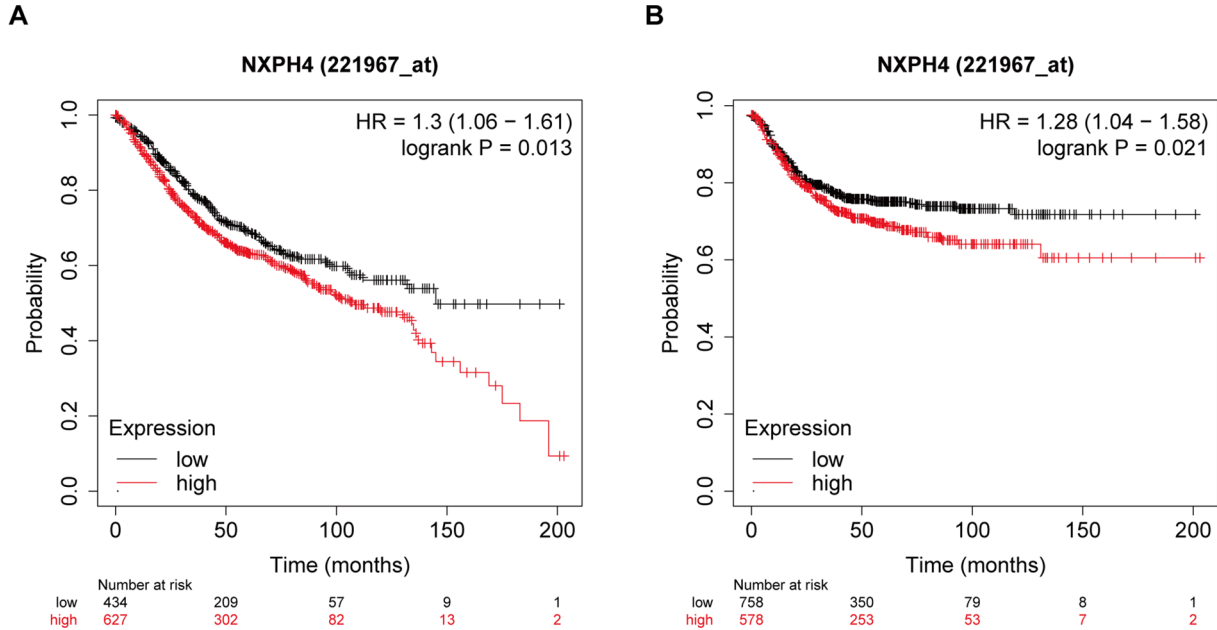
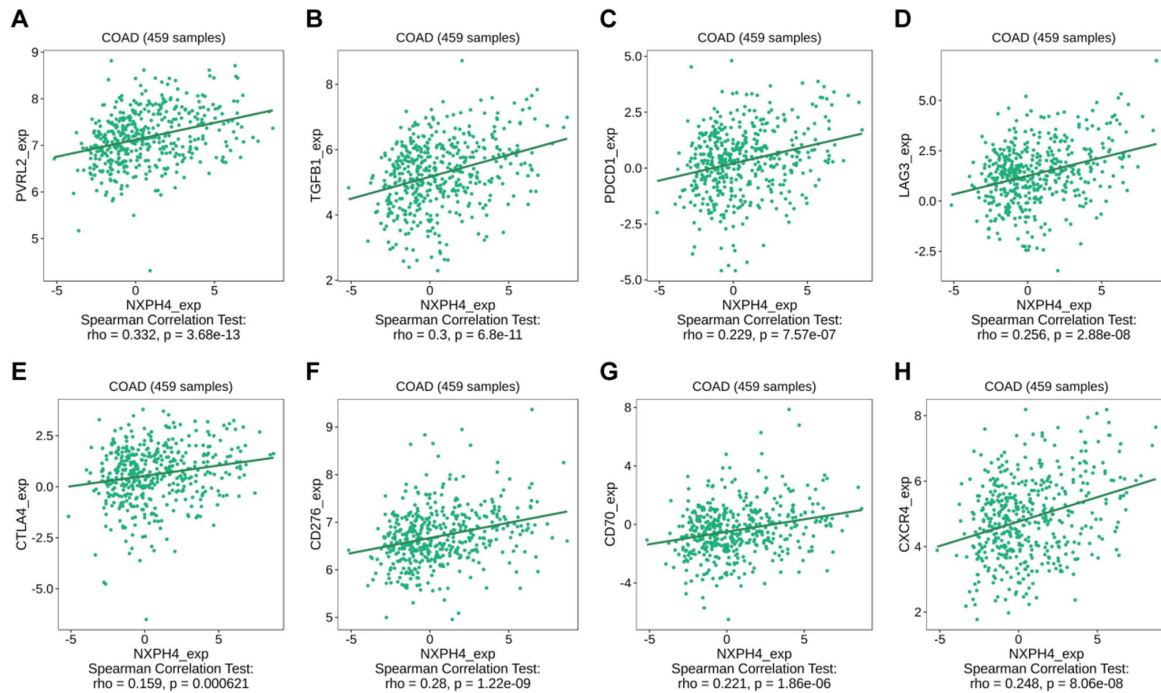


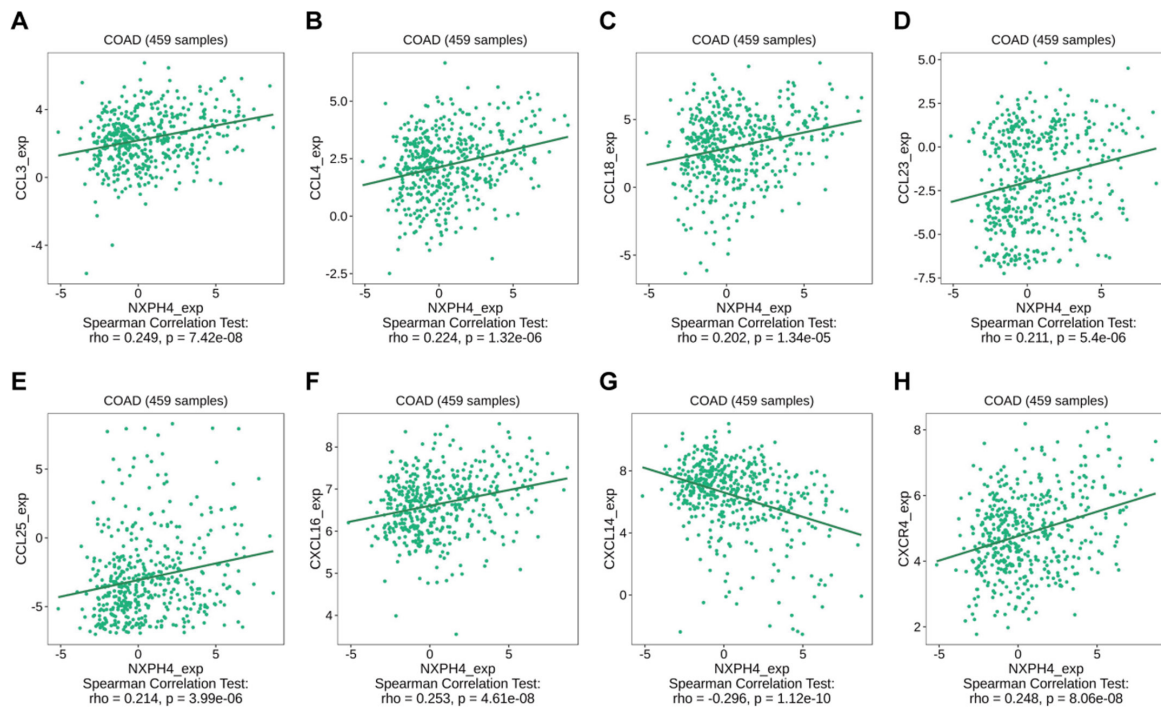
**Figure S1** Flow chart of TCGA data collection and analysis. TCGA, The Cancer Genome Atlas; COAD, colon adenocarcinoma; NXPH4, neurexophilin 4; ROC, receiver operator characteristic; DEGs, differential expressed genes; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; GSEA, gene set enrichment analysis.



**Figure S2** Correlation of NXPH4 expression and prognosis in colon cancer patients via Kaplan-Meier plotter database. (A) OS. (B) RFS. NXPH4, neurexophilin 4; HR, hazard ratio; OS, overall survival; RFS relapse-free survival.



**Figure S3** Correlation analysis of NXPH4 expression with immunomodulators. The correlation between NXPH4 and (A) PVRL2, (B) TGFB1, (C) PDCD1, (D) LAG3, (E) CTLA4, (F) CD276, (G) CD70, and (H) CXCR4. NXPH4, neurexophilin 4; COAD, colon adenocarcinoma.



**Figure S4** Correlation analysis of NXPH4 expression with chemokines and chemokine receptors. The correlation between NXPH4 and (A) CCL3, (B) CCL4, (C) CCL18, (D) CCL23, (E) CCL25, (F) CXCL16, (G) CXCL14, and (H) CXCR4. NXPH4, neurexophilin 4; COAD, colon adenocarcinoma.

**Table S1** Potential upstream miRNAs of NXP4 predicted by both ENCORI and TargetScan

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hsa-miR-15a-5p  
hsa-miR-16-5p  
hsa-miR-24-3p  
hsa-miR-204-5p  
hsa-miR-211-5p  
hsa-miR-214-3p  
hsa-miR-15b-5p  
hsa-miR-141-3p  
hsa-miR-195-5p  
hsa-miR-320a  
hsa-miR-200a-3p  
hsa-miR-375  
hsa-miR-424-5p  
hsa-miR-485-5p  
hsa-miR-497-5p  
hsa-miR-582-5p  
hsa-miR-588  
hsa-miR-625-5p  
hsa-miR-663a  
hsa-miR-654-5p  
hsa-miR-296-3p  
hsa-miR-361-3p  
hsa-miR-541-3p  
hsa-miR-876-5p

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**Table S1** (*continued*)

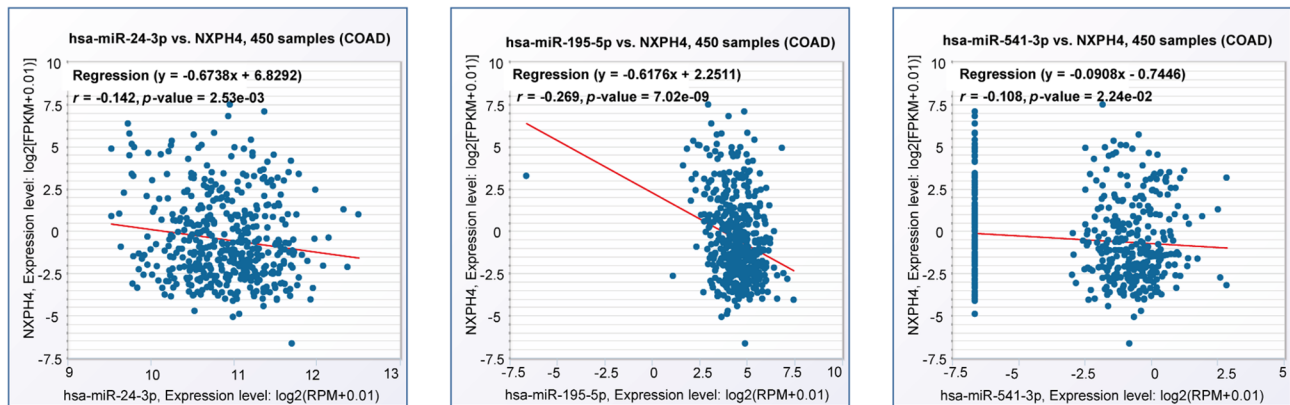
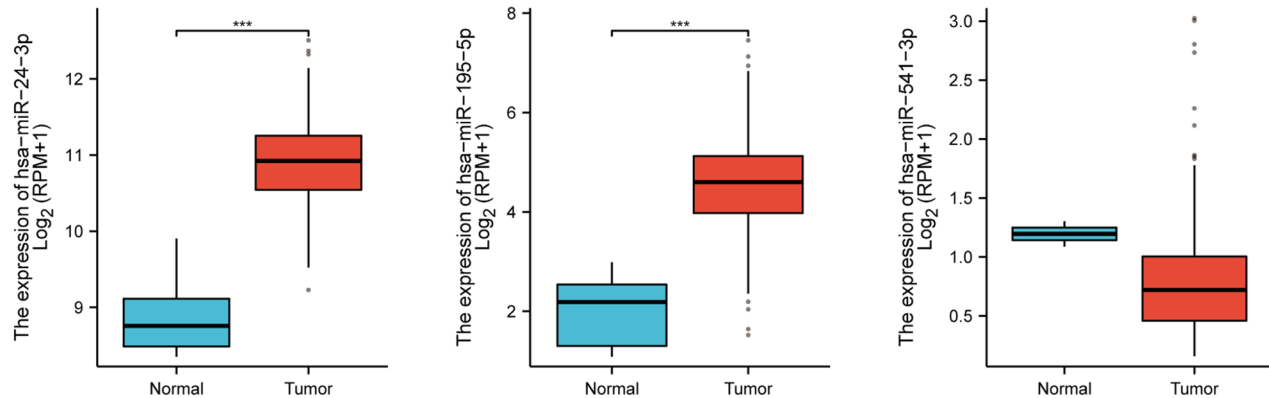
**Table S1** (*continued*)

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hsa-miR-744-5p  
hsa-miR-665  
hsa-miR-320b  
hsa-miR-320c  
hsa-miR-1286  
hsa-miR-1295a  
hsa-miR-1247-5p  
hsa-miR-320d  
hsa-miR-1908-5p  
hsa-miR-3142  
hsa-miR-3167  
hsa-miR-3180-3p  
hsa-miR-3180  
hsa-miR-4429  
hsa-miR-4436a  
hsa-miR-4525  
hsa-miR-4664-3p  
hsa-miR-4701-5p  
hsa-miR-4731-5p  
hsa-miR-1245b-5p  
hsa-miR-5000-3p  
hsa-miR-5010-5p  
hsa-miR-766-5p  
hsa-miR-642b-5p

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miRNAs, microRNAs; NXP4, neurexophilin 4.

**A****B**

**Figure S5** Analysis of the potential upstream miRNAs of NXPH4. (A) Correlation analysis between NXPH4 expression and hsa-miR-24-3p, hsa-miR-195-5p, and hsa-miR-541-3p. (B) Analysis of hsa-miR-24-3p, hsa-miR-195-5p, and hsa-miR-541-3p in tumor tissues and adjacent normal tissues in TCGA-COAD. \*\*\*,  $P < 0.001$ . NXPH4, neurexophilin 4; COAD, colon adenocarcinoma; RPM, reads per million; FPKM, fragments per kilobase per million; TCGA, The Cancer Genome Atlas.

**Table S2** Potential upstream lncRNAs of hsa-miR-204-5p, hsa-miR-485-5p, hsa-miR-497-5p, and hsa-miR-320c

miRNAs	Potential upstream lncRNAs
hsa-miR-204-5p	AL365181.2, WWTR1-AS1, AC093866.1, NPSR1-AS1, FAM225A, AP002954.1, AC023509.3, HOTAIR, DHRS4-AS1, SRRM2-AS1, AC099518.1, LINC02693, MZF1-AS1, DGCR5, MIAT, AL021707.6
hsa-miR-485-5p	AL645608.2, AL645608.7, AL691432.2, PINK1-AS, LINC01750, AL365181.2, AC080013.1, MELTF-AS1, CTBP1-DT, TENM3-AS1, IRF2-DT, ZSCAN16-AS1, AL035446.1, SNHG26, AC069281.2, AC100861.1, MIR31HG, DBH-AS1, SNHG7, AL358394.1, RPARP-AS1, LINC02882, SNHG10, AL135838.1, MIR9-3HG, LINC02348, AL008727.1, SRRM2-AS1, MMP25-AS1, ATP2A1-AS1, SNAI3-AS1, PITPNA-AS1, LINC02693, AC018521.5, AC007998.3, AC027307.2, AC006262.1, NAPA-AS1, AC020915.2, A1BG-AS1, AL109976.1, TSPEAR-AS2, DGCR5, MIAT, OGFRP1, MIRLET7BHG
hsa-miR-497-5p	AL645608.2, AC012073.1, AC093001.1, CTBP1-DT, AFAP1-AS1, AC093866.1, TENM3-AS1, AC025171.1, AC069281.2, AC091182.1, LY6E-DT, LINC02846, MIR210HG, HOXC-AS1, AC012531.1, AGAP2-AS1, LINC02882, LINC02347, LINC00943, TMEM132D-AS1, MIR9-3HG, AL008727.1, MMP25-AS1, AC129492.1, LINC02693, SNHG25, AC139530.1, PCAT19, IGFL2-AS1, AC010327.6, MZF1-AS1, LINC01547, AP000547.3, DGCR5, MIAT, MIRLET7BHG
hsa-miR-320c	AC069281.2, AC090152.1, FAM225A, DBH-AS1, AC012531.1, DHRS4-AS1, LINC01303, AC090181.2, MIR9-3HG, MMP25-AS1, LINC02693, TYMSOS, AC007996.1, LINC00909, AC012313.8, AP000251.1, LINC01547, MIAT, MIRLET7BHG

lncRNAs, long noncoding RNAs.