

SUPPLEMENTARY DATA

Supplementary Figure 1. Ingenuity Pathway Analysis reveals activation of MYC network under hyperglycemic conditions. Cultures of wild-type MEF were labeled for 6 h for pSILAC in Dulbecco’s modified Eagle’s medium containing either 5 mM glucose supplemented with 20 mM mannitol or 25 mM glucose supplemented with 3 mM glucosamine. Cells were harvested, combined, and analyzed by mass spectrometry to compare labeled peptide peaks. The most highly significant transcription factor identified by Ingenuity Pathway Analysis to exhibit altered regulation under these conditions was MYC ($p=9.02E-40$). The network is displayed as nodes (gene products) and edges (biological relationships between nodes). Each node is displayed with a shape representing its functional class, while edges are displayed as direct (solid line) or indirect/unknown interaction (dashed line). Red or green color intensity indicates the degree of downregulation or upregulation, respectively, that was observed under the high glucose condition. In this network, proteins whose expression has been linked to MYC activation, such as METAP2, YBX1, and KIAA0664, exhibited elevated synthetic rates under the high glucose condition; whereas those downregulated by MYC, such as PEX19, were repressed.

