Sh2d1a Cas9-CKO Strategy

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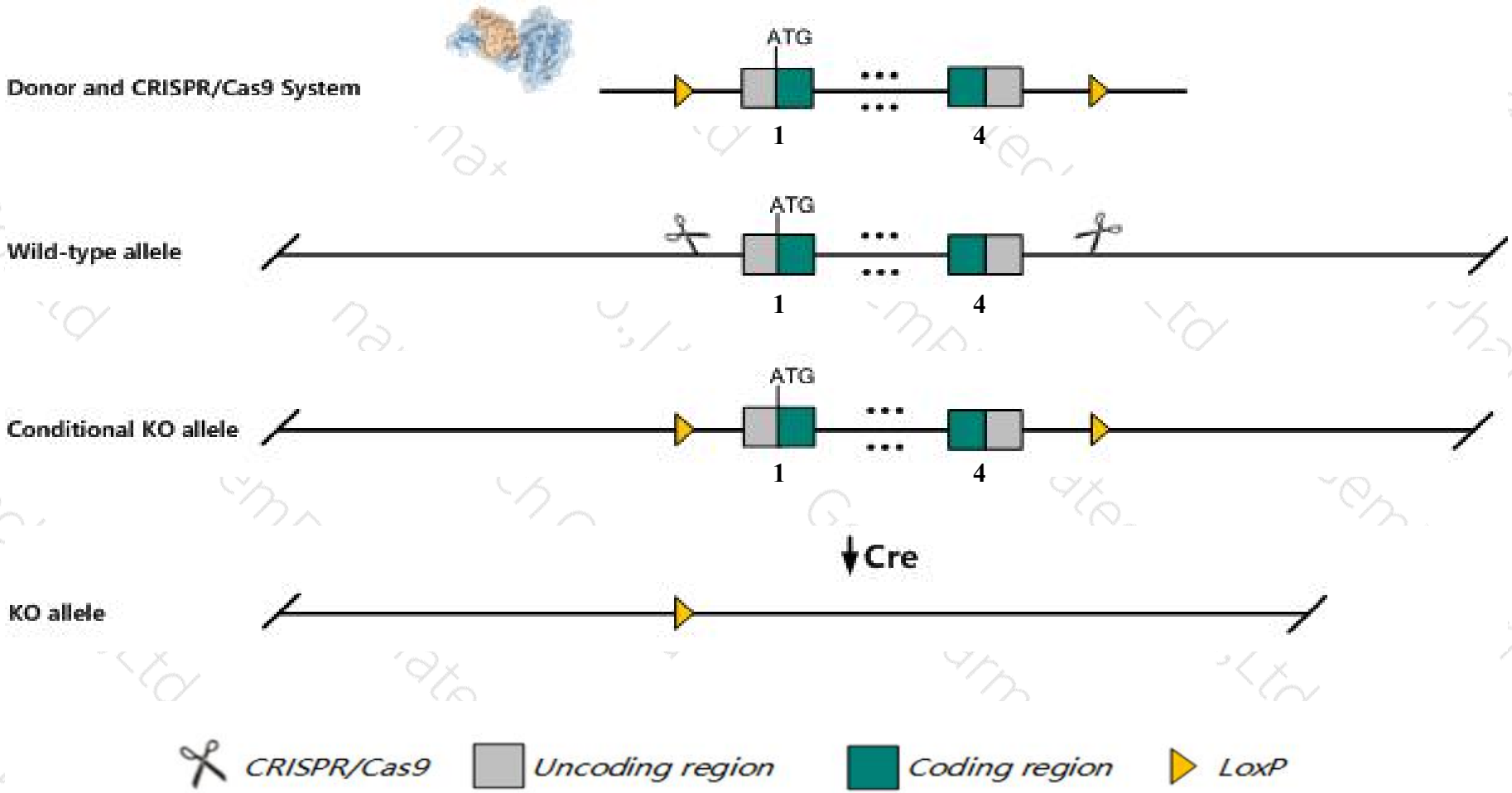
Project Overview

Project Name	***Sh2d1a***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sh2d1a* gene. The schematic diagram is as follows:



Technical routes

- The *Sh2d1a* gene has 7 transcripts. According to the structure of *Sh2d1a* gene, exon1-exon4 of *Sh2d1a-201* (ENSMUST00000005839.10) 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 *Sh2d1a* 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

- According to the existing MGI data,mice homozygous for disruptions in this gene display various immune system abnormalities.
- The *Sh2d1a* gene is located on the ChrX. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Sh2d1a SH2 domain containing 1A [Mus musculus (house mouse)]

Gene ID: 20400, updated on 13-Mar-2020

Summary

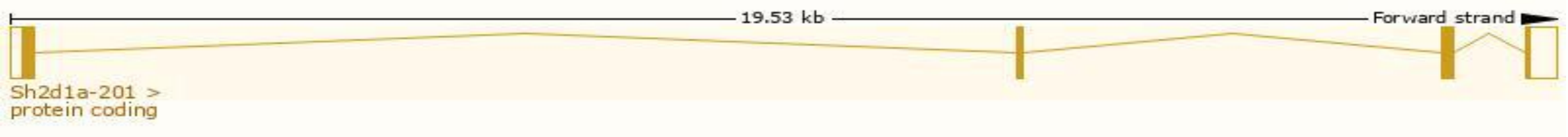
Official Symbol	Sh2d1a provided by MGI
Official Full Name	SH2 domain containing 1A provided byMGI
Primary source	MGI:MGI:1328352
See related	Ensembl:ENSMUSG00000005696
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm686, SAP
Expression	Restricted expression toward thymus adult (RPKM 26.6)See more
Orthologs	human all

Transcript information（Ensembl）

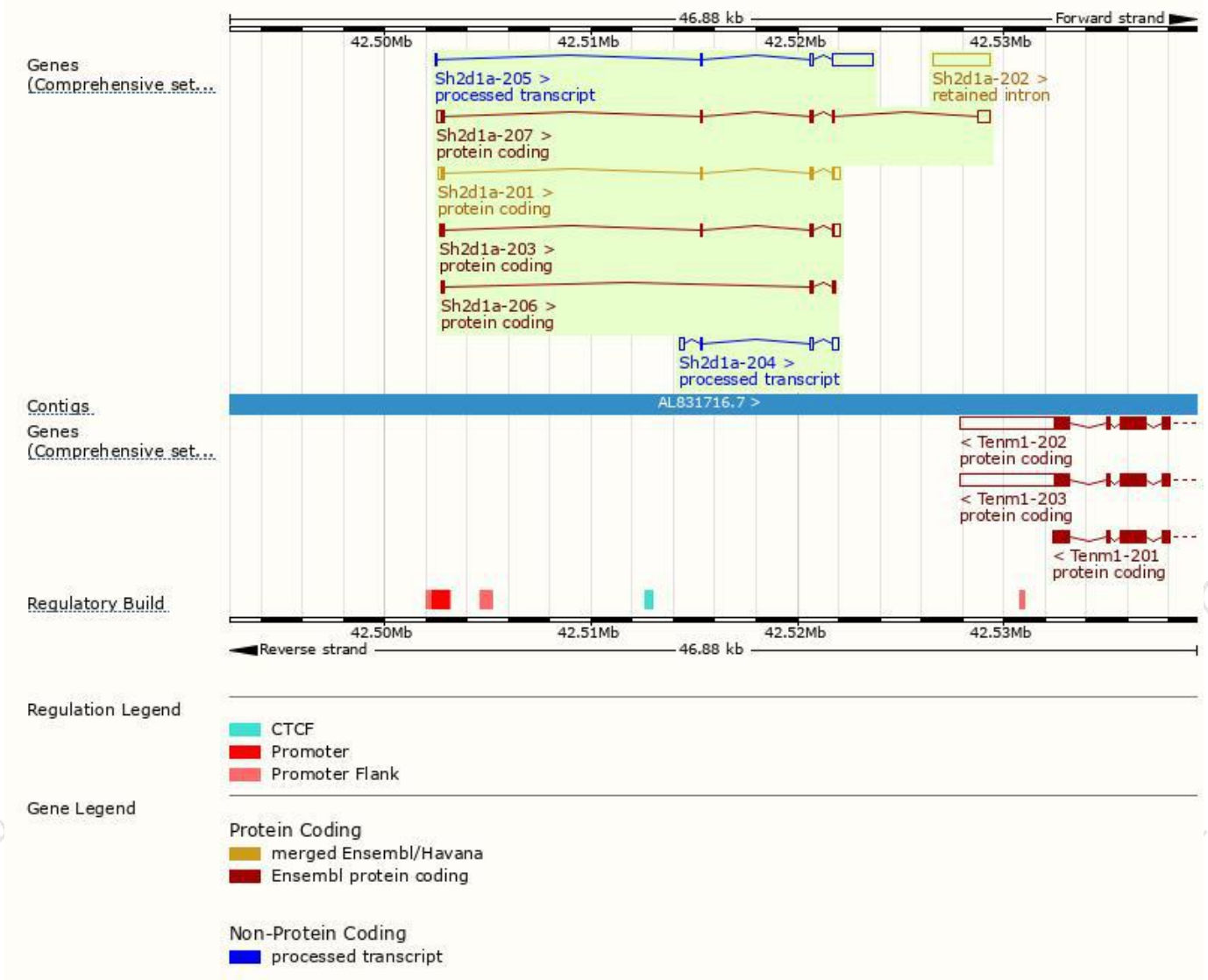
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sh2d1a-207	ENSMUST00000189753.6	1223	126aa	Protein coding	CCDS30099	O88890 Q544F1	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 P1
Sh2d1a-201	ENSMUST00000005839.10	883	126aa	Protein coding	CCDS30099	O88890 Q544F1	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
Sh2d1a-203	ENSMUST00000115070.7	782	123aa	Protein coding	CCDS85770	O88890	TSL:1 GENCODE basic
Sh2d1a-206	ENSMUST00000153948.1	400	93aa	Protein coding	-	S4R2F6	CDS 5' incomplete TSL:3
Sh2d1a-205	ENSMUST00000129855.7	2269	No protein	Processed transcript	-	-	TSL:1
Sh2d1a-204	ENSMUST00000128393.1	625	No protein	Processed transcript	-	-	TSL:3
Sh2d1a-202	ENSMUST00000101619.3	2746	No protein	Retained intron	-	-	TSL:NA

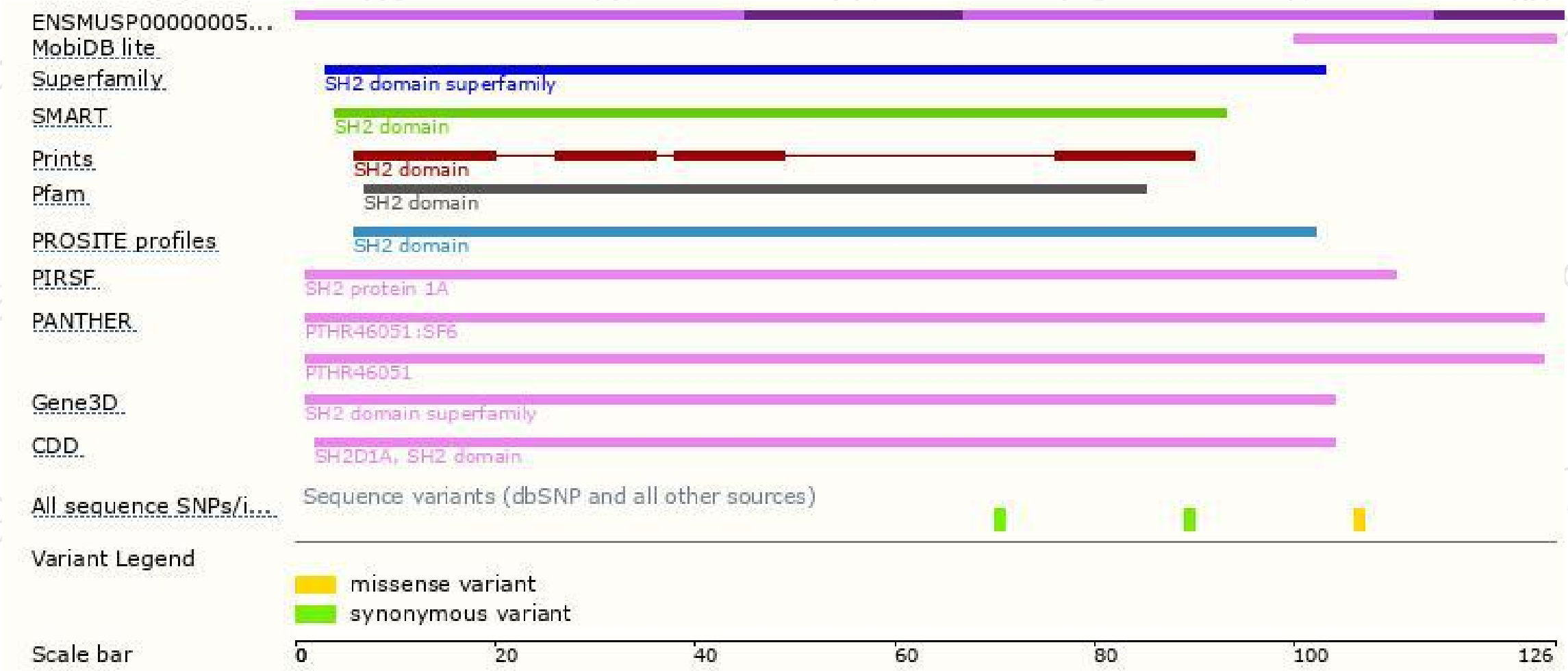
The strategy is based on the design of *Sh2d1a-201* transcript,the transcription is shown below:



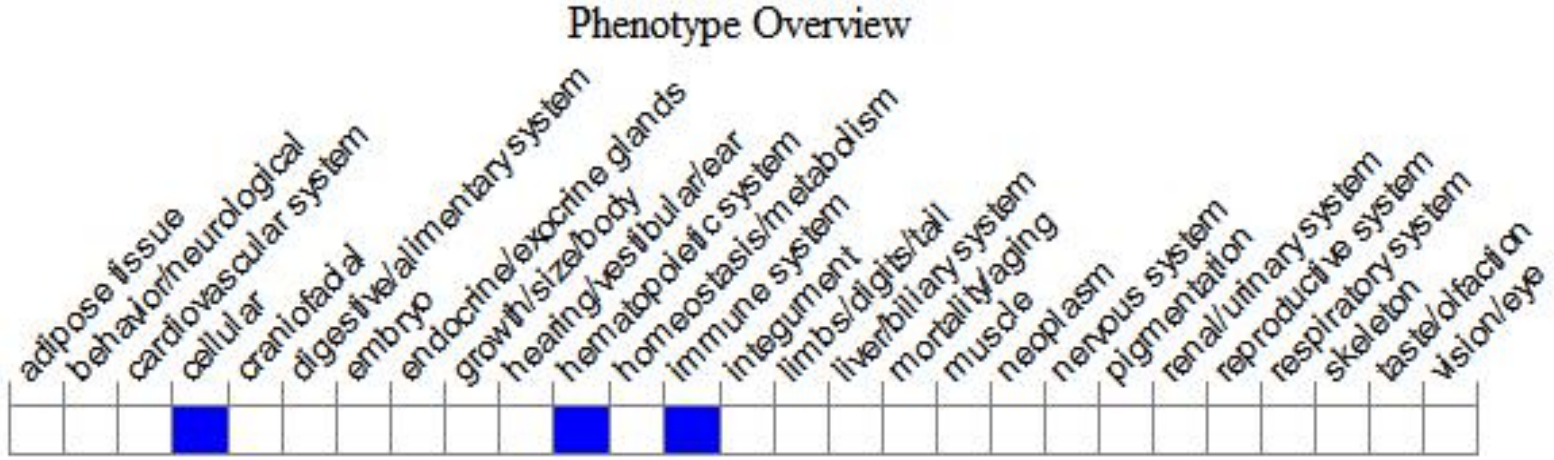
Genomic location distribution



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 disruptions in this gene display various immune system abnormalities.

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

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