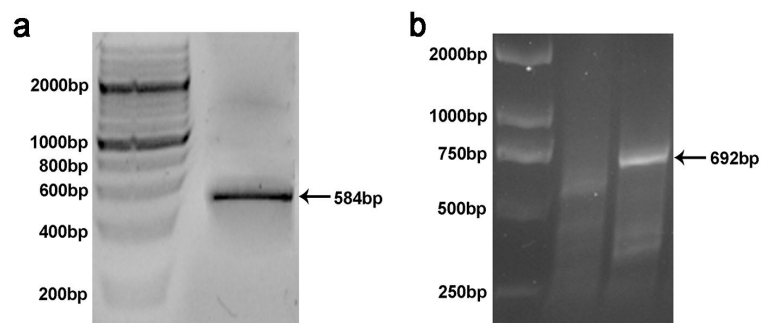
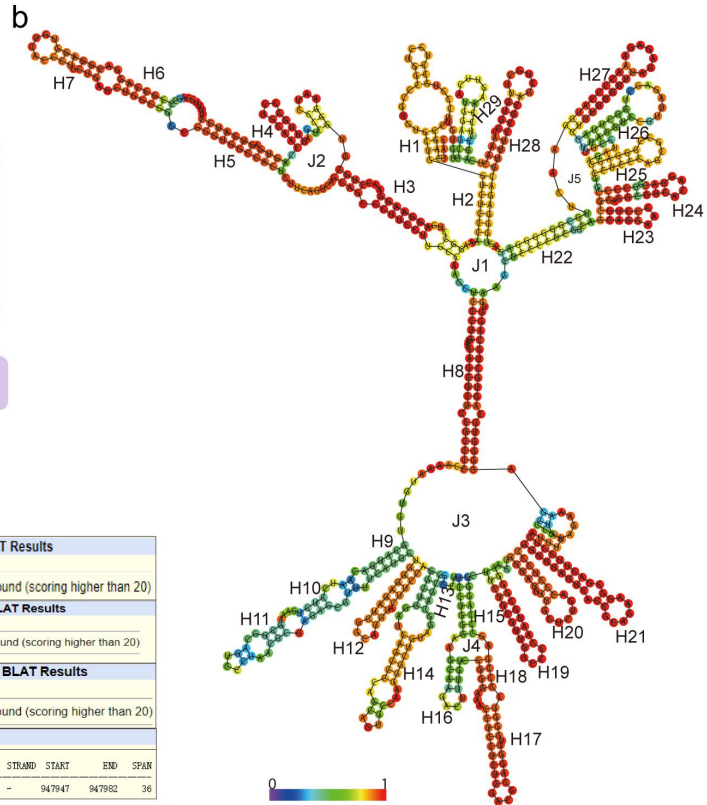
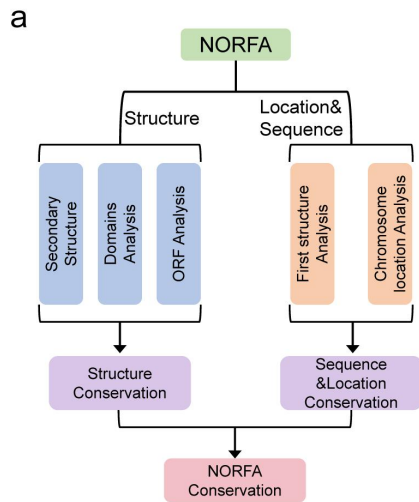


Supplementary Figures

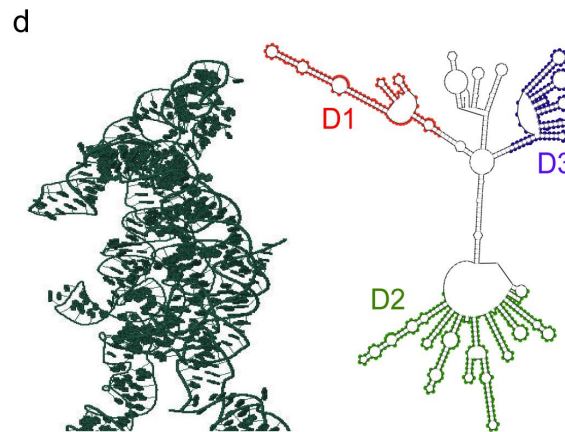


Supplementary Figure 1. 5'- and 3'-RACE analyses for porcine lincRNA-NORFA. Gel images showing the nested PCR amplified products obtained from 5'-RACE (**a**) and 3'-RACE (**b**) analyses. Black arrows indicate the products at 584 bp and 692 bp in length, respectively. DNA molecular weight markers are also represented.



c

Human (hg38) BLAT Results		Mouse (mm10) BLAT Results									
Sorry, no matches found (scoring higher than 20)		Sorry, no matches found (scoring higher than 20)									
Chimp (panTro6) BLAT Results		Sheep (oviAri4) BLAT Results									
Sorry, no matches found (scoring higher than 20)		Sorry, no matches found (scoring higher than 20)									
Cow (bosTau9) BLAT Results		Chicken (galGal6) BLAT Results									
Sorry, no matches found (scoring higher than 20)		Sorry, no matches found (scoring higher than 20)									
Pig (susScr11) BLAT Results											
ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	YourSeq	36	1	36	36	100.0%	chrUn_NW_018084833v1	-	947947	947982	36



D1 domain
Human (hg38) BLAT Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	20	98	117	148	100.0%	chr17	+	10198866	10198885	20

D2 domain
Human (hg38) BLAT Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	33	124	290	292	62.2%	chr2	+	206600434	206603051	108
browser details	NORFA	22	121	143	292	100.0%	chr20	+	51270275	51270301	27
browser details	NORFA	20	122	141	292	100.0%	chr4	-	168879999	168880018	20

D3 domain
Human (hg38) BLAT Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	29	19	56	116	94.2%	chr3	+	181696143	181696188	46

e

ORF Finder results
Results for 739 residue sequence "NORFA" starting "CATCAGCCTC"
No ORFs were found in reading frame 1.

ORF Finder results
Results for 739 residue sequence "NORFA" starting "CATCAGCCTC"
>ORF number 1 in reading frame 1 on the reverse strand extends from base 82 to base 249
ATGGGGTTCCTCTTACAGCCACAGCTAAGCCAGCTTAAAGCCAAAGCGATCTCC
CCCGCGCTCGAGGCCGGGGCCCTCTGTGACGCTCCCGACGGTTCCTGCTGCCAGG
GGAGCTTCACTCGACCACTCCACCTCTTCTTCAGGTAATAATGA
>Translation of ORF number 1 in reading frame 1 on the reverse strand.
MGFLSNPTAKPALDLINGSPPGAGRPFPSCDASAGFLLRGASPALHPSFVRK*

All Genomes BLAT Results

Name	Genome	Assembly	Tiles	Chrom
NORFA	Pig	susScr11	31	chrUn_NW_018084833v1
NORFA	American alligator	allMis1	4	JH734654
NORFA	Bison	bisBis1	4	KN264896v1
NORFA	Cow	bosTau9	4	chr16
NORFA	Horse	equCab3	4	chr24
NORFA	Chicken	galGal6	4	chr19
NORFA	Gorilla	gorGor5	2	CYUI0100003v1
NORFA	Human	hg38	2	chr1
NORFA	Coelacanth	latCha1	2	JH126564
NORFA	Elephant	loxAfr3	2	scaffold_0

Cow (bosTau9) BLAT Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	26	141	166	168	100.0%	chr11	-	105959425	105959450	26
browser details	NORFA	23	129	154	168	96.2%	chr11	+	78399066	78399093	28
browser details	NORFA	20	109	128	168	100.0%	chr24	+	42274447	42274466	20

Chicken (galGal6) BLAT Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	24	120	144	168	100.0%	chr3	+	57619879	57619906	28
browser details	NORFA	23	119	146	168	96.0%	chr14	+	70800696	70800724	29
browser details	NORFA	23	119	146	168	96.0%	chr14	+	7158650	7158608	29
browser details	NORFA	22	120	143	168	95.9%	chr2	+	8027210	8027233	24
browser details	NORFA	20	66	85	168	100.0%	chr25	-	1429916	1429935	20
browser details	NORFA	20	127	146	168	100.0%	chr1	-	663655	663674	20

Human (hg38) BLAT Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	29	58	95	168	94.2%	chr3	-	181696143	181696188	46
browser details	NORFA	23	124	147	168	100.0%	chr17	+	73451838	73451863	26
browser details	NORFA	20	138	157	168	100.0%	chr8	-	18171443	18171462	20

f

All Genomes BLAT Results				
Name	Genome	Assembly	Tiles	Chrom
NORFA Pig		susScr11	144	chrUn_NW_018084833v1
NORFA Cow		bosTau9	8	chr11
NORFA Sheep		oviAri4	6	chr3
NORFA Chicken		galGal6	4	chr1
NORFA Human		hg38	4	chr2
NORFA Mouse		mm10	4	chr16

Cow (bosTau9) BLAT Results

BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	56	50	718	739	49.5%	chr11	+	105958875	105959819	945
browser details	NORFA	22	301	323	739	100.0%	chr21	-	67144106	67144134	29
browser details	NORFA	21	313	333	739	100.0%	chr17	-	67110189	67110209	21
browser details	NORFA	20	576	595	739	100.0%	chr21	+	69527059	69527078	20
browser details	NORFA	20	164	183	739	100.0%	chr13	+	62677480	62677499	20
browser details	NORFA	20	6	25	739	100.0%	chr12	+	35225350	35225369	20

Sheep (oviAri4) BLAT Results

BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	92	50	525	739	47.0%	chr3	-	812354	812897	544
browser details	NORFA	24	1	25	739	100.0%	chr19	-	60265655	60266028	374
browser details	NORFA	24	434	464	739	44.1%	chr18	+	56438471	56438497	27
browser details	NORFA	23	189	216	739	88.0%	chr14	-	14071843	14071869	27
browser details	NORFA	22	441	466	739	92.4%	chr20	+	14229295	14229320	26
browser details	NORFA	22	2	24	739	100.0%	chr2	+	229784821	229784846	26
browser details	NORFA	20	191	210	739	100.0%	chr20	-	48691001	48691020	20
browser details	NORFA	20	164	183	739	100.0%	chr13	+	62004179	62004198	20

Human (hg38) BLAT Results

BLAT Search Results

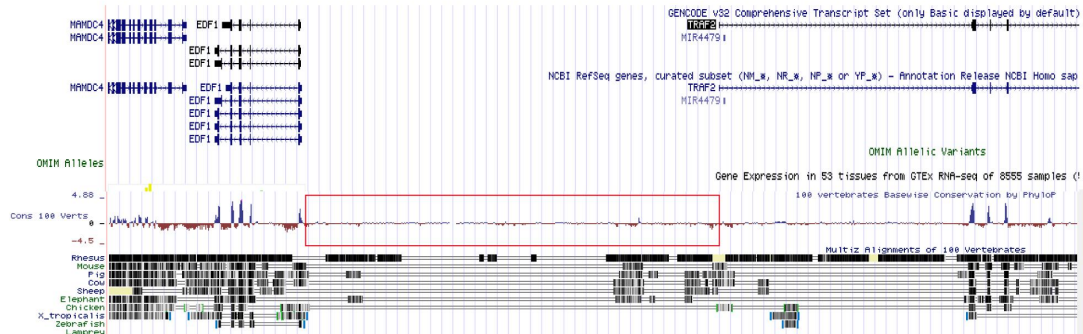
ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	27	31	58	739	100.0%	chr17	+	33333051	33333088	38
browser details	NORFA	24	486	510	739	100.0%	chr15	-	47689554	47689596	43
browser details	NORFA	23	512	535	739	100.0%	chr17	-	73451838	73451863	26
browser details	NORFA	20	141	160	739	100.0%	chr17	+	10198866	10198885	20
browser details	NORFA	20	35	56	739	95.5%	chr11	+	40930981	40931002	22

Mouse (mm10) BLAT Results

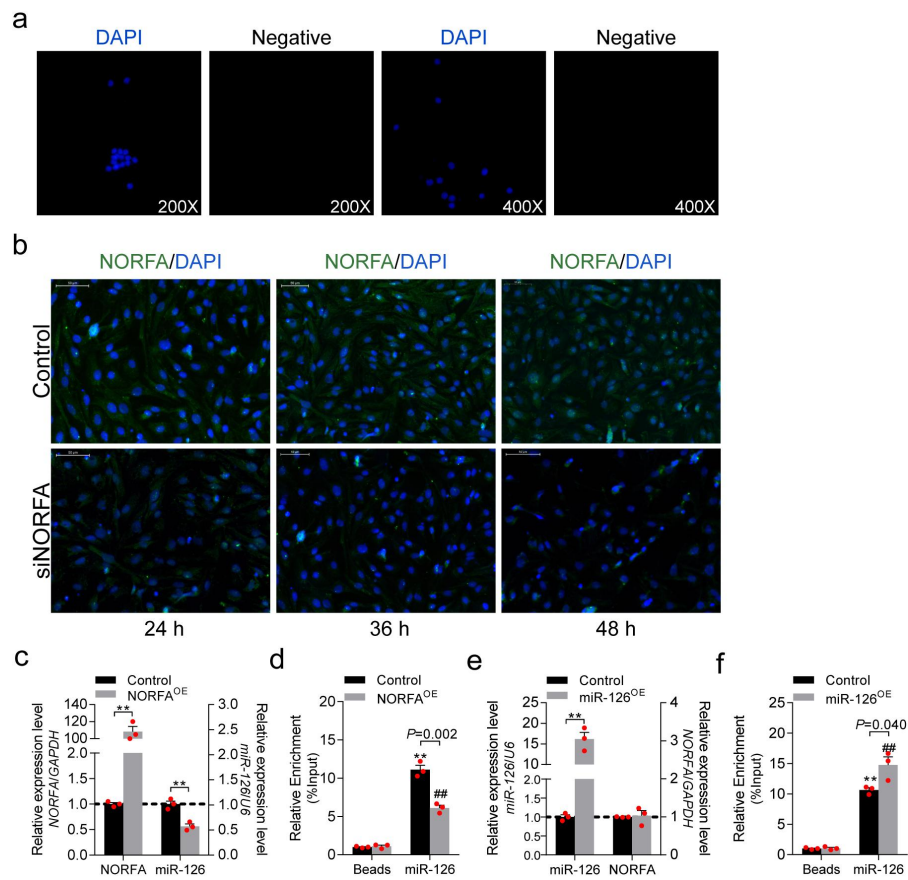
BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHROM	STRAND	START	END	SPAN
browser details	NORFA	28	499	539	739	93.8%	chr14	+	11448625	11448672	48
browser details	NORFA	25	504	539	739	81.5%	chr17	+	46612779	46612811	33
browser details	NORFA	25	633	658	739	100.0%	chr10	+	60738891	60738922	32
browser details	NORFA	24	310	334	739	100.0%	chr13	+	69969870	69969913	44
browser details	NORFA	23	359	382	739	100.0%	chr12	-	71995296	71995331	36
browser details	NORFA	21	223	243	739	100.0%	chr6	+	64452496	64452516	21
browser details	NORFA	21	47	69	739	95.7%	chr13	+	17404261	17404283	23

g



Supplementary Figure 2. Identification of the conservation of pig NORFA structure. (a) Diagram depicting the investigation strategy for pig NORFA conservation. (b) The secondary structure of pig NORFA was analyzed by RNAfold and RNAstructure software. H: helice, J: junction. (c) The conservation of NORFA secondary structure, diagram showing the conservation of H21 of pig NORFA by UCSC database among different species. (d) The tertiary structure and domains of pig NORFA were predicted and the conservation of these domains were detected using UCSC. (e) The potential ORFs within pig NORFA (sense and anti-sense) were predicted and their conservation were detected by UCSC. (f) The conservation of pig NORFA primary structure was detected. (g) The conservation of desert region between *EDF1* and *TRAF2* (red box) among different mammal species were detected.



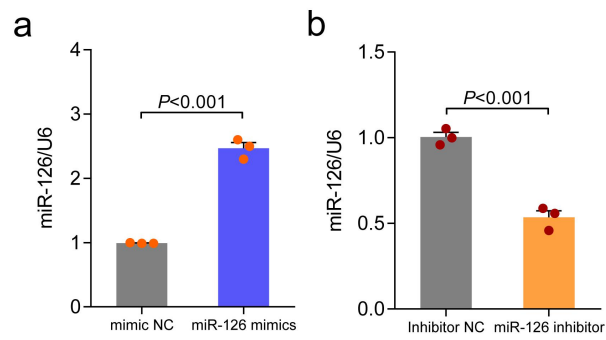
Supplementary Figure 3. NORFA physically interacts with miR-126 in granulosa cells. (a) The negative control for RNA FISH assays. (b) The signals of *NORFA* in porcine granulosa cells after transfection with *NORFA*-siRNA (*siNORFA*) for different time (24 h, 36 h and 48 h) were detected by FISH assays. (c) The expression levels of *NORFA* and miR-126 in *NORFA* overexpressed porcine granulosa cells were detected by qRT-PCR. (d) The enrichment of miR-126 on biotin-labeled *NORFA* in *NORFA* overexpressed porcine granulosa cells was detected by RNA pull-down. (e) The expression levels of miR-126 and *NORFA* in miR-126 overexpressed porcine granulosa cells were detected by qRT-PCR. (f) The enrichment of miR-126 on biotin-labeled *NORFA* in miR-126 overexpressed porcine granulosa cells was detected by RNA pull-down. Data in **c-f** are shown as mean \pm S.E.M. with three independent experiments. *P*-values were calculated by a two-tailed Student's *t*-test. **,###*P* < 0.01.

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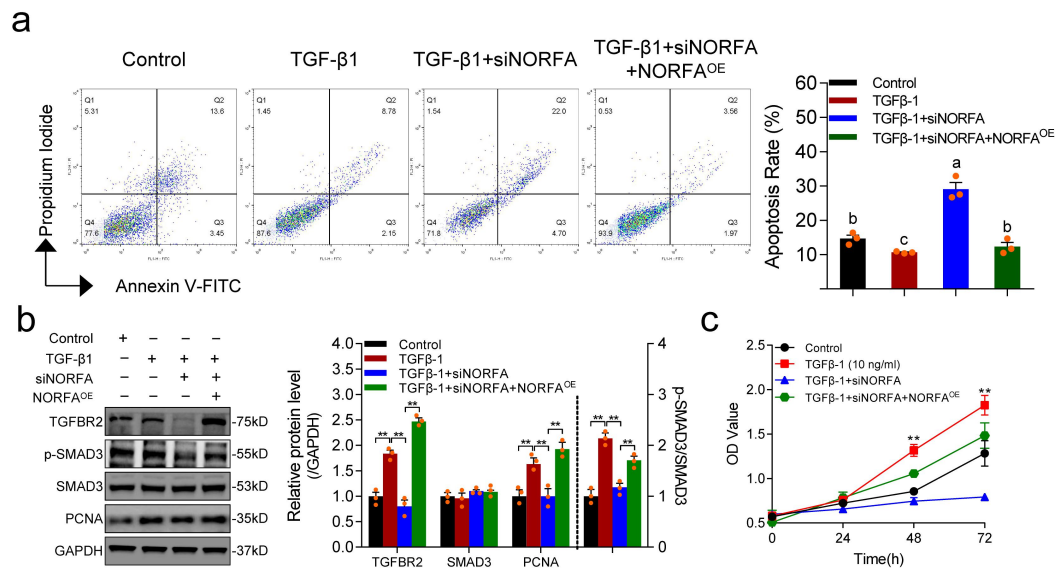
Homo sapiens .....CGCTGGCCGCGGRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCCGTCACGGCA 85
Sus scrofa .....CGCGGRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCTG..... 73
Mus musculus .....CGCTGGTCTGGRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCCACAGCA 86
Rattus norvegicus .....TGACRCRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCA..... 73
Ornithorhynchus anatinus GAAGCATCAGIGACAGCTGGCACTCCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTGGCAGCA 99
Bos taurus .....TGCGGRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCA..... 73
Cricetulus griseus .....CGGTCCRCRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCAGCAG... 80
Capra hircus .....GCTGGTCCGRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCAGCAG... 82
Gallus gallus .....GCTGGTCCGRCATTATTACTTTGGTACGGGCTGTGCACCT..TCAAACTCGTACCGTGAGTAATAATGCGCTCAGCAGCA 84
Taenopygia guttata ...GAGCCATTTTAACIGCTTCCCTTCATTATTACTTTGGTACGGGCTAGCCAGAC..TCAAACTCGTACCGTGAGTAATAATGCACTCTGGCAGIGG 97
*****

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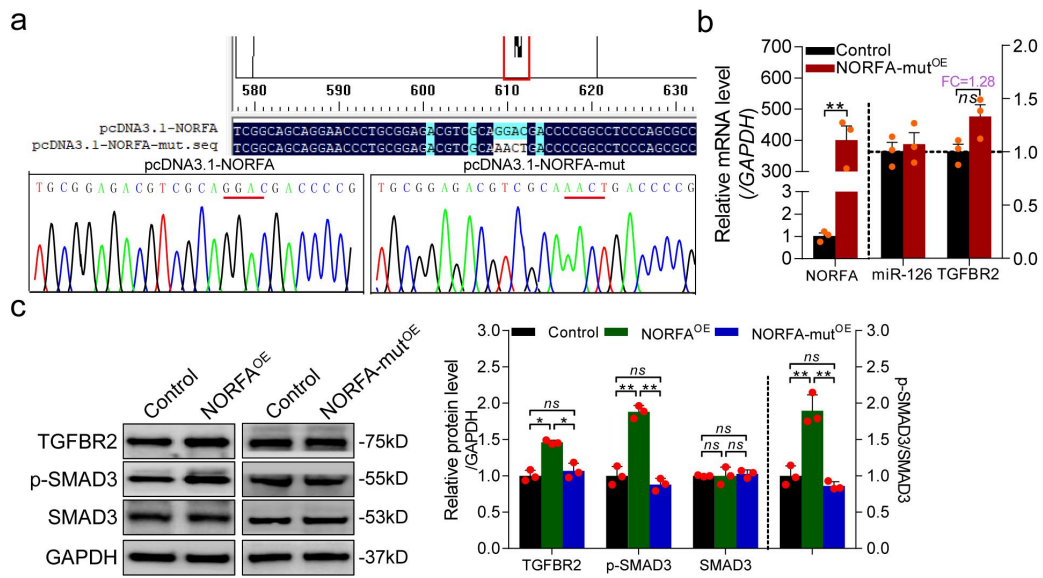
Supplementary Figure 4. Multiple-sequence alignment of pre-miR-126 from different species. The multiple-sequence alignment of pre-miR-126 from 10 different species were shown and asterisks in red indicate the sequence of mature sequence of miR-126.



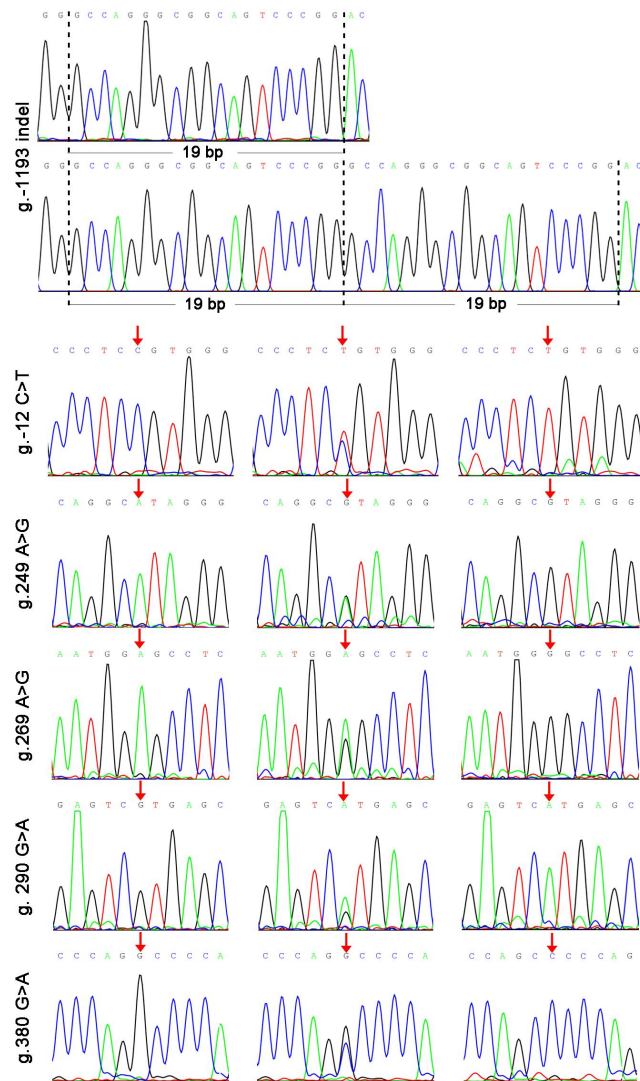
Supplementary Figure 5. Forced expression and silencing of miR-126 in porcine granulosa cells. (a) The expression levels of miR-126 were measured by qRT-PCR after porcine granulosa cells transfection with mimics NC (n=3) or miR-126 mimics (n=3). (b) qRT-PCR was performed and miR-126 expression levels were detected in porcine granulosa cells transfected with inhibitor NC (n=3) or miR-126 inhibitor (n=3). Data are shown as mean \pm S.E.M. by a two-tailed Student's *t*-test.



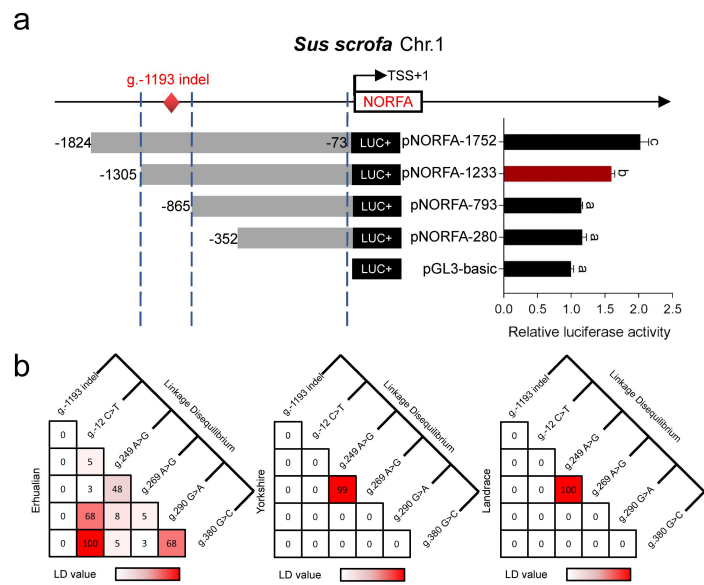
Supplementary Figure 6. NORFA affects the sensitive of porcine granulosa cells to TGF-β1. (a) The apoptosis rate of porcine granulosa cells treated with TGF-β1 and NORFA-siRNA (siNORFA) or/and pcDNA3.1-NORFA (NORFA^{OE}) were measured by FACS. (b) The protein levels of TGFB2, p-SMAD3, SMAD3 and PCNA in porcine granulosa cells treated with TGF-β1 and siNORFA or/and NORFA^{OE} were determined by western blotting and normalized to GAPDH. GAPDH was used as a loading control. (c) The proliferation levels of porcine granulosa cells treated with TGF-β1 and siNORFA or/and NORFA^{OE} were measured by CCK-8. Data are shown as mean ± S.E.M. with three independent experiments. *P*-values were calculated by a two-tailed Student's *t*-test. ***P* < 0.01.



Supplementary Figure 7. NORFA/miR-126/TGFBR2 axis regulates TGF- β signaling pathway in granulosa cells. (a) Construction of pcDNA3.1-NORFA-mut vector with miR-126 response element mutation. (b) The expression levels of NORFA, miR-126 and TGFBR2 in porcine granulosa cells transfected with pcDNA3.1-NORFA-mut vectors were measured by qRT-PCR. (c) The protein levels of TGFBR2 and p-SMAD3 in porcine granulosa cells treated with NORFA^{OE} or NORFA-mut^{OE} were detected by western blot. Data were shown as mean \pm SEM with three independent experiments. *P* values were calculated by using a two-tailed Student's *t*-test. **P*<0.05, ***P*<0.01 and ns indicates no significance.



Supplementary Figure 8. Identification of *NORFA* variants in Erhualian, Yorkshire and Landrace sow groups. A 19-bp duplication (g.-1193 indel) and 5 point variants (g.-12C>T, g.249A>G, g.269A>G, g.290G>A and g.380G>A) were identified within *NORFA*. Sanger sequencing traces for these variants were shown and their locations were indicated by red arrows.



Supplementary Figure 9. Characterization of the 19-bp duplication variant within *NORFA*. (a) Schematic showing the luciferase reporters containing different fragments of *NORFA* 5'-flanking sequences. The core promoter of *NORFA* was identified using dual-luciferase activity assay. The transcription start site (TSS) is indicated with black arrow and the 19-bp duplication is represented with red diamond. (b) The linkage disequilibrium (LD) analyses. The LD values of these six variants within *NORFA* from Erhuanlian, Yorkshire and Landrace sow groups were calculated by SHEsis software.

a

>The core promoter of pig *NORFA*[-1305~-865]

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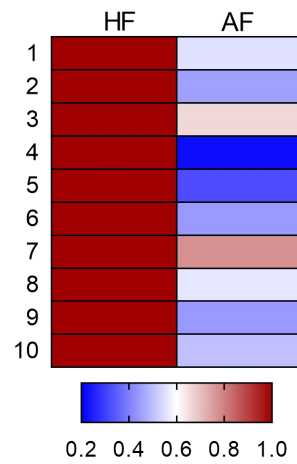
-1305 GGGTTTGTGA GTCCAAAGCA AGGCGGCGGC GCAAAGTCCC CACGGAGACC AGGTGCGCAG
      NRF1
      NFIX
      GCCAGGGCGGCAGTCCCGG
      g.-1193 indel
-1245 CTGTCTCGGC AGGACCTCGG CCCGGAGTCG CGGGCCAGGG CGGCAGTCCC GGACGCGGCC
      MYOD1 NFIX
-1185 GGCAGGGGGC GCCTGAGGAC CCGCCAGGCT CCGCATTGGG GTGGAGGGAA CCGCGGCCCC
      CTCG E2F6
-1125 CTGCCCGGGA GCAGCACCCG GGGGACGACA CAAGCACGCA AACGGGCGCT GGGCGAGGGG
      KLF4
-1065 ACGCACCTAA CGCGGGGCCA CCCGGAGAGA GACCTTCTCC ACTCAATCTT GAGACCCTAA
      ZNF354C
-1005 AACCTGCAGA GGGCGCAGGC TGTGCCCAGC GCCTGGGGGG CAGGGAGCGG GTCTGTGTGA
-1945 GGGACTGGCG GTTGGGGTTG CAAAGGCCCT GGGGCCAGGT CAGCTGGCGA TGGGAGGCGG
      NFIC TCF3
-1885 GACGCCAGGG CGGCCCGGC

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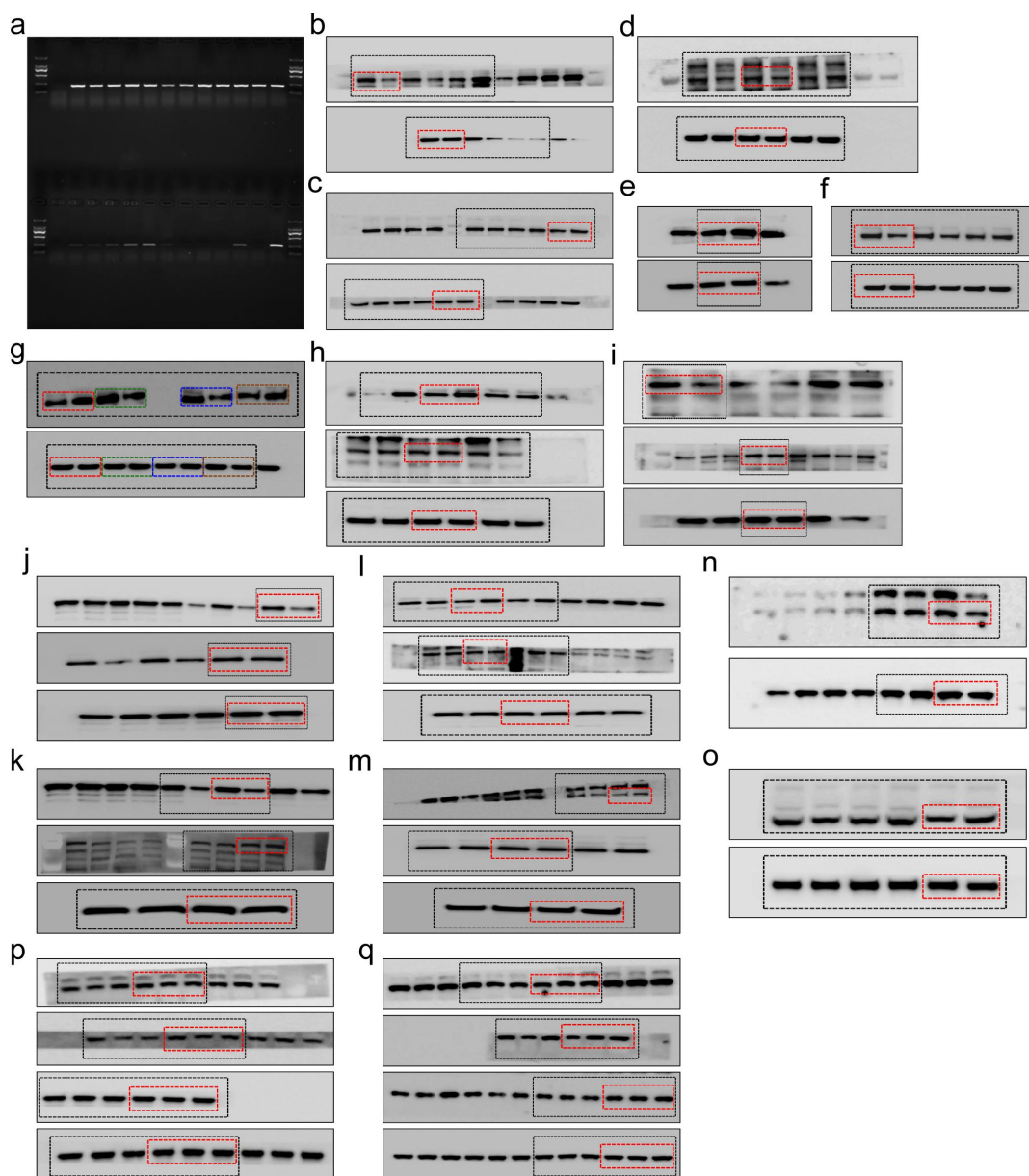
b

TF	del/del Location	ins/ins Location	Score
NFIX	-1215/-1206	-1234/-1225 -1215/-1206	10.687
E2F6	-1207/-1197	-1226/-1217 -1207/-1197	6.606
E2F4	-1208/-1198	-1228/-1217 -1208/-1198	6.584
PAX2	-1201/-1194	-1220/-1213 -1201/-1194	5.548
GABPA	-1206/-1195	-1225/-1214 -1206/-1195	5.396

Supplementary Figure 10. Characterization of the core promoter of porcine *NORFA*. (a) The core promoter sequence of *NORFA* containing 19-bp duplication was shown. The binding motifs of the potential transcription factors (TFs) were labeled with underlines. (b) The binding motifs of TFs within 19-bp duplication alleles were analyzed by JASPAR. 5 novel binding sites for NFIX, E2F6, E2F4, PAX2 and GABPA were identified, and their locations (red) with prediction scores were represented.



Supplementary Figure 11. NFIX is differentially expressed during follicular atresia. Heatmap showing the mRNA levels of NFIX in porcine granulosa cells from healthy follicles (HF) and atretic follicles (AF), analyzed by qRT-PCR (n=10). The expression levels of NFIX in AF were normalized to that in HF.



Supplementary Figure 12. The original images of gels and blots. (a) The original gel image for Figure1e. (b-q) The original blot images in the main figures of this manuscript. Figure6h (b), Figure6i (c), Figure7b (d), Figure7d (e), Figure7e (f), Figure8d-g (g), Figure8h (h), Figure8i (i), Figure8j (j), Figure8k (k), Figure8l (l), Figure8m (m), Figure9e (n, o), Figure10c (p) and Figure10d (q). The dotted rectangles in red, green, blue and brown indicated the representative images in the main text and the dotted rectangles in black showed the original images involved the corresponding experiments in this research.

Supplementary Tables

Supplementary Table 1 Oligonucleotide sequences used in this study

Name	Sequence (5' to 3')	Source
Mimics NC	UUGUACUACACAAAAGUACUG	This study
MiR-126	UCGUACCGUGAGUAAUAAUGCG	This study
Inhibitor NC	CAGUACUUUUGUGUAGUACAA	This study
MiR-126 inhibitor	CGCAUUUUUACUCACGGUACGA	This study
NC-siRNA	Sense: UUCUCCGAACGUGUCACGUTT Anti-Sense: ACGUGACACGUUCGGAGAATT	This study
TGFBR2-siRNA	Sense: GCCAACAAUCAACCACATT Anti-Sense: UGUGGUUGAUGUUGUUGGCTT	This study
NORFA-siRNA	Sense: CAGACAGAUGUGGAUGAAUTT Anti-Sense: AUUCAUCCACAUCUGUCUGTT	This study
NFIX-siRNA	Sense: CCAACCGUUUGUCAGCAUTT Anti-Sense: AUGCUGACAAACCGUUGGTT	This study

Supplementary Table 2. Primers designed for qRT-PCR

Genes	Primer sequence (5'-3')	Usage
<i>miR-126</i>	CCTGTTGTCTCCAGCCACAAAAGAGCACAAATATTCAGGAGAC AACAGGCGCATT	Reverse-transcription ¹
<i>miR-126</i>	F: CGGGCCACCACCTCCCCTGCAA R: CAGCCACAAAAGAGCACAAAT	qRT-PCR
<i>EGFL7</i>	F: TGCCAGACAGATGTGGATGAA R: TCCGCTGTTGTGGGGTTT	qRT-PCR
<i>AGPAT2</i>	F: CGCTCGTGCGTCATCATCT R: TCCAGCACCTCCACCTTGAT	qRT-PCR
<i>LCN12</i>	F: CGTTTCTTTCCCGTTCTGT R: CCTGAGTGATCCTCCCTGTGC	qRT-PCR
<i>C8G</i>	F: CGGACTACCGGAGCTTTGC R: AGCGTCGCAGAAGCCGTAC	qRT-PCR
<i>FBXW5</i>	F: CCAGAATCTCAACGCCAGCAC R: TGCCGCCCAGGTCAAAGA	qRT-PCR
<i>TRAF2</i>	F: AGCCCTTCTCGGCCAGA R: GTTCAGCACGCAGACGATGT	qRT-PCR
<i>EDF1</i>	F: CGAGCACTACAGTGGCGACTCAGAT R: GCTCCACTATGCTGGACAGGCAGT	qRT-PCR
<i>MAMDC4</i>	F: ACCGTTCCGGATGAGGACACA R: GACCCATGCAGATAGTGATAGAAGA	qRT-PCR
<i>PHPT1</i>	F: CCACGGGATTGGTCACAGA R: ACGGCGTGTA CTGAATCAG	qRT-PCR
<i>LCN8</i>	F: CGAGCAATACGCCATCCTG R: CCGTGTCTGCCGTC AACTC	qRT-PCR
<i>LCN5</i>	F: CTGGTACGAGATCGCCTTGG R: ACGATGGCGTAGGTCCTGTA	qRT-PCR
<i>LCN6</i>	F: GACCGCCCTTCTGGCTTTG R: GATGGTTCTGCGGCGTGAG	qRT-PCR
<i>LCN10</i>	F: TGTCAGGCGGCTCTGTGCTT R: CTGAAGAGCAGCAGCGTCTTG	qRT-PCR
<i>FAM69B</i>	F: TTCCGCAAAGGCATCATCTCA R: TGCCCTGCCAGAGCCCACT	qRT-PCR
<i>TMEM141</i>	F: ATCAGGCTGTCTCACGCTCTT R: CCGTCGCCTGTGATTGGTAG	qRT-PCR
<i>CCDC183</i>	F: CCAAGAACAAGGCGACGAT R: ACGCGGTCTGAAGACGTA CTT	qRT-PCR
<i>BAX</i>	F: CCGAAATGTTTGCTGACG R: AGCCGATCTCGAAGGAAGT	qRT-PCR
<i>BCL2</i>	F: TTCTTTGAGTTCGGTGGGG R: CCAGGAGAAATCAAATAGAGGC	qRT-PCR
<i>TGFBR2</i>	F: GTGCCAAGCAGGTCATTCA R: CTCCTCAGGGCTTCGGTCA	qRT-PCR
<i>GAPDH</i>	F: GATGGTGAAGGTCGGAGTG R: CGAAGTTGTCATGGATGACC	qRT-PCR
<i>U6</i>	F: TTATGGGTCCTAGCCTGAC R: CACTATTGCGGGTCTGC	qRT-PCR
<i>Linc-NORFA</i>	F: AGGAACCTGCGTGGGAATC R: CCGATCTCCAGCATGAAA	qRT-PCR
<i>Rplp0</i>	F: TCCAGGCTTAGGCATCACC R: GGCTCCCACTTTGTCTCCAG	qRT-PCR
<i>NFIX</i>	F: CGAGGAGCGAGCGGTGAA R: TGGCGAAGGCAGTCAATCC	qRT-PCR

¹. Stem-loop reverse-transcriptional primers designed for detect the expression level of mature miRNAs.
F: Forward primers; R: Reverse primers.

Supplementary Table 3. Primers used for plasmids construction

Plasmids	Primer sequence (5'-3')	Vector	Usage
NORFA-MRE-wt	F: CCTGGGAAGCAAGACTTTGTC	<i>pmirGLO</i>	vector
	R: GGAGGCTGAGTTGCCACA		construction
NORFA-MRE1-mut	F: AAAATGTGTTTGGTATGAGCGCGCTGAGATTGGCAGTCC	<i>pmirGLO</i>	Mutation
	R: GGGGGCGGAGCGCTGGGGACAGGGAGCTTGCCAAGG		
NORFA-MRE2-mut	F: AGGAACCTTTGGAGGTGGTGTATTGTTGCCGCCCTC	<i>pmirGLO</i>	Mutation
	R: GCTGCCGAGGGGAGCTTCACCTGCAGCACTGCACCCCT		
TGFBR2-MRE-wt	F: TGACCTATAGGACTTGCTCGGA	<i>pmirGLO</i>	vector
	R: CACCTTCACTGTGTGCTAAAATT		construction
TGFBR2-MRE-mut	F: TCTCTGATGCTTCTCCGCGCGGATTGGGACCGTGCAAT	<i>pmirGLO</i>	Mutation
	R: AACCCAACATGAGAGACCATCTATGACATAACTGGTCTGAA		
pNORFA-1752	F: CGGGGTACCGGTCGTCATGGAATATGCTCG	<i>pGL3-basic</i>	
	R: CCGCTCGAGCCTCCAATACGATCTACTTCCTG		
pNORFA-1233	F: CGGGGTACCGGTTTGTGAGTCCAAAGCAA	<i>pGL3-basic</i>	
	R: CCGCTCGAGCCTCCAATACGATCTACTTCCTG		
pNORFA-793	F: CGGGGTACCACCTGTAATCCTGCTGGTGAGA	<i>pGL3-basic</i>	vector
	R: CCGCTCGAGCCTCCAATACGATCTACTTCCTG		construction
pNORFA-280	F: CGGGGTACCCAGCATCGCGTCGCTTTT	<i>pGL3-basic</i>	
	R: CCGCTCGAGCCTCCAATACGATCTACTTCCTG		
pcDNA3.1-NFIX	F: GCCCCCAACTCACAACCTCTG	<i>pcDNA3.1</i>	
	R: GGGGATTTTTCCACGTCTCAA		

F: Forward primers; R: Reverse primers.

Supplementary Table 4. Primers used for CHIP assay

Primers	Sequence (5'-3')	Temp	Product size
NORFA	F: GCAAAGTCCCCACGGAGACCA	62 °C	139 bp for A1/A1
	R: AGCCTGGCGGGTCCTCAGGC		120 bp for A2/A2
SBEX	F:CAGCAAAGGGTGGCAAGGT	60 °C	145 bp
	R:ATGCCTGTGCCACTTTCAACT		

Supplementary Table 5. Primers used for NORFA polymorphism detection

Primers	Sequence (5'-3')	Annealing temp	Product size
NORFA-P1	F: TGGTCCAGGAGGGCAAGC R: CCCCGTTTGCGTGCTTGT	62 °C	637 bp
NORFA-P2	F: GGGTTTGTGAGTCAAAGCAAG R: GGTTTCCACGTCCCTCGGTAT	60 °C	796 bp
NORFA-P3	F: TTCCAGAGCCTCAAAGTGA R: CCTTTGGGAGACCAGCACA	62 °C	730 bp
NORFA-P4	F: GCAGGAAGTAGATCGTATTGGG R: GGGATTCCCACGCAGGT	62 °C	630 bp
NORFA-P5	F: CGTAGGGAGCAGCTAATGGG R: CCAGCTCTAACGGACCTAAACG	62 °C	840 bp
NORFA-P6	F: CCTGGGAAGCAAGACTTTGTC R: GCAGGCTTTGAAGTTCTGTGATT	61 °C	539 bp

Supplementary Methods

FACS analysis

The apoptosis rate of porcine granulosa cells were assessed by FACS, as described in the methods with Annexin V-FITC and PI dyes. For gating strategy, cells without dye label and two single dye label were respectively used to detect the FSC/SSC gates, which is shown in Reference 24. Q1 mainly includes the dead cells, Q2 includes the late apoptotic cells, Q3 mainly includes early apoptotic cells, and Q4 mainly includes healthy cells. Besides, the right part of FSC gating (Q2+Q3) was considered as positive apoptotic cells.