Regulation of gene expression by glucose metabolism in mammary cell lines

Input files

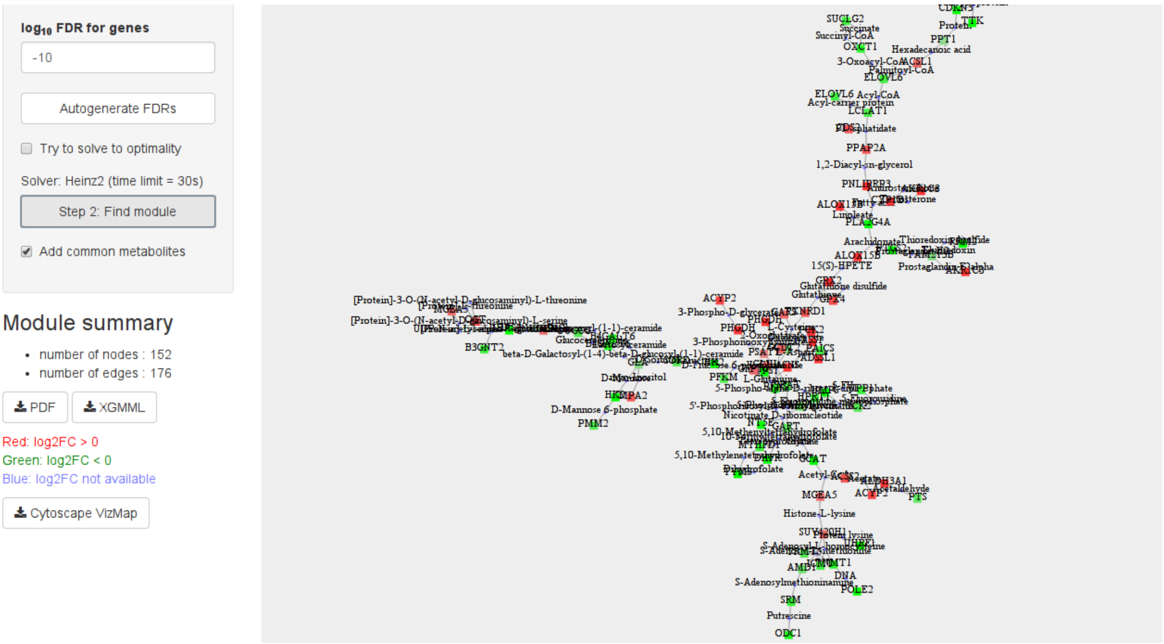
We analyzed control vs 2-deoxy-glucose (2DG) treated mammary epithelial cells (MCF10A). Data was acquired from GEO Omnibus GSE59228.

File with differential expression (DE) for genes: https://artyomovlab.wustl.edu/publications/supp_materials/GAM_2015/MCF10A.Ctrl.vs.2DG.gene.de.tsv

DE table consists of 20285 genes. No cutoff for expression was applied.

Module

We ran GAM analysis with default parameters (reactions as nodes, collapsing reactions, not solving to optimality) and logFDR=-10 (Fig. 1).



$\log_{10}$ FDR for genes

-10

☐ Try to solve to optimality

Solver: Heinz2 (time limit = 30s)

☑ Add common metabolites

Module summary

- number of nodes : 152
- number of edges : 176

Red: log2FC > 0

Green: log2FC < 0

Blue: log2FC not available

Fig. 1. Overview of a module for 2DG treated cells.

2DG treatment blocks glycolysis and results in the same effects as glucose deprivations. The analysis highlighted three major up-regulated features (Fig 2): 1) up-regulation of glutathione redox control locus; and 2) usage of glutamine via glutaminolysis. Importantly, these features have been documented as characteristic for glucose starved cells (http://www.ncbi.nlm.nih.gov/pubmed/12767261, http://www.ncbi.nlm.nih.gov/pubmed/22225880). This illustrates the power of metabolic network based analysis even when only transcriptional data are available.

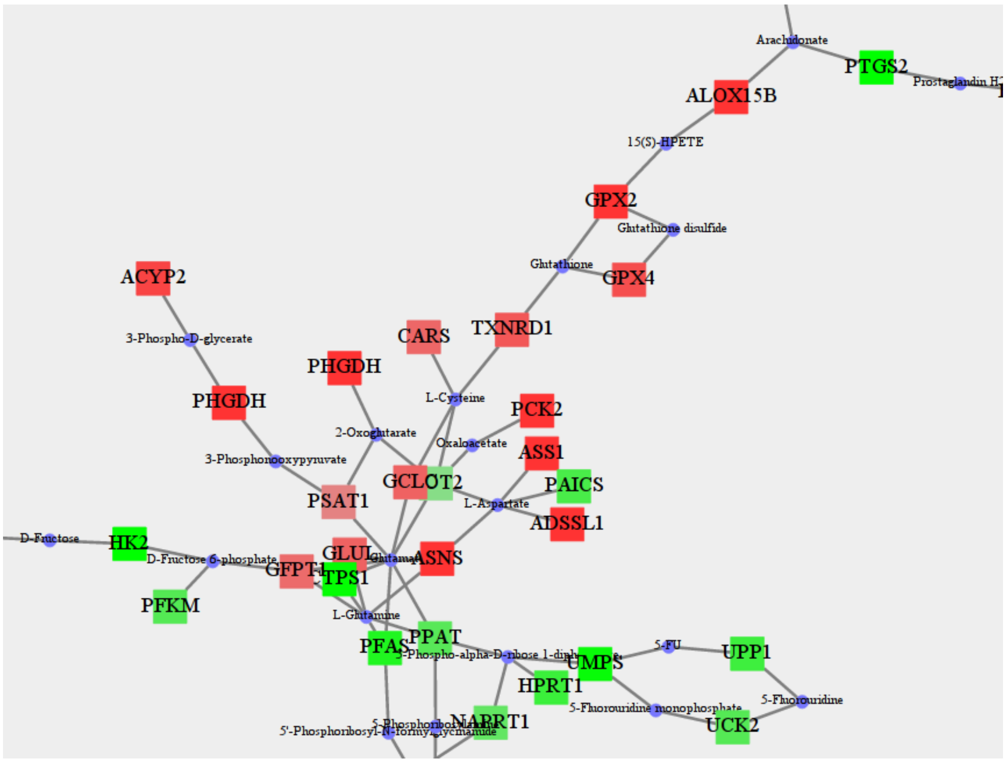


Fig. 2. Fragment of the module with changes in glutathione metabolism and glutaminolysis.