

Ccrl2 Cas9-CKO Strategy

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Project Overview

Project Name

Ccrl2

Project type

Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

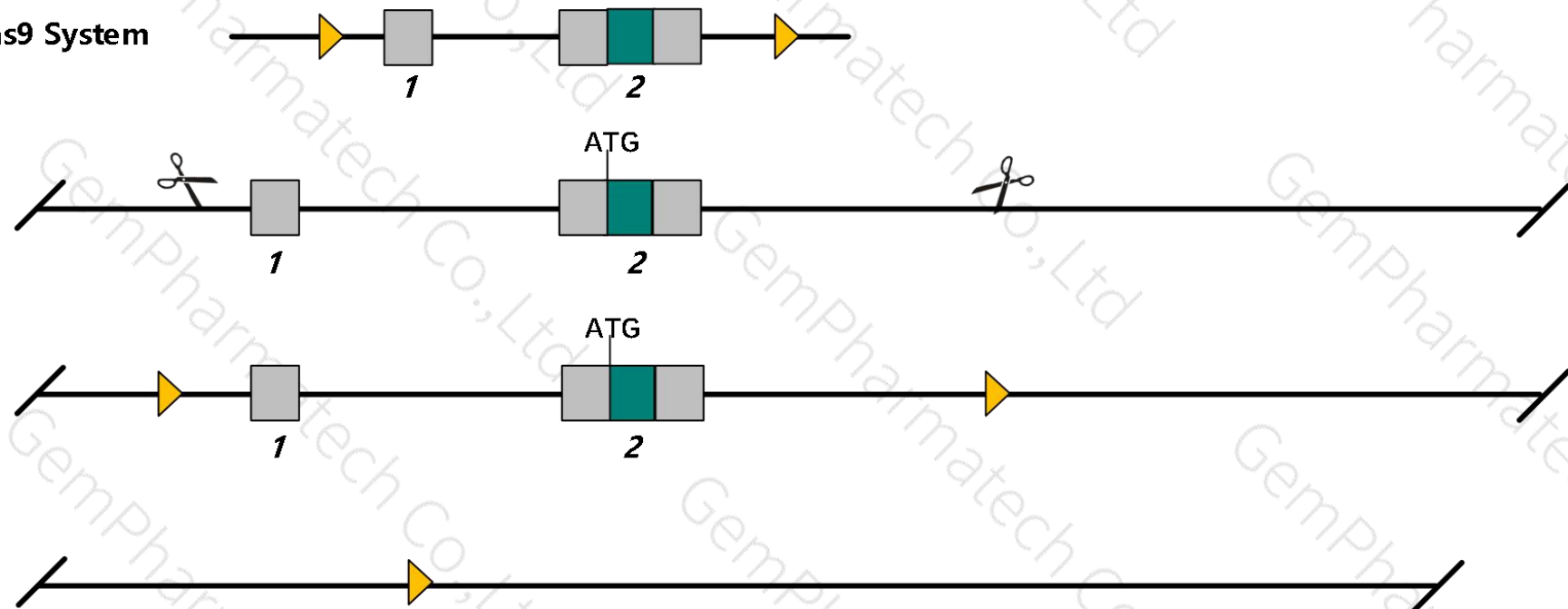
This model will use CRISPR/Cas9 technology to edit the *Ccr12* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Conditional KO allele

KO allele



Cas9/sgRNA



Uncoding region



Coding region



LoxP

- The *Ccrl2* gene has 3 transcripts. According to the structure of *Ccrl2* gene, exon1-exon2 of *Ccrl2-201* (ENSMUST00000111888.2) 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 *Ccrl2* 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 targeted null mutation do not exhibit any significant abnormalities compared to controls.
- The KO region contains functional region of the *Gm43814* gene. Knockout the region may affect the function of *Gm43814* gene.
- The *Ccrl2* gene is located on the Chr9. 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)

Ccr12 chemokine (C-C motif) receptor-like 2 [Mus musculus (house mouse)]

Gene ID: 54199, updated on 31-Jan-2019

Summary



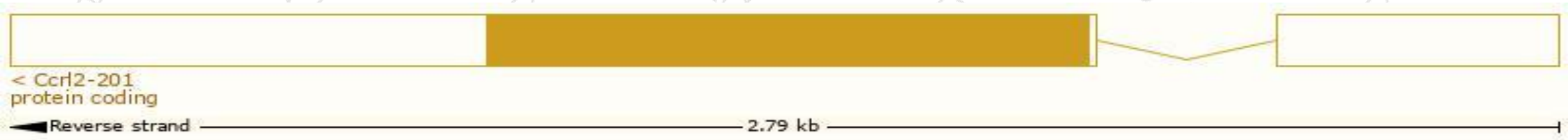
Official Symbol	Ccr12 provided by MGI
Official Full Name	chemokine (C-C motif) receptor-like 2 provided by MGI
Primary source	MGI:MGI:1920904
See related	Ensembl:ENSMUSG00000043953
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810047I05Rik, Ackr5, CCR11, Cmkbr1l2, E01, L-CCR
Expression	Broad expression in lung adult (RPKM 16.6), placenta adult (RPKM 10.7) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

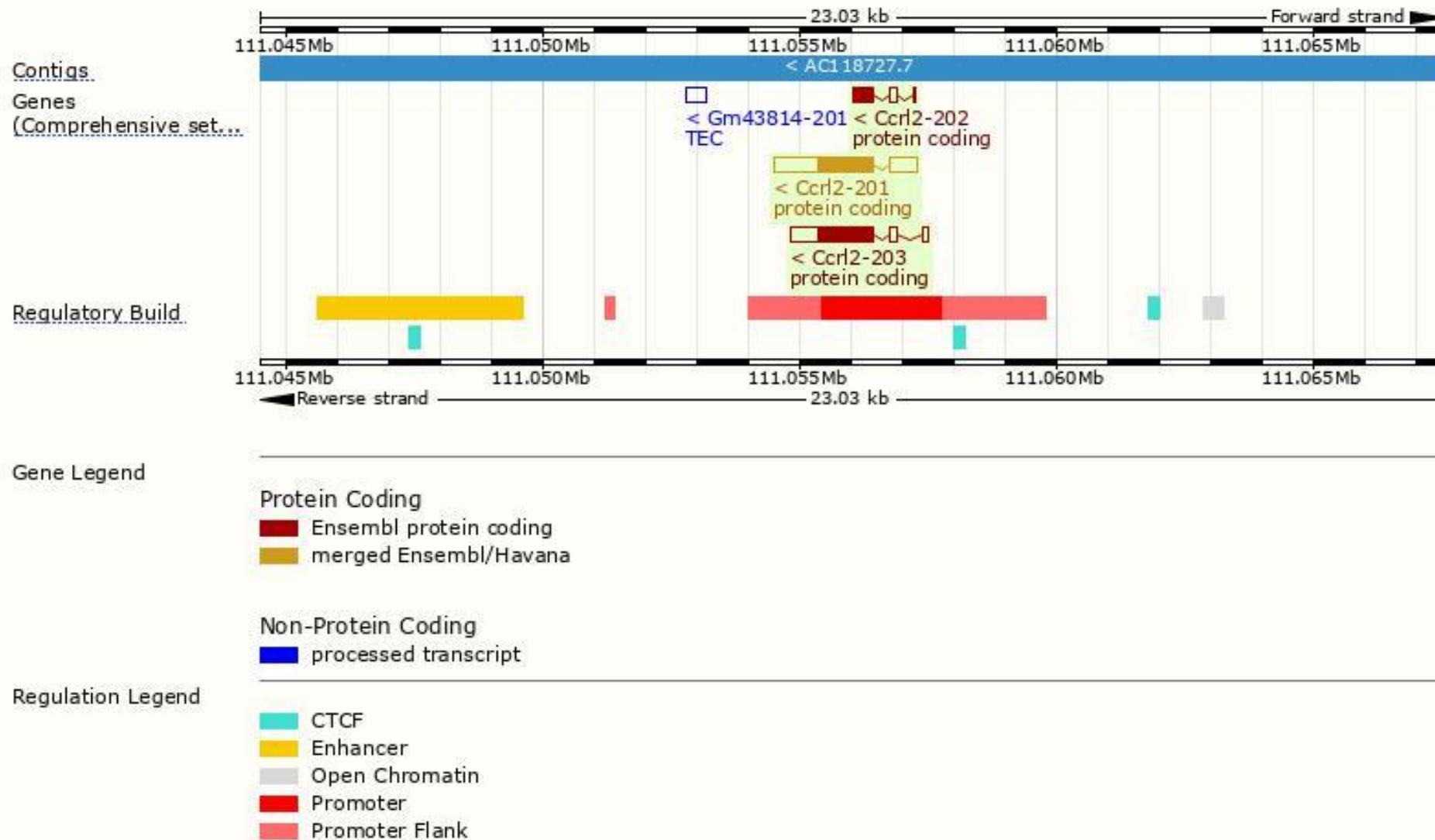
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccrl2-201	ENSMUST00000111888.2	2459	360aa	Protein coding	CCDS23582	Q35457	TSL:1 GENCODE basic APPRIS P1
Ccrl2-203	ENSMUST00000199839.4	1864	360aa	Protein coding	CCDS23582	Q35457	TSL:1 GENCODE basic APPRIS P1
Ccrl2-202	ENSMUST00000195968.1	569	133aa	Protein coding	-	A0A0G2JFB5	CDS 3' incomplete TSL:2

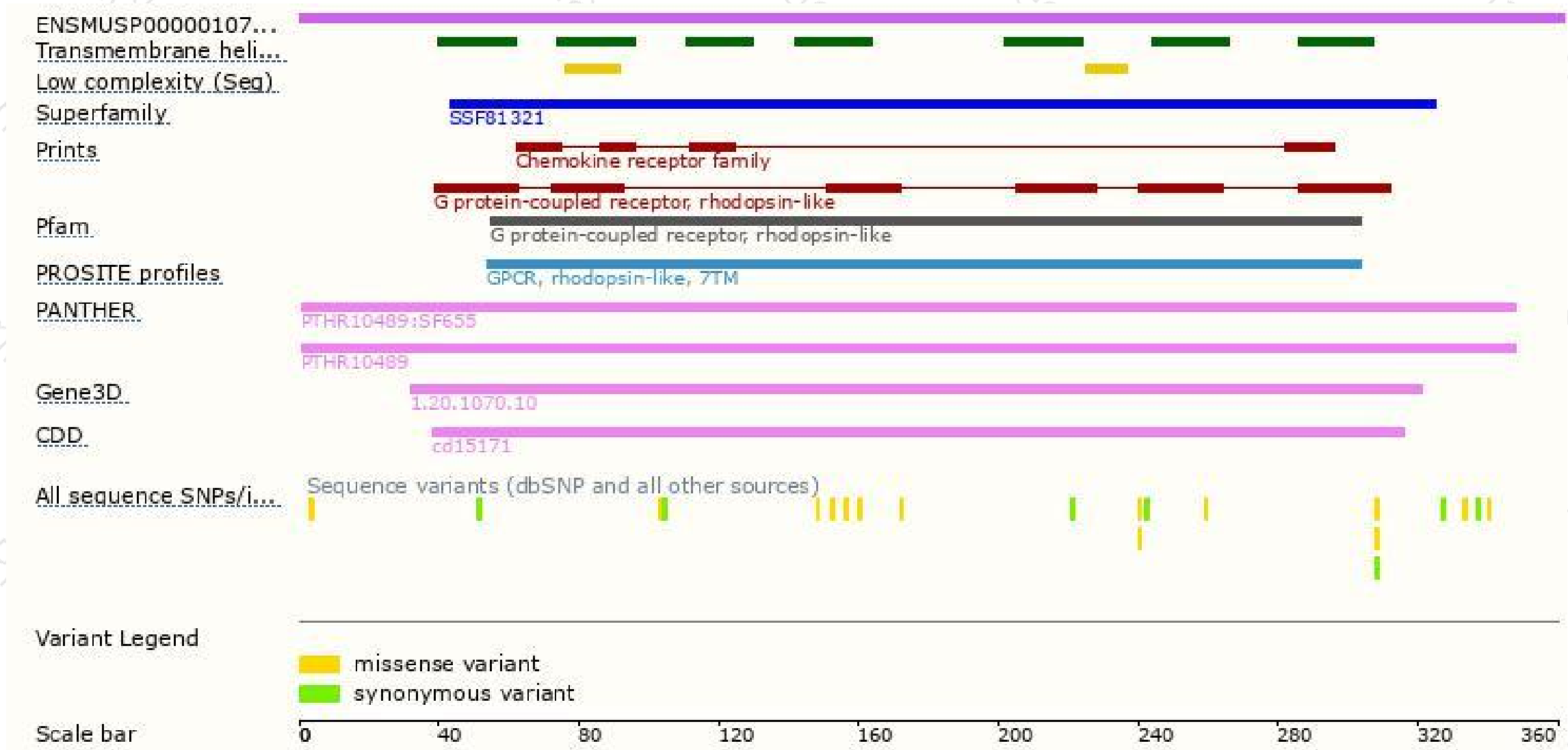
The strategy is based on the design of *Ccrl2-201* transcript,The transcription is shown below



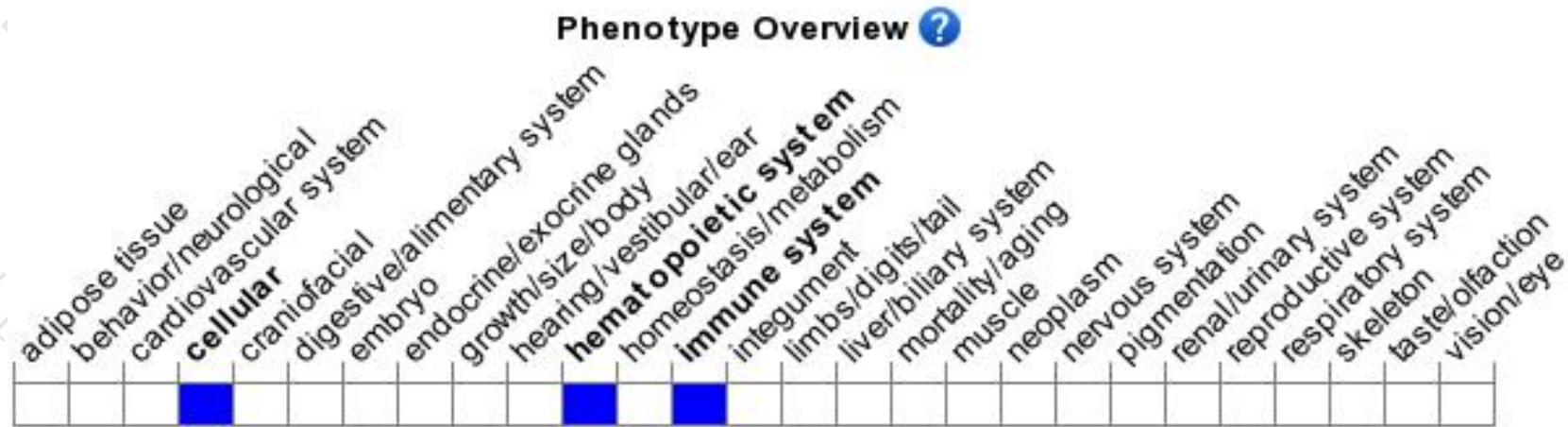
Genomic location distribution



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 targeted null mutation do not exhibit any significant abnormalities compared to controls.

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

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