



Figure 2 Network analyses of gene expression data. **(A)** A heatmap of Edge Flux (EF) values with highest variance across the six conditions (see text and Materials and methods). **(B)** A network plot of the interactions in K1. Nodes are colored by the relative gene expression values of respective genes in resistant cells (see the red-green color key), and edges are colored according to the type of interaction. **(C)** Functional enrichment scores of highest scoring GO functional classes in the network of 500 highest EF values in resistant cells relative to parental cells. Enrichment score was calculated as the $-\log$ of hypergeometric distribution function. **(D)** Heatmap of gene expressions of some genes in our data set previously implicated in glucose deprivation response.