

# *Cacna2d4* Cas9-KO Strategy

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Reviewer: Yanhua Shen

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# Project Overview

**Project Name**

***Cacna2d4***

**Project type**

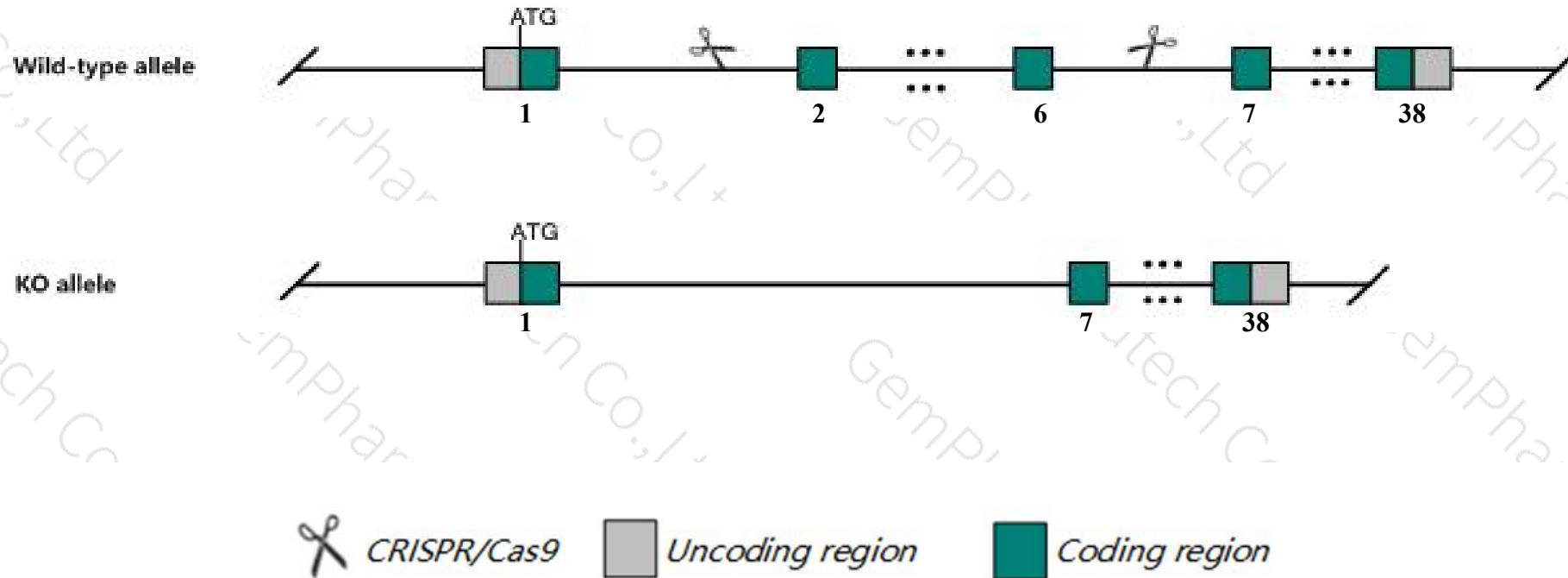
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cacna2d4* gene. The schematic diagram is as follows:



- The *Cacna2d4* gene has 10 transcripts. According to the structure of *Cacna2d4* gene, exon2-exon6 of *Cacna2d4-201* (ENSMUST00000037434.12) transcript is recommended as the knockout region. The region contains 554bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cacna2d4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a spontaneous mutation exhibit severe loss of retinal signaling associated with abnormal photoreceptor ribbon synapses and cone-rod dysfunction.
- Transcript *Cacna2d4*-202&203&204&206&207&208&210 may not be affected.
- The *Cacna2d4* gene is located on the Chr6. 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)

## Cacna2d4 calcium channel, voltage-dependent, alpha 2/delta subunit 4 [ *Mus musculus* (house mouse) ]

Gene ID: 319734, updated on 4-Jan-2020

### Summary

- Official Symbol** Cacna2d4 provided by [MGI](#)
- Official Full Name** calcium channel, voltage-dependent, alpha 2/delta subunit 4 provided by [MGI](#)
- Primary source** [MGI:MGI:2442632](#)
- See related** [Ensembl:ENSMUSG000000041460](#)
- 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** BE686333; 5730412N02Rik
- Expression** Biased expression in thymus adult (RPKM 2.1), lung adult (RPKM 0.6) and 5 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 6; 6 F1 See Cacna2d4 in [Genome Data Viewer](#)

**Exon count:** 40

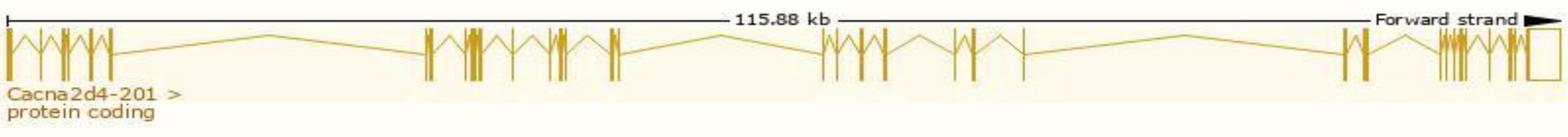
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	6	NC_000072.6 (119236524..119352407)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	6	NC_000072.5 (119186544..119302425)

# Transcript information (Ensembl)

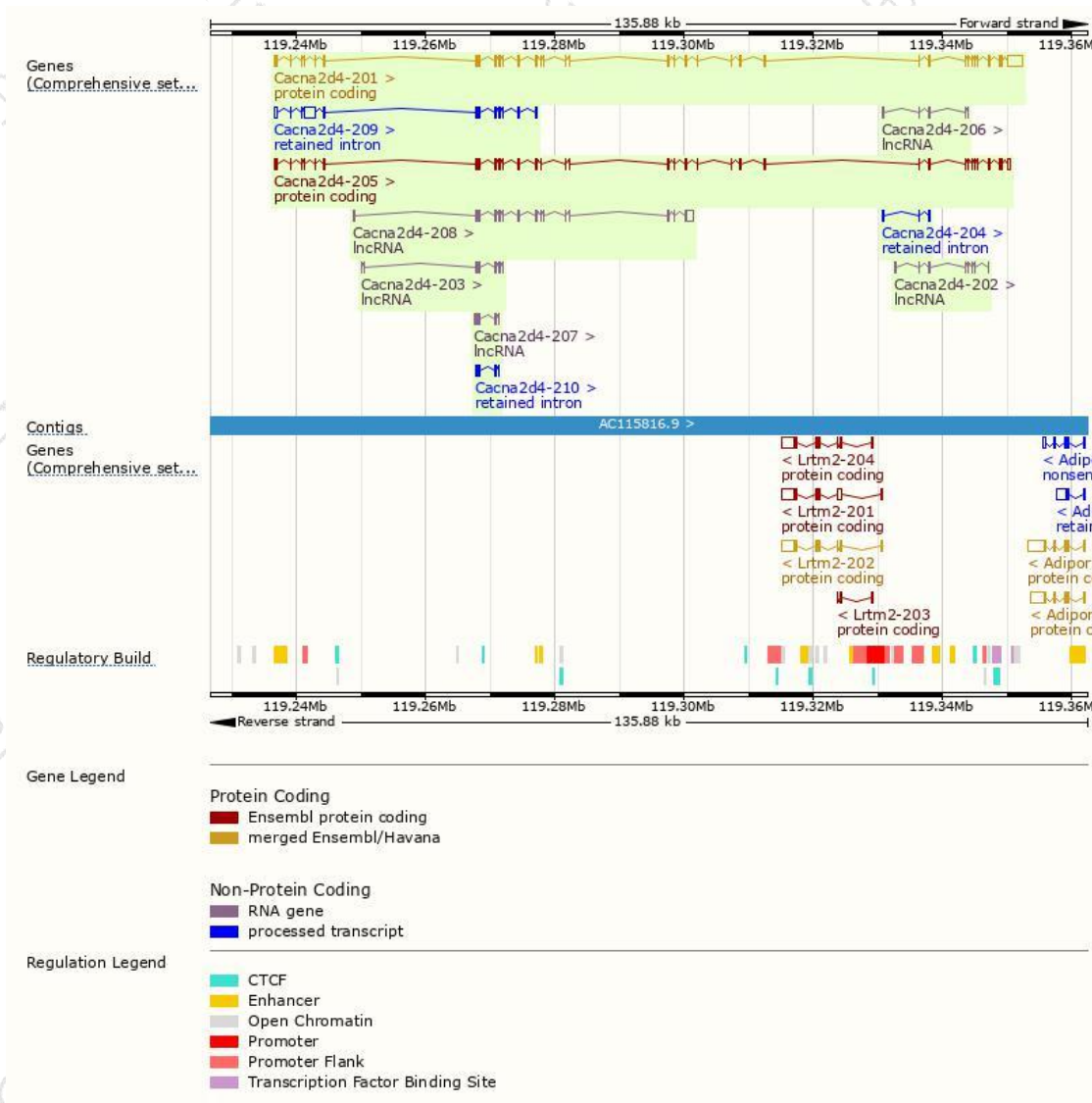
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cacna2d4-201	<a href="#">ENSMUST00000037434.12</a>	5803	<a href="#">1144aa</a>	Protein coding	<a href="#">CCDS51886</a>	<a href="#">F8VPL1</a>	TSL:2 GENCODE basic APPRIS P3
Cacna2d4-205	<a href="#">ENSMUST00000186622.1</a>	3710	<a href="#">1119aa</a>	Protein coding	<a href="#">CCDS85143</a>	<a href="#">A0A087WQH4</a>	TSL:1 GENCODE basic APPRIS ALT2
Cacna2d4-209	<a href="#">ENSMUST00000190015.6</a>	3229	No protein	Retained intron	-	-	TSL:1
Cacna2d4-204	<a href="#">ENSMUST00000186203.6</a>	419	No protein	Retained intron	-	-	TSL:3
Cacna2d4-210	<a href="#">ENSMUST00000191331.1</a>	414	No protein	Retained intron	-	-	TSL:2
Cacna2d4-208	<a href="#">ENSMUST00000188239.6</a>	2578	No protein	lncRNA	-	-	TSL:1
Cacna2d4-202	<a href="#">ENSMUST00000185965.1</a>	761	No protein	lncRNA	-	-	TSL:3
Cacna2d4-203	<a href="#">ENSMUST00000186176.6</a>	748	No protein	lncRNA	-	-	TSL:3
Cacna2d4-206	<a href="#">ENSMUST00000186702.6</a>	448	No protein	lncRNA	-	-	TSL:3
Cacna2d4-207	<a href="#">ENSMUST00000187222.6</a>	404	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Cacna2d4-201* transcript,The transcription is shown below

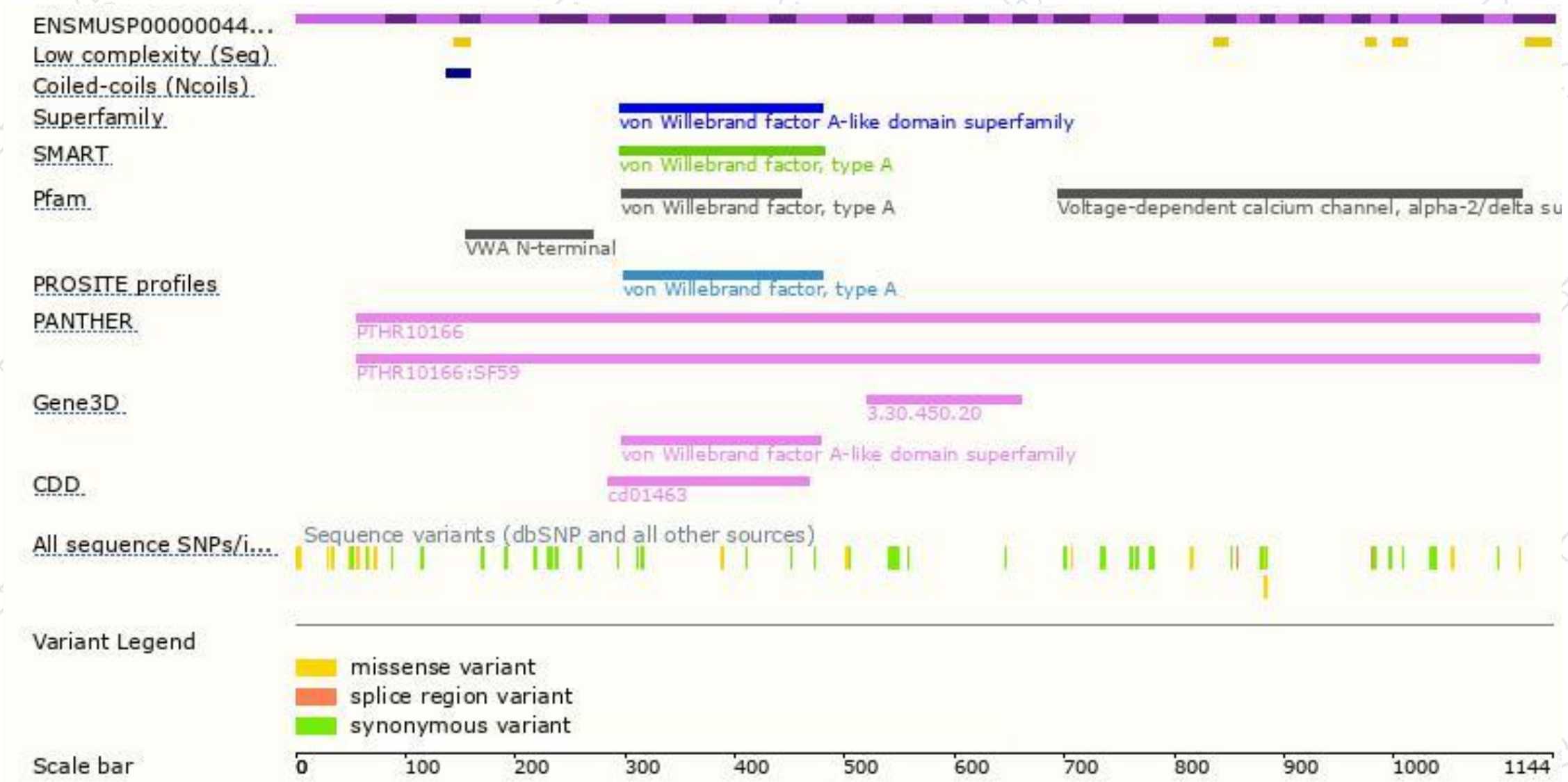


# Genomic location distribution

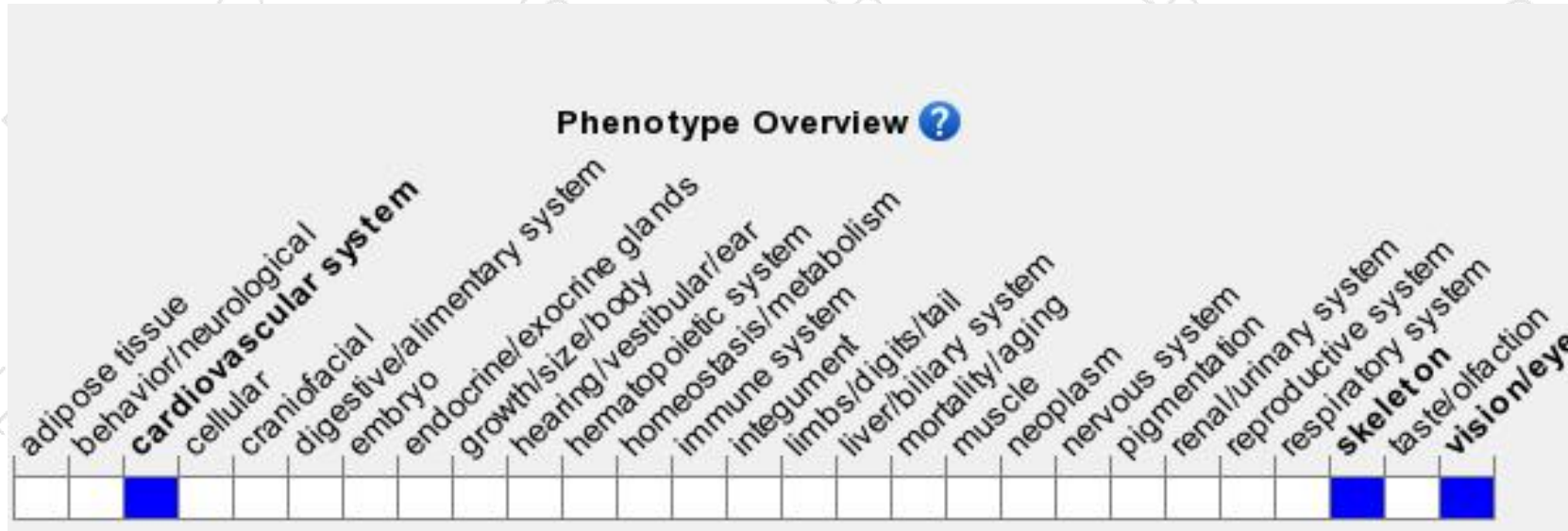




# Protein domain



# 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 spontaneous mutation exhibit severe loss of retinal signaling associated with abnormal photoreceptor ribbon synapses and cone-rod dysfunction.

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

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