

Scn8a Cas9-CKO Strategy

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Project Overview

Project Name

Scn8a

Project type

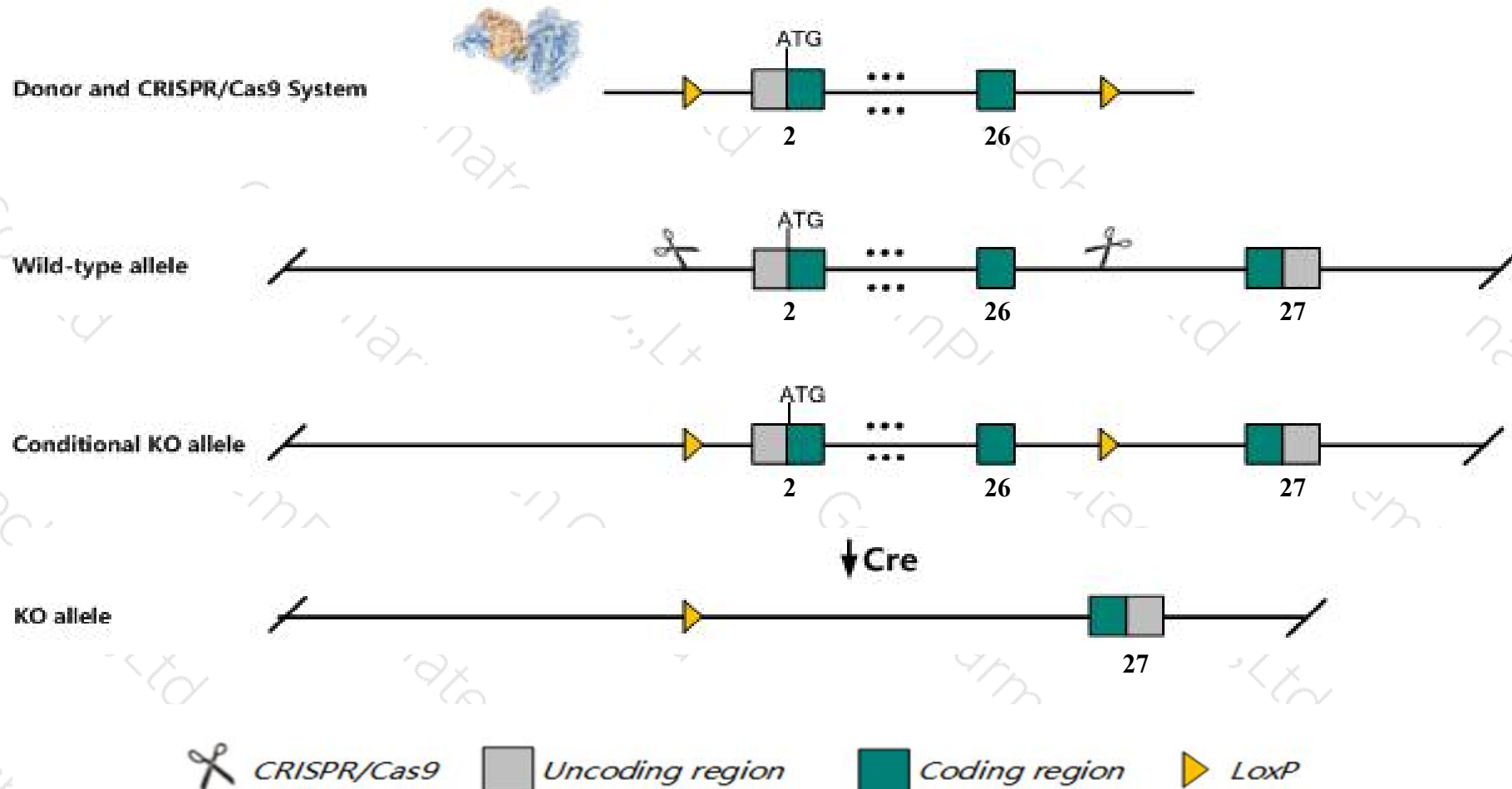
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scn8a* gene. The schematic diagram is as follows:



Technical routes

- The *Scn8a* gene has 20 transcripts. According to the structure of *Scn8a* gene, exon2-exon26 of *Scn8a-201* (ENSMUST00000082209.12) 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 *Scn8a* 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, Spontaneous mutant homozygotes have ataxia, dystonia, muscular atrophy, progressive paralysis, Purkinje cell loss, in some cases severe head-tossing and for severe alleles, juvenile lethality. A mild, semidominant ENU allele causes deafness of variable penetrance and severity and mild tremor.
- The *Scn8a* gene is located on the Chr15. 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)

Scn8a sodium channel, voltage-gated, type VIII, alpha [Mus musculus (house mouse)]

Gene ID: 20273, updated on 19-Feb-2019

Summary



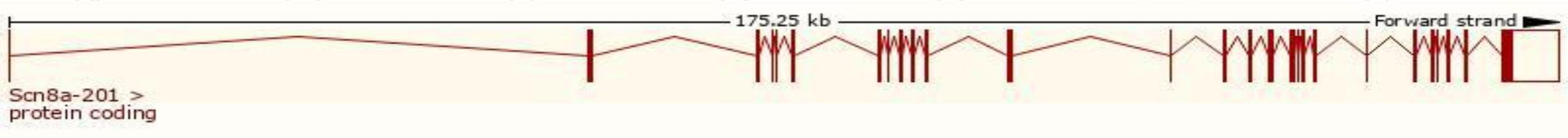
Official Symbol	Scn8a provided by MGI
Official Full Name	sodium channel, voltage-gated, type VIII, alpha provided by MGI
Primary source	MGI:MGI:103169
See related	Ensembl:ENSMUSG00000023033
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI853486, C630029C19Rik, NaCh6, Nav1.6, dmu, med, mnd-2, mnd2, nmf2, nmf335, nmf58, nur14, seal
Expression	Biased expression in cortex adult (RPKM 21.8), cerebellum adult (RPKM 21.1) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

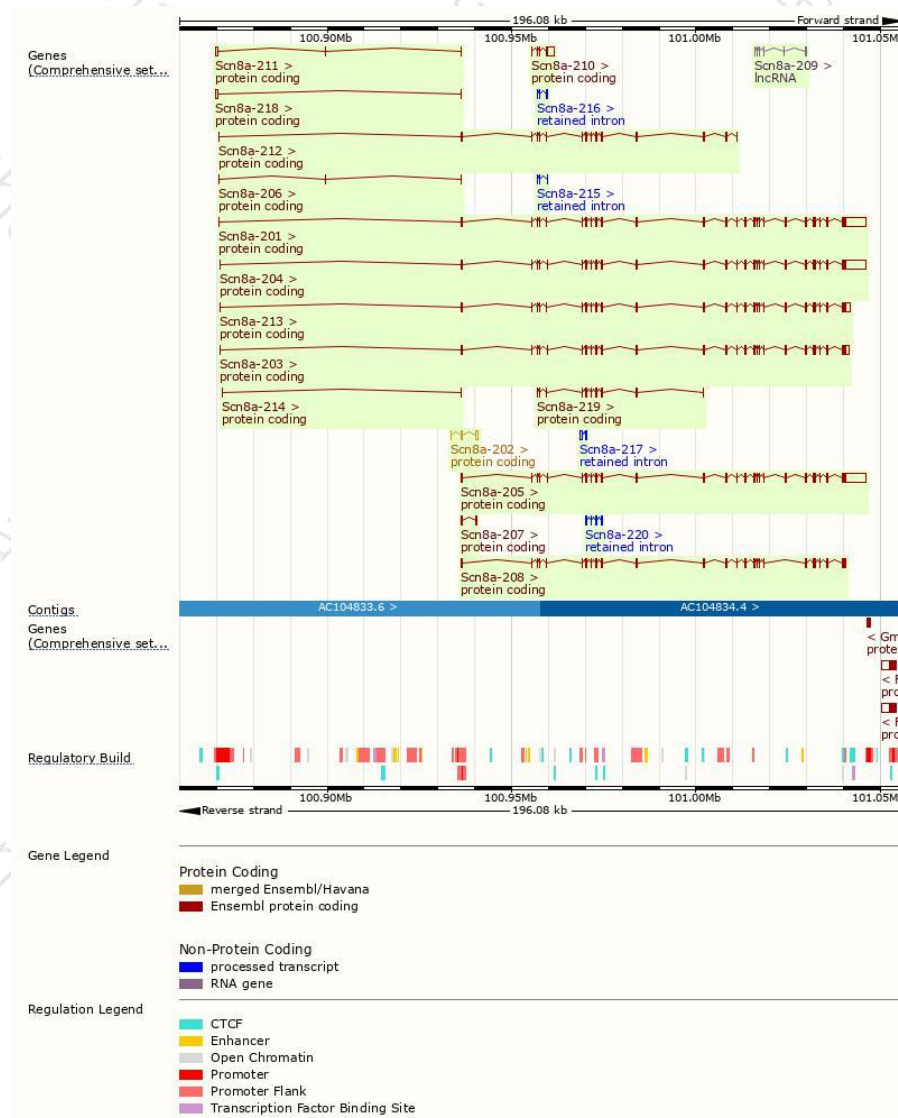
The gene has 20 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scn8a-201	ENSMUST00000082209.12	11293	1978aa	Protein coding	CCDS57010	F6U329	TSL:5 GENCODE basic APPRIS P5
Scn8a-205	ENSMUST00000108910.9	11232	1978aa	Protein coding	CCDS57011	F7D6K4	TSL:1 GENCODE basic APPRIS ALT1
Scn8a-213	ENSMUST00000201549.3	7120	1978aa	Protein coding	CCDS57010	F6U329	TSL:5 GENCODE basic APPRIS P5
Scn8a-203	ENSMUST00000108908.6	7030	1978aa	Protein coding	CCDS57011	F7D6K4	TSL:5 GENCODE basic APPRIS ALT1
Scn8a-204	ENSMUST00000108909.8	11436	1988aa	Protein coding	-	F7D6J5	TSL:5 GENCODE basic
Scn8a-208	ENSMUST00000200963.3	5814	1937aa	Protein coding	-	A0A0J9YUW5	TSL:5 GENCODE basic
Scn8a-212	ENSMUST00000201518.3	2565	804aa	Protein coding	-	A0A0J9YTW4	CDS 3' incomplete TSL:1
Scn8a-210	ENSMUST00000201438.3	2110	132aa	Protein coding	-	A0A0J9YUL0	CDS 5' incomplete TSL:3
Scn8a-219	ENSMUST00000202702.1	1618	539aa	Protein coding	-	A0A0J9YTW2	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Scn8a-202	ENSMUST00000096198.9	1072	102aa	Protein coding	-	Q4KL32	TSL:1 GENCODE basic
Scn8a-211	ENSMUST00000201484.3	683	1aa	Protein coding	-	-	CDS 3' incomplete TSL:1
Scn8a-207	ENSMUST00000200959.1	587	100aa	Protein coding	-	A0A0J9YUK3	TSL:3 GENCODE basic
Scn8a-218	ENSMUST00000202527.3	533	1aa	Protein coding	-	-	CDS 3' incomplete TSL:1
Scn8a-214	ENSMUST00000202071.1	322	1aa	Protein coding	-	-	CDS 3' incomplete TSL:1
Scn8a-206	ENSMUST00000200933.3	290	1aa	Protein coding	-	-	CDS 3' incomplete TSL:1
Scn8a-220	ENSMUST00000202971.1	840	No protein	Retained intron	-	-	TSL:2
Scn8a-217	ENSMUST00000202452.1	681	No protein	Retained intron	-	-	TSL:3
Scn8a-216	ENSMUST00000202349.3	514	No protein	Retained intron	-	-	TSL:2
Scn8a-215	ENSMUST00000202347.1	326	No protein	Retained intron	-	-	TSL:5
Scn8a-209	ENSMUST00000201246.1	903	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Scn8a-201* transcript,The transcription is shown below



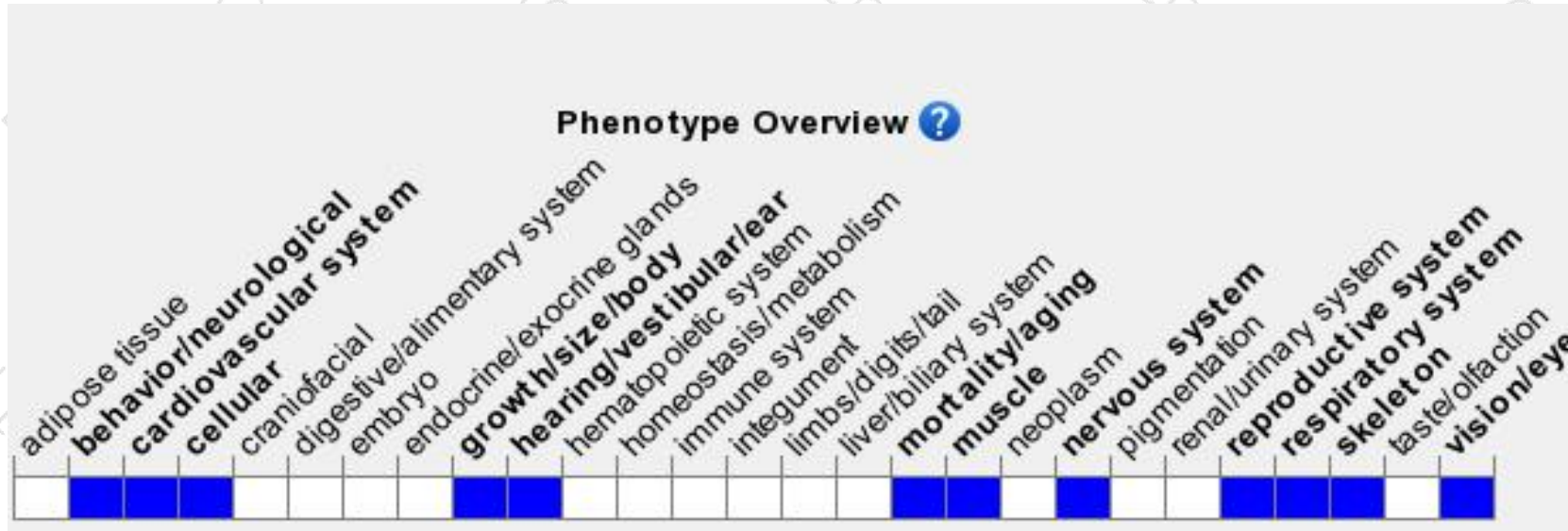
Genomic location distribution



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, Spontaneous mutant homozygotes have ataxia, dystonia, muscular atrophy, progressive paralysis, Purkinje cell loss, in some cases severe head-tossing and for severe alleles, juvenile lethality. A mild, semidominant ENU allele causes deafness of variable penetrance and severity and mild tremor.

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

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