Arhgap26 Cas9-KO Strategy

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Reviewer: Xiaojing Li

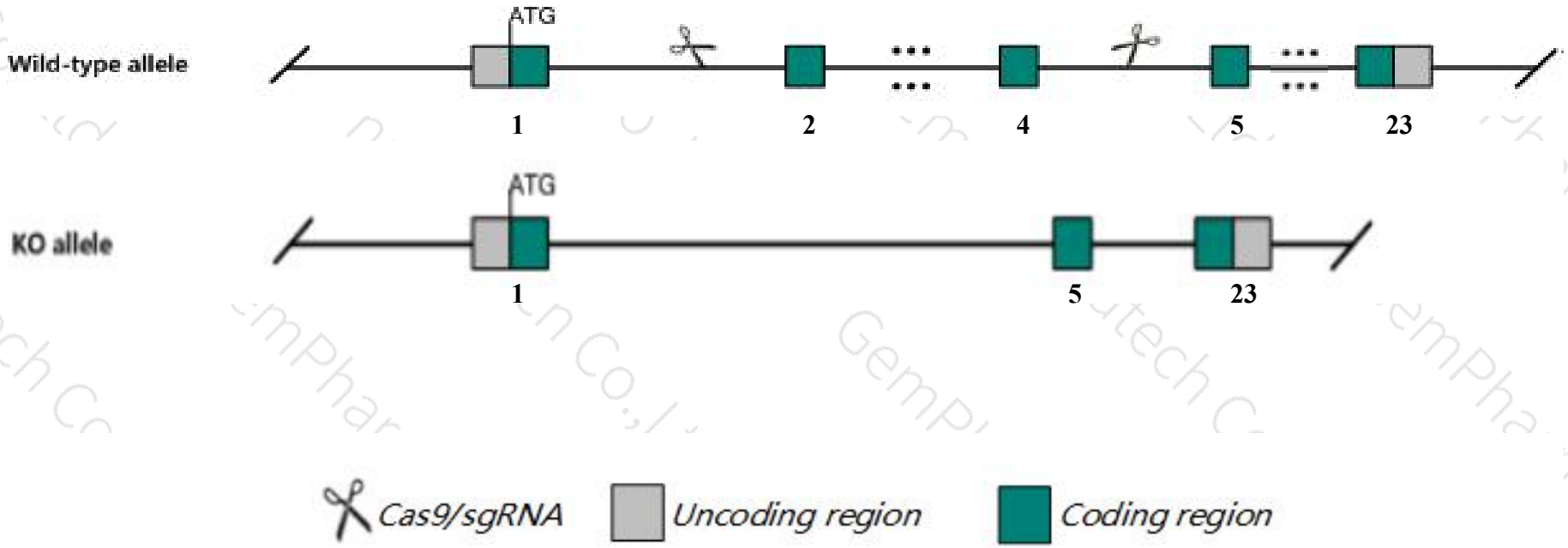
Design Date: 2020-3-5

Project Overview

Project Name	***Arhgap26***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgap26* gene. The schematic diagram is as follows:



Technical routes

➢ The *Arhgap26* gene has 12 transcripts. According to the structure of *Arhgap26* gene, exon2-exon4 of *Arhgap26-201* (ENSMUST00000097593.8) transcript is recommended as the knockout region.The region contains 230bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Arhgap26* gene. The brief process is as follows: CRISPR/Cas9 sys

Notice

➢ According to the existing MGI data, Mice homozygous for a hypomorphic allele display reduced myofiber size, impaired myoblast fusion and abnormal muscle regeneration.

➢Transcript 206,209,211 CDS 5' incomplete the influences is unknown.

➢ The *Arhgap26* gene is located on the Chr18. 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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Arhgap26 Rho GTPase activating protein 26 [*Mus musculus* (house mouse)]

Gene ID: 71302, updated on 13-Mar-2020

Summary

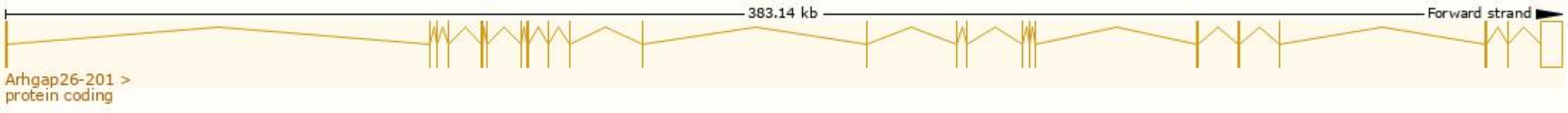
Official Symbol	Arhgap26 provided by MGI
Official Full Name	Rho GTPase activating protein 26 provided by MGI
Primary source	MGI:MGI:1918552
See related	Ensembl:ENSMUSG00000036452
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI853435; mKIAA0621; 1810044B20Rik; 2610010G17Rik; 4933432P15Rik
Expression	Broad expression in cerebellum adult (RPKM 9.3), cortex adult (RPKM 5.9) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

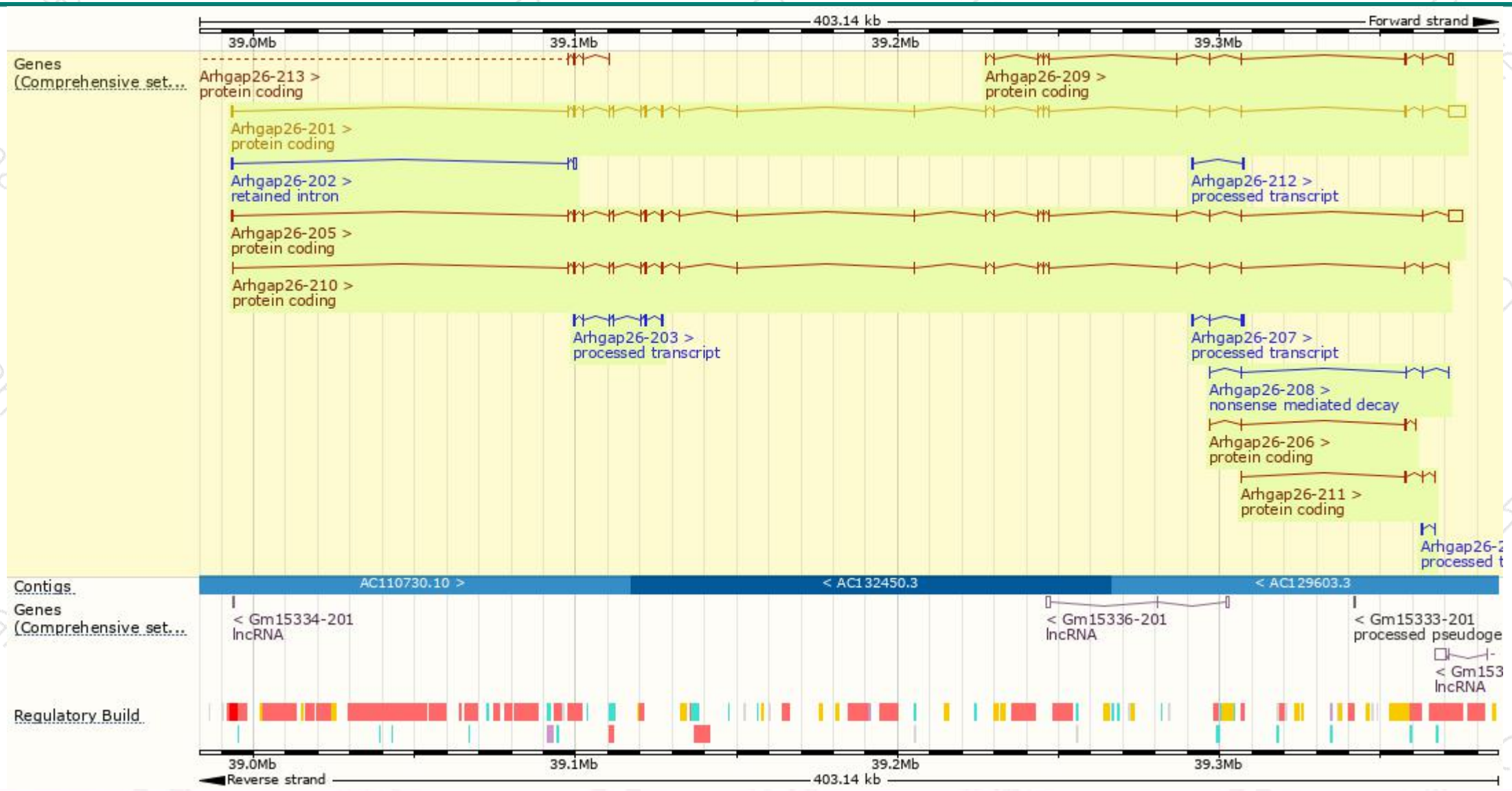
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgap26-201	ENSMUST00000097593.8	7898	814aa	Protein coding	CCDS29205	Q6ZQ82	TSL:5 GENCODE basic APPRIS P2
Arhgap26-205	ENSMUST00000137497.8	6415	722aa	Protein coding	-	F6T836	TSL:1 GENCODE basic APPRIS ALT1
Arhgap26-209	ENSMUST00000154551.7	2515	388aa	Protein coding	-	F6XTB7	CDS 5' incomplete TSL:1
Arhgap26-210	ENSMUST00000155576.7	2280	759aa	Protein coding	-	E9QAQ3	TSL:5 GENCODE basic APPRIS ALT1
Arhgap26-206	ENSMUST00000141058.7	607	144aa	Protein coding	-	F6Q7M1	CDS 5' incomplete TSL:2
Arhgap26-211	ENSMUST00000235660.1	524	132aa	Protein coding	-	A0A494B9M9	CDS 5' incomplete
Arhgap26-208	ENSMUST00000151757.7	529	115aa	Nonsense mediated decay	-	F7D661	CDS 5' incomplete TSL:5
Arhgap26-207	ENSMUST00000148399.1	867	No protein	Processed transcript	-	-	TSL:1
Arhgap26-203	ENSMUST00000123820.1	775	No protein	Processed transcript	-	-	TSL:5
Arhgap26-212	ENSMUST00000235817.1	577	No protein	Processed transcript	-	-	-
Arhgap26-204	ENSMUST00000133247.1	556	No protein	Processed transcript	-	-	TSL:1
Arhgap26-202	ENSMUST00000115574.1	1159	No protein	Retained intron	-	-	TSL:1

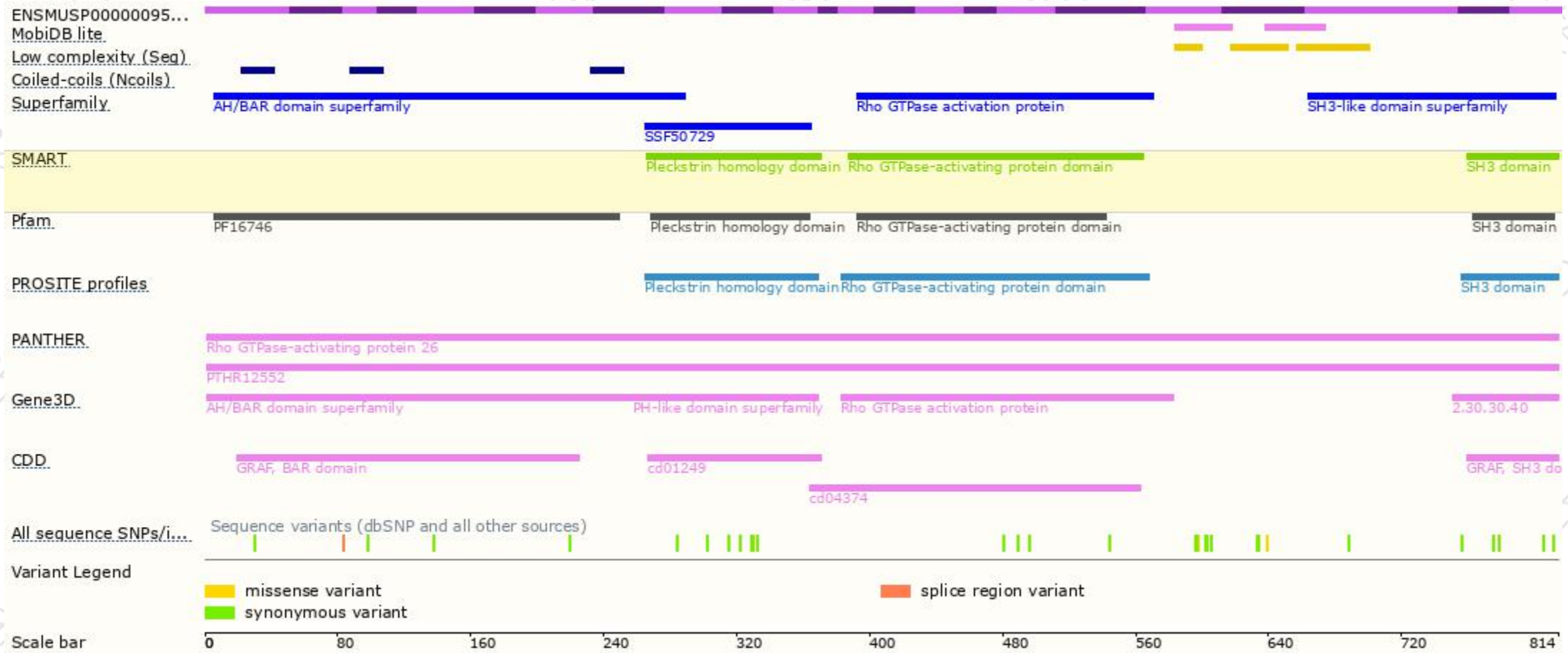
The strategy is based on the design of *Arhgap26-201* transcript,The transcription is shown below



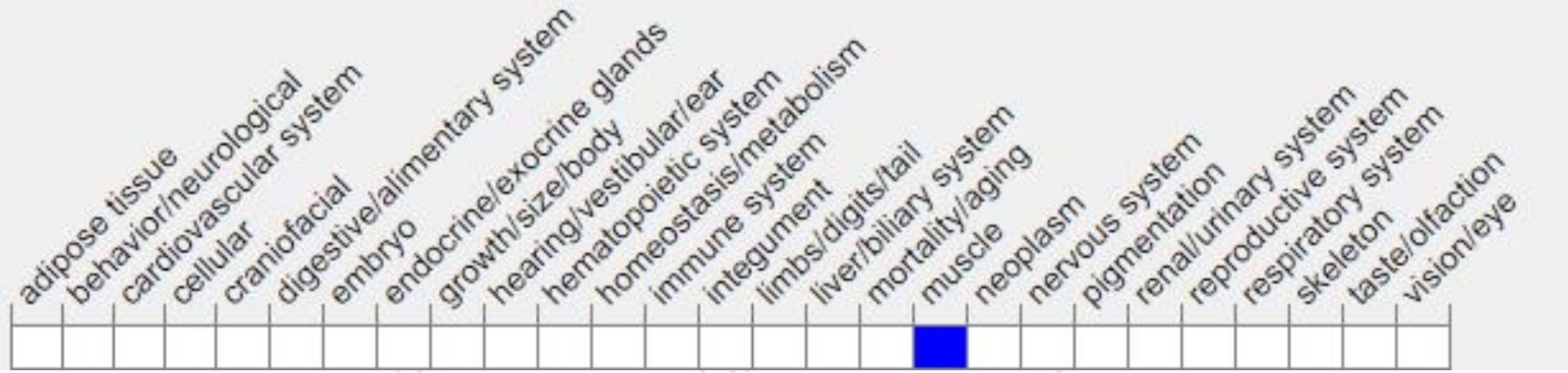
Genomic location distribution



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 hypomorphic allele display reduced myofiber size, impaired myoblast fusion and abnormal muscle regeneration.

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

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