S100a9 Cas9-KO Strategy

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Reviewer: Lingyan Wu

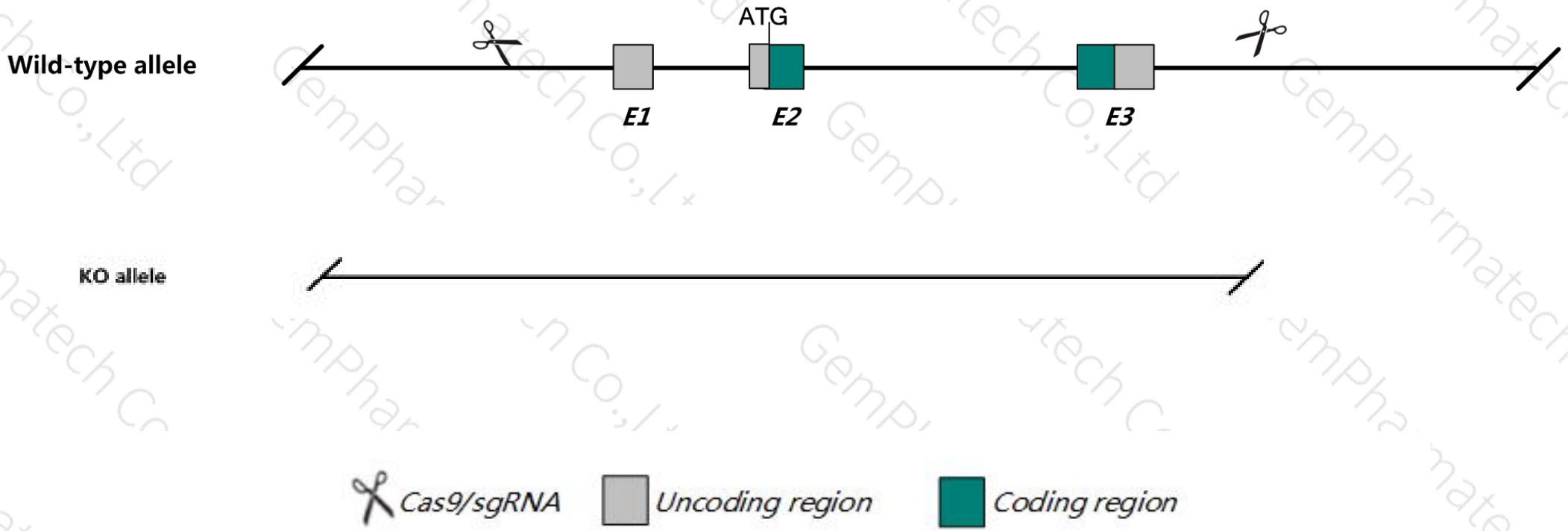
Design Date: 2019-12-17

Project Overview

Project Name	***S100a9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *S100a9* gene. The schematic diagram is as follows:



Technical routes

➢ The *S100a9* gene has 2 transcripts. According to the structure of *S100a9* gene, exon1-exon3 of *S100a9-202* (ENSMUST00000117167.1) transcript is recommended as the knockout region.The region contains most 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 *S100a9* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

➢ According to the existing MGI data,Mice homozygous for one null allele exhibit abnormal immune physiology.

➢ The *S100a9* 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）

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S100a9 S100 calcium binding protein A9 (calgranulin B) [Mus musculus (house mouse)]

Gene ID: 20202, updated on 9-Apr-2019

Summary

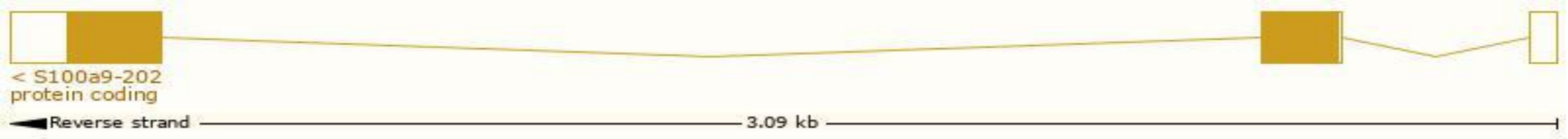
Official Symbol	S100a9 provided by MGI
Official Full Name	S100 calcium binding protein A9 (calgranulin B) provided by MGI
Primary source	MGI:MGI:1338947
See related	Ensembl:ENSMUSG00000056071
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	60B8Ag, AW546964, BEE22, Cagb, GAGB, L1Ag, MRP14, p14
Expression	Biased expression in liver E18 (RPKM 1633.0), liver E14 (RPKM 204.2) and 1 other tissue See more
Orthologs	human all

Transcript information（Ensembl）

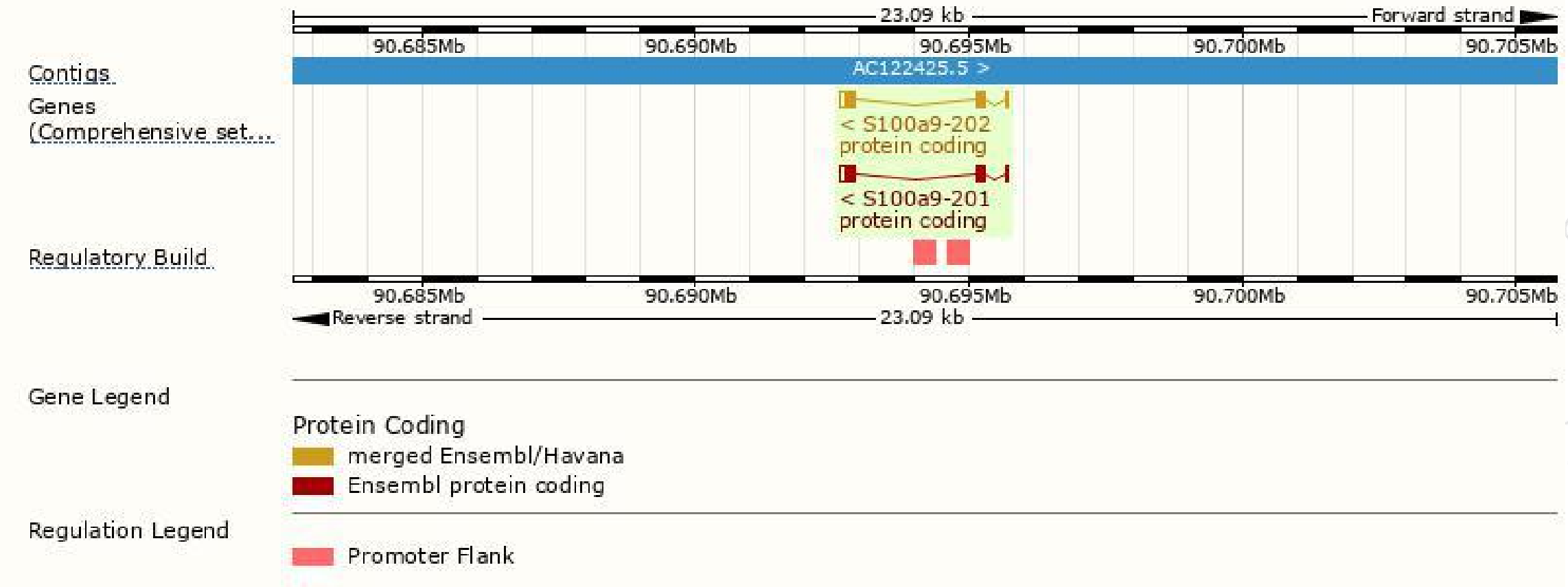
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
S100a9-202	ENSMUST00000117167.1	519	113aa	Protein coding	CCDS17543	P31725 Q3UP42	TSL:1 GENCODE basic APPRIS P1
S100a9-201	ENSMUST00000069960.11	512	113aa	Protein coding	CCDS17543	P31725 Q3UP42	TSL:1 GENCODE basic APPRIS P1

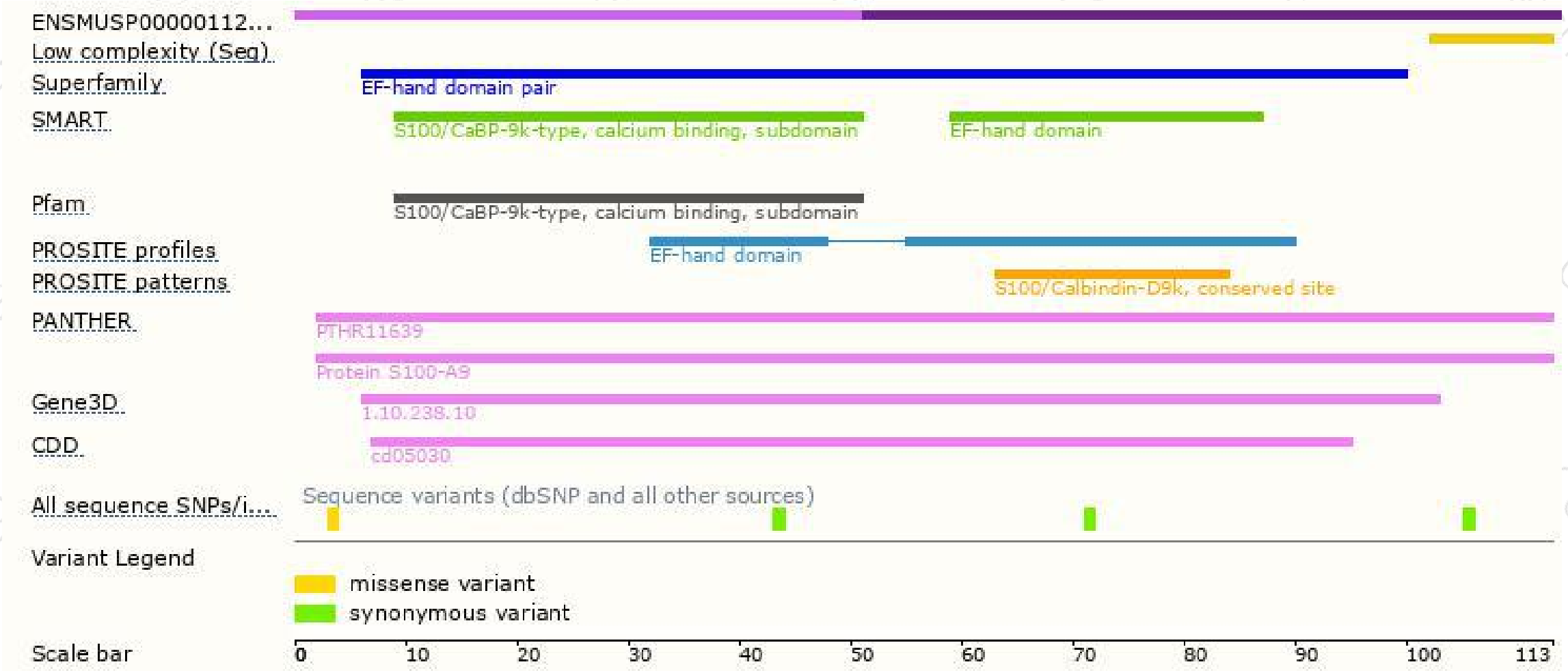
The strategy is based on the design of *S100a9-202* transcript,The transcription is shown below



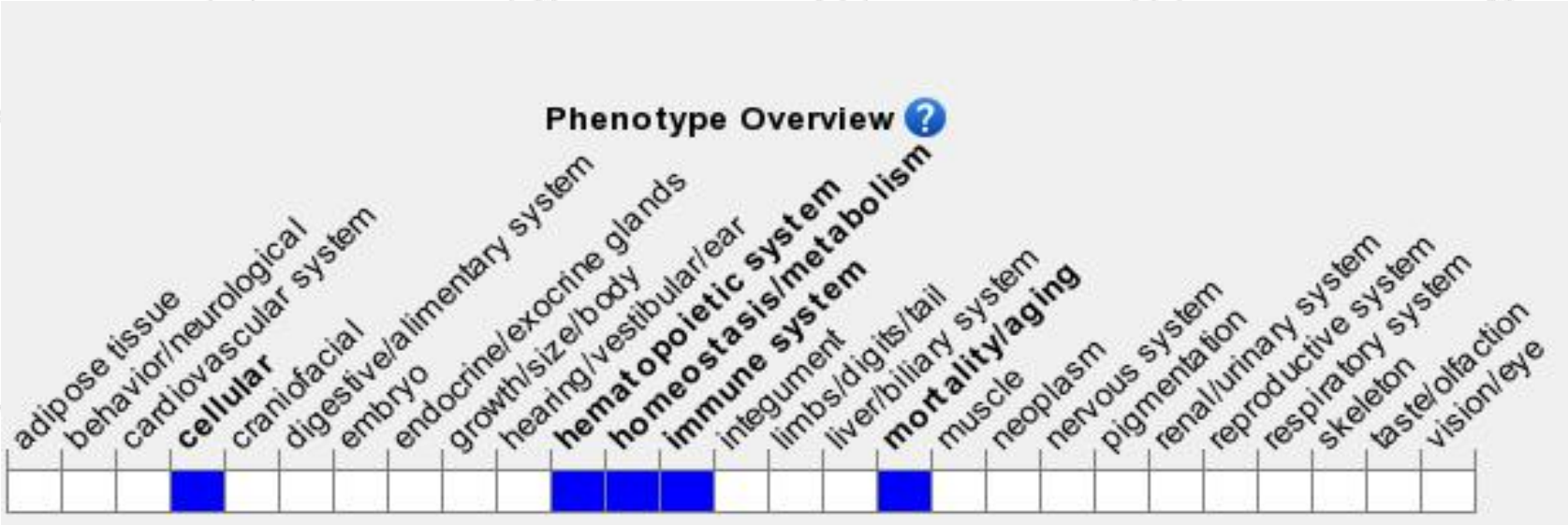
Genomic location distribution



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 null allele exhibit abnormal immune physiology.

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

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