

S100a4 Cas9-KO Strategy

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Project Overview

Project Name

S100a4

Project type

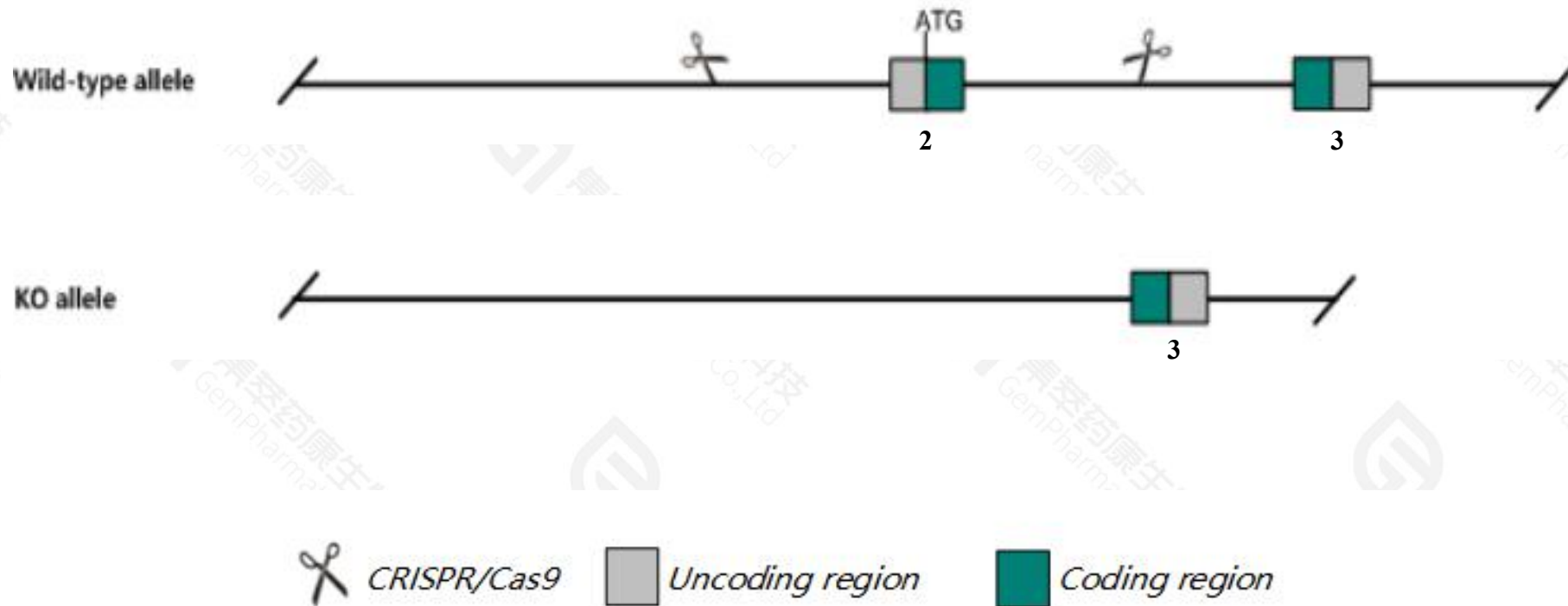
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *S100a4* gene. The schematic diagram is as follows:



Technical routes

- The *S100a4* gene has 2 transcripts. According to the structure of *S100a4* gene, exon2 of *S100a4*-201(ENSMUST00000001046.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *S100a4* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for one knock-out allele exhibit impaired chemotaxis of macrophages. Mice homozygous for another knock-out allele exhibit embryonic lethality resulting in a skewed sex ratio and increased tumor incidence.
- The knockout region contains the *Gm42674* gene. Knockout the region may affect the function of the *Gm42674* gene.
- The *S100a4* gene is located on the Chr3. 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)

S100a4 S100 calcium binding protein A4 [Mus musculus (house mouse)]

Gene ID: 20198, updated on 13-Mar-2020

Summary

Official Symbol S100a4 provided by [MGI](#)

Official Full Name S100 calcium binding protein A4 provided by [MGI](#)

Primary source [MGI:MGI:1330282](#)

See related [Ensembl:ENSMUSG00000001020](#)

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 18A2, 42a, Cap1, FSp1, Mts1, PeL98, metastasin, pk9a

Expression Biased expression in bladder adult (RPKM 53.9), mammary gland adult (RPKM 13.8) and 10 other tissues [See more](#)

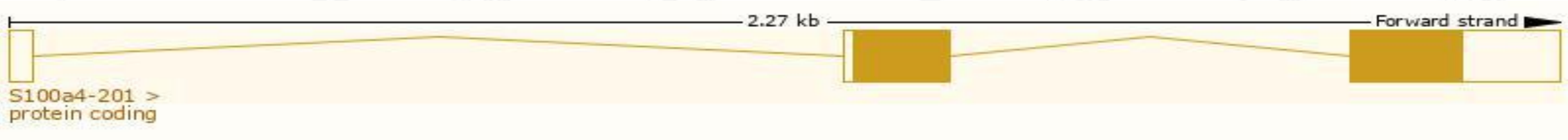
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

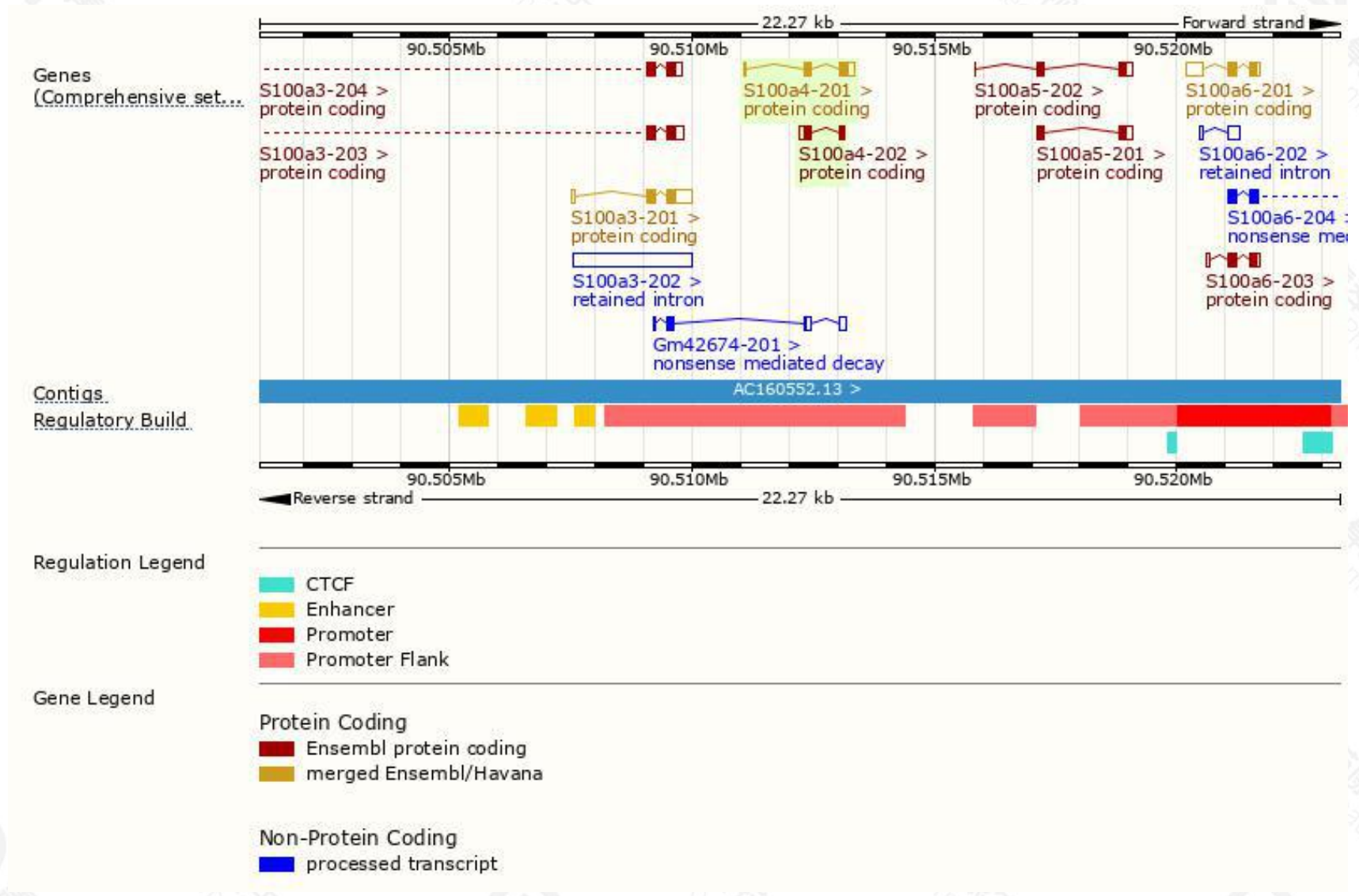
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
S100a4-201	ENSMUST0000001046.6	498	101aa	Protein coding	CCDS17538	P07091 Q545V2	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
S100a4-202	ENSMUST00000142476.1	336	78aa	Protein coding	-	A0A0G2JGD2	CDS 3' incomplete TSL:1

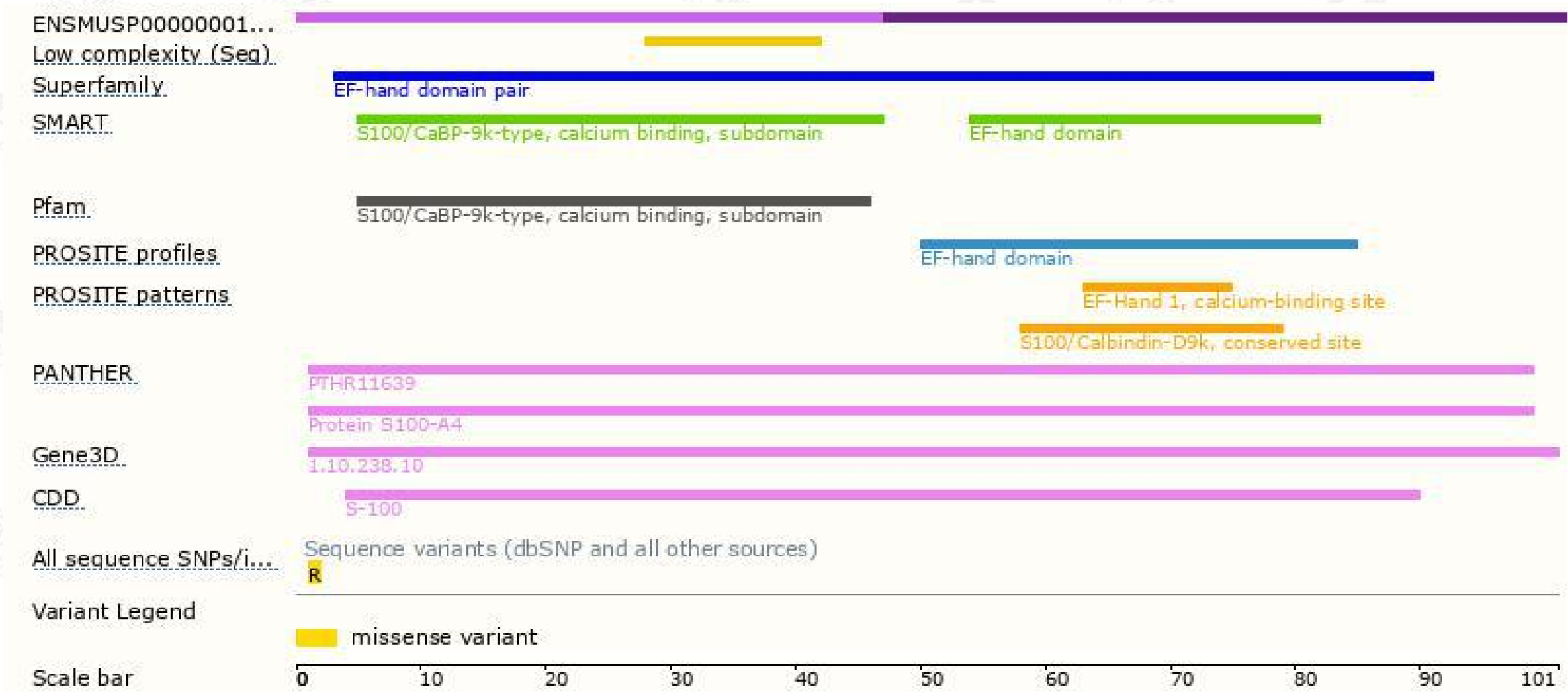
The strategy is based on the design of *S100a4-201* transcript,the transcription is shown below:



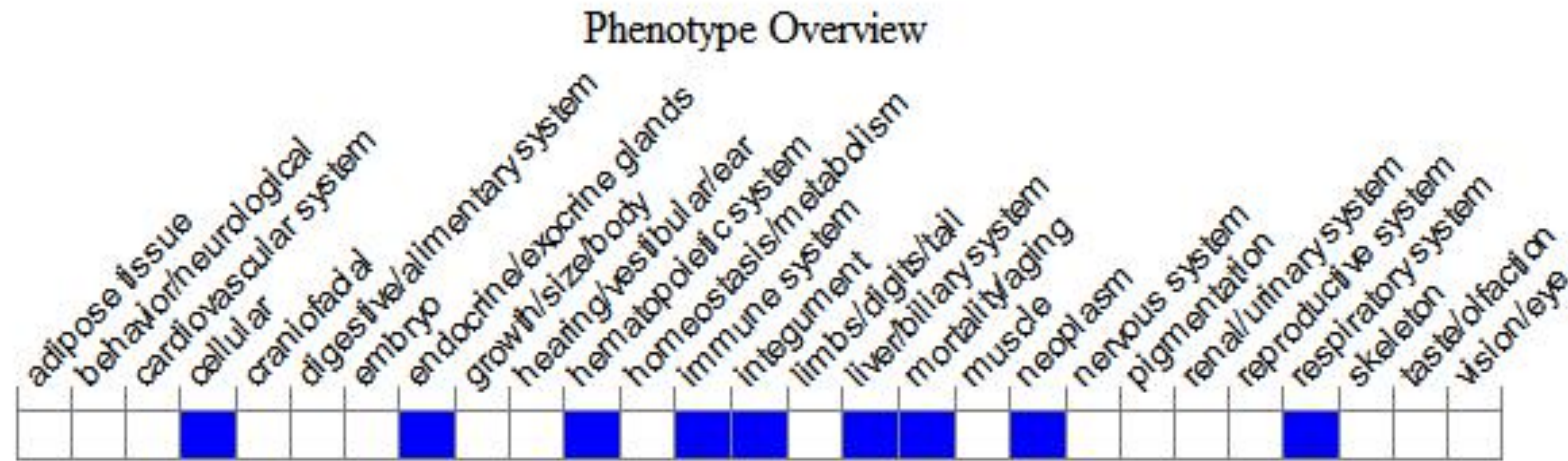
Genomic location distribution



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 one knock-out allele exhibit impaired chemotaxis of macrophages. Mice homozygous for another knock-out allele exhibit embryonic lethality resulting in a skewed sex ratio and increased tumor incidence.

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