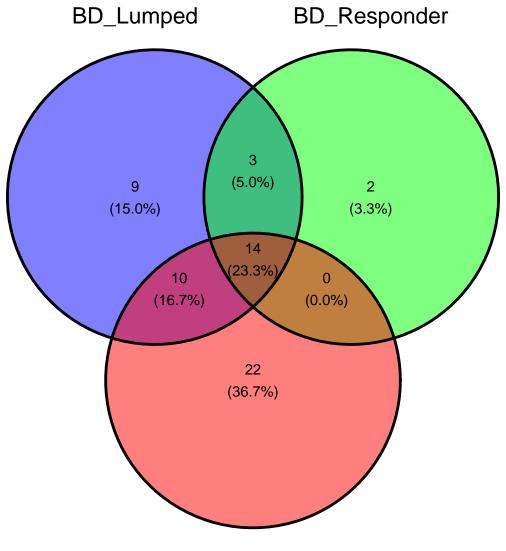
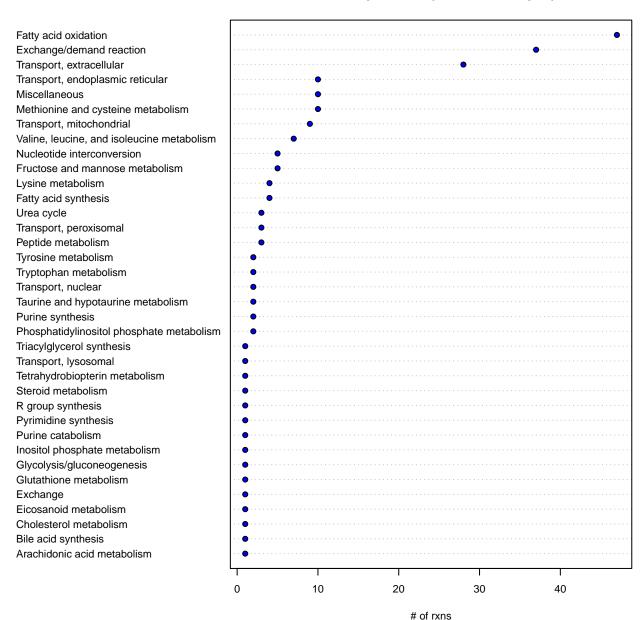


BD_NonResponder



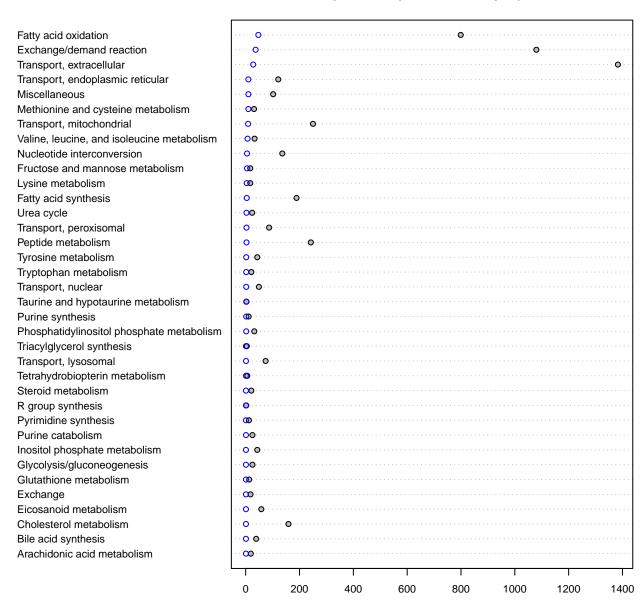
BD_NonResponder

of disrupted rxns (n=212, bd_lumped)



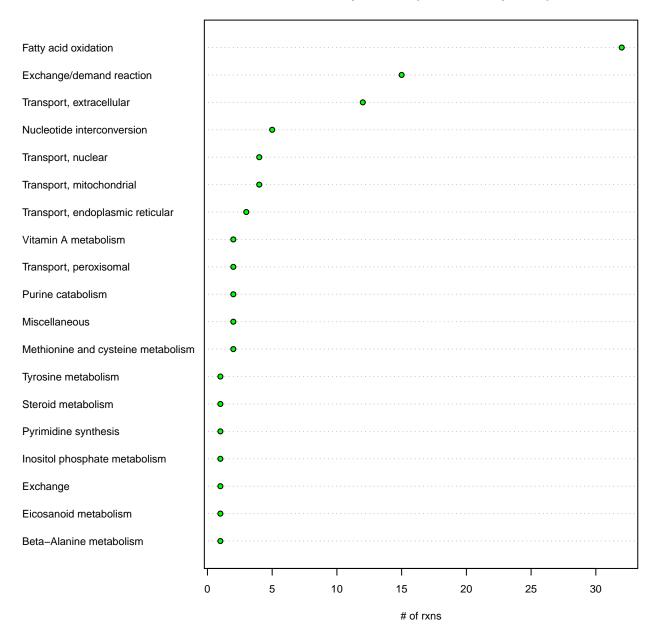
of disrupted rxns (n=212, bd_lumped) vs all rxns

of rxns

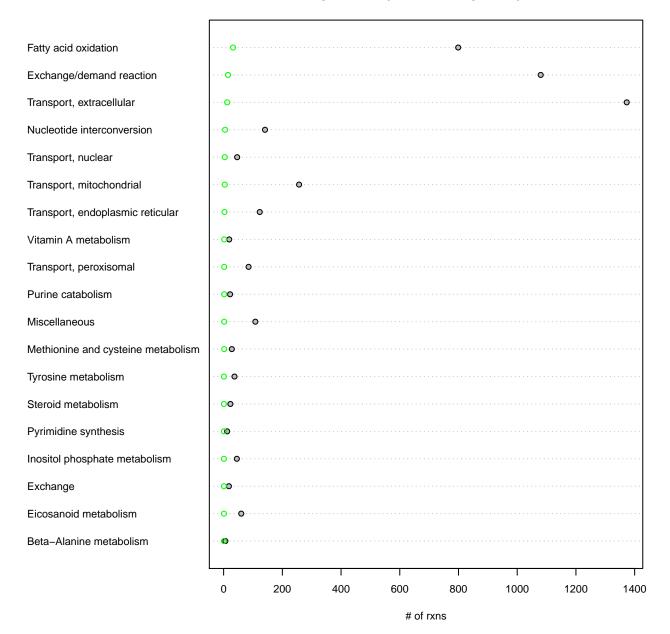


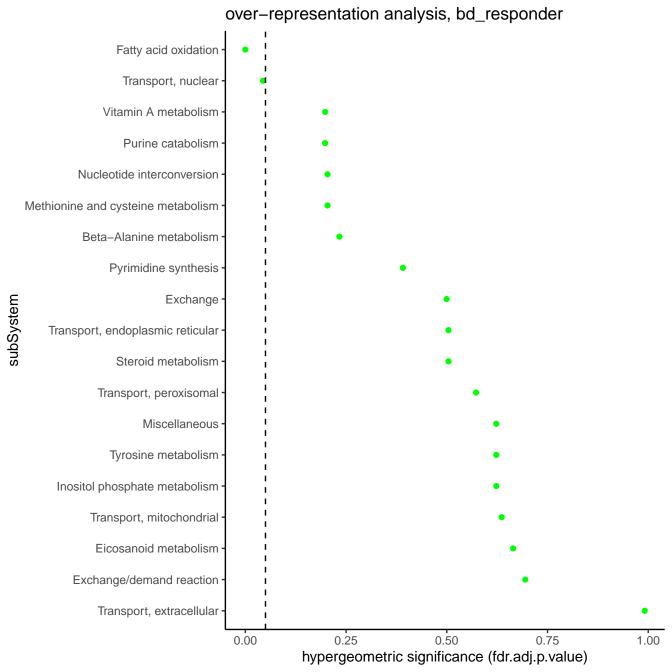
over-representation analysis, bd_lumped Methionine and cysteine metabolism -Fatty acid oxidation Valine, leucine, and isoleucine metabolism Fructose and mannose metabolism Miscellaneous Lysine metabolism Taurine and hypotaurine metabolism Transport, endoplasmic reticular Urea cycle Purine synthesis R group synthesis Triacylglycerol synthesis Tryptophan metabolism Tetrahydrobiopterin metabolism Phosphatidylinositol phosphate metabolism Exchange/demand reaction · subSystem 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 · 0.00 0.25 0.50 0.75 1.00 hypergeometric significance (fdr.adj.p.value)

of disrupted rxns (n=92, bd_responder)



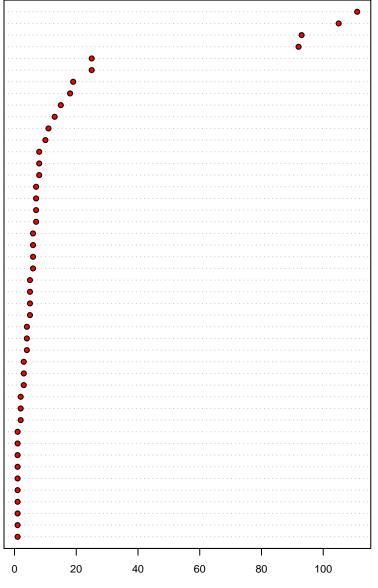
of disrupted rxns (n=92, bd_responder) vs all rxns





of disrupted rxns (n=670, bd_nonresponder)

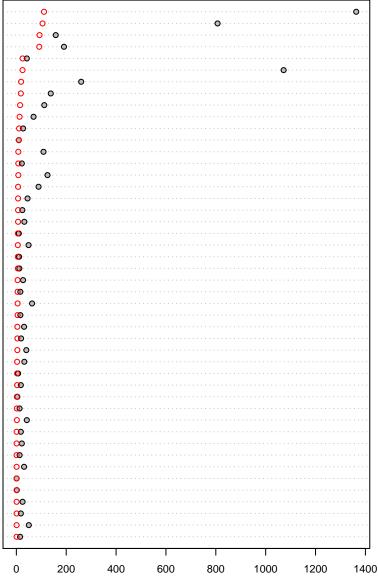




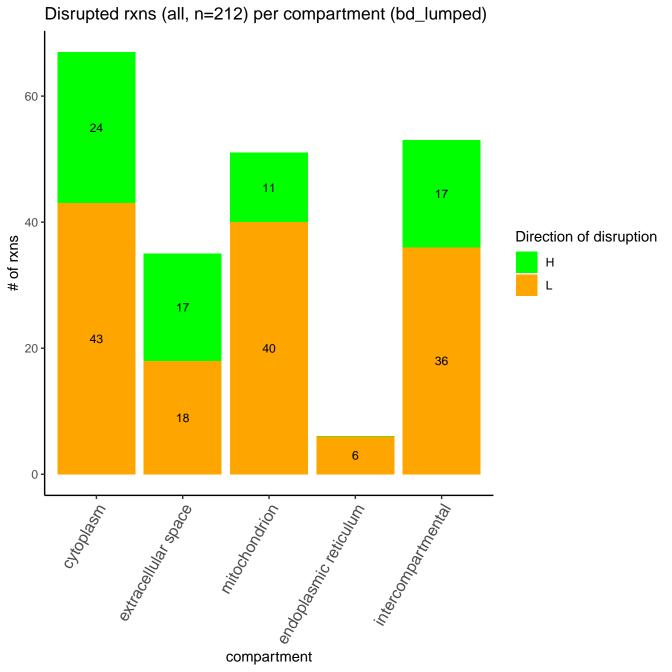
of rxns

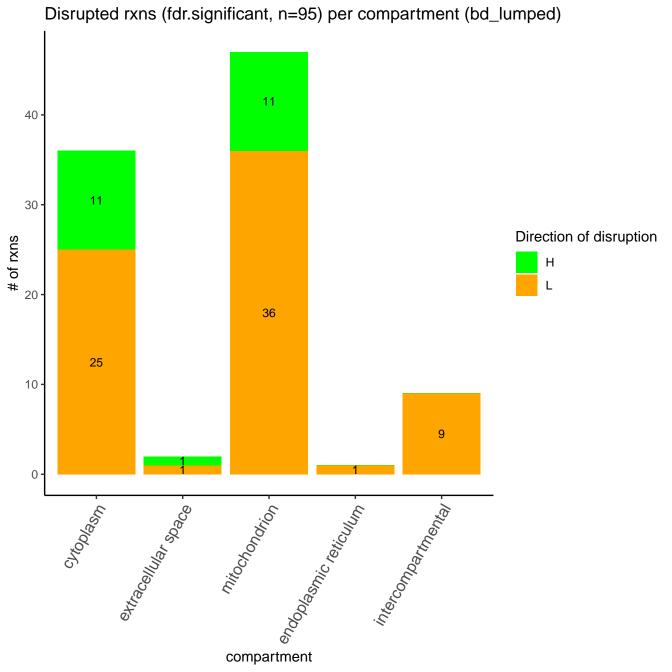
of disrupted rxns (n=670, bd_nonresponder) vs all rxns

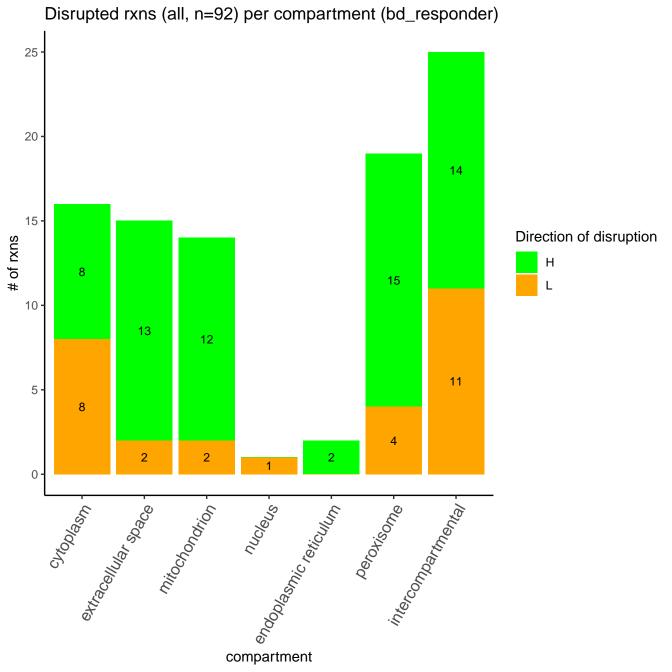


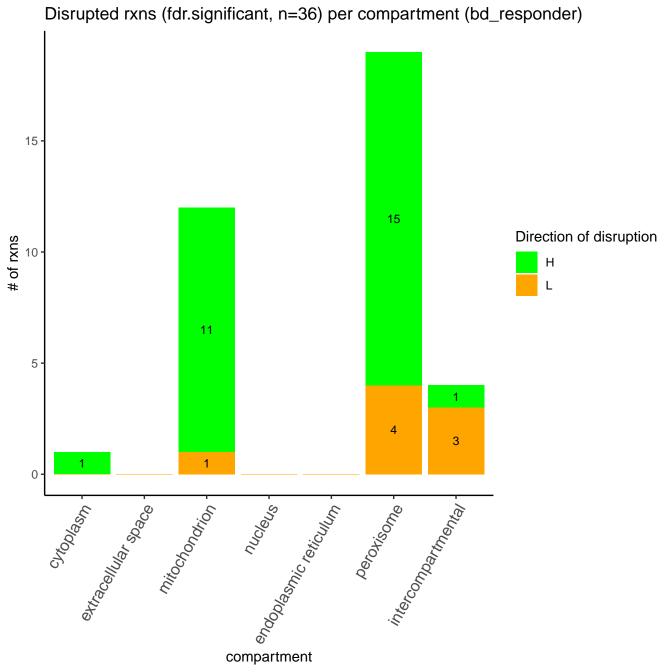


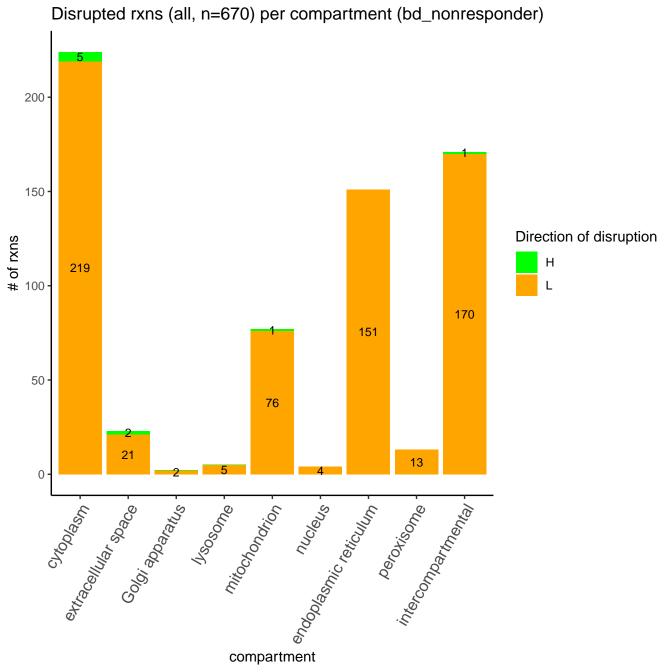
over-representation analysis, bd_nonresponder Cholesterol metabolism -Fatty acid synthesis Inositol phosphate metabolism Biotin metabolism Glycolysis/gluconeogenesis Vitamin B6 metabolism Propanoate metabolism Glutamate metabolism Pyrimidine catabolism Purine catabolism Fatty acid oxidation Starch and sucrose metabolism NAD metabolism Transport, lysosomal Glyoxylate and dicarboxylate metabolism Phosphatidylinositol phosphate metabolism Vitamin B2 metabolism Nucleotide metabolism Citric acid cycle Urea cycle subSystem 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)

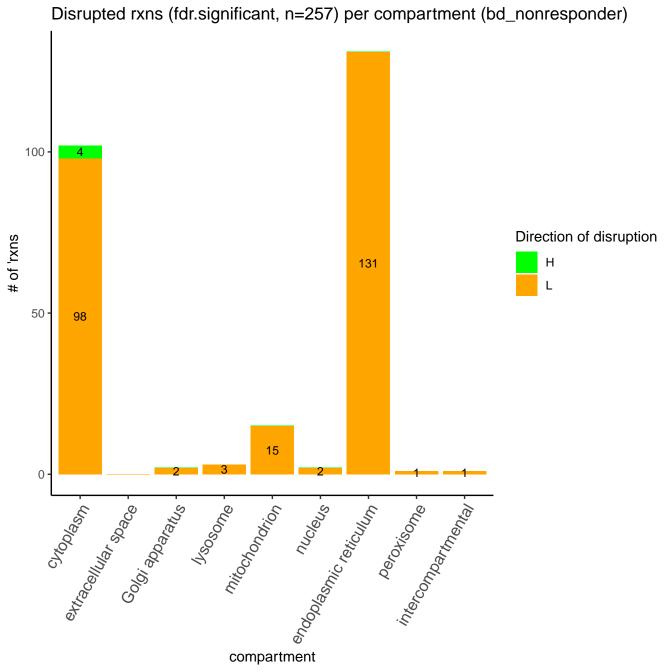


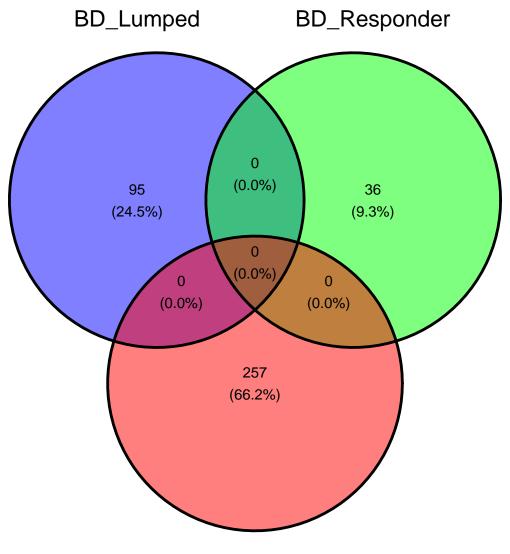




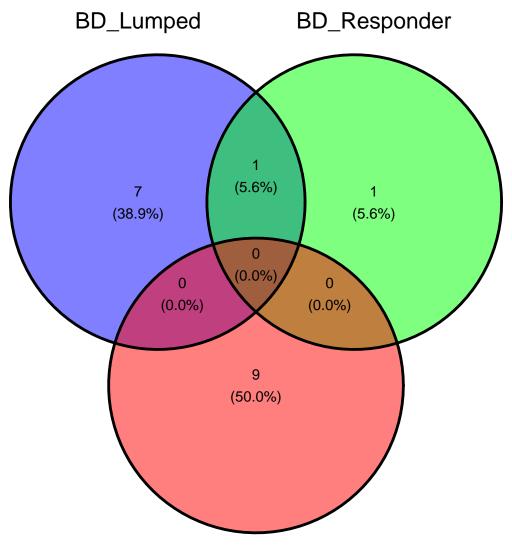








BD_NonResponder



BD_NonResponder