Slc18a1 Cas9-KO Strategy

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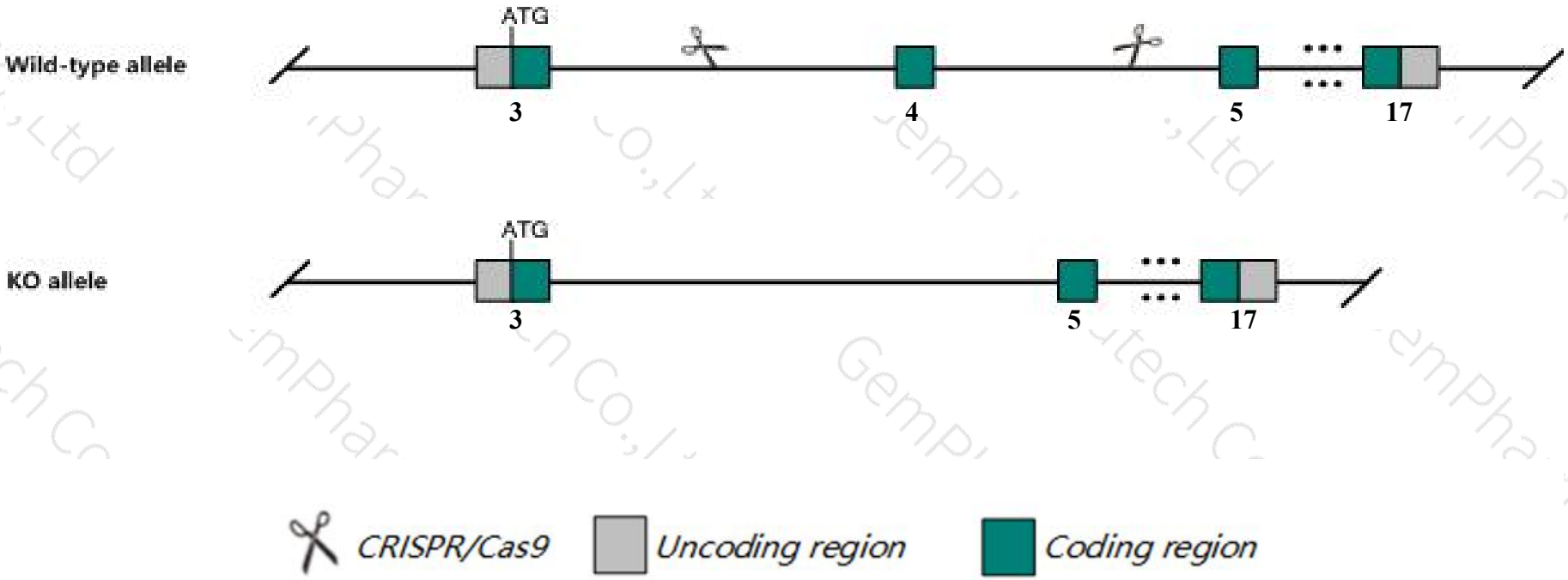
Project Overview

Project Name	***Slc18a1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc18a1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc18a1* gene has 5 transcripts. According to the structure of *Slc18a1* gene, exon4 of *Slc18a1-201* (ENSMUST00000037478.12) transcript is recommended as the knockout region.The region contains 355bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc18a1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit increased neuron apoptosis, decreased neuron proliferation and impaired spatial object recognition.

- The transcript *Slc18a1-205* is incomplete, so the effect on it is unknown.

- The *Slc18a1* gene is located on the Chr8. 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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Slc18a1 solute carrier family 18 (vesicular monoamine), member 1 [*Mus musculus* (house mouse)]

Gene ID: 110877, updated on 12-Aug-2019

Summary

Official Symbol	Slc18a1 provided by MGI
Official Full Name	solute carrier family 18 (vesicular monoamine), member 1 provided by MGI
Primary source	MGI:MGI:106684
See related	Ensembl:ENSMUSG00000036330
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	Vat1; Vmat1; 4832416I10Rik
Expression	Biased expression in kidney adult (RPKM 38.4), adrenal adult (RPKM 4.8) and 2 other tissues See more
Orthologs	human all

Genomic context

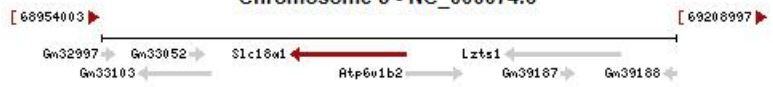
Location: 8 B3.3; 8 33.88 cM

See Slc18a1 in Genome Data Viewer

Exon count: 17

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	8	NC_000074.6 (69037708..69089238, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	8	NC_000074.5 (71561607..71613121, complement)

Chromosome 8 - NC_000074.6

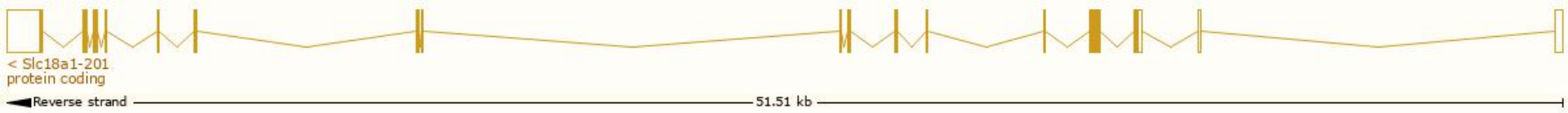


Transcript information（Ensembl）

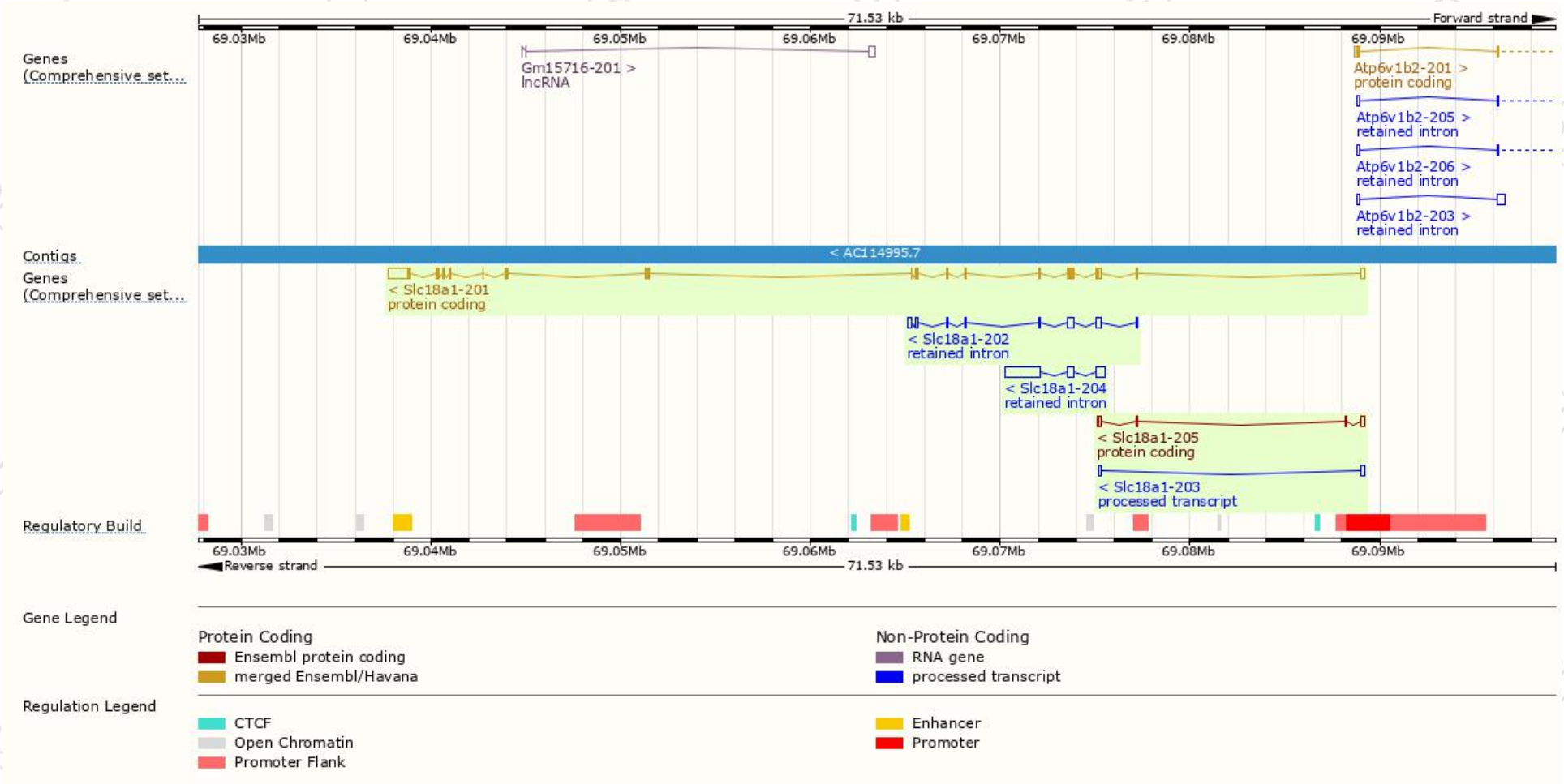
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc18a1-201	ENSMUST00000037478.12	3115	521aa	Protein coding	CCDS22344	Q32XG7 Q8R090	TSL:1 GENCODE basic APPRIS P1
Slc18a1-205	ENSMUST00000148856.1	613	19aa	Protein coding	-	A0A1D5RLM7	CDS 3' incomplete TSL:3
Slc18a1-203	ENSMUST00000142710.1	366	No protein	Processed transcript	-	-	TSL:2
Slc18a1-204	ENSMUST00000147674.1	2697	No protein	Retained intron	-	-	TSL:1
Slc18a1-202	ENSMUST00000142548.7	1221	No protein	Retained intron	-	-	TSL:1

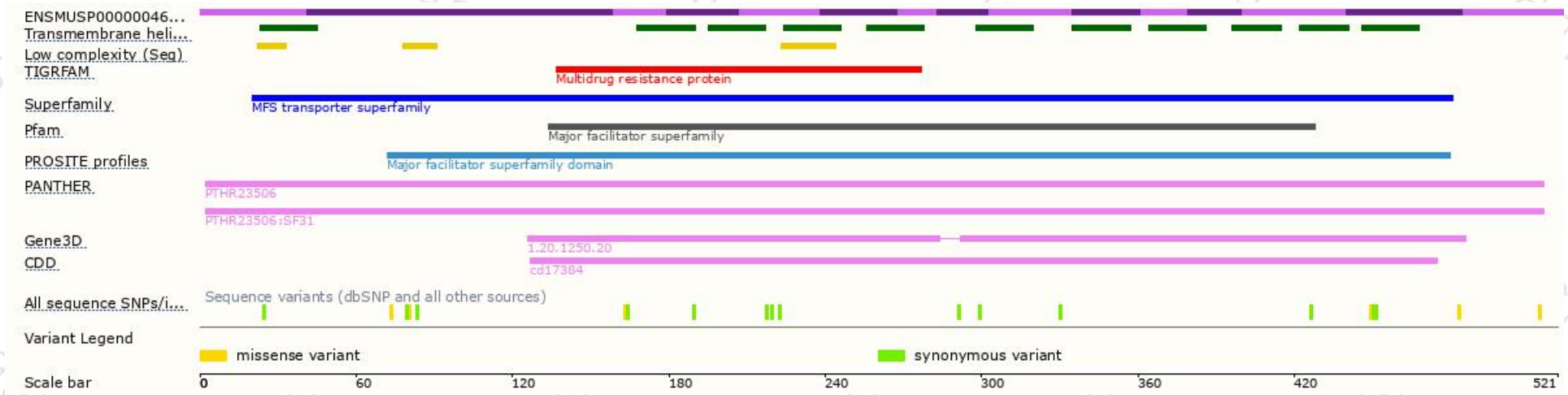
The strategy is based on the design of *Slc18a1-201* transcript,The transcription is shown below



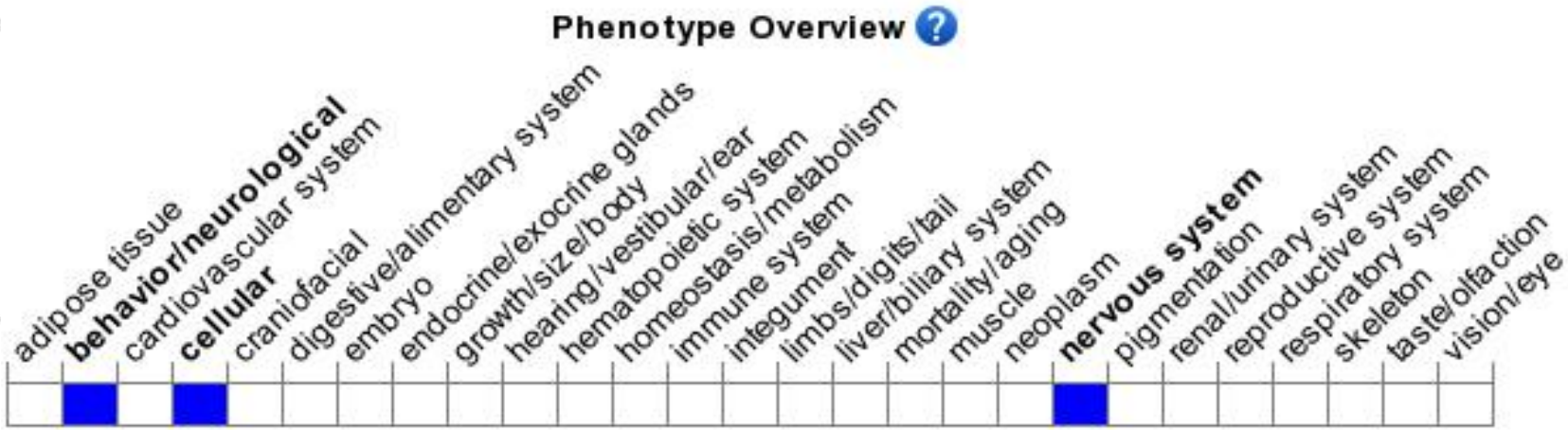
Genomic location distribution



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 knock-out allele exhibit increased neuron apoptosis, decreased neuron proliferation and impaired spatial object recognition.

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

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