Dclre1c Cas9-KO Strategy

Designer: Yang Zeng
Reviewer: Xiaojing Li

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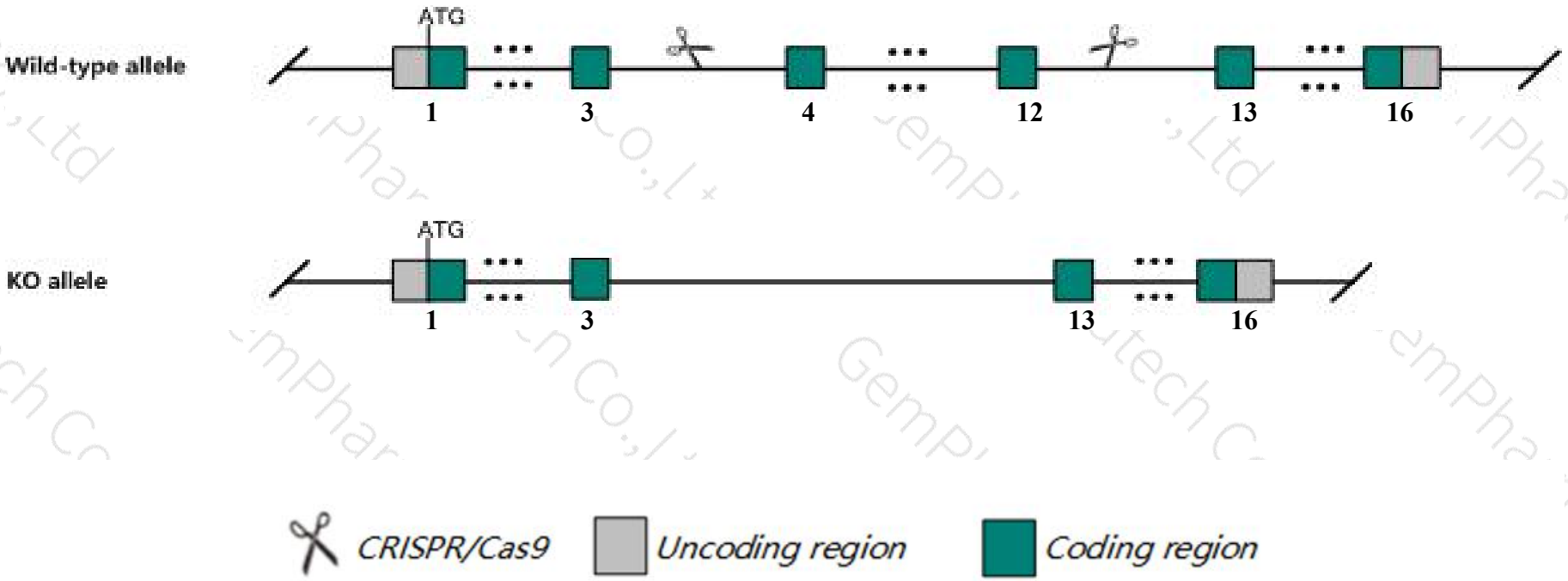
Project Overview

Project Name	***Dclre1c***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dclre1c* gene. The schematic diagram is as follows:



Technical routes

➢ The *Dclre1c* gene has 9 transcripts. According to the structure of *Dclre1c* gene, exon4-exon12 of *Dclre1c-201* (ENSMUST00000061852.11) transcript is recommended as the knockout region.The region contains 815bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Dclre1c* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous mutant mice exhibit a combined immunodeficiency phenotype. While immunoglobulin rearrangement is completely blocked in B cells, the block of V(D)J rearrangement in T cells is partial.

- The *Dclre1c* gene is located on the Chr2. 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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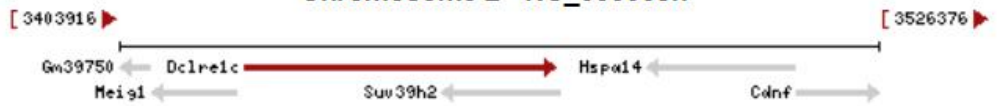
Dclre1c DNA cross-link repair 1C [*Mus musculus* (house mouse)]

Gene ID: 227525, updated on 13-Aug-2019

Summary

Official Symbol	Dclre1c provided by MGI
Official Full Name	DNA cross-link repair 1C provided by MGI
Primary source	MGI:MGI:2441769
See related	Ensembl:ENSMUSG00000026648
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	Art; Snm1l; AI661365; 9930121L06Rik
Summary	This gene encodes a member of the SNM1 family of nucleases and is involved in V(D)J recombination and DNA repair. This protein has single-strand-specific 5'-3' exonuclease activity; it also exhibits endonuclease activity on 5' and 3' overhangs and hairpins. The protein also functions in the regulation of the cell cycle in response to DNA damage. Homozygous knockout mice for this gene exhibit severe combined immunodeficiency with sensitivity to ionizing radiation. Mutations in this gene in humans can cause Athabascan-type severe combined immunodeficiency (SCIDA) and Omenn syndrome. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Nov 2014]
Expression	Ubiquitous expression in CNS E11.5 (RPKM 1.7), CNS E14 (RPKM 1.7) and 26 other tissues See more
Orthologs	human all

Chromosome 2 - NC_000068.7

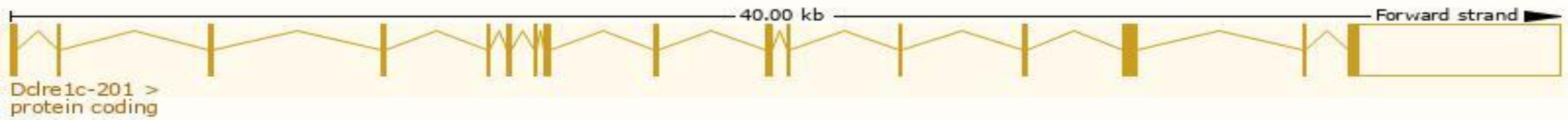


Transcript information（Ensembl）

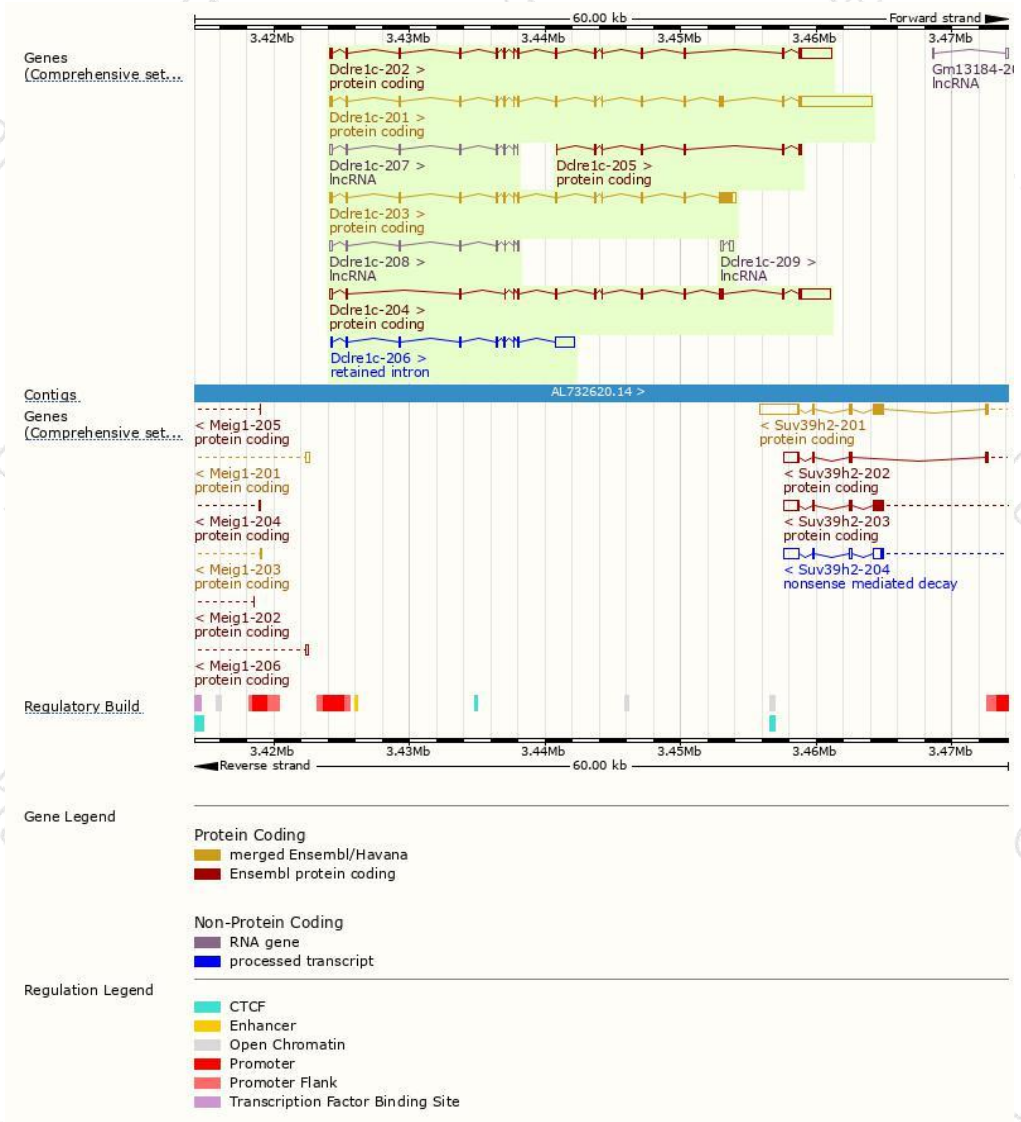
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Dclre1c-201	ENSMUST00000061852.11	7075	603aa	ENSMUSP00000054300.5	Protein coding	CCDS15649	Q8K4J0	TSL:1 GENCODE basic APPRIS ALT2
Dclre1c-204	ENSMUST00000115066.7	3828	473aa	ENSMUSP00000110718.1	Protein coding	CCDS79728	Q8K4J0	TSL:1 GENCODE basic
Dclre1c-202	ENSMUST00000100463.9	3705	486aa	ENSMUSP00000098031.3	Protein coding	CCDS50486	Q32MX8	TSL:1 GENCODE basic APPRIS ALT2
Dclre1c-203	ENSMUST00000102988.9	2469	705aa	ENSMUSP00000100053.3	Protein coding	CCDS15650	Q8K4J0	TSL:1 GENCODE basic APPRIS P4
Dclre1c-205	ENSMUST00000129657.1	679	227aa	ENSMUSP00000116883.1	Protein coding	-	F7BA65	CDS 5' and 3' incomplete TSL:5
Dclre1c-206	ENSMUST00000131433.1	2143	No protein	-	Retained intron	-	-	TSL:2
Dclre1c-207	ENSMUST00000132565.7	655	No protein	-	lncRNA	-	-	TSL:3
Dclre1c-208	ENSMUST00000146027.7	650	No protein	-	lncRNA	-	-	TSL:3
Dclre1c-209	ENSMUST00000152468.1	523	No protein	-	lncRNA	-	-	TSL:3

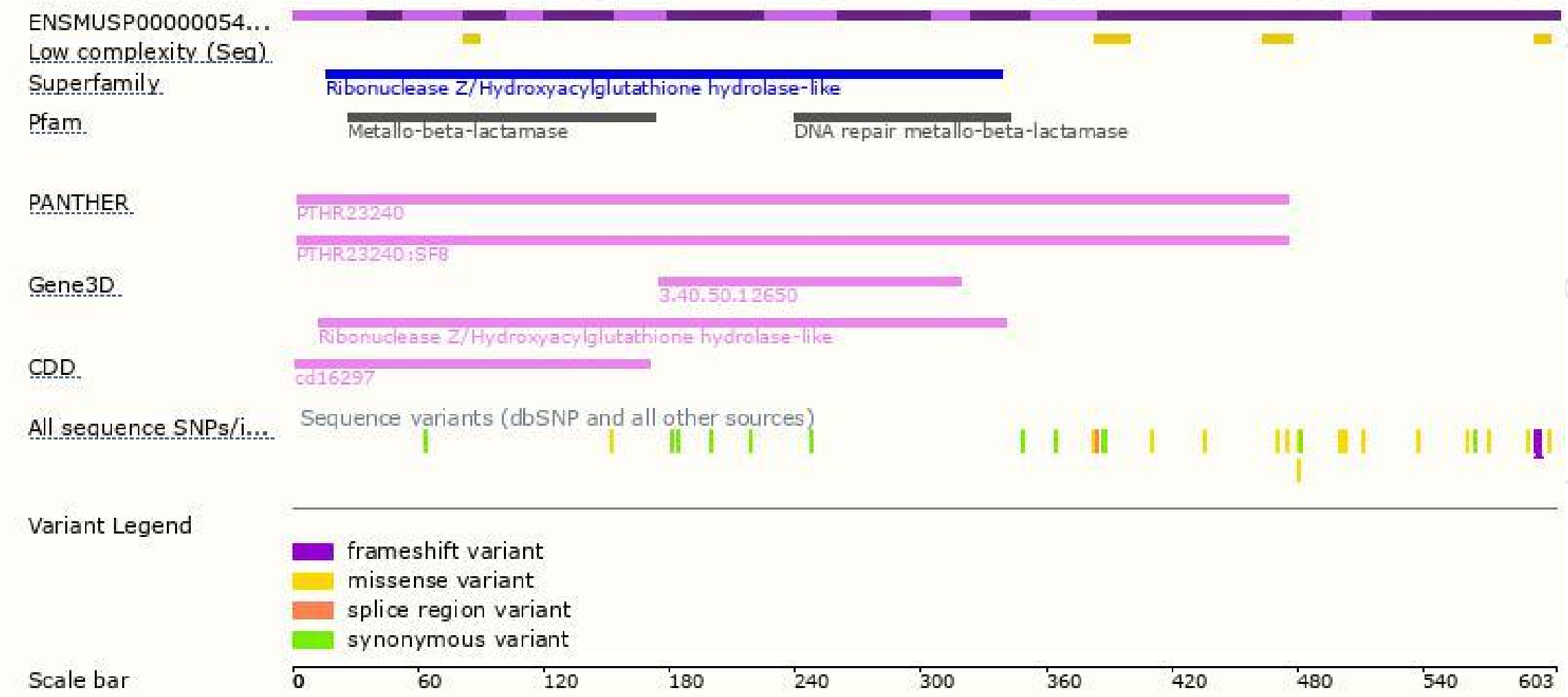
The strategy is based on the design of *Dclre1c-201* transcript,The transcription is shown below



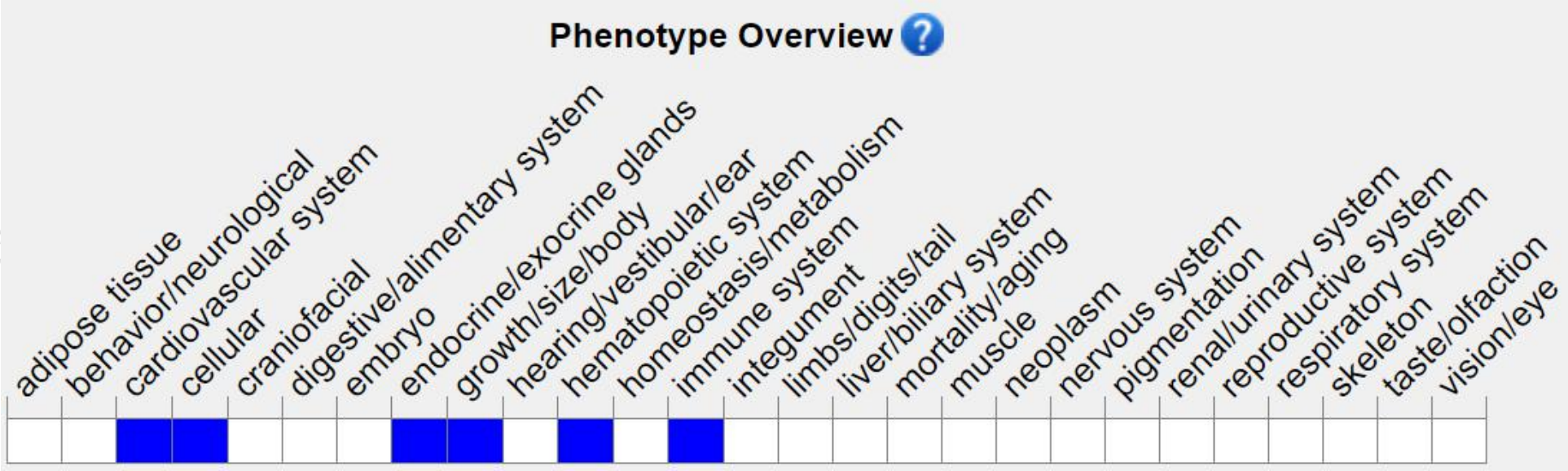
Genomic location distribution



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,Homozygous mutant mice exhibit a combined immunodeficiency phenotype. While immunoglobulin rearrangement is completely blocked in B cells, the block of V(D)J rearrangement in T cells is partial.

集萃药康
GemPharmatech

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd