

Atp6v1c1 Cas9-CKO Strategy

Designer: Jinling Wang

Reviewer: Fengjuan Wang

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Project Overview

Project Name

Atp6v1c1

Project type

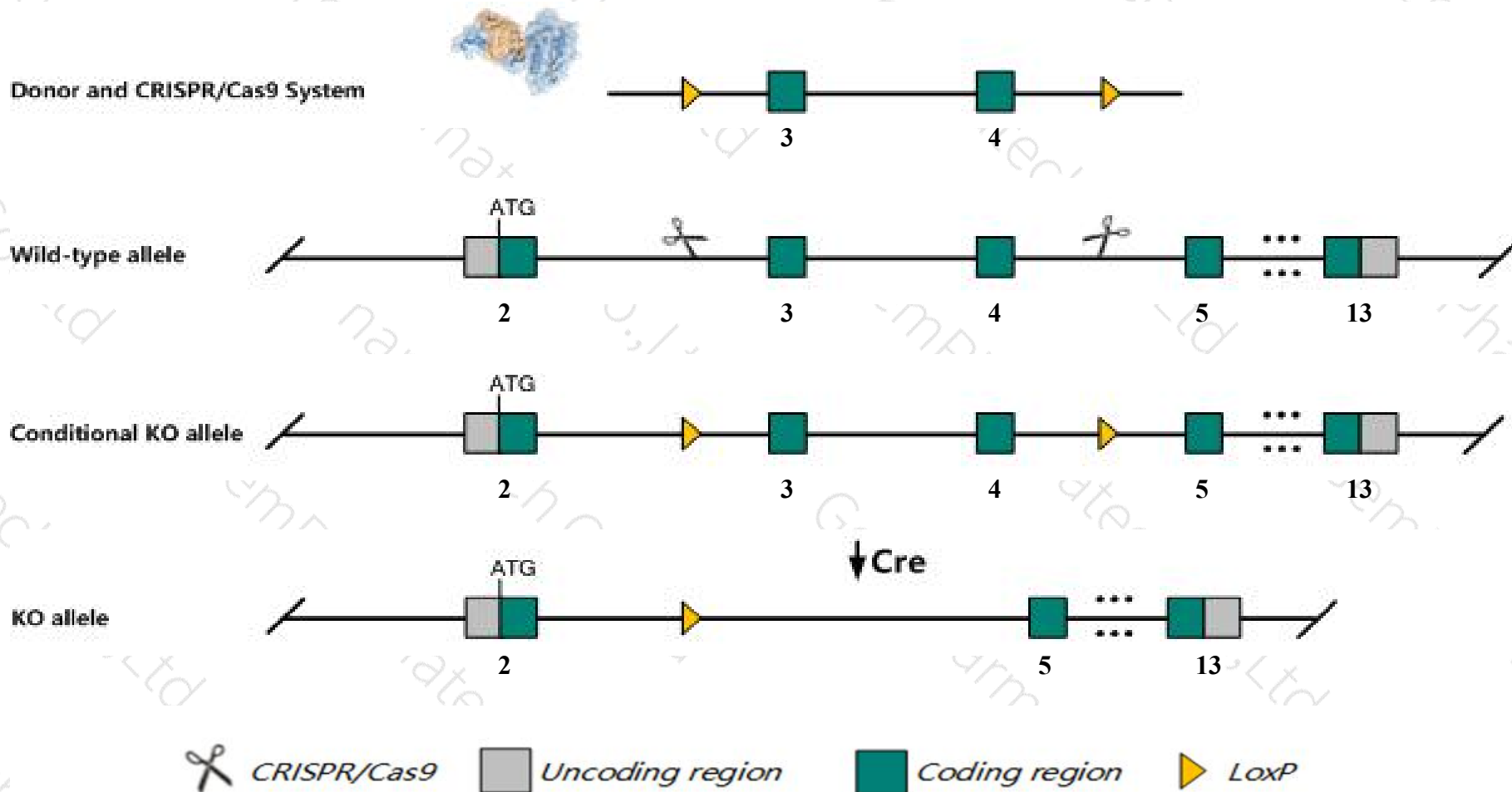
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v1c1* gene. The schematic diagram is as follows:



- The *Atp6v1c1* gene has 7 transcripts. According to the structure of *Atp6v1c1* gene, exon3-exon4 of *Atp6v1c1-201*(ENSMUST00000022904.7) transcript is recommended as the knockout region. The region contains 154bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp6v1c1* 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.

- The *Atp6v1c1* gene is located on the Chr15. 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.
- The 3' UTR region of the *Atp6v1c1-207* are incomplete. The effect of this strategy on them is unknown.
- 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)

Atp6v1c1 ATPase, H⁺ transporting, lysosomal V1 subunit C1 [Mus musculus (house mouse)]

Gene ID: 66335, updated on 13-Mar-2020

Summary



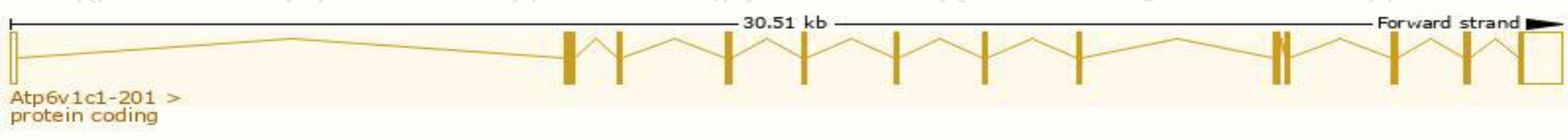
Official Symbol	Atp6v1c1 provided by MGI
Official Full Name	ATPase, H ⁺ transporting, lysosomal V1 subunit C1 provided by MGI
Primary source	MGI:MGI:1913585
See related	Ensembl:ENSMUSG00000022295
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700025B18Rik, U13839
Expression	Ubiquitous expression in cortex adult (RPKM 58.2), frontal lobe adult (RPKM 53.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

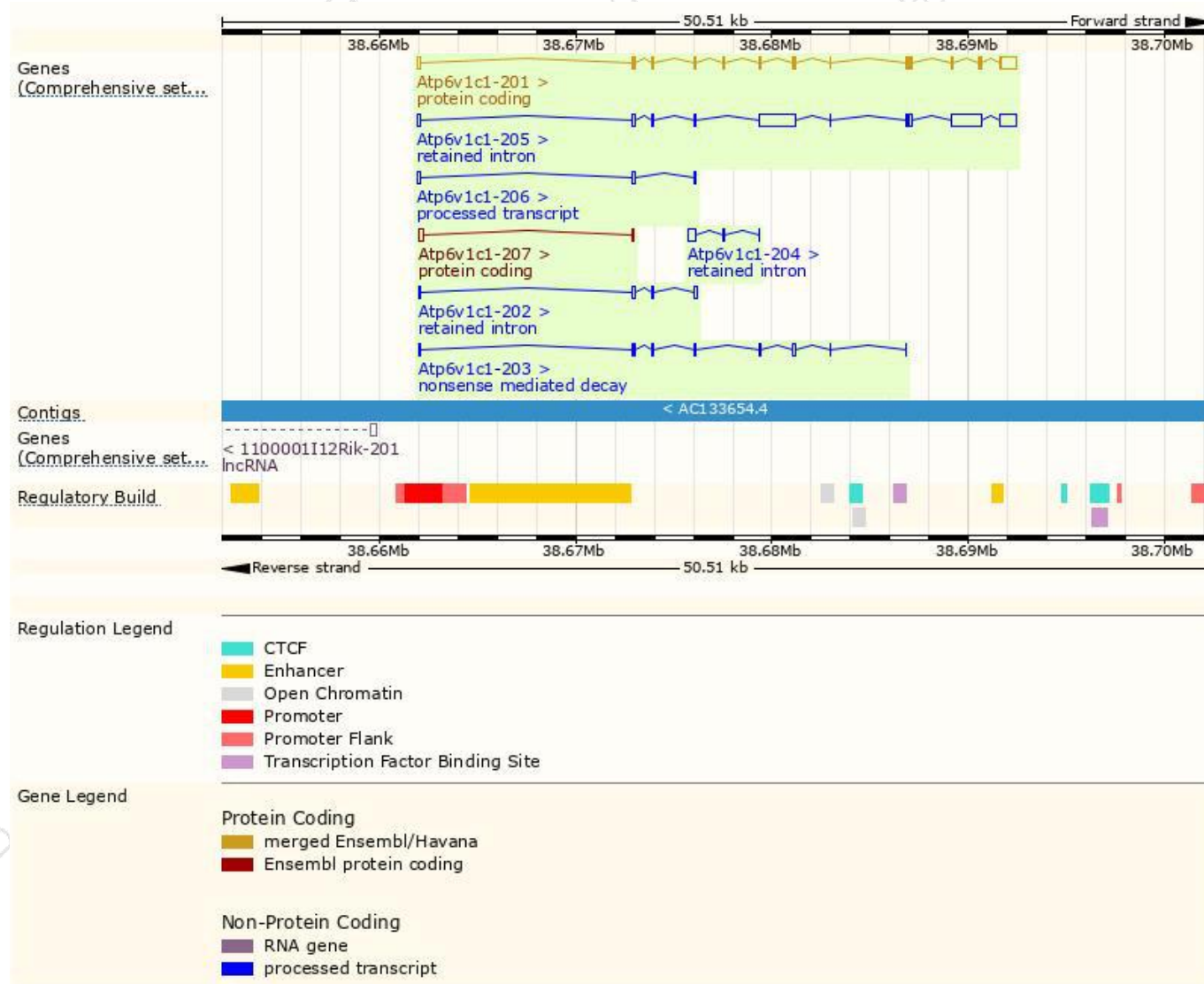
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v1c1-201	ENSMUST00000022904.7	2071	382aa	Protein coding	CCDS27439	Q9Z1G3	TSL:1 GENCODE basic APPRIS P1
Atp6v1c1-207	ENSMUST00000228820.1	373	31aa	Protein coding	-	A0A2I3BQD9	CDS 3' incomplete
Atp6v1c1-203	ENSMUST00000226533.1	728	101aa	Nonsense mediated decay	-	A0A2I3BPD0	
Atp6v1c1-206	ENSMUST00000228486.1	390	No protein	Processed transcript	-	-	
Atp6v1c1-205	ENSMUST00000228475.1	4927	No protein	Retained intron	-	-	
Atp6v1c1-204	ENSMUST00000227482.1	569	No protein	Retained intron	-	-	
Atp6v1c1-202	ENSMUST00000226487.1	506	No protein	Retained intron	-	-	

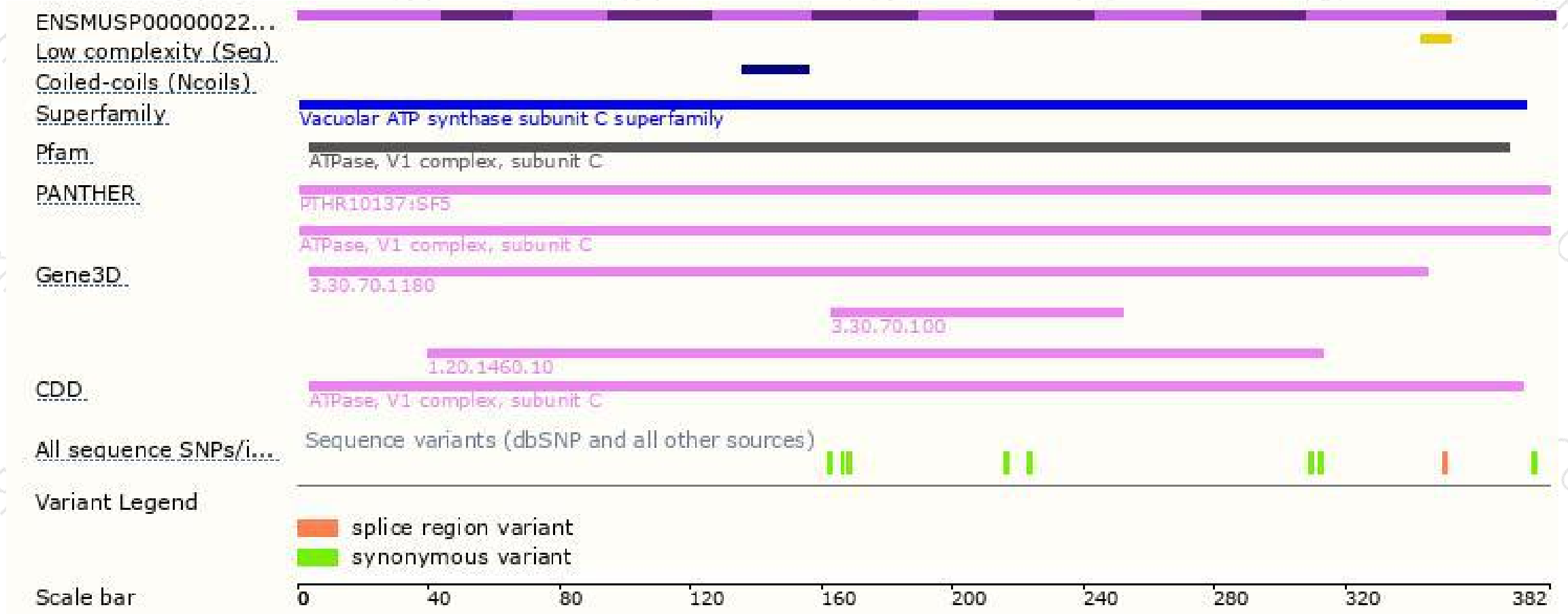
The strategy is based on the design of *Atp6v1c1-201* transcript,the transcription is shown below:



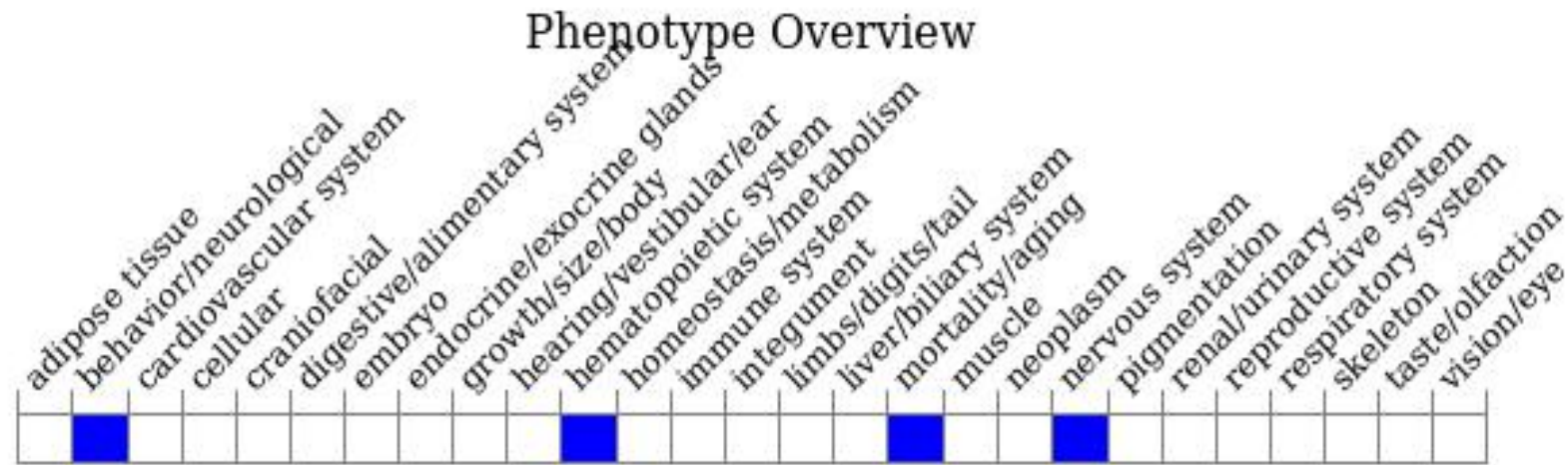
Genomic location distribution



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/>).

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

Tel: 400-9660890

