Akap9 Cas9-KO Strategy

Designer: Xiaojing Li
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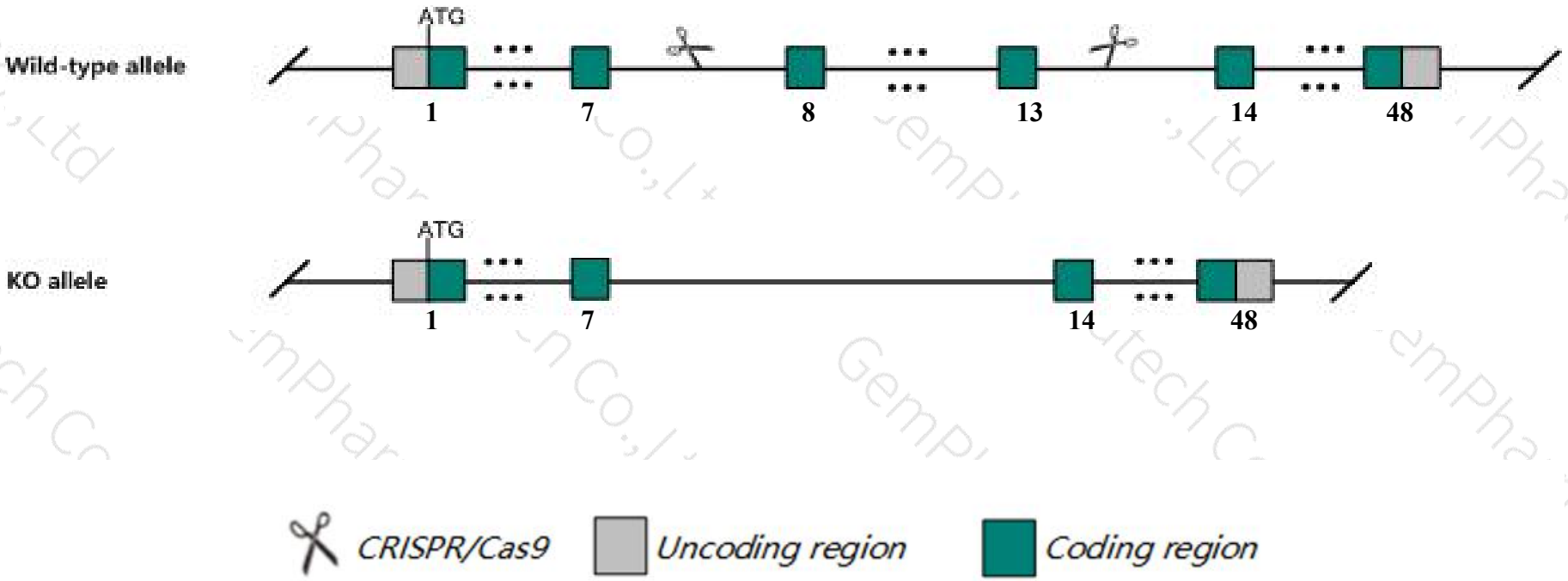
Reviewer: JiaYu

Project Overview

Project Name	***Akap9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Akap9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Akap9* gene has 16 transcripts. According to the structure of *Akap9* gene, exon8-exon13 of *Akap9-201* (ENSMUST00000044492.9) transcript is recommended as the knockout region.The region contains 821bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Akap9* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a chemically induced allele exhibit male infertily with abnormal spermatogenesis and Sertoli maturation.

- The *Akap9* gene is located on the Chr5. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.

- This Strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Akap9 A kinase (PRKA) anchor protein (yotiao) 9 [*Mus musculus* (house mouse)]

Gene ID: 100986, updated on 12-Aug-2019

Summary

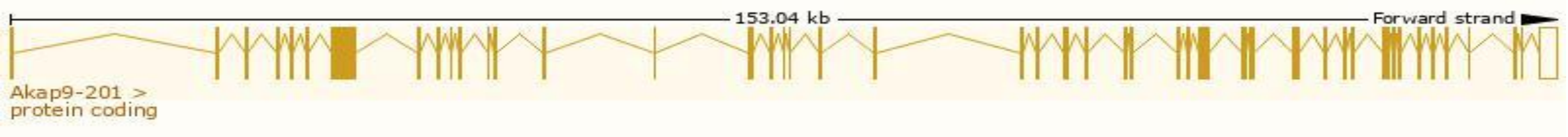
Official Symbol	Akap9 provided by MGI
Official Full Name	A kinase (PRKA) anchor protein (yotiao) 9 provided by MGI
Primary source	MGI:MGI:2178217
See related	Ensembl:ENSMUSG00000040407
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PRKA9; AKAP-9; C79026; mei2-5; AKAP450; repro12; AW545847; G1-448-15; mKIAA0803; 5730481H23Rik
Expression	Broad expression in CNS E14 (RPKM 12.4), CNS E18 (RPKM 10.9) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

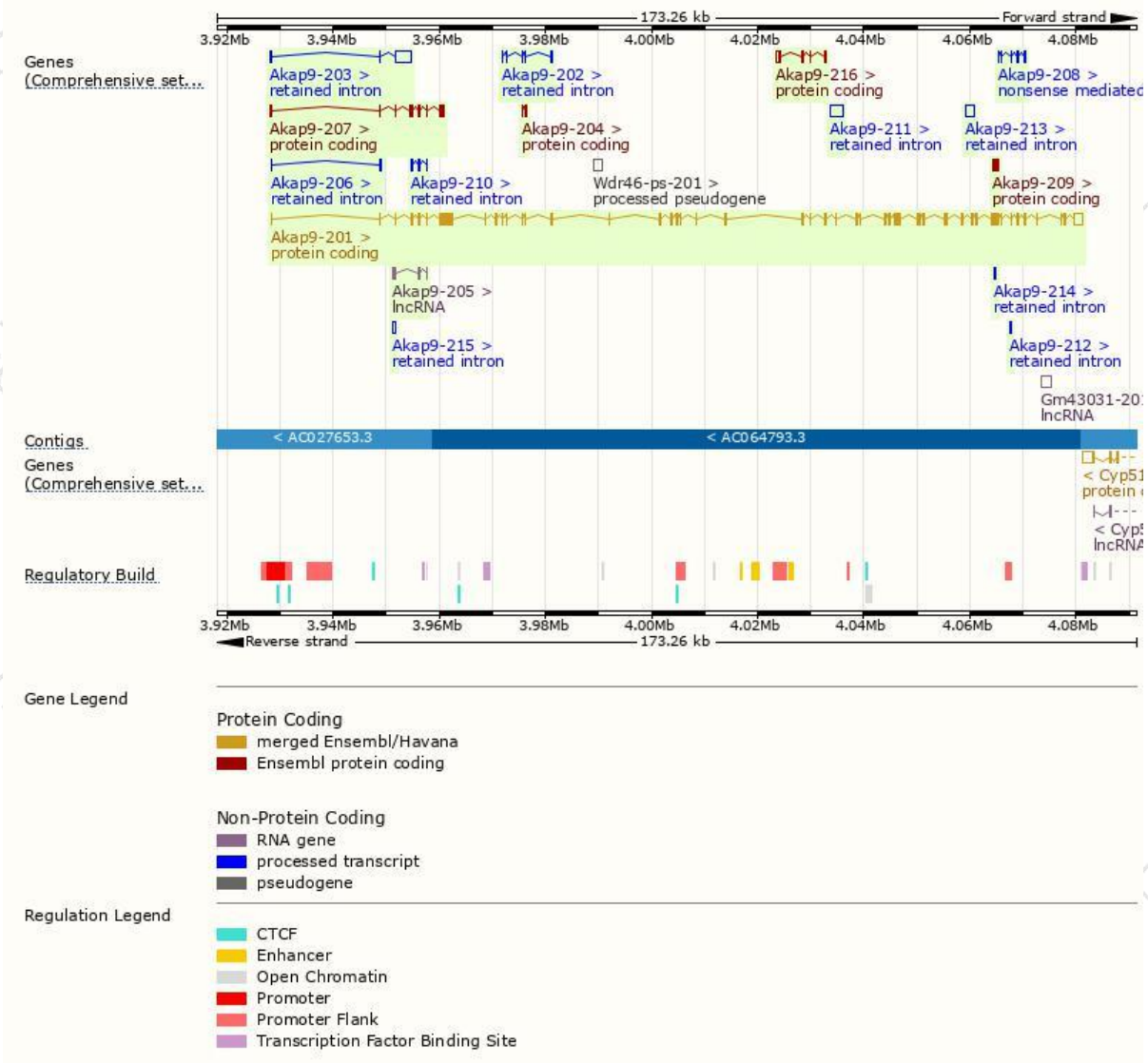
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Akap9-201	ENSMUST00000044492.9	13123	3779aa	Protein coding	CCDS19070	E9QQ10	TSL:1 GENCODE basic APPRIS P1
Akap9-202	ENSMUST00000123119.1	670	No protein	Retained intron	-	-	TSL:3
Akap9-203	ENSMUST00000132058.1	3646	No protein	Retained intron	-	-	TSL:1
Akap9-204	ENSMUST00000133952.1	499	113aa	Protein coding	-	A0A0G2JFW0	CDS 5' incomplete TSL:3
Akap9-205	ENSMUST00000140977.7	375	No protein	lncRNA	-	-	TSL:3
Akap9-206	ENSMUST00000141817.1	491	No protein	Retained intron	-	-	TSL:2
Akap9-207	ENSMUST00000143365.7	2010	581aa	Protein coding	-	A0A140T8S1	CDS 3' incomplete TSL:1
Akap9-208	ENSMUST00000147629.1	718	56aa	Nonsense mediated decay	-	G3UX24	CDS 5' incomplete TSL:5
Akap9-209	ENSMUST00000176863.1	595	198aa	Protein coding	-	H3BLL7	CDS 5' and 3' incomplete TSL:3
Akap9-210	ENSMUST00000177448.1	491	No protein	Retained intron	-	-	TSL:2
Akap9-211	ENSMUST00000196350.1	2323	No protein	Retained intron	-	-	TSL:NA
Akap9-212	ENSMUST00000196837.1	460	No protein	Retained intron	-	-	TSL:NA
Akap9-213	ENSMUST00000196918.1	1676	No protein	Retained intron	-	-	TSL:NA
Akap9-214	ENSMUST00000197366.1	479	No protein	Retained intron	-	-	TSL:NA
Akap9-215	ENSMUST00000198973.1	581	No protein	Retained intron	-	-	TSL:NA
Akap9-216	ENSMUST00000238634.1	1352	282aa	Protein coding	-	-	CDS 3' incomplete

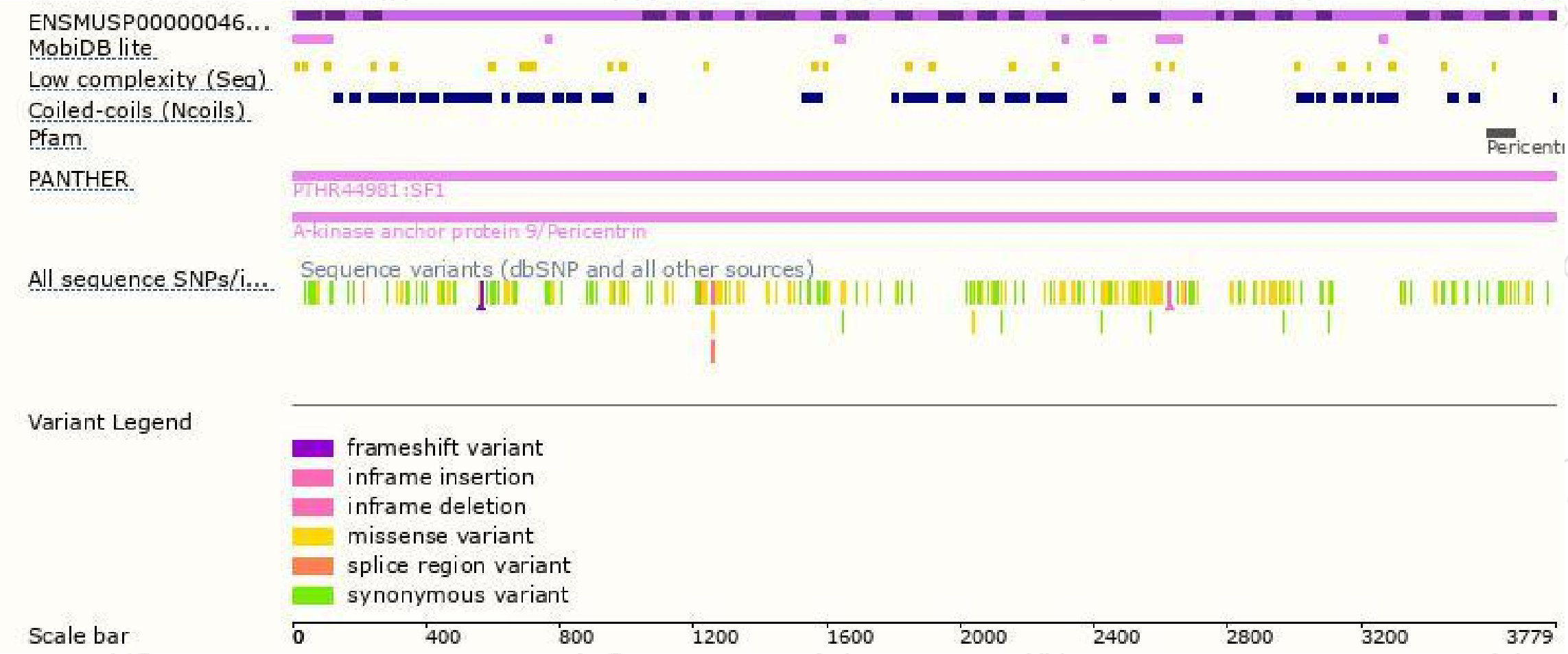
The strategy is based on the design of *Akap9-201* transcript,The transcription is shown below



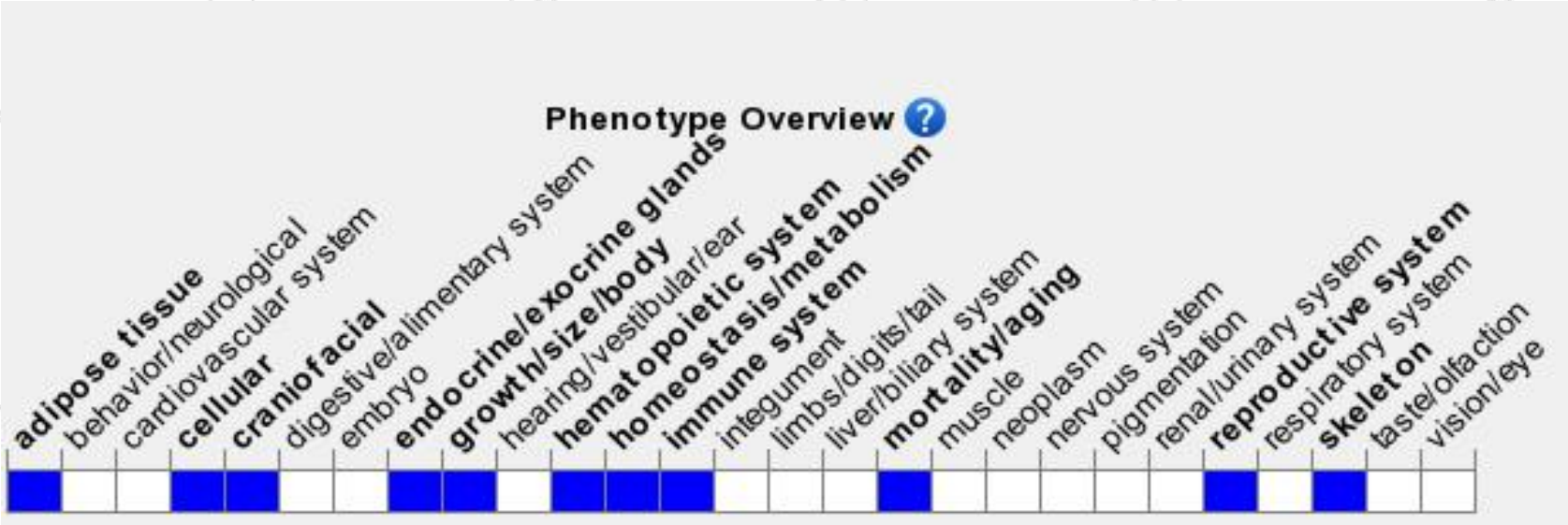
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data,Mice homozygous for a chemically induced allele exhibit male infertily with abnormal spermatogenesis and Sertoli maturation.

集萃药康
GemPharmatech

If you have any questions, you are welcome to inquire.

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd