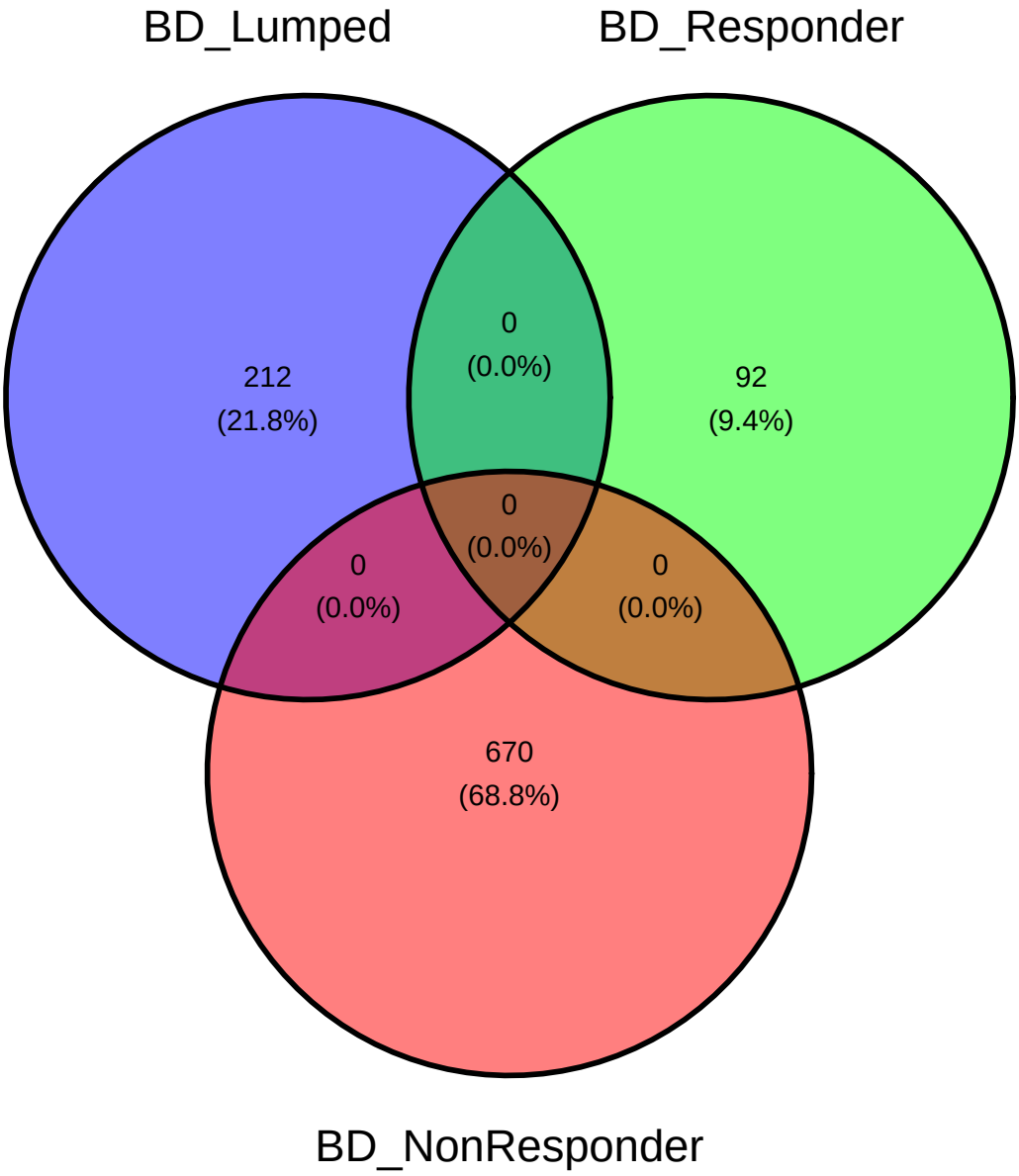
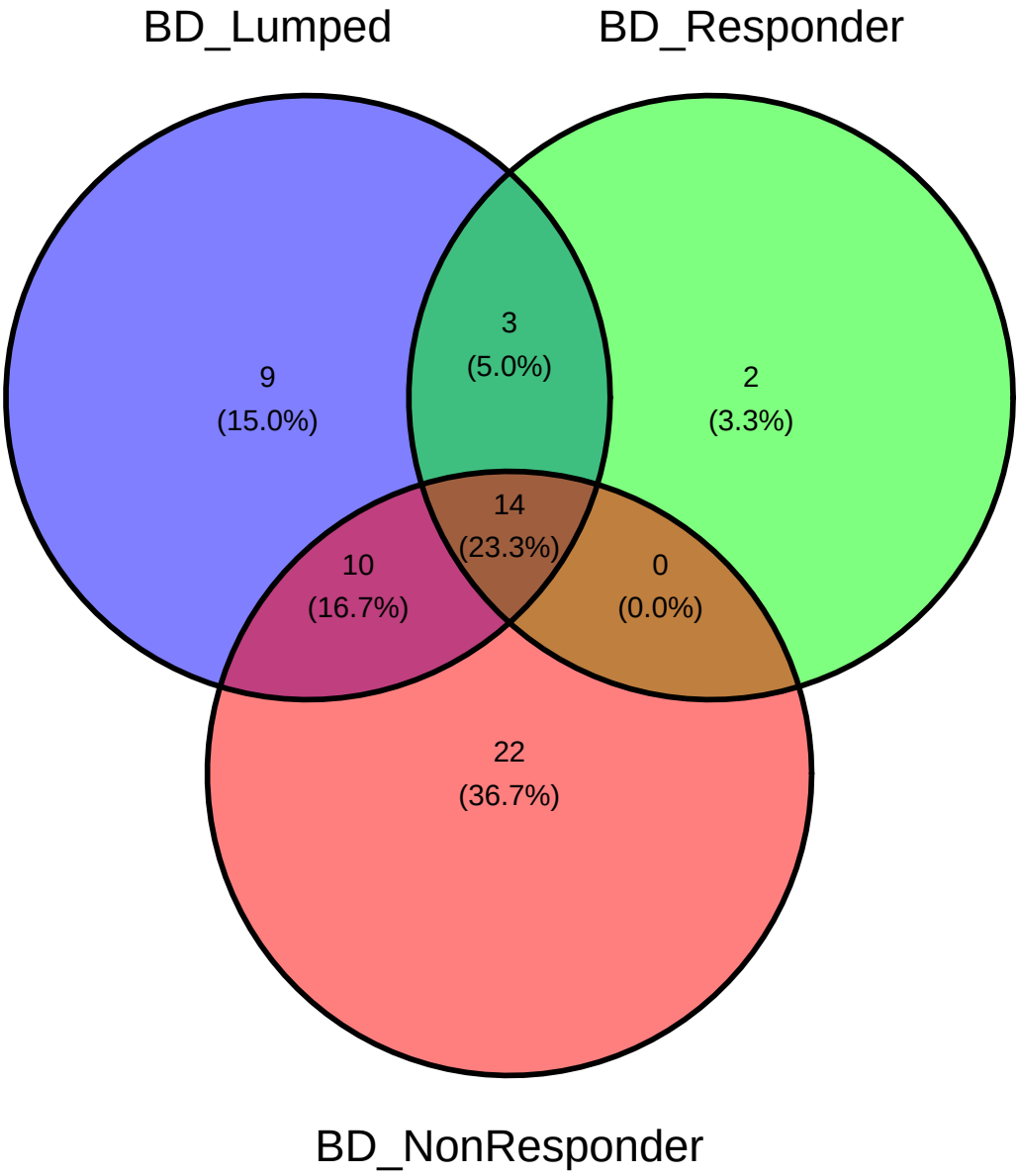
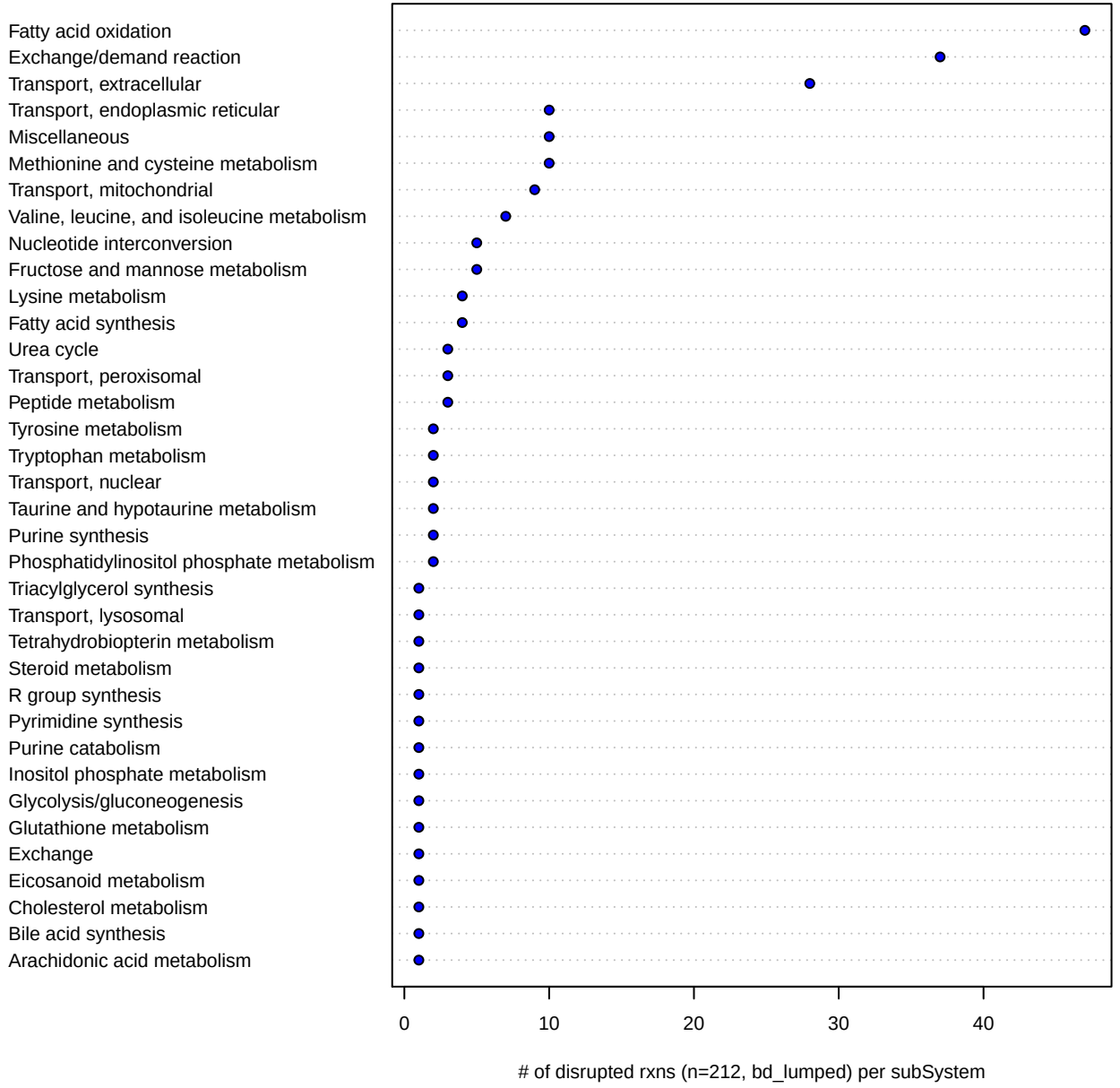
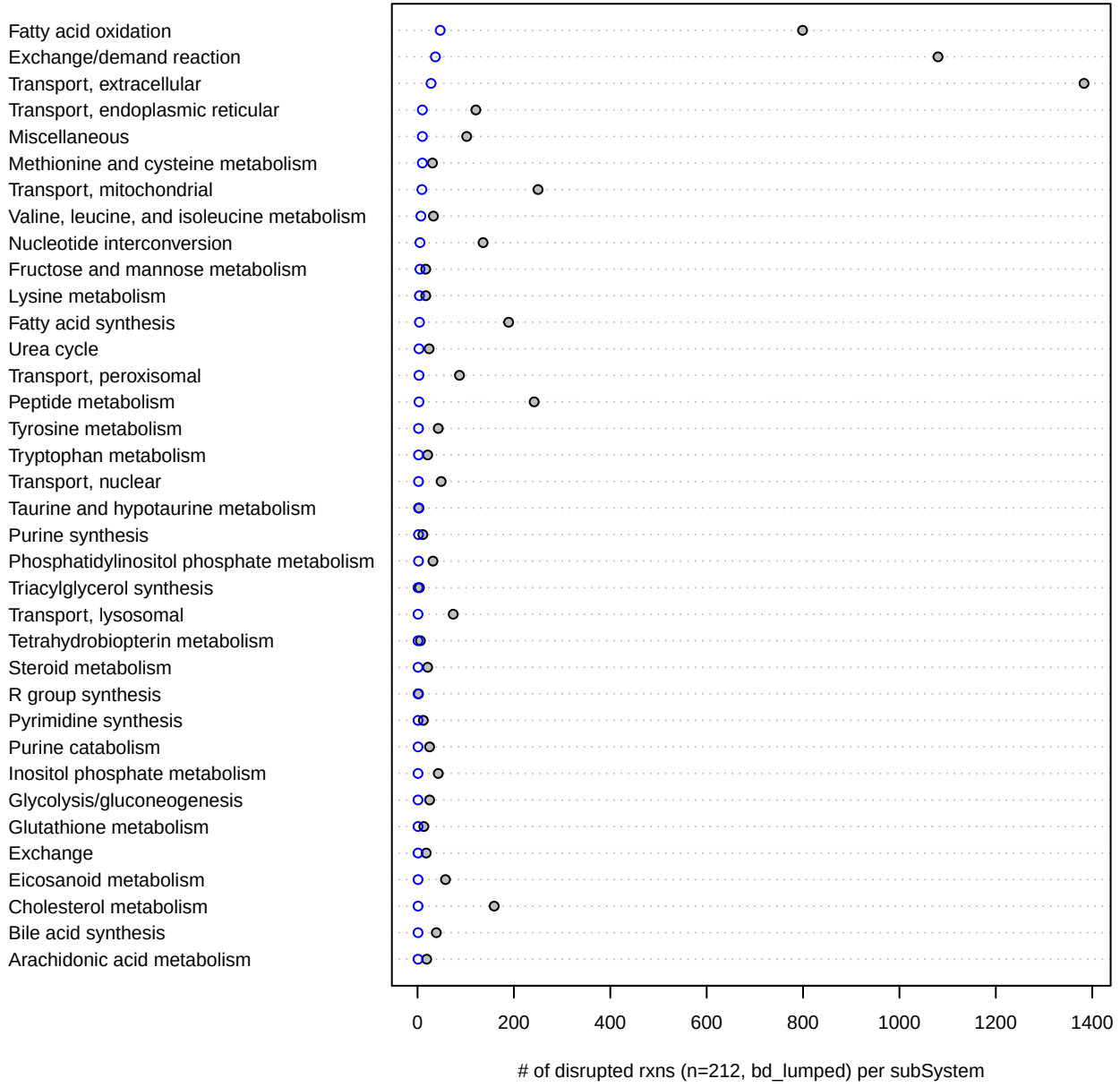
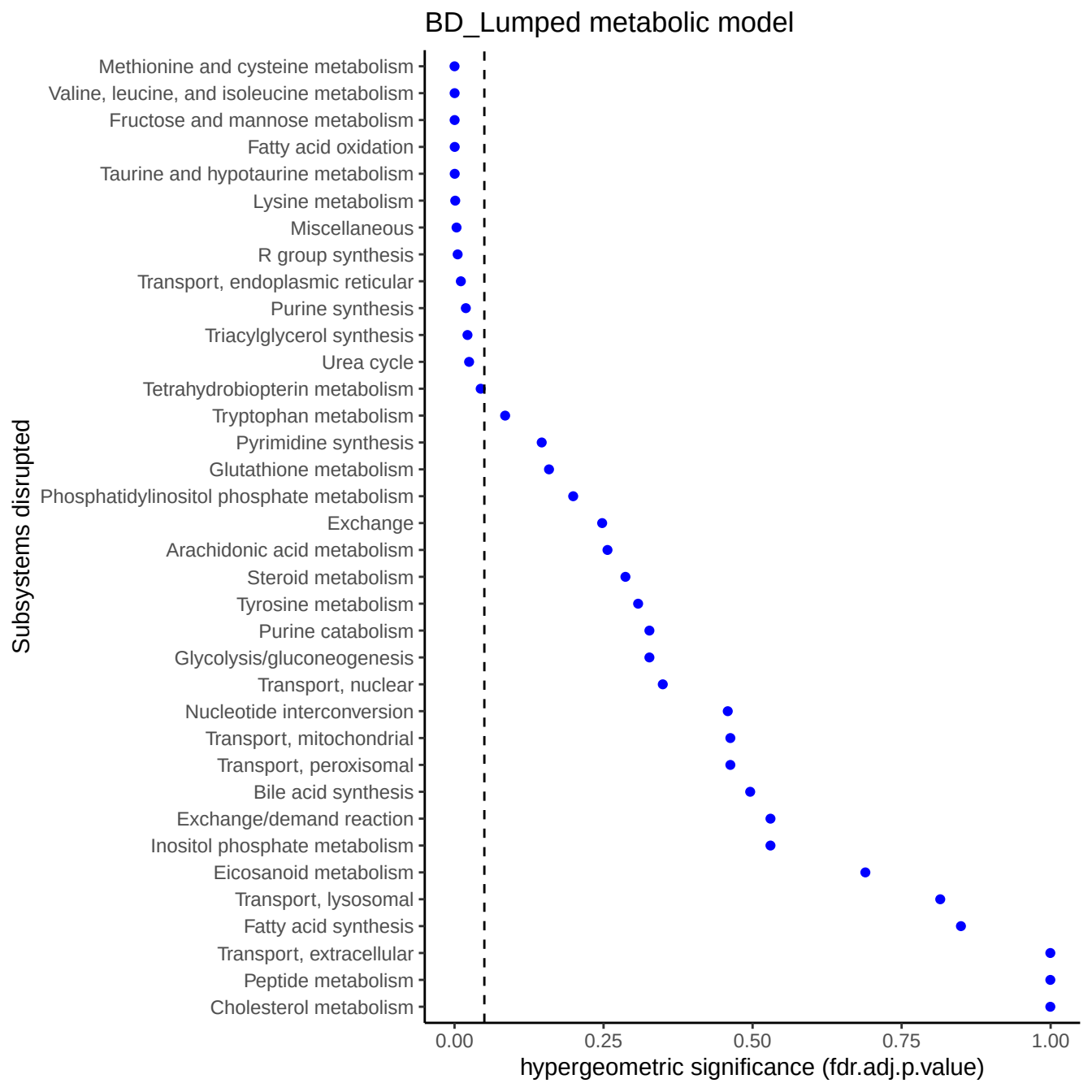
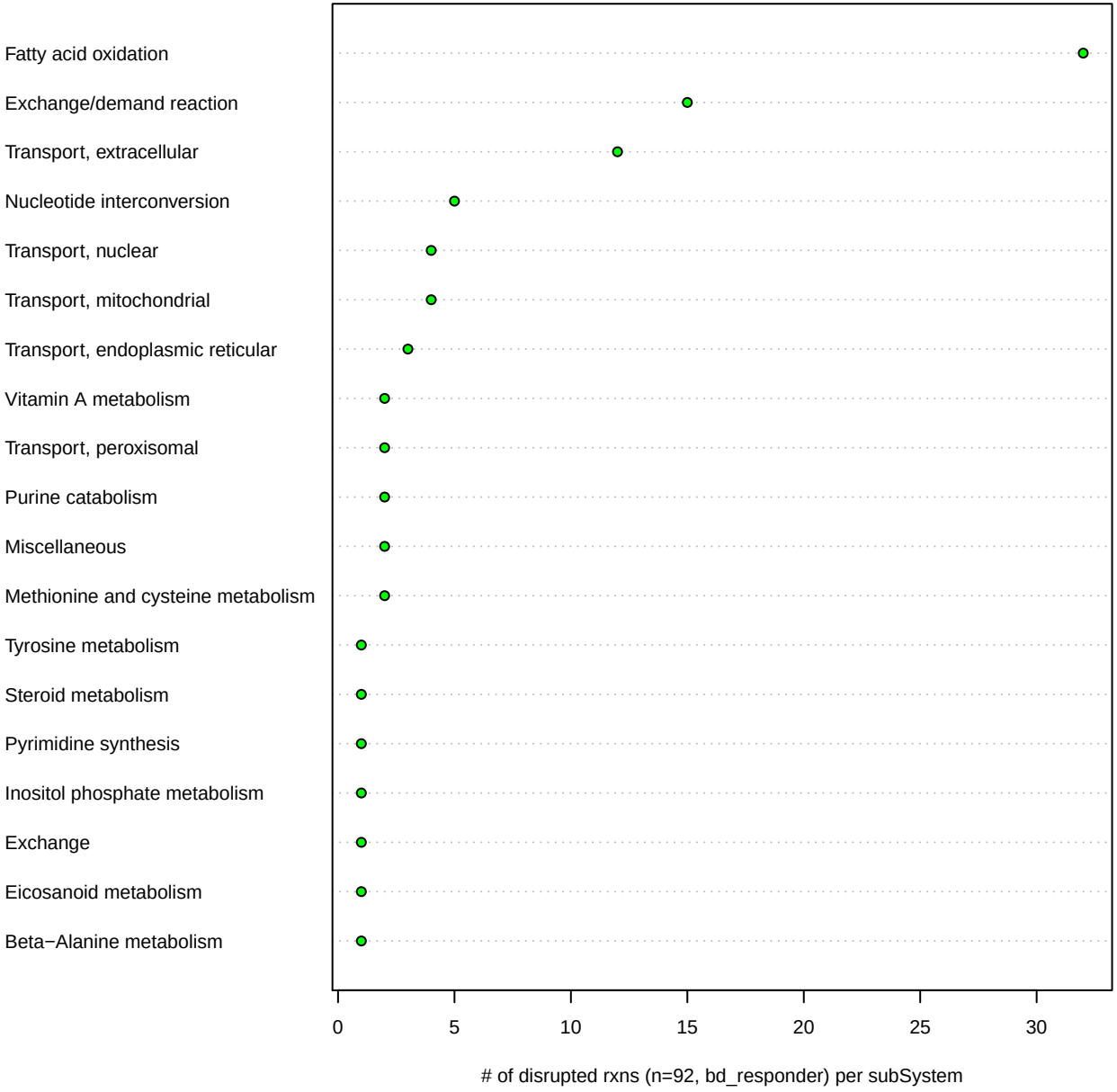

BD_Lumped
BD_Responder
212
(21.8%)
0
(0.0%)
92
(9.4%)
0
(0.0%)
0
(0.0%)
0
(0.0%)
670
(68.8%)
BD_NonResponder

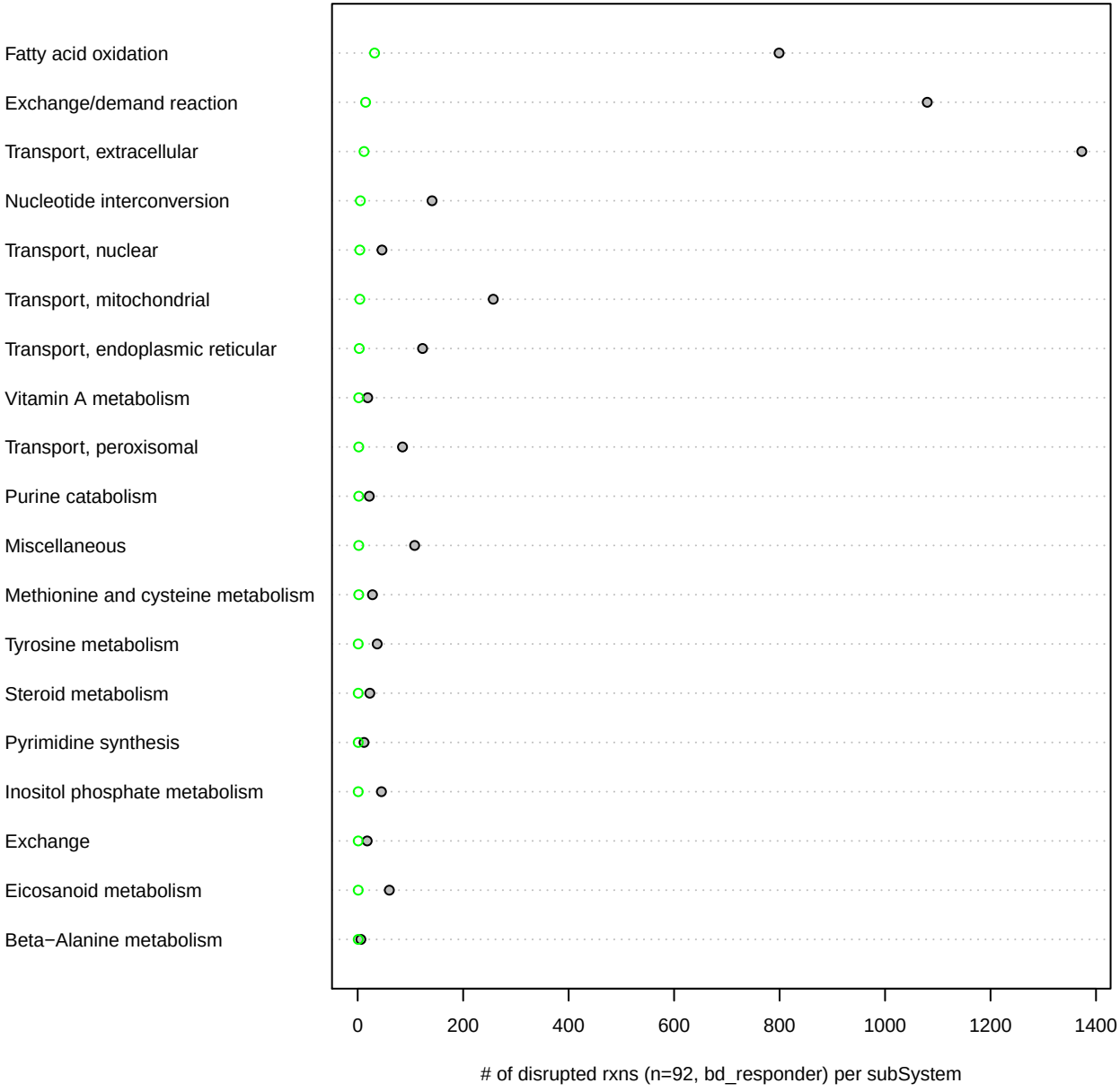

BD_Lumped
BD_Responder
BD_NonResponder
9
(15.0%)
3
(5.0%)
2
(3.3%)
14
(23.3%)
10
(16.7%)
0
(0.0%)
22
(36.7%)

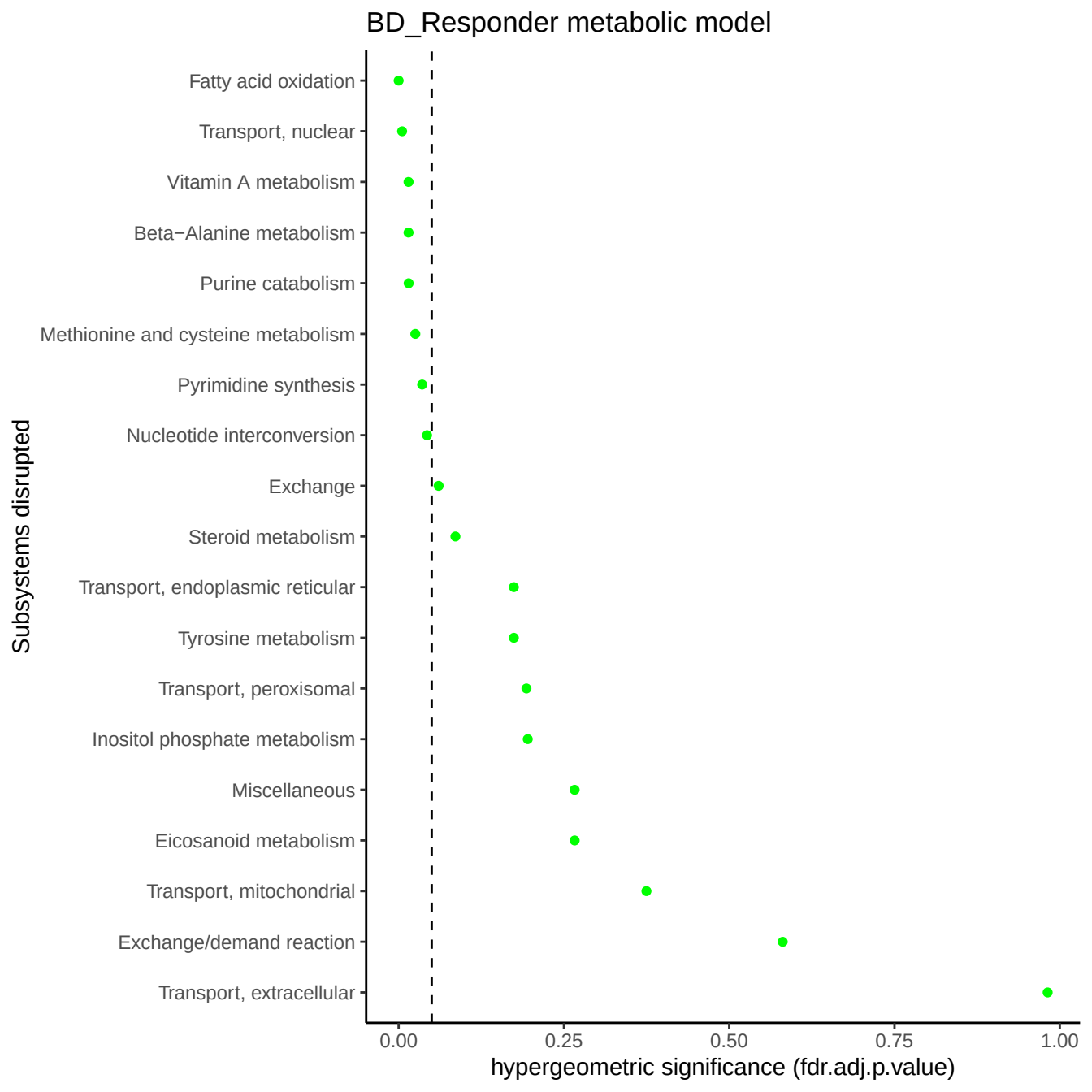

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Transport, endoplasmic reticular
Miscellaneous
Methionine and cysteine metabolism
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose metabolism
Lysine metabolism
Fatty acid synthesis
Urea cycle
Transport, peroxisomal
Peptide metabolism
Tyrosine metabolism
Tryptophan metabolism
Transport, nuclear
Taurine and hypotaurine metabolism
Purine synthesis
Phosphatidylinositol phosphate metabolism
Triacylglycerol synthesis
Transport, lysosomal
Tetrahydrobiopterin metabolism
Steroid metabolism
R group synthesis
Pyrimidine synthesis
Purine catabolism
Inositol phosphate metabolism
Glycolysis/gluconeogenesis
Glutathione metabolism
Exchange
Eicosanoid metabolism
Cholesterol metabolism
Bile acid synthesis
Arachidonic acid metabolism
0
10
20
30
40
# of disrupted rxns (n=212, bd_lumped) per subSystem

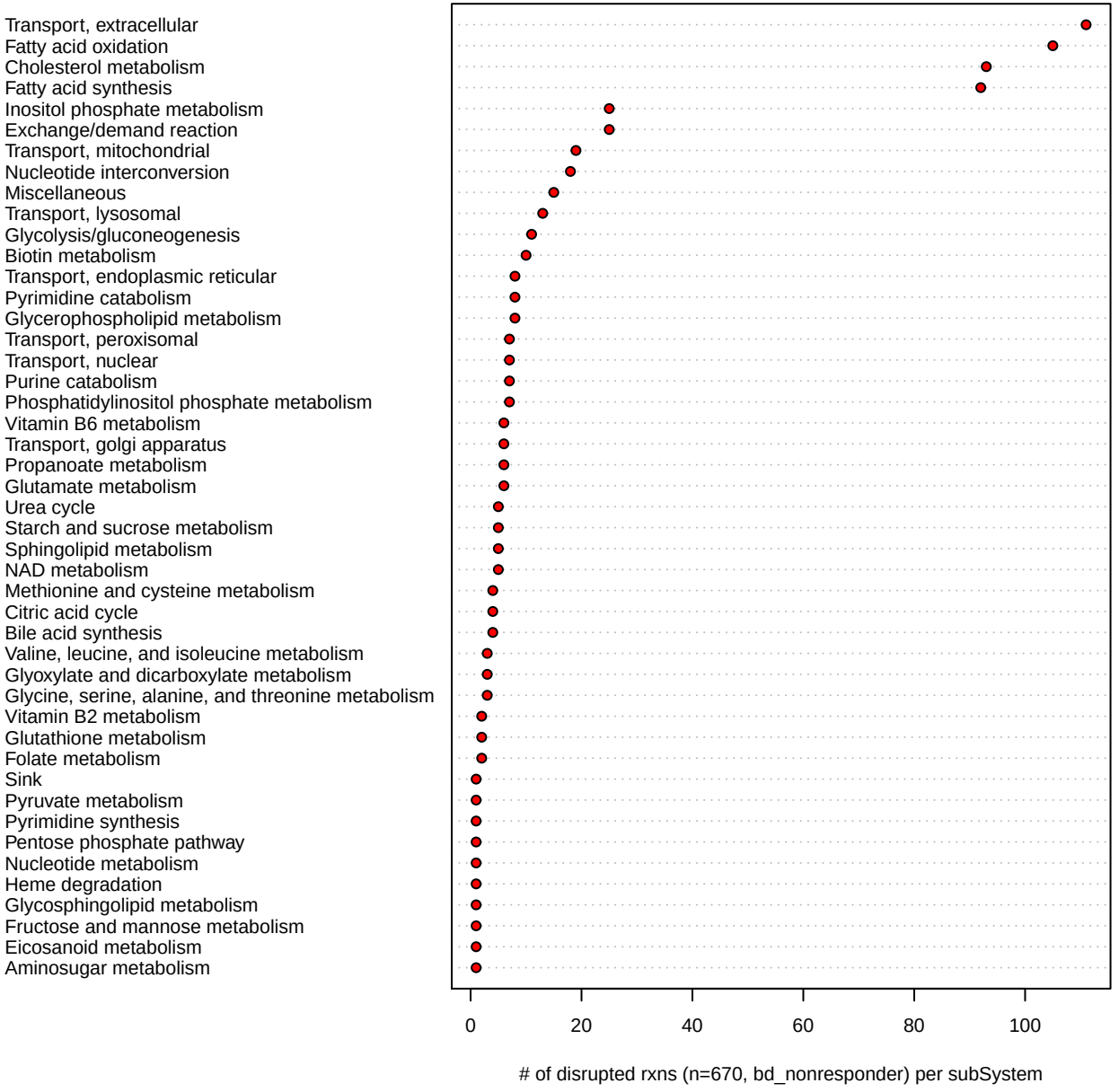

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Transport, endoplasmic reticular
Miscellaneous
Methionine and cysteine metabolism
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose metabolism
Lysine metabolism
Fatty acid synthesis
Urea cycle
Transport, peroxisomal
Peptide metabolism
Tyrosine metabolism
Tryptophan metabolism
Transport, nuclear
Taurine and hypotaurine metabolism
Purine synthesis
Phosphatidylinositol phosphate metabolism
Triacylglycerol synthesis
Transport, lysosomal
Tetrahydrobiopterin metabolism
Steroid metabolism
R group synthesis
Pyrimidine synthesis
Purine catabolism
Inositol phosphate metabolism
Glycolysis/gluconeogenesis
Glutathione metabolism
Exchange
Eicosanoid metabolism
Cholesterol metabolism
Bile acid synthesis
Arachidonic acid metabolism
0
200
400
600
800
1000
1200
1400
# of disrupted rxns (n=212, bd_lumped) per subSystem

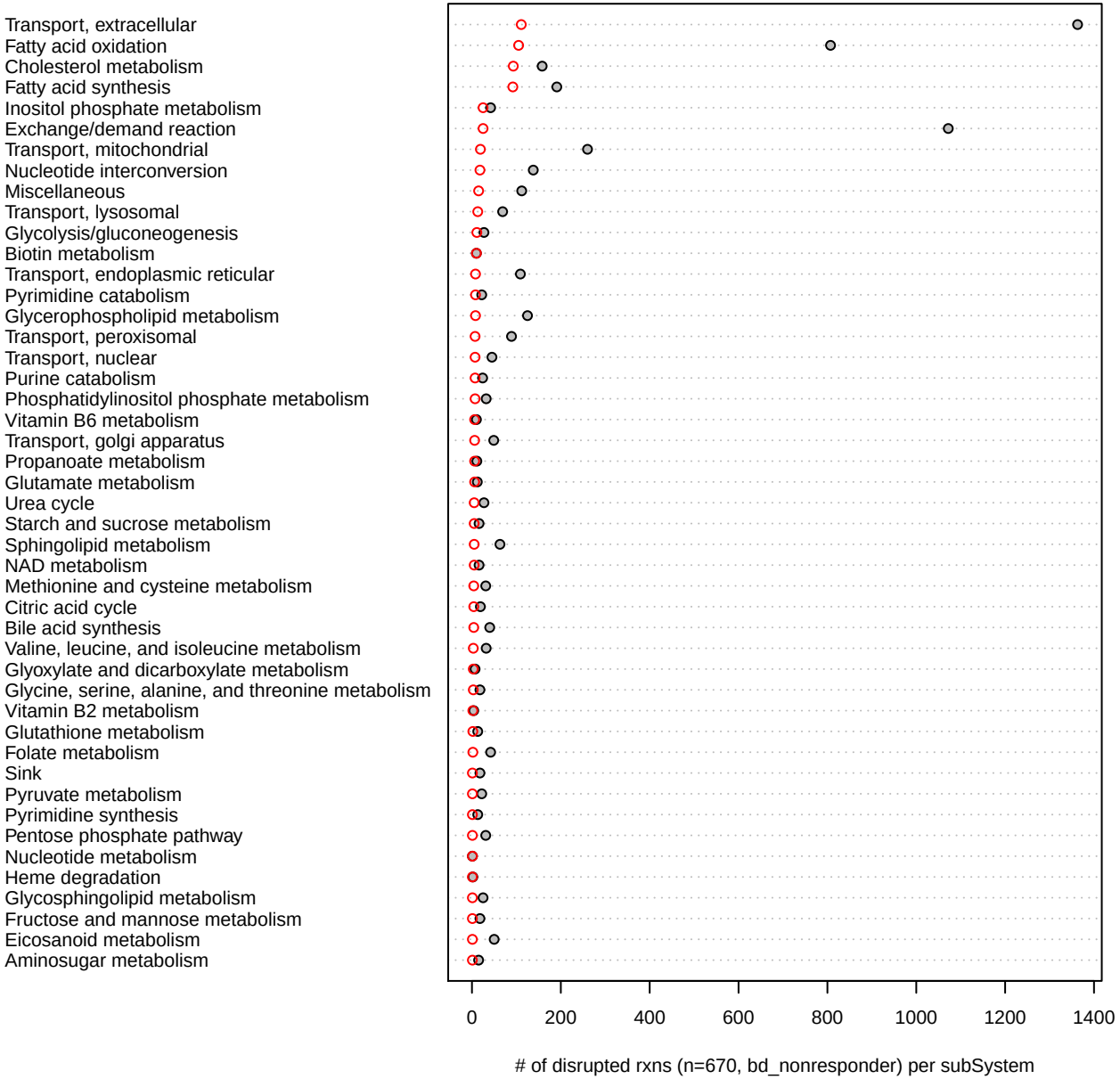

BD_Lumped metabolic model
Methionine and cysteine metabolism
Valine, leucine, and isoleucine metabolism
Fructose and mannose metabolism
Fatty acid oxidation
Taurine and hypotaurine metabolism
Lysine metabolism
Miscellaneous
R group synthesis
Transport, endoplasmic reticular
Purine synthesis
Triacylglycerol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

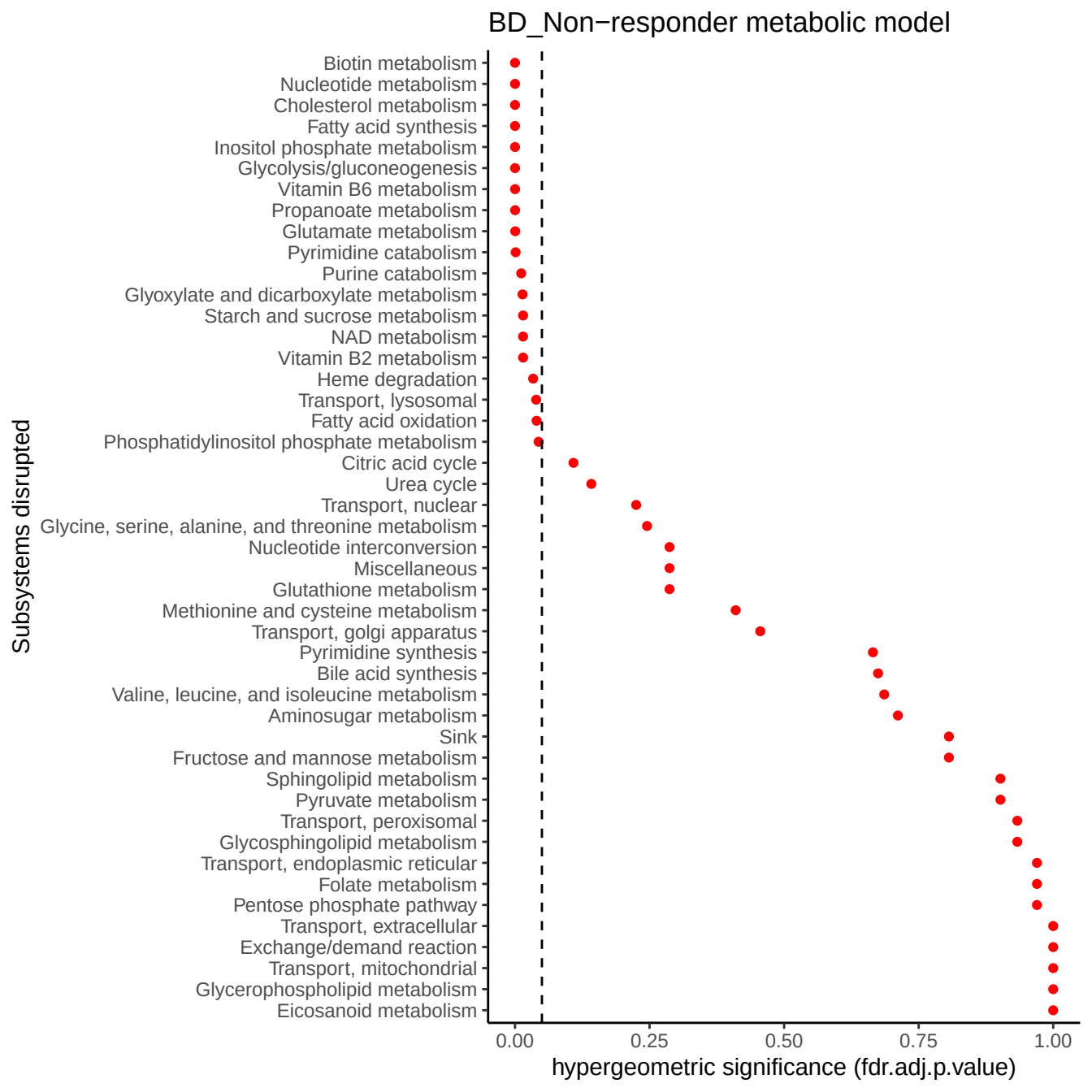

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Nucleotide interconversion
Transport, nuclear
Transport, mitochondrial
Transport, endoplasmic reticular
Vitamin A metabolism
Transport, peroxisomal
Purine catabolism
Miscellaneous
Methionine and cysteine metabolism
Tyrosine metabolism
Steroid metabolism
Pyrimidine synthesis
Inositol phosphate metabolism
Exchange
Eicosanoid metabolism
Beta−Alanine metabolism
0
5
10
15
20
25
30
# of disrupted rxns (n=92, bd_responder) per subSystem

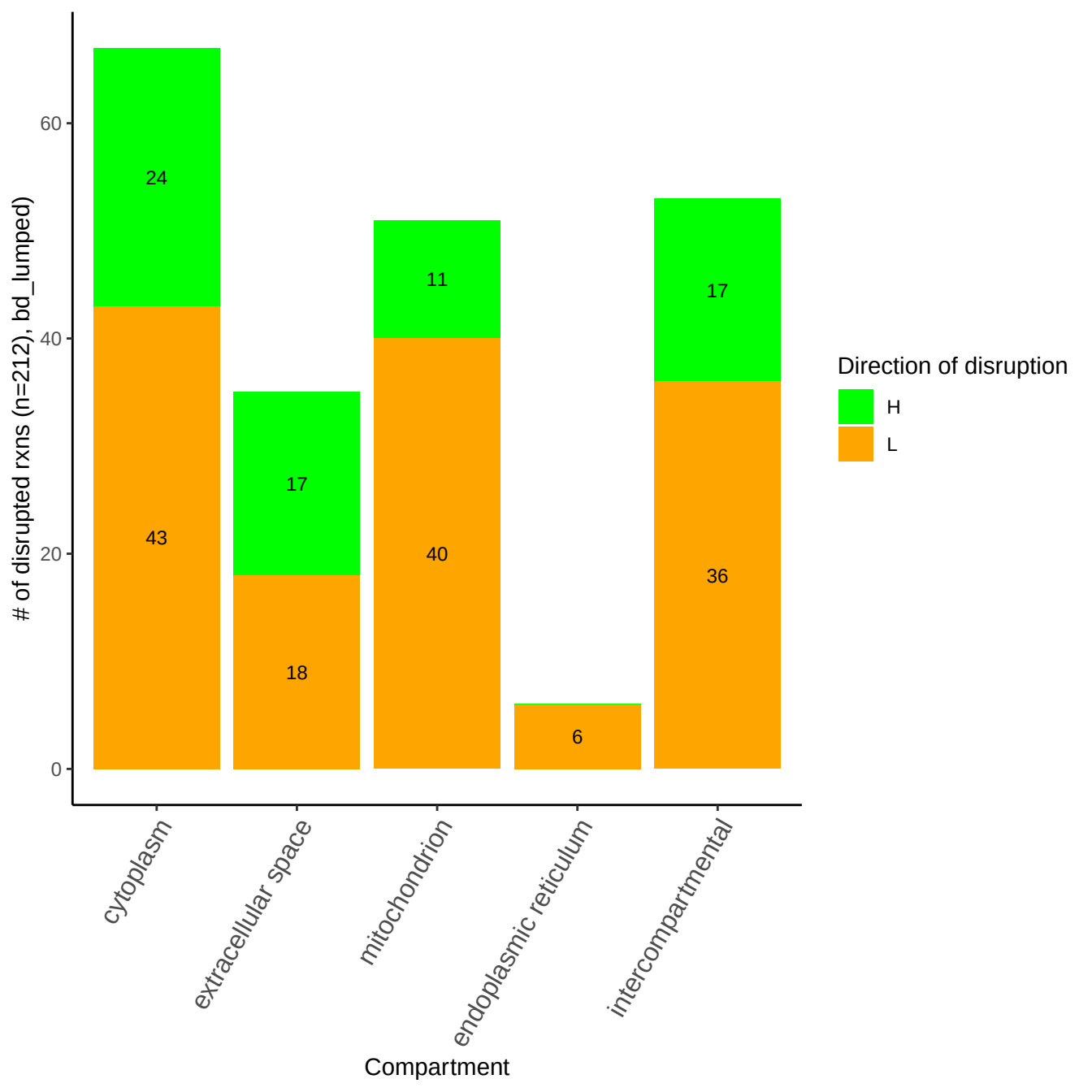

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Nucleotide interconversion
Transport, nuclear
Transport, mitochondrial
Transport, endoplasmic reticular
Vitamin A metabolism
Transport, peroxisomal
Purine catabolism
Miscellaneous
Methionine and cysteine metabolism
Tyrosine metabolism
Steroid metabolism
Pyrimidine synthesis
Inositol phosphate metabolism
Exchange
Eicosanoid metabolism
Beta−Alanine metabolism
0
200
400
600
800
1000
1200
1400
# of disrupted rxns (n=92, bd_responder) per subSystem

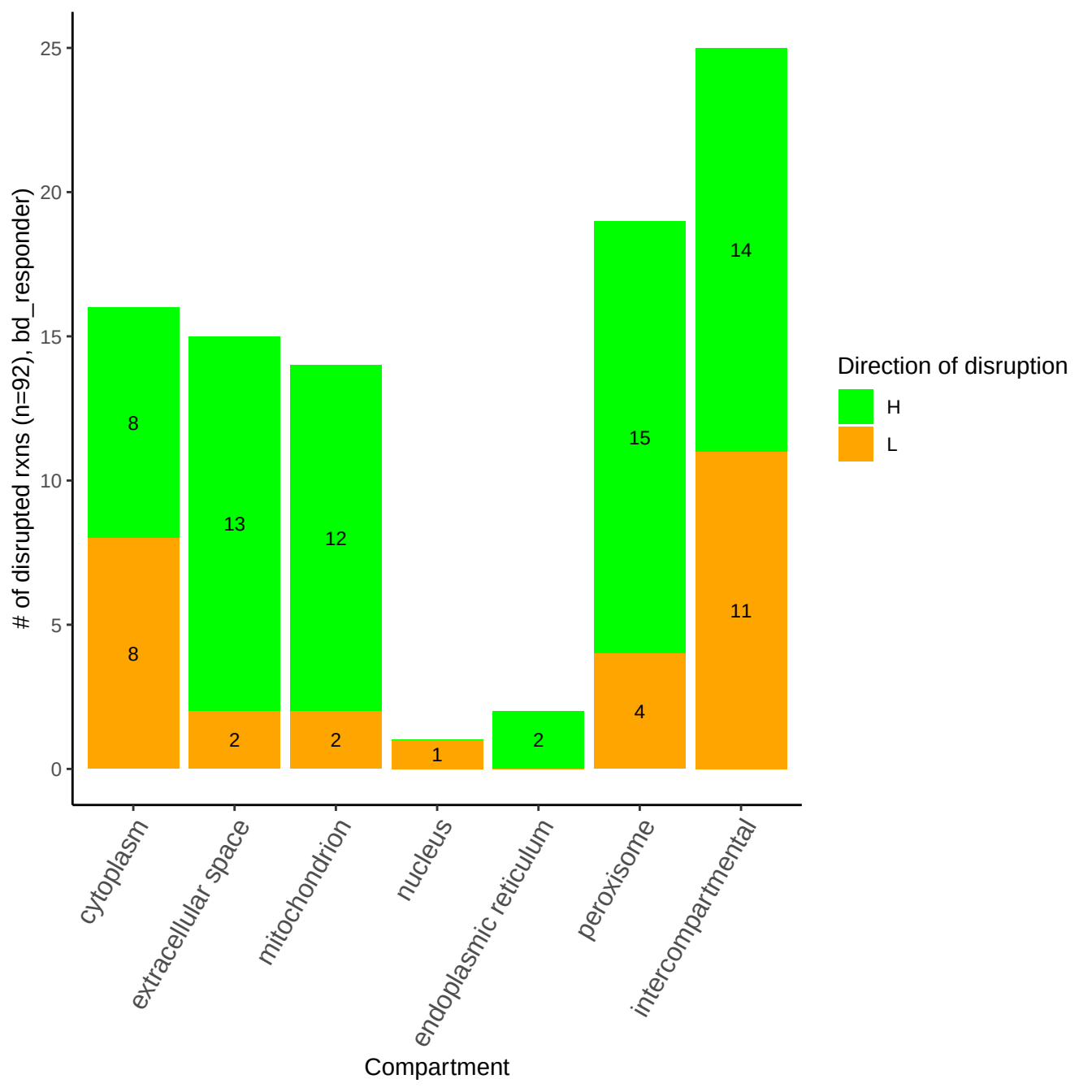

BD_Responder metabolic model
Subsystems disrupted
Fatty acid oxidation
Transport, nuclear
Vitamin A metabolism
Beta−Alanine metabolism
Purine catabolism
Methionine and cysteine metabolism
Pyrimidine synthesis
Nucleotide interconversion
Exchange
Steroid metabolism
Transport, endoplasmic reticular
Tyrosine metabolism
Transport, peroxisomal
Inositol phosphate metabolism
Miscellaneous
Eicosanoid metabolism
Transport, mitochondrial
Exchange/demand reaction
Transport, extracellular
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)

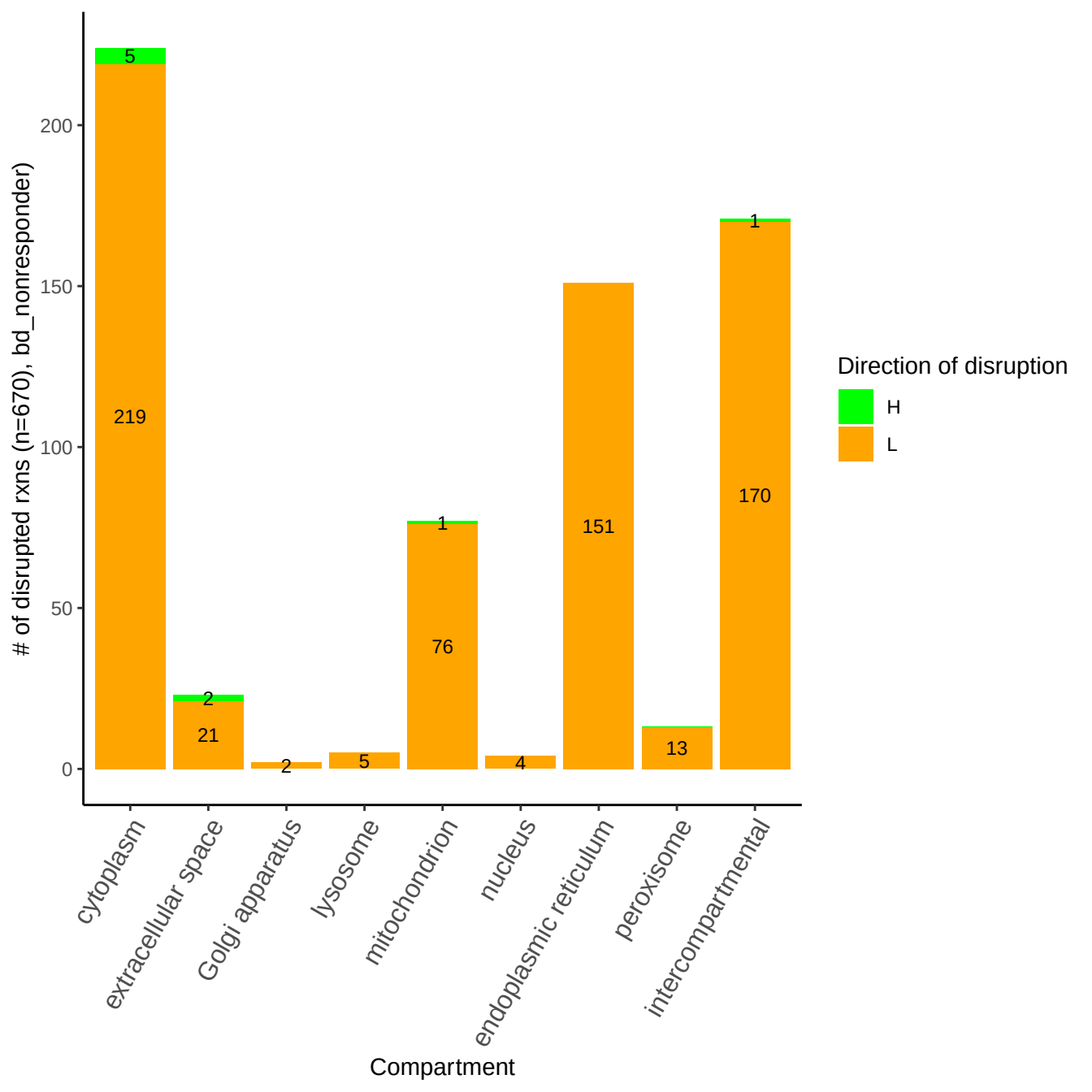

Transport, extracellular
Fatty acid oxidation
Cholesterol metabolism
Fatty acid synthesis
Inositol phosphate metabolism
Exchange/demand reaction
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Biotin metabolism
Transport, endoplasmic reticular
Pyrimidine catabolism
Glycerophospholipid metabolism
Transport, peroxisomal
Transport, nuclear
Purine catabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Transport, golgi apparatus
Propanoate metabolism
Glutamate metabolism
Urea cycle
Starch and sucrose metabolism
Sphingolipid metabolism
NAD metabolism
Methionine and cysteine metabolism
Citric acid cycle
Bile acid synthesis
Valine, leucine, and isoleucine metabolism
Glyoxylate and dicarboxylate metabolism
Glycine, serine, alanine, and threonine metabolism
Vitamin B2 metabolism
Glutathione metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Fructose and mannose metabolism
Eicosanoid metabolism
Aminosugar metabolism
0
20
40
60
80
100
# of disrupted rxns (n=670, bd_nonresponder) per subSystem


Transport, extracellular
Fatty acid oxidation
Cholesterol metabolism
Fatty acid synthesis
Inositol phosphate metabolism
Exchange/demand reaction
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Biotin metabolism
Transport, endoplasmic reticular
Pyrimidine catabolism
Glycerophospholipid metabolism
Transport, peroxisomal
Transport, nuclear
Purine catabolism
Phosphatidylinositol phosphate metabolism
Vitamin B6 metabolism
Transport, golgi apparatus
Propanoate metabolism
Glutamate metabolism
Urea cycle
Starch and sucrose metabolism
Sphingolipid metabolism
NAD metabolism
Methionine and cysteine metabolism
Citric acid cycle
Bile acid synthesis
Valine, leucine, and isoleucine metabolism
Glyoxylate and dicarboxylate metabolism
Glycine, serine, alanine, and threonine metabolism
Vitamin B2 metabolism
Glutathione metabolism
Folate metabolism
Sink
Pyruvate metabolism
Pyrimidine synthesis
Pentose phosphate pathway
Nucleotide metabolism
Heme degradation
Glycosphingolipid metabolism
Fructose and mannose metabolism
Eicosanoid metabolism
Aminosugar metabolism
0
200
400
600
800
1000
1200
1400
# of disrupted rxns (n=670, bd_nonresponder) per subSystem


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


60
40
20
0
# of disrupted rxns (n=212), bd_lumped)
24
43
17
18
11
40
6
17
36
cytoplasm
extracellular space
mitochondrion
endoplasmic reticulum
intercompartmental
Compartment
Direction of disruption
H
L


25
20
15
10
5
0
# of disrupted rxns (n=92), bd_responder)
8
8
13
2
12
2
1
2
15
4
14
11
cytoplasm
extracellular space
mitochondrion
nucleus
endoplasmic reticulum
peroxisome
intercompartmental
Compartment
Direction of disruption
H
L


5
219
2
21
2
5
1
76
4
151
13
1
170
200
150
100
50
0
# of disrupted rxns (n=670), bd_nonresponder)
cytoplasm
extracellular space
Golgi apparatus
lysosome
mitochondrion
nucleus
endoplasmic reticulum
peroxisome
intercompartmental
Compartment
Direction of disruption
H
L