

Sash3 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Sash3

Project type

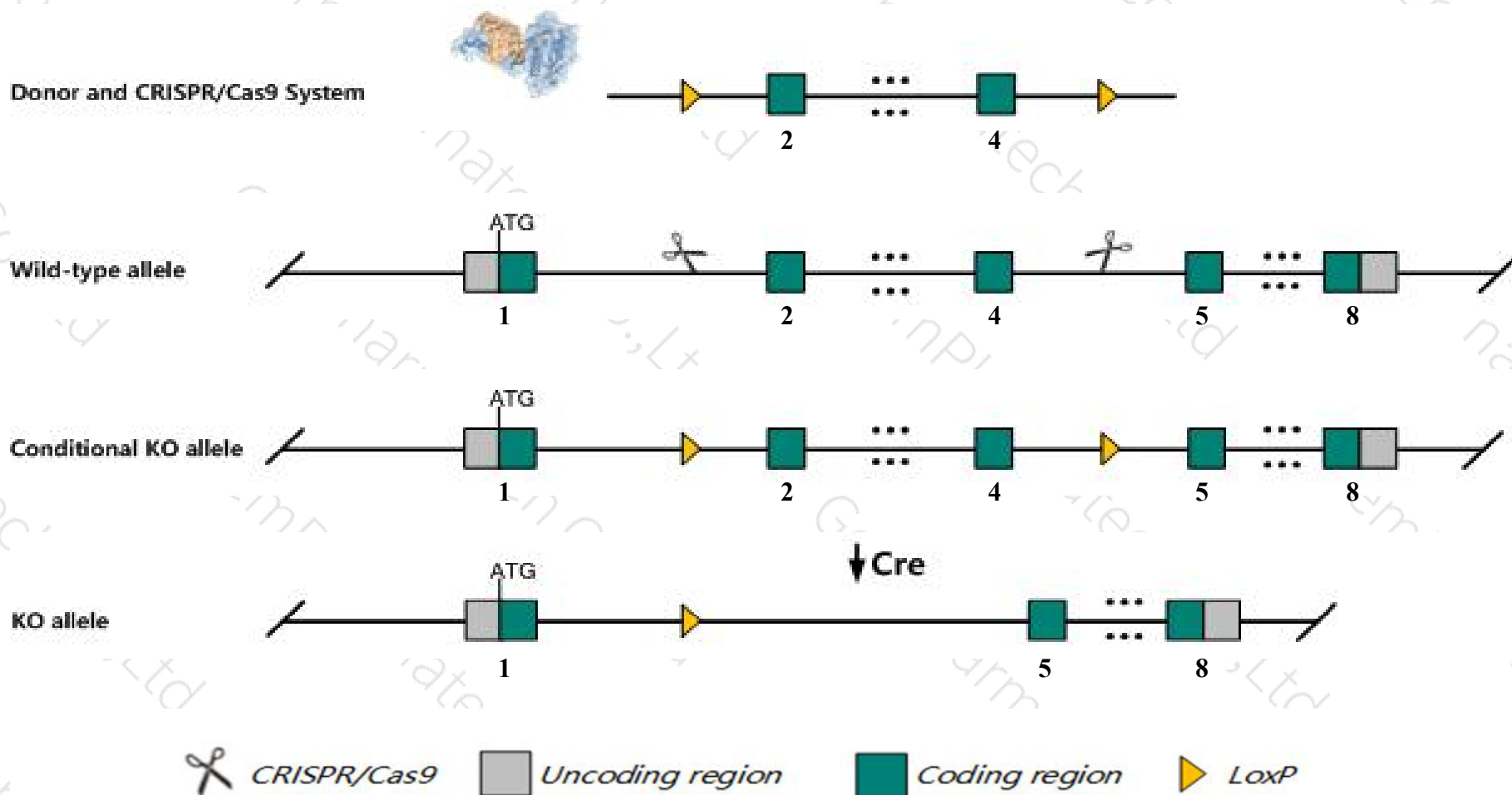
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sash3* gene. The schematic diagram is as follows:



- The *Sash3* gene has 1 transcript. According to the structure of *Sash3* gene, exon2-exon4 of *Sash3-201* (ENSMUST00000033427.6) transcript is recommended as the knockout region. The region contains 385bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sash3* 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.

- According to the existing MGI data, Mice homozygous for a truncation allele exhibit decreased T and B cells, altered B cell physiology and increased length of semi-identical allograft survival.
- The *Sash3* 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)

Sash3 SAM and SH3 domain containing 3 [Mus musculus (house mouse)]

Gene ID: 74131, updated on 31-Jan-2019

Summary



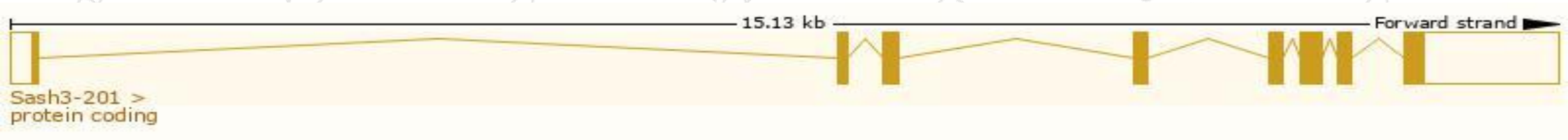
Official Symbol	Sash3 provided by MGI
Official Full Name	SAM and SH3 domain containing 3 provided by MGI
Primary source	MGI:MGI:1921381
See related	Ensembl:ENSMUSG000000031101
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200013B08Rik, AW413946, SLY1
Expression	Biased expression in thymus adult (RPKM 104.2), spleen adult (RPKM 50.8) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

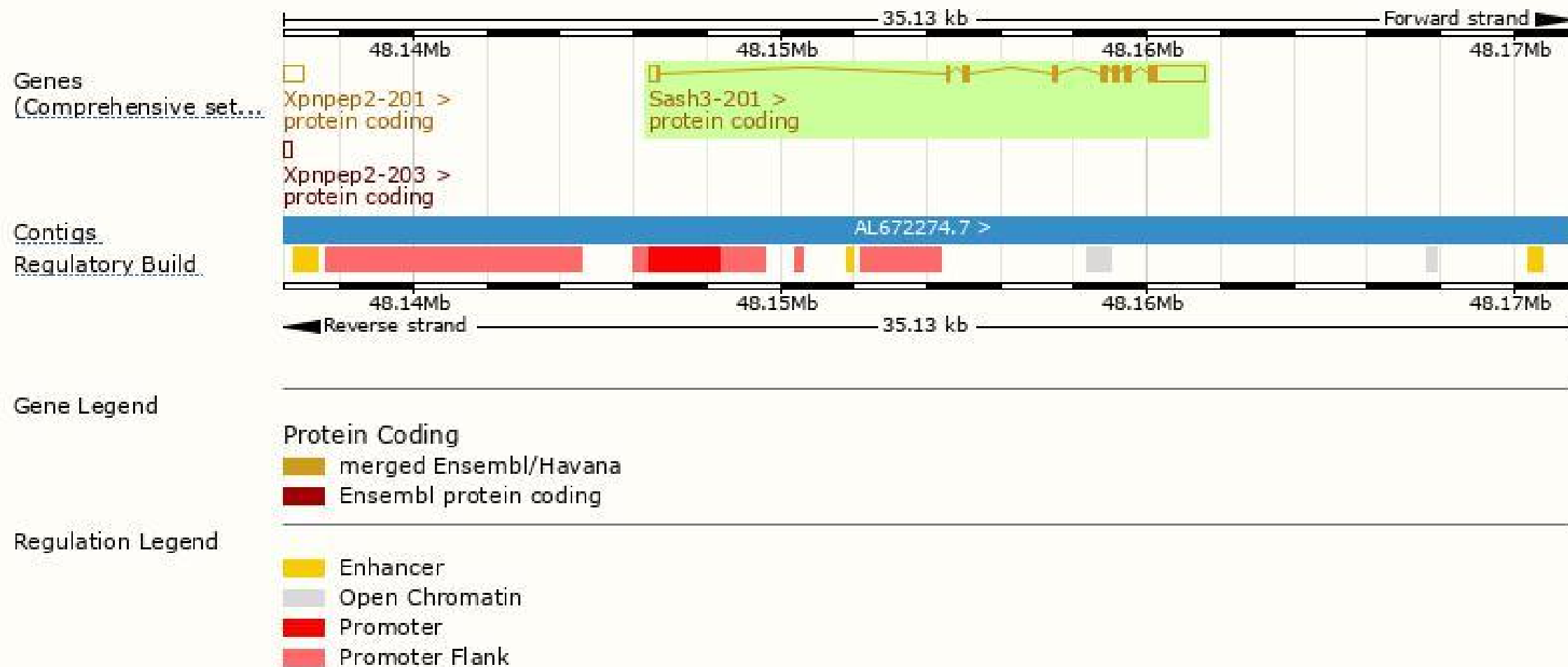
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sash3-201	ENSMUST00000033427.6	2677	380aa	Protein coding	CCDS40959	Q8K352	TSL:1 GENCODE basic APPRIS P1

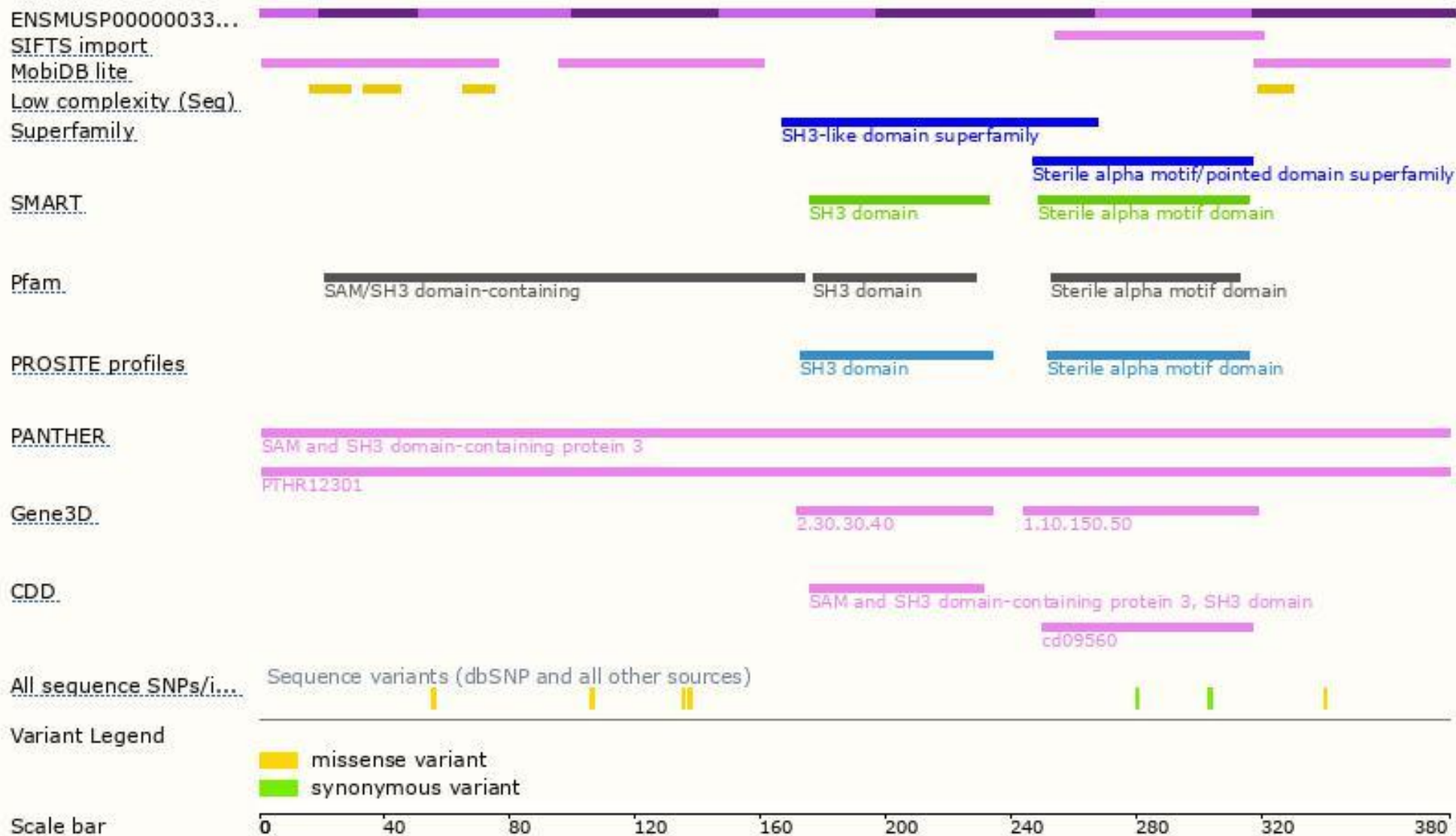
The strategy is based on the design of *Sash3-201* transcript, The transcription is shown below



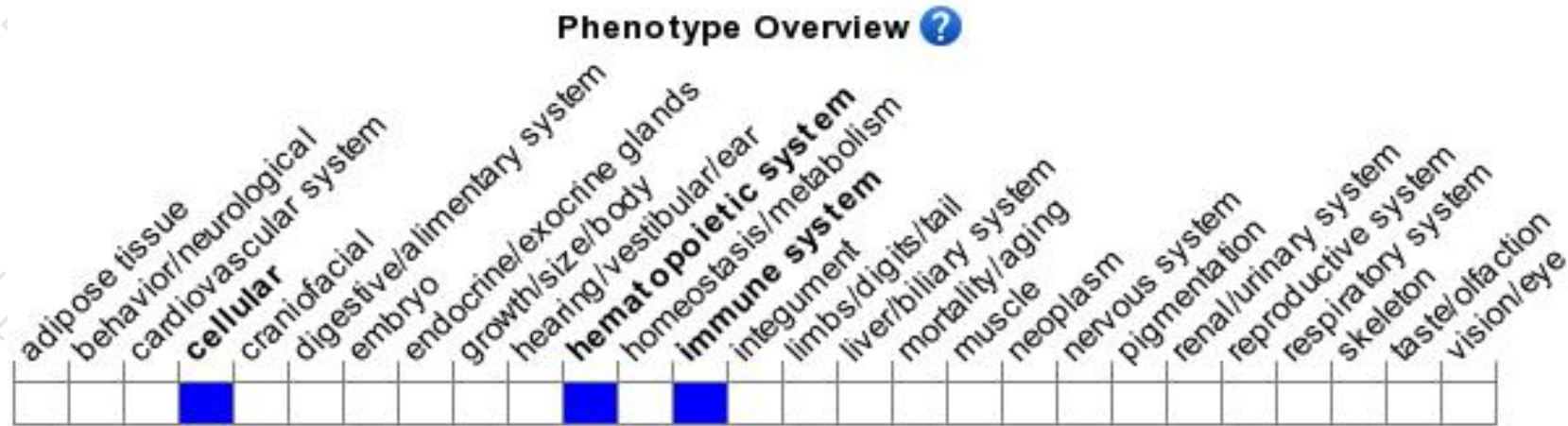
Genomic location distribution



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 a truncation allele exhibit decreased T and B cells, altered B cell physiology and increased length of semi-identical allograft survival.

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

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