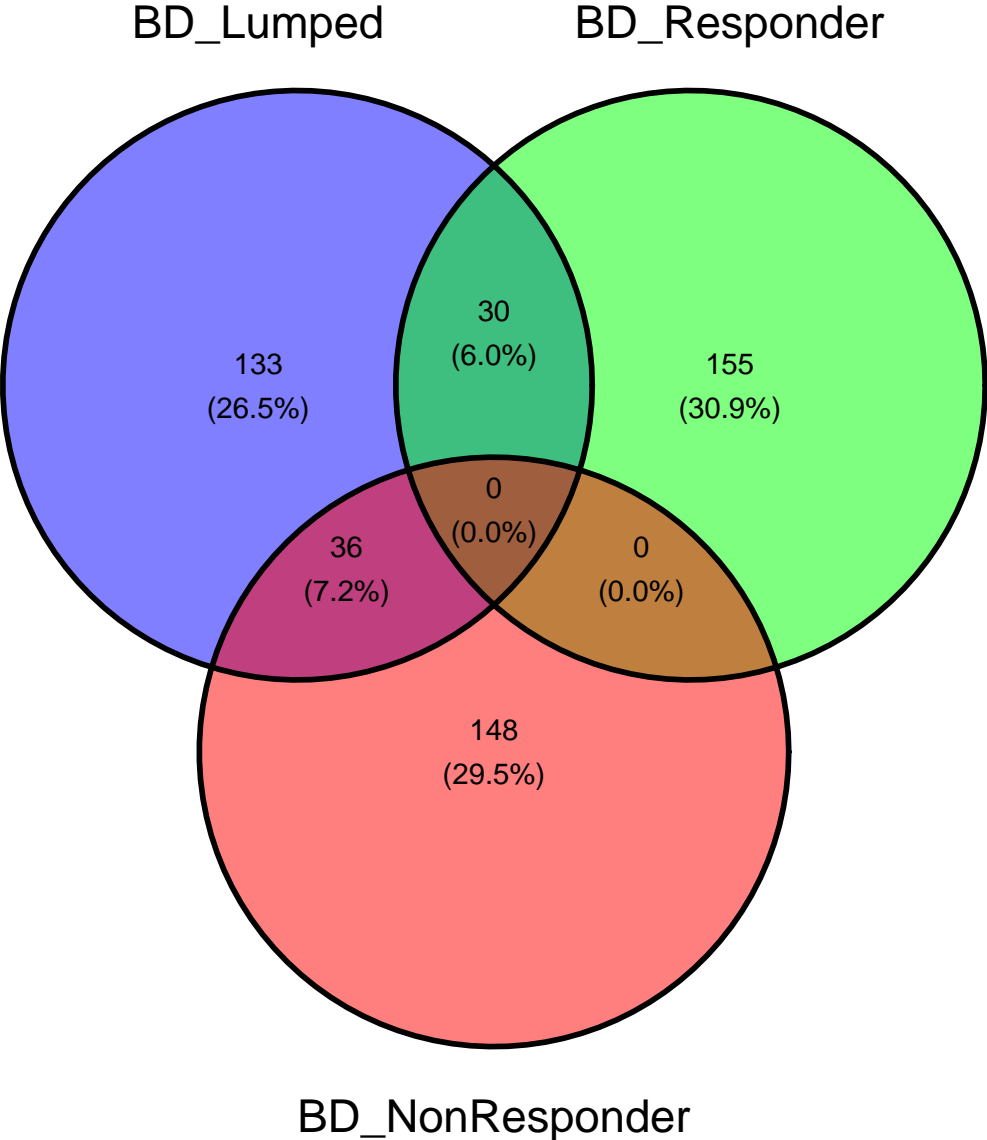
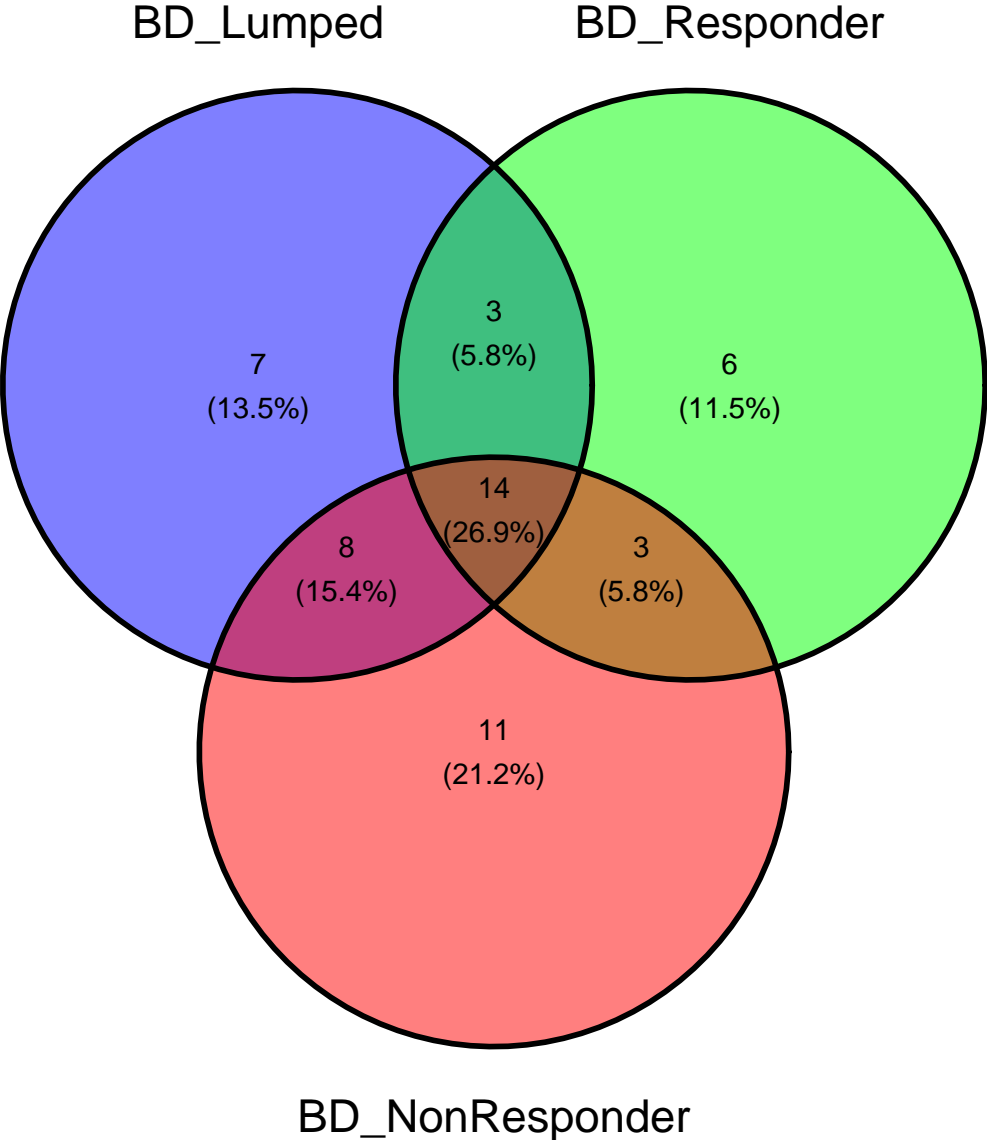


Overlap in rxns disrupted between models

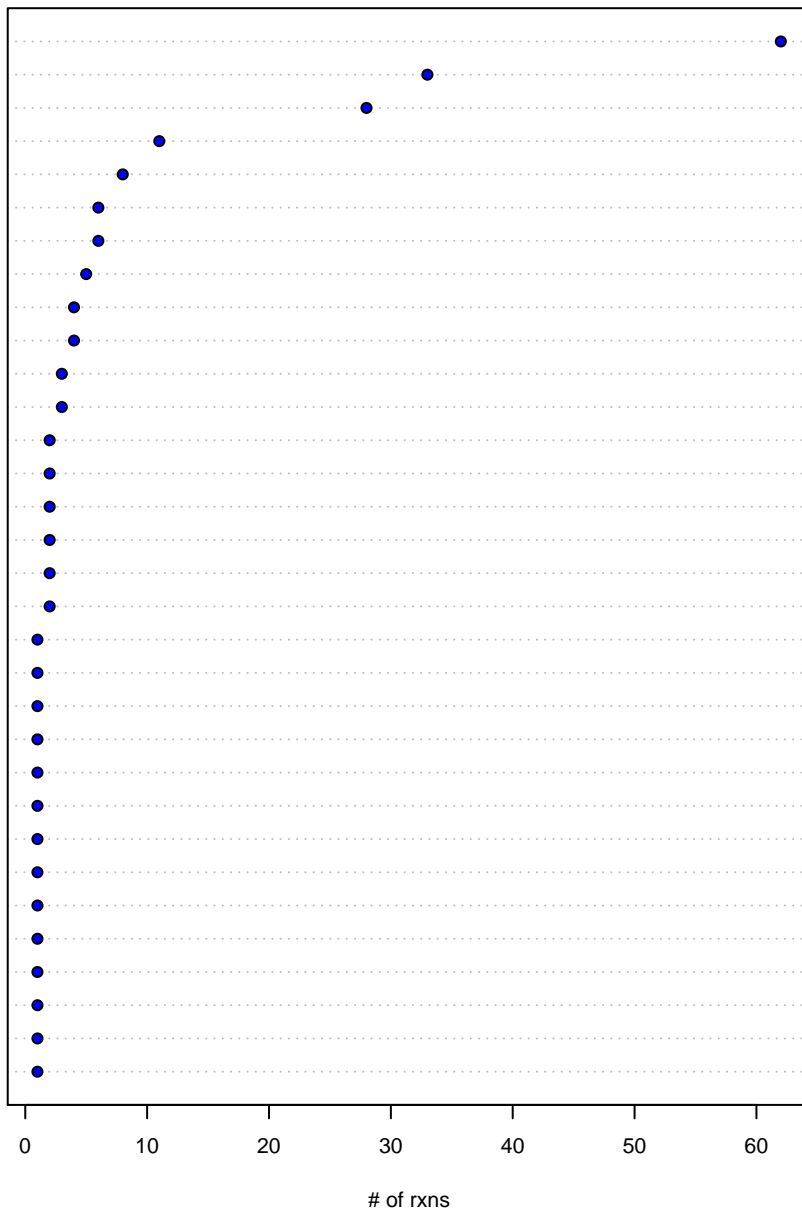


Overlap in subSystems disrupted between models

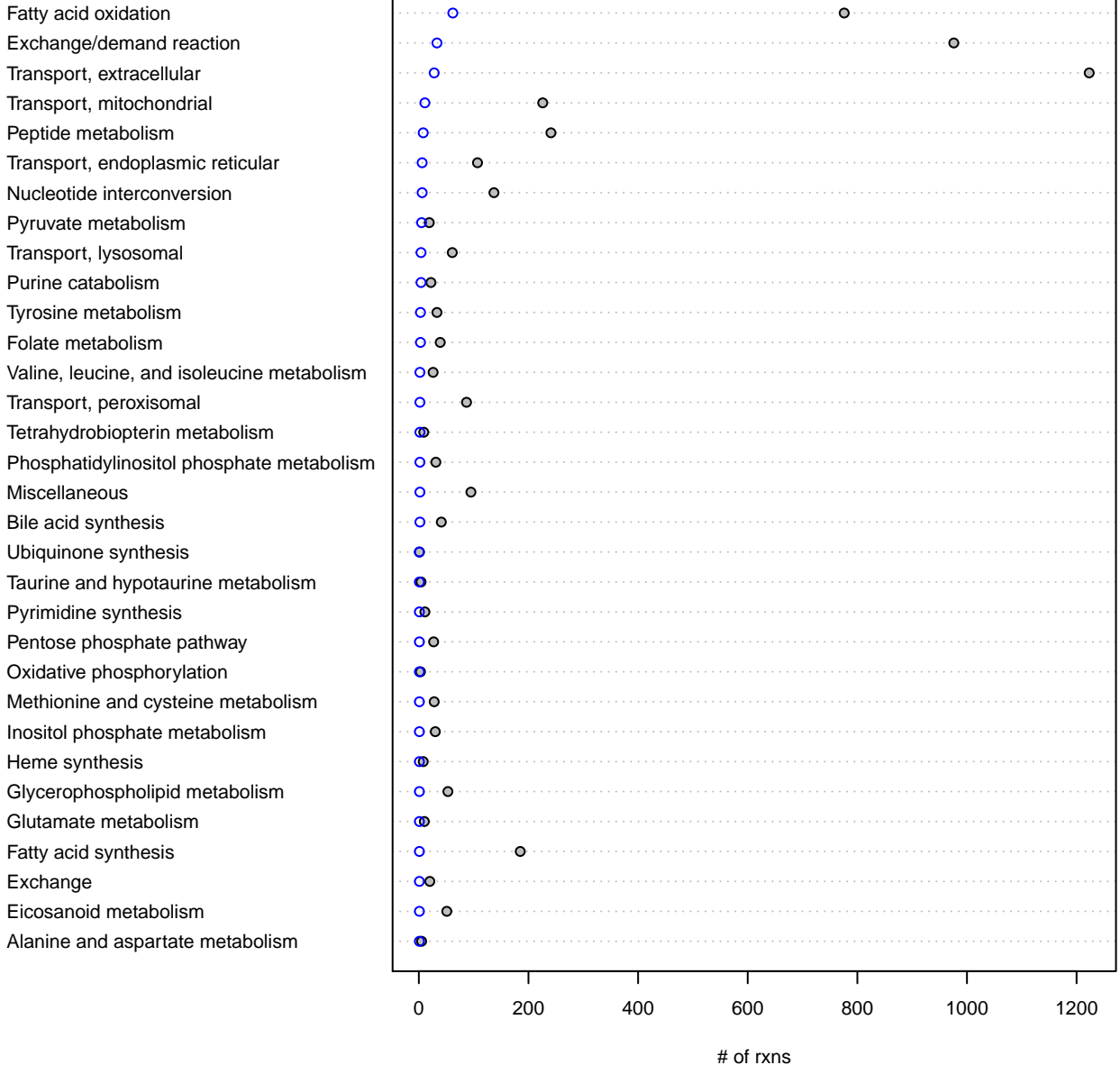


of disrupted rxns (n=199, bd_lumped)

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

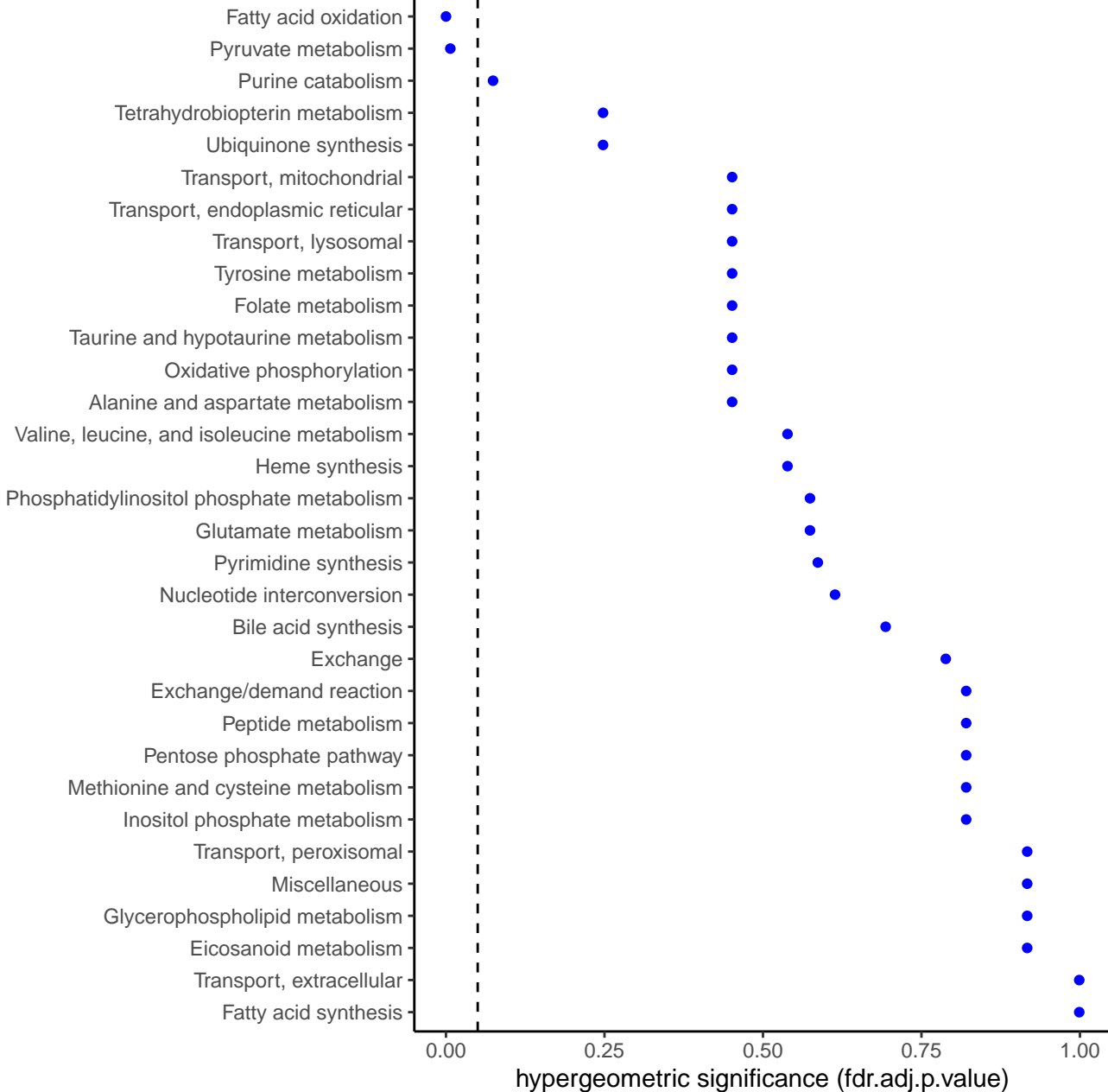


of disrupted rxns (n=199, bd_lumped) vs all rxns

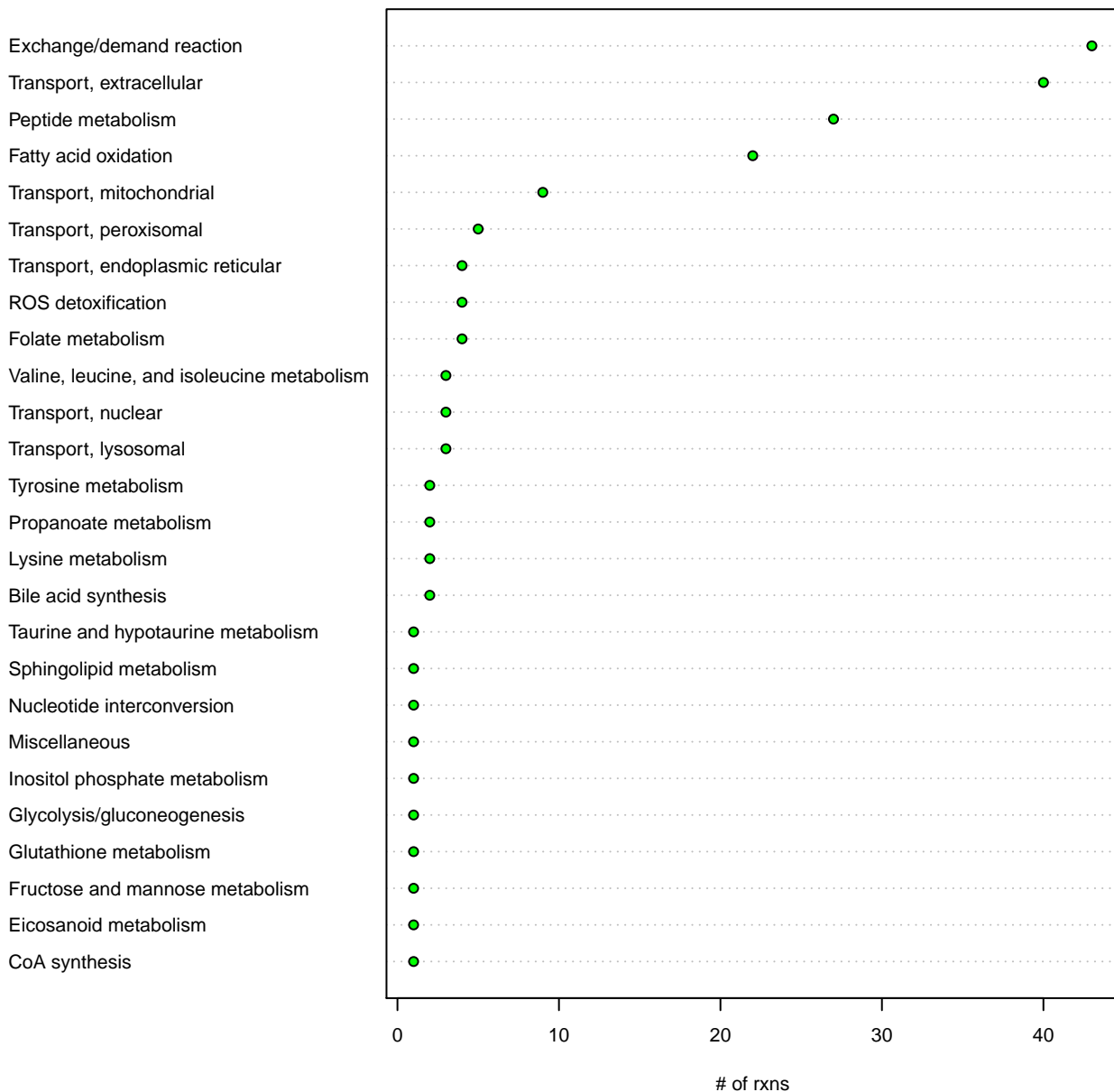


over-representation analysis, bd_lumped

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

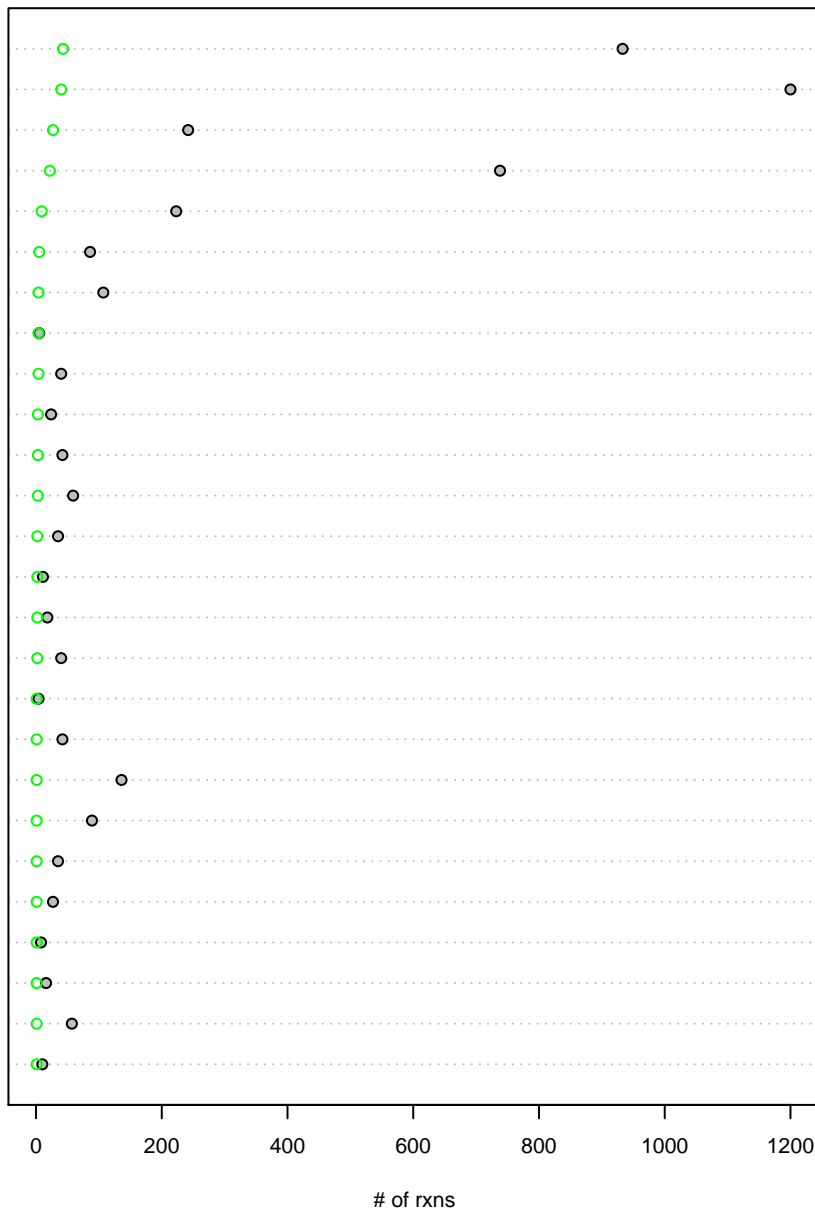
Glycolysis/gluconeogenesis

Glutathione metabolism

Fructose and mannose metabolism

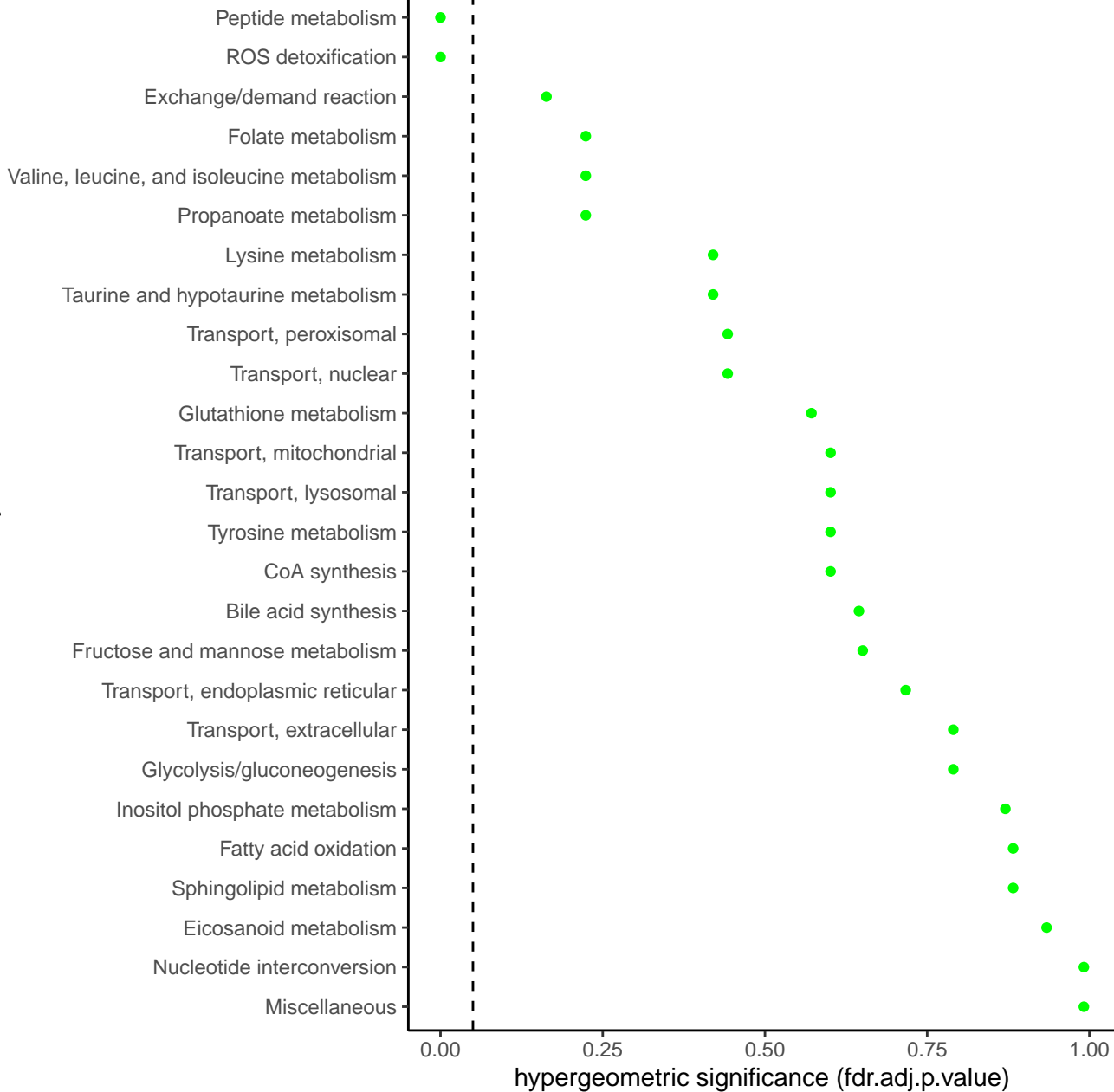
Eicosanoid metabolism

CoA synthesis



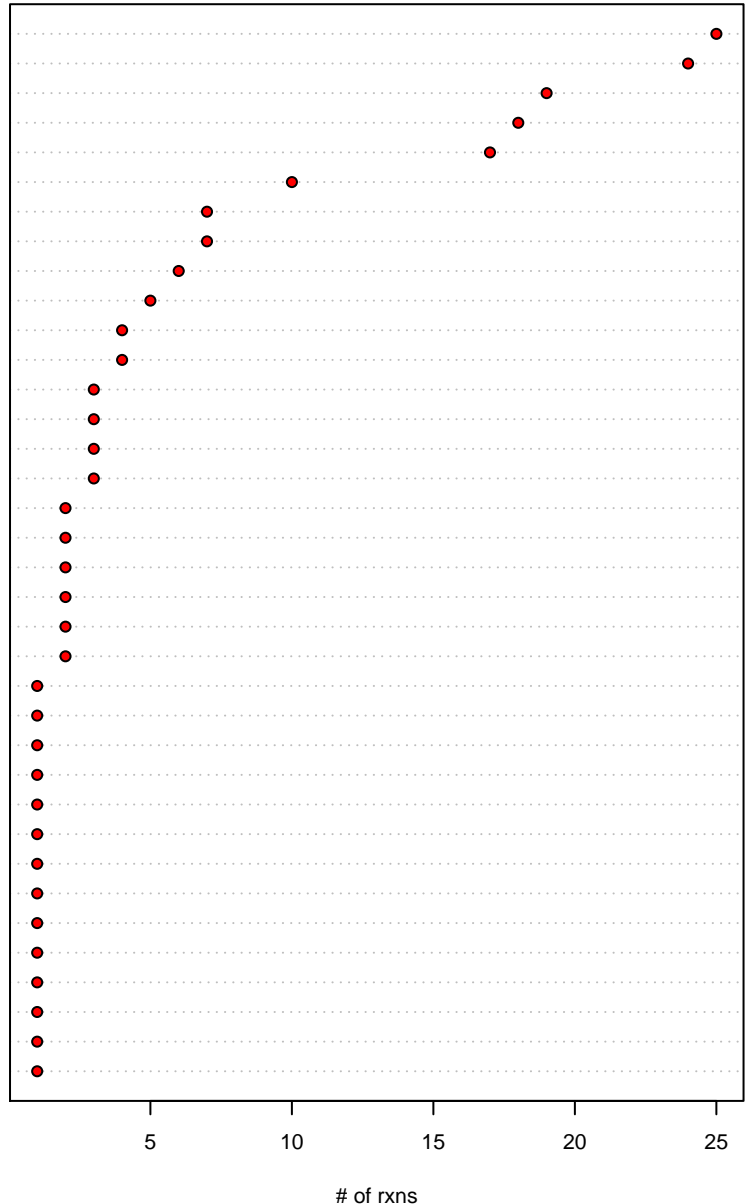
over-representation analysis, bd_responder

subSystem

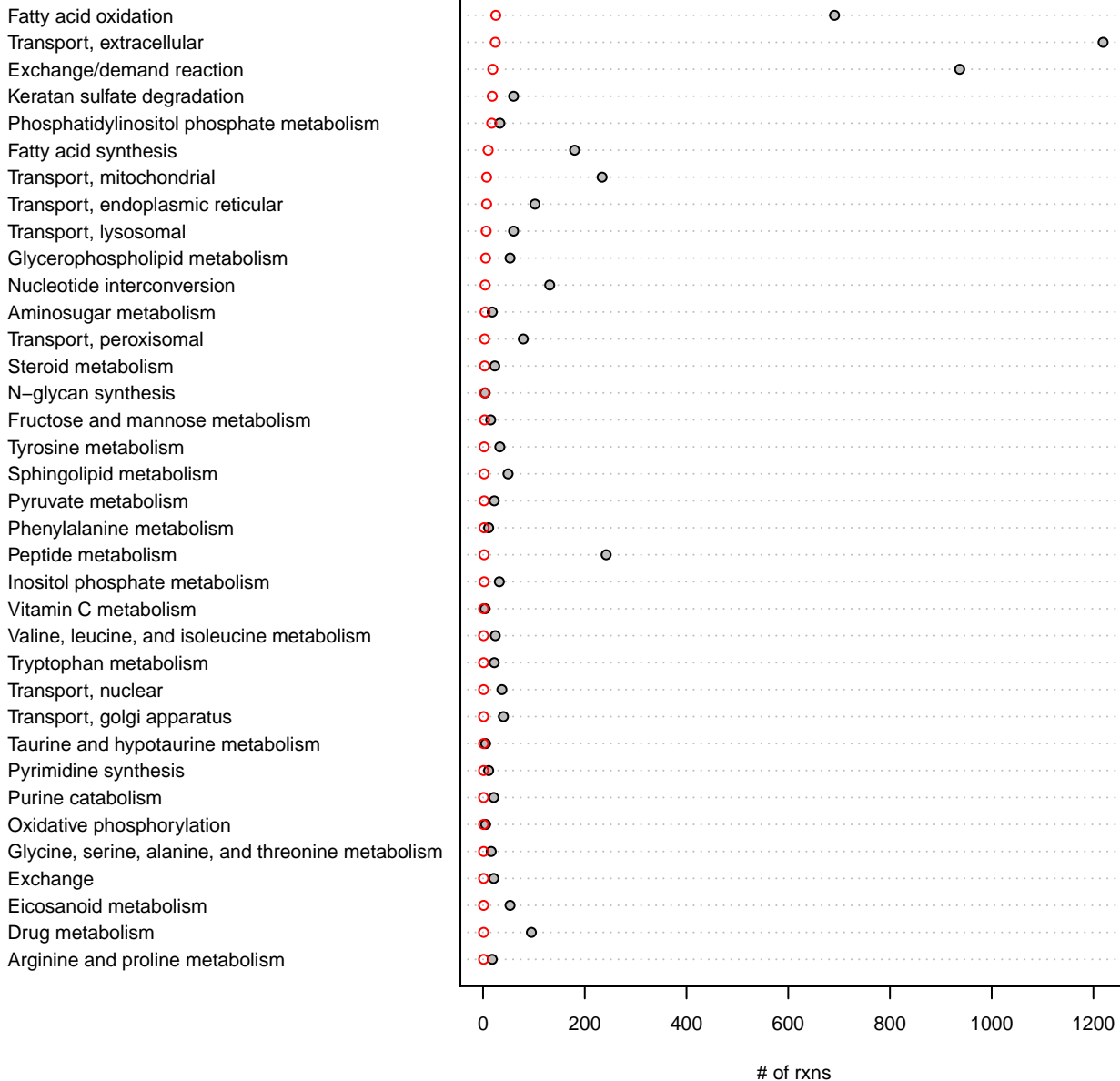


of disrupted rxns (n=184, bd_nonresponder)

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

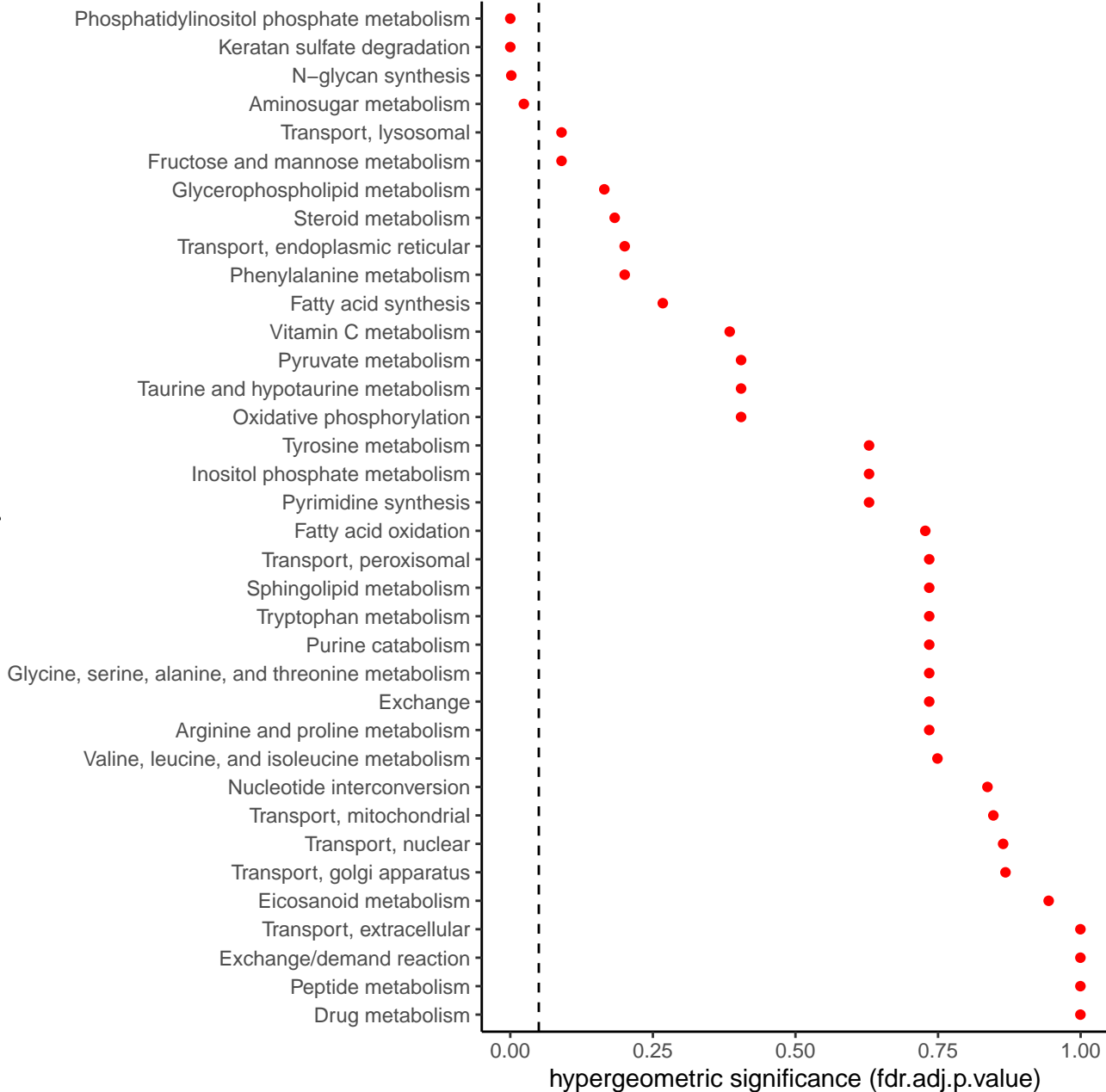


of disrupted rxns (n=184, bd_nonresponder) vs all rxns

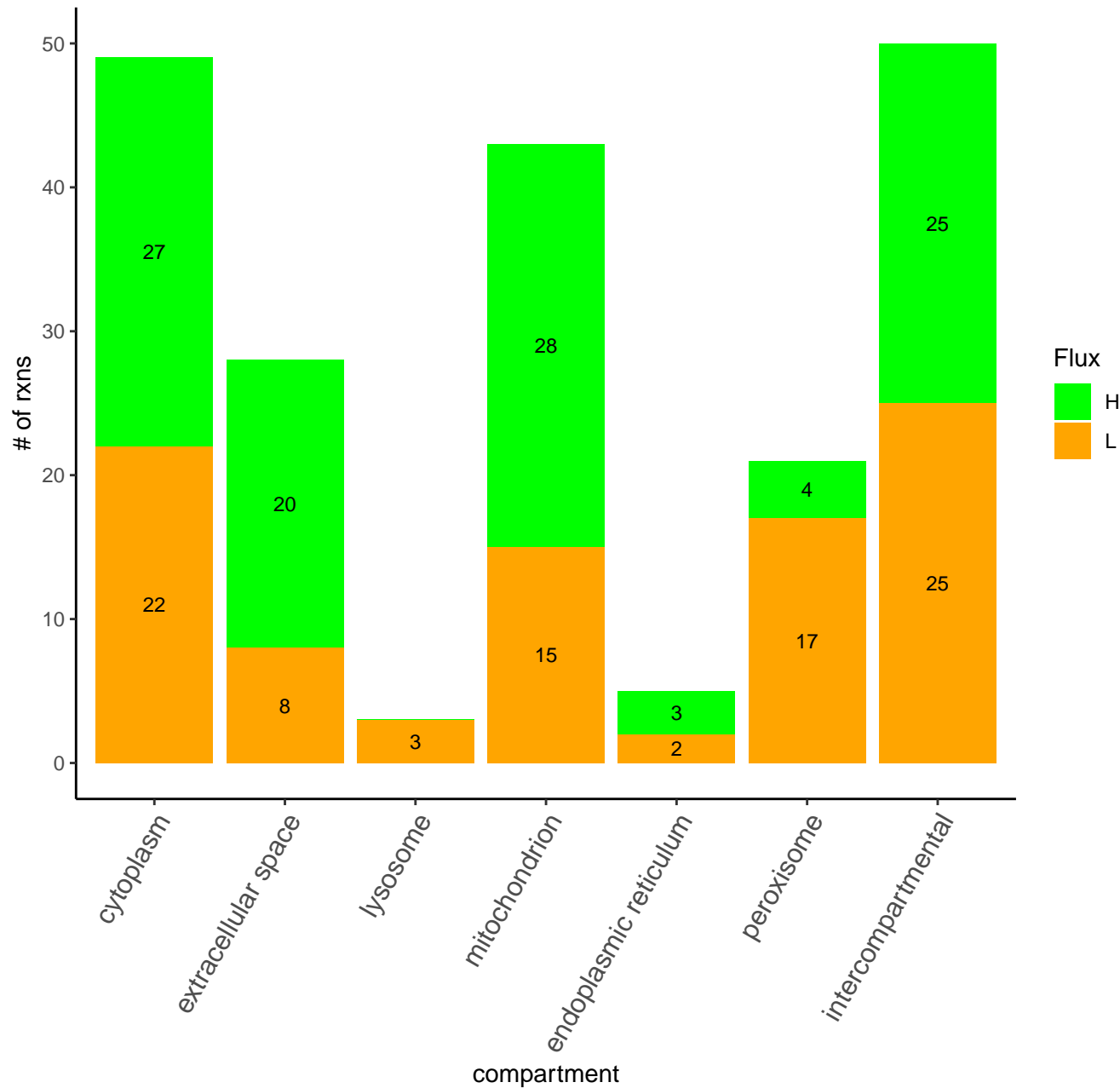


over-representation analysis, bd_nonresponder

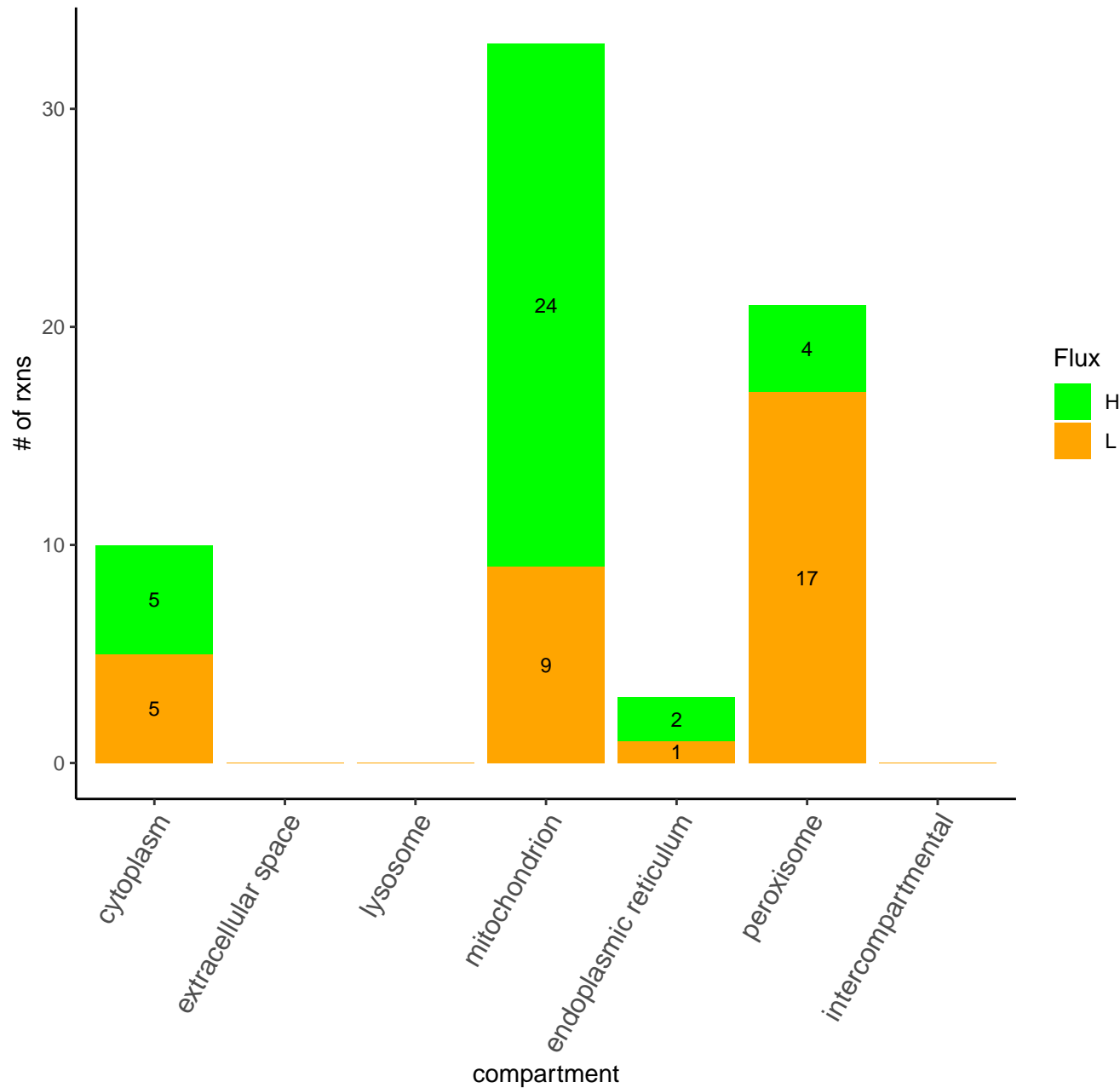
subSystem



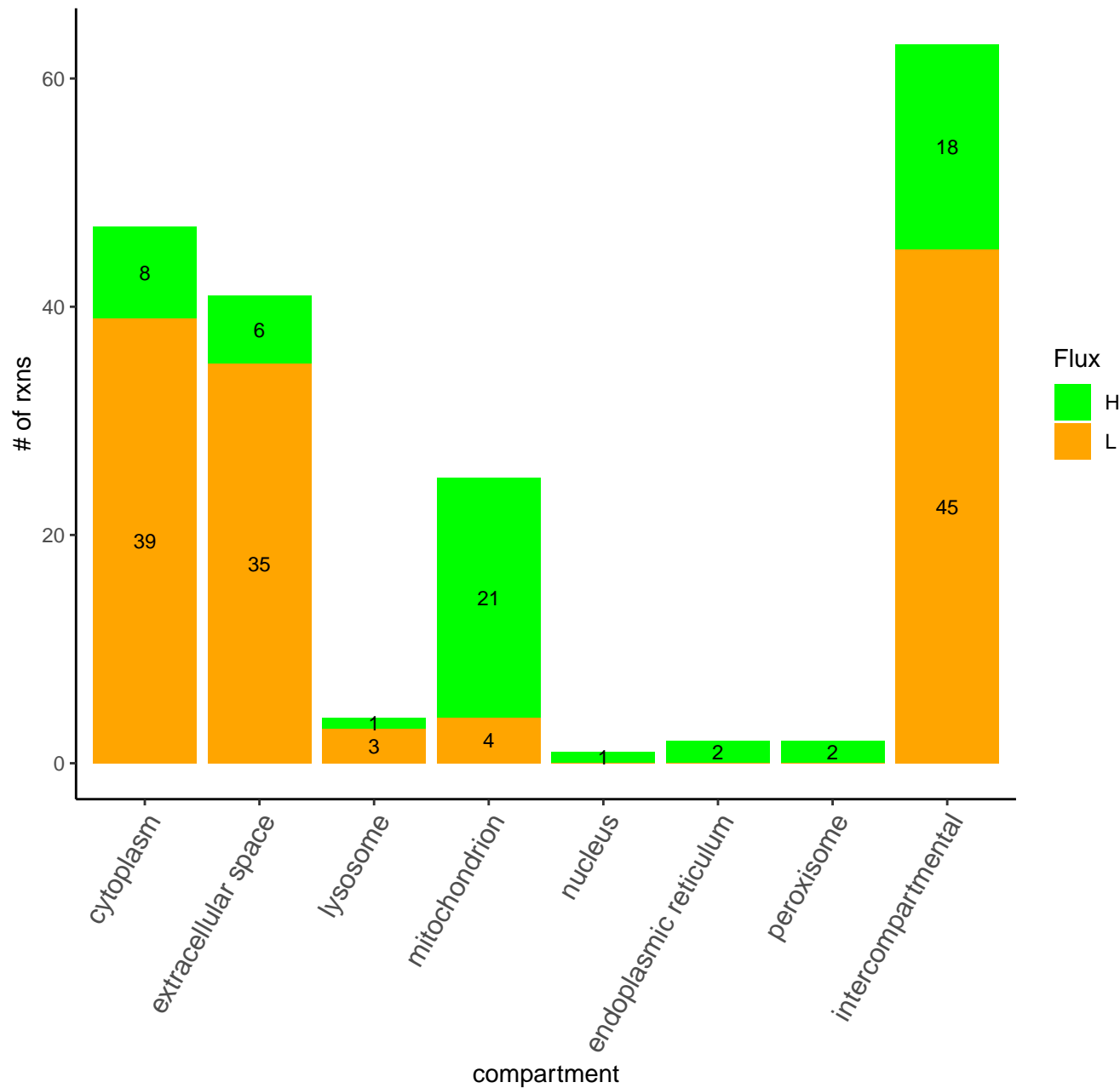
Disrupted rxns (all, n=199) per compartment (bd_lumped)



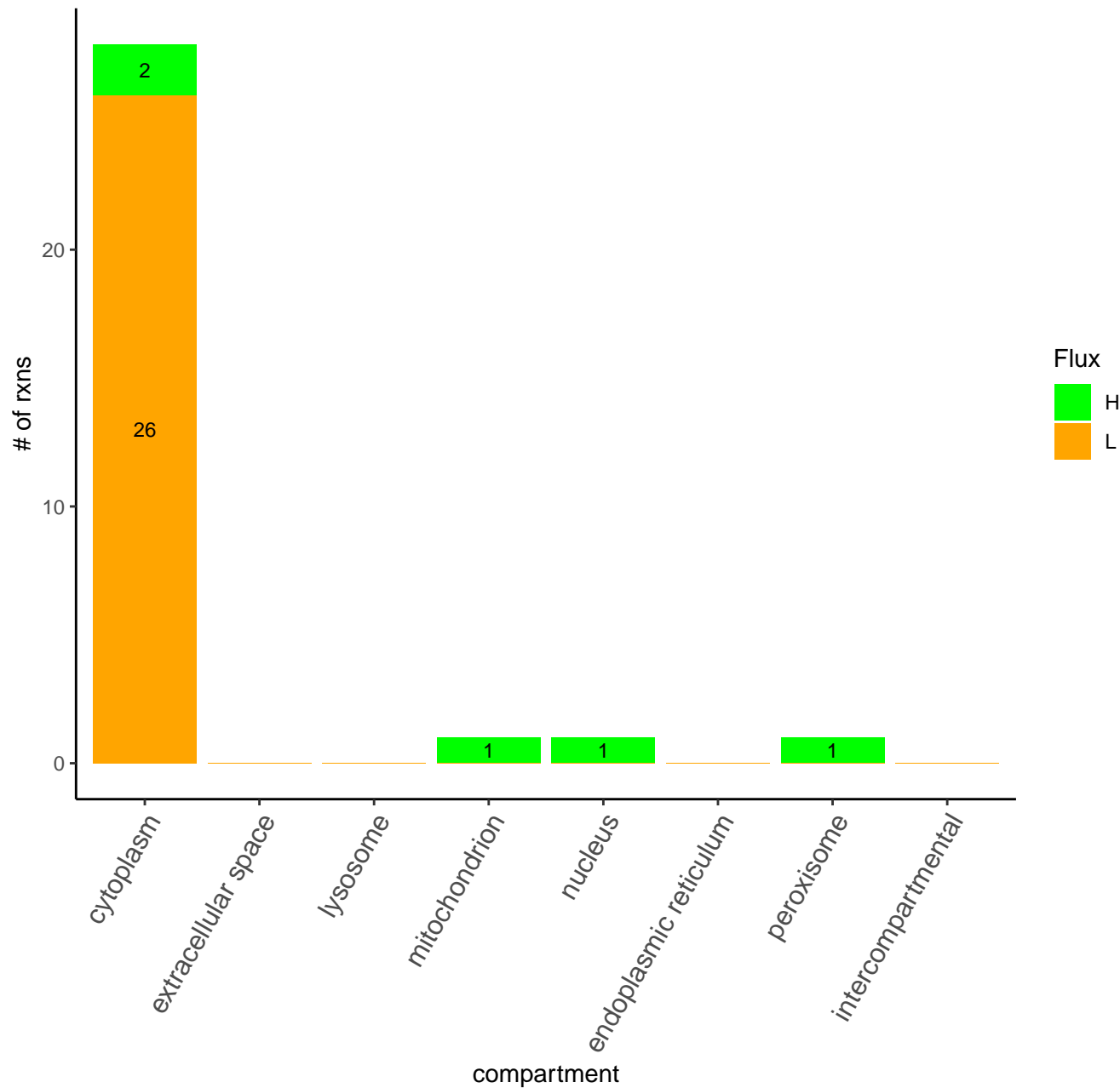
Disrupted rxns (fdr.significant, n=67) per compartment (bd_lumped)



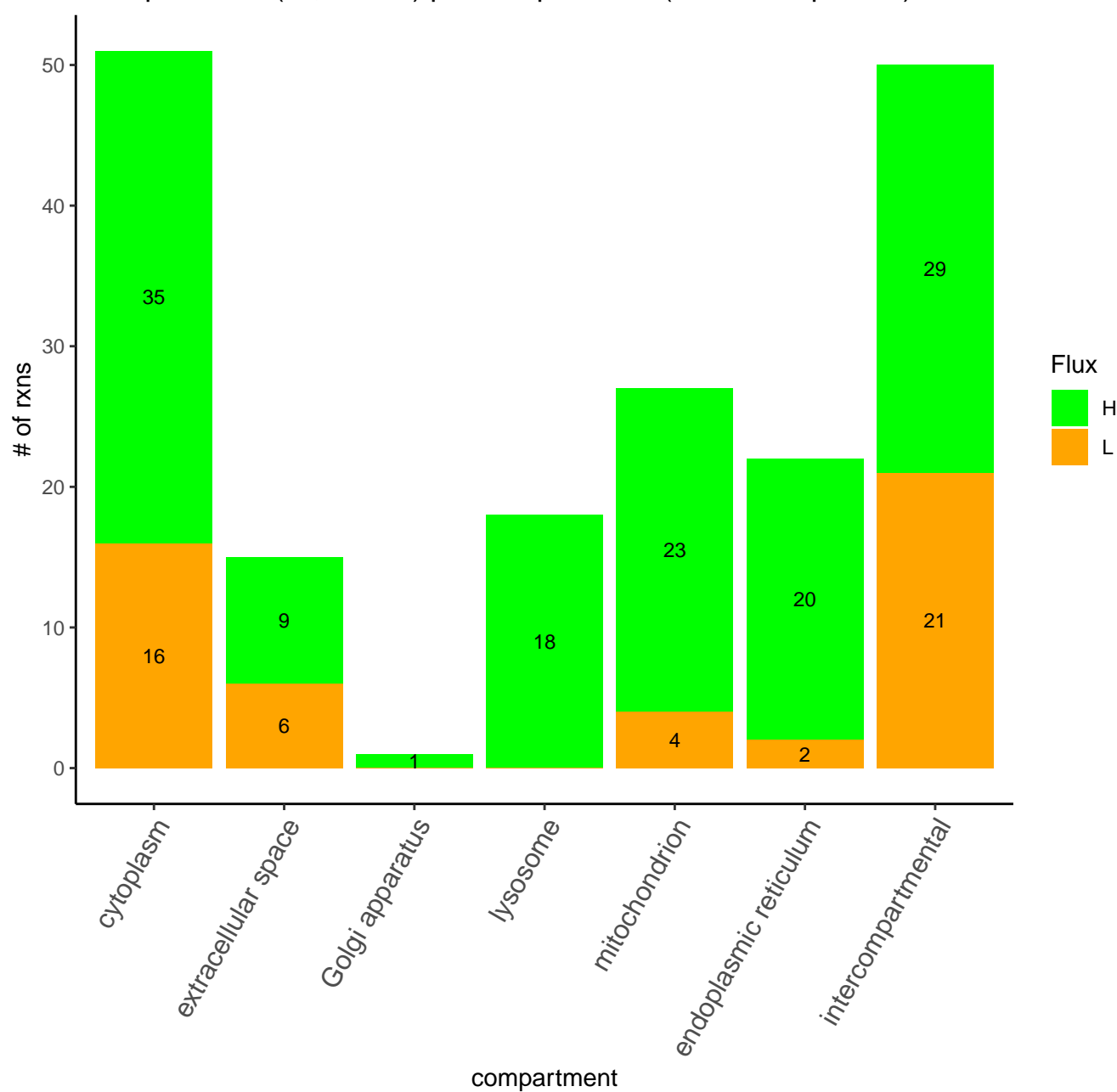
Disrupted rxns (all, n=185) per compartment (bd_responder)



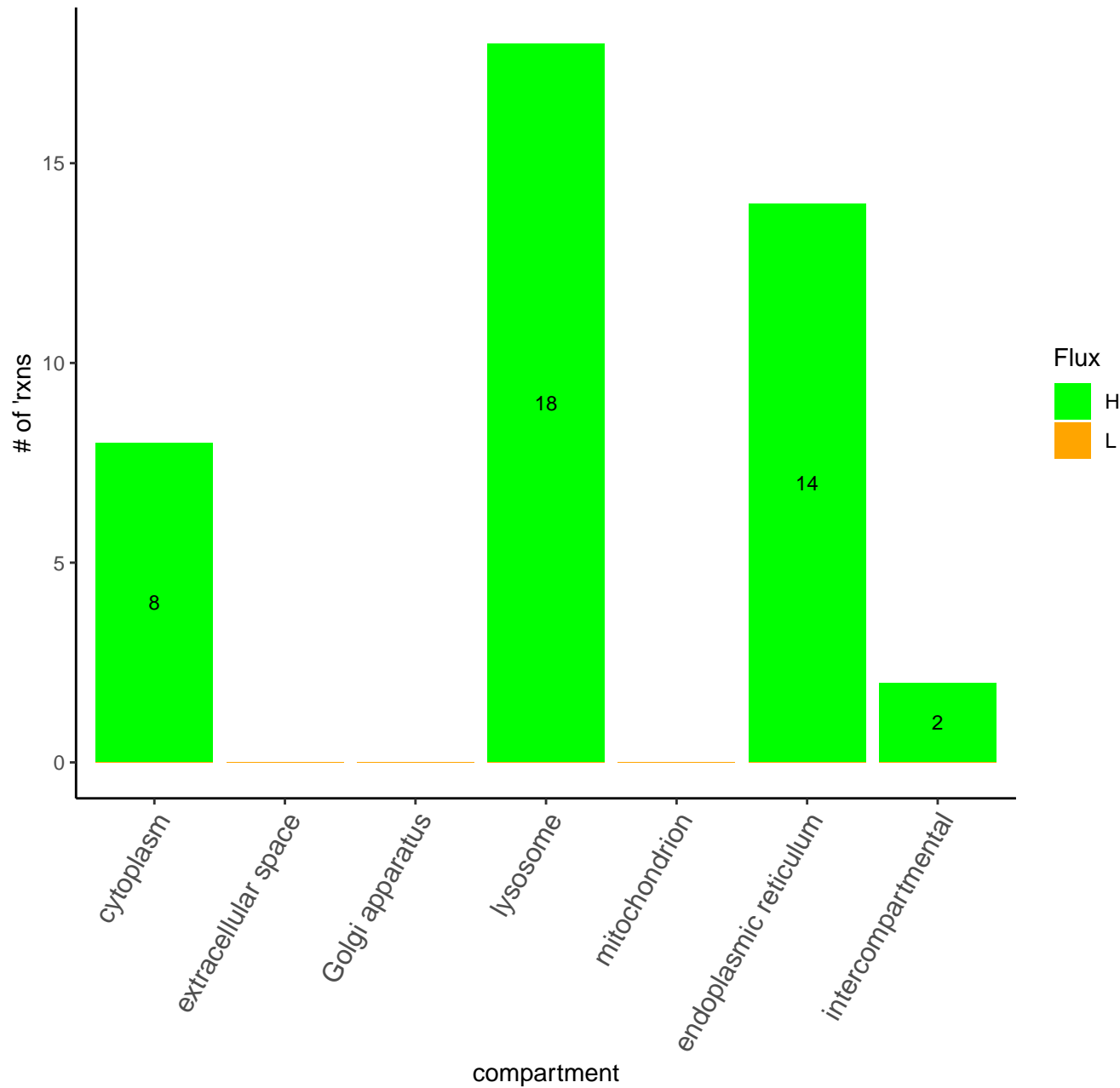
Disrupted rxns (fdr.significant, n=31) per compartment (bd_responder)



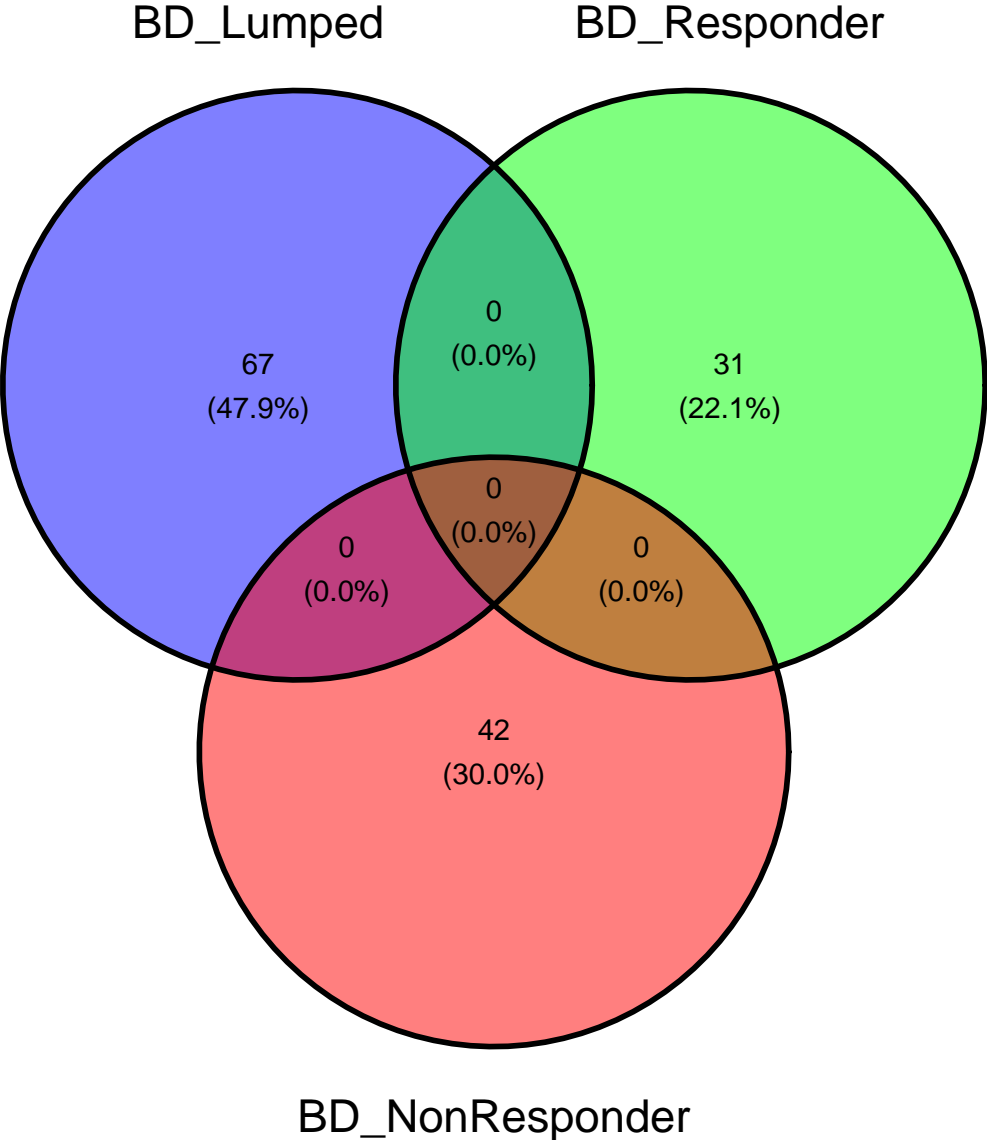
Disrupted rxns (all, n=184) per compartment (bd_nonresponder)



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

