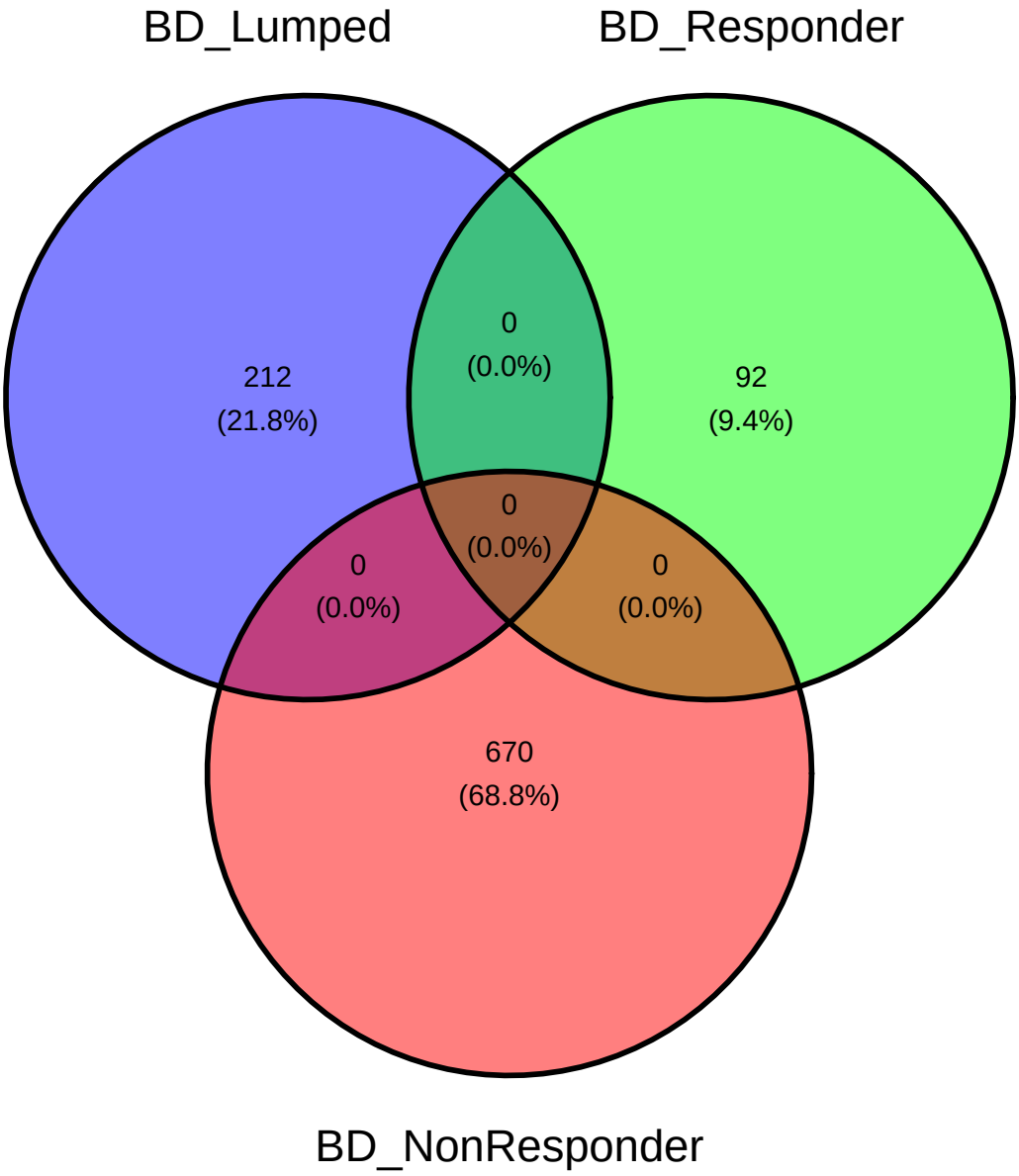
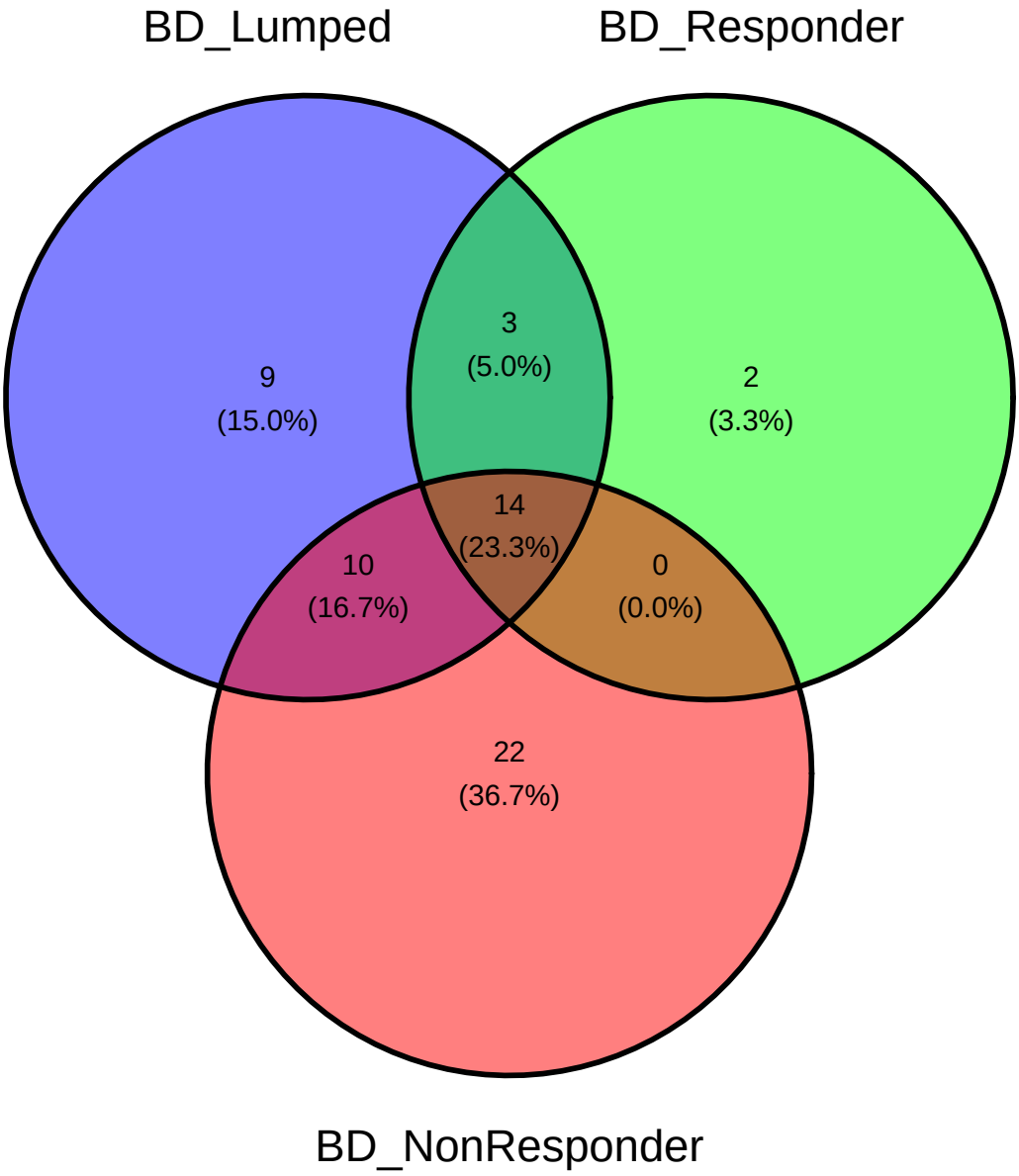
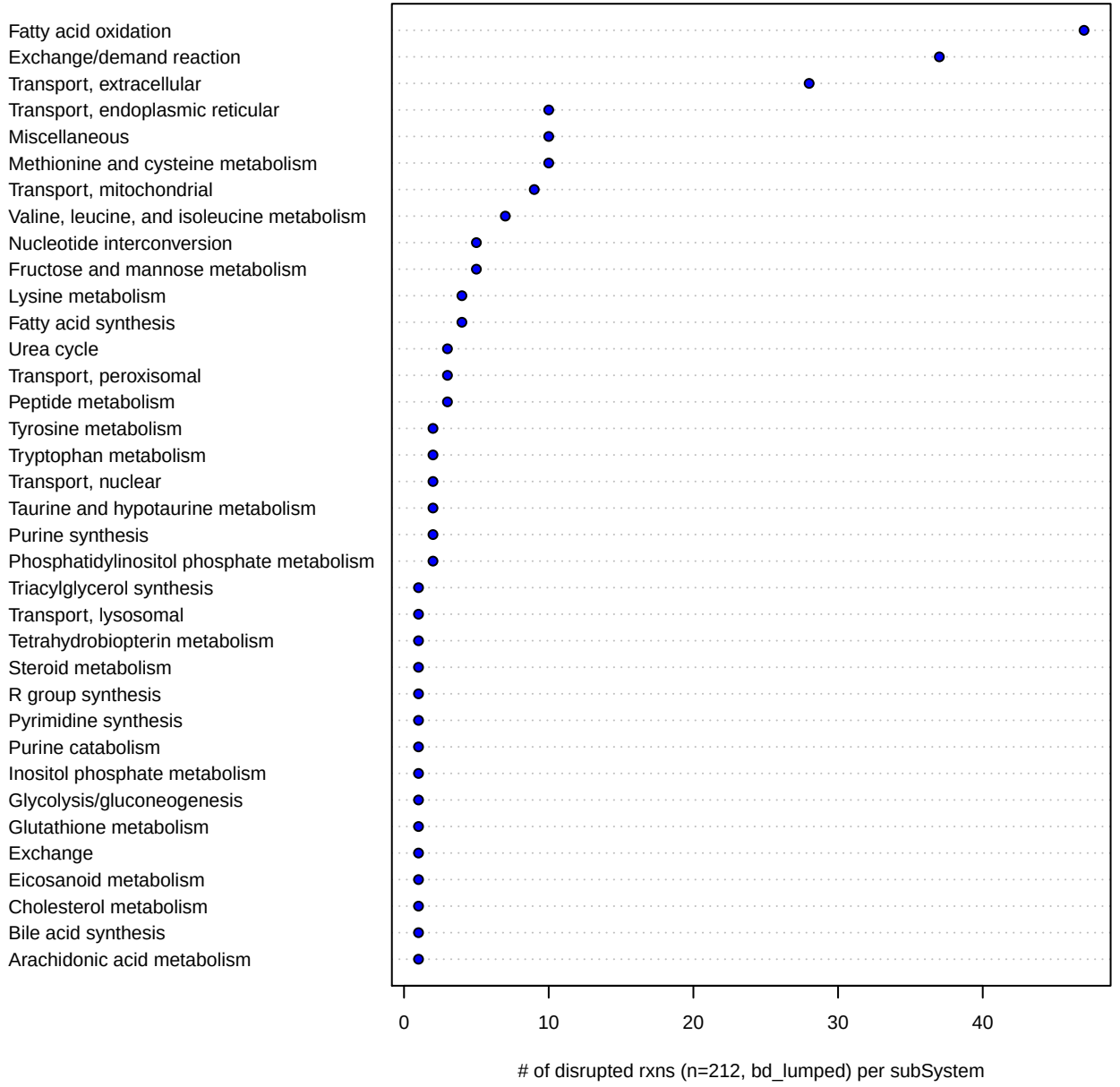
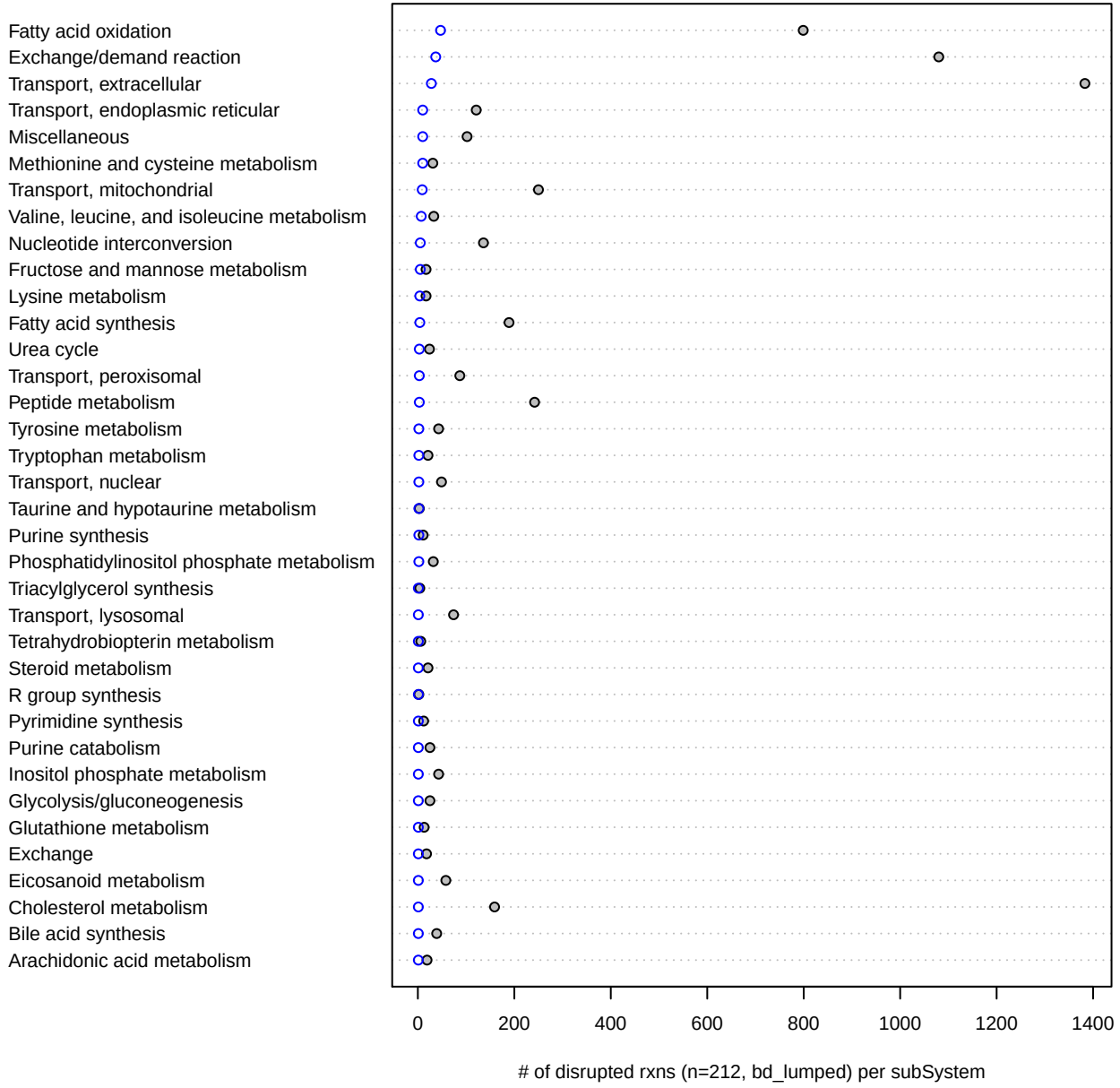
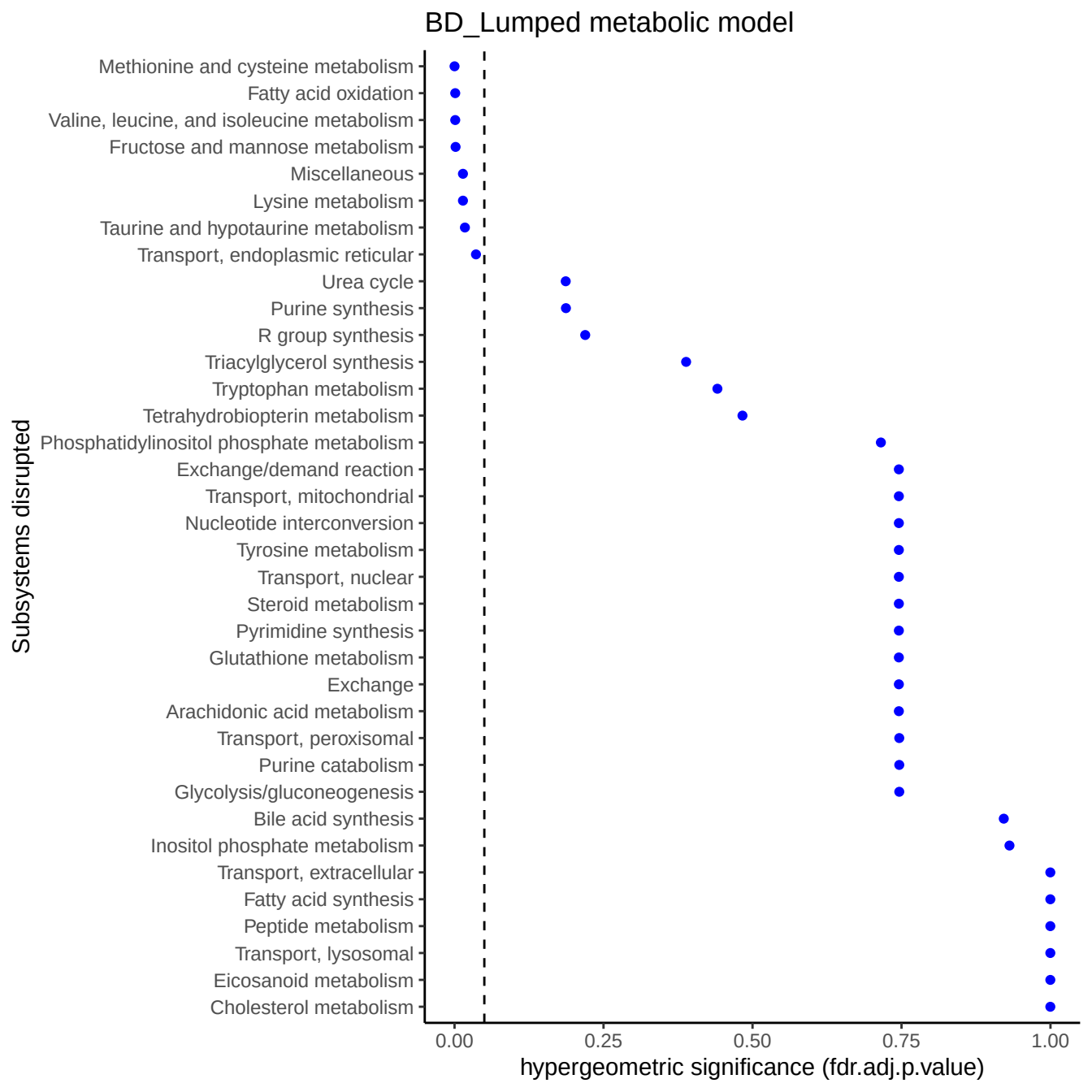
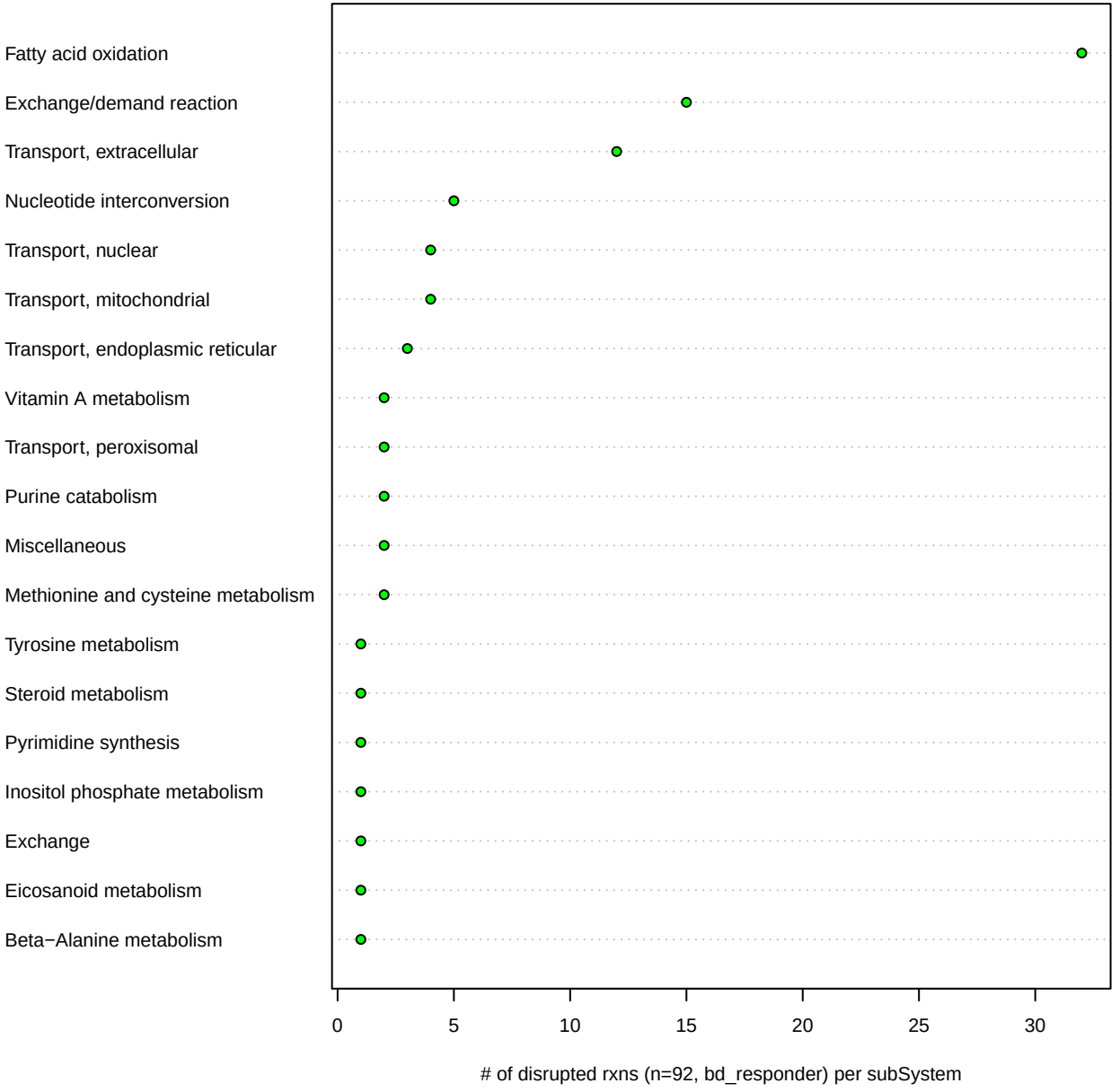

BD_Lumped
BD_Responder
212
(21.8%)
0
(0.0%)
92
(9.4%)
0
(0.0%)
0
(0.0%)
0
(0.0%)
670
(68.8%)
BD_NonResponder

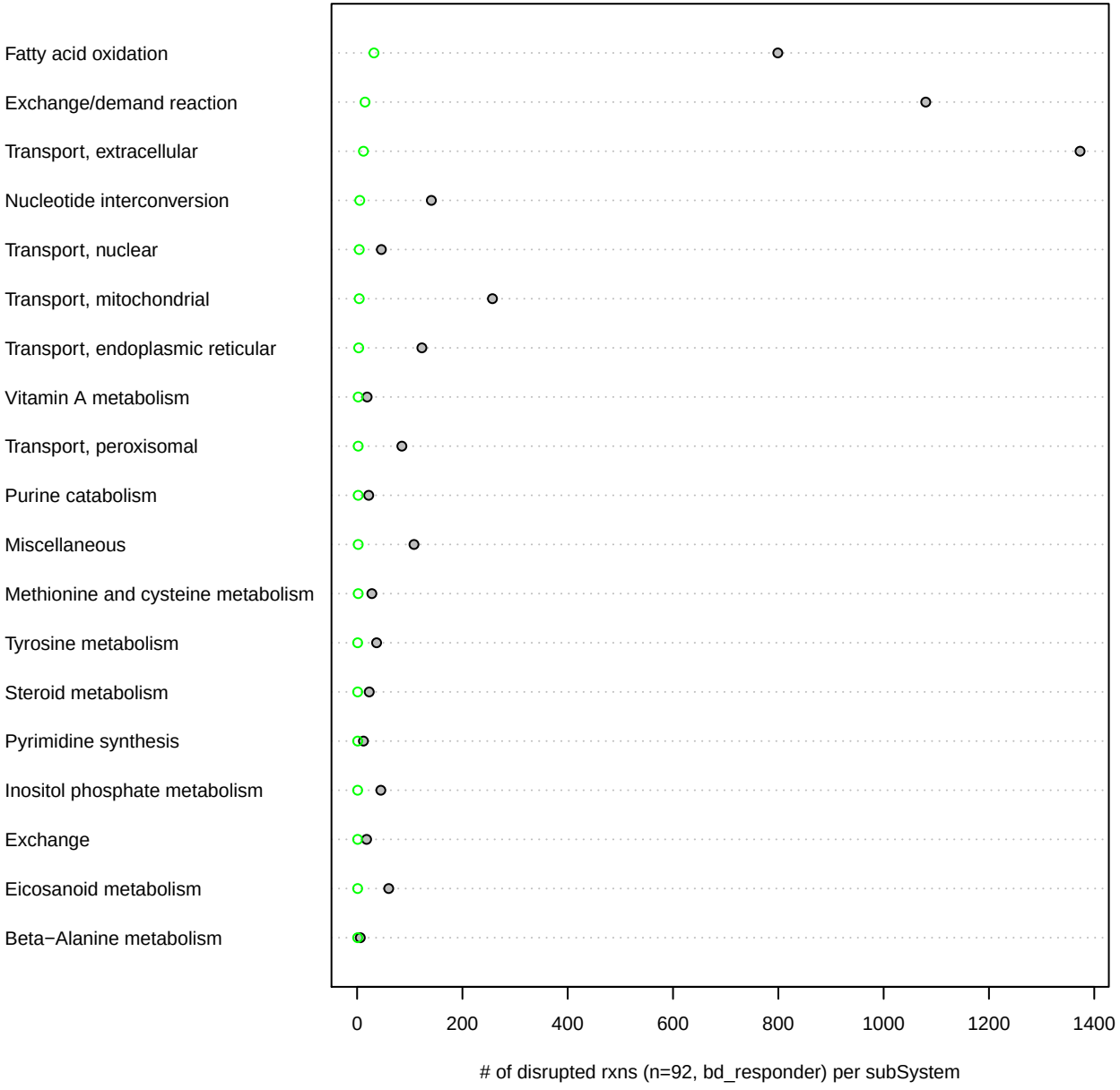

BD_Lumped
BD_Responder
9
(15.0%)
3
(5.0%)
2
(3.3%)
14
(23.3%)
10
(16.7%)
0
(0.0%)
22
(36.7%)
BD_NonResponder

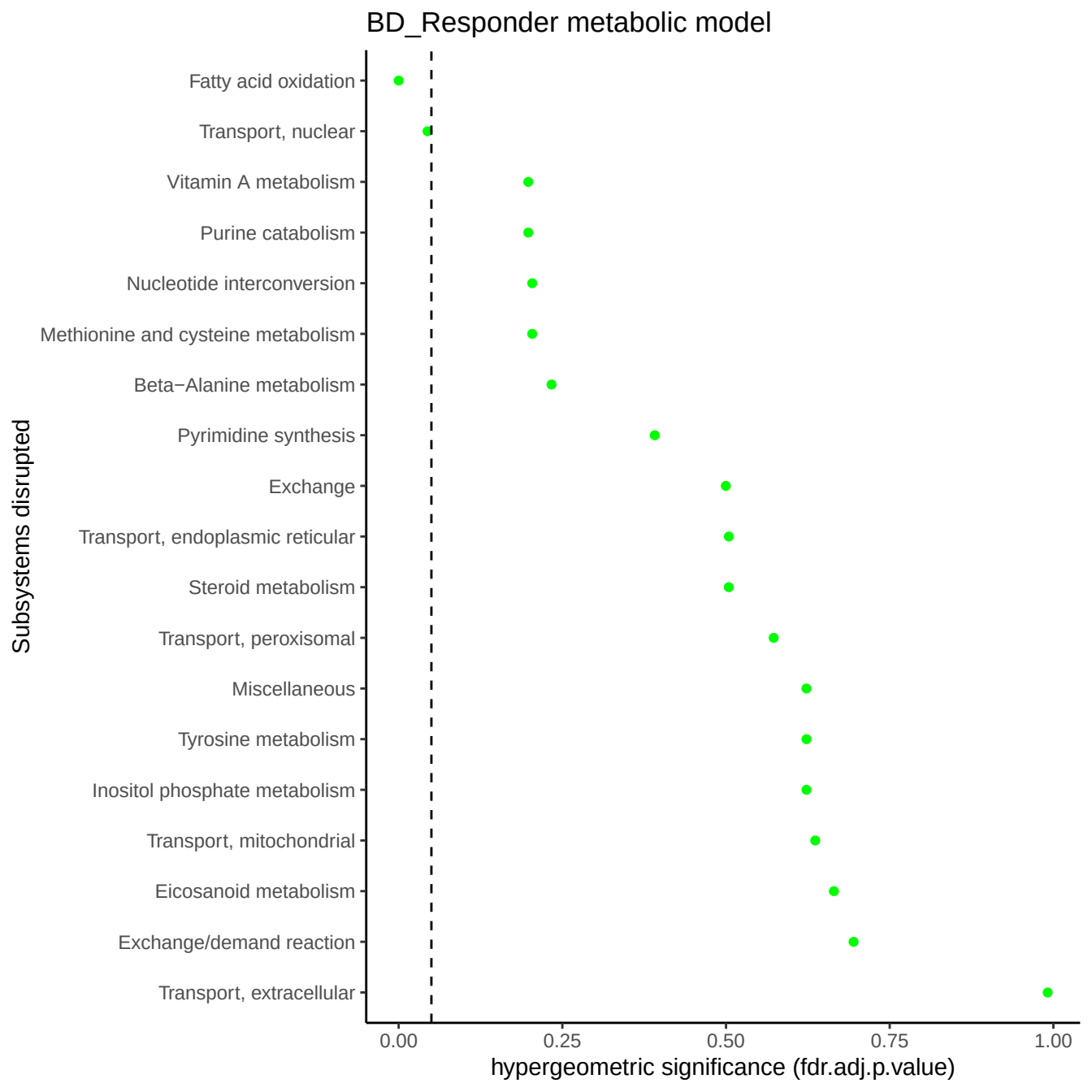

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Transport, endoplasmic reticular
Miscellaneous
Methionine and cysteine metabolism
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose metabolism
Lysine metabolism
Fatty 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

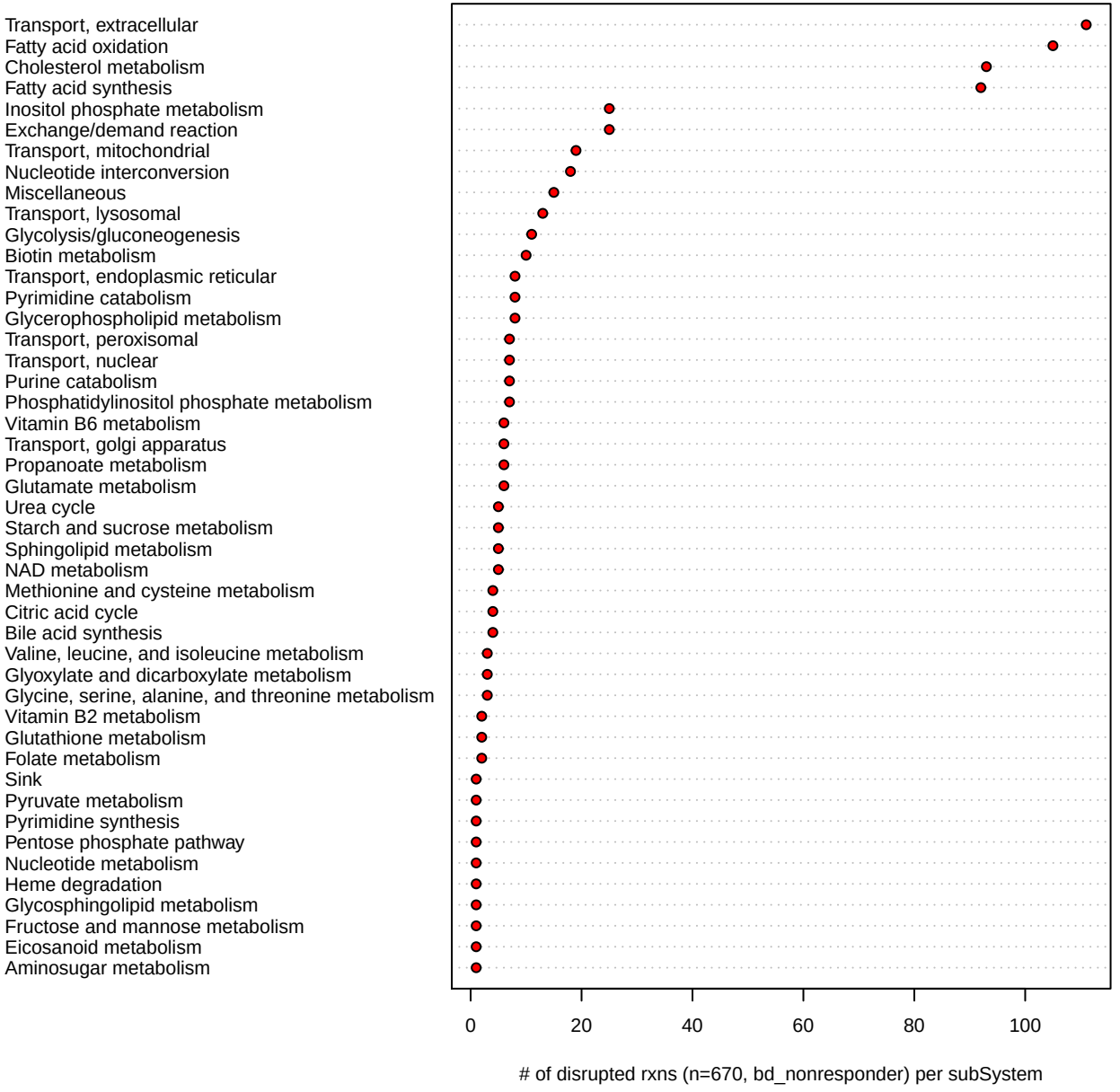

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Transport, endoplasmic reticular
Miscellaneous
Methionine and cysteine metabolism
Transport, mitochondrial
Valine, leucine, and isoleucine metabolism
Nucleotide interconversion
Fructose and mannose metabolism
Lysine metabolism
Fatty 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

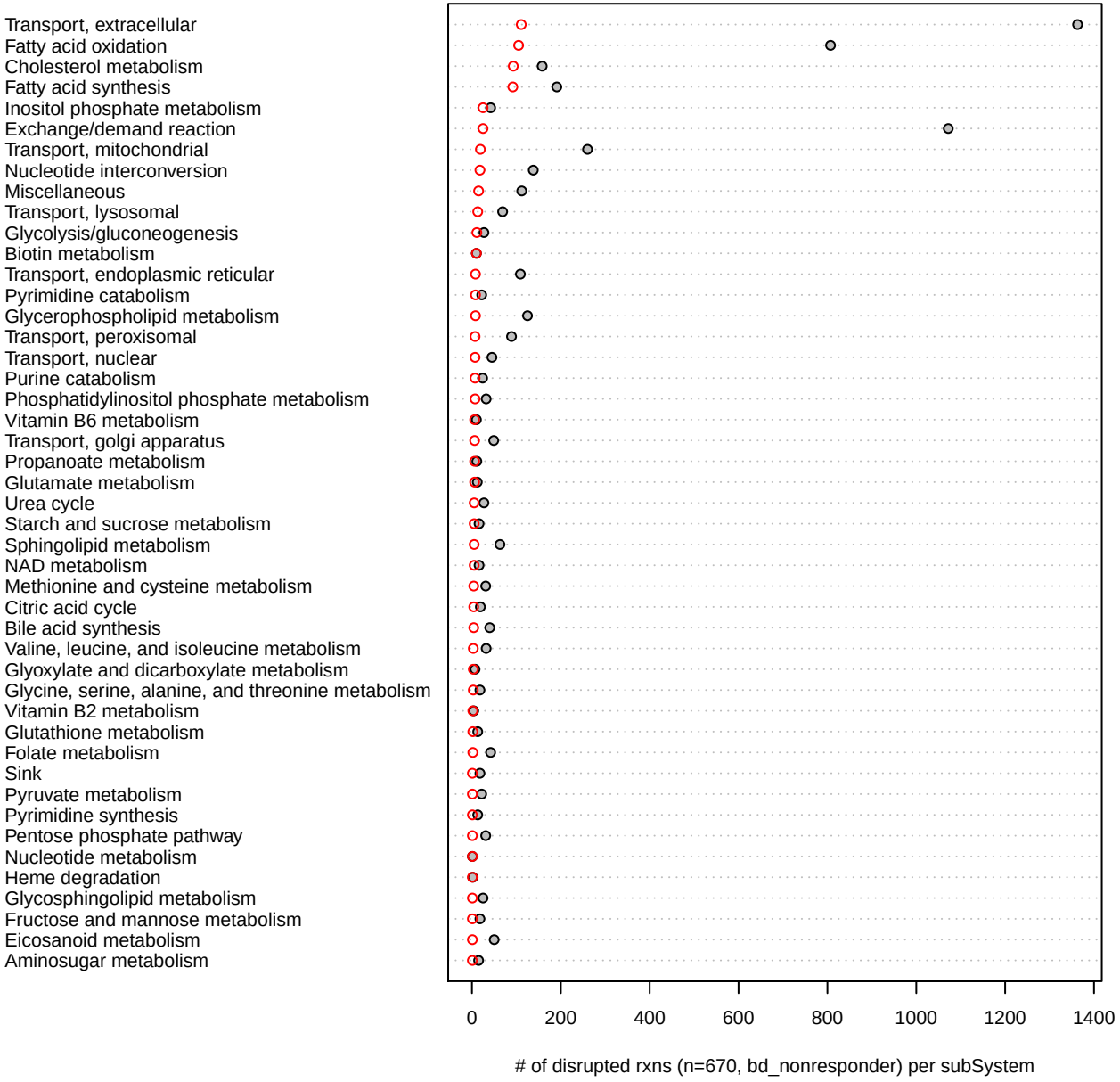

BD_Lumped metabolic model
Methionine and cysteine metabolism
Fatty acid oxidation
Valine, leucine, and isoleucine metabolism
Fructose and mannose metabolism
Miscellaneous
Lysine metabolism
Taurine and hypotaurine metabolism
Transport, endoplasmic reticular
Urea cycle
Purine synthesis
R group synthesis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

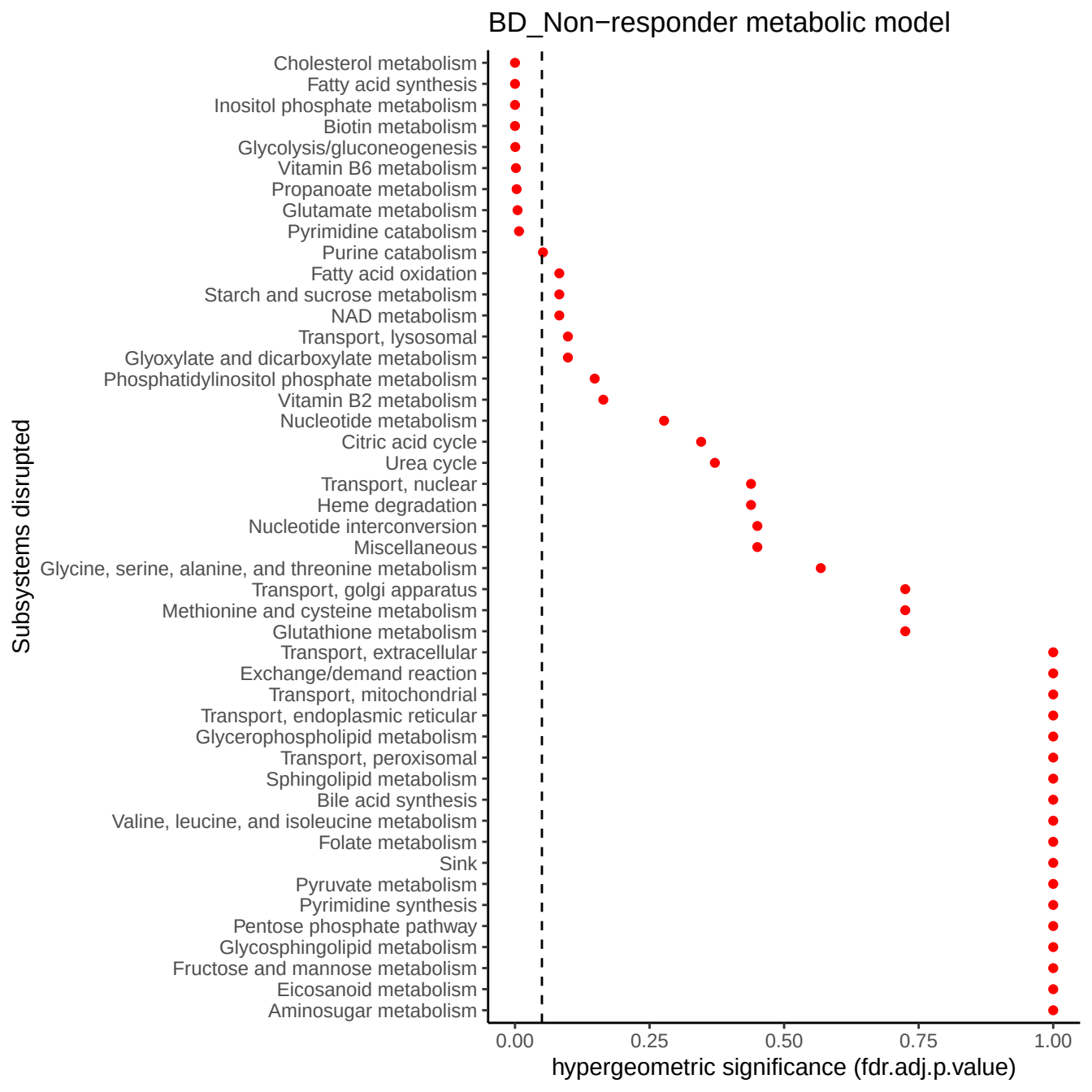

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Nucleotide interconversion
Transport, nuclear
Transport, mitochondrial
Transport, endoplasmic reticular
Vitamin A metabolism
Transport, peroxisomal
Purine catabolism
Miscellaneous
Methionine and cysteine metabolism
Tyrosine metabolism
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

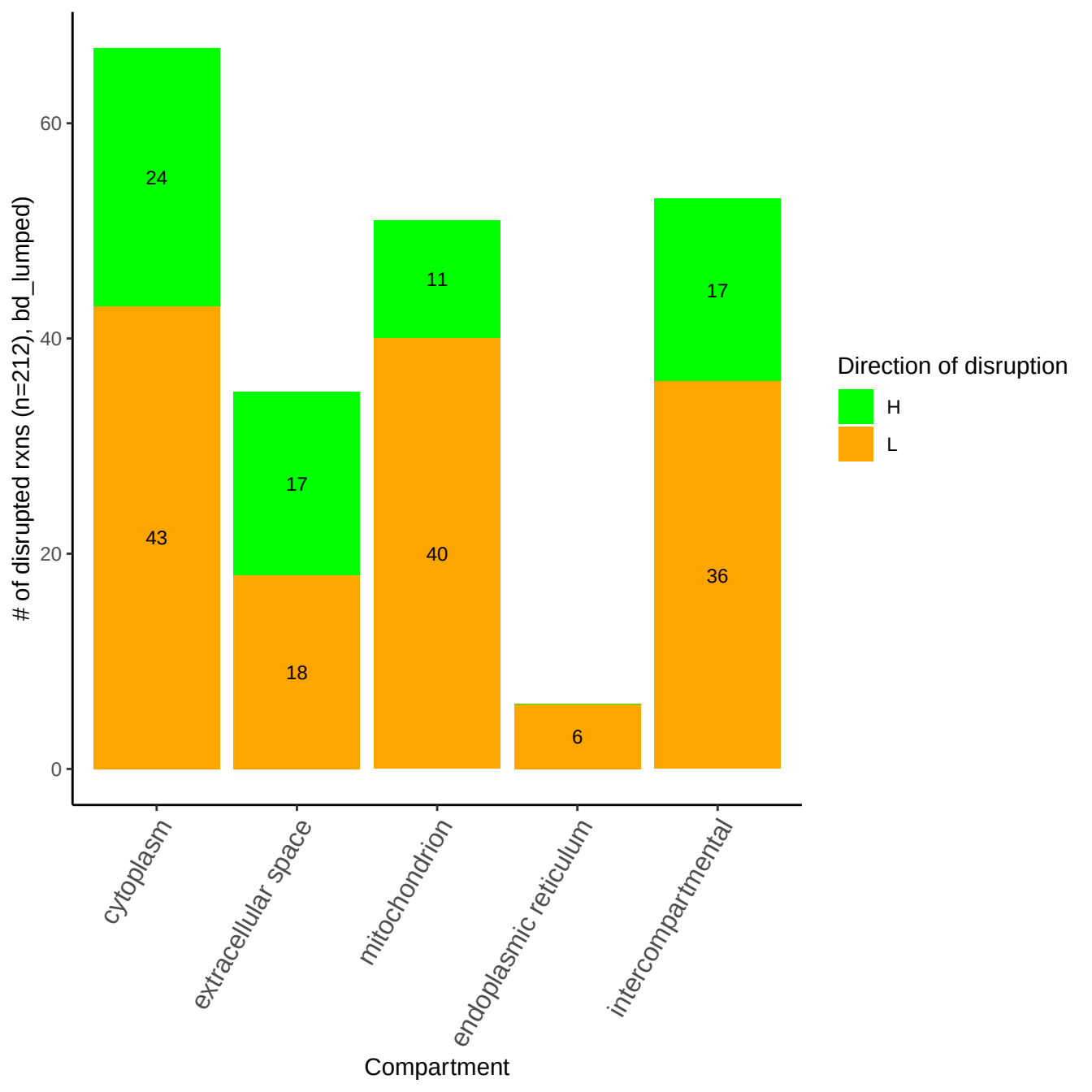

Fatty acid oxidation
Exchange/demand reaction
Transport, extracellular
Nucleotide interconversion
Transport, nuclear
Transport, mitochondrial
Transport, endoplasmic reticular
Vitamin A metabolism
Transport, peroxisomal
Purine catabolism
Miscellaneous
Methionine and cysteine metabolism
Tyrosine metabolism
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

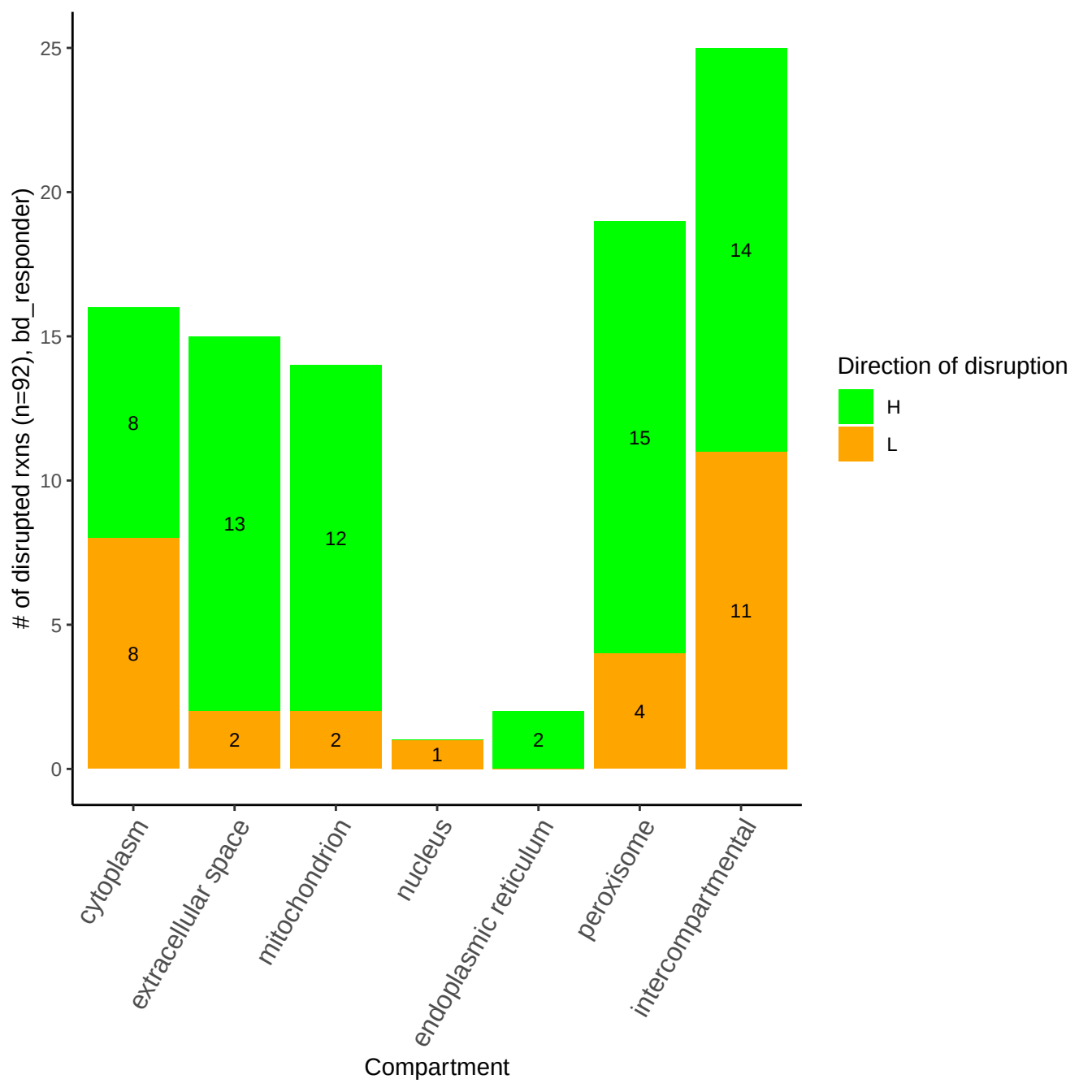

BD_Responder metabolic model
Fatty acid oxidation
Transport, nuclear
Vitamin A metabolism
Purine catabolism
Nucleotide interconversion
Methionine and cysteine metabolism
Beta−Alanine metabolism
Pyrimidine synthesis
Exchange
Transport, endoplasmic reticular
Steroid metabolism
Transport, peroxisomal
Miscellaneous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

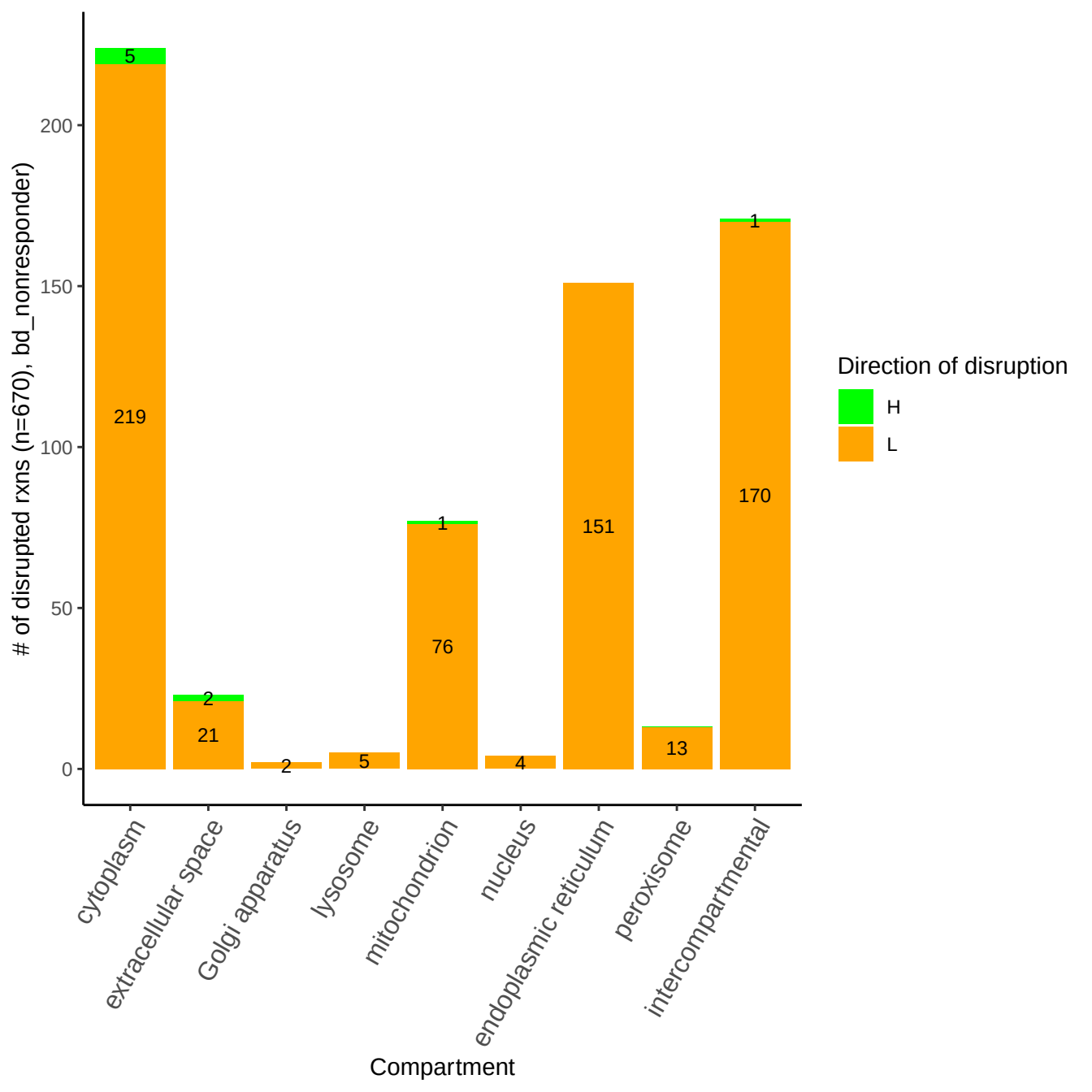

Transport, extracellular
Fatty acid oxidation
Cholesterol metabolism
Fatty acid synthesis
Inositol phosphate metabolism
Exchange/demand reaction
Transport, mitochondrial
Nucleotide interconversion
Miscellaneous
Transport, lysosomal
Glycolysis/gluconeogenesis
Biotin metabolism
Transport, endoplasmic reticular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


# of disrupted rxns (n=92), bd_responder)
25
20
15
10
5
0
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