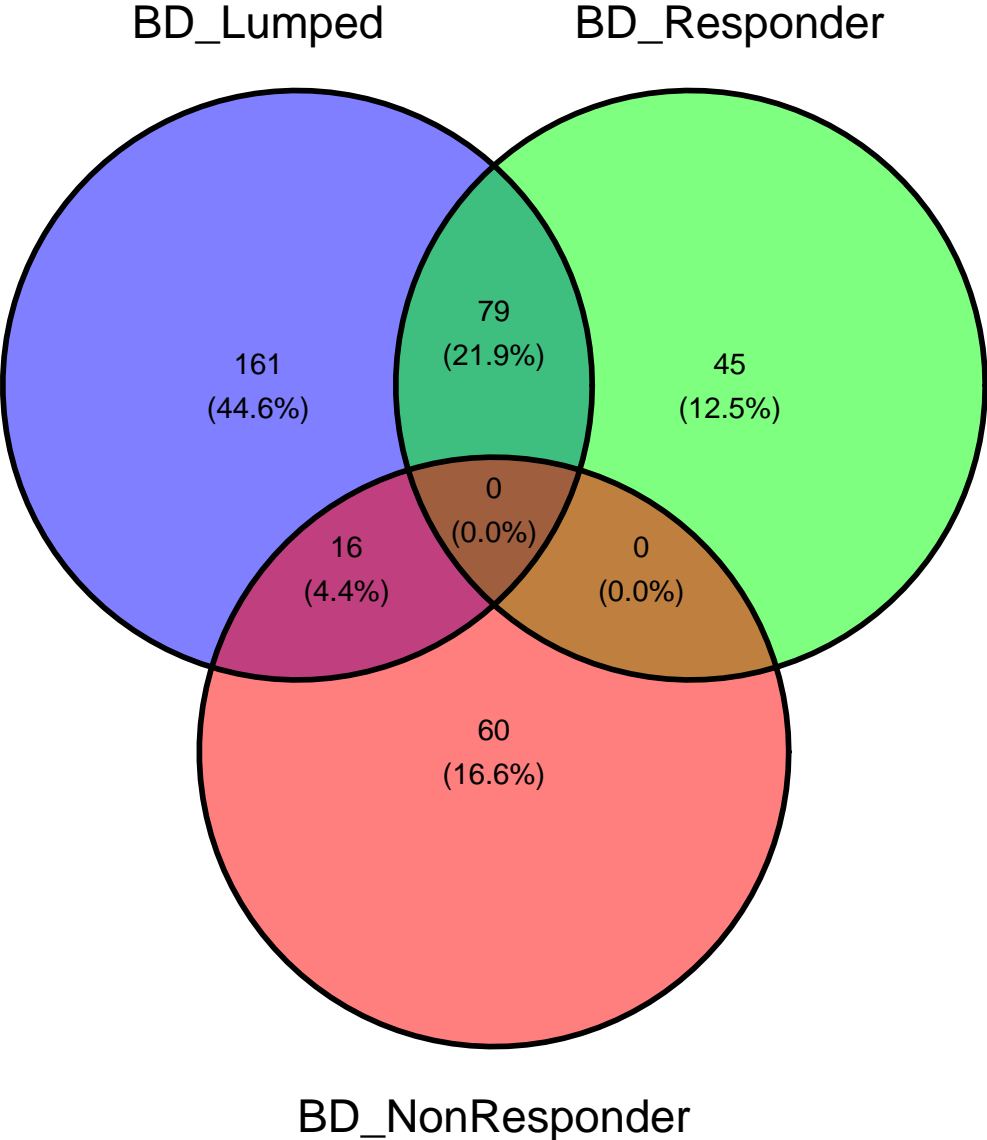Overlap in rxns disrupted between models

Overlap in subSystems disrupted between models

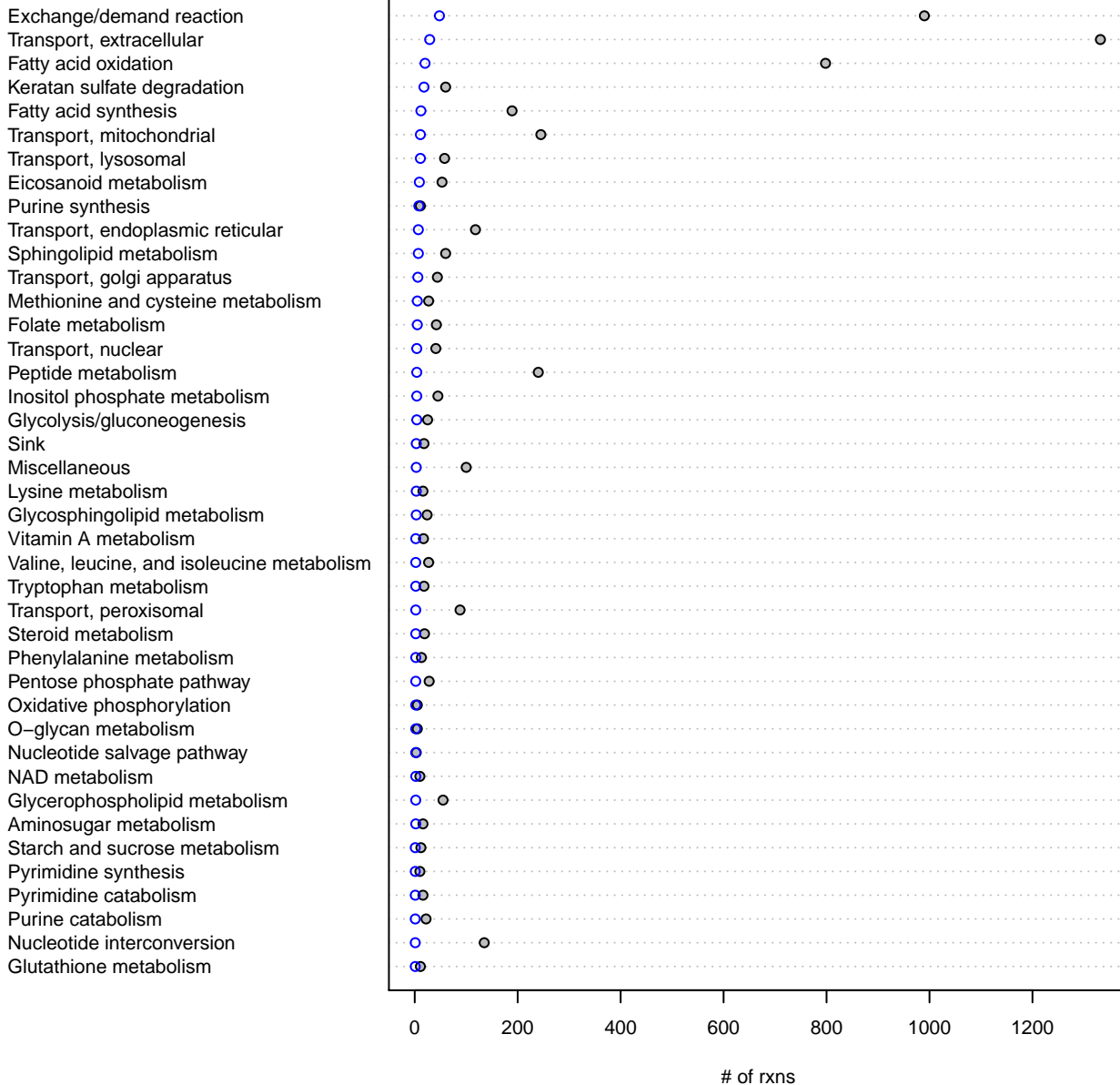BD_Lumped   BD_Responder

11
(22.9%)

13
(27.1%)

3
(6.2%)

7
(14.6%)

10
(20.8%)

1
(2.1%)

3
(6.2%)

BD_NonResponder
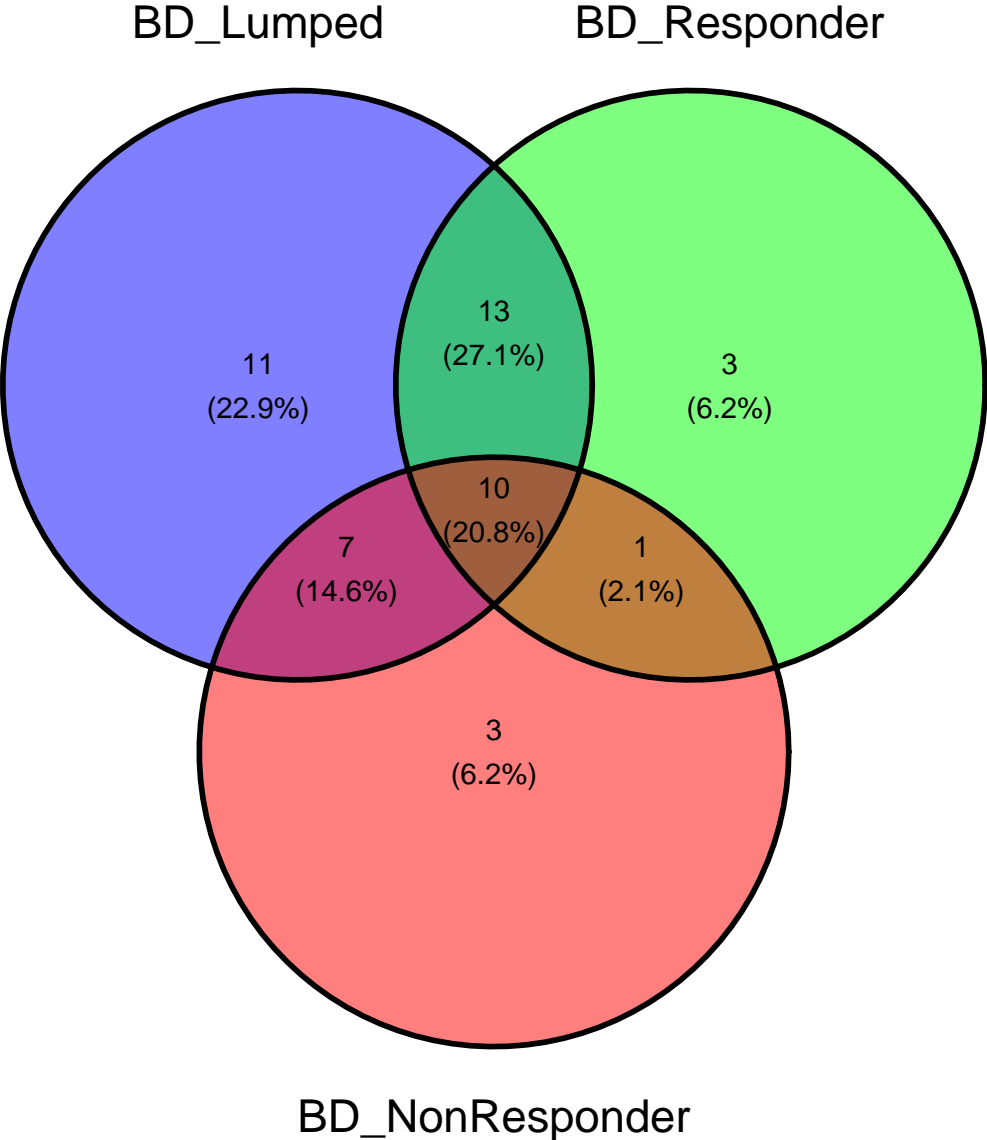
# of disrupted rxns (n=256, bd_lumped)

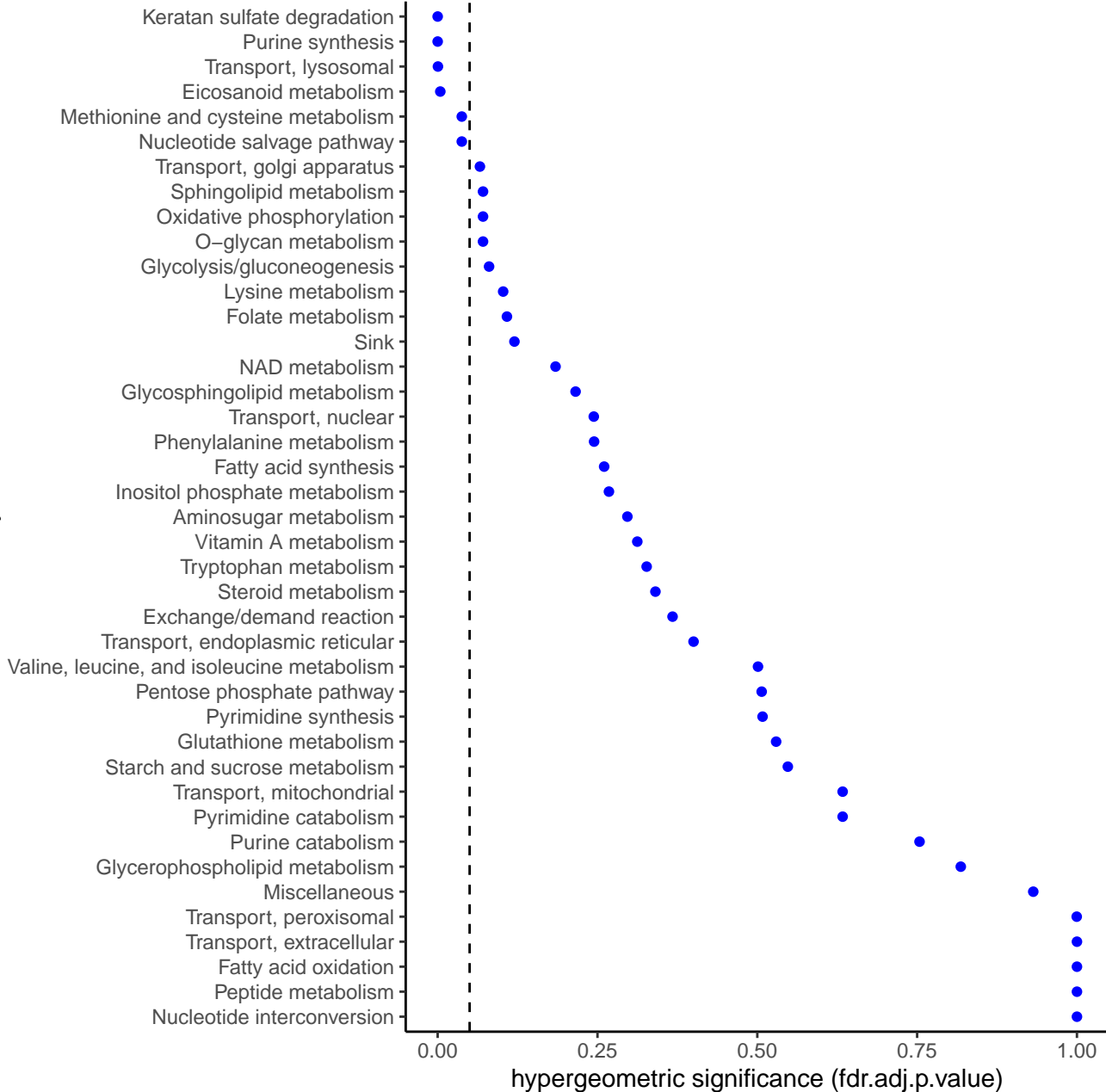| Category	
Exchange/demand reaction	
Transport, extracellular	
Fatty acid oxidation	
Keratan sulfate degradation	
Fatty acid synthesis	
Transport, mitochondrial	
Transport, lysosomal	
Eicosanoid metabolism	
Purine synthesis	
Transport, endoplasmic reticular	
Sphingolipid metabolism	
Transport, golgi 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 rxns
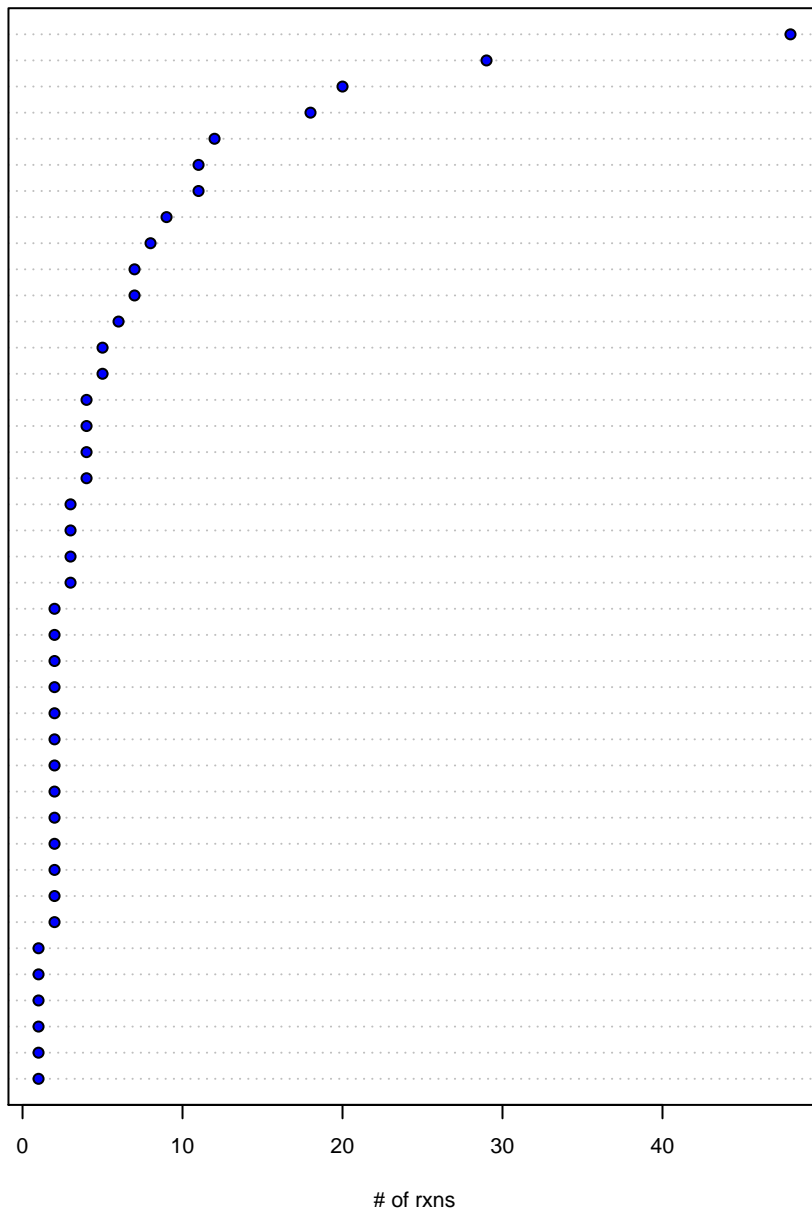
# of disrupted rxns (n=256, bd_lumped) vs all rxns

over−representation analysis, bd_lumped

of disrupted rxns (n=124, bd_responder)

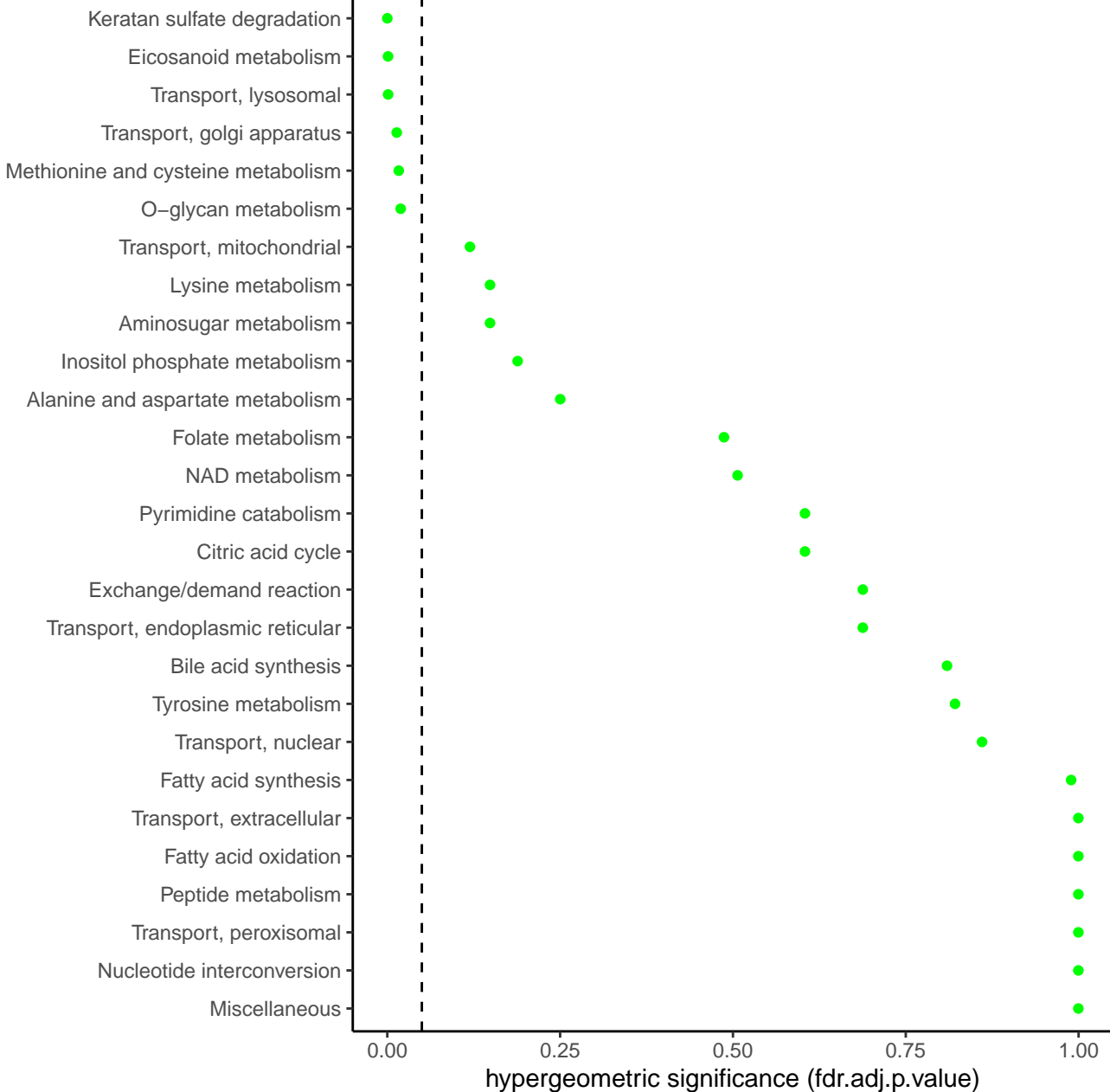| Category	
Exchange/demand reaction	
Keratan sulfate degradation	
Transport, extracellular	
Transport, mitochondrial	
Transport, lysosomal	
Fatty acid oxidation	
Eicosanoid metabolism	
Transport, golgi apparatus	
Methionine and cysteine metabolism	
Transport, endoplasmic reticular	
Peptide metabolism	
Inositol phosphate metabolism	
Fatty acid synthesis	
O−glycan metabolism	
Lysine metabolism	
Folate metabolism	
Aminosugar metabolism	
Tyrosine metabolism	
Transport, peroxisomal	
Transport, nuclear	
Pyrimidine catabolism	
Nucleotide interconversion	
NAD metabolism	
Miscellaneous	
Citric acid cycle	
Bile acid synthesis	
Alanine and aspartate metabolism	

# of rxns

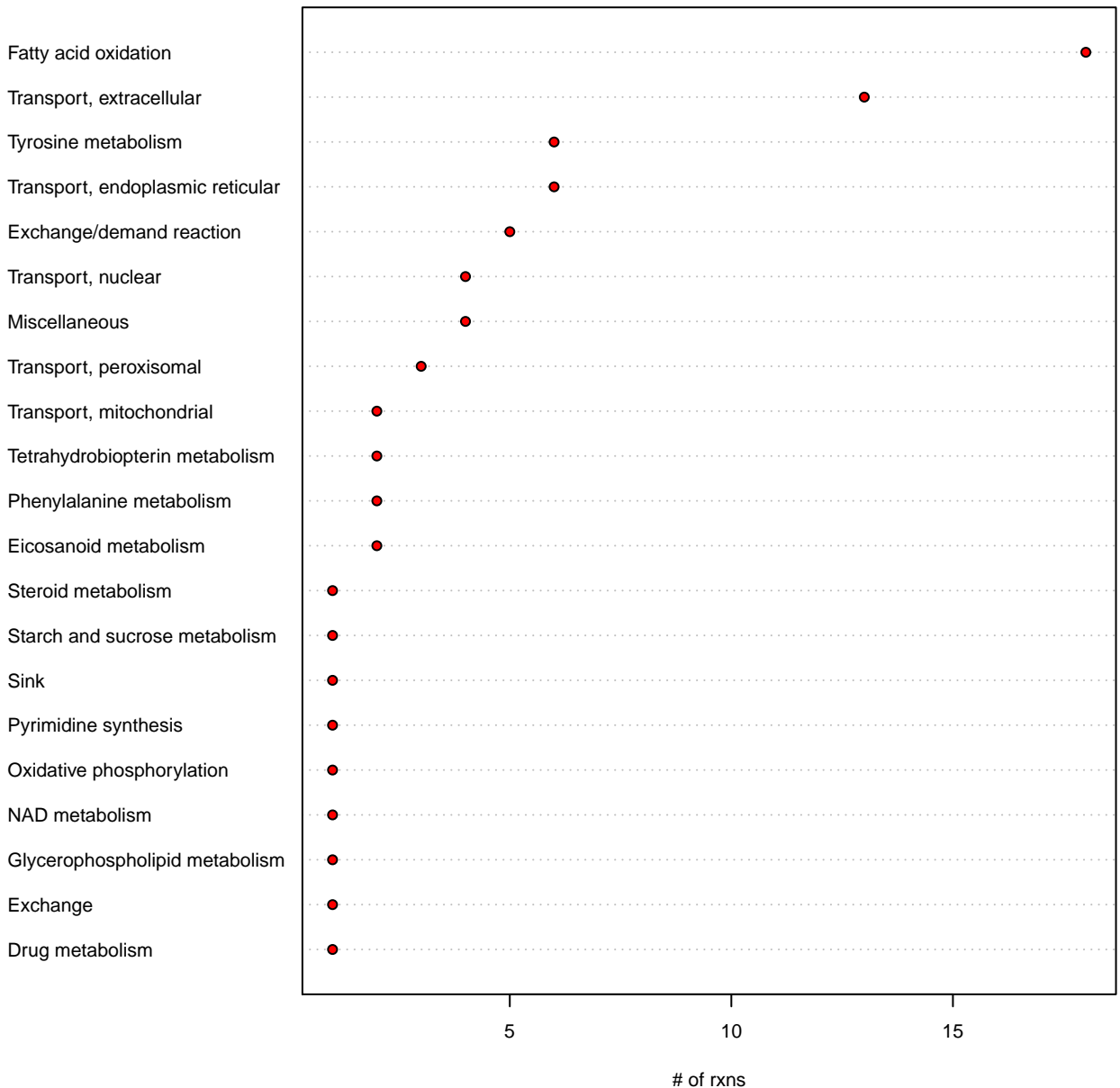# # of disrupted rxns (n=124, bd_responder) vs all rxns

# of rxns
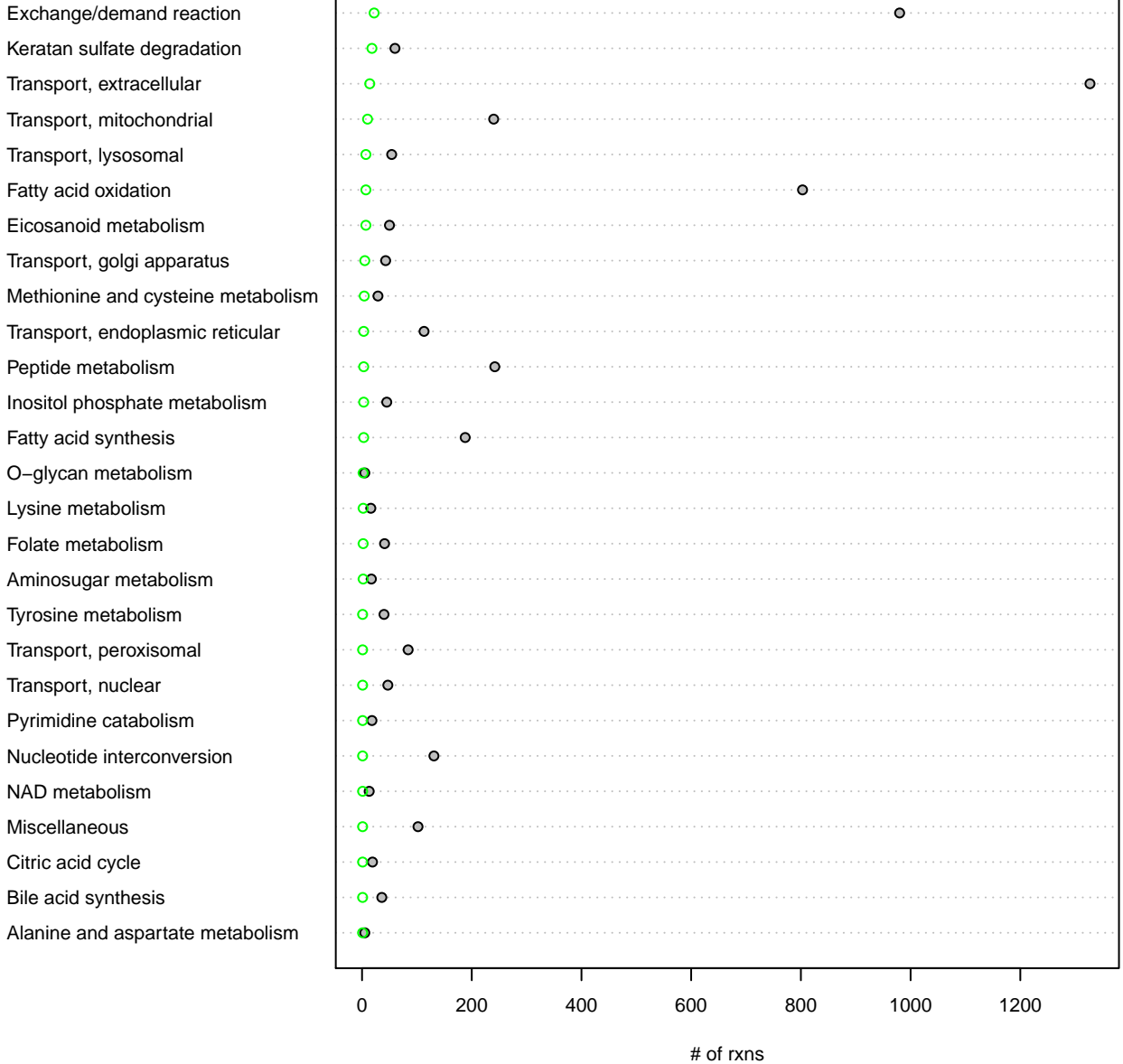
over−representation analysis, bd_responder

# of disrupted rxns (n=76, bd_nonresponder)

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

Category
Fatty acid oxidation
Transport, extracellular
Tyrosine metabolism
Transport, endoplasmic reticular
Exchange/demand reaction
Transport, nuclear
Miscellaneous
Transport, peroxisomal
Transport, mitochondrial
Tetrahydrobiopterin metabolism
Phenylalanine metabolism
Eicosanoid metabolism
Steroid metabolism
Starch and sucrose metabolism
Sink
Pyrimidine synthesis
Oxidative phosphorylation
NAD metabolism
Glycerophospholipid metabolism
Exchange
Drug metabolism

# of rxns

over−representation analysis, bd_nonresponder
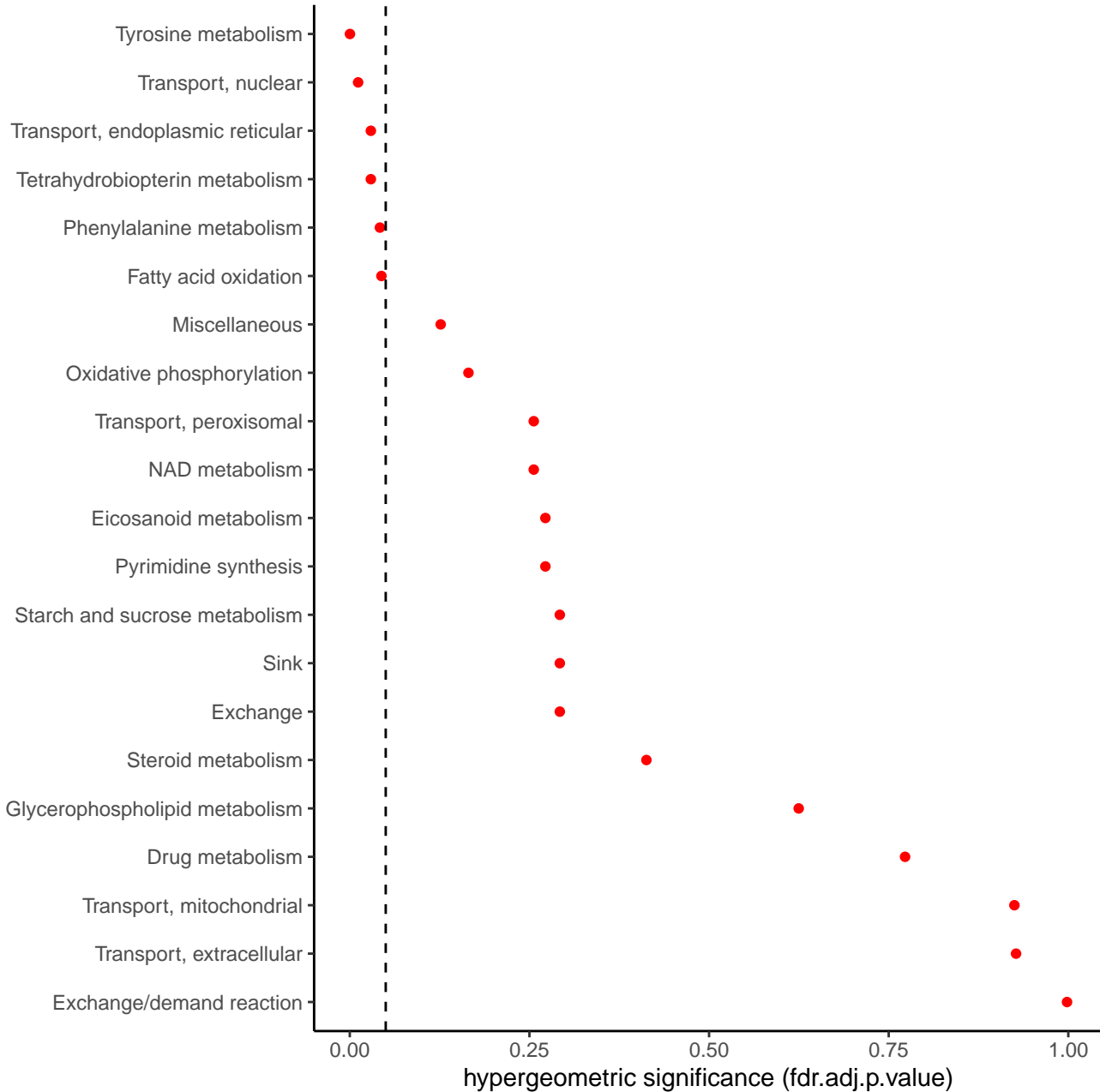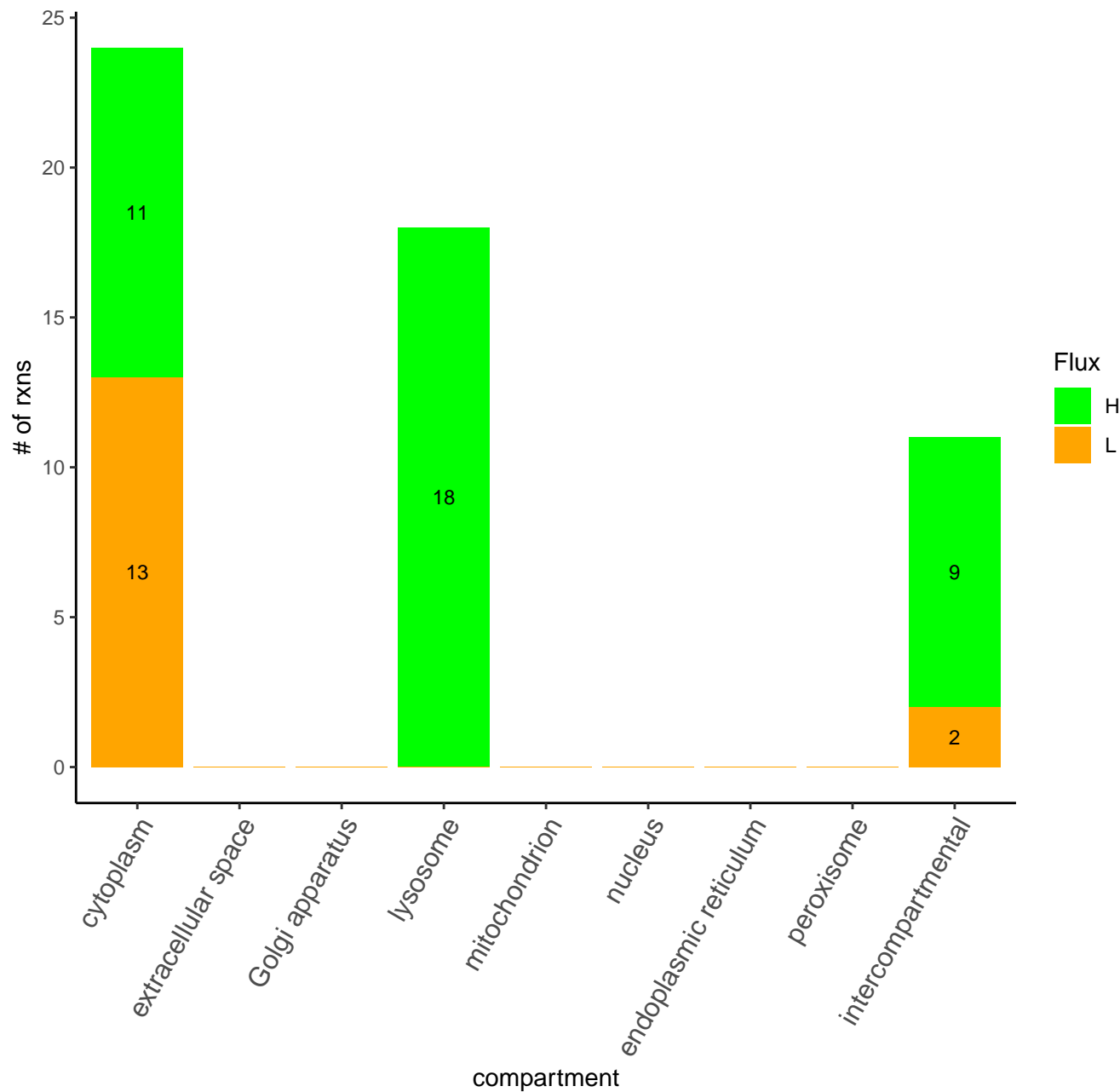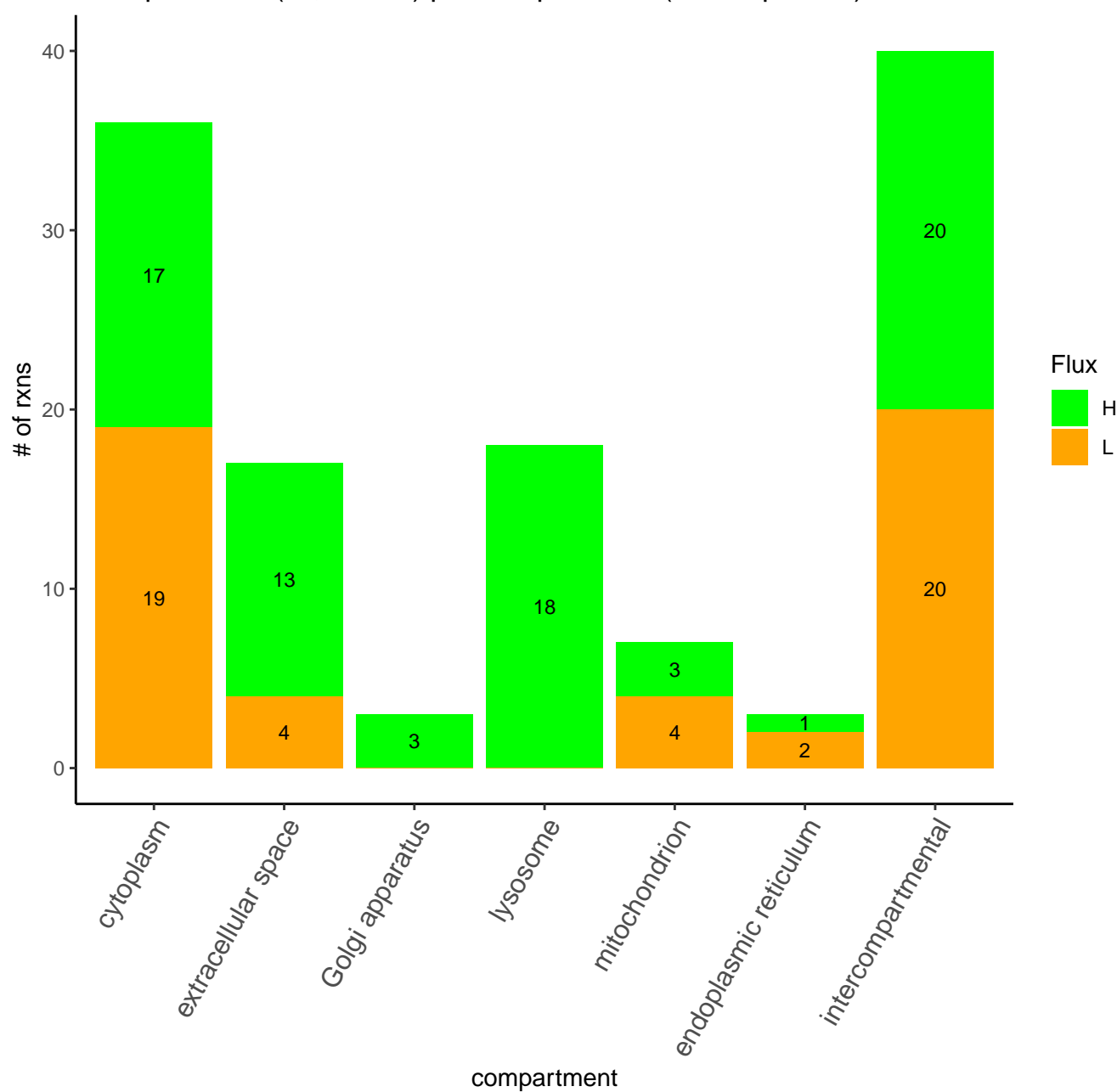
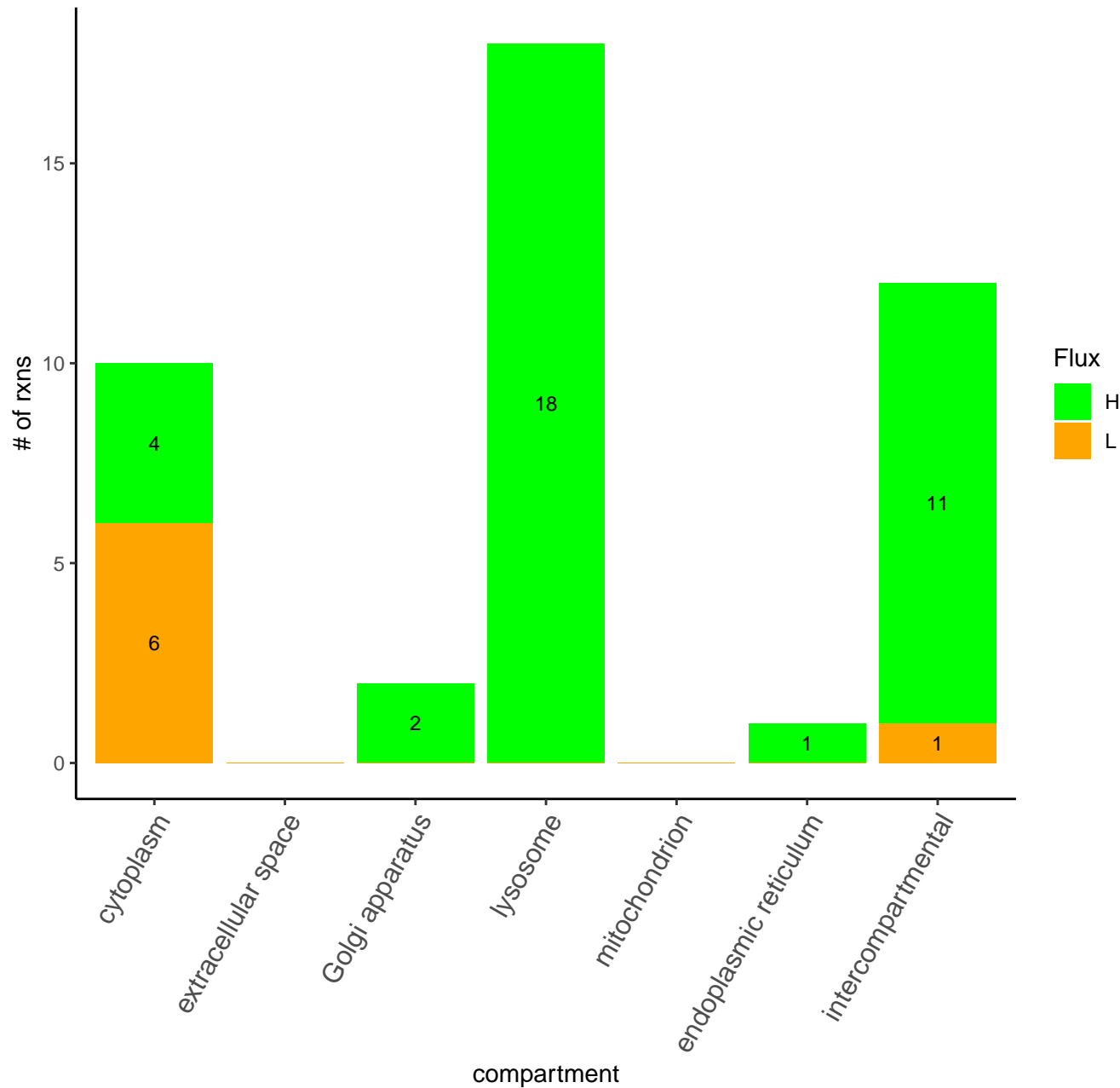Disrupted rxns (all, n=256) per compartment (bd_lumped)
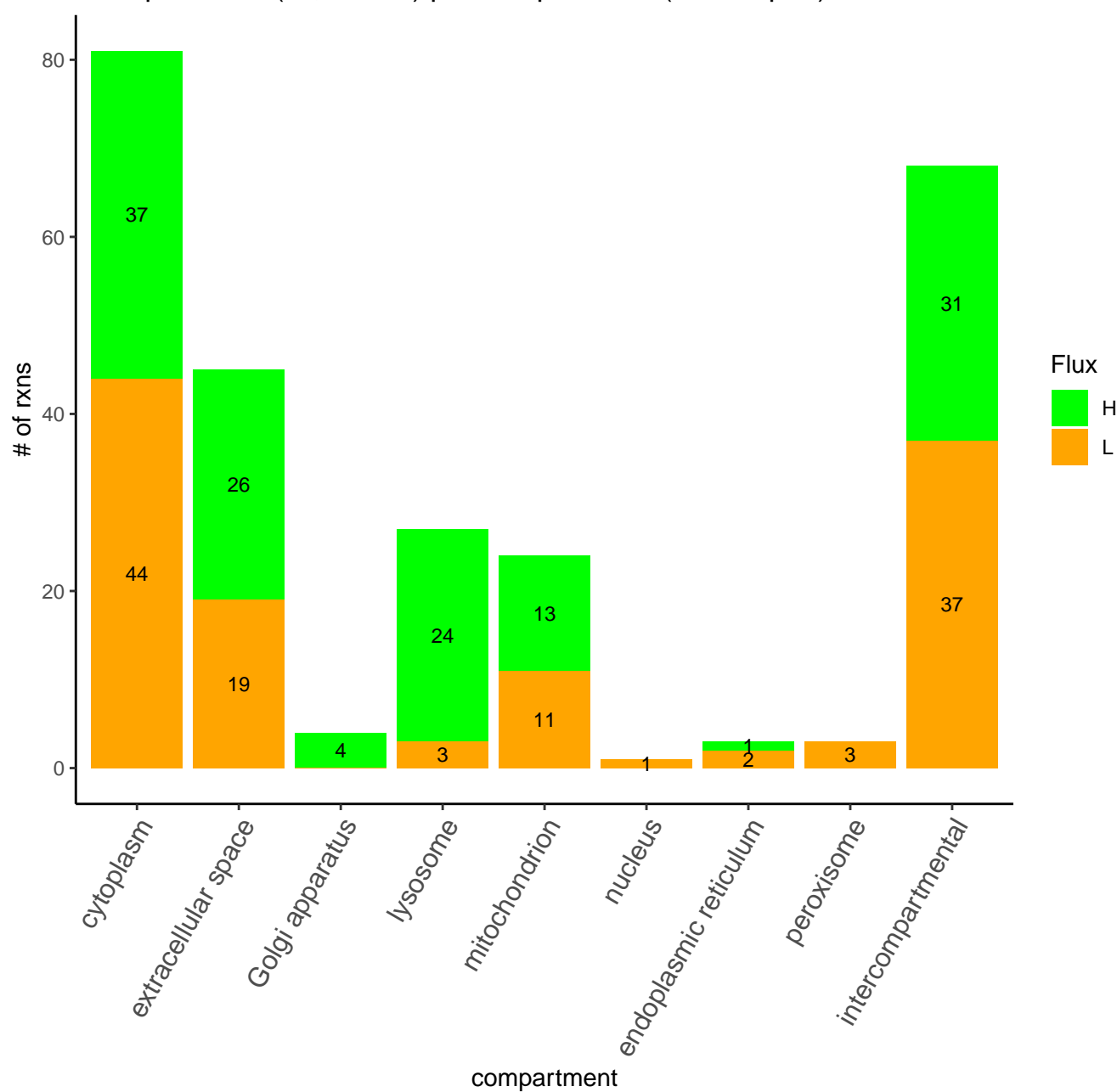
Disrupted rxns (fdr.significant, n=53) per compartment (bd_lumped)
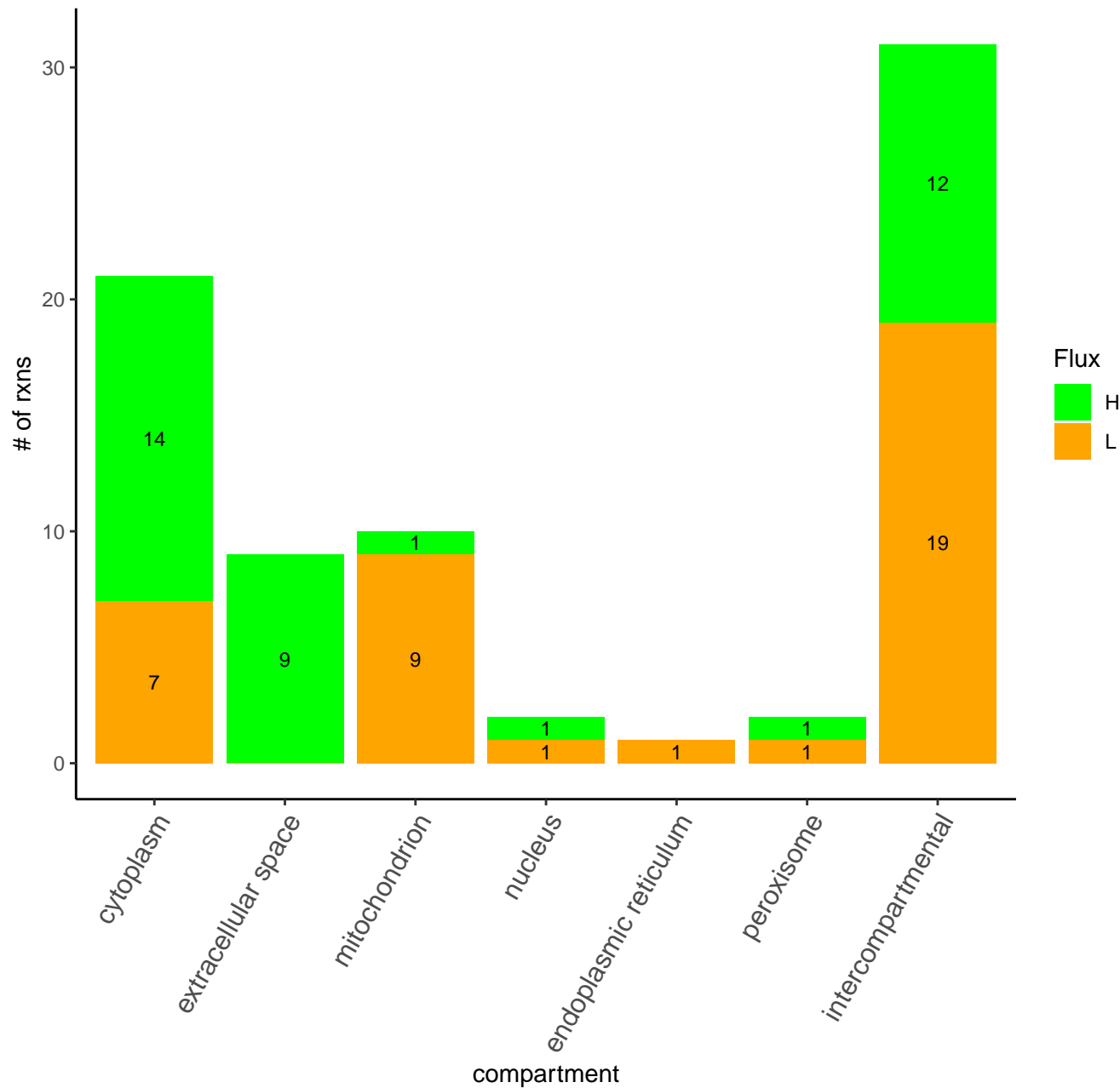
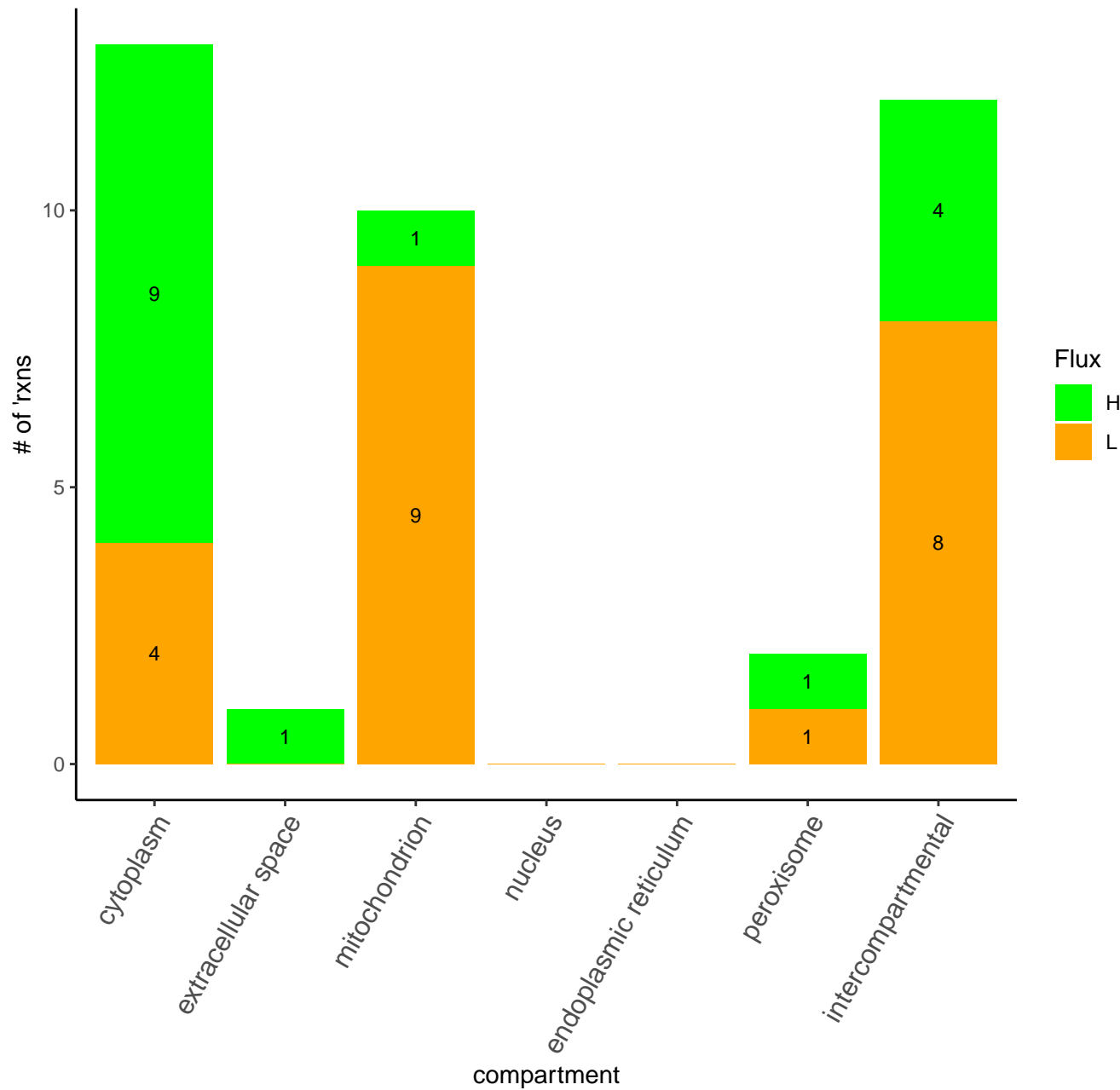Disrupted rxns (all, n=124) per compartment (bd_responder)

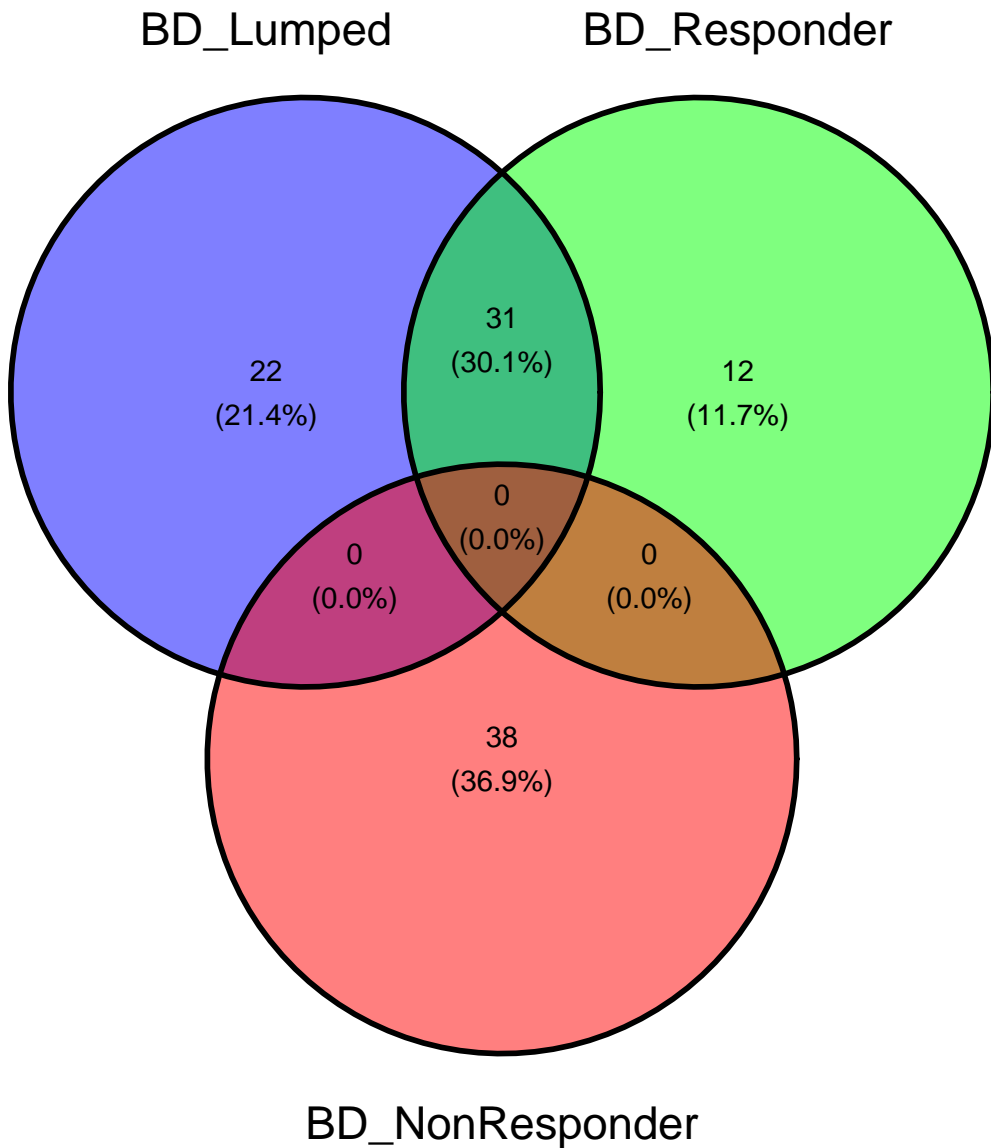Disrupted rxns (fdr.significant, n=43) per compartment (bd_responder)

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

Disrupted rxns (fdr.significant, n=38) per compartment (bd_nonresponder)

Overlp in rxns (fdr.significant) disrupted between models

Overlp in subSystems (fdr.significant) disrupted between models