Nck1 Cas9-KO Strategy

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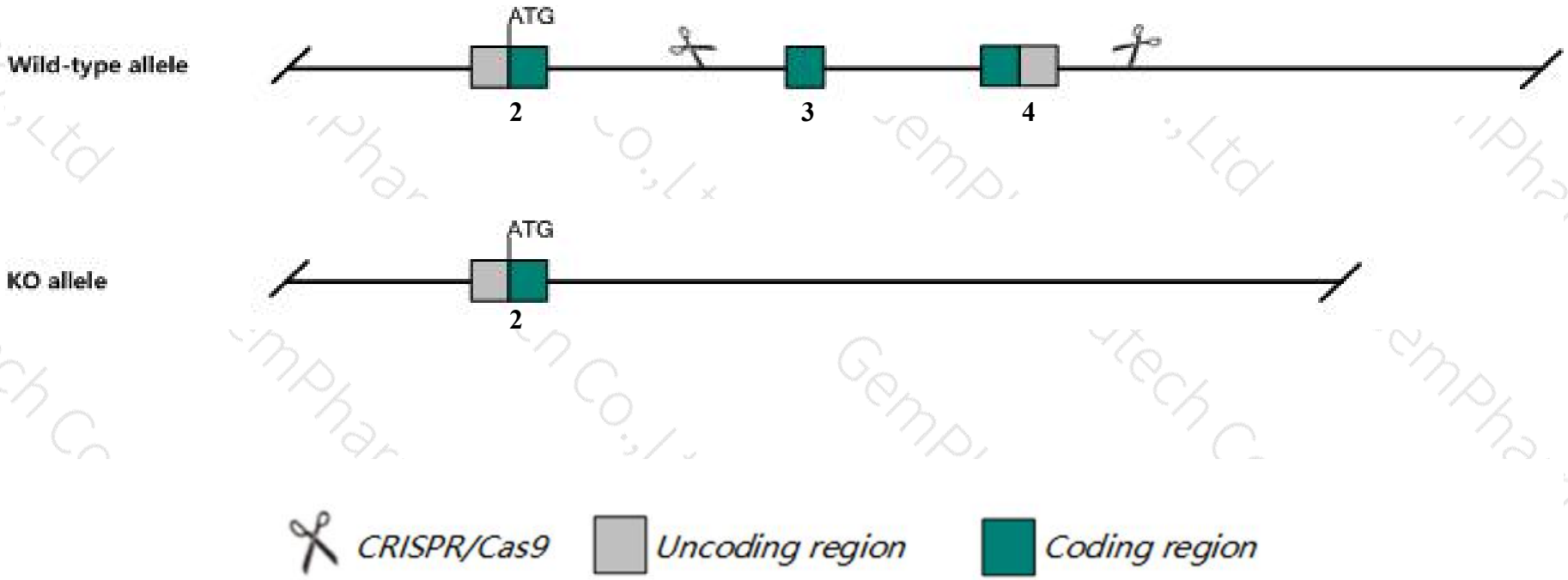
Project Overview

Project Name	***Nck1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nck1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Nck1* gene has 4 transcripts. According to the structure of *Nck1* gene, exon3-exon4 of *Nck1-202* (ENSMUST00000116522.7) 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 *Nck1* gene. The brief process is as follows: CRISPR/Cas9 system were

Notice

- According to the existing MGI data,Mice homozygous for disruption of this gene display no abnormal phenotype.

- The knockout region is near to the N-terminal of *Il20rb* gene,this strategy may influence the regulatory function of the N-terminal of *Il20rb* gene.

- The *Nck1* 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 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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Nck1 non-catalytic region of tyrosine kinase adaptor protein 1 [*Mus musculus* (house mouse)]

Gene ID: 17973, updated on 10-Oct-2019

Summary

Official Symbol	Nck1 provided by MGI
Official Full Name	non-catalytic region of tyrosine kinase adaptor protein 1 provided by MGI
Primary source	MGI:MGI:109601
See related	Ensembl:ENSMUSG00000032475
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	Nck; Nck-1; 6330586M15Rik; D230010O13Rik
Expression	Broad expression in CNS E11.5 (RPKM 10.7), placenta adult (RPKM 9.3) and 24 other tissues See more
Orthologs	human all

Genomic context

Location: 9; 9 E3.3

See Nck1 in Genome Data Viewer

Exon count: 6

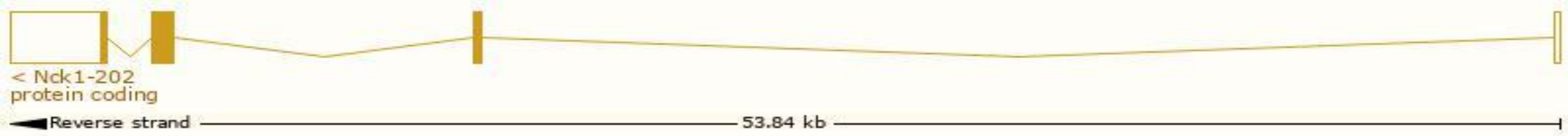
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (100494302..100546134, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (100395422..100446472, complement)

Transcript information（Ensembl）

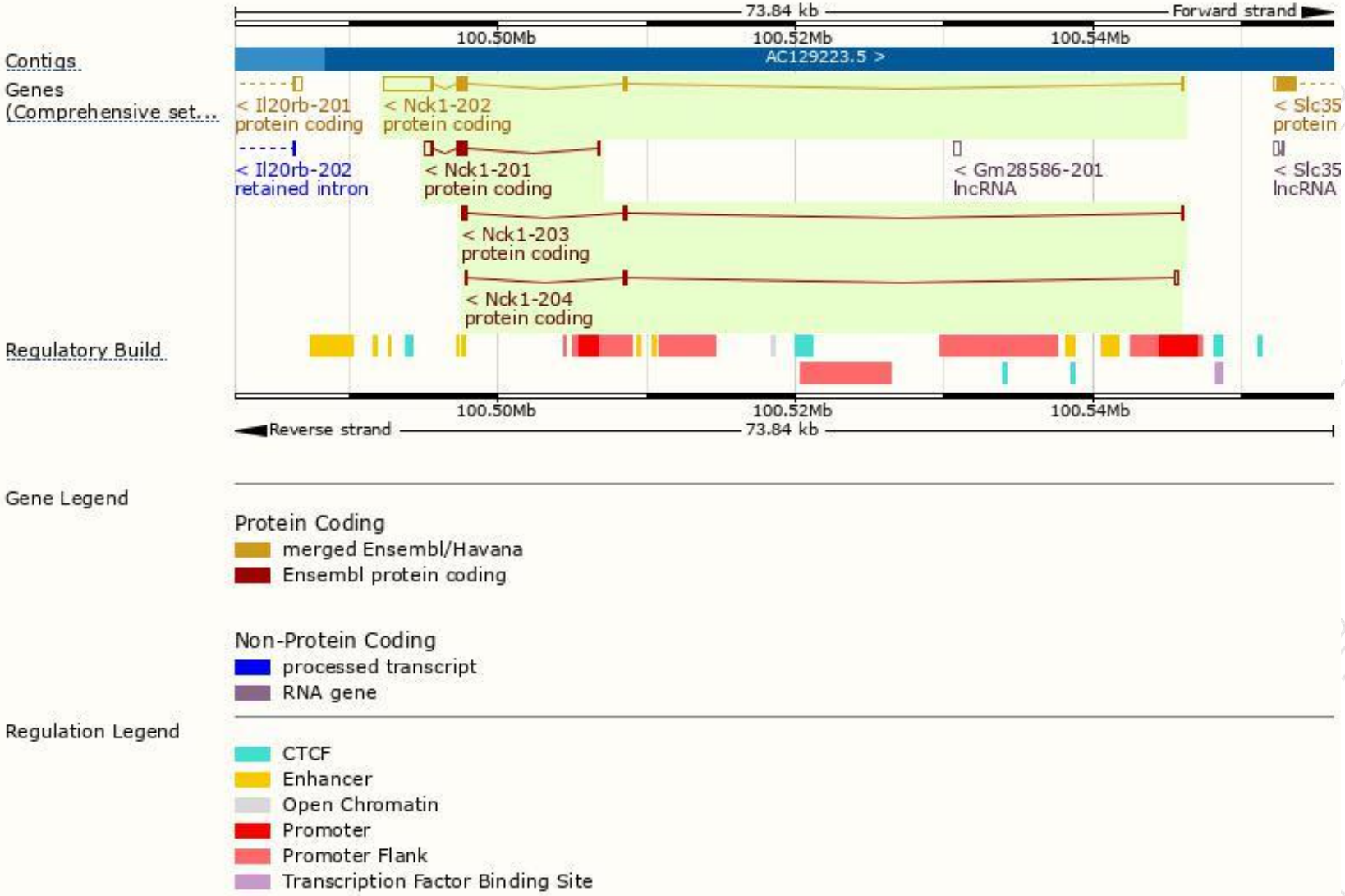
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nck1-202	ENSMUST00000116522.7	4476	377aa	Protein coding	CCDS23440	Q99M51	TSL:1 GENCODE basic APPRIS P1
Nck1-201	ENSMUST00000112874.3	1513	313aa	Protein coding	CCDS85715	Q8BH99	TSL:1 GENCODE basic
Nck1-203	ENSMUST00000186591.6	734	206aa	Protein coding	-	A0A087WSB1	CDS 3' incomplete TSL:2
Nck1-204	ENSMUST00000188670.1	600	132aa	Protein coding	-	A0A087WQD1	CDS 3' incomplete TSL:3

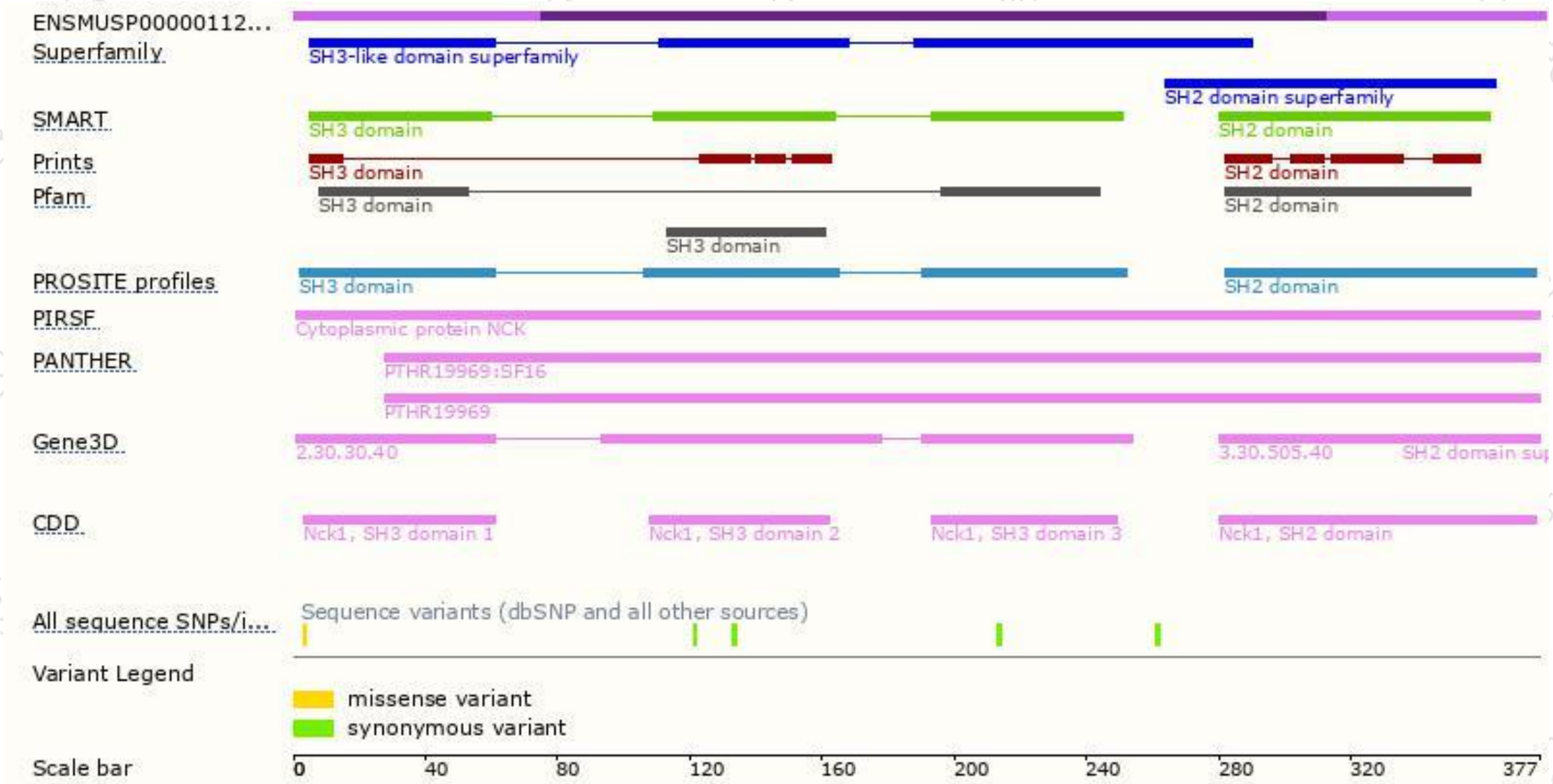
The strategy is based on the design of *Nck1-202* transcript,The transcription is shown below



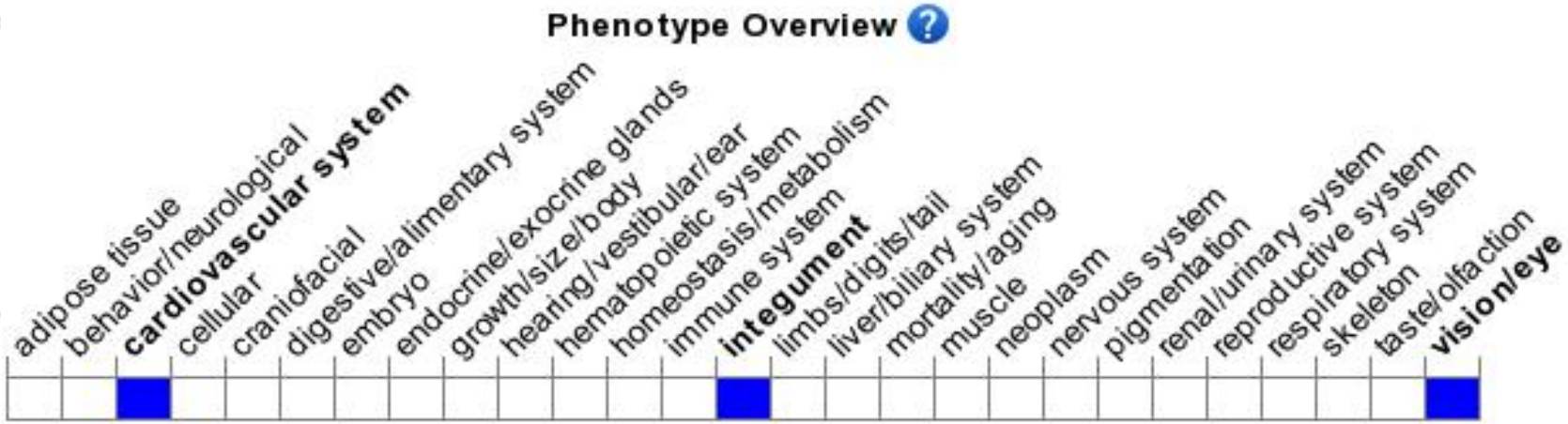
Genomic location distribution



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 disruption of this gene display no abnormal phenotype.

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

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