

Vtn Cas9-CKO Strategy

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Design Date: 2021/2/7

Project Overview

Project Name

Vtn

Project type

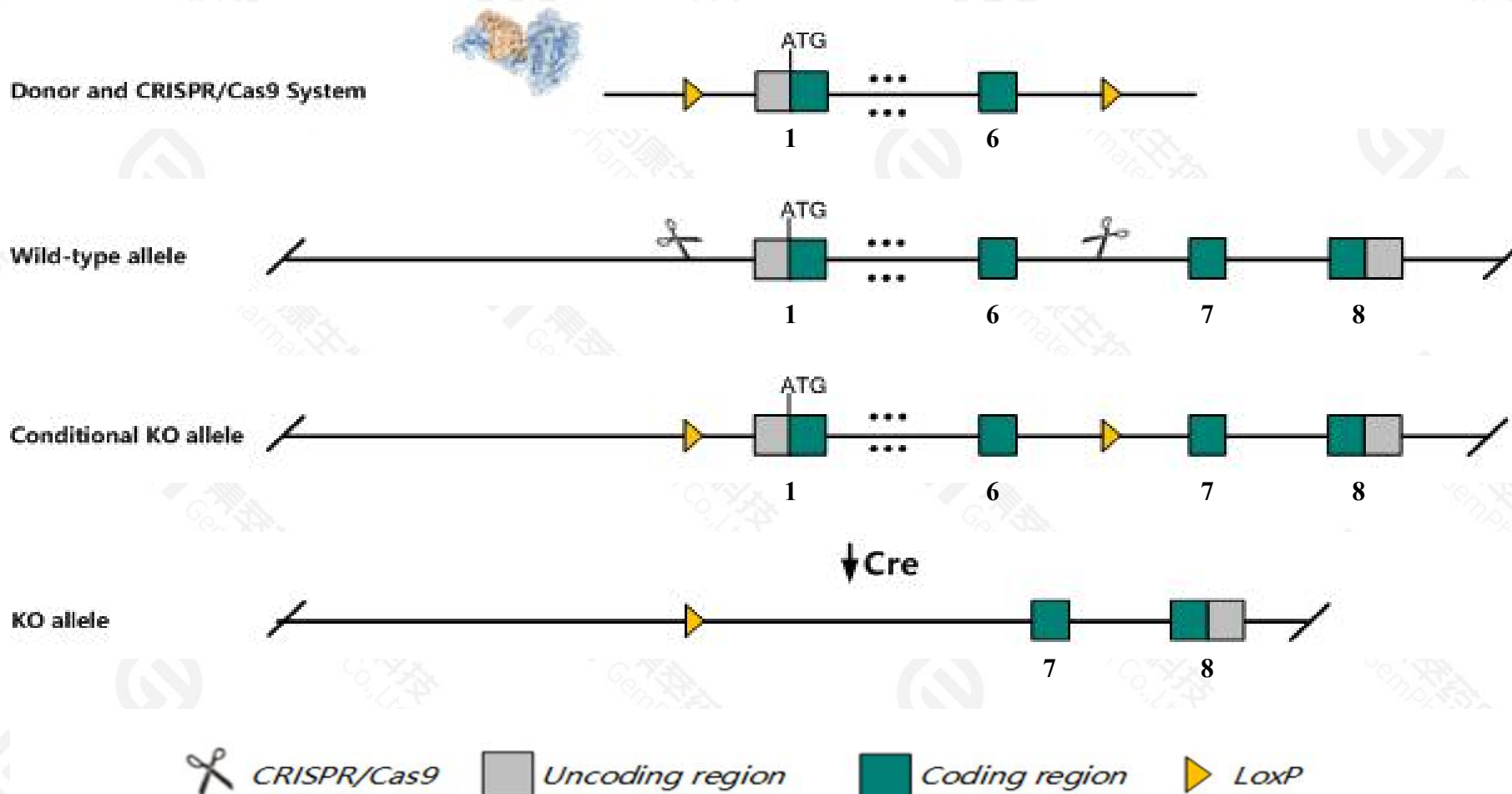
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Vtn* gene has 4 transcripts. According to the structure of *Vtn* gene, exon1-exon6 of *Vtn-201*(ENSMUST00000017488.4) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vtn* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, homozygotes and heterozygotes for a targeted null mutation appear to develop, mature, and reproduce normally.
- The floxed region is near to the N-terminal of *Sarm1* gene and *Sebox* gene, this strategy extremely likely influence the regulatory function of the N-terminal of these genes.
- The *Vtn* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Vtn vitronectin [Mus musculus (house mouse)]

Gene ID: 22370, updated on 13-Mar-2020

Summary



Official Symbol Vtn provided by [MGI](#)

Official Full Name vitronectin provided by [MGI](#)

Primary source [MGI:MGI:98940](#)

See related [Ensembl:ENSMUSG00000017344](#)

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 AI256434, Vn

Expression Biased expression in liver adult (RPKM 833.3), liver E18 (RPKM 554.4) and 2 other tissues [See more](#)

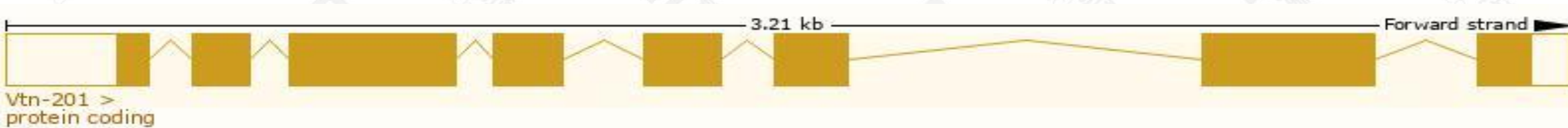
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

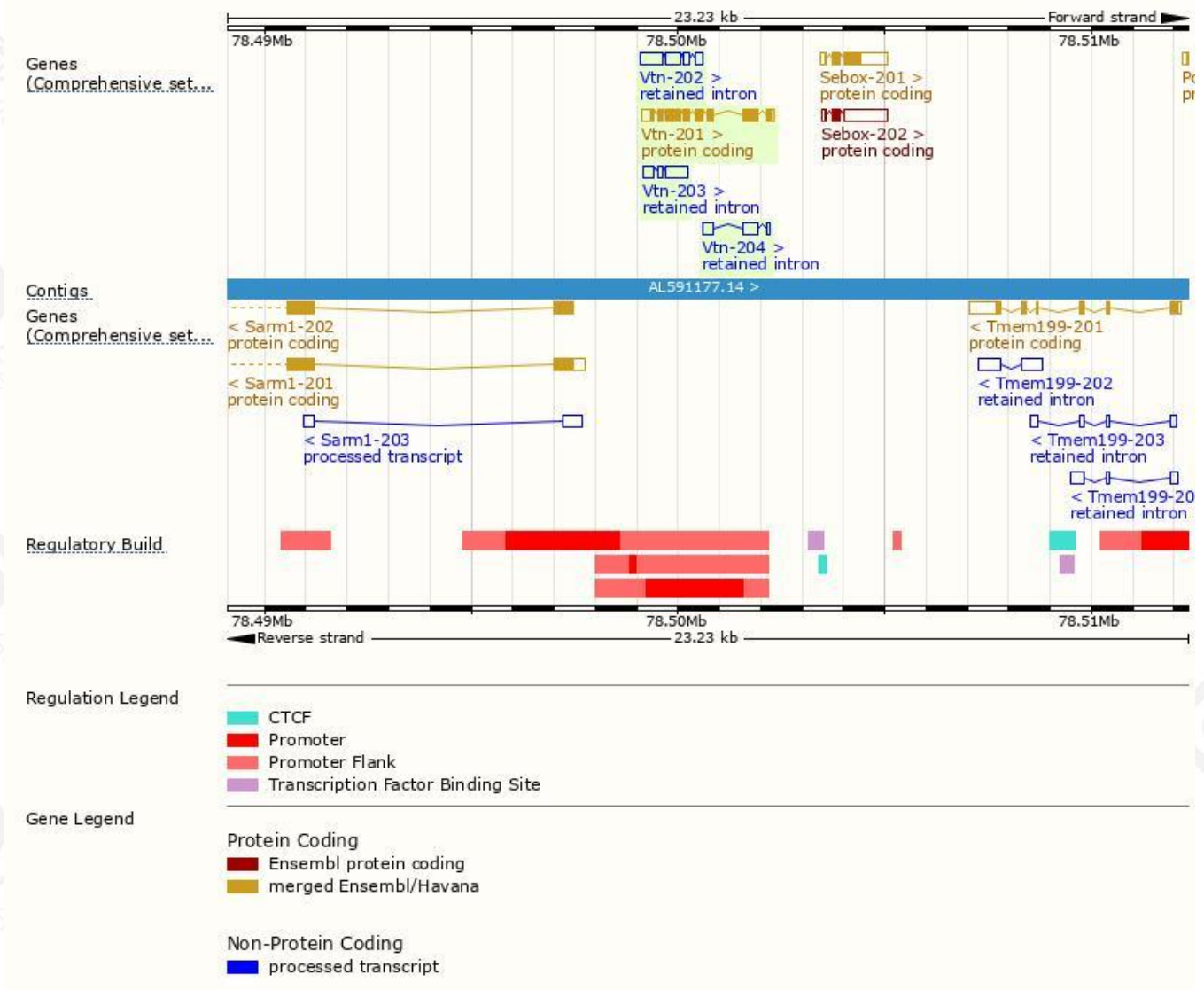
The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vtn-201	ENSMUST00000017488.4	1744	478aa	Protein coding	CCDS25106	P29788	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
Vtn-202	ENSMUST00000128479.1	1171	No protein	Retained intron	-	-	TSL:2
Vtn-203	ENSMUST00000146997.1	906	No protein	Retained intron	-	-	TSL:2
Vtn-204	ENSMUST00000153628.1	678	No protein	Retained intron	-	-	TSL:2

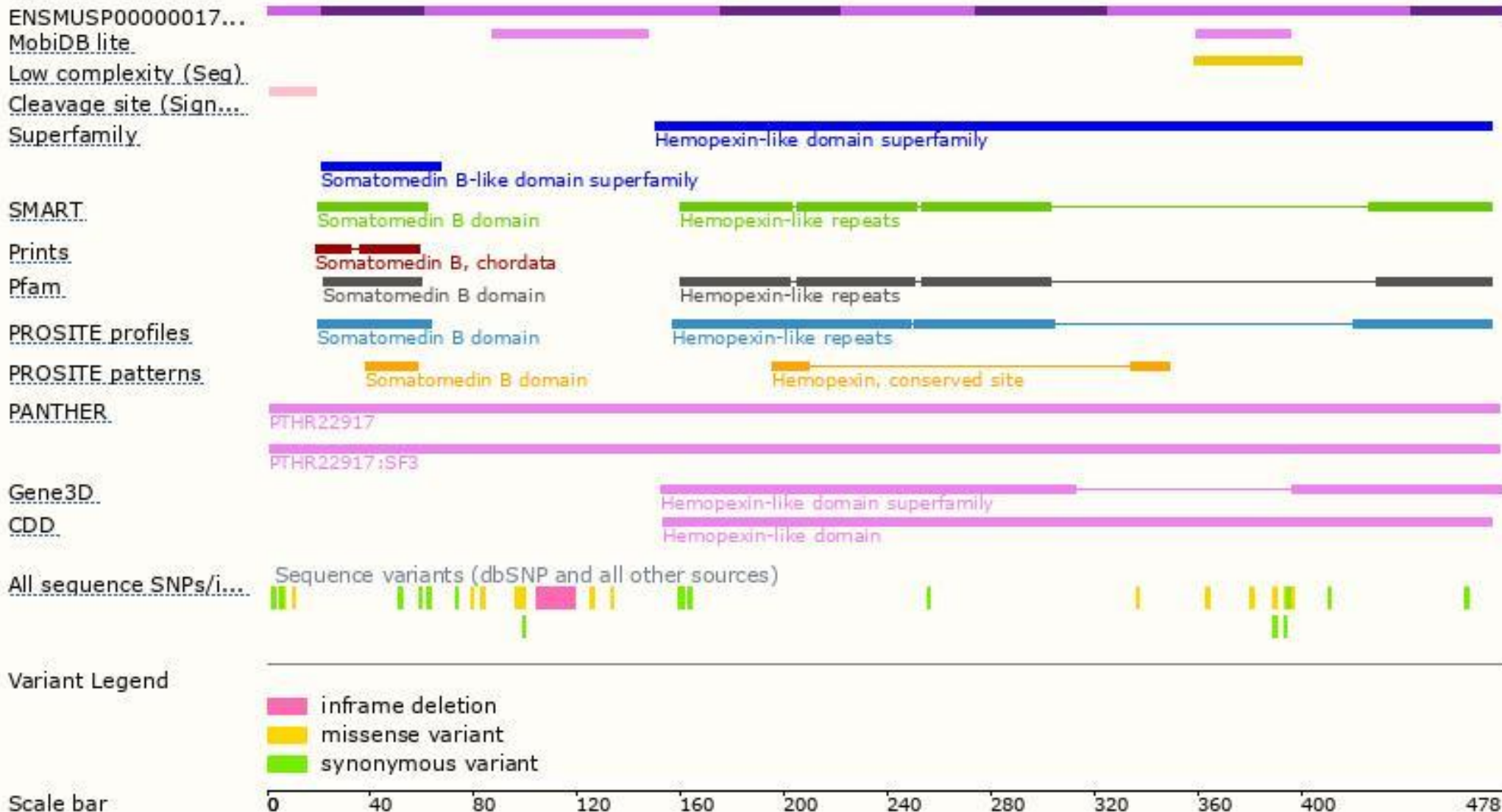
The strategy is based on the design of *Vtn-201* transcript, the transcription is shown below:



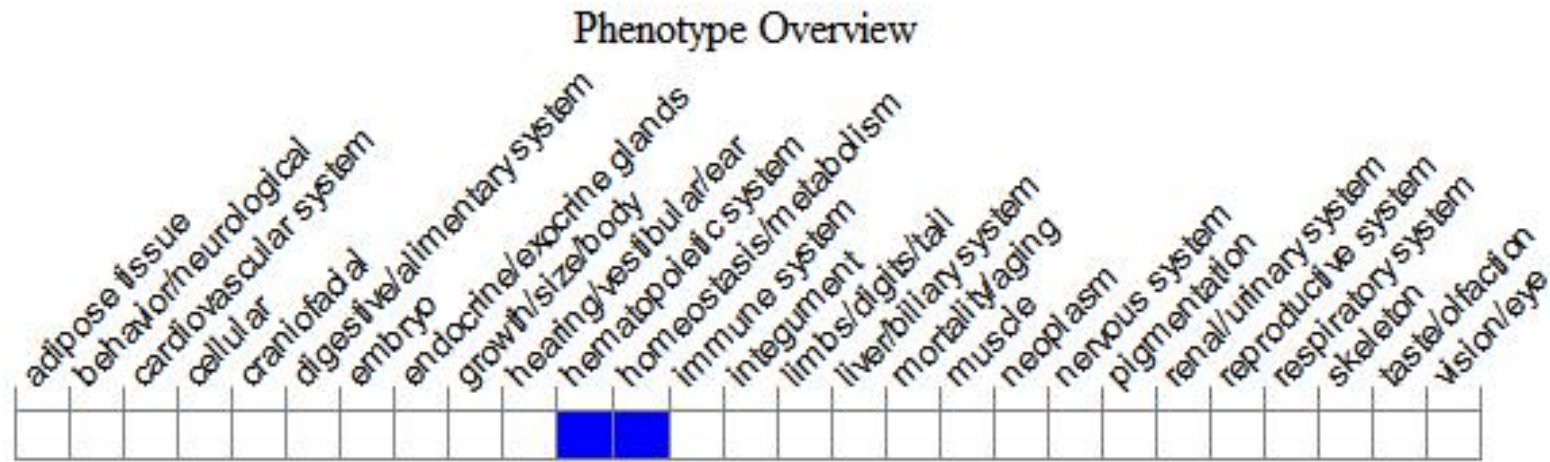
Genomic location distribution



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, homozygotes and heterozygotes for a targeted null mutation appear to develop, mature, and reproduce normally.

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

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