

Cd244a Cas9-CKO Strategy

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Project Overview

Project Name

Cd244a

Project type

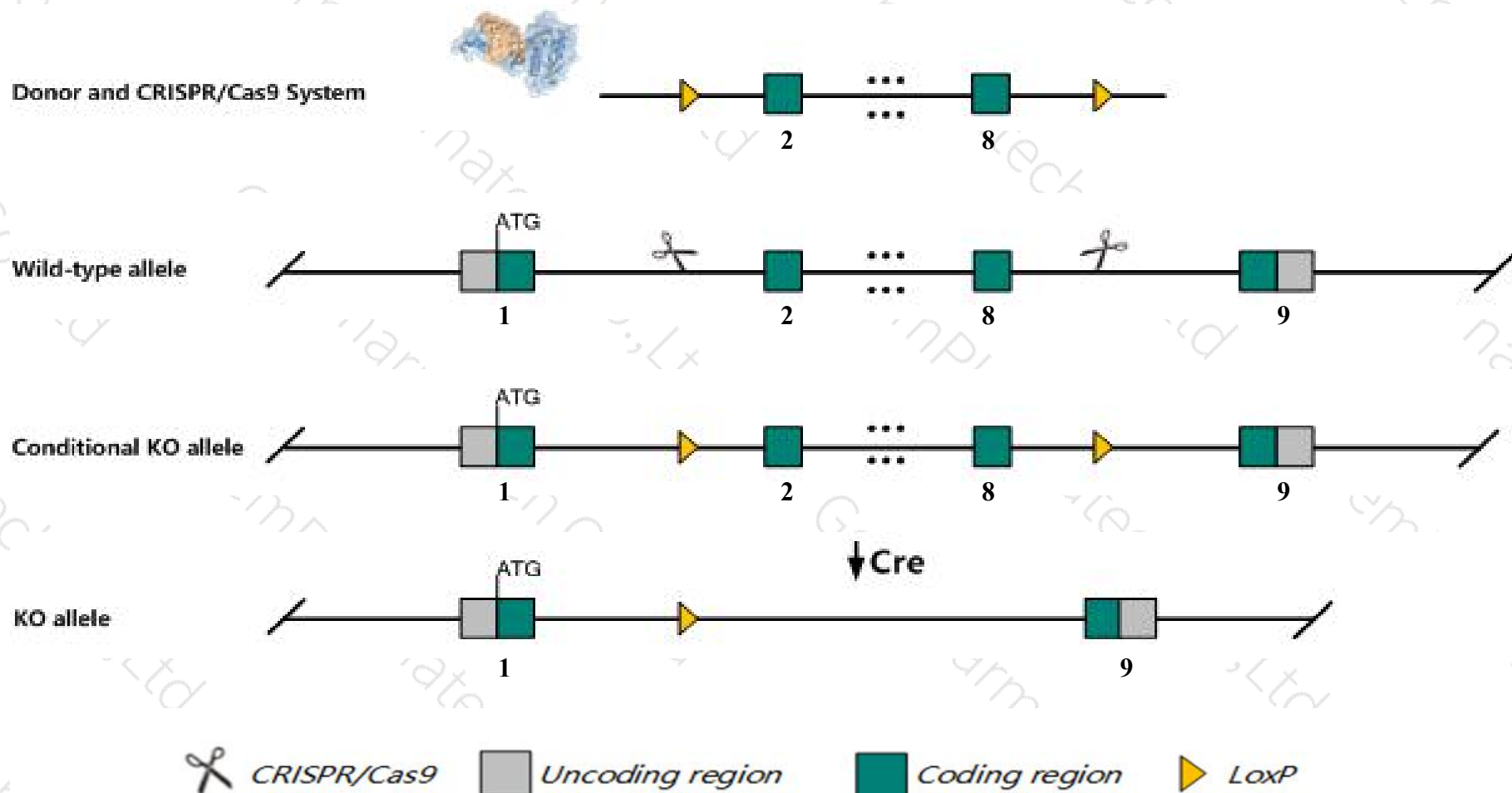
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd244a* gene. The schematic diagram is as follows:



- The *Cd244a* gene has 4 transcripts. According to the structure of *Cd244a* gene, exon2-exon8 of *Cd244a-201* (ENSMUST00000004829.12) transcript is recommended as the knockout region. The region contains 1052bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cd244a* 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 knock-out allele exhibit altered natural killer (NK) cell cytotoxicity. Mice homozygous for an ENU-generated allele exhibit reduced missing-self targets recognition and elimination and increased clearance of B16 melanoma tumors.
- The *Cd244a* gene is located on the Chr1. 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)

Cd244a CD244 molecule A [*Mus musculus* (house mouse)]

Gene ID: 18106, updated on 21-Oct-2019

Summary

Official Symbol	Cd244a provided by MGI
Official Full Name	CD244 molecule A provided by MGI
Primary source	MGI:MGI:109294
See related	Ensembl:ENSMUSG00000004709
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	2B4; C9.1; Ly90; NAIL; Nmrk; Cd244; NKR2B4; SLAMF4; F730046O15Rik
Expression	Biased expression in spleen adult (RPKM 1.6), large intestine adult (RPKM 0.7) and 12 other tissues See more
Orthologs	human all

Genomic context

Location: 1 H3; 1 79.52 cM

See Cd244a in [Genome Data Viewer](#)

Exon count: 9

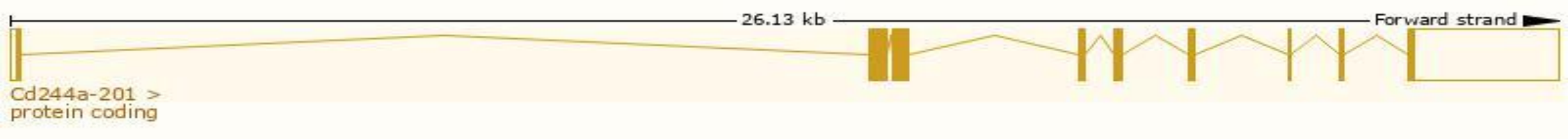
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (171558718..171585316)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (173489324..173515447)

Transcript information (Ensembl)

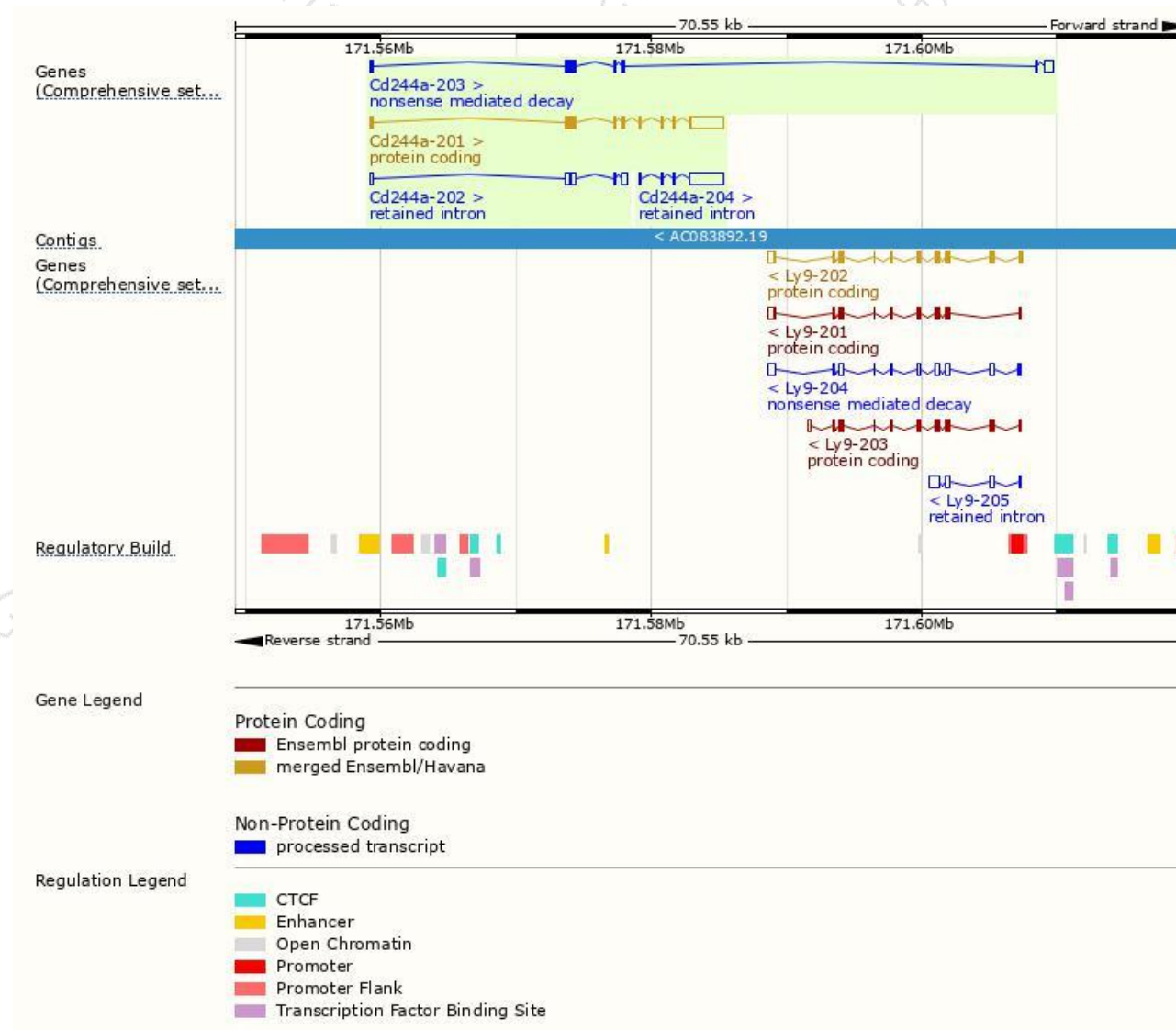
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd244a-201	ENSMUST00000004829.12	3760	397aa	Protein coding	CCDS35778	Q07763	TSL:1 GENCODE basic APPRIS P1
Cd244a-203	ENSMUST00000194797.1	1854	312aa	Nonsense mediated decay	-	Q3TAZ6	TSL:1
Cd244a-204	ENSMUST00000195804.1	2743	No protein	Retained intron	-	-	TSL:1
Cd244a-202	ENSMUST00000194170.1	1331	No protein	Retained intron	-	-	TSL:1

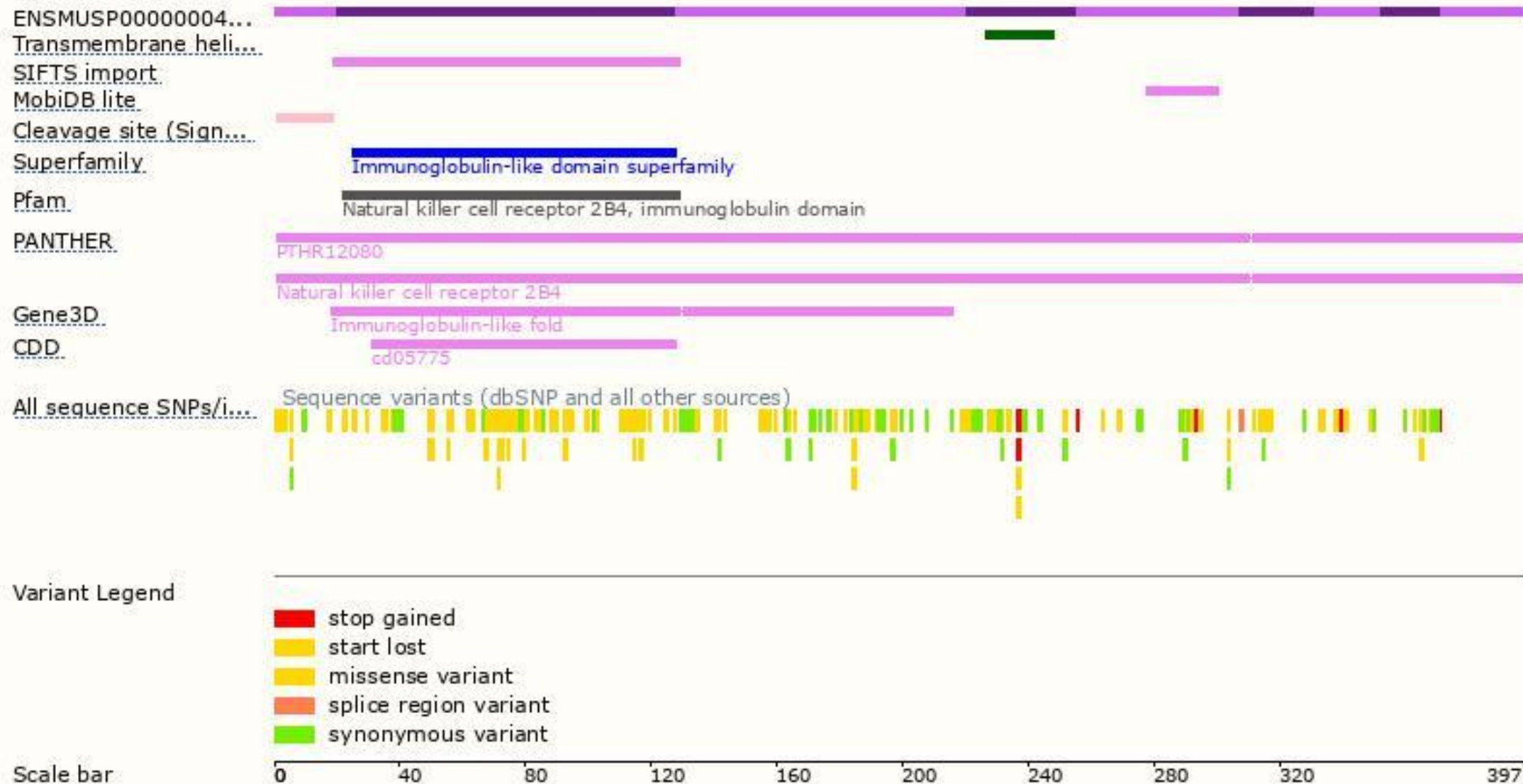
The strategy is based on the design of *Cd244a-201* transcript,The transcription is shown below



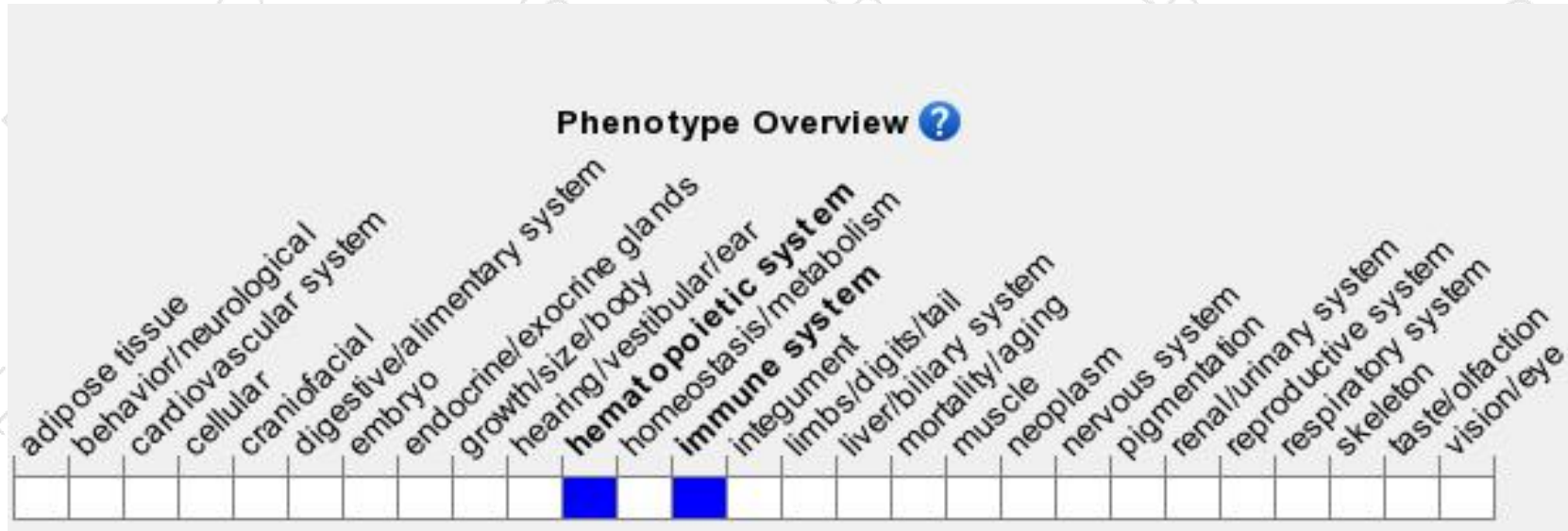
Genomic location distribution



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 knock-out allele exhibit altered natural killer (NK) cell cytotoxicity. Mice homozygous for an ENU-generated allele exhibit reduced missing-self targets recognition and elimination and increased clearance of B16 melanoma tumors.

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

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