

# *Cacna2d2* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Cacna2d2***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cacna2d2* gene. The schematic diagram is as follows:



- The *Cacna2d2* gene has 10 transcripts. According to the structure of *Cacna2d2* gene, exon4-exon23 of *Cacna2d2*-205 (ENSMUST00000168532.7) transcript is recommended as the knockout region. The region contains 1600bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cacna2d2* gene. The brief process is as follows: CRISPR/Cas9 sys

- According to the existing MGI data, Homozygotes for different mutant alleles show variable movement abnormalities including waddling, reeling or very slow gait, ataxia, and mild spike-wave seizures. While gross CNS abnormalities and demyelination are present in some mutant lines, they are not observed in others.
- Transcript *Cacna2d2*-206&210 may not be affected.
- The *Cacna2d2* gene is located on the Chr9. 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)

## Cacna2d2 calcium channel, voltage-dependent, alpha 2/delta subunit 2 [ *Mus musculus* (house mouse) ]

Gene ID: 56808, updated on 11-Sep-2019

### Summary

**Official Symbol** Cacna2d2 provided by [MGI](#)  
**Official Full Name** calcium channel, voltage-dependent, alpha 2/delta subunit 2 provided by [MGI](#)  
**Primary source** [MGI:MGI:1929813](#)  
**See related** [Ensembl:ENSMUSG00000010066](#)  
**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** du; td; a2d2; torpid; Cacna2d; mKIAA0558  
**Expression** Biased expression in cerebellum adult (RPKM 24.9), whole brain E14.5 (RPKM 22.0) and 10 other tissues [See more](#)  
**Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 9 F1; 9 58.02 cM

See Cacna2d2 in [Genome Data Viewer](#)

**Exon count:** 39

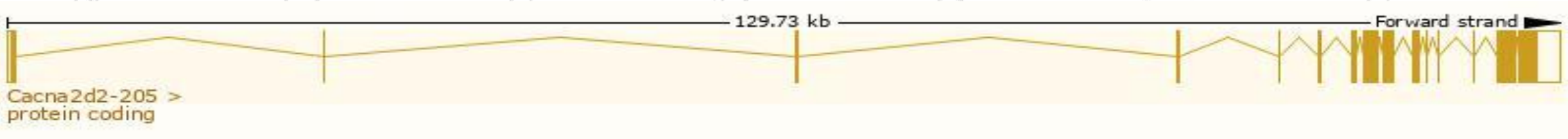
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	9	NC_000075.6 (107399733..107529346)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	9	NC_000075.5 (107302211..107431674)

# Transcript information (Ensembl)

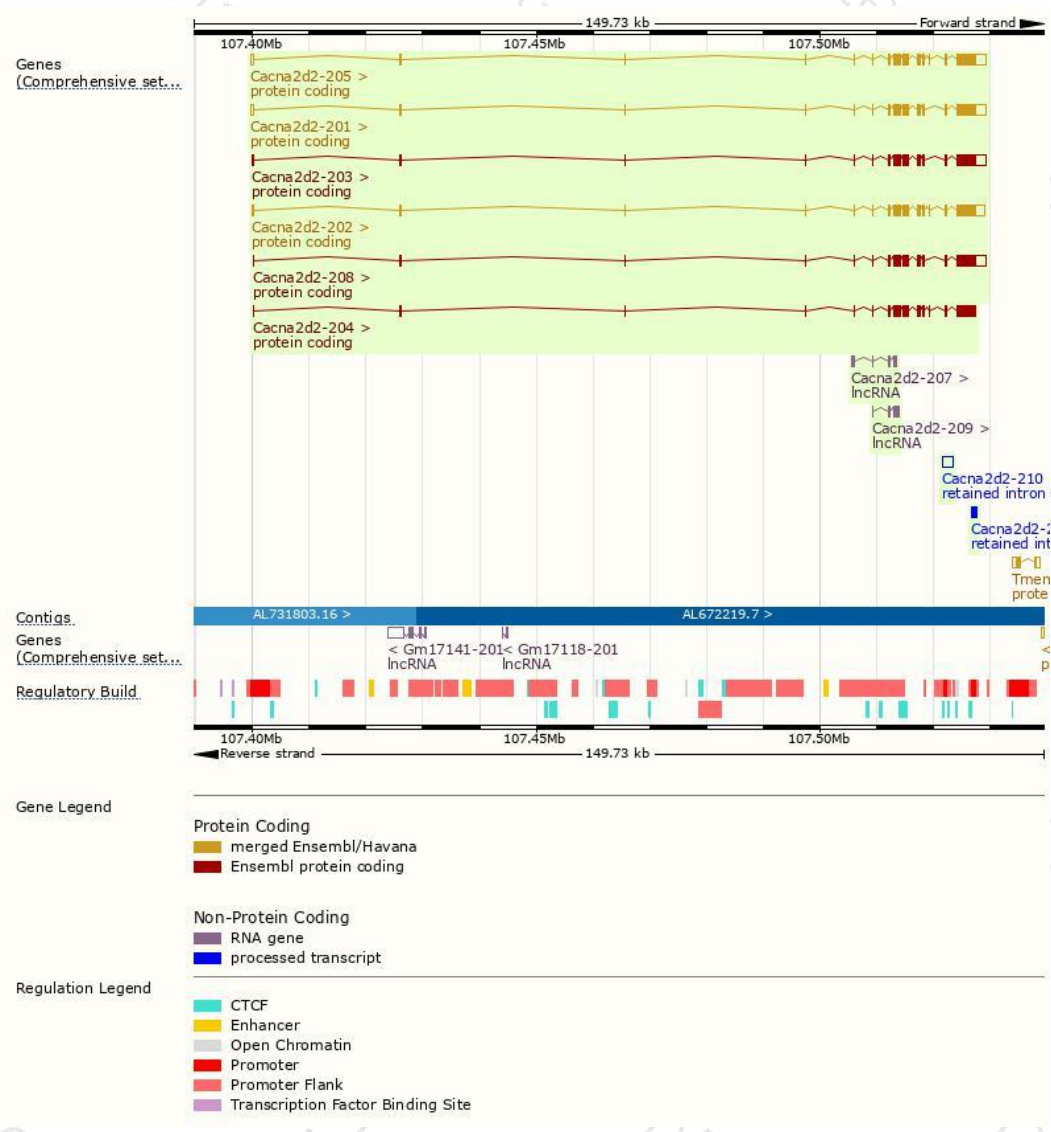
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cacna2d2-205	<a href="#">ENSMUST00000168532.7</a>	5807	<a href="#">1156aa</a>	Protein coding	<a href="#">CCDS72304</a>	<a href="#">Q6PHS9</a>	TSL:1 GENCODE basic APPRIS ALT 2
Cacna2d2-201	<a href="#">ENSMUST0000010210.12</a>	5783	<a href="#">1148aa</a>	Protein coding	<a href="#">CCDS52917</a>	<a href="#">Q6PHS9</a>	TSL:1 GENCODE basic APPRIS ALT 2
Cacna2d2-208	<a href="#">ENSMUST00000170737.2</a>	5332	<a href="#">1150aa</a>	Protein coding	<a href="#">CCDS72305</a>	<a href="#">Q6PHS9</a>	TSL:1 GENCODE basic APPRIS ALT 2
Cacna2d2-202	<a href="#">ENSMUST00000085092.11</a>	5183	<a href="#">1154aa</a>	Protein coding	<a href="#">CCDS52916</a>	<a href="#">Q6PHS9</a>	TSL:5 GENCODE basic APPRIS P4
Cacna2d2-203	<a href="#">ENSMUST00000164988.8</a>	5542	<a href="#">1157aa</a>	Protein coding	-	<a href="#">E9Q683</a>	TSL:5 GENCODE basic APPRIS ALT 2
Cacna2d2-204	<a href="#">ENSMUST00000166799.7</a>	3474	<a href="#">1157aa</a>	Protein coding	-	<a href="#">Q6PHS9</a>	TSL:5 GENCODE basic APPRIS ALT 2
Cacna2d2-210	<a href="#">ENSMUST00000194842.1</a>	1975	No protein	Retained intron	-	-	TSL:NA
Cacna2d2-206	<a href="#">ENSMUST00000168959.1</a>	604	No protein	Retained intron	-	-	TSL:3
Cacna2d2-209	<a href="#">ENSMUST00000171809.1</a>	727	No protein	lncRNA	-	-	TSL:3
Cacna2d2-207	<a href="#">ENSMUST00000169354.7</a>	671	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Cacna2d2-205* transcript,The transcription is shown below

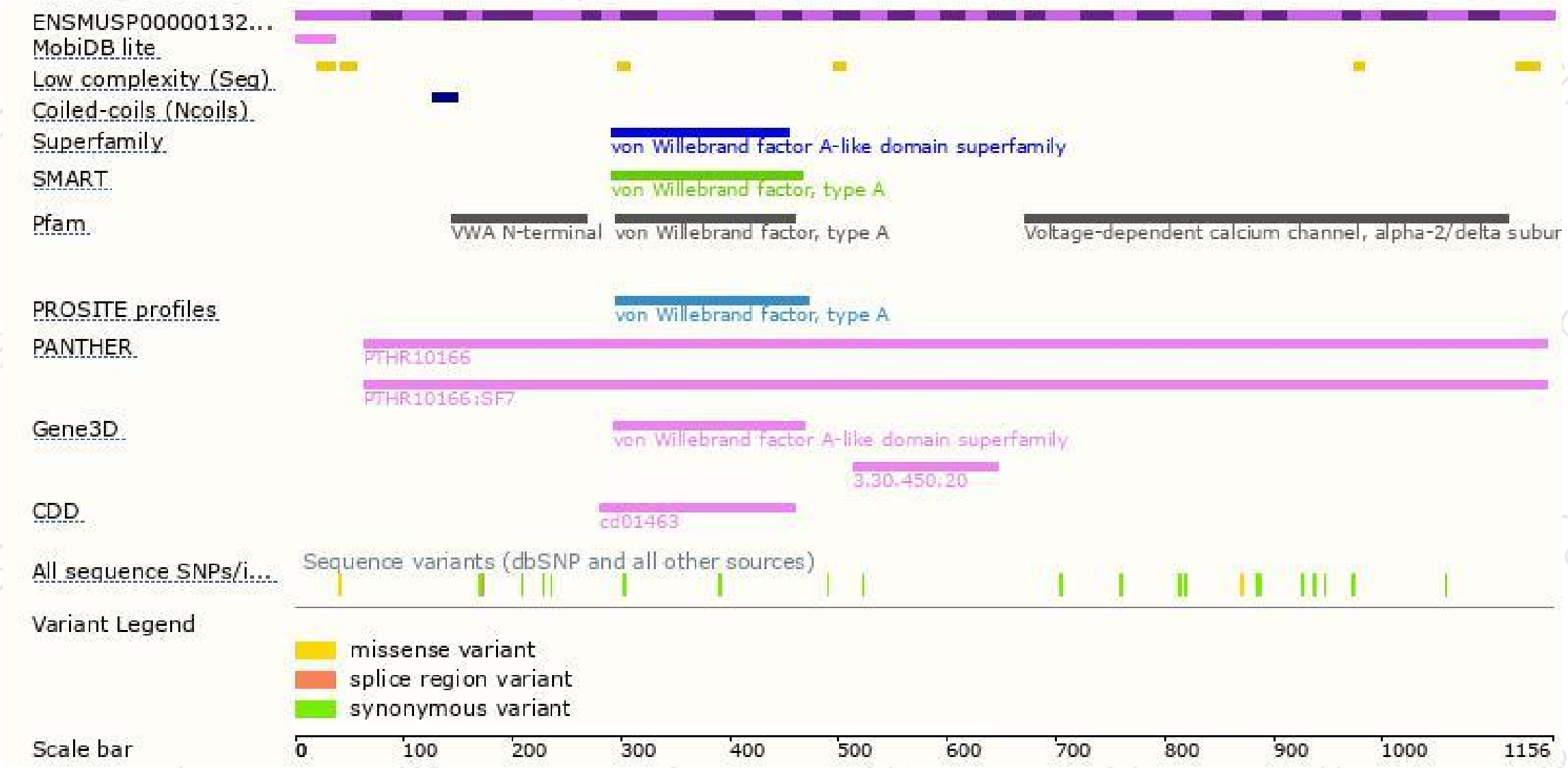


# Genomic location distribution

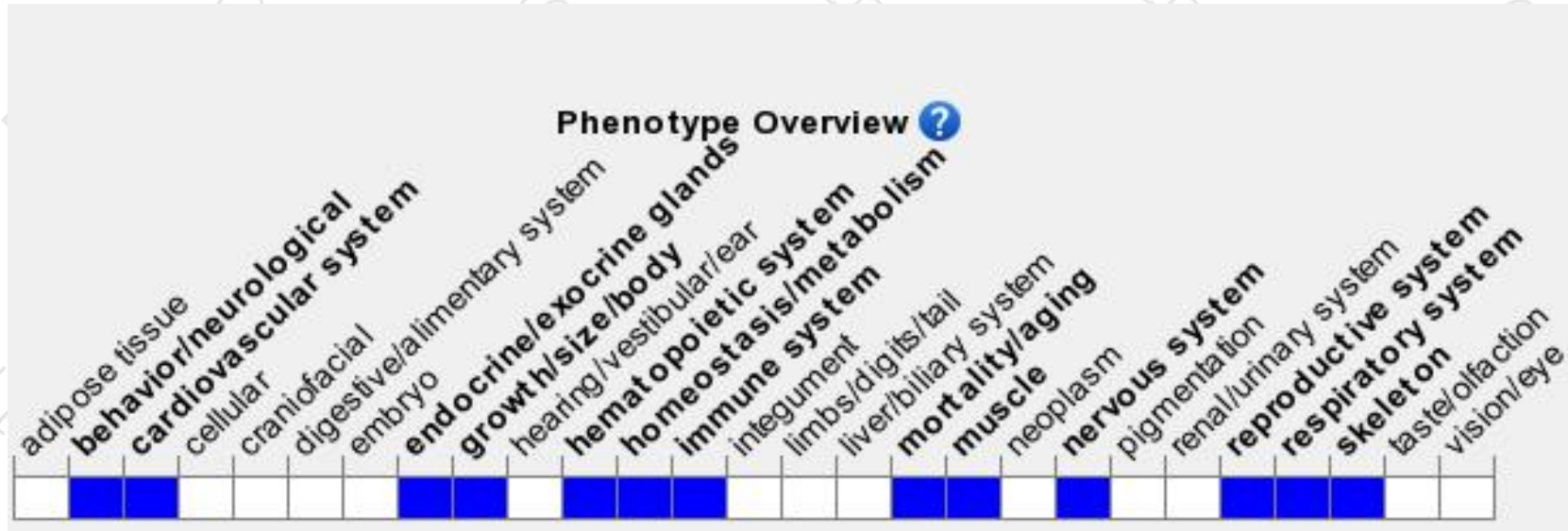




# Protein domain



# 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 different mutant alleles show variable movement abnormalities including waddling, reeling or very slow gait, ataxia, and mild spike-wave seizures. While gross CNS abnormalities and demyelination are present in some mutant lines, they are not observed in others.

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

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