Gene	Node ID	Coordinates
TOP2B	51806	chr3:25639475-25706398
SIDT1	60561	chr3:113251143-113348425
LAPTM5	3123	chr1:31205316-31230667
AKR1B1	136736	chr7:134127127-134144036
BAX	264956	chr19:49458072-49465055
HNRNPA1	200470	chr12:54673977-54680872
PRDX2	261302	chr19:12907634-12912694
RAD23A	261316	chr19:13056654-13064448

Table S2: **Node coordinates for all exemplar genes: SIDT1, AKR1B1, LAPTM5, TOP2B, BAX, HNRNPA1, PRDX2, and RAD23A.** For each gene, the second and third columns list the corresponding node identifiers and the chromosome coordinates, respectively. The fourth column lists the gene's actual chromosomal coordinates. Note that the transcription start site was used as the basis for assigning each gene to a node.

S2 Analysis of exemplar genes

- **SIDT1** encodes a transmembrane dsRNA-gated channel protein and is part of a larger family of proteins necessary for systemic RNA interference (Elhassan et al., 2012; Entrez Gene, 1988). This gene has also been implicated in chemoresistance to the drug gemcitabine in adenocarcinoma cells (Elhassan et al., 2012).

- **AKR1B1** encodes an enzyme that belongs to the aldo-keto reductase family. It has also been identified as a key player in complications associated with diabetes (Donaghue et al., 2005; Entrez Gene, 1988).

- **LAPTM5** encodes a receptor protein that spans the lysosomal membrane (Entrez Gene, 1988). It is highly expressed in immune cells and plays a role in the downregulation of T and B cell receptors and the upregulation of macrophage cytokine production (Glowacka et al., 2012).

- **TOP2B** encodes DNA topoisomerase II beta, a protein that controls the topological state of DNA during transcription and replication (Entrez Gene, 1988). It transiently breaks and then reforms duplex DNA, relieving torsional stress. Mutations in this enzyme can lead to B cell immunodeficiency (Broderick et al., 2019).

- **BAX** encodes a protein that forms a heterodimeric complex with BCL2, which activates apoptosis by aggregating at the mitochondrial membrane and inducing its permeabilization (Entrez Gene, 1988; Pea-Blanco and Garca-Sez, 2018). The tumor suppressor gene P53 plays a role in its regulation.

- **HNRNPA1** encodes a protein that forms part of the heterogeneous nuclear ribonucleoprotein (hnRNP) complex, which binds to nuclear pre-mRNA and helps to regulate RNA transport, metabolism, and splicing (Entrez Gene, 1988; Roy et al., 2017). Mutations in this gene have been linked to the development of amyotrophic lateral sclerosis.

- **PRDX2** encodes an enzyme that reduces hydrogen peroxide and alkyl hydroperoxides (Entrez Gene, 1988). It protects against oxidative stress (Jin et al., 2020) as well as stabilizes hemoglobin, making it a therapeutic target for the treatment of hemolytic anemia.
- **RAD23A** encodes a protein that carries out nucleotide excision repair (Entrez Gene, 1988; Fang et al., 2013). It also plays a role in transporting poly-ubiquitinated proteins to the proteasome for degradation.