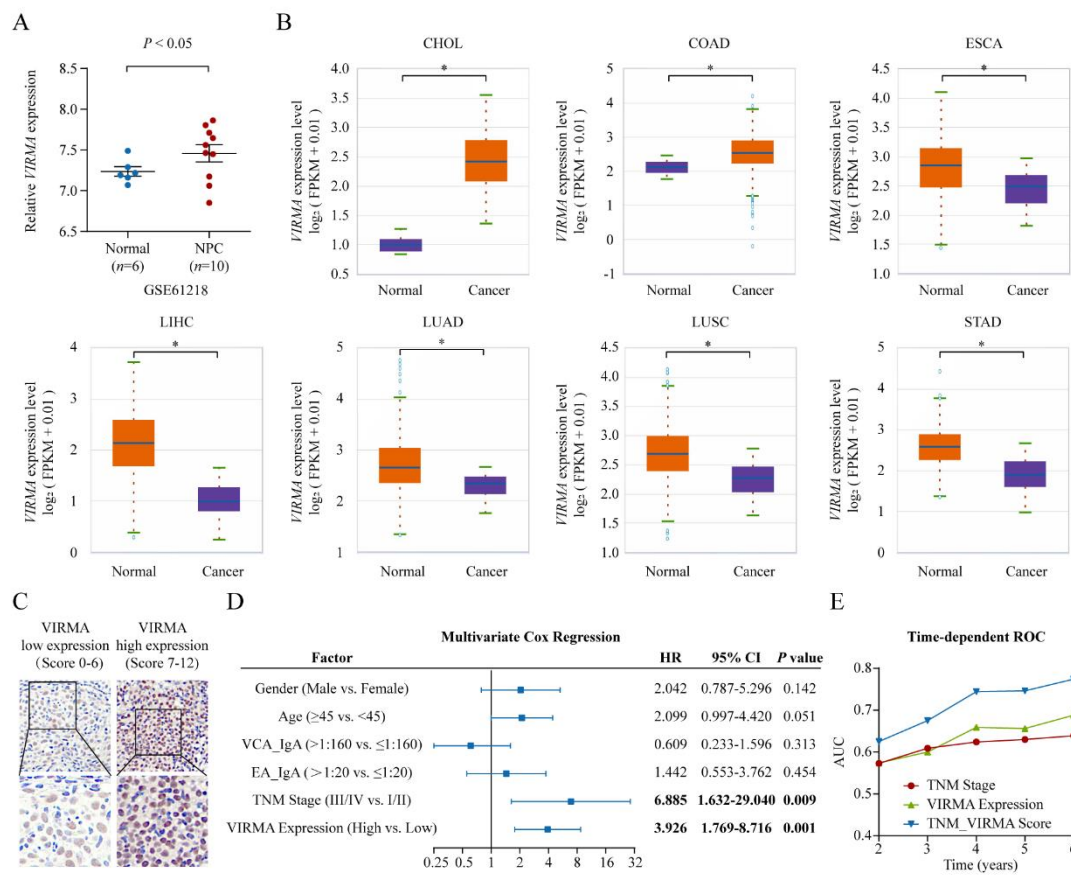


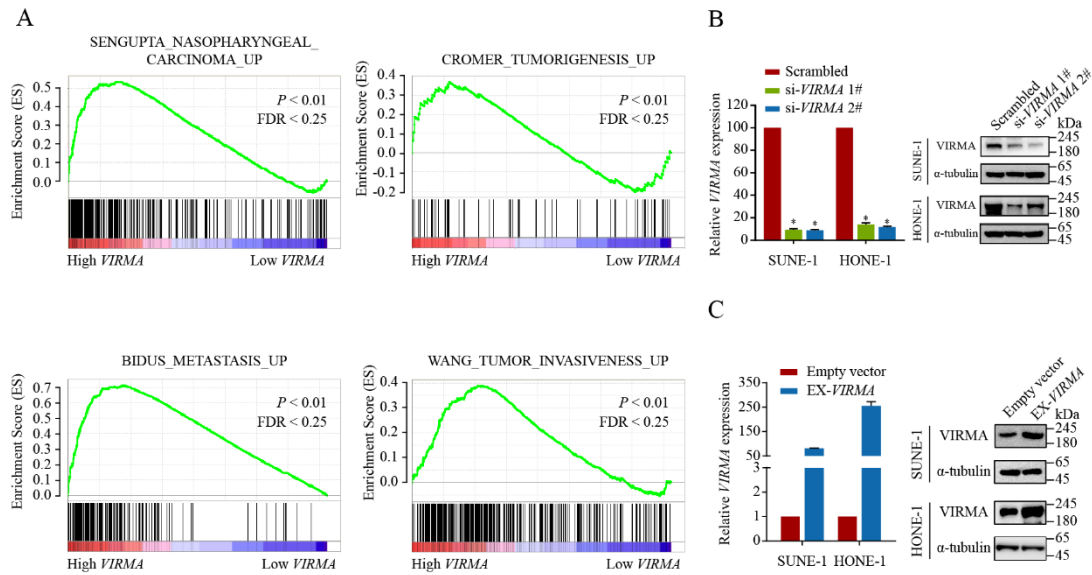
Supplementary Figure 1



Supplementary Figure S1. *VIRMA* is upregulated and predicts an unfavorable prognosis for patients with NPC.

A. Expression levels of *VIRMA* in NPC tissues and normal nasopharyngeal tissues were compared based on the GEO database GSE61218. **B.** *VIRMA* expression levels in various cancer types based on RNA-seq data from TCGA databases. Abbreviations: CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; HNSC, head and neck squamous cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung carcinoma; LUSC, lung squamous carcinoma; STAD, stomach adenocarcinoma. **C.** Representative images of *VIRMA* low (score 0-6) and high (score 8-12) expression stained with IHC assays. **D.** Multivariate Cox regression was used to analyze the prognostic value of *VIRMA* expression. **E.** Time-dependent ROC analysis to determine the predictive ability of *VIRMA* expression of overall survival in NPC patients.

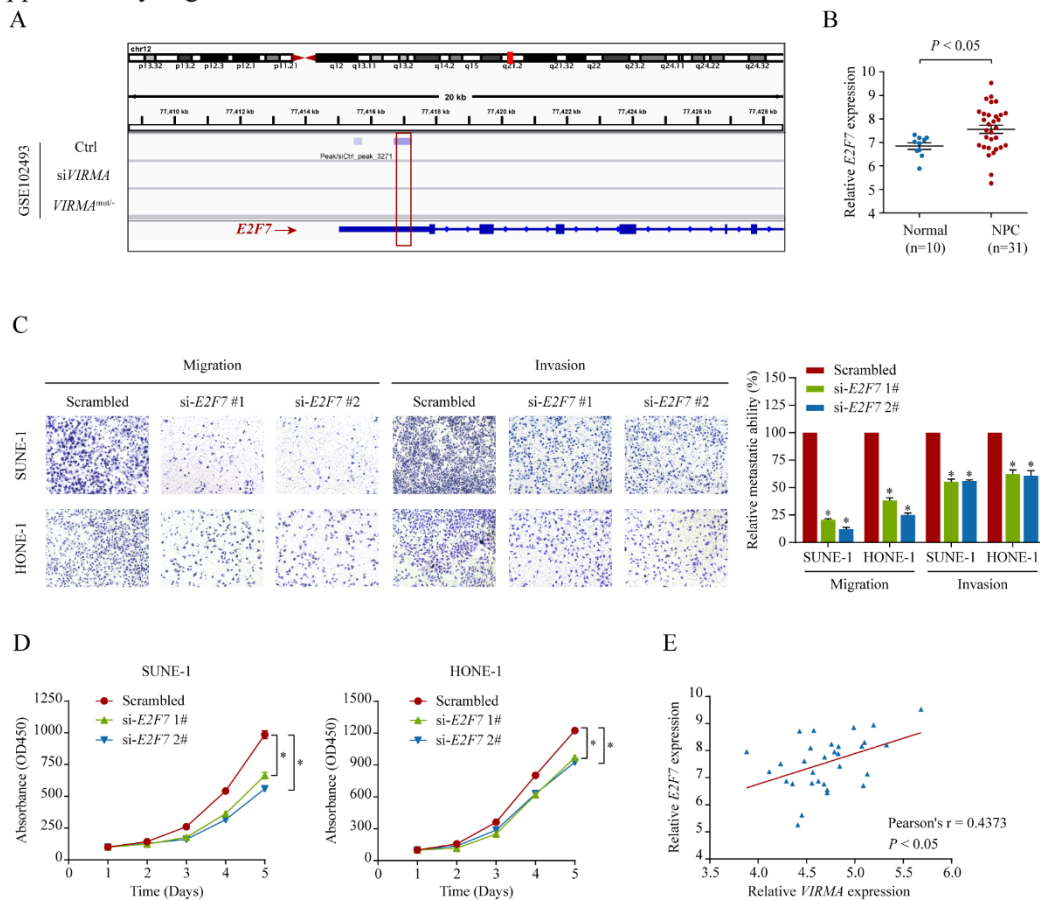
Supplementary Figure 2



Supplementary Figure S2. Overexpression of *VIRMA* promotes NPC progression and metastasis.

A. GSEA analysis of RNA-seq data from GSE12452 revealed that *VIRMA* was closely associated with NPC tumorigenesis and metastasis. **B–C.** Knockdown (**B**) and overexpression (**C**) efficiency of *VIRMA* was validated by qPCR (left panel) and western blotting (right panel). Data are presented as the mean $\pm$ SD. * $P < 0.05$.

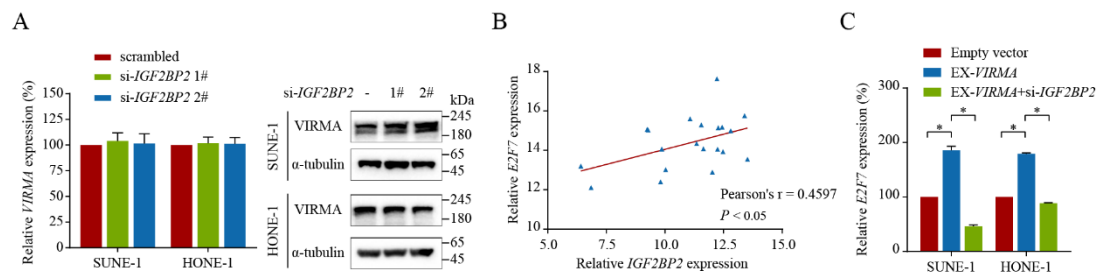
Supplementary Figure 3



Supplementary Figure S3. VIRMA-mediated upregulation of *E2F7* promotes NPC proliferation and metastasis in NPC.

A. m6A peaks in the 3'UTR region of *E2F7* in control, *VIRMA* silencing or *VIRMA*-mutant Hela cells from the GEO database (GSE102493). **B.** Expression levels of *E2F7* in NPC tissues and normal nasopharyngeal tissues were compared using the GEO database (GSE12452). **C.** Migration and invasion capacities of *E2F7*-silencing SUNE-1 and HONE-1 cells were analyzed by Transwell assays. **D.** CCK-8 assays were performed to analyze the proliferation ability of SUNE-1 and HONE-1 cells with *E2F7* silencing. **E.** Pearson correlation analysis of *VIRMA* and *E2F7* expression from GEO database (GSE12452). Data are presented as the mean $\pm$ SD. * $P < 0.05$.

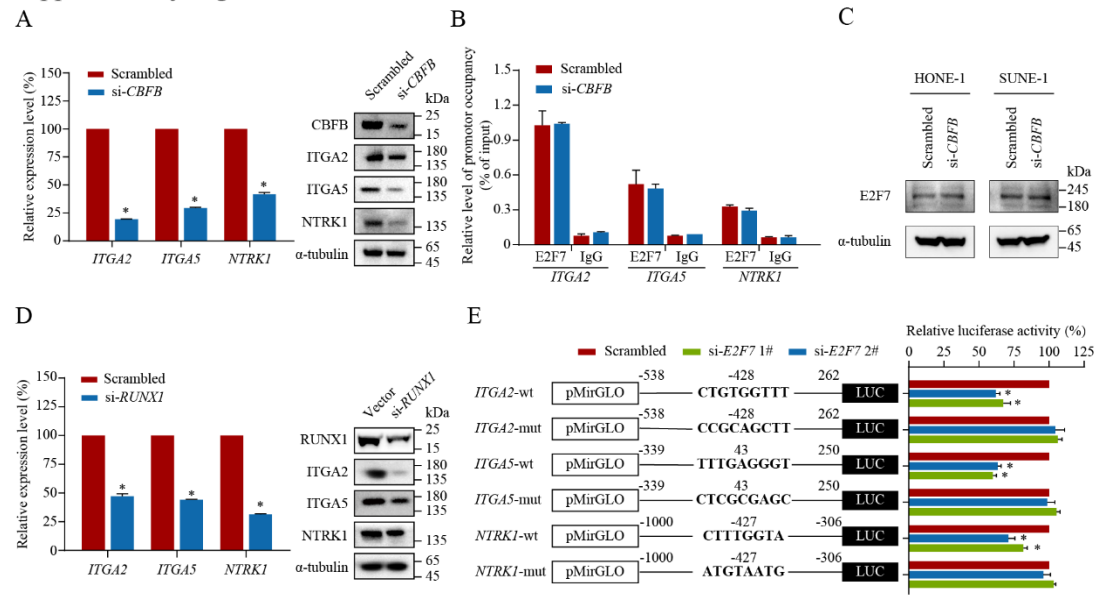
Supplementary Figure 4



Supplementary Figure S4. VIRMA-mediated m6A modification of E2F7 mRNA maintains its IGF2BP2-dependent stability.

A. Quantitative RT-PCR (left) and western blotting (right) analysis of *VIRMA* expressions in SUNE-1 and HONE-1 cells with or without *IGF2BP2* silencing. **B.** Pearson correlation analysis of *IGF2BP2* and *E2F7* expression in 20 NPC tissues. **C.** Relative *E2F7* expression level in SUNE-1 and HONE-1 cells co-transfected with *VIRMA* overexpression vectors and si-*IGF2BP2* or the corresponding control. Data are presented as the mean $\pm$ SD. * $P < 0.05$, ** $P < 0.01$.

Supplementary Figure 5



Supplementary Figure S5. E2F7 transactivates *ITGA2*, *ITGA5*, and *NTRK1* cooperatively with RUNX1.

A. Relative RNA (left panel) and protein (right panel) expression level of *ITGA2*, *ITGA5*, and *NTRK1* upon *CBFB* knockdown. **B.** Relative level of occupancy in *ITGA2*, *ITGA5*, and *NTRK1* promoter regions by E2F7 with or without *CBFB* knockdown. **C.** Relative E2F7 expression upon *CBFB* knockdown. **D.** Relative RNA (left panel) and protein (right panel) expression level of *ITGA2*, *ITGA5*, and *NTRK1* upon *RUNX1* knockdown. **E.** Left, schematic presentation of *ITGA2*, *ITGA5*, and *NTRK1* promoter regions constructed on luciferase reporter expression vectors; Right, relative luciferase activity in HONE-1 cells transfected with wild type or RUNX1-binding-site mutant *ITGA2*, *ITGA5* or *NTRK1* luciferase reporter expression vectors upon *E2F7* silencing. The numbers indicated the distance to transcription start sites (TSS) of the corresponding gene. Data are presented as the mean $\pm$ SD. * $P < 0.05$.