

***Tnks2* Cas9-CKO Strategy**

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Project Overview

Project Name

Tnks2

Project type

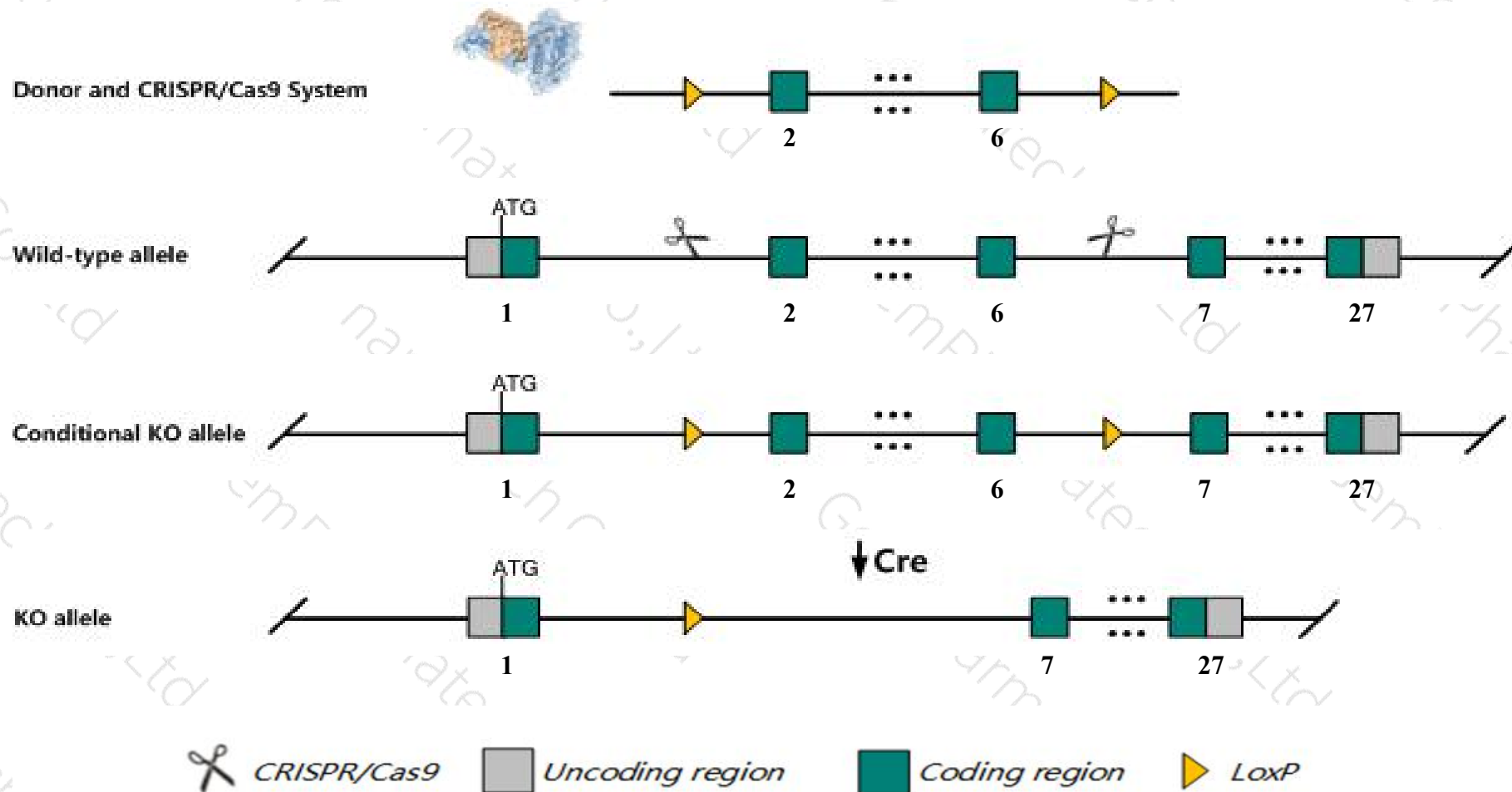
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tnks2* gene. The schematic diagram is as follows:



Technical routes

- The *Tnks2* gene has 9 transcripts. According to the structure of *Tnks2* gene, exon2-exon6 of *Tnks2-201*(ENSMUST00000025729.11) transcript is recommended as the knockout region. The region contains 529bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tnks2* 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 null allele are viable but display decreased body weight and abnormal adipocyte glucose uptake in response to insulin stimulation. Mice homozygous for a different null allele show partial postnatal lethality as well as decreased body weight.
- Transcript 202,205 CDS 5' and 3' incomplete the influences is unknown.
- Transcript 208 CDS 5' incomplete the influences is unknown.
- The *Tnks2* 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)

Tnks2 tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 [Mus musculus (house mouse)]

Gene ID: 74493, updated on 13-Mar-2020

Summary



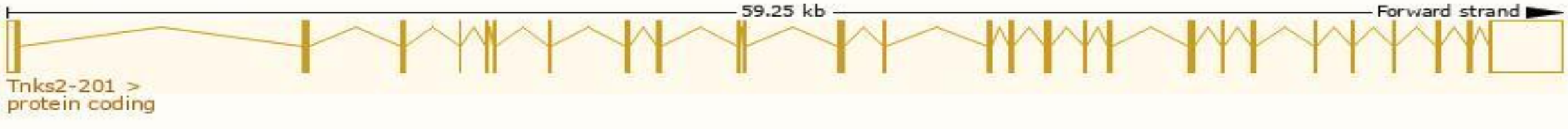
Official Symbol	Tnks2 provided by MGI
Official Full Name	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 provided by MGI
Primary source	MGI:MGI:1921743
See related	Ensembl:ENSMUSG00000024811
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5430432P15Rik, AA517131, AI662480, ARTD6, TNKS-2, Tank2
Expression	Ubiquitous expression in placenta adult (RPKM 24.7), CNS E11.5 (RPKM 20.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

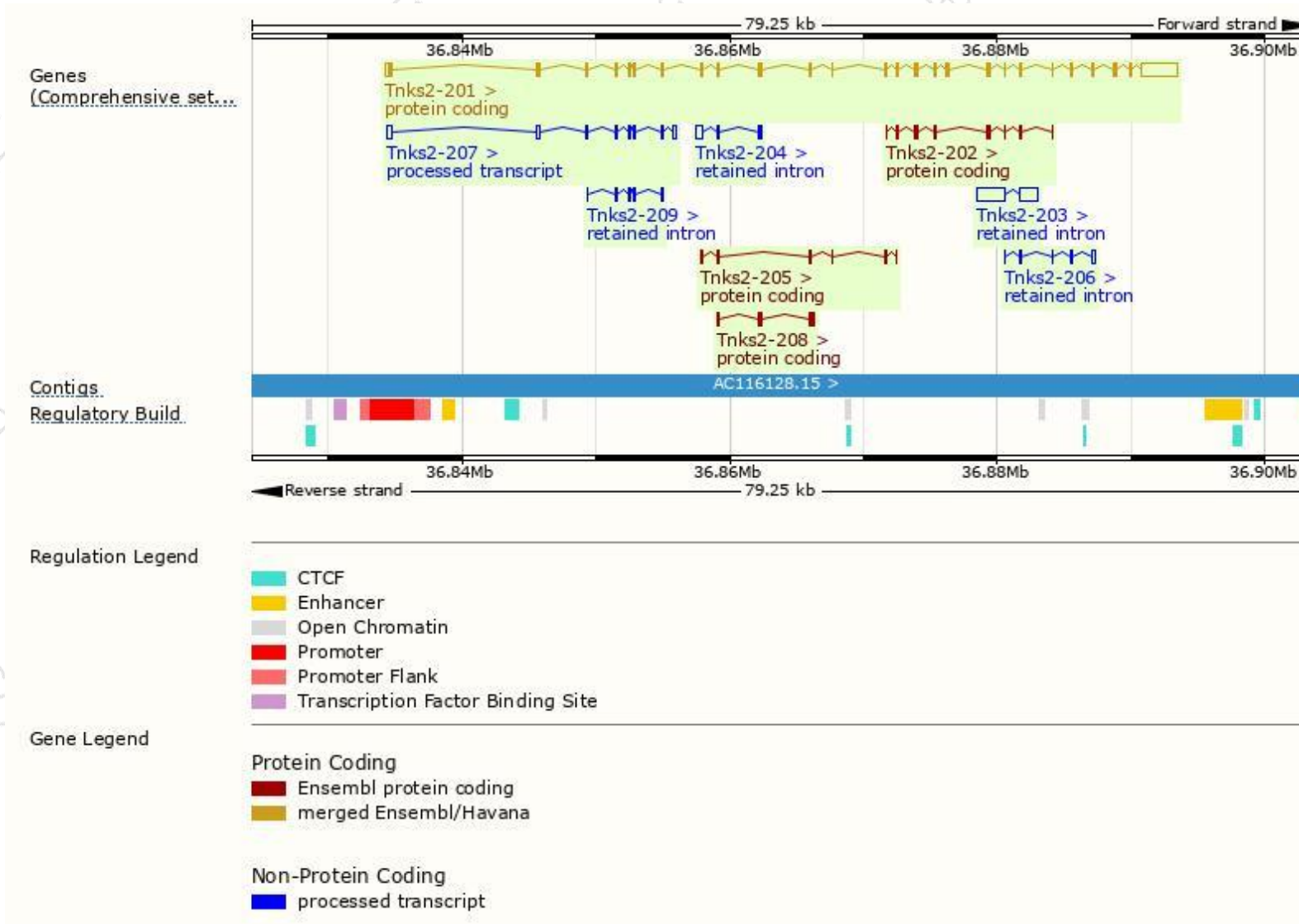
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnks2-201	ENSMUST00000025729.11	6481	1166aa	Protein coding	CCDS50426	Q3UES3	TSL:5 GENCODE basic APPRIS P1
Tnks2-202	ENSMUST00000164665.1	982	327aa	Protein coding	-	F6V619	CDS 5' and 3' incomplete TSL:5
Tnks2-205	ENSMUST00000167724.1	670	223aa	Protein coding	-	F6YVU7	CDS 5' and 3' incomplete TSL:3
Tnks2-208	ENSMUST00000168718.1	606	170aa	Protein coding	-	F6S169	CDS 5' incomplete TSL:2
Tnks2-207	ENSMUST00000168656.7	1078	No protein	Processed transcript	-	-	TSL:1
Tnks2-203	ENSMUST00000166677.1	3491	No protein	Retained intron	-	-	TSL:1
Tnks2-204	ENSMUST00000167533.1	740	No protein	Retained intron	-	-	TSL:3
Tnks2-206	ENSMUST00000168654.1	622	No protein	Retained intron	-	-	TSL:5
Tnks2-209	ENSMUST00000168973.1	344	No protein	Retained intron	-	-	TSL:5

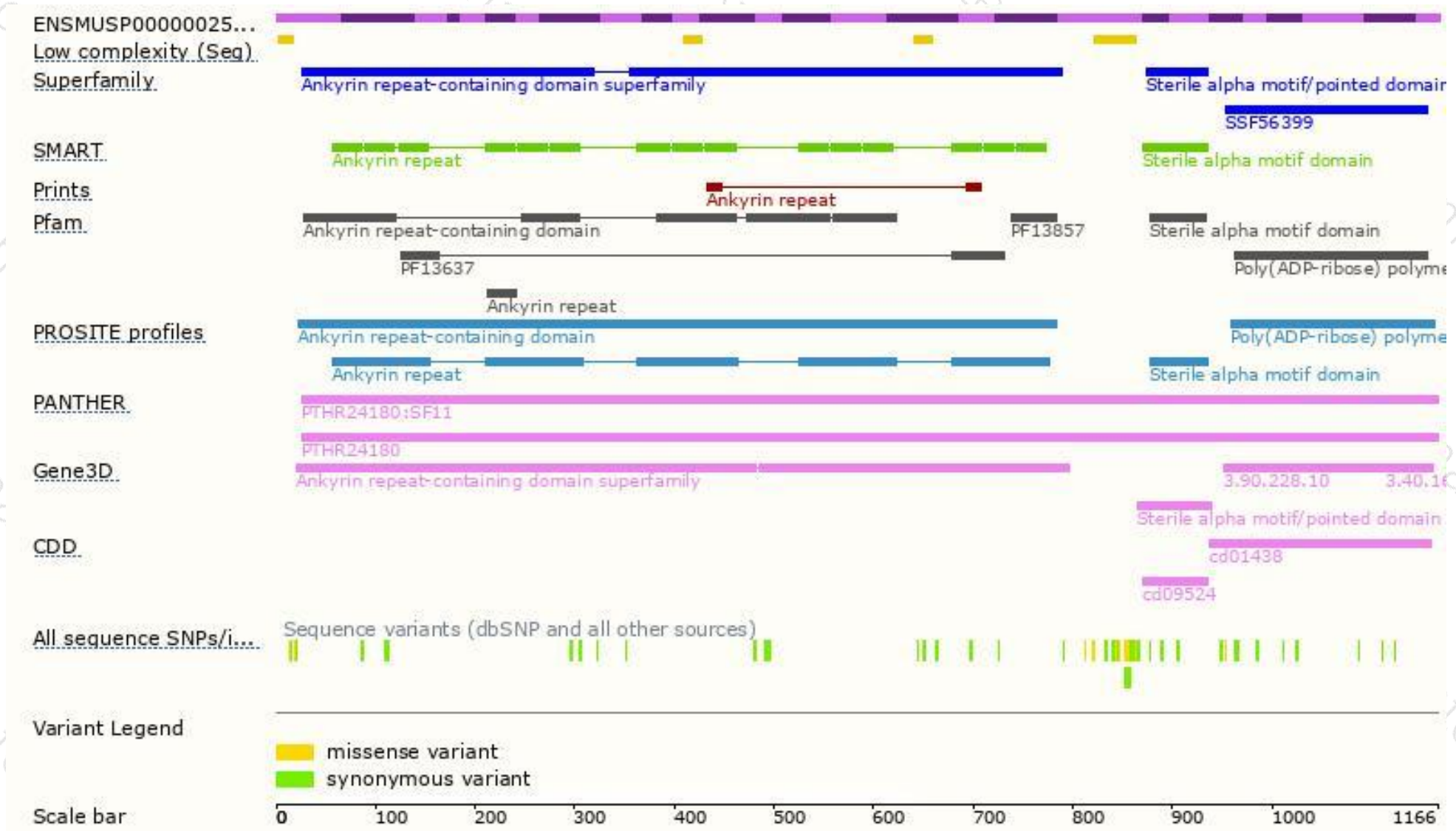
The strategy is based on the design of *Tnks2-201* transcript,the transcription is shown below:



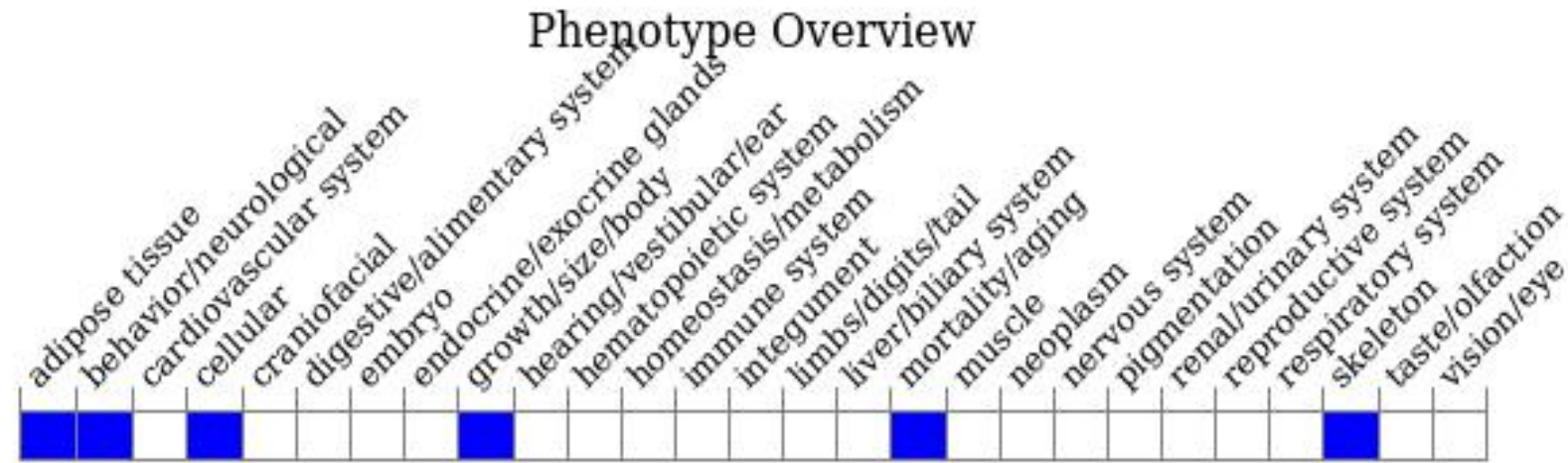
Genomic location distribution



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 null allele are viable but display decreased body weight and abnormal adipocyte glucose uptake in response to insulin stimulation. Mice homozygous for a different null allele show partial postnatal lethality as well as decreased body weight.

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

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