# *Dmpk* Cas9-KO Strategy

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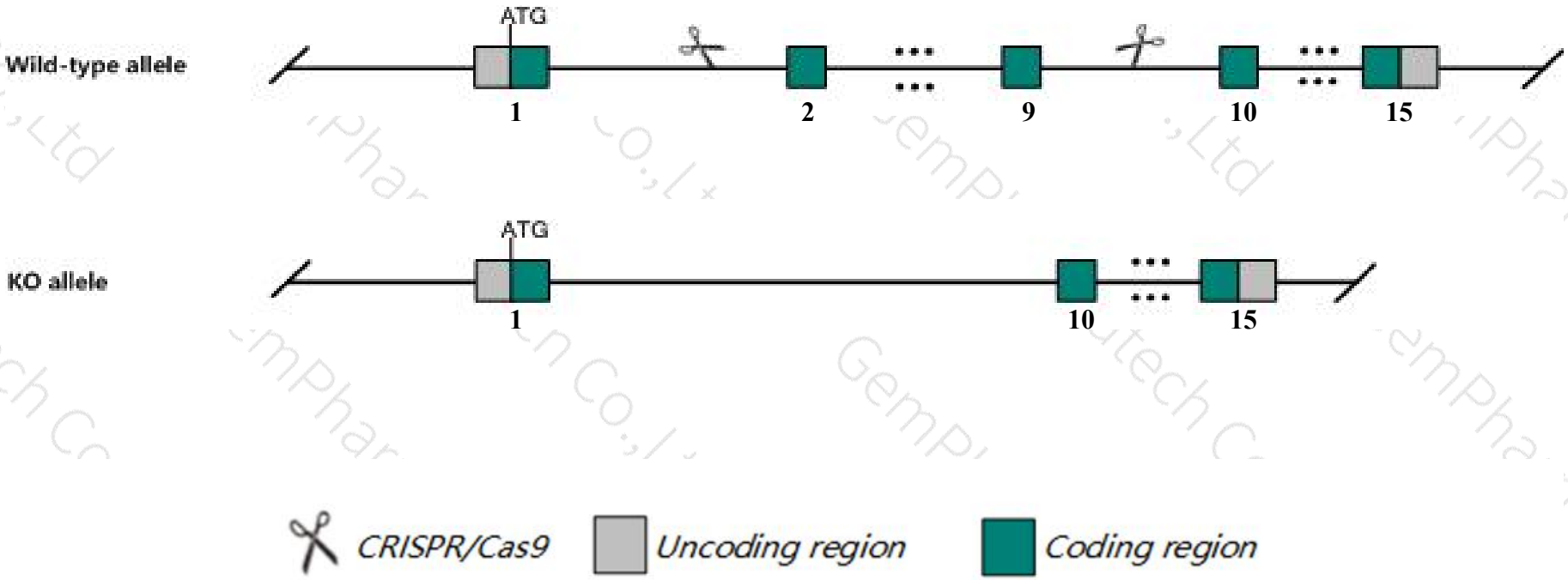
# Project Overview

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

# Knockout strategy

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



# Technical routes

➢ The *Dmpk* gene has 18 transcripts. According to the structure of *Dmpk* gene, exon2-exon9 of *Dmpk-201* (ENSMUST00000032568.13) transcript is recommended as the knockout region.The region contains 1072bp coding sequenc Knock out the region will result in disruption of protein function.

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

# Notice

➢ According to the existing MGI data,Homozygotes for a null mutation exhibit abnormal sodium channel gating in cardiac myocytes, cardiac conduction defects, and late-onset progressive skeletal myopathy. Homozygotes for a second null mutation do not develop skeletal myopathy but do have abnormal muscle intracellular calcium levels.

➢Transcript *Dmpk*-205&210&212&214 may not be affected.

➢*Mir3100* gene will be deleted together in this strategy.

➢The knockout region is near to the N-terminal of *Six5* gene,this strategy may influence the regulatory function of the N-terminal of *Six5* gene.

➢ The *Dmpk* 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.

# Gene information（NCBI）

集萃药康 GemPharmatech

## Dmpk dystrophia myotonica-protein kinase [ *Mus musculus* (house mouse) ]

Gene ID: 13400, updated on 18-Nov-2019

### Summary

| | |
|---|---|
| **Official Symbol** | Dmpk provided by MGI |
| **Official Full Name** | dystrophia myotonica-protein kinase provided by MGI |
| **Primary source** | MGI:MGI:94906 |
| **See related** | Ensembl:ENSMUSG00000030409 |
| **Gene type** | protein coding |
| **RefSeq status** | REVIEWED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | DM; DMK; Dm15; MDPK; MT-PK |
| **Summary** | The protein encoded by this gene is a serine/threonine protein kinase that contains coiled-coil and C-terminal membrane association domains. In the embryonic mouse, it is found in cardiac and skeletal myocytes where it appears to play a role in myogenesis. In adults, the transcript is localized to several tissues including brain, heart, and skeletal and smooth muscle, and a function in cytoskeletal remodeling has been described. Transcripts with expanded CUG repeats in the 3' untranslated region mediate alternative splicing of several genes and sequester RNA binding proteins and RNA transcripts that contain CAG repeats, resulting in myotonic dystrophy, an autosomal dominant neuromuscular disorder. Alternative splicing results in multiple protein coding and non-coding transcript variants. [provided by RefSeq, Oct 2014] |
| **Expression** | Broad expression in heart adult (RPKM 189.9), bladder adult (RPKM 179.2) and 16 other tissues See more |
| **Orthologs** | human all |

### Genomic context

**Location:** 7 A3; 7 9.46 cM

See Dmpk in Genome Data Viewer

**Exon count:** 15

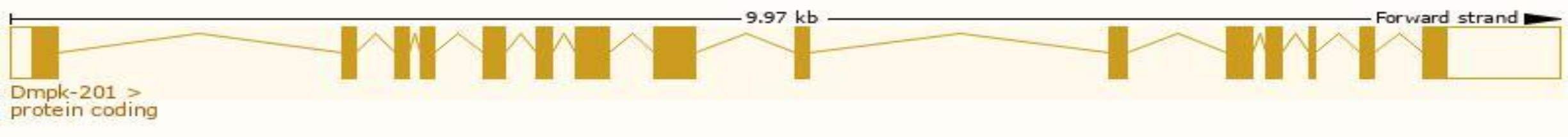
| Annotation release | Status | Assembly | Chr | Location |
|---|---|---|---|---|
| 108 | current | GRCm38.p6 (GCF_000001635.26) | 7 | NC_000073.6 (19083646..19093821) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 7 | NC_000073.5 (19669198..19679170) |

# Transcript information（Ensembl）

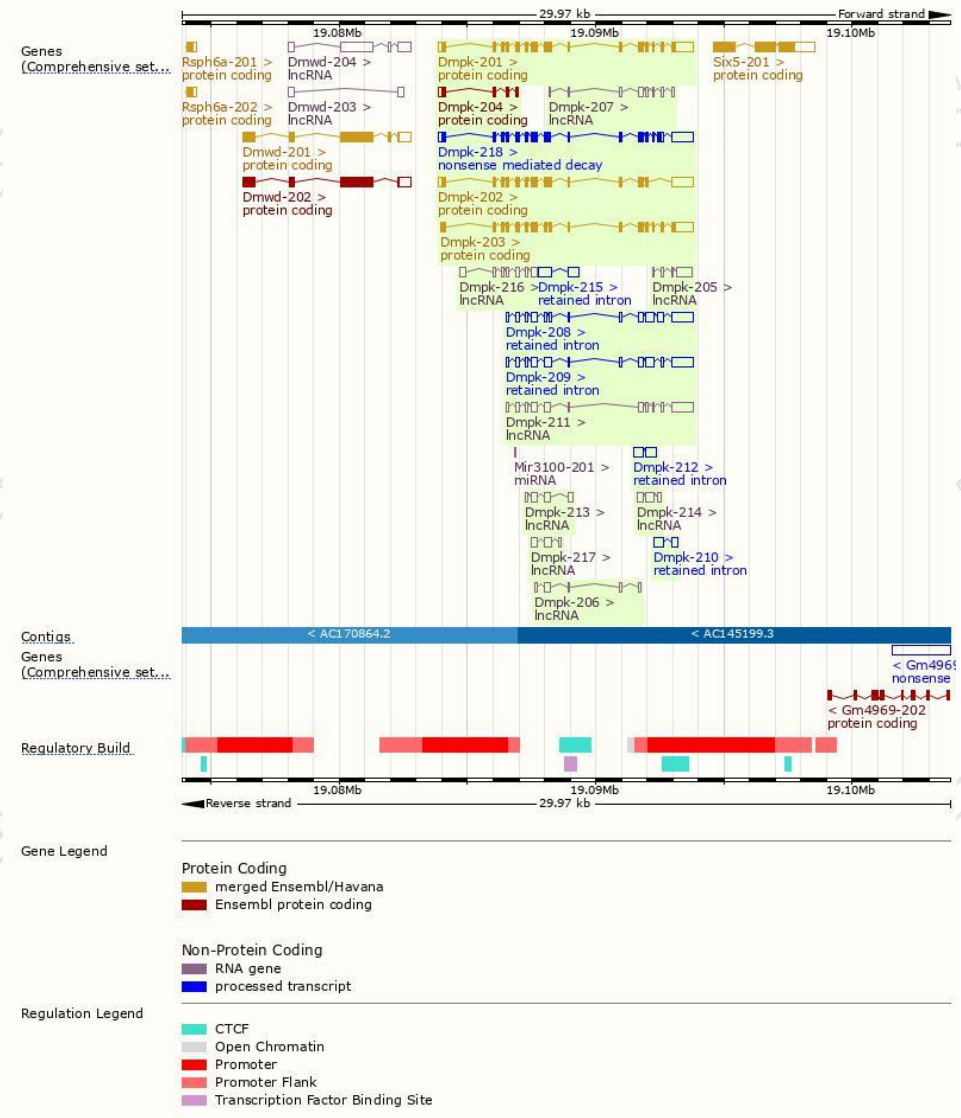
The gene has 18 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Dmpk-201 | ENSMUST00000032568.13 | 2761 | 631aa | Protein coding | CCDS39794 | P54265 | TSL:5 GENCODE basic APPRIS P3 |
| Dmpk-203 | ENSMUST00000108474.1 | 2591 | 605aa | Protein coding | CCDS52053 | E9Q6J9 | TSL:1 GENCODE basic APPRIS ALT2 |
| Dmpk-202 | ENSMUST00000108473.9 | 2588 | 537aa | Protein coding | CCDS52054 | P54265 | TSL:1 GENCODE basic APPRIS ALT2 |
| Dmpk-204 | ENSMUST00000122999.7 | 544 | 139aa | Protein coding | - | D3YYG5 | CDS 3' incomplete TSL:3 |
| Dmpk-218 | ENSMUST00000154199.7 | 2850 | 588aa | Nonsense mediated decay | - | D6RI32 | TSL:1 |
| Dmpk-208 | ENSMUST00000135839.7 | 2475 | No protein | Retained intron | - | - | TSL:1 |
| Dmpk-209 | ENSMUST00000137219.7 | 2433 | No protein | Retained intron | - | - | TSL:1 |
| Dmpk-215 | ENSMUST00000148472.1 | 967 | No protein | Retained intron | - | - | TSL:3 |
| Dmpk-212 | ENSMUST00000143938.1 | 785 | No protein | Retained intron | - | - | TSL:5 |
| Dmpk-210 | ENSMUST00000140742.1 | 592 | No protein | Retained intron | - | - | TSL:2 |
| Dmpk-211 | ENSMUST00000142725.7 | 2135 | No protein | lncRNA | - | - | TSL:1 |
| Dmpk-216 | ENSMUST00000149188.7 | 923 | No protein | lncRNA | - | - | TSL:5 |
| Dmpk-205 | ENSMUST00000126264.1 | 851 | No protein | lncRNA | - | - | TSL:3 |
| Dmpk-207 | ENSMUST00000132115.7 | 757 | No protein | lncRNA | - | - | TSL:5 |
| Dmpk-213 | ENSMUST00000147215.7 | 743 | No protein | lncRNA | - | - | TSL:3 |
| Dmpk-214 | ENSMUST00000148380.1 | 663 | No protein | lncRNA | - | - | TSL:3 |
| Dmpk-206 | ENSMUST00000128422.7 | 650 | No protein | lncRNA | - | - | TSL:3 |
| Dmpk-217 | ENSMUST00000152050.1 | 565 | No protein | lncRNA | - | - | TSL:3 |

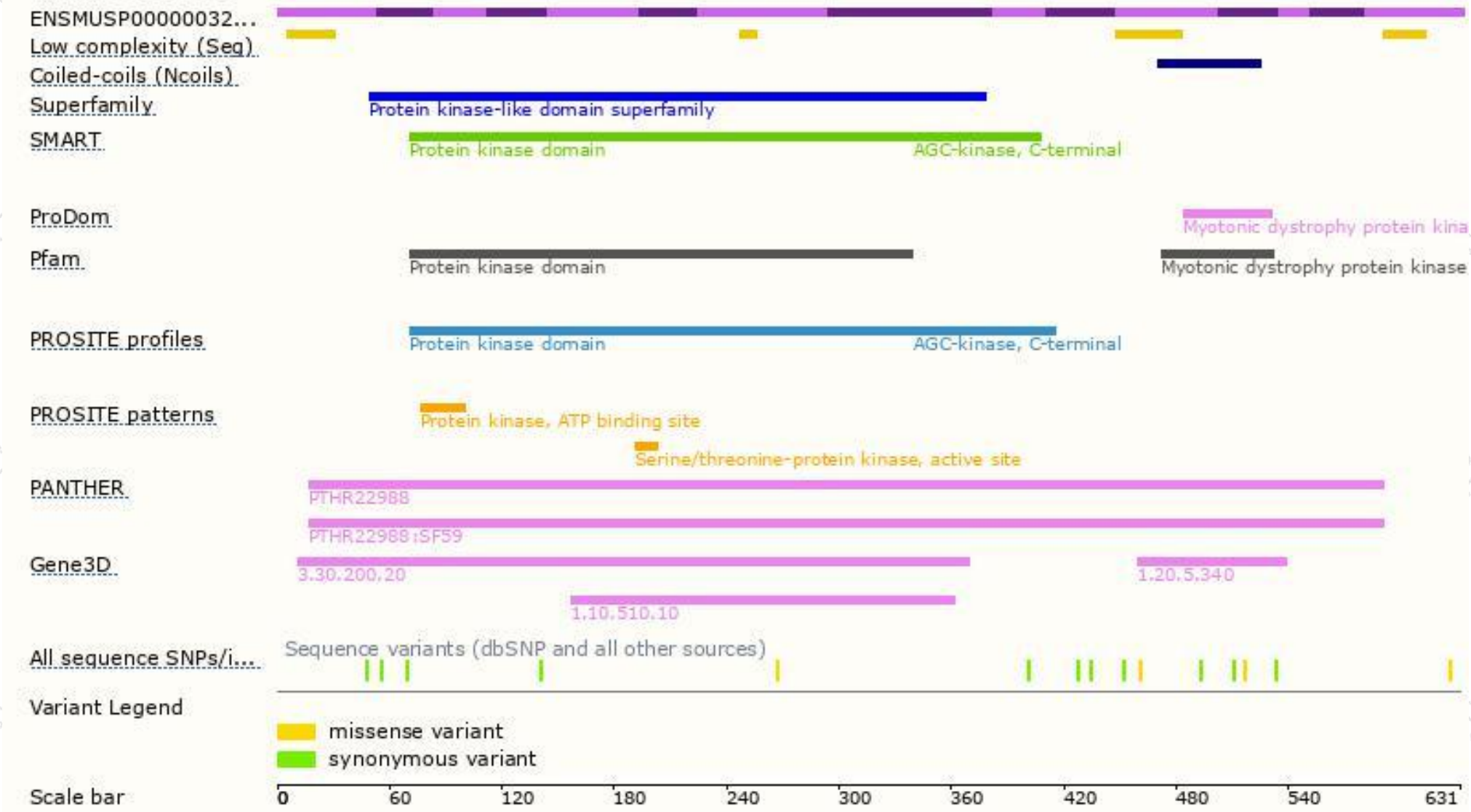
The strategy is based on the design of *Dmpk-201* transcript,The transcription is shown below



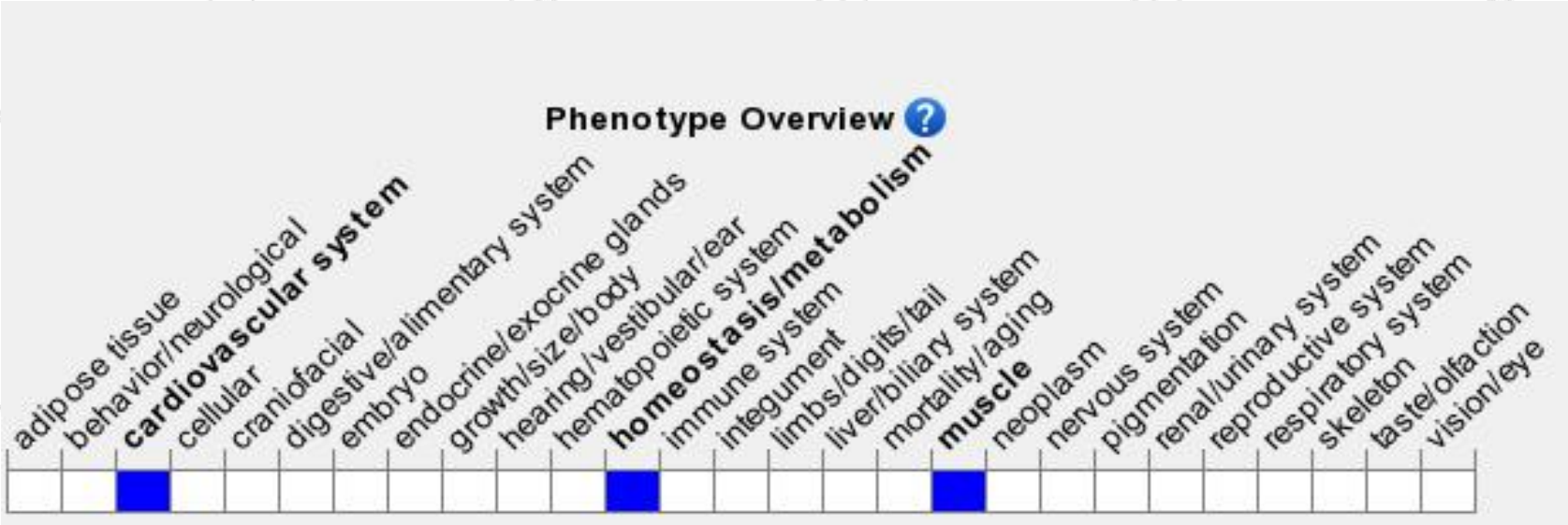
# Genomic location distribution



# 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,Homozygotes for a null mutation exhibit abnormal sodium channel gating in cardiac myocytes, cardiac conduction defects, and late-onset progressive skeletal myopathy. Homozygotes for a second null mutation do not develop skeletal myopathy but do have abnormal muscle intracellular calcium levels.

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

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