

***Rab7* Cas9-KO Strategy**

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Project Overview

Project Name

Rab7

Project type

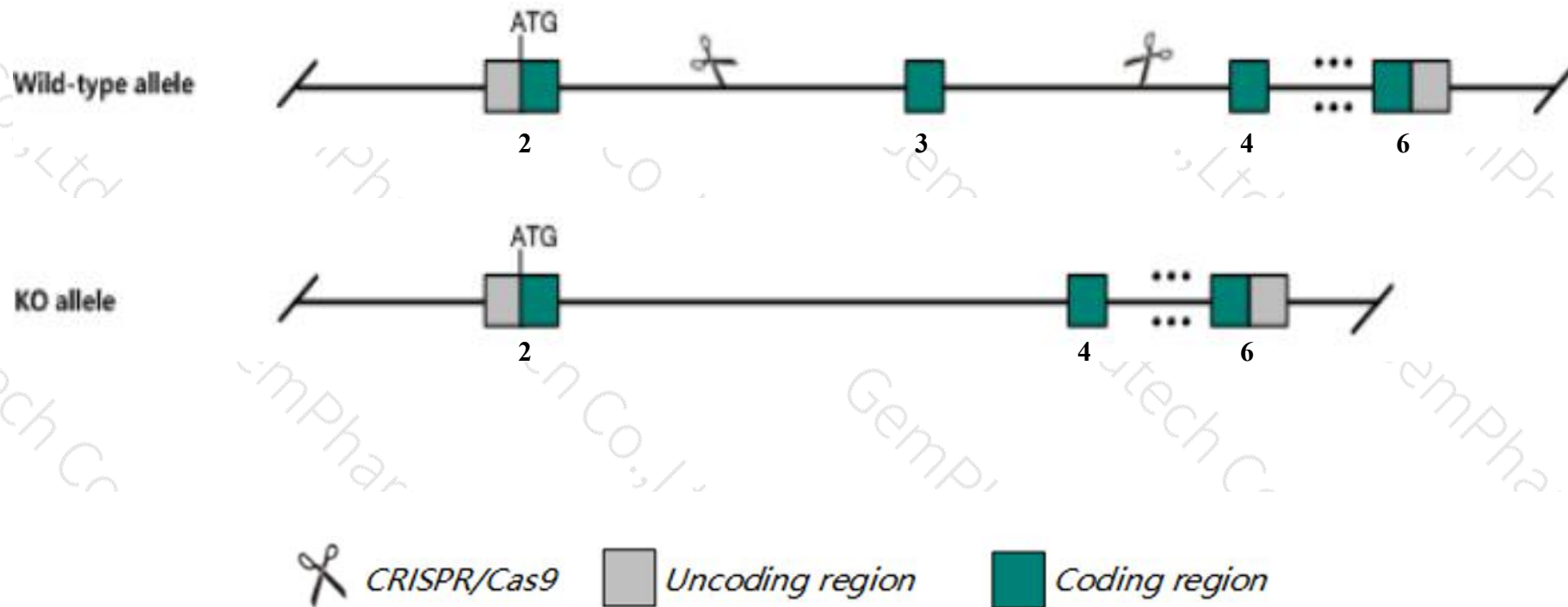
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rab7* gene. The schematic diagram is as follows:



- The *Rab7* gene has 7 transcripts. According to the structure of *Rab7* gene, exon3 of *Rab7-201*(ENSMUST00000095048.5) transcript is recommended as the knockout region. The region contains 127bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rab7* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a targeted alleles exhibit abnormal endocytosis within the visceral endoderm, failure of elongation along the primitive streak and incomplete gastrulation.
- The *Rab7* gene is located on the Chr6. 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)

Rab7 RAB7, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 19349, updated on 13-Mar-2020

Summary

Official Symbol Rab7 provided by [MGI](#)

Official Full Name RAB7, member RAS oncogene family provided by [MGI](#)

Primary source [MGI:MGI:105068](#)

See related [Ensembl:ENSMUSG00000079477](#)

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 Rab7a

Expression Ubiquitous expression in bladder adult (RPKM 76.7), kidney adult (RPKM 66.7) and 28 other tissues [See more](#)

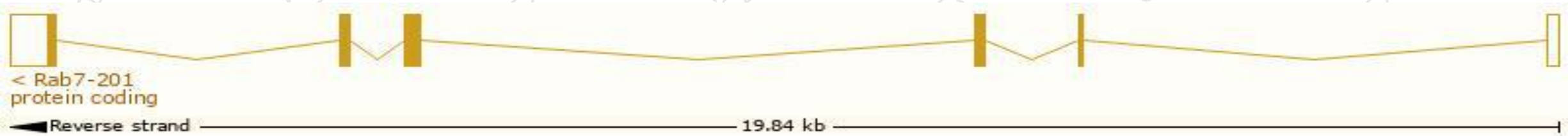
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

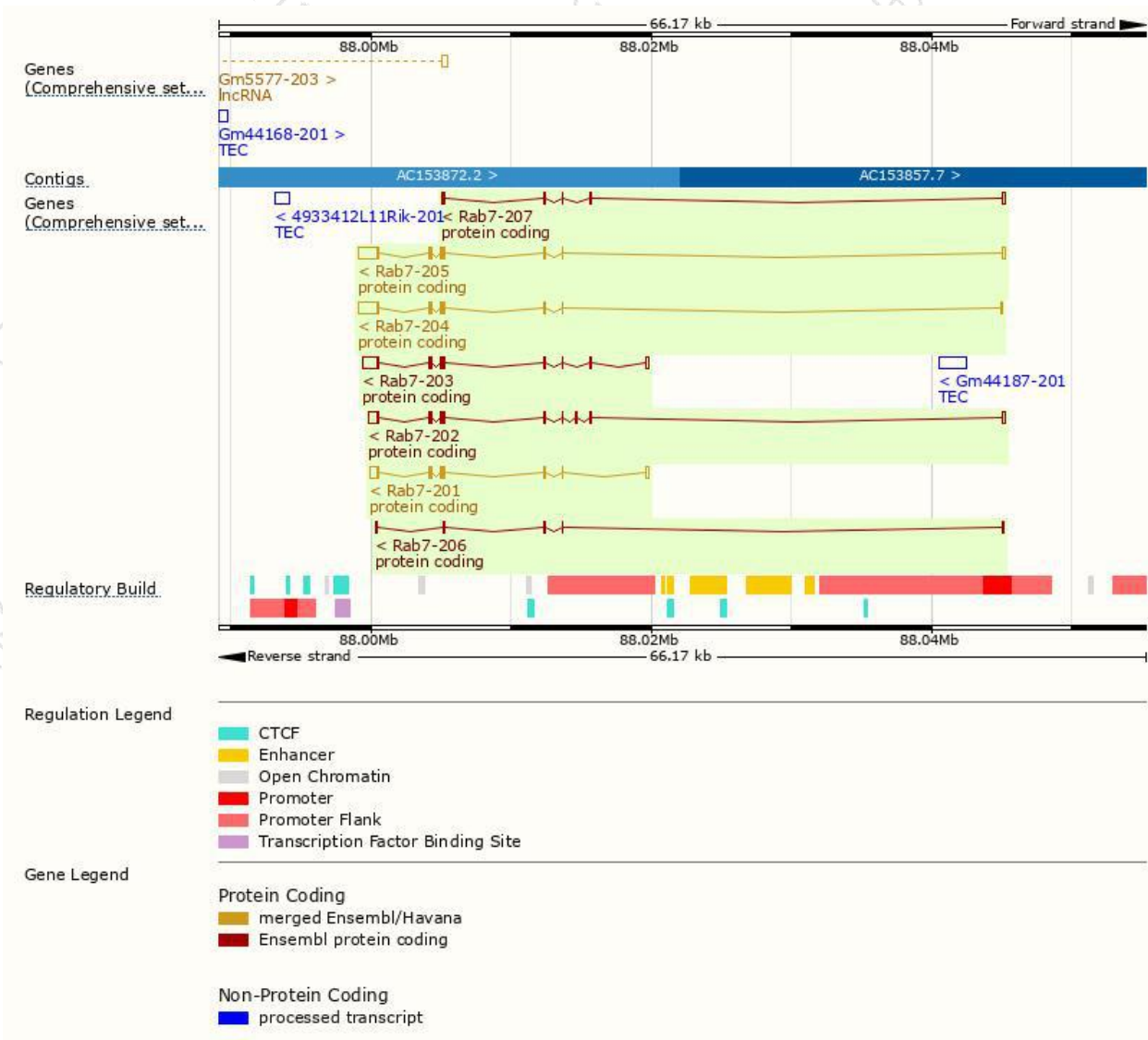
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rab7-205	ENSMUST00000113600.9	2159	207aa	Protein coding	CCDS39552	P51150_Q4FJQ0	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
Rab7-204	ENSMUST00000113598.7	2031	207aa	Protein coding	CCDS39552	P51150_Q4FJQ0	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
Rab7-203	ENSMUST00000113597.7	1859	207aa	Protein coding	CCDS39552	P51150_Q4FJQ0	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
Rab7-202	ENSMUST00000113596.7	1657	207aa	Protein coding	CCDS39552	P51150_Q4FJQ0	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
Rab7-201	ENSMUST00000095048.5	1275	207aa	Protein coding	CCDS39552	P51150_Q4FJQ0	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
Rab7-207	ENSMUST00000204126.1	550	98aa	Protein coding	-	A0A0N4SVG9	CDS 3' incomplete TSL:3
Rab7-206	ENSMUST00000203674.2	424	88aa	Protein coding	-	A0A0N4SVR6	TSL:5 GENCODE basic

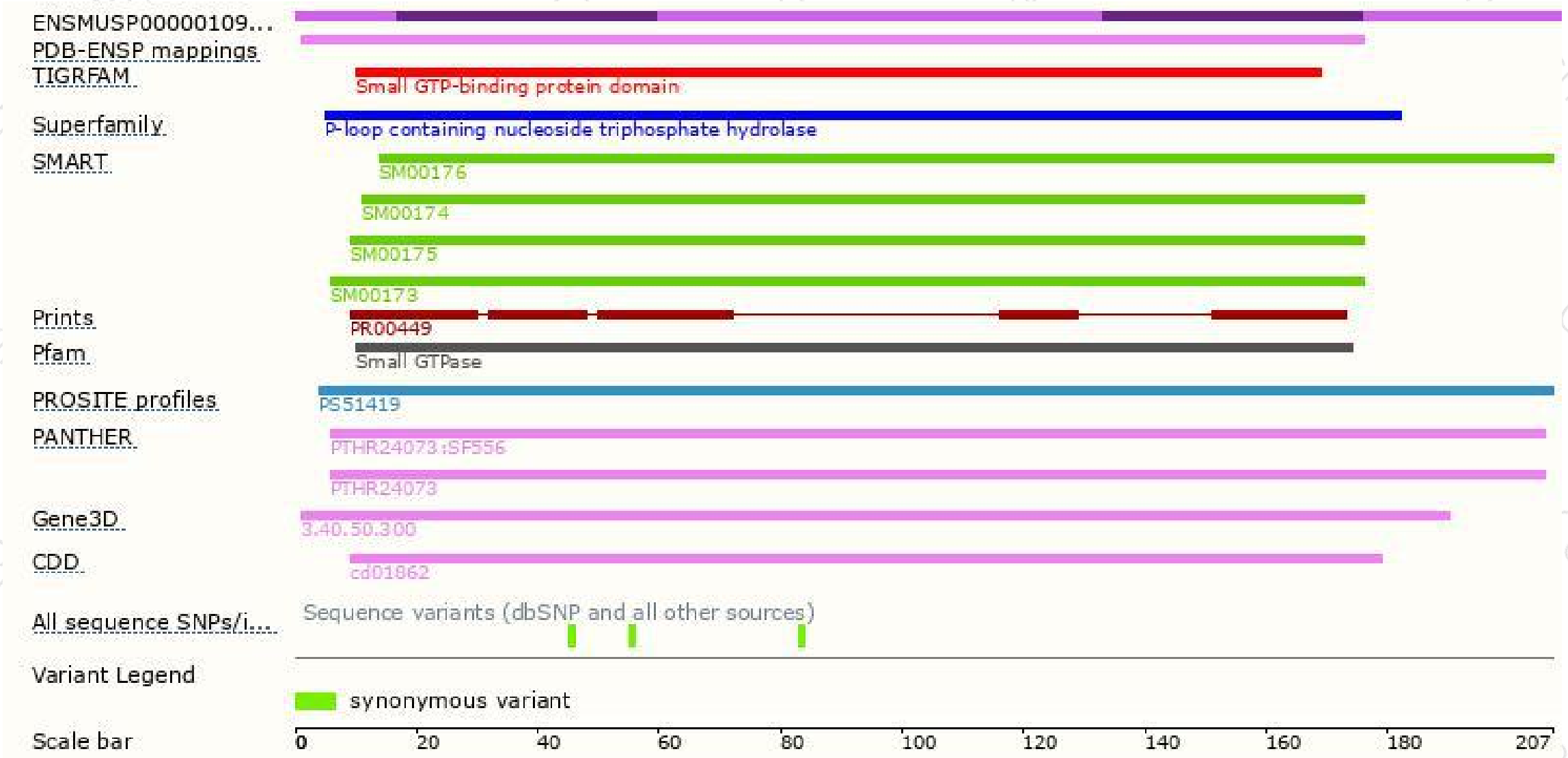
The strategy is based on the design of *Rab7-201* transcript,the transcription is shown below:



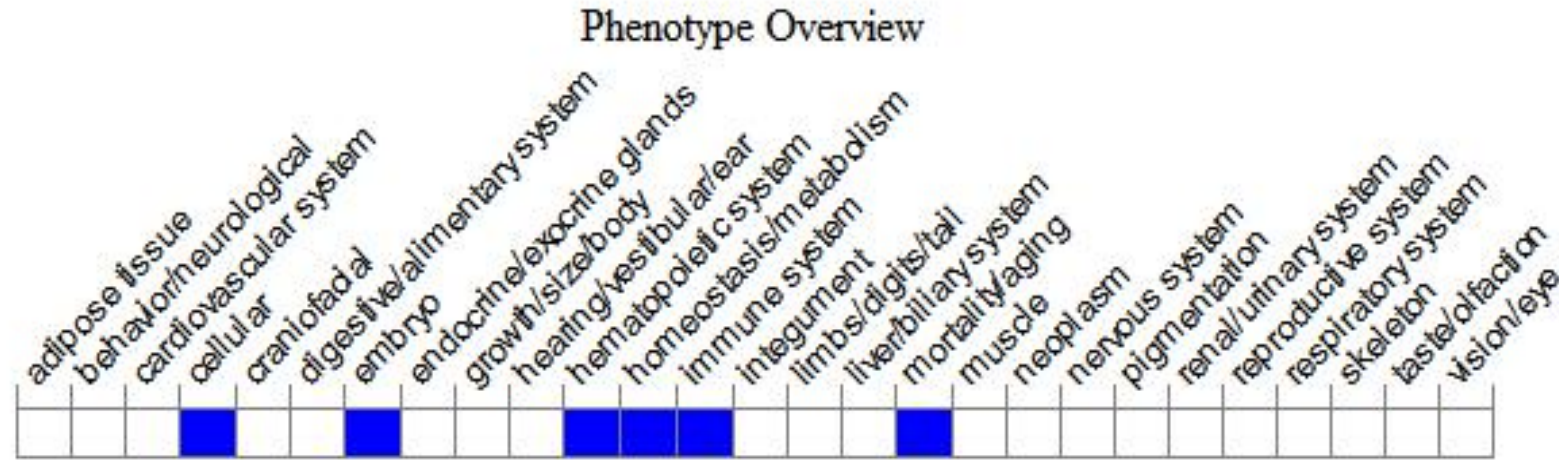
Genomic location distribution



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 targeted alleles exhibit abnormal endocytosis within the visceral endoderm, failure of elongation along the primitive streak and incomplete gastrulation.

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

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