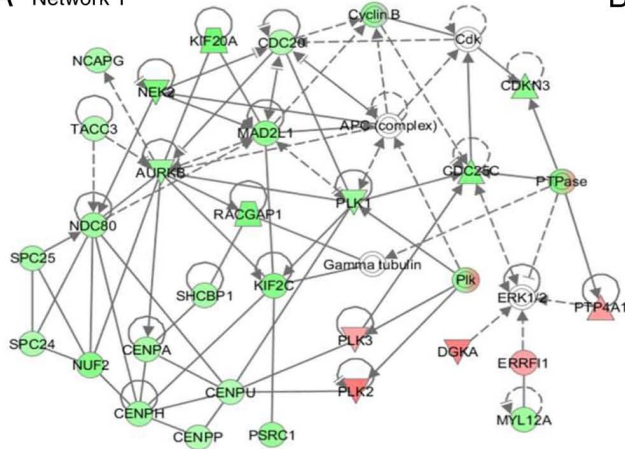
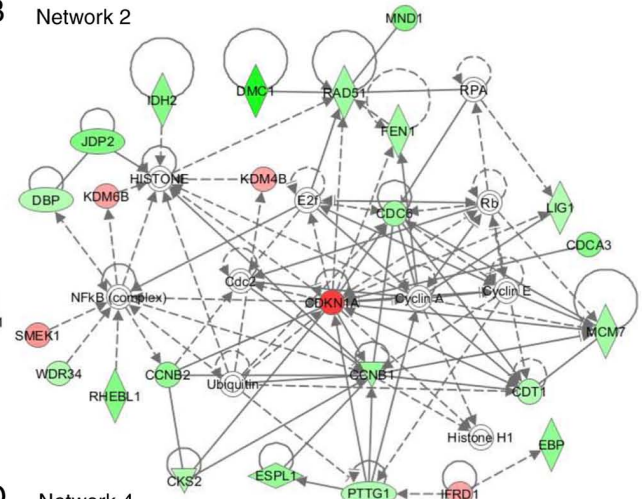


Figure S1. Functional enrichment of 228 commonly dysregulated genes in top five IPA networks. Networks (A) network 1, (B) network 2, (C) network 3, (D) network 4, and (E) network 5 which are generated by IPA. Up- and downregulated genes are shown in red and green, respectively. Genes in gray are associated with dysregulated genes.

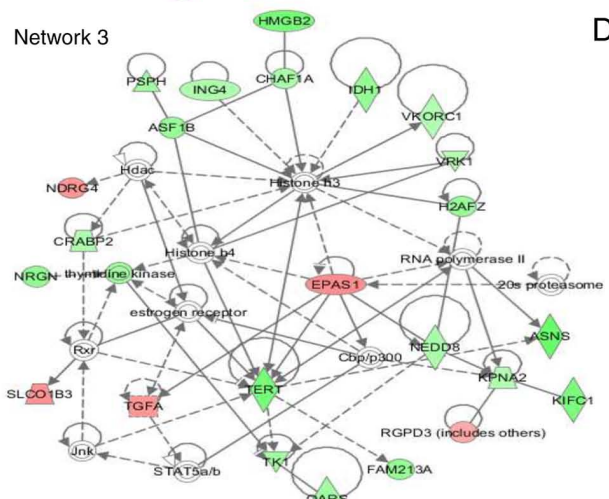
A Network 1



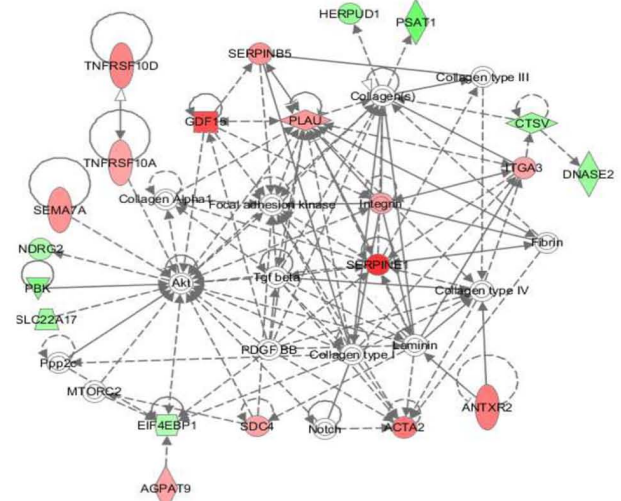
B Network 2



C Network 3



D Network 4



E Network 5

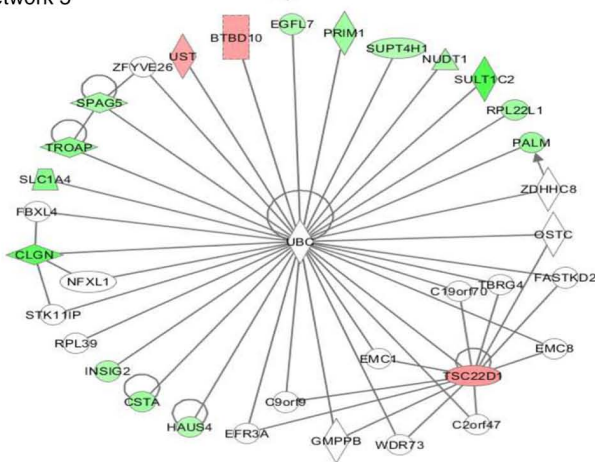


Figure S2. Basal levels of RPL27 and RPL27 overexpression in CRC cells. (A) Relative basal levels of RPL27 mRNA and protein in HCT116 and HT29 cells. RPL27 (B) mRNA and (C) protein expression in HCT116 cells in the presence or absence of Empty or RPL27 vector. **P<0.01, ***P<0.001 vs. NC. si, small interfering; NC, negative control; RPL27, ribosomal protein L27; NT, non-treated; CRC, colorectal cancer.

