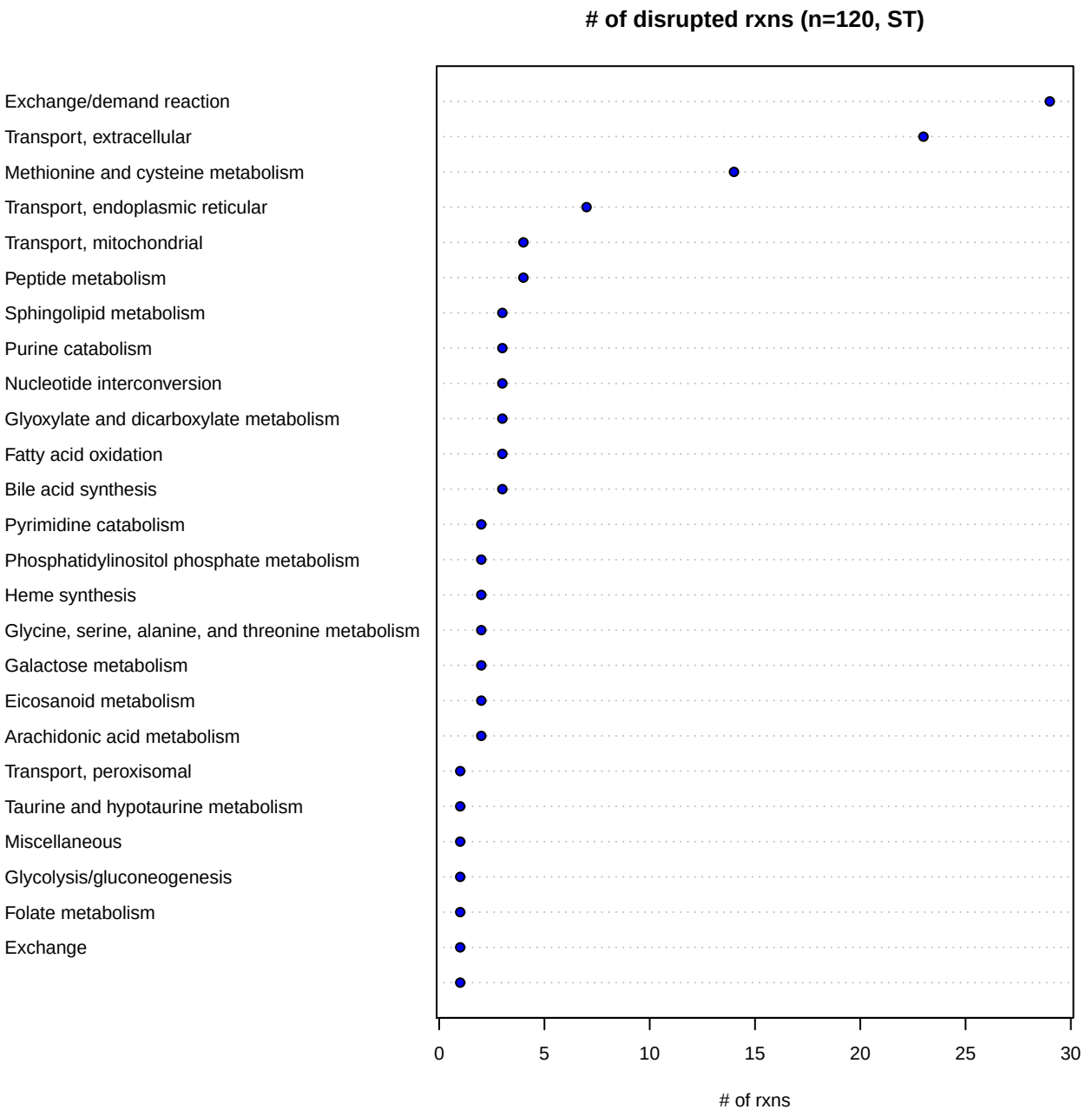
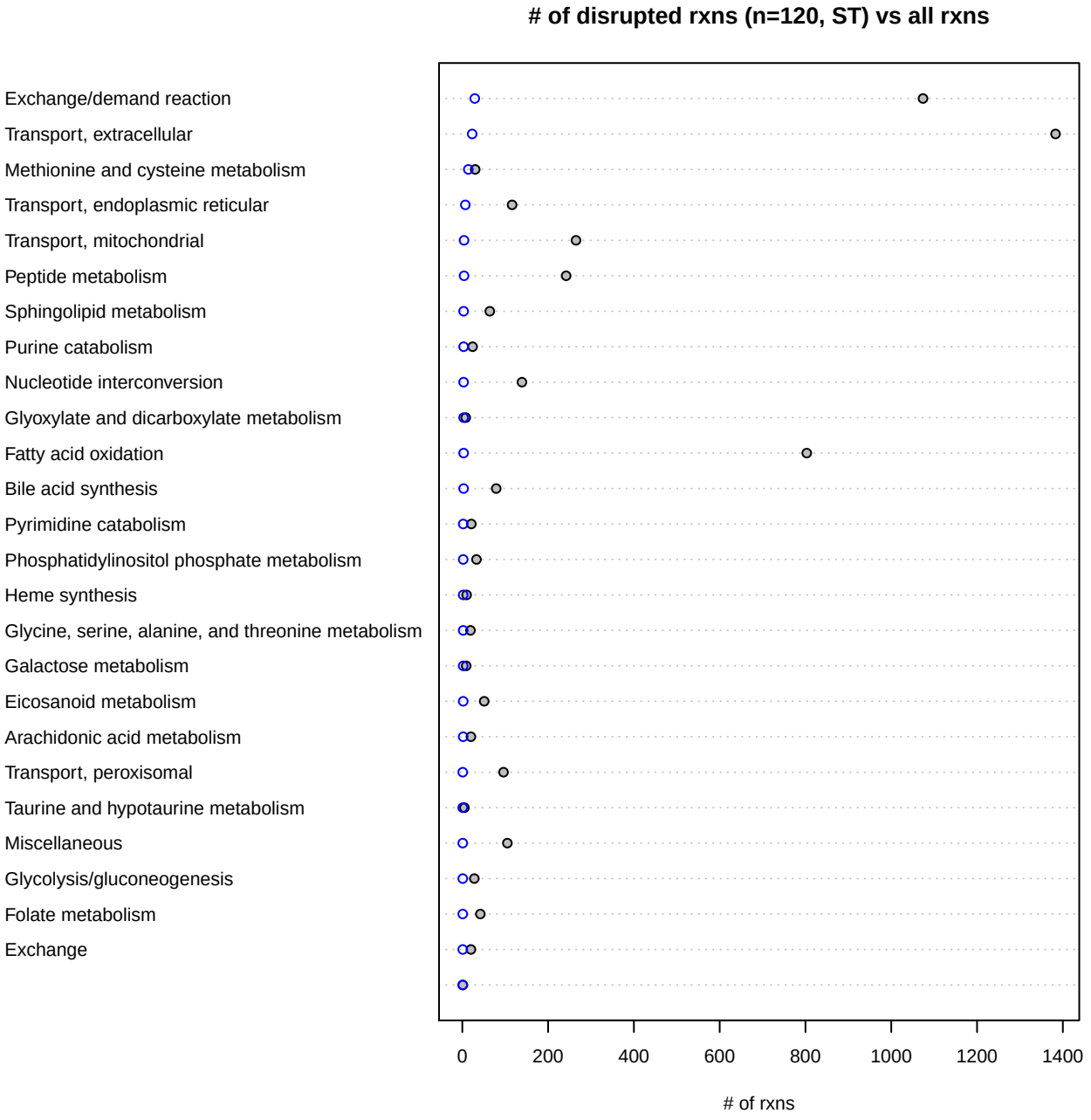
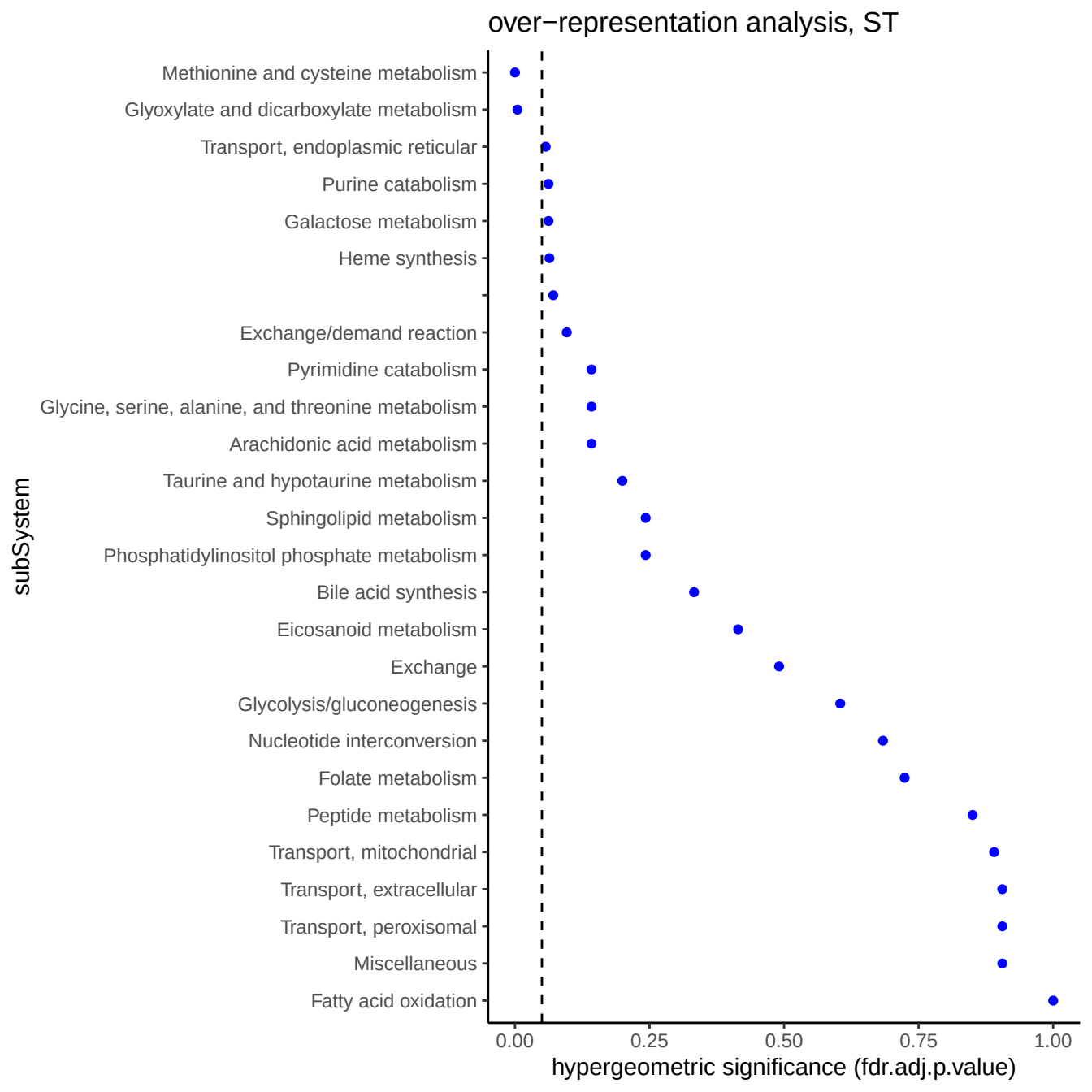
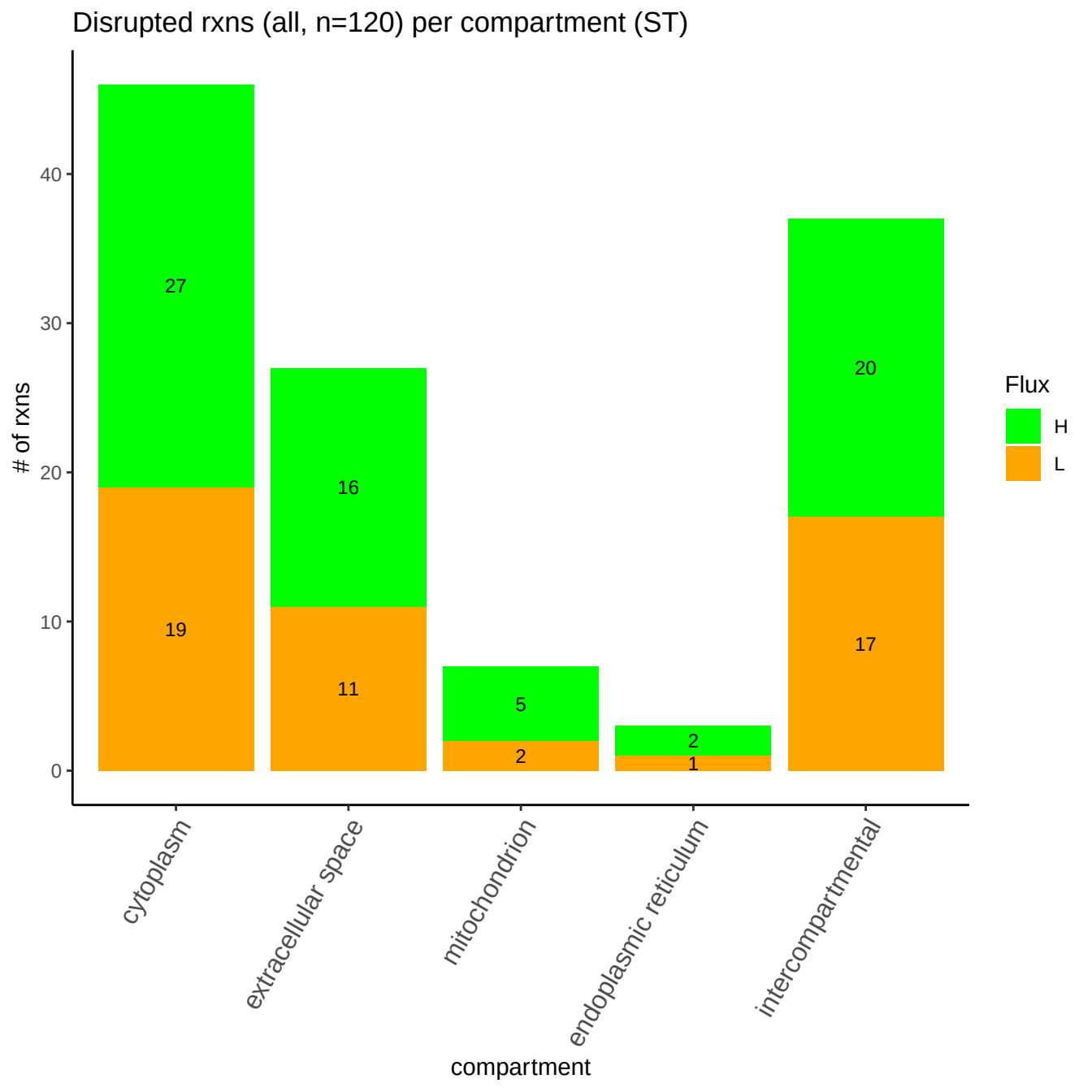
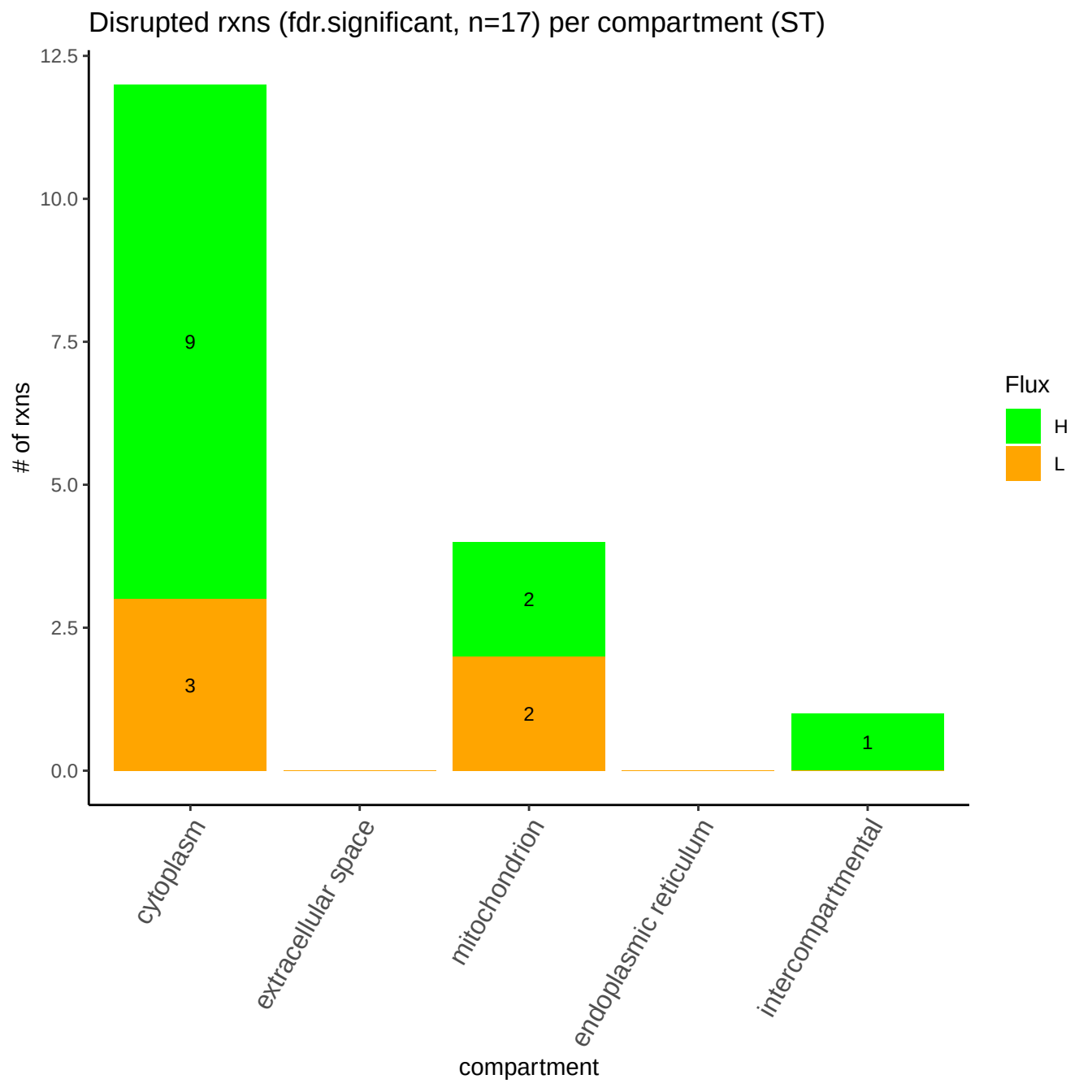

# of disrupted rxns (n=120, ST)
Exchange/demand reaction
Transport, extracellular
Methionine and cysteine metabolism
Transport, endoplasmic reticular
Transport, mitochondrial
Peptide metabolism
Sphingolipid metabolism
Purine catabolism
Nucleotide interconversion
Glyoxylate and dicarboxylate metabolism
Fatty acid oxidation
Bile acid synthesis
Pyrimidine catabolism
Phosphatidylinositol phosphate metabolism
Heme synthesis
Glycine, serine, alanine, and threonine metabolism
Galactose metabolism
Eicosanoid metabolism
Arachidonic acid metabolism
Transport, peroxisomal
Taurine and hypotaurine metabolism
Miscellaneous
Glycolysis/gluconeogenesis
Folate metabolism
Exchange
0
5
10
15
20
25
30
# of rxns


# of disrupted rxns (n=120, ST) vs all rxns
Exchange/demand reaction
Transport, extracellular
Methionine and cysteine metabolism
Transport, endoplasmic reticular
Transport, mitochondrial
Peptide metabolism
Sphingolipid metabolism
Purine catabolism
Nucleotide interconversion
Glyoxylate and dicarboxylate metabolism
Fatty acid oxidation
Bile acid synthesis
Pyrimidine catabolism
Phosphatidylinositol phosphate metabolism
Heme synthesis
Glycine, serine, alanine, and threonine metabolism
Galactose metabolism
Eicosanoid metabolism
Arachidonic acid metabolism
Transport, peroxisomal
Taurine and hypotaurine metabolism
Miscellaneous
Glycolysis/gluconeogenesis
Folate metabolism
Exchange
0
200
400
600
800
1000
1200
1400
# of rxns


over−representation analysis, ST
Methionine and cysteine metabolism
Glyoxylate and dicarboxylate metabolism
Transport, endoplasmic reticular
Purine catabolism
Galactose metabolism
Heme synthesis
Exchange/demand reaction
Pyrimidine catabolism
Glycine, serine, alanine, and threonine metabolism
Arachidonic acid metabolism
Taurine and hypotaurine metabolism
Sphingolipid metabolism
Phosphatidylinositol phosphate metabolism
Bile acid synthesis
Eicosanoid metabolism
Exchange
Glycolysis/gluconeogenesis
Nucleotide interconversion
Folate metabolism
Peptide metabolism
Transport, mitochondrial
Transport, extracellular
Transport, peroxisomal
Miscellaneous
Fatty acid oxidation
subSystem
0.00
0.25
0.50
0.75
1.00
hypergeometric significance (fdr.adj.p.value)


Disrupted rxns (all, n=120) per compartment (ST)
# of rxns
0
10
20
30
40
27
19
16
11
5
2
2
1
20
17
cytoplasm
extracellular space
mitochondrion
endoplasmic reticulum
intercompartmental
compartment
Flux
H
L


Disrupted rxns (fdr.significant, n=17) per compartment (ST)
12.5
10.0
7.5
5.0
2.5
0.0
# of rxns
9
3
2
2
1
Flux
H
L
cytoplasm
extracellular space
mitochondrion
endoplasmic reticulum
intercompartmental
compartment