

Srsf5 Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

Design Date: 2020-11-10

Project Overview

Project Name

Srsf5

Project type

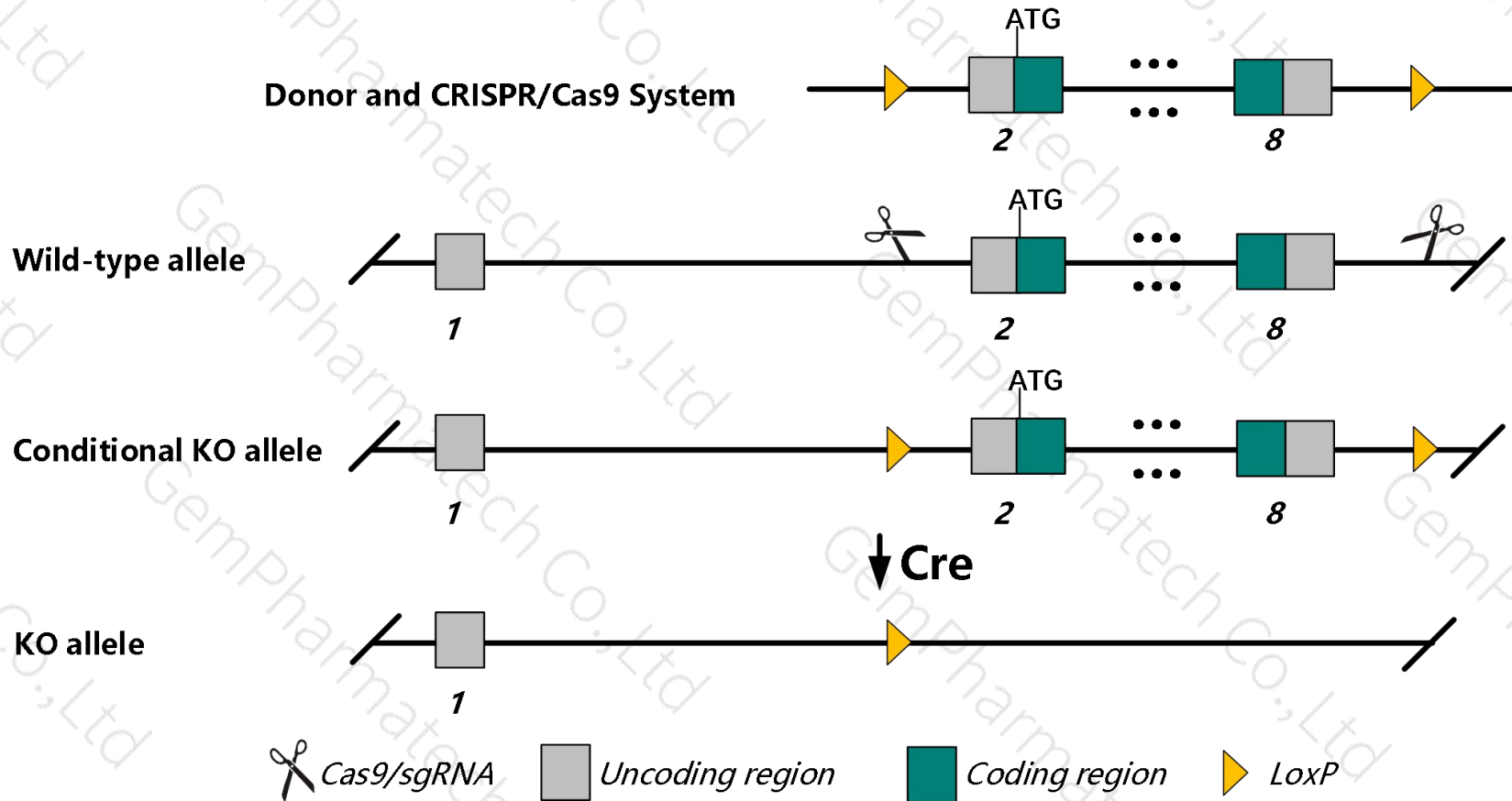
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srsf5* gene. The schematic diagram is as follows:



- The *Srsf5* gene has 12 transcripts. According to the structure of *Srsf5* gene, exon2-exon8 of *Srsf5*-202(ENSMUST00000110351.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Srsf5* 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.

Notice

- The *Srsf5* gene is located on the Chr12. 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.
- The floxed region is near to the N-terminal of *Gm20337* gene, this strategy may influence the regulatory function of the N-terminal of *Gm20337* gene.
- 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)

Srsf5 serine and arginine-rich splicing factor 5 [Mus musculus (house mouse)]

Gene ID: 20384, updated on 13-Mar-2020

Summary

Official Symbol Srsf5 provided by [MGI](#)

Official Full Name serine and arginine-rich splicing factor 5 provided by [MGI](#)

Primary source [MGI:MGI:98287](#)

See related [Ensembl:ENSMUSG00000021134](#)

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 Sfrs5

Summary The protein encoded by this gene is a member of the serine/arginine (SR)-rich family of pre-mRNA splicing factors, which constitute part of the spliceosome. Each of these factors contains an RNA recognition motif (RRM) for binding RNA and an RS domain for binding other proteins. The RS domain is rich in serine and arginine residues and facilitates interaction between different SR splicing factors. In addition to being critical for mRNA splicing, the SR proteins have also been shown to be involved in mRNA export from the nucleus and in translation. [provided by RefSeq, Nov 2016]

Expression Ubiquitous expression in CNS E11.5 (RPKM 229.5), bladder adult (RPKM 197.4) and 28 other tissues [See more](#)

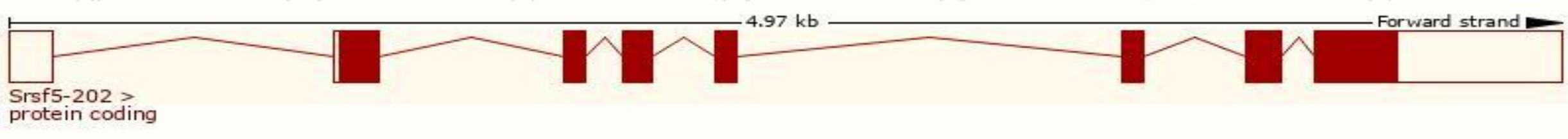
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

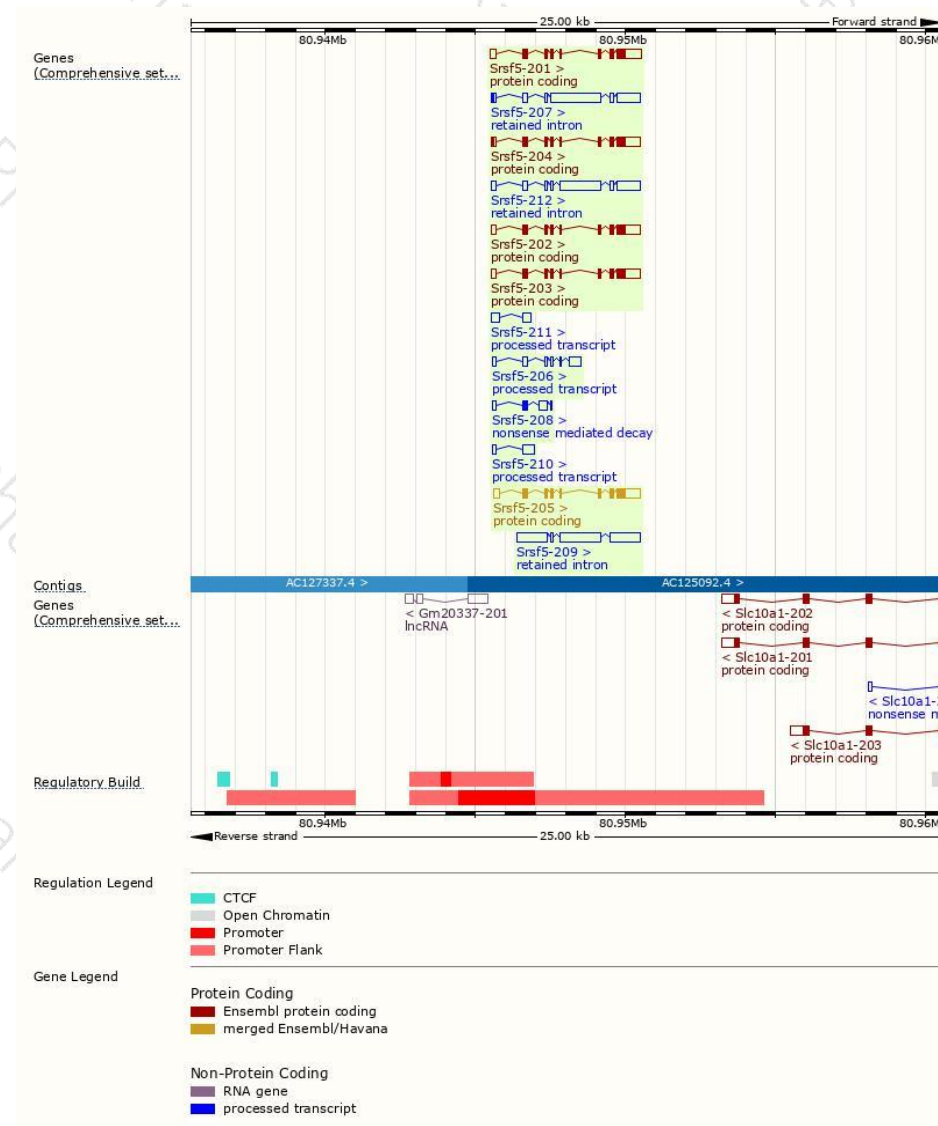
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf5-205	ENSMUST00000110356.2	1568	269aa	Protein coding	CCDS36484	Q35326	TSL:5 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 P3
Srsf5-201	ENSMUST00000094693.10	1527	269aa	Protein coding	CCDS36484	Q35326	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 P3
Srsf5-202	ENSMUST00000110351.7	1498	270aa	Protein coding	CCDS83974	Q9D8S5	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 ALT2
Srsf5-203	ENSMUST00000110352.9	1491	269aa	Protein coding	CCDS36484	Q35326	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 P3
Srsf5-204	ENSMUST00000110354.7	1489	270aa	Protein coding	CCDS83974	Q9D8S5	TSL:5 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 ALT2
Srsf5-208	ENSMUST00000138434.7	547	46aa	Nonsense mediated decay	-	S4R2G3	TSL:3
Srsf5-206	ENSMUST00000125814.8	886	No protein	Processed transcript	-	-	TSL:2
Srsf5-211	ENSMUST00000152662.1	538	No protein	Processed transcript	-	-	TSL:1
Srsf5-210	ENSMUST00000151968.1	489	No protein	Processed transcript	-	-	TSL:2
Srsf5-209	ENSMUST00000151036.1	3482	No protein	Retained intron	-	-	TSL:1
Srsf5-207	ENSMUST00000133783.7	2919	No protein	Retained intron	-	-	TSL:5
Srsf5-212	ENSMUST00000153056.7	2720	No protein	Retained intron	-	-	TSL:5

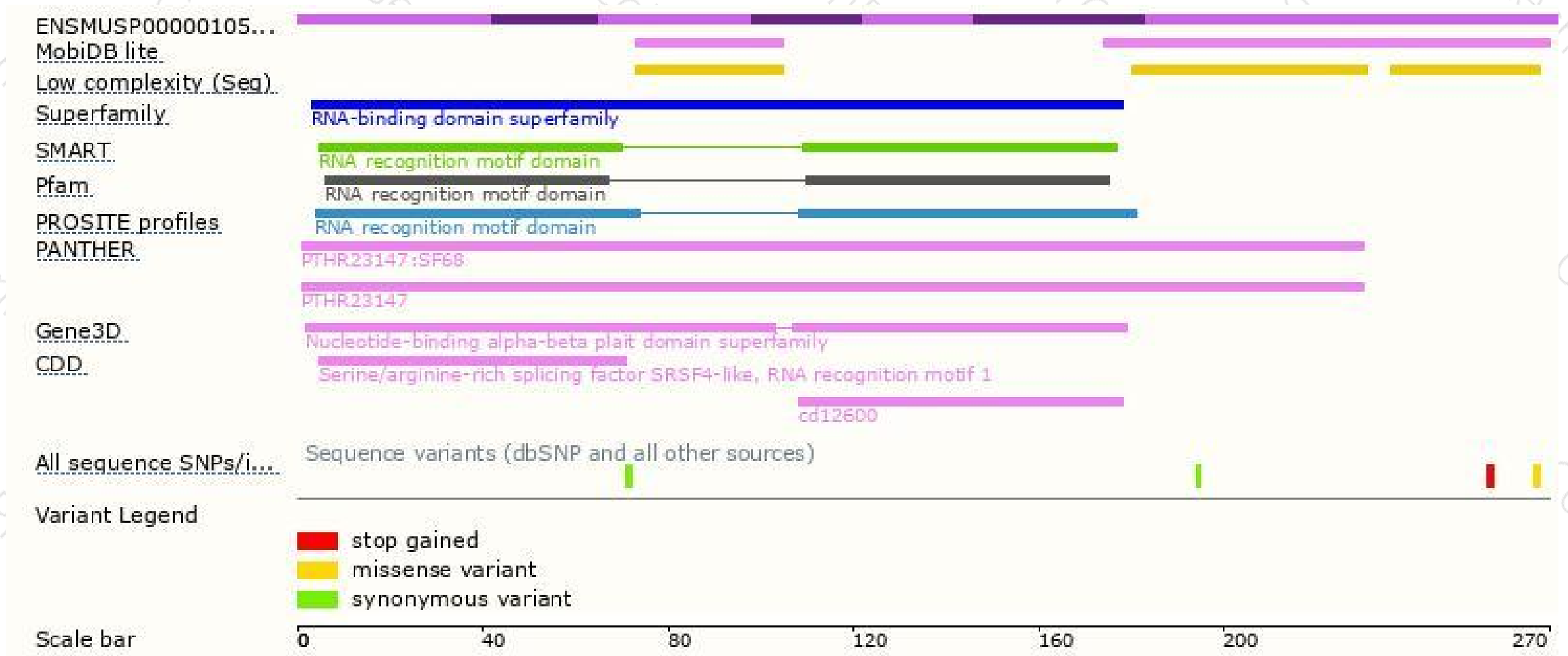
The strategy is based on the design of *Srsf5-202* transcript,the transcription is shown below:



Genomic location distribution

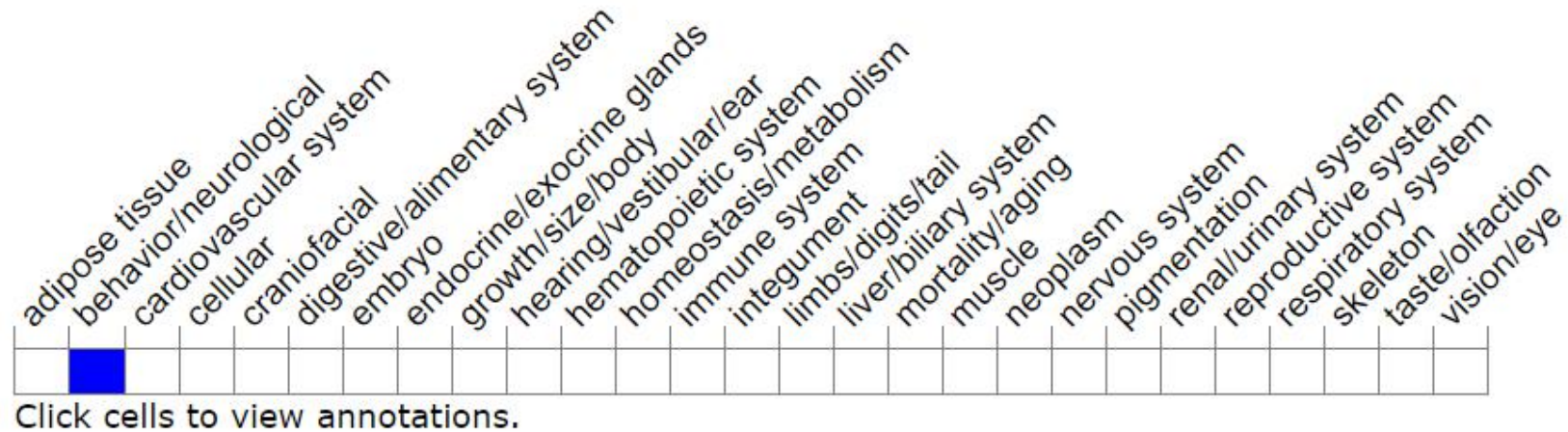


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



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.

Tel: 400-9660890

