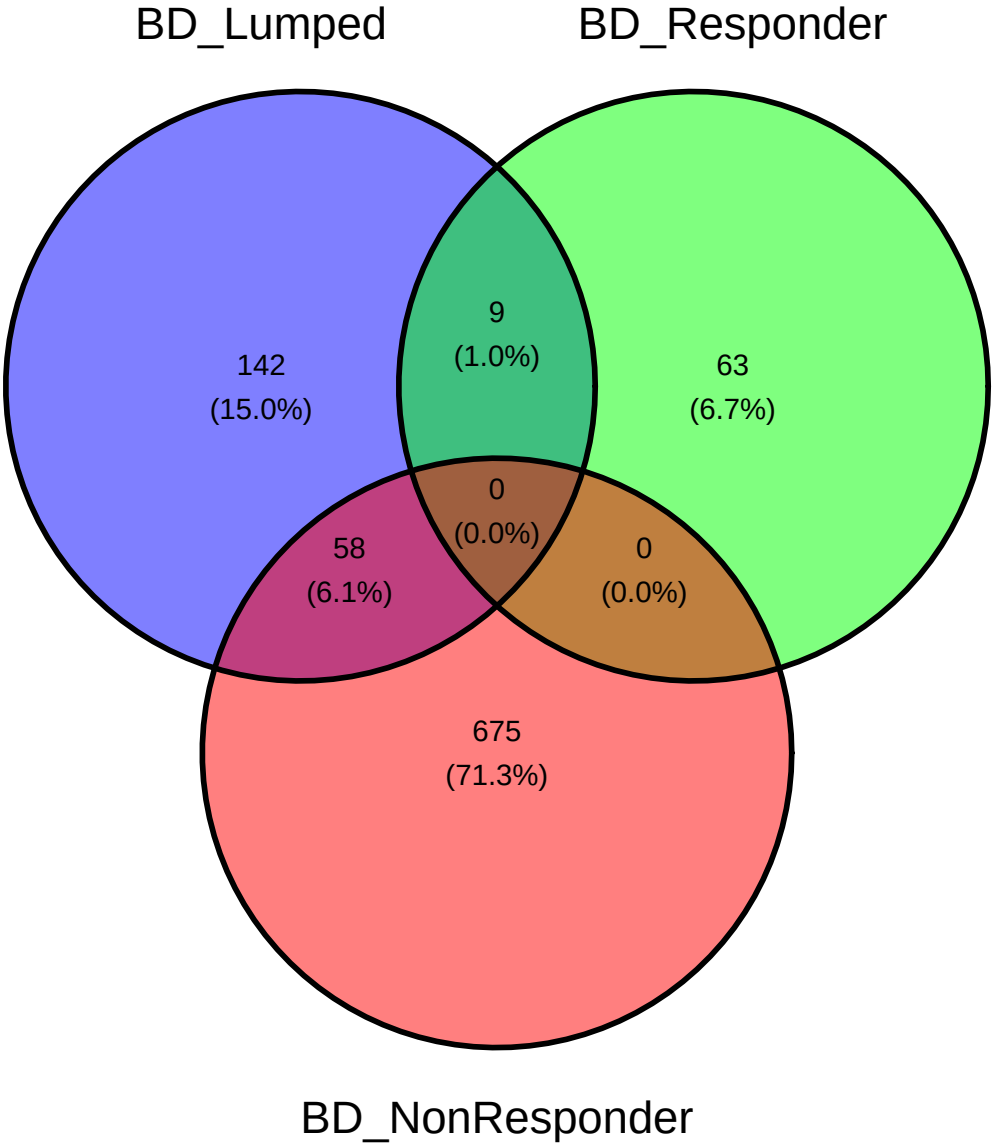
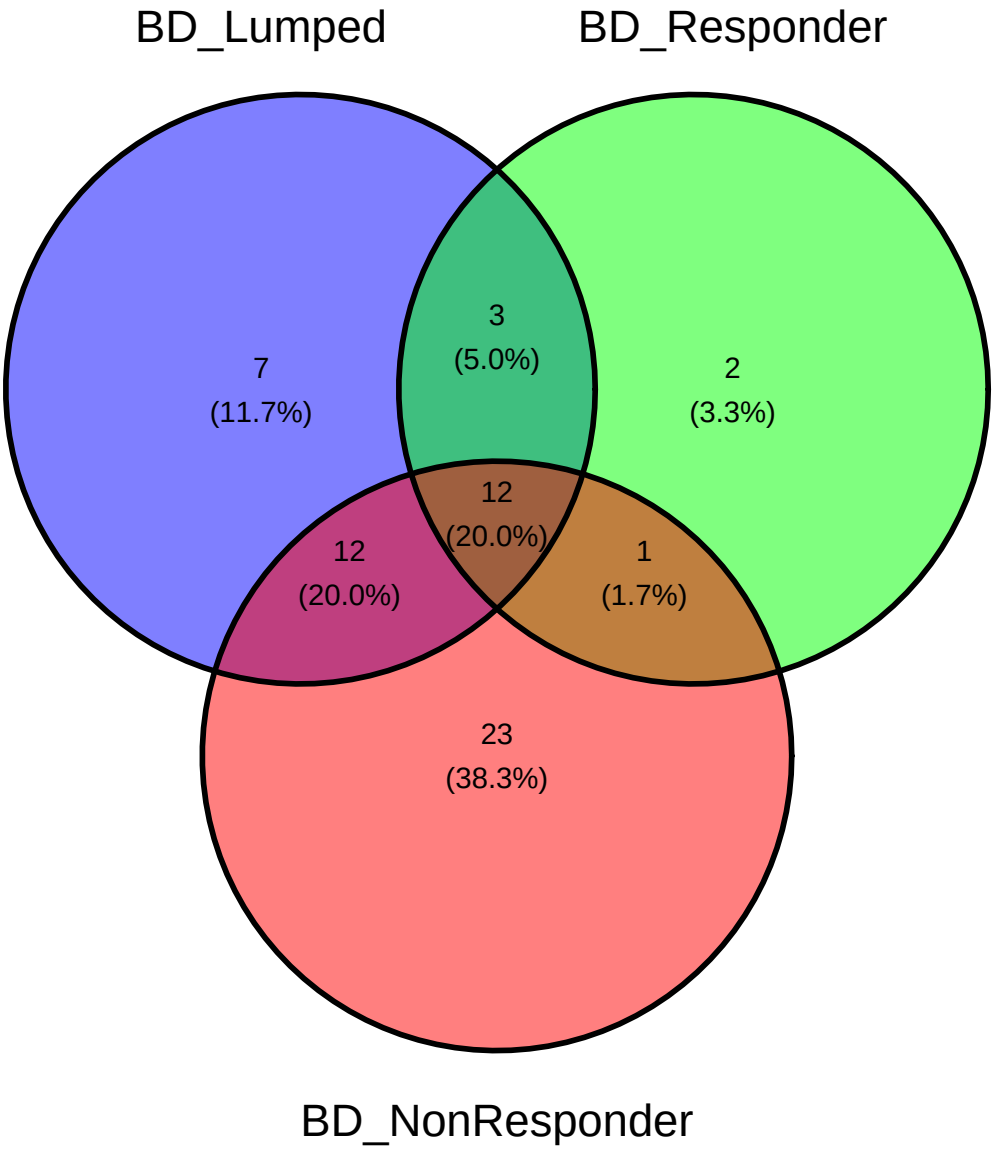
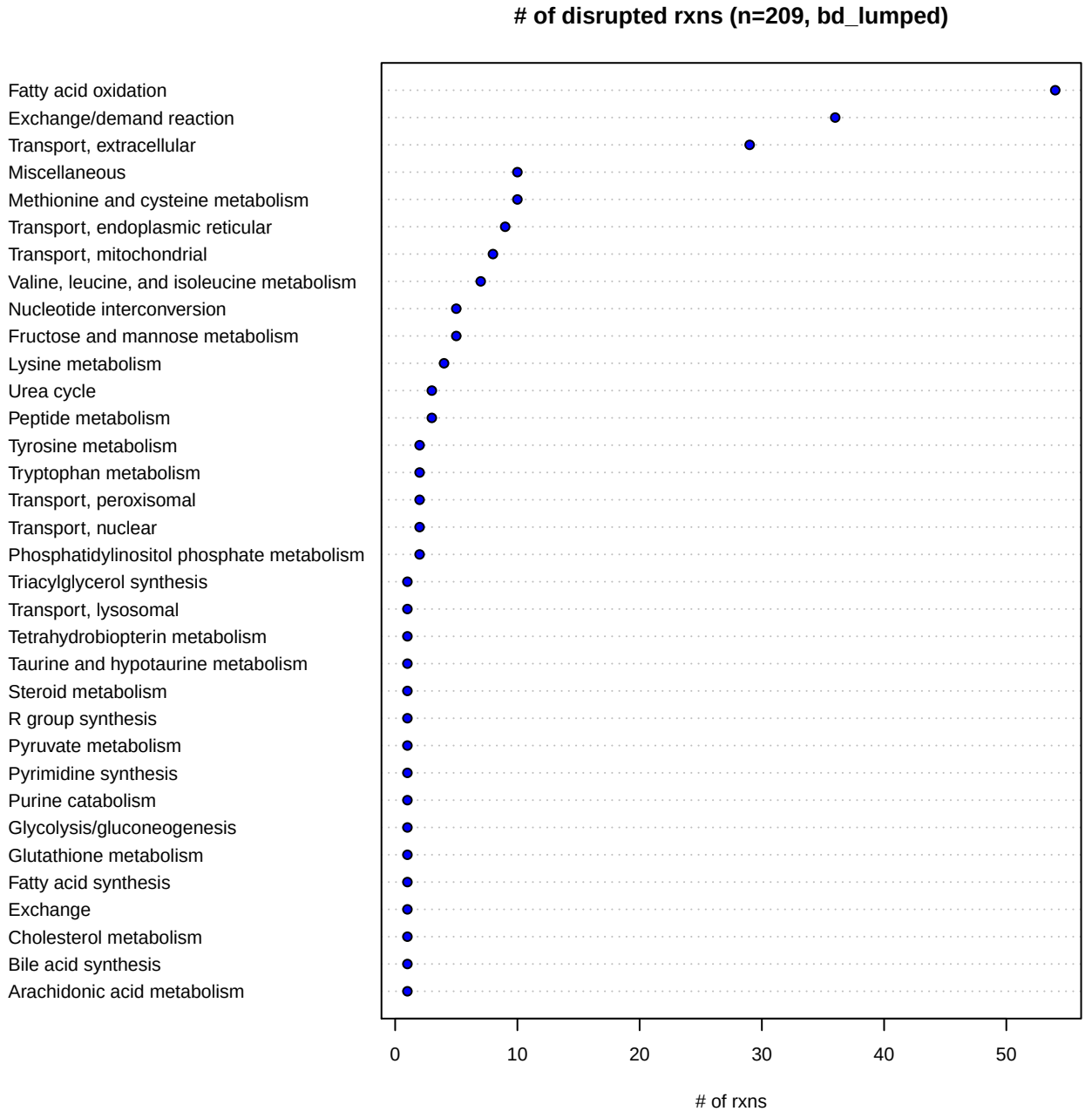
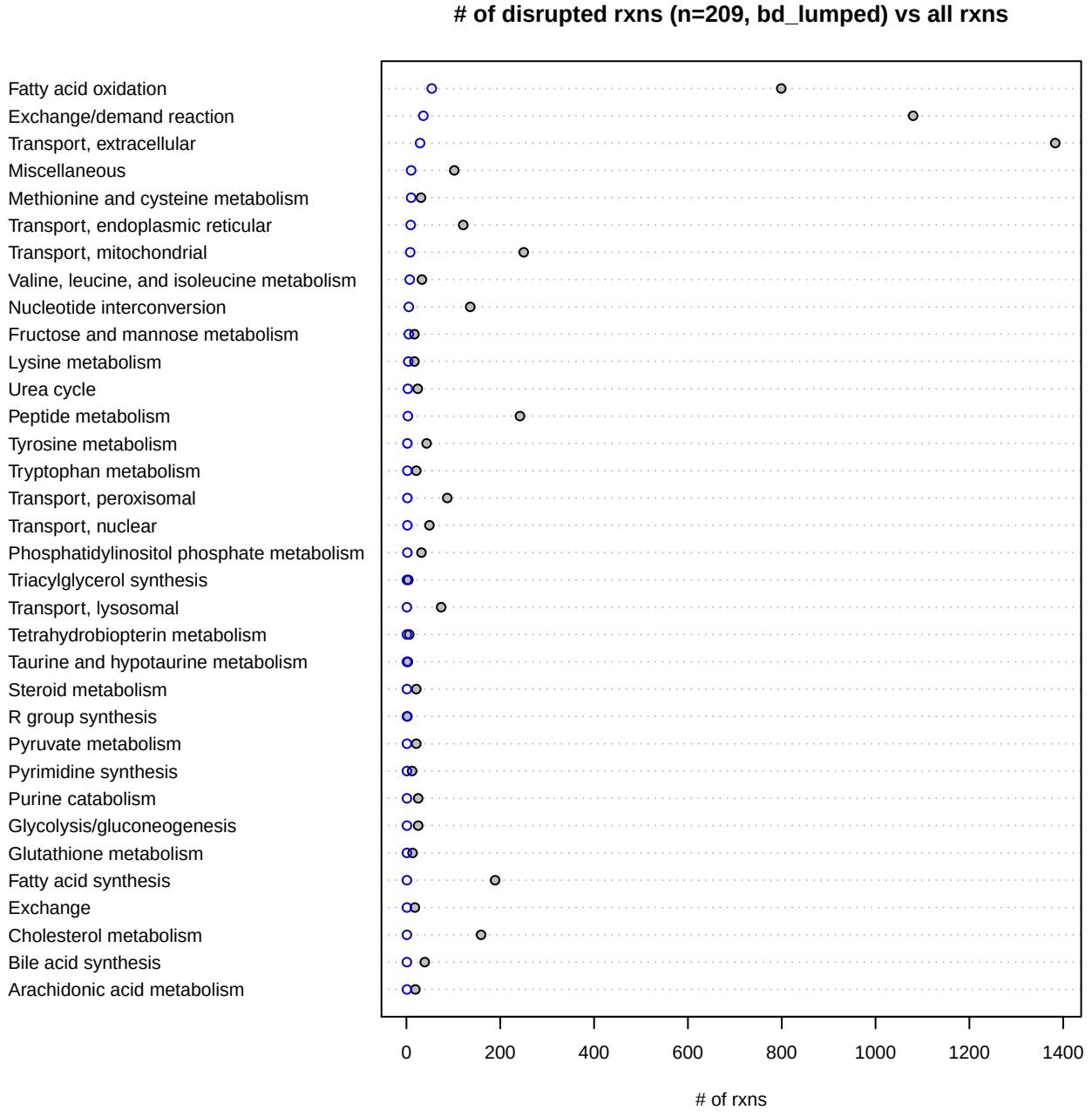
Overlap in rxns disrupted between models

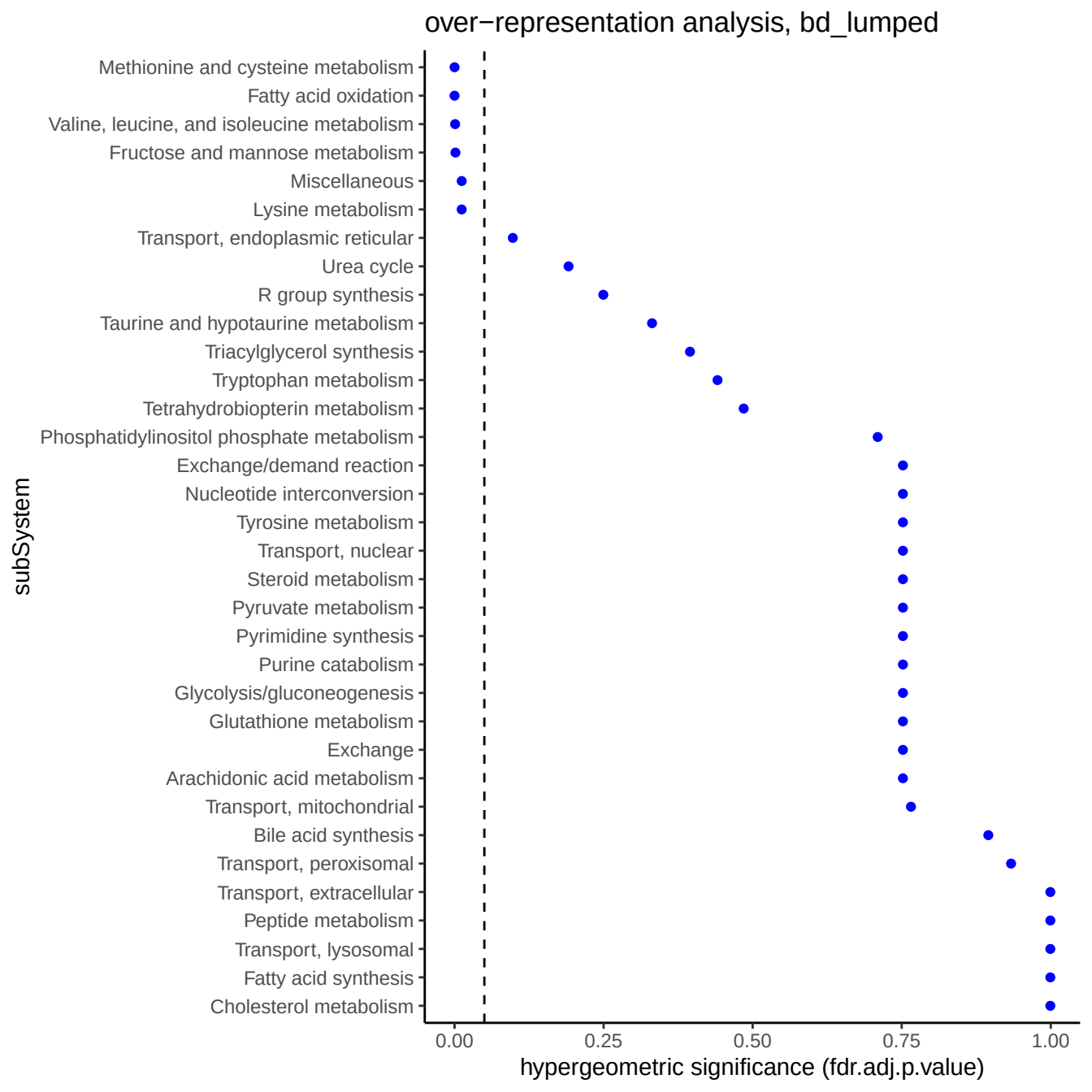


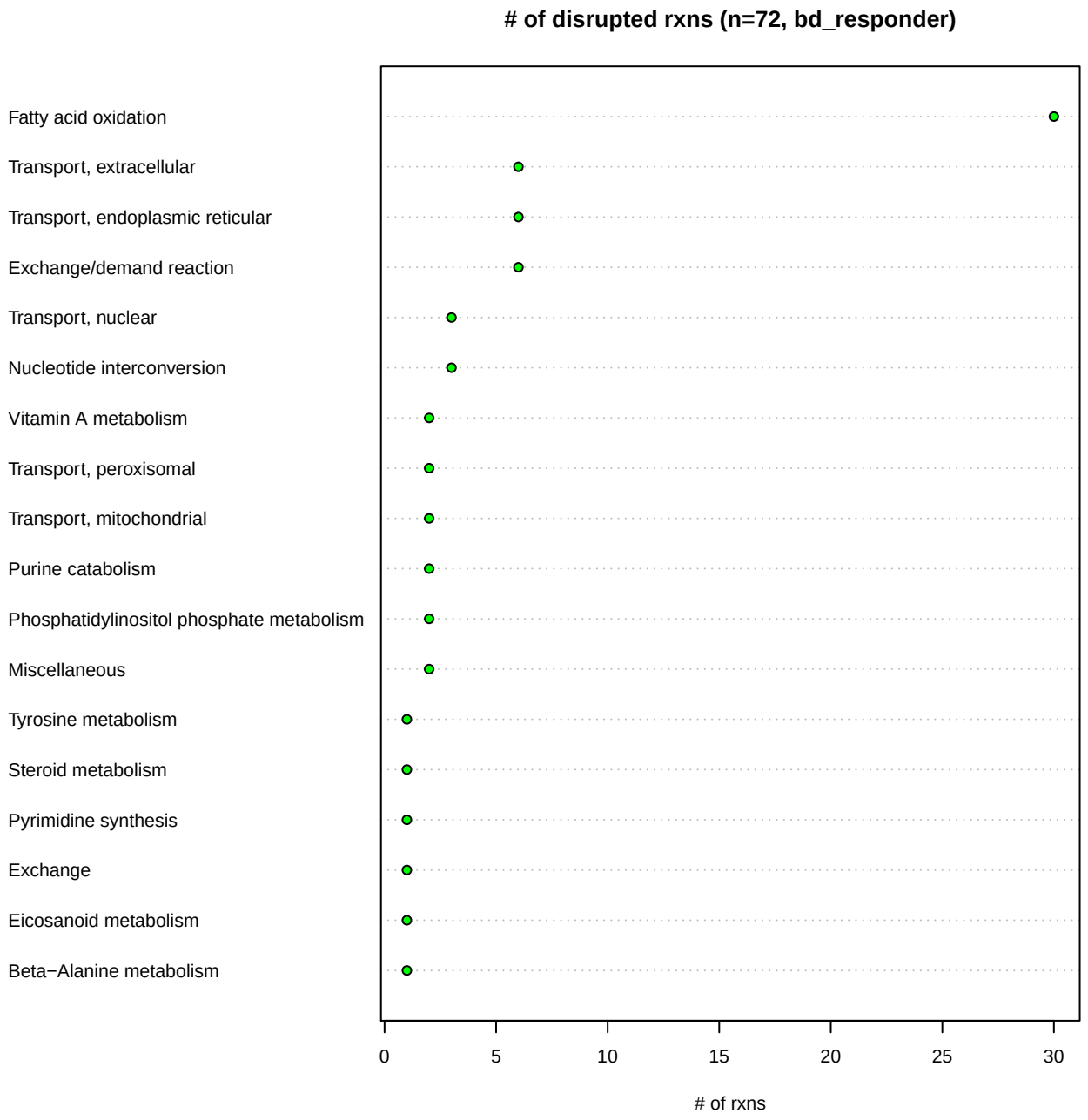
Overlap in subSystems disrupted between models

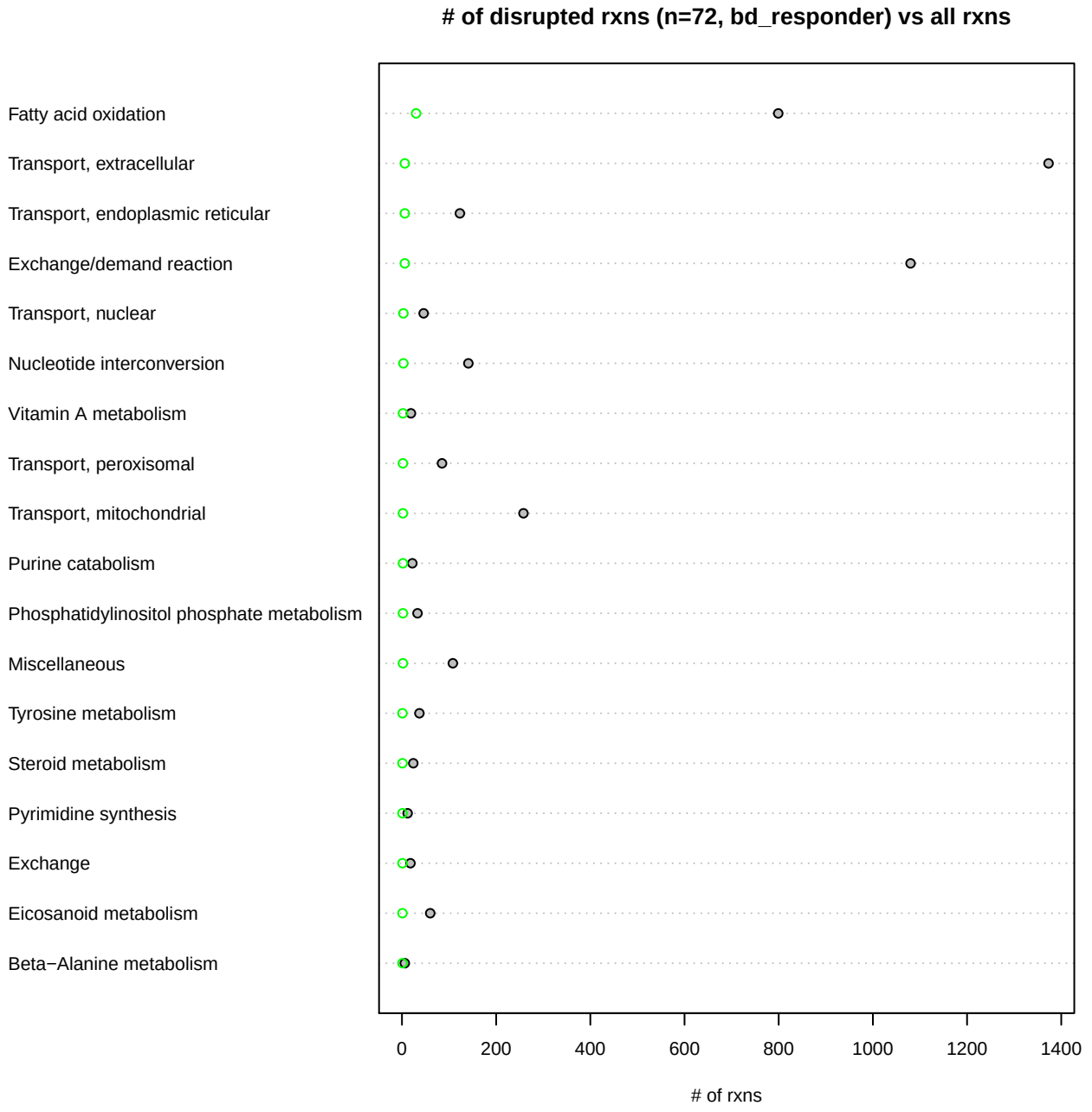


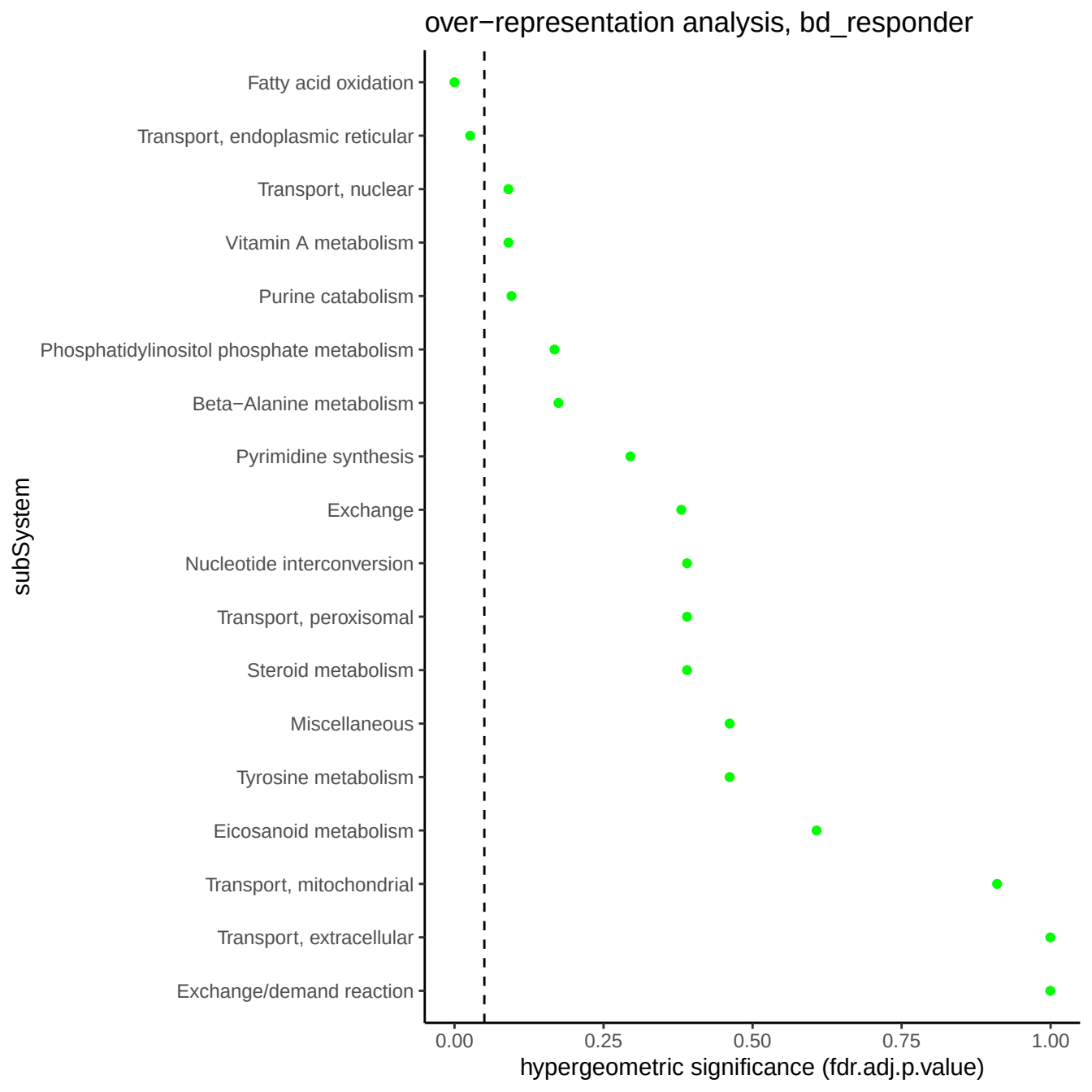

# of disrupted rxns (n=209, bd_lumped)
Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Miscellaneous
Methionine and cysteine metabolism
Transport, endoplasmic reticular
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose 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
0
10
20
30
40
50
# of rxns

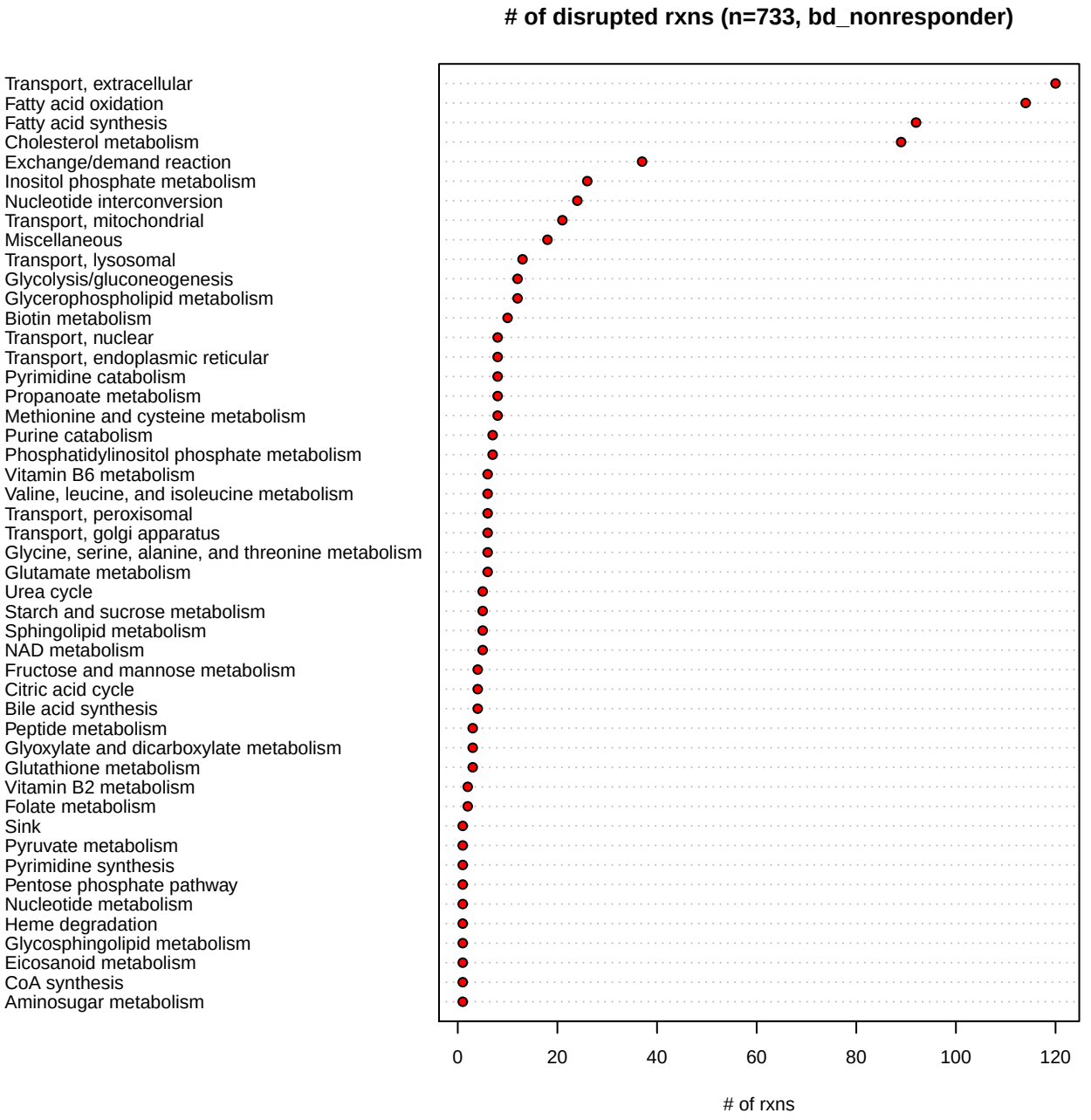

# of disrupted rxns (n=209, bd_lumped) vs all rxns
Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Miscellaneous
Methionine and cysteine metabolism
Transport, endoplasmic reticular
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose 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
0
200
400
600
800
1000
1200
1400
# of rxns

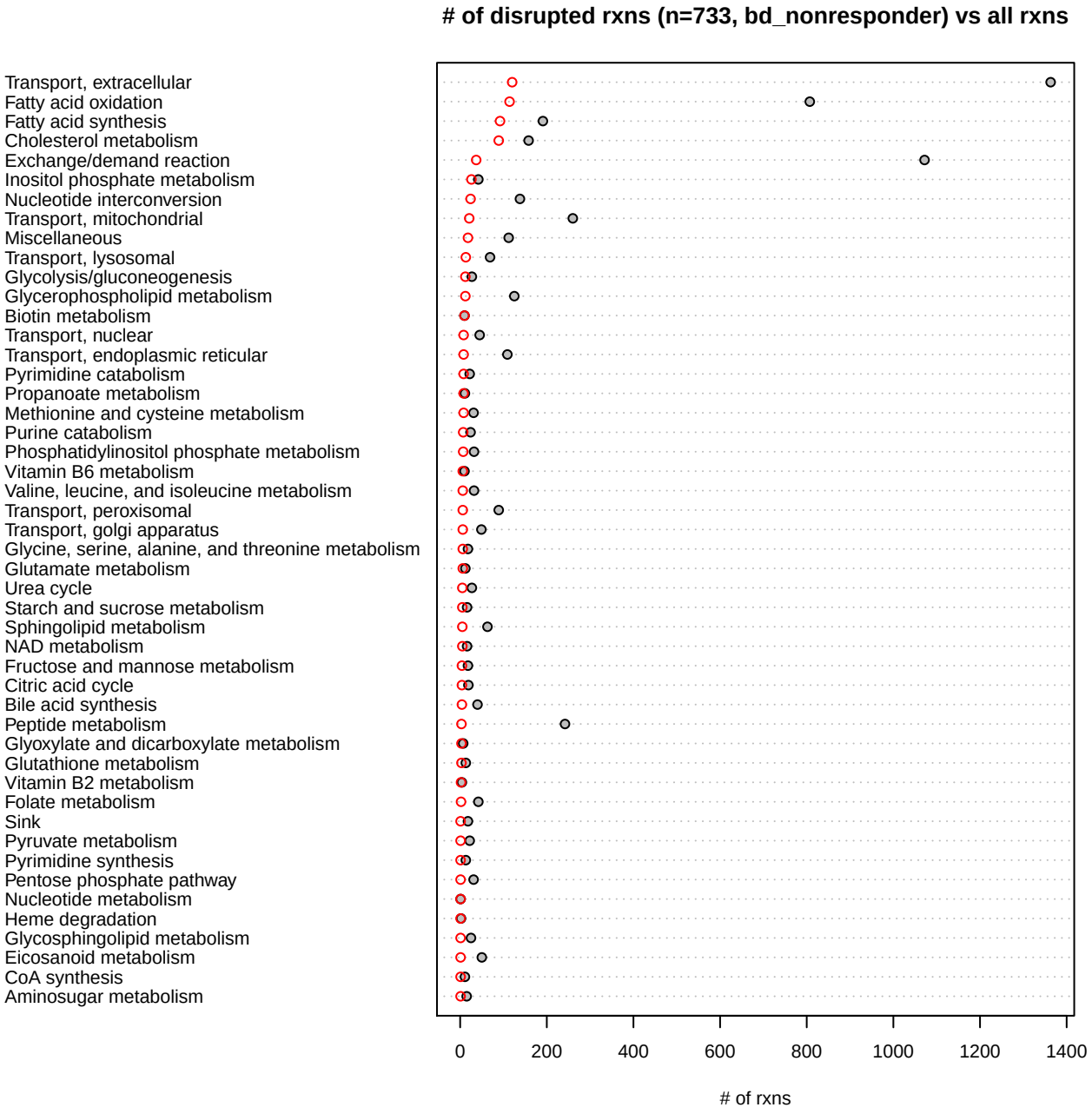

over−representation analysis, bd_lumped
Methionine and cysteine metabolism
Fatty acid oxidation
Valine, leucine, and isoleucine metabolism
Fructose and mannose metabolism
Miscellaneous
Lysine metabolism
Transport, endoplasmic reticular
Urea cycle
R group synthesis
Taurine and hypotaurine metabolism
Triacylglycerol synthesis
Tryptophan metabolism
Tetrahydrobiopterin metabolism
Phosphatidylinositol phosphate metabolism
Exchange/demand reaction
Nucleotide interconversion
Tyrosine metabolism
Transport, nuclear
Steroid metabolism
Pyruvate metabolism
Pyrimidine synthesis
Purine catabolism
Glycolysis/gluconeogenesis
Glutathione metabolism
Exchange
Arachidonic acid metabolism
Transport, mitochondrial
Bile acid synthesis
Transport, peroxisomal
Transport, extracellular
Peptide metabolism
Transport, lysosomal
Fatty acid synthesis
Cholesterol metabolism
subSystem
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

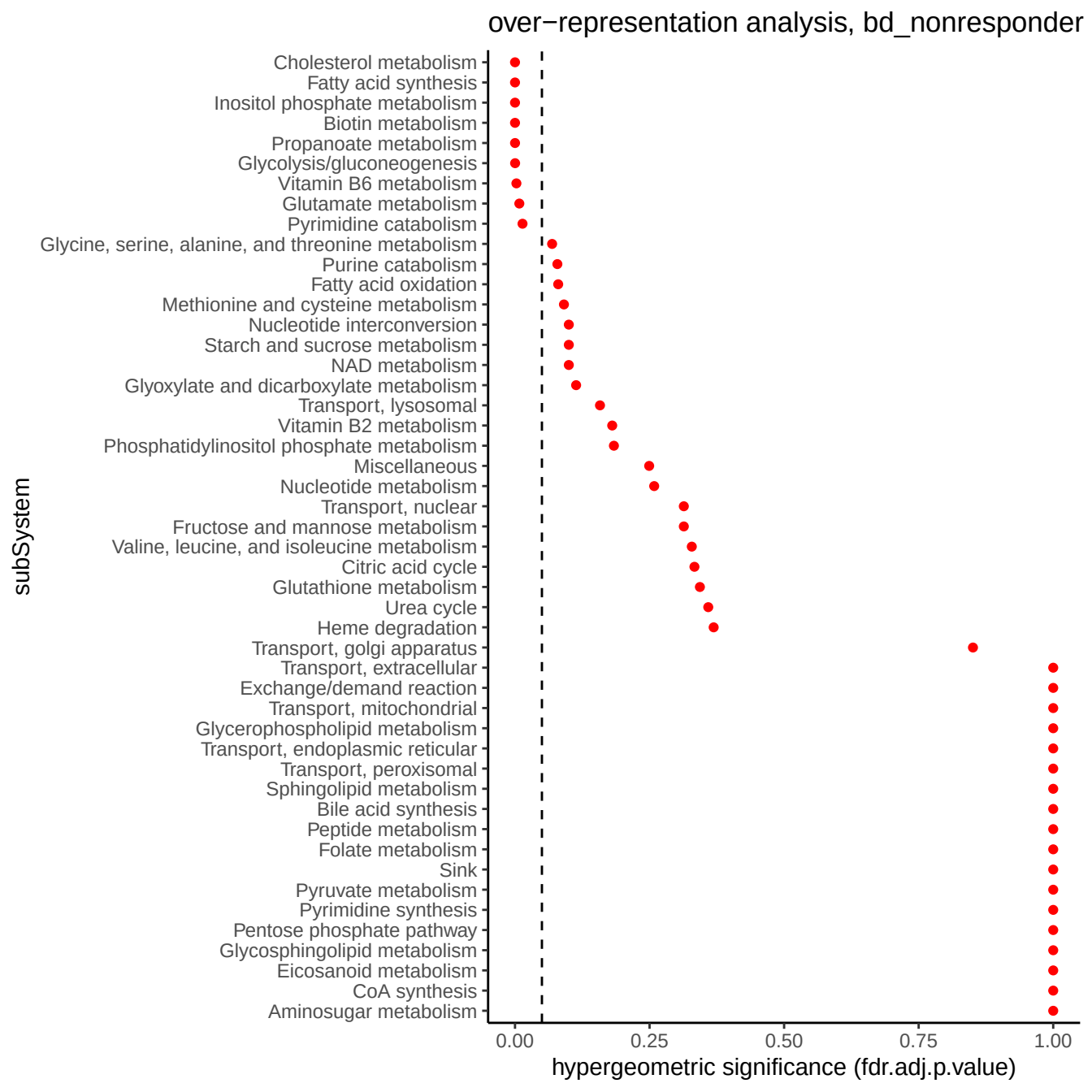

# of disrupted rxns (n=72, bd_responder)
Fatty acid oxidation
Transport, extracellular
Transport, endoplasmic reticular
Exchange/demand reaction
Transport, nuclear
Nucleotide interconversion
Vitamin A metabolism
Transport, peroxisomal
Transport, mitochondrial
Purine catabolism
Phosphatidylinositol phosphate metabolism
Miscellaneous
Tyrosine metabolism
Steroid metabolism
Pyrimidine synthesis
Exchange
Eicosanoid metabolism
Beta−Alanine metabolism
0
5
10
15
20
25
30
# of rxns

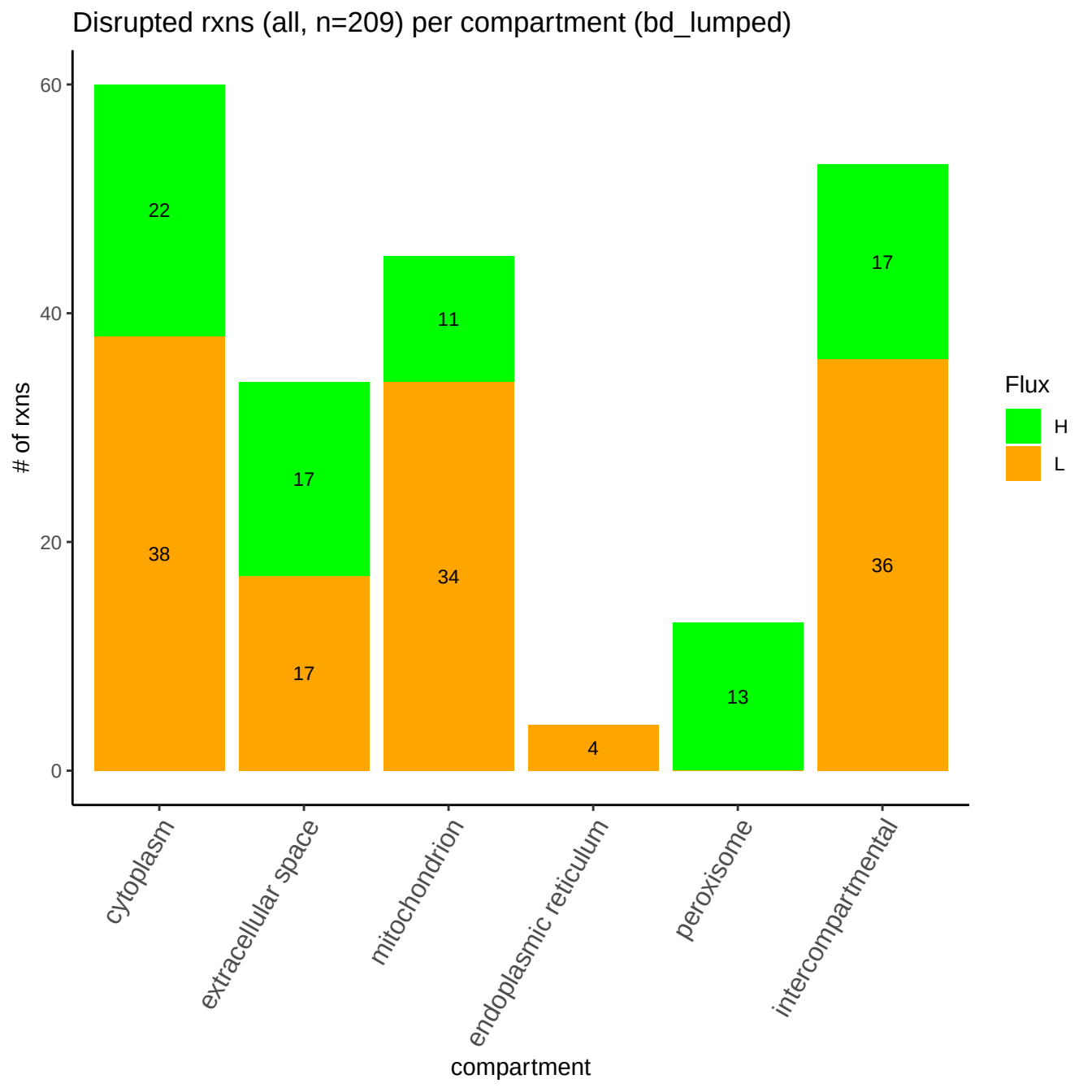

# of disrupted rxns (n=72, bd_responder) vs all rxns
Fatty acid oxidation
Transport, extracellular
Transport, endoplasmic reticular
Exchange/demand reaction
Transport, nuclear
Nucleotide interconversion
Vitamin A metabolism
Transport, peroxisomal
Transport, mitochondrial
Purine catabolism
Phosphatidylinositol phosphate metabolism
Miscellaneous
Tyrosine metabolism
Steroid metabolism
Pyrimidine synthesis
Exchange
Eicosanoid metabolism
Beta−Alanine metabolism
0
200
400
600
800
1000
1200
1400
# of rxns

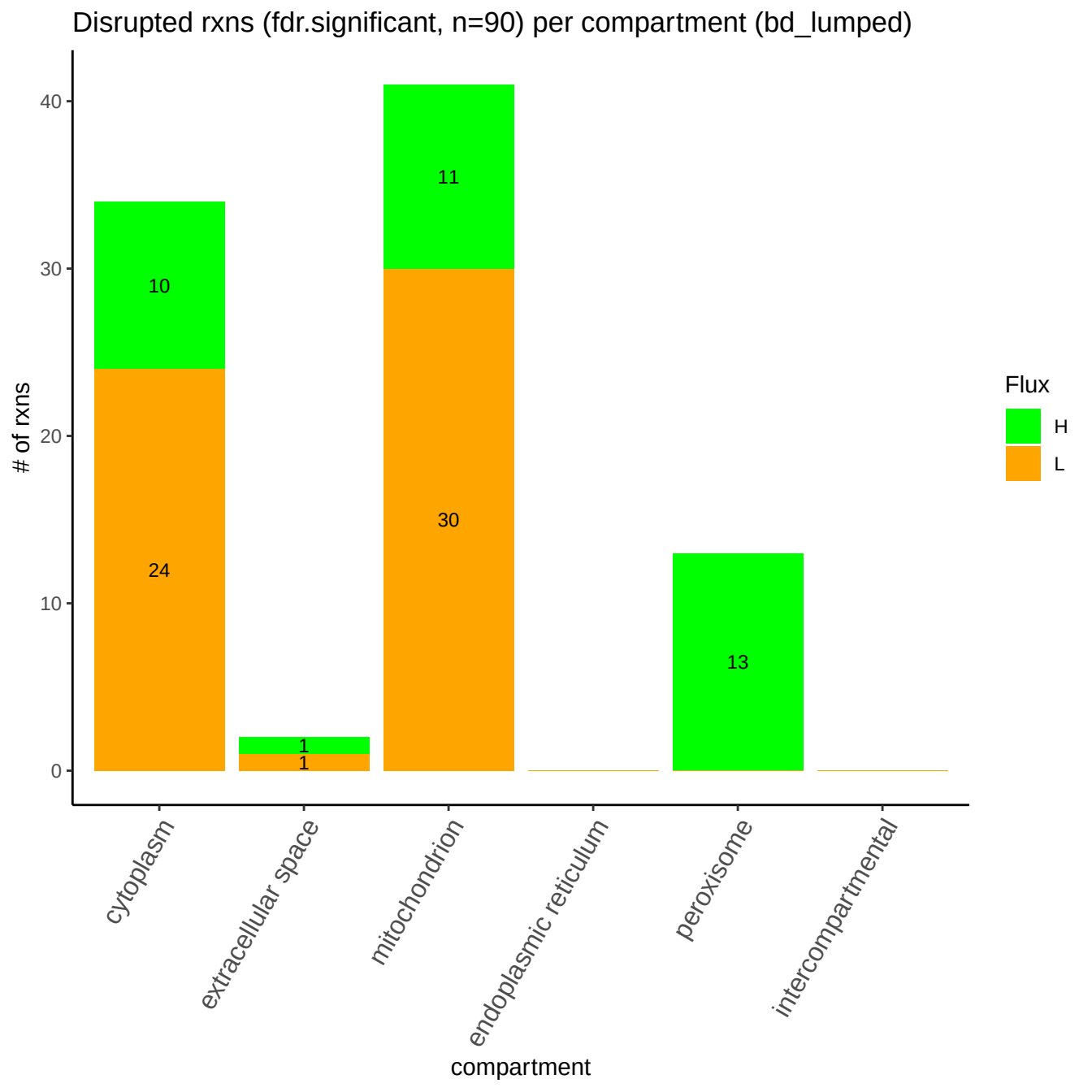

over−representation analysis, bd_responder
Fatty acid oxidation
Transport, endoplasmic reticular
Transport, nuclear
Vitamin A metabolism
Purine catabolism
Phosphatidylinositol phosphate metabolism
Beta−Alanine metabolism
Pyrimidine synthesis
Exchange
Nucleotide interconversion
Transport, peroxisomal
Steroid metabolism
Miscellaneous
Tyrosine metabolism
Eicosanoid metabolism
Transport, mitochondrial
Transport, extracellular
Exchange/demand reaction
subSystem
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

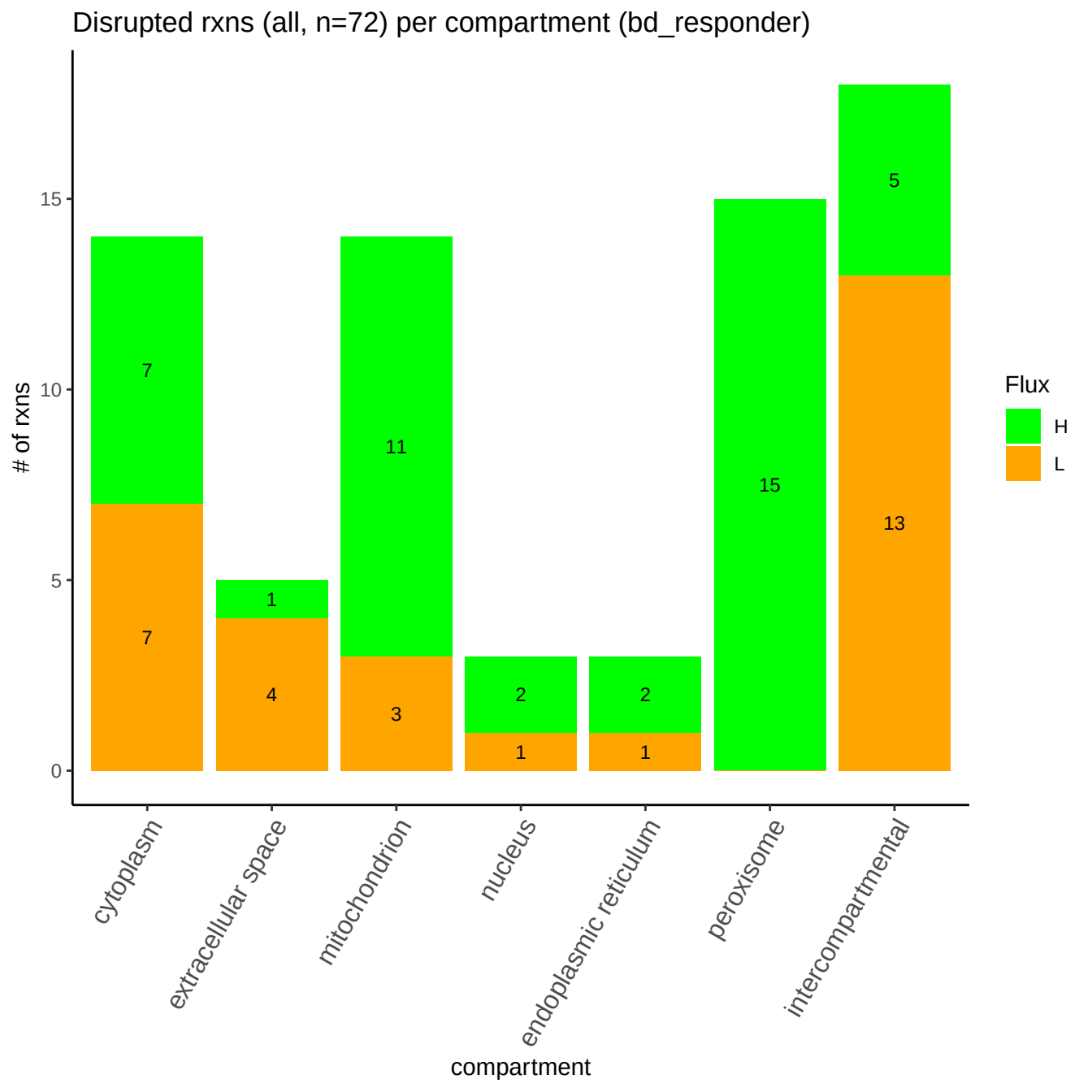

# of disrupted rxns (n=733, bd_nonresponder)
Transport, extracellular
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Exchange/demand reaction
Inositol phosphate metabolism
Nucleotide interconversion
Transport, mitochondrial
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Biotin metabolism
Transport, nuclear
Transport, endoplasmic reticular
Pyrimidine catabolism
Propanoate metabolism
Methionine and cysteine metabolism
Purine catabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Valine, leucine, and isoleucine metabolism
Transport, peroxisomal
Transport, golgi apparatus
Glycine, serine, alanine, and threonine 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
Glutathione metabolism
Vitamin B2 metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Eicosanoid metabolism
CoA synthesis
Aminosugar metabolism
0
20
40
60
80
100
120
# of rxns

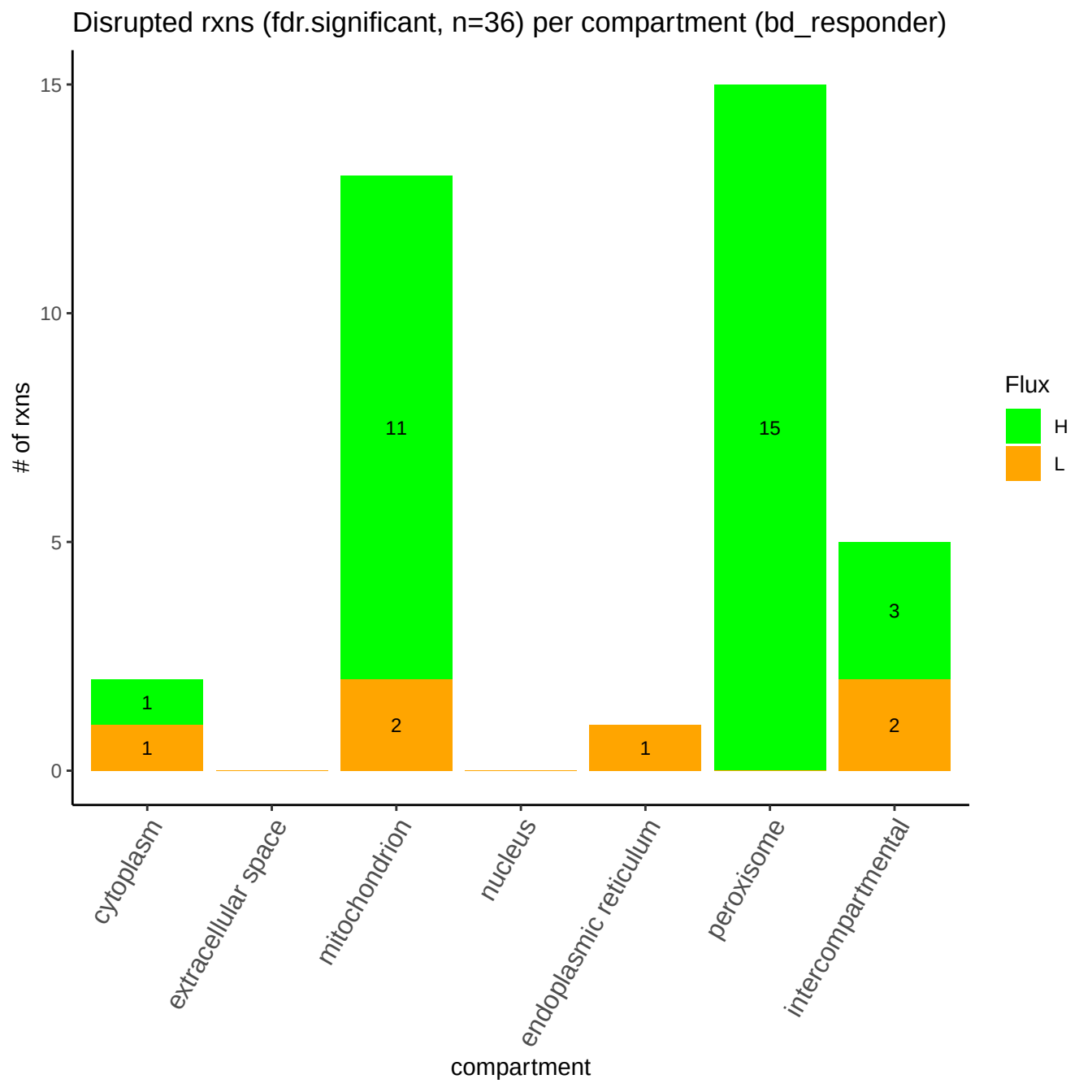

# of disrupted rxns (n=733, bd_nonresponder) vs all rxns
Transport, extracellular
Fatty acid oxidation
Fatty acid synthesis
Cholesterol metabolism
Exchange/demand reaction
Inositol phosphate metabolism
Nucleotide interconversion
Transport, mitochondrial
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Glycerophospholipid metabolism
Biotin metabolism
Transport, nuclear
Transport, endoplasmic reticular
Pyrimidine catabolism
Propanoate metabolism
Methionine and cysteine metabolism
Purine catabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Valine, leucine, and isoleucine metabolism
Transport, peroxisomal
Transport, golgi apparatus
Glycine, serine, alanine, and threonine 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
Glutathione metabolism
Vitamin B2 metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Eicosanoid metabolism
CoA synthesis
Aminosugar metabolism
0
200
400
600
800
1000
1200
1400
# of rxns

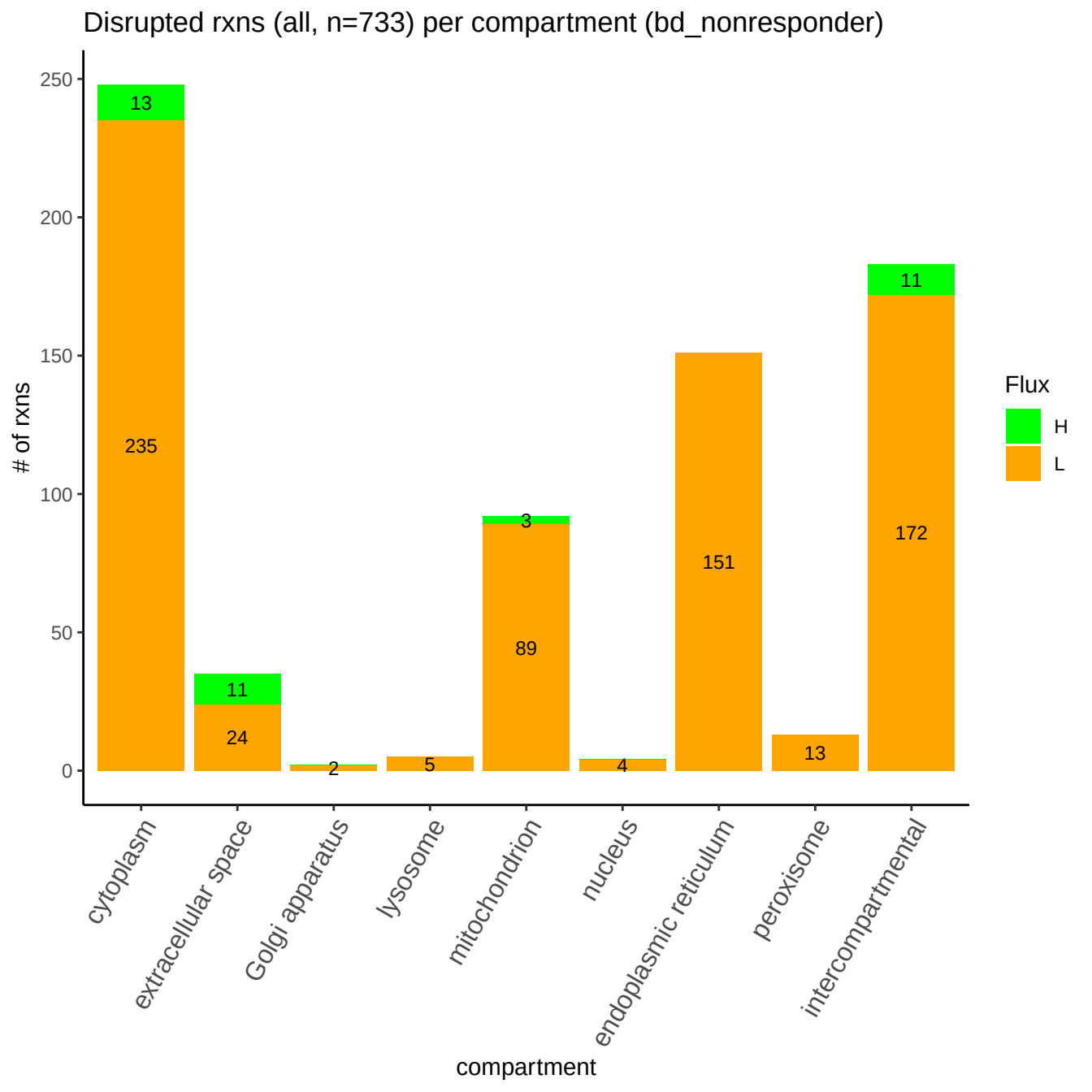

over−representation analysis, bd_nonresponder
Cholesterol metabolism
Fatty acid synthesis
Inositol phosphate metabolism
Biotin metabolism
Propanoate metabolism
Glycolysis/gluconeogenesis
Vitamin B6 metabolism
Glutamate metabolism
Pyrimidine catabolism
Glycine, serine, alanine, and threonine metabolism
Purine catabolism
Fatty acid oxidation
Methionine and cysteine metabolism
Nucleotide interconversion
Starch and sucrose metabolism
NAD metabolism
Glyoxylate and dicarboxylate metabolism
Transport, lysosomal
Vitamin B2 metabolism
Phosphatidylinositol phosphate metabolism
Miscellaneous
Nucleotide metabolism
Transport, nuclear
Fructose and mannose metabolism
Valine, leucine, and isoleucine metabolism
Citric acid cycle
Glutathione metabolism
Urea cycle
Heme degradation
Transport, golgi apparatus
Transport, extracellular
Exchange/demand reaction
Transport, mitochondrial
Glycerophospholipid metabolism
Transport, endoplasmic reticular
Transport, peroxisomal
Sphingolipid metabolism
Bile acid synthesis
Peptide metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Glycosphingolipid metabolism
Eicosanoid metabolism
CoA synthesis
Aminosugar metabolism
subSystem
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

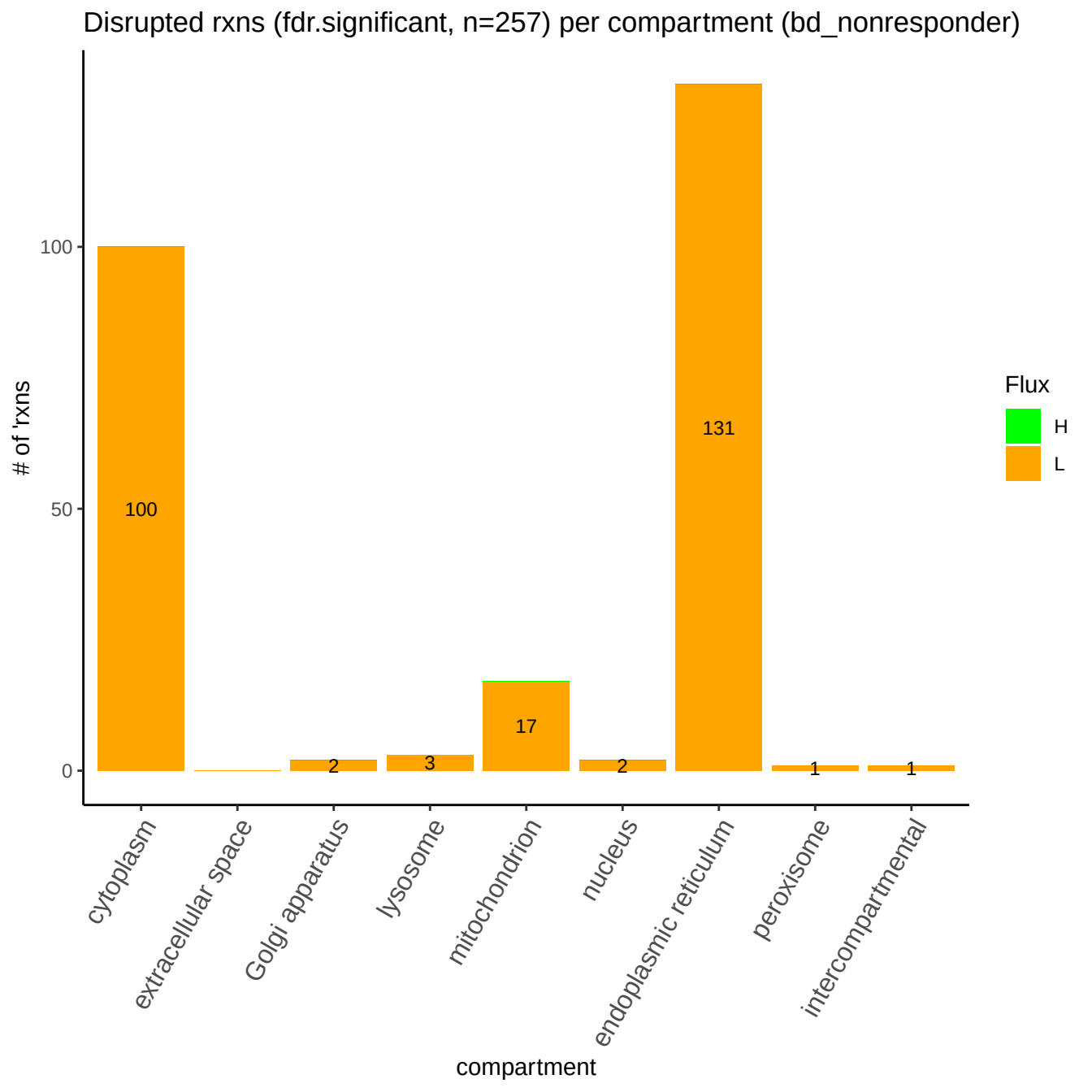

Disrupted rxns (all, n=209) per compartment (bd_lumped)
# of rxns
60
40
20
0
22
38
17
17
11
34
4
13
17
36
cytoplasm
extracellular space
mitochondrion
endoplasmic reticulum
peroxisome
intercompartmental
compartment
Flux
H
L


Disrupted rxns (fdr.significant, n=90) per compartment (bd_lumped)
# of rxns
40
30
20
10
0
10
24
1
1
11
30
13
Flux
H
L
cytoplasm
extracellular space
mitochondrion
endoplasmic reticulum
peroxisome
intercompartmental
compartment

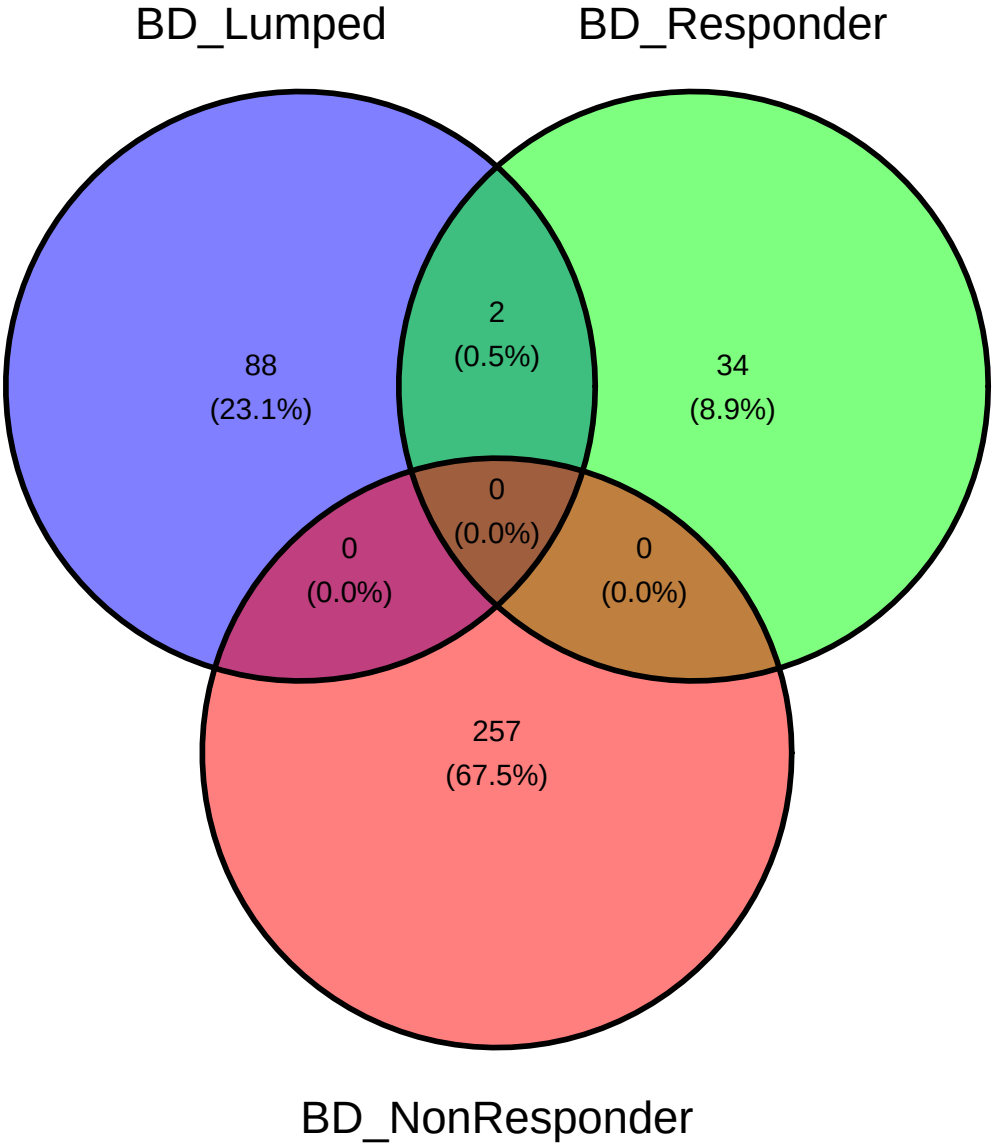

Disrupted rxns (all, n=72) per compartment (bd_responder)
# of rxns
0
5
10
15
7
7
1
4
11
3
2
1
2
1
15
5
13
Flux
H
L
cytoplasm
extracellular space
mitochondrion
nucleus
endoplasmic reticulum
peroxisome
intercompartmental
compartment


Disrupted rxns (fdr.significant, n=36) per compartment (bd_responder)
# of rxns
15
10
5
0
1
1
11
2
1
15
3
2
cytoplasm
extracellular space
mitochondrion
nucleus
endoplasmic reticulum
peroxisome
intercompartmental
compartment
Flux
H
L


Disrupted rxns (all, n=733) per compartment (bd_nonresponder)
# of rxns
250
200
150
100
50
0
13
235
11
24
2
5
3
89
4
151
13
11
172
cytoplasm
extracellular space
Golgi apparatus
lysosome
mitochondrion
nucleus
endoplasmic reticulum
peroxisome
intercompartmental
compartment
Flux
H
L


Disrupted rxns (fdr.significant, n=257) per compartment (bd_nonresponder)
of 'rxns
100
50
0
100
2
3
17
2
131
1
1
cytoplasm
extracellular space
Golgi apparatus
lysosome
mitochondrion
nucleus
endoplasmic reticulum
peroxisome
intercompartmental
compartment
Flux
H
L

Overlp in rxns (fdr.significant) disrupted between models



Overlp in subSystems (fdr.significant) disrupted between models