

## Supplemental Information

### Supplementary Figures

**Fig.S1 MIDEAS-AS1 is lowly expressed in TNBC.** (A) Heat map shows the significantly expressed lncRNAs in breast cancer samples compared to normal tissues according to The Cancer Genome Atlas (TCGA) database. The red shades represent high expression, and blue shades represent low expression. (B) Schematic view of the chromosomal location of MIDEAS-AS1. (C) The protein-coding ability of MIDEAS-AS1 is predicted by CPC2 (<http://cpc2.gao-lab.org>). (D) The expression level of MIDEAS-AS1 in different subtypes of breast cancer tissues by using GSE21653 database. Statistical analysis was performed with the R language. Data were shown as mean  $\pm$  SD. (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ).

**Fig.S2 Knock down of MIDEAS-AS1 contributes to TNBC cell proliferation and migration in vitro.** (A-B) The efficiency of MIDEAS-AS1 overexpression (A) and knockdown (B) were examined by qRT-PCR. (C) Flow cytometry was performed to measure the effect of MIDEAS-AS1 overexpression and knockdown on cell cycle in vitro. (D) Wound-healing assays were used to evaluate the motility of MDA-MB-231 and MDA-MB-468 cells transfected with MIDEAS-AS1-overexpressing vector or control vector and si-NC or si-MIDEAS-AS1. Data were shown as mean  $\pm$  SD. (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ).

**Fig.S3 Effect of overexpression or knockdown of MIDEAS-AS1 on MATR3.** (A)

Interaction sites of MIDEAS-AS1 and MATR3 genes were analyzed from the catRAPID database. (B) The influence of knockdown or overexpression MIDEAS-AS1 on the expression level of MATR3 in MDA-MB-231 and MDA-MB-468 cells was determined by qRT-PCR and western blot analysis.

**Fig.S4 NCALD is downregulated in breast cancer tissues.** (A) qRT-PCR analysis was used to verify the relative expression of 9 candidate genes in MDA-MB-231 and MDA-MB-468 cells with knockdown or overexpression MIDEAS-AS1. (B) Effect of overexpression and knockdown of MIDEAS-AS1 on expression of its sense gene (MIDEAS) by qRT-PCR assay in MDA-MB-231 and MDA-MB-468 cells. (C) Relative expression of NCALD in tumor tissue and adjacent normal breast tissues from TCGA data. (D) Relative expression of NCALD in tumor tissue and adjacent normal breast tissues from a BCIP cohort. (E) Expression of NCALD in tumor and normal breast tissues detected by IHC from Human Protein Atlas (<https://www.proteinatlas.org/>). (F) The efficiency of knockdown and overexpression of MATR3 was confirmed by qRT-PCR and Western blot in MDA-MB-231 and MDA-MB-468 cells. Data were shown as mean  $\pm$  SD. (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ).

**Fig.S5 Knock down of NCALD promotes TNBC cell proliferation and migration in vitro.** (A) Flow cytometry was performed to measure the effect of NCALD overexpression and knockdown on cell cycle in vitro. (B) Wound-healing assays were

used to evaluate the motility of MDA-MB-231 and MDA-MB-468 cells transfected with NCALD-overexpressing vector or control vector and si-NC or si-NCALD. Data were shown as mean  $\pm$  SD. (\* $p$ <0.05, \*\* $p$ <0.01, \*\*\* $p$ <0.001).

## Supplementary Tables

**Table S1. si-RNA and plasmids used for transfection.**

<b>Name</b>	<b>Sequence (5'-3')</b>
MIDEAS-AS1	F CGGAATCCCCCTCGGCTGCGGGGTAG R CGGGATCCTGCCAAAATGAACACTACTGTCATG
MIDEAS-AS1(for organoid)	F GCTCTAGACCCTCGGCTGCGGGGTAG R CGGGATCCTGCCAAAATGAACACTACTGTCATG
NCLAD	F CCCTCGAGATGGGGAAACAGAACAGCAAGCT R GCTCTAGATCAGAACTGGCCGGCACTGCTC
MATR3	F CGCAAATGGGCGGTAGGCGTG R CCTCTACAAATGTGGTATGGC
NCALD-Luc1	F GGGGTACCCTGGTTTGGGAAAAGGTATGGC R CCCTCGAGTTCCTTCTTTCCCAACCCC
NCALD-Luc2	F GGGGTACCTGAGTGCTAATAGGTGTGGGAT R CCCTCGAGTTCACGTTTAATGTGAACTCTTC
NCALD-Luc3	F GGGGTACCCTTCTGGCTTCTCTTGGGGGCA R CCCTCGAGAGAGAATCTAATCTAATTGTTA
NCALD-Luc4	F GGGGTACCCGGGGTCGGGCCTAGTATTAAG R CCCTCGAGGCCTTCCTCGTTGTAATGTTTGC
NCALD-Luc5	F GGGGTACCCAGGTCACGGTGCCTTTGCAGCCT R CCCTCGAGTGCTTTTGTCTAACTAGTGCTTTC
NCALD-all length (Luc)	F GGGGTACCCTGGTTTGGGAAAAGGTATGGCA R CCCTCGAGTGCTTTTGTCTAACTAGTGCTTTC
MIDEAS-AS1-Sense	F TAATACGACTCACTTACATAGGGCCCTCGGCTGCGGGGTAG R TGCCAAAATGAACACTACTGTCATG
MIDEAS-AS1-Antisense	F TAATACGACTCACTTACATAGGGTGCCAAAATGAACACTACTGTCATG R CCCTCGGCTGCGGGGTAG
MIDEAS-AS1- $\Delta$ 1-sense	F1 TAATACGACTCACTATAGGGCCTGCCAATGATCTCTGCCTCCA
MIDEAS-AS1- $\Delta$ 2	R2 AGTTCTCAATGTTGCCTCATGGGCGCATCTTAGAGGCTGT
MIDEAS-AS1- $\Delta$ 2-sense	F2 ACAGCCTCTAAGATGCGCCCATGAGGCAACATTGAGAA
MIDEAS-AS1- $\Delta$ 3	R3 TGCTGTGCTGCCAGCAGCCAGCTCA
si-MIDEAS-AS1	Sense CCAUUUCUCCACUUUGGAATT Antisense UCCAAAGUGGAGAAAUGGTT
si-MATR3	Sense GCCAGUGAGAGUUUCAUUUATT Antisense UAAAUGAACUCUCACUGGCTT
si-NCALD	Sense UUCUCCGAACGUGUCACGUTT Antisense ACGUGACACGUUCGGAGAA
si-NC	Sense UUCUCCGAACGUGUCACGUTT Antisense ACGUGACACGUUCGGAGAATT

**Table S2. Primers used for qRT-PCR.**

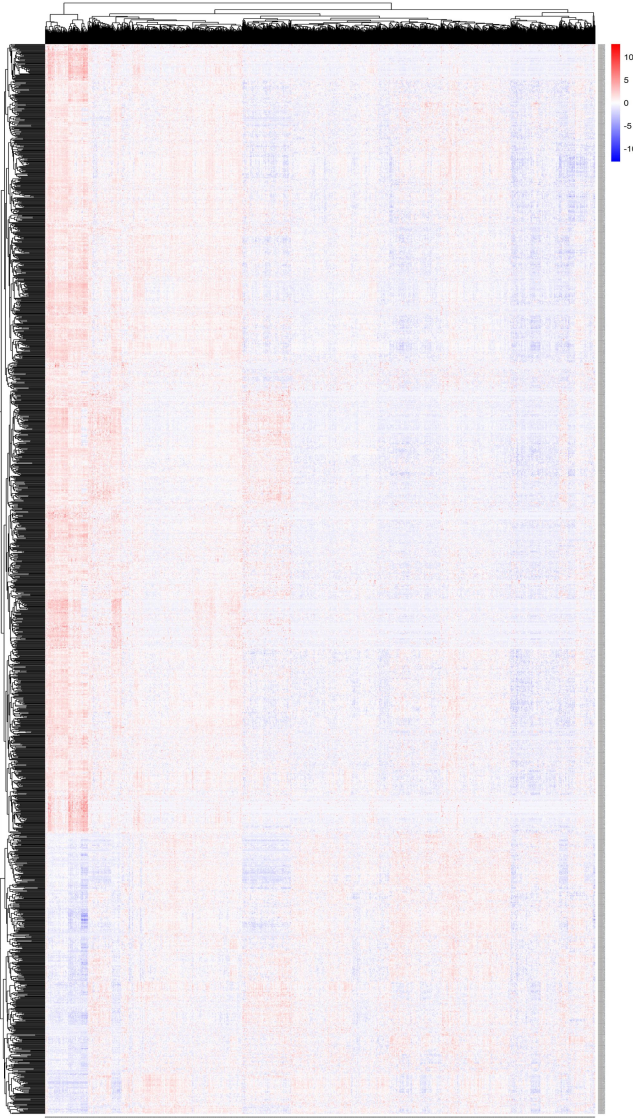
<b>Name</b>	<b>Sequence (5'-3')</b>
MIDEAS-AS1	F TTCCCATCCCAGAAGATAAAG R TTGCCTCATTGCTGTGCTG
U6	F CTCGCTTCGGCAGCACAA R AACGCTTCACGAATTTGCGT
GAPDH	F GTCTCCTCTGACTTCAACAGCG R ACCACCCTGTTGCTGTAGCCAA
MATR3	F CAGCAGTCTACAAATCCAGCACC R CTGCATGTGTCTAGGTCCTTGC
NCALD	F TCATCATCGCCTTGAGTGT R TTGACTCATCTTCAGGCATT
HBB	F AGGAGAAGTCTGCCGTTACTG R CCGAGCACTTTCTTGCCATGA
ADHFE1	F TGGACTTTCACCTTCTGGGAA R GGAGAGGTTCTTGTCTGTCATCA
MAPK10	F CAGATGGAATTAGACCATGAGCG R TCAATGTGCAATCAGACTTGACT
EDAR	F CGAGCGGAATACTCAAAGTGGC R TAGTCCTCGTCTTTGGTGCCGT
AF131215.5	F AGCCAGGGGAACAAGGTAAAAG R ATCTGATCACCTTACCACCTCCA
CXCL1	F AGCTTGCTCAATCCTGCATCC R TCCTTCAGGAACAGCCACCAGT
DAPL1	F AGAAATTGGCACCTTGGAAGACA R GCTTCTCCAGTGCGTCATTGAG
ARHGAP40	F AGCCTTCAACATGGACTCTGC R TTTGGGGACGGTAAACTTCGG
NCALD-P1	F CTGGTTTGGGAAAAGGTATGG R TATCCATTTATCAGTTGACAGACA
NCALD-P2	F TGACATCGTTTGTTCATAAAGAG R CCAACTTCCAGTGACCACTTATC
NCALD-P3	F TGGGGAAAGAAGGGAATGA R GTGATTTTTCTTTAATGATCTCTAC
NCALD-P4	F CAATAAAGAAAAGTAGATAAAGTGG R TTCACGTTTAATGTGAACTCTTCTA
NCALD-P5	F TCTGGCTTCTCTTGGGGGCAG R GACAAACTGAGAAGGGCACAA
NCALD-P6	F CTTTATCCTTCAGGGACATTTG R CAGGGGTGTCCAGCTTTGTA
NCALD-P7	F TTAGATTAGATTCTCTCGGGGTCGG R TTAGCAGGTTAGCCCAGCAT
NCALD-P8	F TGATGGTTTAAACAGCCTCCTAGA

	R GCCTTCCTCGTTGTAATGTTTG
NCALD-P9	F TGCCTTTGCAGCCTTGTTA
	R CCAGCACCTGTTTCCTGTCTT
NCALD-P10	F ATTGGGTGAATGAATTGACAAGA
	R GGCTGCTTTTGTCTAACTAGTGCTT
MIDEAS	F AGCGGAAAAGTGTATTGGCCT
	R GCTCAGCAGGGTTCTGTTCA
Actin	F CATGTACGTTGCTATCCAGGC
	R CTCCTTAATGTCACGCACGAT

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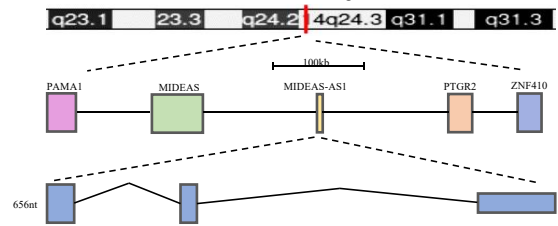
**Figure S1**

**A**

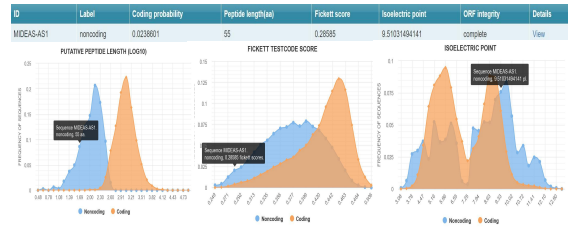


**B**

Chromosome14:73,787,360-73,803,300 (hg38)

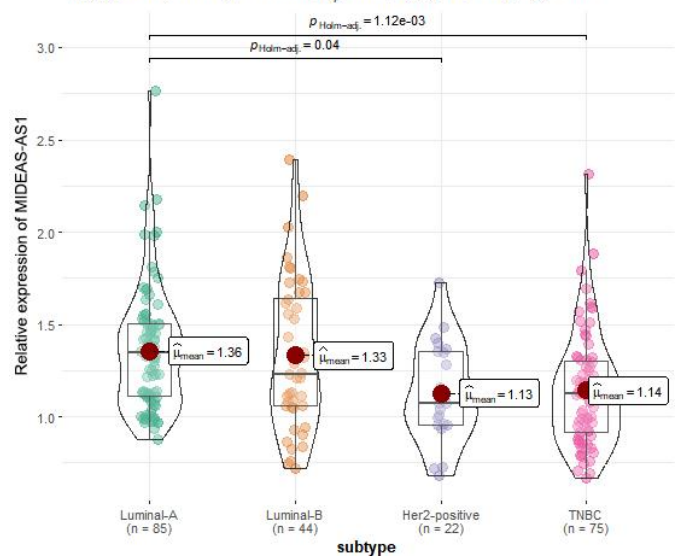


**C**



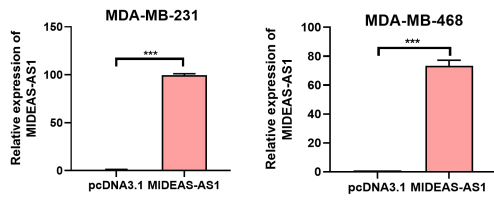
**D**

$$F_{\text{Welch}}(3, 79, 19) = 8.03, p = 9.72e-05, \hat{\alpha}_p^2 = 0.20, CI_{95\%} [0.07, 1.00], n_{\text{obs}} = 226$$

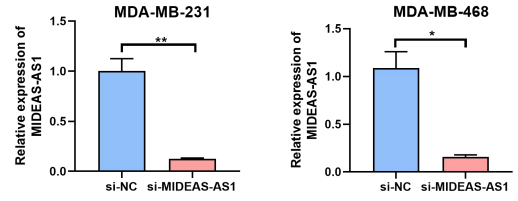


**Figure S2**

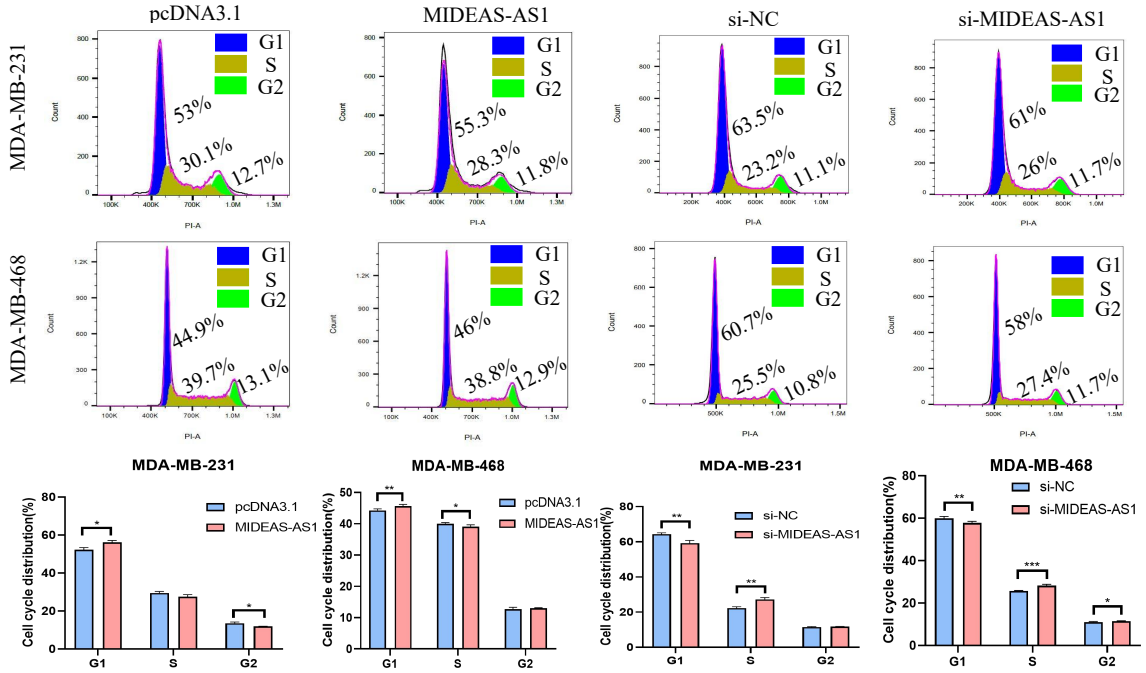
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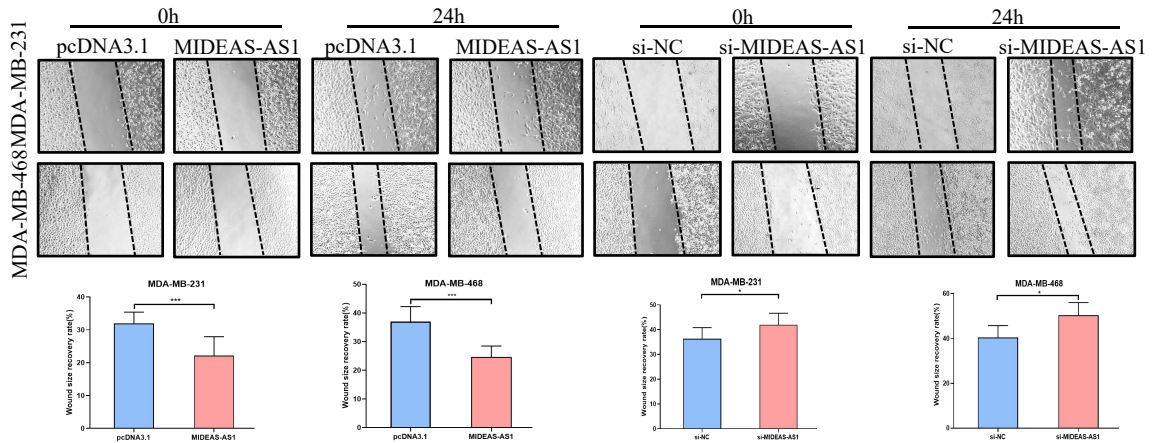
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**C**



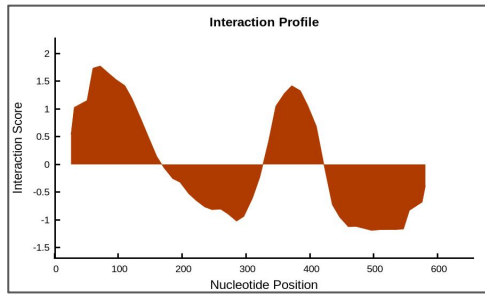
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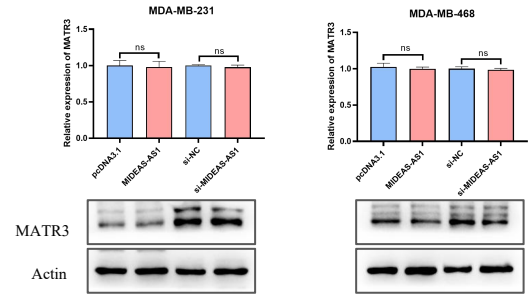


**Figure S3**

**A**

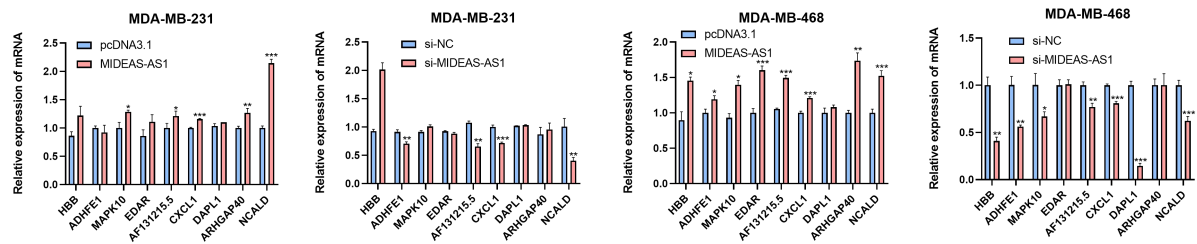


**B**

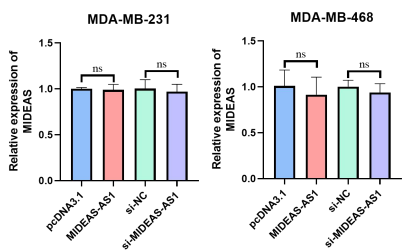


# Figure S4

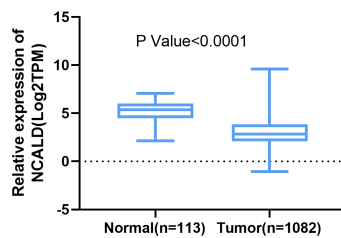
A



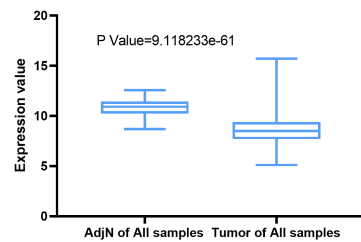
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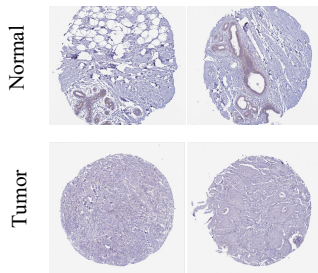
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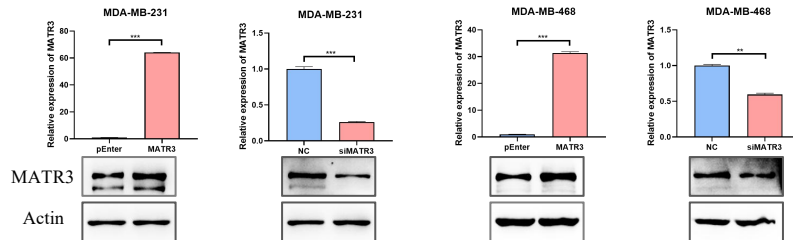
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E

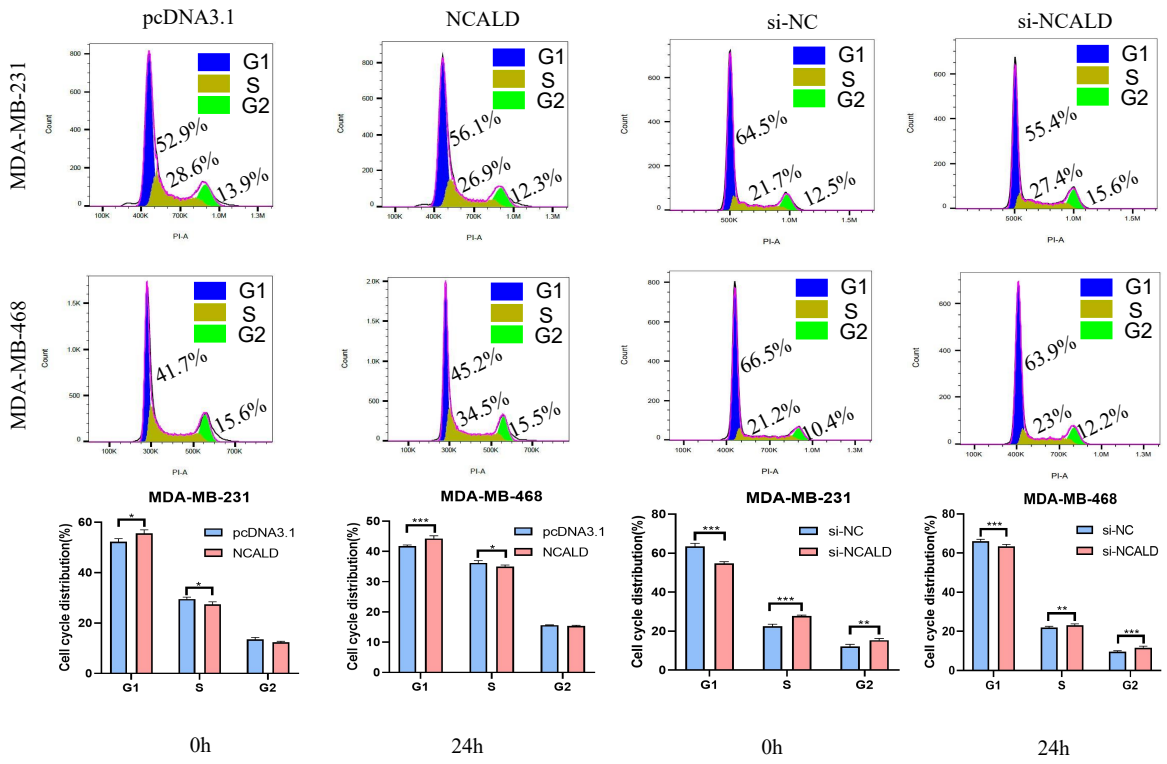


F



**Figure S5**

**A**



**B**

