Nalcn Cas9-KO Strategy

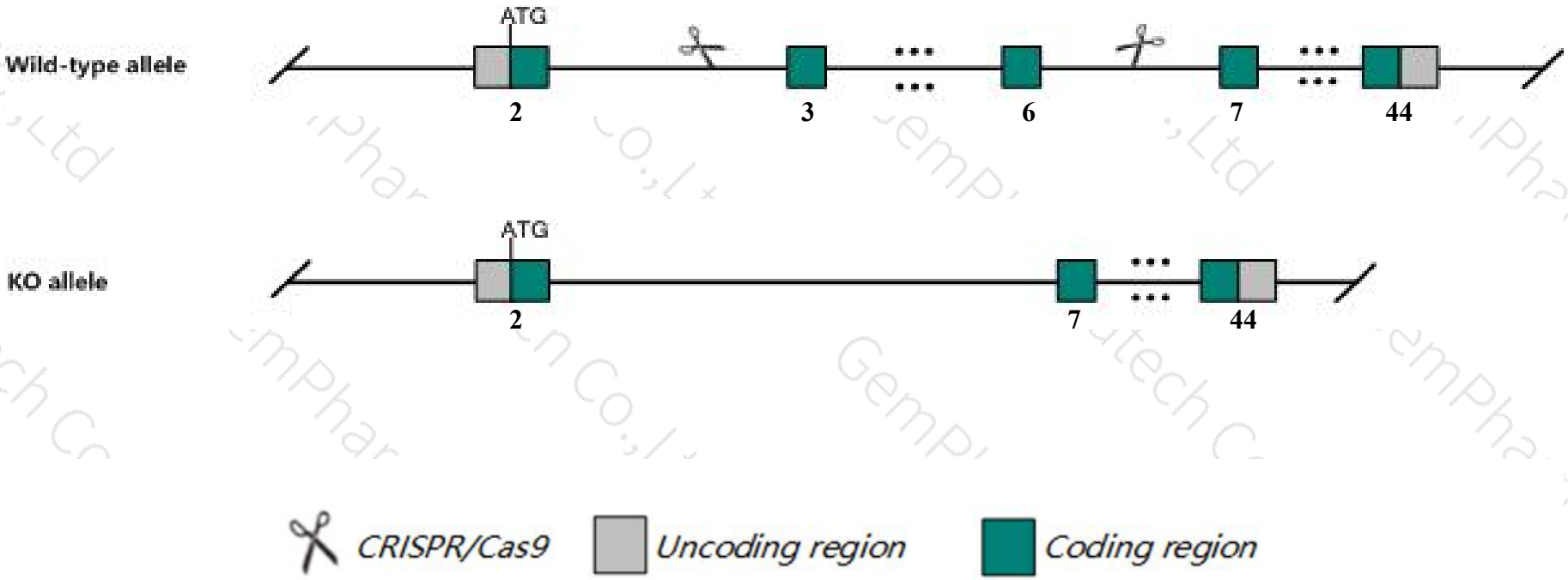
Designer: JiaYu

Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Nalcn* gene has 7 transcripts. According to the structure of *Nalcn* gene, exon3-exon6 of *Nalcn-201* (ENSMUST00000000201.6) transcript is recommended as the knockout region.The region contains 536bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nalcn* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a null allele exhibit abnormal breathing at birth and die within 24 hours. Mice homozygous for a gain of function ENU mutation exhibit reduced the total amount and episode duration of REMS.

➢ The *Nalcn* gene is located on the Chr14. 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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Nalcn sodium leak channel, non-selective [Mus musculus (house mouse)]

Gene ID: 338370, updated on 31-Jan-2019

Summary

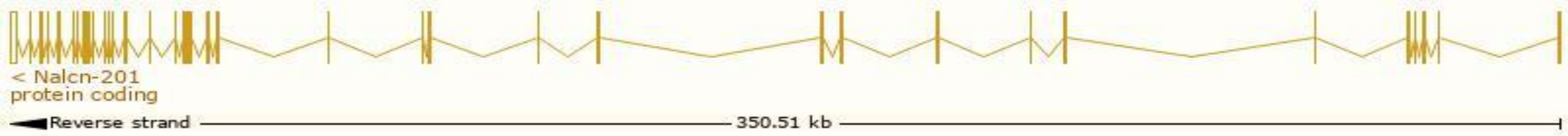
Official Symbol	Nalcn provided by MGI
Official Full Name	sodium leak channel, non-selective provided by MGI
Primary source	MGI:MGI:2444306
See related	Ensembl:ENSMUSG00000000197
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A530023G15Rik, AI849508, Vgcnl1
Expression	Biased expression in frontal lobe adult (RPKM 7.8), cerebellum adult (RPKM 7.7) and 8 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

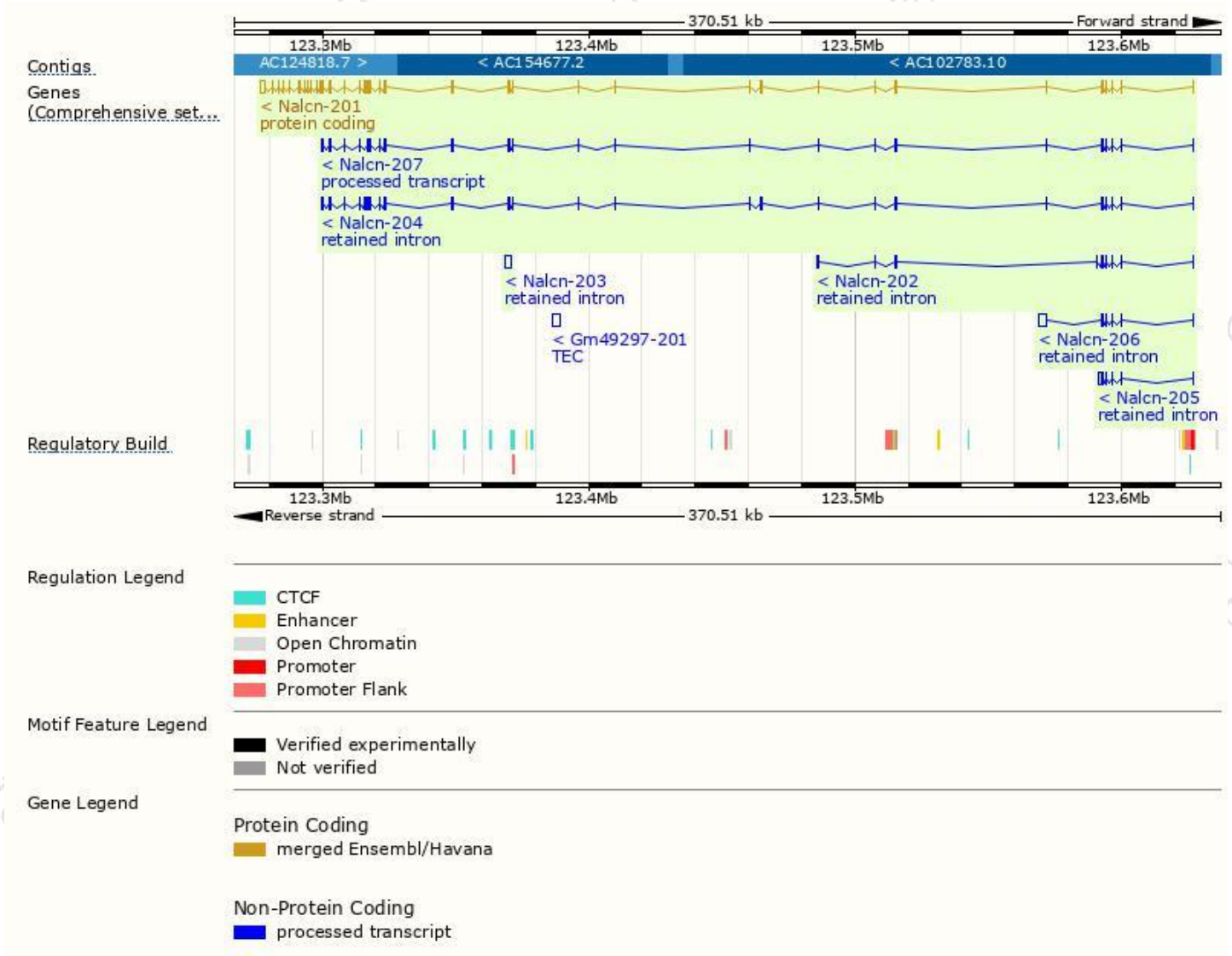
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nalcn-201	ENSMUST00000000201.6	7122	1739aa	Protein coding	CCDS37023	E9QLE4	TSL:5 GENCODE basic APPRIS P1
Nalcn-207	ENSMUST00000228860.1	3802	No protein	Processed transcript	-	-	
Nalcn-206	ENSMUST00000228789.1	3933	No protein	Retained intron	-	-	
Nalcn-204	ENSMUST00000227818.1	3862	No protein	Retained intron	-	-	
Nalcn-202	ENSMUST00000226617.1	2327	No protein	Retained intron	-	-	
Nalcn-203	ENSMUST00000227541.1	2307	No protein	Retained intron	-	-	
Nalcn-205	ENSMUST00000228766.1	2051	No protein	Retained intron	-	-	

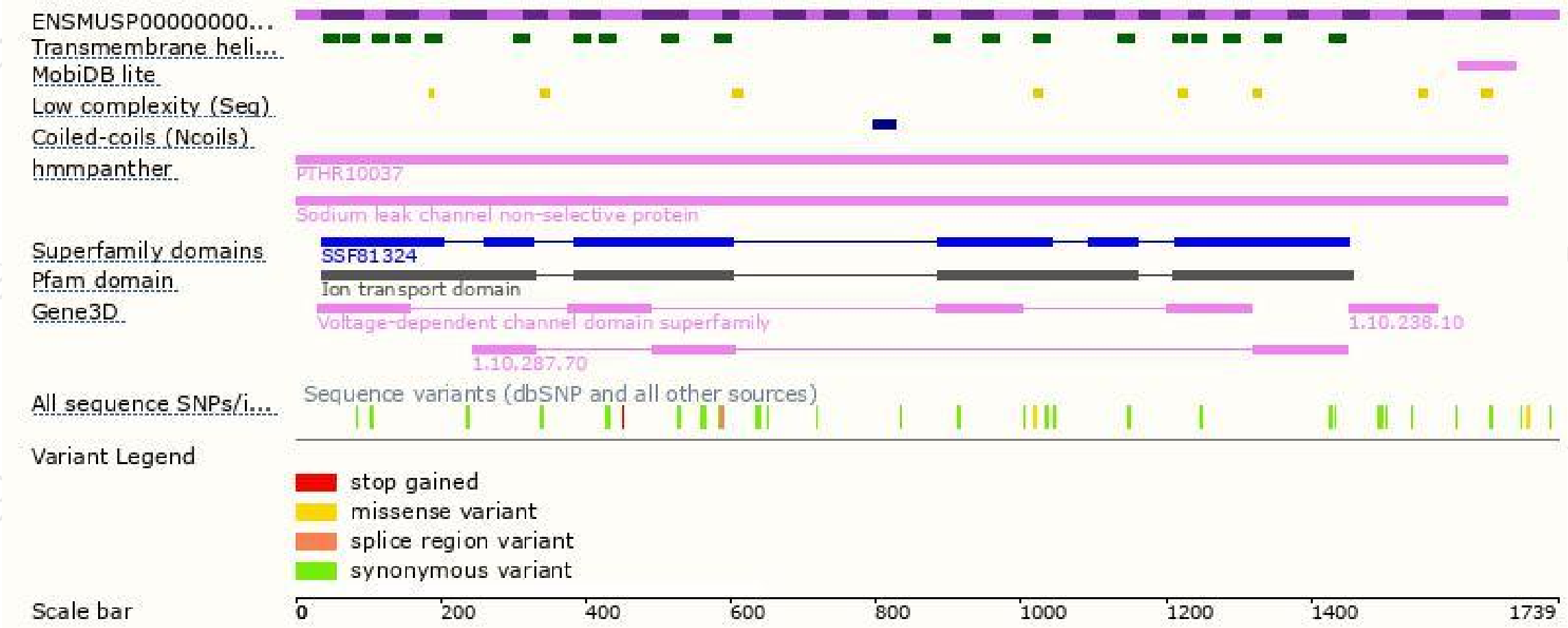
The strategy is based on the design of *Nalcn-201* transcript,The transcription is shown below



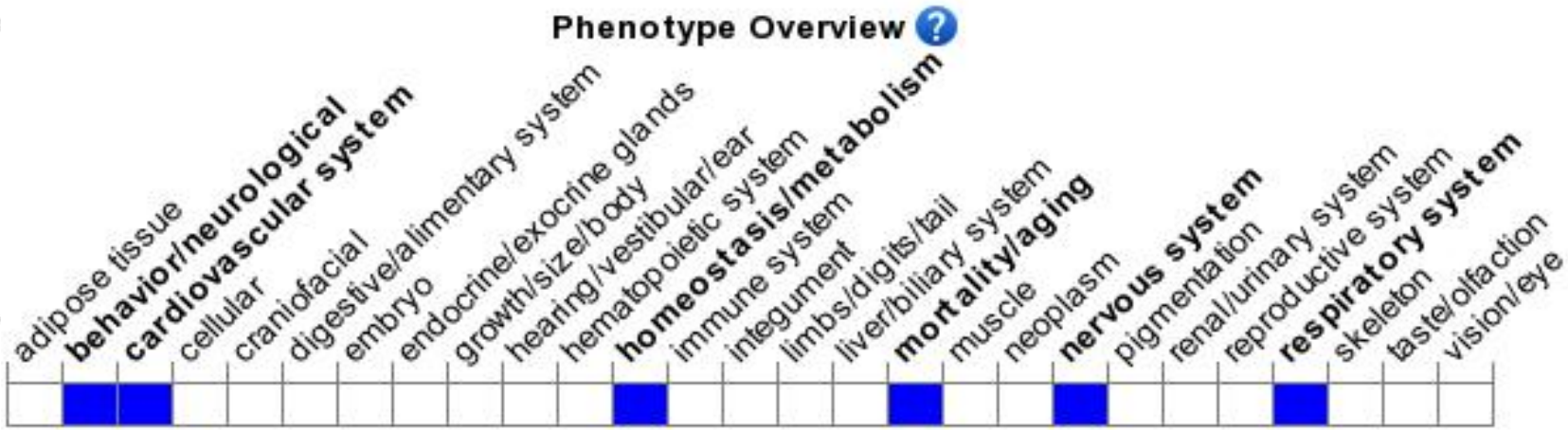
Genomic location distribution



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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