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.