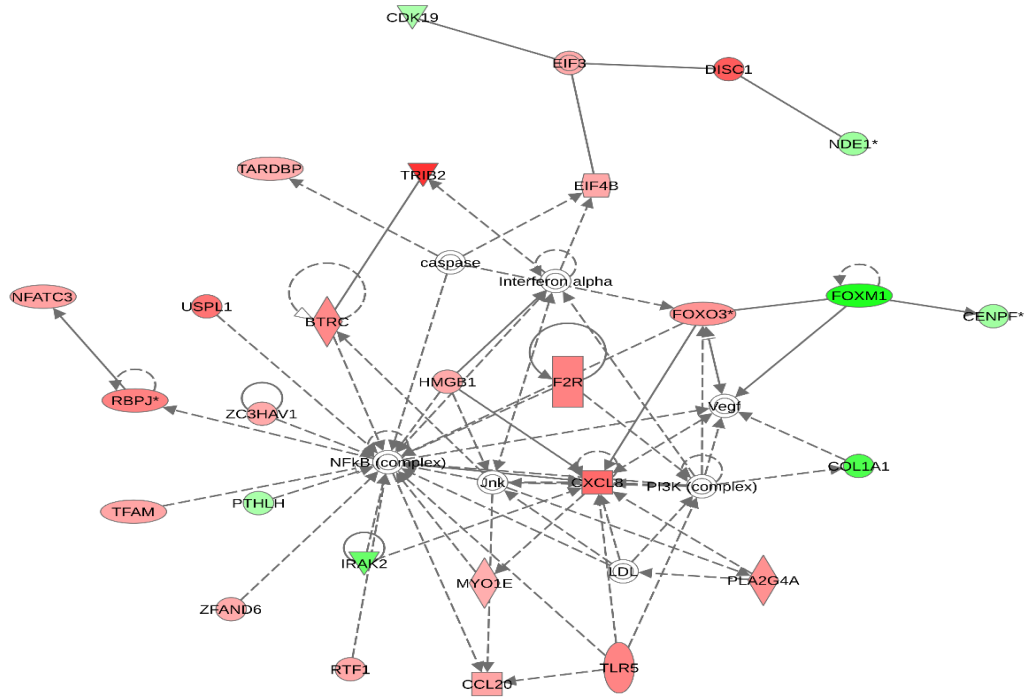
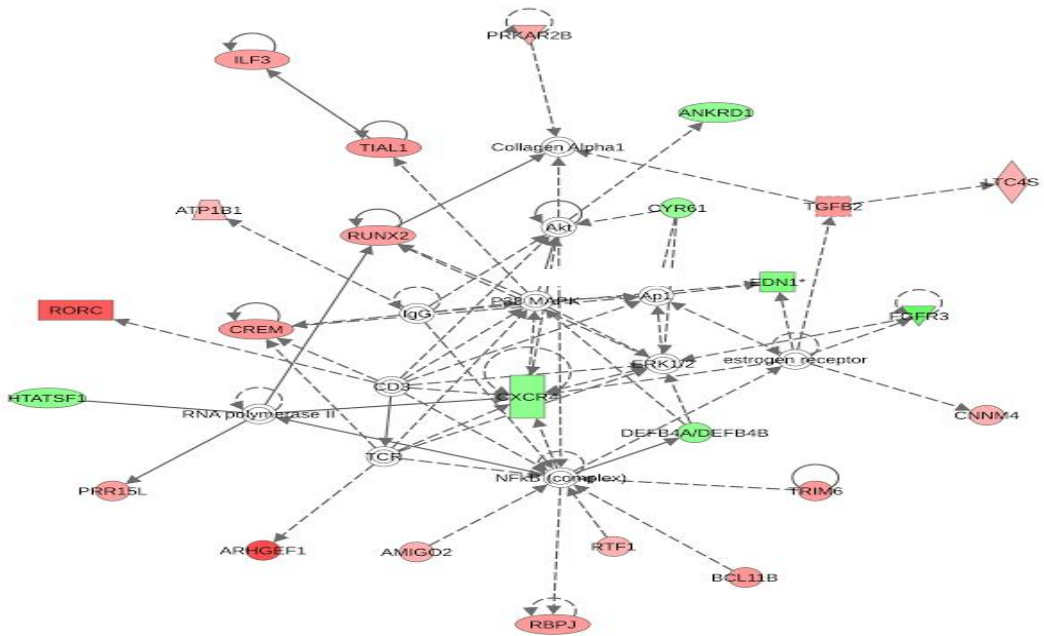


A



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B



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Figure S7. Functional analysis of the genome-wide transcriptional response in FOXM1-silenced EOC cells. Putative network reconstruction on EOC-CC1 cells (A) and on OSPC2 cells (B). Red, up-regulated genes (siFOXM1 versus scramble); green, down-regulated genes. The intensity of the node color indicated the degree of dysregulation. Genes in uncolored notes were not identified as differentially expressed in our experiments and were integrated into the computationally generated networks on the basis of evidence stored in IPA database indicating a relevance to the network. Solid lines indicate direct relationships, while dashed lines indicate indirect relationships (Ingenuity® Pathway Analysis, Qiagen).