Ing2 Cas9-KO Strategy

Designer: Yanhua Shen

Reviewer: Xueting Zhang

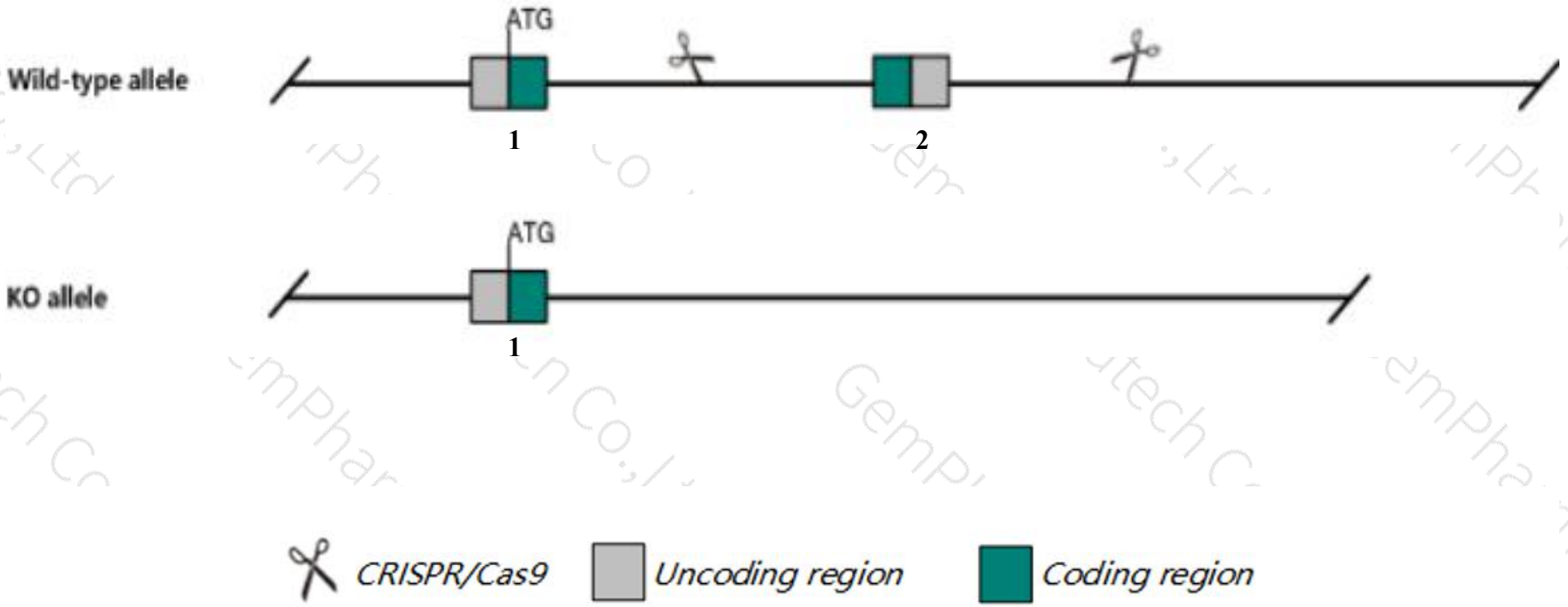
Design Date: 2020-4-26

Project Overview

Project Name	***Ing2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ing2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ing2* gene has 3 transcripts. According to the structure of *Ing2* gene, exon2 of *Ing2-201* (ENSMUST00000080353.2) transcript is recommended as the knockout region.The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ing2* gene. The brief process is as follows: CRISPR/Cas9 system wer

Notice

- According to the existing MGI data,homozygous inactivation of this gene causes impaired spermatogenesis and male infertility associated with teratozoospermia, seminiferous tubule degeneration, germ cell depletion, arrest of male meiosis and enhanced testicular apoptosis, and leads to an increased incidence of soft tissue sarcomas.
- The *Ing2* gene is located on the Chr8. 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）

集萃药康 GemPharmatech

Ing2 inhibitor of growth family, member 2 [Mus musculus (house mouse)]

Gene ID: 69260, updated on 13-Mar-2020

Summary

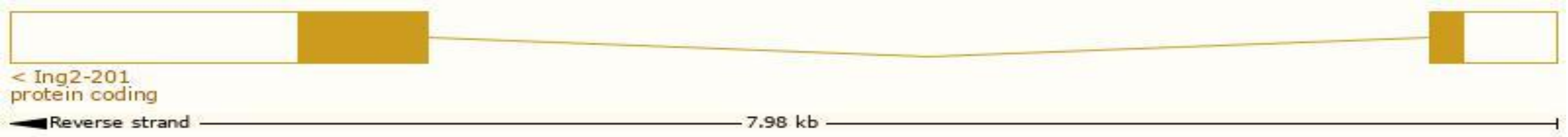
Official Symbol	Ing2 provided by MGI
Official Full Name	inhibitor of growth family, member 2 provided by MGI
Primary source	MGI:MGI:1916510
See related	Ensembl:ENSMUSG00000063049
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810011M06Rik, Ing1l, Ing2b, P33ING2
Expression	Ubiquitous expression in placenta adult (RPKM 8.8), cortex adult (RPKM 5.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

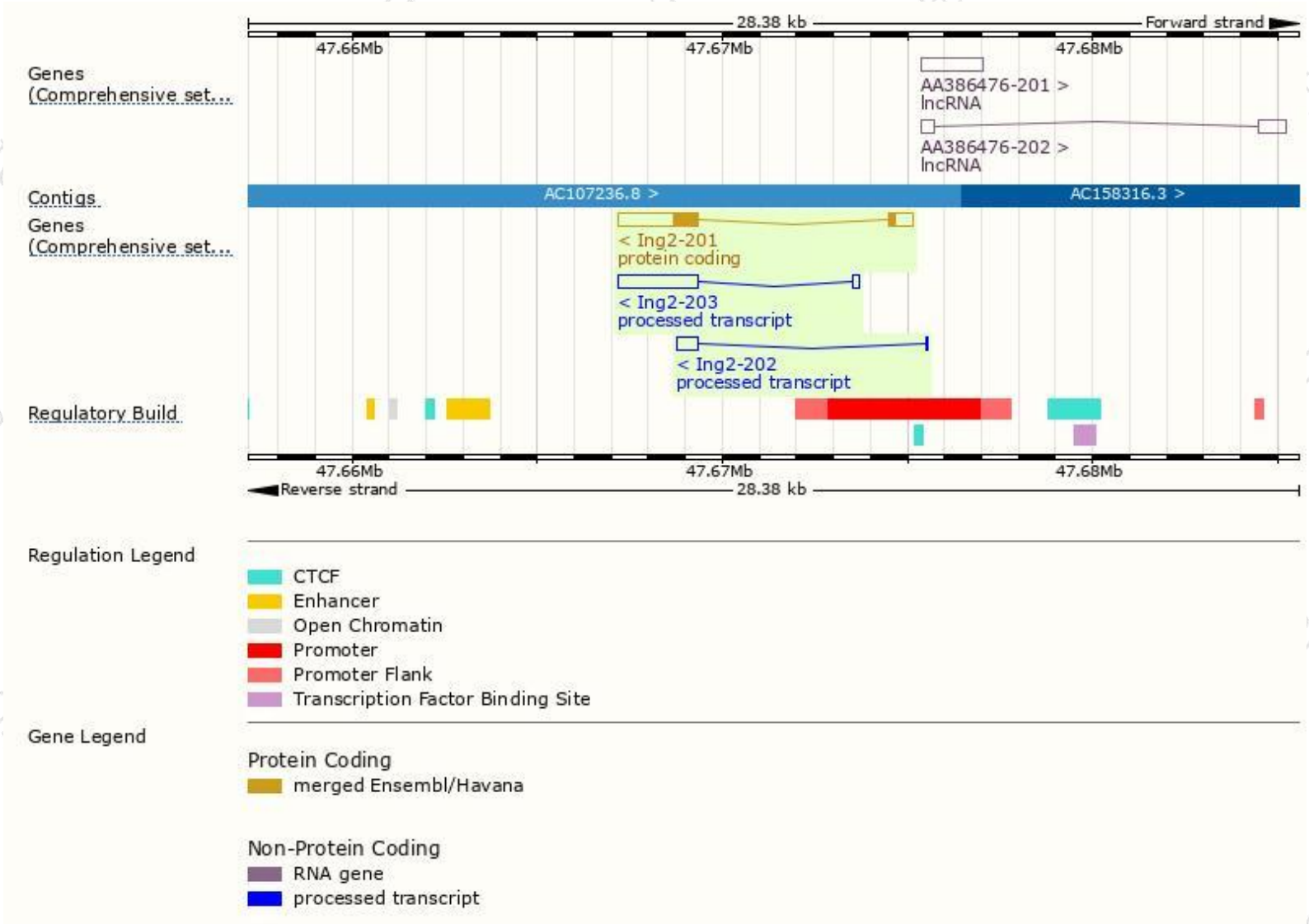
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ing2-201	ENSMUST00000080353.2	2812	281aa	Protein coding	CCDS22298	Q9ESK4	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Ing2-203	ENSMUST00000146625.2	2320	No protein	Processed transcript	-	-	TSL:1
Ing2-202	ENSMUST00000125536.1	628	No protein	Processed transcript	-	-	TSL:3

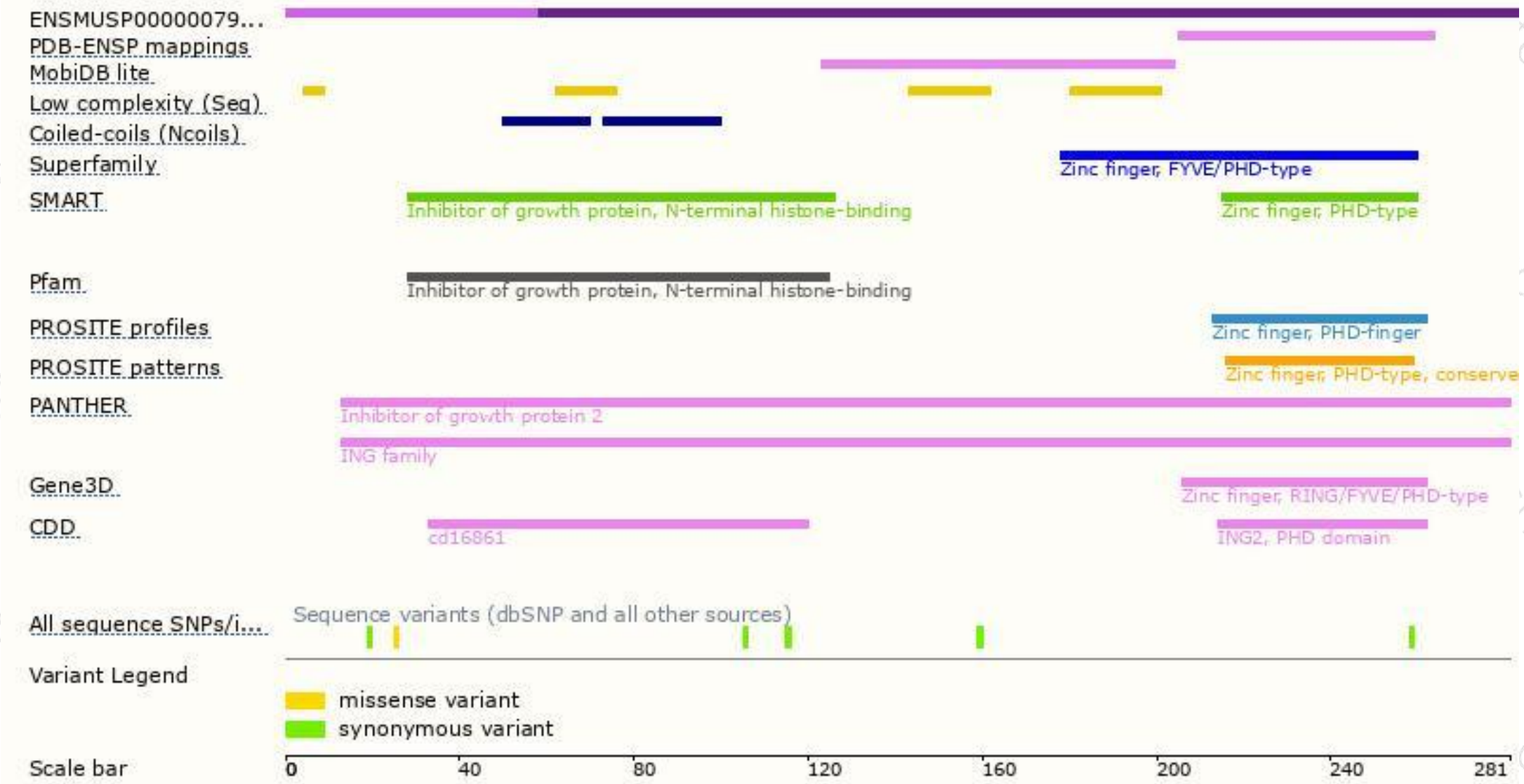
The strategy is based on the design of *Ing2-201* transcript,the transcription is shown below:



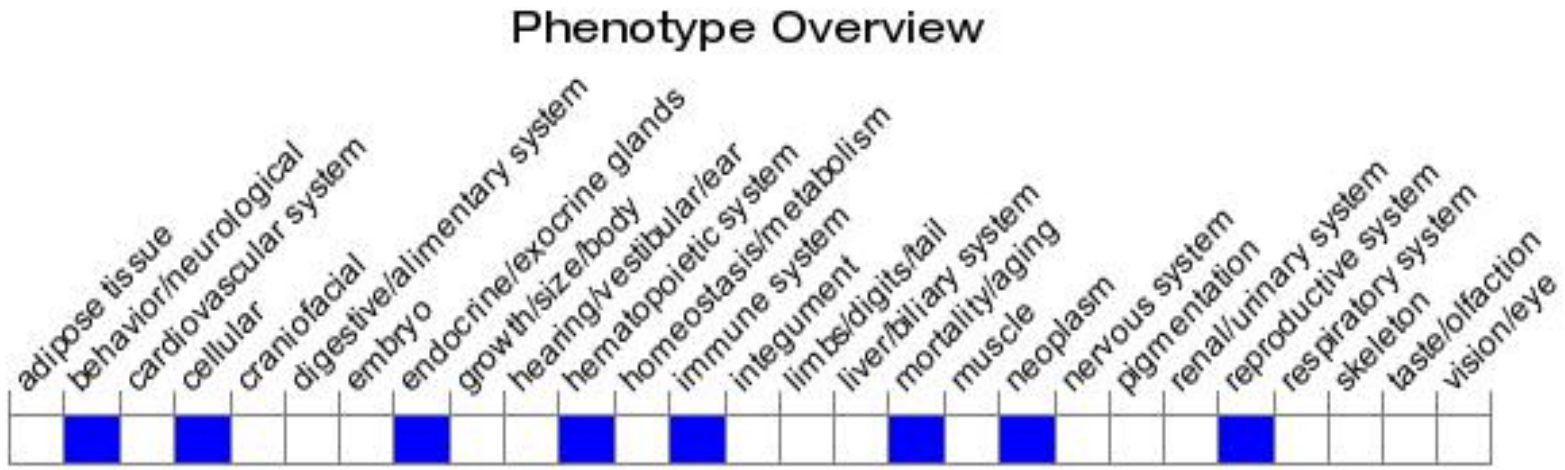
Genomic location distribution



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,homozygous inactivation of this gene causes impaired spermatogenesis and male infertility associated with teratozoospermia, seminiferous tubule degeneration, germ cell depletion, arrest of male meiosis and enhanced testicular apoptosis, and leads to an increased incidence of soft tissue sarcomas.

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