**Supplementary Table II. Description of tools and databases used in our analysis.**

Database/ Tool	Full Name	Use Description	Link
UniProt	The Universal Protein Resource	Used for obtaining protein names and accessions	http://www.uniprot.org/
HGNC	HUGO Gene Nomenclature Committee	Used for obtaining gene names and accessions	http://www.genenames.org/
DAVID	The Database for Annotation, Visualization and Integrated Discovery	Used for functional annotation of the curated accessions and enrichment analysis	http://david.abcc.ncifcrf.gov/
GO	Gene Ontology	Used for annotation of biological processes and cellular components for different accessions	http://geneontology.org/
KEGG Pathway	Kyoto Encyclopedia of Genes and Genomes	Used for annotation of KEGG pathways enriched in the network and rich-club	www.genome.jp/kegg/
STRING	Search Tool for the Retrieval of Interacting Genes/Proteins	Used for retreiving information on protein-protein interactions	http://string-db.org/
PANTHER	Panther Classification System	Used to obtain distribution of genes across different enriched GO categories.	http://pantherdb.org/
Cytoscape	Cytoscape	Used for network visualization	http://www.cytoscape.org/
SBEToolbox	MATLAB Systems Biology & Evolution Toolbox	MATLAB toolbox used for network analysis	http://www.bioinformatics.org/sbetoolbox/