

Alpk3 Cas9-KO Strategy

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Project Overview

Project Name

Alpk3

Project type

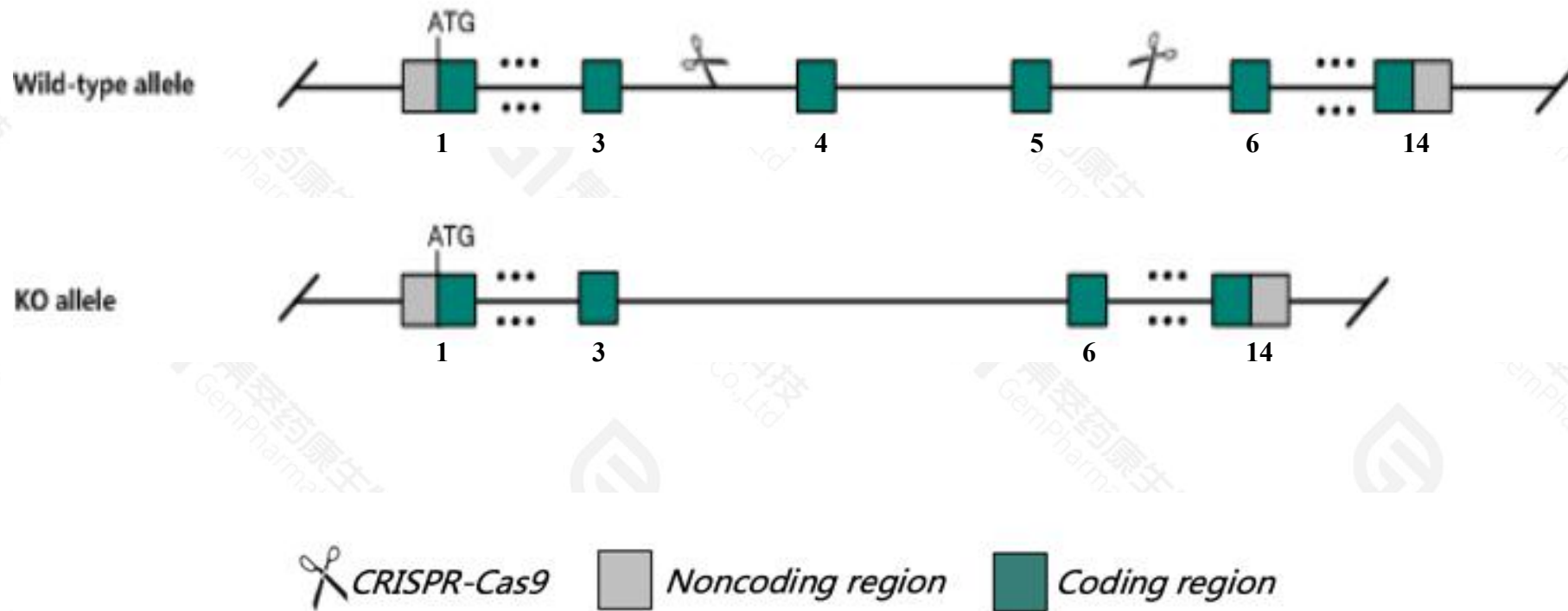
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Alpk3* gene. The schematic diagram is as follows:



- The *Alpk3* gene has 2 transcripts. According to the structure of *Alpk3* gene, exon4-exon5 of *Alpk3-201*(ENSMUST00000107348.2) transcript is recommended as the knockout region. The region contains 1406bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Alpk3* 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 gene-trapped allele exhibit altered cardiomyocyte architecture and develop a non-progressive cardiomyopathy that presents features of both hypertrophic and dilated forms of cardiomyopathy,
- The *Alpk3* gene is located on the Chr7. 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.

Alpk3 alpha-kinase 3 [Mus musculus (house mouse)]

Gene ID: 116904, updated on 17-Dec-2020

Summary



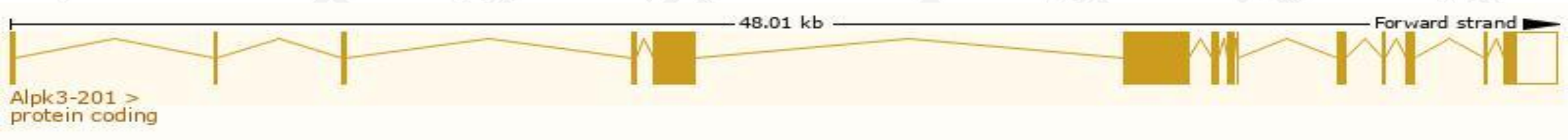
Official Symbol	Alpk3 provided by MGI
Official Full Name	alpha-kinase 3 provided by MGI
Primary source	MGI:MGI:2151224
See related	Ensembl:ENSMUSG00000038763
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW319487, D330016D04, MAK, Mi, Midori, mKIAA1330
Expression	Biased expression in heart adult (RPKM 12.1), limb E14.5 (RPKM 1.2) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

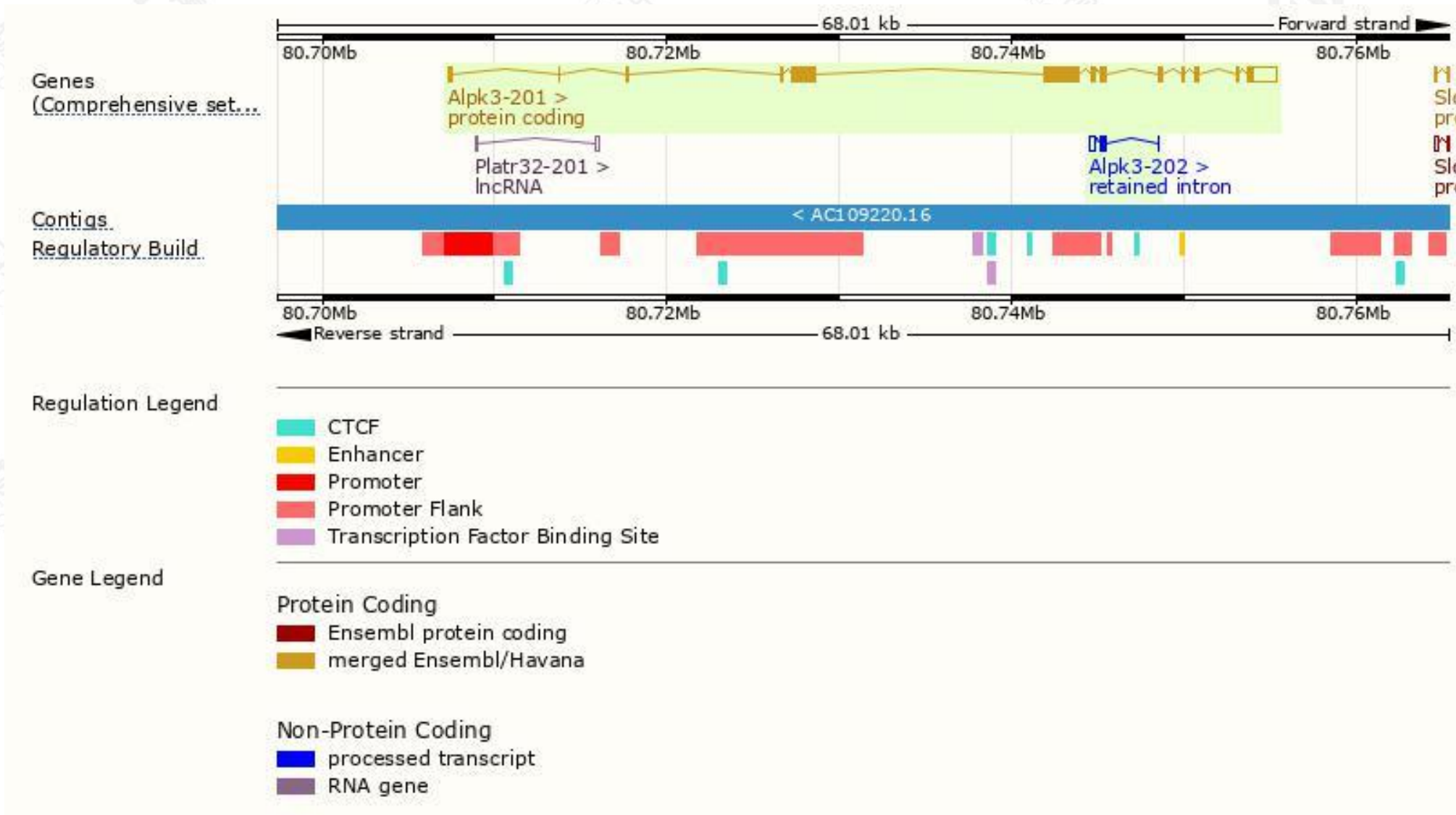
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Alpk3-201	ENSMUST00000107348.2	6369	1680aa	Protein coding	CCDS40004		TSL:1 , GENCODE basic , APPRIS P1 ,
Alpk3-202	ENSMUST00000151115.3	460	No protein	Retained intron	-		TSL:3 ,

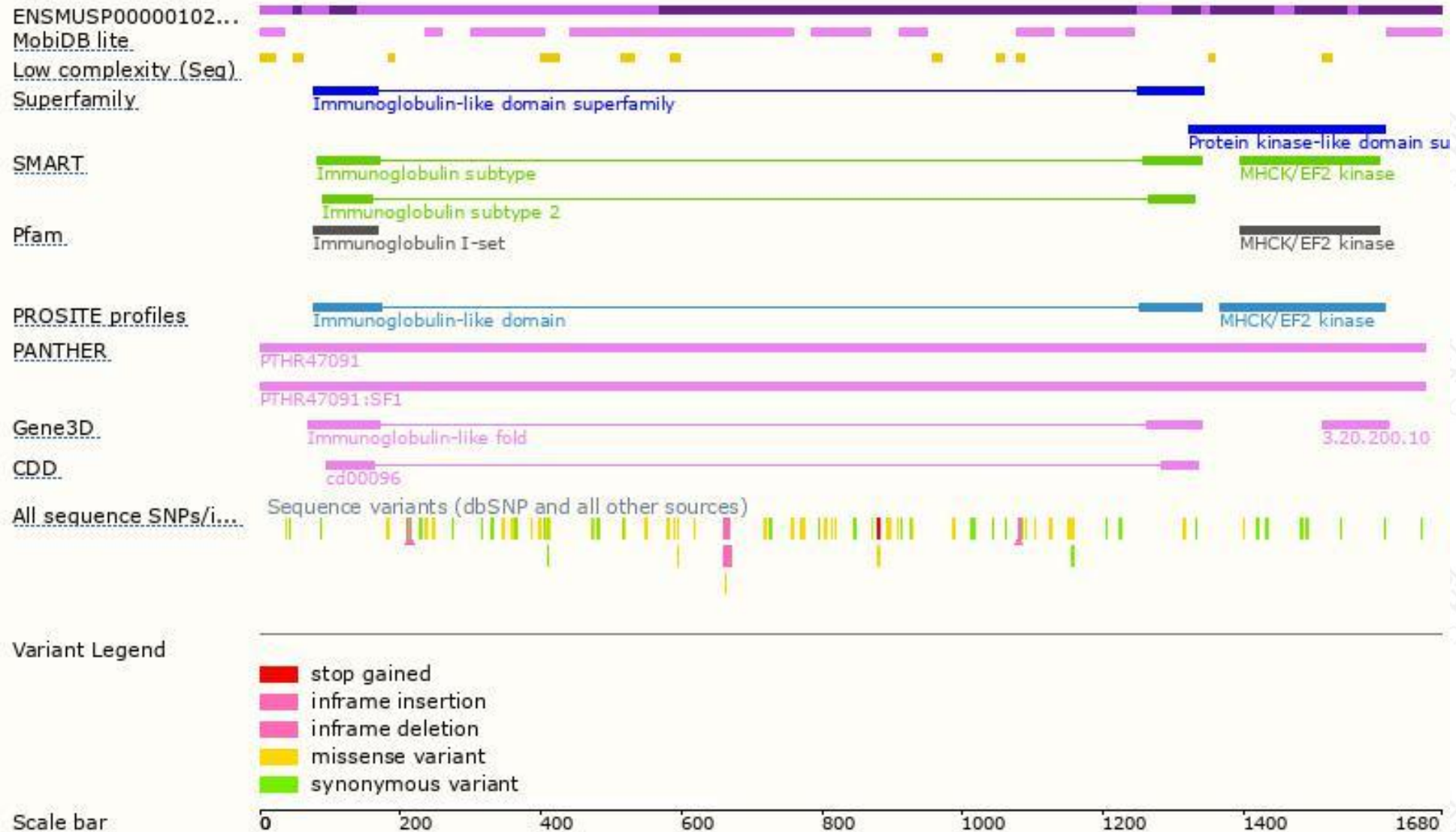
The strategy is based on the design of *Alpk3-201* transcript,the transcription is shown below:



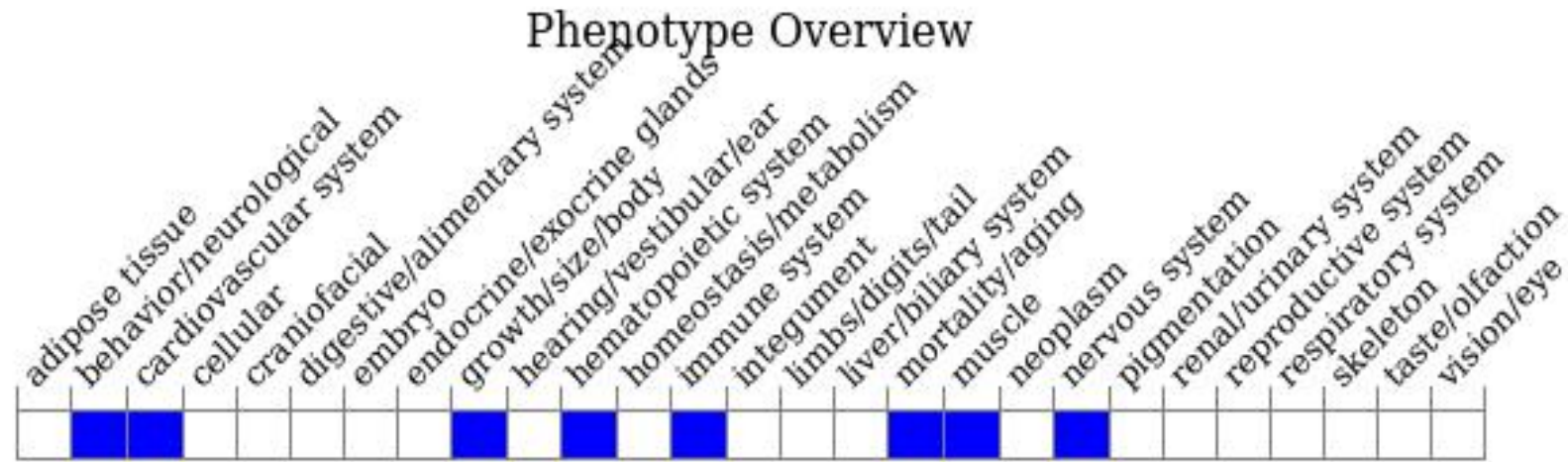
Genomic location distribution



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 altered cardiomyocyte architecture and develop a non-progressive cardiomyopathy that presents features of both hypertrophic and dilated forms of cardiomyopathy,

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