# *Myh14* Cas9-CKO Strategy

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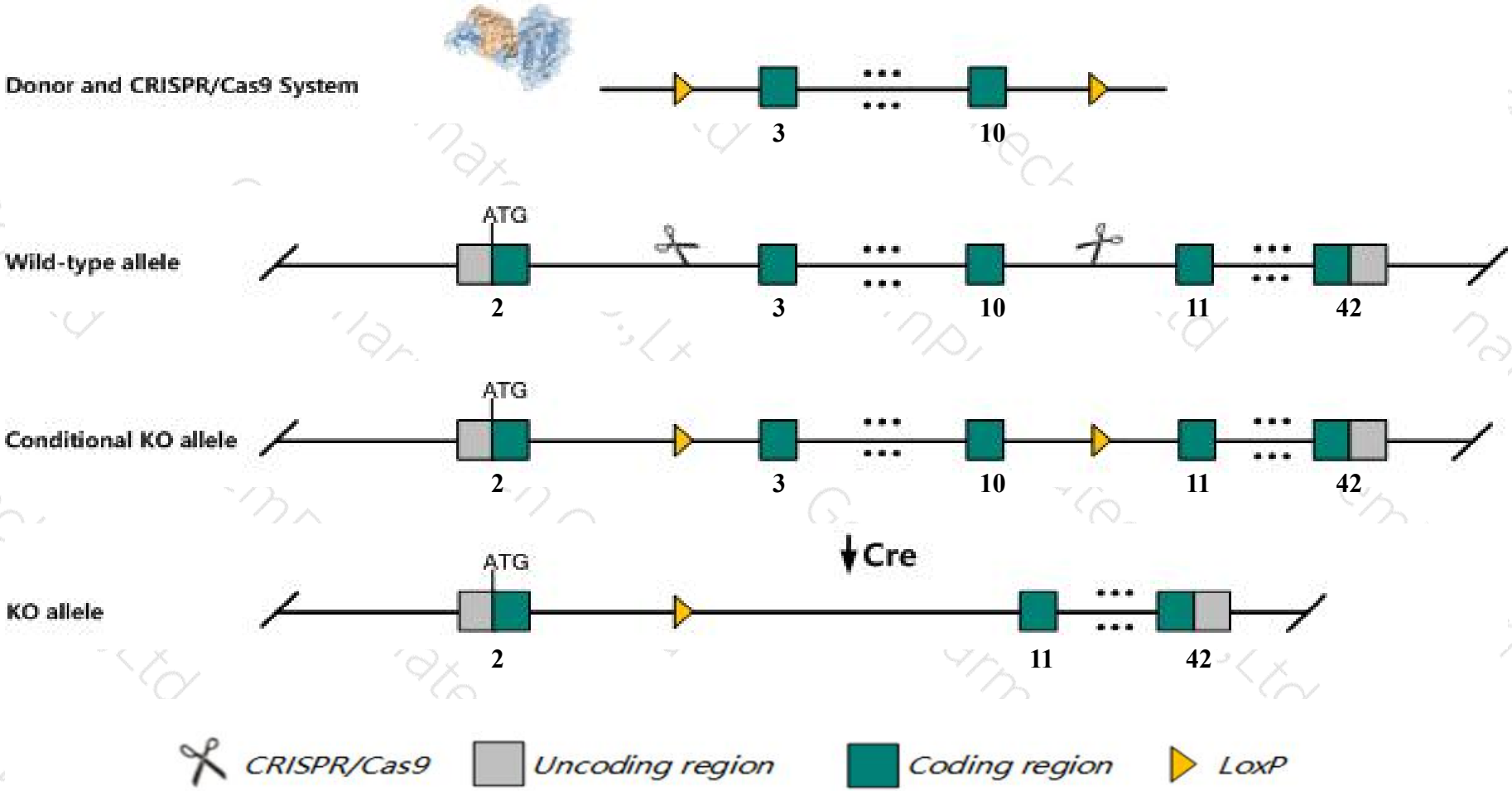
**Design Date:** 2020-1-31

# Project Overview

| | |
|---|---|
| **Project Name** | ***Myh14*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myh14* gene. The schematic diagram is as follows:



# Technical routes

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- The *Myh14* gene has 9 transcripts. According to the structure of *Myh14* gene, exon3-exon10 of *Myh14-201* (ENSMUST00000048102.14) transcript is recommended as the knockout region.The region contains 709bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Myh14* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele are healthy and survive to adulthood with no apparent defects. About 30% of knock-in mice either heterozygous or homozygous for a single amino acid mutation exhibit increased lymphoma incidence.

➢ Transcript *Myh14-207* may not be affected.

➢ The *Myh14* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# Gene information （NCBI）

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## Myh14 myosin, heavy polypeptide 14 [Mus musculus (house mouse)]

Gene ID: 71960, updated on 31-Jan-2019

### Summary

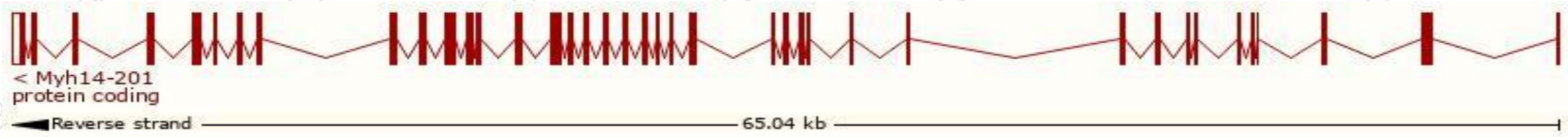
| | |
|---|---|
| **Official Symbol** | Myh14 provided by MGI |
| **Official Full Name** | myosin, heavy polypeptide 14 provided by MGI |
| **Primary source** | MGI:MGI:1919210 |
| **See related** | Ensembl:ENSMUSG00000030739 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | 2400004E04Rik, II-C, NHMCII, NMHC II-C |
| **Expression** | Biased expression in small intestine adult (RPKM 46.6), colon adult (RPKM 41.7) and 8 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

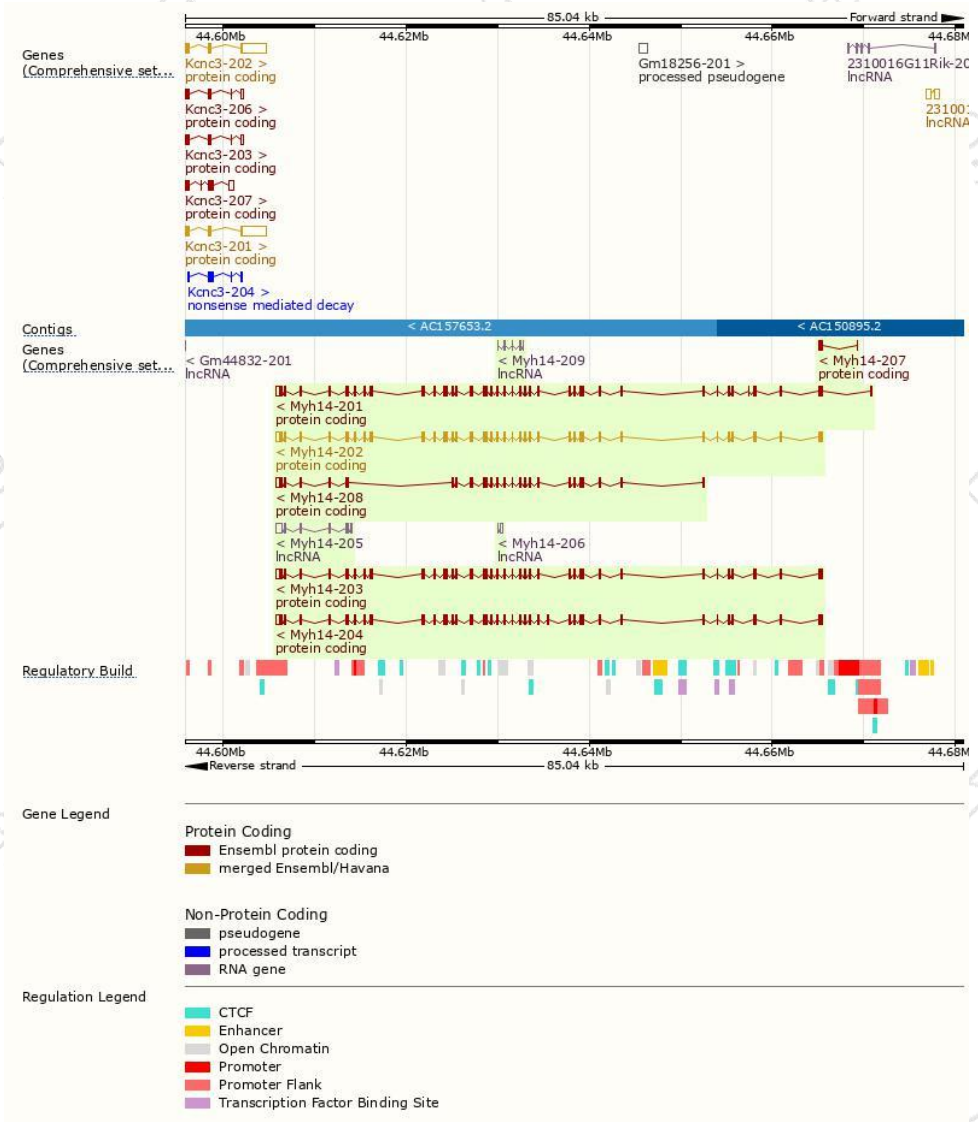
The gene has 9 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Myh14-201 | ENSMUST00000048102.14 | 6457 | 2000aa | Protein coding | CCDS71951 | Q6URW6 | TSL:1 GENCODE basic APPRIS ALT2 |
| Myh14-202 | ENSMUST00000107899.9 | 6390 | 1992aa | Protein coding | CCDS39943 | Q6URW6 | TSL:1 GENCODE basic APPRIS P3 |
| Myh14-204 | ENSMUST00000207775.1 | 6499 | 2033aa | Protein coding | - | Q6URW6 | TSL:5 GENCODE basic APPRIS ALT2 |
| Myh14-203 | ENSMUST00000107900.3 | 6400 | 2000aa | Protein coding | - | K3W4R2 | TSL:5 GENCODE basic APPRIS ALT2 |
| Myh14-208 | ENSMUST00000208200.1 | 4143 | 1245aa | Protein coding | - | A0A140LI60 | CDS 5' incomplete TSL:1 |
| Myh14-207 | ENSMUST00000208131.1 | 471 | 120aa | Protein coding | - | A0A140LHX1 | CDS 3' incomplete TSL:2 |
| Myh14-205 | ENSMUST00000208044.1 | 1438 | No protein | lncRNA | - | - | TSL:1 |
| Myh14-209 | ENSMUST00000209024.1 | 535 | No protein | lncRNA | - | - | TSL:3 |
| Myh14-206 | ENSMUST00000208085.1 | 380 | No protein | lncRNA | - | - | TSL:3 |

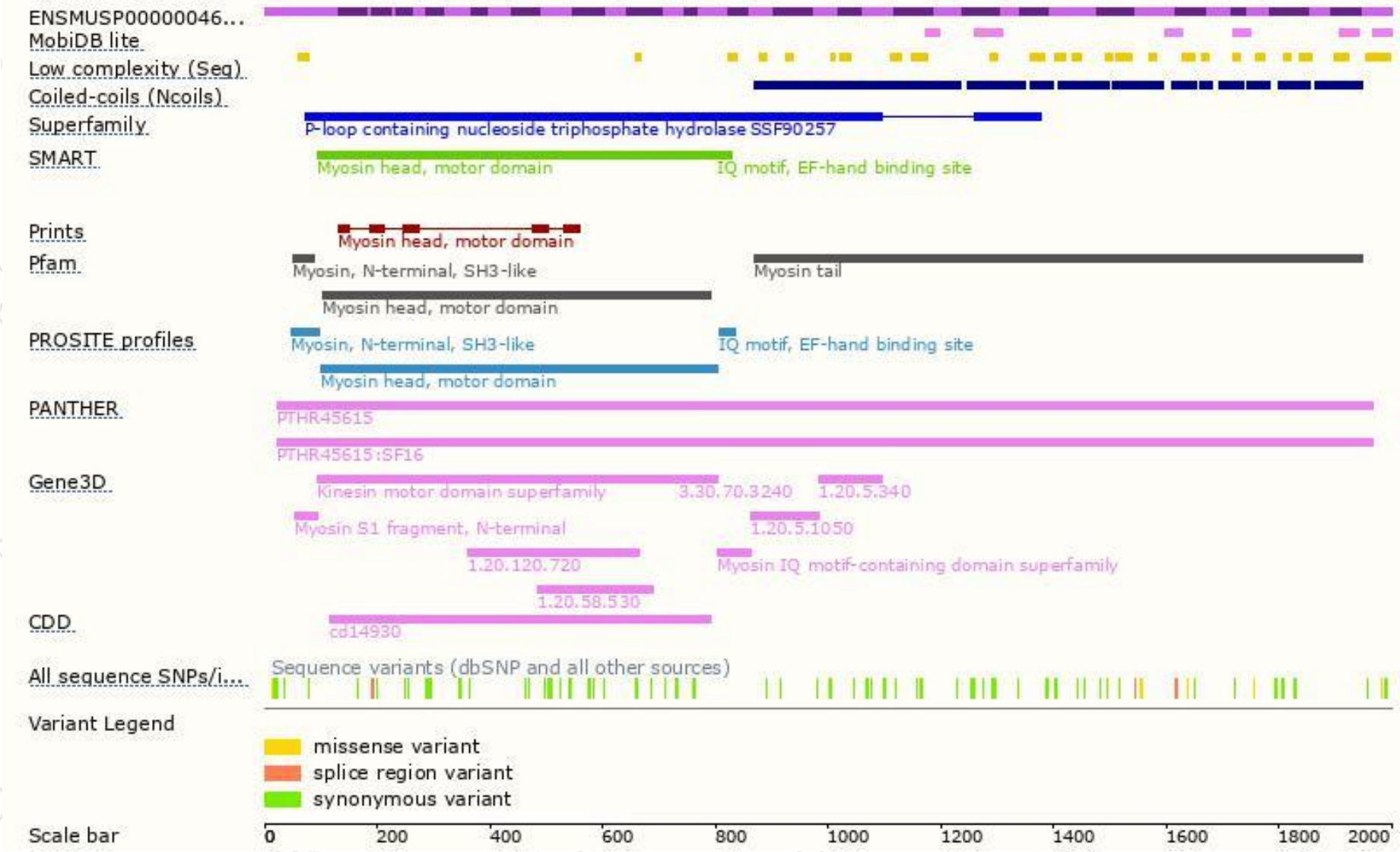
The strategy is based on the design of *Myh14-201* transcript,The transcription is shown below



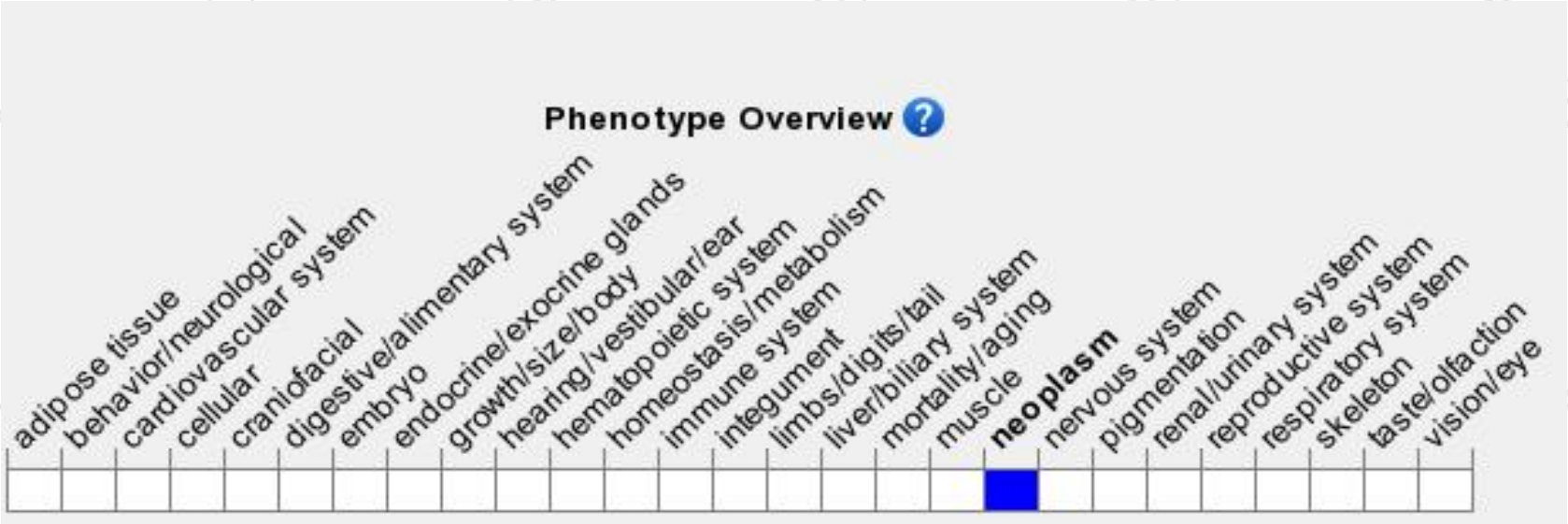
# Genomic location distribution



# 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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