

Supplementary material

Table S1. Semen quality of high and low cleavage rate group (*GAPDH* normalised semen samples)

a,bValues with different letters within the same column are significantly different ($P < 0.05$)

Group	Semen concentration ($\times 10^9$ cells/mL)	Motility (% \pm SEM)
High cleavage group ($n = 3$)	6.82 ± 0.57^a	$80.90 \pm 1.55 \%^a$
Low cleavage group ($n = 3$)	4.53 ± 1.15^b	$81.57 \pm 0.50 \%^a$

Table S2. Development of *in vitro*-cultured porcine embryos fertilized with semen samples whose mRNA quantity was normalised by *GAPDH*

†Embryos developed to the 2-4 cell stage during 2 days incubation after insemination were considered cleaved embryos

*Percentage of blastocysts relative to cleaved embryos

a,bValues with different letters within the same column are significantly different ($P < 0.05$)

Group	No. of embryos cultured	No. of embryos cleaved† (% \pm SEM)	No. of blastocysts (% \pm SEM)	Blastocysts / cleaved embryos* (% \pm SEM)
High cleavage group ($n = 3$)	398	328 ($82.29 \pm 5.94\%^a$)	134 ($33.46 \pm 7.72\%^a$)	$40.37 \pm 7.00\%^a$
Low cleavage group ($n = 3$)	283	163 ($61.76 \pm 13.28\%^b$)	34 ($15.52 \pm 10.55\%^b$)	$23.22 \pm 14.00\%^a$

Fig. S1. Quantitative analysis of MYC, CYP19, ADAM2, PRM1, and PRM2 from porcine spermatozoa of the two groups that differed in cleavage rate.

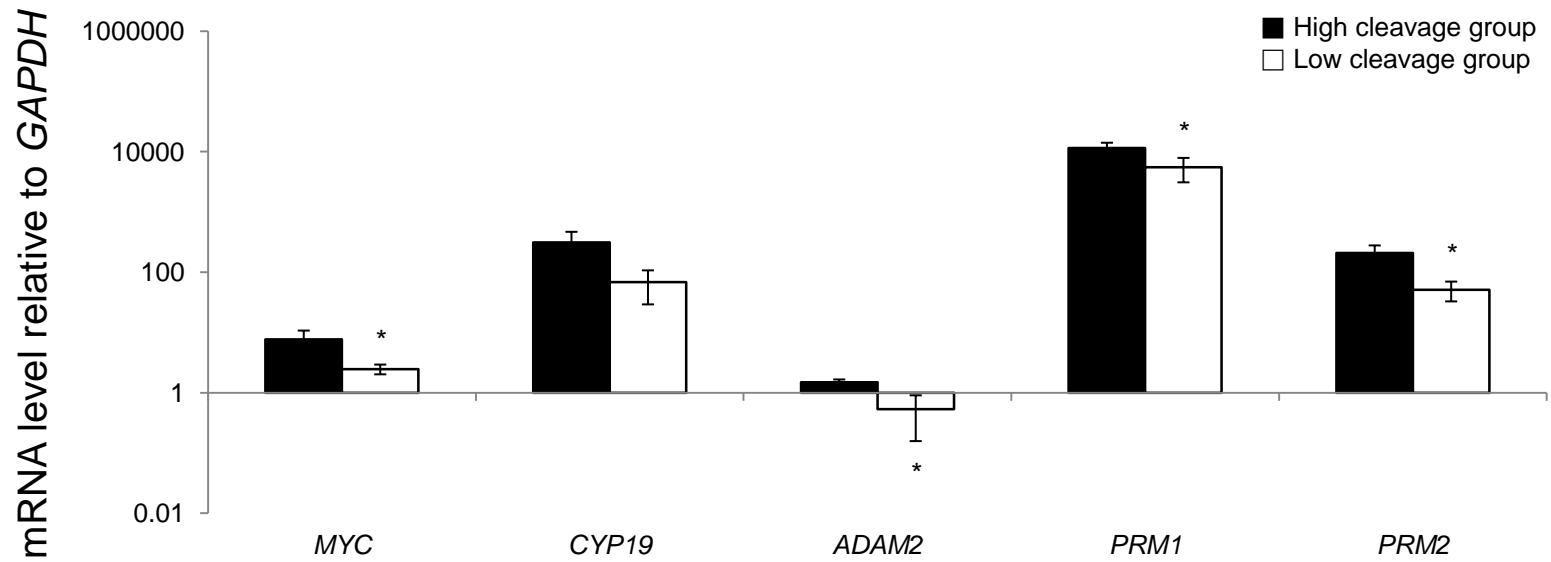


Fig. S2. Comparison of the changes in the amounts of mRNA coding for the selected genes in porcine spermatozoa after capacitation between the two groups that differed in cleavage results.

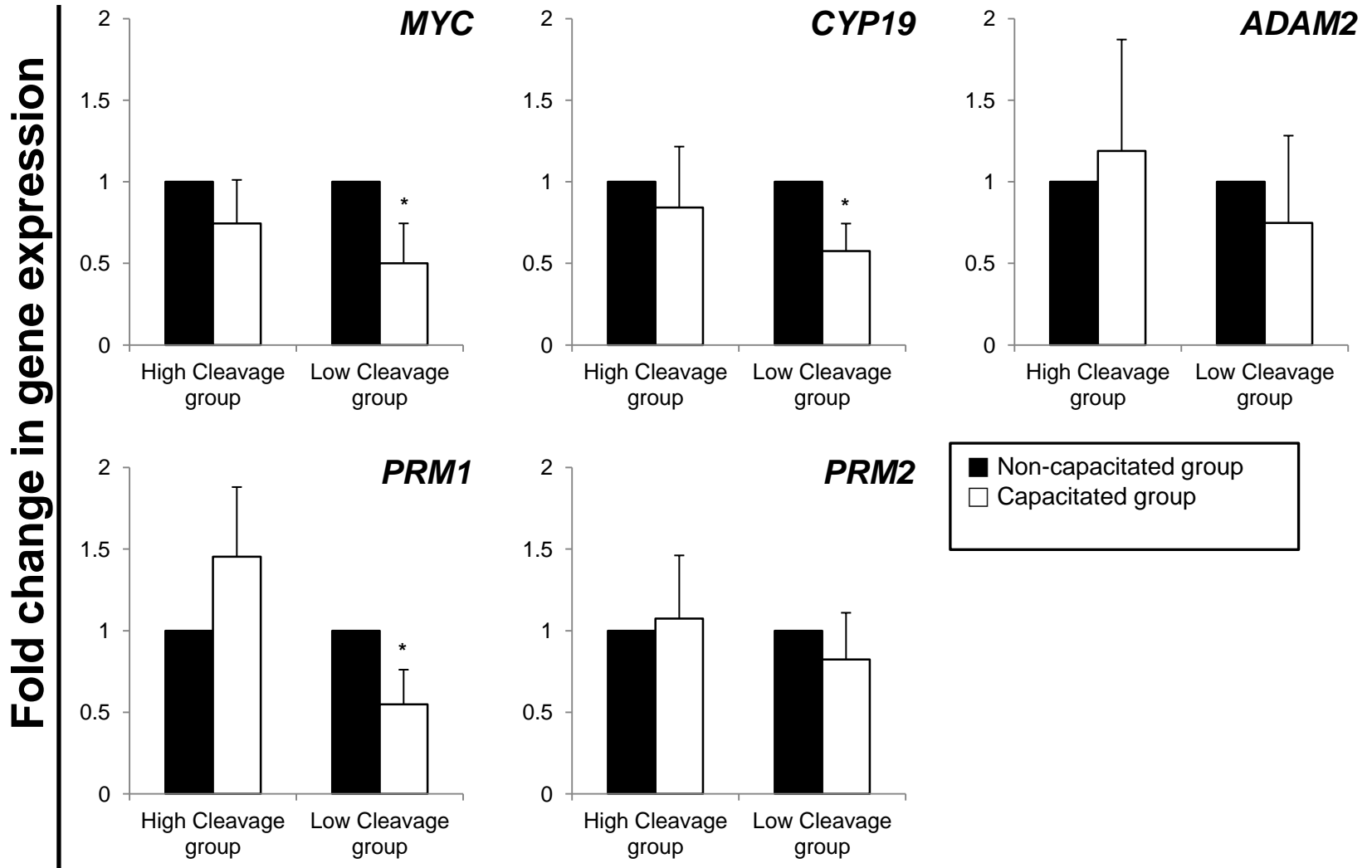


Fig. S3. Correlation analysis between mRNA abundance of 5 genes and cleavage rate of *in vitro* fertilised embryo

