

Slc24a2 Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

Design Date:

2020-2-19

Project Overview

Project Name

Slc24a2

Project type

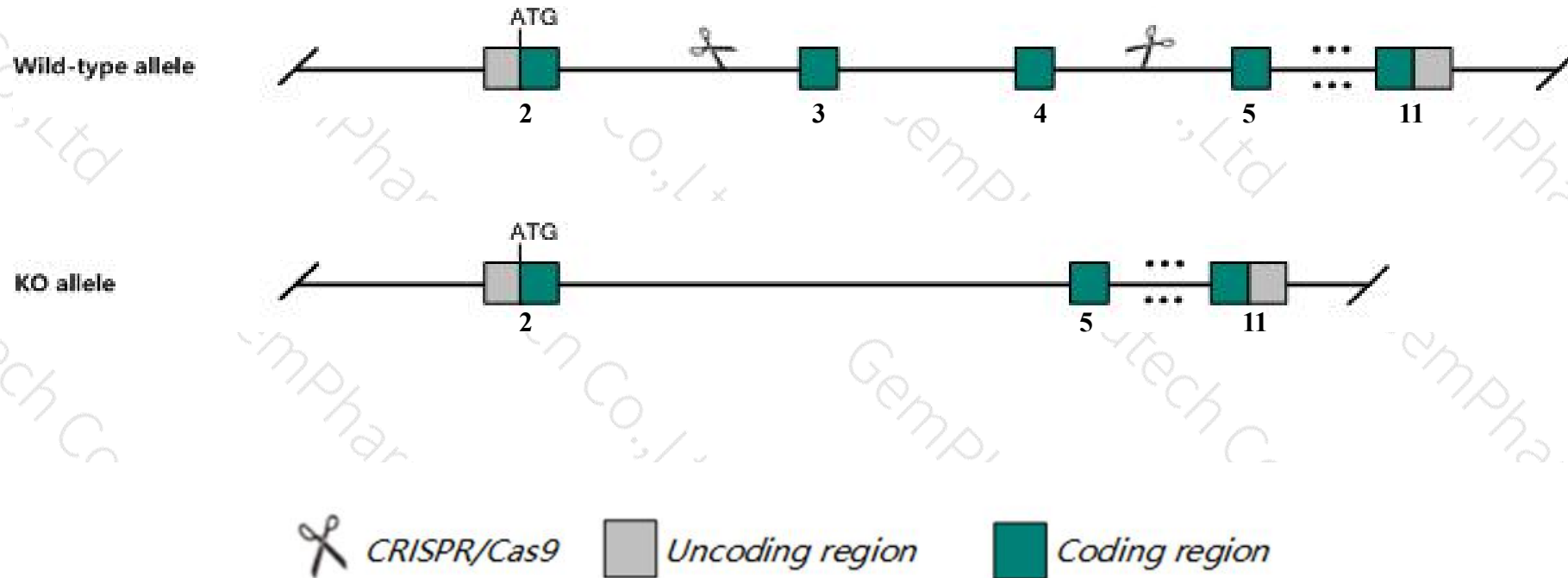
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc24a2* gene. The schematic diagram is as follows:



- The *Slc24a2* gene has 9 transcripts. According to the structure of *Slc24a2* gene, exon3-exon4 of *Slc24a2-203* (ENSMUST00000107157.8) transcript is recommended as the knockout region. The region contains 148bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc24a2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutation of this gene results in loss of long term potentiation and an increase in long term depression and deficits in motor learning and spatial working memory.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Slc24a2* gene is located on the Chr4. 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)

Slc24a2 solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 [Mus musculus (house mouse)]

Gene ID: 76376, updated on 5-Mar-2019

Summary



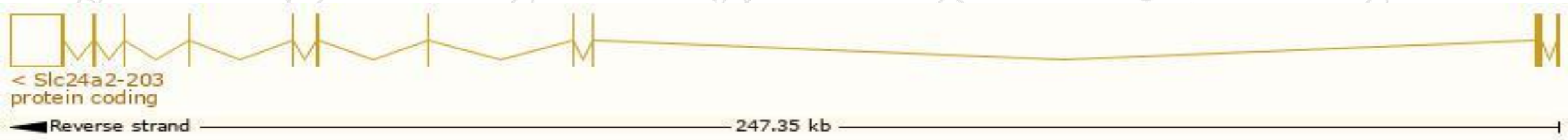
Official Symbol	Slc24a2 provided by MGI
Official Full Name	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 provided by MGI
Primary source	MGI:MGI:1923626
See related	Ensembl:ENSMUSG000000037996
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810021B17Rik, 6330417K15Rik, AI847460, Nckx2
Expression	Biased expression in cortex adult (RPKM 27.0), cerebellum adult (RPKM 20.2) and 2 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

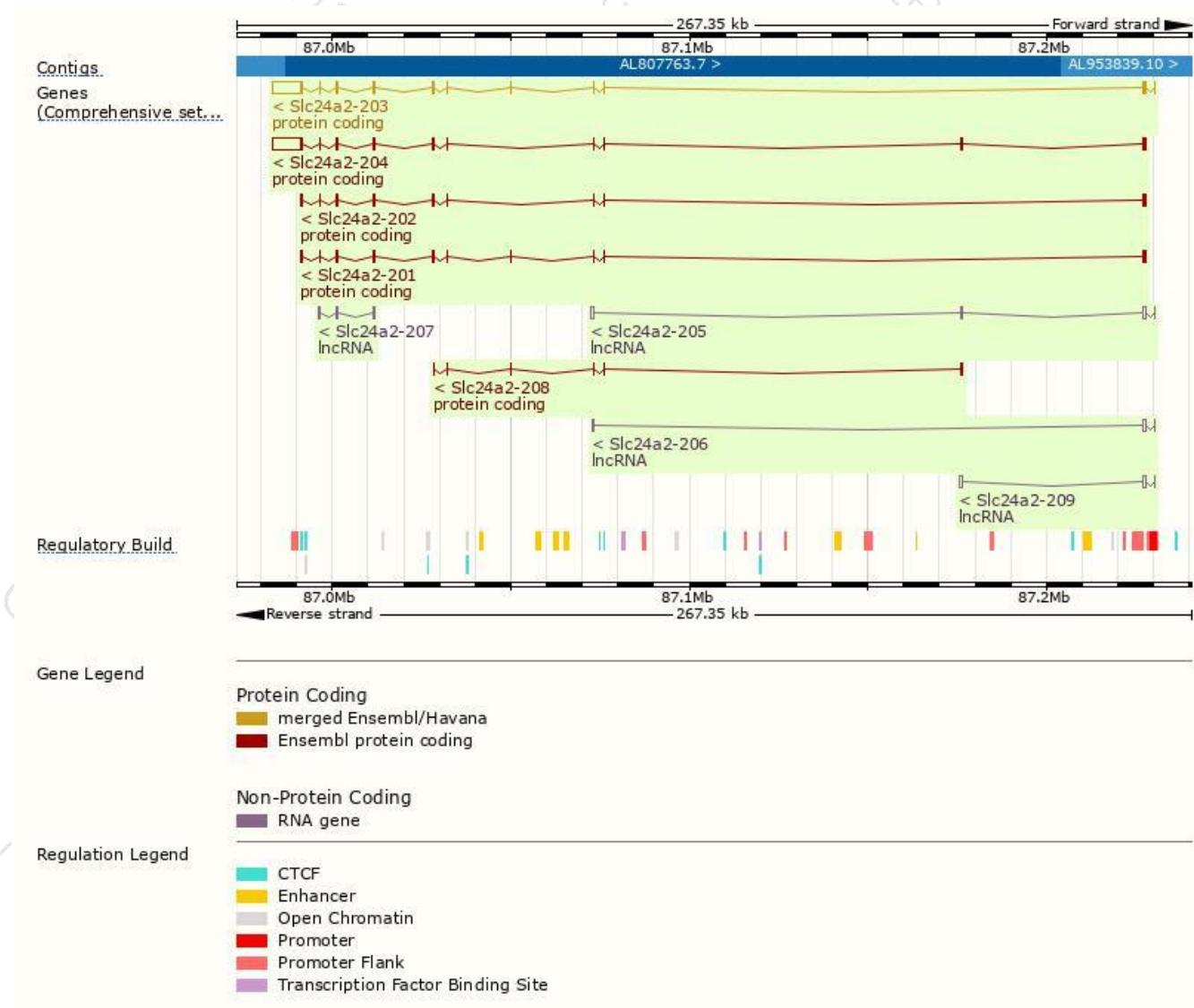
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc24a2-203	ENSMUST00000107157.8	10531	666aa	Protein coding	CCDS18312	Q8BUN9	TSL:1 GENCODE basic APPRIS P2
Slc24a2-204	ENSMUST00000107158.8	10499	711aa	Protein coding	CCDS51220	Q14BI1	TSL:1 GENCODE basic
Slc24a2-201	ENSMUST00000044990.10	2218	662aa	Protein coding	-	B1AXF2	TSL:5 GENCODE basic APPRIS ALT 1
Slc24a2-202	ENSMUST00000107155.7	2171	645aa	Protein coding	-	B1AXF3	TSL:5 GENCODE basic APPRIS ALT 1
Slc24a2-208	ENSMUST00000146815.1	504	168aa	Protein coding	-	F6RT95	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
Slc24a2-205	ENSMUST00000134248.7	2230	No protein	lncRNA	-	-	TSL:2
Slc24a2-209	ENSMUST00000155361.1	1796	No protein	lncRNA	-	-	TSL:2
Slc24a2-206	ENSMUST00000134643.7	1655	No protein	lncRNA	-	-	TSL:2
Slc24a2-207	ENSMUST00000140780.1	679	No protein	lncRNA	-	-	TSL:3

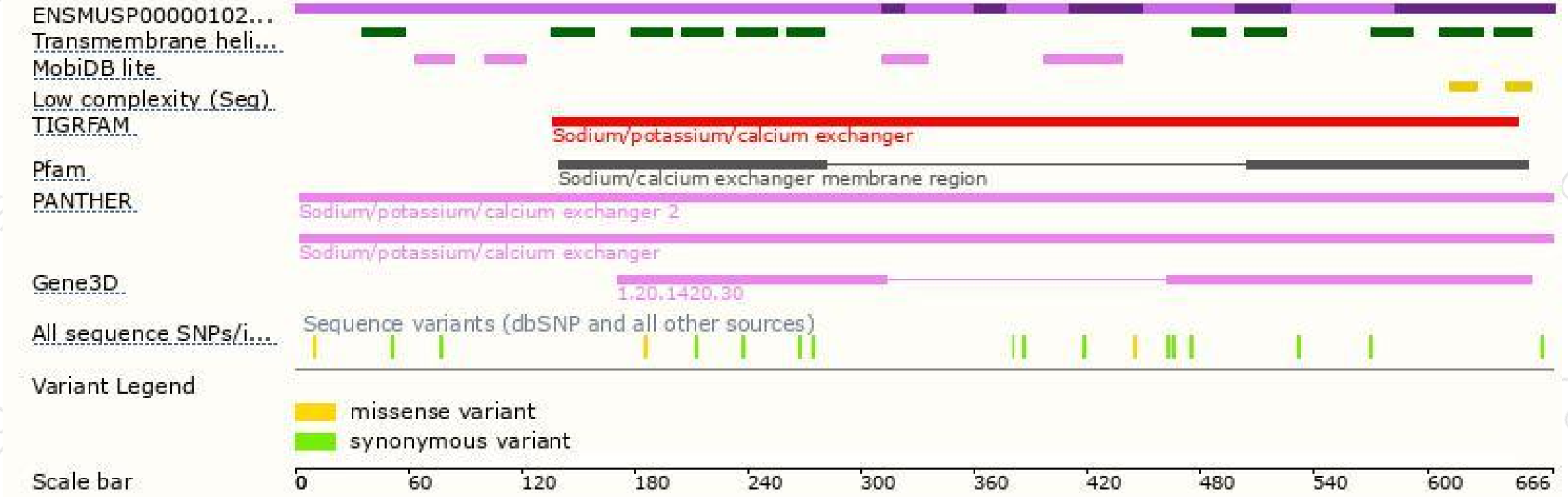
The strategy is based on the design of *Slc24a2-203* transcript,The transcription is shown below



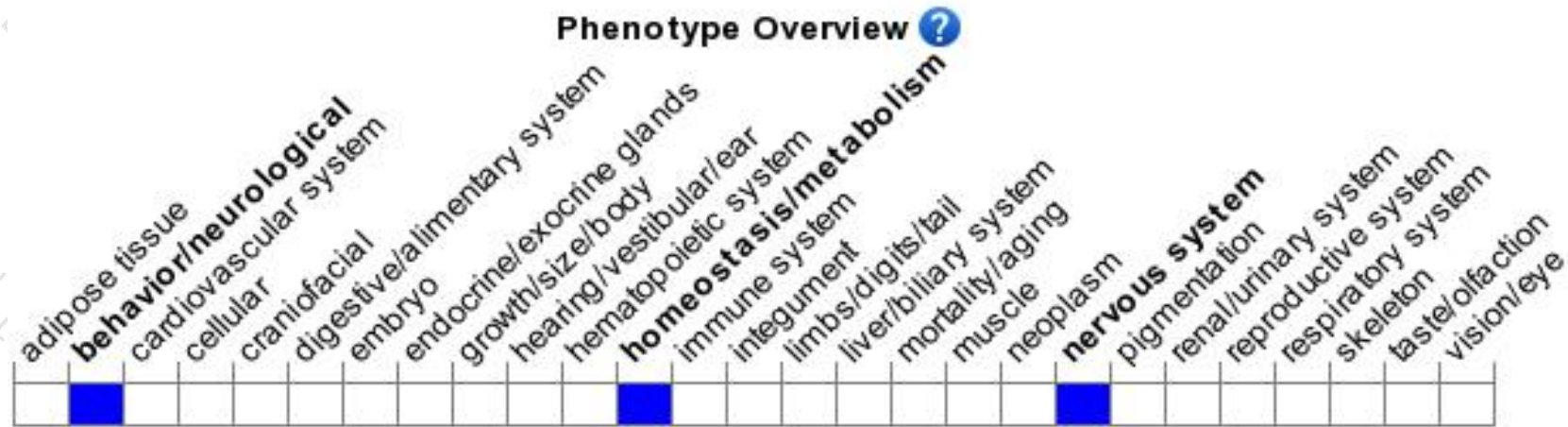
Genomic location distribution



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 loss of long term potentiation and an increase in long term depression and deficits in motor learning and spatial working memory.

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

Tel: 400-9660890

