

Supplementary Materials

Supplementary Table 1. Detail of primers for bisulfite sequencing

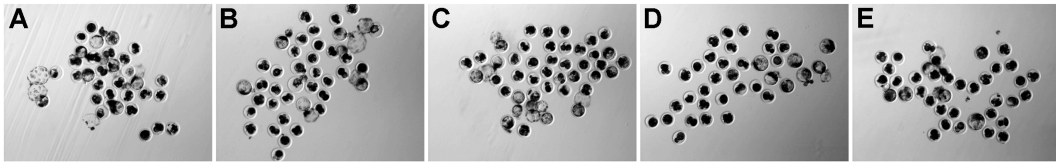
Gene	Primer sequence (5'-3')	Length (bp)	Accession number
CenRep	F: GGTATTGTTGTTTGTGGTGATT R: AAAATTTATTCCTCAAACCCAATTT	231	Z75640
	Outer		
Thy1	F: GGTAGGGAGGTTATGGAAGTTA R: TAAATTCATTTACATTATAATACAACC	497	NC_010451
	Inner		
Oct4	F: GGAAAGGTTTTGGTTTTAAGG R: TCCAAAACCTCTTAACATCCTACA	395	NC_010449
	Outer		
Oct4	F: ATTAGATTTGTGTGAGGATTTGAGAG R: AAAACCCAATAAAAACCAAAACTCTC	409	NC_010449
	Inner		
Igf2/H19	F: GTGTATAGAGTAGTGGAGAGGG R: CCCAATCCCACCCACTAA	249	AY044827
	Outer		
Igf2/H19	F: GGTTTTAGGGGGATATTTTTT R: TTAAAAAACATTACTIONCATATAC	384	AY044827
	Inner		
Igf2/H19	F: GATTTTTAGGTTTGTATTATTT R: CAAATATTCAATAAAAAAACC	208	AY044827
	Outer		

Note: primers for CenRep or Igf2/H19 were from published papers [1, 2].

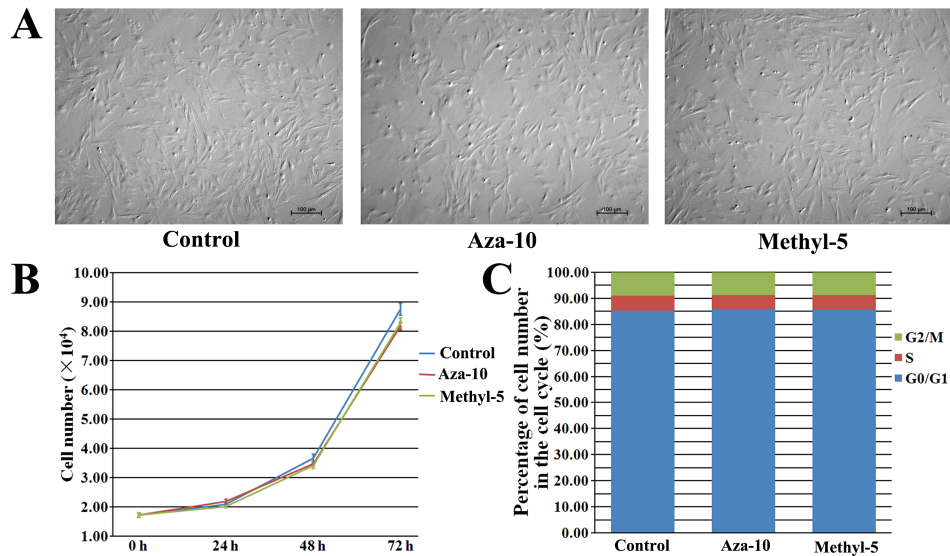
Supplementary Table 2. Detail of primers for quantitative real-time PCR

Gene	Primer sequence (5'-3')	Length (bp)	Accession number
<i>Oct4</i>	F: GAAGGTGTTTCAGCCAAACGAC	185	NM_001113060
	R: CGATACTTGTCCGCTTTC		
<i>Nanog</i>	F: CCTCCATGGATCTGCTTATTC	209	NM_001129971
	R: CATCTGCTGGAGGCTGAGGT		
<i>Sox2</i>	F: AACCAGAAGAACAGCCCAGAC	155	NM_001123197
	R: TCCGACAAAAGTTTCCACTCG		
<i>Dnmt1</i>	F: GCGTCTTGCAGGCTGGTCAGTA	152	NM_001032355
	R: CTTCTTATCATCGACCACGACGCT		
<i>Dnmt3a</i>	F: ATGTGGTTCGGAGACGGCAAGT	195	NM_001097437
	R: GCTCTCGTCGTTGTCATGGCA		
<i>Igf2</i>	F: CCGTGGCATCGTGGAAGAGTG	170	NM_213883
	R: TCCAGGTGTCATAGCGGAAGAAC		
<i>Thy1</i>	F: AACCTACCATTGGCATCGCT	143	NM_001146129
	R: TGAATGGGCAGGTTGGTGGT		
<i>Col5a2</i>	F: AGATGTACTIONAACAGGGACATTTG	124	NM_001105289
	R: GTTATGGGGTCAGCACATTCAAGC		
<i>Eif1a</i>	F: AGATGAGGCTAGAAGTCTGAAGGC	113	NM_001243218
	R: CAATGTCATCAAACACTGGATTCATC		
<i>ATP1b1</i>	F: CCACCAGGATTAACACAGATTCC	185	NM_001001542
	R: TCTTTGAGTTCGCTGGGCAC		
<i>Cdx2</i>	F: GACAAGGACGTGAGCATGTATCC	220	XM_003130908
	R: CGTAGCCGTTCCAGTCCTCG		

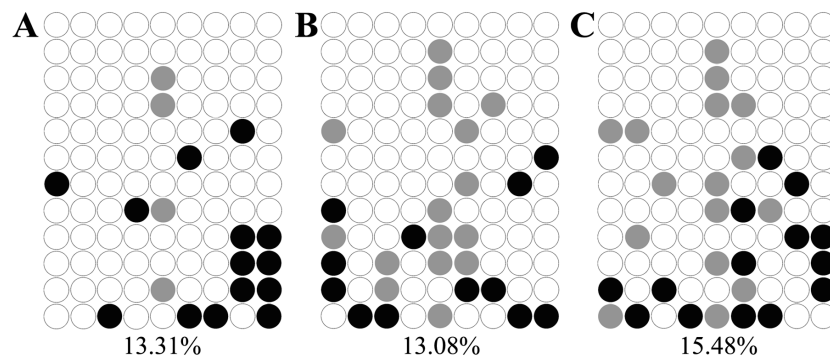
<i>Bax</i>	F: CAGTAACATGGAGCTGCAGAGG R: GCCTTGAGCACCAGTTTACTGG	159	AJ_606301
<i>Bcl2l1</i>	F: CTGGTGGTTGACTTTCTCTCCTAC R: GTTCCGCTTCTGATTCAGTCC	119	NM_214285
<i>β2m</i>	F: CTTTCTACCTTCTGGTCCACACTG R: GTGGTCTCGATCCCACTTAACTATC	116	NM_213978
<i>18s</i>	F: AATCTCGGGTGGCTGAACGC R: CCGTTCTTAGTTGGTGGAGCGAT	143	NR_002170



Supplementary Fig. 1. Cloned blastocysts ($\times 40$) derived from untreated PFFs (A), PFFs treated with 10 nM 5-aza-dC (B) or PFFs treated with 1 uM (C), 2 uM (D) or 5 uM (E) 5-methyl-dCTP.

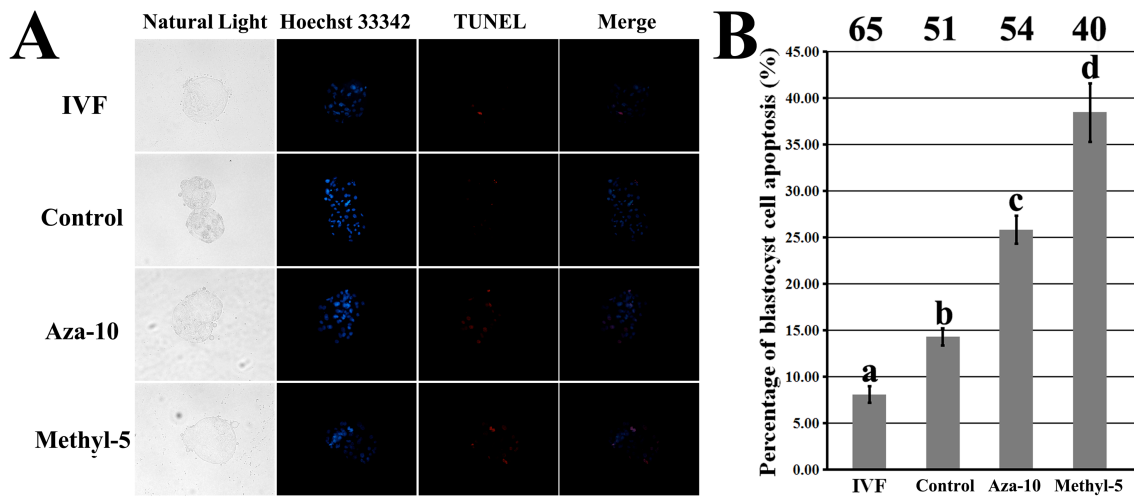


Supplementary Fig. 2. Cell morphology (A), cell proliferation (B) and cell cycle (C) of donor cells after treatment with 10 nM 5-aza-dC (aza-10) or 5 uM 5-methyl-dCTP (methyl-5).



Supplementary Fig. 3. Methylation status of the *CenRep* region in cloned blastocysts of the control (A), aza-10 (B) or methyl-5 (C) group. Black or white circles represent methylated or unmethylated CpG sites, and gray circles represent mutated and/or single nucleotide polymorphism (SNP) variation

at certain CpG sites.



Supplementary Fig. 4. Blastocyst cell apoptosis after 5-aza-dC (aza-10) or 5-methyl-dCTP (methyl-5) treatment. A, the status of blastocyst cell apoptosis in the IVF, control, aza-10 or methyl-10 group; B, the percentage of blastocyst cell apoptosis in the IVF, control, aza-10 or methyl-10 group.

The images of blastocyst cell apoptosis were magnified (200×).

The number of blastocysts detected are indicated at the top of the column chart.

^{a-d}Percentages (% ± SEM) in columns with different superscripts differed significantly ($P < 0.05$).

References

1. **Park CH, Kim HS, Lee SG, and Lee CK.** Methylation status of differentially methylated regions at *Igf2/H19* locus in porcine gametes and preimplantation embryos. *Genomics* 2009; 93: 179-186.
2. **Zhao MT, Rivera RM, and Prather RS.** Locus-specific DNA methylation reprogramming during early porcine embryogenesis. *Biol Reprod* 2013; 88: 48.