Supplementary Figure 1

A, Correlation between LHX1 expression and DFI in HNSCC patients. **B,** Correlation between LHX1 expression and DSS in HNSCC patients. **C,** Correlation between LHX1 expression and tumor size in HNSCC patients. **D,** Correlation between LHX1 expression and lymph node metastasis in HNSCC. **E,** Correlation between LHX1 expression and distant metastasis in HNSCC patients. **F,** Correlation between LHX1 expression and clinical stage in HNSCC. **G,** Correlation of LHX1 expression with pathological grade in HNSCC. **H,** Correlation between LHX1 expression and age in HNSCC patients. **I,** Correlation between LHX1 expression and gender in HNSCC patients. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, not significant.

Supplementary Figure 2

A, GSEA was performed following *LHX1* knockout, revealing the downregulated pathways. **B,** Immunoblotting of LHX1 following the LHX1 overexpression. **C,** RT-qPCR analysis of *LHX1* following LHX1 overexpression. $n = 3$, unpaired *t* test. **D,** RT-qPCR analysis of *ALDH1A1, SOX2, POU5F1,* and *NANOG* following LHX1 overexpression. **E,** TIF of tumor cells assessed by the ELDA method following LHX1 overexpression. $n = 8$, $\chi 2$ test. Data are shown as mean ± SD. **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.

Supplementary Figure 3

A, The protein levels of IL-1α, IL-6, and IL-8 measured by ELISA in *LHX1*-knockout cells following treatment with SASP inhibitors. **B,** RT-qPCR analysis of *IL1A, IL6, IL8,*

and *CXCL10* following LHX1 overexpression. n = 3, unpaired t test. **C,** Immunoblotting of pRb, p21, and p16 following LHX1 overexpression. **D,** Colony formation assay in *LHX1*-knockout cells following treatment with SASP inhibitors. **E,** Quantification of the colony numbers in *LHX1*-knockout cells following treatment with SASP inhibitors. n = 3, one-way ANOVA. **F,** RT-qPCR analysis of *SOX2, POU5F1,* and *NANOG* in *LHX1*-knockout cells following treatment with SASP inhibitors. n = 3, one-way ANOVA. Data are shown as mean ± SD. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ns, not significant.

Supplementary Figure 4

A, Colony formation assay in recipient cells following treatment with CM from *LHX1*-knockout cells. **B,** Quantification of the colony numbers. n = 3, unpaired t test. **C,** Sphere formation assay in recipient cells following treatment with conditioned medium from *LHX1*-knockout cells. Scale bar, 100 μm. **D,** Quantification of the sphere numbers in recipient cells. n = 3, unpaired t test. **E,** RT-qPCR analysis of *ALDHA1, SOX2, POU5F1,* and *NANOG* in recipient cells following treatment with CM from *LHX1*-knockout cells. n = 3, unpaired t test. **F,** Immunoblotting of pRb, p21, and p16 in *LHX1*-knockout cells following treatment with neutralizing-antibodies. **G,** Colony formation assay in *LHX1*-knockout cells following treatment with neutralizing-antibodies. **H,** Sphere formation assay in *LHX1*-knockout cells following treatment with neutralizing-antibodies. Scale bar, 100 μm. **I,** Quantification of the colony numbers. n = 3, one-way ANOVA. **J,** Quantification of the sphere numbers. n = 3, one-way ANOVA. Data are shown as mean ± SD. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns,

not significant.

Supplementary Figure 5

A, The counts value of *cGAS* and *STING* following *LHX1* knockout. **B,** RT-qPCR analysis of *STING* in *LHX1* knockout FaDu cells. n = 3, one-way ANOVA. **C,** Immunoblotting analysis of STING, P-TBK1, TBK1, P-IRF3, and IRF3 in *LHX1* knockout FaDu cells. **D,** RT-qPCR analysis of *STING* following LHX1 overexpression. n = 3, unpaired t test. **E,** Immunoblotting analysis of STING following LHX1 overexpression. **F,** RT-qPCR analysis of *cGAS* following *LHX1* knockout. n = 3, one-way ANOVA. **G,** RT-qPCR analysis of *cGAS* following LHX1 overexpression. n = 3, unpaired t test. **H,** ELISA analysis of cGAMP in normal epithelial cells (HIOEC and HaCaT) and HNSCC cells (CAL27 and FaDu). **I,** ELISA analysis of cGAMP following *LHX1* knockout. **J,** ELISA analysis of cGAMP following LHX1 overexpression. **K,** Immunoblotting analysis of STING following re-expression of LHX1-WT, LHX1-ΔLIM, and LHX1-ΔHOX in *LHX1* knockout FaDu cells. **L,** RT-qPCR analysis of *STING* following re-expression of LHX1-WT, LHX1-ΔLIM, and LHX1-ΔHOX in *LHX1* knockout FaDu cells. n = 3, one-way ANOVA. **M,** ChIP-PCR analysis of LHX1 binding to different regions of the *STING* promoter in FaDu cells. **N,** ChIP-qPCR analysis of LHX1 binding to different regions of the *STING* promoter in FaDu cells. n = 3, unpaired t test. Data are shown as mean ± SD. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, not significant.

Supplementary Figure 6

A, Expression of *STING* in HNSCC and normal tissues from the TCGA database. n = 518 for tumors, n = 44 for normal tissues, unpaired t test. **B,** Promoter methylation level of *STING* in HNSCC and normal tissues from the TCGA database. n = 50 for normal tissues, n = 528 for tumors, unpaired t test. **C,** ChIP-qPCR analysis of H3K9me3 and H3K27me3 at the *STING* promoter following *LHX1*-knockout. n = 3, unpaired t test. **D,** Immunoblotting of pRb, p21, and p16 in *LHX1*-knockout cells following treatment with cGAMP. **E,** Colony formation assay in *LHX1*-knockout cells following treatment with cGAMP. F, Quantification of the colony numbers. n = 3, one-way ANOVA. Data are shown as mean ± SD. ***, $P < 0.001$; ns, not significant.

Supplementary Figure 7

A, The amino acid sequences of the LIM1 and LIM2 domains, as well as the sequences of the designed TAT, TAT-AE, and TAT-VM peptides. **B,** RT-qPCR analysis of *STING* in FaDu cells following treatment with different concentrations of TAT. **C,** RT-qPCR analysis of *STING* expression in FaDu cells when treated with different concentrations of TAT-AE and TAT-VM peptides. **D,** Co-IP results of HA-LDB1 and FLAG-LHX1 in 293T cells when treated with TAT-AE and TAT-VM peptides. **E,** RT-qPCR analysis of *STING* in HNSCC cells when treated with TAT-AE or TAT-VM peptides. n = 3, unpaired t test. **F,** Immunoblotting analysis of STING in HNSCC cells treated with TAT-AE and TAT-VM peptides. **G,** Colony formation assay following treatment with TAT-AE-DRI and TAT-VM-DRI peptides. **H,** Quantification of the colony numbers. n = 3,

one-way ANOVA. **I,** Effect of TAT-AE-DRI and TAT-VM-DRI peptides on the growth of CAL27-derived subcutaneous xenografts. n = 8, unpaired t test. **J,** Impact of TAT-AE-DRI and TAT-VM-DRI peptides on the survival of mice in the MOC2 orthotopic tongue tumor model. n = 8, Kaplan-Meier curve. Data are shown as mean ± SD. *** $P < 0.001$; **** $P < 0.0001$.

Supplementary Figure 8

A, Immunoblotting analysis of STING following LDB1 overexpression. **B,** RT-qPCR analysis of *STING* following LDB1 overexpression. n = 3, unpaired t test. **C,** Immunoblotting analysis of STING following *LDB1*-knockout. **D,** RT-qPCR analysis of *STING* following *LDB1*-knockout. n = 3, one-way ANOVA. **E,** Co-IP results of FLAG-LHX1 and HA-LDB1 in 293T cells, with FLAG-LHX1 serving as the bait protein. **F,** Co-IP results of HA-LDB1 and FLAG-LHX1 in 293T cells, with HA-LDB1 serving as the bait protein. **G,** Sequence diagram of the LDB1-WT and LDB1-ΔLID mutant. **H,** RT-qPCR analysis of *STING* following re-expression of LDB1-WT and LDB1-ΔLID mutant in *LDB1*-knockout FaDu cells. n = 3, one-way ANOVA. **I,** Immunoblotting analysis of STING following re-expression of LDB1-WT and LDB1-ΔLID mutant in *LDB1*-knockout FaDu cells. **J,** ChIP-PCR analysis of the binding of LHX1-WT and LHX1-3m mutant to the site1 region of *STING* promoter in FaDu cells. **K,** ChIP-qPCR analysis of the binding of LHX1-WT and LHX1-3m mutant to the site1 region of *STING* promoter in FaDu cells. n = 3, one-way ANOVA. **L,** RT-qPCR analysis of *STING* following re-expression of LHX1-WT or LHX1-3m mutant in *LHX1*

knockout FaDu cells. $n = 3$, one-way ANOVA. **M,** Immunoblotting analysis of STING following re-expression of LHX1-WT or LHX1-3m mutant in *LHX1* knockout FaDu cells. Data are shown as mean ± SD. **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, not significant.

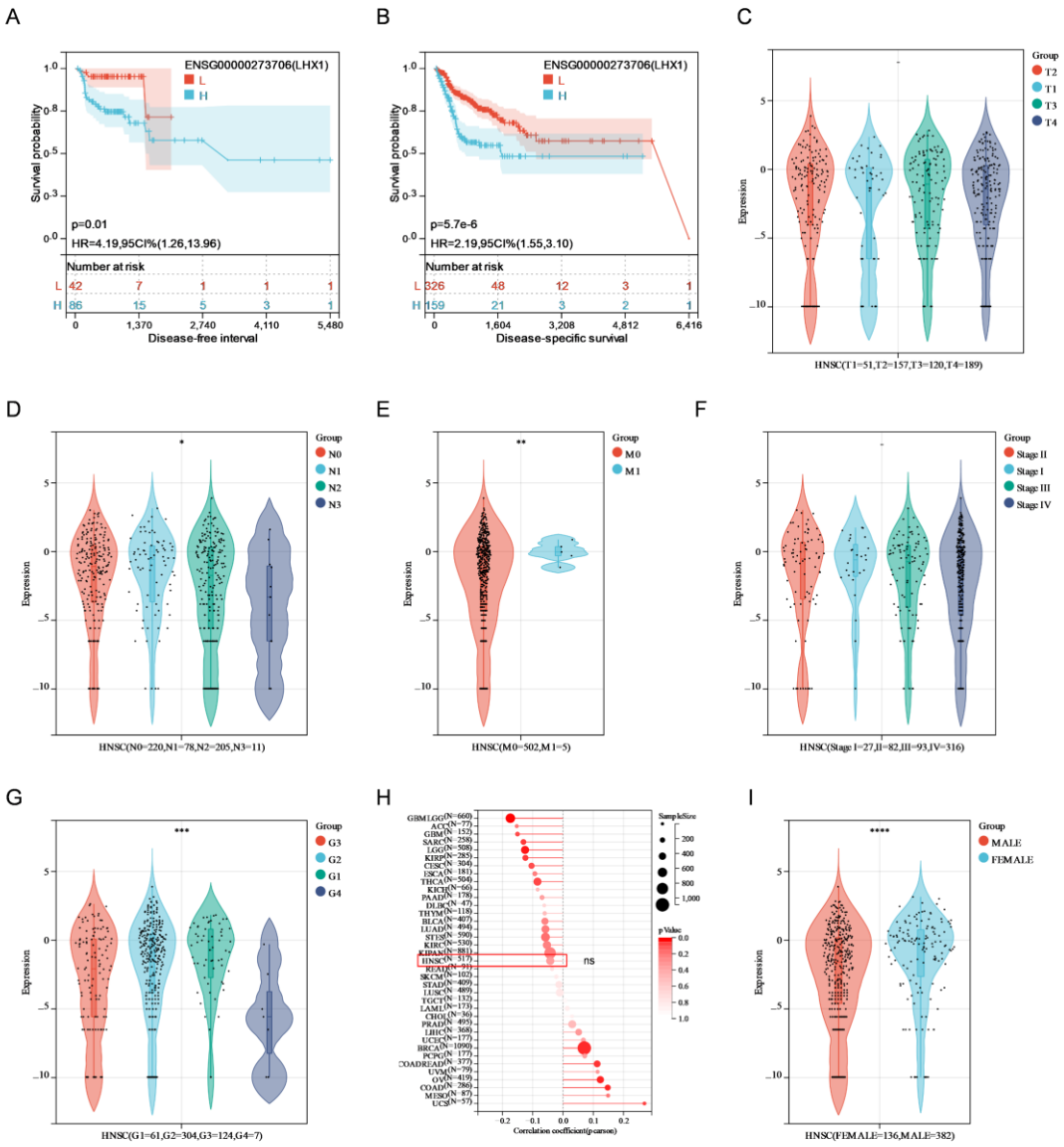
Supplementary Figure 9

A, The amino acid sequences of the LIM1 and LIM2 domains, as well as the sequences of the designed TAT, TAT-AE, and TAT-VM peptides. **B,** Fluorescence microscopy images of FaDu with peptides conjugated to GFP protein. Scale bar, 50 μm. **C,** RT-qPCR analysis of *STING* in FaDu cells following treatment with different concentrations of TAT. **D,** RT-qPCR analysis of *STING* expression in FaDu cells when treated with different concentrations of TAT-AE and TAT-VM peptides. **E,** Co-IP results of HA-LDB1 and FLAG-LHX1 in 293T cells when treated with TAT-AE and TAT-VM peptides. **F,** RT-qPCR analysis of *STING* in HNSCC cells when treated with TAT-AE or TAT-VM peptides. $n = 3$, unpaired *t* test. **G,** Immunoblotting analysis of STING in HNSCC cells treated with TAT-AE and TAT-VM peptides. **H,** Co-IP results of LDB1 and LHX1, LMO1, LMO2 in FaDu cells when treated with TAT-AE-DRI and TAT-VM-DRI peptides. **I,** Colony formation assay following treatment with TAT-AE-DRI and TAT-VM-DRI peptides. **J,** Quantification of the colony numbers. $n = 3$, one-way ANOVA. $n = 8$, Kaplan-Meier curve. Data are shown as mean ± SD. *** $P < 0.001$; **** $P < 0.0001$.

Supplementary Figure 10

A, Effect of TAT-AE-DRI and TAT-VM-DRI peptides on the growth of CAL27-derived subcutaneous xenografts. n = 8, unpaired t test. **B,** Impact of TAT-AE-DRI and TAT-VM-DRI peptides on the survival of mice in the MOC2 orthotopic tongue tumor model. n = 8, Kaplan-Meier curve. **C,** IHC staining of Ki67, Cleaved Caspase-3, STING, p-TBK1, and p-IRF3 in tumor tissues from mice in the MOC1 orthotopic tongue tumor model. Scale bar, 50 μm. **D,** Statistical analysis of relative repression of Ki67, Cleaved Caspase-3, STING, p-TBK1, and p-IRF3. n = 8, unpaired t test. Data are shown as mean ± SD. **** $P < 0.0001$; ns, not significant.

Figure S1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L
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HR=4.19,95CI%(1.26,13.96)
Number at risk
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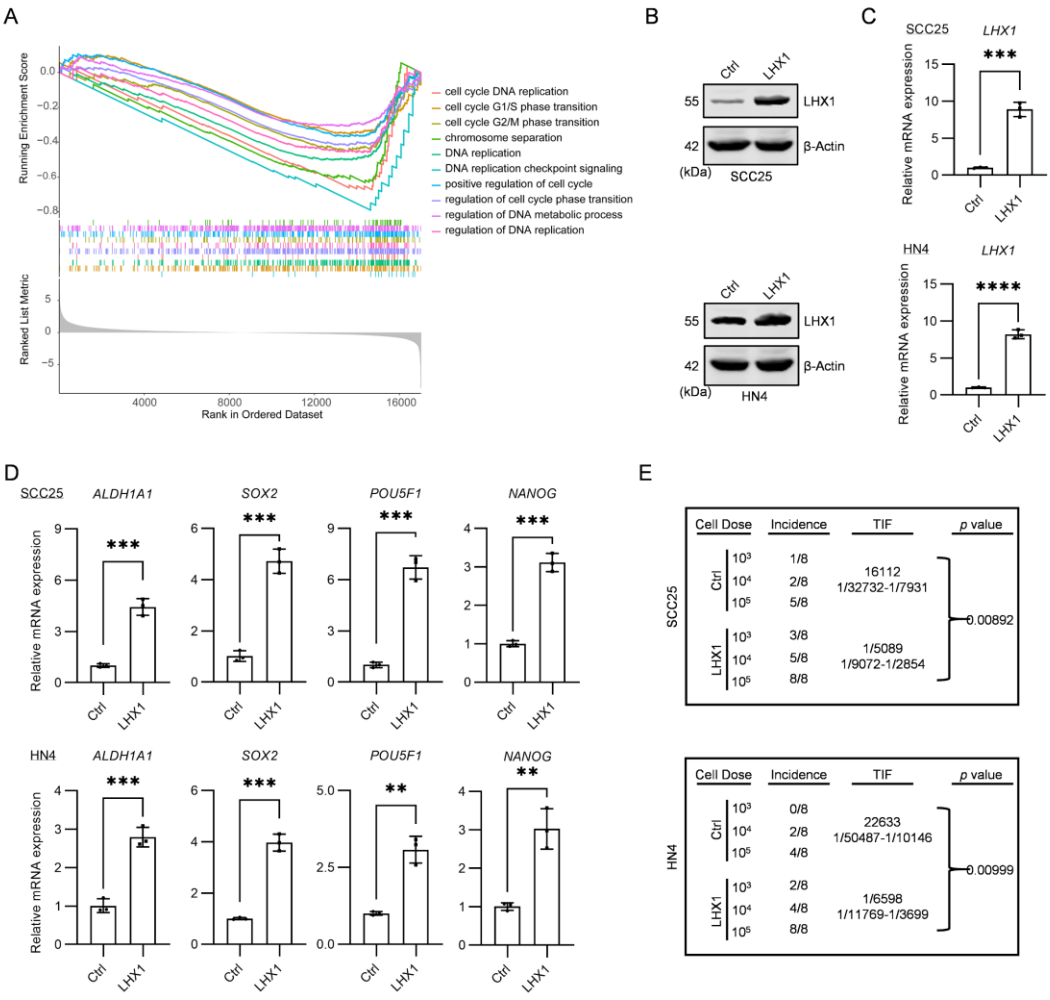
H 86 15 5 3 1
0 1,370 2,740 4,110 5,480
Disease-free interval
B
ENSG00000273706(LHX1)
L
H
Survival probability
p=5.7e-6
HR=2.19,95CI%(1.55,3.10)
Number at risk
L 326 48 12 3 1
H 159 21 3 2 1
0 1,604 3,208 4,812 6,416
Disease-specific survival
C
Group
T2
T1
T3
T4
Expression
HNSC(T1=51,T2=157,T3=120,T4=189)
D
Group
N0
N1
N2
N3
Expression
HNSC(N0=220,N1=78,N2=205,N3=11)
E
Group
M0
M1
Expression
HNSC(M0=502,M1=5)
F
Group
Stage II
Stage I
Stage III
Stage IV
Expression
HNSC(Stage I=27,II=82,III=93,IV=316)
G
Group
G3
G2
G1
G4
Expression
HNSC(G1=61,G2=304,G3=124,G4=7)
H
SampleSize
pValue
ns
Correlation coefficient(pearson)
I
Group
MALE
FEMALE
Expression
HNSC(FEMALE=136,MALE=382)

Figure S2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Running Enrichment Score
Ranked List Metric
Rank in Ordered Dataset
cell cycle DNA replication
cell cycle G1/S phase transition
cell cycle G2/M phase transition
chromosome separation
DNA replication
DNA replication checkpoint signaling
positive regulation of cell cycle
regulation of cell cycle phase transition
regulation of DNA metabolic process
regulation of DNA replication
B
Ctrl
LHX1
55
42
(kDa)
LHX1
β-Actin
SCC25
HN4
C
SCC25
LHX1
HN4
Relative mRNA expression
***
****
D
SCC25
HN4
ALDH1A1
SOX2
POU5F1
NANOG
Relative mRNA expression
***
**
E
Cell Dose
Incidence
TIF
p value
SCC25
HN4
Ctrl
LHX1
10³
10⁴
10⁵
1/8
2/8
5/8
3/8
5/8
8/8
0/8
2/8
4/8
2/8
4/8
8/8
16112
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1/5089
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0.00999

Figure S3

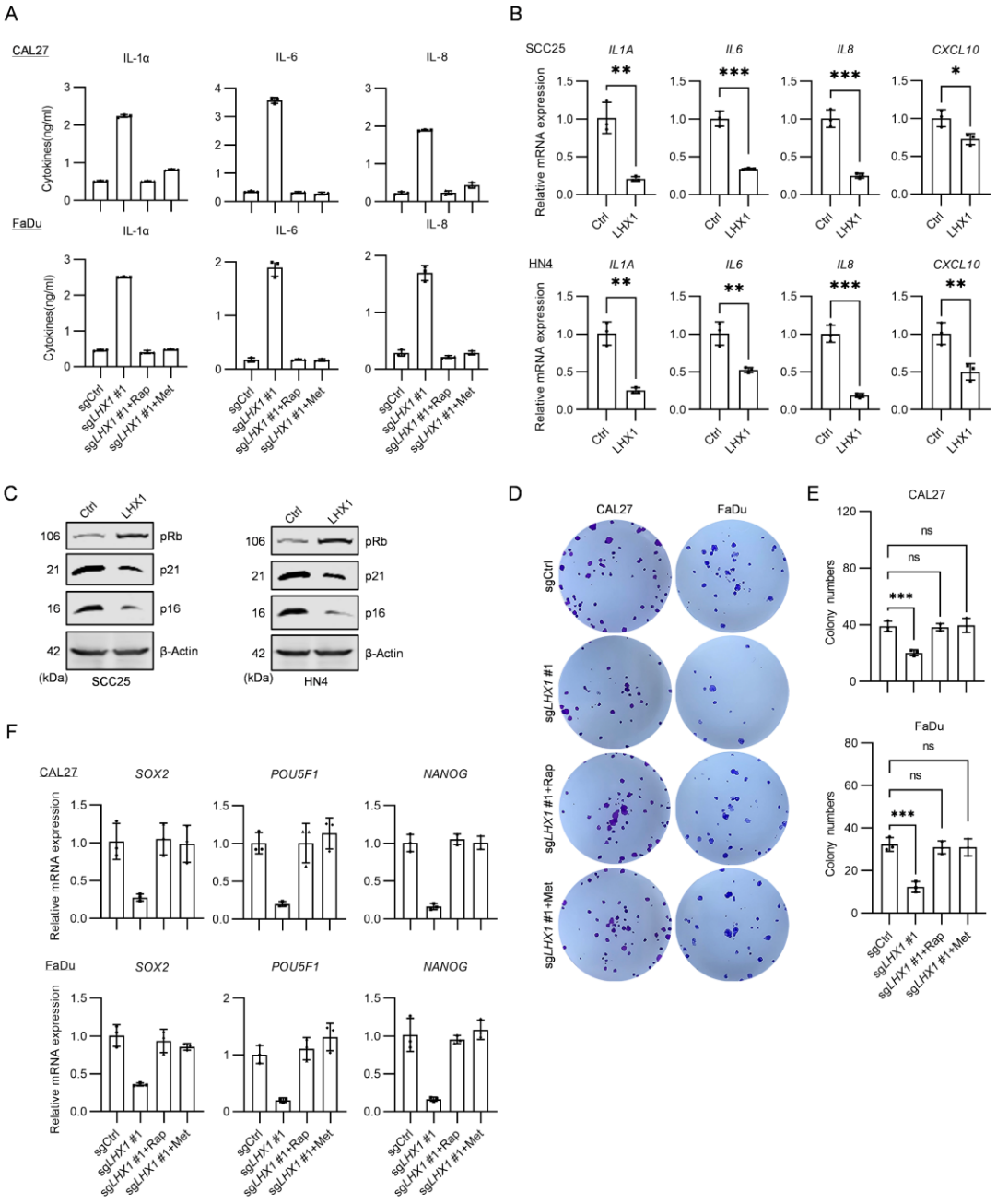

A
CAL27
IL-1α
IL-6
IL-8
Cytokines(ng/ml)
FaDu
sgCtrl
sgLHX1 #1
sgLHX1 #1+Rap
sgLHX1 #1+Met
B
SCC25
IL1A
IL6
IL8
CXCL10
Relative mRNA expression
Ctrl
LHX1
HN4
C
Ctrl
LHX1
106
pRb
21
p21
16
p16
42
β-Actin
(kDa)
SCC25
HN4
D
CAL27
FaDu
sgCtrl
sgLHX1 #1
sgLHX1 #1+Rap
sgLHX1 #1+Met
E
Colony numbers
ns
F
SOX2
POU5F1
NANOG

Figure S4

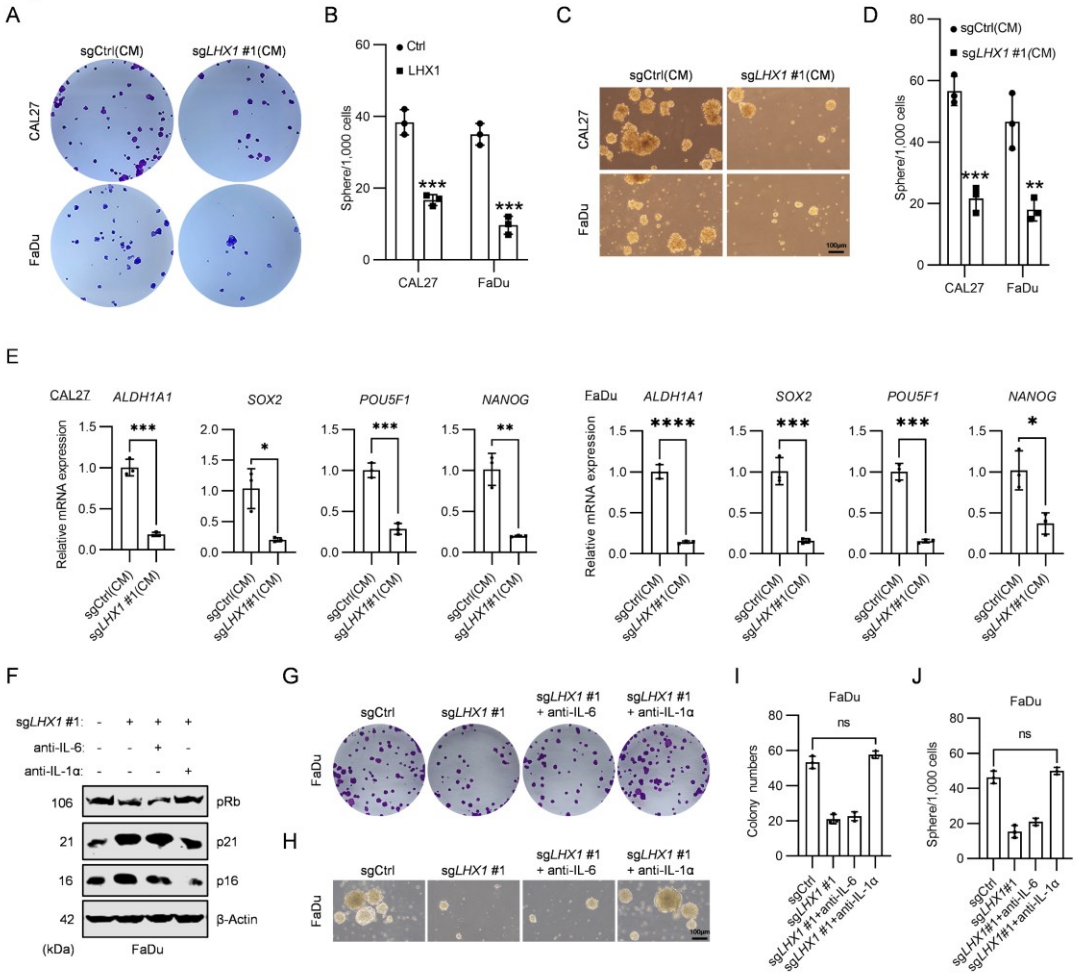

A
sgCtrl(CM)
sgLHX1 #1(CM)
CAL27
FaDu
B
Ctrl
LHX1
Sphere/1,000 cells
CAL27
FaDu
C
sgCtrl(CM)
sgLHX1 #1(CM)
CAL27
FaDu
D
sgCtrl(CM)
sgLHX1 #1(CM)
Sphere/1,000 cells
CAL27
FaDu
E
CAL27
ALDH1A1
SOX2
POU5F1
NANOG
FaDu
Relative mRNA expression
sgCtrl(CM)
sgLHX1#1(CM)
F
sgLHX1 #1:
anti-IL-6:
anti-IL-1α:
106
pRb
21
p21
16
p16
42
β-Actin
(kDa)
FaDu
G
sgCtrl
sgLHX1 #1
sgLHX1 #1 + anti-IL-6
sgLHX1 #1 + anti-IL-1α
FaDu
H
sgCtrl
sgLHX1 #1
sgLHX1 #1 + anti-IL-6
sgLHX1 #1 + anti-IL-1α
FaDu
I
FaDu
ns
Colony numbers
sgCtrl
sgLHX1 #1
sgLHX1 #1+anti-IL-6
sgLHX1 #1+anti-IL-1α
J
FaDu
ns
Sphere/1,000 cells
sgCtrl
sgLHX1#1
sgLHX1#1+anti-IL-6
sgLHX1#1+anti-IL-1α

Figure S5

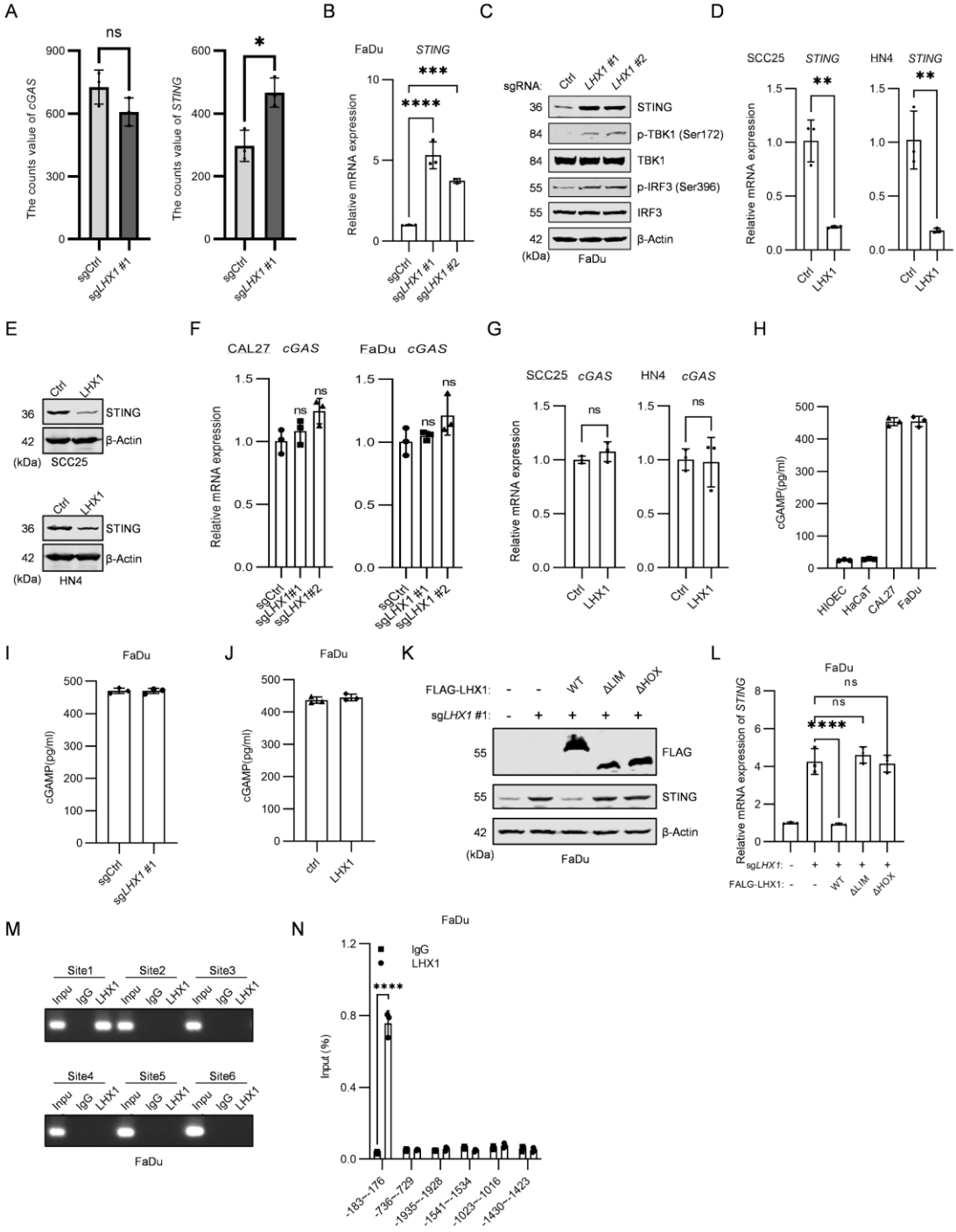

A
ns
*
The counts value of cGAS
The counts value of STING
sgCtrl
sgLHX1 #1
B
FaDu
STING
***
****
Relative mRNA expression
sgCtrl
sgLHX1 #1
sgLHX1 #2
C
sgRNA:
Ctrl
LHX1 #1
LHX1 #2
STING
p-TBK1 (Ser172)
TBK1
p-IRF3 (Ser396)
IRF3
β-Actin
(kDa)
FaDu
D
SCC25
STING
HN4
STING
**
Relative mRNA expression
Ctrl
LHX1
E
Ctrl
LHX1
STING
β-Actin
(kDa)
SCC25
HN4
F
CAL27 cGAS
FaDu cGAS
ns
Relative mRNA expression
sgCtrl
sgLHX1#1
sgLHX1#2
G
SCC25 cGAS
HN4 cGAS
ns
Relative mRNA expression
H
cGAMP(pg/ml)
HIOEC
HaCaT
CAL27
FaDu
I
FaDu
cGAMP(pg/ml)
sgCtrl
sgLHX1 #1
J
FaDu
cGAMP(pg/ml)
ctrl
LHX1
K
FLAG-LHX1:
WT
ΔLIM
ΔHOX
sgLHX1 #1:
FLAG
STING
β-Actin
(kDa)
FaDu
L
FaDu
ns
****
Relative mRNA expression of STING
sgLHX1:
FALG-LHX1:
WT
ΔLIM
ΔHOX
M
Site1
Site2
Site3
Site4
Site5
Site6
Inpu
IgG
LHX1
FaDu
N
FaDu
IgG
LHX1
****
Input (%)
-183~-176
-736~-729
-1935~-1928
-1541~-1534
-1023~-1016
-1430~-1423

Figure S6

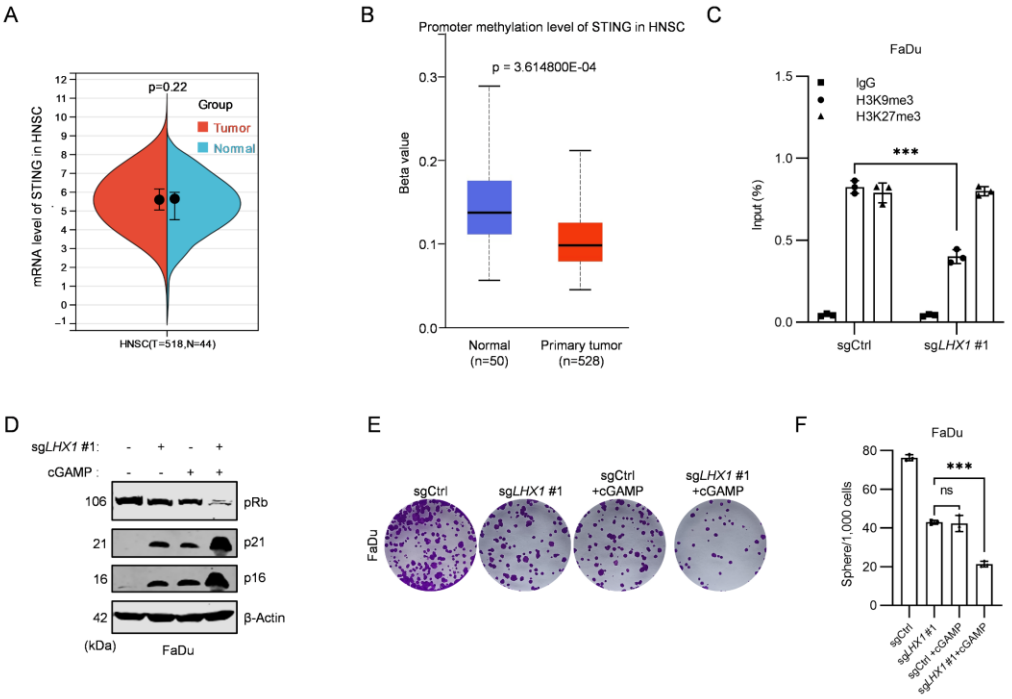

A
p=0.22
Group
Tumor
Normal
mRNA level of STING in HNSC
HNSC(T=518,N=44)
B
Promoter methylation level of STING in HNSC
p = 3.614800E-04
Beta value
Normal (n=50)
Primary tumor (n=528)
C
FaDu
IgG
H3K9me3
H3K27me3
***
Input (%)
sgCtrl
sgLHX1 #1
D
sgLHX1 #1:
cGAMP :
106
pRb
21
p21
16
p16
42
β-Actin
(kDa)
FaDu
E
sgCtrl
sgLHX1 #1
sgCtrl +cGAMP
sgLHX1 #1 +cGAMP
FaDu
F
FaDu
***
ns
Sphere/1,000 cells
sgCtrl
sgLHX1 #1
sgCtrl +cGAMP
sgLHX1 #1+cGAMP

Figure S7

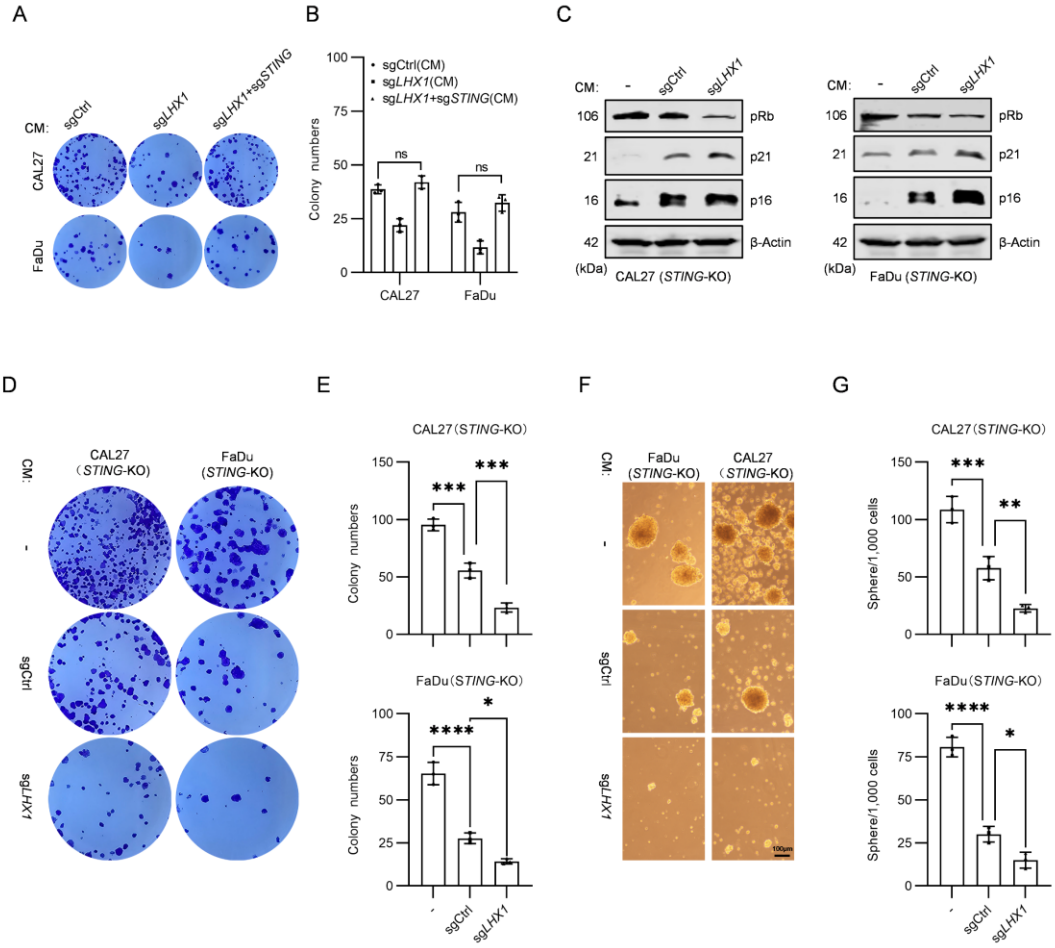

A
CM:
sgCtrl
sgLHX1
sgLHX1+sgSTING
CAL27
FaDu
B
sgCtrl(CM)
sgLHX1(CM)
sgLHX1+sgSTING(CM)
Colony numbers
ns
ns
CAL27
FaDu
C
CM:
-
sgCtrl
sgLHX1
106
21
16
42
pRb
p21
p16
β-Actin
(kDa)
CAL27 (STING-KO)
FaDu (STING-KO)
D
CM:
CAL27 (STING-KO)
FaDu (STING-KO)
-
sgCtrl
sgLHX1
E
CAL27(STING-KO)
Colony numbers
***
***
FaDu(STING-KO)
****
*
F
CM:
FaDu (STING-KO)
CAL27 (STING-KO)
-
sgCtrl
sgLHX1
100μm
G
CAL27(STING-KO)
Sphere/1,000 cells
***
**
FaDu(STING-KO)
****
*

Figure S8

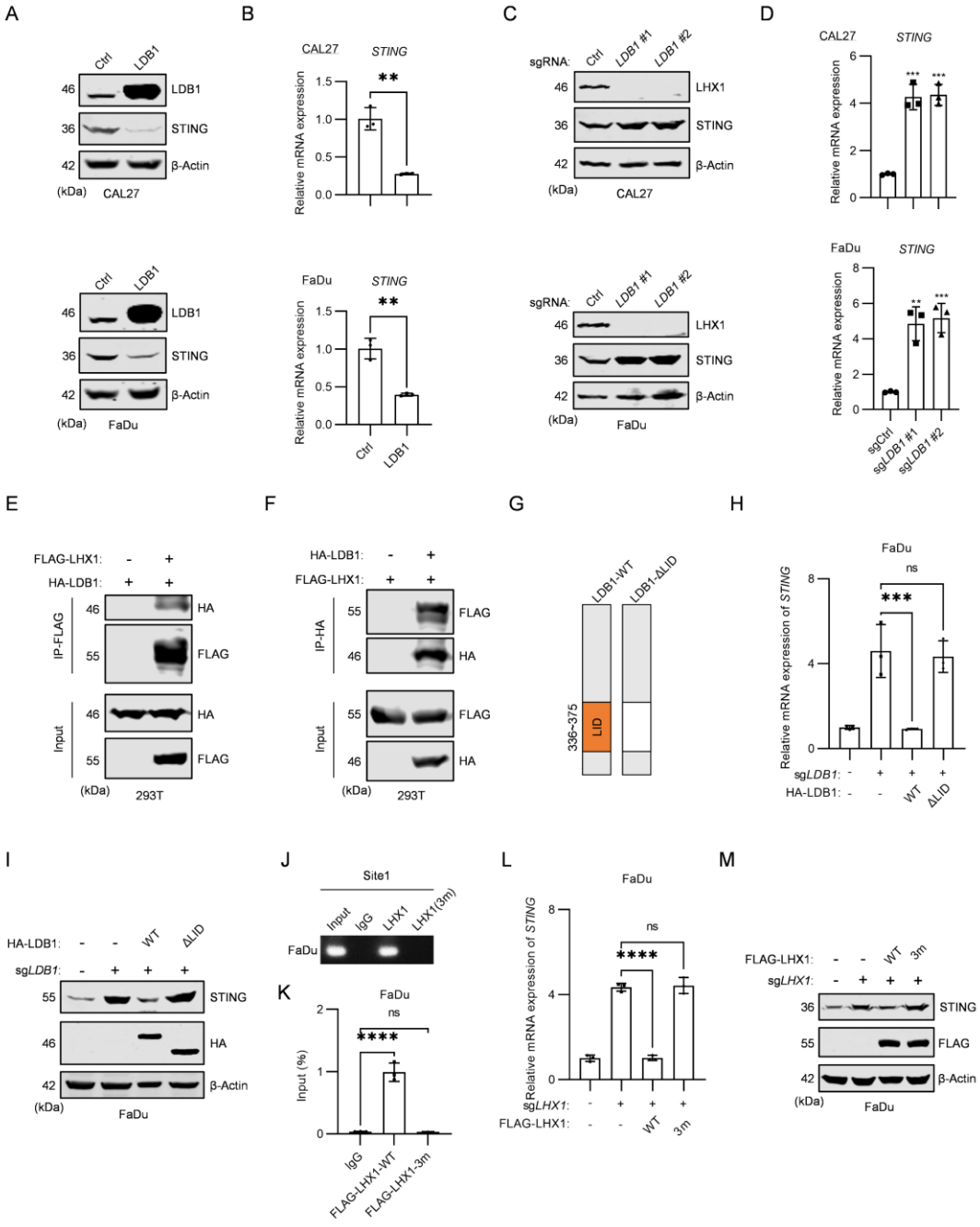
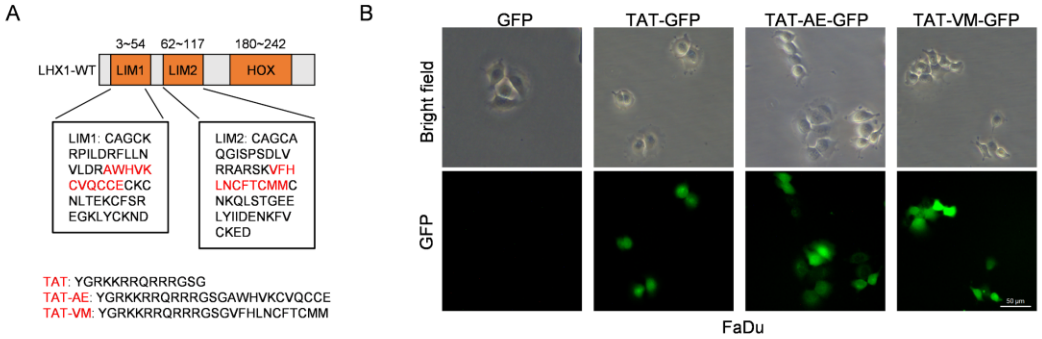
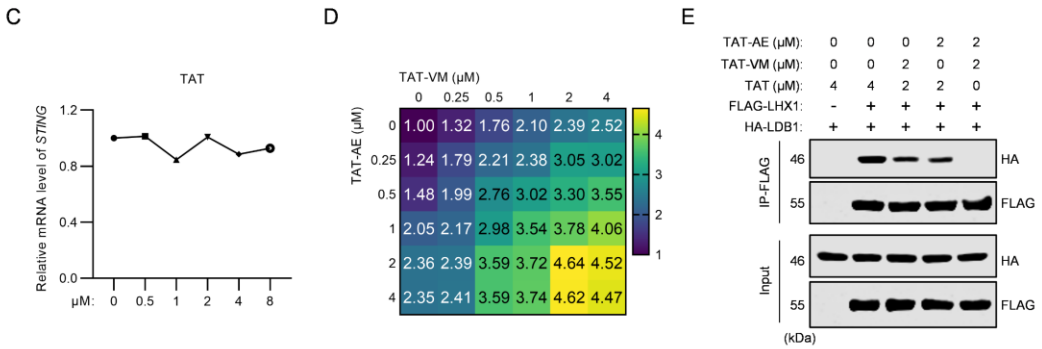
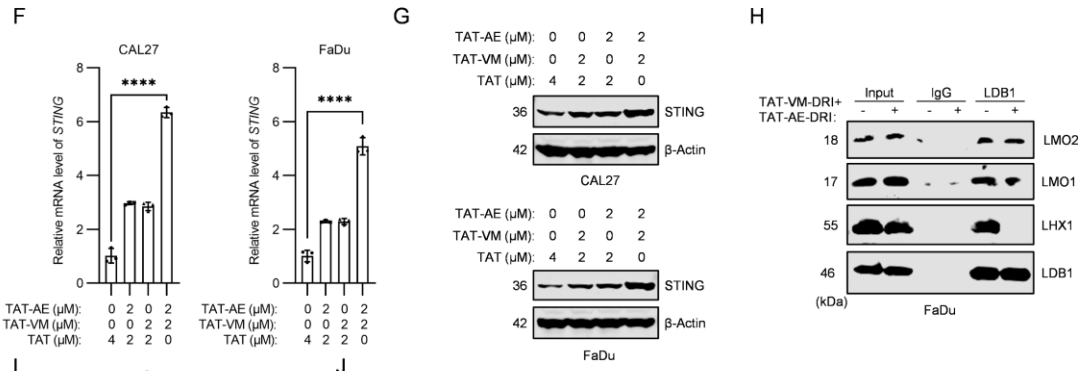

A
Ctrl
LDB1
46
LDB1
36
STING
42
β-Actin
(kDa)
CAL27
FaDu
B
CAL27
STING
Relative mRNA expression
**
Ctrl
LDB1
C
sgRNA:
Ctrl
LDB1 #1
LDB1 #2
LHX1
D
***
sgCtrl
sgLDB1 #1
sgLDB1 #2
E
FLAG-LHX1:
HA-LDB1:
IP-FLAG
Input
HA
FLAG
293T
F
IP-HA
G
LDB1-WT
LDB1-ΔLID
336-375
LID
H
ns
Relative mRNA expression of STING
sgLDB1:
WT
ΔLID
I
sgLDB1:
ΔLID
J
Site1
Input
IgG
LHX1
LHX1(3m)
K
Input (%)
FLAG-LHX1-WT
FLAG-LHX1-3m
L
****
sgLHX1:
M
3m
sgLHX1:

Figure S9


A
3~54
62~117
180~242
LHX1-WT
LIM1
LIM2
HOX
LIM1: CAGCK RPILDRFLLN VLDRAWHVK CVQCCECKC NLTEKCFSR EGKLYCKND
LIM2: CAGCA QGISPSDLV RRARSKVFH LNCFTCMMC NKQLSTGEE LYIIDENKFV CKED
TAT: YGRKKRRQRRRGSG
TAT-AE: YGRKKRRQRRRGSGAWHVKCVQCCE
TAT-VM: YGRKKRRQRRRGSGVFHLNCFTCMM
B
GFP
TAT-GFP
TAT-AE-GFP
TAT-VM-GFP
Bright field
GFP
FaDu


C
TAT
Relative mRNA level of STING
μM: 0 0.5 1 2 4 8
D
TAT-VM (μM)
TAT-AE (μM)
E
TAT-AE (μM): 0 0 0 2 2
TAT-VM (μM): 0 0 2 0 2
TAT (μM): 4 4 2 2 0
FLAG-LHX1: - + + + +
HA-LDB1: + + + + +
IP-FLAG
Input
HA
FLAG
(kDa)


F
CAL27
FaDu
Relative mRNA level of STING
****
G
STING
β-Actin
H
Input
IgG
LDB1
LMO2
LMO1
LHX1
LDB1
(kDa)

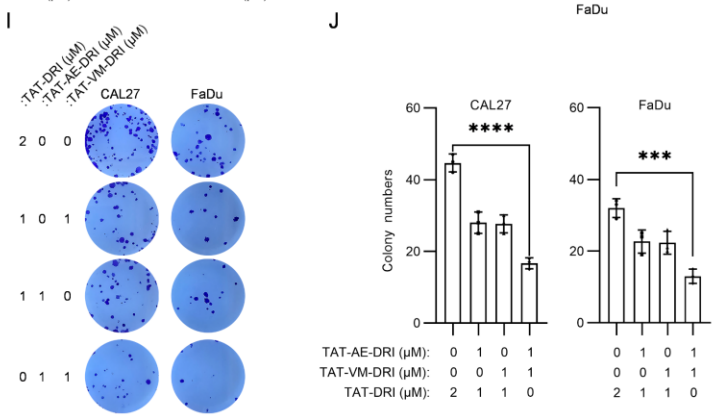

I
TAT-DRI (μM)
TAT-AE-DRI (μM)
TAT-VM-DRI (μM)
CAL27
FaDu
J
Colony numbers
****
***
TAT-AE-DRI (μM):
TAT-VM-DRI (μM):
TAT-DRI (μM):

Figure S10

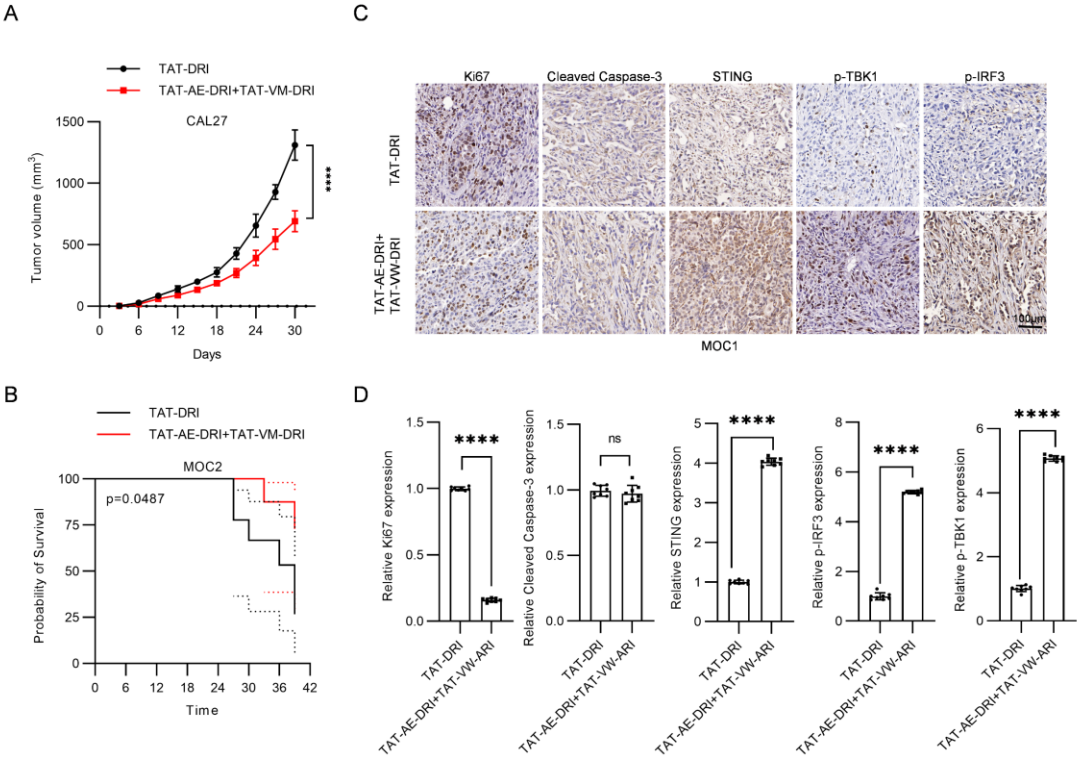

A
TAT-DRI
TAT-AE-DRI+TAT-VM-DRI
CAL27
Tumor volume (mm3)
Days
****
B
TAT-DRI
TAT-AE-DRI+TAT-VM-DRI
MOC2
p=0.0487
Probability of Survival
Time
C
Ki67
Cleaved Caspase-3
STING
p-TBK1
p-IRF3
TAT-DRI
TAT-AE-DRI+ TAT-VW-DRI
100 μm
MOC1
D
Relative Ki67 expression
Relative Cleaved Caspase-3 expression
Relative STING expression
Relative p-IRF3 expression
Relative p-TBK1 expression
****
ns
TAT-DRI
TAT-AE-DRI+TAT-VW-ARI

Table S1. Detailed information of patients.

Patients	Age	Location	TNM	Relapse	Grade
1	53	Mouth Floor	T3N0M0	NO	II-III
2	55	Buccal Mucosa	T2N1M0	NO	II
3	67	Buccal Mucosa	T2N0M0	NO	I-II
4	46	Tongue	T2N1M0	YES	III
5	39	Tongue	T3N1M0	NO	III
6	72	Gingiva	T2N0M0	NO	II
7	73	Buccal Mucosa	T1N0M0	NO	I-II
8	71	Gingiva	T2N0M0	YES	II-III
9	71	Tongue	T3N0M0	YES	III
10	48	Tongue	T1N0M0	NO	I-II
11	62	Buccal Mucosa	T2N0M0	NO	II
12	57	Buccal Mucosa	T2N0M0	NO	II
13	37	Tongue	T3N1M0	NO	III
14	32	Tongue	T3N0M0	YES	II-III
15	75	Tongue	T2N0M0	NO	II
16	34	Tongue	T2N0M0	NO	II
17	48	Tongue	T1N0M0	NO	I
18	69	Soft Palate	T2N1M0	NO	III
19	49	Tongue	T1N2M0	NO	IV
20	44	Buccal Mucosa	T3N1M0	NO	III
21	36	Tongue	T3N0M0	YES	II-III

Table S2. The primers for sgRNAs.

Genes	Species	Primers
Ctrl	Human	F: CACCGACGGAGGCTAAGCGTCGCAA
		R: AAACTTGCGACGCTTAGCCTCCGTC
LHX1 #1	Human	F: CACCGTCTCCGCACCAGGTCGCTAG
		R: AAACCTAGCGACCTGGTGCGGAGAC
LHX1 #2	Human	F: CACCGCGGCTGCAAAAGGCCCATCC
		R: AAACGGATGGGCCTTTTGCAGCCGC
STING	Human	F: CACCGCTGGGACTGCTGTTAAACG
		R: AAACCGTTTAACAGCAGTCCCAGC
LDB1 #1	Human	F: CACCGGAAAGGCGTTGCCGTTCGG
		R: AAACCCGAACGGCAACGCCTTTCC
LDB1 #2	Human	F: CACCGGAGTGTGACAATCTCTGGT
		R: AAACACCAGAGATTGTCACACTCC

Table S3. The primers used for RT-qPCR.

Genes	Species	Primers
ACTB	Human	F: CCTGGCACCCAGCACAAT
		R: GGGCCGGACTCGTCATAC
LHX1	Human	F: GCCCACCCGCCACATCC
		R: TGCTTCATCCTCCGCTCCTTG
ALDH1A1	Human	F: CCGTGGCGTACTATGGATGC
		R: GCAGCAGACGATCTCTTTCGAT
SOX2	Human	F: GCCGAGTGGAAACTTTTGTCG
		R: GGCAGCGTGTACTTATCCTTCT
POU5F1	Human	F: CTGGGTTGATCCTCGGACCT
		R: CCATCGGAGTTGCTCTCCA
NANOG	Human	F: CCCCAGCCTTTACTCTTCCTA
		R: CCAGGTTGAATTGTTCCAGGTC
IL1A	Human	F: TGGTAGTAGCAACCAACGGGA
		R: ACTTTGATTGAGGGCGTCATTC
IL6	Human	F: ACTCACCTCTTCAGAACGAATTG
		R: CCATCTTTGGAAGGTTCAGGTTG
IL8	Human	F: TTTTGCCAAGGAGTGCTAAAGA
		R: AACCCTCTGCACCCAGTTTTC
CXCL10	Human	F: CACCATGAATCAAACTGCGA
		R: GCTGATGCAGGTACAGCGT
STING1	Human	F: CTAGGAGAGCCACCAGAGCAC
		R: AGAAATAGATGGACAGCAGCAACAG
cGAS	Human	F: AAGAAGAAACATGGCGGCTATCC
		R: AAGGCTGAGGCAGGAGAATGG

Table S4. The primers used in the ChIP assay.

Binding sites	Binding sequence	Primers
Site1	GCAATTAC	F: CGGCCTCCCAAAGCGCTGGG
		R: GGTTTCTGCCCAGAAGGCGG
Site2	TCAATTAC	F: CAGAGCAAGCTGGGCTTTGG
		R: TTTTATAGATGGATAATCCG
Site3	CCAATTAT	F: GTCTATTTTTACGTTTAGGT
		R: GGCTGGGTTTCCCCACTCAT
Site4	GCCATCAC	F: AAGCAGTTCTCCTGCCTCAG
		R: CAACATGGAGAAACCCCATC
Site5	GCCATCAC	F: TTTTTTTGAGATAGGGTATC
		R: CTGAGGTGGGAGCATCACTT
Site6	GCAATTTG	F: AGGATGGTCTTGAACTCCTG
		R: CGGCAACAAGAGTCAAACTC