

Lhx2 Cas9-KO Strategy

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Project Overview

Project Name

Lhx2

Project type

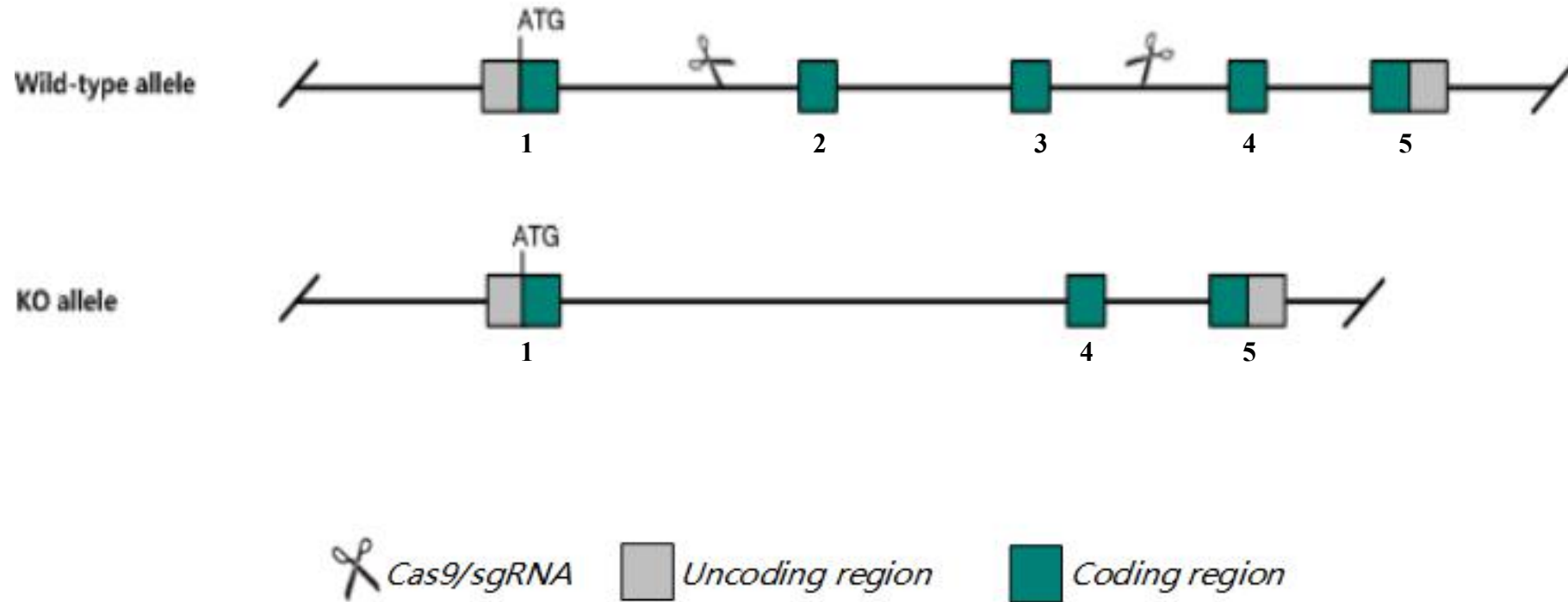
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lhx2* gene. The schematic diagram is as follows:



The *Lhx2* gene has 7 transcripts. According to the structure of *Lhx2* gene, exon2-exon3 of *Lhx2*-201(ENSMUST00000000253.6) transcript is recommended as the knockout region. The region contains 607bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Lhx2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

According to the existing MGI data, mice homozygous for a knock-out allele exhibit lethality during fetal development and the perinatal period with abnormal liver, telencephalon, olfactory bulb, basal ganglion, and eye morphology.

The *Lhx2* gene is located on the Chr2. 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.

Lhx2 LIM homeobox protein 2 [Mus musculus (house mouse)]

Gene ID: 16870, updated on 12-Feb-2021

Summary



Official Symbol Lhx2 provided by [MGI](#)

Official Full Name LIM homeobox protein 2 provided by [MGI](#)

Primary source [MGI:MGI:96785](#)

See related [Ensembl:ENSMUSG00000000247](#)

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 LH, LH2A, Lh-, Lh-2, Lim2, ap, apt, apterous

Expression Biased expression in CNS E14 (RPKM 42.9), whole brain E14.5 (RPKM 35.2) and 6 other tissues [See more](#)

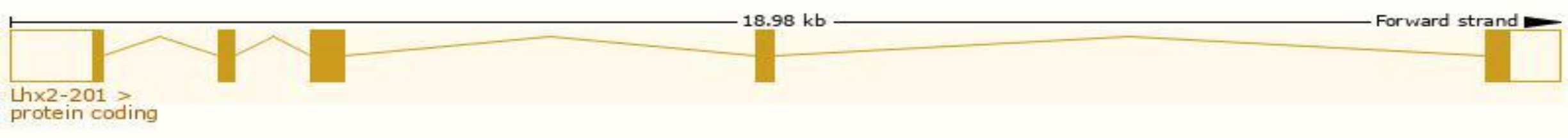
Orthologs [human](#) [all](#)

Transcript information Ensembl

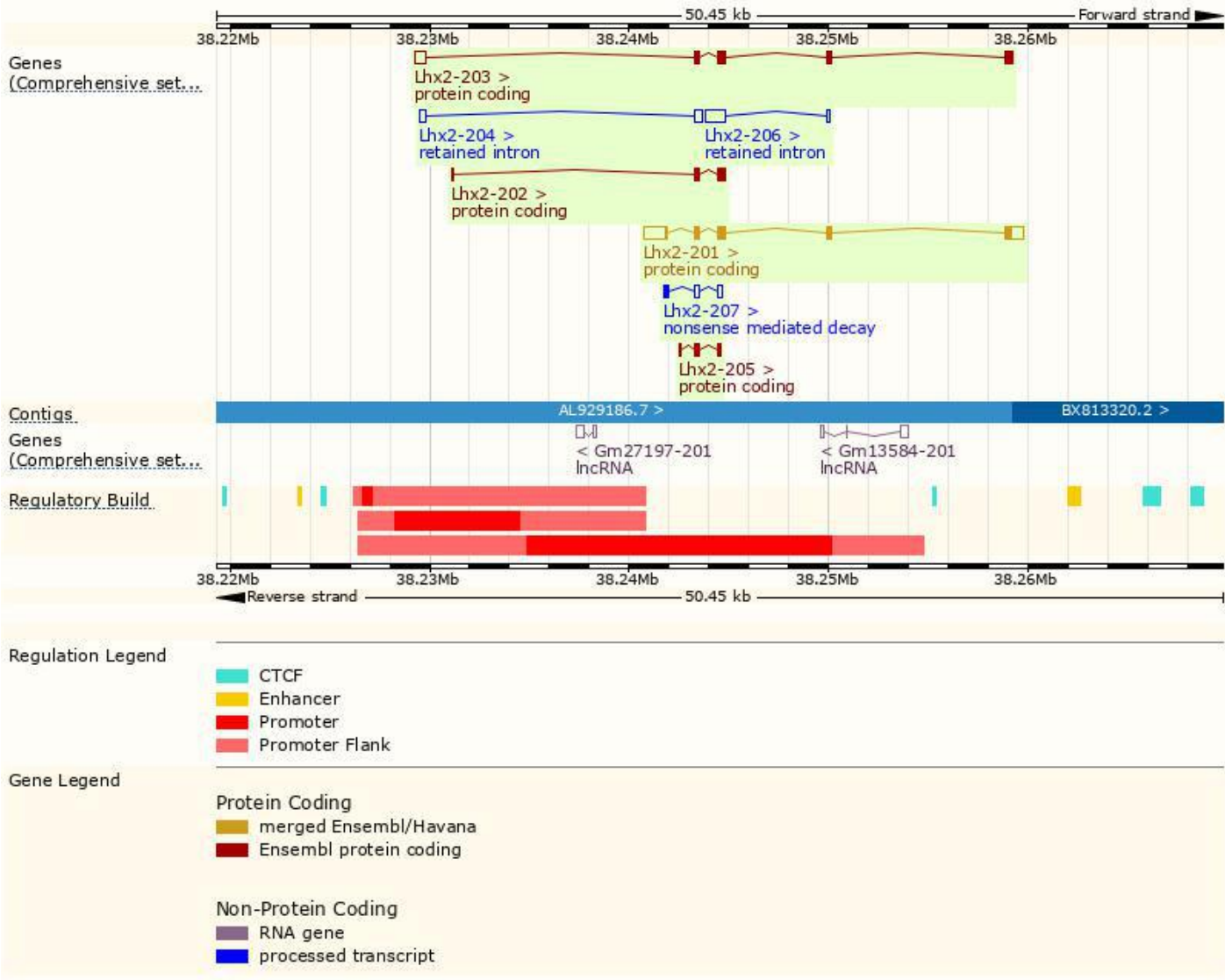
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lhx2-201	ENSMUST00000000253.6	2840	406aa	Protein coding	CCDS16008		TSL:1 , GENCODE basic , APPRIS P1 ,
Lhx2-203	ENSMUST00000143783.9	1696	365aa	Protein coding	CCDS71048		TSL:1 , GENCODE basic ,
Lhx2-202	ENSMUST00000133661.8	654	192aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Lhx2-205	ENSMUST00000155964.3	375	108aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Lhx2-207	ENSMUST00000176229.2	592	49aa	Nonsense mediated decay	-		TSL:3 ,
Lhx2-206	ENSMUST00000175896.2	1243	No protein	Retained intron	-		TSL:2 ,
Lhx2-204	ENSMUST00000149664.2	701	No protein	Retained intron	-		TSL:2 ,

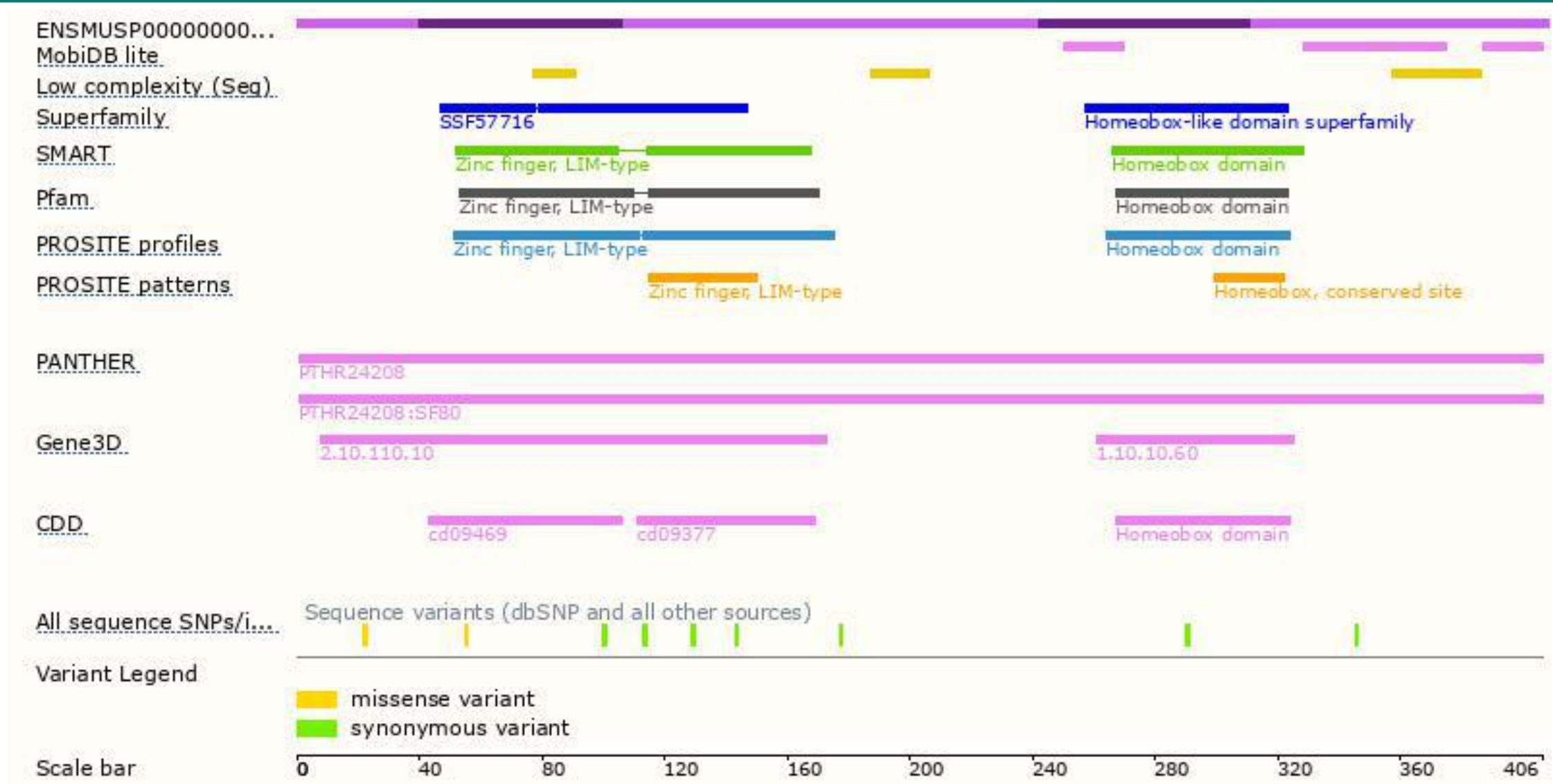
The strategy is based on the design of *Lhx2-201* transcript,the transcription is shown below:



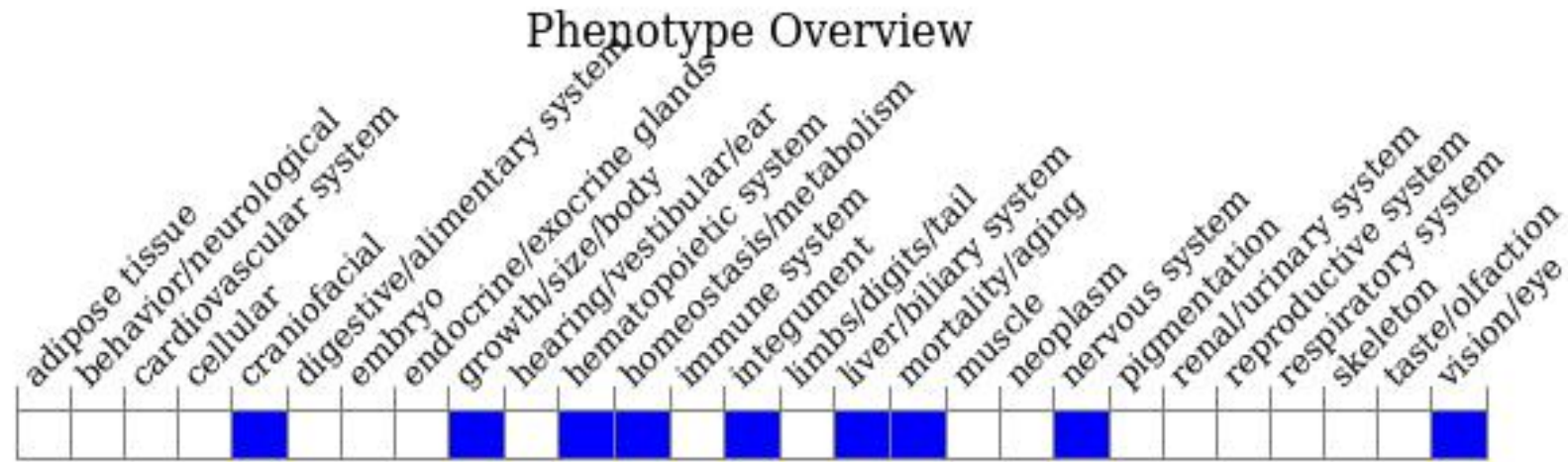
Genomic location distribution



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 a knock-out allele exhibit lethality during fetal development and the perinatal period with abnormal liver, telencephalon, olfactory bulb, basal ganglion, and eye morphology.

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

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