

Reactome

The Reactome database was used for pathway enrichment analysis. Reactome is an open-source, open access, manually curated and peer-reviewed pathway database.

Pathway enrichment was determined through the Reactome FI plug-in (1) for Cytoscape, which uses a binomial test. The *p*-value enrichment is determined from the hypergeometric distribution. The significance of each pathway was calculated by computing the fraction of genes within the pathway, the size of the pathway, and the probability of success determined by considering all genes. False-discovery rates were calculated based on 1000 permutations on all genes in the FI network. Pathways with $FDR \leq 0.05$ were considered significant.

In supplementary table 3 we show all pathways attaining $FDR \leq 0.05$ for the identified sets of proteins. In addition to these analyses, and to create and visualize gene set interaction networks, we used a functional interaction (FI) network generated by curated interactions extracted from reactions and complexes annotated in pathways, combined with bimolecular interactions predicted using a Naïve Bayes Classifier (NBC). The final diagrams were drawn in Cytoscape and the functional interactions annotated by a Cytoscape plug-in developed for the FI network (Fig 1 supplementary).

References

- 1) http://wiki.reactome.org/index.php/Reactome_FI_Cytoscape_Plugin

Fig 1 supplementary

