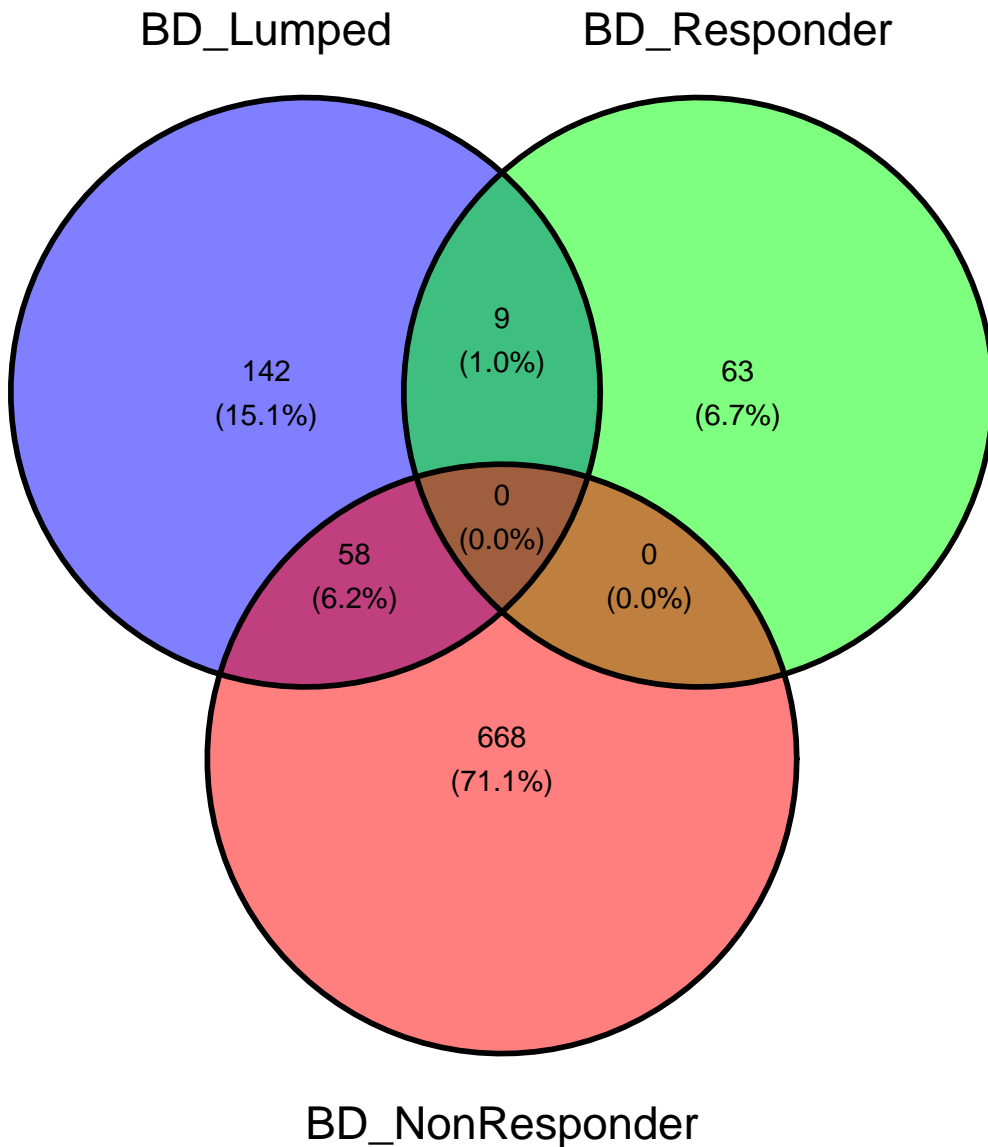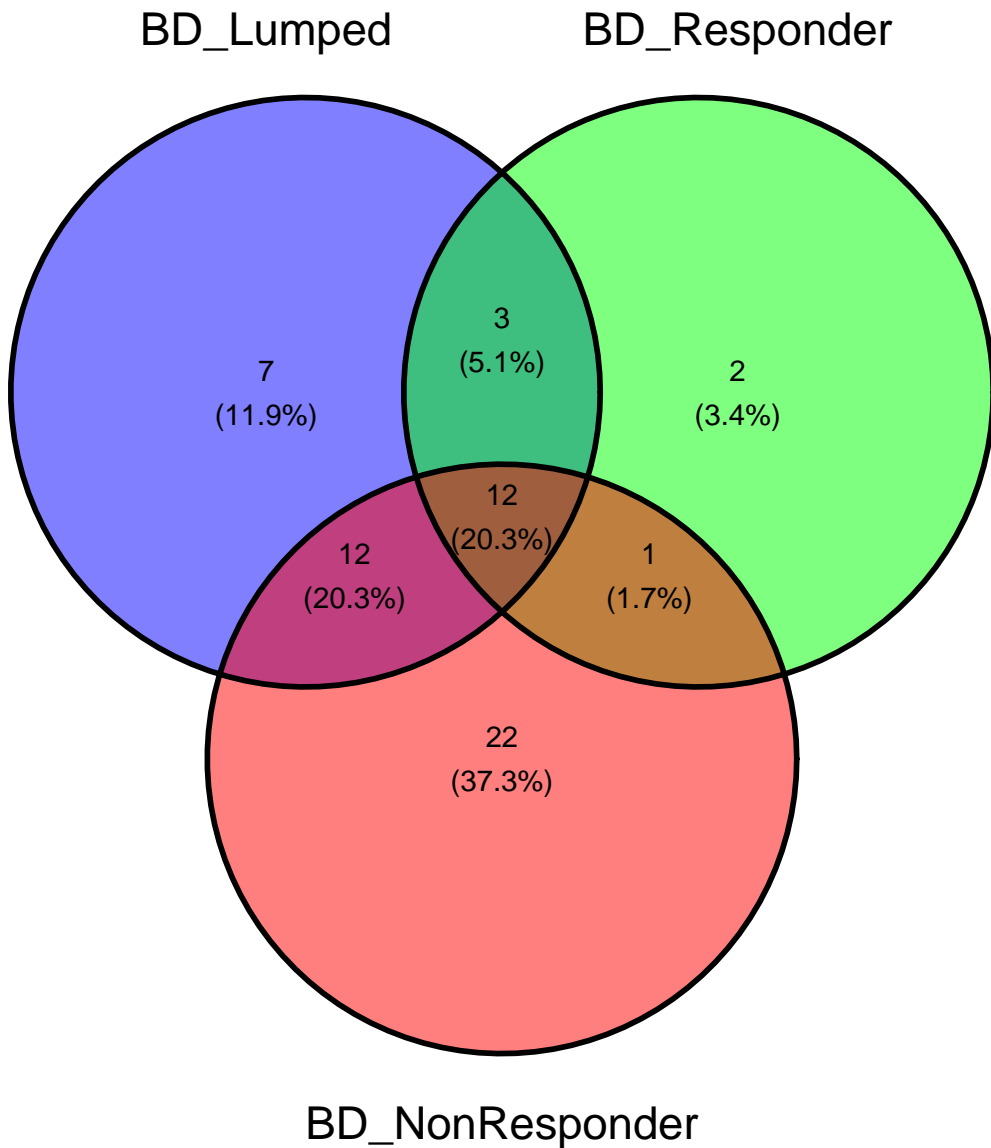Overlap in rxns disrupted between models

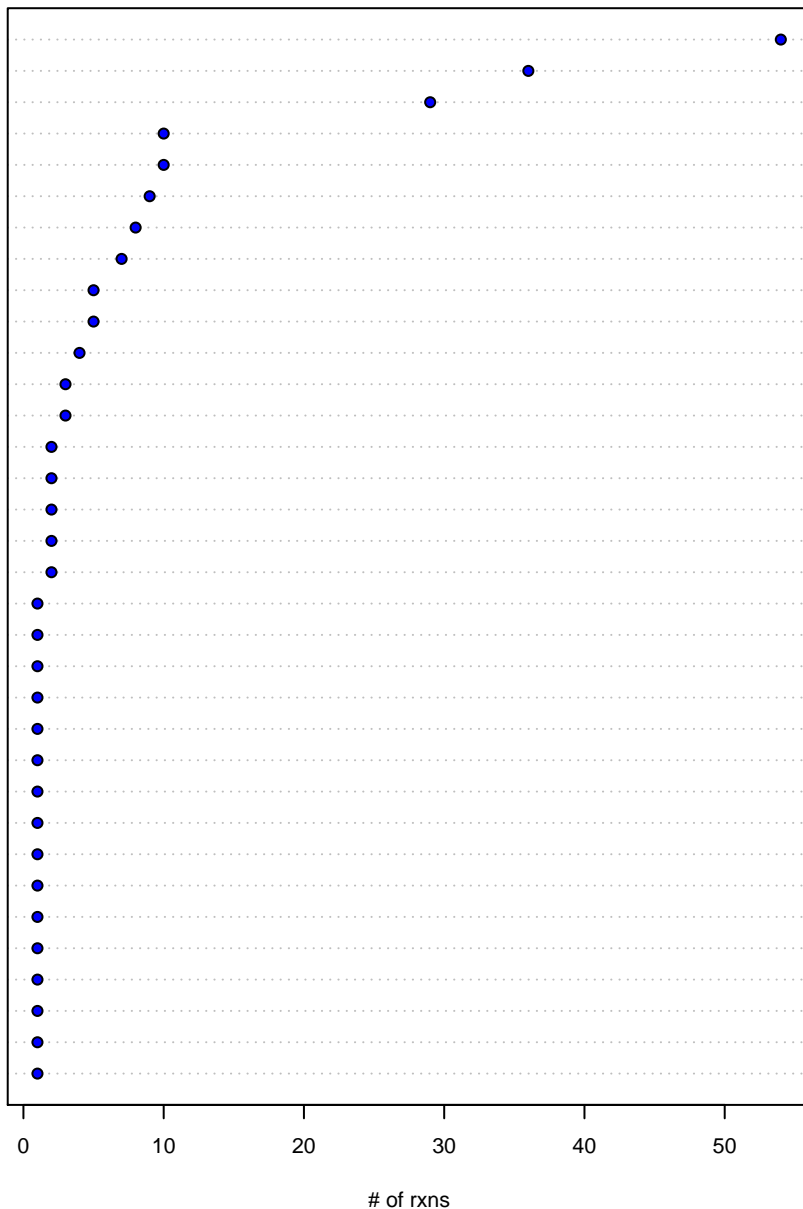Overlap in subSystems disrupted between models

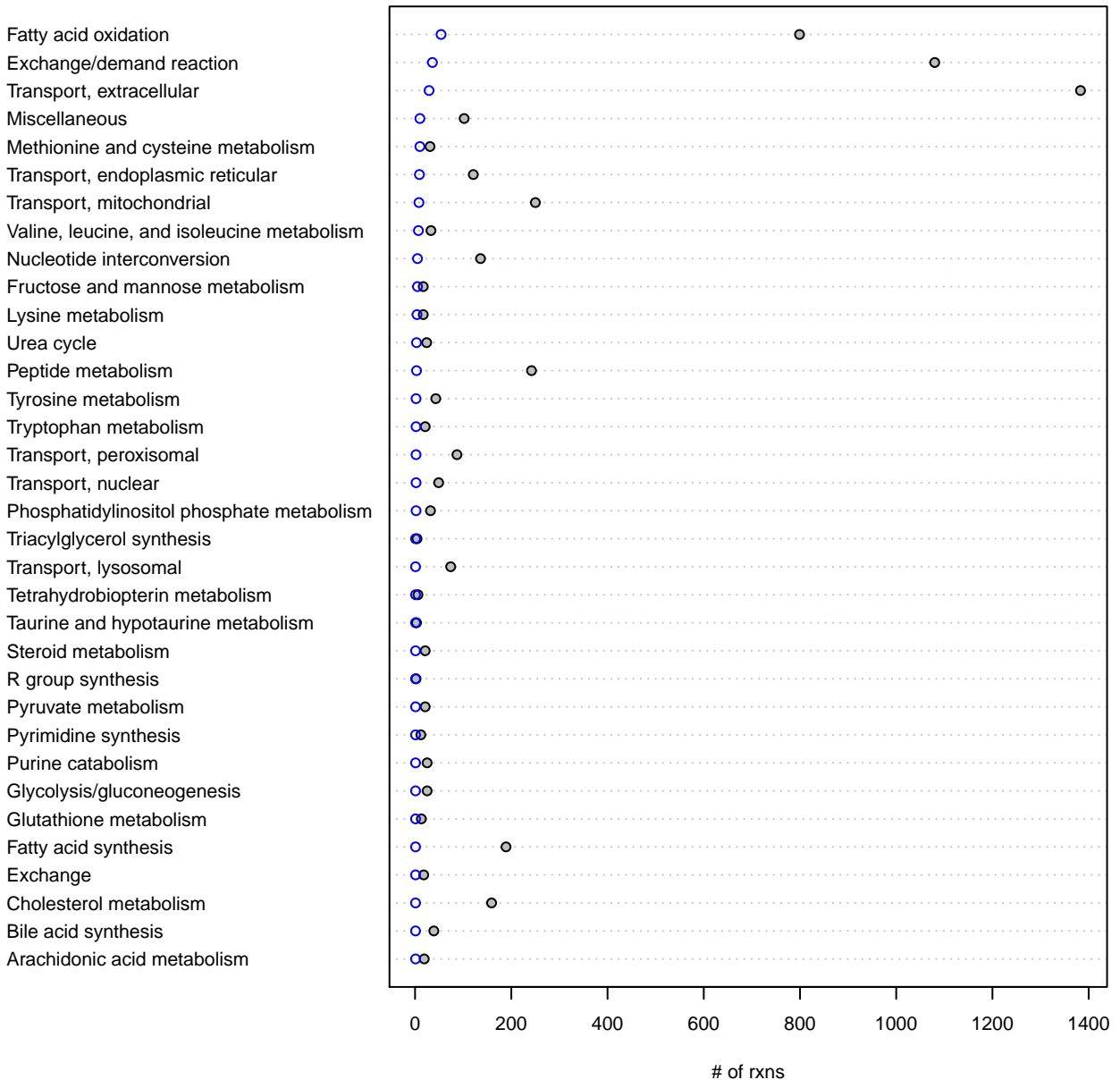**# of disrupted rxns (n=209, bd_lumped)**

Label
Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Miscellaneous
Methionine and cysteine metabolism
Transport, endoplasmic reticular
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose metabolism
Lysine metabolism
Urea cycle
Peptide metabolism
Tyrosine metabolism
Tryptophan metabolism
Transport, peroxisomal
Transport, nuclear
Phosphatidylinositol phosphate metabolism
Triacylglycerol synthesis
Transport, lysosomal
Tetrahydrobiopterin metabolism
Taurine and hypotaurine metabolism
Steroid metabolism
R group synthesis
Pyruvate metabolism
Pyrimidine synthesis
Purine catabolism
Glycolysis/gluconeogenesis
Glutathione metabolism
Fatty acid synthesis
Exchange
Cholesterol metabolism
Bile acid synthesis
Arachidonic acid metabolism

# of rxns

# of disrupted rxns (n=209, bd_lumped) vs all rxns

Fatty acid oxidation	
Exchange/demand reaction	
Transport, extracellular	
Miscellaneous	
Methionine and cysteine metabolism	
Transport, endoplasmic reticular	
Transport, mitochondrial	
Valine, leucine, and isoleucine metabolism	
Nucleotide interconversion	
Fructose and mannose metabolism	
Lysine metabolism	
Urea cycle	
Peptide metabolism	
Tyrosine metabolism	
Tryptophan metabolism	
Transport, peroxisomal	
Transport, nuclear	
Phosphatidylinositol phosphate metabolism	
Triacylglycerol synthesis	
Transport, lysosomal	
Tetrahydrobiopterin metabolism	
Taurine and hypotaurine metabolism	
Steroid metabolism	
R group synthesis	
Pyruvate metabolism	
Pyrimidine synthesis	
Purine catabolism	
Glycolysis/gluconeogenesis	
Glutathione metabolism	
Fatty acid synthesis	
Exchange	
Cholesterol metabolism	
Bile acid synthesis	
Arachidonic acid metabolism	

# of rxns

over−representation analysis, bd_lumped

# of disrupted rxns (n=72, bd_responder)

Metabolic category	# of rxns
Fatty acid oxidation	30
Transport, extracellular	6
Transport, endoplasmic reticular	6
Exchange/demand reaction	6
Transport, nuclear	3
Nucleotide interconversion	3
Vitamin A metabolism	2
Transport, peroxisomal	2
Transport, mitochondrial	2
Purine catabolism	2
Miscellaneous	2
Methionine and cysteine metabolism	2
Tyrosine metabolism	1
Steroid metabolism	1
Pyrimidine synthesis	1
Exchange	1
Eicosanoid metabolism	1
Beta−Alanine metabolism	1

# of rxns

# of disrupted rxns (n=72, bd_responder) vs all rxns

Fatty acid oxidation

Transport, extracellular

Transport, endoplasmic reticular

Exchange/demand reaction

Transport, nuclear

Nucleotide interconversion

Vitamin A metabolism

Transport, peroxisomal

Transport, mitochondrial

Purine catabolism

Miscellaneous

Methionine and cysteine metabolism

Tyrosine metabolism

Steroid metabolism

Pyrimidine synthesis

Exchange

Eicosanoid metabolism

Beta−Alanine metabolism

0   200   400   600   800   1000   1200   1400
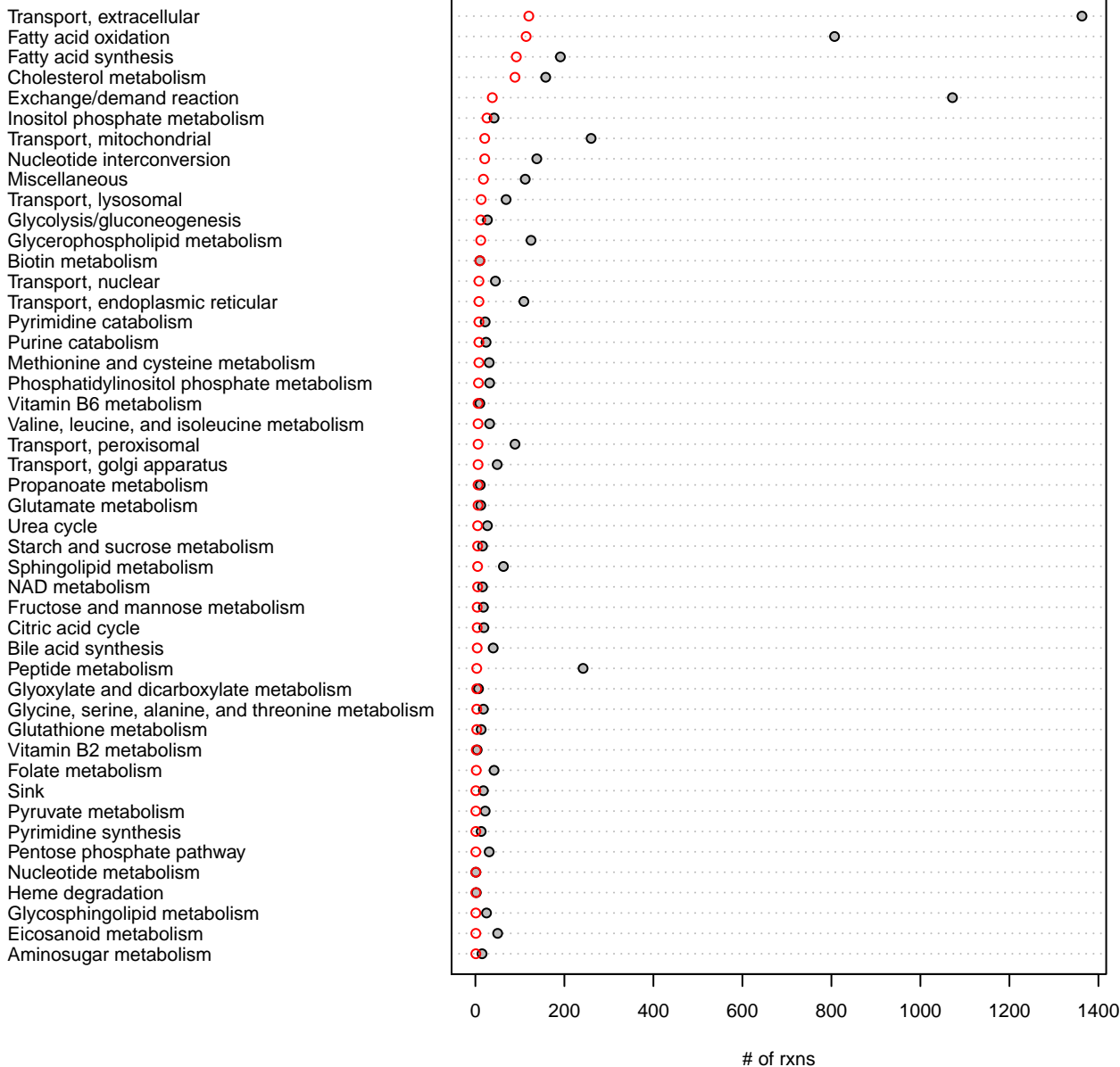
# of rxns

over−representation analysis, bd_responder
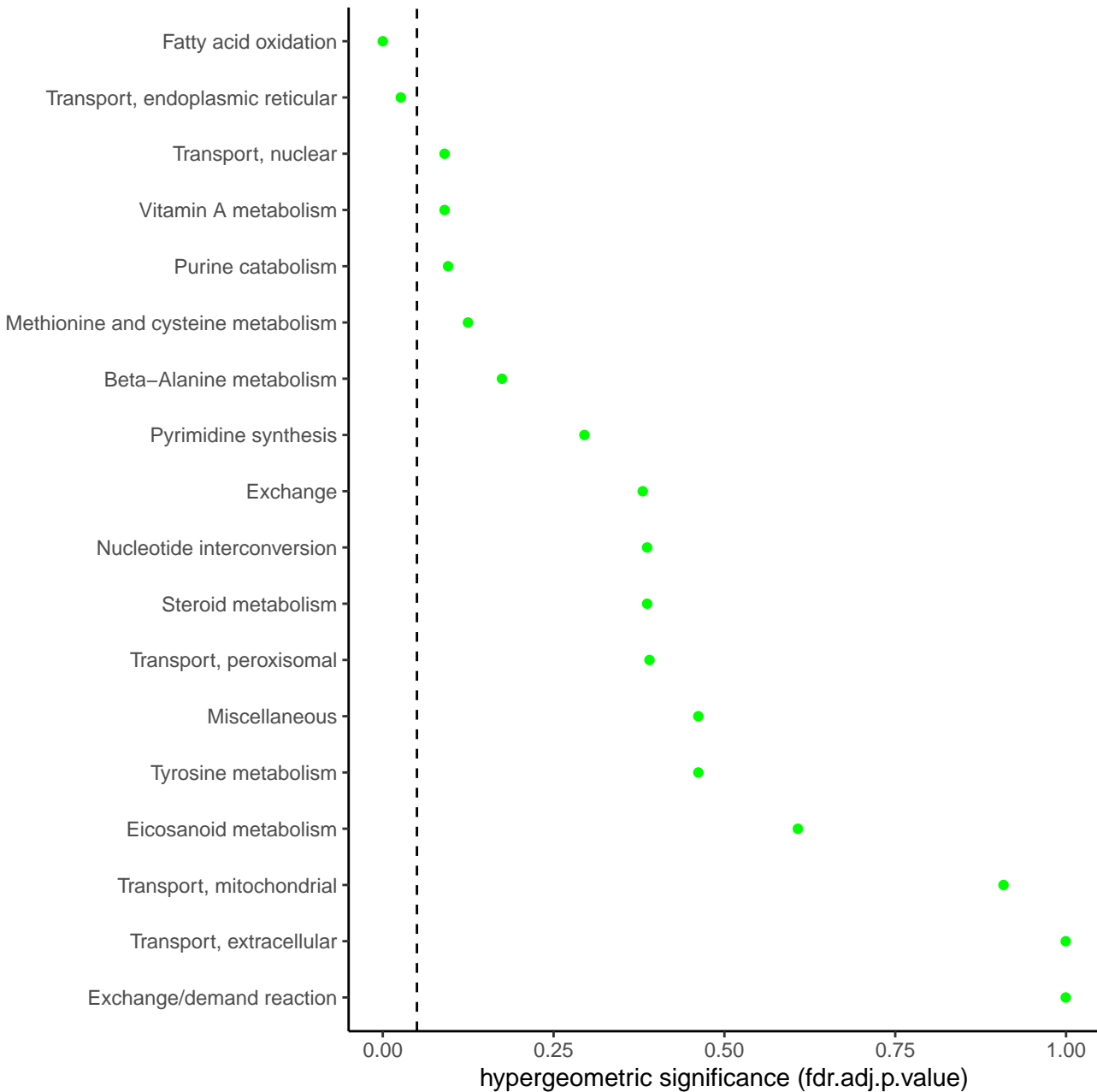
# of disrupted rxns (n=726, bd_nonresponder)

Transport, extracellular
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Exchange/demand reaction
Inositol phosphate metabolism
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Biotin metabolism
Transport, nuclear
Transport, endoplasmic reticular
Pyrimidine catabolism
Purine catabolism
Methionine and cysteine metabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Valine, leucine, and isoleucine metabolism
Transport, peroxisomal
Transport, golgi apparatus
Propanoate metabolism
Glutamate metabolism
Urea cycle
Starch and sucrose metabolism
Sphingolipid metabolism
NAD metabolism
Fructose and mannose metabolism
Citric acid cycle
Bile acid synthesis
Peptide metabolism
Glyoxylate and dicarboxylate metabolism
Glycine, serine, alanine, and threonine metabolism
Glutathione metabolism
Vitamin B2 metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Eicosanoid metabolism
Aminosugar metabolism

# of rxns

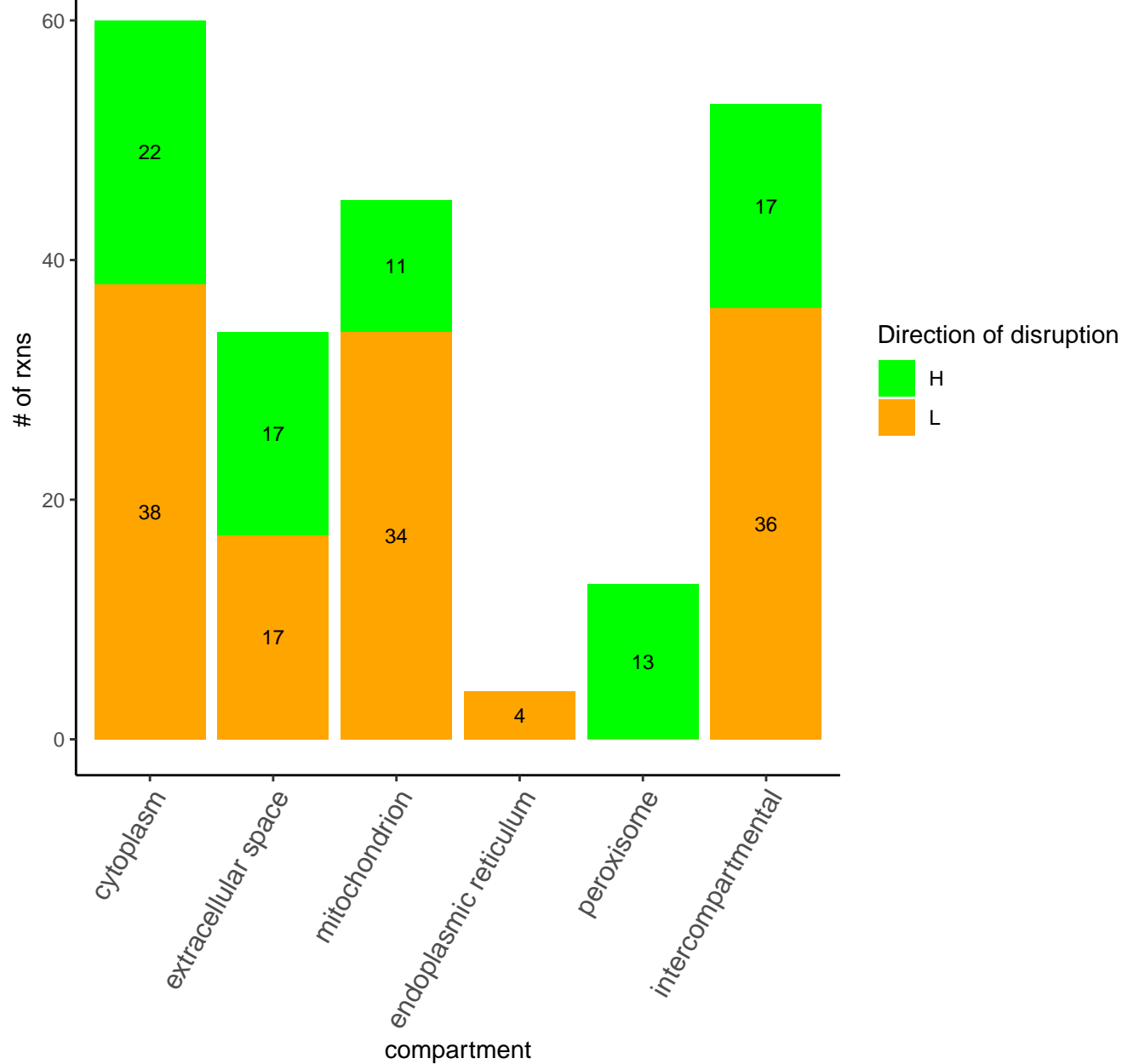**# of disrupted rxns (n=726, bd_nonresponder) vs all rxns**

Transport, extracellular
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Exchange/demand reaction
Inositol phosphate metabolism
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Biotin metabolism
Transport, nuclear
Transport, endoplasmic reticular
Pyrimidine catabolism
Purine catabolism
Methionine and cysteine metabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Valine, leucine, and isoleucine metabolism
Transport, peroxisomal
Transport, golgi apparatus
Propanoate metabolism
Glutamate metabolism
Urea cycle
Starch and sucrose metabolism
Sphingolipid metabolism
NAD metabolism
Fructose and mannose metabolism
Citric acid cycle
Bile acid synthesis
Peptide metabolism
Glyoxylate and dicarboxylate metabolism
Glycine, serine, alanine, and threonine metabolism
Glutathione metabolism
Vitamin B2 metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Eicosanoid metabolism
Aminosugar metabolism

0   200   400   600   800   1000   1200   1400
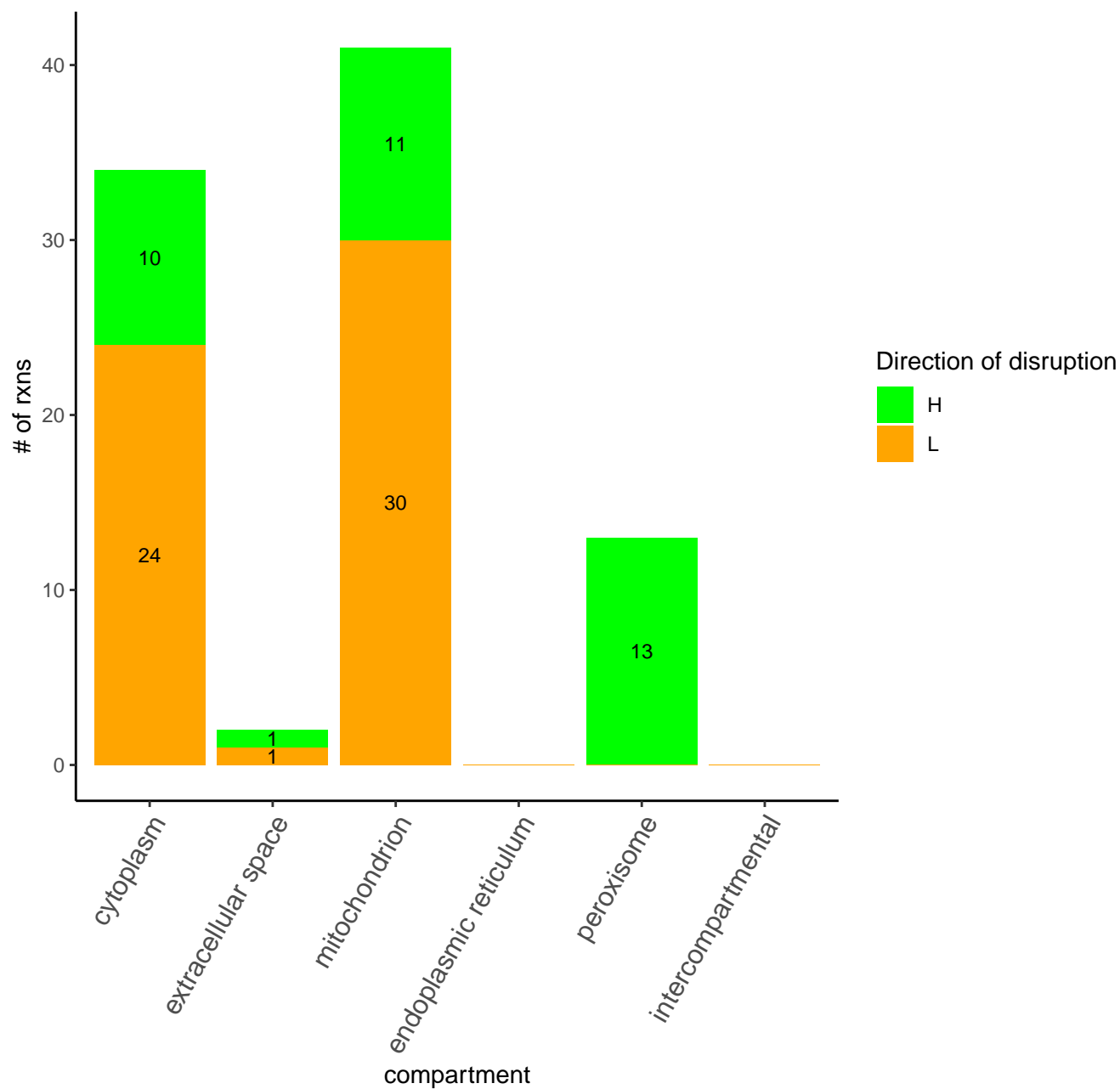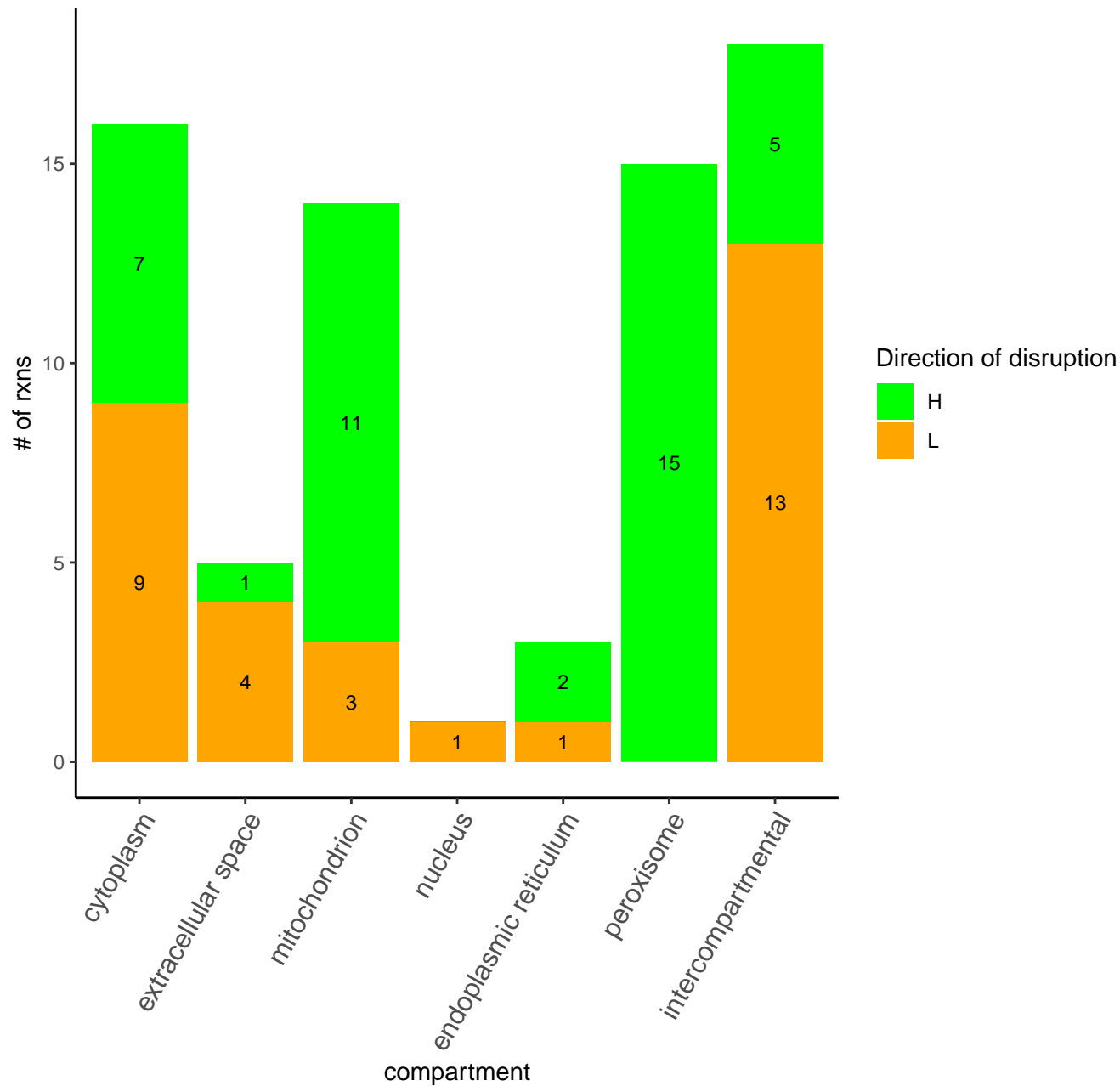
# of rxns

over−representation analysis, bd_nonresponder
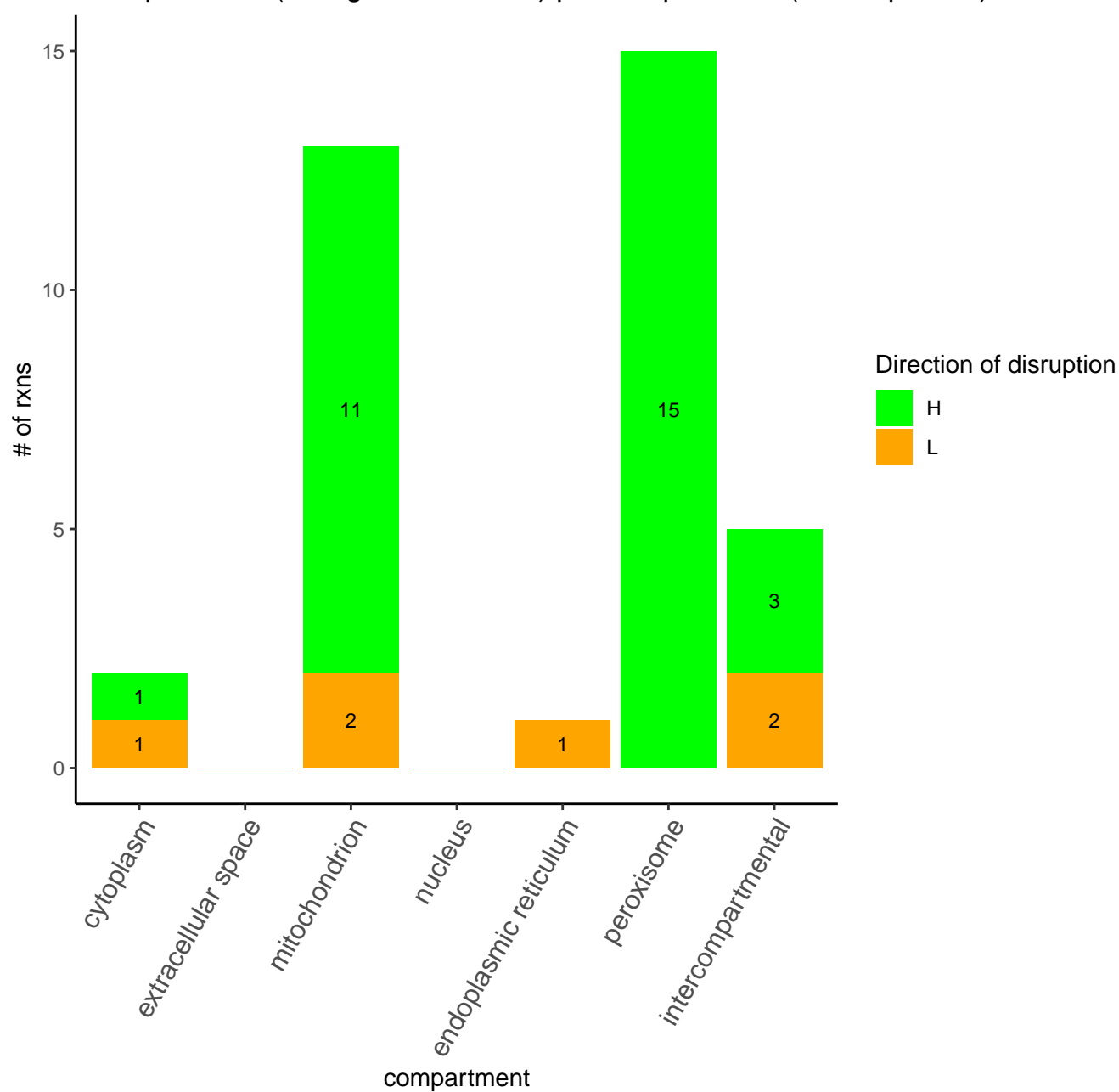
Disrupted rxns (all, n=209) per compartment (bd_lumped)

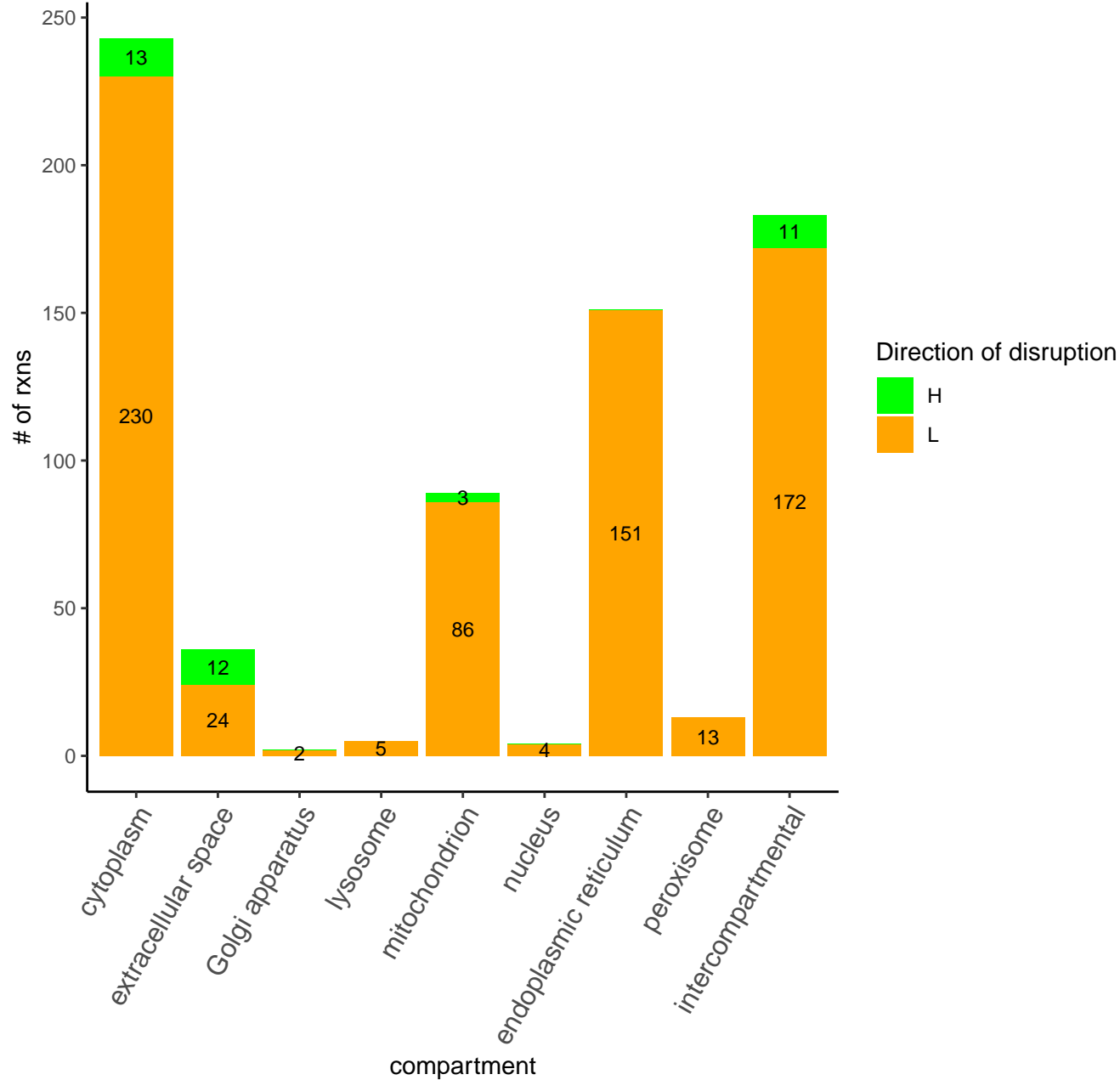Disrupted rxns (fdr.significant, n=90) per compartment (bd_lumped)

Disrupted rxns (all, n=72) per compartment (bd_responder)

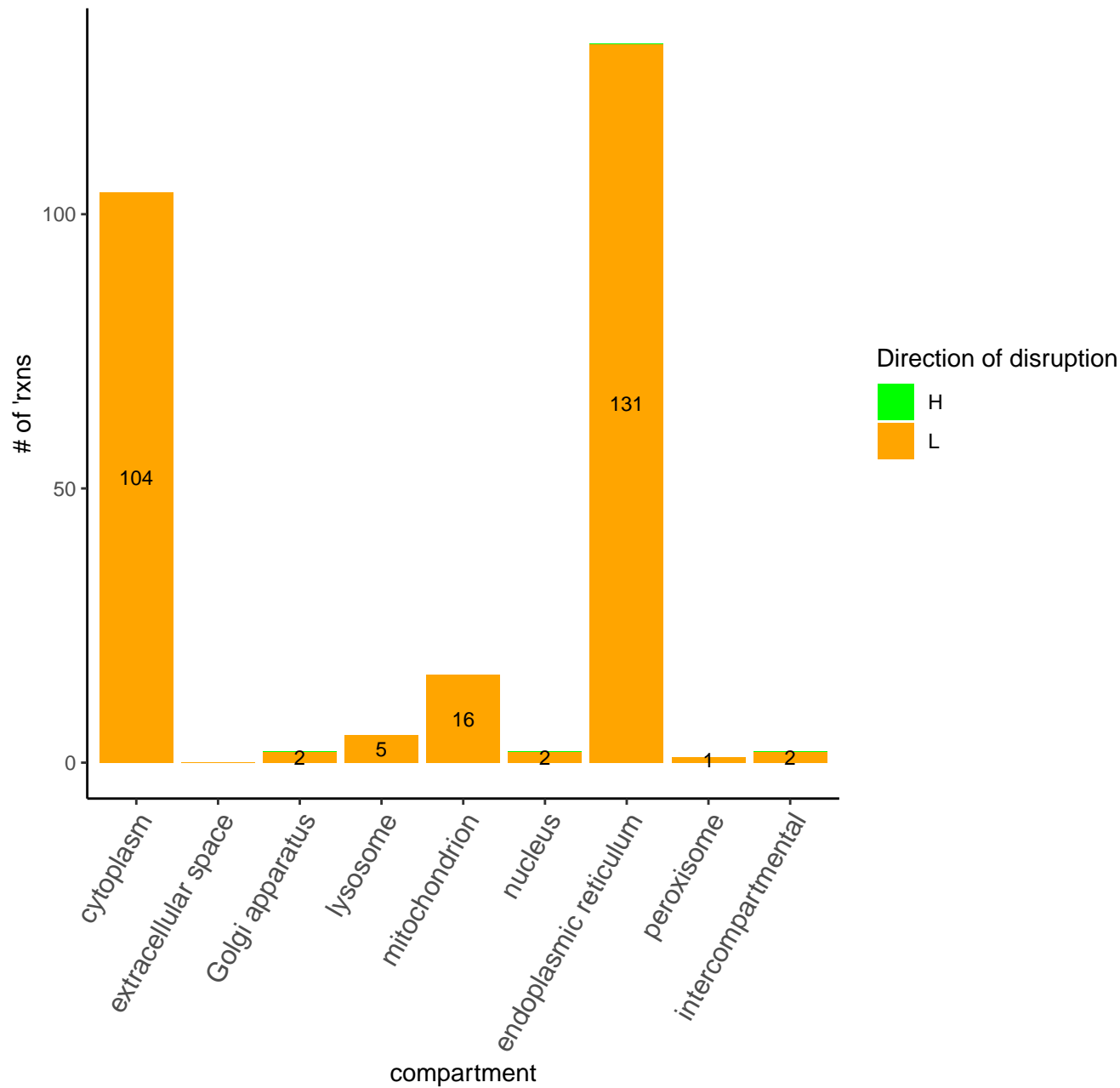Disrupted rxns (fdr.significant, n=36) per compartment (bd_responder)

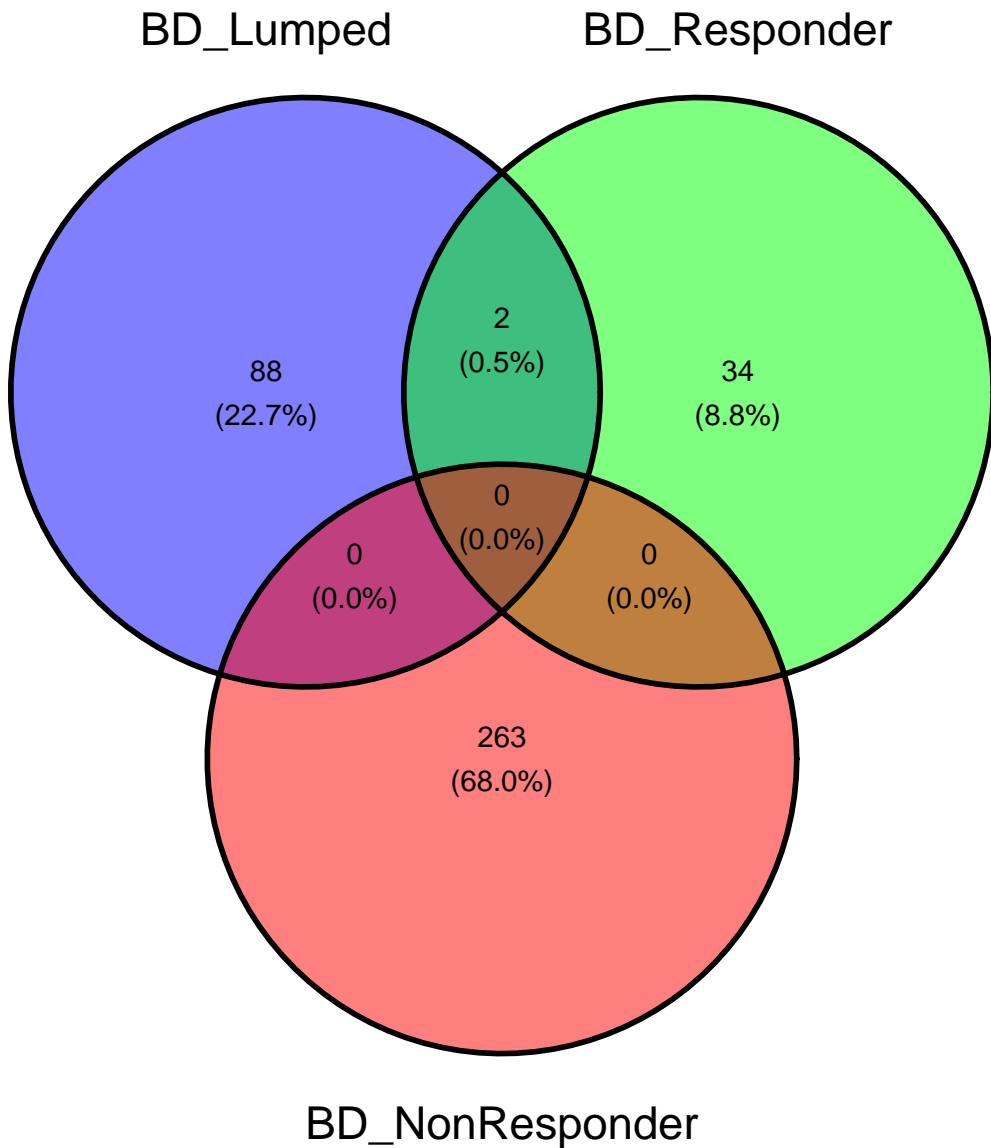Disrupted rxns (all, n=726) per compartment (bd_nonresponder)

Disrupted rxns (fdr.significant, n=263) per compartment (bd_nonresponder)

Overlp in rxns (fdr.significant) disrupted between models

Overlp in subSystems (fdr.significant) disrupted between models