Sh3glb1 Cas9-CKO Strategy

Designer: Huan Wang

Reviewer: Huan Fan

Design Date: 2020-5-6

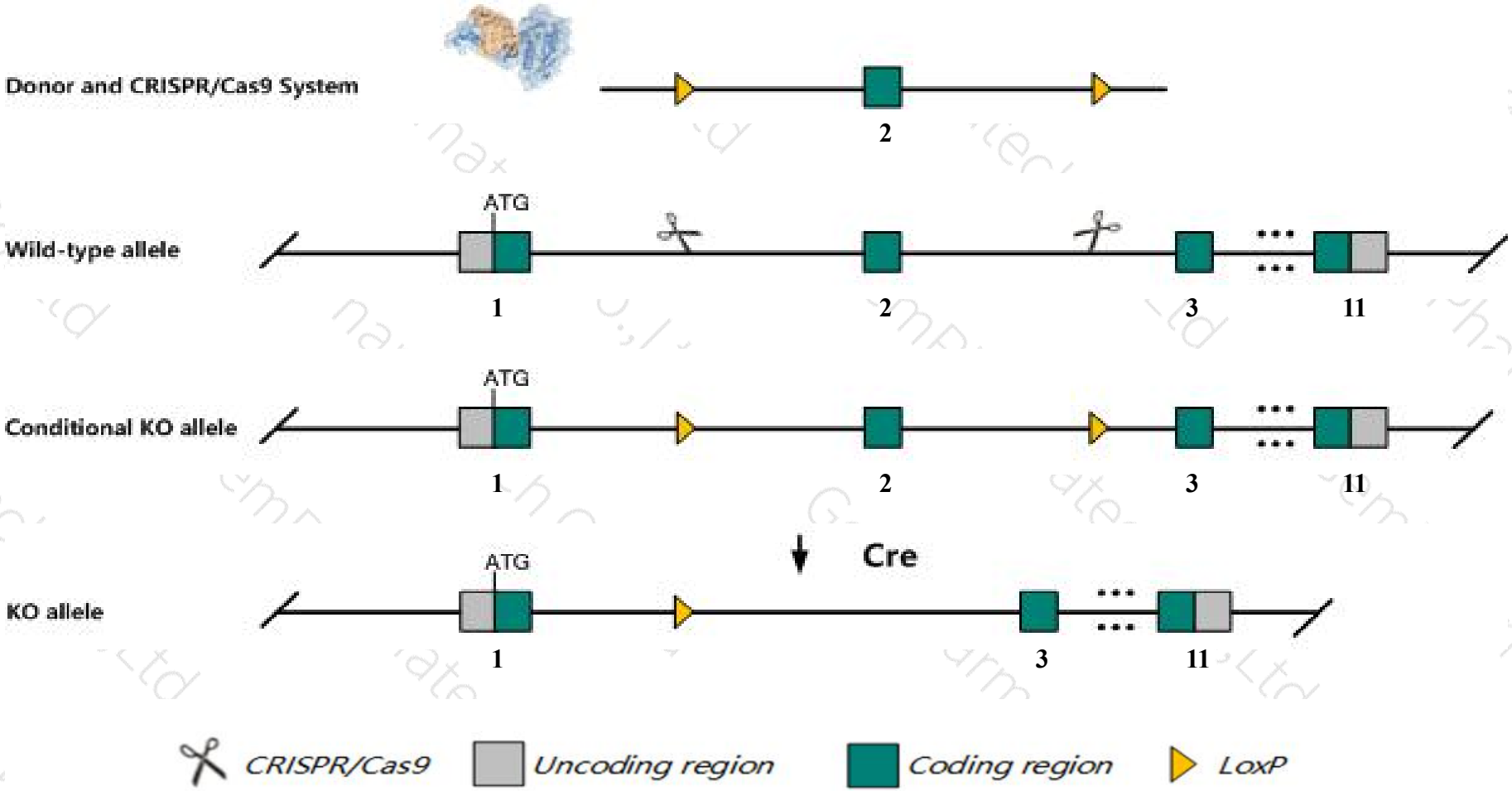
GemPharmatech Co.,Ltd

Project Overview

Project Name	***Sh3glb1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sh3glb1* gene. The schematic diagram is as follows:



Technical routes

- The *Sh3glb1* gene has 6 transcripts. According to the structure of *Sh3glb1* gene, exon2 of *Sh3glb1-202* (ENSMUST00000198254.4) transcript is recommended as the knockout region.The region contains 142bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Sh3glb1* 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.

Notice

- According to the existing MGI data,homozygous mutation of this gene results in delayed apoptosis of embryonic fibroblasts in response to serum withdrawal or treatment with a mitochondrial stress inducer.
- Transcript *Sh3glb1-206* may not be affected.
- The *Sh3glb1* gene is located on the Chr3. 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）

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Sh3glb1 SH3-domain GRB2-like B1 (endophilin) [Mus musculus (house mouse)]

Gene ID: 54673, updated on 25-Mar-2020

Summary

Official Symbol	Sh3glb1 provided by MGI
Official Full Name	SH3-domain GRB2-like B1 (endophilin) provided by MGI
Primary source	MGI:MGI:1859730
See related	Ensembl:ENSMUSG00000037062
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	AA409932, AI314629, AU015566, Bif-1, mKIAA0491
Expression	Ubiquitous expression in testis adult (RPKM 28.5), CNS E18 (RPKM 9.1) and 27 other tissues See more
Orthologs	human all

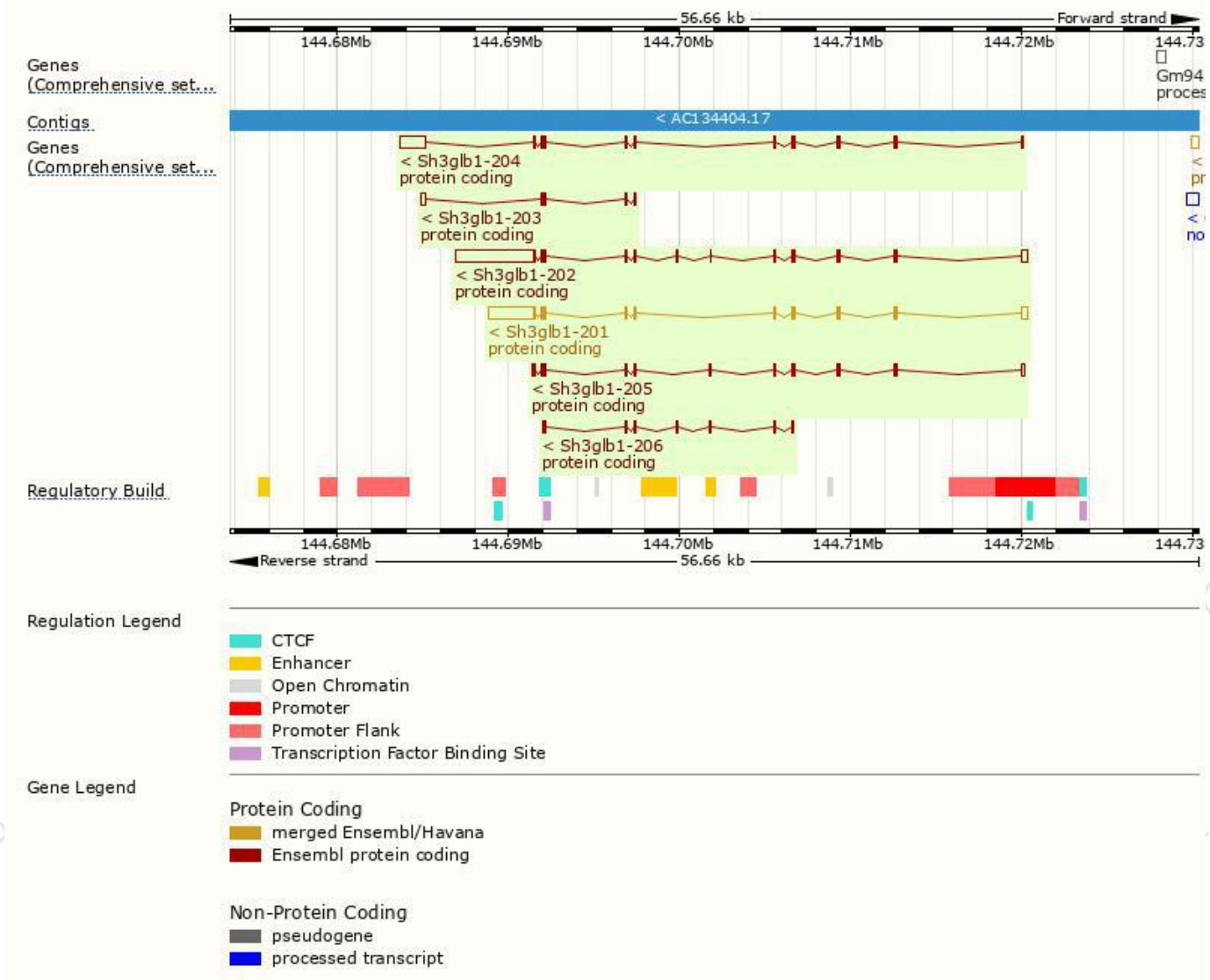
Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sh3glb1-202	ENSMUST00000198254.4	5945	386aa	Protein coding	CCDS80043	Q9JK48	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 ALT1
Sh3glb1-201	ENSMUST00000163279.5	3961	365aa	Protein coding	CCDS17885	Q9JK48	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 P3
Sh3glb1-204	ENSMUST00000199531.4	2584	355aa	Protein coding	CCDS80042	Q9JK48	TSL:1 GENCODE basic
Sh3glb1-205	ENSMUST00000199854.4	1416	394aa	Protein coding	-	A0A0G2JEC4	TSL:5 GENCODE basic
Sh3glb1-203	ENSMUST00000199350.4	665	140aa	Protein coding	-	A0A0G2JF57	CDS 5' incomplete TSL:3
Sh3glb1-206	ENSMUST00000200532.1	582	194aa	Protein coding	-	A0A0G2JE45	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

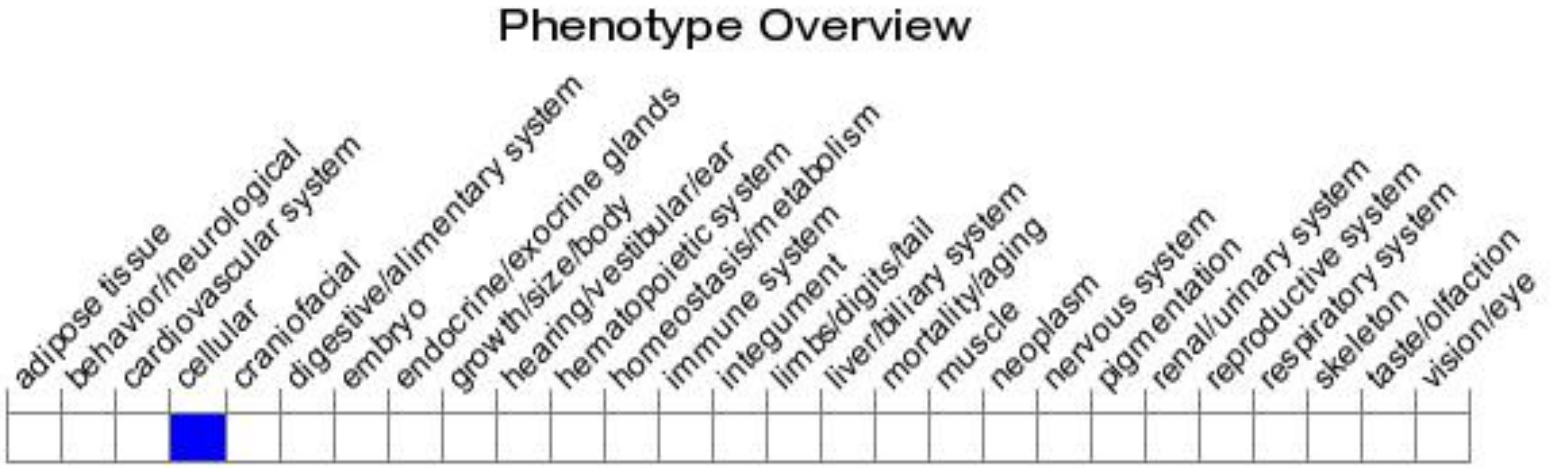
The strategy is based on the design of *Sh3glb1-202* transcript,the transcription is shown below:

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,homozygous mutation of this gene results in delayed apoptosis of embryonic fibroblasts in response to serum withdrawal or treatment with a mitochondrial stress inducer.

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd

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