Cwc27 Cas9-KO Strategy

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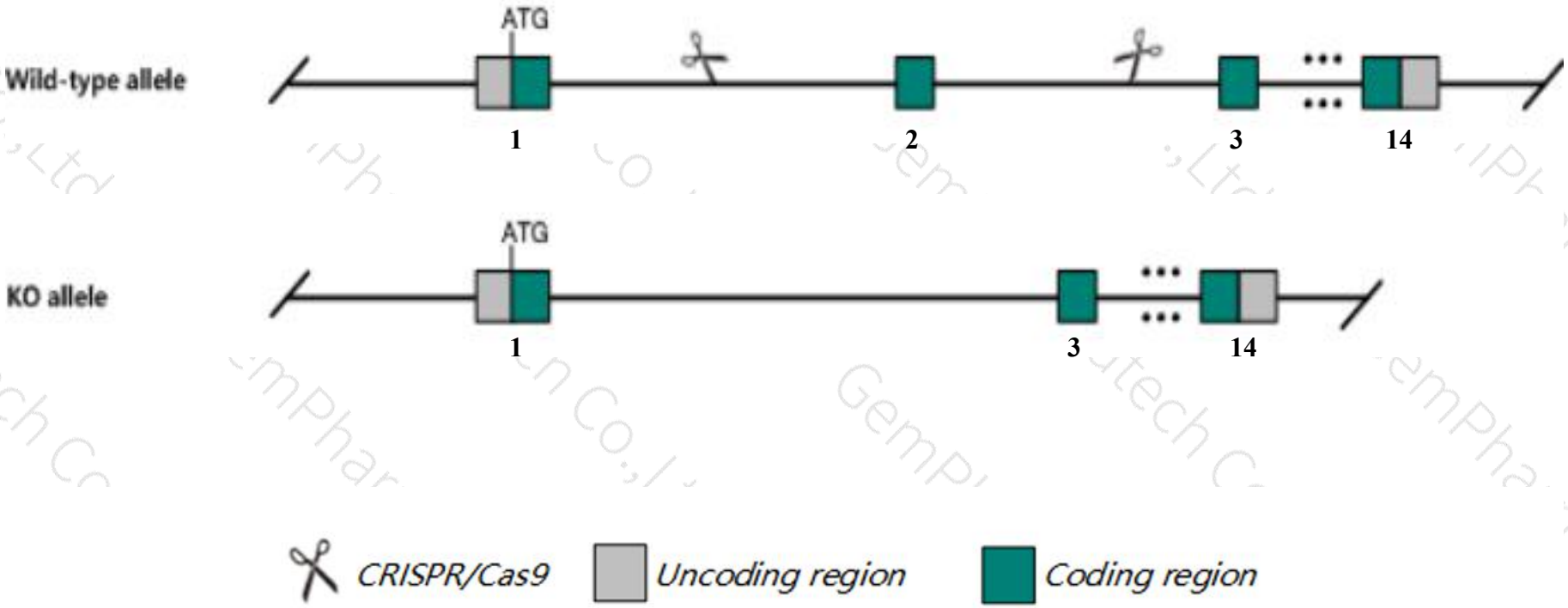
Design Date: 2020-4-15

Project Overview

Project Name	***Cwc27***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cwc27* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cwc27* gene has 4 transcripts. According to the structure of *Cwc27* gene, exon2 of *Cwc27-201* (ENSMUST00000022228.12) transcript is recommended as the knockout region.The region contains 97bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cwc27* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

- According to the existing MGI data,homozygous mutant mice exhibit reduced viability. Surviors after birth show signs of growth retardation and retinal depigmentation, along with numerous neurological, immunological, and blood chemistry abnormalities.
- The partial intron of transcript *Srek1ip1*-203 will be deleted together in this strategy.
- The knockout region is near to the N-terminal of *Srek1ip1* gene,this strategy may influence the regulatory function of the N-terminal of *Srek1ip1* gene.
- Transcript *Cwc27*-202&203 may not be affected.
- The *Cwc27* gene is located on the Chr13. 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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Cwc27 CWC27 spliceosome-associated protein [Mus musculus (house mouse)]

Gene ID: 67285, updated on 13-Mar-2020

Summary

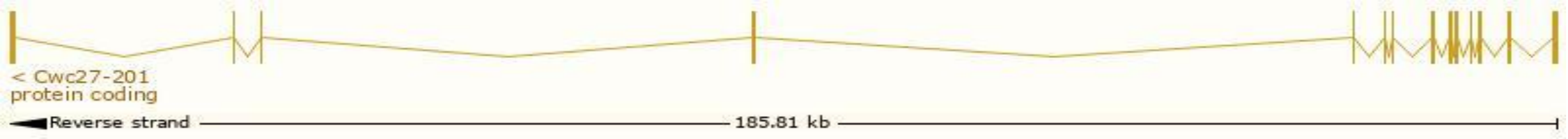
Official Symbol	Cwc27 provided by MGI
Official Full Name	CWC27 spliceosome-associated protein provided byMGI
Primary source	MGI:MGI:1914535
See related	Ensembl:ENSMUSG00000021715
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110009E13Rik, NY-CO-10, Sdccag10
Expression	Broad expression in CNS E11.5 (RPKM 1.3), CNS E14 (RPKM 0.7) and 21 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

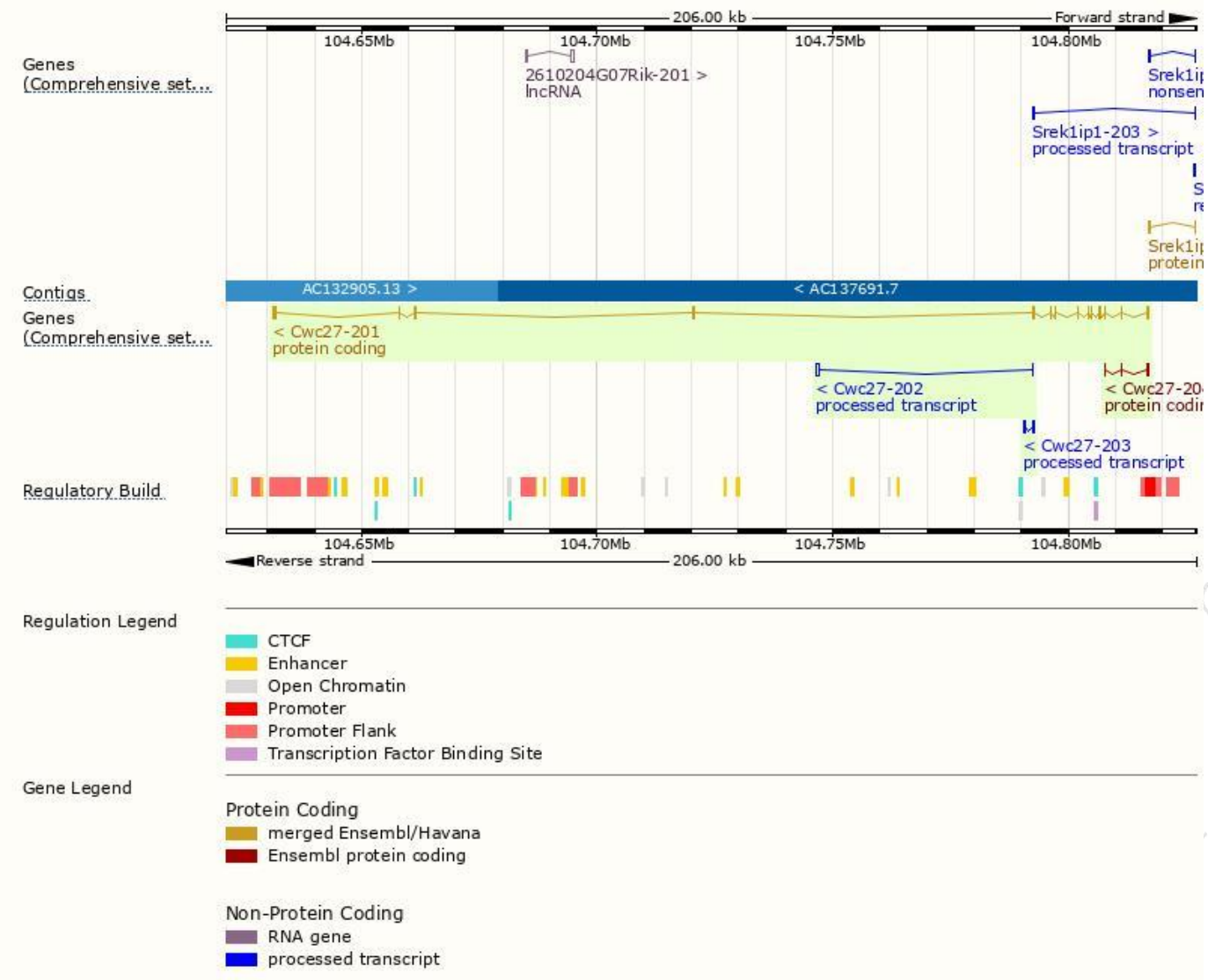
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cwc27-201	ENSMUST00000022228.12	2071	469aa	Protein coding	CCDS26752	Q3TKY6	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
Cwc27-204	ENSMUST00000154165.1	353	83aa	Protein coding	-	D3Z2U3	CDS 3' incomplete TSL:3
Cwc27-202	ENSMUST00000141495.1	588	No protein	Processed transcript	-	-	TSL:3
Cwc27-203	ENSMUST00000147514.1	451	No protein	Processed transcript	-	-	TSL:3

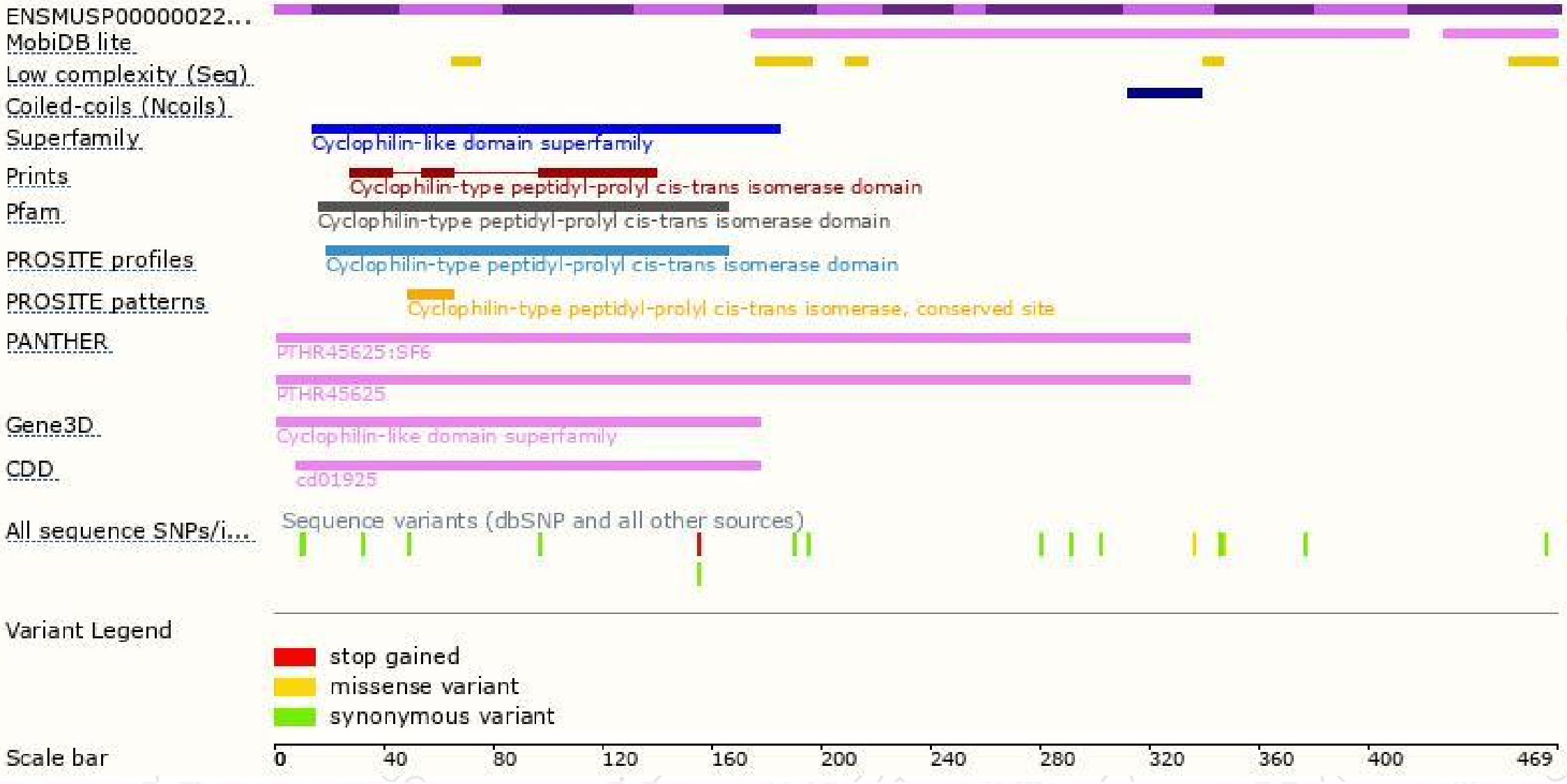
The strategy is based on the design of *Cwc27-201* transcript,the transcription is shown below



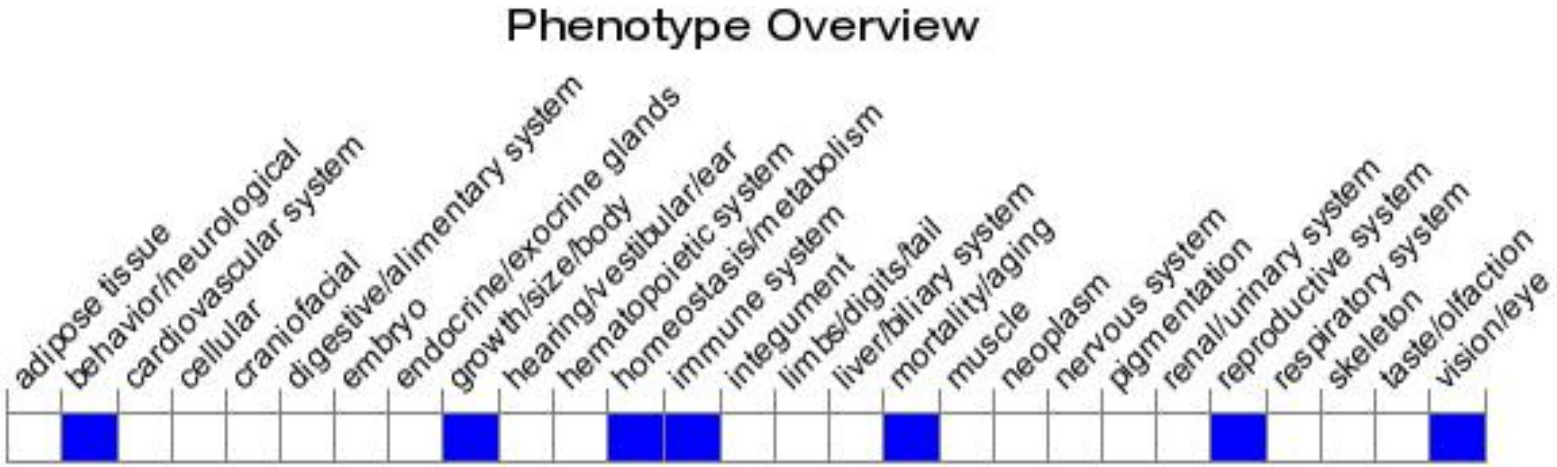
Genomic location distribution



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/).

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

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