Scn10a Cas9-KO Strategy

Designer: Yupeng Yang

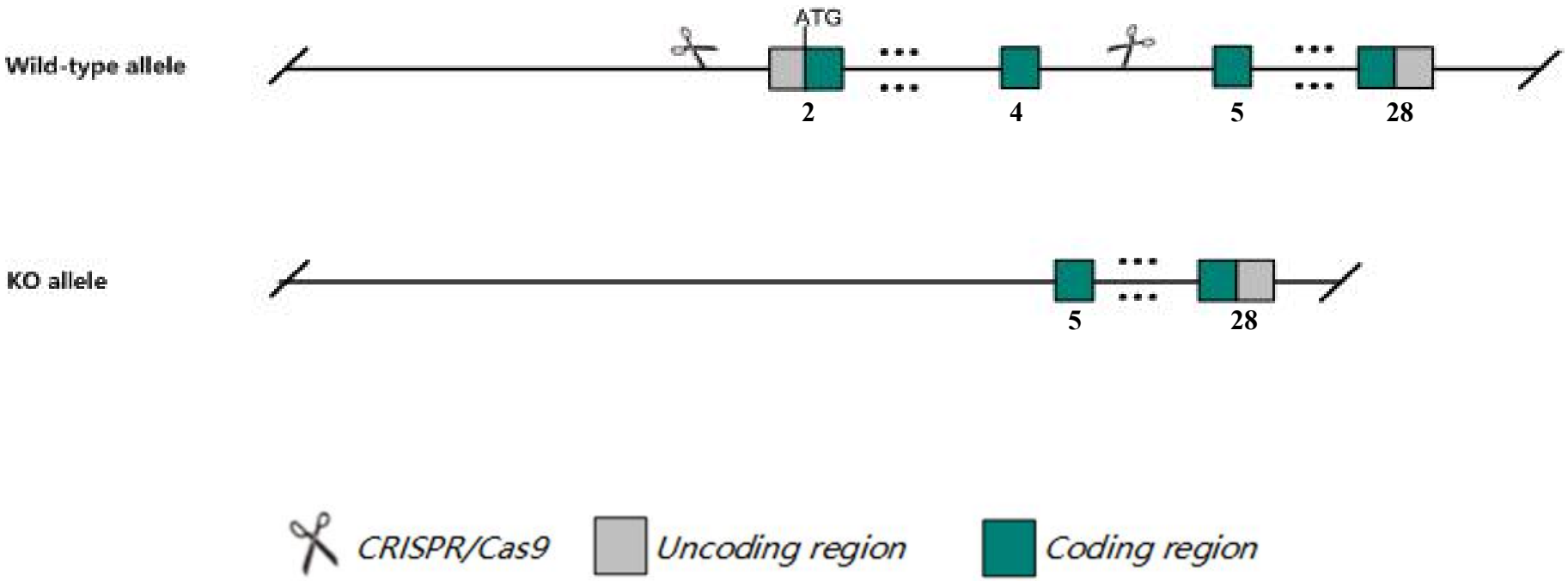
Design Date: 2019-7-24

Project Overview

Project Name	***Scn10a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scn10a* gene. The schematic diagram is as follows:



Technical routes

The *Scn10a* gene has 5 transcripts. According to the structure of *Scn10a* gene, exon2-exon4 of *Scn10a-201* (ENSMUST00000084787.5) 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 *Scn10a* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

According to the existing MGI data,Homozygotes for a targeted null mutation exhibit impaired perception of pain. Mice homozygous or heterozygous for an ENU-induced allele exhibit a catalepsy phenotype following scruffing and increased sensitivity to cold pain.

The *Scn10a* gene is located on the Chr9. 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

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Scn10a sodium channel, voltage-gated, type X, alpha [Mus musculus (house mouse)]

Gene ID: 20264, updated on 12-Mar-2019

Summary

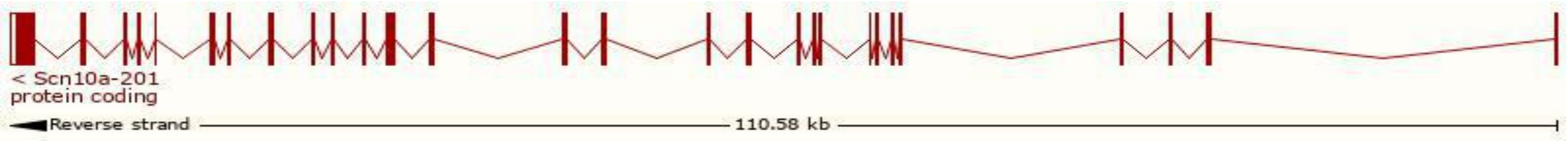
Official Symbol	Scn10a provided by MGI
Official Full Name	sodium channel, voltage-gated, type X, alpha provided by MGI
Primary source	MGI:MGI:108029
See related	Ensembl:ENSMUSG00000034533
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Nav1.8, PN3, SNS
Expression	Biased expression in heart adult (RPKM 1.0), CNS E18 (RPKM 0.5) and 9 other tissues See more
Orthologs	human all

Transcript information Ensembl

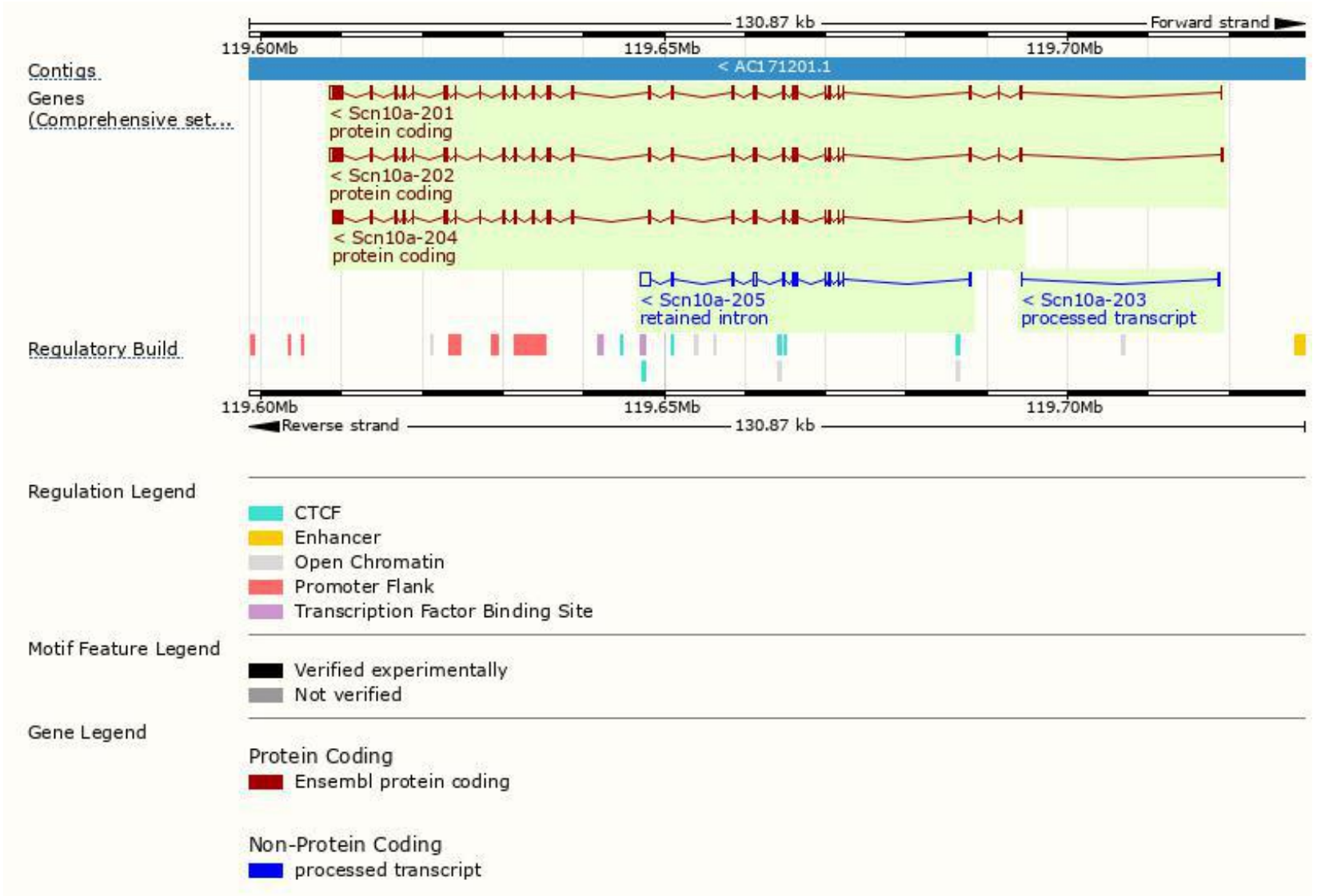
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scn10a-201	ENSMUST00000084787.5	6416	1958aa	Protein coding	CCDS57716	K3W4P8	TSL:5 GENCODE basic APPRIS P2
Scn10a-204	ENSMUST00000214408.1	5877	1958aa	Protein coding	CCDS57716	K3W4P8	TSL:1 GENCODE basic APPRIS P2
Scn10a-202	ENSMUST00000213392.1	6692	1957aa	Protein coding	-	Q6QIY3	TSL:1 GENCODE basic APPRIS ALT2
Scn10a-203	ENSMUST00000213401.1	299	No protein	Processed transcript	-	-	TSL:1
Scn10a-205	ENSMUST00000216583.1	2880	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Scn10a-201* transcript,The transcription is shown below

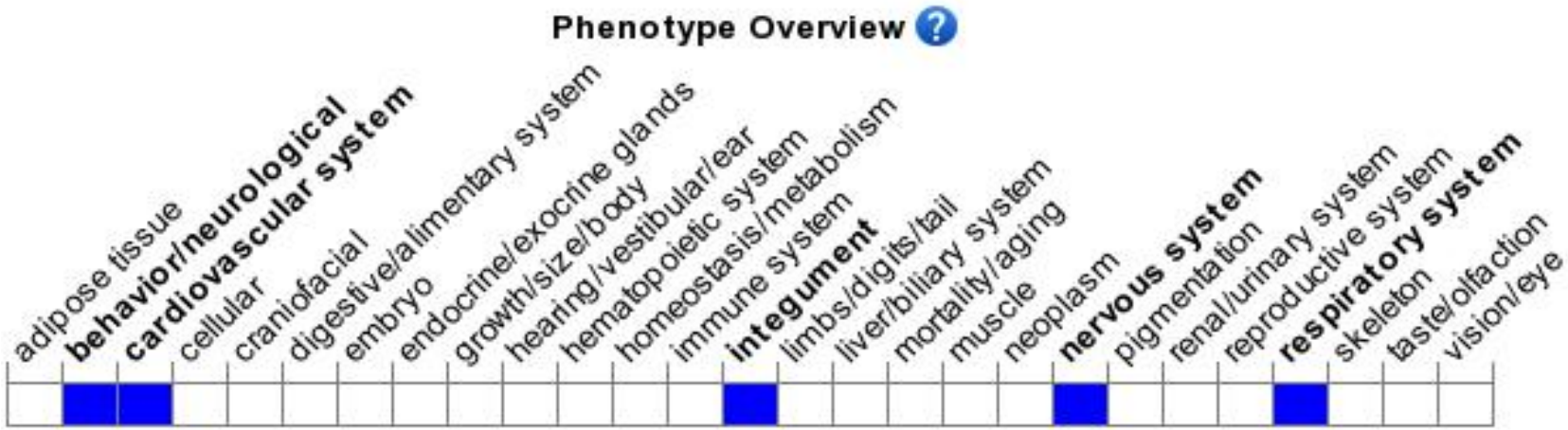


Genomic location distribution



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/).

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