

***Kcnab1* Cas9-CKO Strategy**

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Reviewer:

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Project Overview

Project Name

Kcnab1

Project type

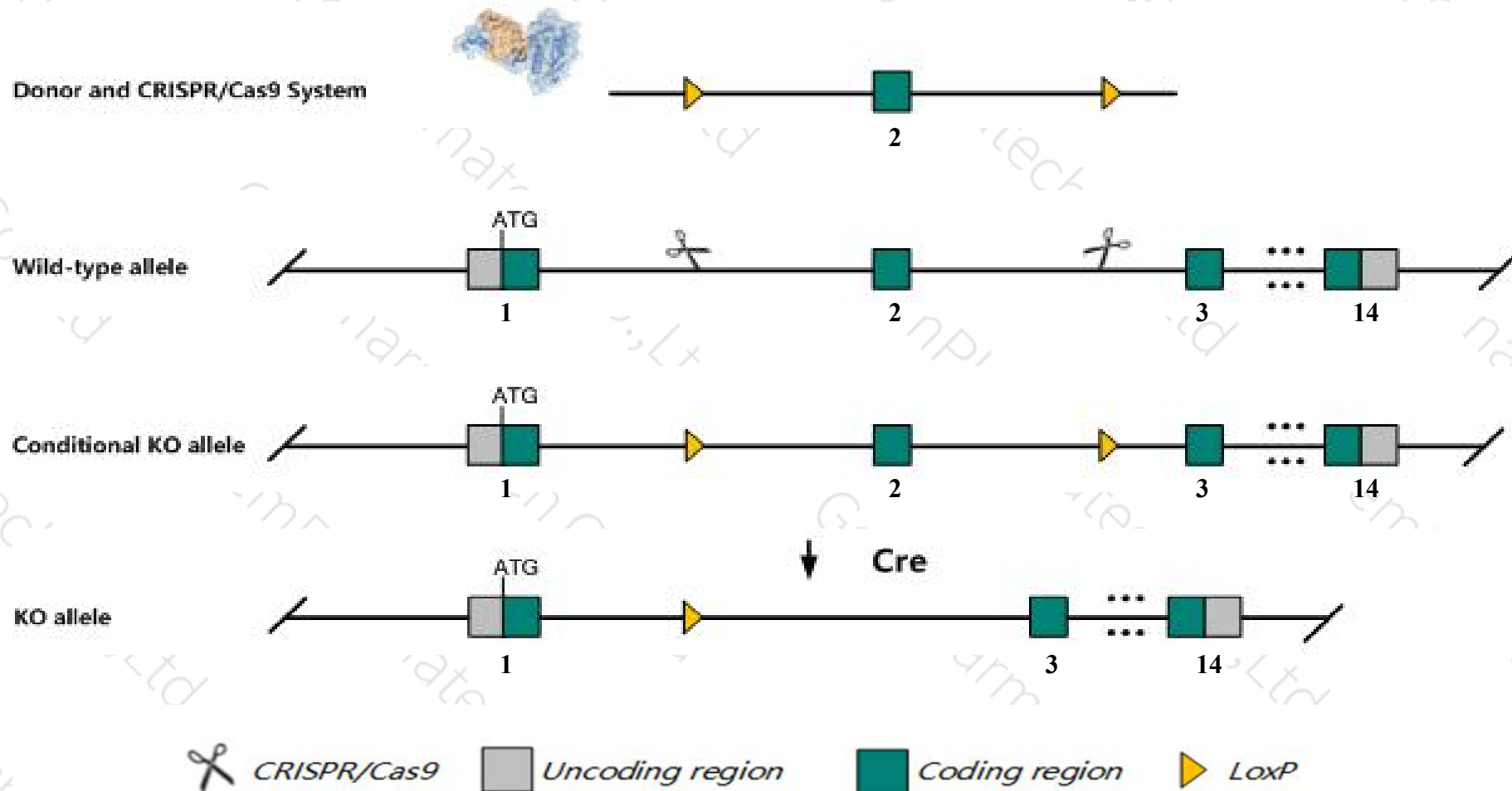
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnab1* gene. The schematic diagram is as follows:



Technical routes

- The *Kcnab1* gene has 9 transcripts. According to the structure of *Kcnab1* gene, exon2 of *Kcnab1-201* (ENSMUST00000049230.10) transcript is recommended as the knockout region. The region contains 44bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnab1* 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, Mice homozygous for disruptions in this gene experience some learning defects but are otherwise normal.
- The flox region is in the intron of the A330015K06Rik gene, which may affect the regulation of this gene.
- The *Kcnab1* gene is located on the Chr3. 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)

Kcnab1 potassium voltage-gated channel, shaker-related subfamily, beta member 1 [*Mus musculus* (house mouse)]

Gene ID: 16497, updated on 13-Mar-2020

Summary

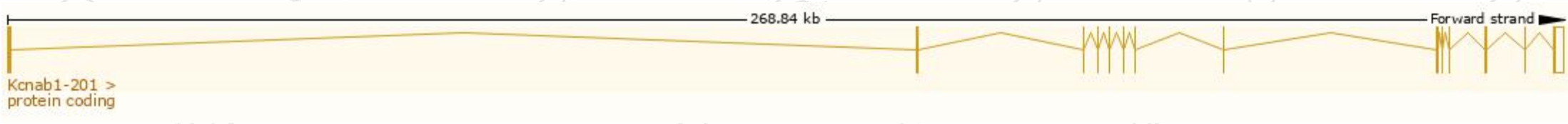
Official Symbol	Kcnab1 provided by MGI
Official Full Name	potassium voltage-gated channel, shaker-related subfamily, beta member 1 provided by MGI
Primary source	MGI:MGI:109155
See related	Ensembl:ENSMUSG00000027827
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Akr8a8; Kvbeta1.1; mKv(beta)1
Expression	Biased expression in cerebellum adult (RPKM 15.7), cortex adult (RPKM 8.2) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

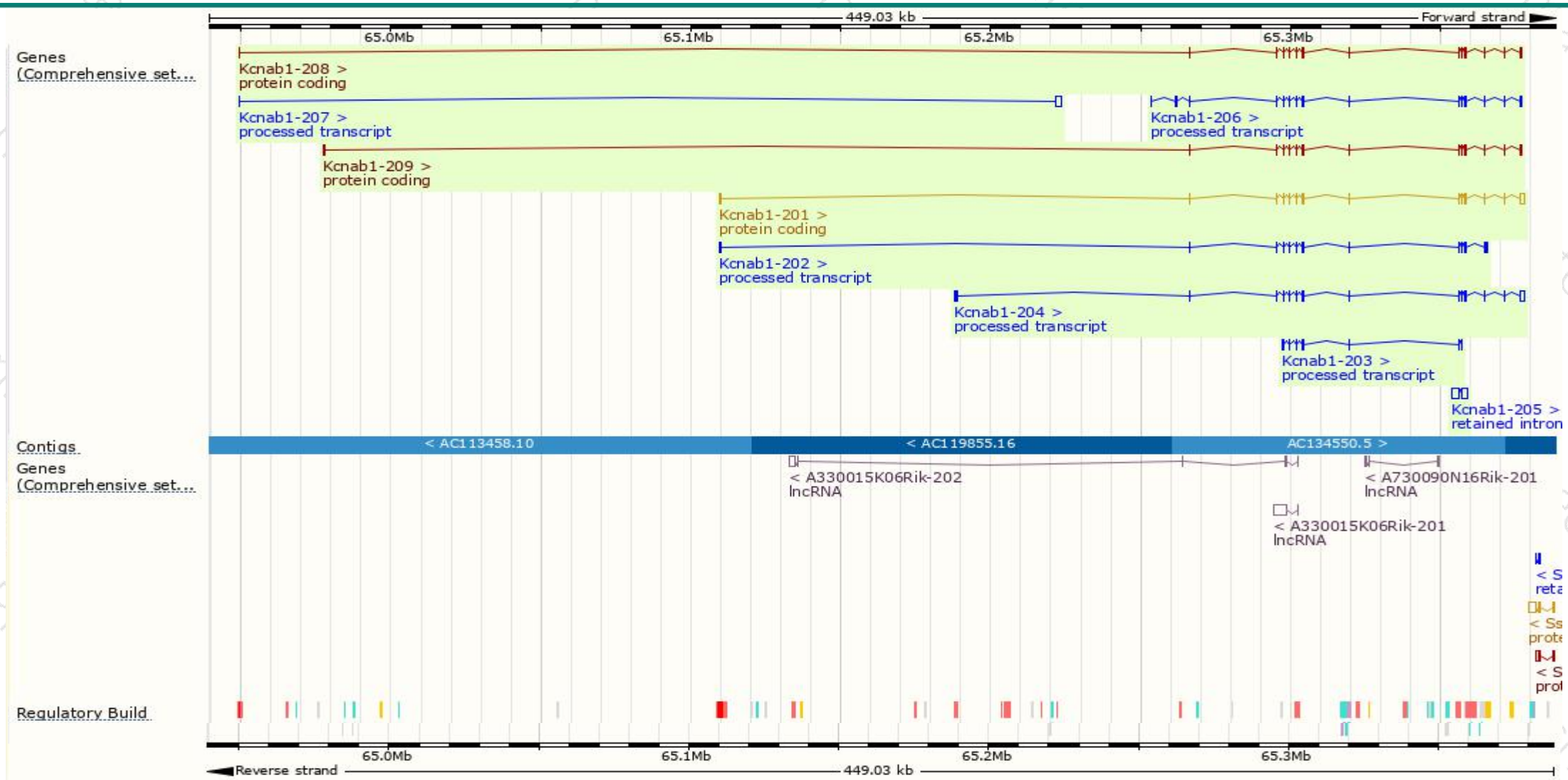
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnab1-201	ENSMUST00000049230.10	3245	401aa	Protein coding	CCDS38447	P63143	TSL:1 GENCODE basic APPRIS P2
Kcnab1-209	ENSMUST00000239069.1	1677	408aa	Protein coding	-	-	GENCODE basic APPRIS ALT1
Kcnab1-208	ENSMUST00000238901.1	1635	419aa	Protein coding	-	-	GENCODE basic
Kcnab1-204	ENSMUST00000161404.7	2849	No protein	Processed transcript	-	-	TSL:1
Kcnab1-207	ENSMUST00000193778.1	2174	No protein	Processed transcript	-	-	TSL:1
Kcnab1-206	ENSMUST00000161979.7	1965	No protein	Processed transcript	-	-	TSL:1
Kcnab1-202	ENSMUST00000159525.7	1923	No protein	Processed transcript	-	-	TSL:1
Kcnab1-203	ENSMUST00000160136.2	534	No protein	Processed transcript	-	-	TSL:5
Kcnab1-205	ENSMUST00000161956.1	4382	No protein	Retained intron	-	-	TSL:1

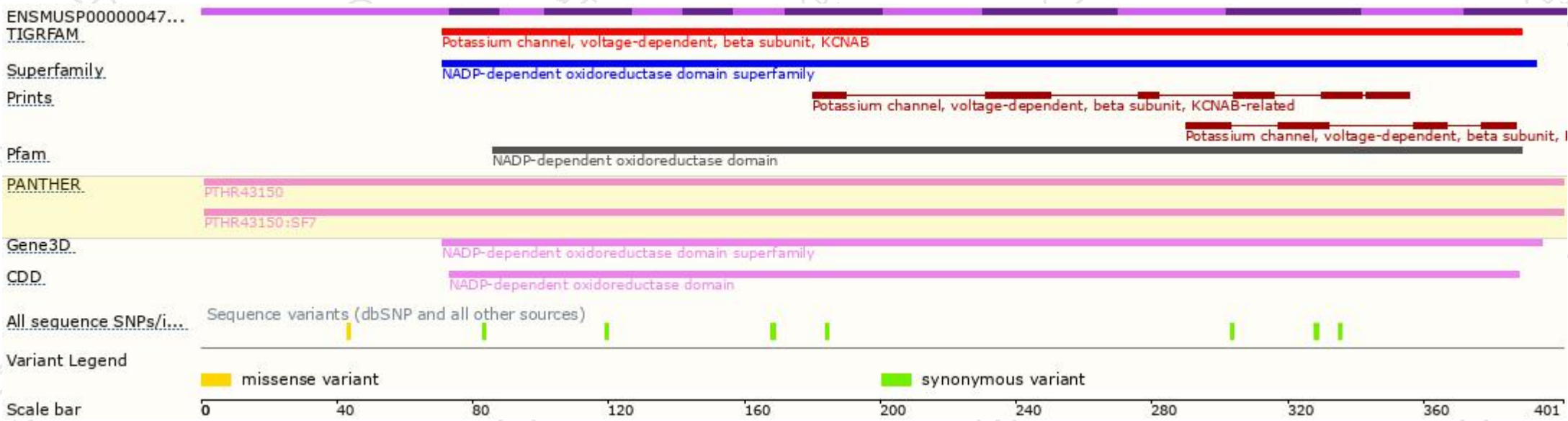
The strategy is based on the design of *Kcnab1-201* transcript,The transcription is shown below



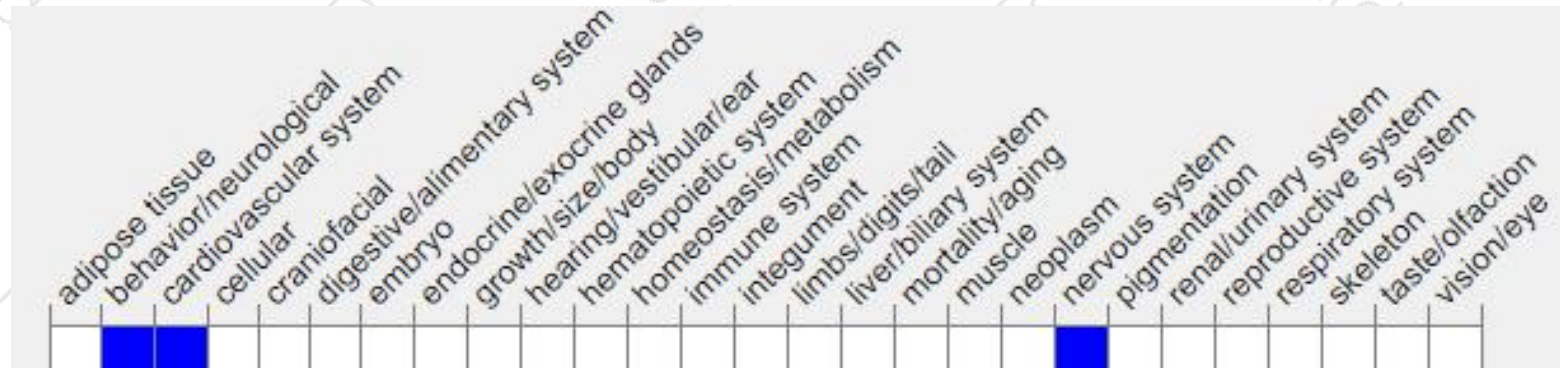
Genomic location distribution



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 disruptions in this gene experience some learning defects but are otherwise normal.

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

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