

***Kcnk16* Cas9-CKO Strategy**

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Project Overview

Project Name

Kcnk16

Project type

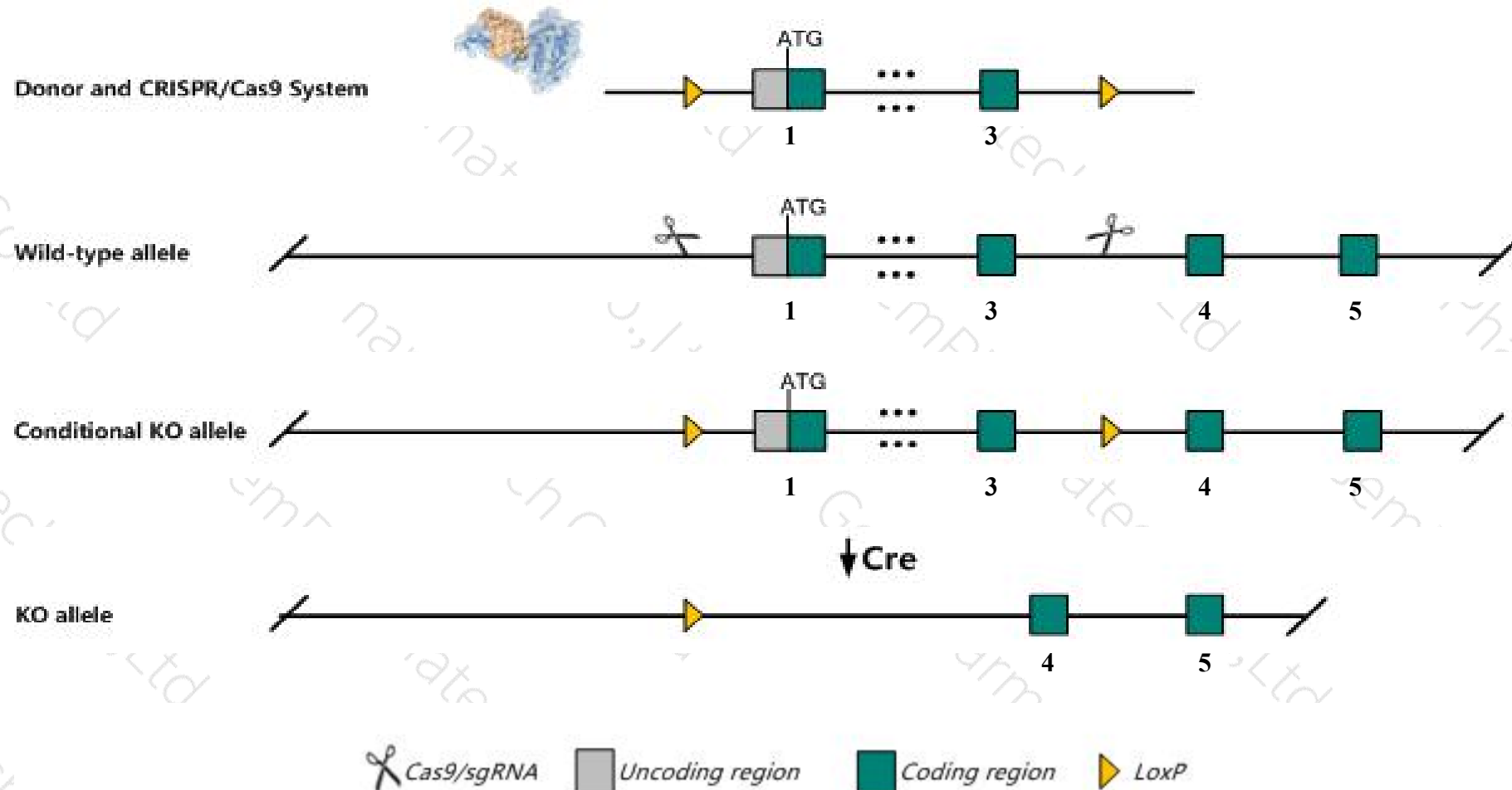
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnk16* gene. The schematic diagram is as follows:



- The *Kcnk16* gene has 2 transcripts. According to the structure of *Kcnk16* gene, exon1-exon3 of *Kcnk16-201*(ENSMUST00000024155.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnk16* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit altered beta cell electrical excitability, second-phase insulin secretion and glucose homeostasis.
- The floxed region is near to the N-terminal of *Gm2048* gene, this strategy may influence the regulatory function of the N-terminal of *Gm2048* gene.
- The *Kcnk16* gene is located on the Chr14. 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)

Kcnk16 potassium channel, subfamily K, member 16 [Mus musculus (house mouse)]

Gene ID: 74571, updated on 13-Mar-2020

Summary



Official Symbol Kcnk16 provided by [MGI](#)

Official Full Name potassium channel, subfamily K, member 16 provided by [MGI](#)

Primary source [MGI:MGI:1921821](#)

See related [Ensembl:ENSMUSG00000023387](#)

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 4731413G05Rik, TALK-1, TALK1

Expression Biased expression in placenta adult (RPKM 5.7), liver E14.5 (RPKM 4.8) and 8 other tissues [See more](#)

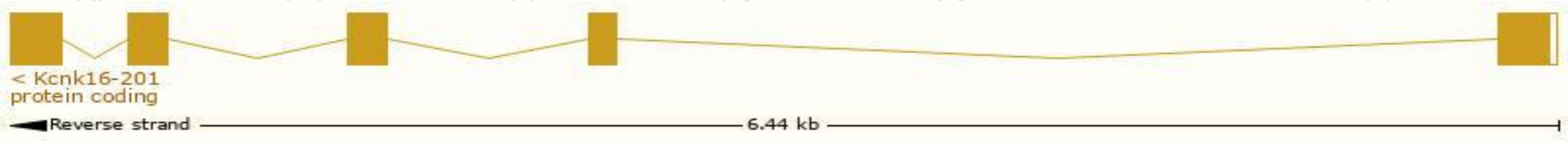
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

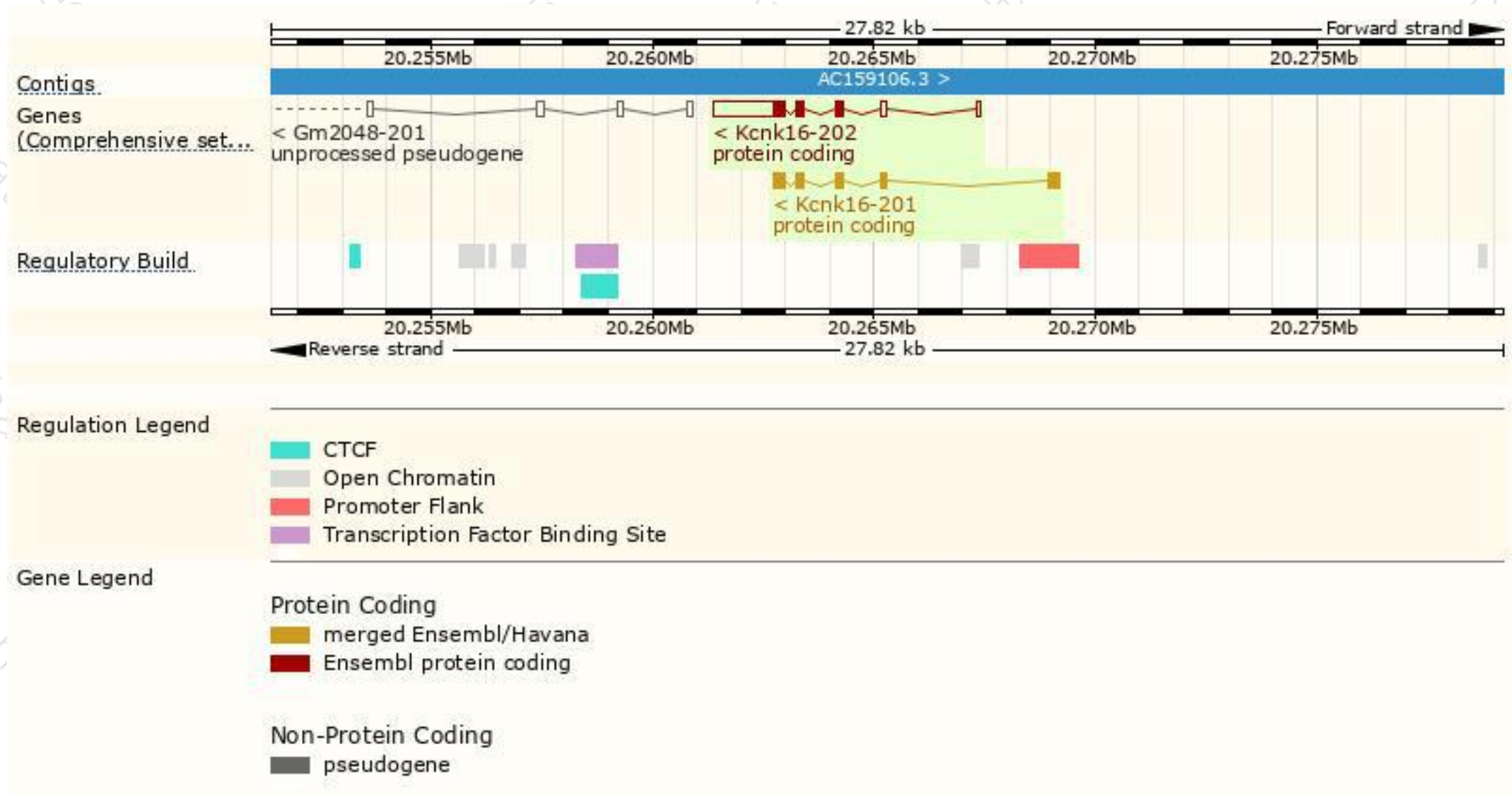
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnk16-201	ENSMUST00000024155.8	916	292aa	Protein coding	CCDS49407	G5E845	TSL:5 GENCODE basic APPRIS P1
Kcnk16-202	ENSMUST000000225596.1	2127	162aa	Protein coding	-	A0A286YDH8	GENCODE basic

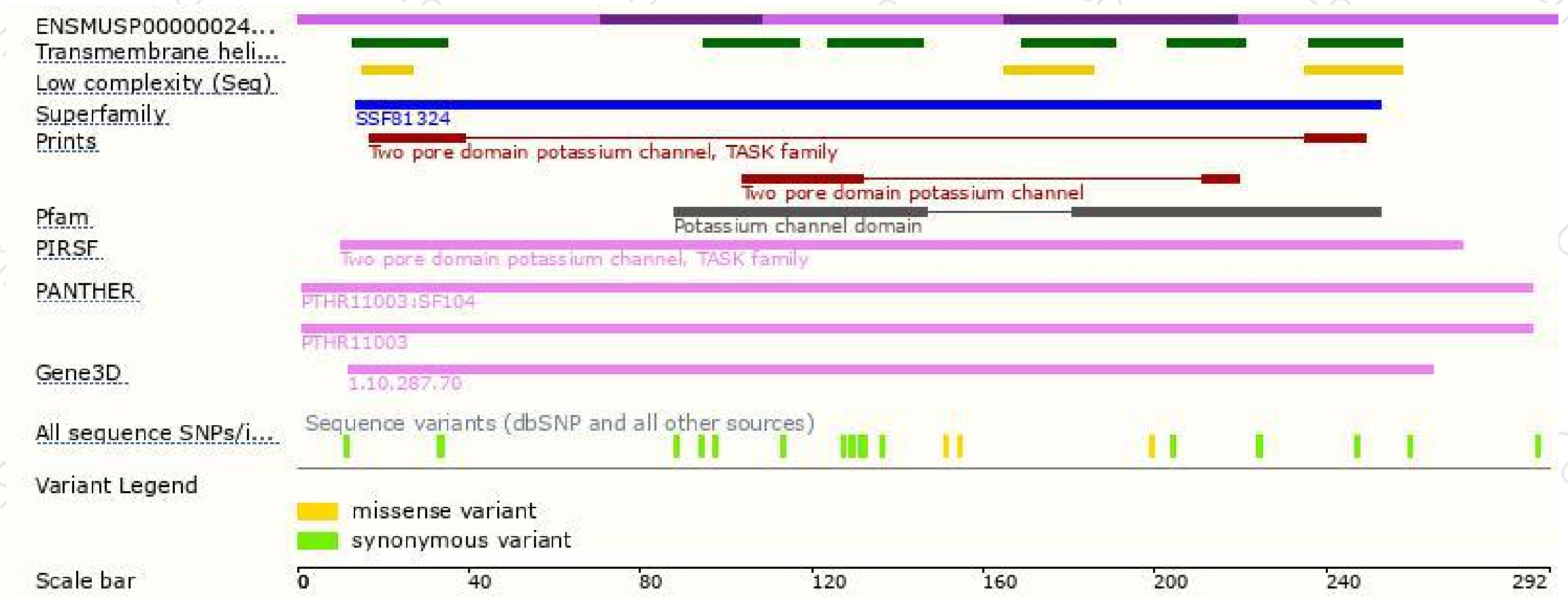
The strategy is based on the design of *Kcnk16-201* transcript,the transcription is shown below:



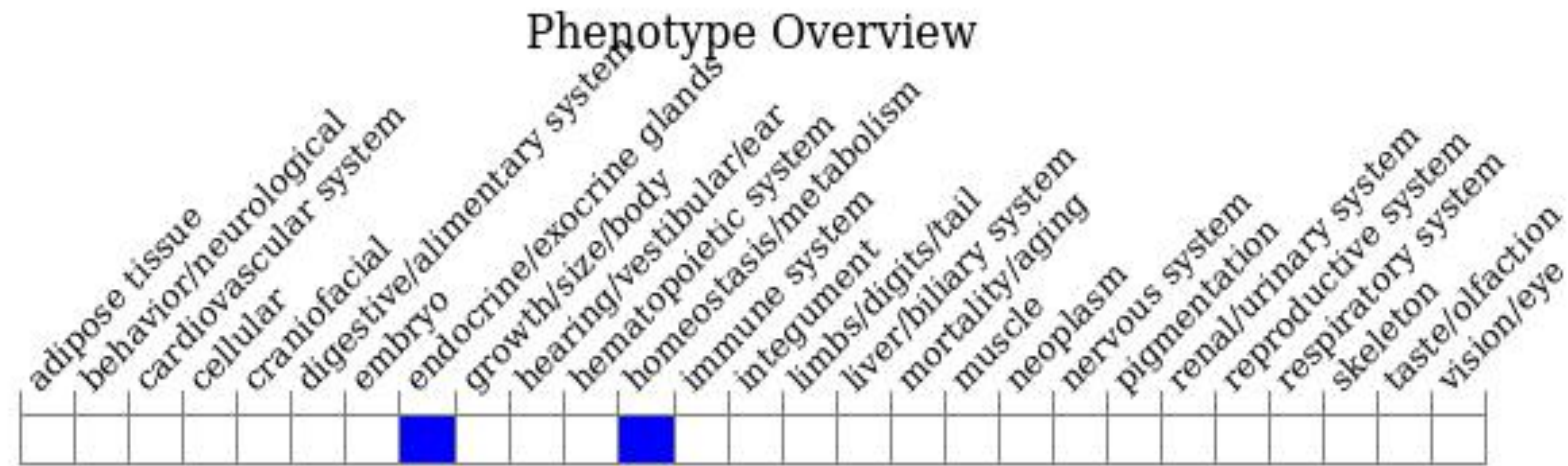
Genomic location distribution



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 knock-out allele exhibit altered beta cell electrical excitability, second-phase insulin secretion and glucose homeostasis.

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

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