

Selenot Cas9-KO Strategy

Designer:	Huan Wang
Reviewer:	Huan Fan
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Project Overview

Project Name

Selenot

Project type

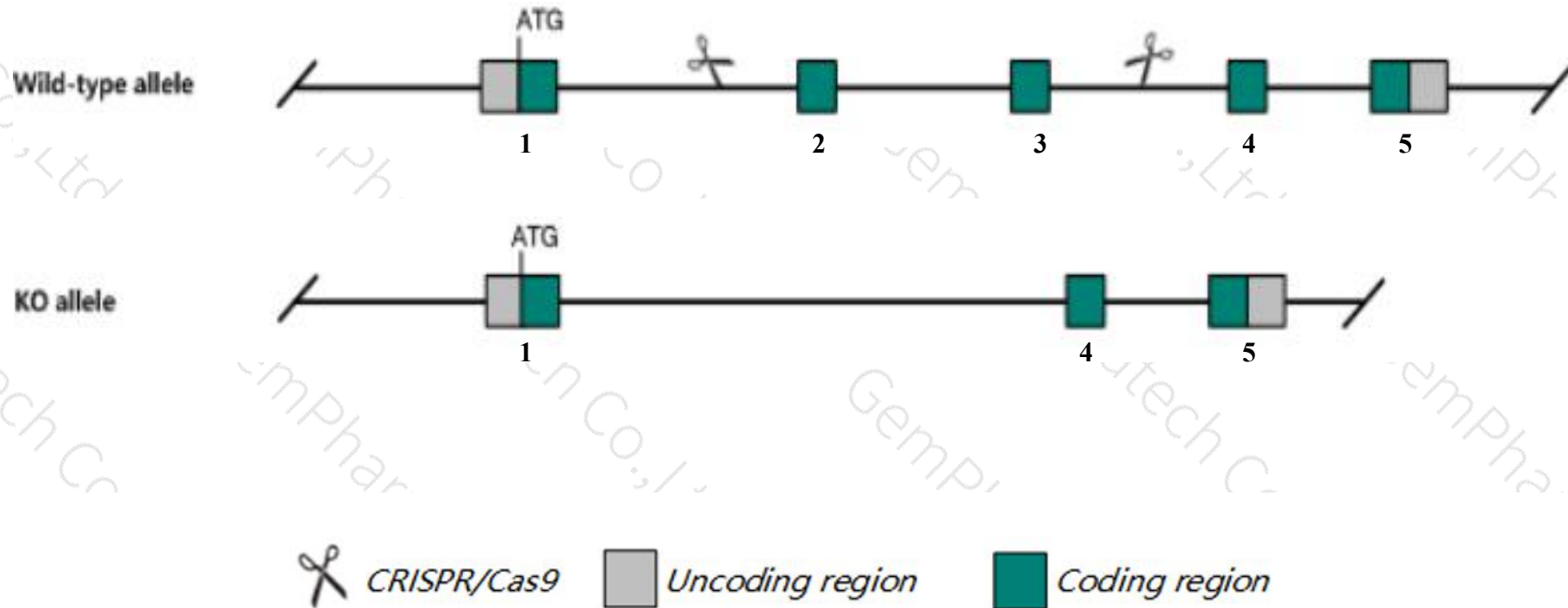
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Selenot* gene has 2 transcripts. According to the structure of *Selenot* gene, exon2-exon3 of *Selenot-201* (ENSMUST00000107924.1) transcript is recommended as the knockout region. The region contains 238bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Selenot* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a conditional allele activated in beta cells exhibit impaired glucose tolerance, increased circulating glucose levels, decreased circulating insulin levels, decreased insulin secretion and an increase in smaller islets.
- The *Selenot* gene is located on the Chr3. 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)

Selenot selenoprotein T [Mus musculus (house mouse)]

Gene ID: 69227, updated on 13-Mar-2020

Summary

Official Symbol Selenot provided by [MGI](#)

Official Full Name selenoprotein T provided by [MGI](#)

Primary source [MGI:MGI:1916477](#)

See related [Ensembl:ENSMUSG00000075700](#)

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 2810407C02Rik, 5730408P04Rik, Selt

Summary This gene encodes a selenoprotein, containing a selenocysteine (Sec) residue at the active site. Sec is encoded by the UGA codon that normally signals translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, the Sec insertion sequence (SECIS) element, that is necessary for the recognition of UGA as a Sec codon rather than as a stop signal. This protein is localized in the endoplasmic reticulum. It belongs to the SelWTH family that possesses a thioredoxin-like fold and a conserved CxxU (C is cysteine, U is Sec) motif found in several redox active proteins. Studies in mice indicate a crucial role for this gene in the protection of dopaminergic neurons against oxidative stress in Parkinson's disease, and in the control of glucose homeostasis in pancreatic beta-cells. A pseudogene of this locus has been identified on chromosome 8. [provided by RefSeq, Aug 2017]

Expression Ubiquitous expression in kidney adult (RPKM 32.3), placenta adult (RPKM 31.3) and 28 other tissues [See more](#)

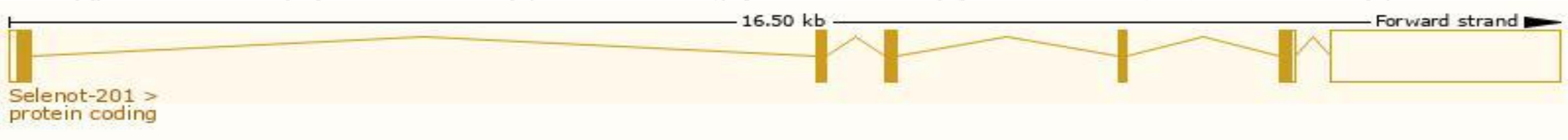
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

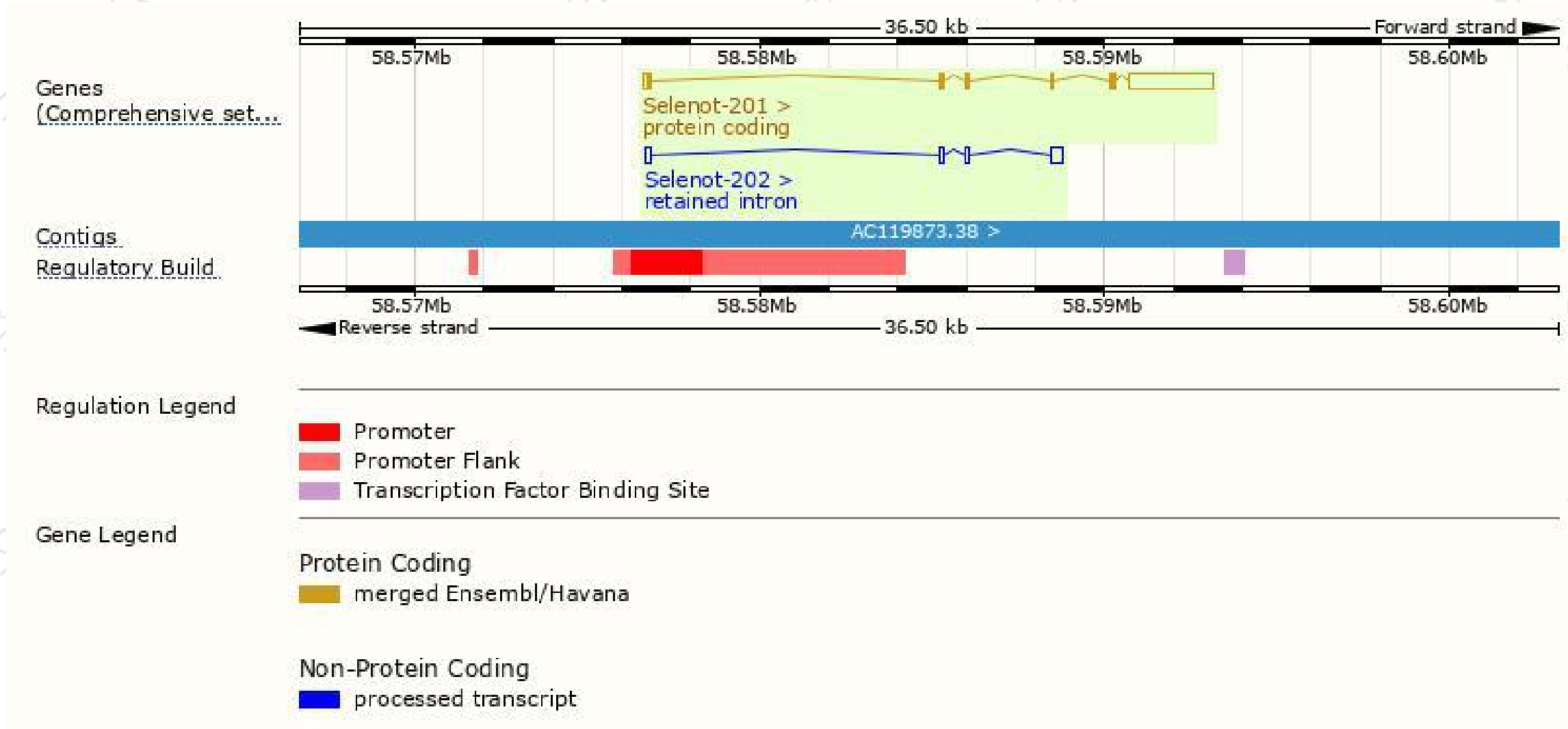
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Selenot-201	ENSMUST00000107924.1	3157	195aa	Protein coding	CCDS38437	P62342	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Selenot-202	ENSMUST00000125815.1	781	No protein	Retained intron	-	-	TSL:2

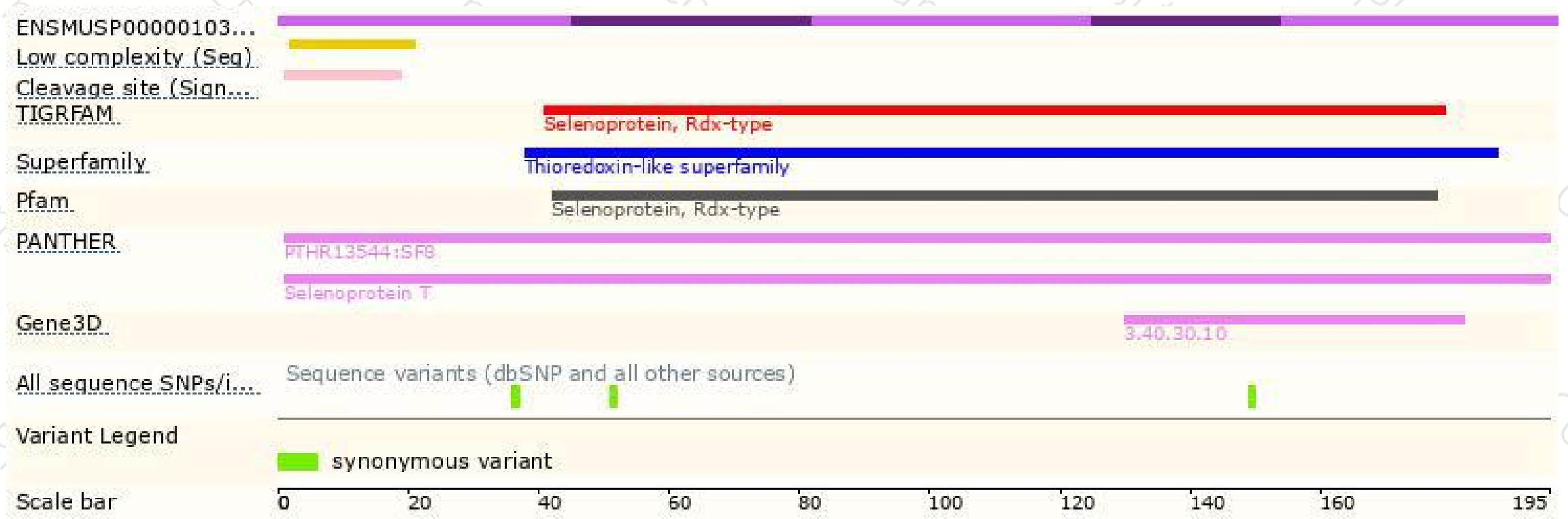
The strategy is based on the design of *Selenot-201* transcript,the transcription is shown below:



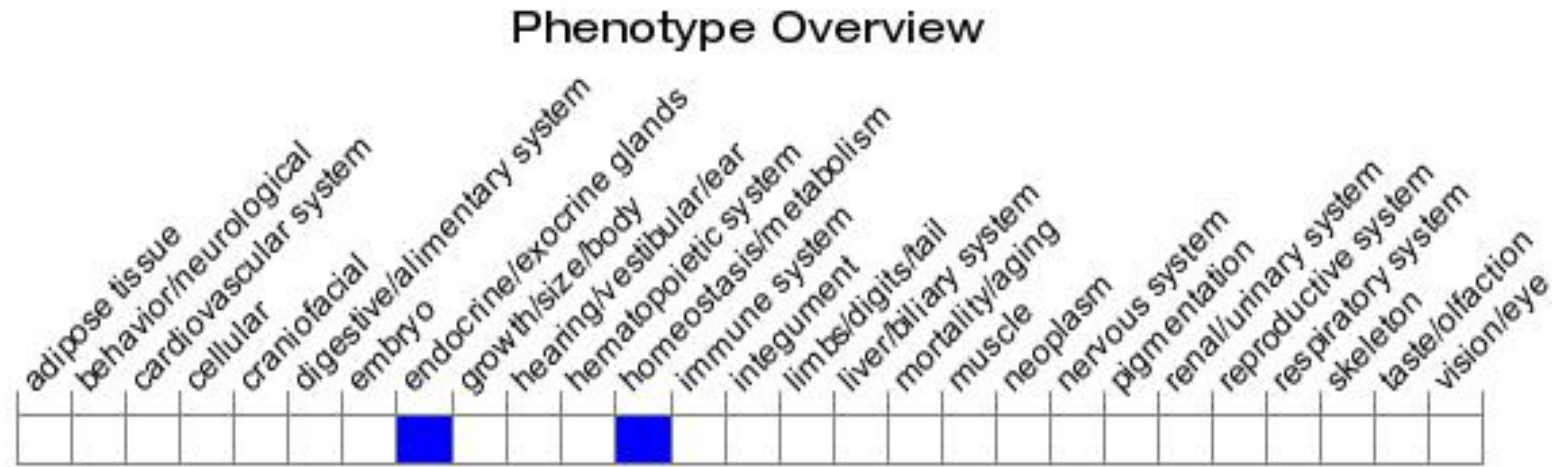
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a conditional allele activated in beta cells exhibit impaired glucose tolerance, increased circulating glucose levels, decreased circulating insulin levels, decreased insulin secretion and an increase in smaller islets.

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

Tel: 400-9660890

