

Figure S1. The 2nd significant module from the PPI module. PPIs with high confidence scores are presented as nodes (90% confidence intervals) and the genes selected for subsequent experiments were marked in red. PPI, protein-protein interaction.

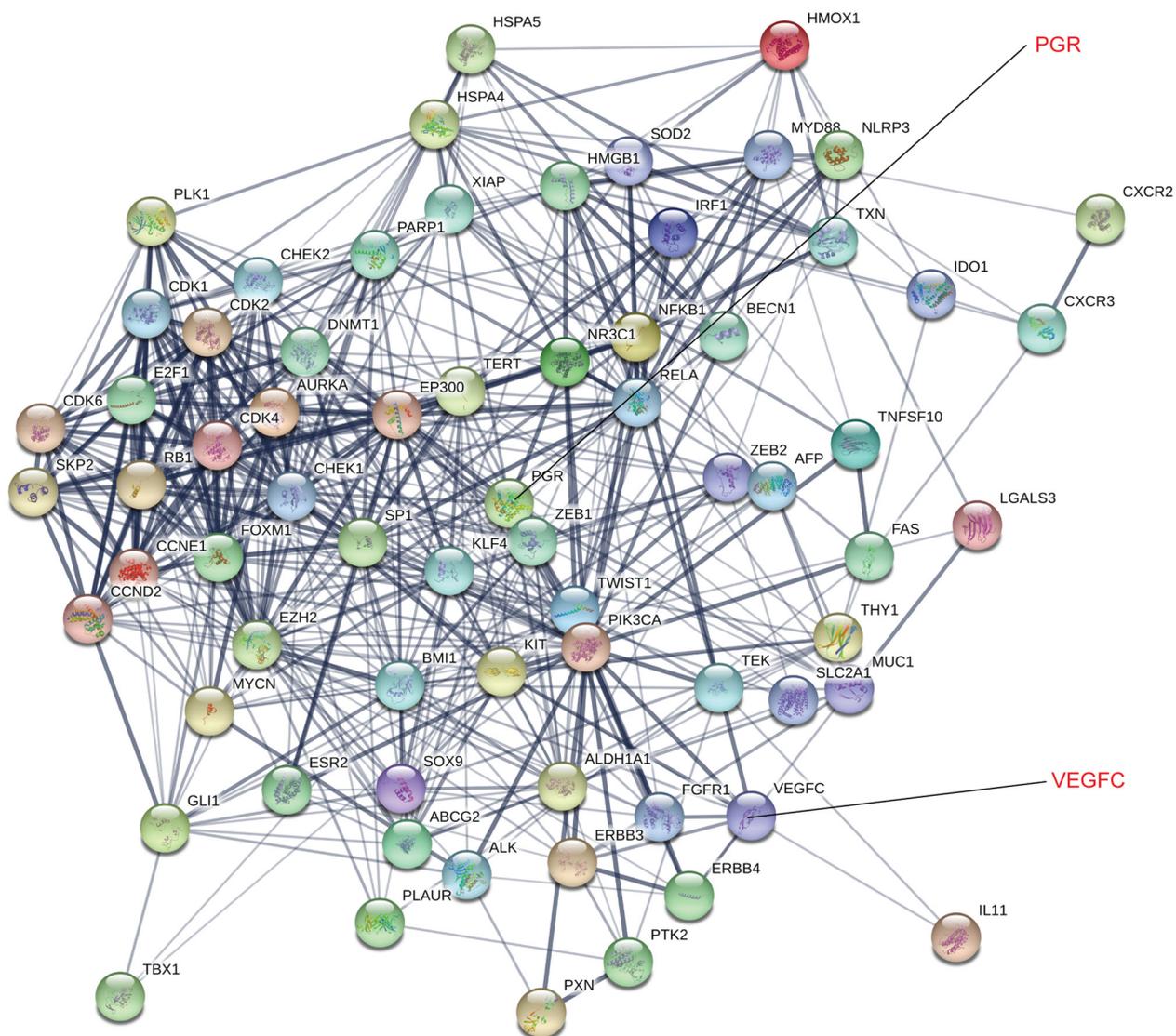


Figure S2. The 3rd significant module from the PPI module. PPIs with high confidence scores are represented as nodes (90% confidence intervals) and the genes selected for subsequent experiments were marked in red. PPI, protein-protein interaction.

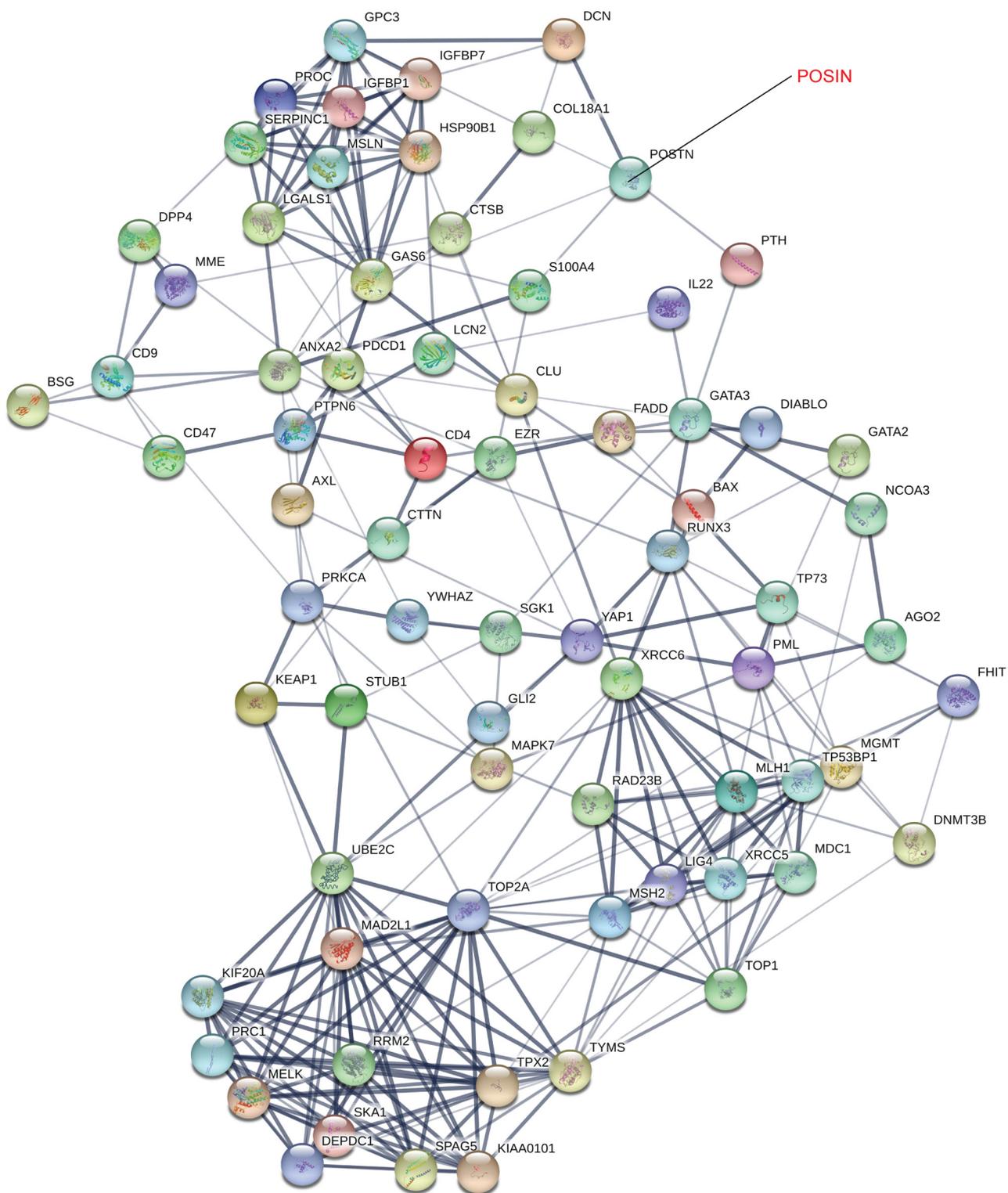


Figure S3. The 4th significant module from the PPI module. PPIs with high confidence scores are represented as nodes (90% confidence intervals) and the genes selected for subsequent experiments were marked in red. PPI, protein-protein interaction.

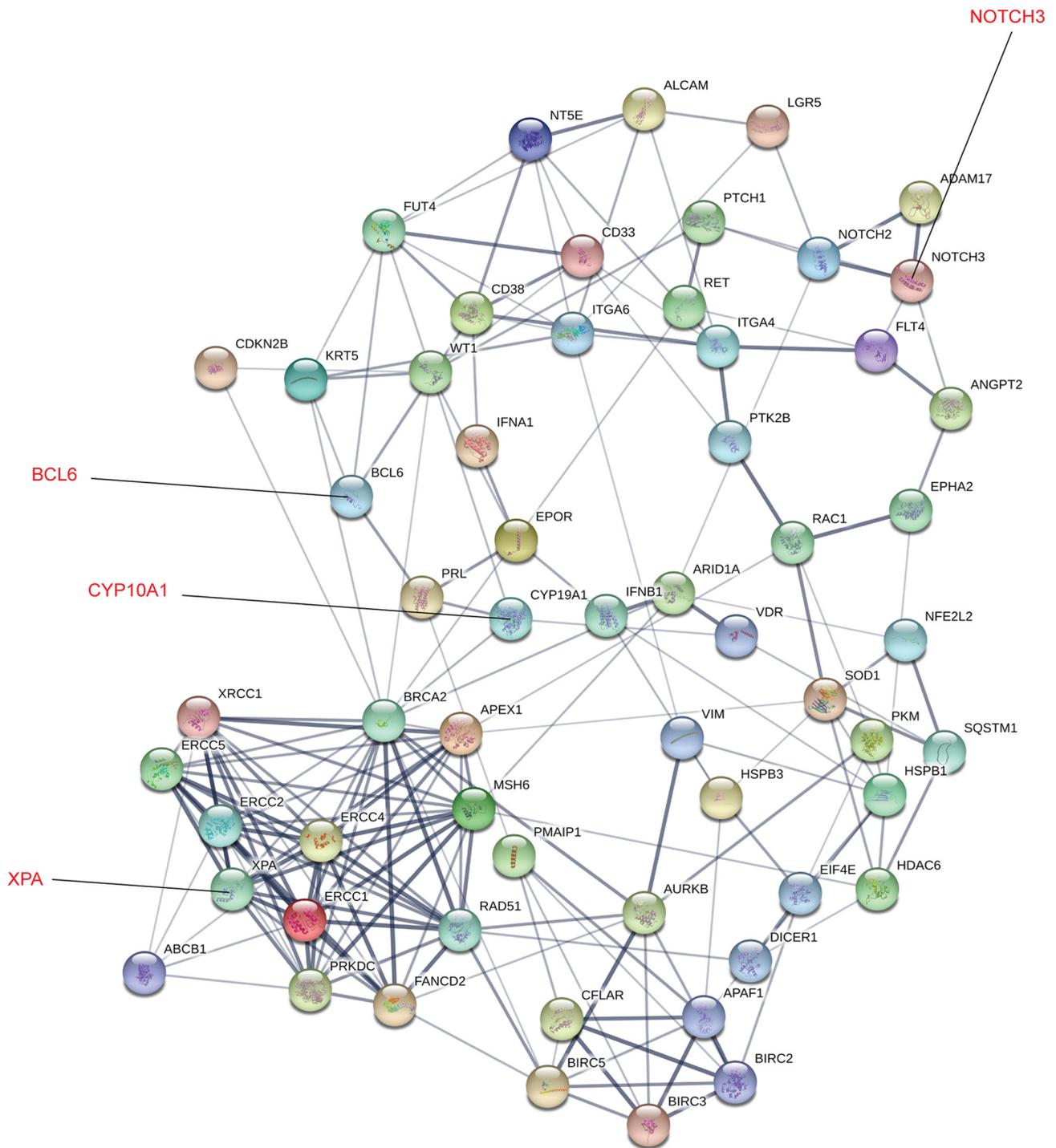


Figure S4. Expression levels of BCL6, EPO, CYP19A1, TGFB1, NOTCH3 and XPA in 33 paired colon cancer tissues and adjacent normal tissues. (A) Representative images and statistical analysis of the expression of the target genes using IHC in 33 paired colon cancer samples. Scale bar, 200 μ m. The data was analyzed using a Wilcoxon signed-rank test and expressed as the median \pm interquartile range. (B) The mRNA expression levels of target genes were detected using reverse transcription-quantitative PCR in 33 paired colon cancer tissues. The data was analyzed using a paired Student's t-test and expressed as mean \pm SD. (C) Survival analysis between the expression level of target genes and patient survival time in 33 paired colon cancer tissues. Each assay was performed independently from 3 repeats. N, normal adjacent tissue; T, tumor tissue; IHC, immunohistochemistry.

