

Ppp1r12a Cas9-CKO Strategy

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Project Overview

Project Name

Ppp1r12a

Project type

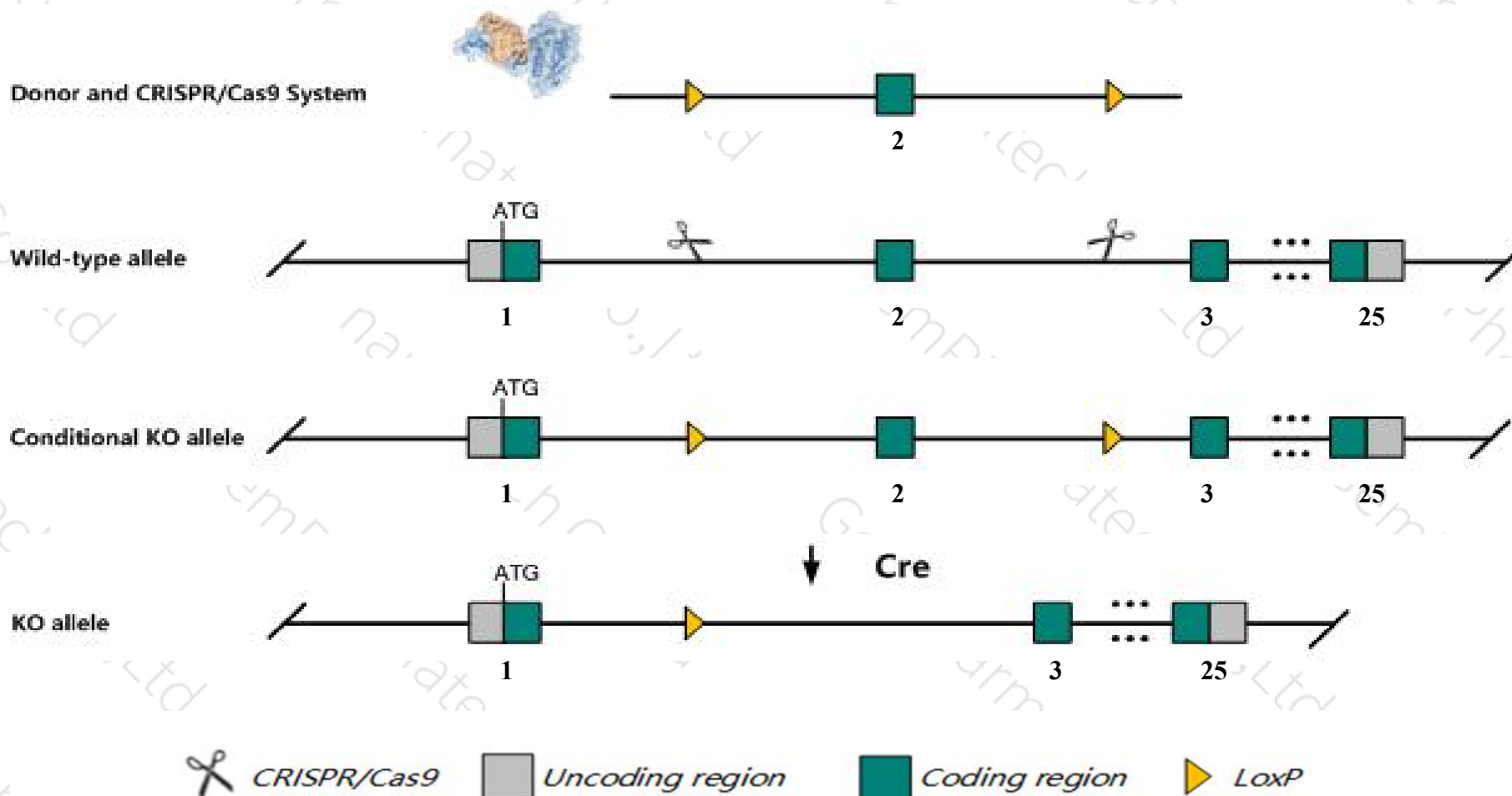
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppp1r12a* gene. The schematic diagram is as follows:



- The *Ppp1r12a* gene has 8 transcripts. According to the structure of *Ppp1r12a* gene, exon2 of *Ppp1r12a*-205(ENSMUST00000219263.1) transcript is recommended as the knockout region. The region contains 131bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppp1r12a* 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, homozygous null mice die before E7.5. Mice homozygous for a floxed allele activated in smooth muscle exhibit altered intestinal smooth muscle contractility.
- The *Ppp1r12a* gene is located on the Chr10. 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)

Ppp1r12a protein phosphatase 1, regulatory subunit 12A [Mus musculus (house mouse)]

Gene ID: 17931, updated on 13-Mar-2020

Summary



Official Symbol Ppp1r12a provided by [MGI](#)

Official Full Name protein phosphatase 1, regulatory subunit 12A provided by [MGI](#)

Primary source [MGI:MGI:1309528](#)

See related [Ensembl:ENSMUSG00000019907](#)

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 1200015F06Rik, 5730577I22Rik, AA792106, AV099298, D10Ert625e, Mypt1

Expression Biased expression in bladder adult (RPKM 144.2), CNS E11.5 (RPKM 14.0) and 11 other tissues [See more](#)

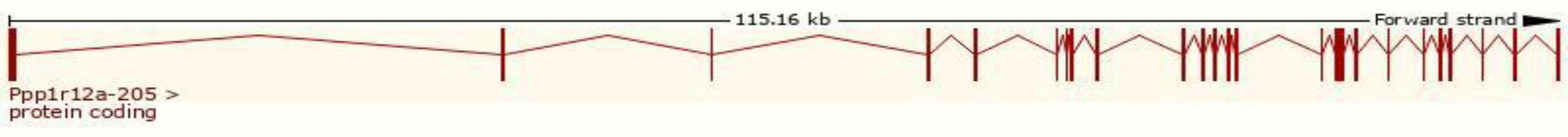
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

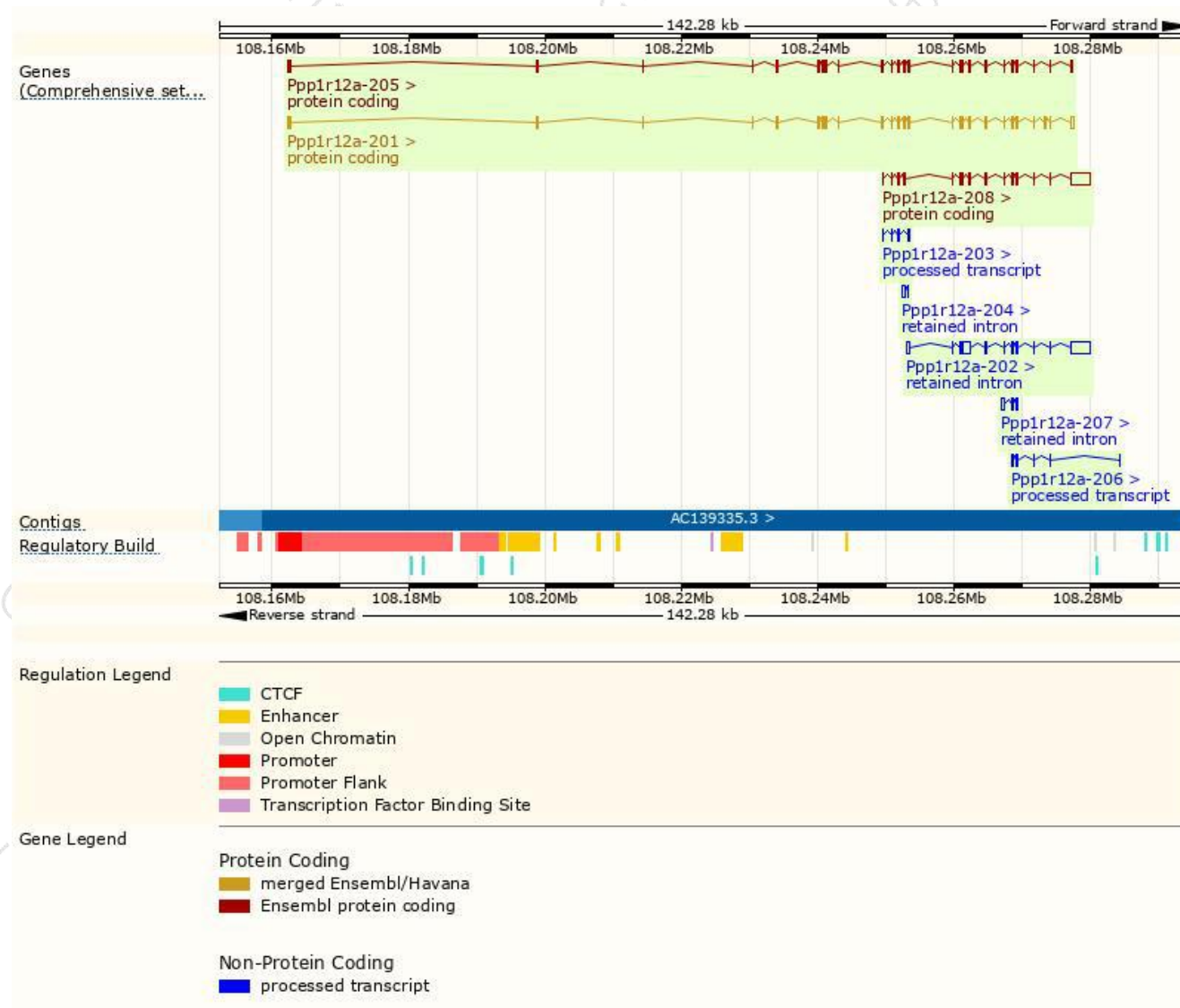
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp1r12a-201	ENSMUST00000070663.5	3403	1004aa	Protein coding	CCDS36052	Q9DBR7	TSL:1 GENCODE basic
Ppp1r12a-208	ENSMUST00000219759.1	4212	506aa	Protein coding	-	A0A1W2P750	CDS 5' incomplete TSL:1
Ppp1r12a-205	ENSMUST00000219263.1	3355	1029aa	Protein coding	-	Q9DBR7	TSL:5 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
Ppp1r12a-206	ENSMUST00000219559.1	541	No protein	Processed transcript	-	-	TSL:3
Ppp1r12a-203	ENSMUST00000218773.1	386	No protein	Processed transcript	-	-	TSL:2
Ppp1r12a-202	ENSMUST00000218161.1	5066	No protein	Retained intron	-	-	TSL:2
Ppp1r12a-204	ENSMUST00000219068.1	590	No protein	Retained intron	-	-	TSL:3
Ppp1r12a-207	ENSMUST00000219653.1	563	No protein	Retained intron	-	-	TSL:3

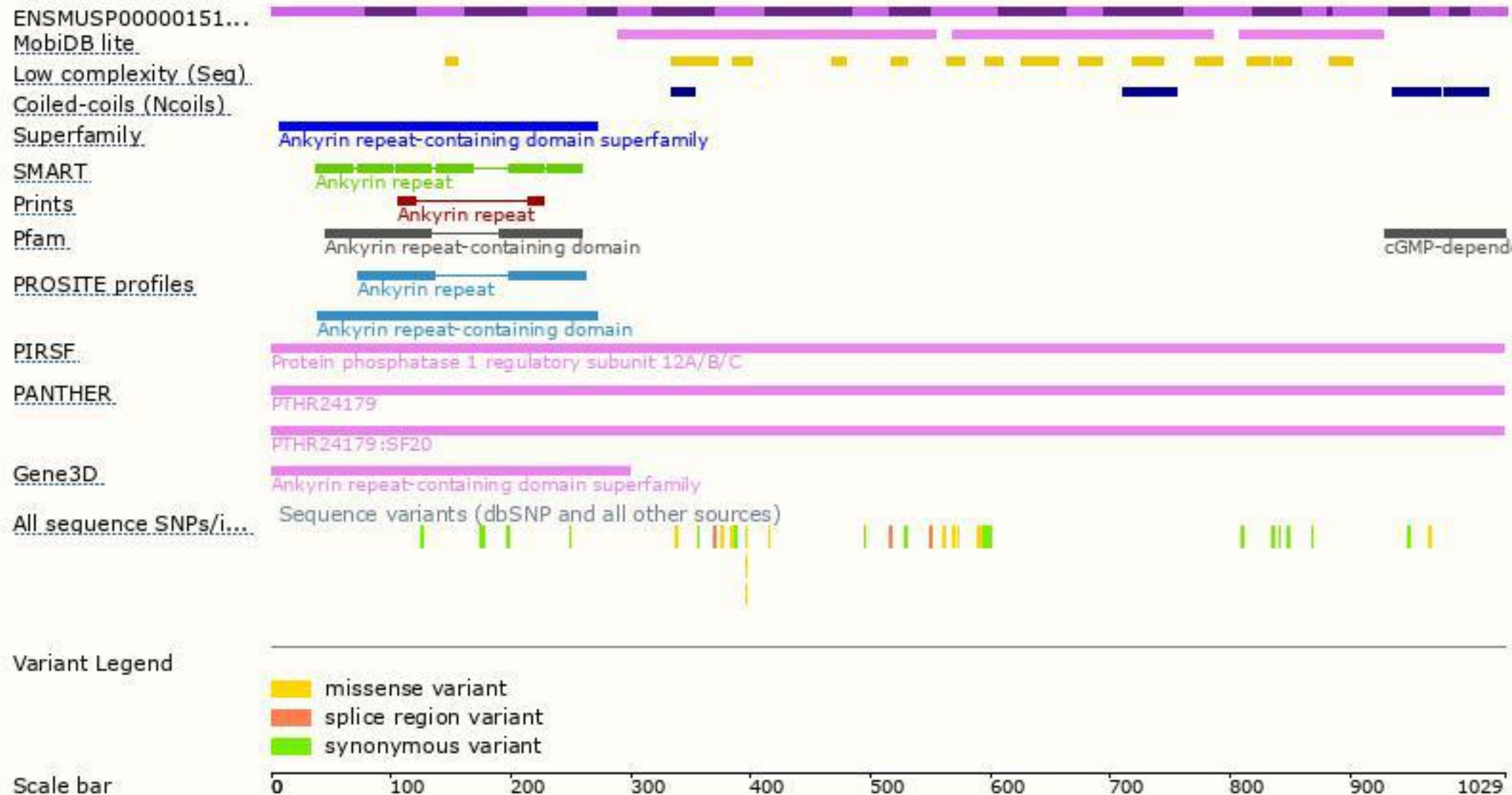
The strategy is based on the design of *Ppp1r12a-205* transcript,the transcription is shown below:



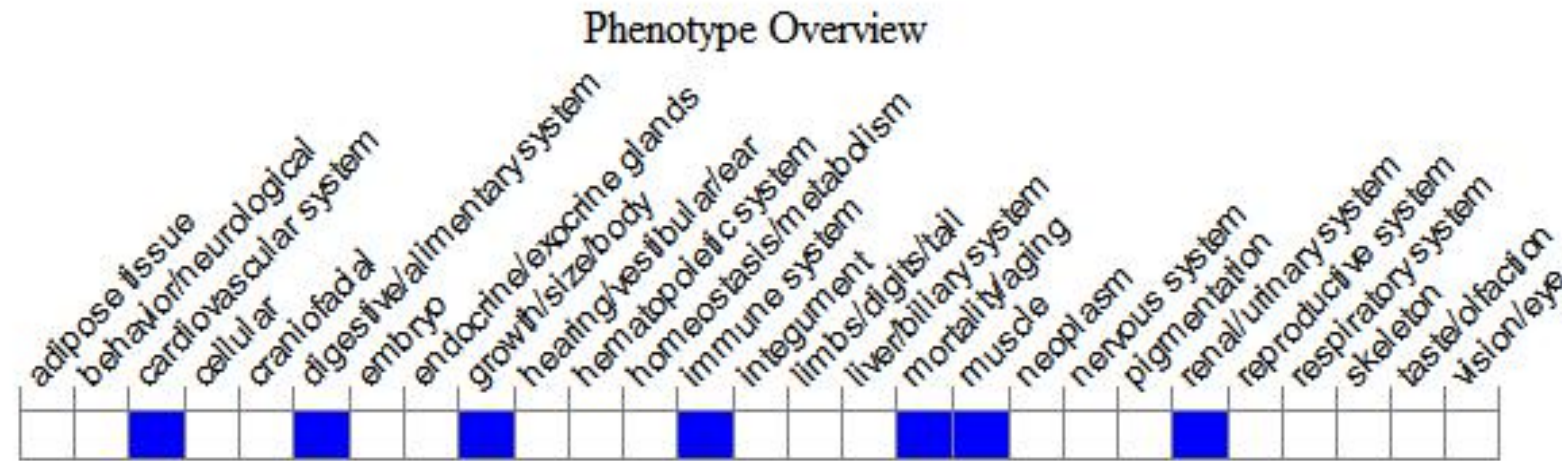
Genomic location distribution



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, homozygous null mice die before E7.5. Mice homozygous for a floxed allele activated in smooth muscle exhibit altered intestinal smooth muscle contractility.

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

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