

## Supporting Information

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HSF5 Deficiency Causes Male Infertility Involving Spermatogenic Arrest at Meiotic Prophase I in Humans and Mice

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## Supplementary information

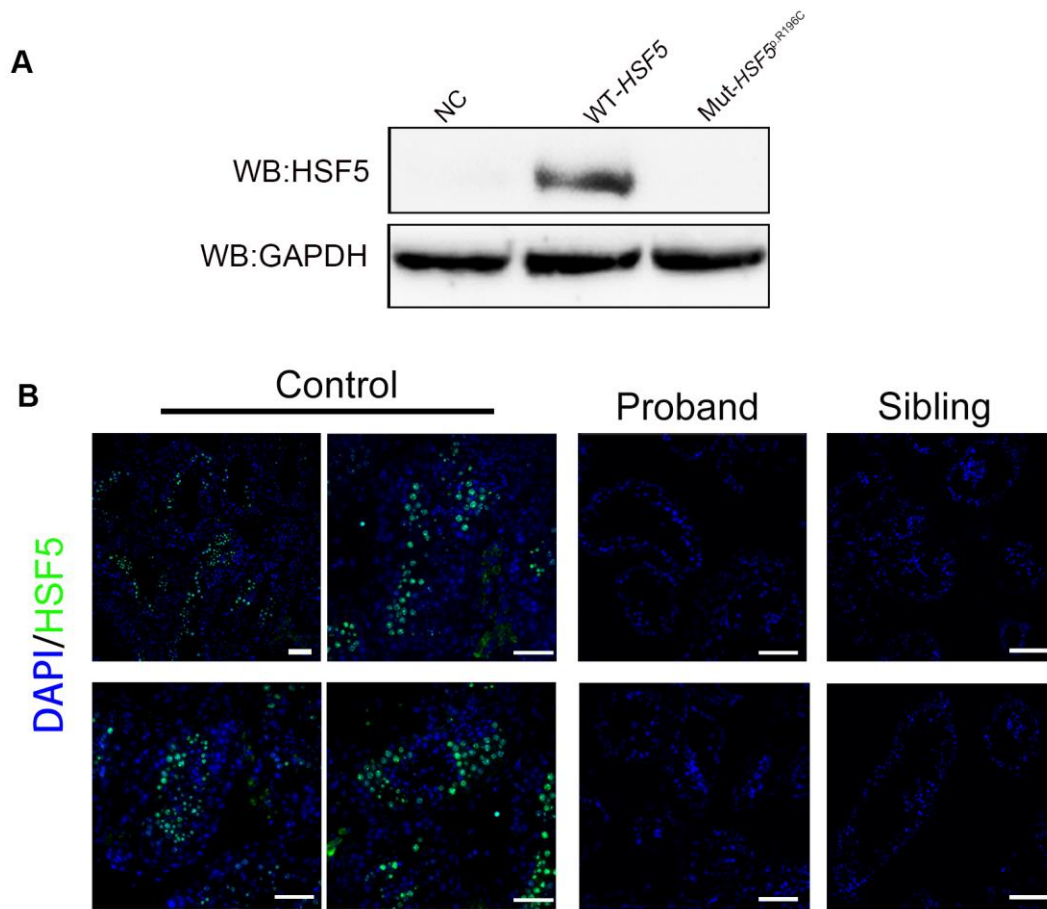


Figure S1. Expression analysis of the *HSF5*<sup>R196C</sup> variant. A) Western blotting analysis detected no HSF5 expression in the cells transfected with the mut-*HSF5*<sup>R196C</sup> plasmid. Three independent experiments were performed. B) Absent expression of HSF5 was observed in the testes from patients by immunofluorescence staining. Three independent experiments were performed (Blue, DAPI; green, HSF5; scale bars, 100  $\mu$ m).

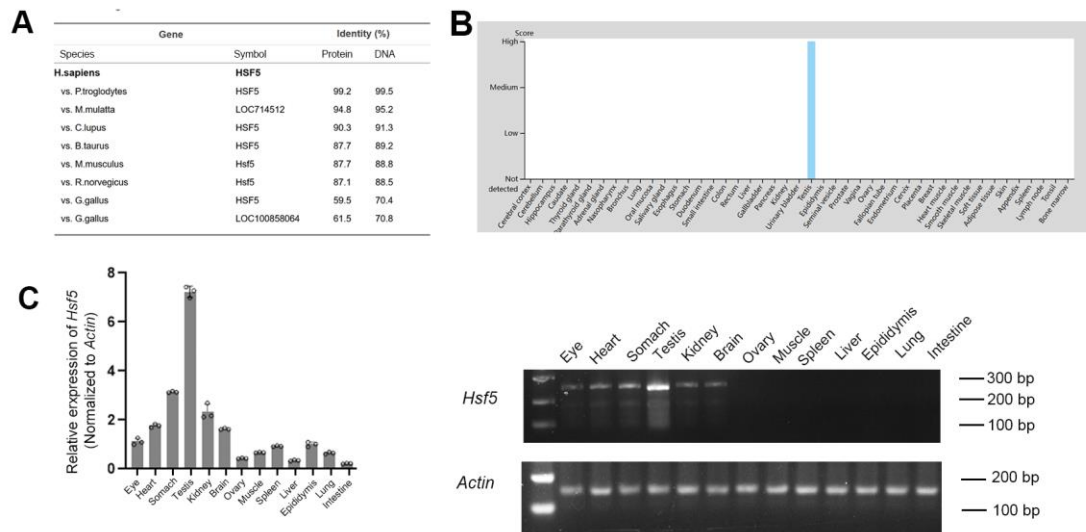


Figure S2. The tissue-specific expression pattern of HSF5/*Hsf5*. A) Homology of *HSF5*/HSF5 among different species ([https://www.ncbi.nlm.nih.gov/homologene?cmd=Retrieve&dopt=AlignmentScores&list\\_uids=52701](https://www.ncbi.nlm.nih.gov/homologene?cmd=Retrieve&dopt=AlignmentScores&list_uids=52701)). B) The relative expression level of HSF5 in different human tissues (<https://www.proteinatlas.org/ENSG00000176160-HSF5/tissue>). C) qPCR revealed that *Hsf5* is predominantly expressed in the mouse testes (N = 3 biologically independent WT mice; error bars, mean  $\pm$  SEM).

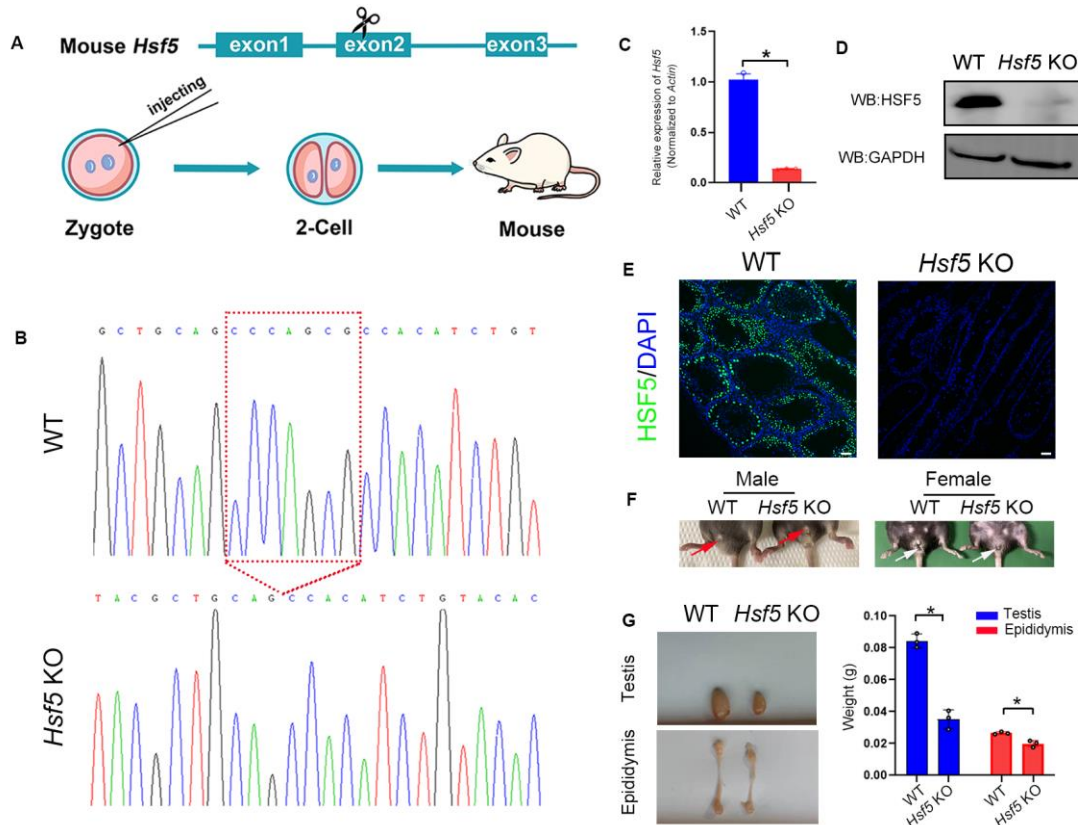


Figure S3. Targeted inactivation of *Hsf5* in mice. A) Schematic illustration of the targeting strategy for generating *Hsf5* KO mice. B) Results of PCR-seq genotyping using tail DNA from *Hsf5* KO mice. The red line designates the deleted bases in the KO mice. C) qPCR analysis of *Hsf5* expression in WT and *Hsf5* KO mouse testes (N = 3 biologically independent WT mice and KO mice; two-sided Student's *t* test; \*  $P < 0.05$ ; error bars, mean  $\pm$  SEM). D) Western blotting showed the absence of HSF5 in *Hsf5* KO testes (N = 3 biologically independent WT mice and KO mice). E) Immunofluorescence staining of HSF5 in testis sections from WT and *Hsf5* KO mice (N = 3 biologically independent WT mice and KO mice; scale bars, 50  $\mu$ m). F) Representative photographs of the reproductive organs of WT mice and KO mice. The red arrows indicate the penises, and the white arrows indicate the female reproductive organs (N = 3 biologically independent WT mice and KO mice). G) Dramatic size reduction in testes

and epididymides from the adult *Hsf5* KO mice (N = 3 biologically independent WT mice and KO mice; two-sided Student's *t* test; \*  $P < 0.05$ ; error bars, mean  $\pm$  SEM).

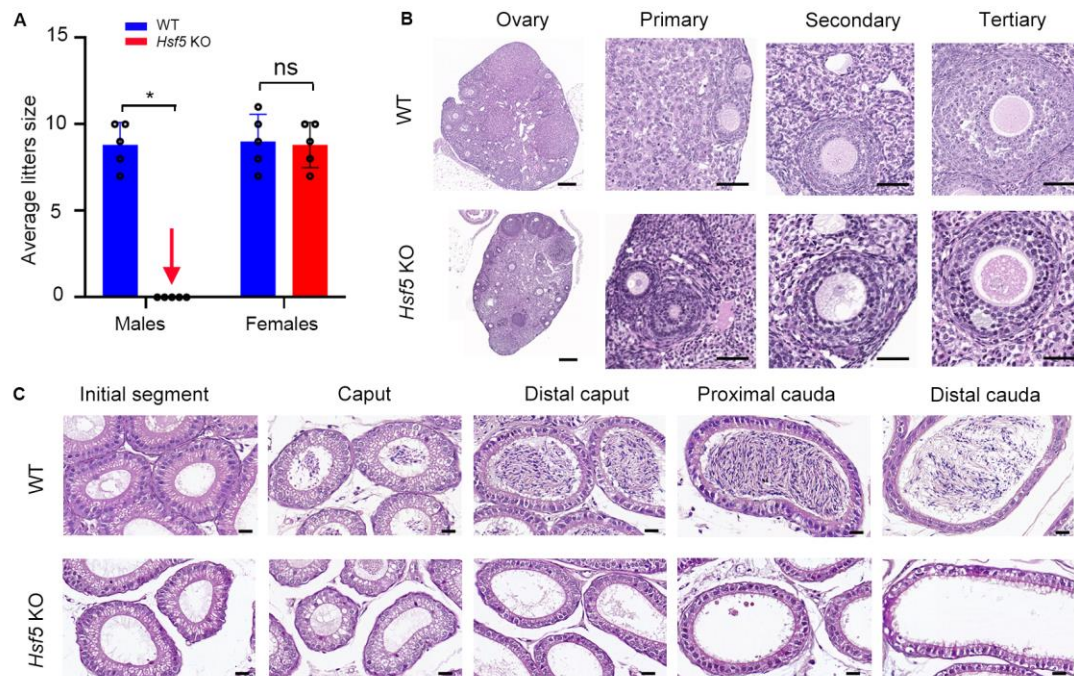


Figure S4. Fertility of *Hsf5* KO mice. A) Fertility in WT and *Hsf5* KO mice. *Hsf5* KO males were completely sterile, while the females showed normal fertility (N = 5 biologically independent WT mice and KO mice; two-sided Student's *t* test; ns, not significant; \*  $P < 0.05$ ; error bars, mean  $\pm$  SEM). B) H&E staining of sections from WT and *Hsf5* KO mouse ovaries (8 weeks old) (N = 3 biologically independent WT mice and KO mice; scale bars, 50  $\mu$ m). C) No spermatozoa were observed in individual fields of the epididymides in *Hsf5* KO mice compared to WT mice (8 weeks old) (N = 3 biologically independent WT mice and KO mice; scale bars, 100  $\mu$ m).

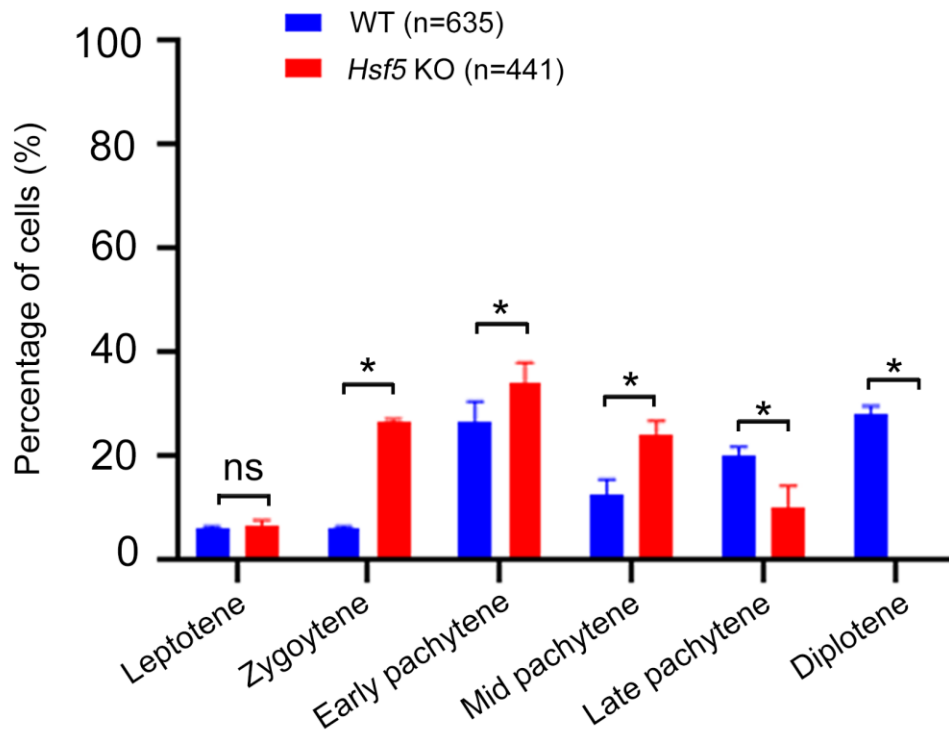


Figure S5. Percentages of substages of spermatocytes in *Hsf5* KO mice. Quantification of the proportion of spermatocytes from Fig. 4 (N = 3 biologically independent WT mice and KO mice; n, the total number of nuclei analyzed; two-sided Student's t test; \* P<0.05; error bars, mean  $\pm$  SEM).

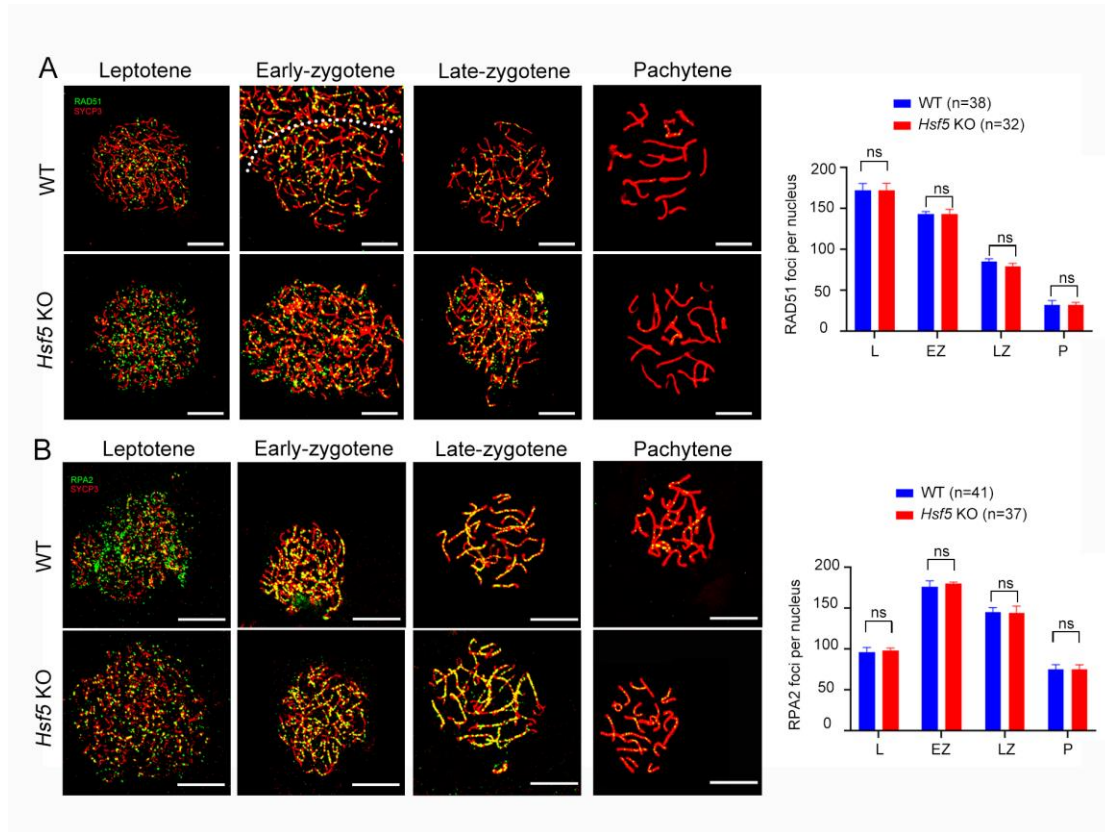


Figure S6. HSF5 is dispensable for early recombination. A) Immunofluorescence staining showed RAD51 foci in spread spermatocytes from 8-week-old WT and *Hsf5* KO mice. RAD51 focus counts were not significantly different between spermatocytes from WT and *Hsf5* KO mice (N = 3 biologically independent WT mice and KO mice; n, the total number of nuclei analyzed; two-sided Student's t test; ns, not significant; error bars, mean  $\pm$  SEM; green, RAD51; red, SYCP3; scale bars, 10  $\mu$ m). B) RPA2 signals were analyzed in WT and *Hsf5* KO spermatocytes. The RPA2 foci exhibited no significant difference between spermatocytes from WT and *Hsf5* KO mice (N = 3 biologically independent WT mice and KO mice; n, the total number of nuclei analyzed; two-sided Student's t test; ns, not significant; error bars, mean  $\pm$  SEM; green, RPA2; red, SYCP3; scale bars, 10  $\mu$ m).

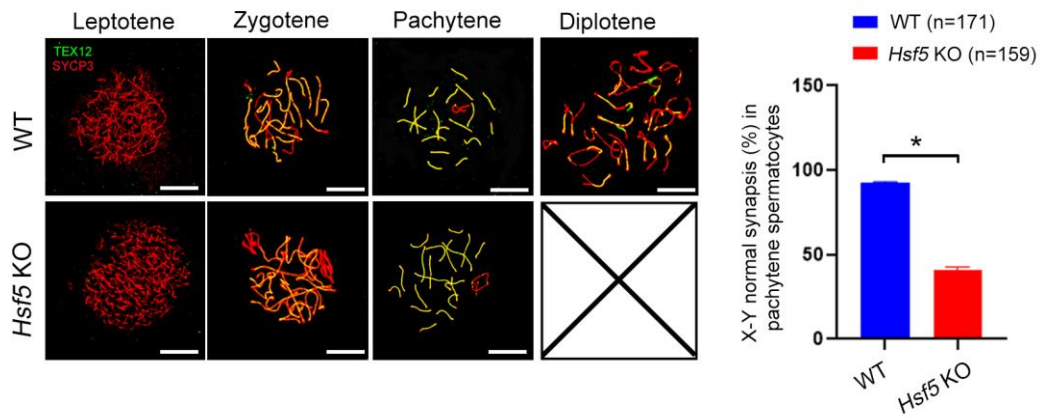


Figure S7. *Hsf5* KO spermatocytes fail to complete sex chromosome synapsis.

Immunofluorescence staining of TEX12 and SYCP3 was analyzed in spread spermatocytes from 8-week-old WT and *Hsf5* KO mice. Quantification of normal synapsis in spermatocytes from WT and *Hsf5* KO mice (N = 3 biologically independent WT mice and KO mice; n, the total number of nuclei analyzed; two-sided Student's t test; \*  $P < 0.05$ ; error bars, mean  $\pm$  SEM; green, TEX12; red, SYCP3; scale bars, 10  $\mu$ m).



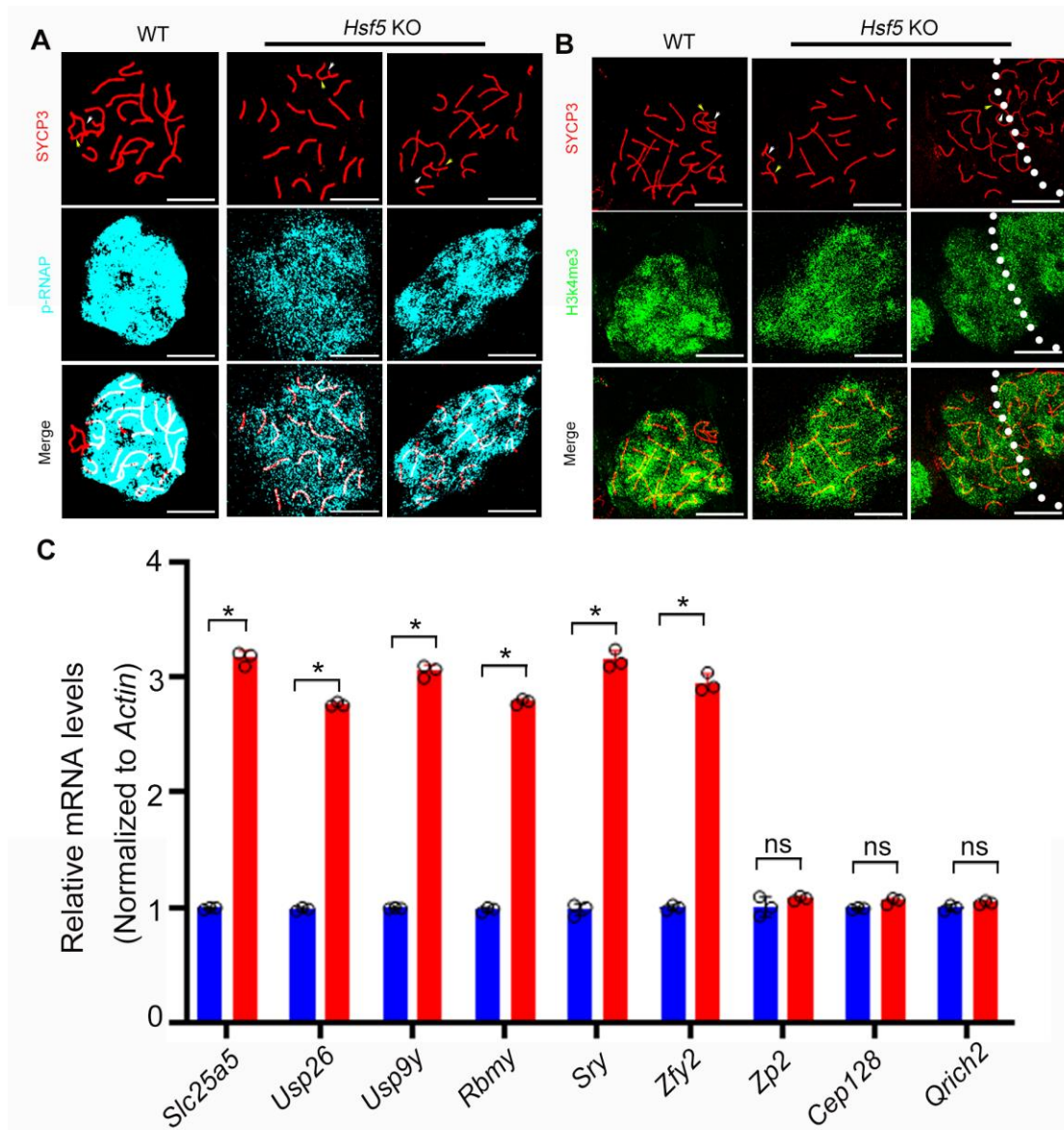


Figure S8. *Hsf5* KO mice show impaired MSCI. A) Spread spermatocytes from 8-week-old WT and *Hsf5* KO mice stained for SYCP3 and p-RNAP. In WT spermatocytes, p-RNAP staining was absent from the sex chromosomes, whereas it was present in that of *Hsf5* KO spermatocytes. Yellow arrow indicates X chromosome and white arrow indicates Y chromosome (N = 3 biologically independent WT mice and KO mice; sky blue, p-RNAP; red, SYCP3; scale bars, 10  $\mu$ m). B) Spread spermatocytes from 8-week-old WT and *Hsf5* KO mice stained for SYCP3 and H3k4me3. H3k4me3 was not excluded in the sex chromosomes of *Hsf5* KO pachytene spermatocytes. Yellow arrow

indicates X chromosome and white arrow indicates Y chromosome (N = 3 biologically independent WT mice and KO mice; green, H3k4me3; red, SYCP3; scale bars, 10  $\mu$ m).

C) qPCR analysis of gene expression in sex chromosomes and autosomes in total RNA from isolated pachytene spermatocytes from WT and *Hsf5* KO testes (N = 3 biologically independent WT mice and KO mice; two-sided Student's *t* test; \*  $P < 0.05$ ; ns, not significant; error bars, mean  $\pm$  SEM).

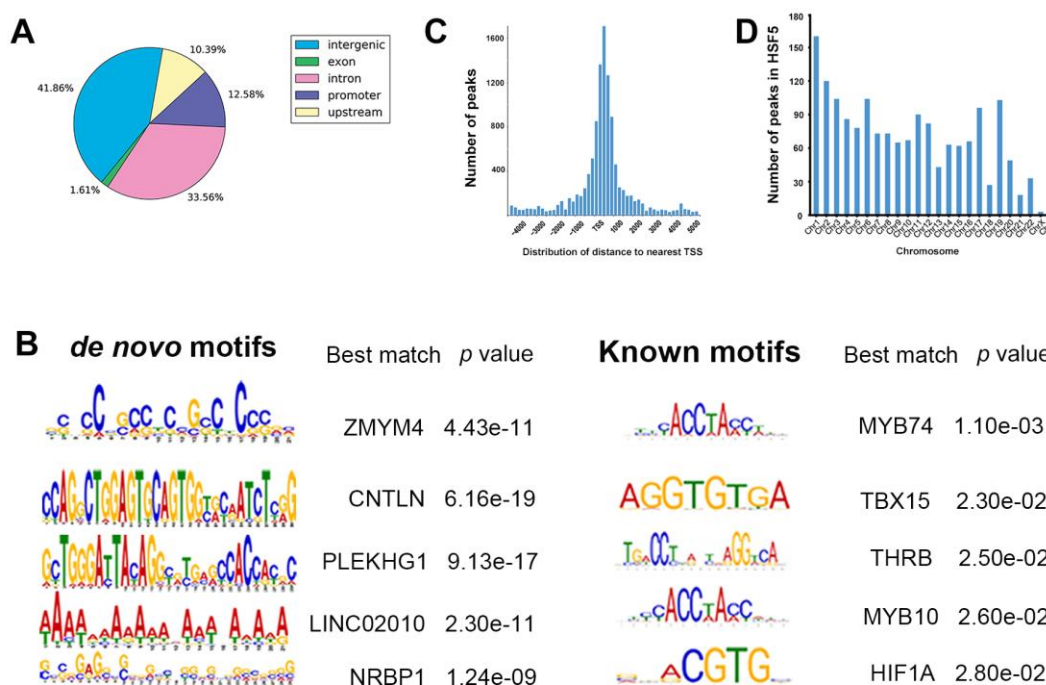


Figure S9. The DNA-binding activity of HSF5 in testes. A) Genomic localization of HSF5 occupancy sites by ChIP-seq. B) Identification of HSF5 binding motif(s) in known and *de novo* motif analysis. C) Density distribution of HSF5 ChIP-seq peaks. D) The HSF5 binding strength for each chromosome.

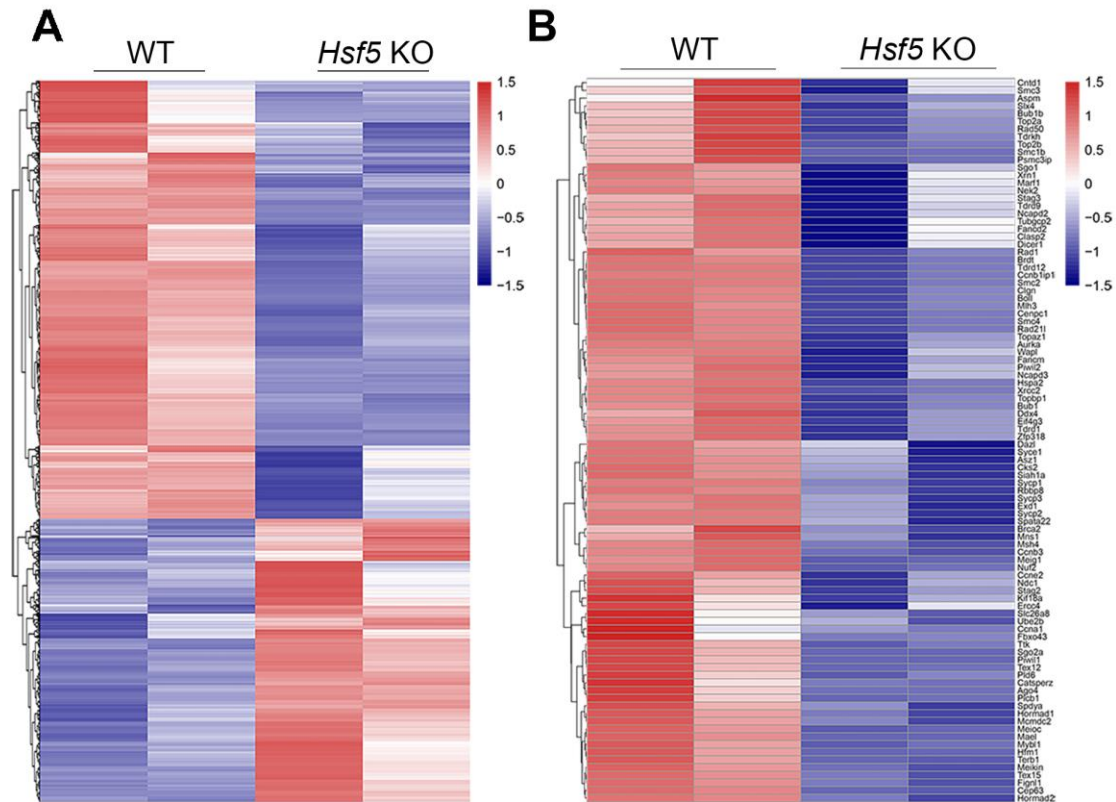


Figure S10. The transcriptome of *Hsf5* KO testes is substantially different from that of WT testes. A) Heatmap of genes differentially expressed in testes between WT and *Hsf5* KO mice at 20 dpp as determined by RNA-seq (N = 2 biologically independent WT mice and KO mice). B) Heatmap of genes associated with spermatogenesis differentially expressed between WT and *Hsf5* KO male mice by RNA-seq analysis (N = 2 biologically independent WT mice and KO mice).

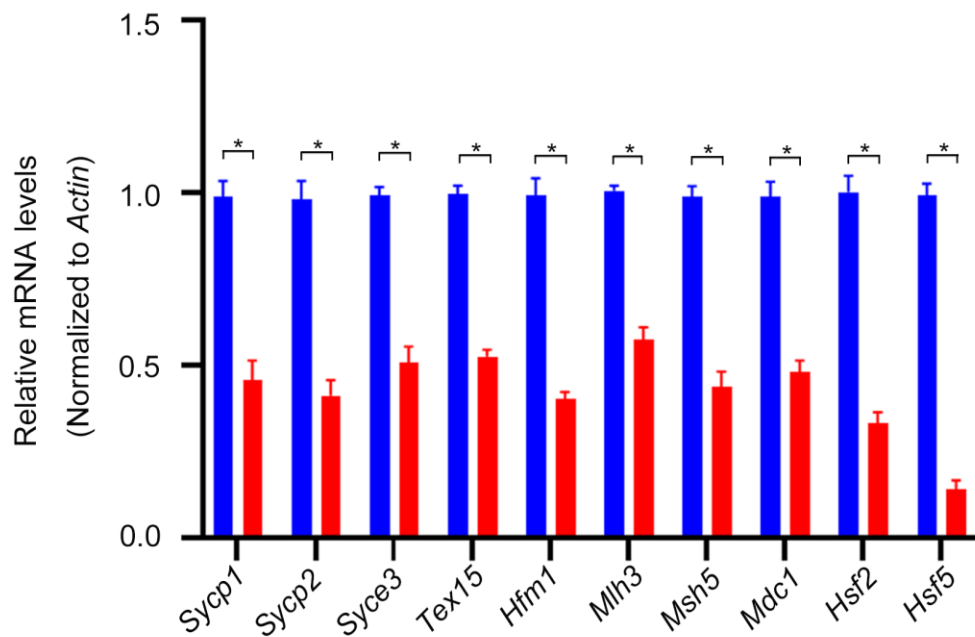


Figure S11. Downregulated mRNA expression of meiosis-related genes is detected in *Hsf5* KO testes. The mRNA levels of *Sycp1*, *Sycp2*, *Syce3*, *Tex15*, *Mdc1*, *Hfm1*, *Mlh3*, *Msh5*, *Hsf2* and *Hsf5* in the testes of WT and *Hsf5* KO mice (N = 3 biologically independent WT mice and KO mice; two-sided Student's *t* test; \*  $P < 0.05$ ; error bars, mean  $\pm$  SEM).

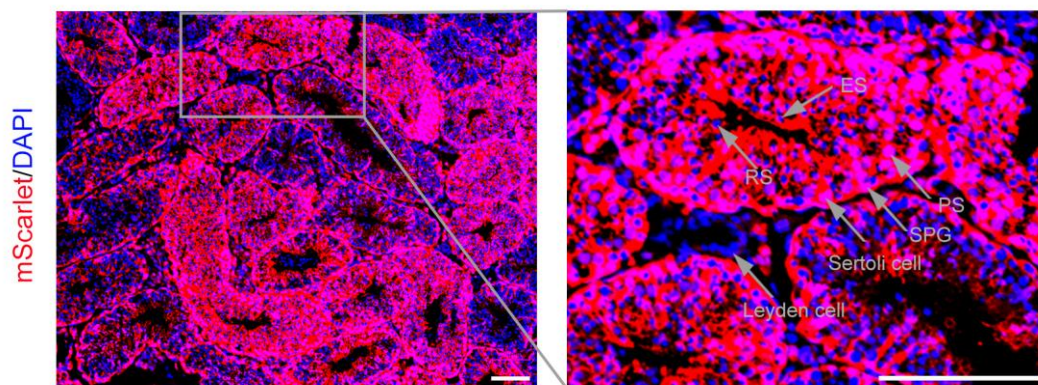


Figure S12. Optimal AAV concentration. WT mouse testes after microinjection with

8\*10<sup>10</sup> gc mScarlet-expressing AAV9 for one week. SPG, spermatogonium; PS, primary spermatocyte; RS, round spermatid; ES, elongating/elongated spermatid (N = 3 biologically independent 8-week-old WT mice; blue, DAPI; red, mScarlet; scale bars, 125  $\mu$ m).

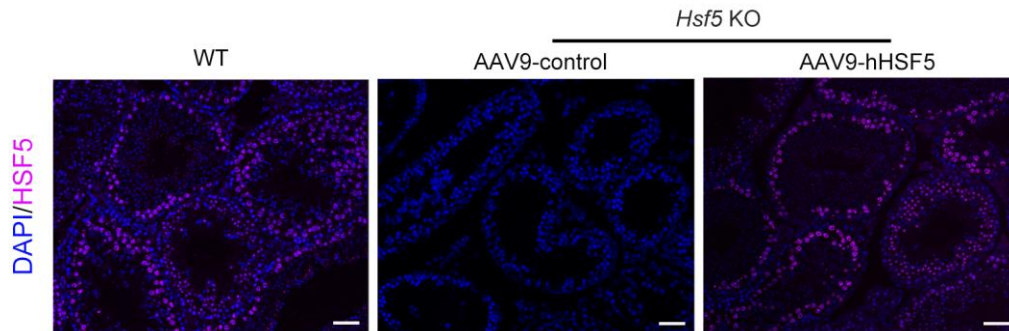


Figure S13. Testicular injection of AAV-hHSF5 rescues HSF5 expression in *Hsf5* KO mice. Immunofluorescence staining of HSF5 in the testes of *Hsf5* KO mice microinjected with AAV9-control and AAV9-hHSF5 compared to WT mice with AAV9-control (N = 3 biologically independent WT mice and KO mice; scale bars, 125  $\mu$ m).

**Table S1. Analysis of c.586C>T variant in *HSF5*.**

<b>Variants</b>	cDNA mutation	c.586C>T
	Protein changes	p.R196C
	Mutation type	Missense
	Genotype	Homozygous
<b>Allele frequency</b>	in ExAC Browser	0.00000845
	GnomAD	0.000004053
	1000 Genomes Project	NA
<b>Function prediction</b>	SIFT	Deleterious
	Polyphen-2	Probably damaging
	CADD	Deleterious

Note: RefSeq accession number of *HSF5*: NM\_001080439.2; NA: Not available

**Table S2. Overview of the primer sequences used in qPCR in mice.**

Primers	Sequences
<i>β-actin</i>	F: 5'-CCCAGGCATTGCTGACAGG-3'
(141 bp)	R: 5'-TGGAAGGTGGACAGTGAGGC-3'
<i>Hsf5</i>	F: 5'-TTTTGCACGAAGTCAGTTGGG-3'
(288 bp)	R: 5'-GGTTTCCGAAGTCGTTCTGT-3'
<i>Sycp1</i>	F: 5'-CTGACAACGGCCCAGGAG-3'
(123 bp)	R: 5'-AGTTGGAGTCTCCTCCCGC-3'
<i>Mdc1</i>	F: 5'-CTGTCCCTGAACTGGCTGTACCAG-3'
(426 bp)	R: 5'-GGTAGATGACATTTCCAAATTGGA-3'
<i>Tex15</i>	F: 5'-TCATACCCACTGGTAACACAG-3'
(220 bp)	R: 5'-GGCAAACATCACTCAAACCTG-3'
<i>Hsf2</i>	F: 5'-AAGGCCAGGATGACCTGTTG-3'
(441 bp)	R: 5'-TCAGTCCTGCTGTGTGGAAC-3'
<i>Sycp2</i>	F: 5'-AGGATGAGATCACTACACCTAGC-3'
(208 bp)	R: 5'-GGTGACGCAGCATAATCCATT-3'
<i>Syce3</i>	F: 5'-CTGATTCCGATCCTGGGAAA-3'
(116 bp)	R: 5'-GGTTGCCTGCACTGAGATTTT-3'
<i>Mlh3</i>	F: 5'-CAGGACAGCAACAACAGTGC-3'
(176 bp)	R: 5'-TGATGCATTTGGATGGGGCT-3'
<i>Hfm1</i>	F: 5'-GTTGCACAAAAGCCGGAAGT-3'
(300 bp)	R: 5'-ACCCAGA ACTTCTTTGTCACG-3'
<i>Msh5</i>	F: 5'-CCTTCTTTCCATTCCCCGCT-3'
(319 bp)	R: 5'-GGGAGAGTAATGCGGTCTCG-3'
<i>Cep128</i>	F: 5'-GATGCTGAAGGCAGAAAGC-3'

(178 bp)	R: 5'-CTCCTTCTTGTCTAGTTCCTCC-3'
<i>Qrich2</i>	F: 5'-CTCTGTCTCTGAGGCGTCTC-3'
(206 bp)	R: 5'-GCAGACTGACTTGGTGGCTC-3'
<i>Usp26</i>	F: 5'-GCACAAGTGCACAGGAGTTG-3'
(462 bp)	R: 5'-ATTCATGCCACTCTAGGCCG-3'
<i>Slc25a5</i>	F: 5'-AGGGCATCATAGACTGCGTG-3'
(170 bp)	R: 5'-CTGGGTCCTCTTGTCCACAC-3'
<i>Usp9y</i>	F: 5'-AAGCCGTTTGGACAGTGCTA-3'
(392 bp)	R: 5'-TCTGTCATTCGCTCAACGGT-3'
<i>Rbmy</i>	F: 5'-TGAGGCACCATCTGCAAGAG-3'
(208 bp)	R: 5'-ATGCCCTCTTTCCTGTCTGC-3'
<i>Zfy2</i>	F: 5'-TAGGAGCTGATGCAGTACACA -3'
(443 bp)	R: 5'-TGAAATGTCCGGCTGTCAAAGG-3'
<i>Sry</i>	F: 5'-GCCTCATCGGAGGGCTAAAG-3'
(91 bp)	R: 5'-GTCCCACTGCAGAAGGTTGT-3'
<i>Zp2</i>	F: 5'-GCATCACTGAGGAGCAAACG-3'
(144 bp)	R: 5'-GAAAAAGGTACCACAGCACCAG-3'

**Table S3. Overview of the primer sequences used in ChIP-PCR and ChIP-qPCR.**

Primers	Sequences
<i>SYCP1</i>	F: 5'-AGAGCCACTTTGCCTACGTC-3'
(318 bp)	R: 5'-ACGGCTAAATAACCGTCGCT-3'
<i>SYCP2</i>	F: 5'-TTTTGCACGAAGTCAGTTGGG-3'
(288 bp)	R: 5'-GGTTCCGAAGTCGTTCTGT-3'
<i>SYCE3</i>	F: 5'-CTCCTCCCAGCCAGAGCTTTCTG-3'
(515 bp)	R: 5'-CTCATTGGGTGTCCTCGGGAAAAG-3'
<i>MDC1</i>	F: 5'-GAGGTGGGGACCAAAGATGG-3'
(379 bp)	R: 5'-CTTCACACTCACCCACCTCC-3'

<i>TEX15</i>	F: 5'-CCCTAAGTGCACTGATTGCTTTTGG-3'
(346 bp)	R: 5'-CGTGGCAACACATCAGCTAATTTTC-3'
<i>HSF5</i>	F: 5'-TCTGCCGGGGTGTCTAAGT-3'
(157 bp)	R: 5'-CCTTTGGTCCCCAGAACGAC-3'
<i>HSF2</i>	F: 5'- TGAACCCCCTGAATAACCGC-3'
(438 bp)	R: 5'-TCGCTGAGGTAAAGATCGCC-3'
<i>MSH5</i>	F: 5'-GTTGGGAAGAGCTGGGCAAG-3'
(291 bp)	R: 5'-GAAGCTTGAGGCTCTCGTGG-3'
<i>HFM1</i>	F: 5'-TAAGCCGAGCTCCAAGCAAT-3'
(204 bp)	R: 5'-TGGGGGTAGAGAAGCAGGTT-3'
<i>MLH3</i>	F: 5'-GTGTTAGAAGAGACCCCGGC-3'
(217 bp)	R: 5'-CTTGGCTGGAACAACCTGGTG-3'

**Table S4. Overview of the primer sequences used in plasmid construction for dual-luciferase reporter assay.**

Primers	Sequences
<i>TEX15</i> promoter (2063 bp)	F: 5'-TTACATGGCATTATTTGGCACTCA -3' R: 5'-GGGAGTCTCAGACGCTACTCT-3'
<i>SYCP2</i> promoter (1917 bp)	F: 5'-AACGACTTCGGAAACCGAGA-3' R: 5'-GGCGTTCATCAGGAGAGCATA-3'
<i>SYCP1</i> promoter (1813 bp)	F: 5'-CACTTAATCCTCACACAGAACGC-3' R: 5'-TGCCTACACAATAATGCTCACTG-3'
<i>SYCE3</i> promoter (1802 bp)	F: 5'-CCTTTCCGTTAGCGAACCT-3' R: 5'-GGGAAGACCAGCCTGACATC-3'
<i>HSF2</i> promoter (1942 bp)	F: 5'-GTGCAAACCACACTTTGCCT-3' R: 5'-CCCCTACTCAACTCCAAGCA-3'
<i>MDC1</i> promoter	F: 5'-CCCCAGTCTTCGAACACACT-3'



(1865 bp)	R: 5'-GGTGGGGACAGCCTTTAAGA-3'
<i>HSF5</i> promoter	F: 5'-GGGGAAGTTGTTGGGGTTGA-3'
(751 bp)	R: 5'-TGGGCAGGCACACAAGATAG-3'
<i>MSH5</i> promoter	F: 5'- GAATCGTTGCTCCGAACCG-3'
(922 bp)	R: 5'-ACATCTGCAATCCCAGAGAGC-3'
<i>HFM1</i> promoter	F: 5'-GGCCTGGGAAAGGACCATAC-3'
(937 bp)	R: 5'-GGTTGTGGGGGTAGAGAAGC-3'
<i>MLH3</i> promoter	F: 5'-CTCCATCAGTGAGAGCCACG-3'
(1031 bp)	R: 5'-TCTCAGCCTTTTCCAGCTCC-3'

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