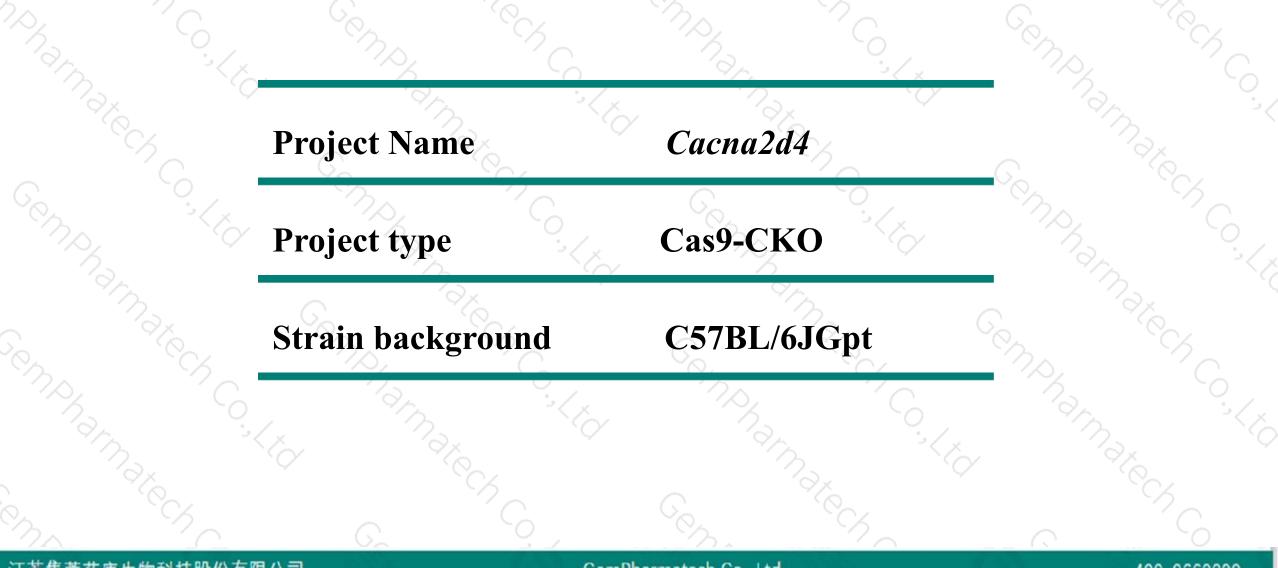


# Cacna2d4 Cas9-CKO Strategy

Designer:Xueting Zhang Reviwer:Yanhua Shen Date:2020-02-20

# **Project Overview**





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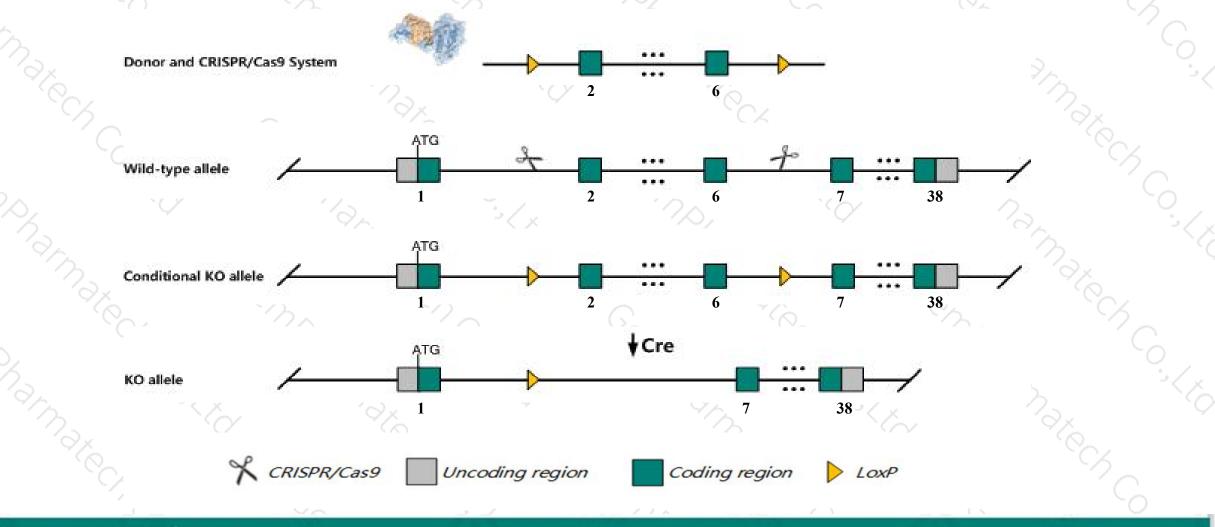
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### **Conditional Knockout strategy**



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



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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 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.



- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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

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Official Full Namecalcium channel, voltage-dependent, alpha 2/delta subunit 4 provided by MGIPrimary sourceMGI:MGI:2442632See relatedEnsembl:ENSMUSG0000041460Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; MusAlso known asBE686333; 5730412N02RikExpressionBiased expression in thymus adult (RPKM 2.1), lung adult (RPKM 0.6) and 5 other tissues See more human all	Official Symbol	Cacna2d4 provided by MGI
See related       Ensembl:ENSMUSG0000041460         Gene type       protein coding         RefSeq status       VALIDATED         Organism       Mus musculus         Lineage       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; 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	Official Full Name	calcium channel, voltage-dependent, alpha 2/delta subunit 4 provided by MGI
Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Murinae; Mus; MusAlso known asBE686333; 5730412N02RikExpressionBiased expression in thymus adult (RPKM 2.1), lung adult (RPKM 0.6) and 5 other tissues See more	Primary source	MGI:MGI:2442632
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	See related	Ensembl:ENSMUSG00000041460
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	Gene type	protein coding
Lineage       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; 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	RefSeq status	VALIDATED
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 <u>See more</u>	Organism	Mus musculus
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	Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Expression Biased expression in thymus adult (RPKM 2.1), lung adult (RPKM 0.6) and 5 other tissues See more		Muroidea; Muridae; Murinae; Mus; Mus
	Also known as	BE686333; 5730412N02Rik
Orthologs human all	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

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See Cacna2d4 in Genome Data Viewer

Location: 6; 6 F1

Exon count: 40

 Annotation release
 Status
 Assembly
 Chr
 Location

 108
 current
 GRCm38.p6 (GCF\_000001635.26)
 6
 NC\_000072.6 (119236524..119352407)

 Build 37.2
 previous assembly
 MGSCv37 (GCF\_000001635.18)
 6
 NC\_000072.5 (119186544..119302425)

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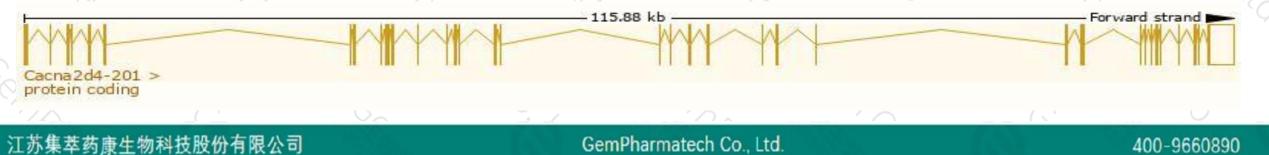
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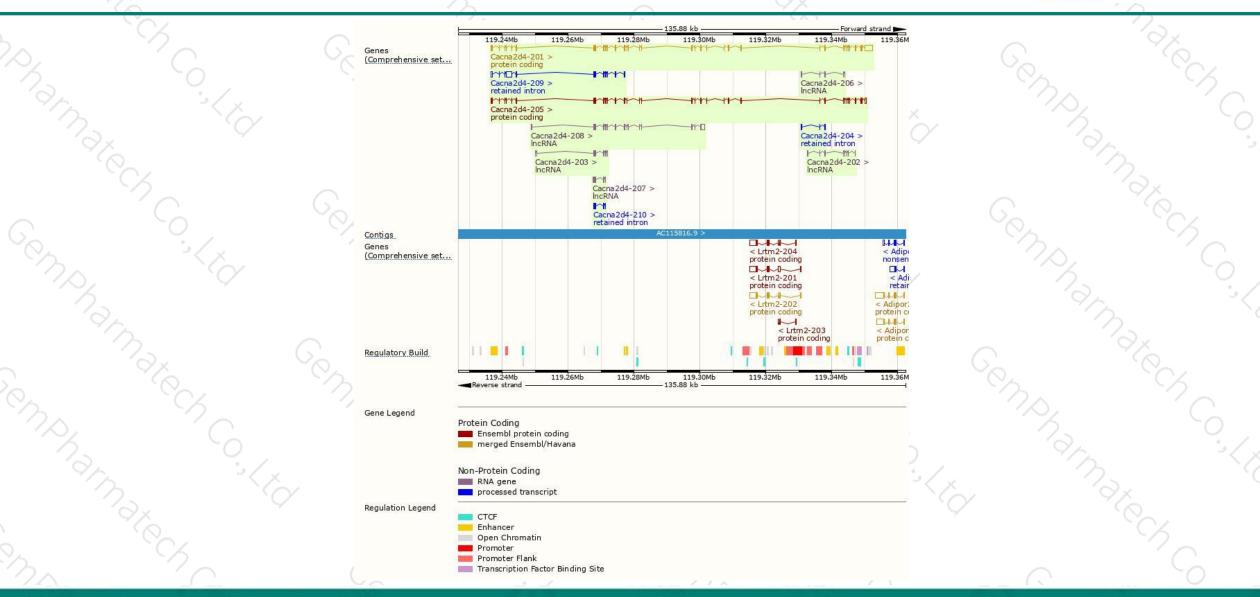
### The gene has 10 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cacna2d4-201	ENSMUST00000037434.12	5803	<u>1144aa</u>	Protein coding	CCDS51886	F8VPL1	TSL:2 GENCODE basic APPRIS P3
Cacna2d4-205	ENSMUST00000186622.1	3710	<u>1119aa</u>	Protein coding	CCDS85143	A0A087WQH4	TSL:1 GENCODE basic APPRIS ALT2
Cacna2d4-209	ENSMUST00000190015.6	3229	No protein	Retained intron	(44)	(2)	TSL:1
Cacna2d4-204	ENSMUST00000186203.6	419	No protein	Retained intron	1.20	323	TSL:3
Cacna2d4-210	ENSMUST00000191331.1	414	No protein	Retained intron			TSL:2
Cacna2d4-208	ENSMUST00000188239.6	2578	No protein	IncRNA	-	1.0	TSL:1
Cacna2d4-202	ENSMUST00000185965.1	761	No protein	IncRNA	(12)	(2)	TSL:3
Cacna2d4-203	ENSMUST00000186176.6	748	No protein	IncRNA	19 <u>9</u> 0	323	TSL:3
Cacna2d4-206	ENSMUST00000186702.6	448	No protein	IncRNA	1.51	1.57	TSL:3
Cacna2d4-207	ENSMUST00000187222.6	404	No protein	IncRNA	19	240	TSL:3

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



### **Genomic location distribution**



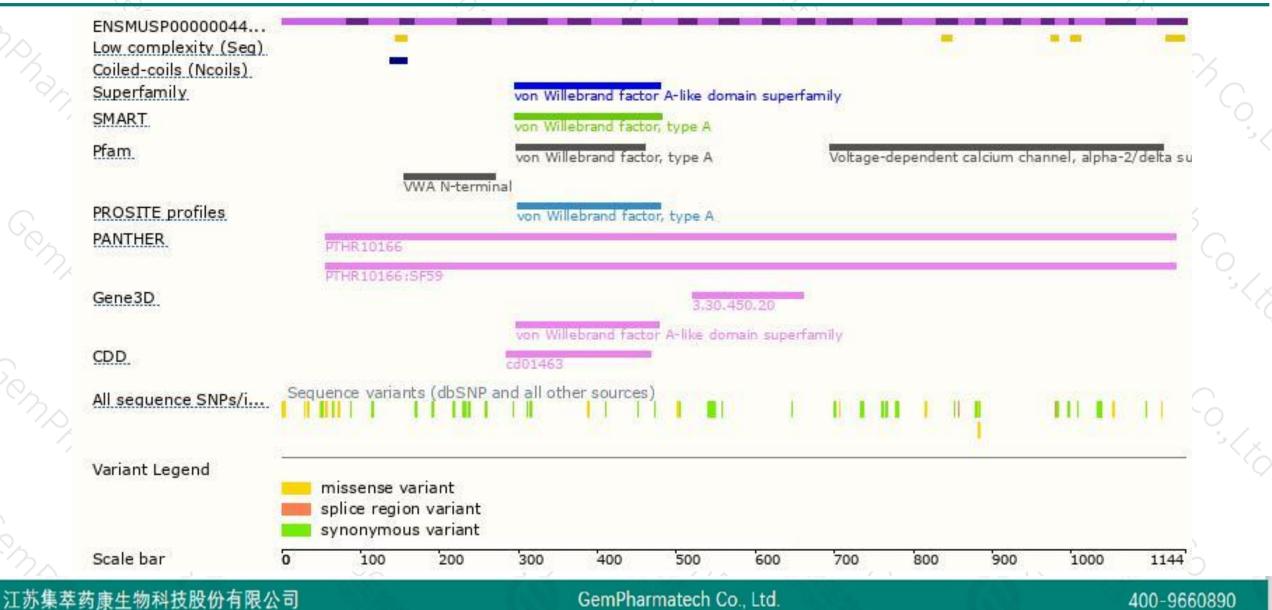
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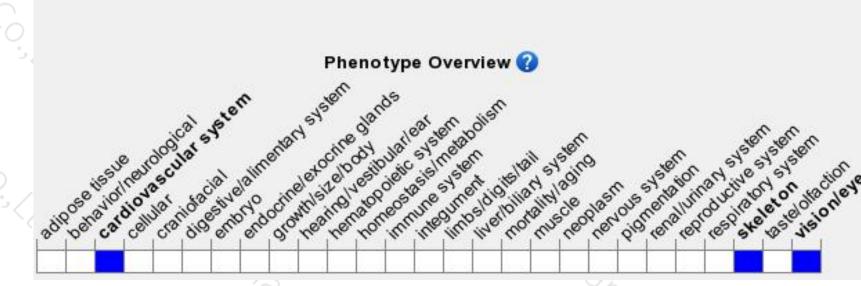
### **Protein domain**





### 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. Tel: 400-9660890



