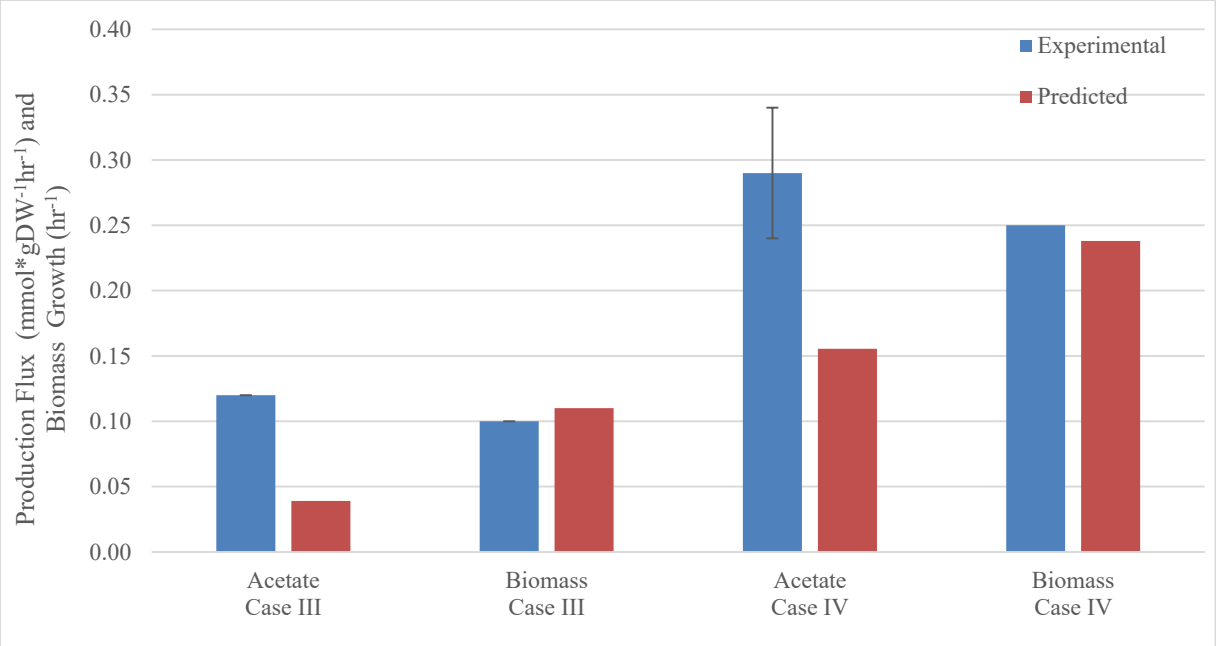
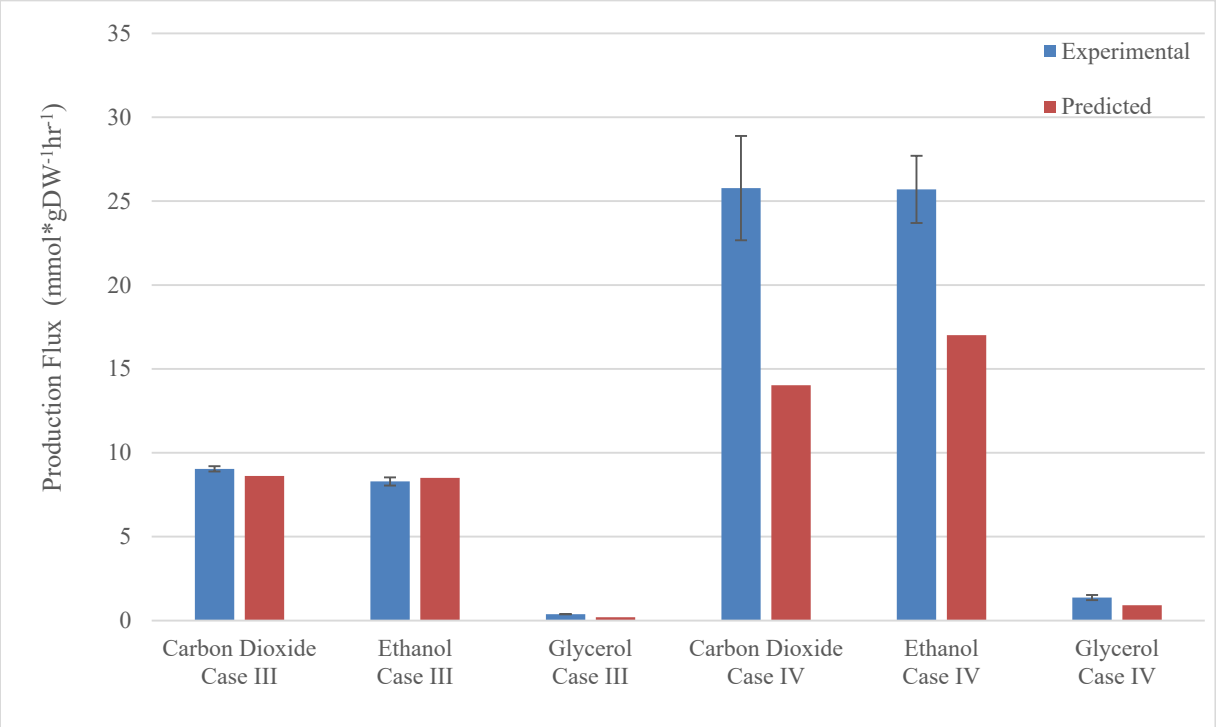

Production Flux (mmol*gDW-1hr-1) and Biomass Growth (hr-1)
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Experimental
Predicted
Acetate Case III
Biomass Case III
Acetate Case IV
Biomass Case IV


Production Flux (mmol*gDW-1hr-1)
35
30
25
20
15
10
5
0
Experimental
Predicted
Carbon Dioxide Case III
Ethanol Case III
Glycerol Case III
Carbon Dioxide Case IV
Ethanol Case IV
Glycerol Case IV

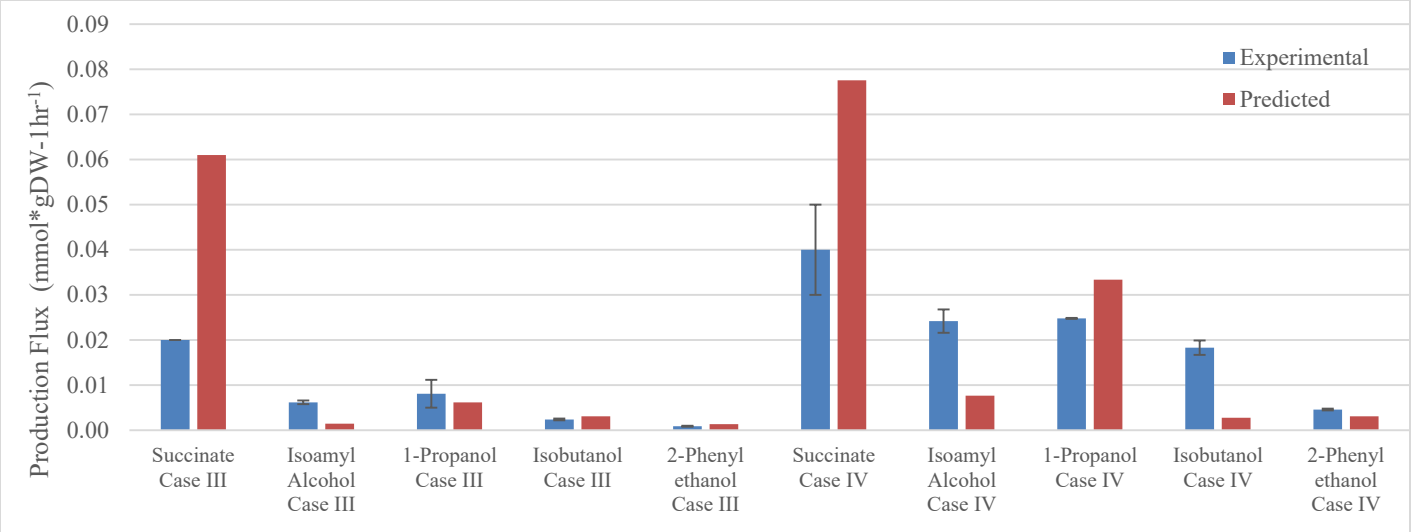


Figure S1. Comparison of GSMM simulations (Red bars) with experimental data [30] (Blue bars). Model predicted and experimental values for biomass growth rates, primary metabolite production fluxes, and secondary metabolite production fluxes represent conditions for Case III and Case IV . Experimental data are shown with standard deviation error bars.

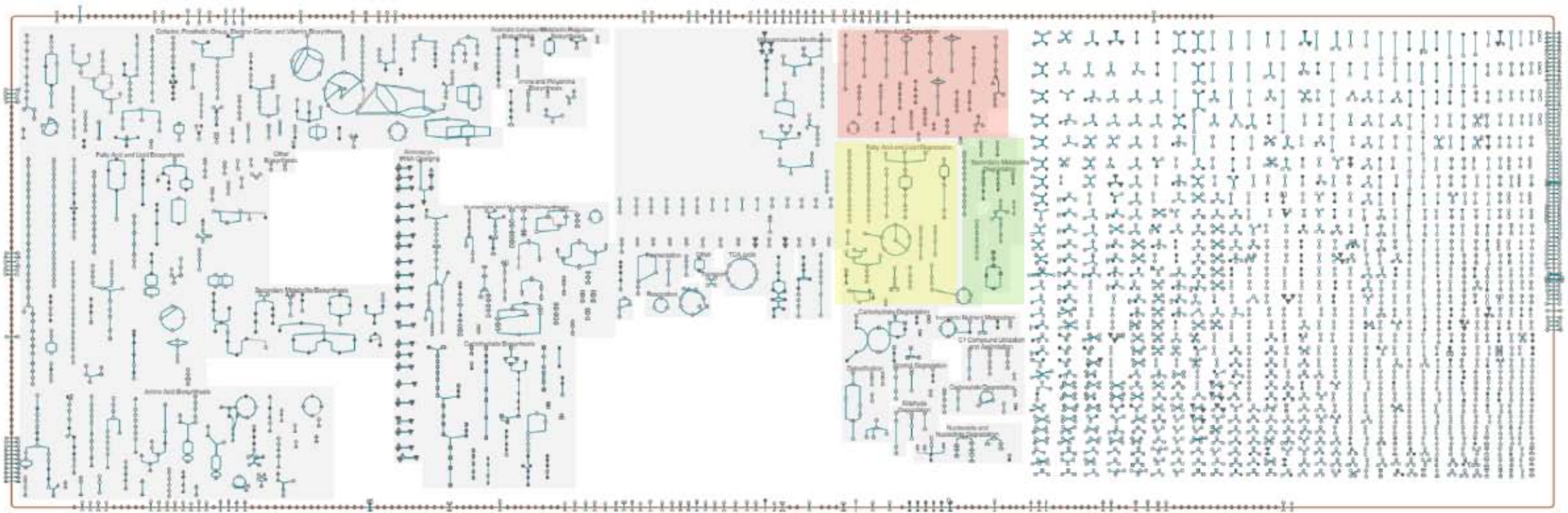
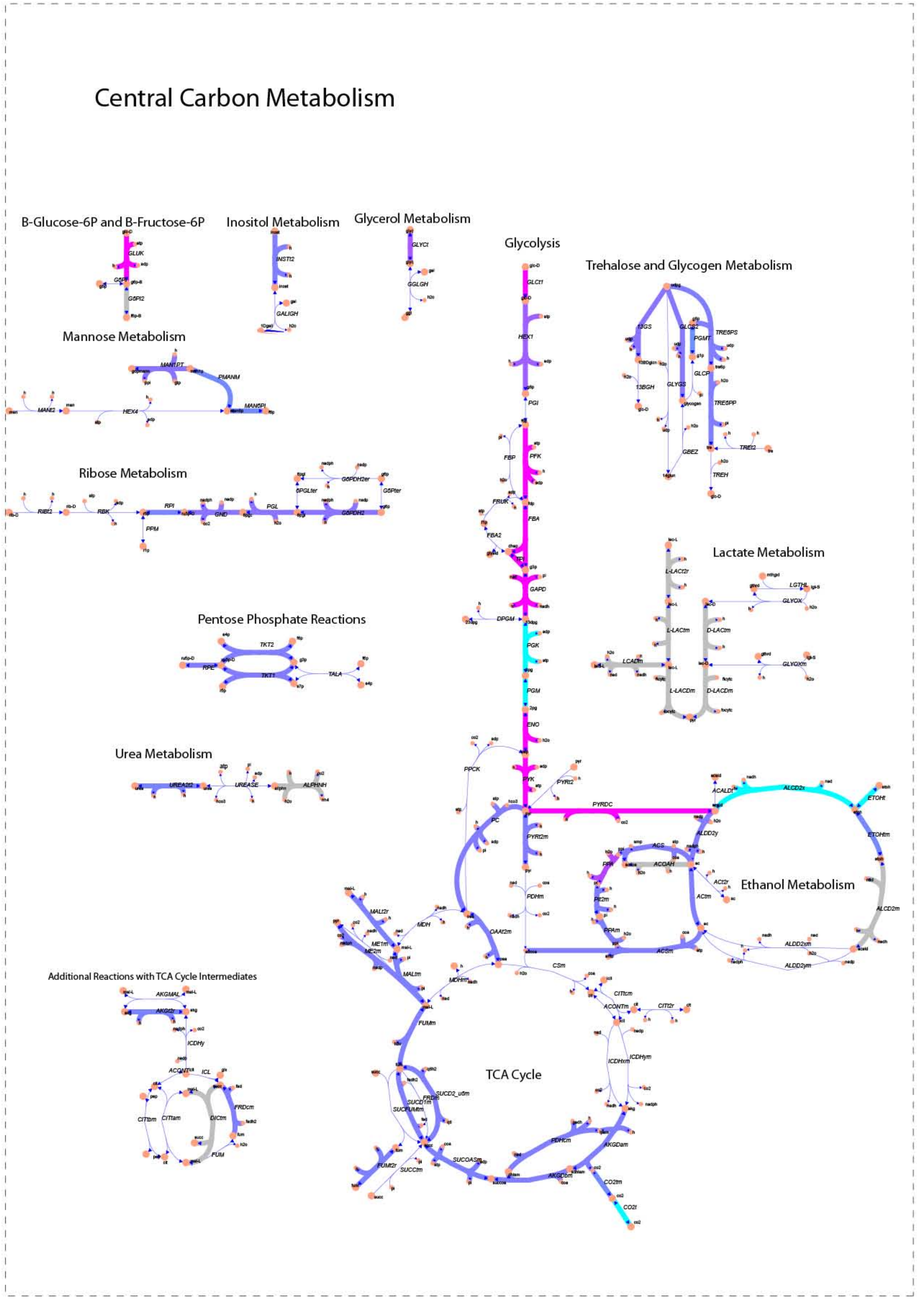


Figure S2. Comprehesive Metabolic Network Map of Yeast (*S. cerevisiae*)



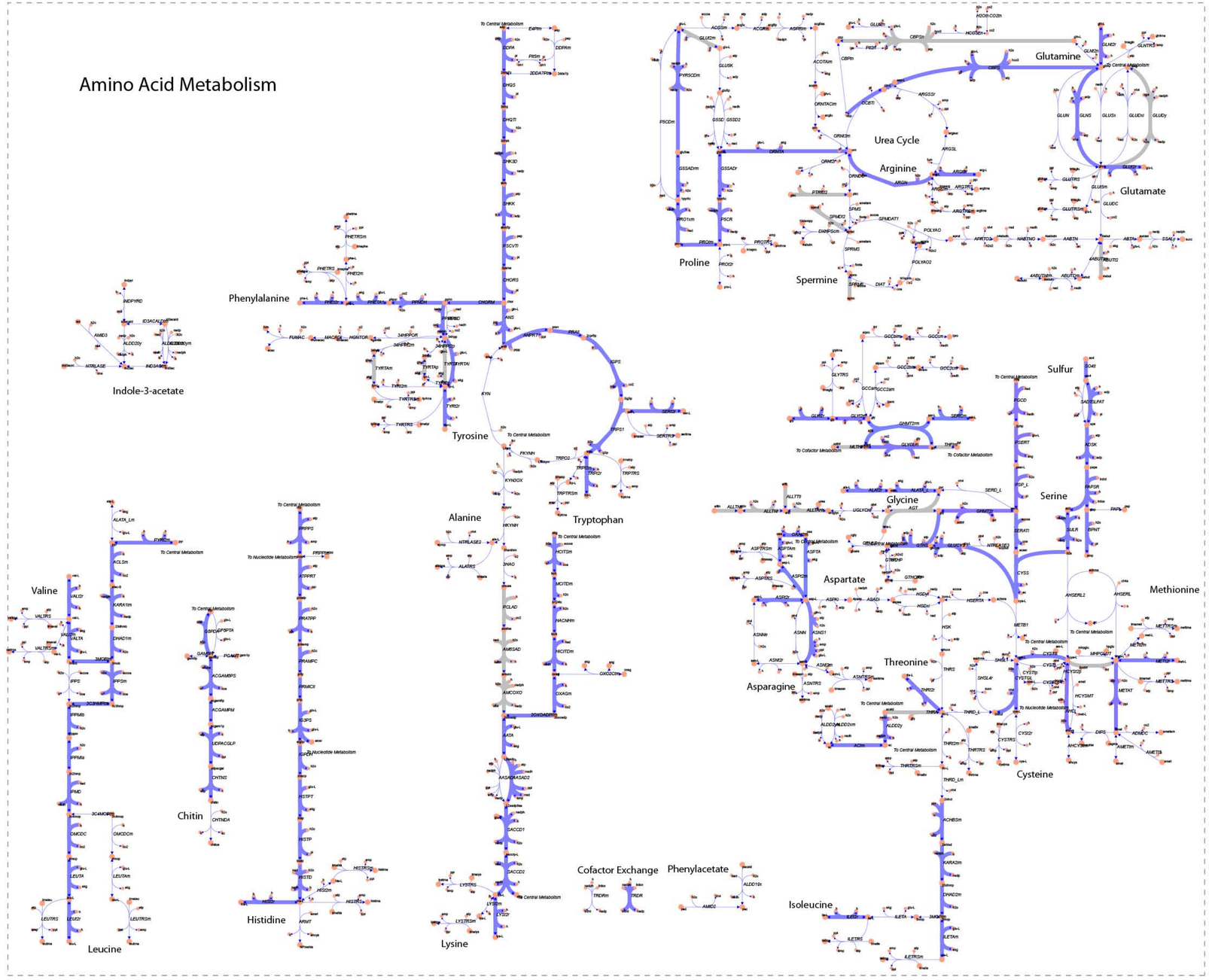
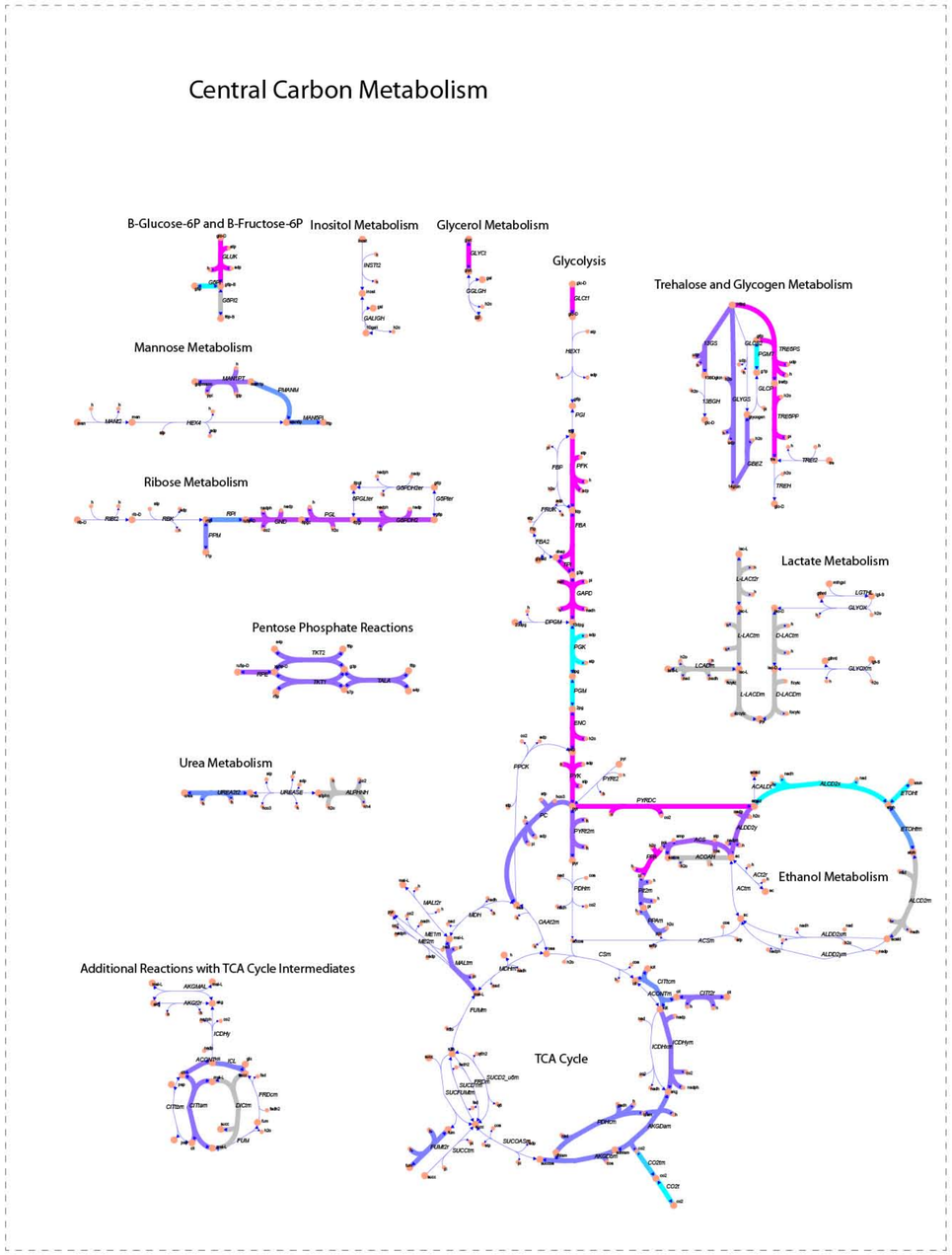


Figure S3. Network map of central carbon metabolism (left) and amino acid metabolism (right). Network fluxes were determined using data from Case I where the network illustrates the optimal solution from FBA. The fluxes were scaled between -1 and +1 for ease of visualization.



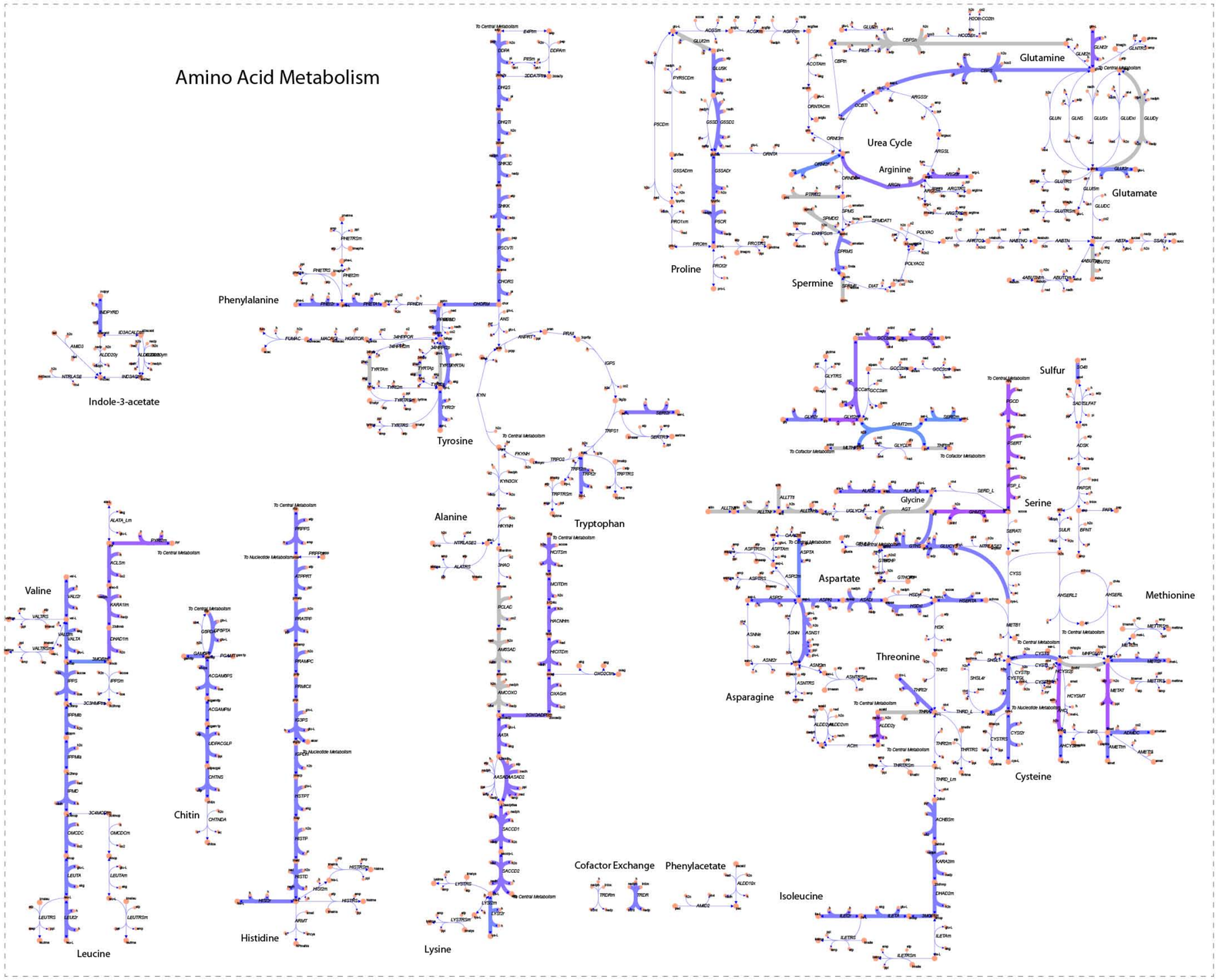


Figure S4. Network map of central carbon metabolism (left) and amino acid metabolism (right). Network fluxes were determined using data from Case II where the network illustrates the optimal solution from FBA. The fluxes were scaled between -1 and +1 for ease of visualization.