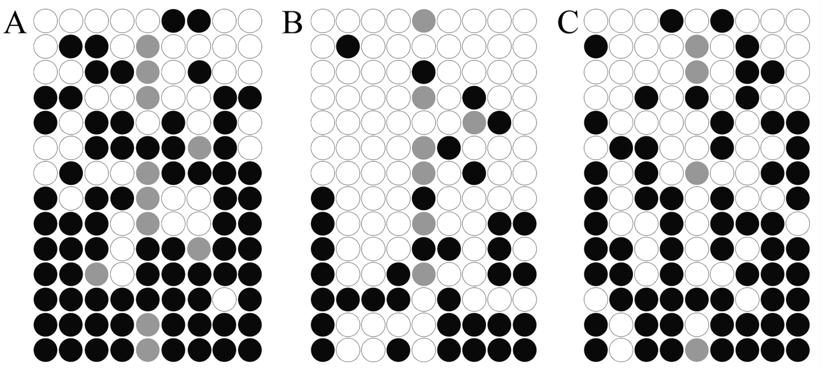
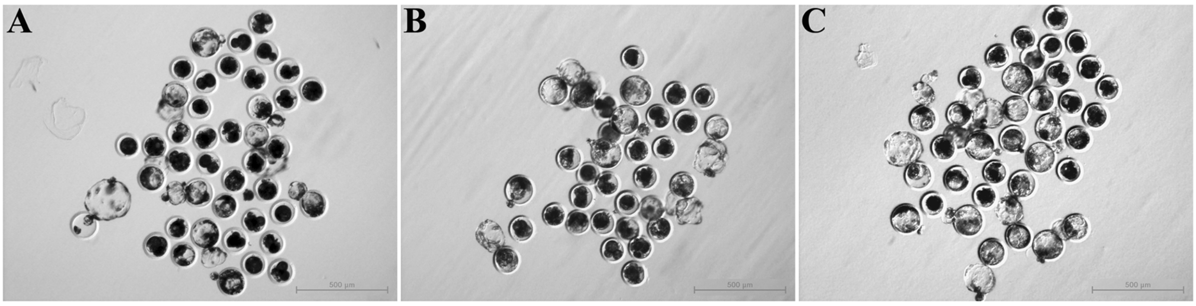
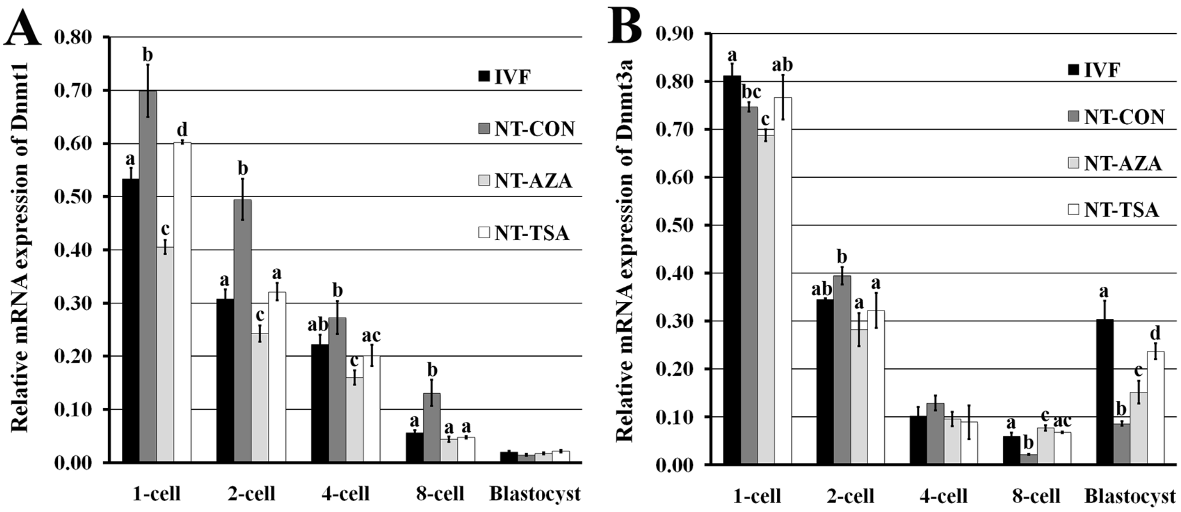


Supplementary Fig. 1. CenRep methylation status in sperm (A), oocytes (B) and PFFs (C).

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. 2. Blastocysts derived from cloned embryos that were untreated (A), treated with 25 nM 5-aza-dC (B) or treated with 40 nM TSA (C).



Supplementary Fig. 3. Relative mRNA expression of Dnmt1 (A) and Dnmt3a (B) in IVF, NT-CON, NT-AZA and NT-TSA embryos.

The transcript abundance in MII oocytes was considered the control.

The data are expressed as means ± SEM.

$^{a\text{-}d}$ Values for a given gene at a certain stage in columns with different superscripts differ significantly ($p < 0.05$).