Atp1b1 Cas9-CKO Strategy

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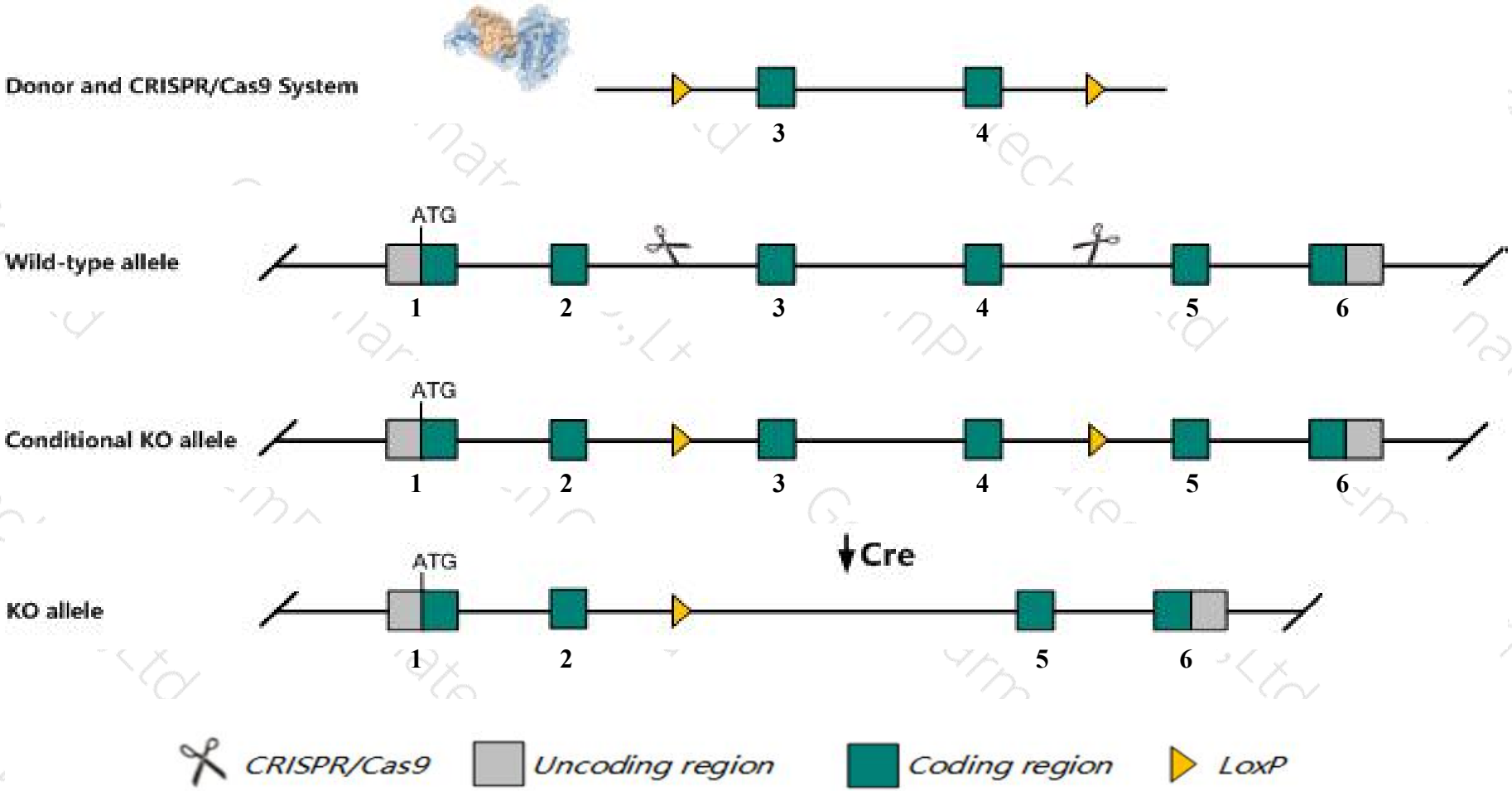
Reviewer:	**Xueting Zhang**
Design Date:	**2019-11-29**

Project Overview

Project Name	***Atp1b1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp1b1* gene. The schematic diagram is as follows:



Technical routes

- The *Atp1b1* gene has 4 transcripts. According to the structure of *Atp1b1* gene, exon3-exon4 of *Atp1b1-201* (ENSMUST00000027863.12) transcript is recommended as the knockout region.The region contains 341bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Atp1b1* 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.

Notice

- According to the existing MGI data,Mice homozygous for a conditional allele activated in cardiac tissue exhibit age-related cardiac hypertrophy and reduced cardiac function, insensitivity to ouabain, and increased heart dysfunction following aortic constriction.

- The *Atp1b1* 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）

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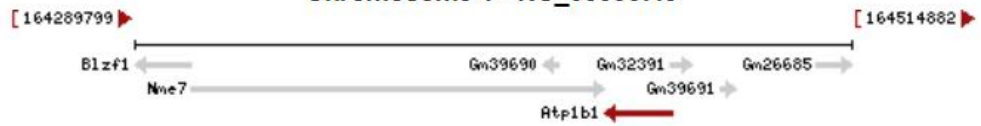
Atp1b1 ATPase, Na+/K+ transporting, beta 1 polypeptide [*Mus musculus* (house mouse)]

Gene ID: 11931, updated on 24-Sep-2019

Summary

Official Symbol	Atp1b1 provided by MGI
Official Full Name	ATPase, Na+/K+ transporting, beta 1 polypeptide provided by MGI
Primary source	MGI:MGI:88108
See related	Ensembl:ENSMUSG00000026576
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	Atpb; Atp4b; Atpb-1; NKbeta1
Summary	This gene encodes an integral membrane protein that comprises a subunit of an ATP-metabolizing enzyme responsible for transporting sodium and potassium ions across the plasma membrane. This enzyme regulates the electrochemical gradient of these ions in cells, and plays a central role in osmoregulation and signal transmission in nerves and muscles, among other biological processes. The encoded protein is the non-catalytic beta subunit; it works together with a catalytic alpha subunit and a gamma subunit. [provided by RefSeq, Mar 2013]
Expression	Biased expression in cerebellum adult (RPKM 397.4), kidney adult (RPKM 397.3) and 13 other tissues See more
Orthologs	human all

Chromosome 1 - NC_000067.6



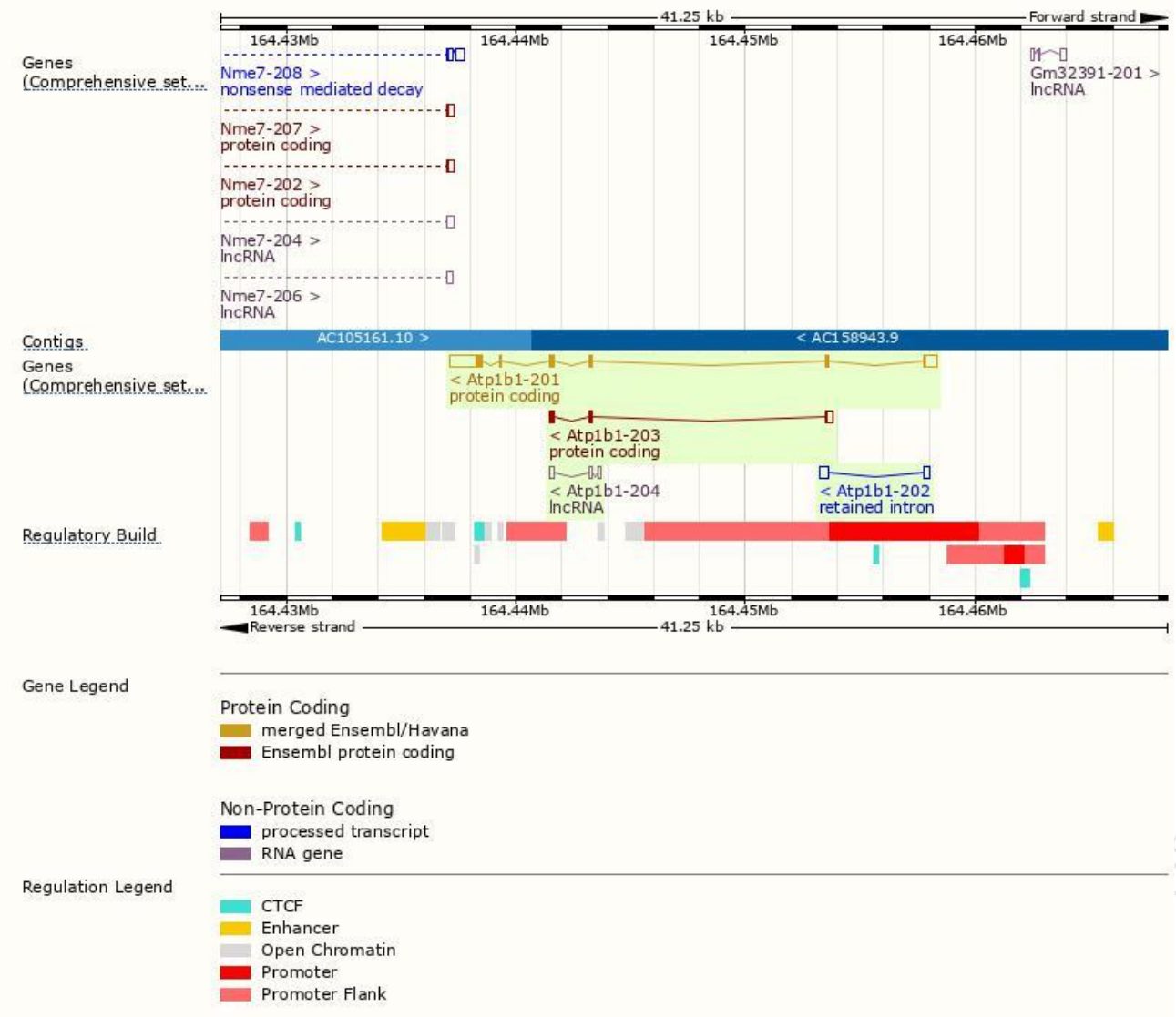
Transcript information（Ensembl）

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

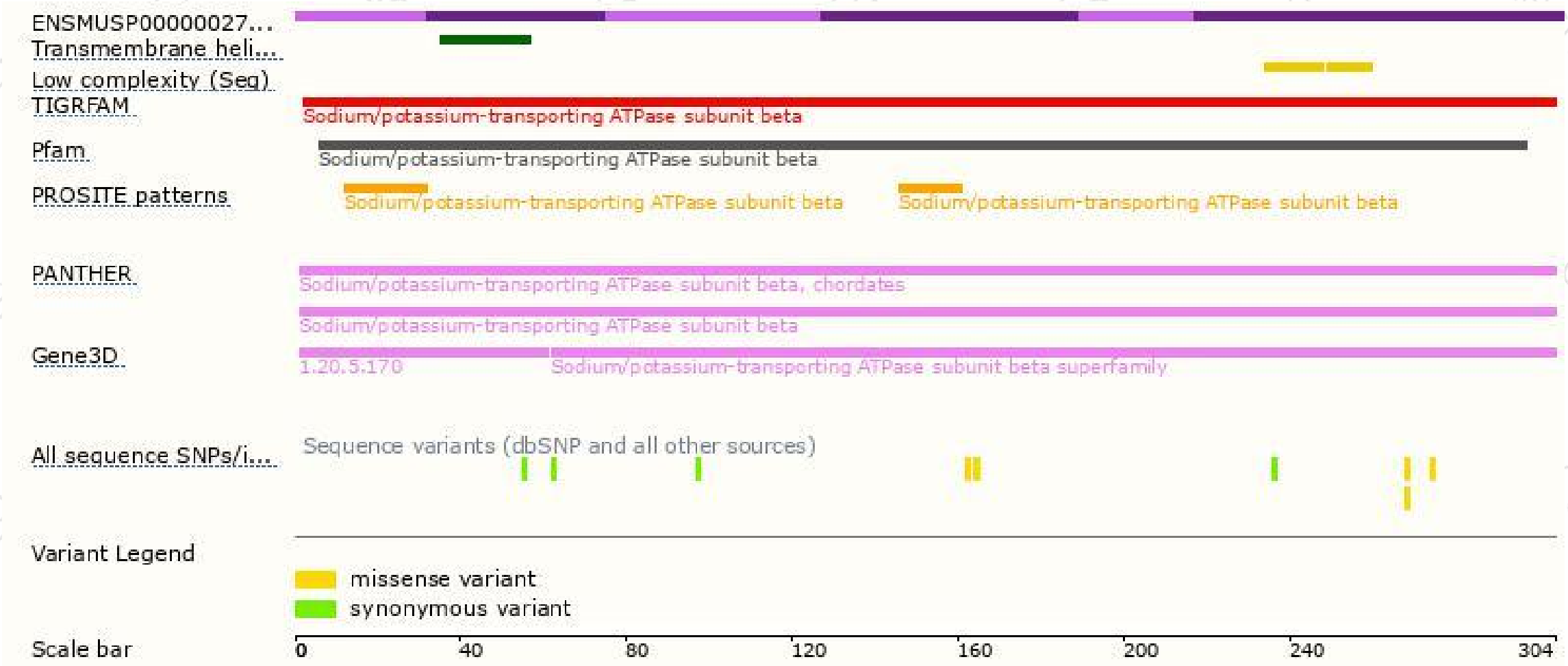
Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Atp1b1-201	ENSMUST00000027863.12	2580	304aa	ENSMUSP00000027863.7	Protein coding	CCDS35755	P14094 Q545P0	TSL:1 GENCODE basic APPRIS P1
Atp1b1-203	ENSMUST00000193367.1	628	132aa	ENSMUSP00000141777.1	Protein coding	-	A0A0A6YX05	CDS 3' incomplete TSL:2
Atp1b1-202	ENSMUST00000192522.1	618	No protein	-	Retained intron	-	-	TSL:2
Atp1b1-204	ENSMUST00000193980.1	453	No protein	-	lncRNA	-	-	TSL:5

The strategy is based on the design of *Atp1b1-201* transcript,The transcription is shown below

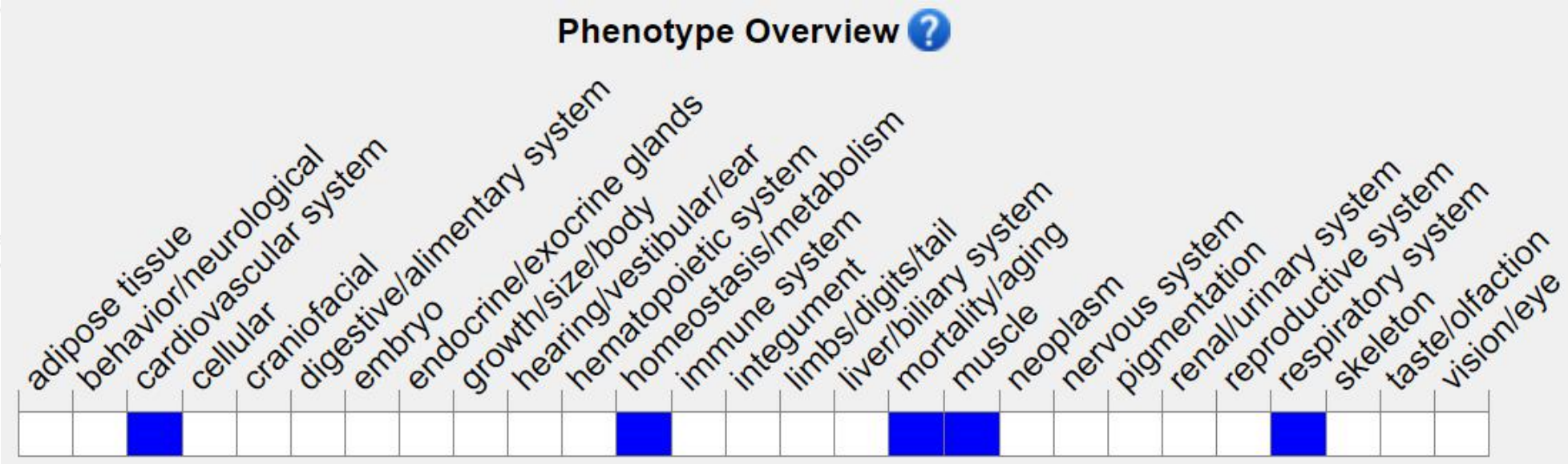
Genomic location distribution



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/).

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

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