

Supplementary Figures

Figure S1. Protein-protein interaction network. The network was constructed using STRING with a high confidence minimum interaction score (0.700) and visualized using Cytoscape. Nodes forming part of the main interaction network are shown, disconnected nodes in the network were omitted, edges indicate functional and physical protein associations, line thickness indicates strength of data support

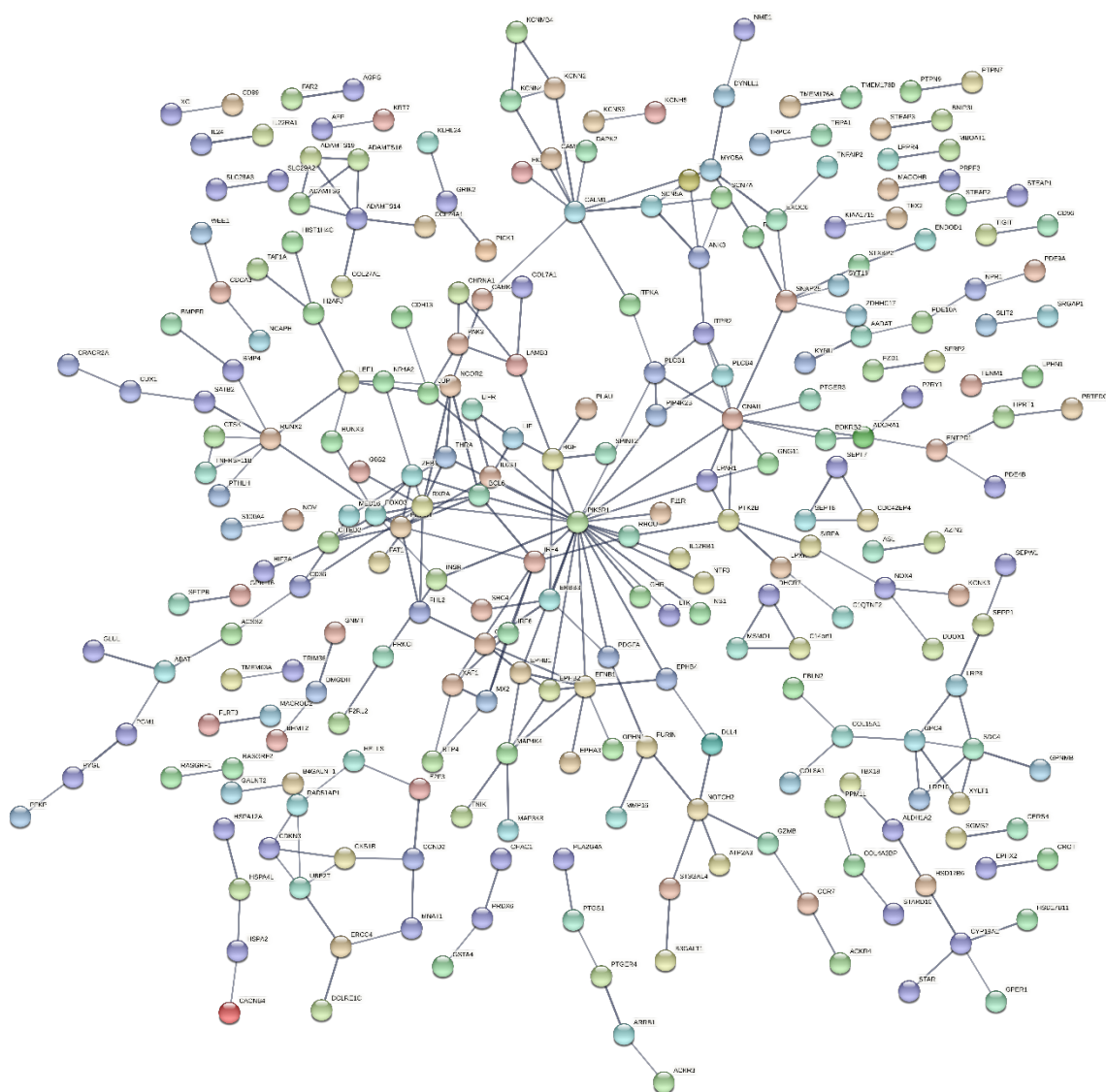


Figure S2. mRNA-lncRNA coexpression network. Yellow rectangles represent lncRNA, blue circles represent mRNA, correlation coefficients were calculated with the Pearson's quick correlation calculations function of the WGCNA package in R Studio, $p > 0.9$ (positive) or $p < -0.9$ (negative) were considered significant. The coexpression network was visualized using Cytoscape.

