Srsf1 Cas9-CKO Strategy

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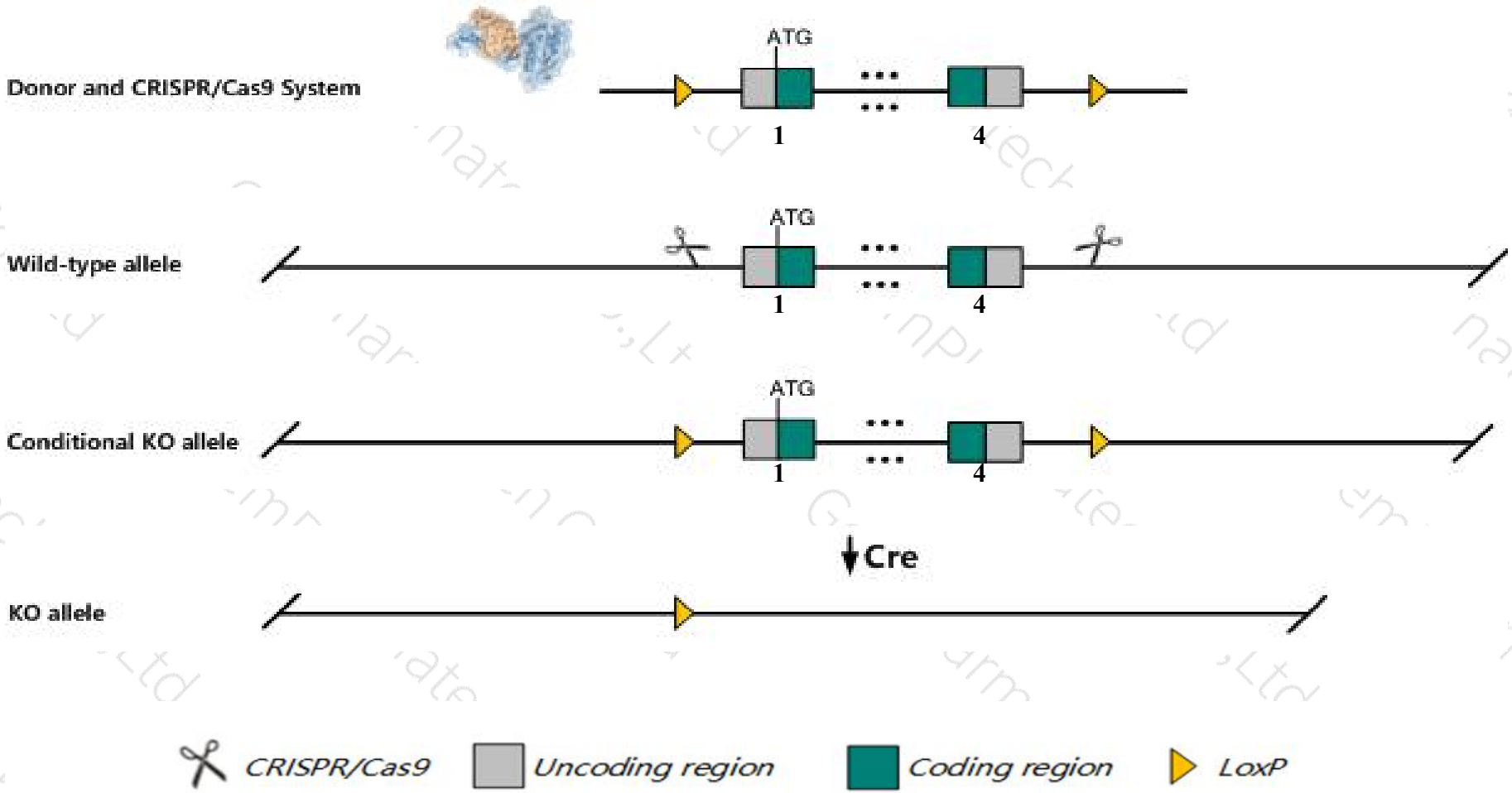
Project Overview

Project Name	***Srsf1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srsf1* gene. The schematic diagram is as follows:



Technical routes

- The *Srsf1* gene has 7 transcripts. According to the structure of *Srsf1* gene, exon1-exon4 of *Srsf1-205* (ENSMUST00000139129.8) 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 *Srsf1* 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,Homozygous null mice display early embryonic lethality. Cardiac specific conditional deletion mutants shows cardiac malfunction and premature death.

- The *Srsf1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Srsf1 serine/arginine-rich splicing factor 1 [Mus musculus (house mouse)]

Gene ID: 110809, updated on 31-Jan-2019

Summary

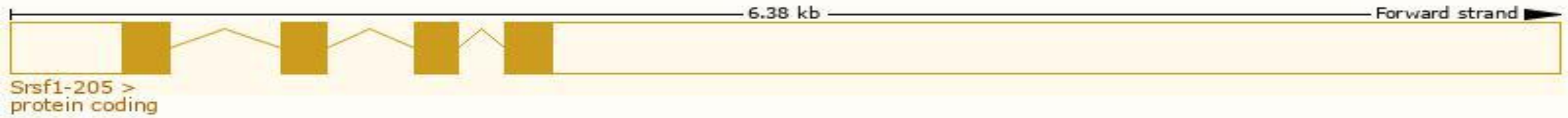
Official Symbol	Srsf1 provided by MGI
Official Full Name	serine/arginine-rich splicing factor 1 provided by MGI
Primary source	MGI:MGI:98283
See related	Ensembl:ENSMUSG00000018379
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110054N12Rik, 5730507C05Rik, 6330415C05Rik, AI482334, AW491331, Asf, Sf2, Sfrs1
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. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2010]
Expression	Ubiquitous expression in CNS E11.5 (RPKM 77.9), CNS E14 (RPKM 62.5) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

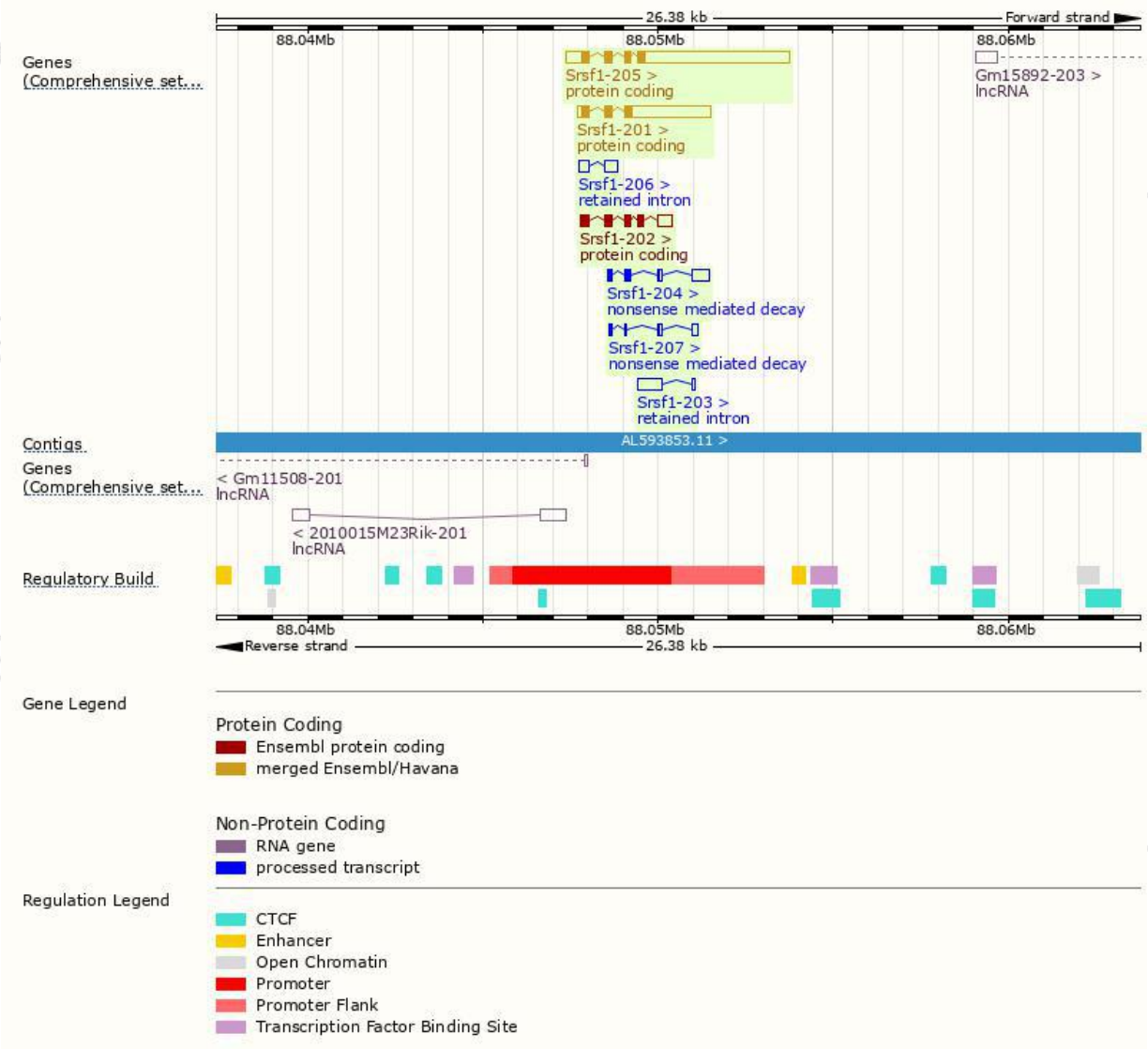
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srsf1-205	ENSMUST00000139129.8	5362	248aa	Protein coding	CCDS36273	Q6PDM2	TSL:1 GENCODE basic APPRIS P1
Srsf1-201	ENSMUST00000079866.10	2948	201aa	Protein coding	CCDS36274	Q6PDM2	TSL:1 GENCODE basic
Srsf1-202	ENSMUST00000107920.9	1209	253aa	Protein coding	-	H7BX95	TSL:5 GENCODE basic
Srsf1-204	ENSMUST00000134824.8	896	106aa	Nonsense mediated decay	-	F7AI47	CDS 5' incomplete TSL:3
Srsf1-207	ENSMUST00000172186.1	401	58aa	Nonsense mediated decay	-	F6QXN3	CDS 5' incomplete TSL:5
Srsf1-203	ENSMUST00000132983.2	759	No protein	Retained intron	-	-	TSL:2
Srsf1-206	ENSMUST00000171976.1	645	No protein	Retained intron	-	-	TSL:2

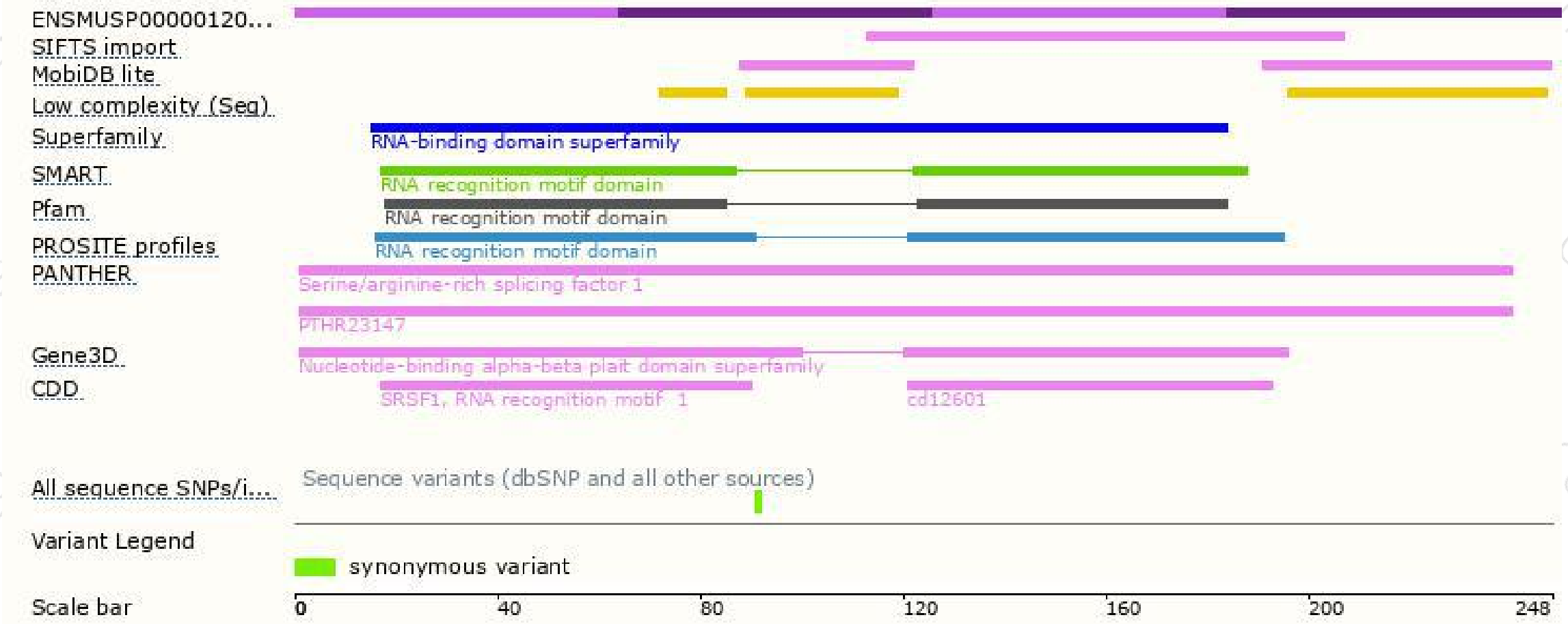
The strategy is based on the design of *Srsf1-205* transcript,The transcription is shown below



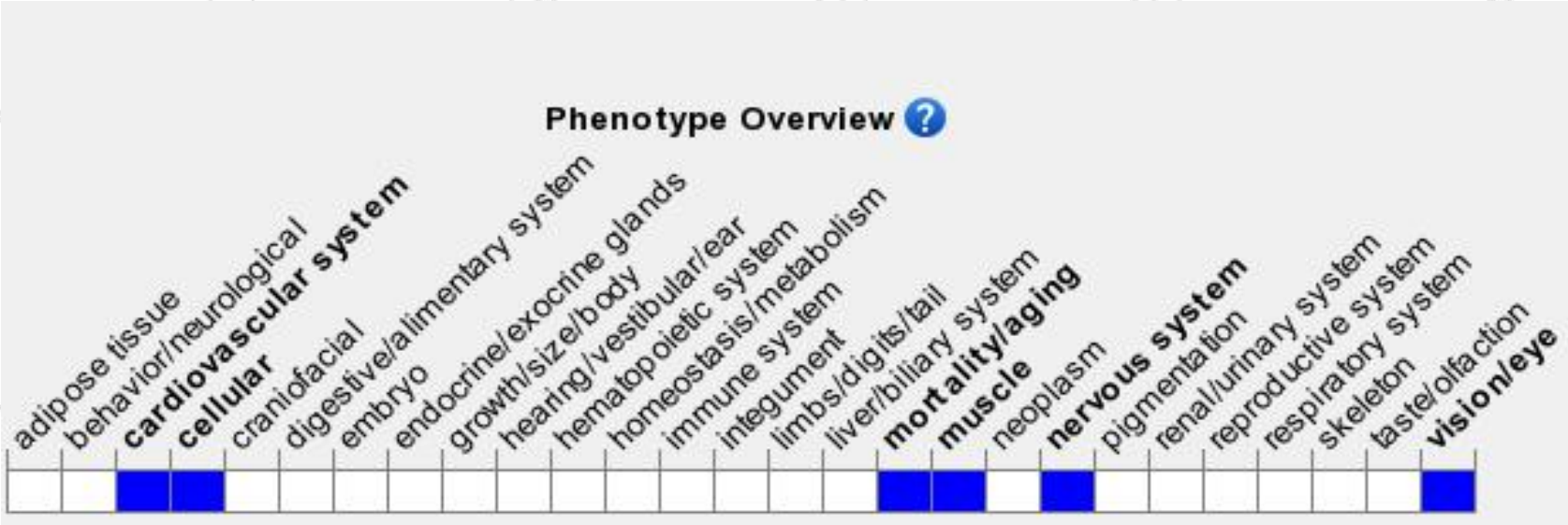
Genomic location distribution



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 null mice display early embryonic lethality. Cardiac specific conditional deletion mutants shows cardiac malfunction and premature death.

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

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