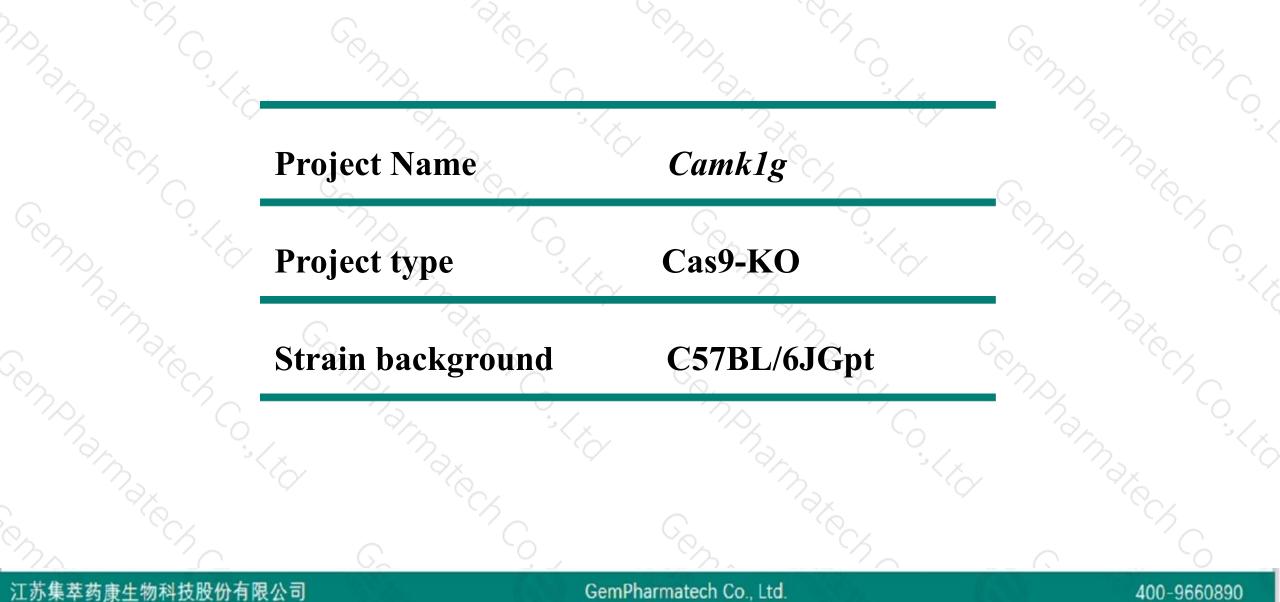


# Camk1g Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-2-26

### **Project Overview**

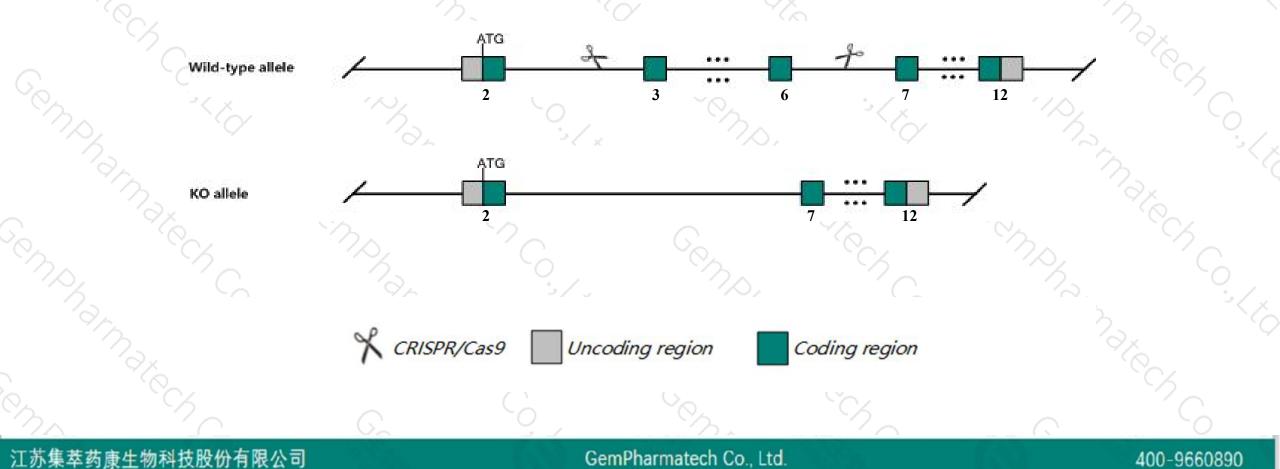




# **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the *Camk1g* gene. The schematic diagram is as follows:





- The Camk1g gene has 4 transcripts. According to the structure of Camk1g gene, exon3-exon6 of Camk1g-201 (ENSMUST00000016323.10) transcript is recommended as the knockout region. The region contains 467bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Camk1g gene. The brief process is as follows: CRISPR/Cas9 syste



- > According to the existing MGI data, Mice homozygous for a knock-out allele exhibit impaired dendritogenesis.
- The Camk1g gene is located on the Chr1. 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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### Camk1g calcium/calmodulin-dependent protein kinase I gamma [Mus musculus (house mouse)]

Gene ID: 215303, updated on 31-Jan-2019

#### Summary

Official Symbol	Camk1g provided by MGI
	calcium/calmodulin-dependent protein kinase I gamma provided byMGI
Primary source	MGI:MGI:2388073
See related	Ensembl:ENSMUSG0000016179
Gene type	protein coding
<b>RefSeq status</b>	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	CLICK-III, CaMKIgamma
Expression	Biased expression in CNS E18 (RPKM 15.3), whole brain E14.5 (RPKM 12.6) and 12 other tissues See more
Orthologs	human all

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## **Transcript information (Ensembl)**



### The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Camk1g-201	ENSMUST00000016323.10	2469	<u>477aa</u>	Protein coding	CCDS15638	Q91VB2	TSL:1 GENCODE basic APPRIS P1
Camk1g-204	ENSMUST00000169907.7	1968	<u>359aa</u>	Protein coding	<del>.</del>	<u>E9Q679</u>	TSL:5 GENCODE basic
Camk1g-202	ENSMUST00000163202.1	754	<u>252aa</u>	Protein coding	24	F6YRI7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Camk1g-203	ENSMUST00000165718.3	783	No protein	Retained intron	č <u>e</u>	20	TSL:3

The strategy is based on the design of *Camk1g-201* transcript, The transcription is shown below

#### < Camk1g-201 protein coding

Reverse strand -

- 23.95 kb --

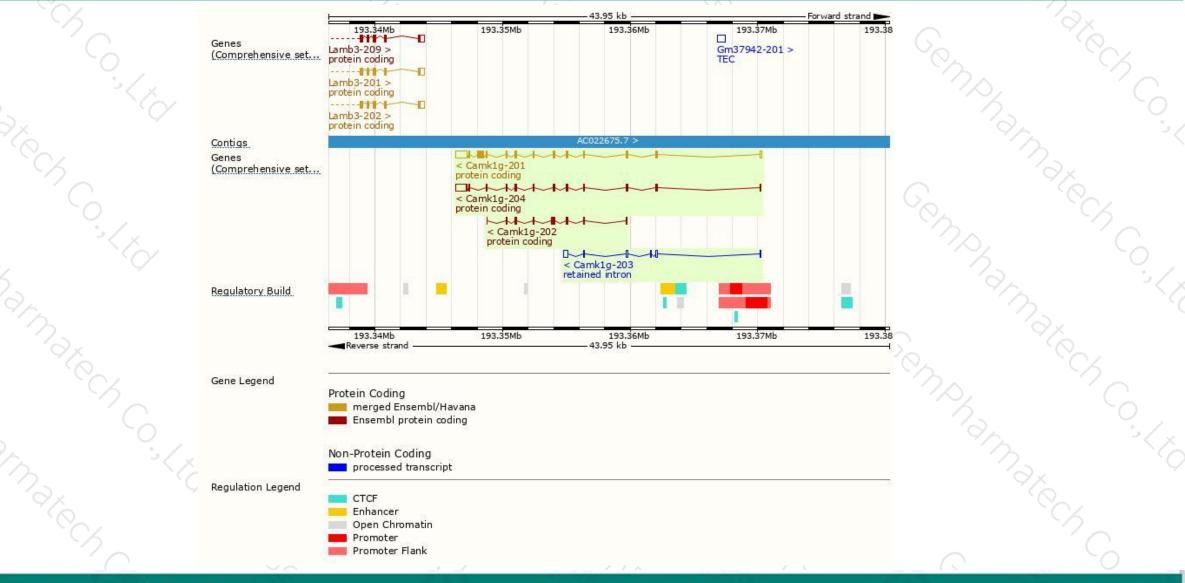
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### **Genomic location distribution**





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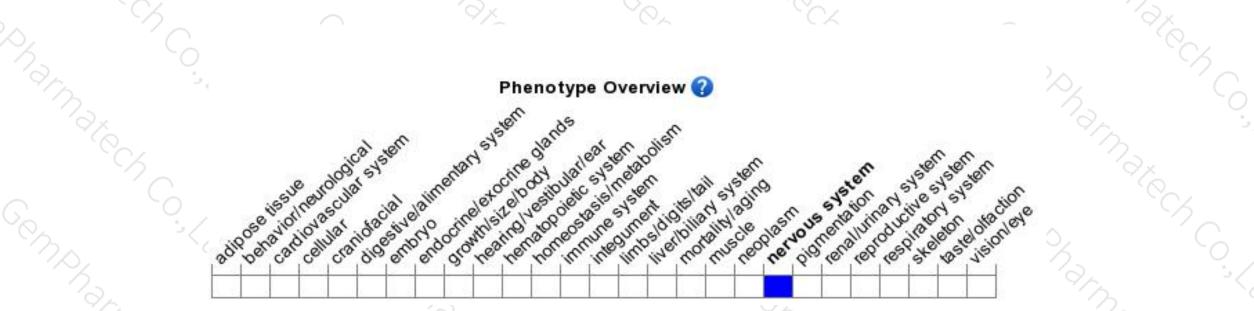
### **Protein domain**



	CDD All sequence SNPs/i		4166			ther source	5-X			•				3
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	PROSITE profiles PROSITE patterns	Pro	otein kinas	e domain	Se	rine/threor	ine-proteir	kinase, a	ctive site					
	Pfam.	100	an and a serie of	se domain										
10	Superfamily SMART	Pr	otein kinaso otein kinas	e domain	in superta	mily			-					

### 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 knock-out allele exhibit impaired dendritogenesis.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



