

SUPPLEMENTARY DATA

Supplementary Figure S1. Mapped 3' and 5' ends of lnc-pri-miR-181a2/b2.

(A) Sequencing results of lnc-pri-miR-181a2/b2 3'RACE products amplified by poly(A) polymerase dependent method. On the left, sequencing of PCR products revealed the boundary between the adaptor primer and lnc-Nr6a1 sequences. On the right, schematic illustration showing location of used primers (black arrowheads) and 3' end cleavage sites based on sequence analysis (green arrows). (B) On the right, a representative image of PCR product from 5'-RACE procedure; on the left, sequencing of PCR product revealed the boundary between the adaptor primer and lnc-Nr6a1 sequence.

Supplementary Figure S2. 3'-end mapping and lnc-Nr6a1 sequences.

(A) and (B) Location of mapped 3'-end cleavage products are shown by green arrows on the lnc-pri-miR-181a2/b2. (C) lnc-Nr6a1-1 isoform cDNA sequence; exons 1, 2 and 3 are colored yellow, blue and gray respectively (D) lnc-pri-miR-181a2/b2 sequence; exons 1, 2 and 3 are colored yellow, blue and gray respectively and mir-181a2 and mi-181b2 in red.

Supplementary Figure S3.

Coding capacity of lnc-Nr6a1-1 and lnc-Nr6a1-2 as well as other known coding and noncoding RNAs was predicted by analysis with Coding Potential Calculator software and Coding Potential Assessment Tool.

Supplementary Figure S4. LNC-NR6A1 human orthologue.

(A) Schematic illustration of the genomic location and transcript structure of the LNC-NR6A1 human orthologue gene. (B) Expression of LNC-NR6A1 orthologue gene in MCF10A human breast epithelial cells and primary human omental mesothelial cells after 24 h of TGF- β treatment. Error bars represent S.D. *** $P < 0.001$ by two-tailed Student's t -test.

Supplementary Figure S5

(A) Screenshot of H3K4me3, H3K27ac, ATAC-seq and RNA-seq tracks at lnc-Nr6a1 genomic region of NMuMG cells. Position of mir-181a2 and mir-181b2 are shown. (B) Scatter plot of expression of miR-181a2-3p and its host gene LNC-NR6A1 in human cancers. BLCA (Bladder Urothelial Carcinoma), BRCA (Breast invasive carcinoma), COAD (Colon adenocarcinoma), CESC (Cervical squamous cell carcinoma and endocervical adenocarcinoma), PADD (Pancreatic adenocarcinoma), OV (Ovarian serous cystadenocarcinoma), LIHC (Liver hepatocellular carcinoma), HNSC (Head and Neck squamous cell carcinoma) and THCA (Thyroid carcinoma).

Supplementary Figure S6.

Validation by RT-qPCR of expression of genes in lnc-Nr6a1-depleted cells compared to control cells. For each mRNA, results are presented relative to the average value of *Hprt* reference gene. Experiments were performed in triplicate samples. Error bars represent S.D. *** $P < 0.001$ by two-tailed Student's t -test.

Supplementary Figure S7. Cell cycle analysis and cell proliferation.

(A) Cell cycle profiles of control cells and lnc-Nr6a1-depleted cells. (B) Real-time monitoring of *in vitro* proliferation of lnc-Nr6a1-depleted cells and control cells using the exCELLigence system. The system measures electric impedance across interdigitated microelectrodes integrated on the bottom of tissue culture plates. Error bars represent S.D. (C) Rate of proliferation by analysing the slopes of the cell proliferation curves. Error bars represent S.D. ns, not significant by two-tailed Student's t -test.

Supplementary Figure S8. Cell cycle analysis and cell proliferation.

(A) Cell cycle profiles of control, lnc-Nr6a1-1-overexpressing and lnc-Nr6a1-2-overexpressing cells. (B) Real-time monitoring of *in vitro* proliferation of control, lnc-Nr6a1-1-over-expressed and lnc-Nr6a1-2-over-expressed cells using the exCELLigence system. Data are from three replicates. Error bars represent S.D. (C) Rate of proliferation by analysing the slopes of the cell proliferation curves. Error bars represent S.D. ns, not significant by two-tailed Student's t -test.

Supplementary Figure S9. Proliferation and cell adhesion.

(A) Real-time monitoring of *in vitro* proliferation of control cells and two independent clones (guide 2 and guide 8) over-expressing the lnc-Nr6a1 precursor using the exCELLigence system. Data are from three replicates. Error bars represent S.D. (B) Rate of proliferation by analysing the slopes of the cell proliferation curves. Error bars represent S.D. ns, not significant by two-tailed Student's t -test. (C) Substrate cell adhesion assay and (D) quantification of crystal violet staining at OD₅₉₀ nm of control and lnc-Nr6a1-1-overexpressing cells and clones of guide 2 and guide 8 over-expressing the lnc-Nr6a1 gene.

Supplementary Figure S10. Lamin A/C-associated domains.

(A) UCSC Genome Browser overview of lamin A/C ChIP-seq profiles in NMuMG control cells (red) and in *Lnc-Nr6a1*-depleted cells (red) and the corresponding identified LADs. From top to bottom: the complete chromosome 1 (mm9) and representative regions of chromosome 1, chromosome 16 and chromosome 11. (B) Gene ontology analysis of genes associated to LADs partially lost in *Lnc-Nr6a1*-depleted cells. (C) Venn diagrams showing the intersection of deregulated genes and LADs associated genes in *Lnc-Nr6a1*-depleted cells. Probability of overlapping based on hypergeometric distribution is provided.

Supplementary Figure S11. Human *LNC-Nr6A1* expression in tumors and normal tissues.

Expression levels of human *Lnc-Nr6a1* gene in different primary tumors versus the corresponding adjacent normal tissues. Expression data were downloaded from the GP1A2 dataset. ACC, adrenocortical carcinoma; BLCA, bladder urothelial carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangio carcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; LAML, acute myeloid leukemia; LGG, brain lower grade glioma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; SARC, sarcoma; STAD, stomach adenocarcinoma; THCA, thyroid carcinoma; THYM, thymoma; UCEC, uterine corpus endometrial carcinoma; UCS, uterine carcinosarcoma. In brackets are shown the number of primary tumor (T) and adjacent normal tissue (N) samples.

Table S1. Transcriptomic analysis of control and *Lnc-Nr6a1*-depleted NMuMG cells. List contains only genes whose expression (fold change > [1.5]) significantly changed ($P\text{-adj} < 0.05$).

Table S2. Gene Ontology enrichment analysis of downregulated genes in *Lnc-Nr6a1*-depleted cells.

Table S3. Transcriptomic profile of control NMuMG cells treated with TGF- β for 2 hours.

Table S4. Transcriptomic profile of *Lnc-Nr6a1*-depleted NMuMG cells treated with TGF- β for 2 hours.

Table S5. The *lnc-Nr6a1-1* protein interactome. Results of iDRiP-mass spectrometry analysis.

Table S6. Genes in LADS lost and LADS gain in *Lnc-Nr6a1*-depleted NMuMG cells

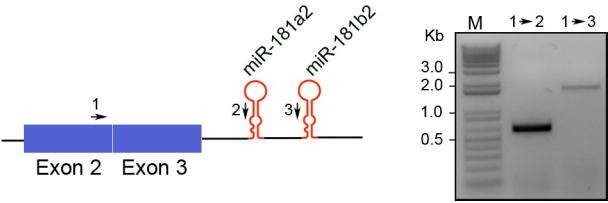
Table S7. Peptide-spectrum match counting for enolase1 coimmunoprecipitation assay

Table S8. Primers and oligonucleotides related to experimental procedures

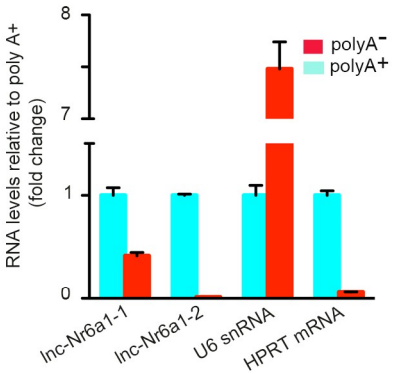
Movie S1. Wound-healing assay. Time-lapse video microscopy of control, *Lnc-Nr6a1*-depleted, *lnc-Nr6a1-1* overexpressing and *lnc-Nr6a1-2* overexpressing NMuMG cells.

Movie S2. Wound-healing assay. Time-lapse video microscopy of control, *lnc-Nr6a1-1* overexpressing and *Lnc-Nr6a1* gene-upregulated (Guide 2) NMuMG cells.

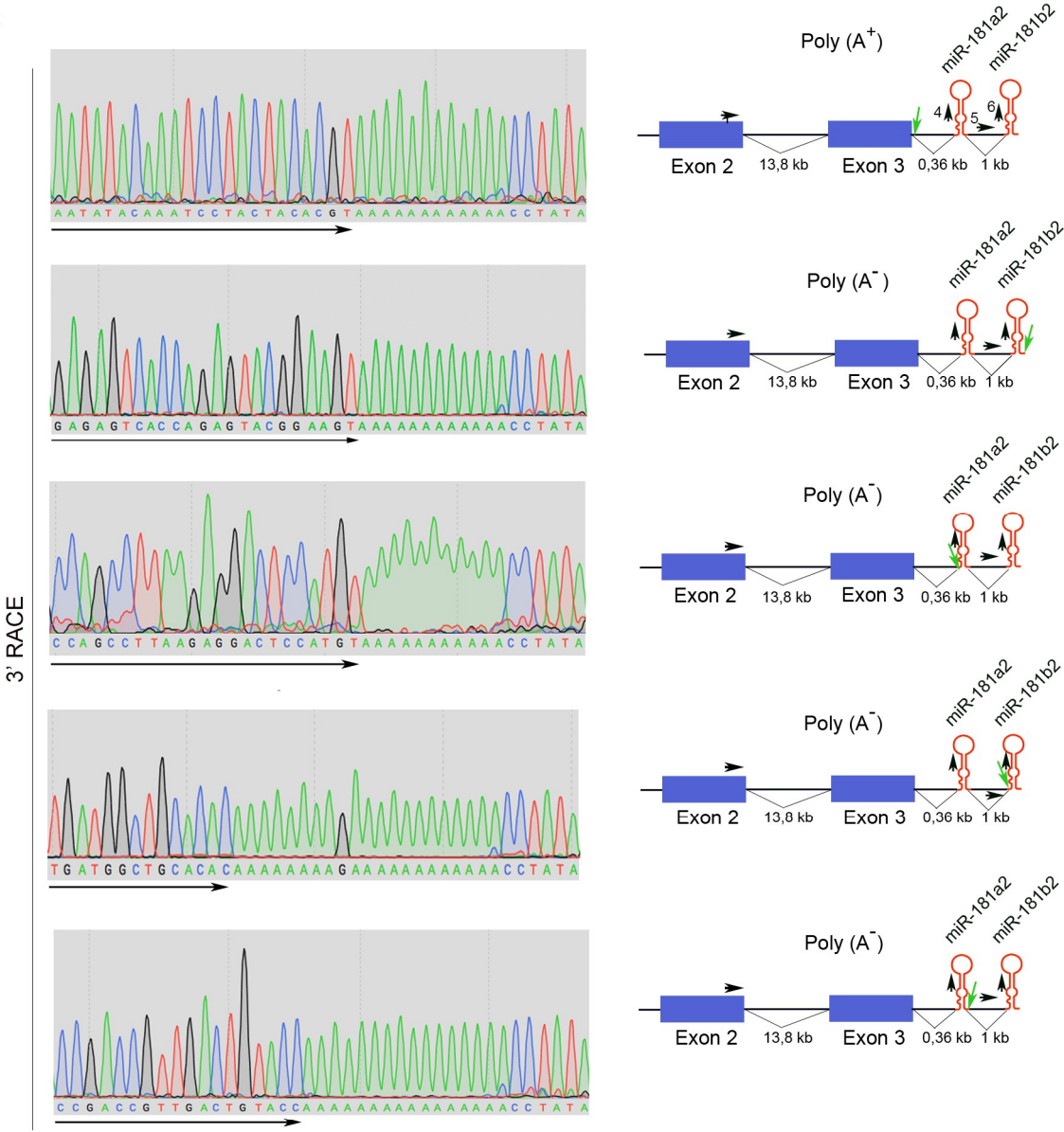
A



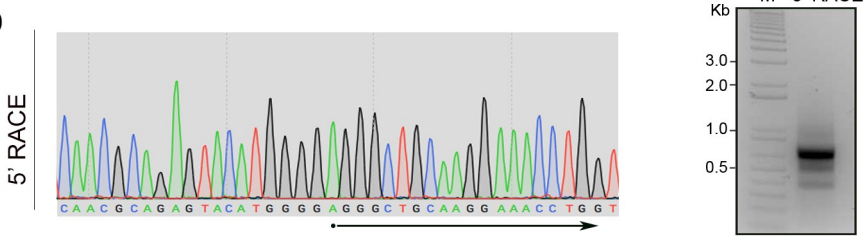
B



C

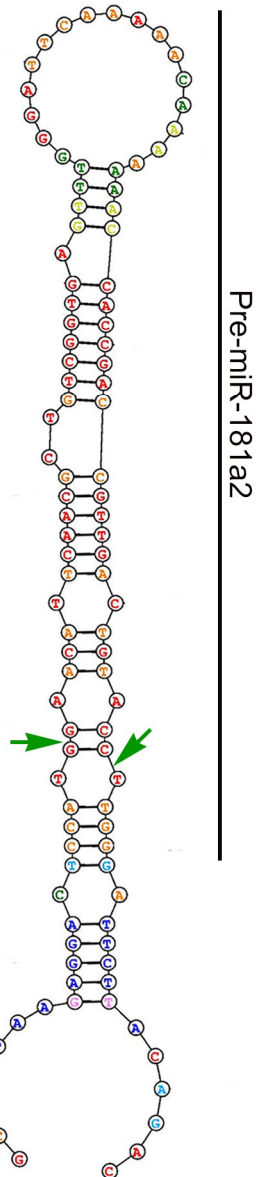


D

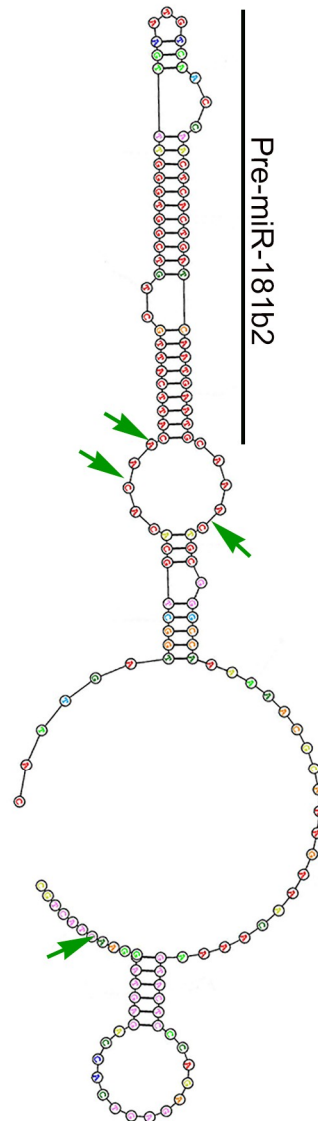


Supplementary Figure S1

A



B



C

Lnc-Nr6a1-1 isoform cDNA sequence

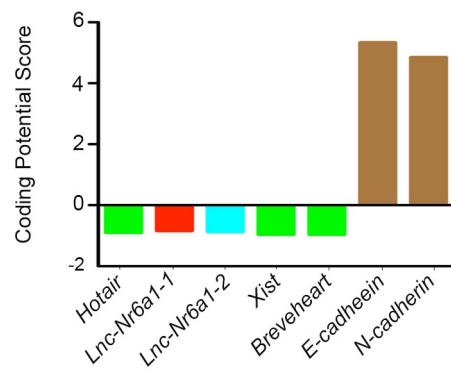
5' agggctgcaaggaaacctgggtgcggttcaataccttgtctagcctgggctccaggatcttttttttttttttttaactgacaaac
tcatttttctactgggacaggatgctgtgctggctgaagttccatttctacagcaagaatcctatctggaagcacagaagtgtcctcta
gccacagcagctccaactttttgtgttgctgctttcttctatcaccccttcccctttgacaaagatccaactgtagaaagtcttacgt
aacagttcaggactacttcggttctttaccggtgaaatgaagctgtgataatgtggtaaatatggggagacaccaagctgtggctctt
gcggacttcagcagcaactgaaatgcaacactgtgggctttggcagctgcattccgtactctgaaattcttatatcattactctggcaaac
aagaaggaatttgctgtttgatttagctctgcagtaaagggtcaaactgagactggtaaaggaaggagaaagcaacatatccaacc
aatactggaacaatgaactctggtgttcaagttctggctatggaactccgggtaagtctctgtttcttaaggaaaaacggttggaatt
aaatatacaaatcctactacac 3'

D

Lnc-pri-miR-181a2/b2 sequence

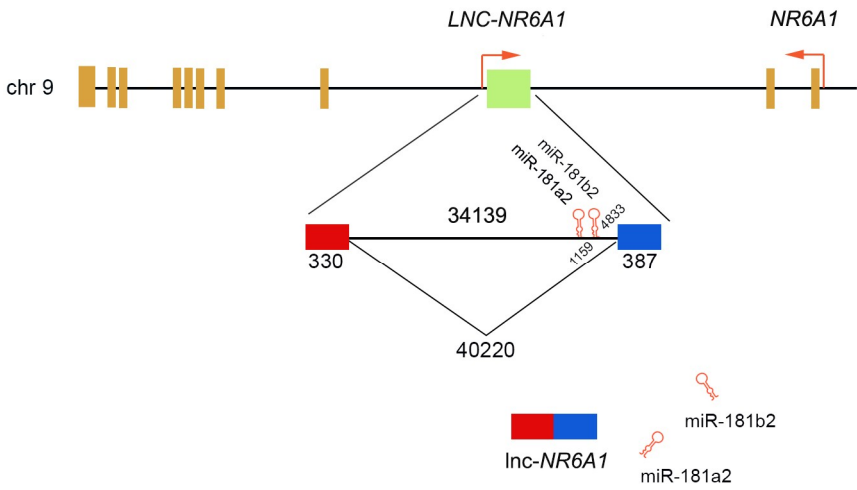
5' agggctgcaaggaaacctggtgcggttcaataccttgtctagcctgggctccaggatcttttttttttttttttaaaactgacaaac
tcatttttctactgggacaggatgctgtgctggctgaagttcattttctacagcaagaatcctatctggaagcacagaagtgtcctcta
gccacagcagctccaactttttgtgttgctgctttcttctatcaccccttccccttttgacaaagatccaactgtagaaagtcttacgt
aacagttcaggactacttcggttctttaccggtgaaatgaagctgtgataatgtggtaaataatggggagacaccaagctgtggctctt
gcggaacttcagcagcactgaaatgcaacactgtgggctttggcagctgcattccgtactctgaaattcttatcattactctggcaaac
aagaaggaatttgcctgtttgatttagctctgcagtaaaggttcaaactcgagactggtaaaggaaggagaaagcaacatatccaacc
aatactggaacaatgaactctggtgttcaagttctggctatggaactccgggtaagtctctgtttcttaaggaaaacacggttgaatt
aaatatacaaatcctactacacataaagtcccagcatgtgttatggcttttctgtttttgtacattaataattaaagtattactacaaaa
ttgctatattgatgtttcagaatgatagcattgaaaaatatttccacagatatccacttttagtcagcaatgtaaactgcagtctcaca
atctctgcagctcatttctgctttatgcaactaacttcacagtgtgaagtactgttaactgaaatttgggaagaatgtgagagacccaa
cagcagtggtccttagaatatgagagcaggccaaagatgggcaaccaagccagccttaagaggactccatggaacattcaacgctg
tcggtgagtttgggattcaaaaaacaaaaaacccgaccgttgactgtaccttgggattcttacagacaacaagtttctgaagcaa
aggagtaggctgtacagatatatcatgtgacagacatcacagatacagtcctgtggcctcttttctaaagggaaccagcaagttttt
tttaagcttccatgtatttatattgtctatttttgtaatttcttgataaataagtgtttcattttaacaatttatgggaagtgccatcatag
taccaaatgcactcaaatatcttctagaaatgtgtcattctagtgcagaaatagggtgtattaaaaatgtctatttactgtaggaaaaaa
atctagttaagctttttattctcatttcttctacgtcctttcaaatttttgccttagggtaagagatttactcagcaaaaaatactcacaga
gttactcactgtctatacaaatcatattgtgcctccagtttcagttactgcggttagggatttgacatctccatgagagaaccagataca
ttccatctccatgtgctaatttaaggaattctgggtcatctctgagcctccgtatccaagtatgttttctcaaagttagaataaggagagg
agagaacctcagagttttaatttaatgagaagatataggggtactttgaacagtttctggctcacagcaaatgtttactacaaaaat
tttacttaactgcaatcataatctatactgctttaccttgaaaagggcacttaacgtctcagcttgaaacaaaagatgaagcaatgtct
ctgagggctcctttacagacatcaacatccaagtctcagccatgtgatcagagctacttacaaggttctcacatagtccttcttctc
acaacttttctgtcttgaacaagttcttgctatacagtcaaggtgatctataattatgagtcacacacatacagatgactagttactaa
catacaacagacttcaaagaaccatagtggaagaagagccaggagatagaaaagaccaagacaatttcatcaaaaggaaacatt
gatggctgcacacaacattcattgctgtcggtgggtttgaatgtcaaccaactcactgatcaatgaatgcaaaactgcgggccaaaaa
cgcaaaagaaacaaaagtactcccagagagtcaccagagtcacgaagt

Supplementary Figure S2

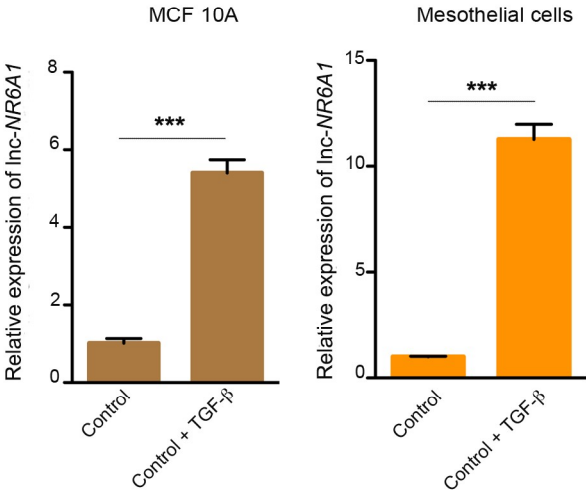


Supplementary Figure S3

A

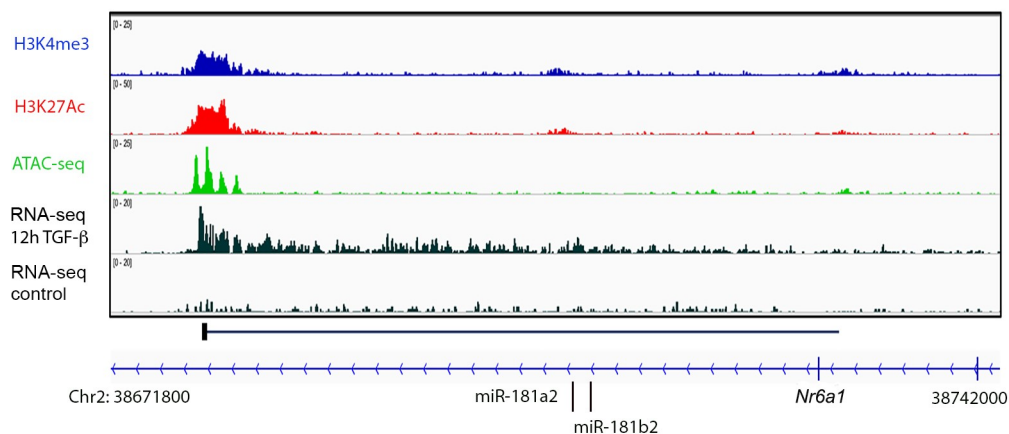


B

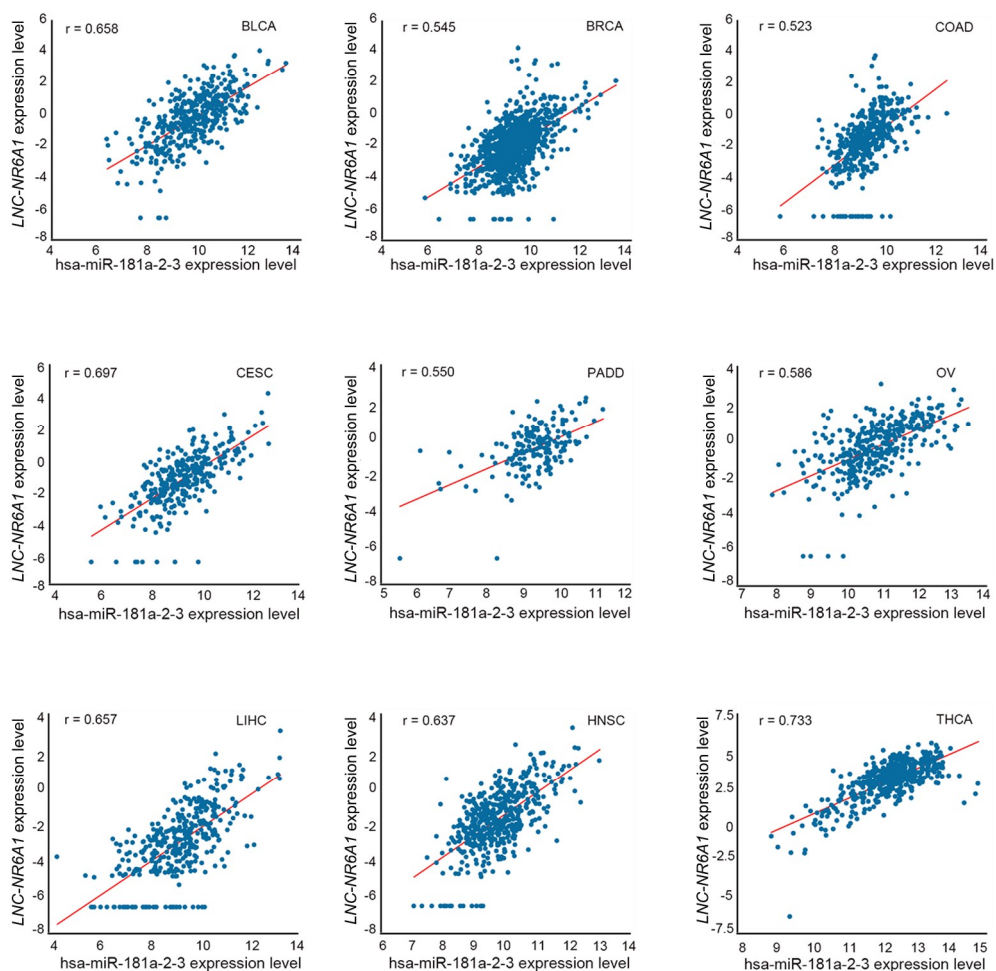


Supplementary Figure S4

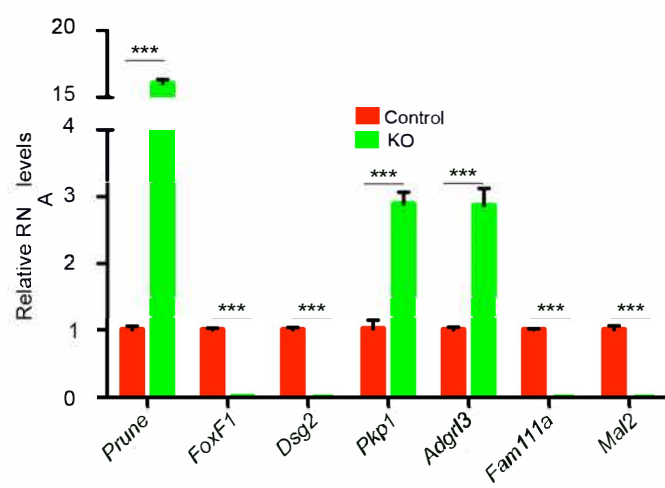
A



B

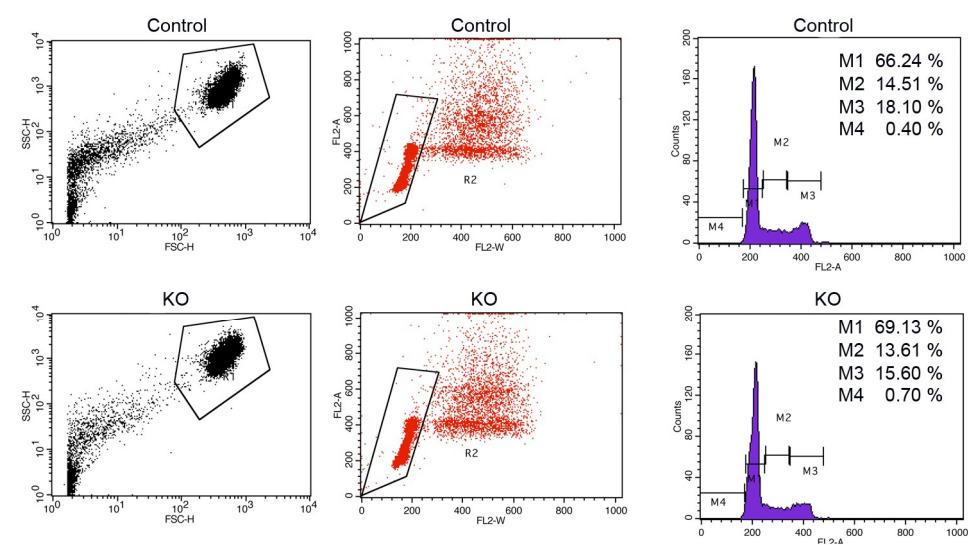


Supplementary Figure S5

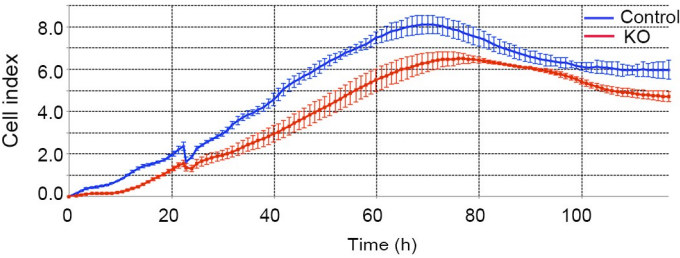


Supplementary Figure S6

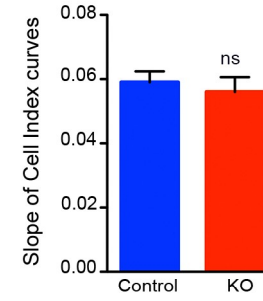
A



B

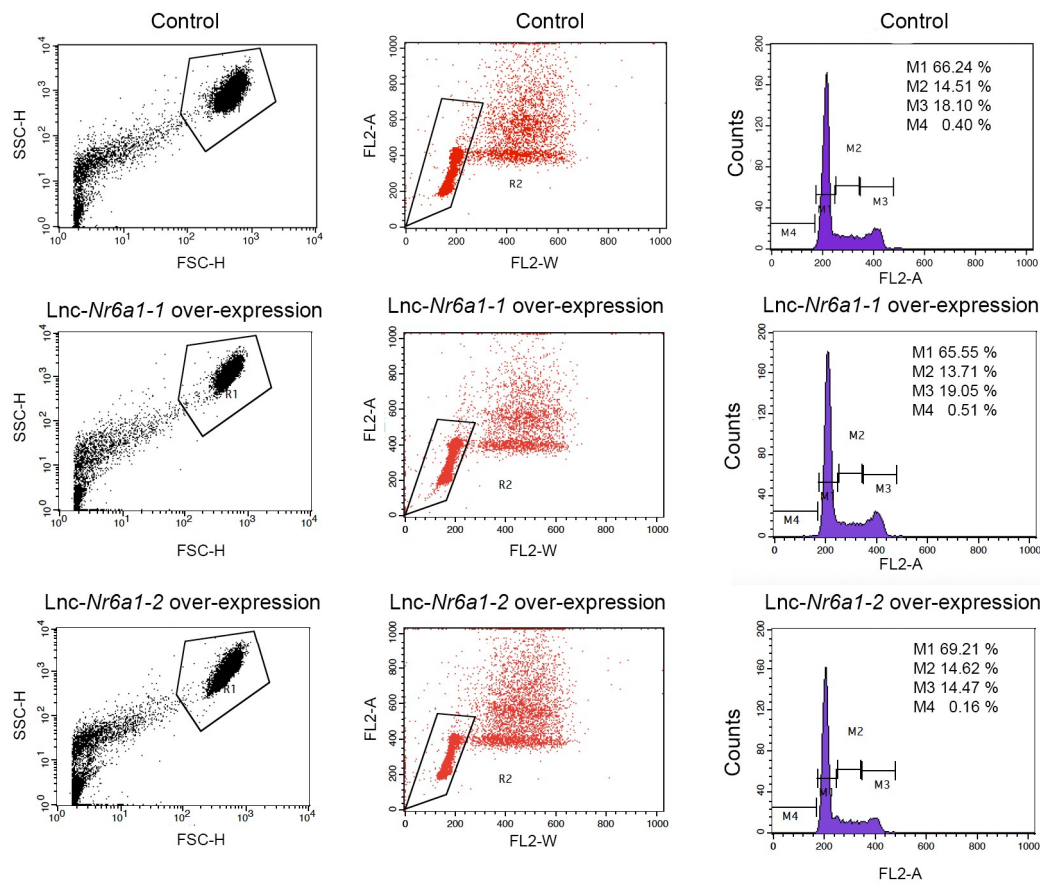


C

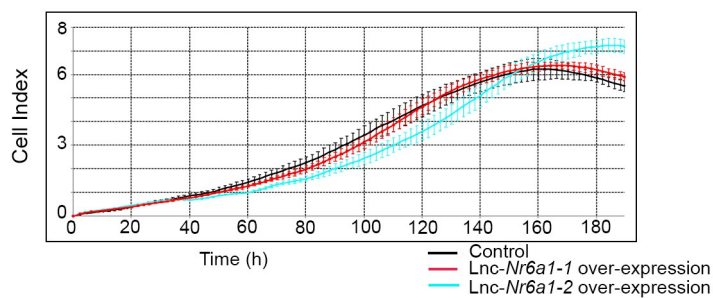


Supplementary Figure S7

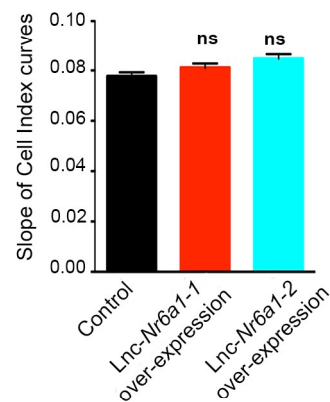
A



B

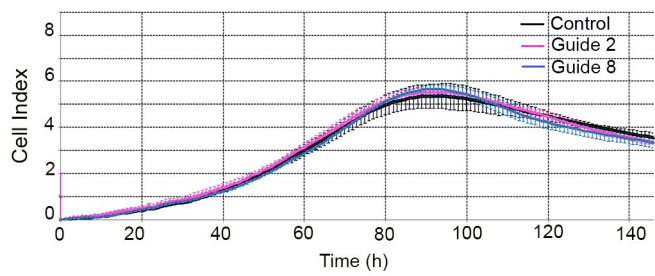


C

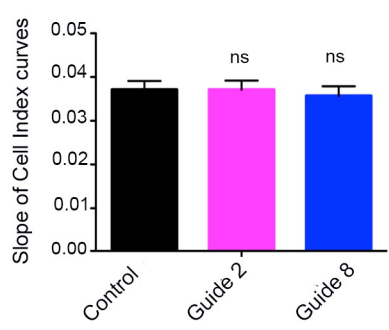


Supplementary Figure S8

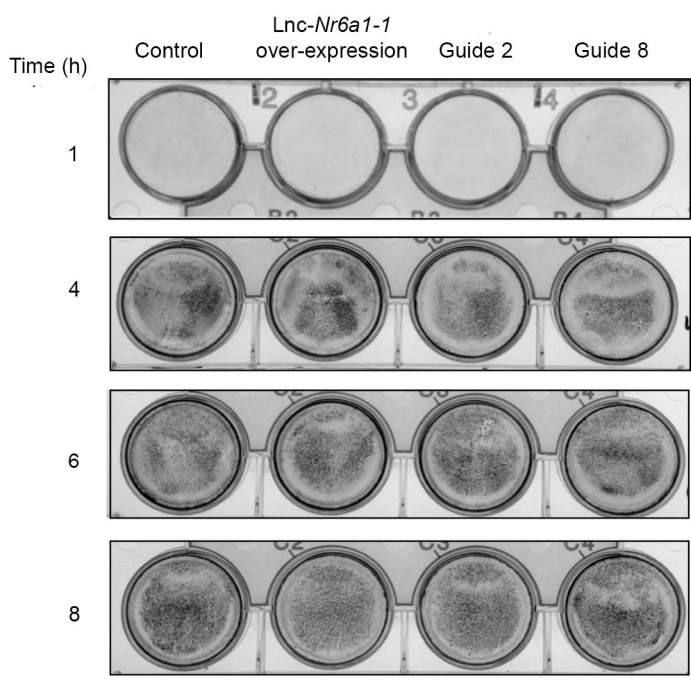
A



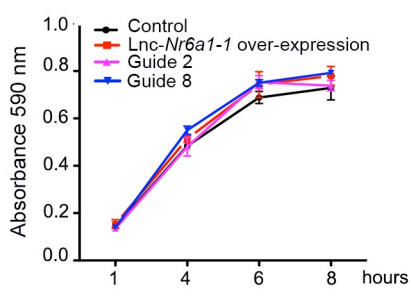
B



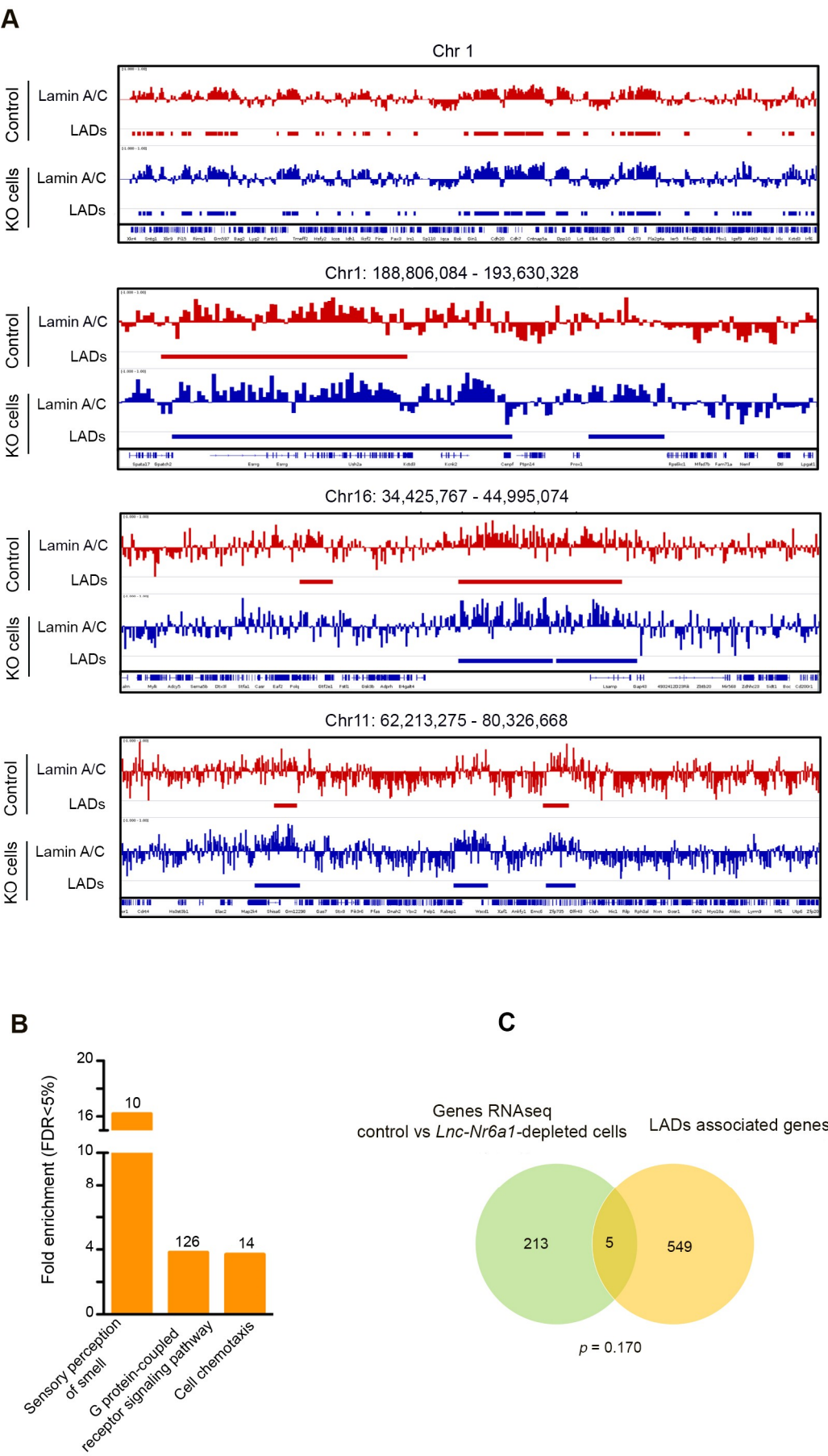
C



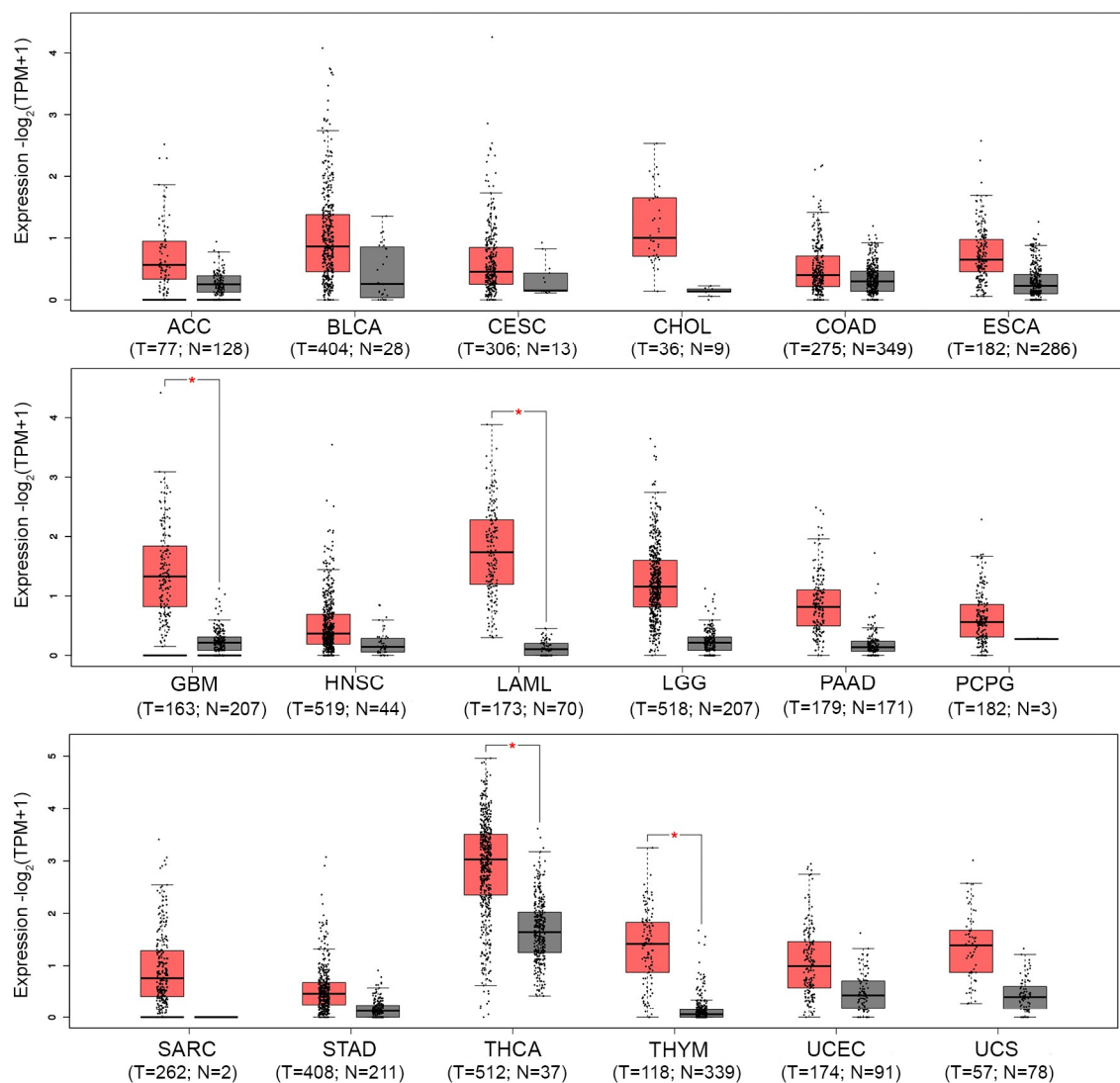
D



Supplementary Figure S9



Supplementary Figure S10



Supplementary Figure S11