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Supplementary Material: Mining metabolic pathways through gene expression

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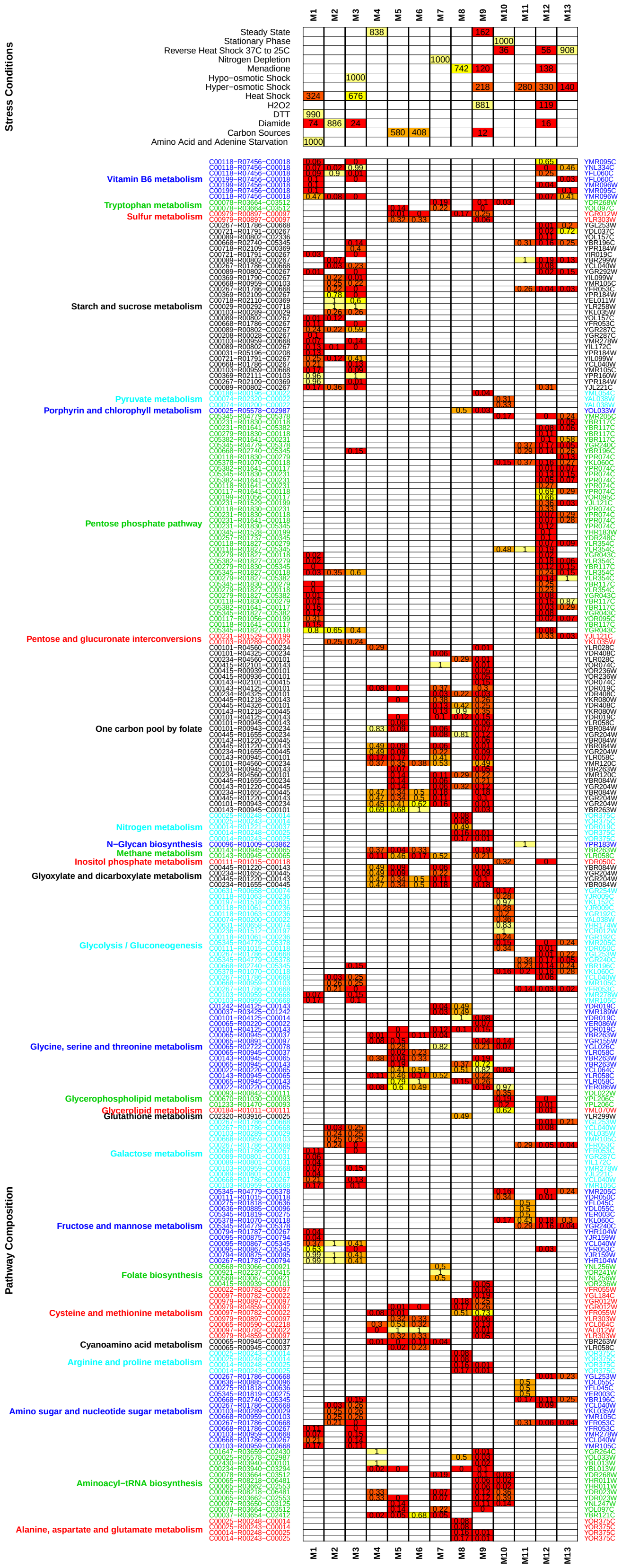
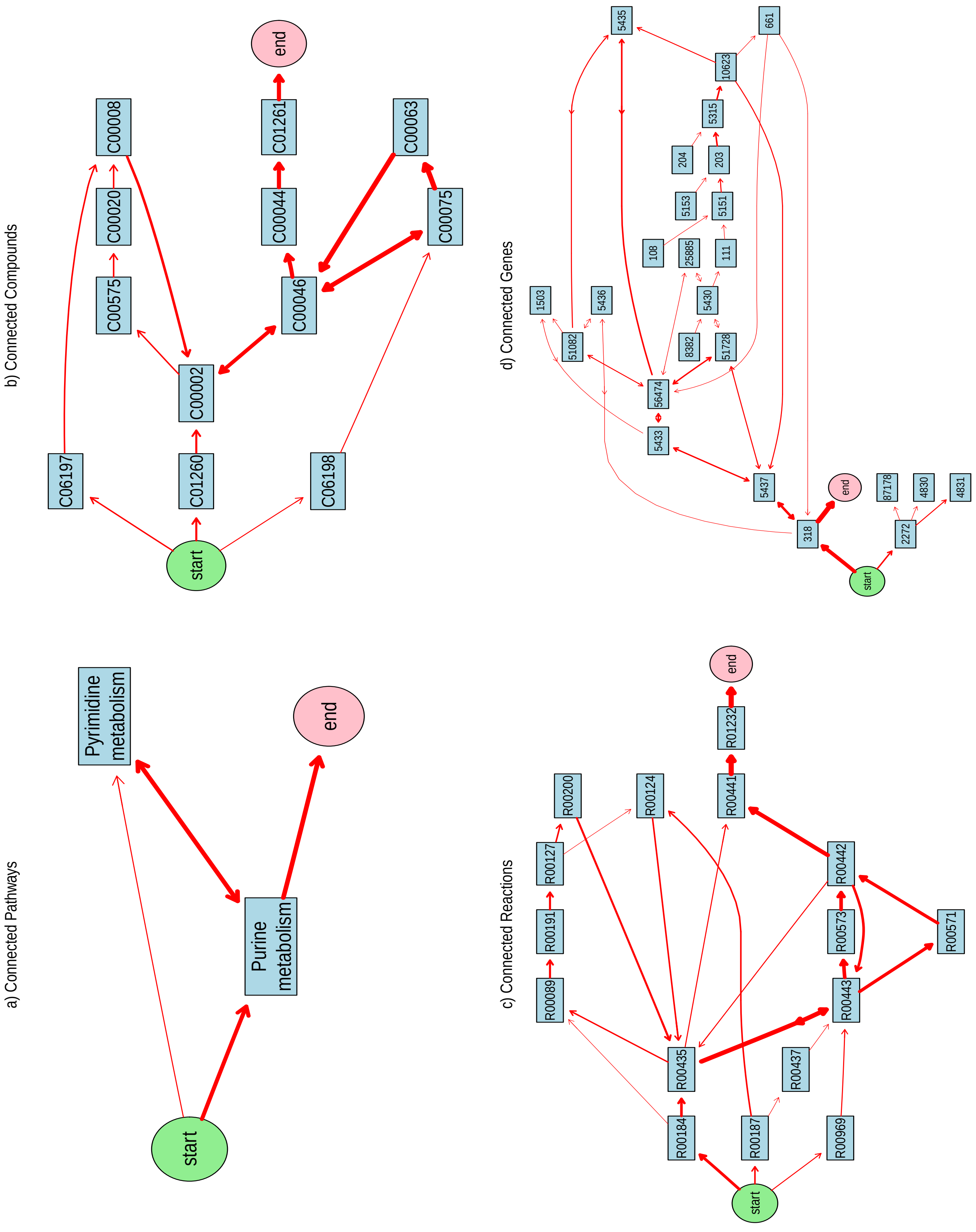


Fig. 1. The 3M pathway clustering results for clustering yeast stress conditions. The left image represents the cluster structure annotated by KEGG pathway, to-compound, reaction, from-compound on the top axis and gene on the bottom axis. The right image represents the confusion matrix between stress condition and cluster. Throughout both images yellow represent highly important cluster features and red represents less important features.


a) Connected Pathways

b) Connected Compounds

c) Connected Reactions

d) Connected Genes

Fig. 2. The most connected components separated by connected pathways, compounds, reactions and genes identified by HME3M to classify insulin resistance. For all images the edge thickness represents the importance of that edge to the overall network.

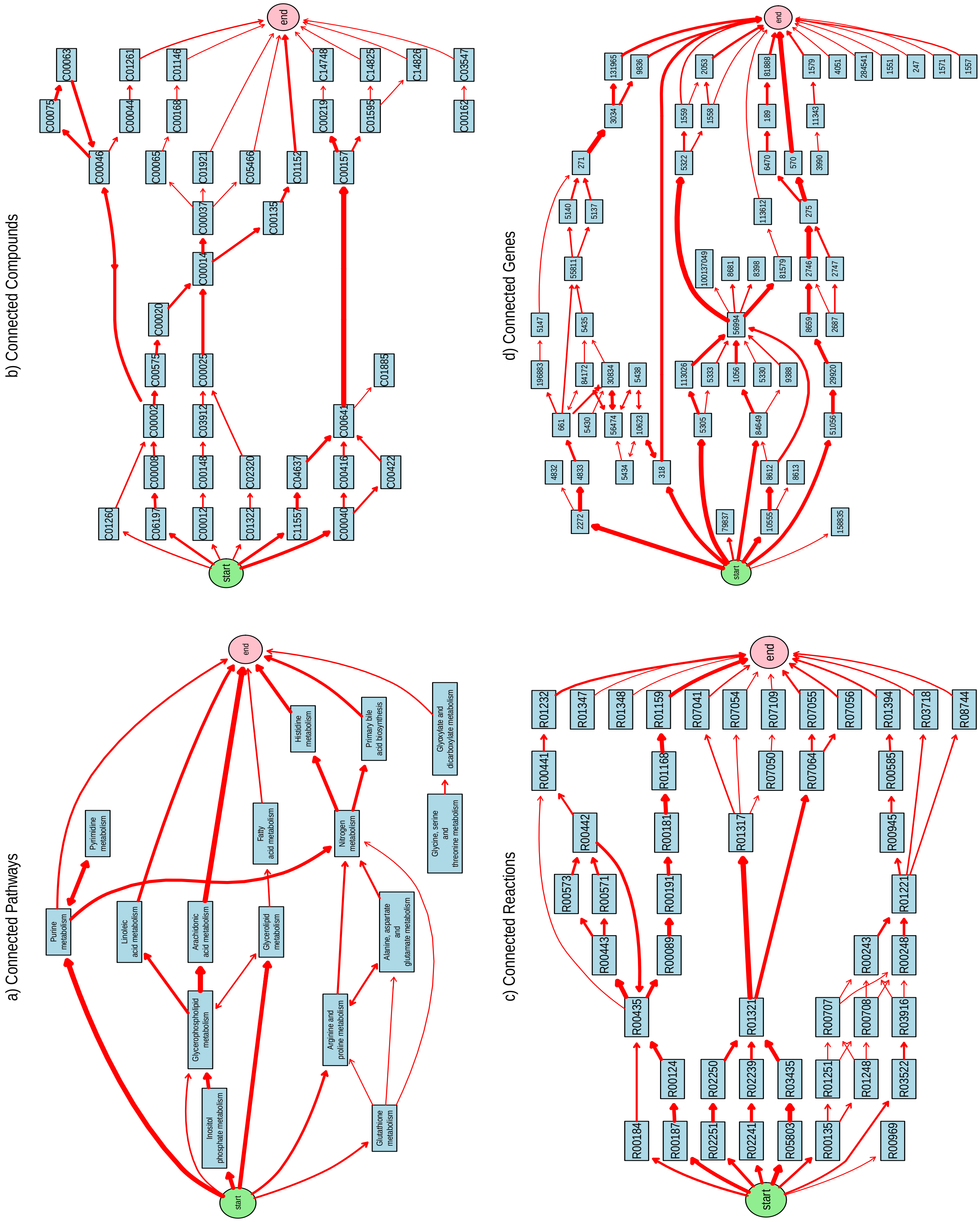


Fig. 3. The most connected components separated by connected pathways, compounds, reactions and genes identified by HME3M to classify insulin sensitivity. For all images the edge thickness represents the importance of that edge to the overall network.