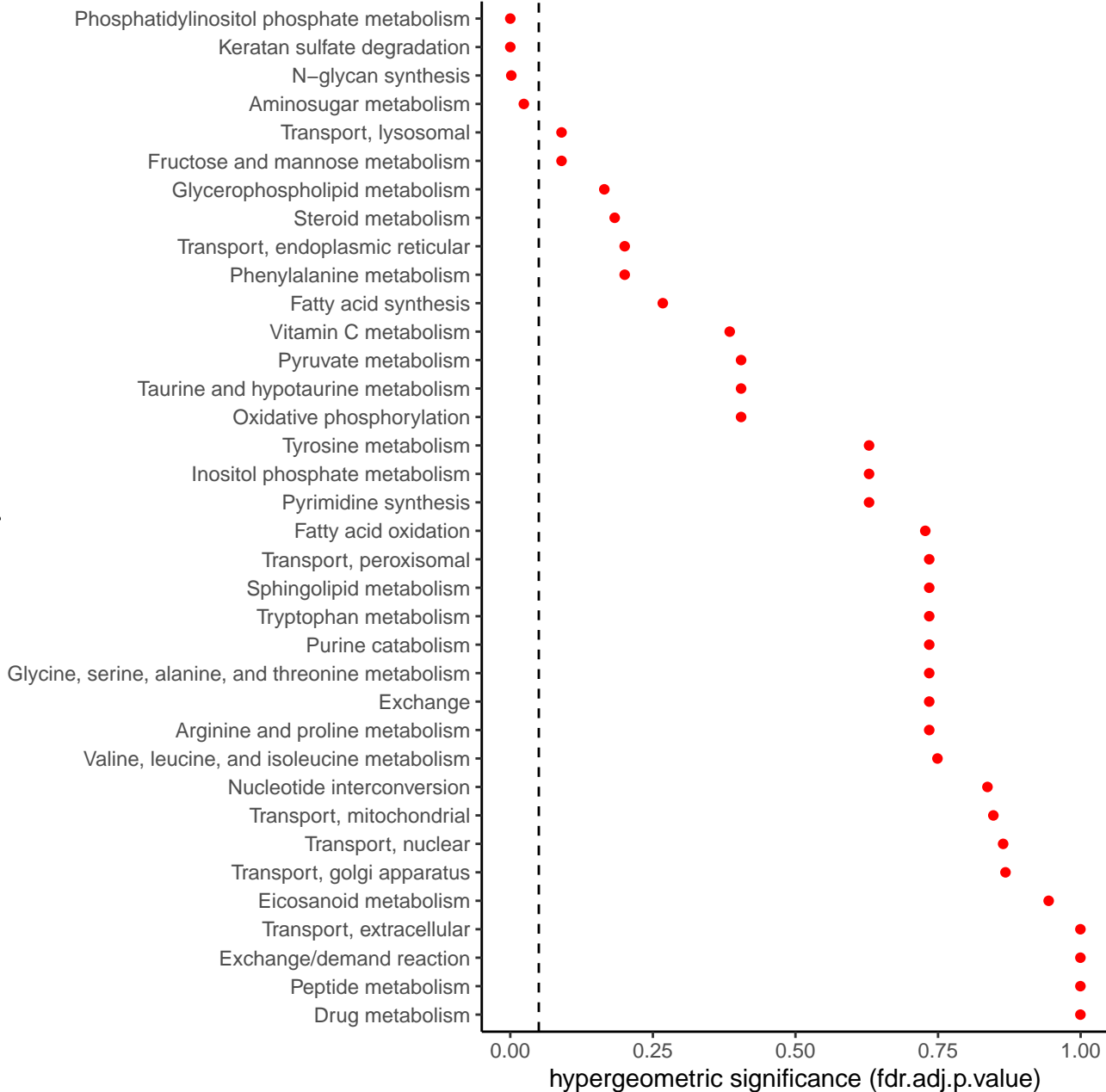


# of disrupted rxns (n=184, bd\_nonresponder) vs all rxns

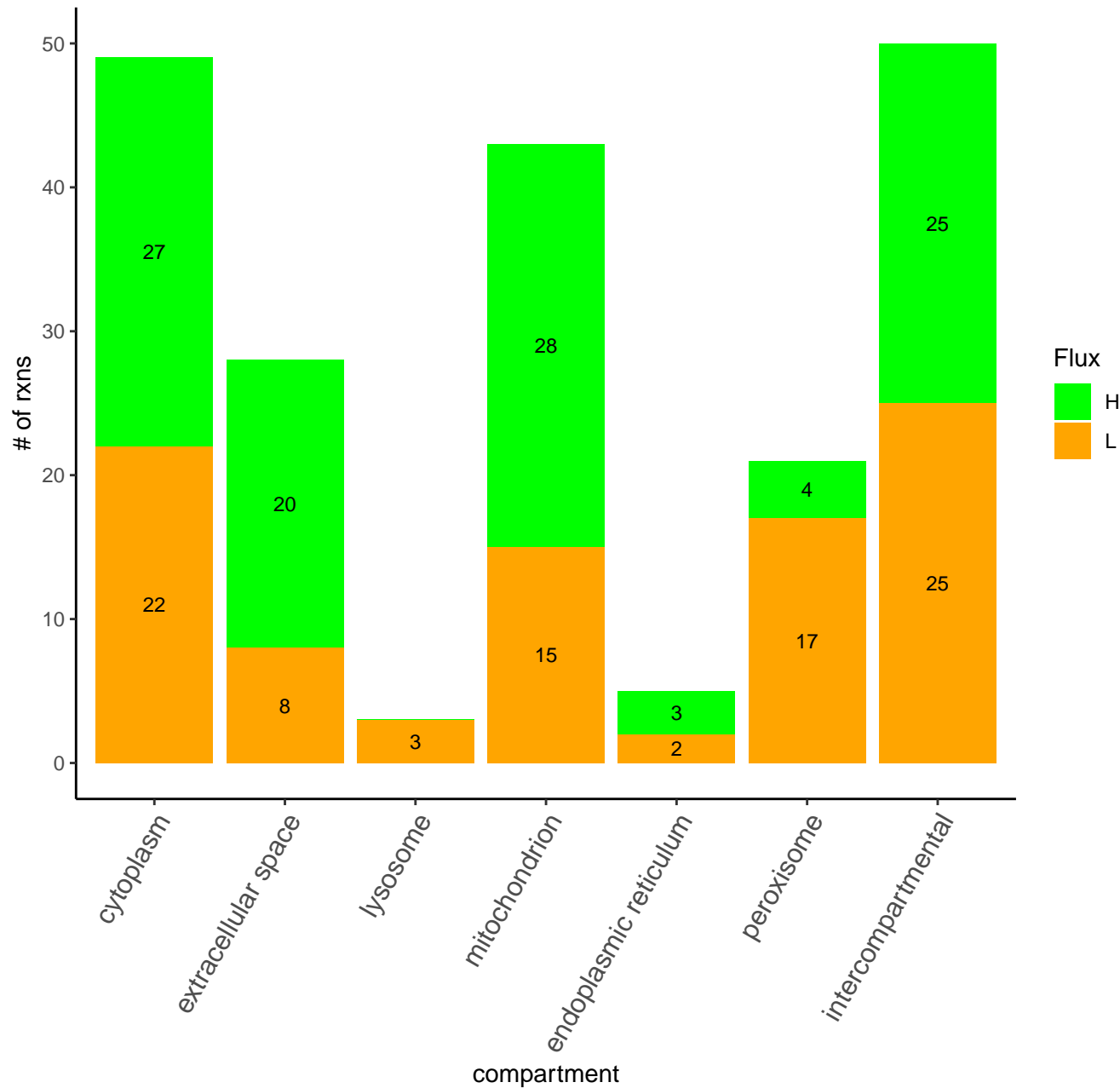


# over-representation analysis, bd\_nonresponder

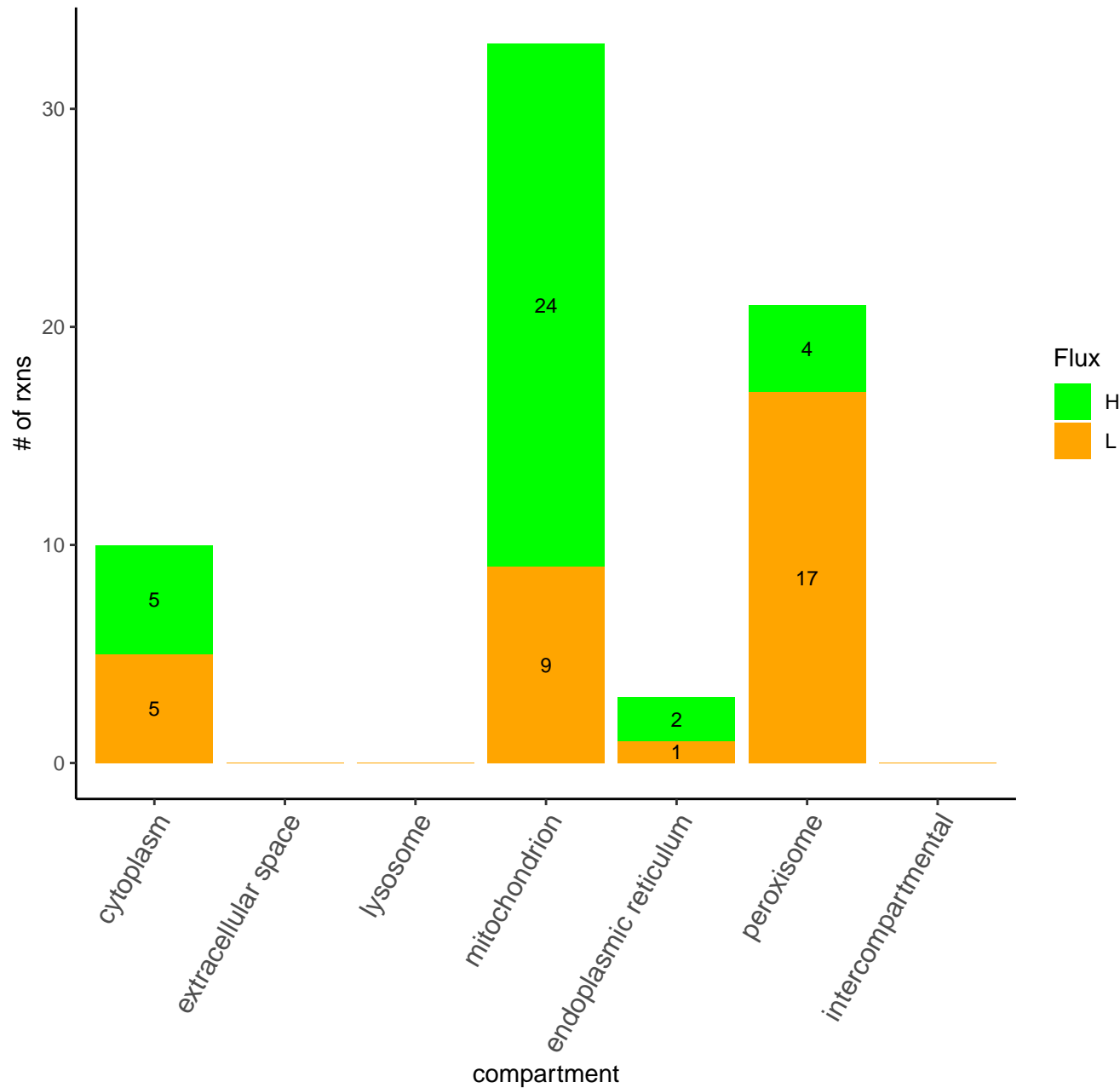
subSystem



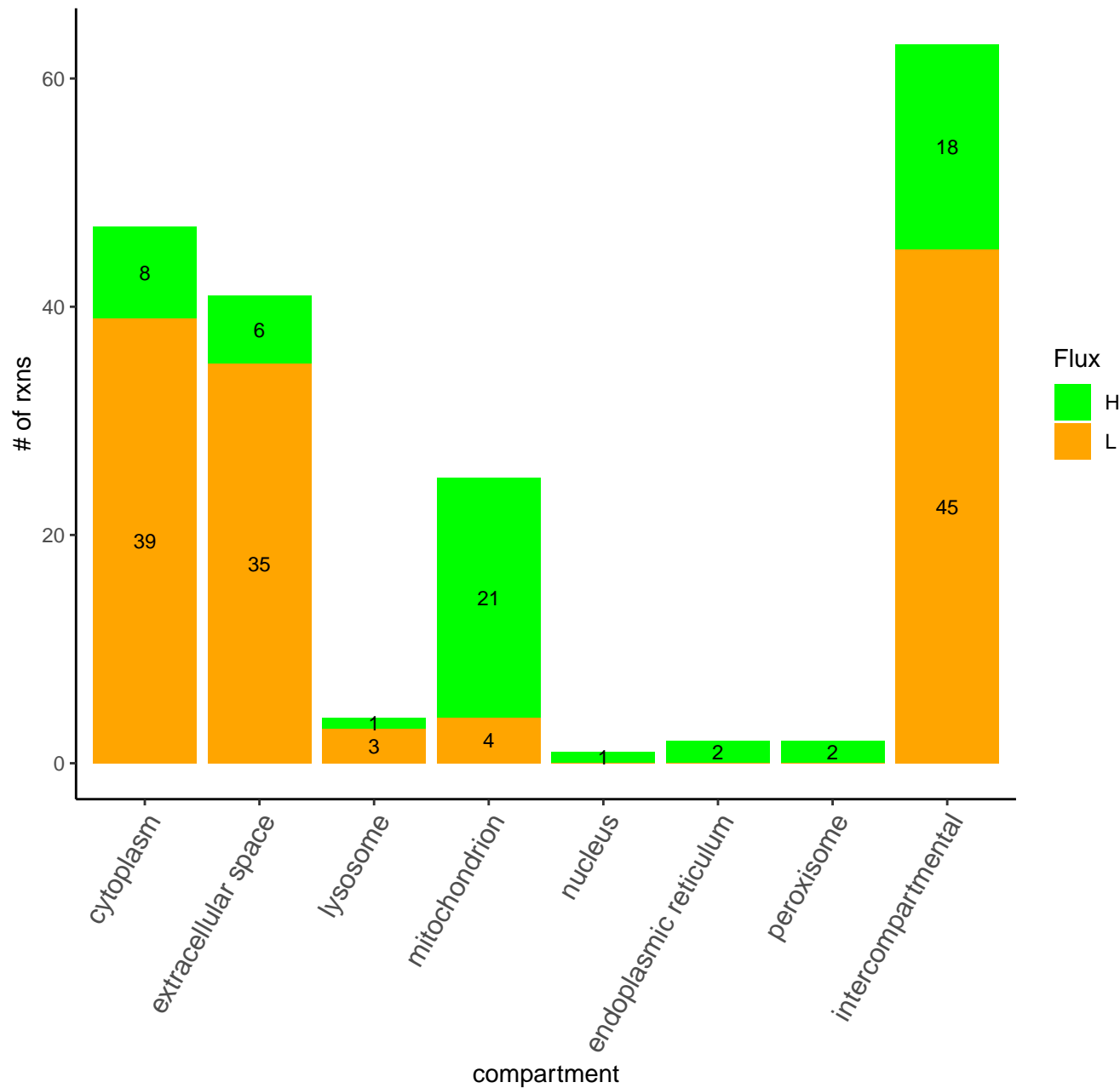
Disrupted rxns (all, n=199) per compartment (bd\_lumped)



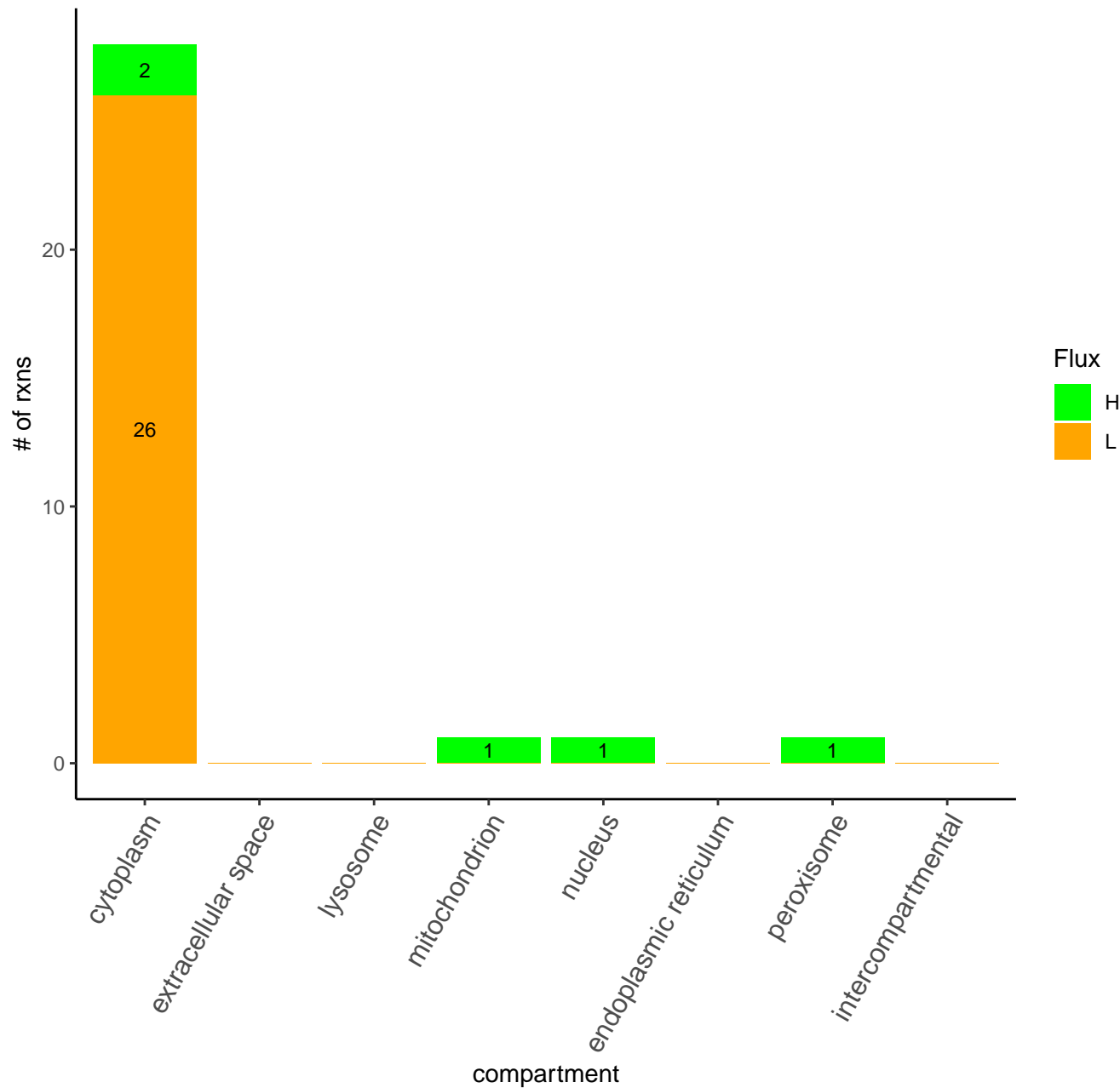
Disrupted rxns (fdr.significant, n=67) per compartment (bd\_lumped)



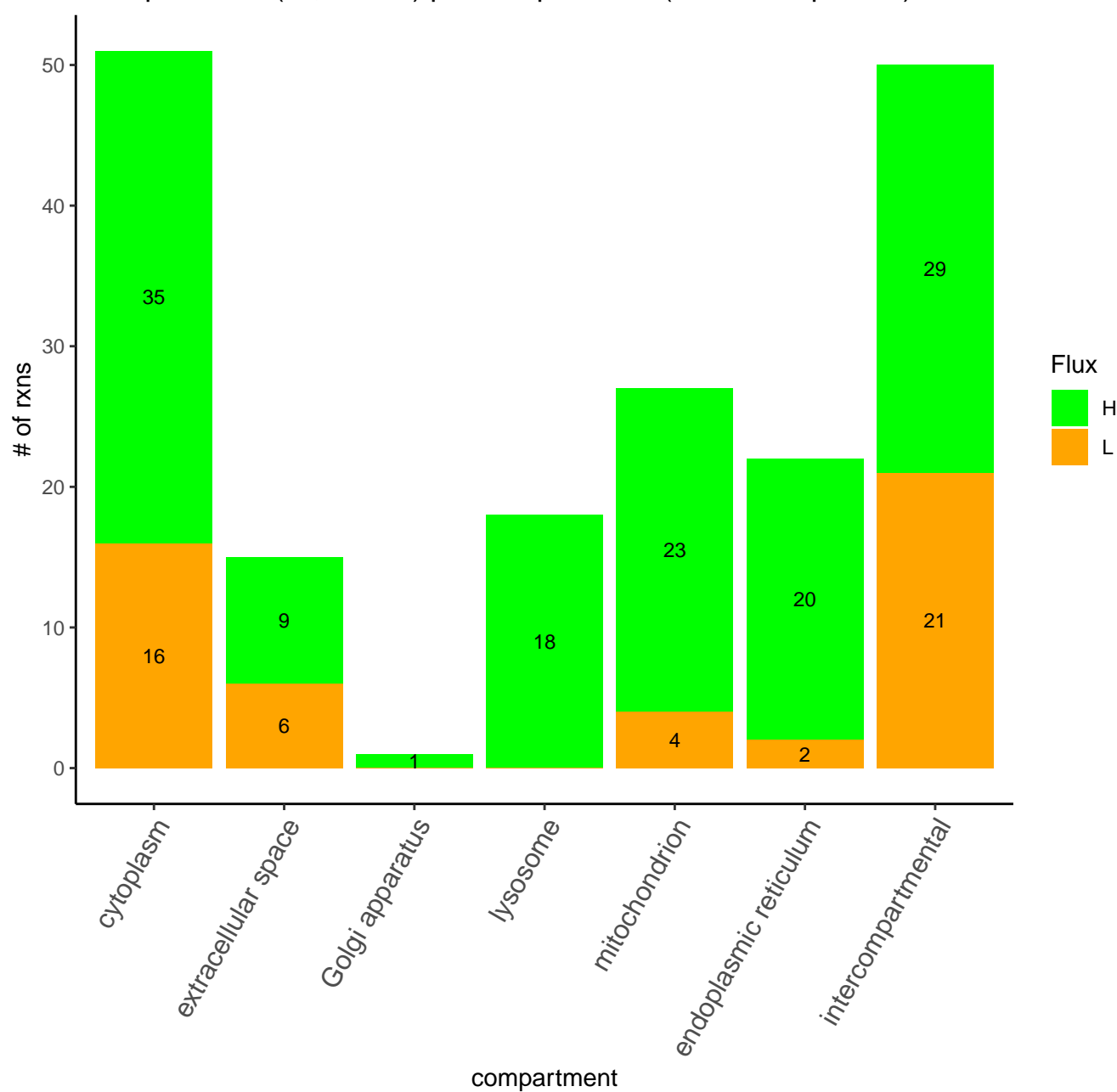
Disrupted rxns (all, n=185) per compartment (bd\_responder)



Disrupted rxns (fdr.significant, n=31) per compartment (bd\_responder)

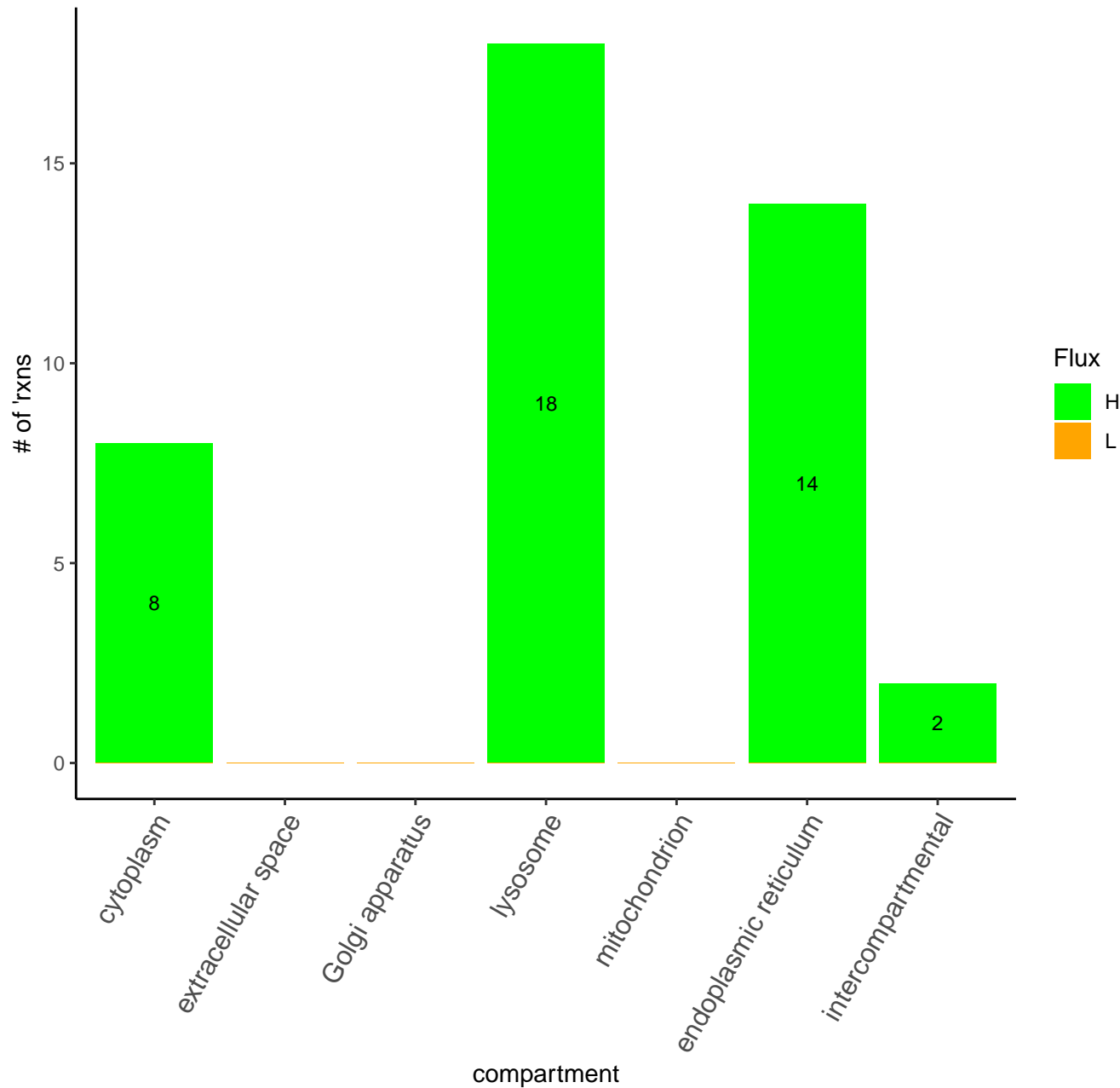


Disrupted rxns (all, n=184) per compartment (bd\_nonresponder)

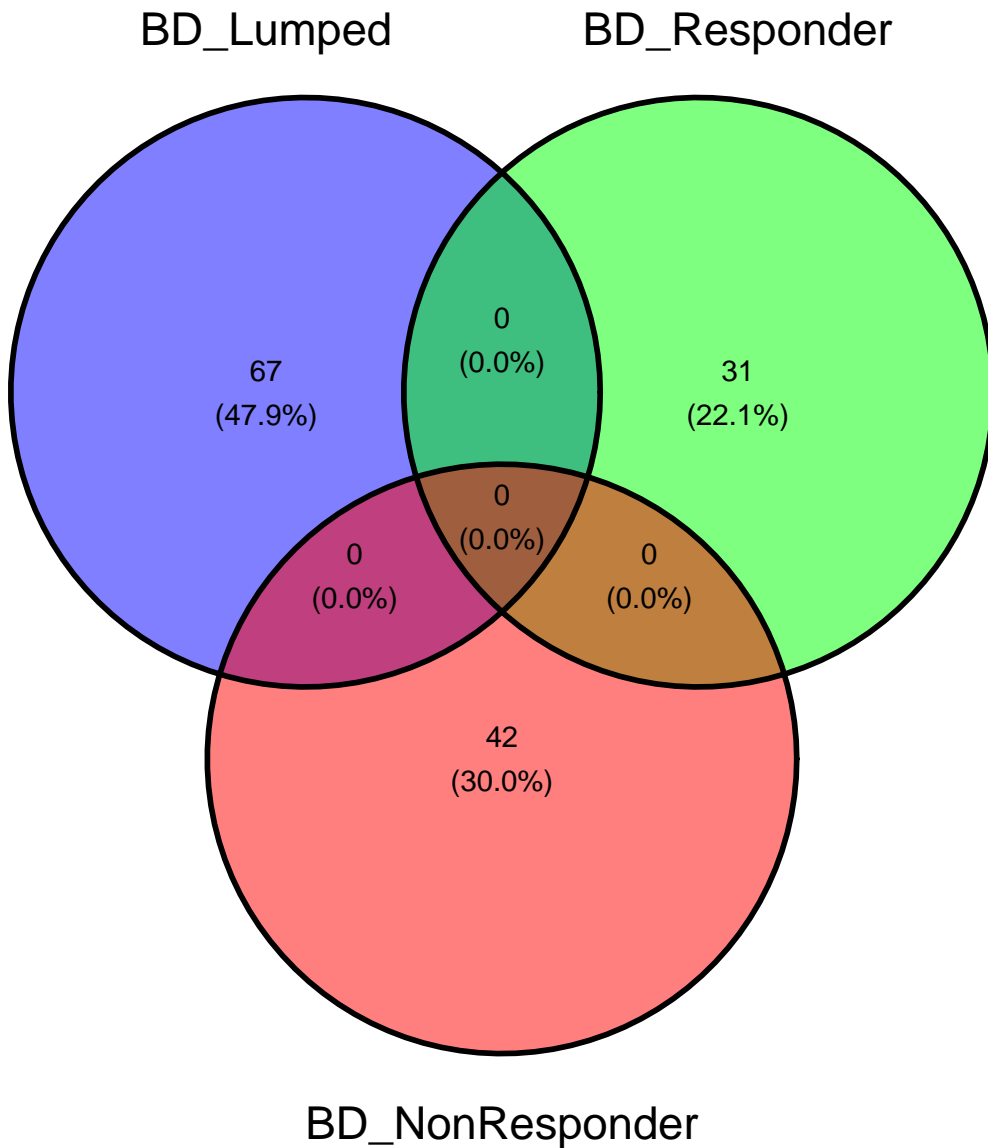




Disrupted rxns (fdr.significant, n=42) per compartment (bd\_nonresponder)



Overlap in rxns (fdr.significant) disrupted between models



Overlap in subSystems (fdr.significant) disrupted between models

