Myf5 Cas9-KO Strategy

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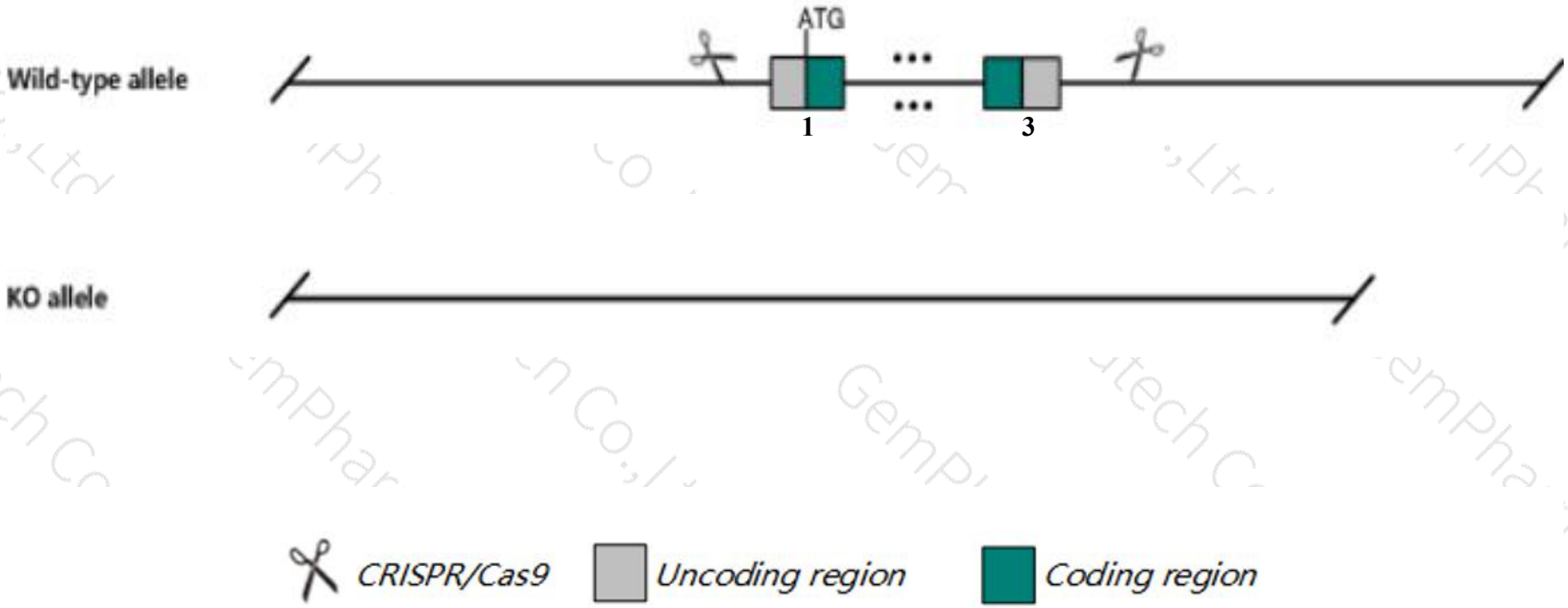
Project Overview

Project Name	***Myf5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myf5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Myf5* gene has 1 transcript. According to the structure of *Myf5* gene, exon1-exon3 of *Myf5-201* (ENSMUST00000000445.1) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Myf5* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,homozygotes for targeted null mutations exhibit delayed appearance of myotomal cells in somites, and lack the distal portion of ribs resulting in inability to breathe and lethality at birth. other mutants lack the rib phenotype.
- The *Myf5* 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 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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Myf5 myogenic factor 5 [Mus musculus (house mouse)]

Gene ID: 17877, updated on 13-Mar-2020

Summary

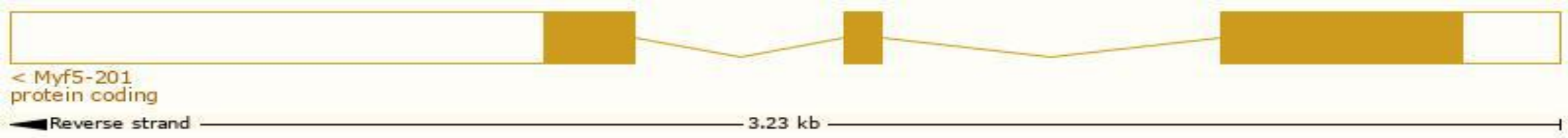
Official Symbol	Myf5 provided by MGI
Official Full Name	myogenic factor 5 provided byMGI
Primary source	MGI:MGI:97252
See related	Ensembl:ENSMUSG00000000435
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B130010J22Rik, Myf-5, bHLHc2
Expression	Biased expression in limb E14.5 (RPKM 2.7), ovary adult (RPKM 0.6) and 1 other tissueSee more
Orthologs	human all

Transcript information（Ensembl）

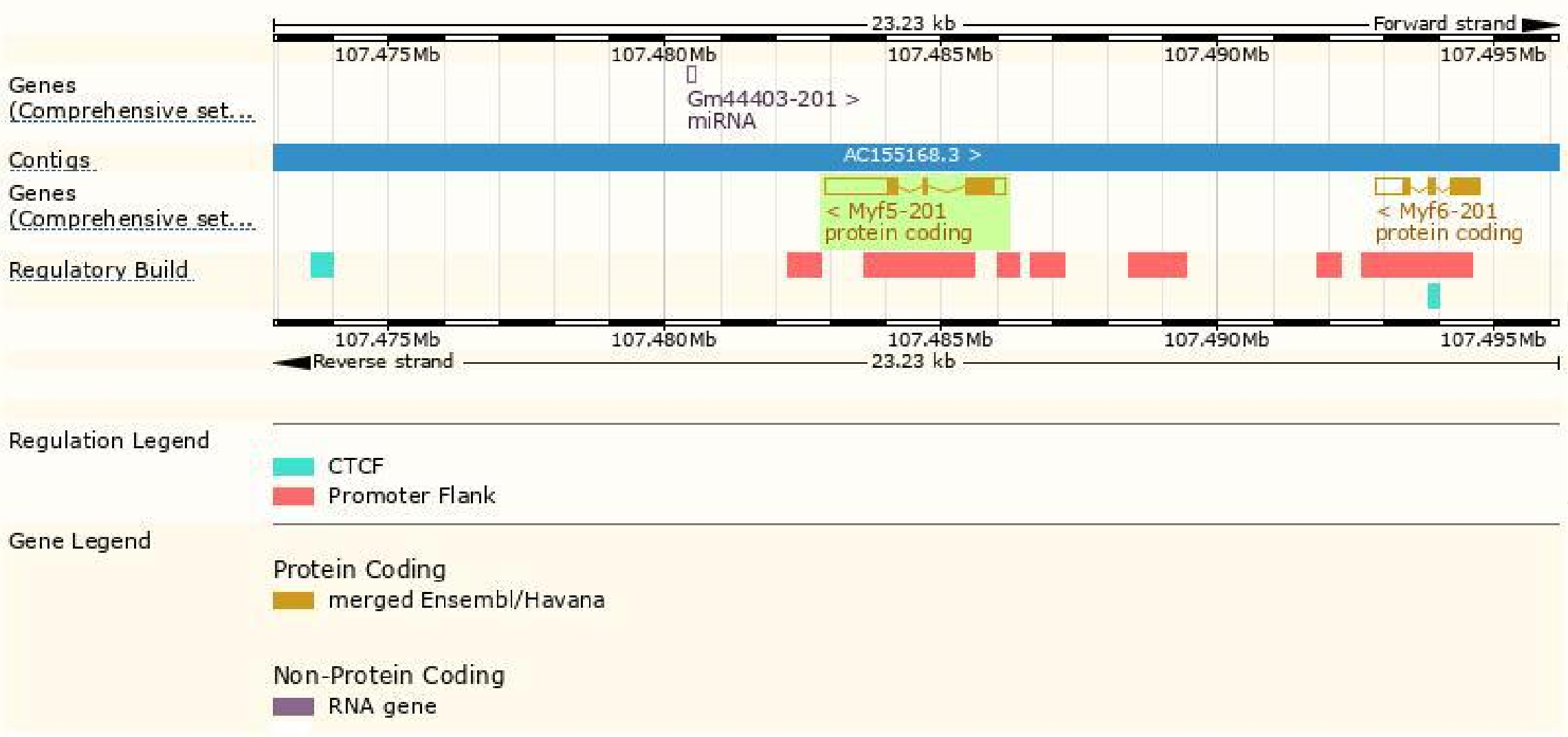
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myf5-201	ENSMUST00000000445.1	2083	255aa	Protein coding	CCDS24161	A2RSK4 P24699	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

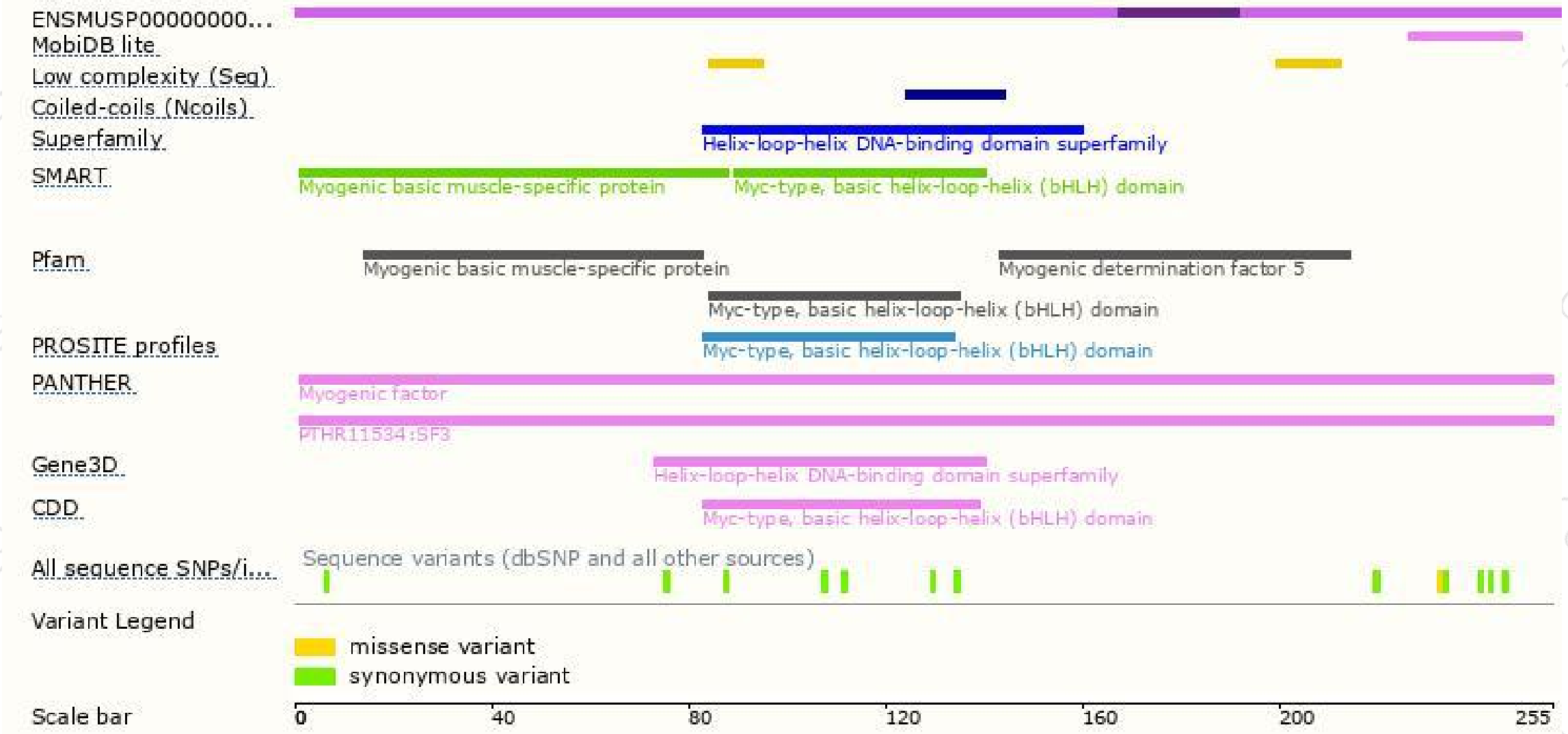
The strategy is based on the design of *Myf5-201* transcript,the transcription is shown below



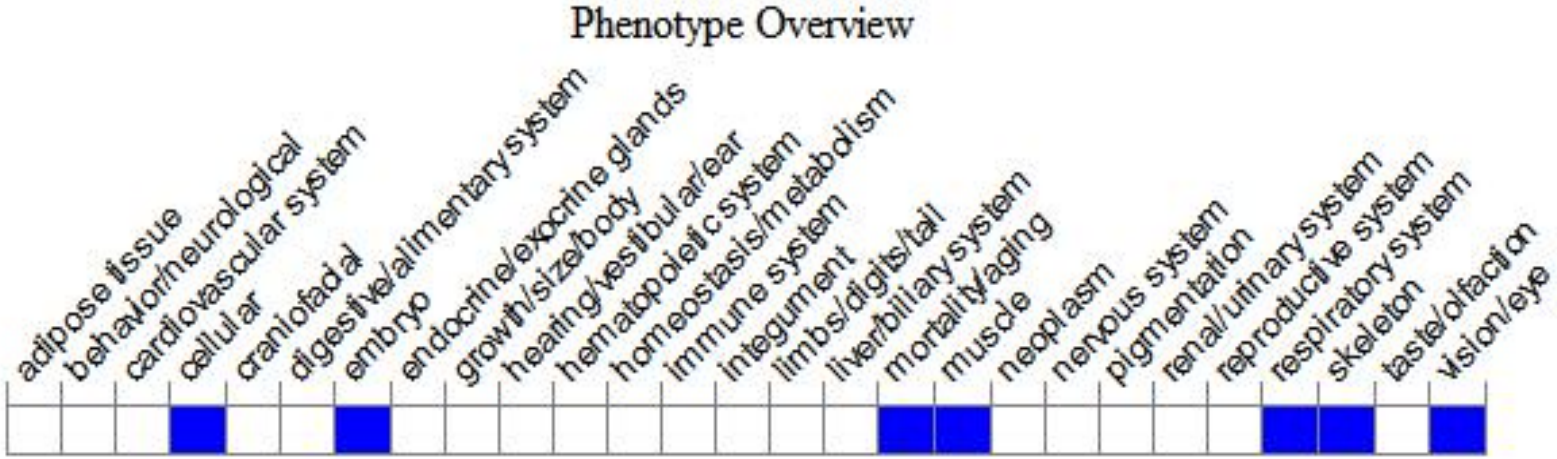
Genomic location distribution



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/).

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

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