

# Camk2a Cas9-KO Strategy

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# **Project Overview**



**Project Name** 

Camk2a

**Project type** 

Cas9-KO

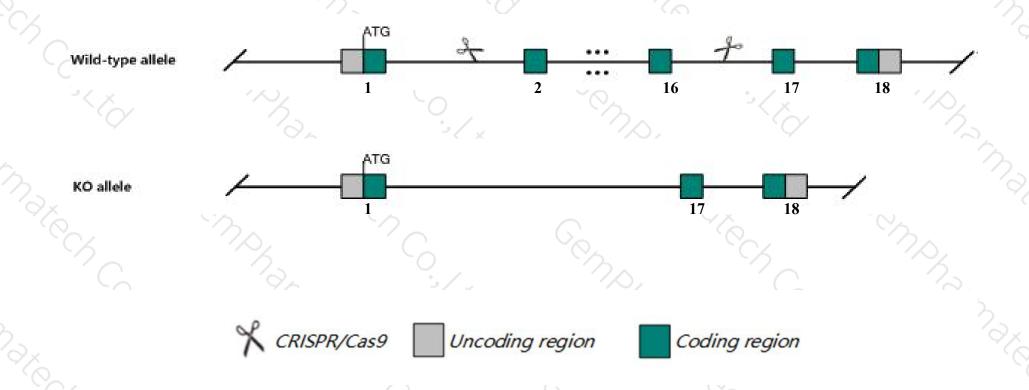
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Camk2a* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Camk2a* gene has 7 transcripts. According to the structure of *Camk2a* gene, exon2-exon16 of *Camk2a-203* (ENSMUST00000102888.9) transcript is recommended as the knockout region. The region contains 1142bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Camk2a* gene. The brief process is as follows: CRISPR/Cas9 systematically systems.

### **Notice**



- ➤ According to the existing MGI data, Homozygous targeted mutants display deficient long-term hippocampal potentiation (LTP) and specific impairment in spatial learning; heterozygotes show decreased fear response and increased defensive aggression, which is more pronounced in homozygotes.
- The *Camk2a* gene is located on the Chr18. 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)



#### Camk2a calcium/calmodulin-dependent protein kinase II alpha [Mus musculus (house mouse)]

Gene ID: 12322, updated on 9-Apr-2019

#### Summary

☆ ?

Official Symbol Camk2a provided by MGI

Official Full Name calcium/calmodulin-dependent protein kinase II alpha provided by MGI

Primary source MGI:MGI:88256

See related Ensembl: ENSMUSG00000024617

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 CaMKII, R74975, mKIAA0968

Expression Biased expression in cortex adult (RPKM 365.9) and frontal lobe adult (RPKM 310.4)See more

Orthologs <u>human</u> all

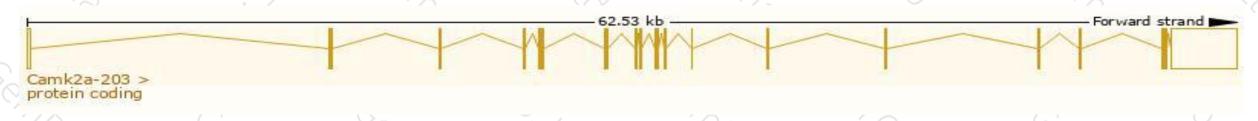
# Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

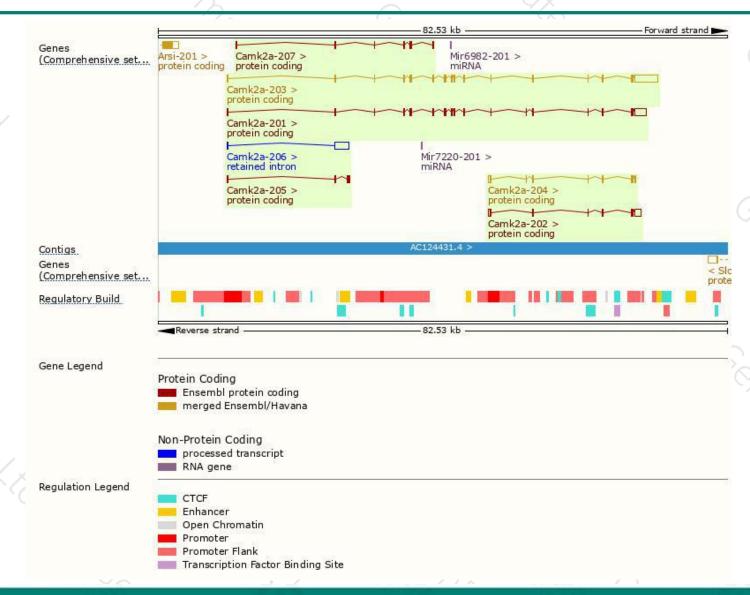
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000102888.9	4970	478aa	Protein coding	CCDS29276	P11798	TSL:1 GENCODE basic APPRIS P2
ENSMUST00000039904.6	1734	<u>189aa</u>	Protein coding	CCDS70898	F8WHB5	TSL:5 GENCODE basic
ENSMUST00000115295.8	979	200aa	Protein coding	CCDS29277	P11798	TSL:1 GENCODE basic
ENSMUST00000025519.10	3244	489aa	Protein coding	Č.	F8WIS9	TSL:5 GENCODE basic APPRIS ALT1
ENSMUST00000137805.2	530	<u>177aa</u>	Protein coding	15	F6WHR9	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
ENSMUST00000115297.7	499	<u>108aa</u>	Protein coding	1 <del>-</del>	D3Z7K9	TSL:2 GENCODE basic
ENSMUST00000134496.1	2301	No protein	Retained intron	¥4	-	TSL:2
	ENSMUST00000102888.9 ENSMUST00000039904.6 ENSMUST00000115295.8 ENSMUST00000025519.10 ENSMUST00000137805.2 ENSMUST00000115297.7	ENSMUST00000102888.9 4970 ENSMUST00000039904.6 1734 ENSMUST00000115295.8 979 ENSMUST00000025519.10 3244 ENSMUST00000137805.2 530 ENSMUST00000115297.7 499	ENSMUST00000102888.9 4970 478aa  ENSMUST00000039904.6 1734 189aa  ENSMUST00000115295.8 979 200aa  ENSMUST00000025519.10 3244 489aa  ENSMUST00000137805.2 530 177aa  ENSMUST00000115297.7 499 108aa	ENSMUST00000102888.9         4970         478aa         Protein coding           ENSMUST00000039904.6         1734         189aa         Protein coding           ENSMUST00000115295.8         979         200aa         Protein coding           ENSMUST00000025519.10         3244         489aa         Protein coding           ENSMUST00000137805.2         530         177aa         Protein coding           ENSMUST00000115297.7         499         108aa         Protein coding	ENSMUST00000102888.9         4970         478aa         Protein coding         CCDS29276           ENSMUST00000039904.6         1734         189aa         Protein coding         CCDS70898           ENSMUST00000115295.8         979         200aa         Protein coding         CCDS29277           ENSMUST00000025519.10         3244         489aa         Protein coding         -           ENSMUST00000137805.2         530         177aa         Protein coding         -           ENSMUST00000115297.7         499         108aa         Protein coding         -	ENSMUST00000102888.9         4970         478aa         Protein coding         CCDS29276         P11798           ENSMUST00000039904.6         1734         189aa         Protein coding         CCDS70898         F8WHB5           ENSMUST00000115295.8         979         200aa         Protein coding         CCDS29277         P11798           ENSMUST00000025519.10         3244         489aa         Protein coding         -         F8WIS9           ENSMUST00000137805.2         530         177aa         Protein coding         -         F6WHR9           ENSMUST00000115297.7         499         108aa         Protein coding         -         D3Z7K9

The strategy is based on the design of *Camk2a-203* transcript, The transcription is shown below



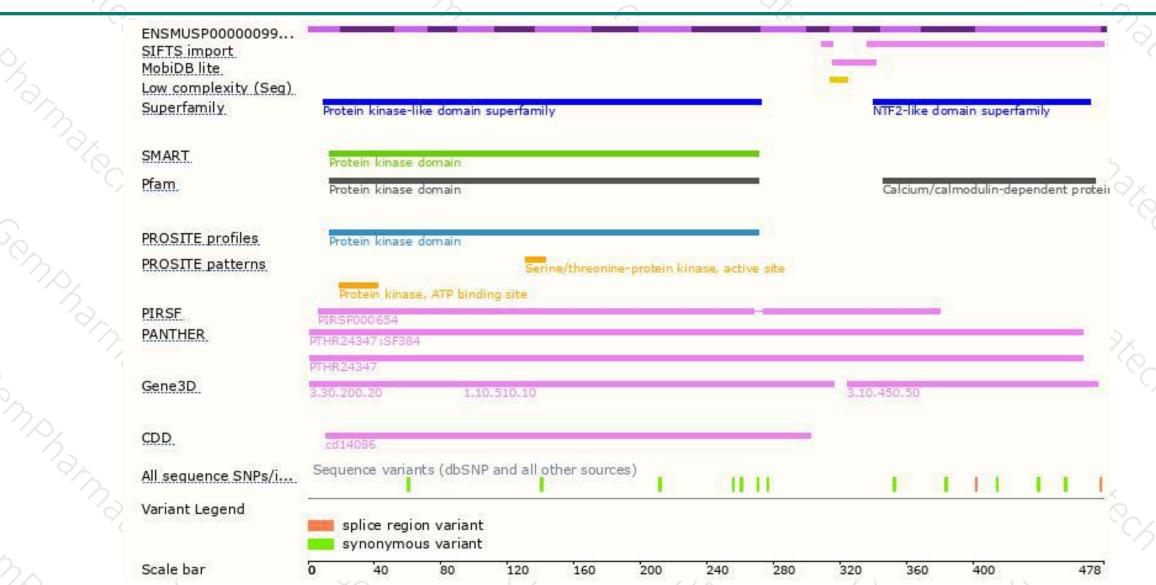
### Genomic location distribution





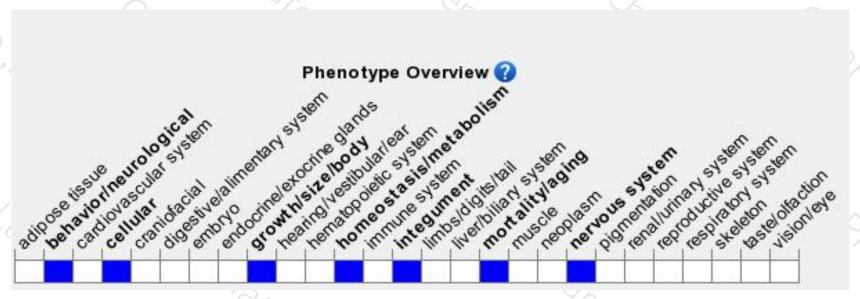
### Protein domain





## 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, Homozygous targeted mutants display deficient long-term hippocampal potentiation (LTP) and specific impairment in spatial learning; heterozygotes show decreased fear response and increased defensive aggression, which is more pronounced in homozygotes.



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





