

Rars Cas9-KO Strategy

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Design Date:

2020-5-7

Project Overview

Project Name

Rars

Project type

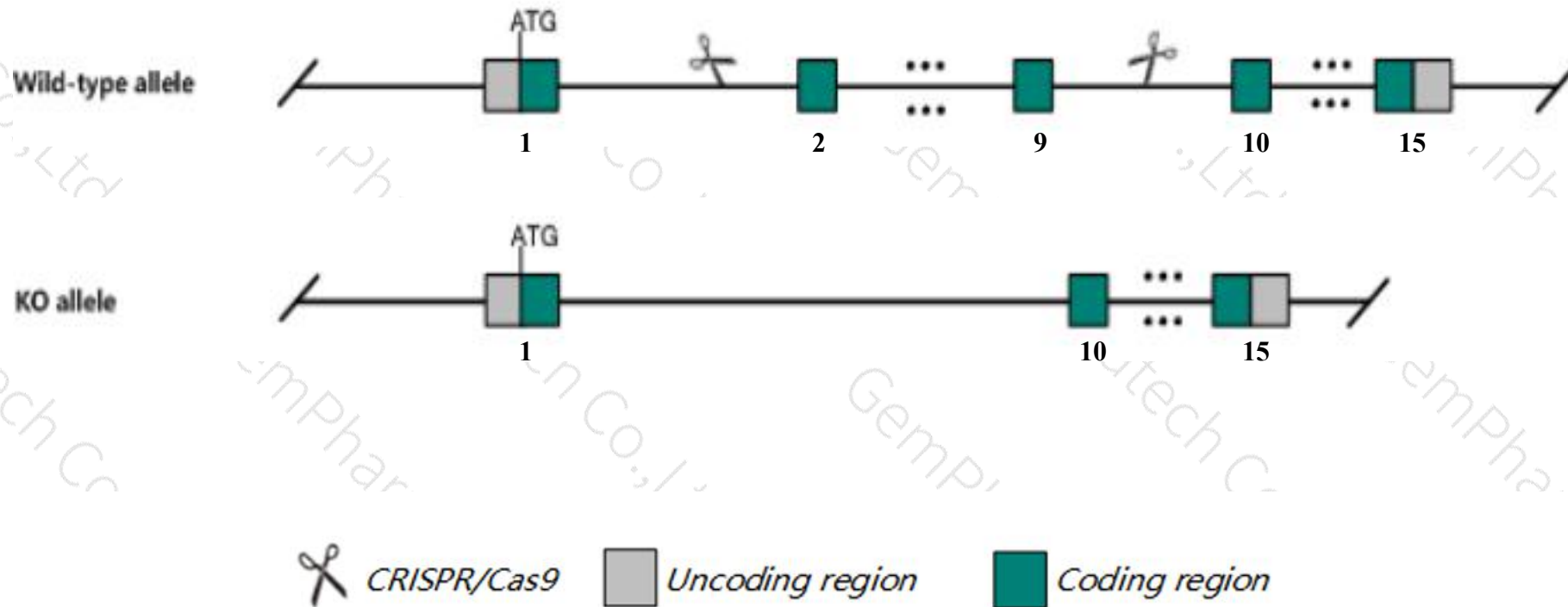
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Rars* gene has 5 transcripts. According to the structure of *Rars* gene, exon2-exon9 of *Rars-201* (ENSMUST00000018992.3) transcript is recommended as the knockout region. The region contains 1012bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rars* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Rars* gene is located on the Chr11. 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)

Rars arginyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 104458, updated on 13-Mar-2020

Summary



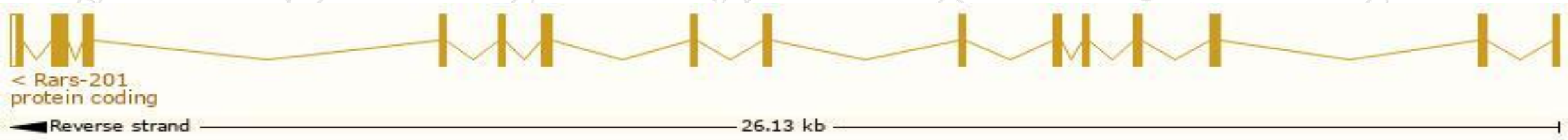
Official Symbol	Rars provided by MGI
Official Full Name	arginyl-tRNA synthetase provided by MGI
Primary source	MGI:MGI:1914297
See related	Ensembl:ENSMUSG00000018848
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610011N19Rik, 2610037E21Rik, AL033339, AW985894
Expression	Ubiquitous expression in placenta adult (RPKM 41.2), CNS E11.5 (RPKM 34.3) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

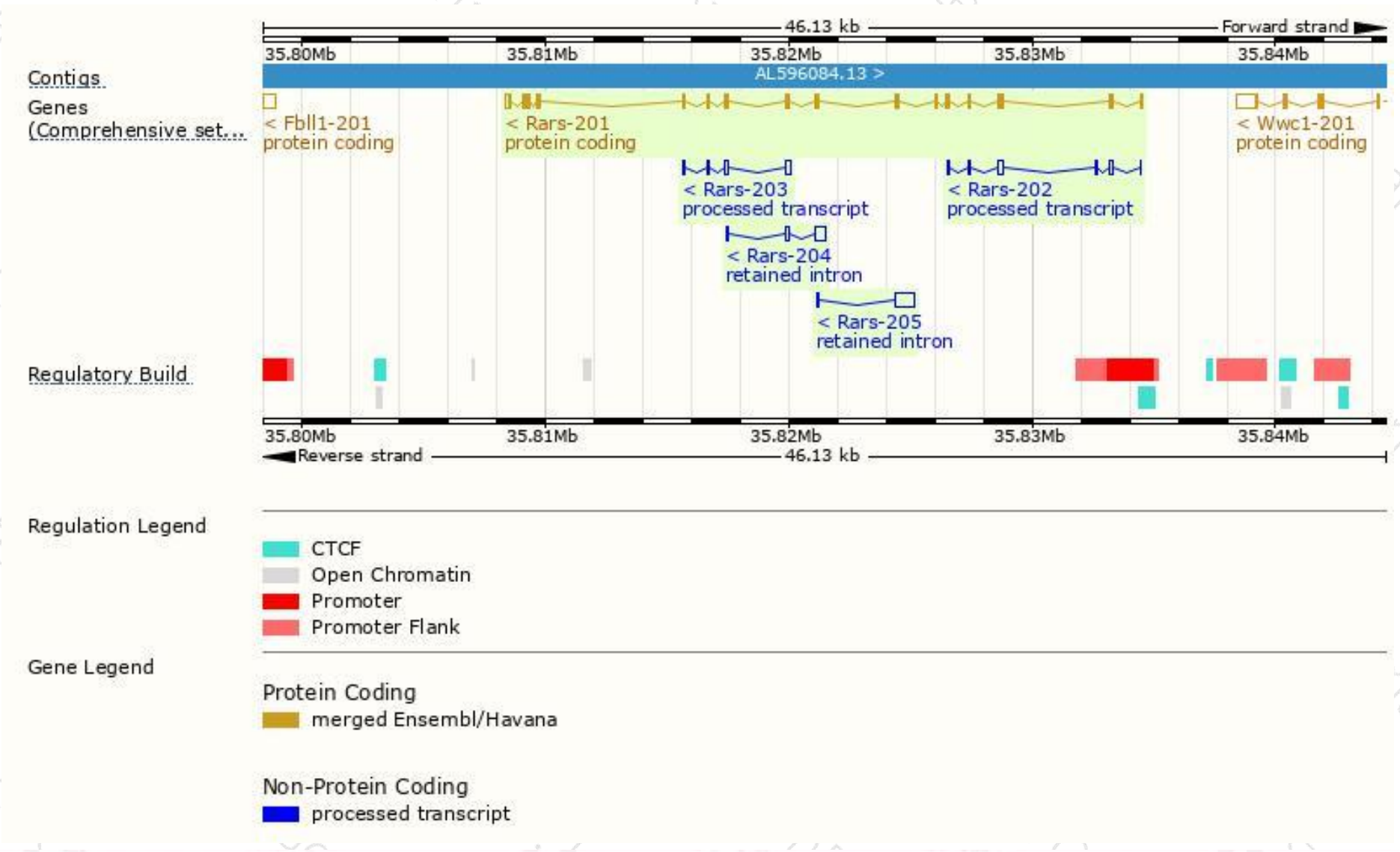
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rars-201	ENSMUST00000018992.3	2109	660aa	Protein coding	CCDS24544	Q9D0I9	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 P1
Rars-202	ENSMUST00000137815.1	634	No protein	Processed transcript	-	-	TSL:5
Rars-203	ENSMUST00000143205.1	602	No protein	Processed transcript	-	-	TSL:2
Rars-205	ENSMUST00000166122.1	827	No protein	Retained intron	-	-	TSL:5
Rars-204	ENSMUST00000165817.1	614	No protein	Retained intron	-	-	TSL:2

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



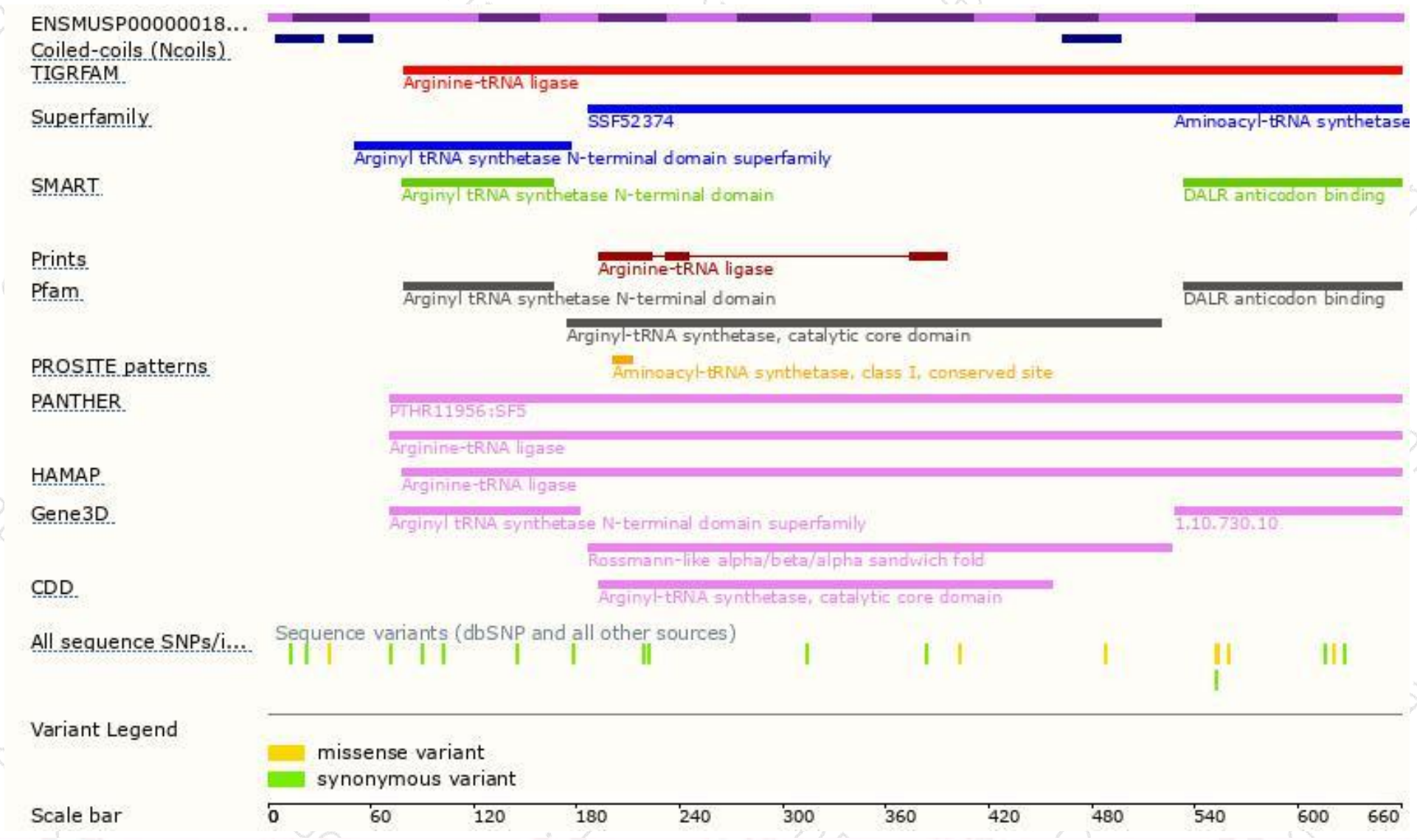
Genomic location distribution



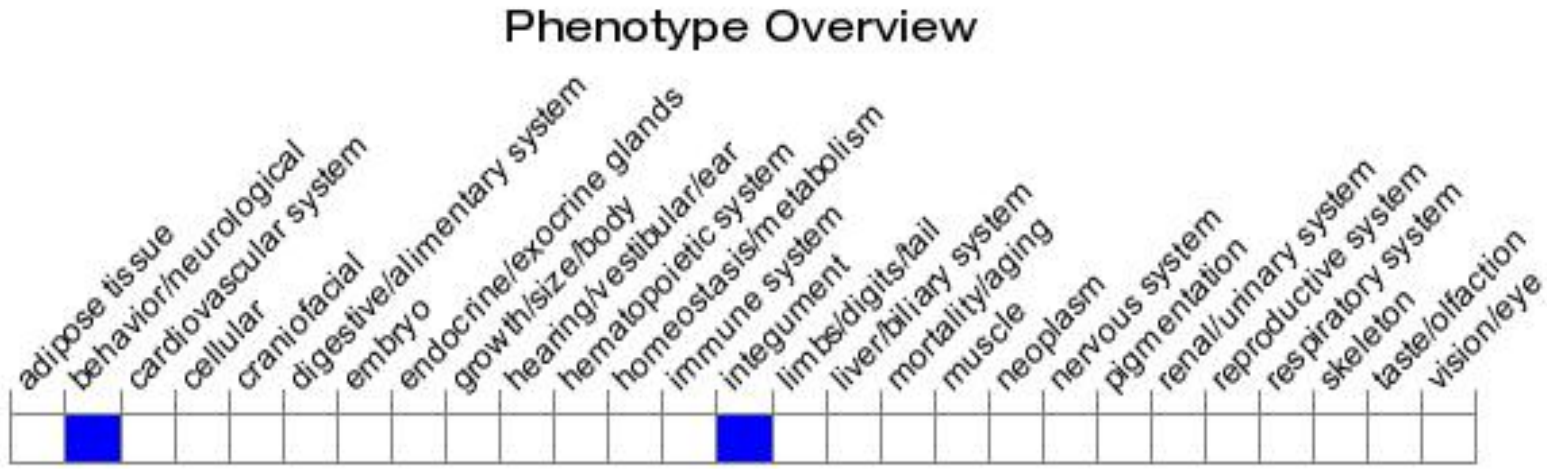
Protein domain



集萃药康
GemPharmatech



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.

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