

AMBIENT: Active Modules for Bipartite Networks. Using high-throughput transcriptomic data to dissect metabolic response.

Supplementary Figures S1-S4

Each diagram represents a single module inferred by either ambient or GiGA, being areas of significantly affected areas of up- and down-regulation in the metabolic network of *S. cerevisiae*. In each diagram, reactions found by both methods are colour-coded, and up- and down-regulated reactions identified by DeRisi and coworkers have black borders. Arrow directions on edges indicate the conventional direction assigned to each reaction; where an arrow points from a reaction to a metabolite, that metabolite is a product of that reaction, and where the arrow points from a metabolite to a reaction it is a substrate. A key can be found below the figure legends.

Figure S1 - statistically significant up-regulated modules found by ambient

Shows modules 2, 3 and 4, panels A, B and C respectively, inferred by ambient to be up-regulated (module 1 is shown in the main text, Figure 1).

Figure S2 - statistically significant down-regulated modules found by ambient

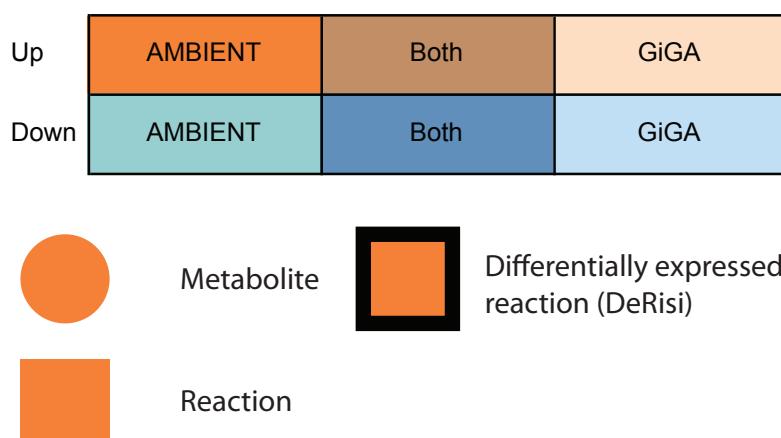
Shows the single down-module inferred by ambient.

Figure S3 - statistically significant up-regulated modules found by GiGA

Shows the two modules inferred by GiGA to be up-regulated.

Figure S4 - statistically significant down-regulated modules found by GiGA

Shows the six modules inferred by GiGA to be down-regulated.



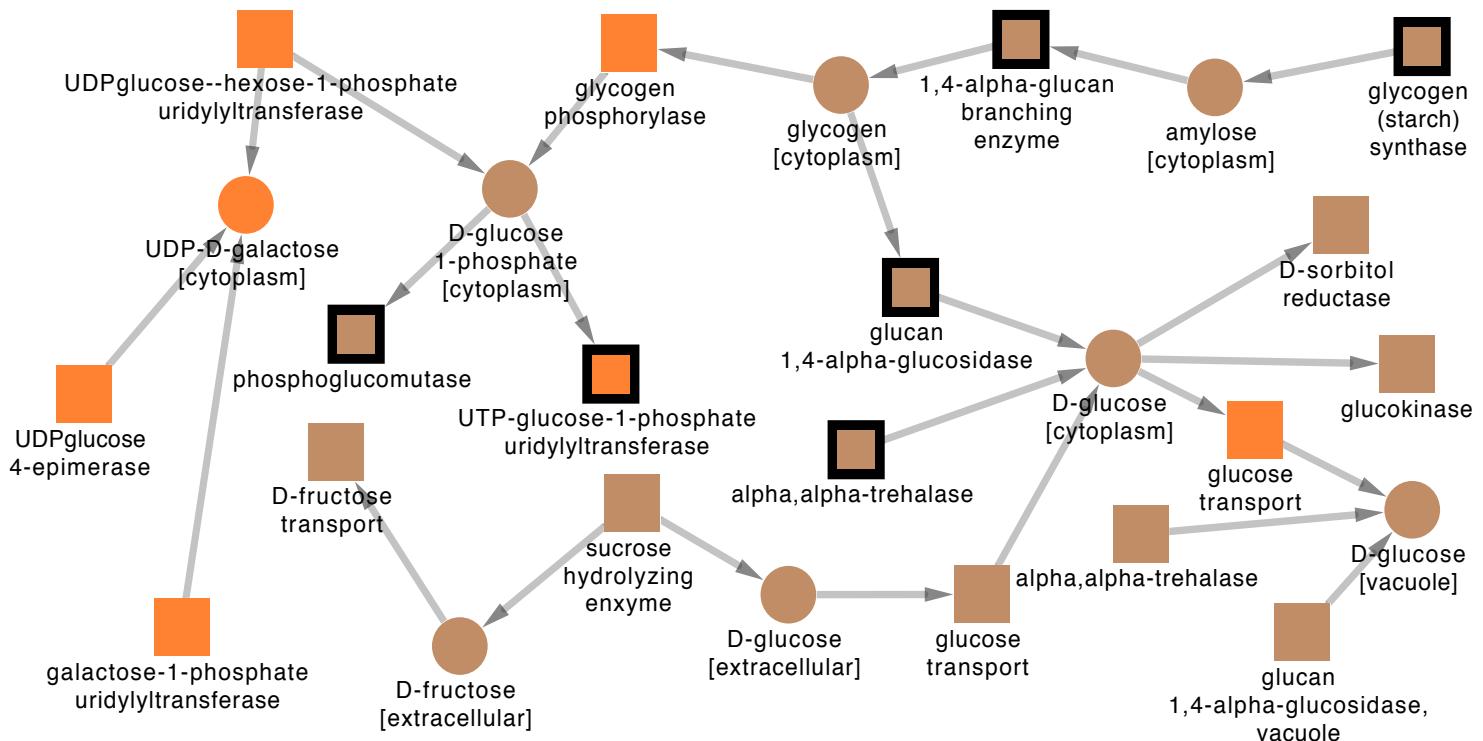


Figure S1A - u2

Figure S1B - u3

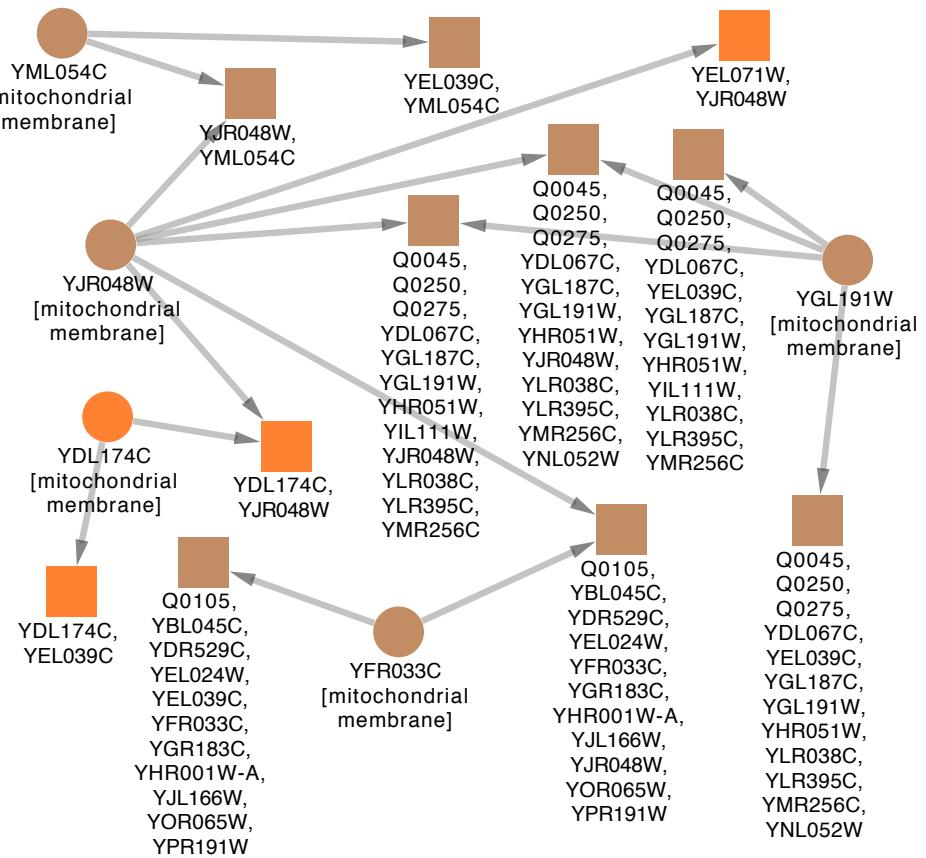
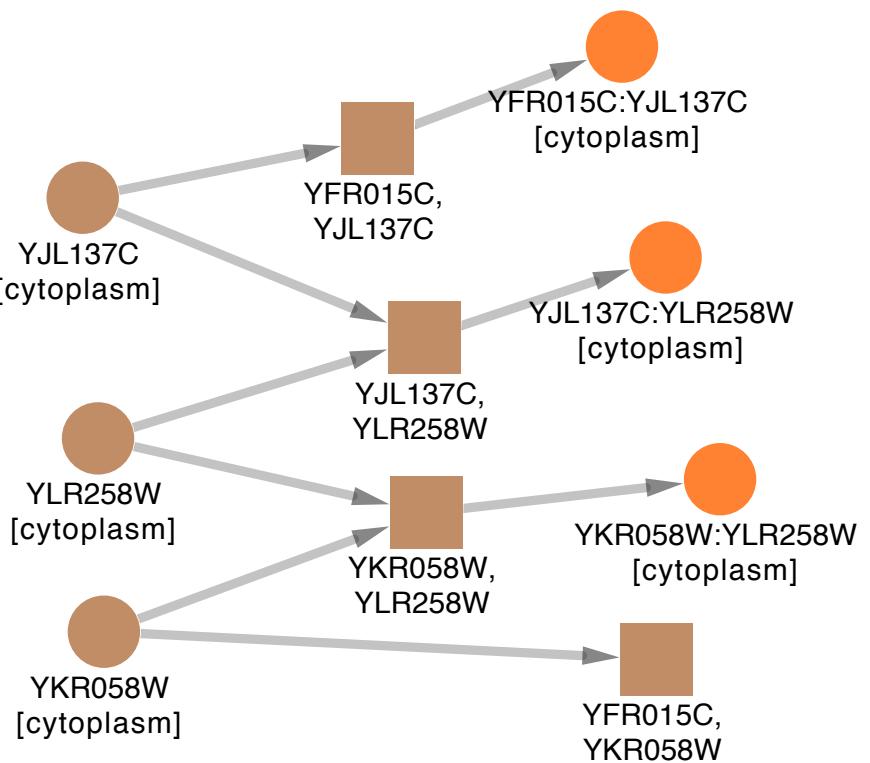


Figure S1C - u4



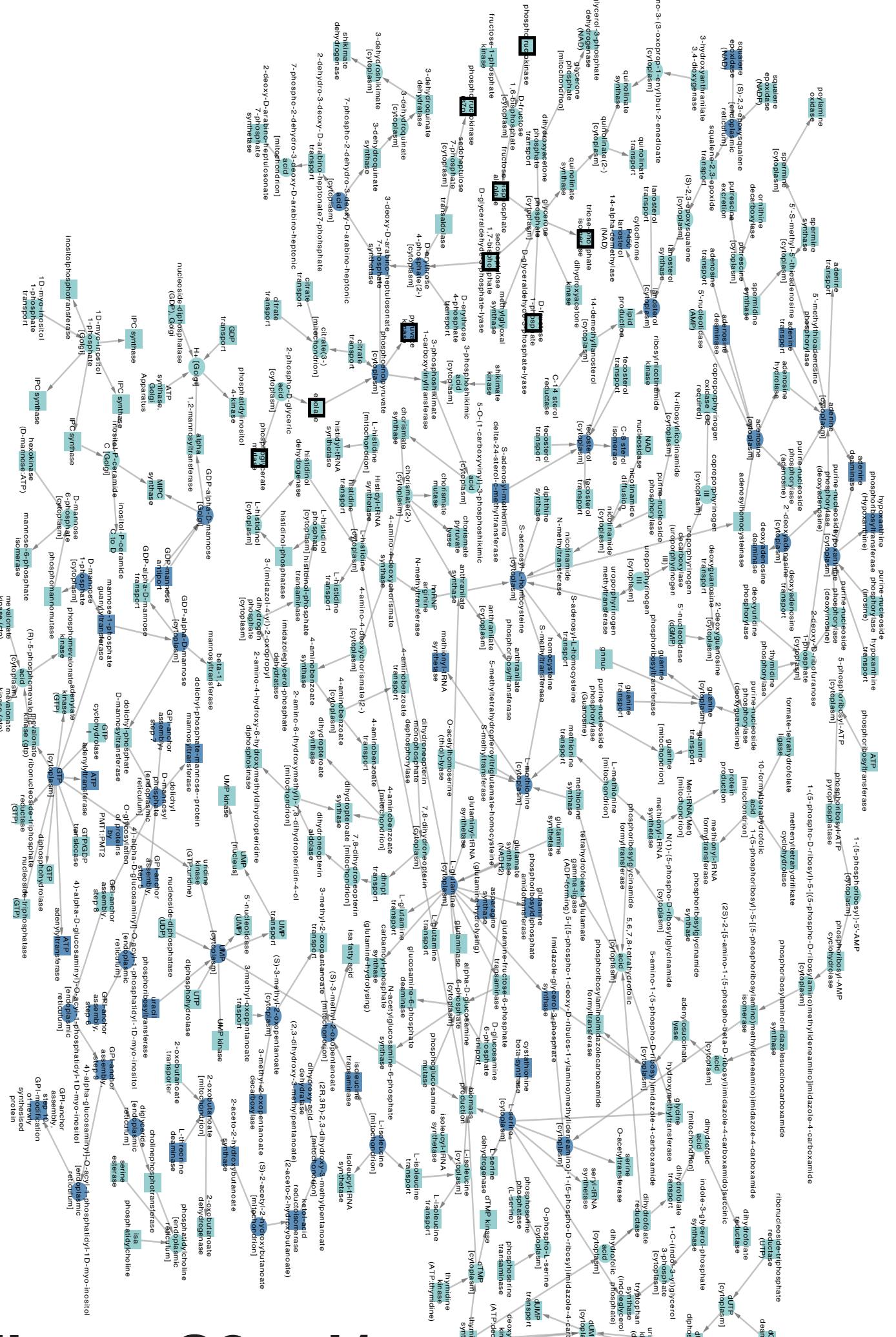


Figure S2 - d1

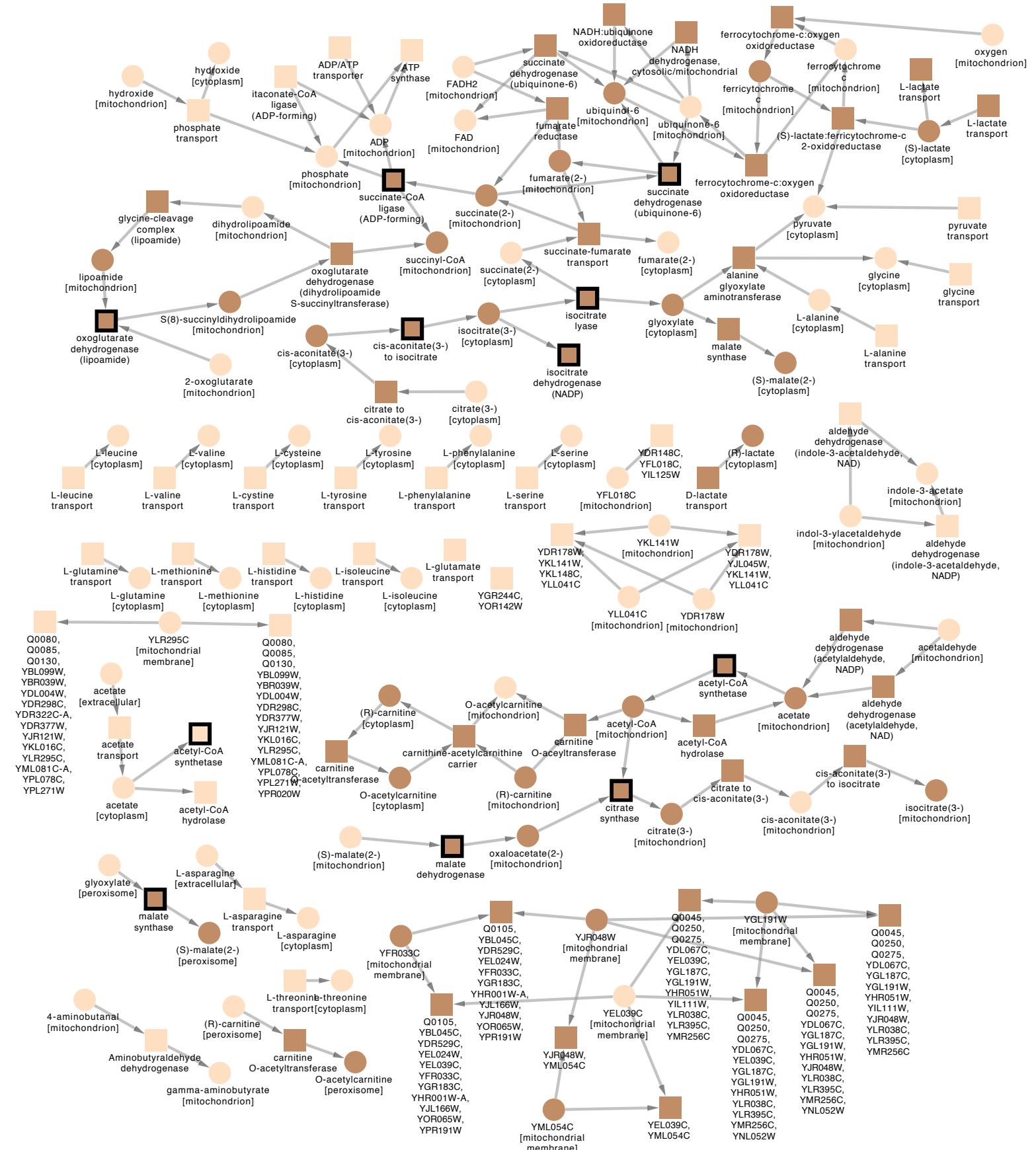


Figure S3A - GiGA up 1

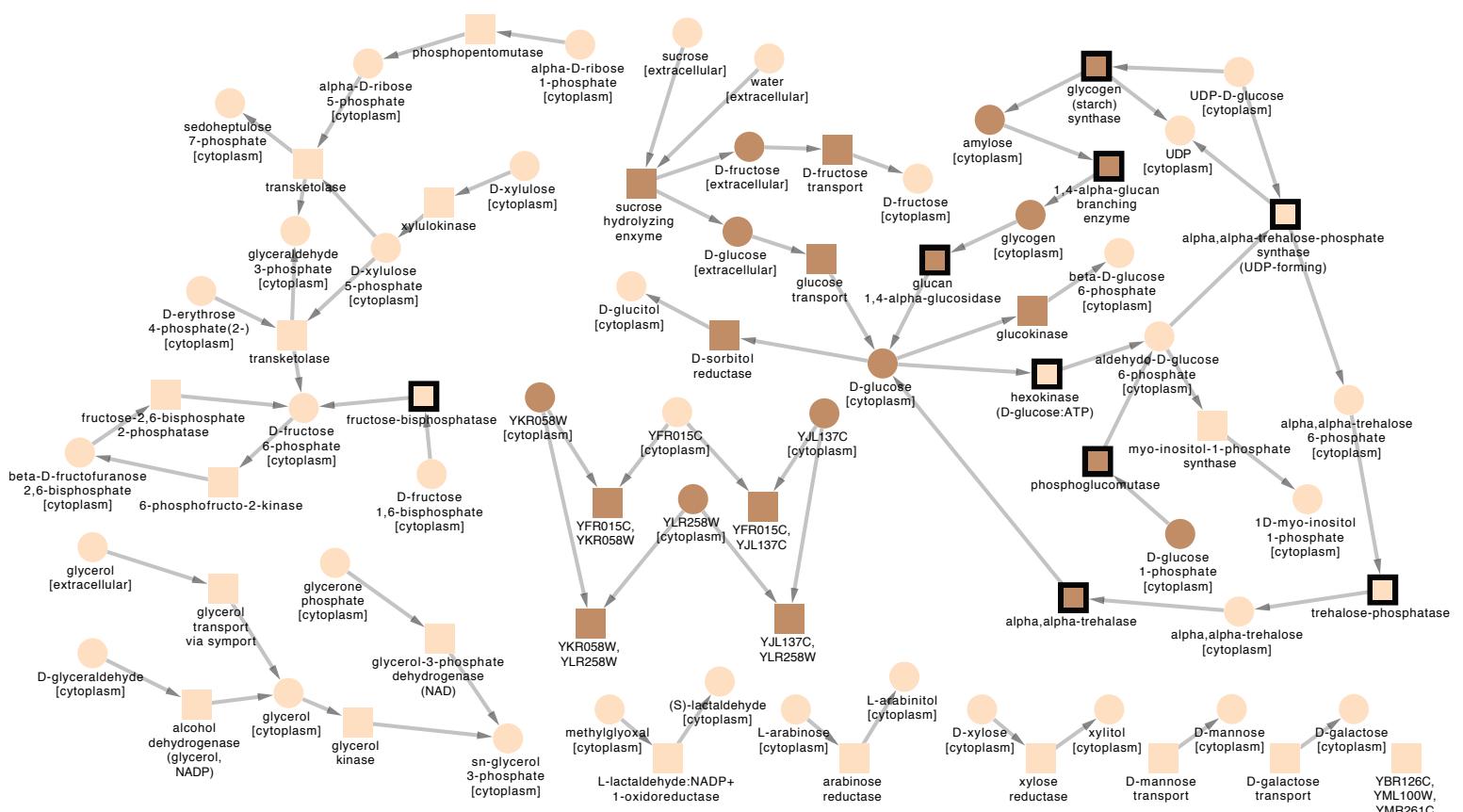


Figure S3B - GiGA up 2

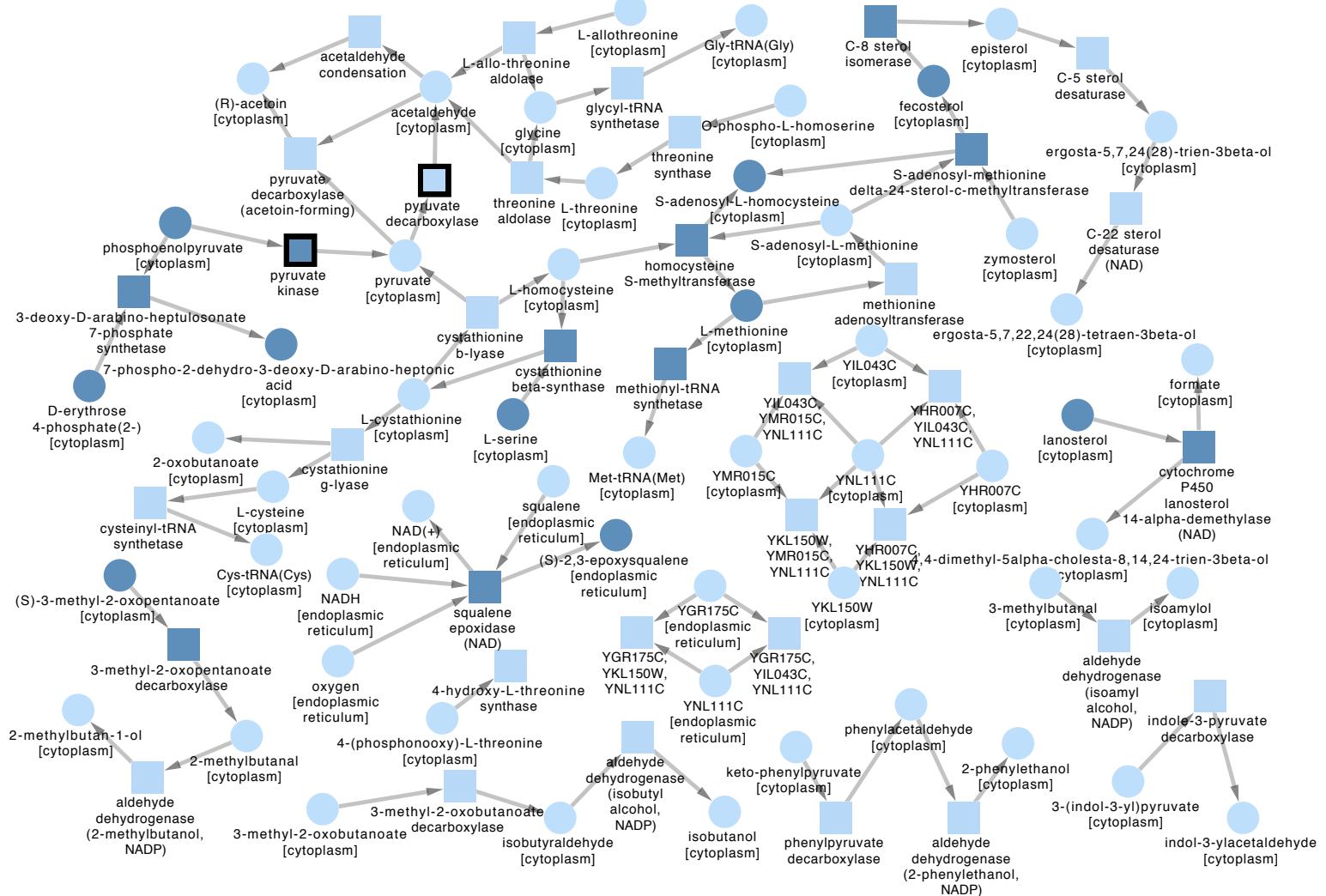


Figure S4A - GiGA down 1

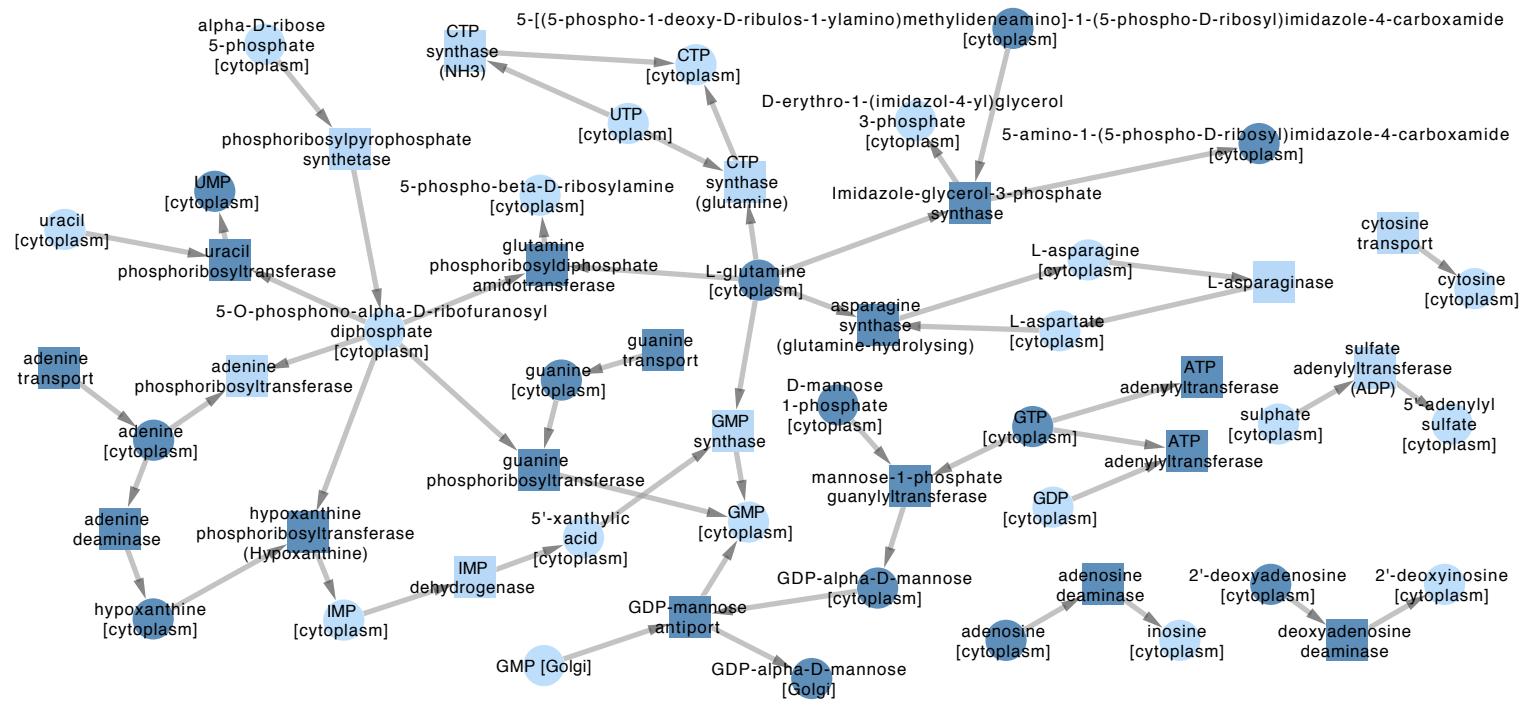


Figure S4B - GiGA down 2

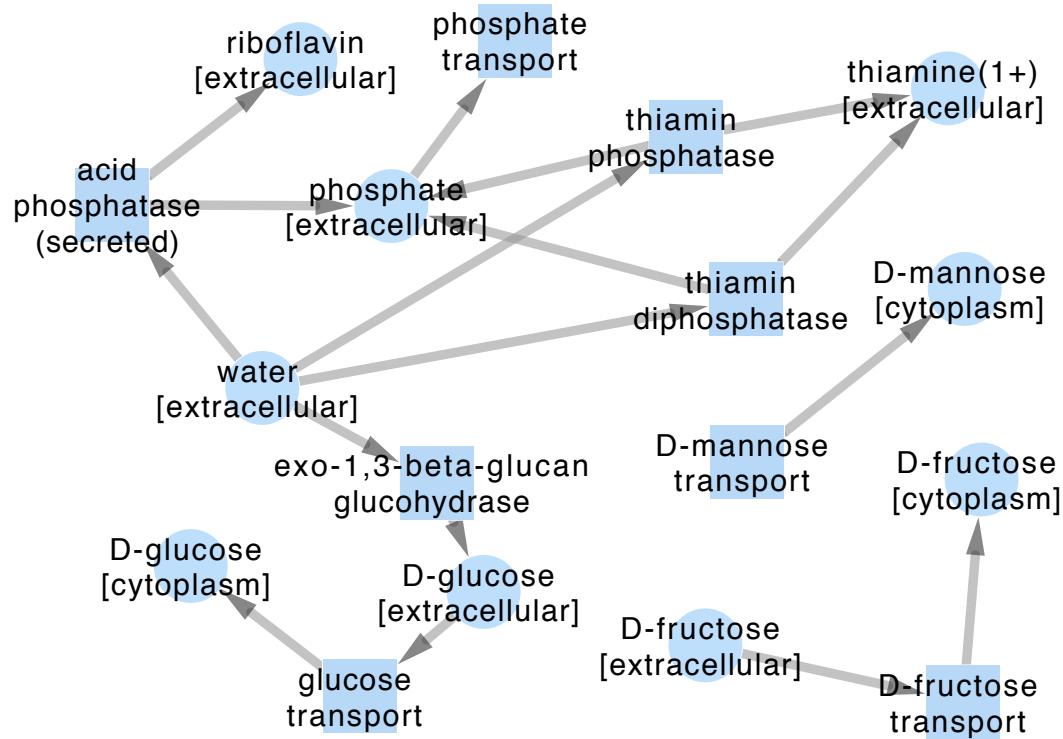


Figure S4C - GiGA down 3

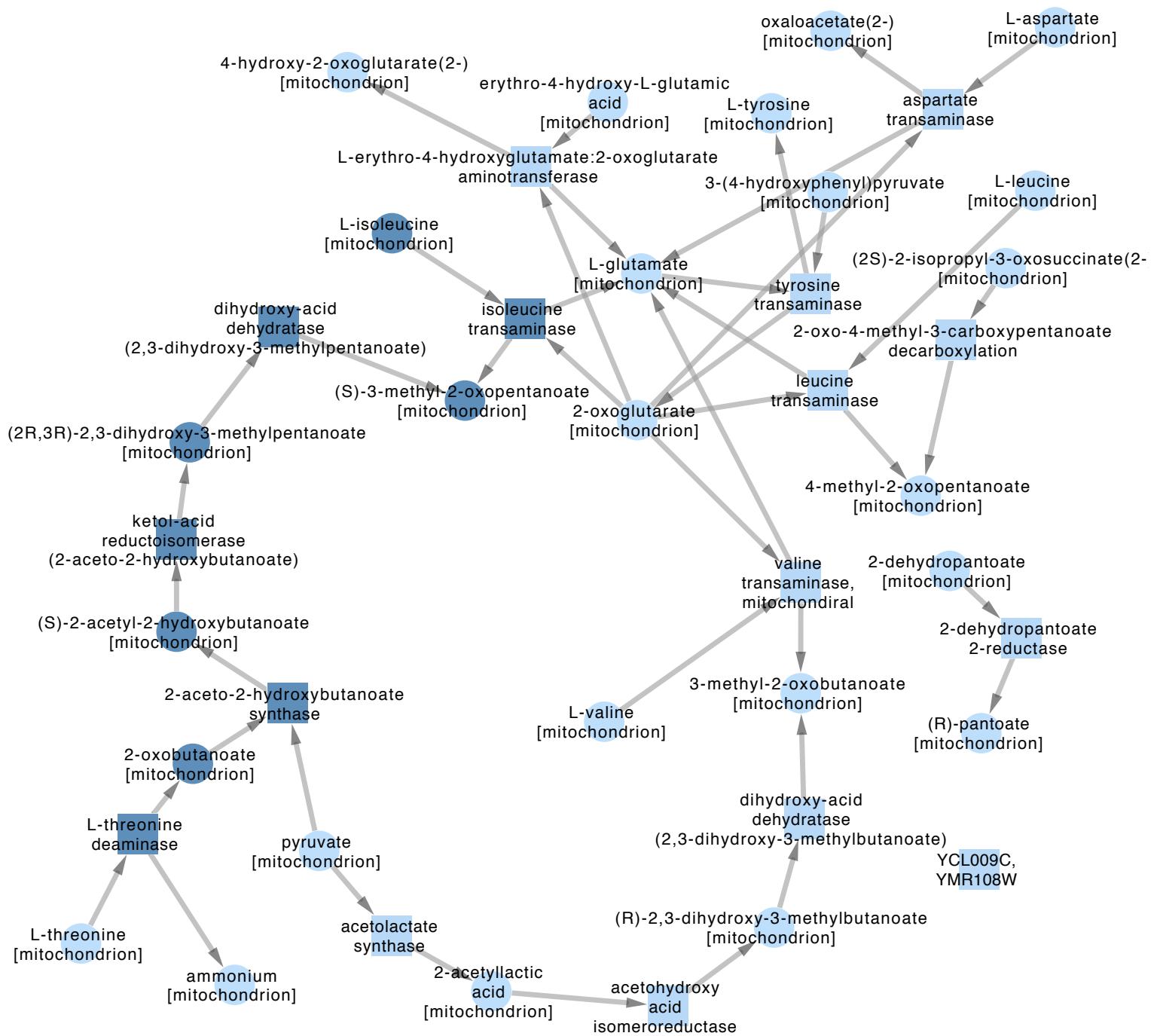


Figure S4D - GiGA down 4

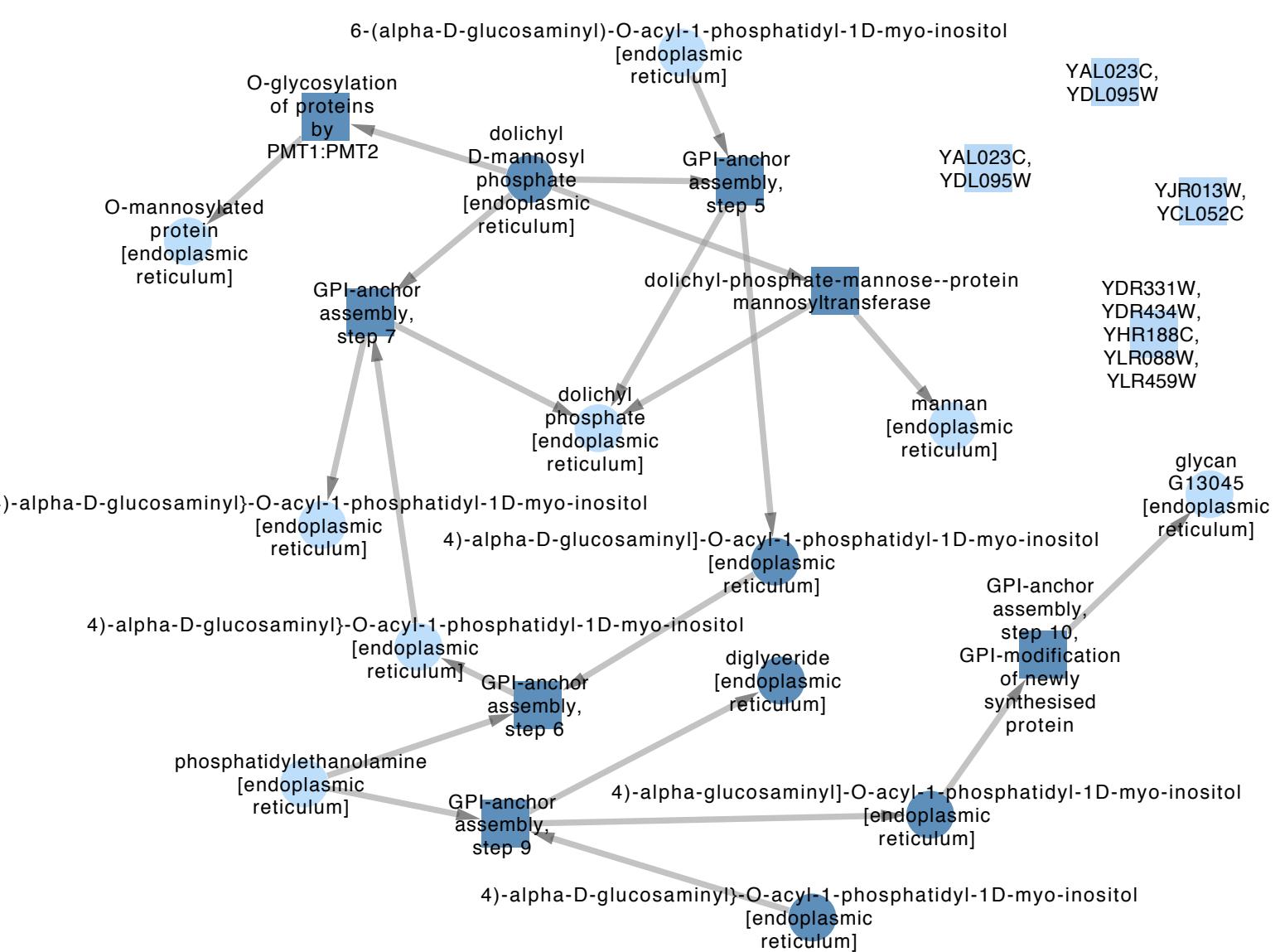


Figure S4E - GiGA down 5

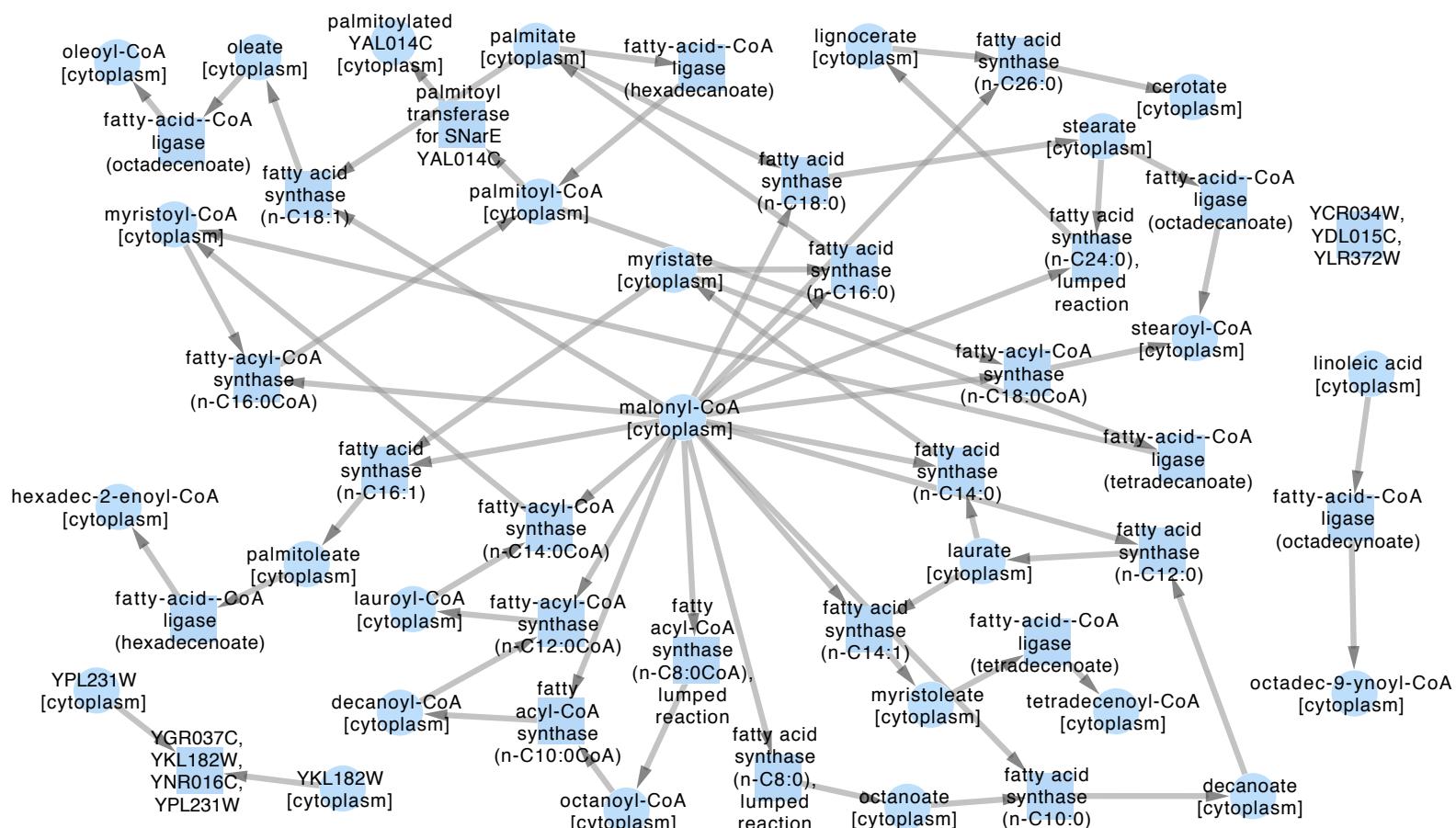


Figure S4F - GiGA down 6