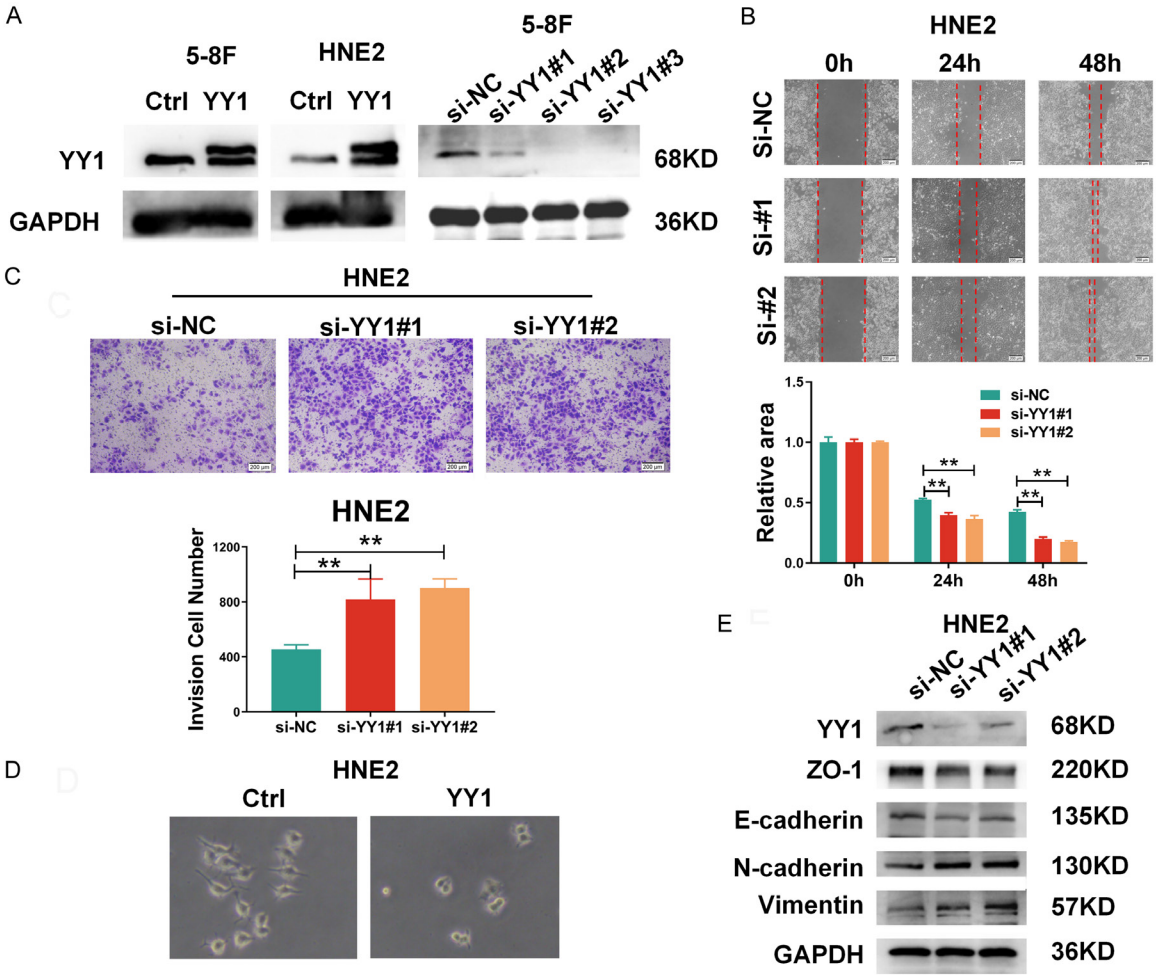

Figure S1. YY1 inhibits migration, invasion and EMT process as a tumor suppressor gene in nasopharyngeal carcinoma. A. Western blotting using antibody against YY1 to confirm YY1 protein levels. GAPDH served as an internal control. B. Cell migration assay was performed with the scratch wound healing analysis in HNE2 cells, and quantification of the wound recovery rate of the three groups. C. Matrigel invasion analysis of cell invasive capabilities in HNE2 with transfection of YY1 siRNAs or negative control, scale bar, 200 μm. D. Photographs of cell morphology from a representative experiment in HNE2 cells stably transfected with YY1 expression plasmid or control. E. Western blotting to verify the significantly differently expressed proteins involved in EMT progression in HNE2 cells with YY1 siRNAs or negative control. Error bars represent the mean ± SD. $^{**}P<0.01$.

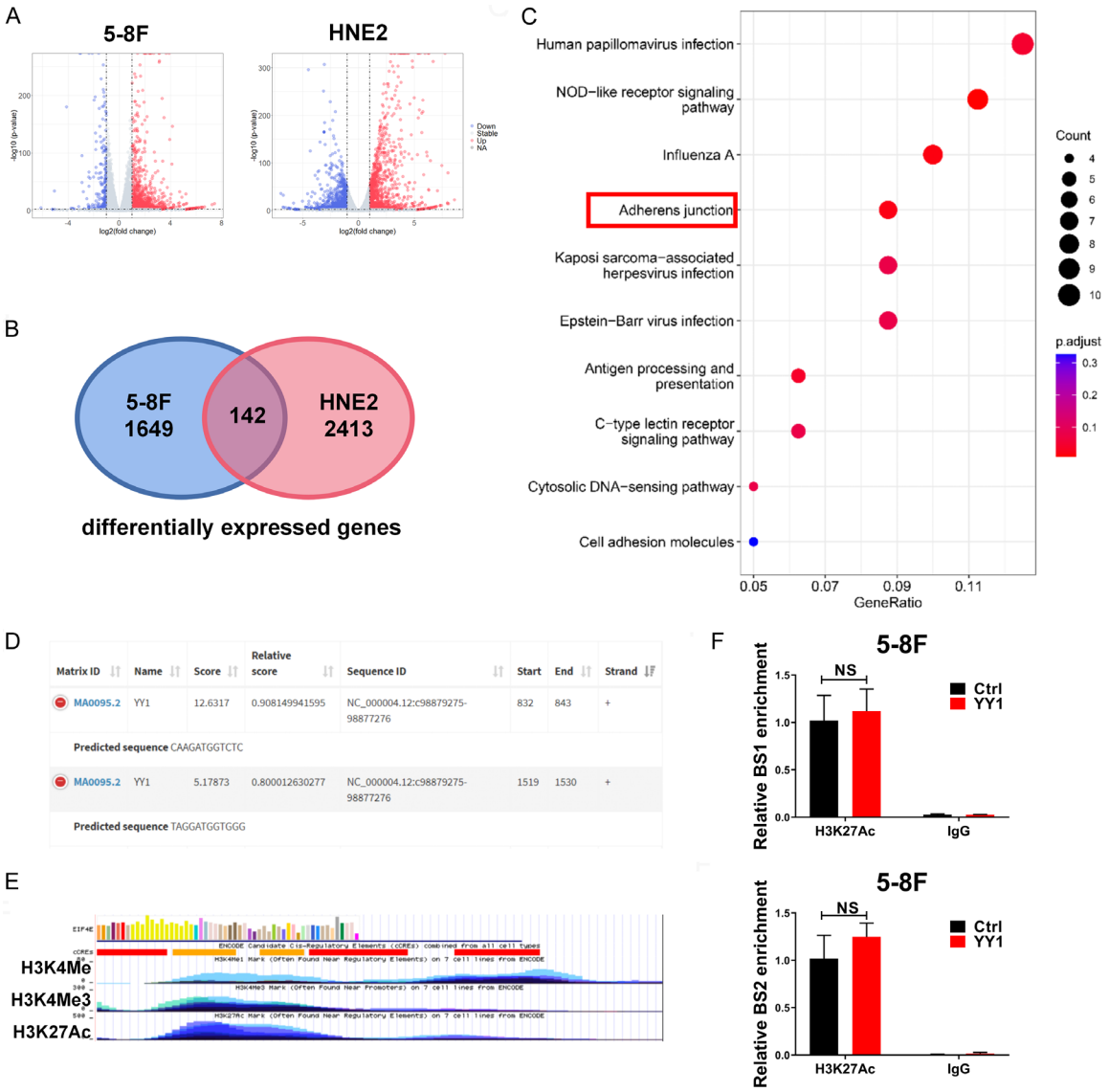

Figure S2. eIF4E is a downstream target gene of the YY1 that negatively regulates its promoter activity. A. The volcano map of differentially expressed proteins after YY1 overexpressed in 5-8F and HNE2 cells. B. The intersection Venn diagram shows the the number of intersecting differentially expressed proteins in 5-8F and HNE2 cells after YY1 overexpression. C. KEGG pathway enrichment results for the differential expressed proteins in the signaling pathway terms. D. JASPER web predicted the binding site of YY1 on the eIF4E promoter. E. USUC web predicts the enrichment of H3K27AC at the eIF4E promoter region. F. ChIP-PCR assays using antibodies specific for H3K27Ac validated the enrichment of H3K27AC at the eIF4E promoter region. Error bars represent the mean ± SD. NS, no significance.

Table S1. The list of overlapped genes by combined analysis of GTRD, HTF target database, and RNA-seq data (with $P<0.001$)

Gene name	Description	Average log2 (fold change)
EIF4E	Eukaryotic translation initiation factor 4E	-1.92337
SNAI1	Snail family transcriptional repressor 1	-1.77311
PTPRH	Protein tyrosine phosphatase receptor type H	1.168943
PLA2G4C	Phospholipase A2 group IVC	1.195911
HMOX1	Heme oxygenase 1	1.211928
APOL3	Apolipoprotein L3	1.224812
REC8	REC8 meiotic recombination protein	1.467768
PLCG2	Phospholipase C gamma 2	1.482419
TJP3	Tight junction protein 3	1.504335
PATL2	PAT1 homolog 2	1.585259
AIM2	Absent in melanoma 2	1.652675
SERPINB9P1	Serpin family B member 9 pseudogene 1	1.674563
ISG15	ISG15 ubiquitin like modifier	1.938478
LAPTM5	Lysosomal protein transmembrane 5	1.944392
RASGRP3	RAS guanyl releasing protein 3	2.169333
EPSTI1	Epithelial stromal interaction 1	2.170507
ADAM19	ADAM metallopeptidase domain 19	2.197979
IRF9	Interferon regulatory factor 9	2.222717
SSC5D	Scavenger receptor cysteine rich family member with 5 domains	2.226573
TNFRSF8	TNF receptor superfamily member 8	2.374073
IGSF23	Immunoglobulin superfamily member 23	2.590725
IFI6	Interferon alpha inducible protein 6	3.00205
CCL5	C-C motif chemokine ligand 5	3.135662
YY1	YY1 transcription factor	4.218289

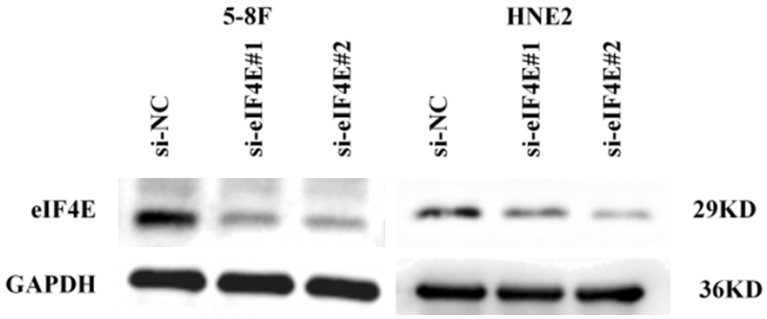

Figure S3. The silencing effect of siRNA targeting eIF4E. Western blotting using antibody against eIF4E to confirm eIF4E protein levels. GAPDH served as an internal control.

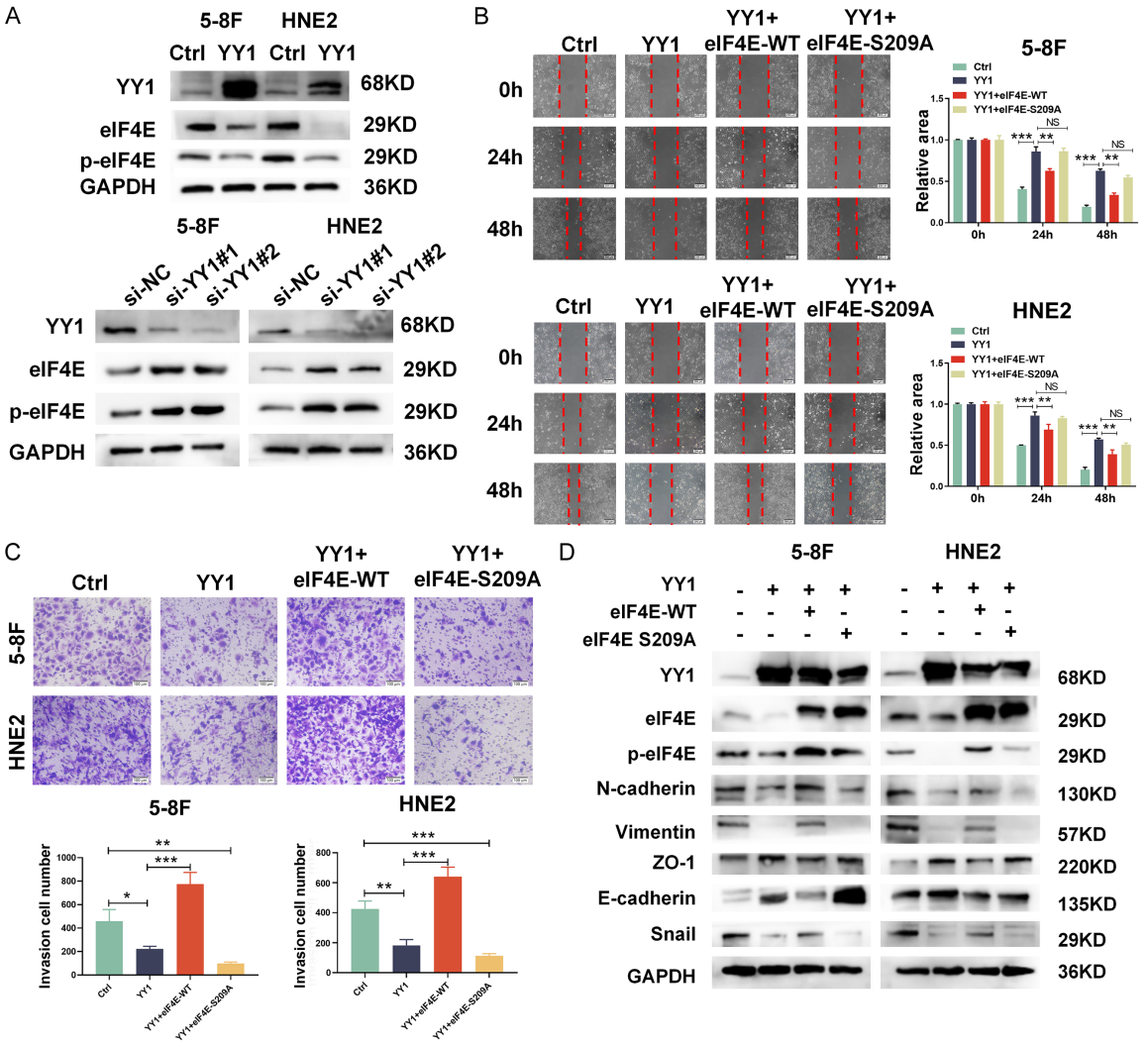

Figure S4. Effect of YY1 on cell migration and invasion is dependent on the phosphorylation of eIF4E at S209. A. Western blotting using antibodies against YY1 and p-eIF4E to confirm YY1 and p-eIF4E protein levels. GAPDH served as an internal control. B. Scratch wound healing analysis of cell migration in 5-8F and HNE2 cells stably with YY1 overexpression, YY1 and eIF4E-WT simultaneous overexpression, YY1 and eIF4E-S209A simultaneous overexpression or control (left), quantification of the wound recovery rate of the four groups (right). C. Matrigel invasion analysis of cell invasive capabilities in 5-8F and HNE2 cells stably with YY1 overexpression, YY1 and eIF4E-WT simultaneous overexpression, YY1 and eIF4E-S209A simultaneous overexpression or control. D. Significantly differently expressed proteins involved in EMT progression (E-cadherin, N-cadherin, Vimentin, ZO-1, Snail) in YY1 overexpression, eIF4E-wt or eIF4E-S209A restoration cells, respectively. GAPDH served as an internal control. Error bars represent the mean ± SD. *P<0.05; **P<0.01; ***P<0.001; NS, no significance.

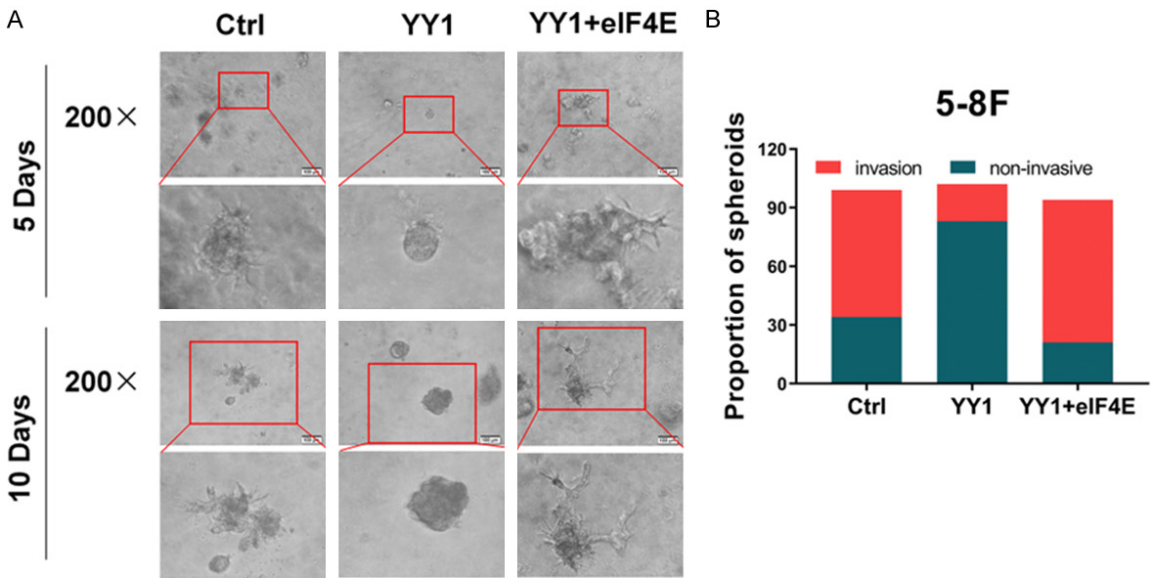

Figure S5. YY1 inhibits cell invasive capabilities in 5-8F cells. A. Three-dimensional invasion analysis of cell invasive capabilities in 5-8F cells stably transfected with YY1 expression plasmid or eIF4E restoration. The white arrows represent prominent protrusions, scale bar, 100 μm. B. Quantification of invasive and non-invasive clonal spheroids in YY1 overexpression and control group.