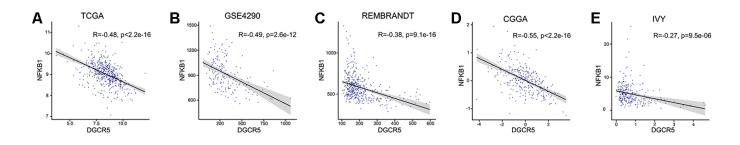
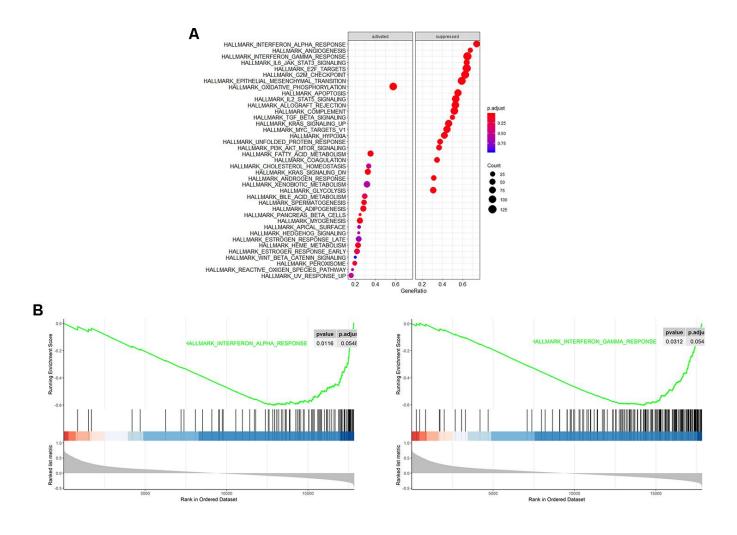
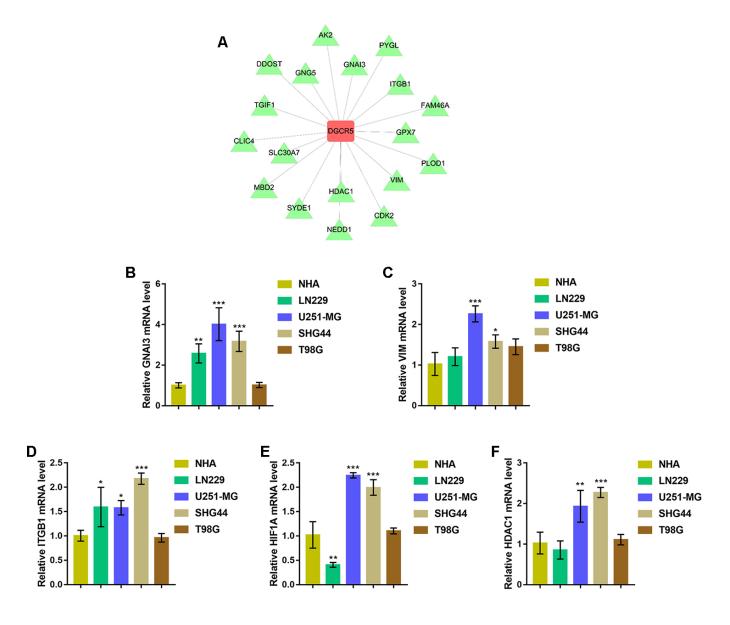
SUPPLEMENTARY FIGURES



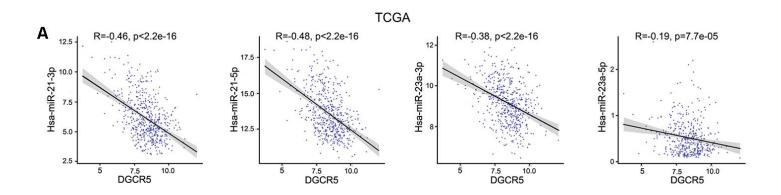
Supplementary Figure 1. Correlation between DGCR5 and NF-κB1 according to (A) TCGA data, (B) GSE4290, (C) REMBRANDT, (D) CGGA, and (E) IVY.



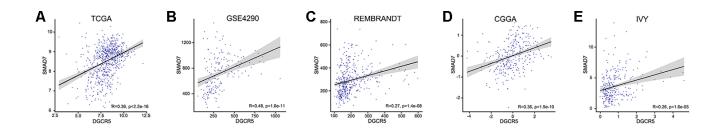
Supplementary Figure 2. Kyoto Encyclopedia of Genes and Genomes (KEGG) (A) and Gene Set Enrichment Analysis (GSEA) (B) on DGCR5.



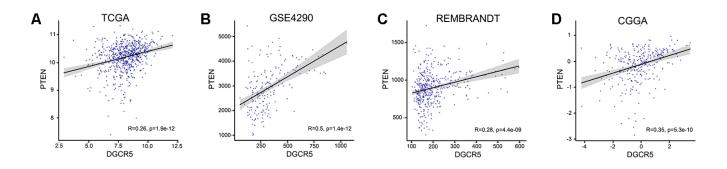
Supplementary Figure 3. Co-expression network consists of DGCR5 and its negatively-correlated genes (**A**) Co-expression network consists of DGCR5 and its negatively-correlated genes. (**B**–**F**) Expression of genes negatively-correlated with DGCR5 in NHA, LN229, U251-MG, SHG44, and T98G cells. **P*<0.05, ***P*<0.01, ****P*<0.005.



Supplementary Figure 4. Correlation between DGCR5, miR-21, and miR-23a according to TCGA data.



Supplementary Figure 5. Correlation between DGCR5 and Smad7 according to (A) TCGA data, (B) GSE4290, (C) REMBRANDT, (D) CGGA, and (E) IVY.



Supplementary Figure 6. Correlation between DGCR5 and PTEN according to (A) TCGA data, (B) GSE4290, (C) REMBRANDT, and (D) CGGA.