Slc9a9 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

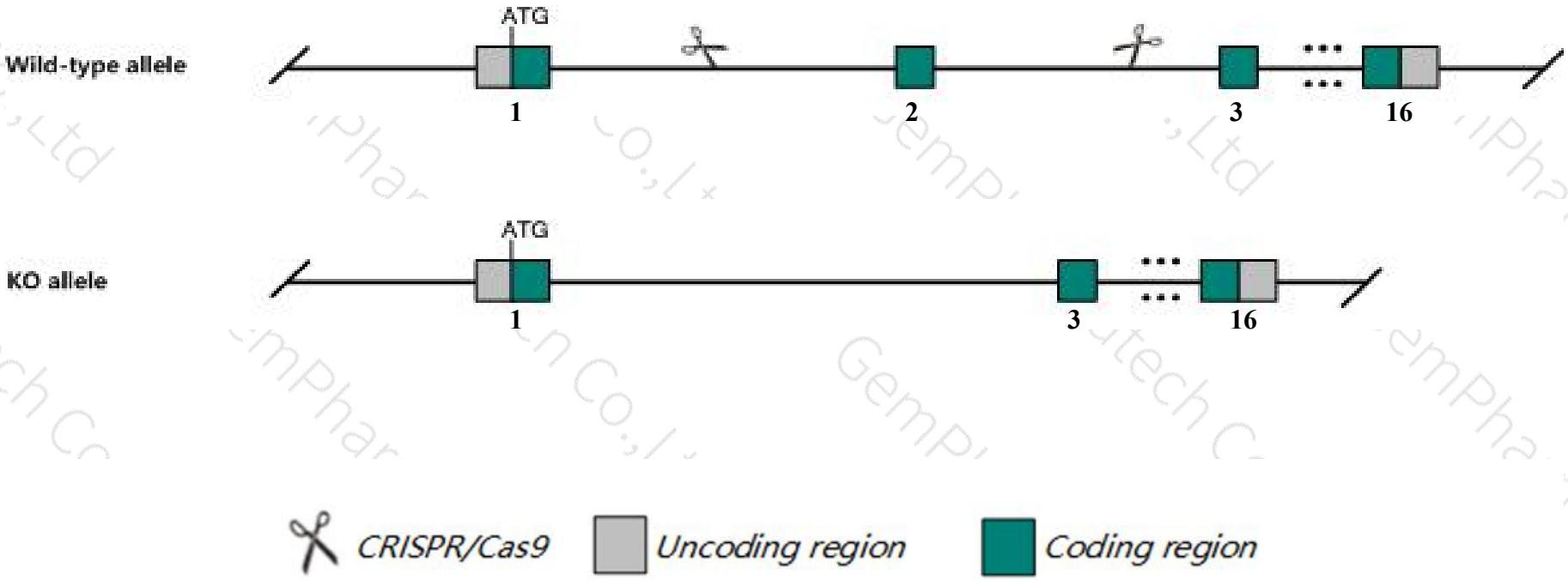
Design Date: 2020-2-21

Project Overview

Project Name	***Slc9a9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc9a9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc9a9* gene has 3 transcripts. According to the structure of *Slc9a9* gene, exon2 of *Slc9a9-201* (ENSMUST00000033463.9) transcript is recommended as the knockout region.The region contains 203bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc9a9* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a null allele display abnormal social and olfactory behavior, abnormal CNS synaptic transmission, impaired synaptic vesicle exocytosis, impaired presynaptic calcium entry, and decreased synaptic vescile pH.

- The *Slc9a9* 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）

集萃药康 GemPharmatech

Slc9a9 solute carrier family 9 (sodium/hydrogen exchanger), member 9 [Mus musculus (house mouse)]

Gene ID: 331004, updated on 5-Feb-2019

Summary

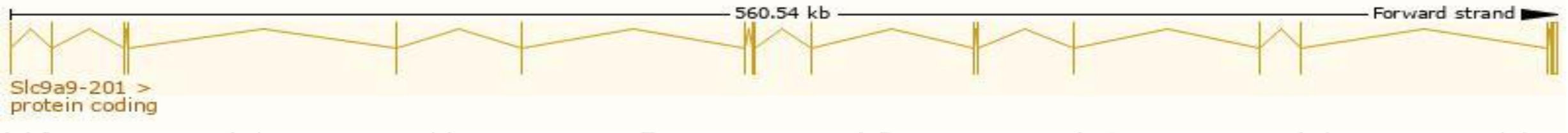
Official Symbol	Slc9a9 provided by MGI
Official Full Name	solute carrier family 9 (sodium/hydrogen exchanger), member 9 provided by MGI
Primary source	MGI:MGI:2679732
See related	Ensembl:ENSMUSG00000031129
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730527A11Rik, 9930105B05, AI854429, Nhe9
Expression	Broad expression in thymus adult (RPKM 14.4), frontal lobe adult (RPKM 5.0) and 20 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

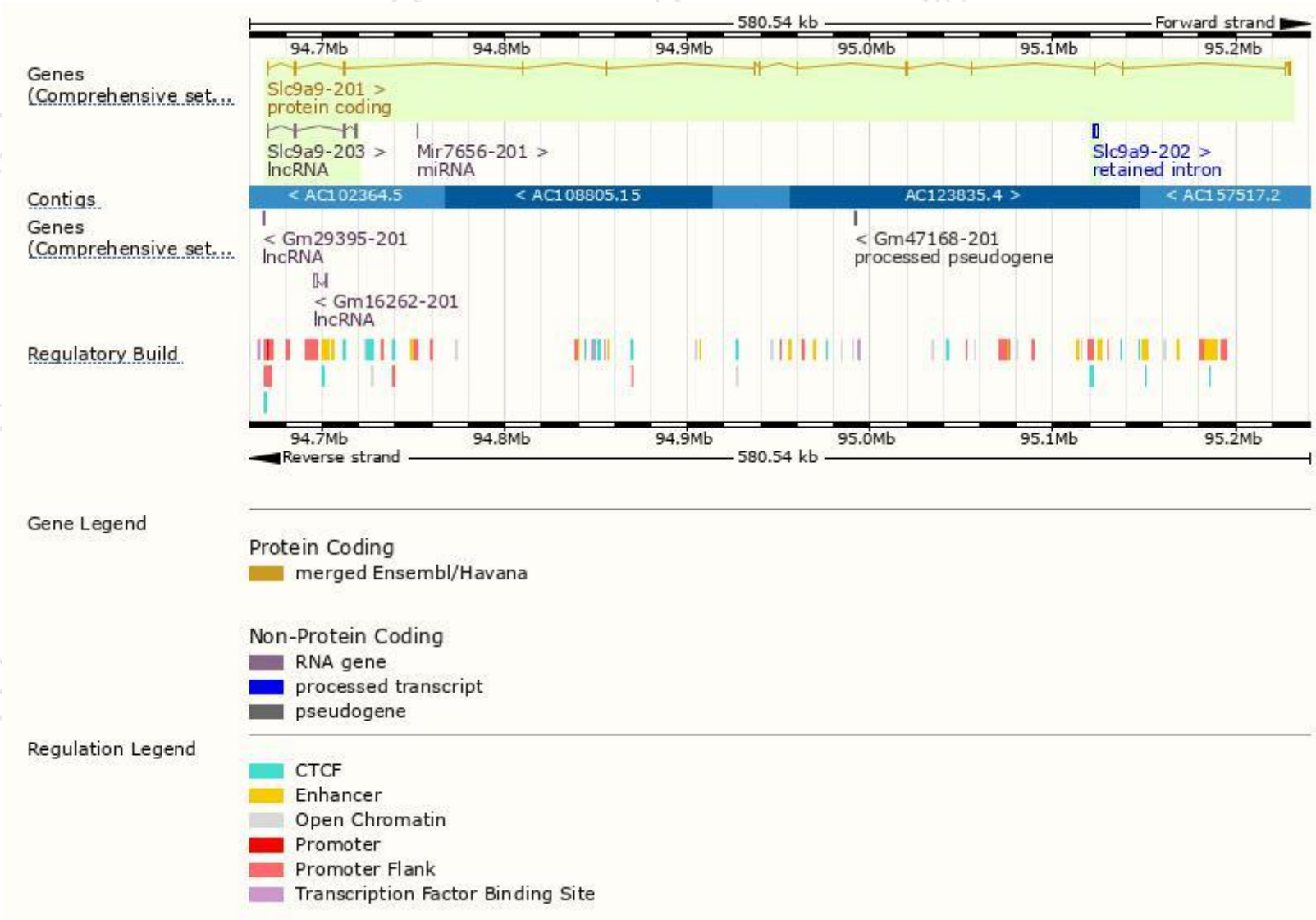
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc9a9-201	ENSMUST00000033463.9	3468	644aa	Protein coding	CCDS40726	Q8BZ00	TSL:1 GENCODE basic APPRIS P1
Slc9a9-202	ENSMUST00000162329.1	1828	No protein	Retained intron	-	-	TSL:1
Slc9a9-203	ENSMUST00000162870.1	1098	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Slc9a9-201* transcript,The transcription is shown below

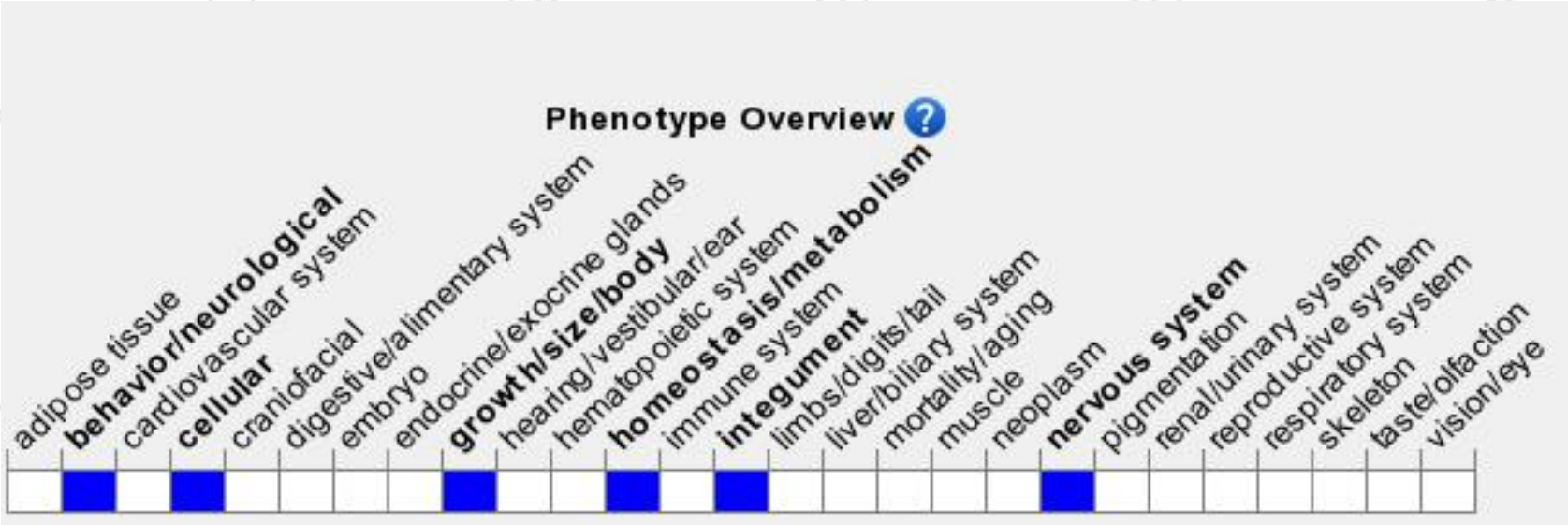


Genomic location distribution



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,Mice homozygous for a null allele display abnormal social and olfactory behavior, abnormal CNS synaptic transmission, impaired synaptic vesicle exocytosis, impaired presynaptic calcium entry, and decreased synaptic vescile pH.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd