

Camta2 Cas9-CKO Strategy

Designer:

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Design Date:

2019-7-19

Project Overview

Project Name

Camta2

Project type

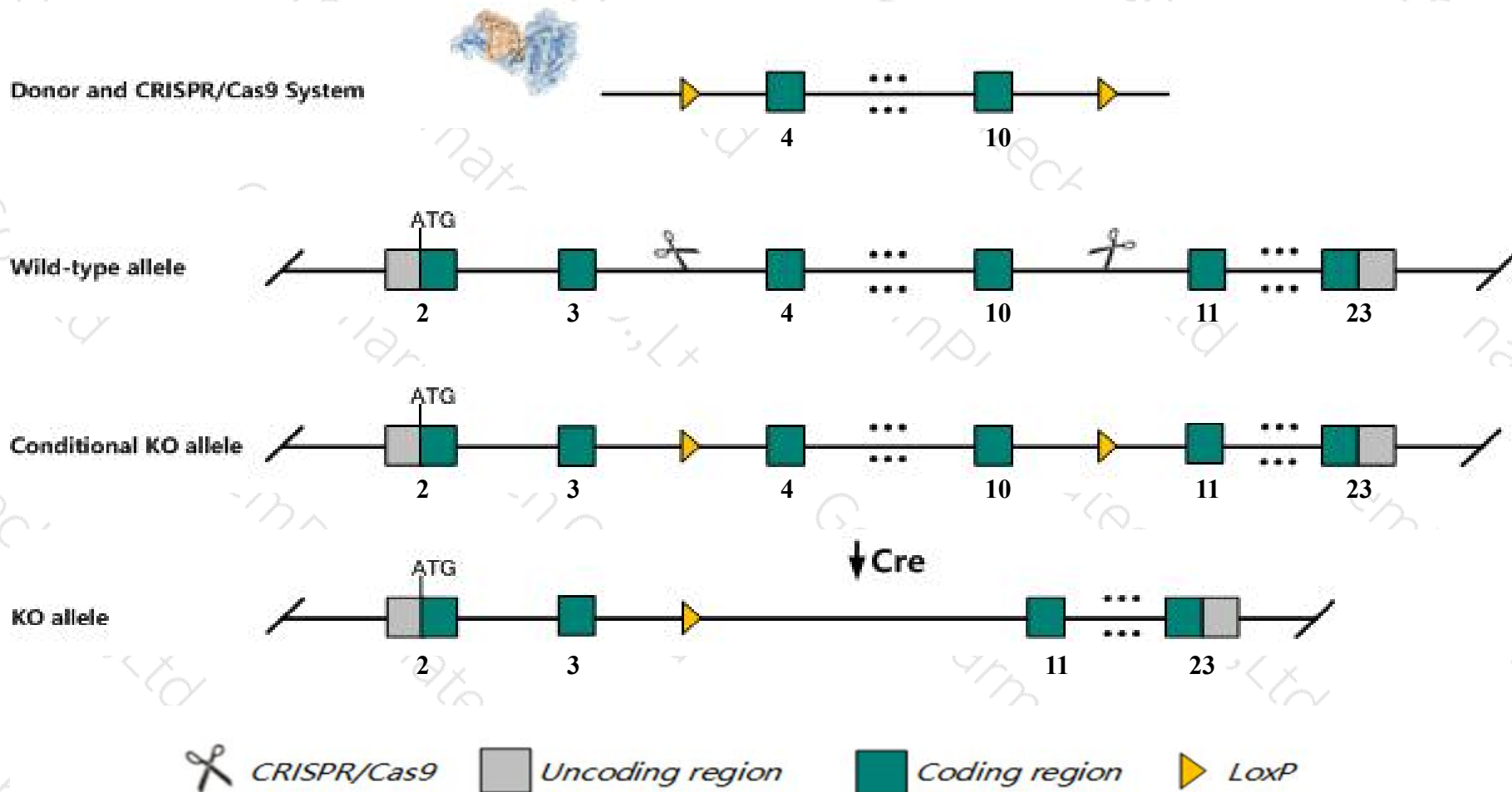
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Camta2* gene. The schematic diagram is as follows:



Technical routes

- The *Camta2* gene has 9 transcripts. According to the structure of *Camta2* gene, exon4-exon10 of *Camta2-201* (ENSMUST00000036299.13) transcript is recommended as the knockout region. The region contains 1636bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Camta2* 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 knock-out allele are viable, fertile and free of obvious cardiac defects, but show reduced pathophysiologic cardiac hypertrophy in response to diverse stress stimuli.
- The *Camta2* gene is located on the Chr11. 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)

Camta2 calmodulin binding transcription activator 2 [Mus musculus (house mouse)]

Gene ID: 216874, updated on 31-Jan-2019

Summary



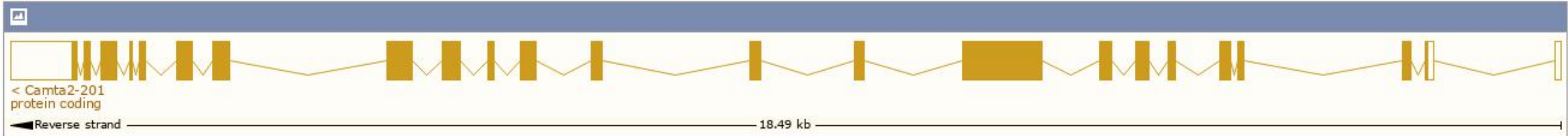
Official Symbol	Camta2 provided by MGI
Official Full Name	calmodulin binding transcription activator 2 provided by MGI
Primary source	MGI:MGI:2135957
See related	Ensembl:ENSMUSG00000040712
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Kiaa0909-hp, mKIAA0909
Expression	Ubiquitous expression in cortex adult (RPKM 27.2), duodenum adult (RPKM 25.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

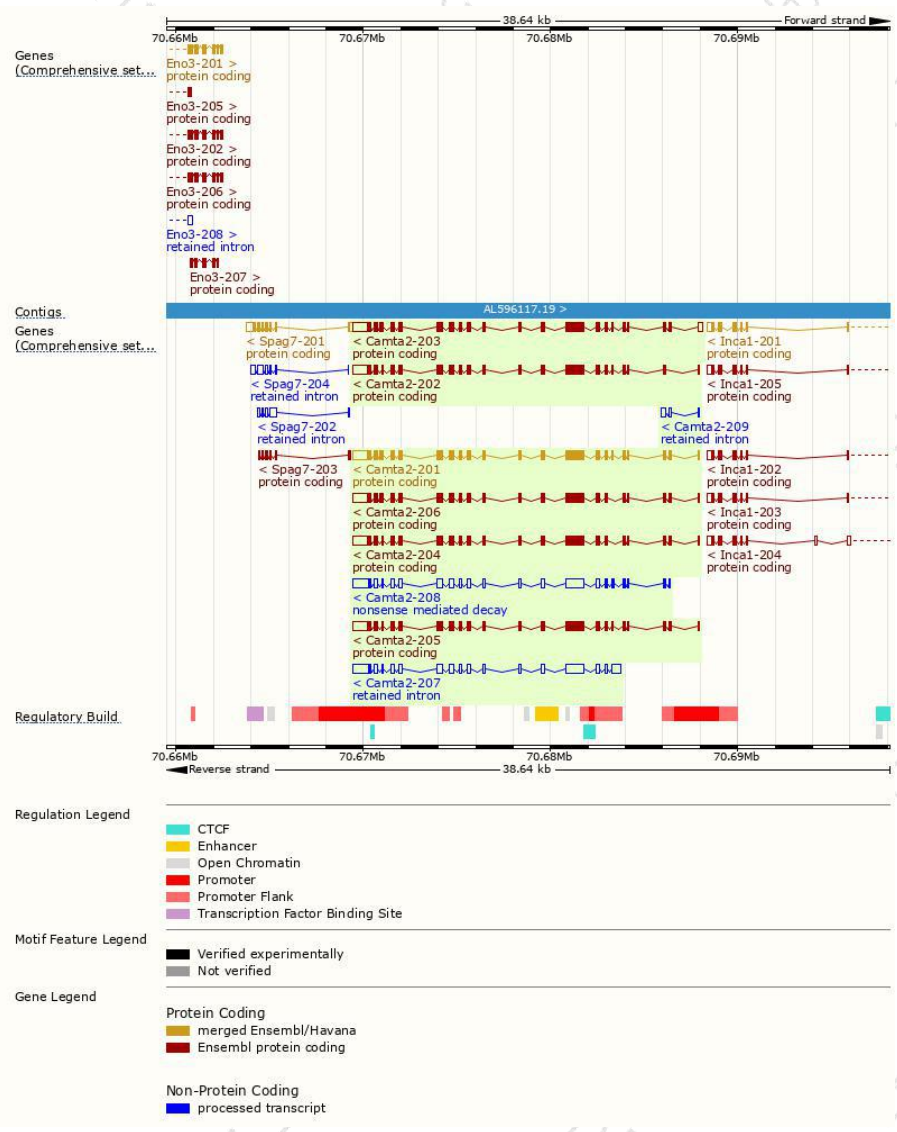
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Camta2-203	ENSMUST00000108544.7	4632	1203aa	Protein coding	CCDS56788	Q80Y50	TSL:1 GENCODE basic APPRIS ALT2
Camta2-201	ENSMUST00000036299.13	4495	1208aa	Protein coding	CCDS24963	Q80Y50	TSL:1 GENCODE basic APPRIS P3
Camta2-205	ENSMUST00000119120.1	4460	1196aa	Protein coding	CCDS56787	B0QZH4	TSL:1 GENCODE basic APPRIS ALT2
Camta2-204	ENSMUST00000108545.8	4377	1172aa	Protein coding	CCDS56786	Q80Y50	TSL:1 GENCODE basic
Camta2-206	ENSMUST00000120261.7	4398	1179aa	Protein coding	-	B0QZH6	TSL:5 GENCODE basic
Camta2-202	ENSMUST00000100933.9	4383	1198aa	Protein coding	-	Q80Y50	TSL:5 GENCODE basic APPRIS ALT2
Camta2-208	ENSMUST00000145823.7	4406	181aa	Nonsense mediated decay	-	D6RCU2	TSL:1
Camta2-207	ENSMUST00000125687.1	4411	No protein	Retained intron	-	-	TSL:1
Camta2-209	ENSMUST00000150224.1	411	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Camta2-201* transcript,The transcription is shown below



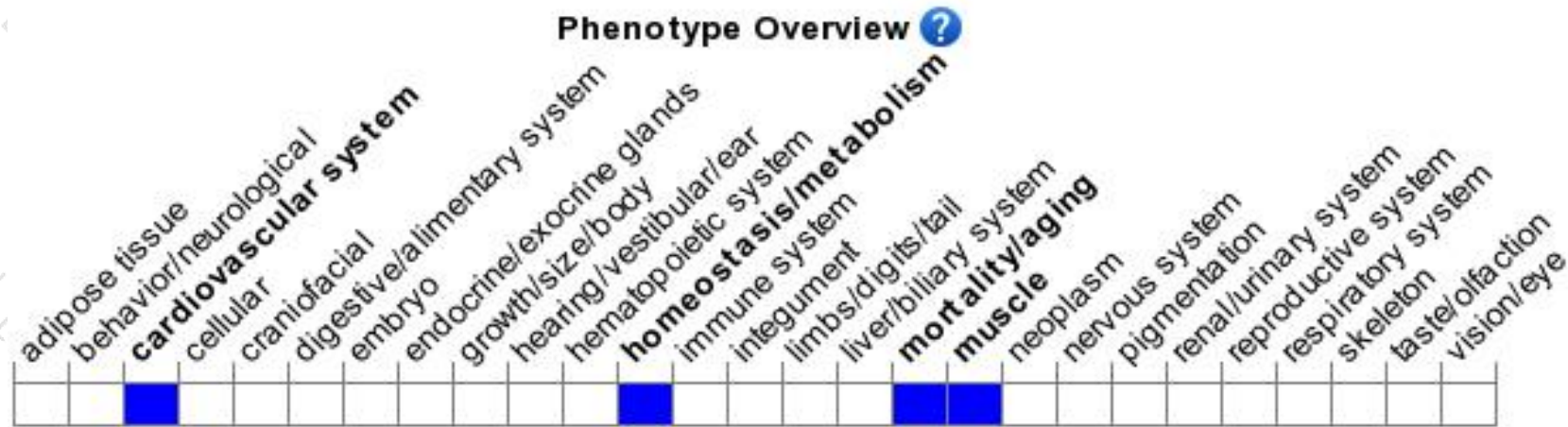
Genomic location distribution



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 knock-out allele are viable, fertile and free of obvious cardiac defects, but show reduced pathophysiologic cardiac hypertrophy in response to diverse stress stimuli.

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

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