Large1 Cas9-KO Strategy

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Design Date: 2019-10-18

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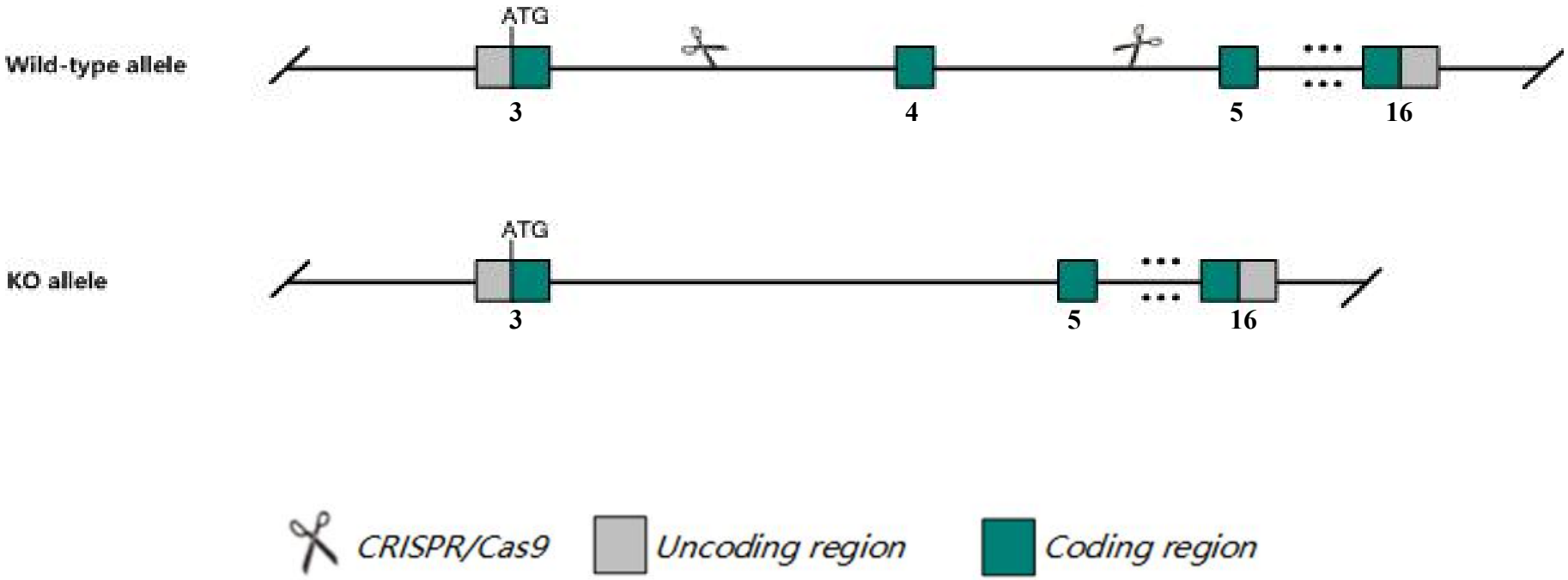
Project Overview

Project Name	***Large1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Large1* gene. The schematic diagram is as follows:



Technical routes

The *Large1* gene has 4 transcripts. According to the structure of *Large1* gene, exon4 of *Large1-204* (ENSMUST00000212459.1) transcript is recommended as the knockout region.The region contains 302bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Large1* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

According to the existing MGI data,Homozygotes exhibit a progressive myopathy, abnormal posture, thoracic kyphosis, calcium deposits in muscle, loss of Schwann cells and myelin, eye and CNS defects, deafness, reduced growth, and death around 4 months.

The *Large1* gene is located on the Chr8. 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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Large1 LARGE xylosyl- and glucuronyltransferase 1 [Mus musculus (house mouse)]

Gene ID: 16795, updated on 31-Jan-2019

Summary

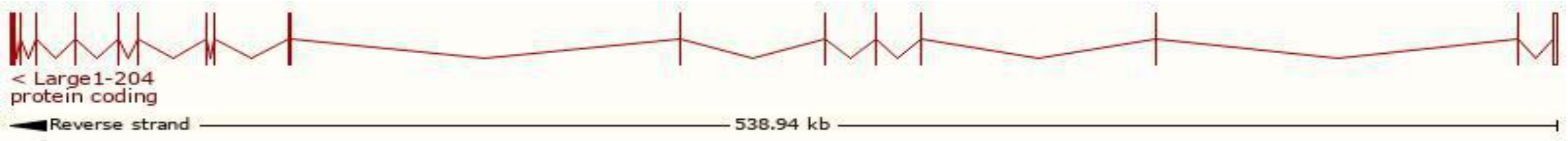
Official Symbol	Large1 provided by MGI
Official Full Name	LARGE xylosyl- and glucuronyltransferase 1 provided by MGI
Primary source	MGI:MGI:1342270
See related	Ensembl:ENSMUSG00000004383
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BPFD#36, Gyltl1a, Large, Mbp-1, Mbp1, enr, fg, froggy, myd
Expression	Broad expression in cortex adult (RPKM 16.0), frontal lobe adult (RPKM 14.9) and 24 other tissues See more
Orthologs	human all

Transcript information Ensembl

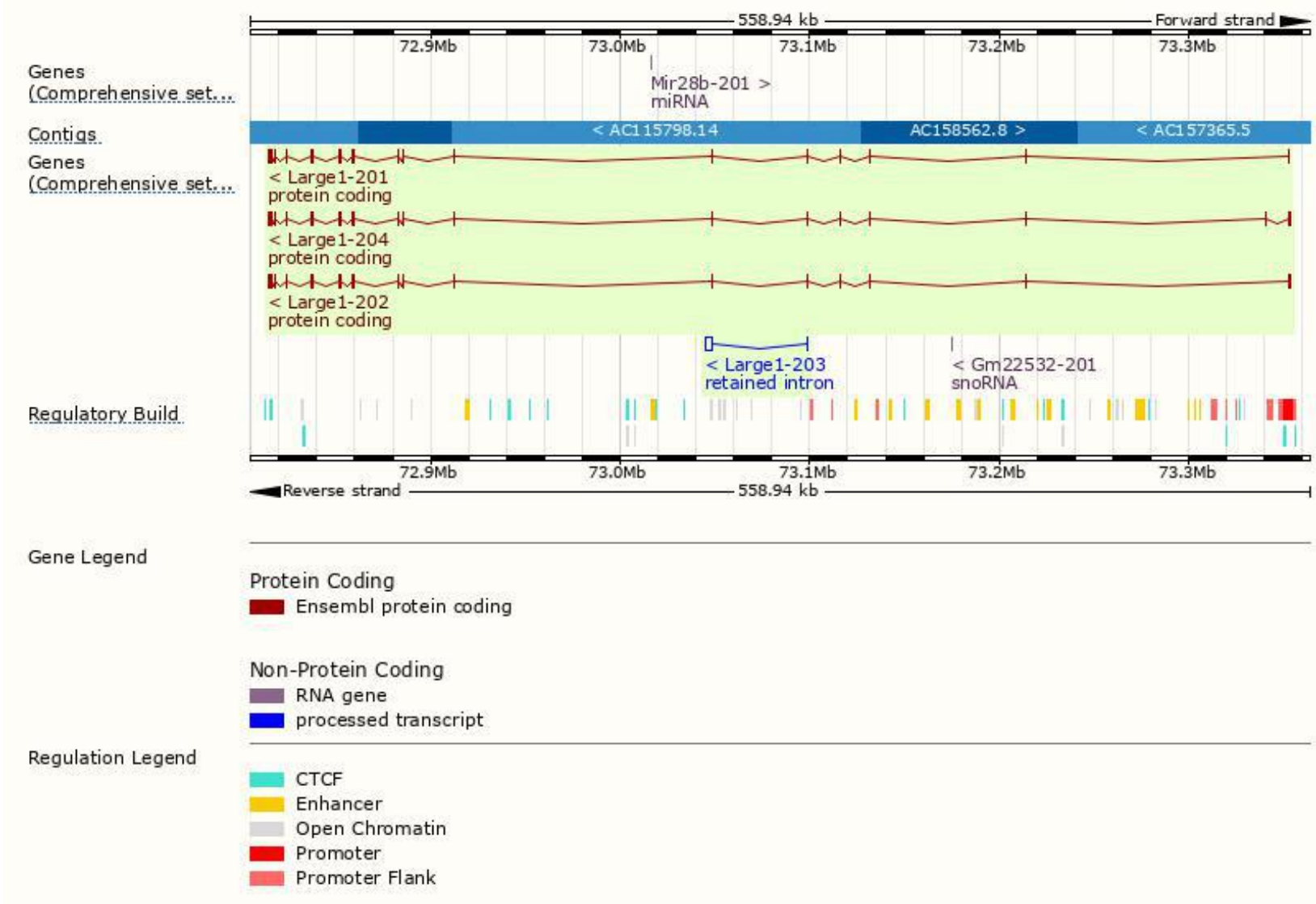
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Large1-204	ENSMUST00000212459.1	4746	756aa	Protein coding	CCDS22420	Q059X9 Q9Z1M7	TSL:1 GENCODE basic APPRIS P1
Large1-202	ENSMUST00000119826.6	4647	756aa	Protein coding	CCDS22420	Q059X9 Q9Z1M7	TSL:5 GENCODE basic APPRIS P1
Large1-201	ENSMUST00000004497.10	3669	756aa	Protein coding	CCDS22420	Q059X9 Q9Z1M7	TSL:1 GENCODE basic APPRIS P1
Large1-203	ENSMUST00000146249.1	3486	No protein	Retained intron	-	-	TSL:1

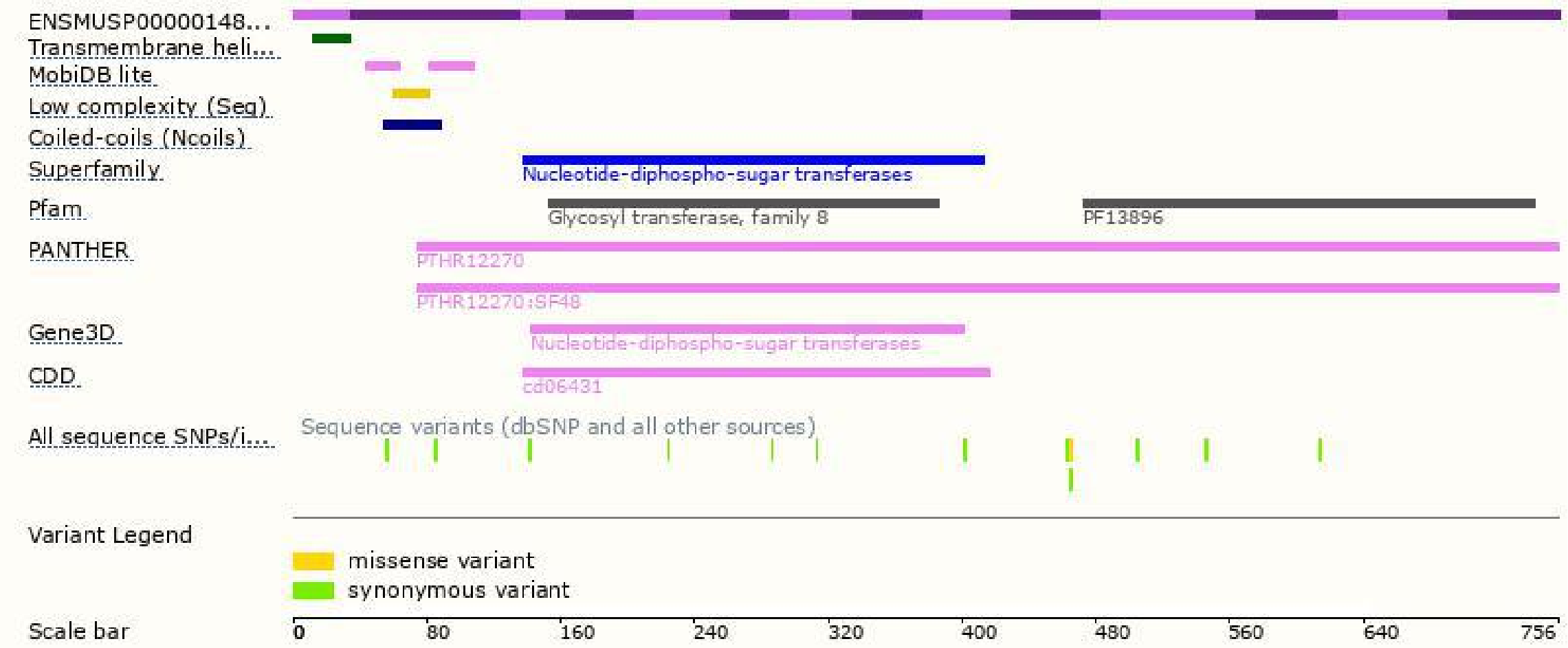
The strategy is based on the design of *Large1-204* transcript,The transcription is shown below



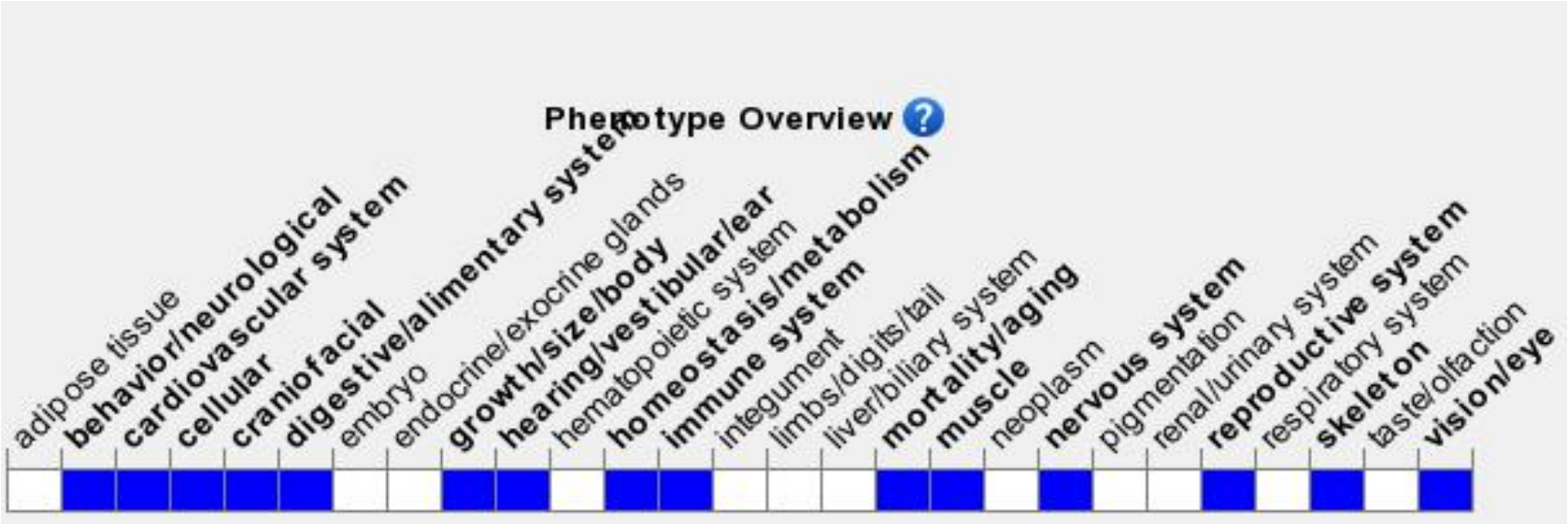
Genomic location distribution



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 exhibit a progressive myopathy, abnormal posture, thoracic kyphosis, calcium deposits in muscle, loss of Schwann cells and myelin, eye and CNS defects, deafness, reduced growth, and death around 4 months.

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