# *Prokr2* Cas9-KO Strategy

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Design Date: 2019-8-5

# Project Overview

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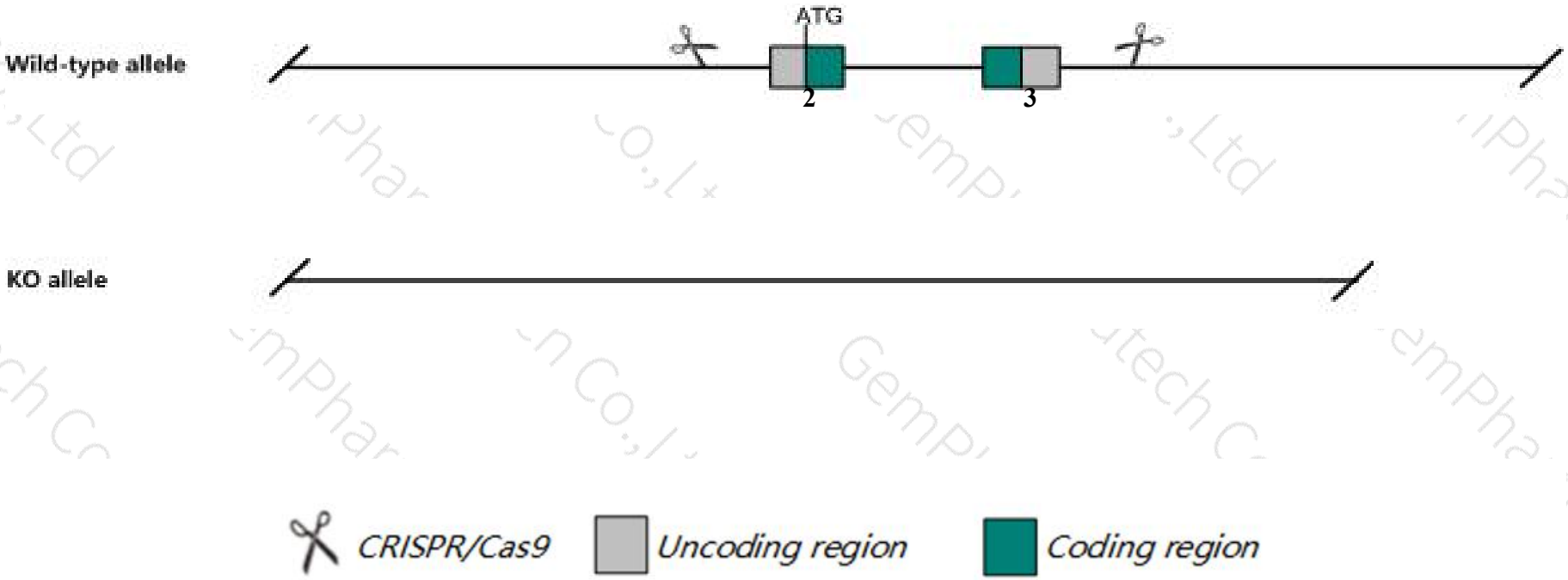
|---|---|
| **Project Name** | ***Prokr2*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prokr2* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Prokr2* gene has 5 transcripts. According to the structure of *Prokr2* gene, exon2-exon3 of *Prokr2-201* (ENSMUST00000049997.13) 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 *Prokr2* gene. The brief process is as follows: CRISPR/Cas9 systen

# Notice

- According to the existing MGI data,Homozygotes for a null allele show 50% neonatal lethality, olfactory bulb malformation, and reproductive system atrophy related to a lack of hypothalamic gonadotropin-releasing hormone synthesizing neurons. Homozygotes for another null allele show impaired circadian behavior and thermoregulation.

- The *Prokr2* gene is located on the Chr2. 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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## Prokr2 prokineticin receptor 2 [Mus musculus (house mouse)]

Gene ID: 246313, updated on 31-Jan-2019

### Summary

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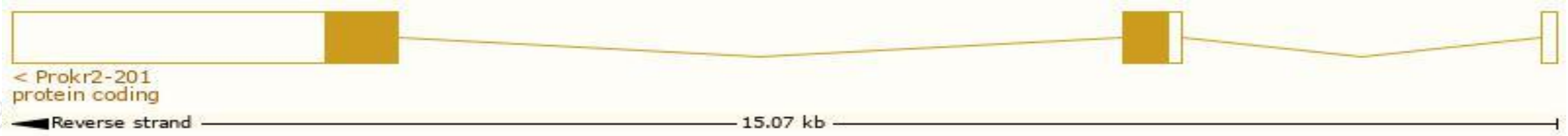
|---|---|
| **Official Symbol** | Prokr2 provided by MGI |
| **Official Full Name** | prokineticin receptor 2 provided by MGI |
| **Primary source** | MGI:MGI:2181363 |
| **See related** | Ensembl:ENSMUSG00000050558 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | B830005M06Rik, EG-VEGRF2, Gpcr73l1, Gpr73l1, PKR2 |
| **Expression** | Biased expression in frontal lobe adult (RPKM 1.4), CNS E18 (RPKM 1.3) and 7 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

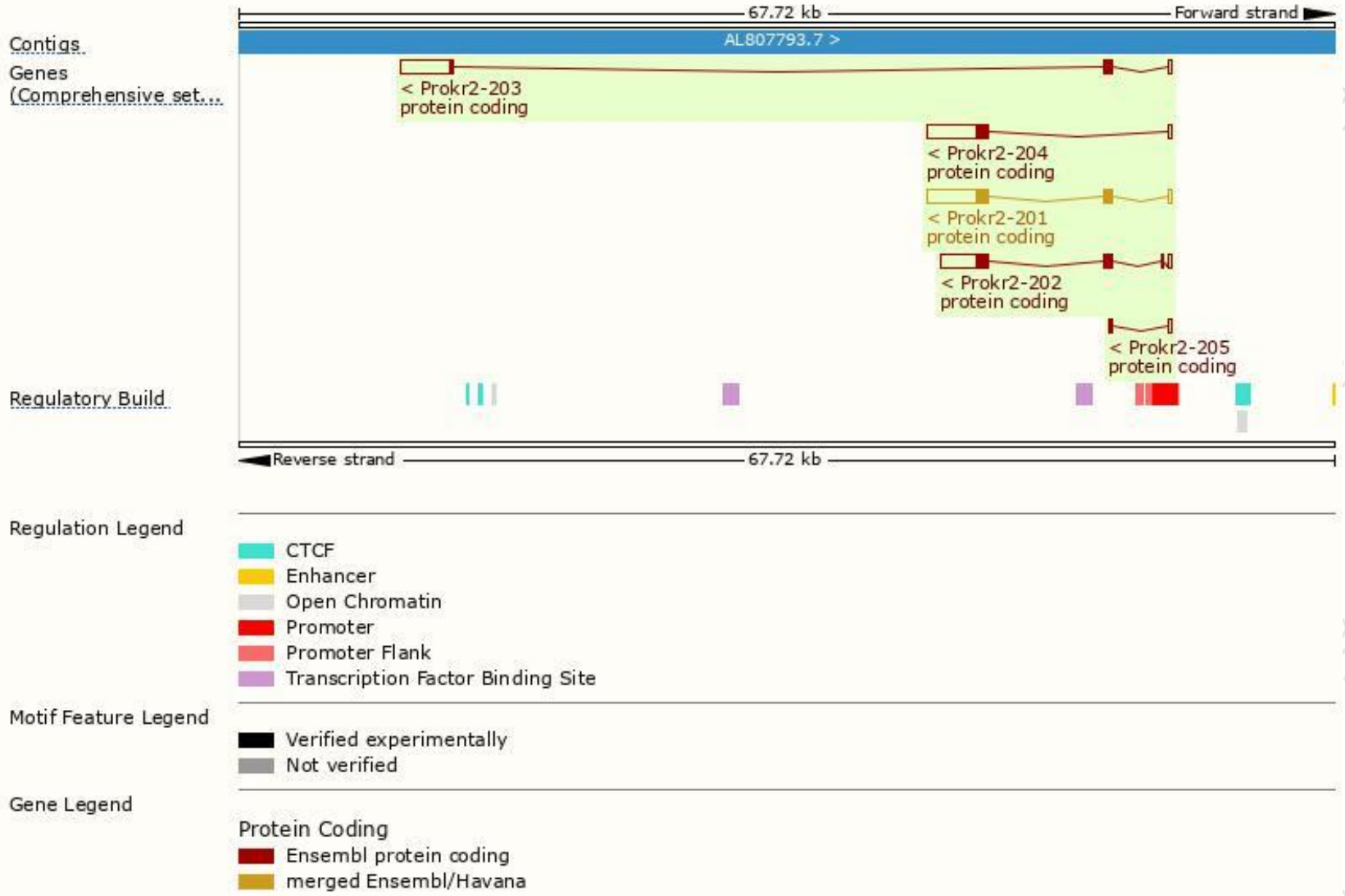
The gene has 5 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| **Prokr2-201** | ENSMUST00000049997.13 | 4486 | 381aa | Protein coding | CCDS16773 | Q8K458 | TSL:1 GENCODE basic APPRIS P1 |
| **Prokr2-202** | ENSMUST00000110156.1 | 3829 | 381aa | Protein coding | CCDS16773 | Q8K458 | TSL:5 GENCODE basic APPRIS P1 |
| **Prokr2-203** | ENSMUST00000110157.8 | 4005 | 198aa | Protein coding | - | A2AMQ7 | TSL:1 GENCODE basic |
| **Prokr2-204** | ENSMUST00000142766.1 | 3932 | 220aa | Protein coding | - | E0CY28 | TSL:1 GENCODE basic |
| **Prokr2-205** | ENSMUST00000145995.1 | 345 | 17aa | Protein coding | - | A2AMQ9 | CDS 3' incomplete TSL:3 |

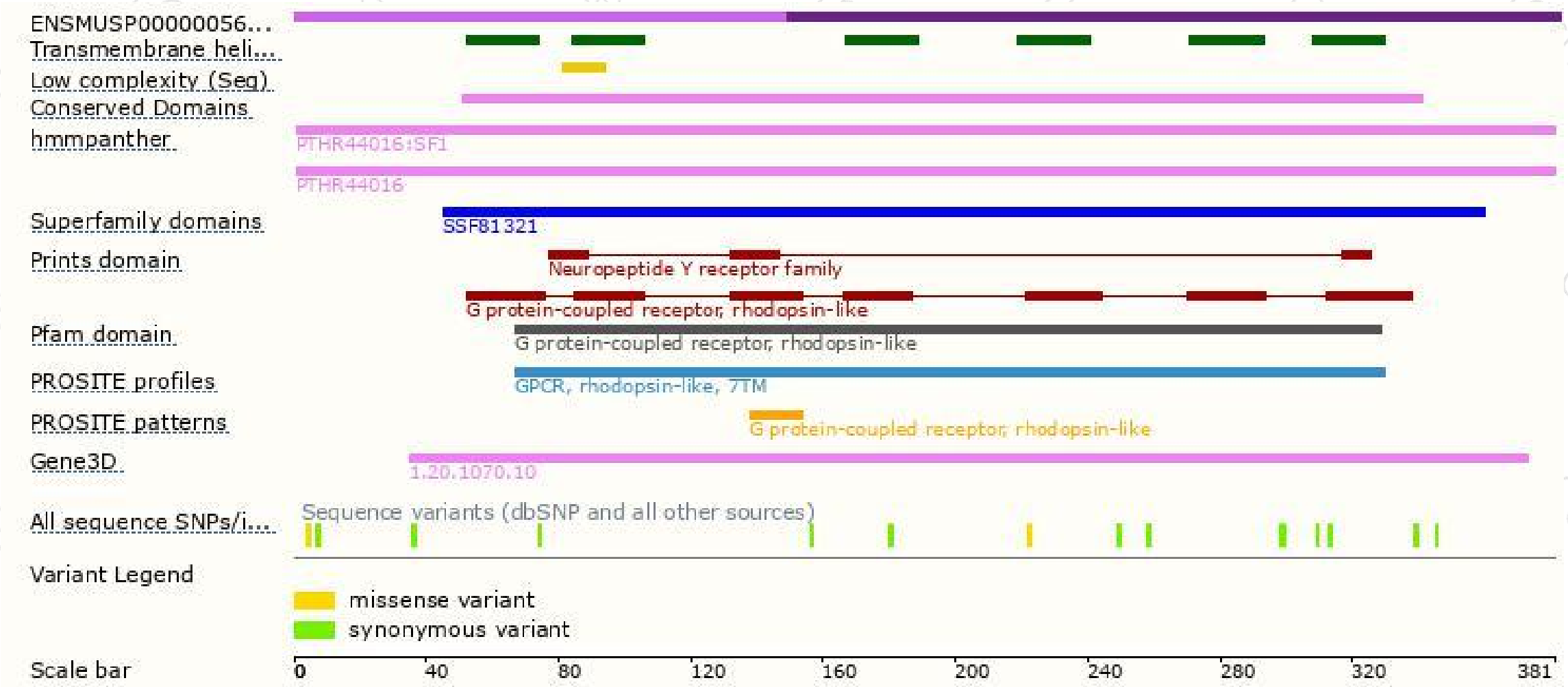
The strategy is based on the design of *Prokr2-201* transcript,The transcription is shown below



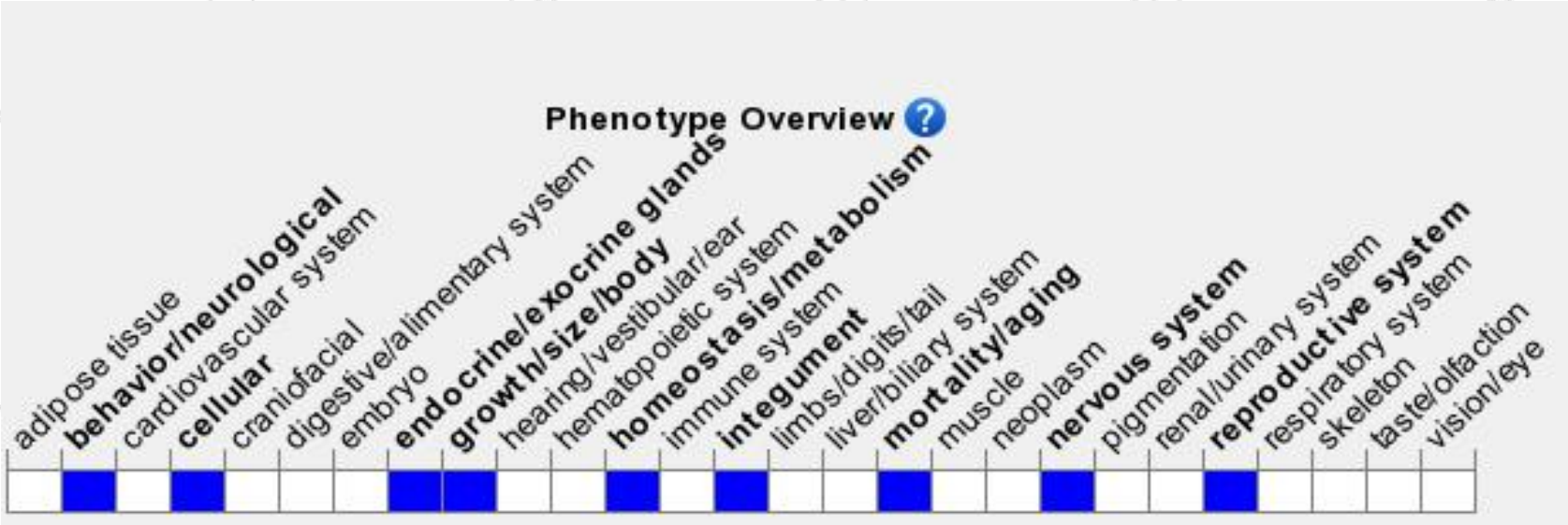
# Genomic location distribution



# 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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