Kcmf1 Cas9-KO Strategy

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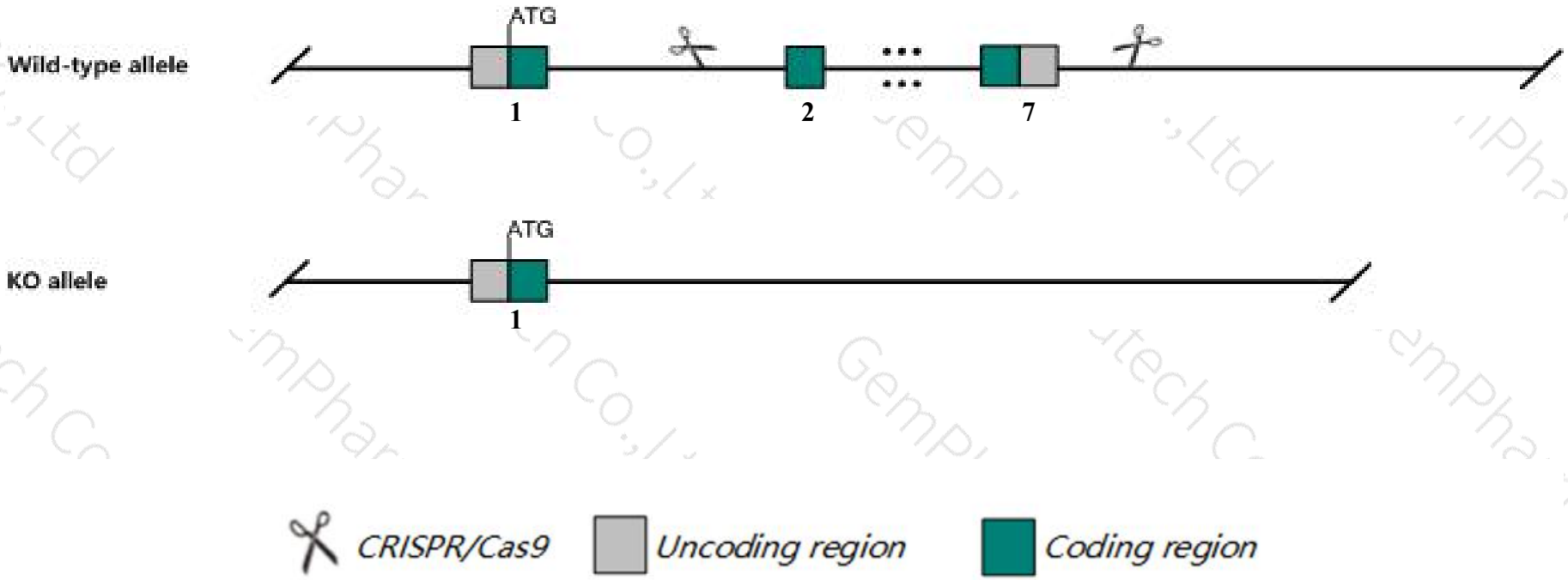
Design Date: 2020-2-5

Project Overview

Project Name	***Kcmf1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcmf1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcmf1* gene has 6 transcripts. According to the structure of *Kcmf1* gene, exon2-exon7 of *Kcmf1-201* (ENSMUST00000068697.10) transcript is recommended as the knockout region.The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Kcmf1* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Mice homozygous for a gene trapped allele exhibit some perinatal and postnatal lethality but mice that survive to adulthood exhibit normal lethality.

- The *Kcmf1* 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）

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Kcmf1 potassium channel modulatory factor 1 [*Mus musculus* (house mouse)]

Gene ID: 74287, updated on 12-Aug-2019

Summary

Official Symbol	Kcmf1 provided by MGI
Official Full Name	potassium channel modulatory factor 1 provided by MGI
Primary source	MGI:MGI:1921537
See related	Ensembl:ENSMUSG00000055239
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	Pmcf; Debt91; 1700094M07Rik
Expression	Ubiquitous expression in testis adult (RPKM 46.7), ovary adult (RPKM 17.8) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 6 C1; 6 32.3 cM

See Kcmf1 in Genome Data Viewer

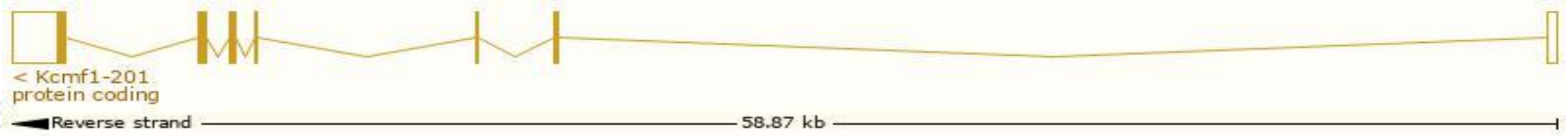
Exon count: 9

Transcript information（Ensembl）

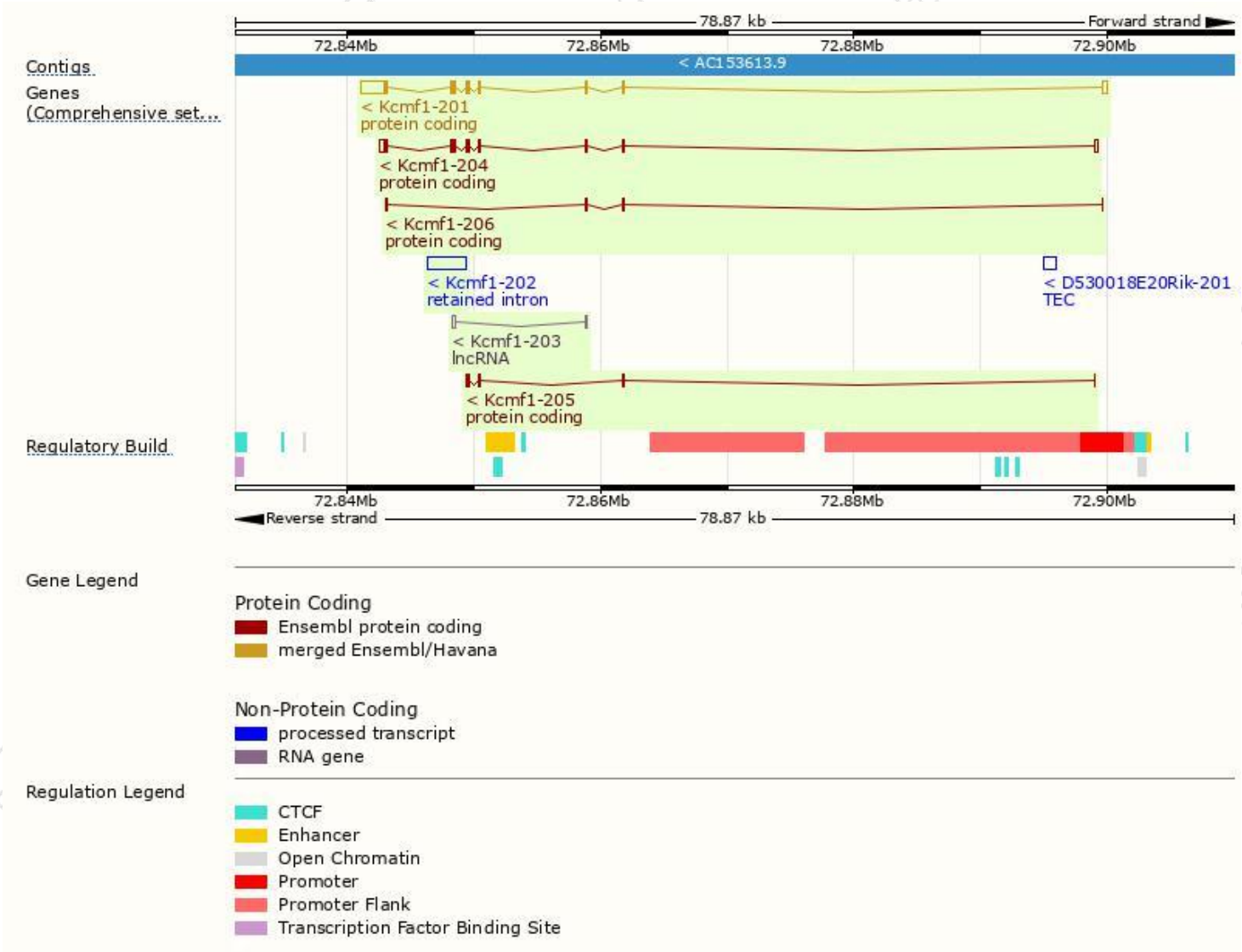
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcmf1-201	ENSMUST00000068697.10	3251	381aa	Protein coding	CCDS39518	Q80UY2	TSL:1 GENCODE basic APPRIS P1
Kcmf1-204	ENSMUST00000204598.2	1743	330aa	Protein coding	CCDS85066	A0A0N4SV15	TSL:1 GENCODE basic
Kcmf1-205	ENSMUST00000204708.1	549	47aa	Protein coding	-	A0A0N4SV12	CDS 3' incomplete TSL:3
Kcmf1-206	ENSMUST00000206378.1	544	110aa	Protein coding	-	A0A0U1RNG8	TSL:5 GENCODE basic
Kcmf1-202	ENSMUST00000203004.1	3044	No protein	Retained intron	-	-	TSL:NA
Kcmf1-203	ENSMUST00000203431.1	393	No protein	lncRNA	-	-	TSL:3

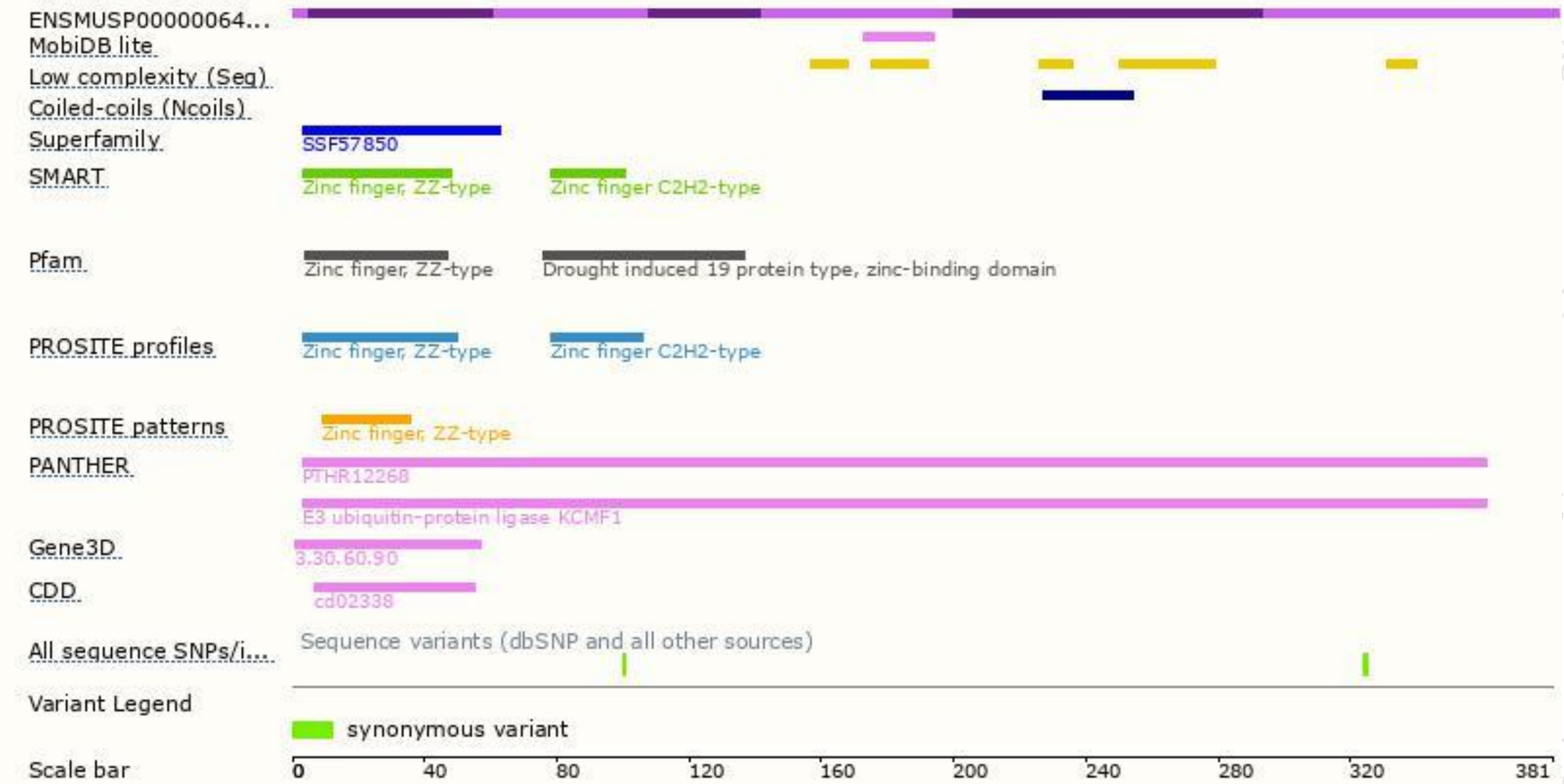
The strategy is based on the design of *Kcmf1-201* transcript,The transcription is shown below



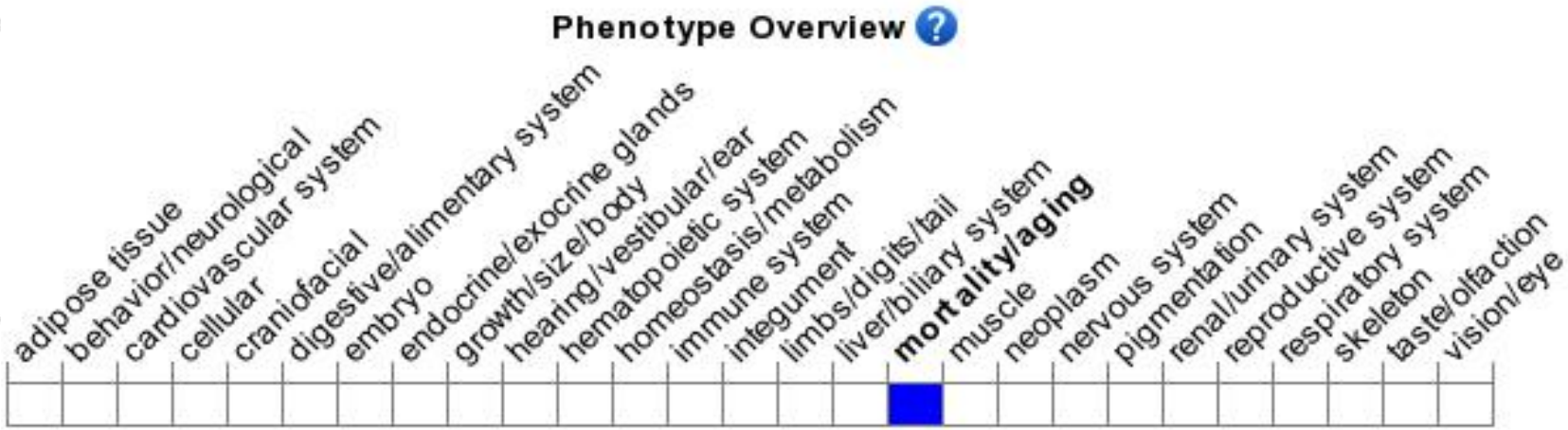
Genomic location distribution



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 gene trapped allele exhibit some perinatal and postnatal lethality but mice that survive to adulthood exhibit normal lethality.

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

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