

Nol9 Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Nol9

Project type

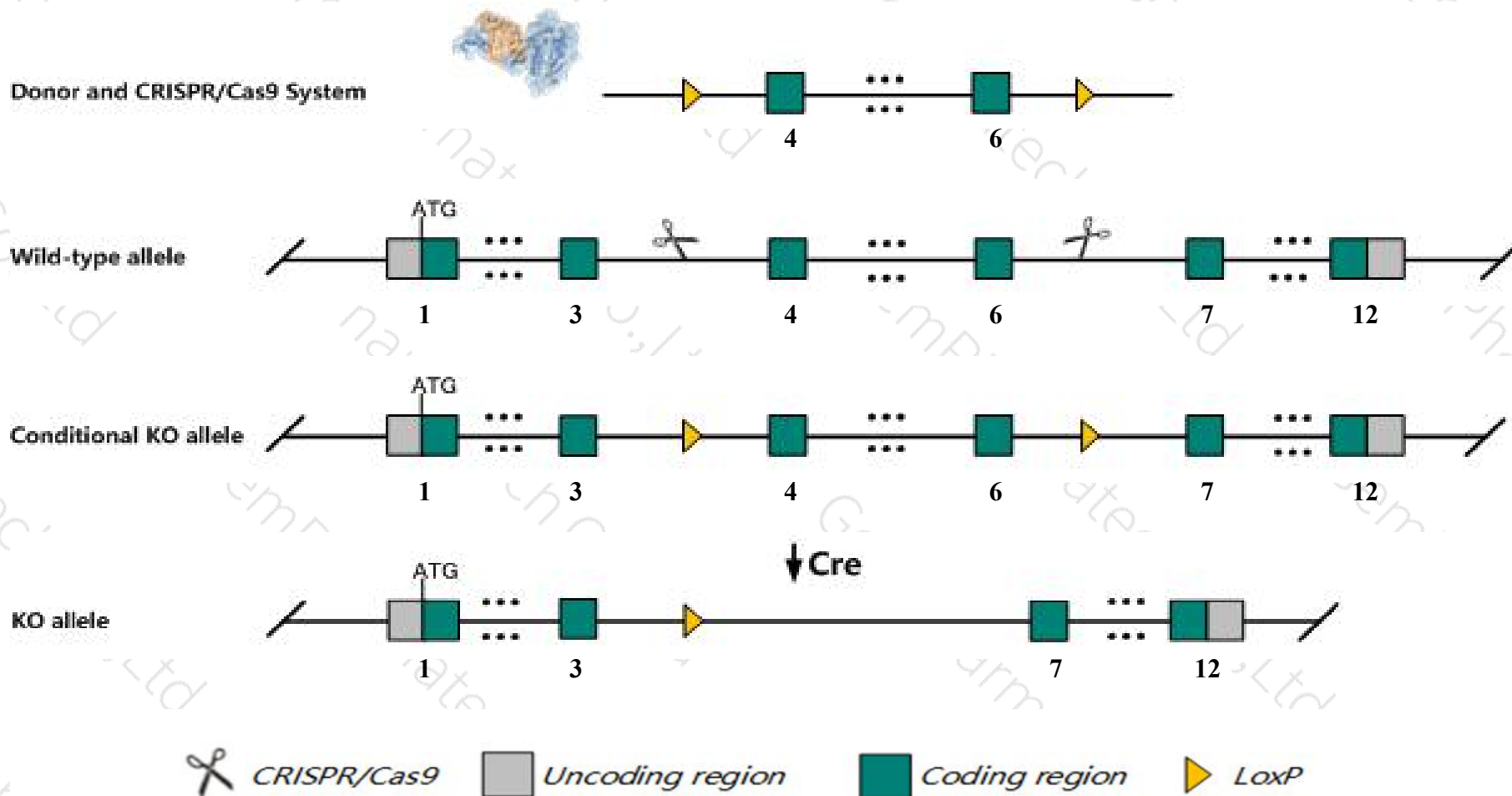
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *No19* gene. The schematic diagram is as follows:



- The *Nol9* gene has 5 transcripts. According to the structure of *Nol9* gene, exon4-exon6 of *Nol9-201* (ENSMUST00000084116.12) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nol9* 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.

- The N-terminal of *Nol9* gene will remain several amino acids ,it may remain the partial function of *Nol9* gene.
- The floxed region is near to the N-terminal of *Tas1r1* gene,this strategy may influence the regulatory function of the N-terminal of *Tas1r1* gene.
- The *Nol9* gene is located on the Chr4. 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)

Nol9 nucleolar protein 9 [Mus musculus (house mouse)]

Gene ID: 74035, updated on 13-Mar-2020

Summary



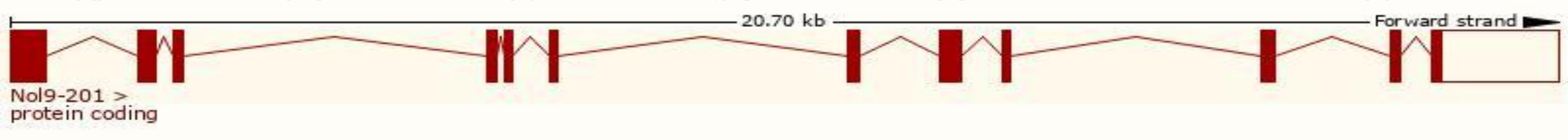
Official Symbol	Nol9 provided by MGI
Official Full Name	nucleolar protein 9 provided by MGI
Primary source	MGI:MGI:1921285
See related	Ensembl:ENSMUSG00000028948
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4632412I24Rik, 6030462G04Rik, A1449622, AW490720
Expression	Ubiquitous expression in ovary adult (RPKM 14.1), thymus adult (RPKM 12.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

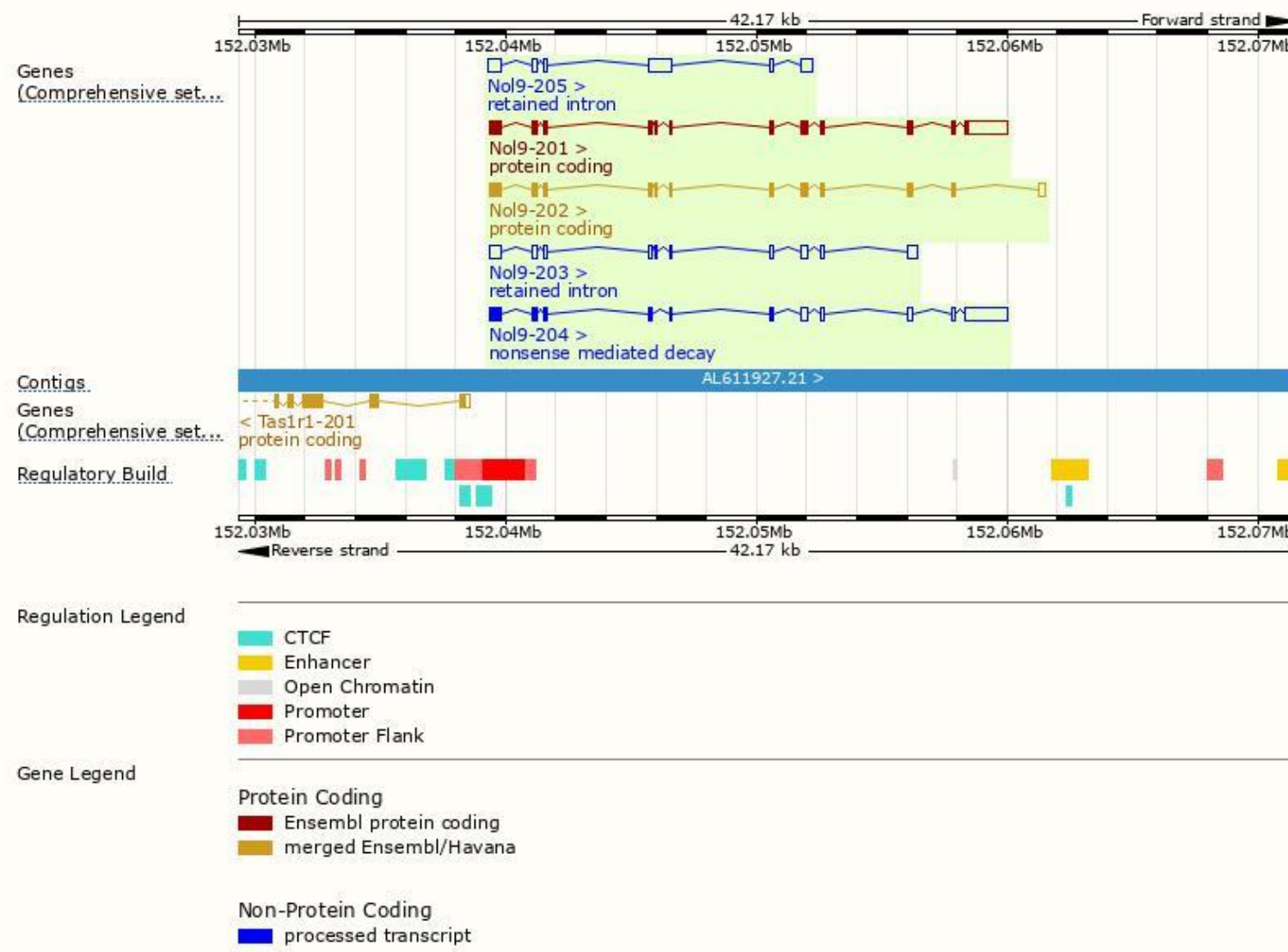
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
NoI9-201	ENSMUST00000084116.12	3722	714aa	Protein coding	CCDS51389	Q3TZX8	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 ALT2
NoI9-202	ENSMUST00000103197.4	2271	671aa	Protein coding	CCDS18986	Q3TZX8	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 P3
NoI9-204	ENSMUST00000131696.2	3616	361aa	Nonsense mediated decay	-	A0A0U1RPVZ	CDS 5' incomplete TSL:1
NoI9-205	ENSMUST00000147797.7	2419	No protein	Retained intron	-	-	TSL:2
NoI9-203	ENSMUST00000105663.7	2064	No protein	Retained intron	-	-	TSL:1

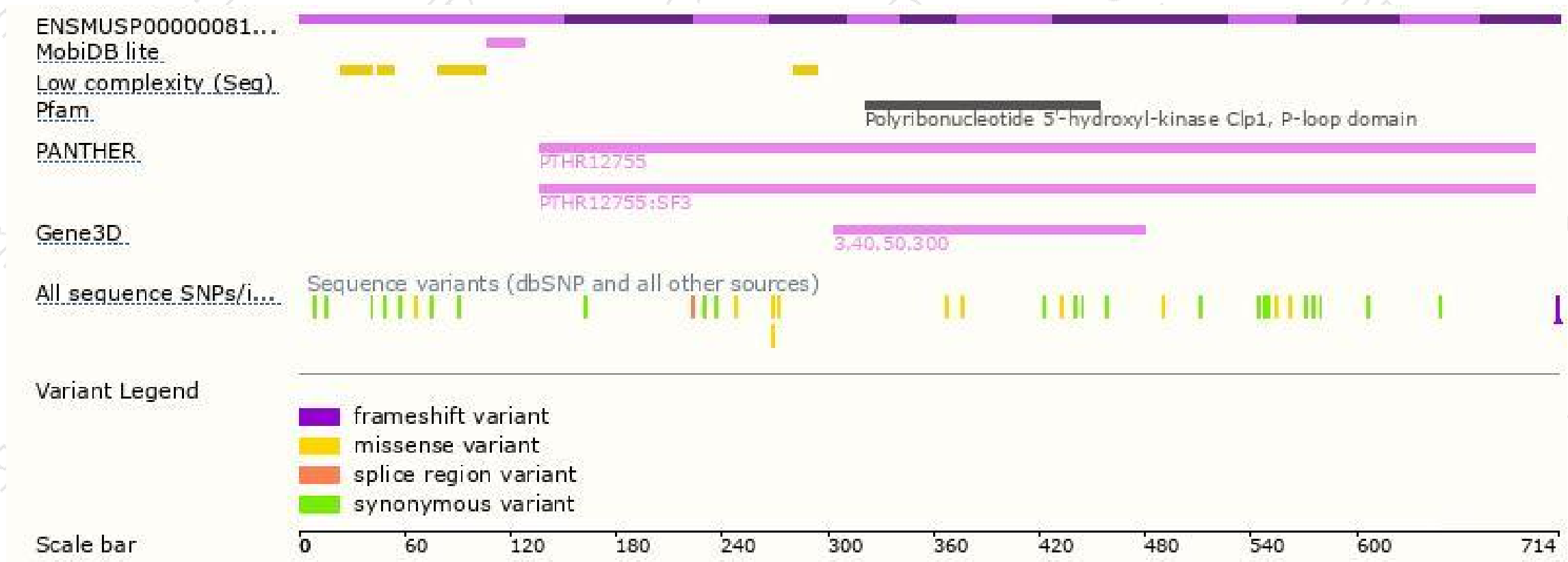
The strategy is based on the design of *NoI9-201* transcript,the transcription is shown below:



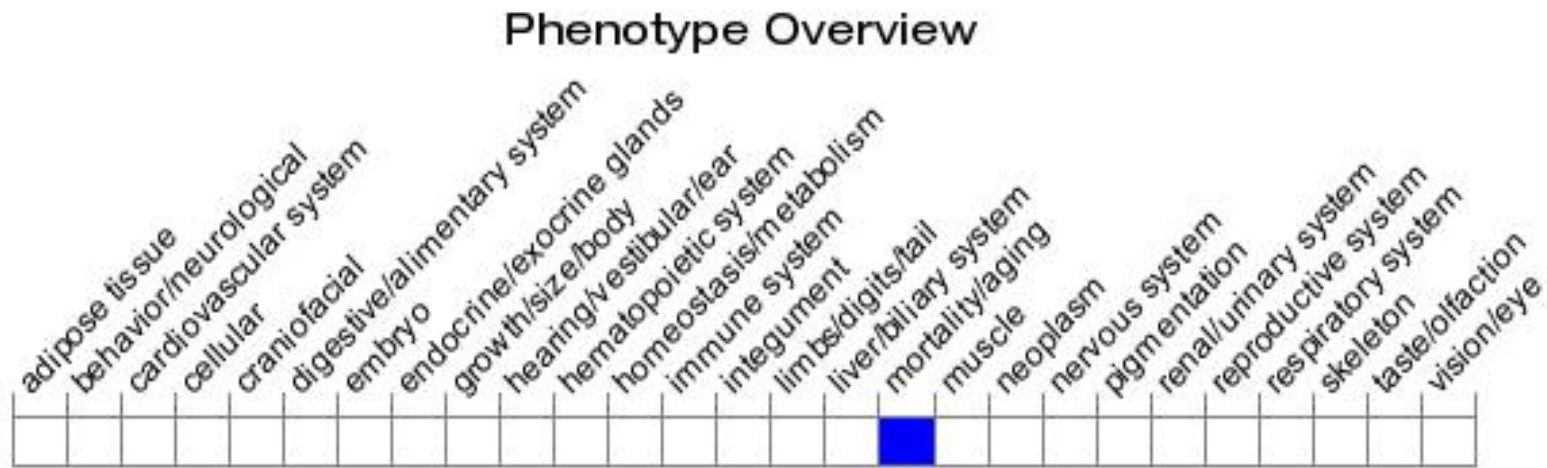
Genomic location distribution



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/>).

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

Tel: 400-9660890

