

Atl3 Cas9-CKO Strategy

Designer: Miaomiao Cui

Reviewer: Lingyan Wu

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Project Overview

Project Name

Atl3

Project type

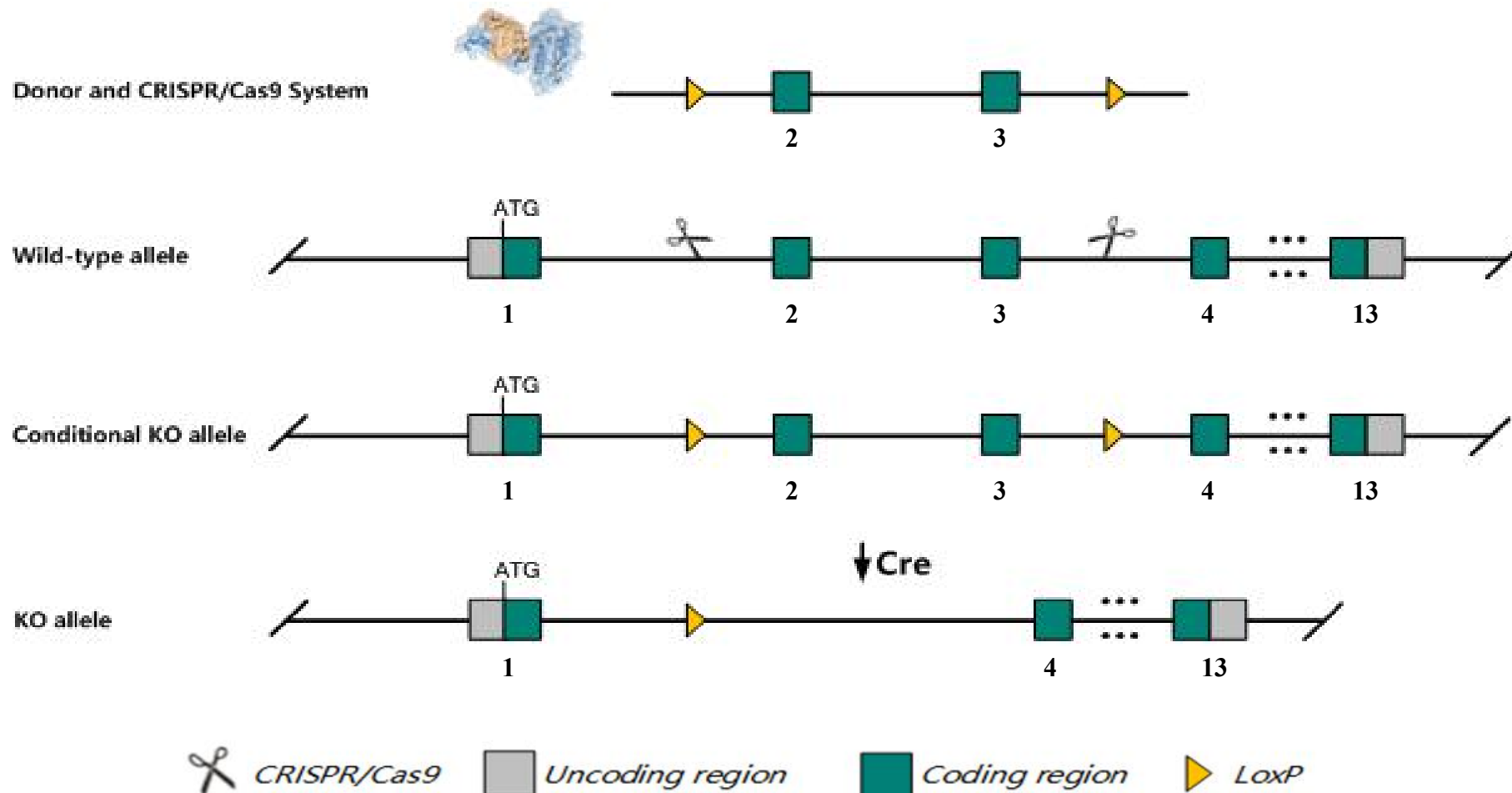
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atl3* gene. The schematic diagram is as follows:



The *Atl3* gene has 7 transcripts. According to the structure of *Atl3* gene, exon2-exon3 of *Atl3-201*(ENSMUST00000025668.9) transcript is recommended as the knockout region. The region contains 359bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Atl3* 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 *At13* 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.

Atl3 atlastin GTPase 3 [Mus musculus (house mouse)]

Gene ID: 109168, updated on 17-Dec-2020

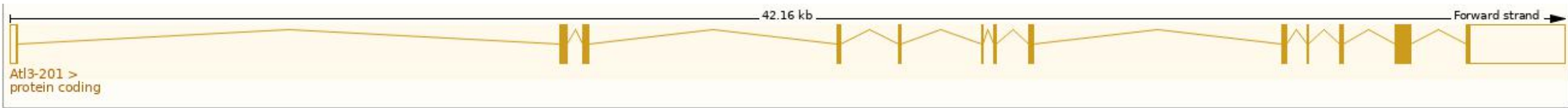
Summary**Official Symbol** Atl3 provided by [MGI](#)**Official Full Name** atlastin GTPase 3 provided by [MGI](#)**Primary source** [MGI:MGI:1924270](#)**See related** [Ensembl:ENSMUSG00000024759](#)**Gene type** protein coding**RefSeq status** VALIDATED**Organism** [Mus musculus](#)**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus**Also known as** 4633402C03Rik, 5730596K20Rik, AI465397, AW228836**Expression** Ubiquitous expression in testis adult (RPKM 31.9), bladder adult (RPKM 16.2) and 26 other tissues [See more](#)**Orthologs** [human](#) [all](#)

Transcript information Ensembl

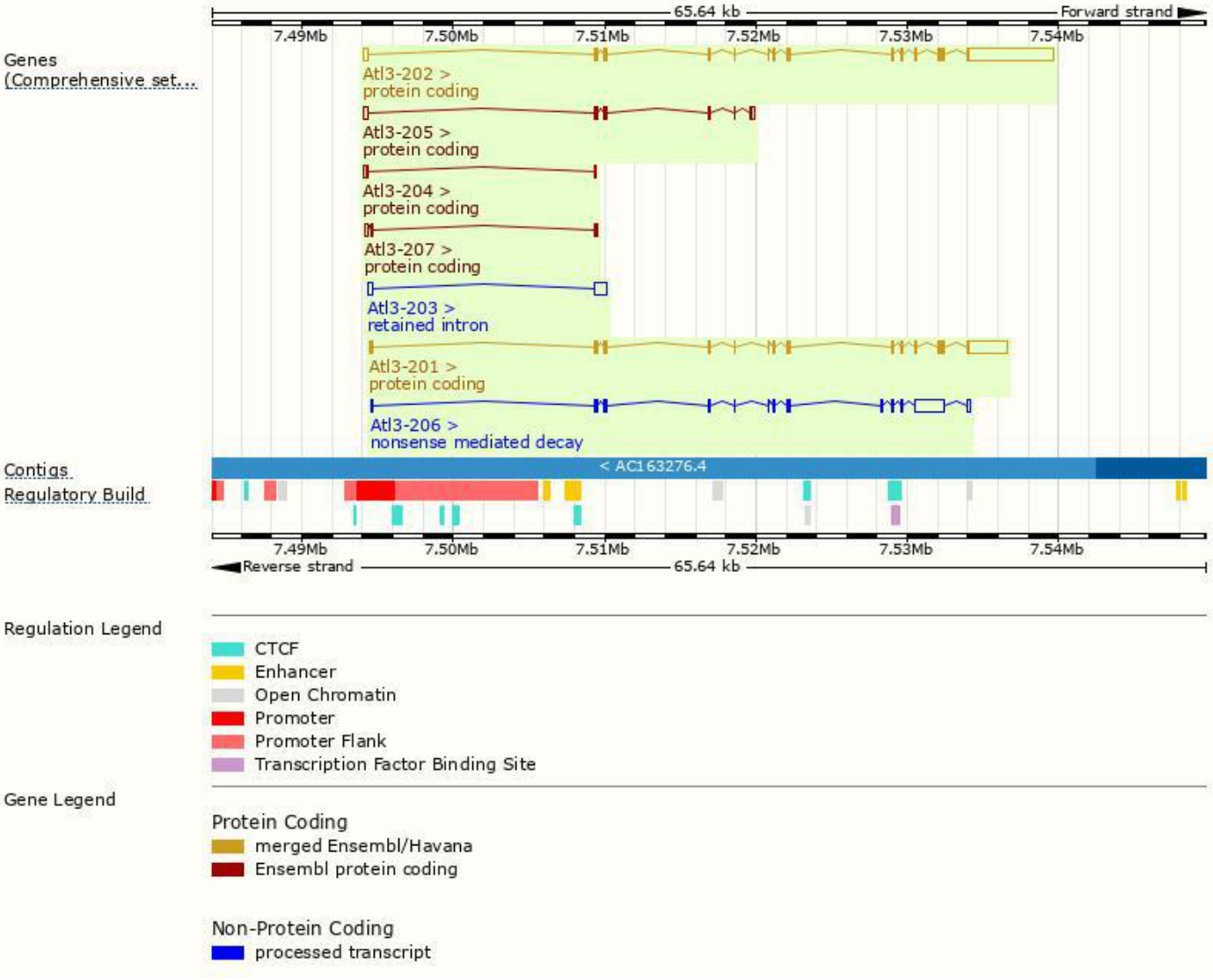
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atl3-202	ENSMUST00000170373.9	7540	536aa	Protein coding	CCDS50379		TSL:5 , GENCODE basic ,
Atl3-201	ENSMUST00000025668.9	4368	541aa	Protein coding	CCDS29527		TSL:1 , GENCODE basic , APPRIS P1 ,
Atl3-205	ENSMUST00000236308.2	1180	232aa	Protein coding	-		GENCODE basic ,
Atl3-207	ENSMUST00000237998.2	437	100aa	Protein coding	-		CDS 3' incomplete ,
Atl3-204	ENSMUST00000235557.2	348	58aa	Protein coding	-		CDS 3' incomplete ,
Atl3-206	ENSMUST00000236382.2	3342	323aa	Nonsense mediated decay	-		CDS 5' incomplete ,
Atl3-203	ENSMUST00000235260.2	1091	No protein	Retained intron	-		

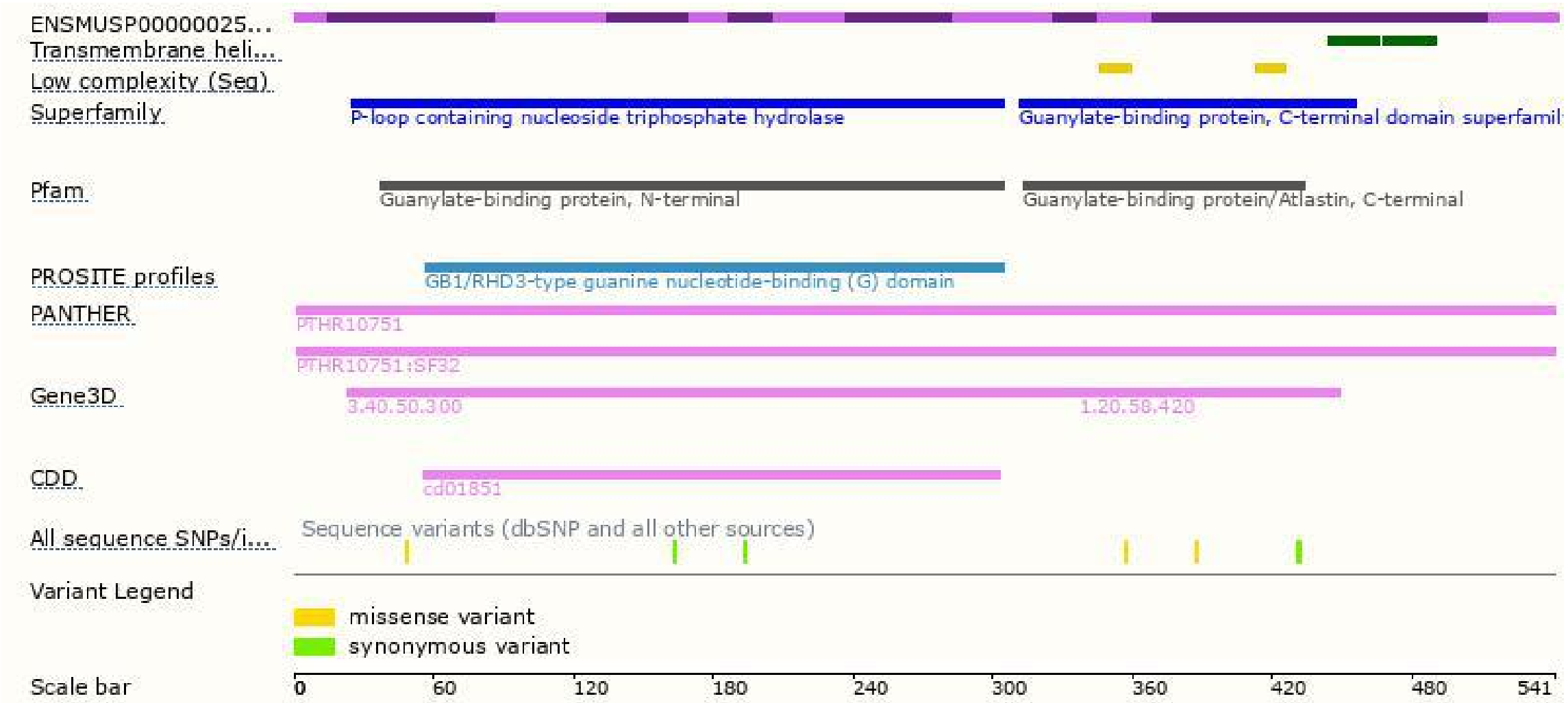
The strategy is based on the design of *Atl3-201* transcript,the transcription is shown below:



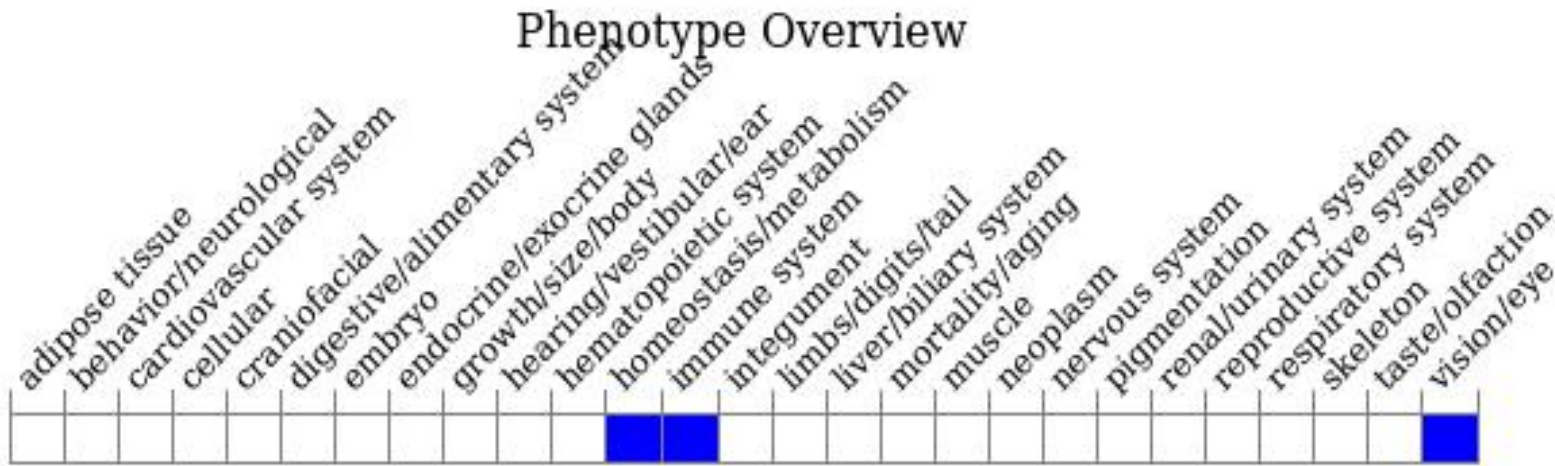
Genomic location distribution



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

