Supplemental Table 1. Primer sequences of the q-PCR experiments

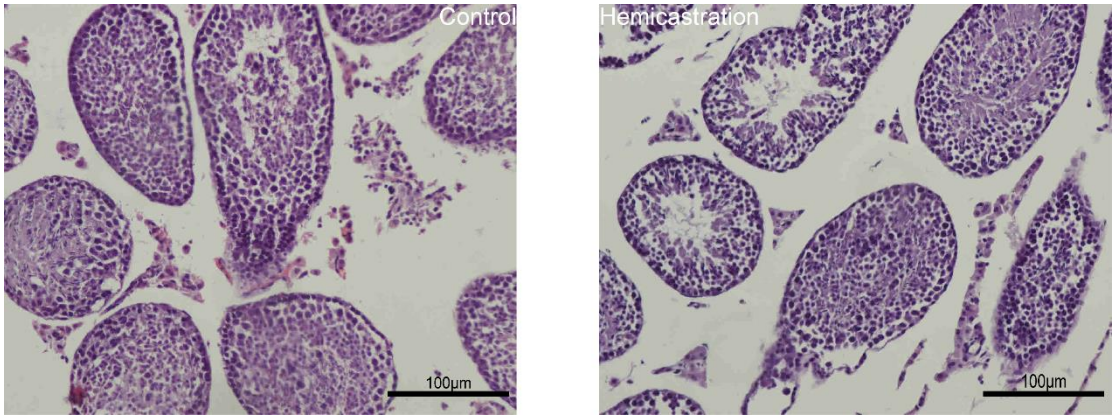
Gene symbol	Primer sequences (5'-3')	Tm (°C)	Product length (bp)
SYCP1	F:AACCCCCAAACAGACTCCTT	59	91
	R:TGTCCAACGGTCCTCTCTCA		
PTGS1	F:GATTGGTGGAGGTAGGAACTTTGA	60	73
	R:CTCTCGGGACTCCTTGATGACA		
PTGS2	F:AATCCTTGCTGTTCCAATCCAT	59	64
	R:ACTGGTCAAATCCTGTGCTCATAC		
PTGES	F:TCCAGTATTACAGGAGTGACCCAG	60	91
	R:CCGAGGAAGAGGAAAGGATAGATT		
EEF2	F:AAAAAACTTCCCCGCACCTTCT	61	96
	R:CTTGGCTGTCTCCTCCTTCCTG		
PPIA	F:ACCAAACACAAACGGTTCCCAG	60	96
	R:ATGCCTTCTTTCACCTTCCCAA		
β-*ACTIN*	F:TCCAGCCTTCCTTCTTGGGTAT	60	91
	R:TCTTTACGGATGTCAACGTCACA		

Supplemental Table 2. Summary of reduced representation bisulfite sequencing read alignment to the reference genome

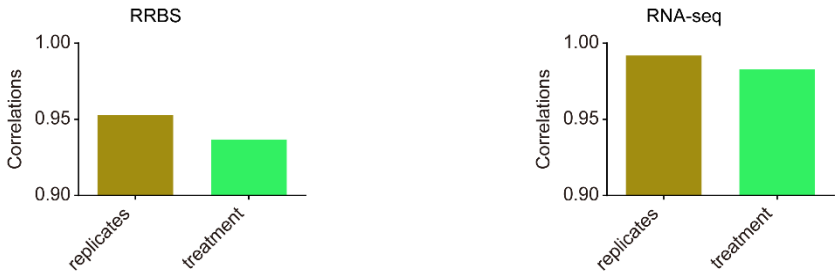
Individual	Read leghth (bp）	Clean data	GC (%)	Aligned (%)	Unique (%)
Control 1	100	52,392,308	32.72	83.96	67.05
Control 2	100	55,624,298	32.22	86.53	67.83
Control 3	100	45,291,032	32.62	83.85	66.45
Hemicastration 1	100	52,549,728	31.54	85.41	67.85
Hemicastration 2	100	47,571,928	32.33	83.55	66.72
Hemicastration 3	100	56,508,314	33.01	82.60	65.30

Supplemental Table 3. Summary of RNA sequencing read alignment to the reference genome

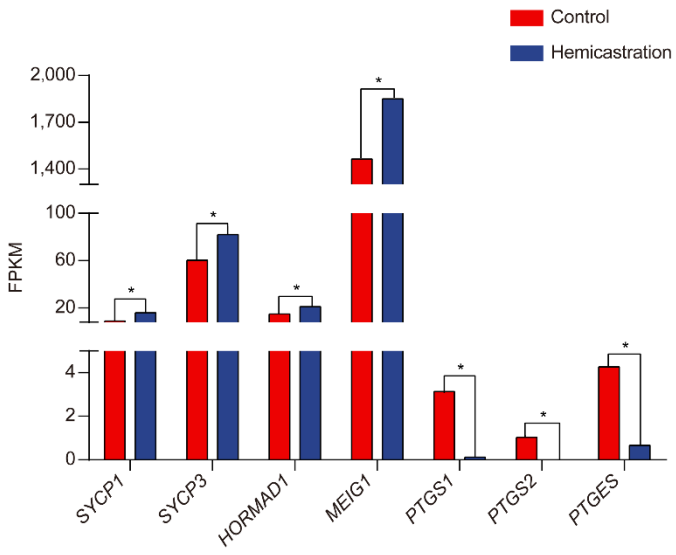
Individual	Raw datas	Clean datas	Raw bases(G)	Clean bases (G)	Q20 (%)	GC (%)	Aligned (%)
Control 1	27,012,852	26,666,541	6.75	6.67	95.16	50.81	87.4
Control 2	22,662,951	22,396,332	5.67	5.6	95.21	50.74	88.2
Hemicastration 1	19,702,382	19,436,926	4.93	4.86	95.66	50.72	87.3
Hemicastration 2	22,284,017	21,970,907	5.57	5.49	95.37	50.31	87.9



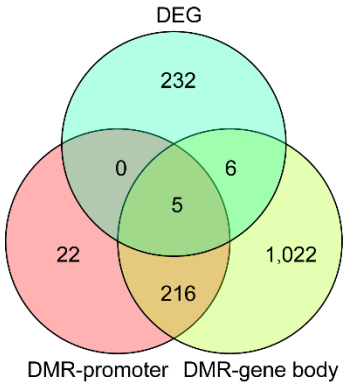
Supplemental Figure S1. Hematoxylin & Eosin (H&E) staining of paraffin sections of right testis from 72 days-old control (left) and hemicastrated (right) mice. Scale bar: 100 µm



Supplemental Figure S2. Comparison of pairwise Pearson's correlation for DMR methylation profiles (left) and gene expression profiles (right) between samples. The correlation between every two samples was calculated by methylation level values and FPKM gene expression values, respectively. Then, these correlation rates were grouped into the following categories: biological replicates (n = 6 for RRBS and n =2 for RNA-seq), the treatment (n = 9 for RRBS and n = 4 for RNA-seq).



Supplemental Figure S3. Fragments per kilobase of transcript per million mapped reads (FPKM) value of typical genes in enrichment analysis of genes that were upregulated and downregulated after hemicastration (*$p < 0.05$).



Supplemental Figure S4. Overlap among differentially expressed genes (DEGs), genes with a differentially methylated region (DMR) in their promoter, and genes with a DMR in their gene body.