

## Appendix

### **M1AP interacts with the mammalian ZZS complex and promotes male meiotic recombination**

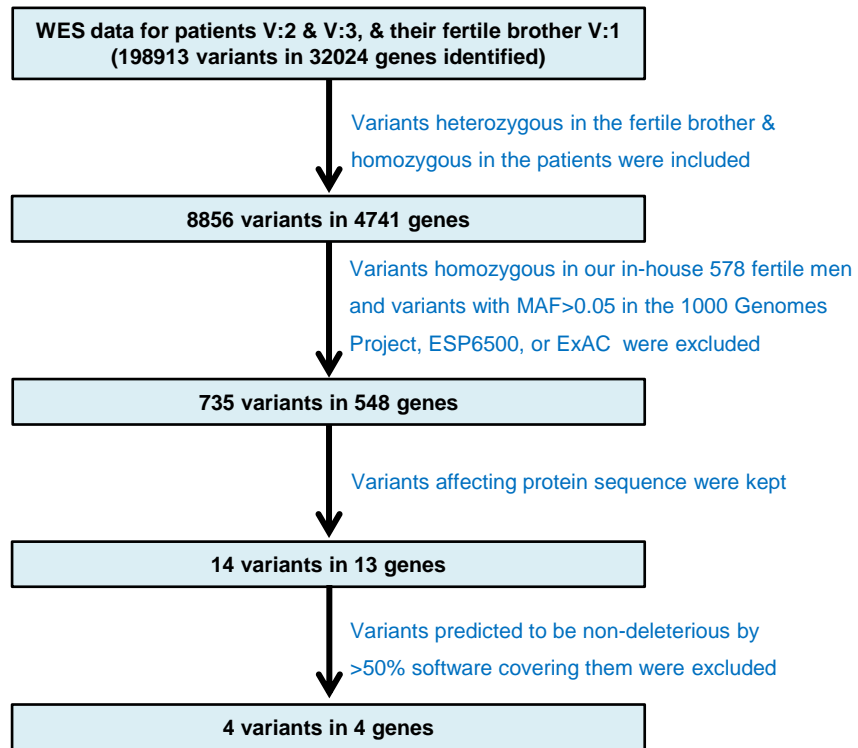
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# Appendix Figure S1

A



B

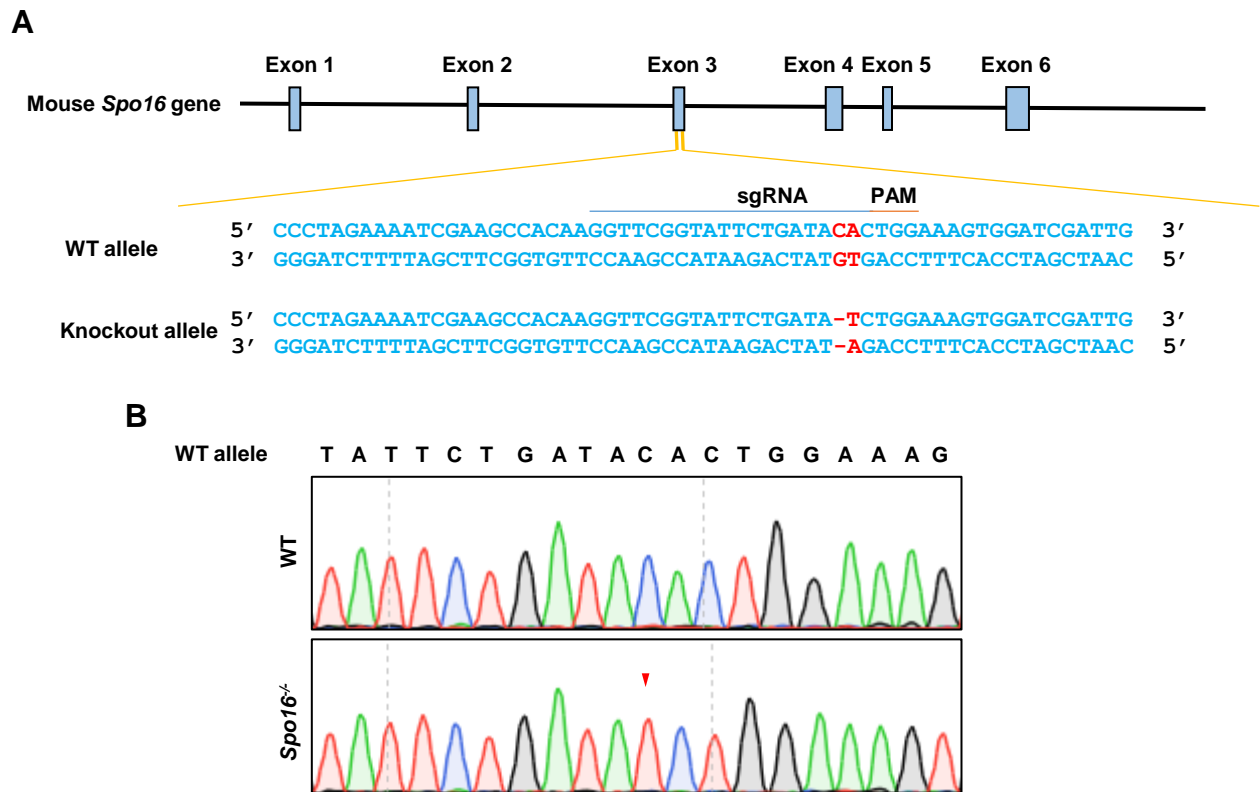
Human gene symbol	Mouse gene symbol	Mutation type	cDNA change	Predicted protein change	Remark
<i>MIAP</i>	<i>Mlap</i>	splicing	1074+2T>C	Not applicable	Mice homozygous for a hypomorphic allele exhibit severe oligozoospermia and infertility (PMID:23269666).
<i>MCEE</i>	<i>Mcee</i>	missense	G428A	R143H	No mention of reproductive phenotype after knockout of this gene in MGI (MGI:1920974).
<i>DYSF</i>	<i>Dysf</i>	nonframeshift substitution	3181delinsC AGGCGG	1062insAE	No mention of reproductive phenotype after knockout of this gene in MGI (MGI:1349385).
<i>AHCTF1P1</i>	-	missense	G1381A	E461K	This gene is a pseudogene.

## Appendix Figure S1. Whole-exome sequencing data analysis for the consanguineous Pakistani family

A. Whole-exome sequencing (WES) data analysis pipeline. MAF, minor allele frequency.

B. Information on the variants identified following bioinformatic analysis of WES data. MGI, mouse genome informatics.

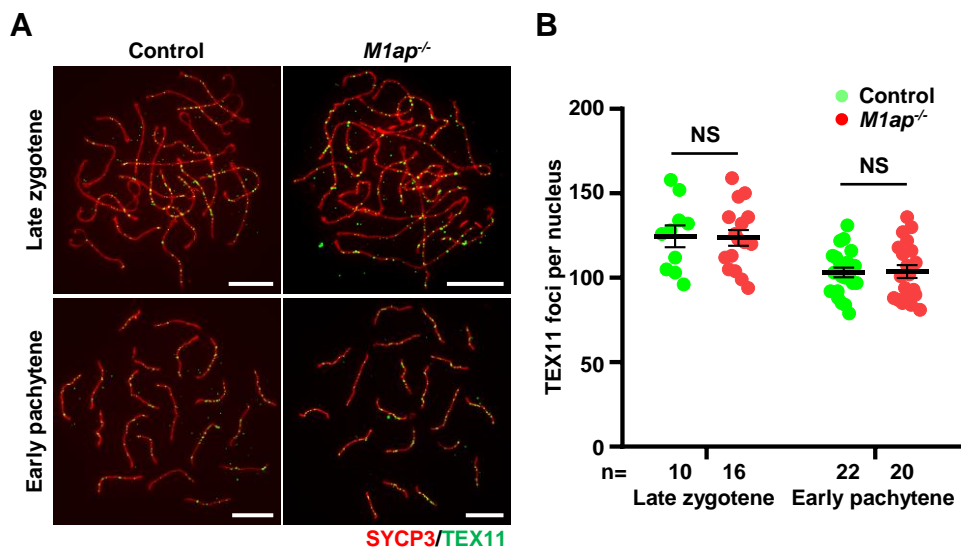
## Appendix Figure S2



### Appendix Figure S2. Generation of *Spo16*<sup>-/-</sup> mice

- A. The strategy to generate *Spo16*<sup>-/-</sup> mice. The single guide RNA (underlined) was designed to target exon 3 of the *Spo16* gene. The mutation site is written in red, where “CA” is replaced by “T”. WT, wild-type. PAM, protospacer adjacent motif.
- B. Sanger sequencing confirmed the mutation in the *Spo16*<sup>-/-</sup> mice at the genomic DNA level. The arrowhead indicates the mutation site.

## Appendix Figure S3



**Appendix Figure S3. No obvious differences were observed in the number of TEX11 foci between control and *M1ap*<sup>-/-</sup> oocytes**

A. Immunofluorescence staining with antibodies against SYCP3 (red) and TEX11 (green) on oocyte spreads from 16.5 days postcoitus (dpc) control and *M1ap*<sup>-/-</sup> fetal mice. Scale bars, 10  $\mu\text{m}$ .

B. The mean number of TEX11 foci per cell in control and *M1ap*<sup>-/-</sup> oocytes at the indicated stages. Data are presented as mean  $\pm$  SEM. n shows the number of cells examined for at least two mice per genotype. NS, not significant; two-tailed Student's *t*-test.