

Shisa9 Cas9-CKO Strategy

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Design Date: 2020-4-8

Project Overview

Project Name

Shisa9

Project type

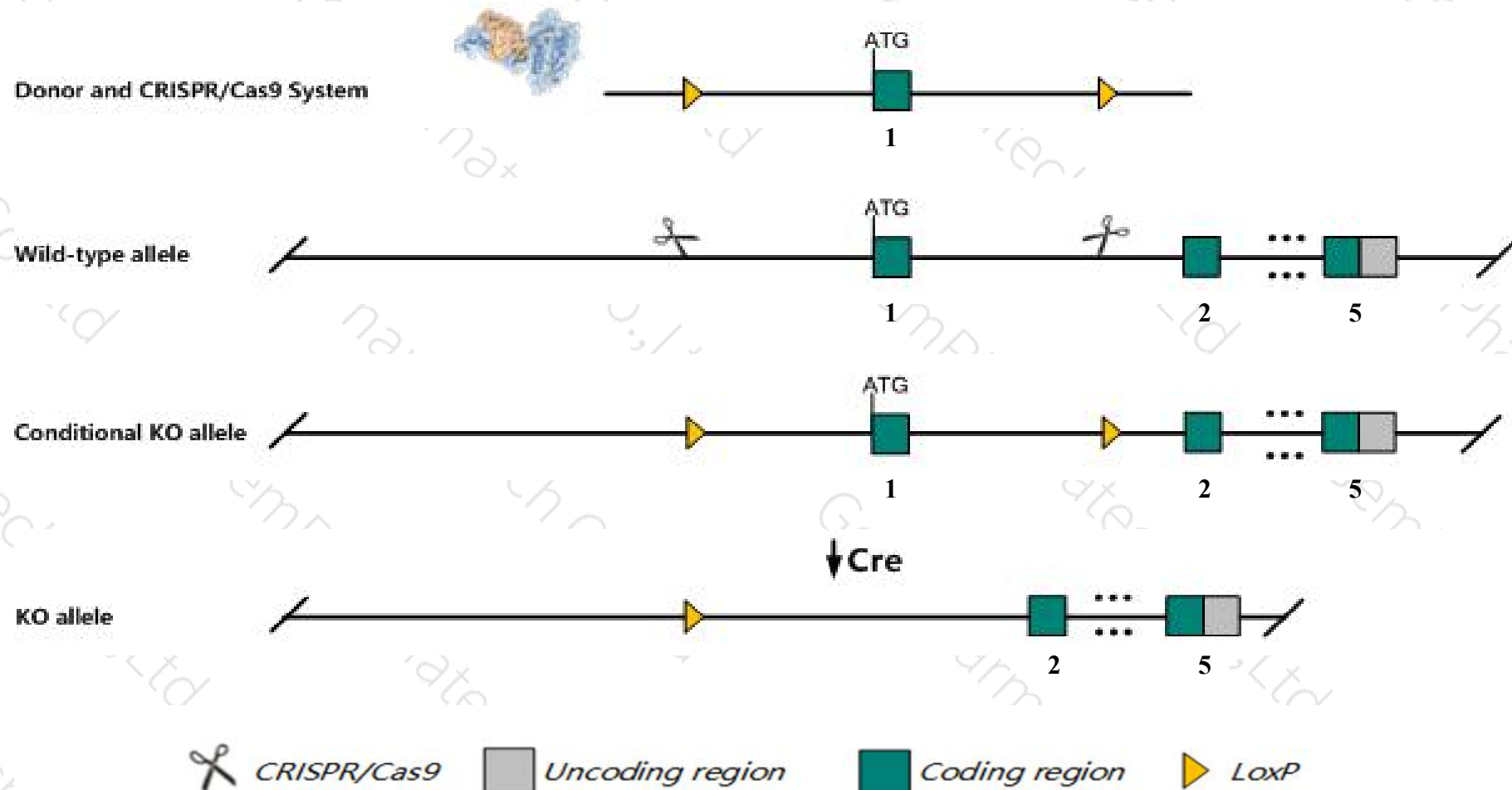
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Shisa9* gene. The schematic diagram is as follows:



- The *Shisa9* gene has 6 transcripts. According to the structure of *Shisa9* gene, exon1 of *Shisa9-202* (ENSMUST00000170672.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Shisa9* 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 exhibit reduced AMPA-mediated synaptic currents in retinogeniculate and corticogeniculate synapses, enhanced paired-pulse facilitation in retinogeniculate synapses and decreased synaptic depression.
- The *Shisa9* gene is located on the Chr16. 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)

Shisa9 shisa family member 9 [Mus musculus (house mouse)]

Gene ID: 72555, updated on 13-Mar-2020

Summary



Official Symbol	Shisa9 provided by MGI
Official Full Name	shisa family member 9 provided by MGI
Primary source	MGI:MGI:1919805
See related	Ensembl:ENSMUSG00000022494
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	2700045P11Rik, Ckamp44
Expression	Biased expression in frontal lobe adult (RPKM 7.4), CNS E18 (RPKM 4.4) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)



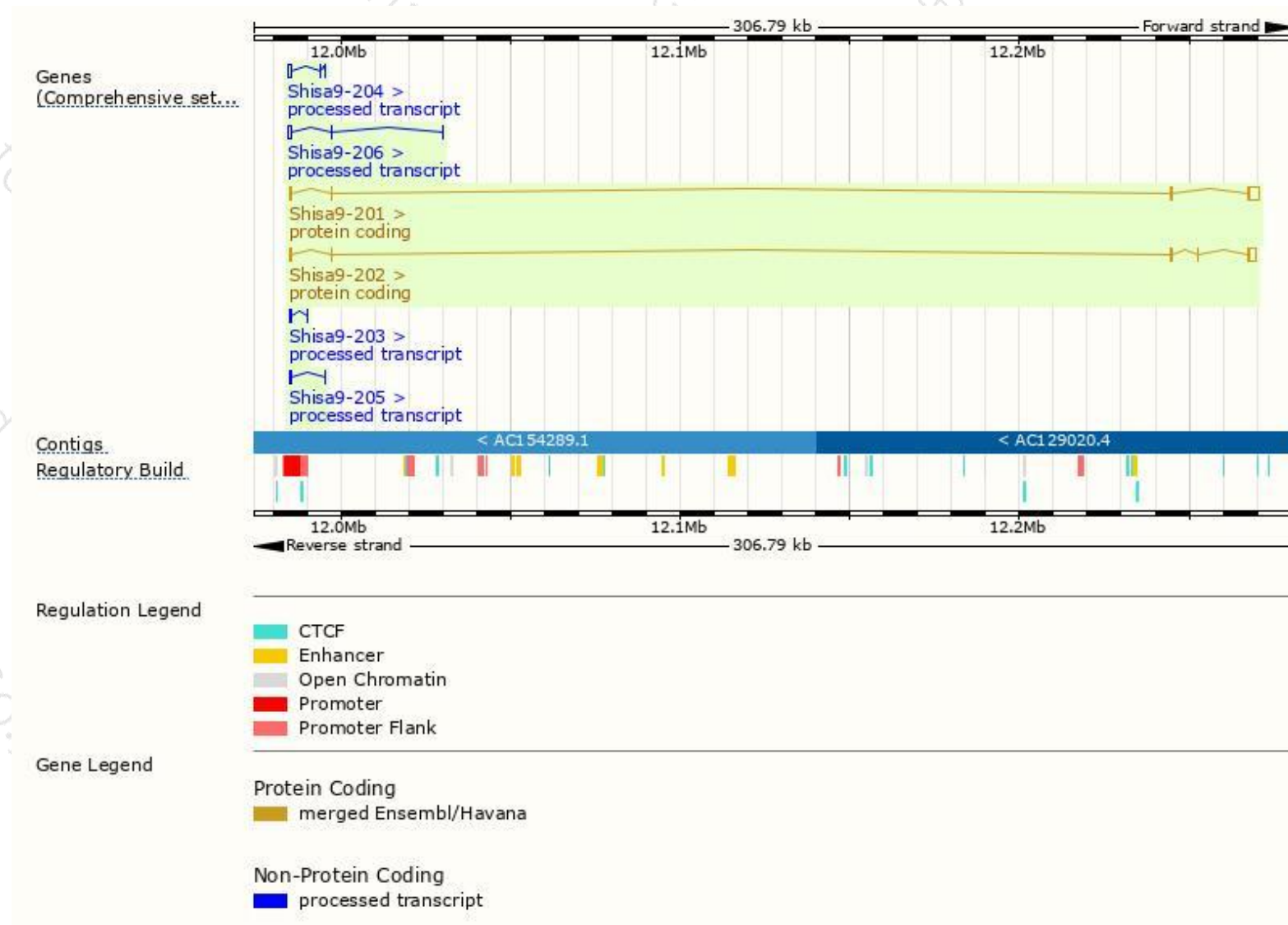
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Shisa9-201	ENSMUST00000023138.7	4326	408aa	Protein coding	CCDS49767	E9QN38	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Shisa9-202	ENSMUST00000170672.8	3421	424aa	Protein coding	CCDS49766	Q9CZN4	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P4
Shisa9-204	ENSMUST00000182889.1	1196	No protein	Processed transcript	-	-	TSL:1
Shisa9-206	ENSMUST00000232469.1	951	No protein	Processed transcript	-	-	
Shisa9-203	ENSMUST00000182154.1	558	No protein	Processed transcript	-	-	TSL:3
Shisa9-205	ENSMUST00000229804.1	538	No protein	Processed transcript	-	-	

The strategy is based on the design of *Shisa9-202* transcript,The transcription is shown below



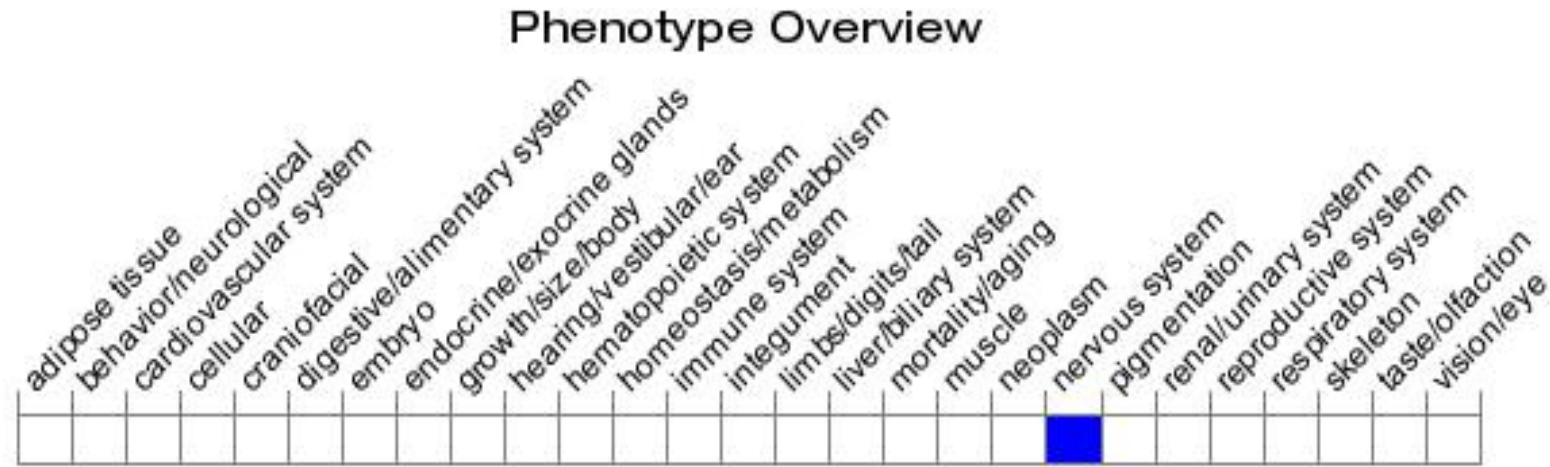
Genomic location distribution



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 exhibit reduced AMPA-mediated synaptic currents in retinogeniculate and corticogeniculate synapses, enhanced paired-pulse facilitation in retinogeniculate synapses and decreased synaptic depression.

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

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