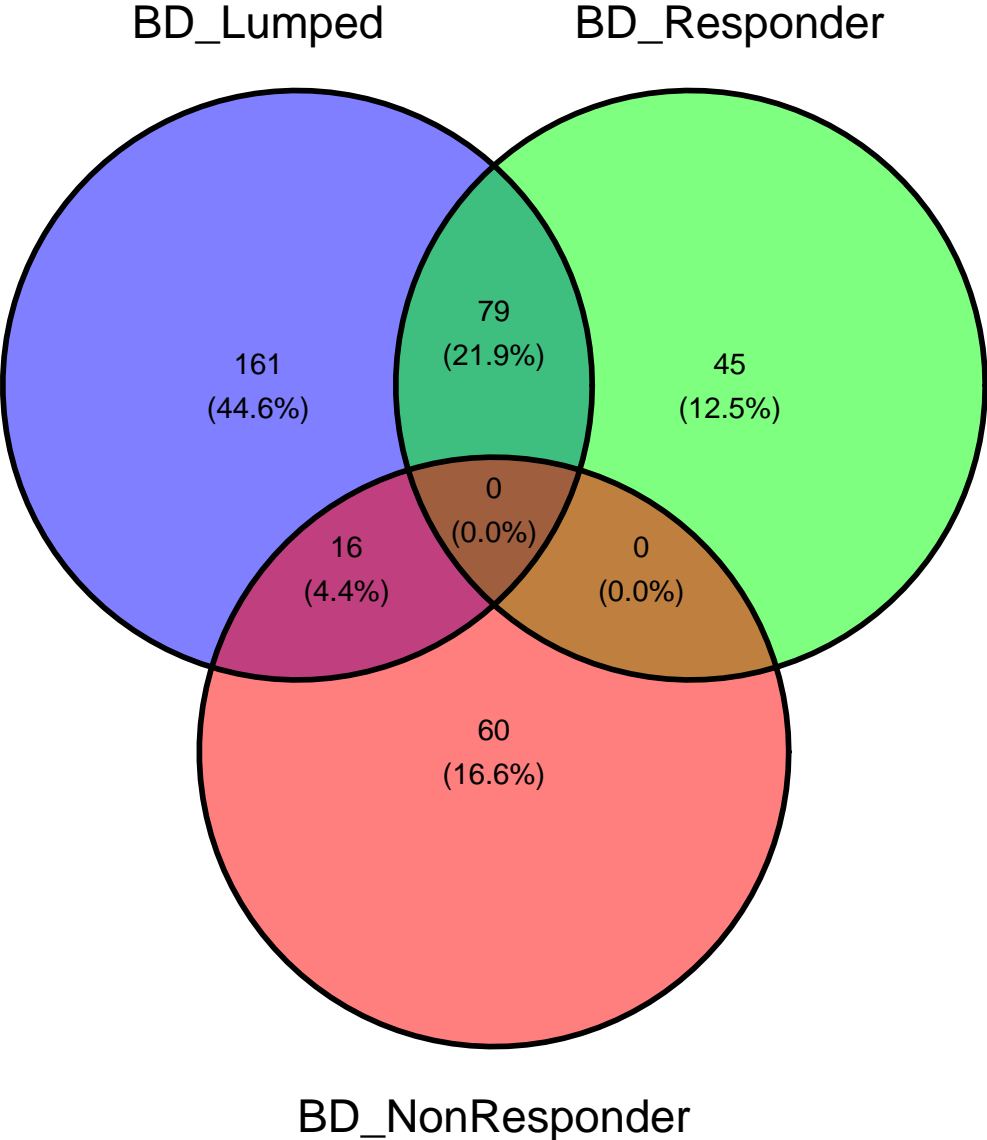
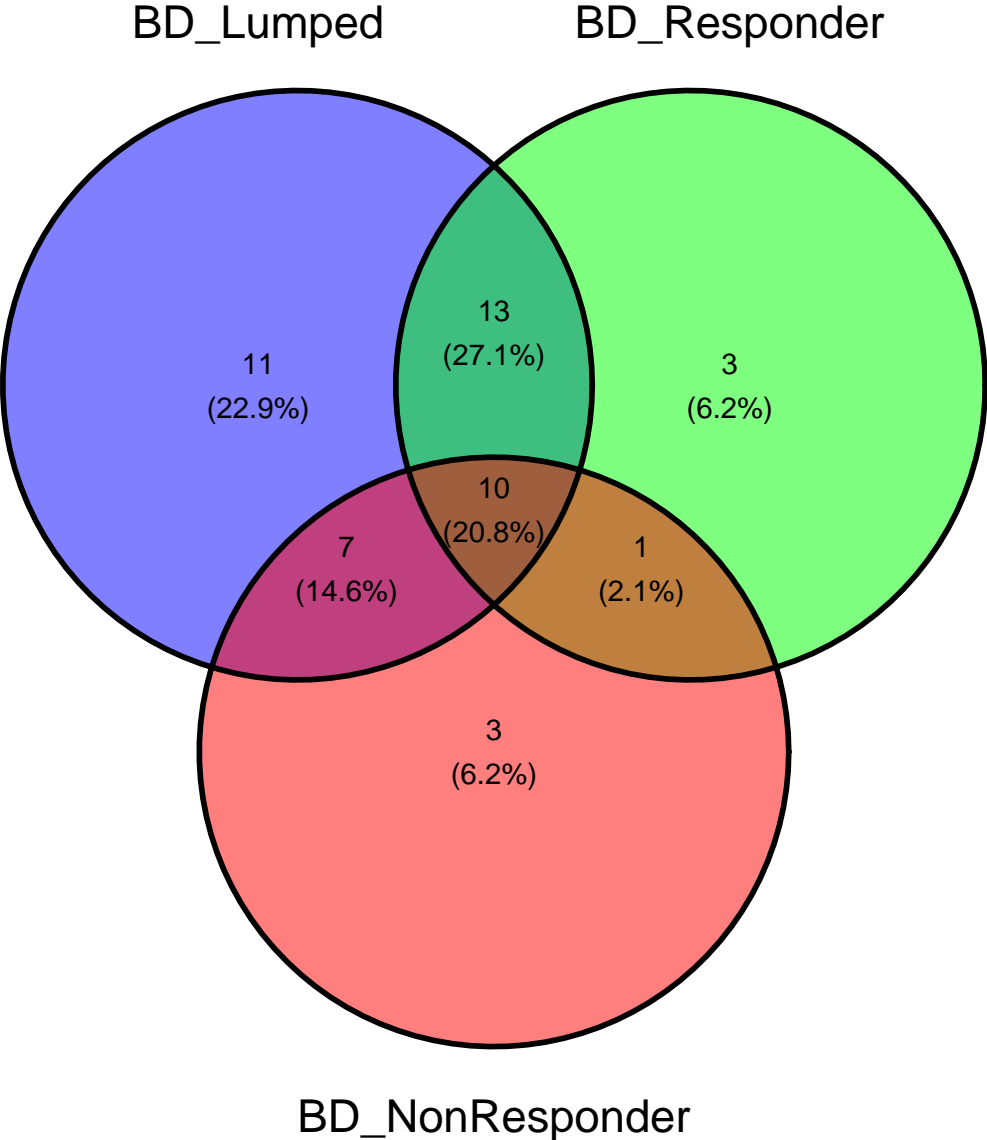


Overlap in rxns disrupted between models

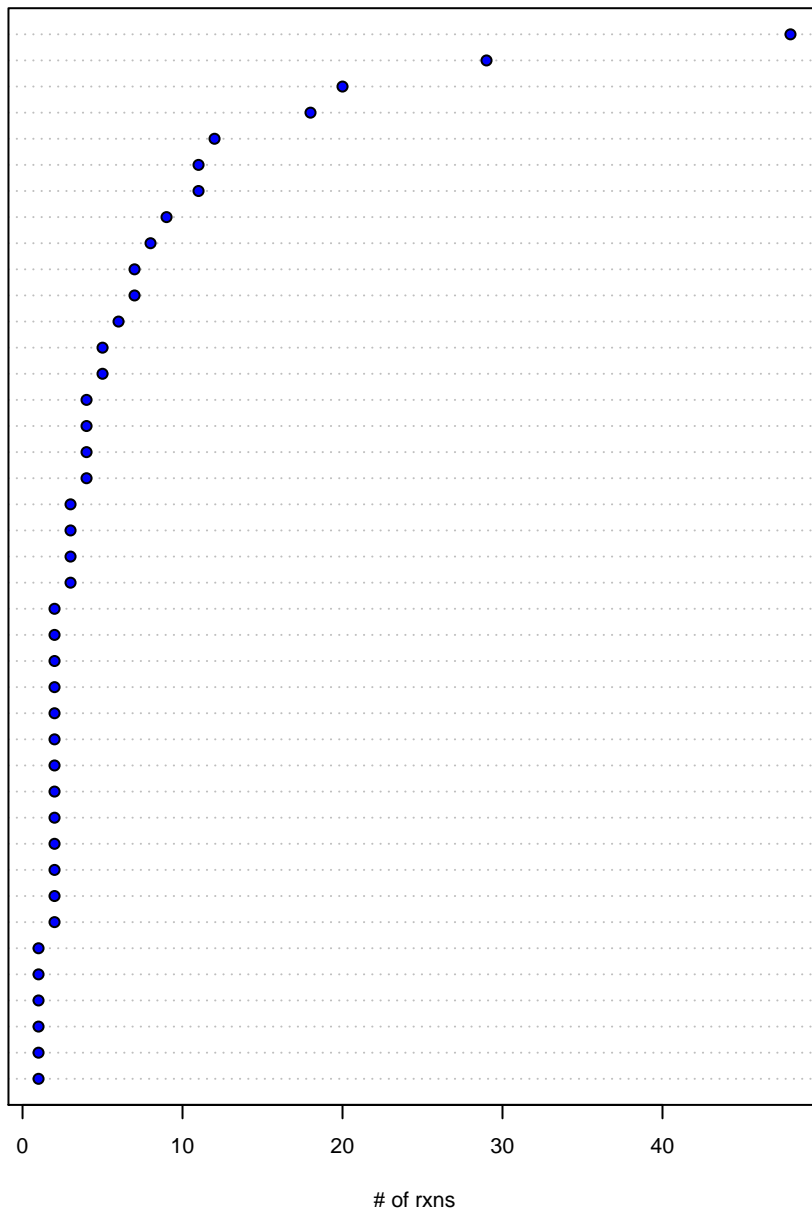


Overlap in subSystems disrupted between models



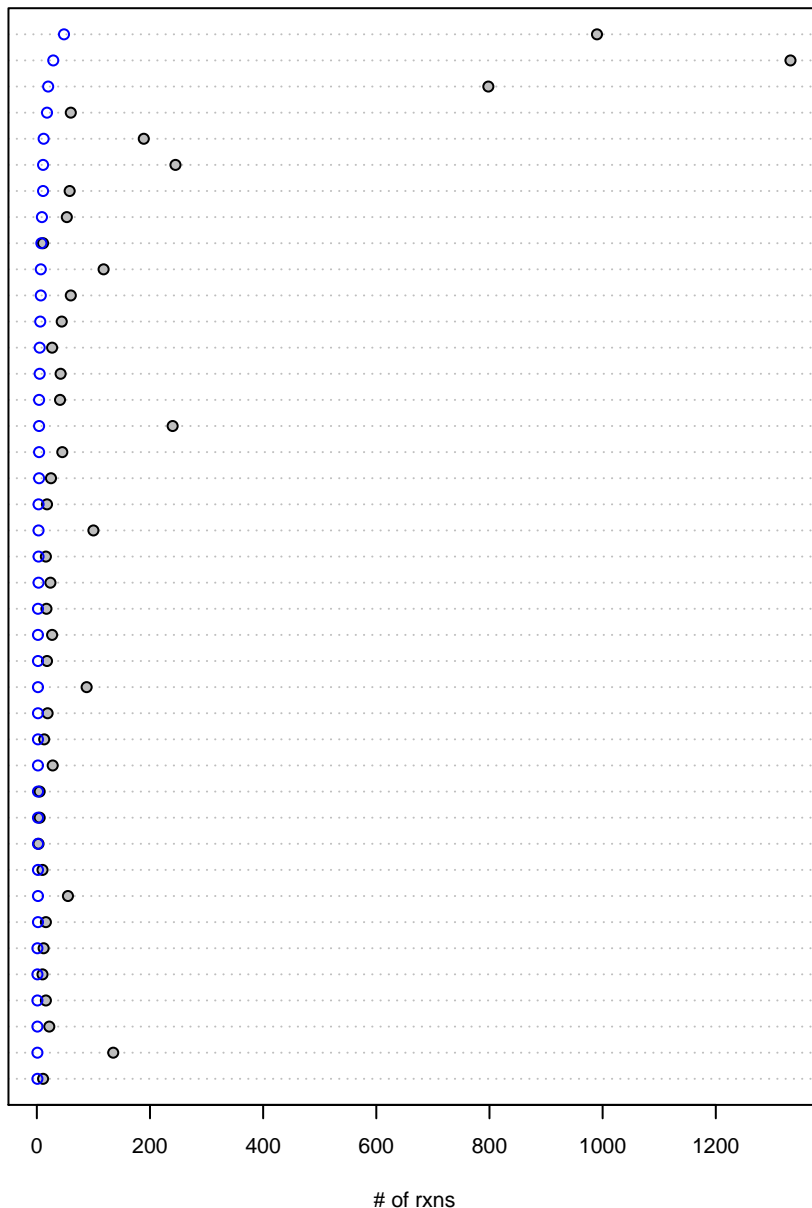
of disrupted rxns (n=256, bd_lumped)

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



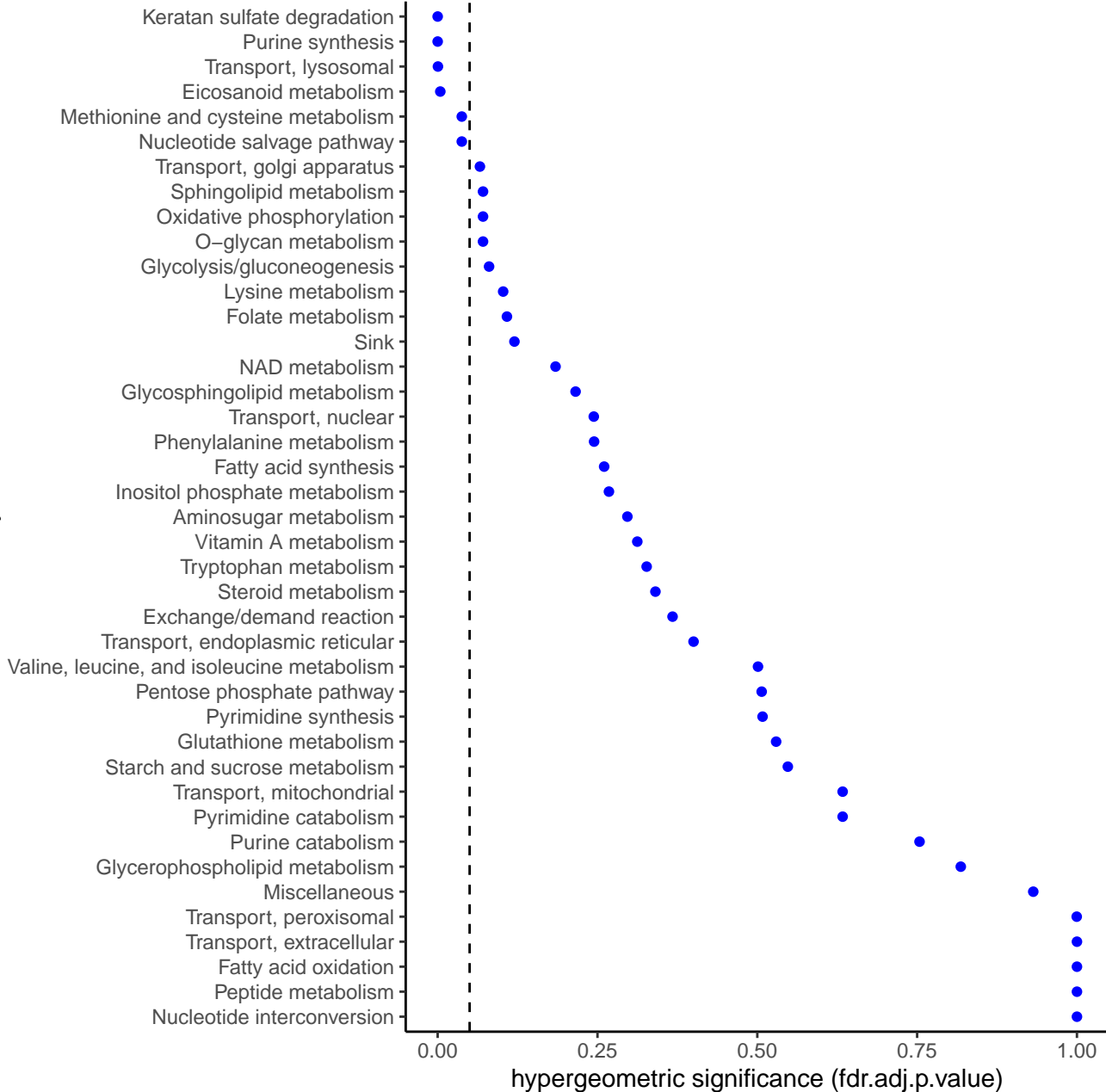
of disrupted rxns (n=256, bd_lumped) vs all rxns

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

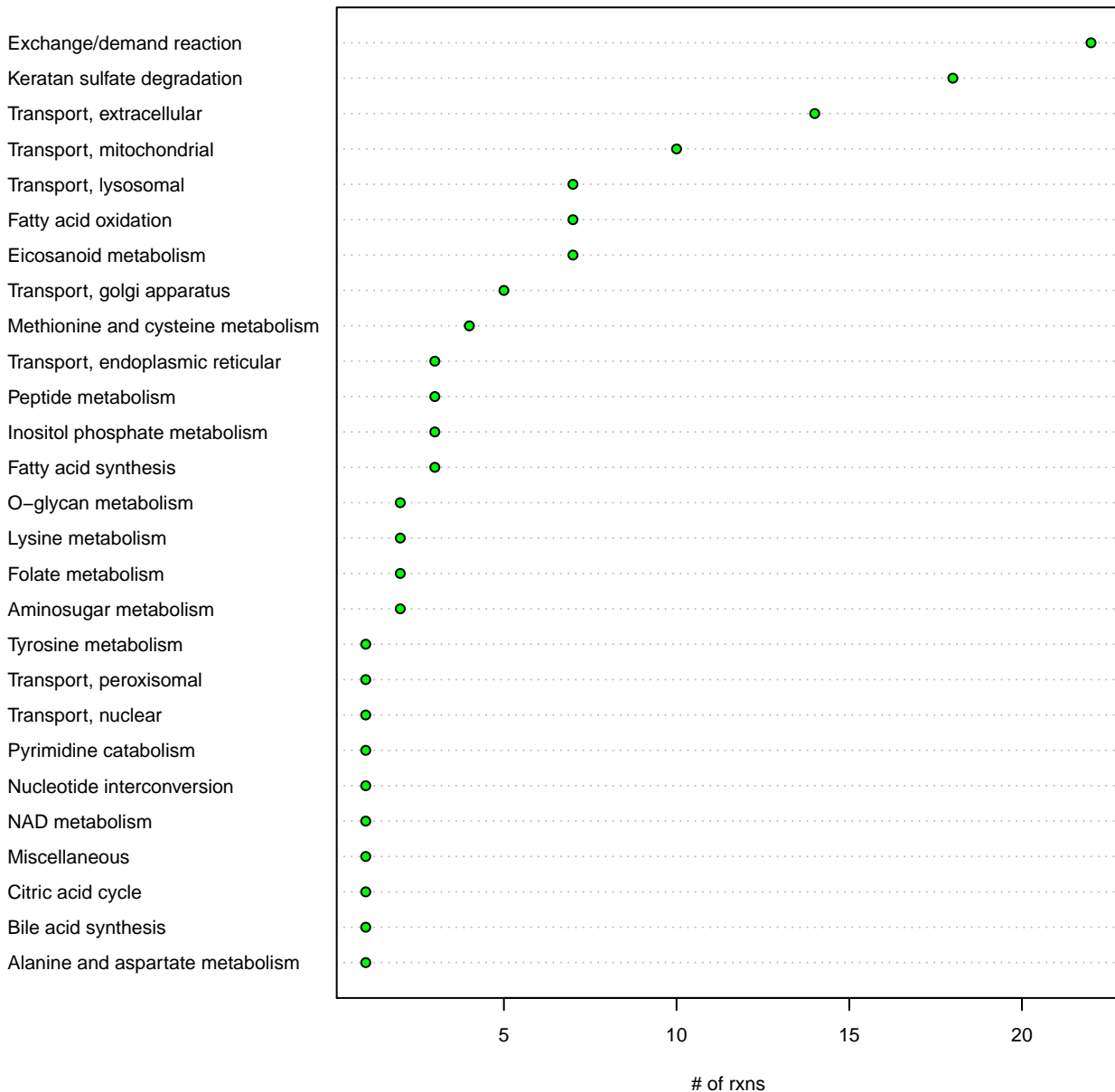


over-representation analysis, bd_lumped

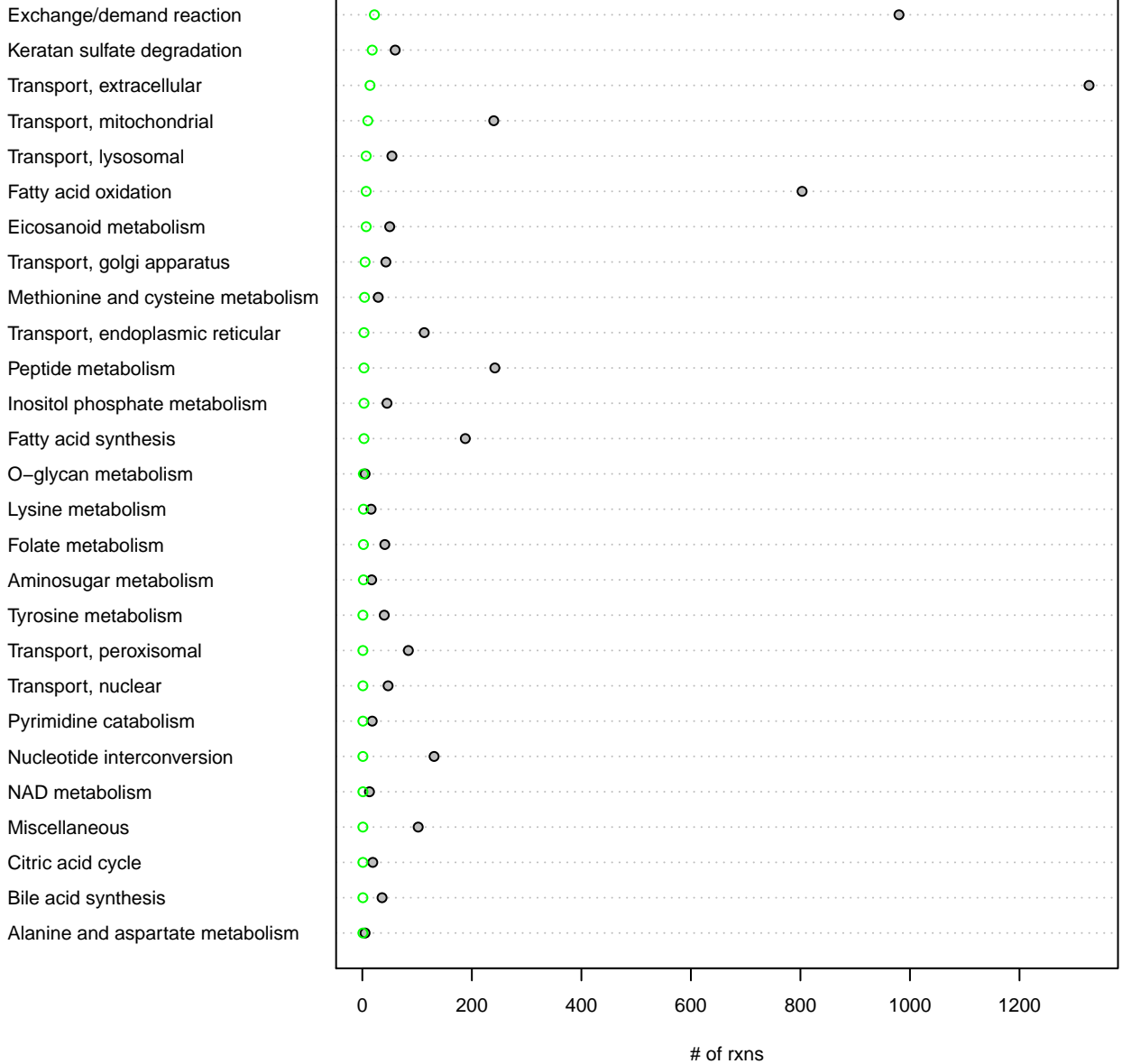
subSystem



of disrupted rxns (n=124, bd_responder)

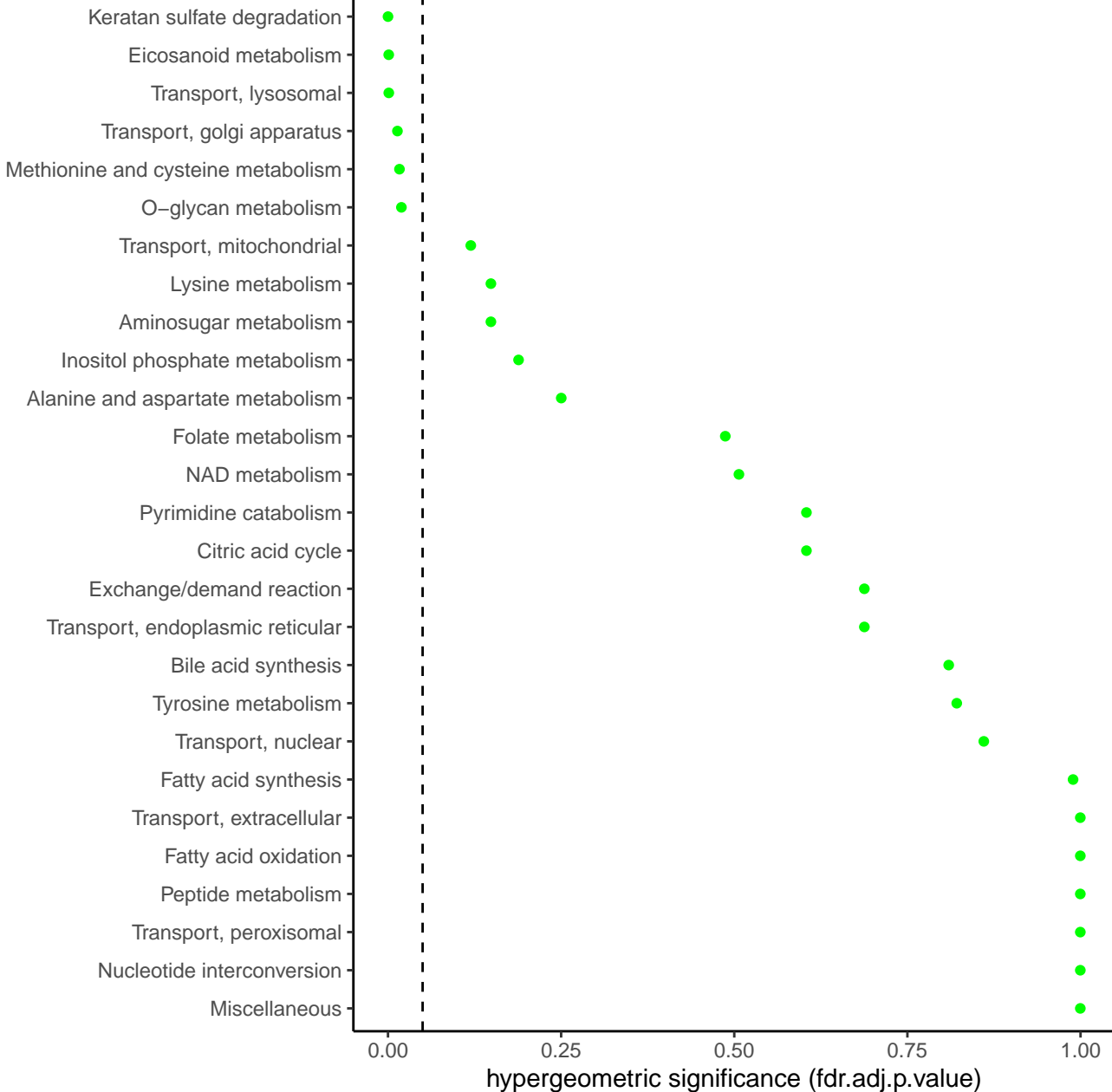


of disrupted rxns (n=124, bd_responder) vs all rxns

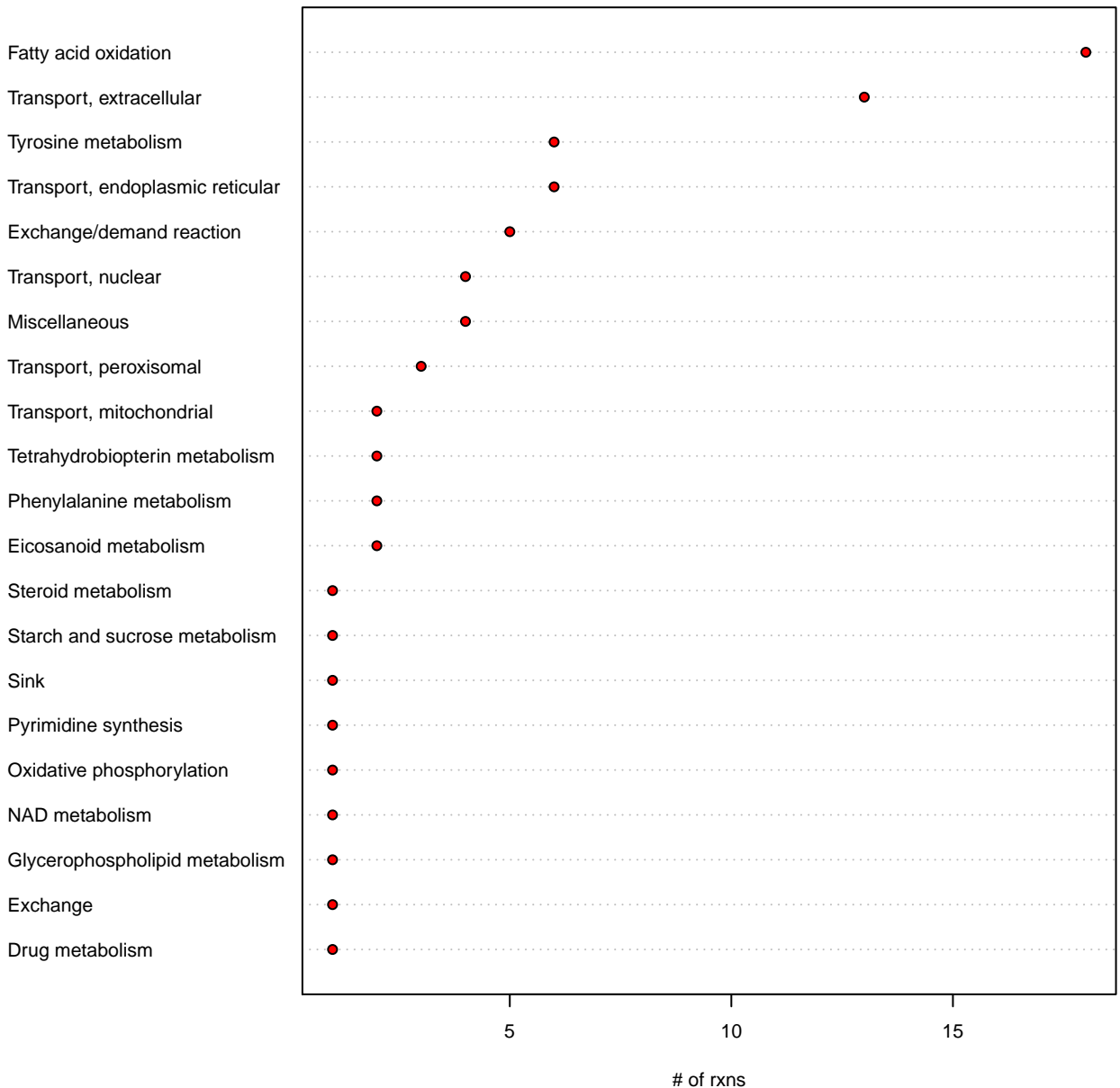


over-representation analysis, bd_responder

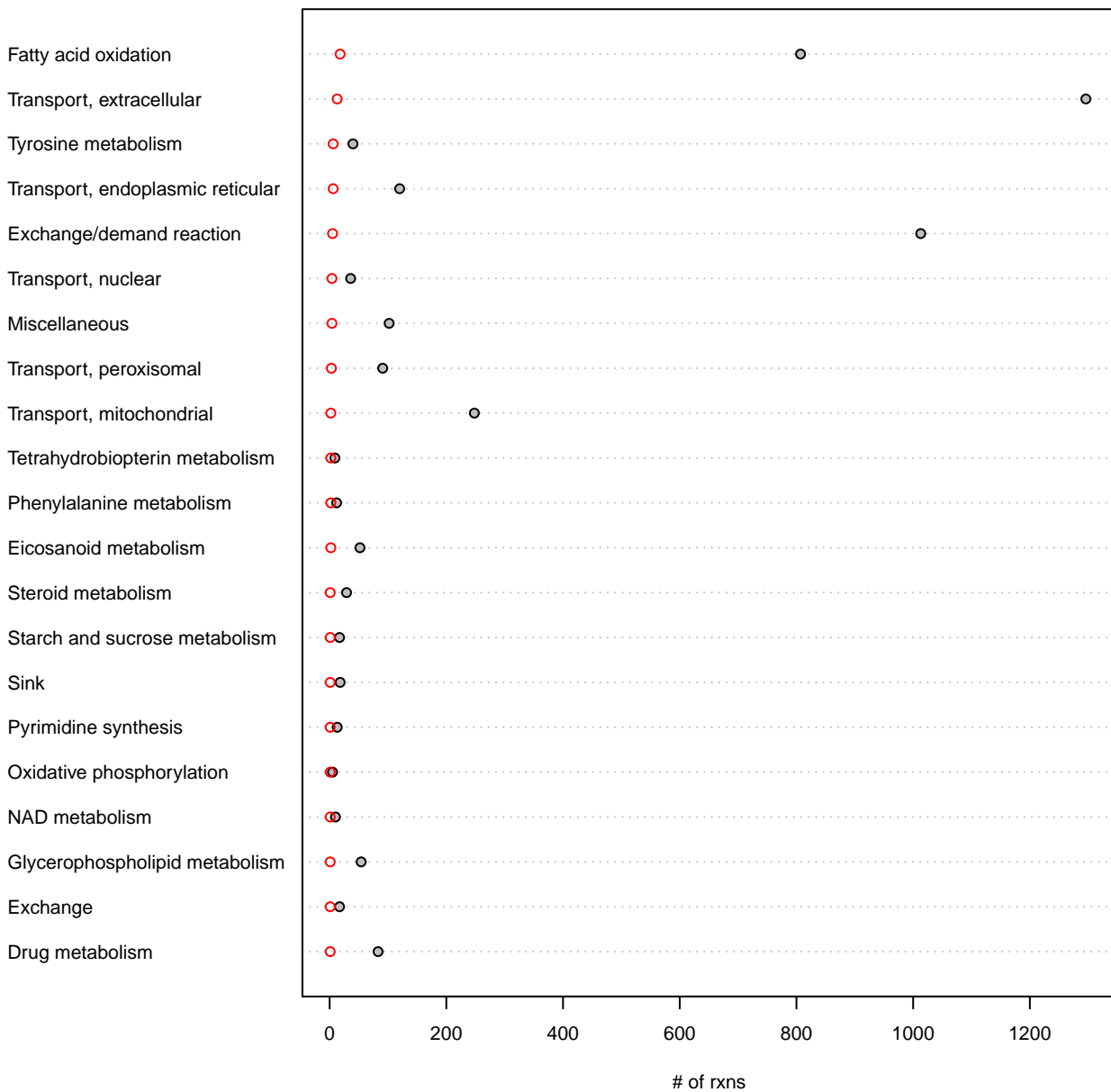
subSystem



of disrupted rxns (n=76, bd_nonresponder)

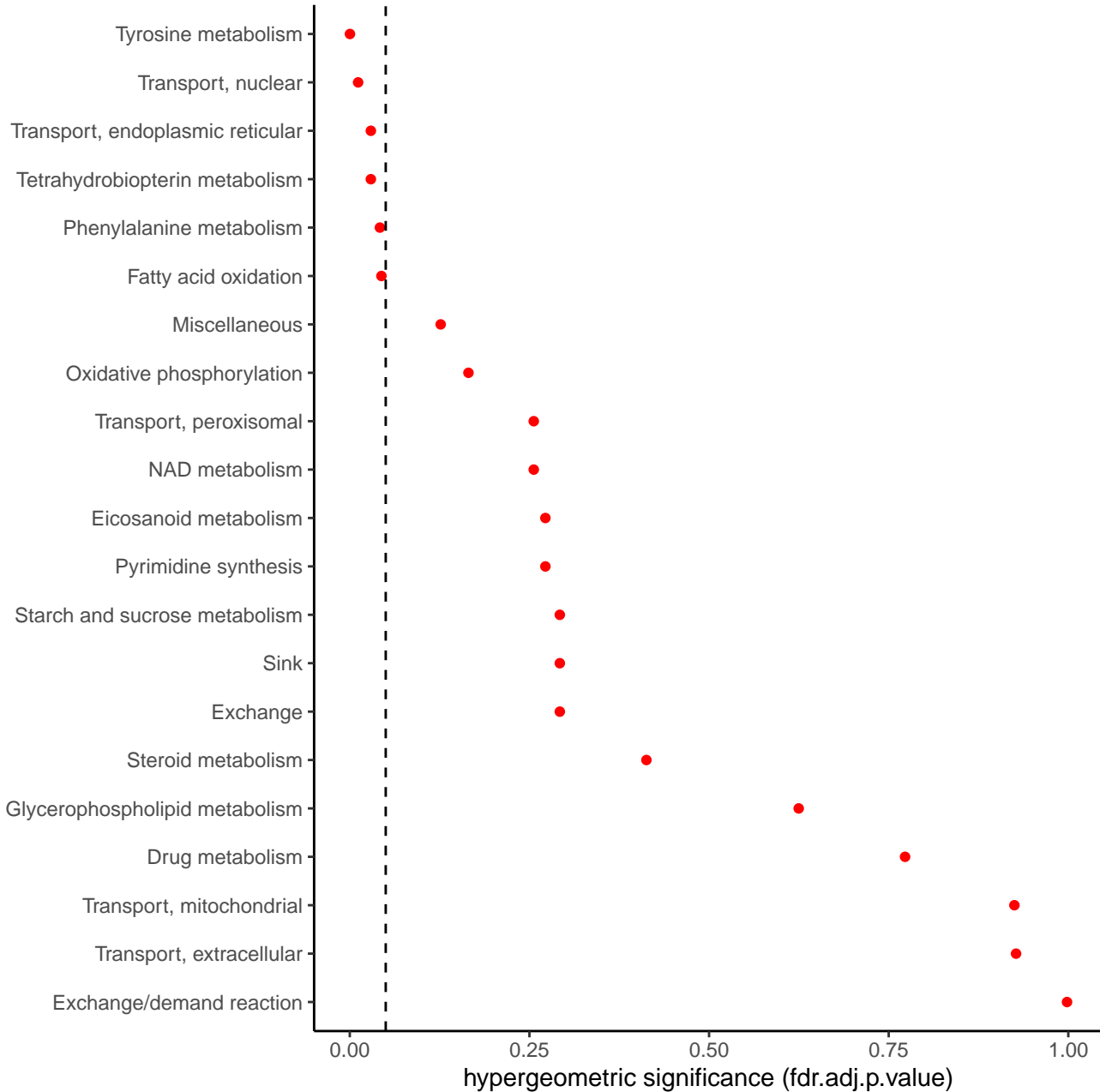


of disrupted rxns (n=76, bd_nonresponder) vs all rxns

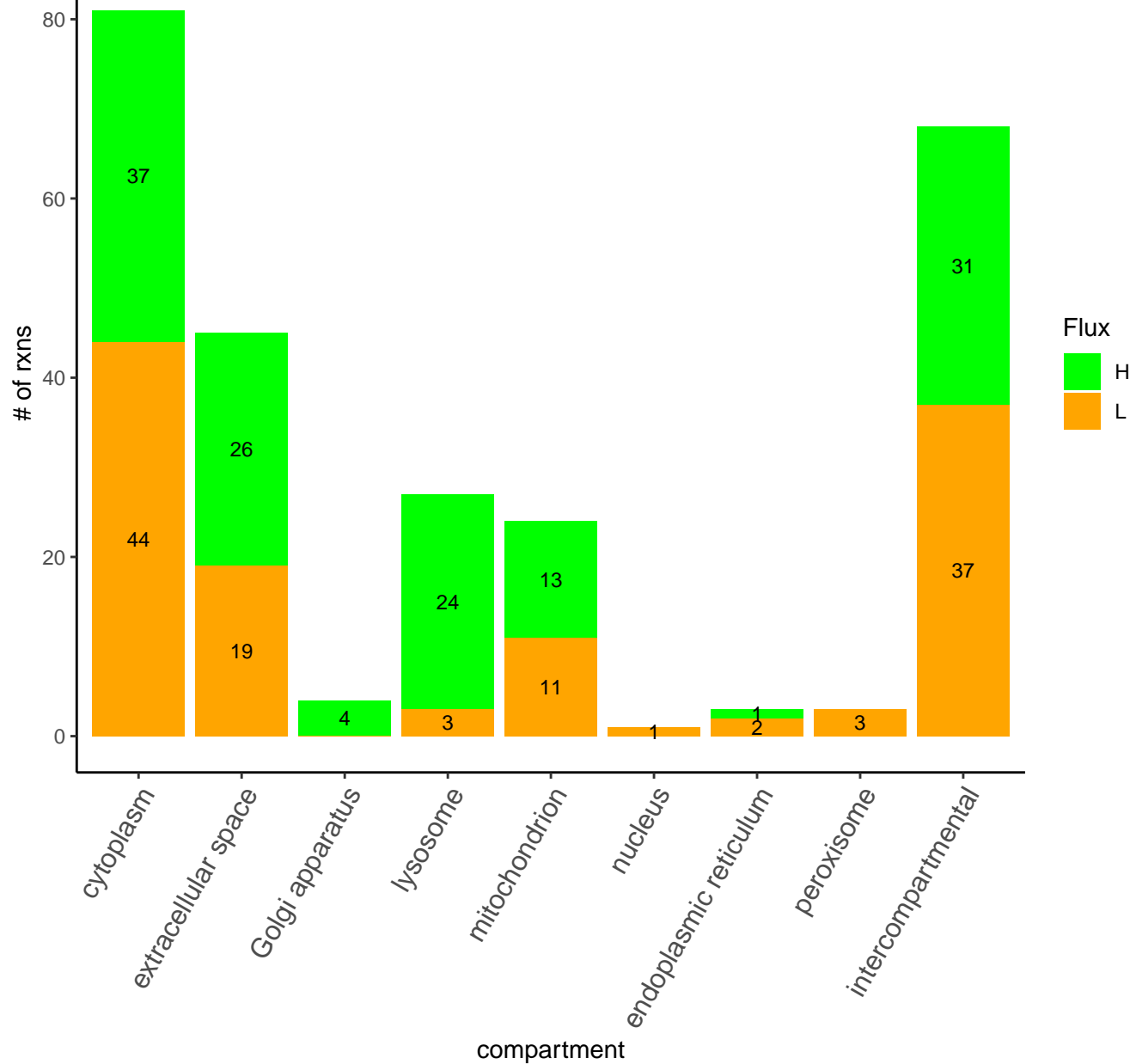


over-representation analysis, bd_nonresponder

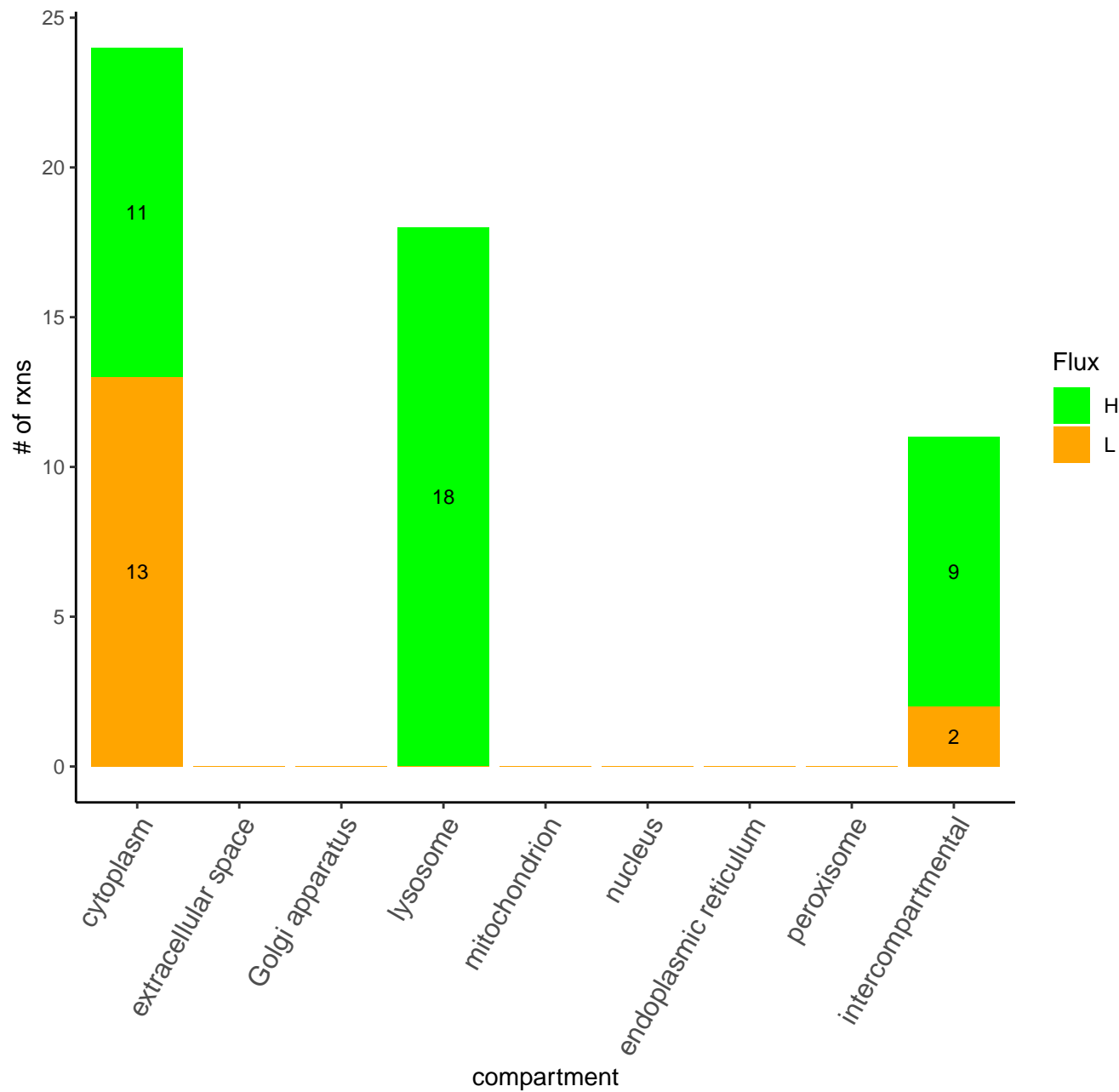
subSystem



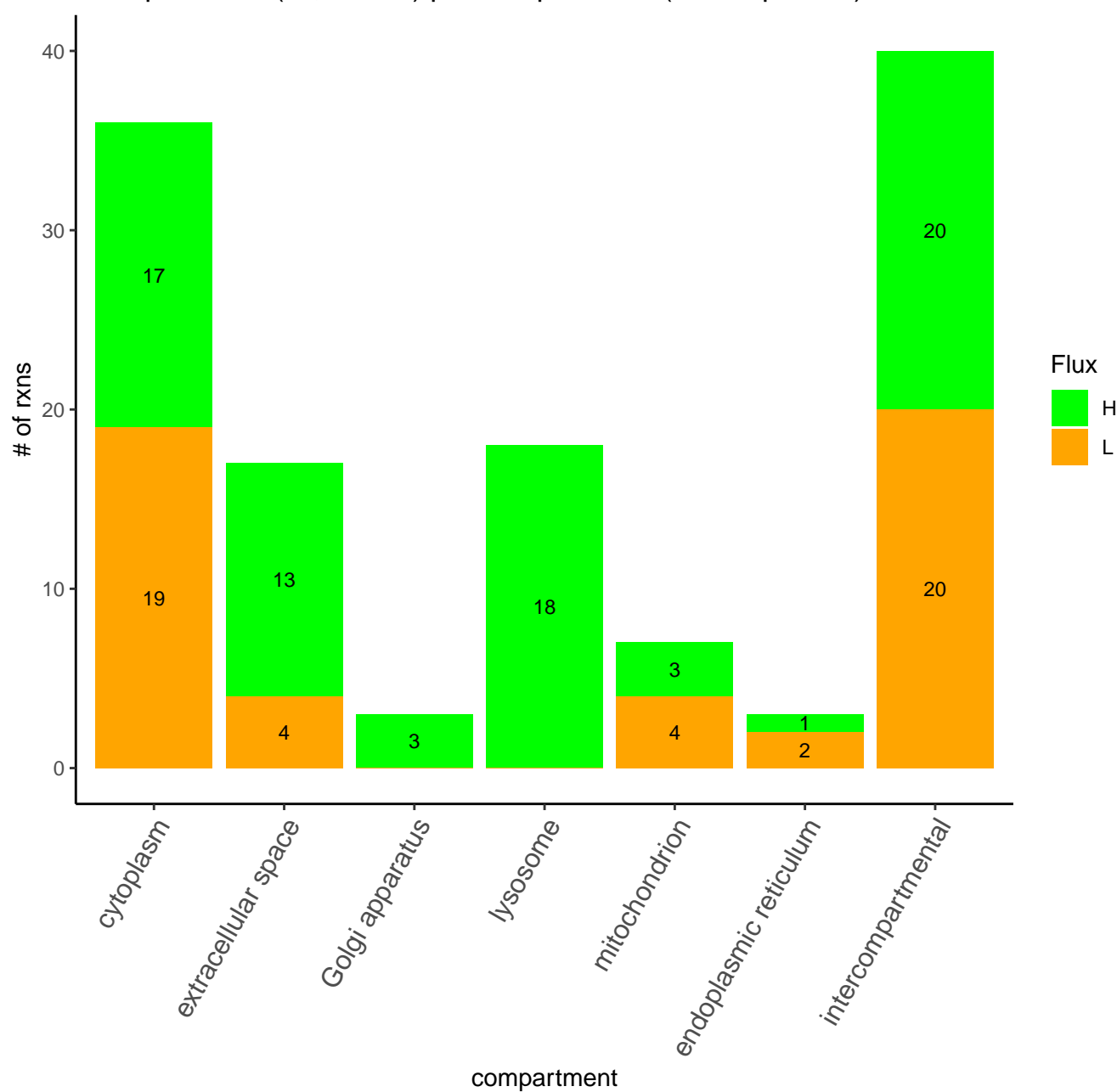
Disrupted rxns (all, n=256) per compartment (bd_lumped)



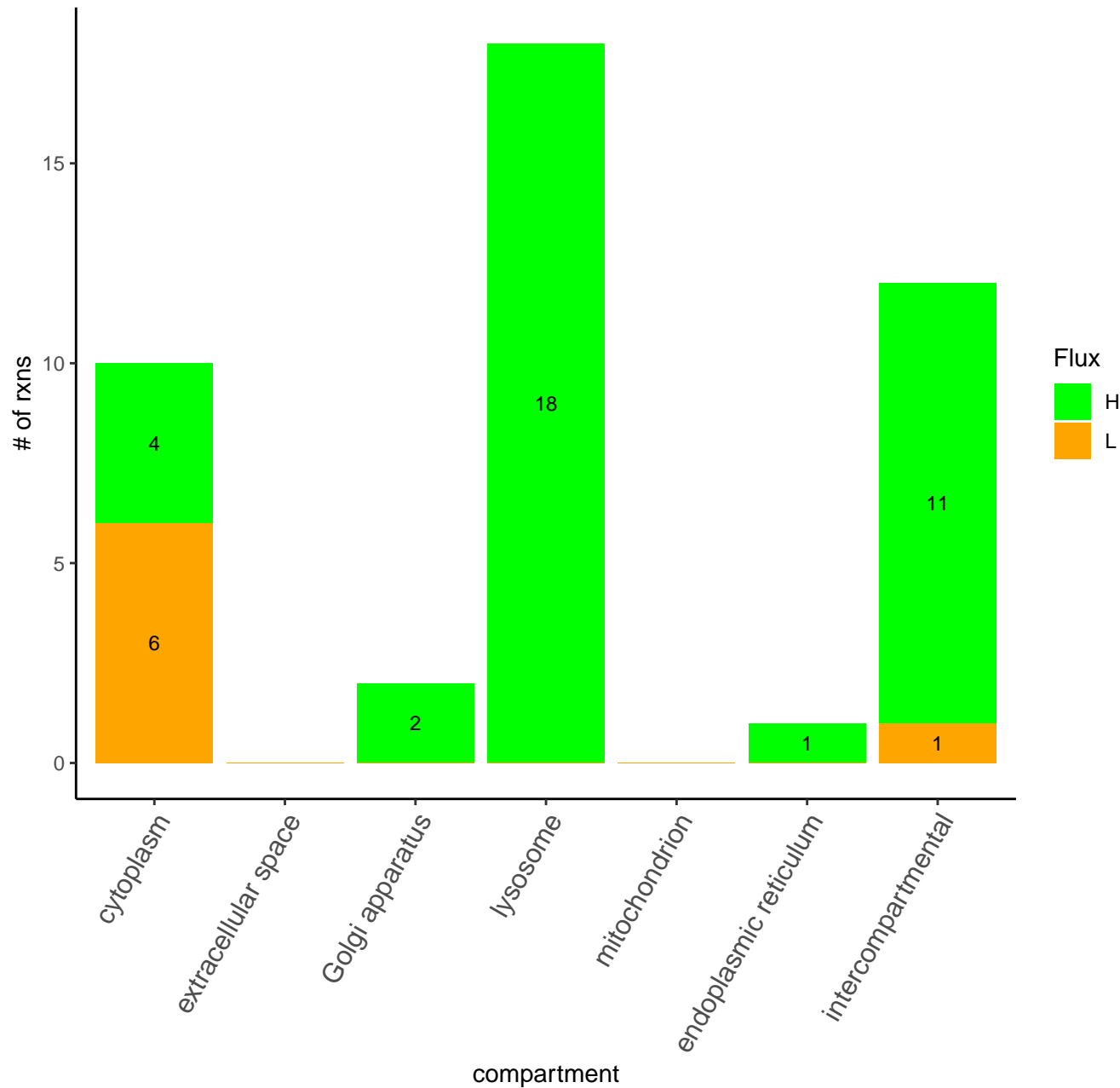
Disrupted rxns (fdr.significant, n=53) per compartment (bd_lumped)



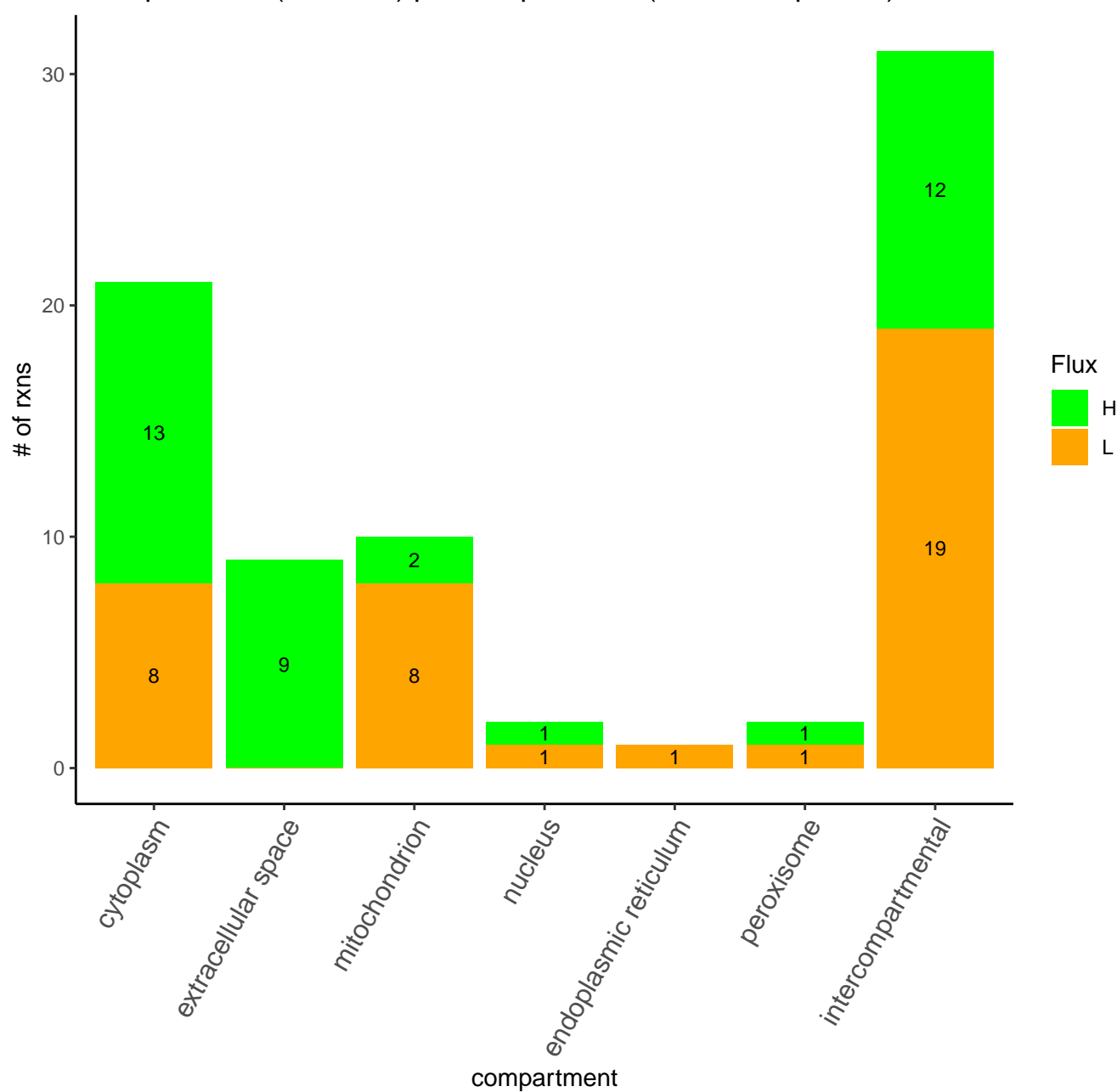
Disrupted rxns (all, n=124) per compartment (bd_responder)



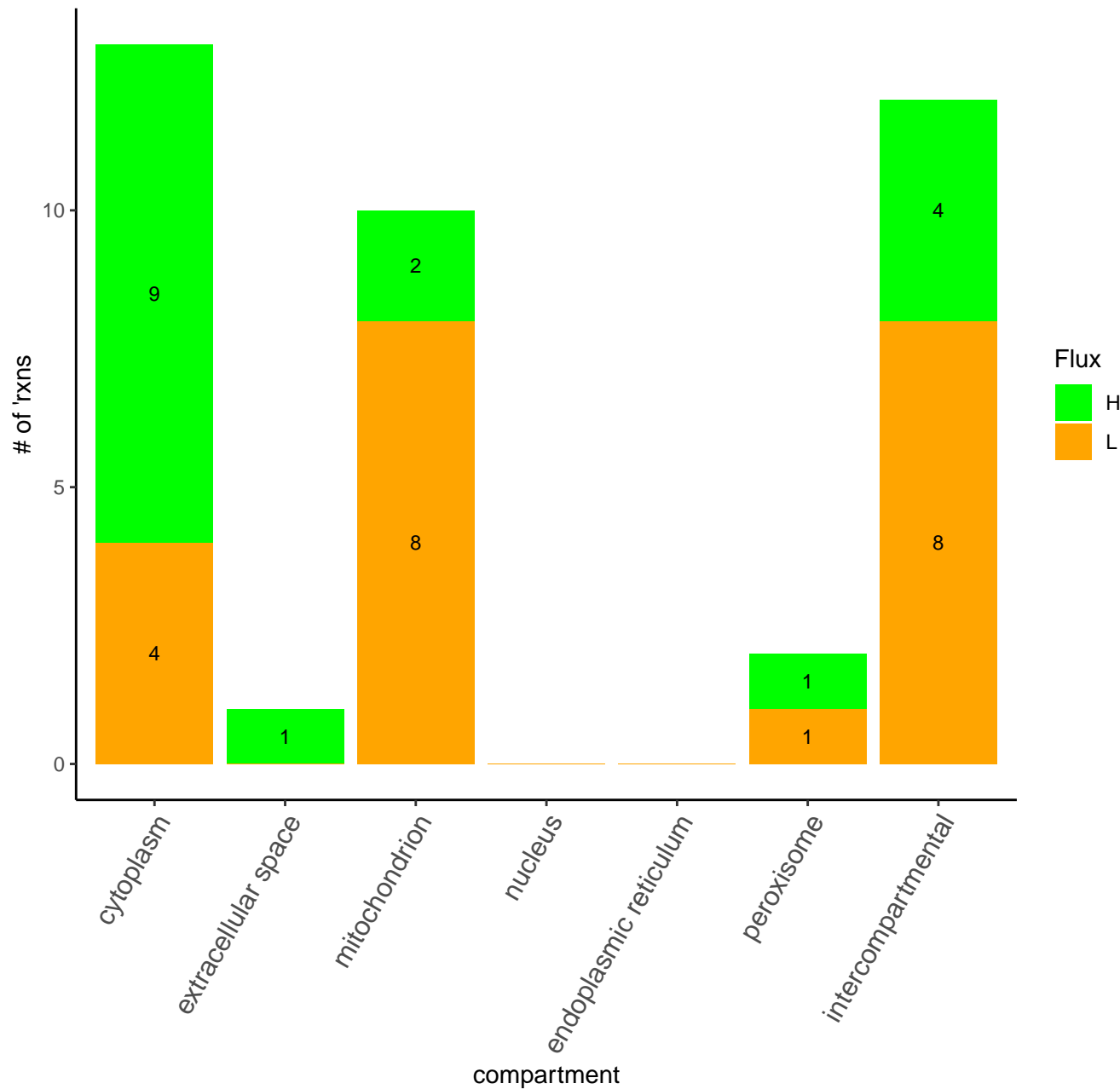
Disrupted rxns (fdr.significant, n=43) per compartment (bd_responder)



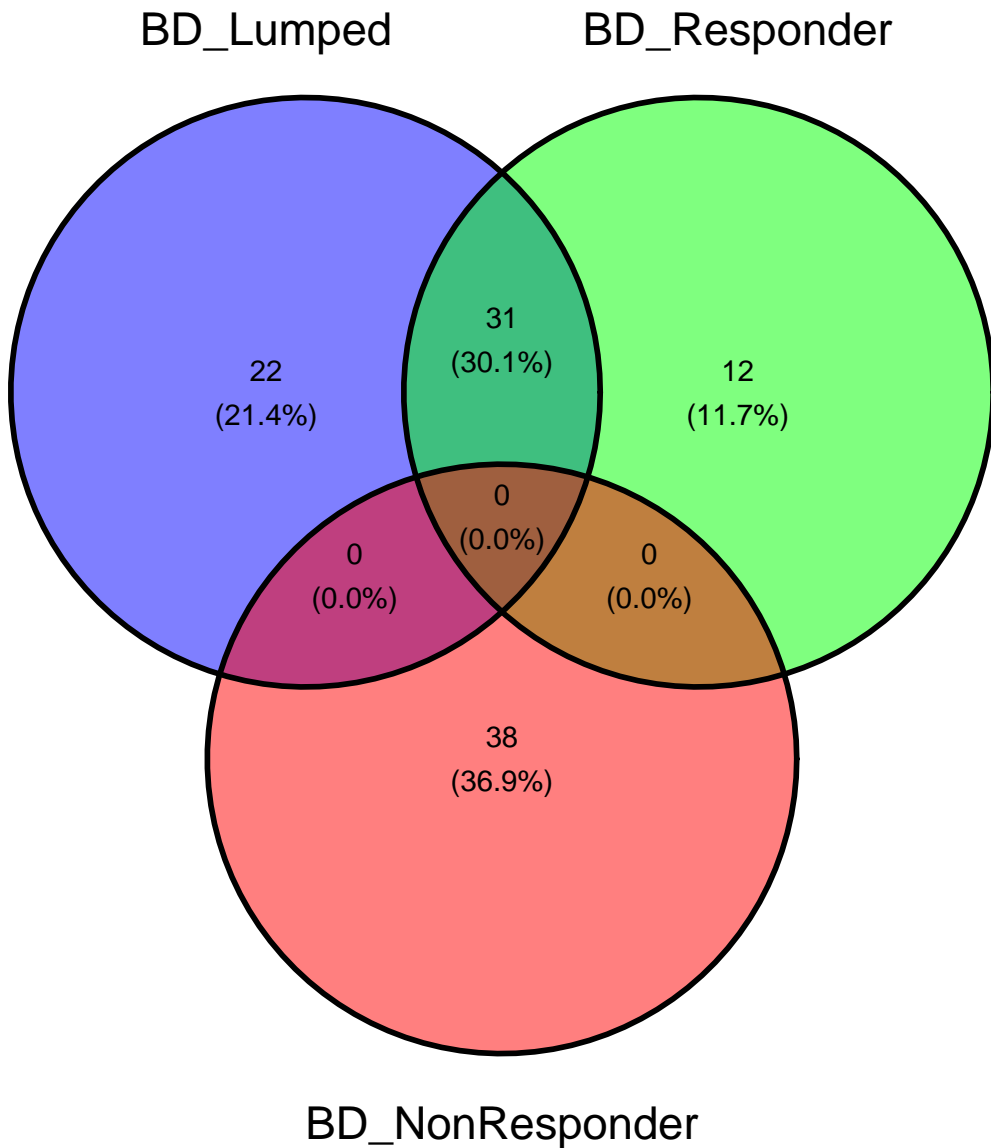
Disrupted rxns (all, n=76) per compartment (bd_nonresponder)



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

