GemPharmatech™

Slc29a4 Cas9-KO Strategy

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Overview

Target Gene Name

- Slc29a4

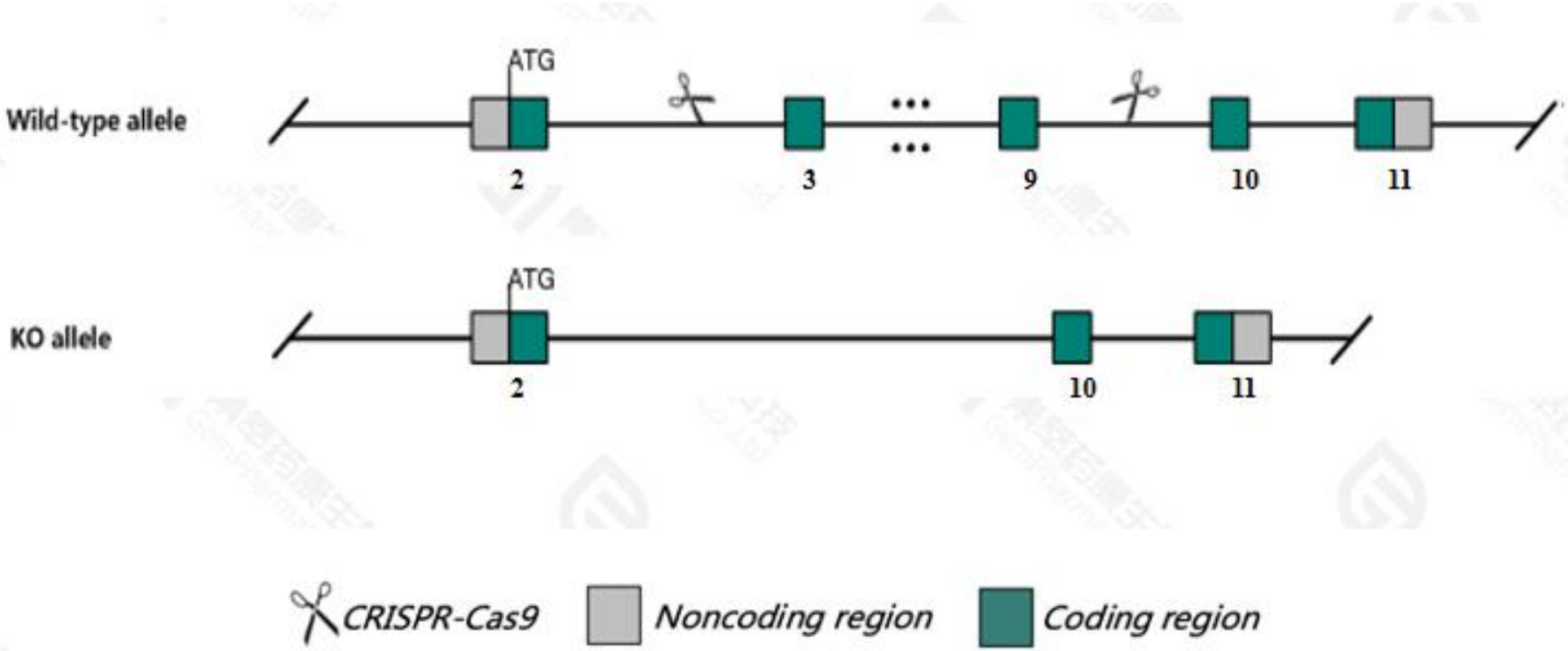
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Slc29a4* gene.

Technical Information

- The *Slc29a4* gene has 2 transcripts. According to the structure of *Slc29a4* gene, exon3-exon9 of *Slc29a4-201*(ENSMUST00000058418.8) transcript is recommended as the knockout region. The region contains 1025bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Slc29a4* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Slc29a4 solute carrier family 29 (nucleoside transporters), member 4 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 243328, updated on 4-Apr-2023

Summary

Official Symbol	Slc29a4 provided by MGI
Official Full Name	solute carrier family 29 (nucleoside transporters), member 4 provided by MGI
Primary source	MGI:MGI:2385330
See related	Ensembl:ENSMUSG00000050822 AllianceGenome:MGI:2385330
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	ENT4; mPMAT
Summary	Enables several functions, including monoamine transmembrane transporter activity; neurotransmitter transmembrane transporter activity; and toxin transmembrane transporter activity. Involved in several processes, including monoamine transport; toxin transport; and xenobiotic transport. Located in apical plasma membrane and basolateral plasma membrane. Is expressed in brain and male reproductive gland or organ. Orthologous to human SLC29A4 (solute carrier family 29 member 4). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in whole brain E14.5 (RPKM 34.0), CNS E14 (RPKM 29.0) and 11 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 5; 5 G2 — See Slc29a4 in Genome Data Viewer

Exon count: 12

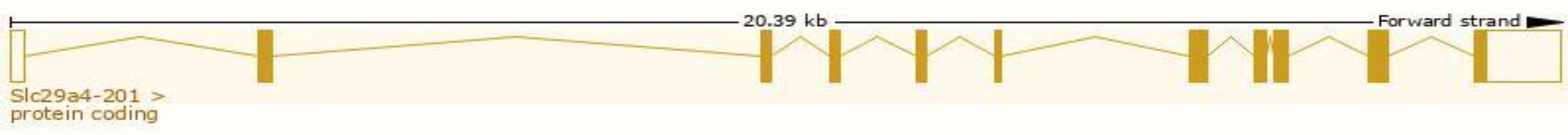
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 2 transcripts, all transcripts are shown below:

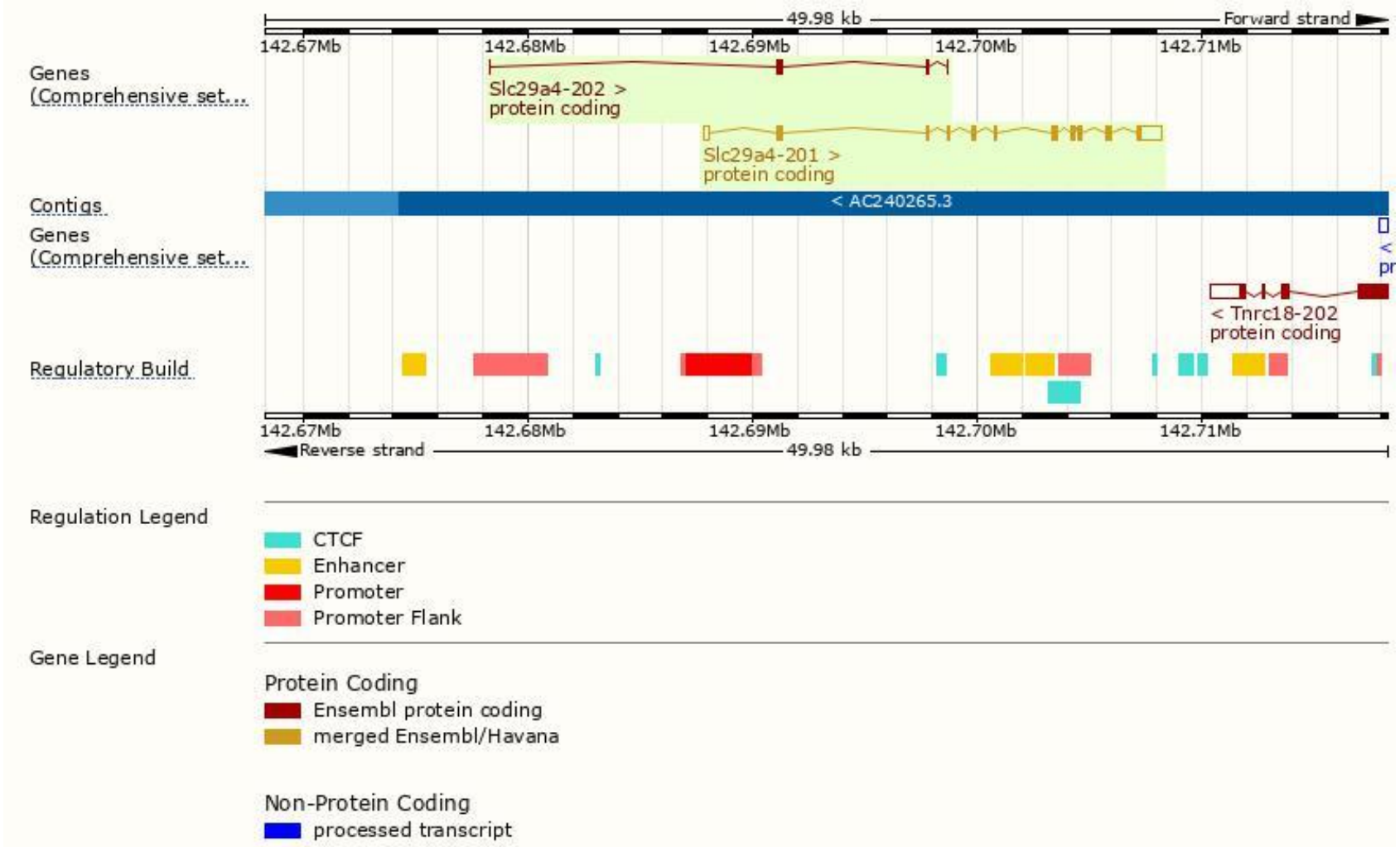
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000058418.8	Slc29a4-201	2789	528aa	Protein coding	CCDS39364	Q8R139	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000198728.5	Slc29a4-202	406	107aa	Protein coding		A0A0G2JE87	TSL:5 CDS 3' incomplete

The strategy is based on the design of *Slc29a4-201* transcript, the transcription is shown below:



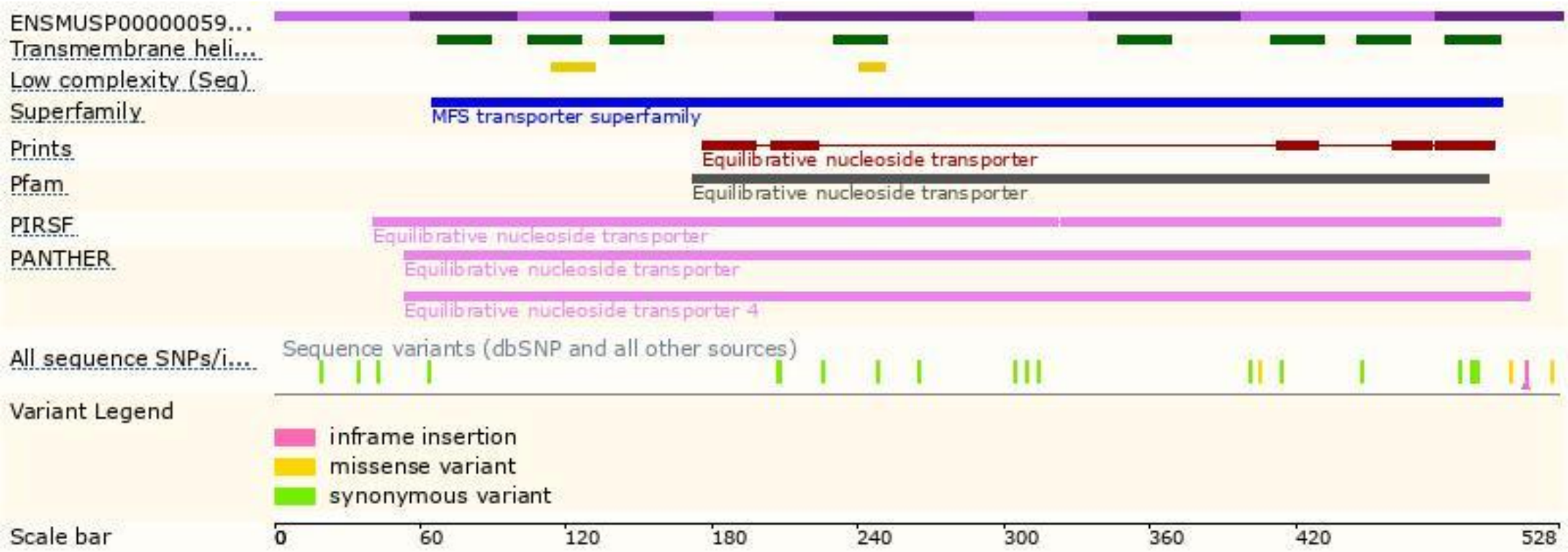
Source: https://www.ensembl.org

Genomic Information



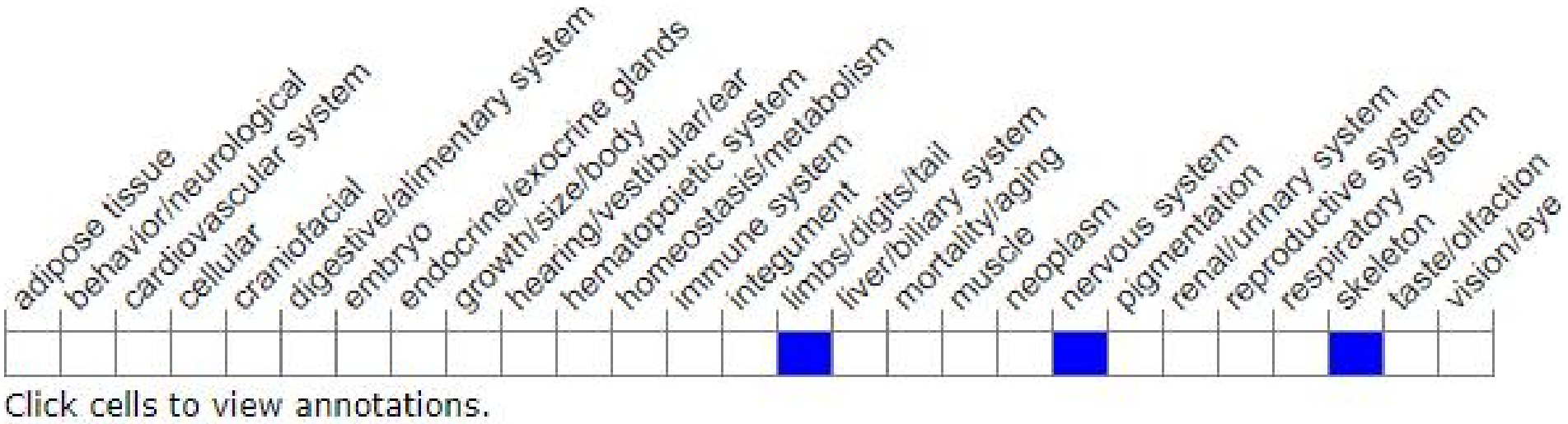
Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Slc29a4* gene are marked in blue. Mice homozygous for a knock-out allele exhibit impaired organic cation and monoamine uptake in the choroid plexus.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data,mice homozygous for a knock-out allele exhibit impaired organic cation and monoamine uptake in the choroid plexus.
- The *Slc29a4* gene is located on the Chr5. 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.