

Klc2 Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Date: 2020-02-14

Project Overview

Project Name

Klc2

Project type

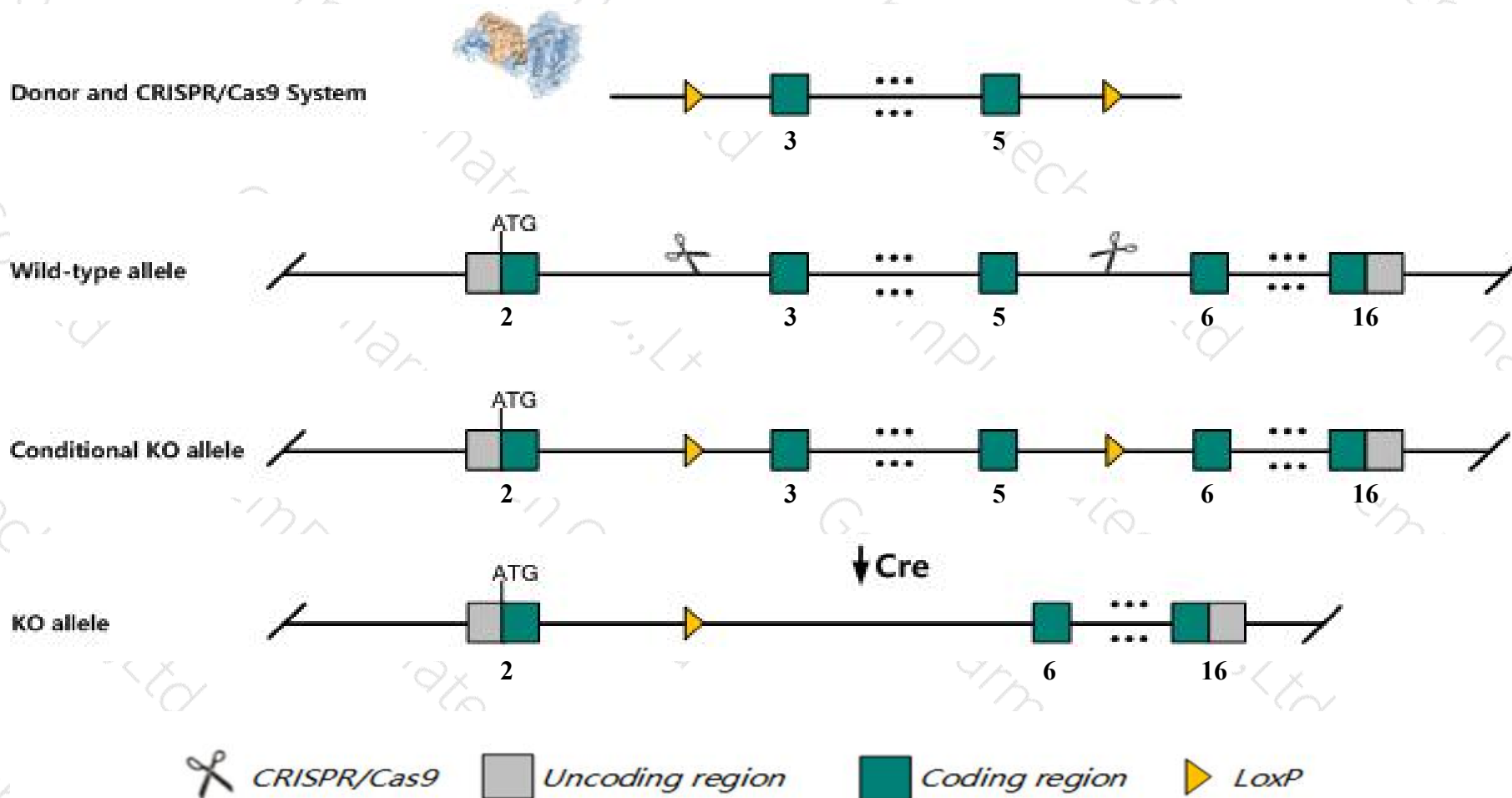
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Klc2* gene. The schematic diagram is as follows:



- The *Klc2* gene has 9 transcripts. According to the structure of *Klc2* gene, exon3-exon5 of *Klc2-204* (ENSMUST00000116563.7) transcript is recommended as the knockout region. The region contains 524bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Klc2* 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

- Transcript *Klc2*-209 may not be affected.
- The effect on transcript *Klc2*-206&207&208 is unknown.
- The floxed region is near to the N-terminal of *Rab1b* gene and *Gm10817* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- The *Klc2* gene is located on the Chr19. 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)

Klc2 kinesin light chain 2 [*Mus musculus* (house mouse)]

Gene ID: 16594, updated on 21-Jan-2020

Summary

Official Symbol	Klc2 <small>provided by MGI</small>
Official Full Name	kinesin light chain 2 <small>provided by MGI</small>
Primary source	MGI:MGI:107953
See related	Ensembl:ENSMUSG00000024862
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	KLC 2; KLC-2; AW212649; 8030455F02Rik
Expression	Broad expression in cerebellum adult (RPKM 59.4), cortex adult (RPKM 42.0) and 24 other tissues See more
Orthologs	human all

Genomic context

Location: 19 A; 19 4.25 cM

See Klc2 in [Genome Data Viewer](#)

Exon count: 16

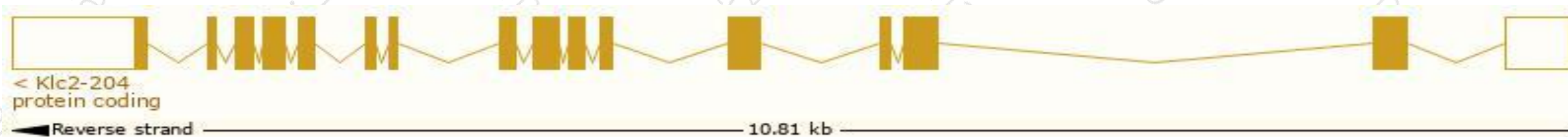
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (5107746..5118298, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (5107746..5118408, complement)

Transcript information (Ensembl)

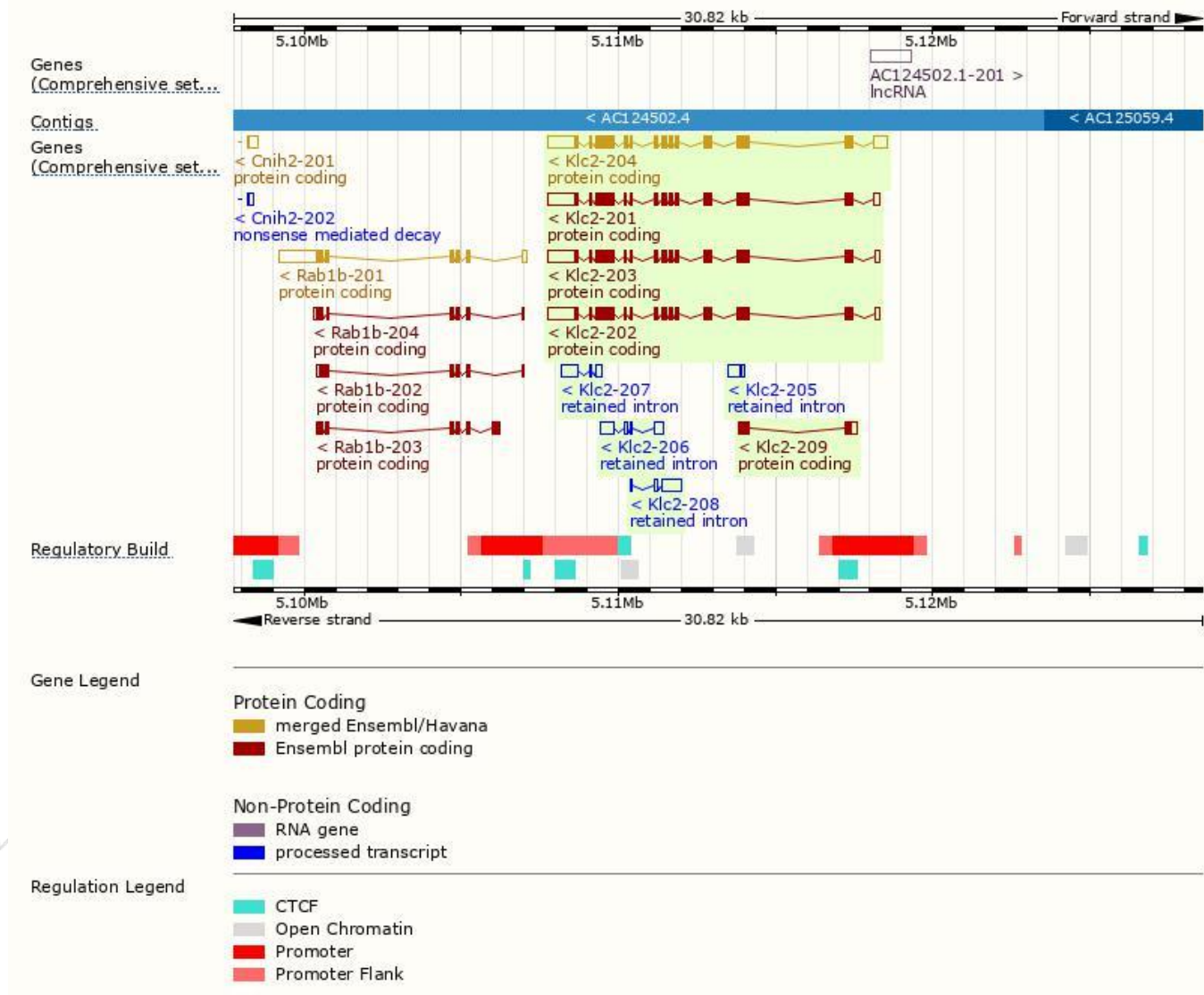
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Klc2-204	ENSMUST00000116563.7	3169	619aa	Protein coding	CCDS37889	Q91YS4	TSL:1 GENCODE basic APPRIS P1
Klc2-201	ENSMUST00000025798.12	2940	617aa	Protein coding	-	D3YXZ3	TSL:5 GENCODE basic
Klc2-202	ENSMUST00000113727.7	2874	617aa	Protein coding	-	D3YXZ3	TSL:5 GENCODE basic
Klc2-203	ENSMUST00000113728.7	2838	617aa	Protein coding	-	D3YXZ3	TSL:5 GENCODE basic
Klc2-209	ENSMUST00000156717.1	665	166aa	Protein coding	-	D3Z5Y7	CDS 3' incomplete TSL:5
Klc2-206	ENSMUST00000137403.7	841	No protein	Retained intron	-	-	TSL:2
Klc2-208	ENSMUST00000149806.1	770	No protein	Retained intron	-	-	TSL:2
Klc2-207	ENSMUST00000142255.1	758	No protein	Retained intron	-	-	TSL:2
Klc2-205	ENSMUST00000135827.1	411	No protein	Retained intron	-	-	TSL:5

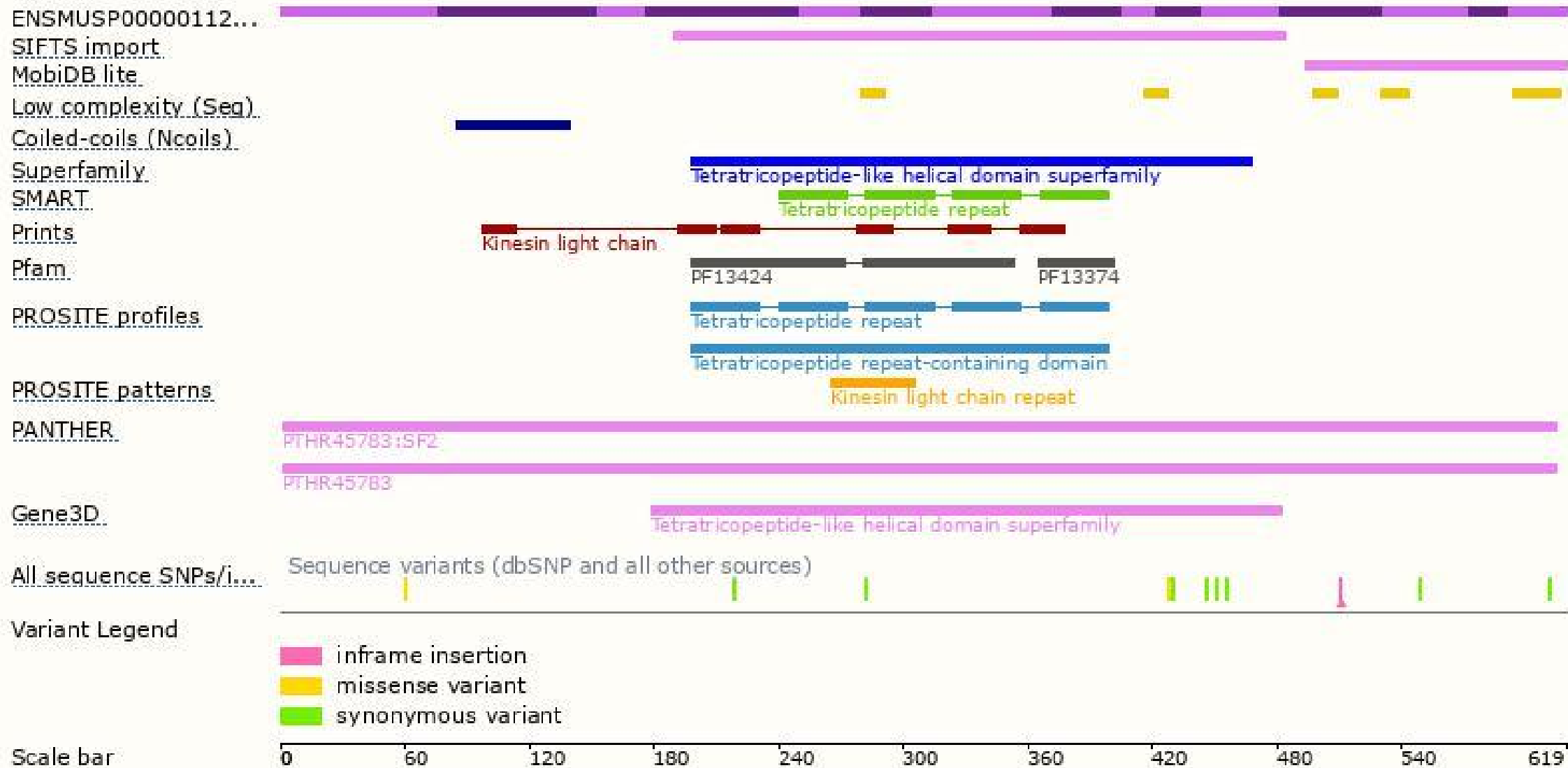
The strategy is based on the design of *Klc2-204* transcript, The transcription is shown below



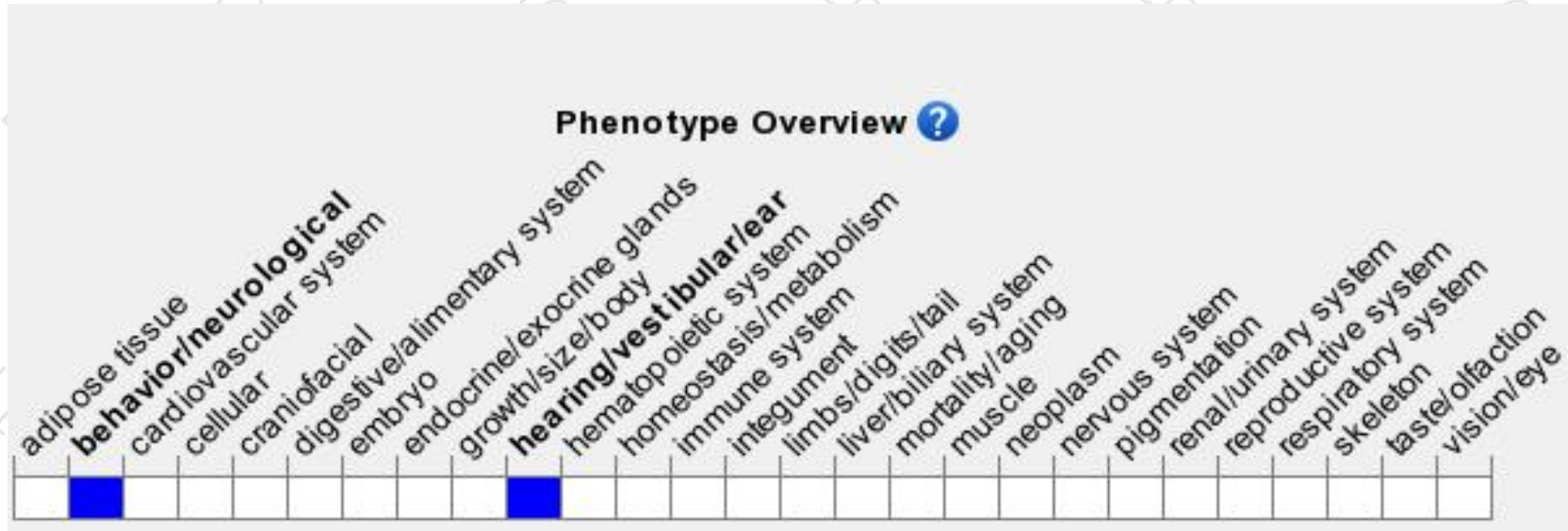
Genomic location distribution



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

