

## Supporting Information

### **Hypoxia-driven TNS4 fosters HNSCC tumorigenesis by stabilizing integrin $\alpha 5\beta 1$ complex and triggering FAK-mediated Akt and TGF $\beta$ signaling pathways**

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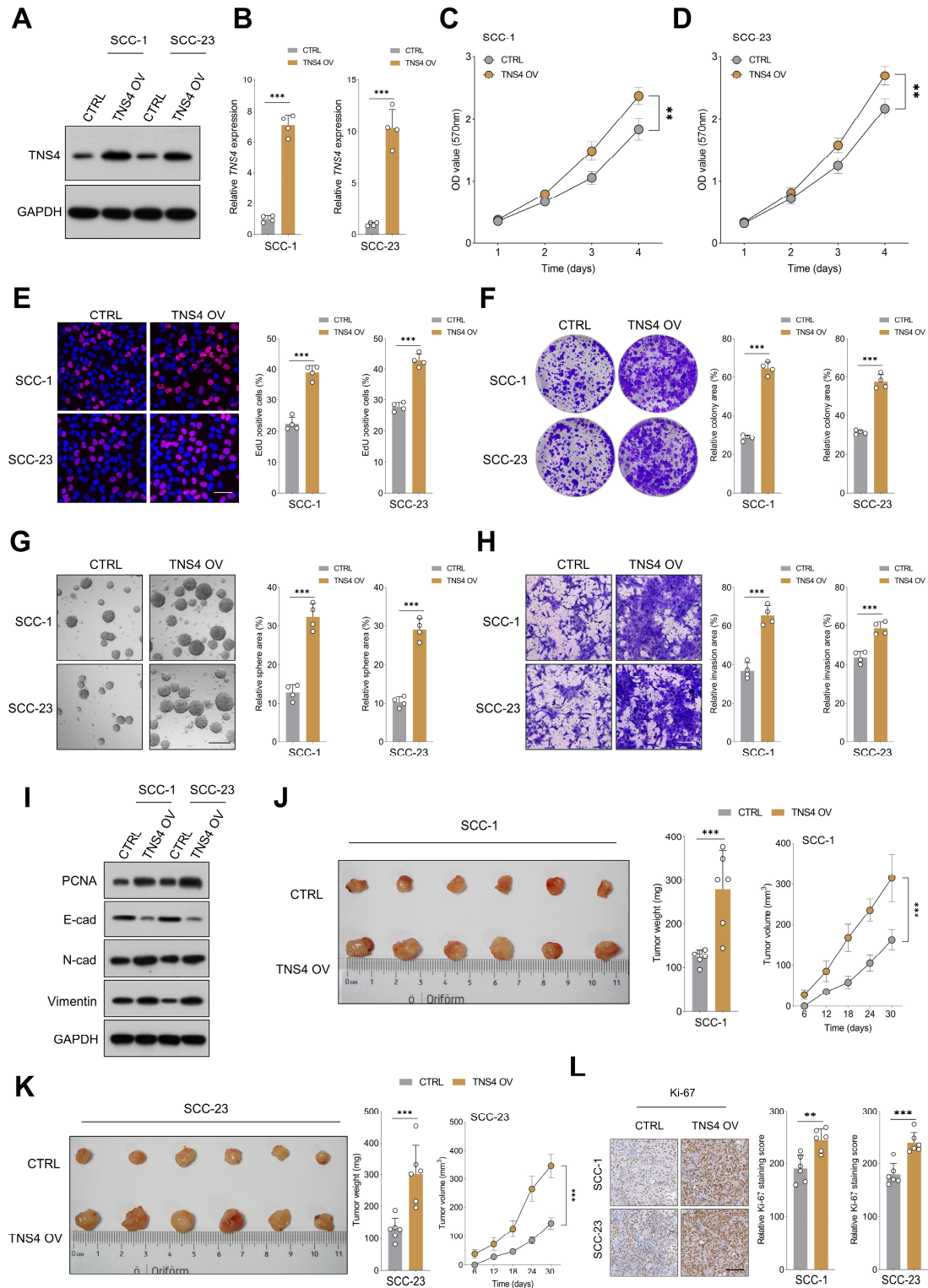
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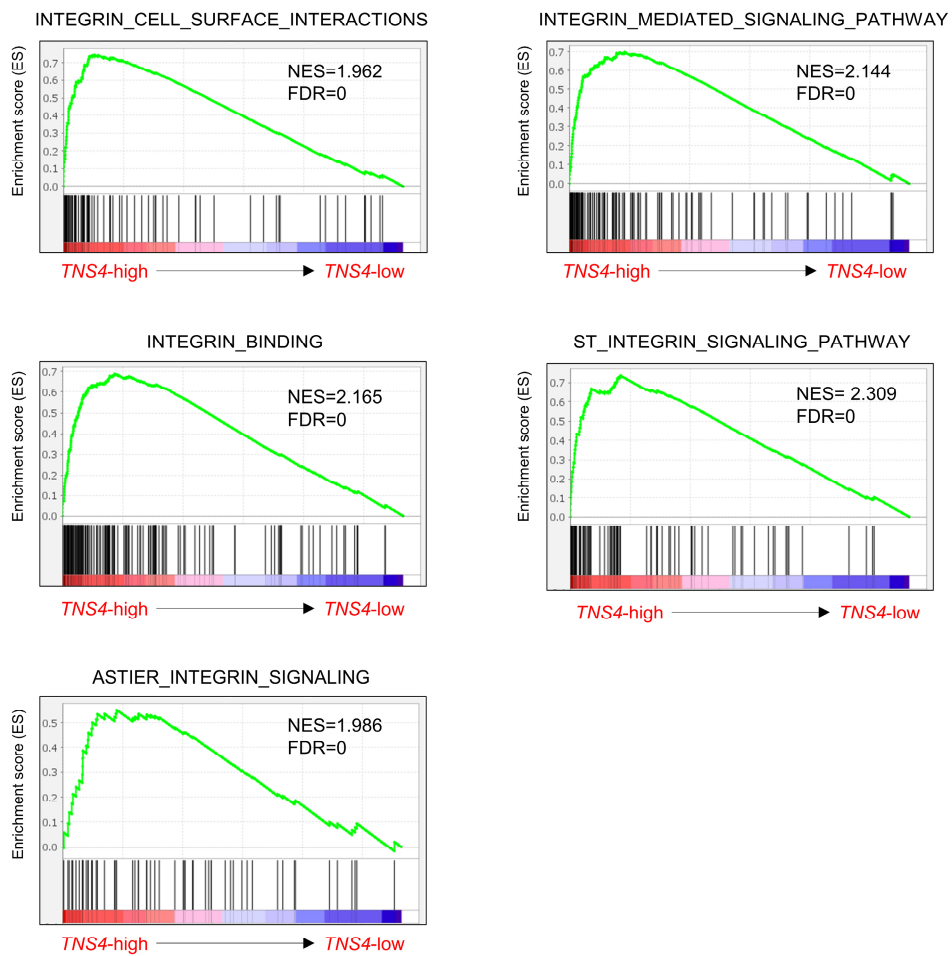
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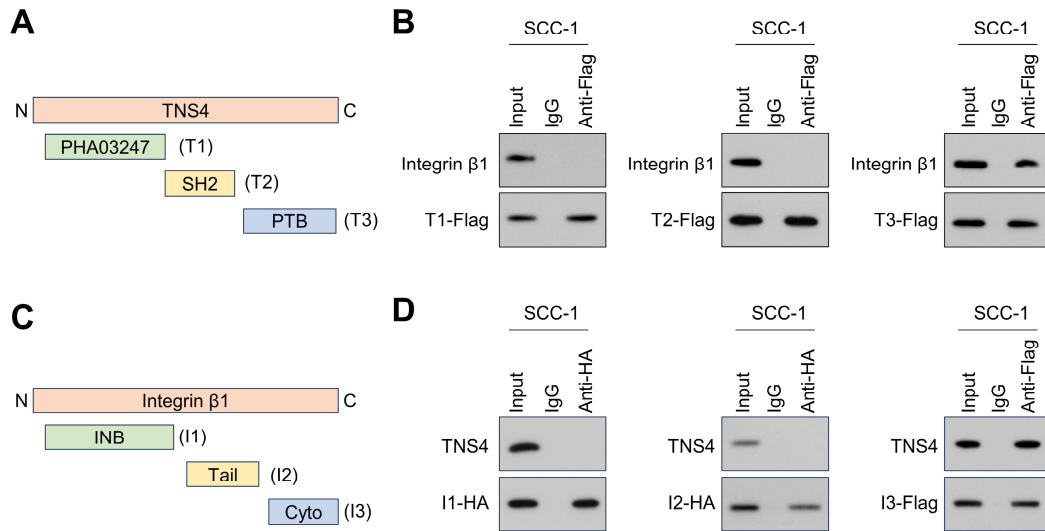


**Figure S1.** TNS4 overexpression enhances malignant features of HNSCC cells *in vitro* and *in vivo*. (A-B) Validation of TNS4 overexpression in HNSCC cells *via* western blotting and qPCR following specific treatments. (C-D) Measurement of OD values at different time intervals for cells with enforced TNS4 expression and their control

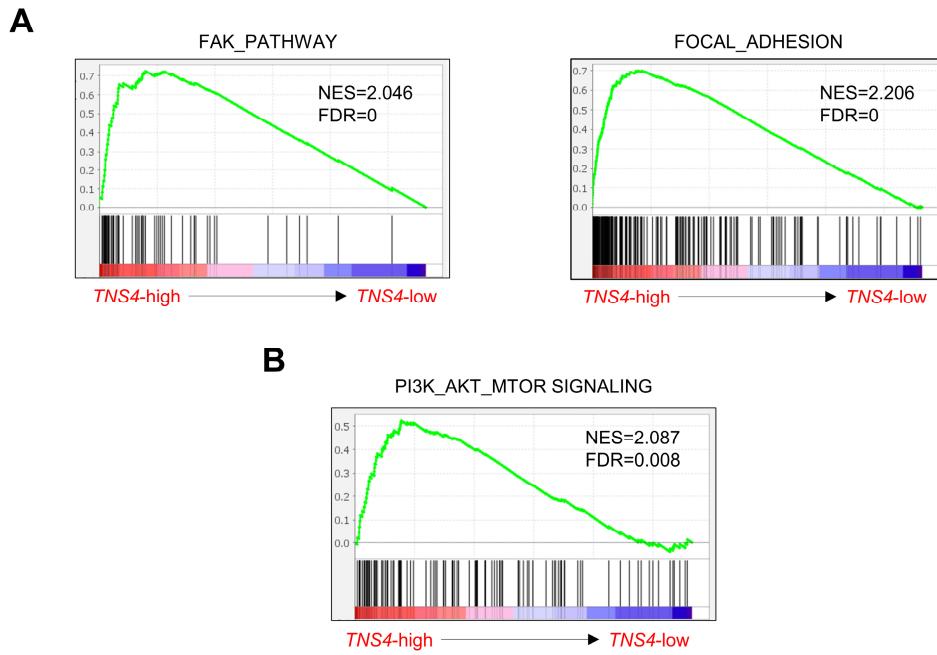
counterparts. (E) Assessment of the proportion of EdU-positive cells in TNS4-overexpressing group versus control group (scale bar=50  $\mu\text{m}$ ). (F-G) Comparative analysis of the colony and sphere formation capabilities in cells with TNS4 overexpression and control cells (scale bar=200  $\mu\text{m}$ ). (H) Examination of the invasion potential of HNSCC cells following TNS4 overexpression (scale bar=200  $\mu\text{m}$ ). (I) Western blot analysis to assess PCNA, E-cadherin, N-cadherin, and vimentin levels in cells with elevated TNS4 expression and control cells. (J-K) Comparison of tumor size, weight, and volume between the group overexpressing TNS4 and the control group. (L) Comparative Ki-67 staining intensity in xenograft tissues generated from cells with TNS4 overexpression and control cells (scale bar=100  $\mu\text{m}$ ).



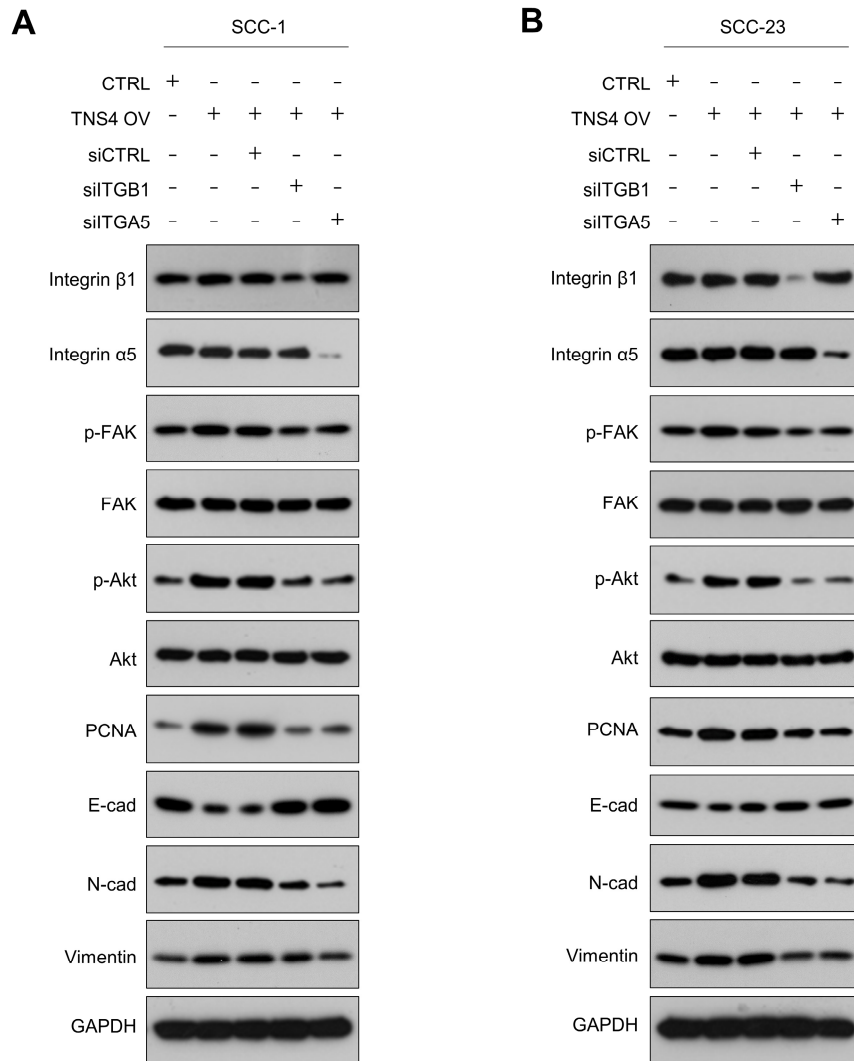
**Figure S2.** Significant enrichment of integrin-related pathways in the *TNS4*-high subgroup from the TCGA HNSCC cohort.



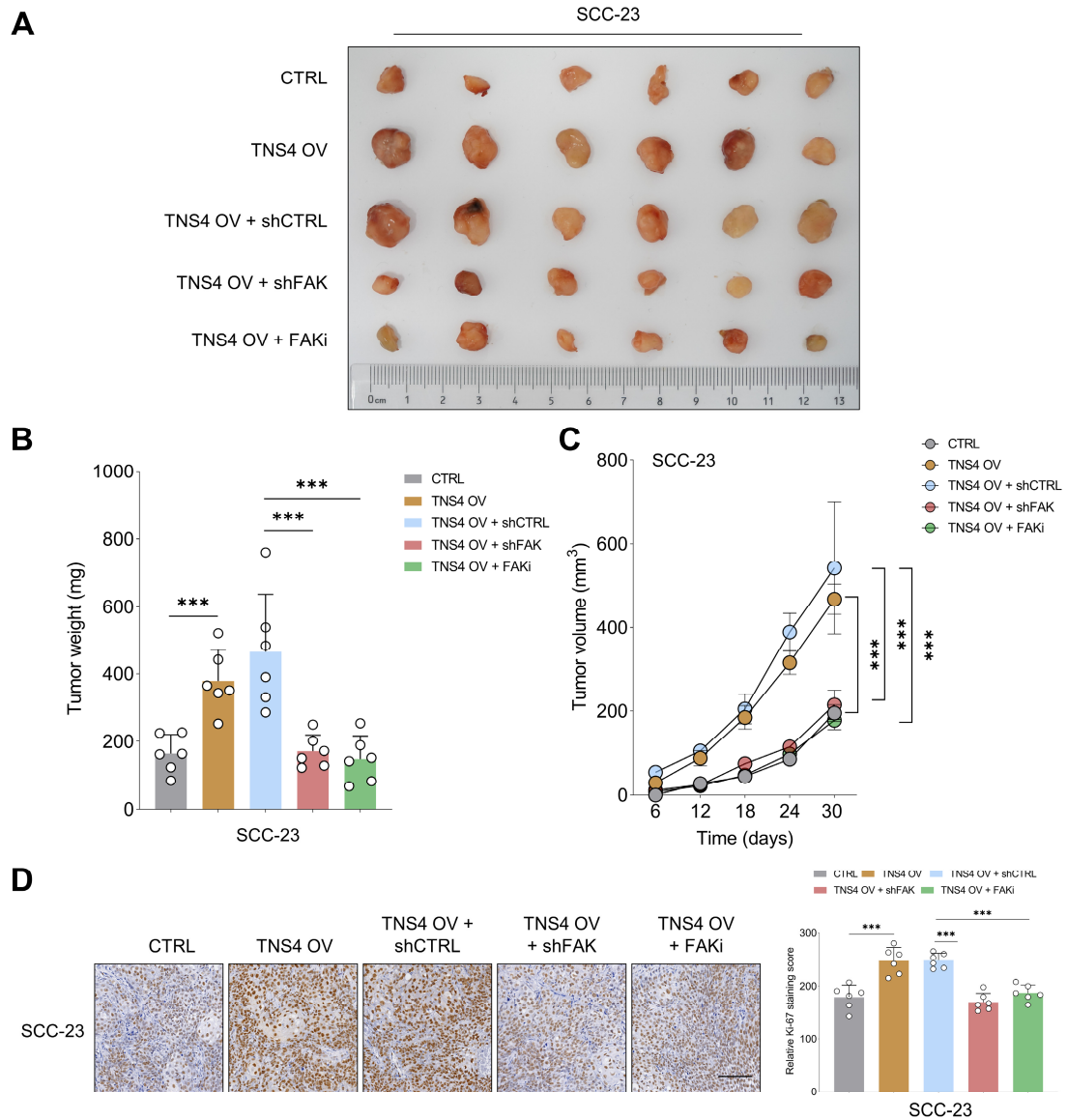
**Figure S3.** The PTB domain of TNS4 physically interacts with the cytoplasmic domain of integrin  $\beta$ 1 in HNSCC cells. (A) Schematic representation of TNS4 domains. (B) Interactions between TNS4 domains and integrin  $\beta$ 1 in HNSCC cells as revealed by Co-IP assays. (C) Schematic diagram depicting the domain structure of integrin  $\beta$ 1. (D) Interactions between integrin  $\beta$ 1 domains and TNS4 in HNSCC cells as revealed by Co-IP assays.



**Figure S4.** Significant enrichment of FAK pathway, focal adhesion pathway, and PI3K-AKT-mTOR pathway in the *TNS4*-high subgroup from the TCGA HNSCC cohort.

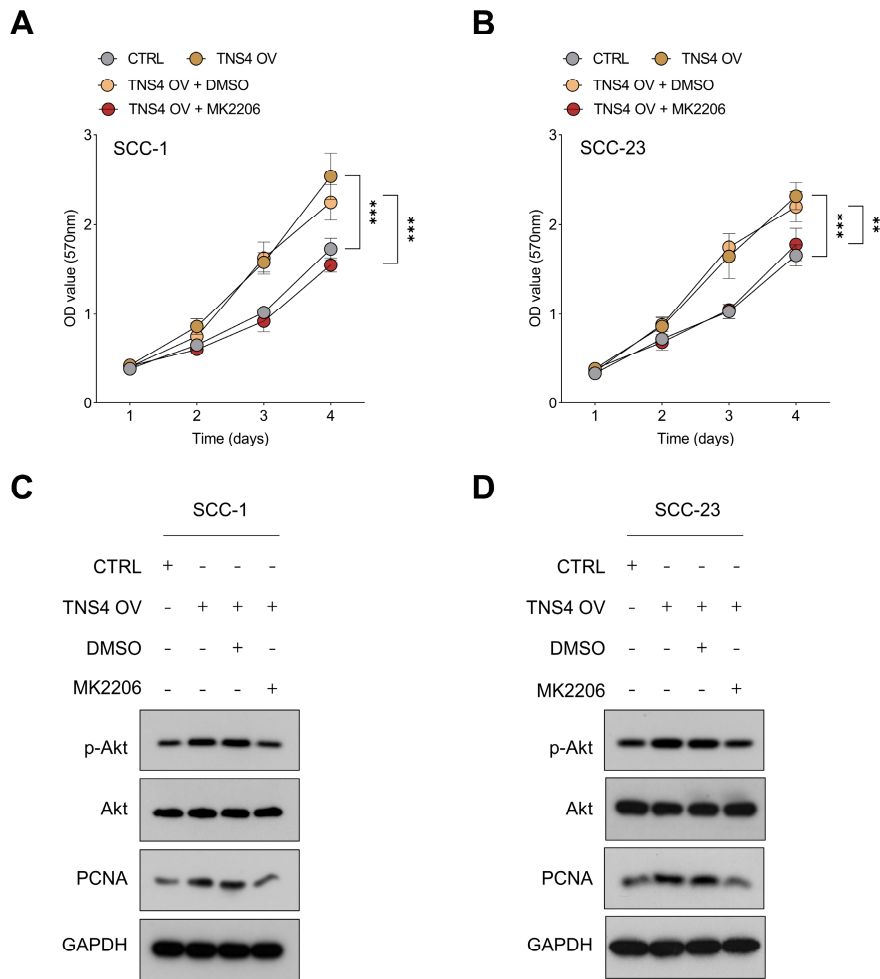


**Figure S5.** The effects of integrin  $\alpha 5$  or integrin  $\beta 1$  depletion on indicated protein expression in TNS4-overexpressing cells. (A-B) Evaluation of protein levels for integrin  $\beta 1$ , integrin  $\alpha 5$ , p-FAK, FAK, p-Akt, Akt, PCNA, E-cadherin, N-cadherin, and vimentin in SCC-1 and SCC-23 cells subjected to specified treatments.

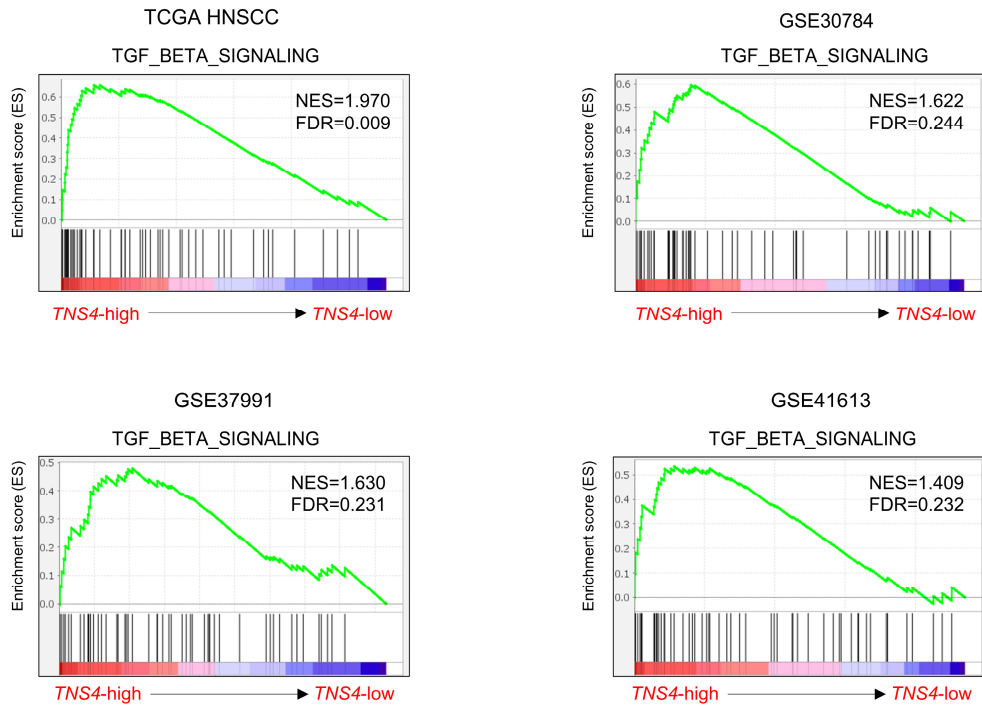


**Figure S6.** Reduction of tumorigenic potential in TNS4-overexpressing SCC-23 cells through FAK inhibition *in vivo*. (A-C) Comparative analysis of tumor size, weight, and volume among different treatment groups. (D) Evaluation of Ki-67 staining intensity in xenograft tumor tissues derived from SCC-23 cells subjected to specified treatments (scale bar=100  $\mu$ m).

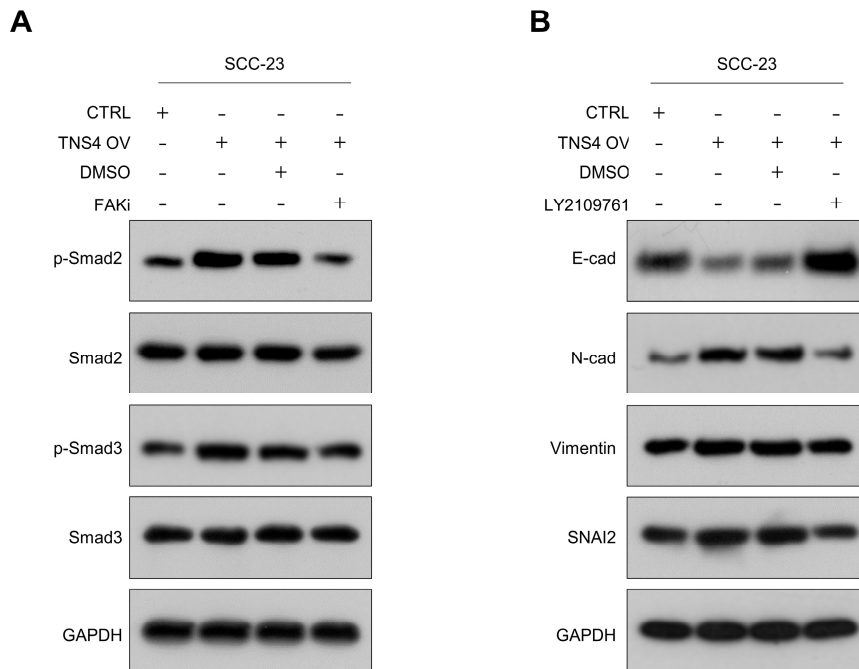




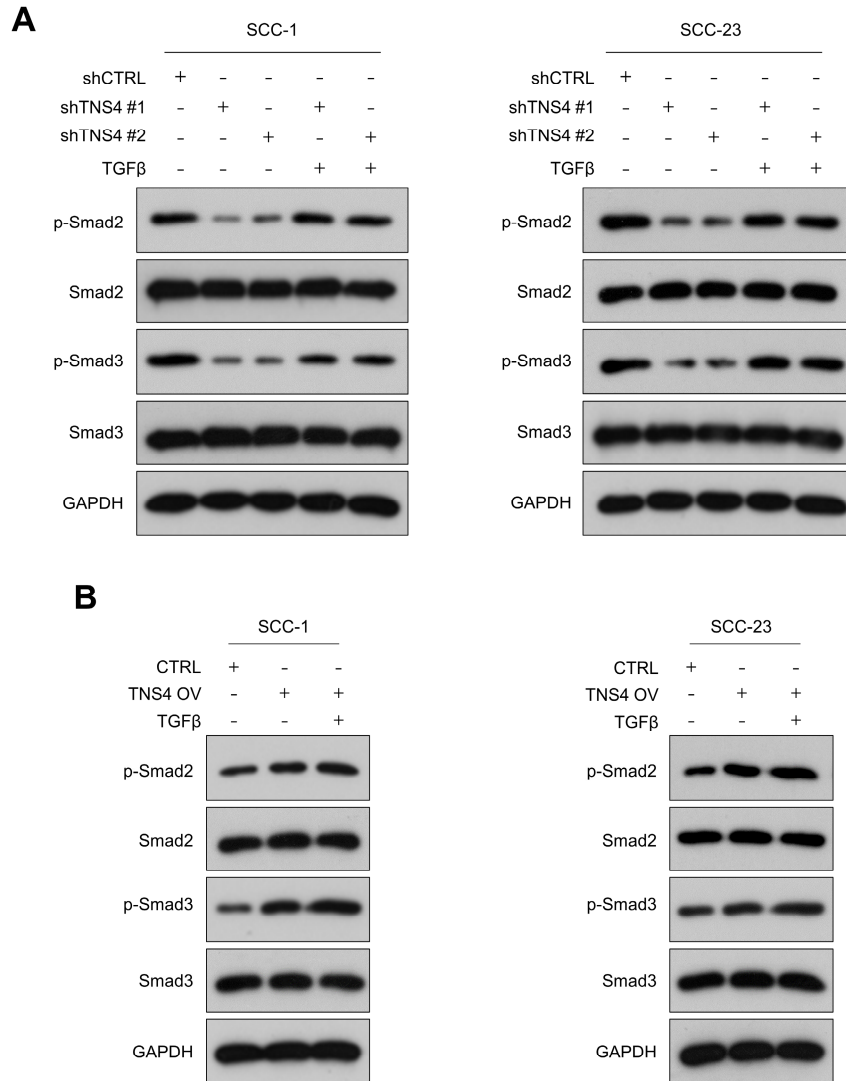
**Figure S7.** Akt inhibition effectively counteracts TNS4 overexpression-enhanced proliferation in HNSCC cells. (A-B) MTT assay demonstrating the proliferative capacity of HNSCC cells subjected to specified treatments. (C-D) Expression levels of p-Akt, Akt, and PCNA in SCC-1 and SCC-23 cells following respective modifications.



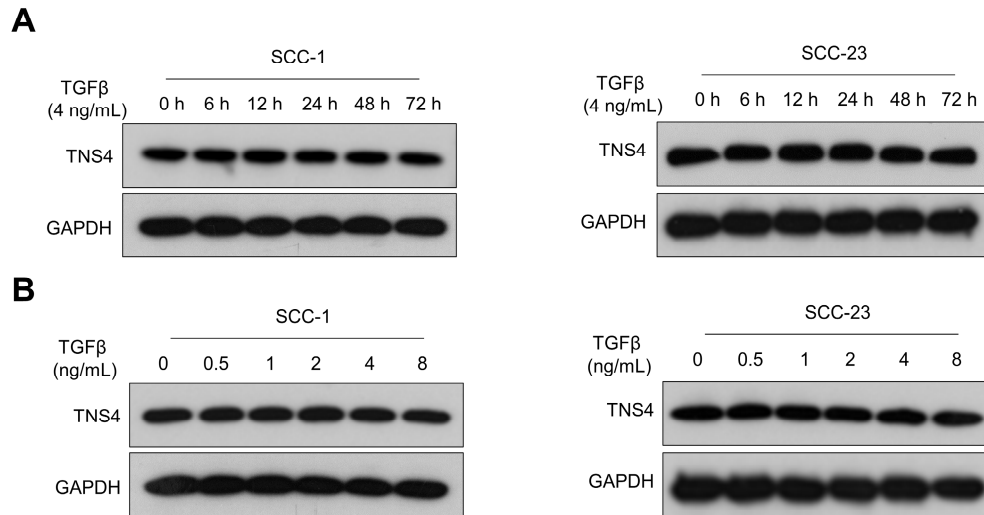
**Figure S8.** GSEA analysis revealing enrichment of the TGF $\beta$  signaling signature in high-*TNS4*-expressing HNSCC tumors across multiple independent cohorts, including TCGA HNSCC, GSE30784, GSE37991, and GSE41613.



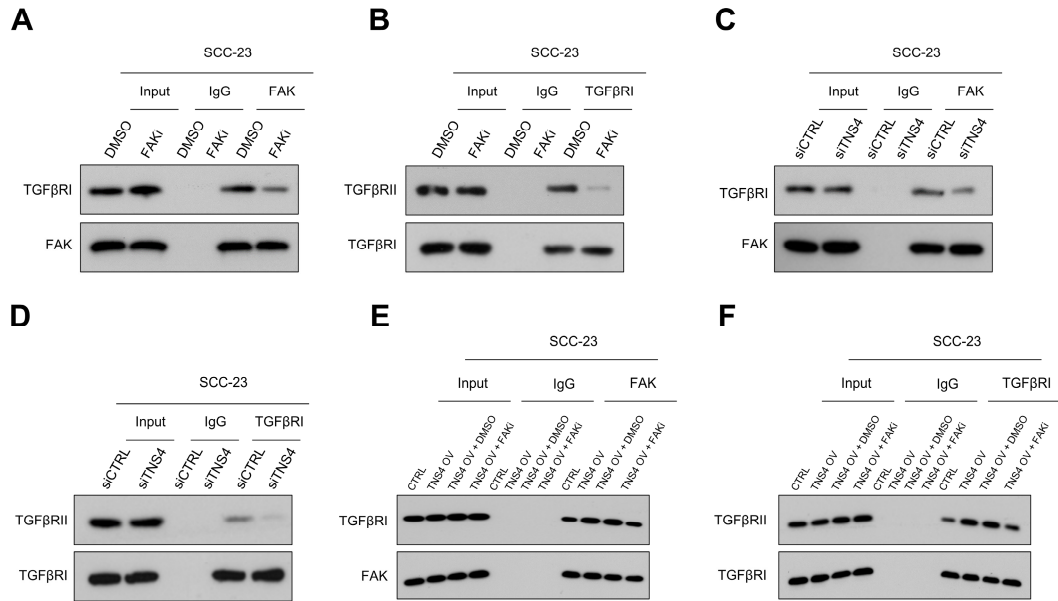
**Figure S9.** Alterations in TGF $\beta$  signaling and EMT marker expression in TNS4-overexpressing SCC-23 cells with indicated treatments. (A) Western blot analysis assessing the expression levels of p-Smad2, Smad3, p-Smad3, and Smad2 in SCC-23 cells subjected to the indicated modifications. (B) Assessment of E-cadherin, N-cadherin, vimentin, and SNAI2 expression levels in TNS4-overexpressing cells following treatment with LY2109761.



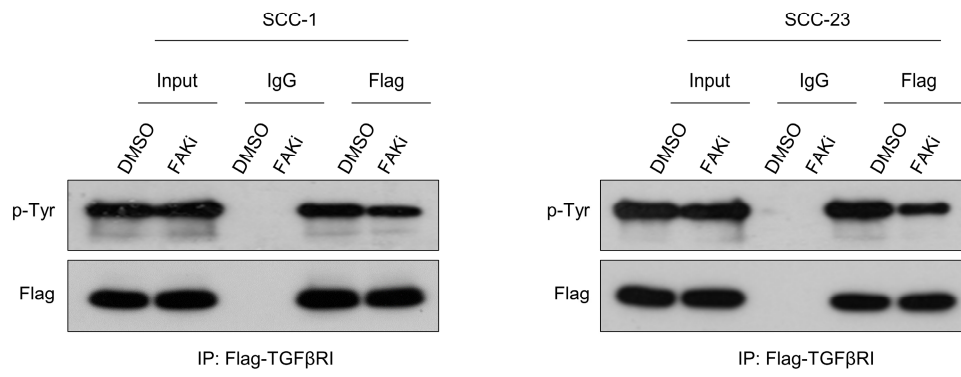
**Figure S10.** Impact of TNS4 depletion or overexpression on key components of TGFβ signaling in HNSCC cells, with or without TGFβ supplementation. (A-B) Assessment of p-Smad2, Smad2, p-Smad3, and Smad3 expression levels in SCC-1 and SCC-23 cells following the indicated treatments.



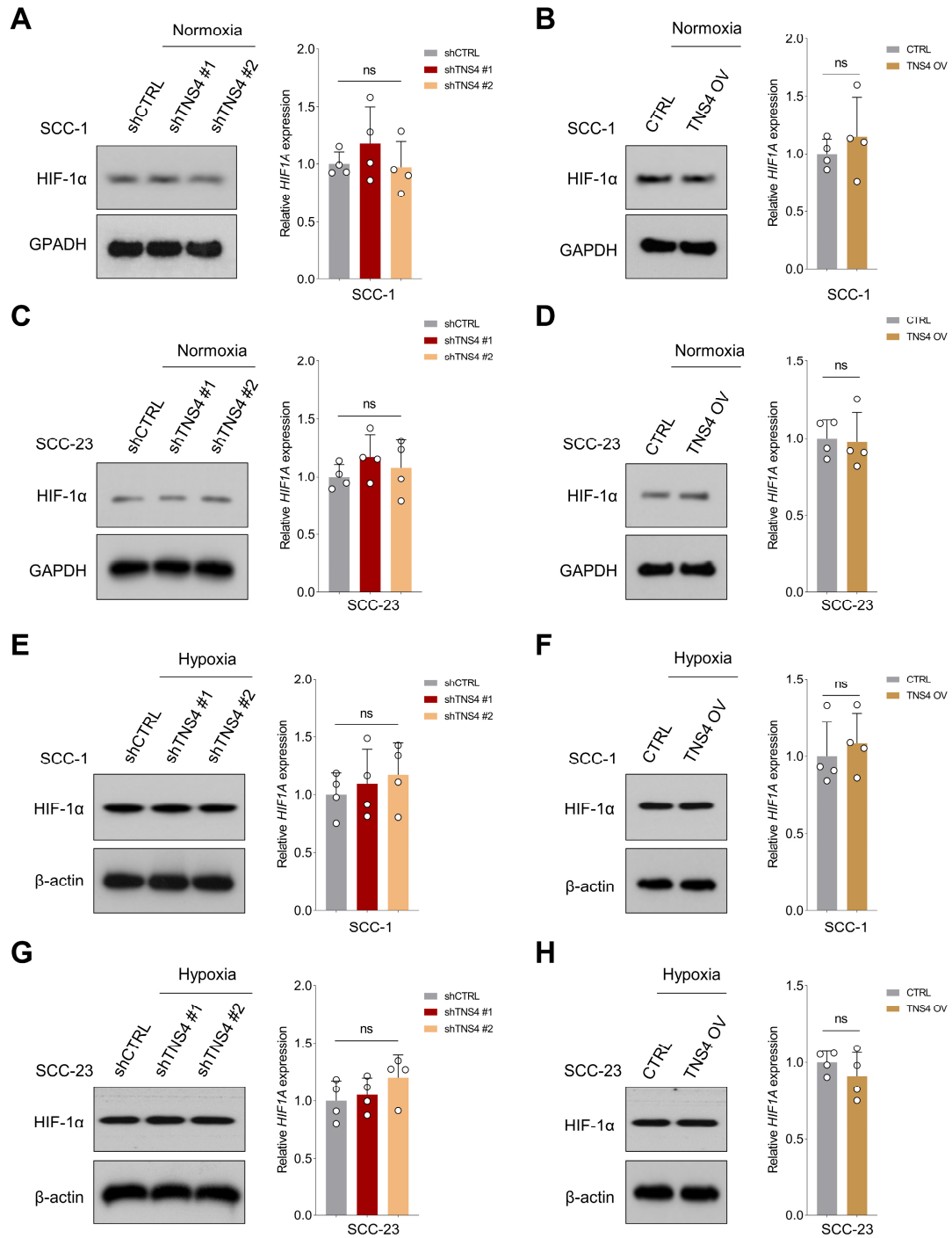
**Figure S11.** Impact of TGF $\beta$  supplementation on TNS4 expression level in HNSCC cells. (A) Temporal variation in TNS4 expression following different durations of TGF $\beta$  exposure. (B) Dose-dependent effects of TGF $\beta$  on TNS4 expression levels in HNSCC cells.



**Figure S12.** The TNS4-FAK axis enhances TGF $\beta$  signaling by facilitating the interaction between TGF $\beta$ RI and TGF $\beta$ RII in SCC-23 cells. (A-B) Analysis of the FAK inhibitor's impact on the interaction between FAK and TGF $\beta$ RI, and between TGF $\beta$ RI and TGF $\beta$ RII. (C-D) Effects of TNS4 depletion on the interaction between FAK and TGF $\beta$ RI, and between TGF $\beta$ RI and TGF $\beta$ RII. (E-F) Effects of TNS4 overexpression on the interaction between FAK and TGF $\beta$ RI, and between TGF $\beta$ RI and TGF $\beta$ RII.



**Figure S13.** Inhibition of FAK markedly reduced the levels of tyrosine phosphorylation on TGFβRI in both SCC-1 and SCC-23 cell lines.



**Figure S14.** Effects of TNS4 depletion or overexpression on HIF-1 $\alpha$  expression in normoxic and hypoxic conditions. (A-D) Comparative analysis of HIF-1 $\alpha$  expression in TNS4-depleted and TNS4-overexpressing cells relative to their respective control cells under normoxic conditions. (E-H) Comparative analysis of HIF-1 $\alpha$  expression in TNS4-depleted and TNS4-overexpressing cells relative to their respective control cells under hypoxic conditions.



**Table S1. The clinicopathological information of in-house HNSCC cohort.**

<b>Clinicopathological parameters</b>	<b>Number of patients (n, %)</b>
<b>Age</b>	
≥60	68 (56.20%)
<60	53 (43.80%)
<b>Gender</b>	
Male	85 (70.25%)
Female	36 (29.75%)
<b>Smoking</b>	
Yes	72 (59.50%)
No	49 (40.50%)
<b>Alcohol intake</b>	
Yes	45 (37.19%)
No	76 (62.81%)
<b>TNM stage</b>	
I-II	66 (54.55%)
III-IV	55 (45.45%)
<b>Lymph node metastasis</b>	
Negative	81 (66.94%)
Positive	40 (33.06%)

**Table S2. Sequences of primers and oligos used in this study.**

<b>Gene/Oligos</b>	<b>Sequence (5'-3')</b>
TNS4	F: AGGACACCAGAACTCCGTTCA R: TCTCGGGTGATGTTTGGCTTA
GAPDH	F: TGCACCACCAACTGCTTAGC R: GGCATGGACTGTGGTCATGAG
ACTB	F: CACCATTGGCAATGAGCGGTTC R: AGGTCTTTGCGGATGTCCACGT
siHIF-1 $\alpha$	CUGAUGACCAGCAACUUGATT
shTNS4 #1	GGACCTTGACTCCTACATTGA
shTNS4 #2	GAAGTGGCAGAAGTACTGCAA