**Accompanying note for supp.zip**

This compressed folder (supp.zip) contains two Microsoft Excel (.xlsx) files, ‘Supplementary Item for Fig S2.xlsx ‘ and ‘Supplementary Item for Fig S3.xlsx’ respectively. Below we provide brief descriptions of the contents of these files.

**Supplementary Item for Fig S2.xlsx**

Supplementary Item for Fig S2.xlsx describes the network that was generated to make **Figure S2** in Supplementary Note 3. It has three tabs ‘GoldStandardNetwork’, ‘WildtypeSteadyState’ and ‘knockdowns’. The ‘GoldStandardNetwork’ tab contains the edges of a 100 node gene regulatory network which was randomly generated using GeneNetWeaver software. The ‘WildtypeSteadyState’ tab contains simulated steady state gene expression levels of the above network. The ‘knockdown’ tab contains simulated steady state gene expression levels of the above network following knockdowns of each of its genes. The knockdown data is presented in a matrix (of dimension 100 x 100) format. Each column of the matrix represents the steady state gene expression levels of the network following knockdown of one gene (shown in the column header). All simulations were performed using GeneNetWeaver software.

**Supplementary Item for Fig S3.xlsx**

Supplementary Item for Fig S2.xlsx contains detailed information about the network that was used to produce **Figure S3** in Supplementary Note 4. It contains the adjacency matrix of a randomly created 100 gene scale-free gene regulatory network. The network was simulated using the method described by Barzel and Barabasi (1). The initial concentrations of the genes of this network were randomly generated using the MATLAB rand() function.

**References:**

1. Barzel, B. & Barabasi, A. L. Network link prediction by global silencing of indirect correlations. *Nat Biotechnol*, doi:10.1038/nbt.2601 (2013).