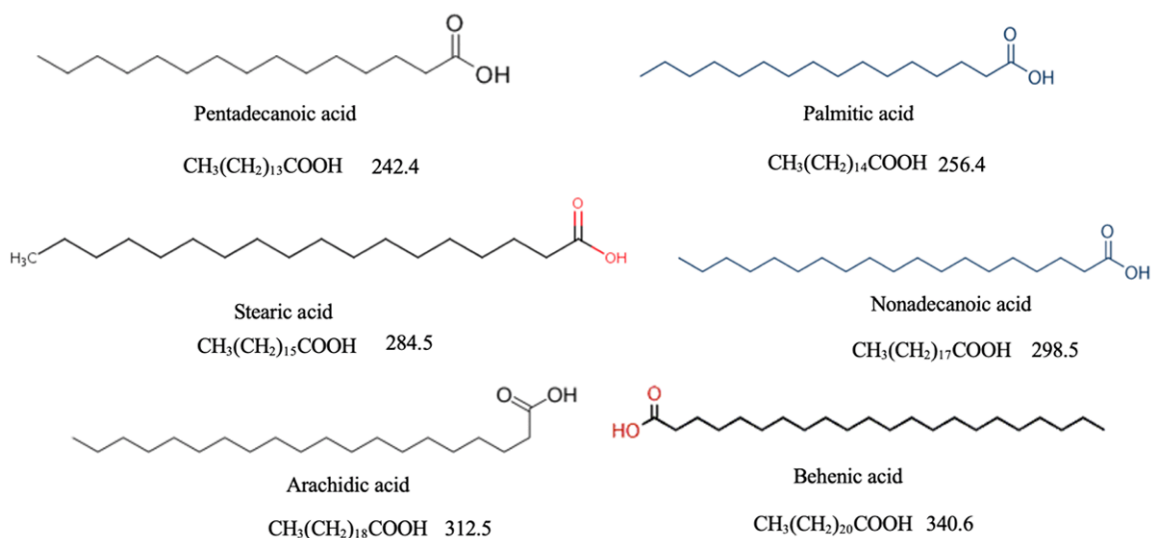


## The pathological role of PDA

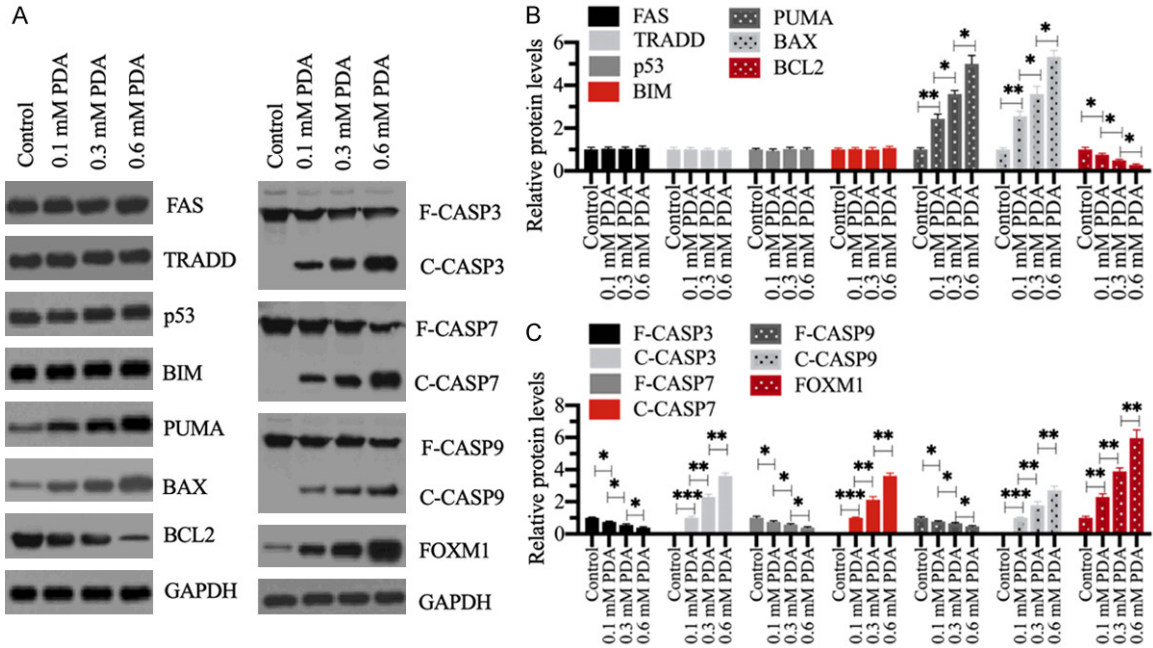
**Supplementary Table 1.** Primers used for RT-qPCR analyses to examine gene expression levels

Gene	Forward Primers (5'→3')	Reverse primers (5'→3')
FOXM1	TGTGCTCAAGCTGTCCACCATCC	ACACAAGGTCCCAGCAGTGGC
PUMA	GACTTTCTCTGCACCATGTAGCA	GTCCCTCTCCTGGCTTCTTGCCAG
APAF1	TCACAGCACCATCCAGTACTG	CCCAACTTAAATGTCCTCTGCAAT
KAT5	TGTTTGGGCACTGATGAGGACT	CTCAATGCACTCAATGTTCTTCA
MSH6	GATTAGACAGTGTCCAGCACC	ATCAGGGACATGATGTAGAG
BCL2	CCAGAGACATCAGCATGGCTC	GATGTCCCTACCAACCAGAAG
BIRC5	GTCTGTCAGCCCAACCTTAC	ACCCTGCAGCTCTATGACAG
NPM1	GGAAGATGCAGAGTCAGAAGA	TCCTTTCATCATCATCGTCA
NOD1	GCAGATGCGTTACAGAGCAACA	GAAACAGATAATCCGCTTCTC
FAS	GGCAAGACTGCCCTTAGAAT	AGCAGGTTTTACATGGACAT
TRADD	TGGAGGCACTCGAGGAGAACGA	AGGAACCCTAAGGCCATCCA
P53	AAGGGCCTGACTCAGACTGAC	GAAGTCCTGGGTGCTTCTGAC
BIM	GTGTGGAGAATGCATTGACAG	CTGAAACGTCACCTGCCCCCT
BAX	TCTGAGCAGATCATGAAGACA	ACACTCGCTCAGCTTCTTGGTG
BAK1	AGATGGTCACCTTACCTCTGCA	TTCTCTGCCGTGGGCTGCAGGT
NCOR1	GGGTCTTAAGCTATTCTGAGT	AGGCTGAGGATGAGAAGGGGTT
β-Actin	CAGGTCATCACCATTGGCAAT	GTCTTTGCCGATGTCCACGTC



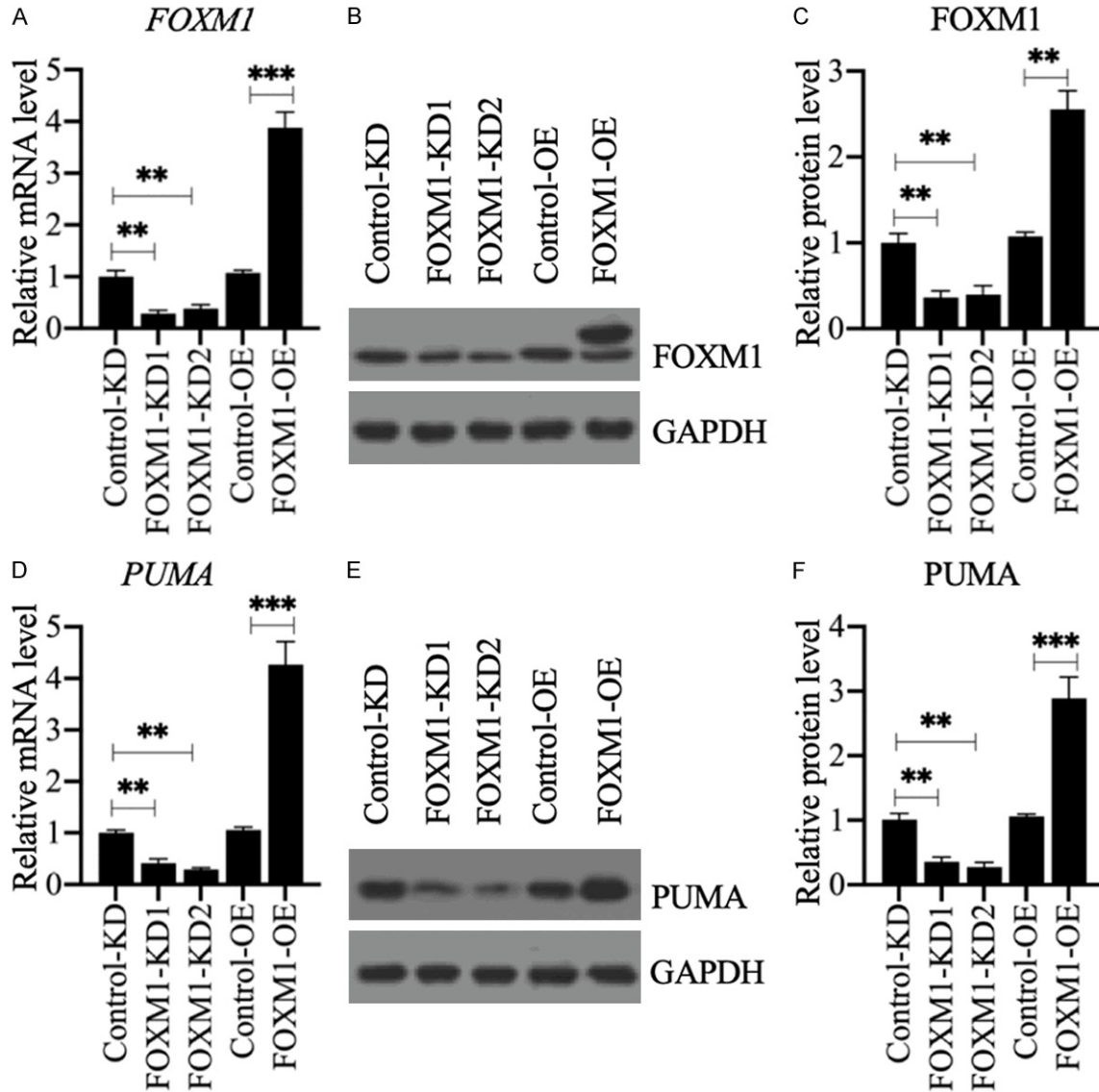
**Supplementary Figure 1.** The chemical structures of LCFAs identified by GC-MS. The chemical structures of six LCFAs (PDA, stearic acid, palmitic acid, nonadecanoic acid, arachidic acid and behenic acid) as shown in **Figure 1** and their molecular weights.

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**Supplementary Figure 2.** The protein levels of genes involved in apoptotic signaling in PDA-treated cells. A. Immunoblot results. Total cell extracts from cells treated with different doses of PDA (0, 0.1, 0.3 and 0.6 mM) were subjected to western blotting to examine the protein levels of FAS, TRADD, p53, BIM, PUMA, BAX, BCL2, CASP3, CASP7, CASP9, and FOXM1. F: full length; C: cleaved form. B and C. Quantification of protein band signals. The protein band signals in A were quantified using Image J software. Statistical significance is denoted by \* for  $P < 0.05$ , \*\* for  $P < 0.01$ , and \*\*\* for  $P < 0.001$ .

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**Supplementary Figure 3.** The effects of *FOXM1* knockdown and overexpression on *PUMA* expression. (A) The relative mRNA level of *FOXM1*. Total RNA from Control-KD, FOXM1-KD1, FOXM1-KD2, Control-OE, and FOXM1-OE1 cells was applied to RT-qPCR analysis to examine the *FOXM1* mRNA level. \*\* $P < 0.01$  and \*\*\* $P < 0.001$ . (B and C) The protein level of *FOXM1*. Total cell extracts from cells used in (A) were applied to western blotting to examine the protein levels of *FOXM1* and GAPDH (loading control) (B). The *FOXM1* protein signals were quantified using ImageJ software and normalized to their corresponding GAPDH levels (C). \*\* $P < 0.01$ . (D) The relative *PUMA* mRNA level. The same RNA samples as used in (A) were subjected to RT-qPCR analysis to examine the expression of *PUMA*. \*\* $P < 0.01$  and \*\*\* $P < 0.001$ . (E and F) *PUMA* protein levels. The same cell extracts as used in (B) were applied to western blotting to examine the protein levels of *PUMA* and GAPDH (loading control) (E). The *PUMA* protein signals were quantified using ImageJ software and normalized to their corresponding GAPDH levels (F). \*\* $P < 0.01$  and \*\*\* $P < 0.001$ .

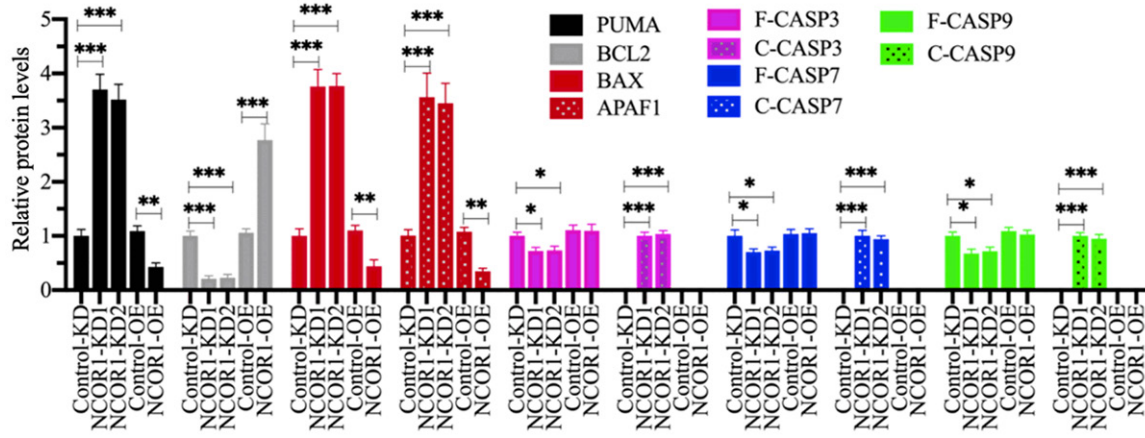
**Supplementary Table 2.** The *FOXM1*-associated proteins by LC-MS/MS analysis

Protein	Protein description	Percolator score	Molecular weight
FOXM1	Forkhead Box M1	7436	84283
NPM1	Nucleophosmin 1	65543	32575
NRIP2	Nuclear Receptor Interacting Protein 2	5231	31331
KIF2A	Kinesin Family Member 2A	5012	79955
HSPA4	Heat Shock Protein Family A (Hsp70) Member 4	4657	94331

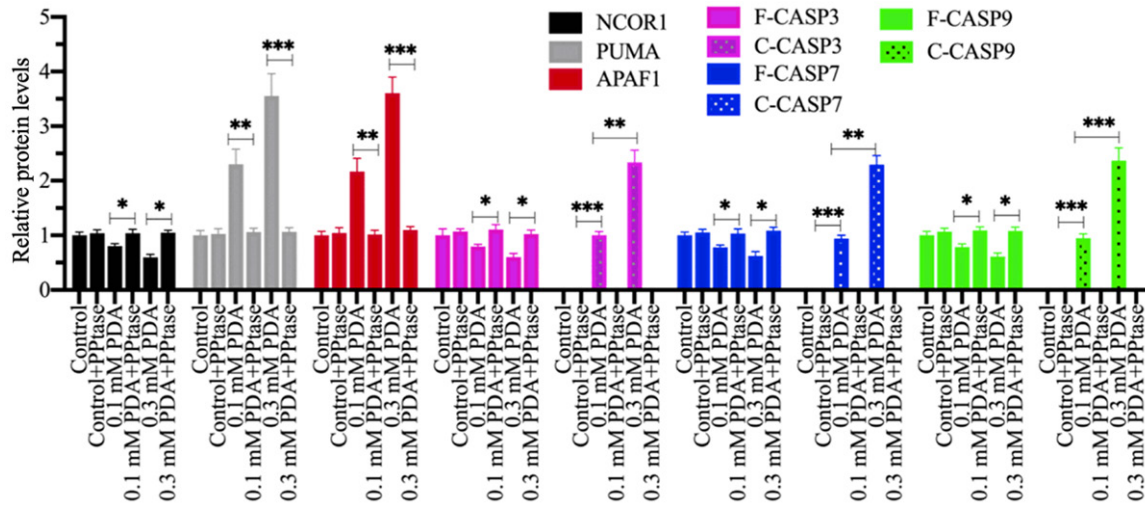
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UHRF1	Ubiquitin Like With PHD And Ring Finger Domains 1	4332	89814
IFI27	Interferon Alpha Inducible Protein 27	3678	11542
RRM1	Ribonucleotide Reductase Catalytic Subunit M1	3212	90070
PPP2CA	Protein Phosphatase 2 Catalytic Subunit Alpha	3094	35594
PCLAF	PCNA Clamp Associated Factor	2778	11986
RPA2	Replication Protein A2	2543	29247
SPC25	SPC25 Component Of NDC80 Kinetochore Complex	2123	26153
SMC4	Structural Maintenance Of Chromosomes 4	2094	147182
NSCAN12	Zinc Finger And SCAN Domain Containing 12	1965	70222
DMAP1	DNA Methyltransferase 1 Associated Protein 1	1932	52993
MKS1	MKS Transition Zone Complex Subunit 1	1902	64528
CALM2	Calmodulin 2	1854	16838
PIGL	Phosphatidylinositol Glycan Anchor Biosynthesis Class L	1823	28531
NCOR1	Nuclear Receptor Corepressor 1	1793	270210
NR1D2	Nuclear Receptor Subfamily 1 Group D Member 2	1744	64625
SIAH2	Siah E3 Ubiquitin Protein Ligase 2	1732	34615
TBL1X	Transducin Beta Like 1 X-Linked	1657	62496
MECP2	Methyl-CpG Binding Protein 2	1432	52441
PRMT1	Protein Arginine Methyltransferase 1	1335	42462
BAZ1A	Bromodomain Adjacent To Zinc Finger Domain 1A	1207	178702
PLD6	Phospholipase D Family Member 6	1184	28273
BAZ2A	Bromodomain Adjacent To Zinc Finger Domain 2A	1034	211198
TEKT3	Tektin 3	1021	56636
PBRM1	Polybromo 1	968	192948
DDX20	DEAD-Box Helicase 20	903	92241
MED19	Mediator Complex Subunit 19	887	26273
ERBB2	Erb-B2 Receptor Tyrosine Kinase 2	834	137910
DDX46	DEAD-Box Helicase 46	812	117362
EWSR1	EWS RNA Binding Protein 1	789	68478
RPS11	Ribosomal Protein S11	764	18431
MED9	Mediator Complex Subunit 9	692	16403
POLR1C	RNA Polymerase I And III Subunit C	632	39250
DVL2	Dishevelled Segment Polarity Protein 2	587	78948
DAP3	Death Associated Protein 3	532	45566
TAF9	TATA-Box Binding Protein Associated Factor 9	511	28974
CORO2A	Coronin 2A	489	59763
CDRT4	CMT1A Duplicated Region Transcript 4	463	17643
NR2C1	Nuclear Receptor Subfamily 2 Group C Member 1	411	67315
DUS3L	Dihydrouridine Synthase 3 Like	406	72594
MTMR3	Myotubularin Related Protein 3	394	133619
XPO5	Exportin 5	365	136311
NUP160	Nucleoporin 160	342	162121
FLNA	Filamin A	322	280739
H2BC5	H2B Clustered Histone 5	312	13936
UPF1	UPF1 RNA Helicase And ATPase	287	124345
SMYD3	SET And MYND Domain Containing 3	265	49097
SND1	Staphylococcal Nuclease And Tudor Domain Containing 1	243	101997
MYL6	Myosin Light Chain 6	225	16930
SCAP	SREBF Chaperone	212	139729

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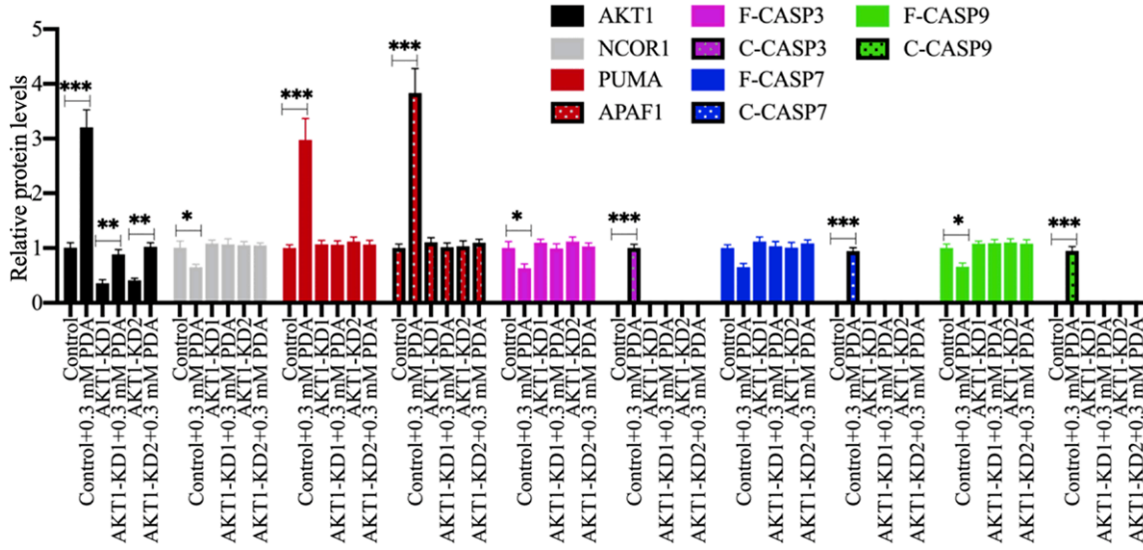


**Supplementary Figure 4.** The relative protein levels of apoptotic proteins in NCOR1-KD cells. The protein signals shown in **Figure 7F** were quantified using ImageJ software and normalized to their corresponding GAPDH level. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\* $P < 0.001$ .

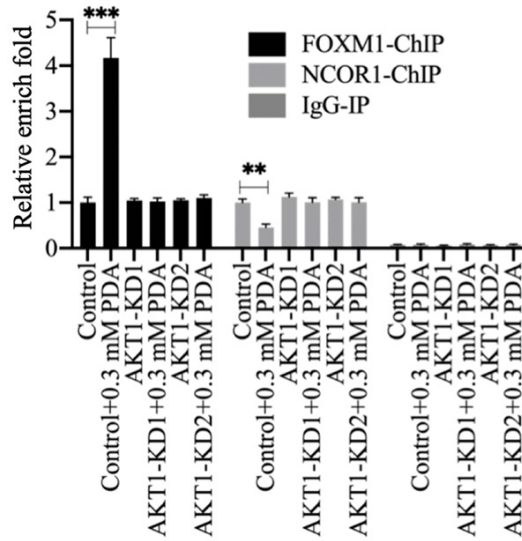


**Supplementary Figure 5.** The relative protein levels of apoptotic proteins in cells treated with or without PDA and PPtase. The protein signals shown in **Figure 8D** were quantified using ImageJ software and normalized to their corresponding GAPDH level. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\* $P < 0.001$ .

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**Supplementary Figure 6.** The relative protein levels of apoptotic proteins in AKT-KD cells treated with or without PDA. The protein signals shown in **Figure 8F** were quantified using ImageJ software and normalized to their corresponding GAPDH level. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\* $P < 0.001$ .



**Supplementary Figure 7.** The occupancies of NCOR1 and FOXM1 on the promoter of *PUMA*. Cells used in **Figure 8F** were subjected to ChIP assays using anti-NCOR1, anti-FOXM1 and IgG (negative control). The purified input and output DNA samples were subjected to RT-qPCR analysis to examine the occupancy of NCOR1 and FOXM1 on the promoter of *PUMA*. \*\* $P < 0.01$  and \*\*\* $P < 0.001$ .