Nfib Cas9-KO Strategy

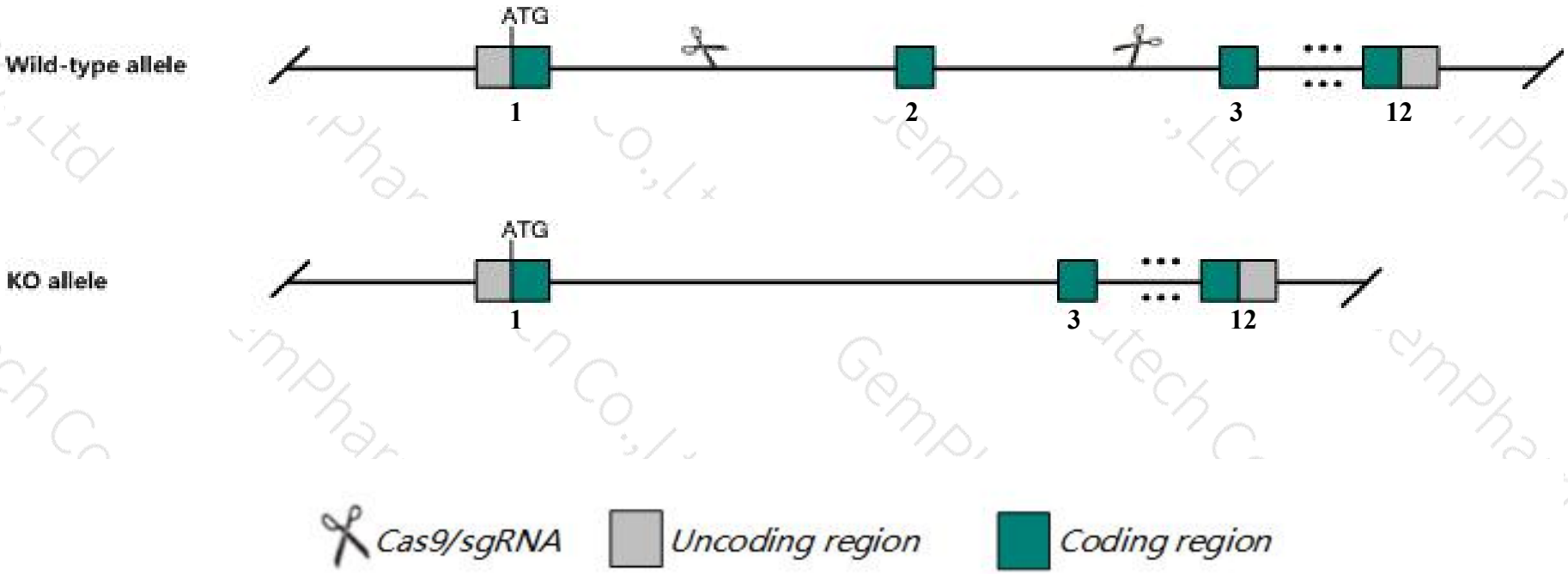
Designer: Ruirui Zhang

Project Overview

Project Name	***Nfib***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

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



Technical routes

- The *Nfib* gene has 12 transcripts. According to the structure of *Nfib* gene, exon2 of *Nfib-201* (ENSMUST00000050872.14) transcript is recommended as the knockout region.The region contains 532bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Nfib* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

- According to the existing MGI data,homozygous inactivation of this gene causes severe lung defects and neonatal death from respiratory failure. Homozygotes for a null allele show callosal agenesis and abnormalities in forebrain, basilar pons, hippocampus, and submandibular gland development, as well as lung maturation defects.

- The *Nfib* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

集萃药康 GemPharmatech

Nfib nuclear factor I/B [Mus musculus (house mouse)]

Gene ID: 18028, updated on 24-Feb-2019

Summary

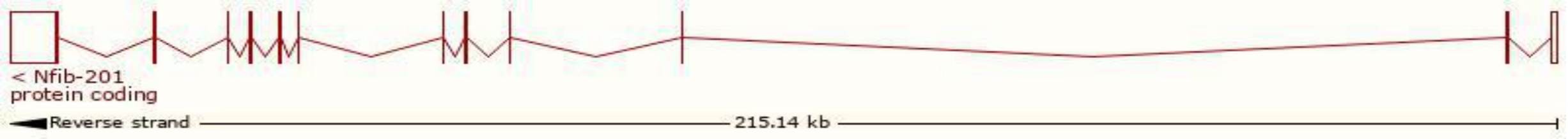
Official Symbol	Nfib provided by MGI
Official Full Name	nuclear factor I/B provided by MGI
Primary source	MGI:MGI:103188
See related	Ensembl:ENSMUSG00000008575
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6720429L07Rik, CTF, E030026I10Rik, NF-I/B, NF1-B, NFI-B
Expression	Broad expression in CNS E14 (RPKM 21.2), whole brain E14.5 (RPKM 17.6) and 21 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

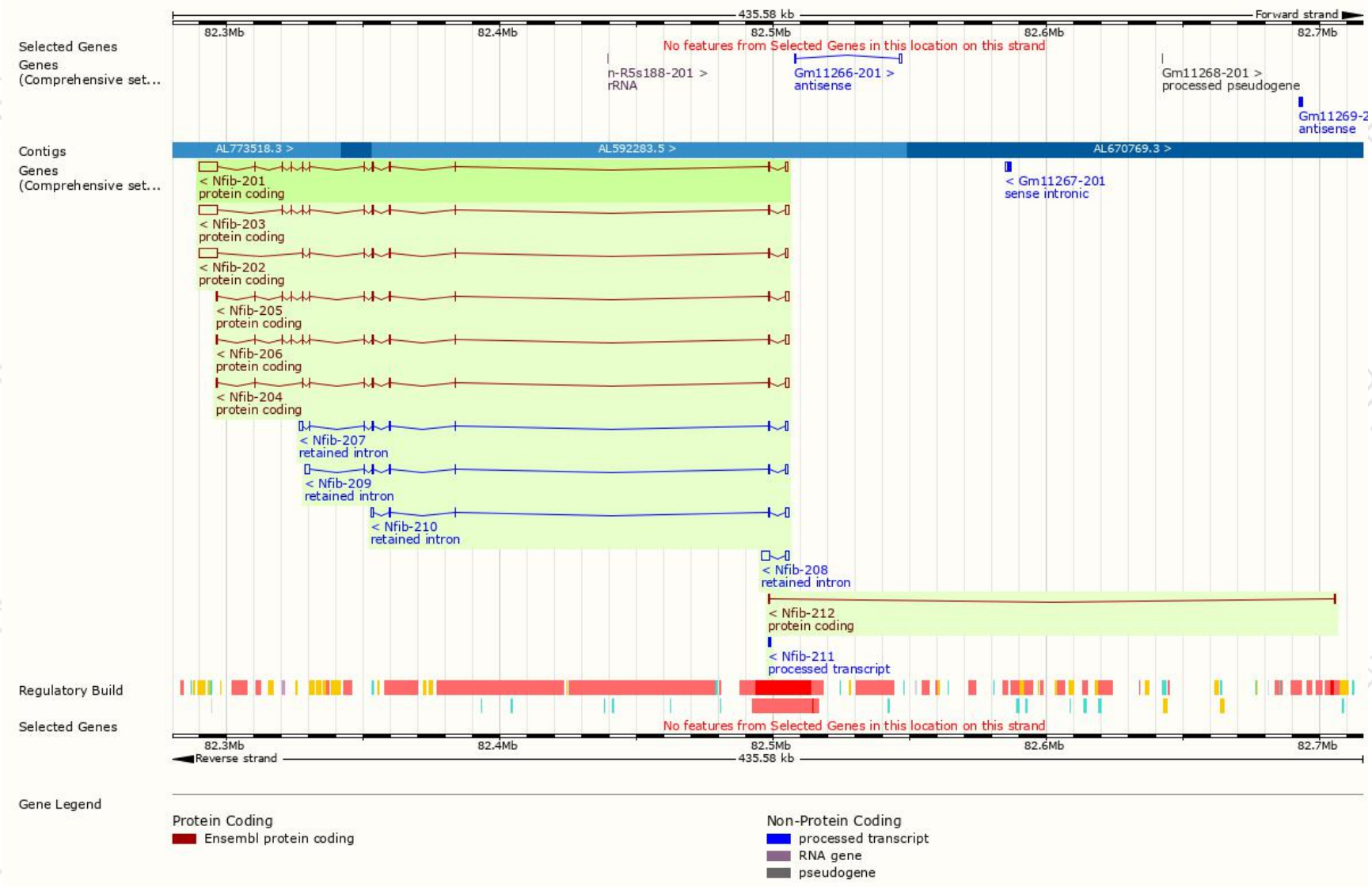
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfib-201	ENSMUST00000050872.14	8770	570aa	Protein coding	CCDS51213	P97863	TSL:1 GENCODE basic APPRIS P2
Nfib-202	ENSMUST00000064770.8	8429	420aa	Protein coding	CCDS38790	P97863 Q6GSP7	TSL:1 GENCODE basic
Nfib-203	ENSMUST00000107245.8	9116	493aa	Protein coding	-	I7HIP8	TSL:1 GENCODE basic
Nfib-206	ENSMUST00000107248.7	3294	569aa	Protein coding	-	A2BG77	TSL:1 GENCODE basic APPRIS ALT1
Nfib-205	ENSMUST00000107247.7	3267	560aa	Protein coding	-	A2BG75	TSL:5 GENCODE basic APPRIS ALT1
Nfib-204	ENSMUST00000107246.1	3075	486aa	Protein coding	-	A2BG76	TSL:1 GENCODE basic
Nfib-212	ENSMUST00000155821.1	685	174aa	Protein coding	-	A2ADI3	CDS 3' incomplete TSL:3
Nfib-211	ENSMUST00000152588.1	379	No protein	Processed transcript	-	-	TSL:5
Nfib-208	ENSMUST00000135024.1	3835	No protein	Retained intron	-	-	TSL:1
Nfib-209	ENSMUST00000140874.7	3308	No protein	Retained intron	-	-	TSL:1
Nfib-207	ENSMUST00000122918.7	2699	No protein	Retained intron	-	-	TSL:1
Nfib-210	ENSMUST00000148982.1	2281	No protein	Retained intron	-	-	TSL:1

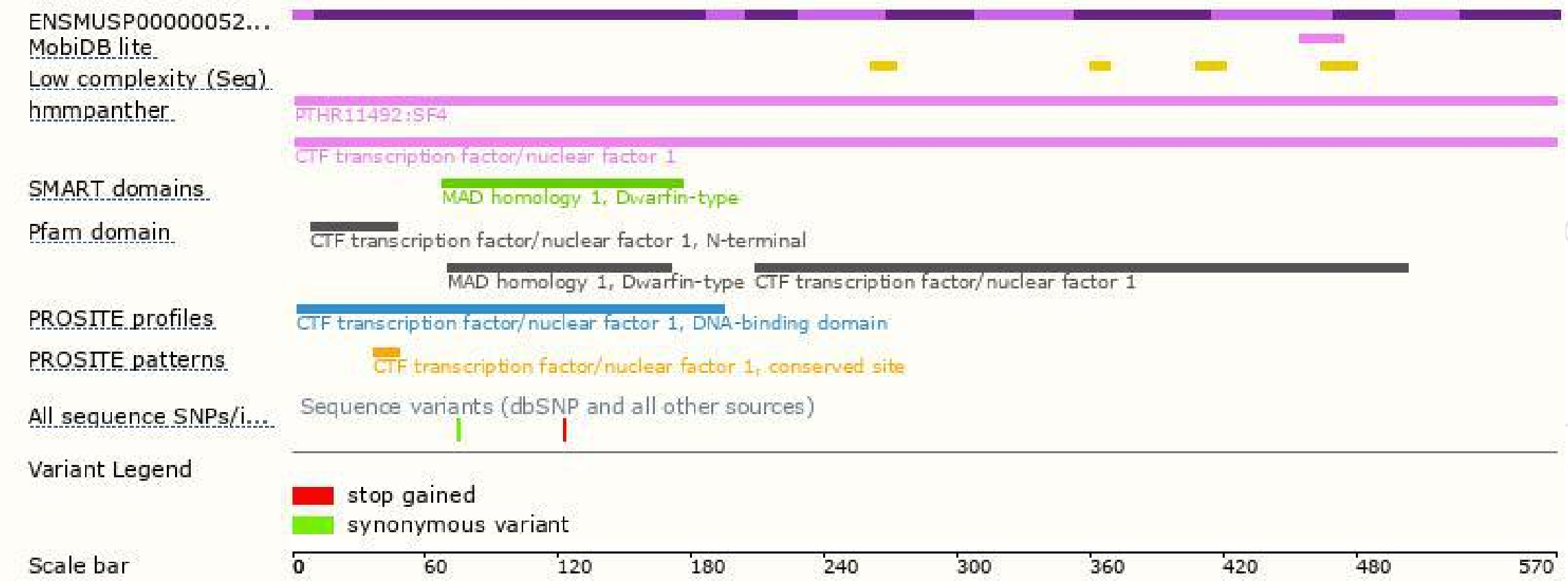
The strategy is based on the design of *Nfib-201* transcript,The transcription is shown below:



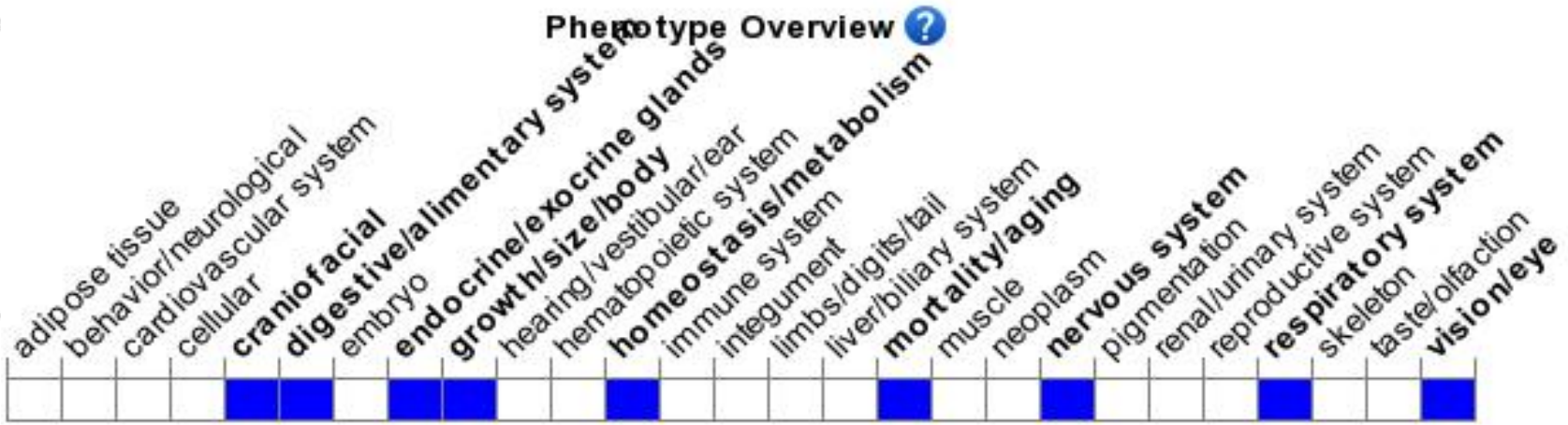
Genomic location distribution



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,Homozygous inactivation of this gene causes severe lung defects and neonatal death from respiratory failure. Homozygotes for a null allele show callosal agenesis and abnormalities in forebrain, basilar pons, hippocampus, and submandibular gland development, as well as lung maturation defects.

集萃药康
GemPharmatech

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

Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd