

Lrrc8c Cas9-CKO Strategy

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Project Overview

Project Name

Lrrc8c

Project type

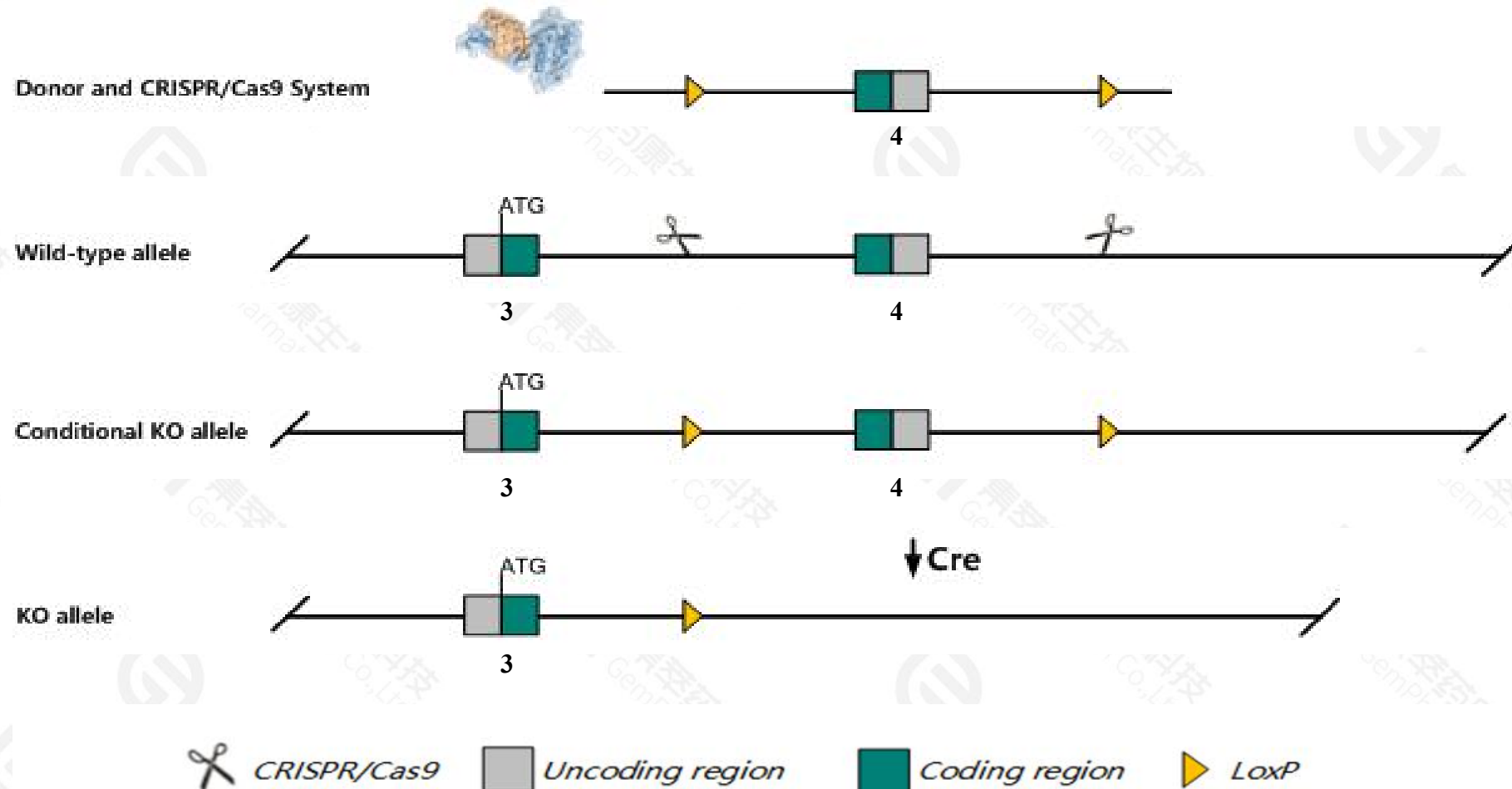
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lrrc8c* gene. The schematic diagram is as follows:



- The *Lrrc8c* gene has 4 transcripts. According to the structure of *Lrrc8c* gene, exon4 of *Lrrc8c-201*(ENSMUST00000067924.13) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lrrc8c* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit a reduction in body weight, white adipose tissue weight, and insulin resistance on a high-fat diet, indicating protection from diet-induced obesity and insulin resistance.
- This strategy deletes most of the coding sequence, but does not result in frameshift.
- The *Lrrc8c* gene is located on the Chr5. 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)

Lrrc8c leucine rich repeat containing 8 family, member C [Mus musculus (house mouse)]

Gene ID: 100604, updated on 3-Jan-2021

Summary



Official Symbol Lrrc8c provided by [MGI](#)

Official Full Name leucine rich repeat containing 8 family, member C provided by [MGI](#)

Primary source [MGI:MGI:2140839](#)

See related [Ensembl:ENSMUSG00000054720](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AD158, AI326115, E430036I04Rik, fad158

Expression Ubiquitous expression in lung adult (RPKM 8.8), thymus adult (RPKM 7.7) and 27 other tissues [See more](#)

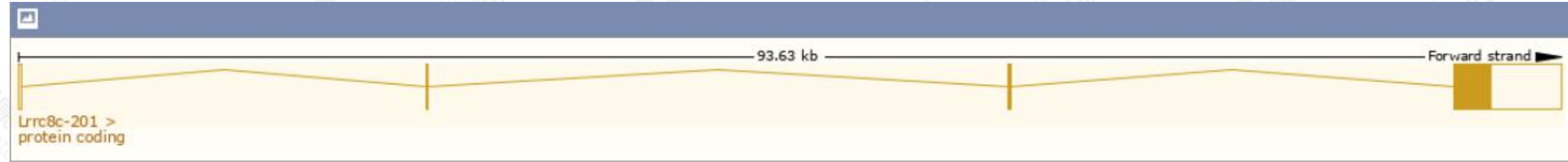
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

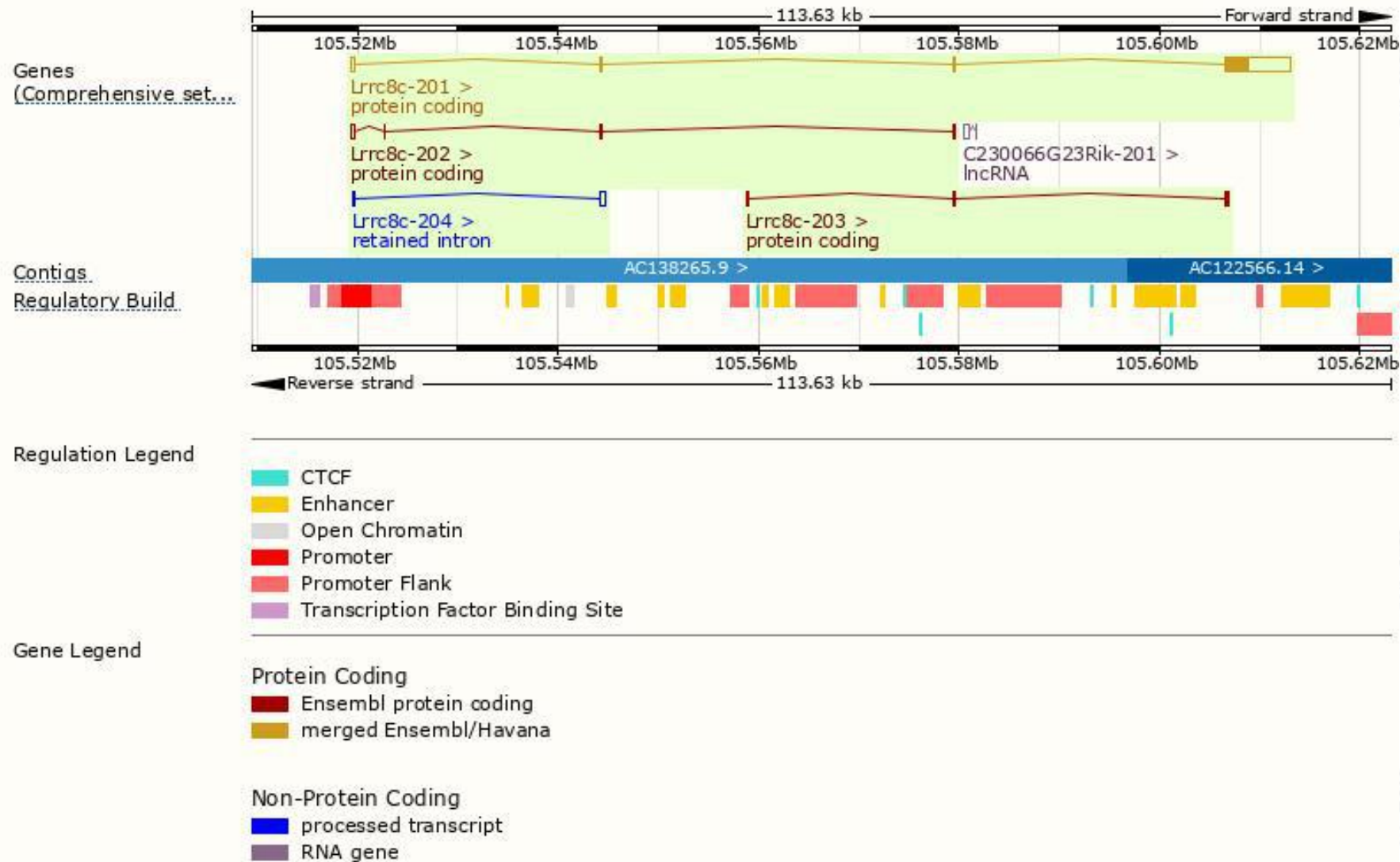
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrrc8c-201	ENSMUST00000067924.13	6976	803aa	Protein coding	CCDS19493		TSL:1 , GENCODE basic , APPRIS P1 ,
Lrrc8c-203	ENSMUST00000153754.2	702	170aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Lrrc8c-202	ENSMUST00000150981.2	510	32aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Lrrc8c-204	ENSMUST00000153955.2	599	No protein	Retained intron	-		TSL:2 ,

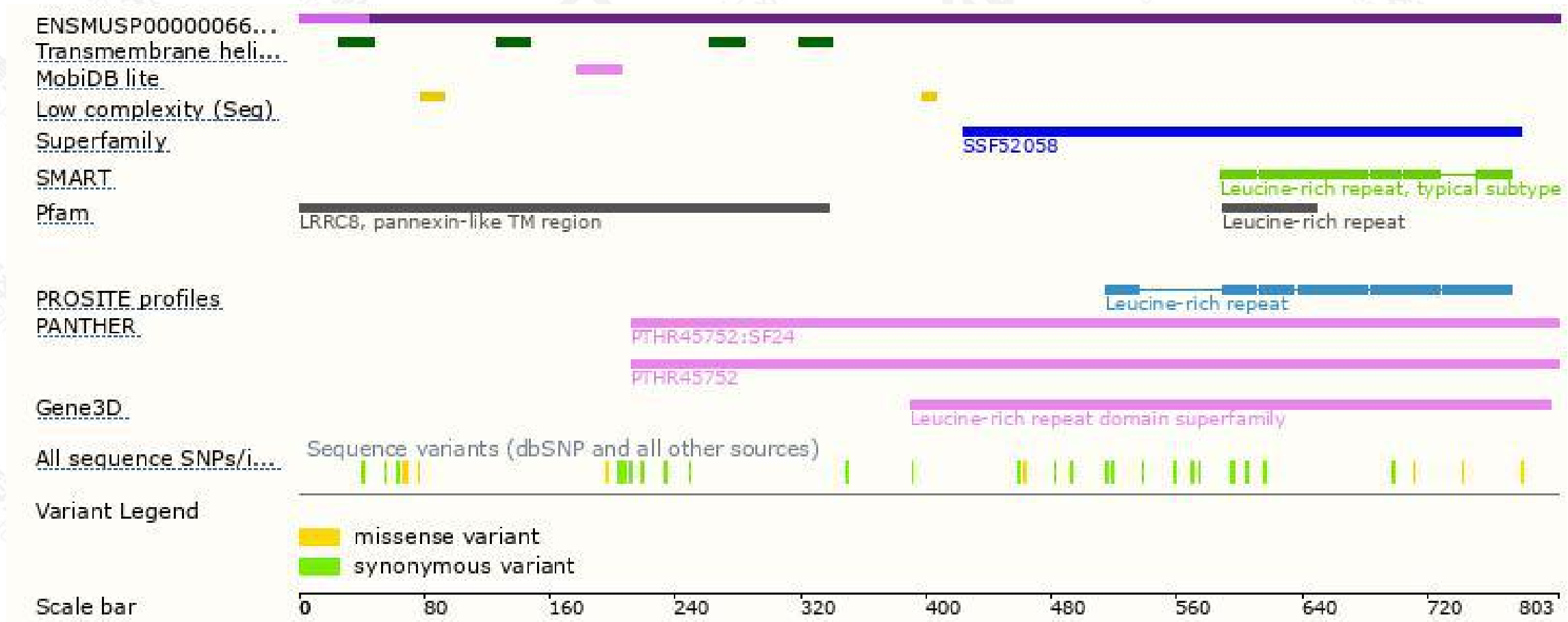
The strategy is based on the design of *Lrrc8c-201* transcript,the transcription is shown below:



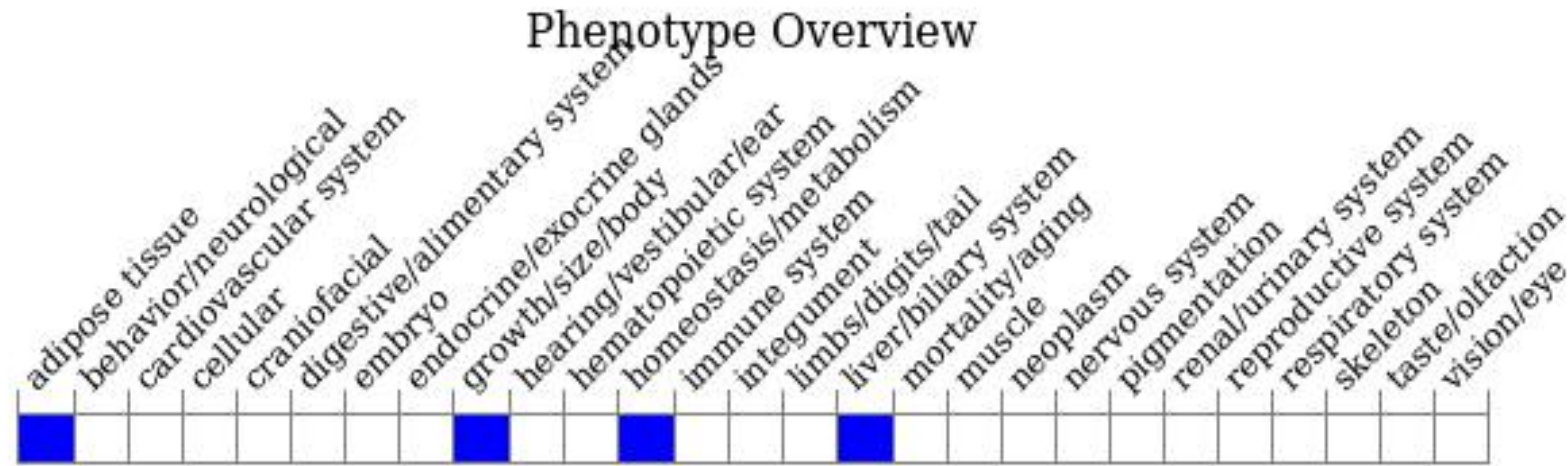
Genomic location distribution



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 a reduction in body weight, white adipose tissue weight, and insulin resistance on a high-fat diet, indicating protection from diet-induced obesity and insulin resistance.

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