

Slc18a2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Slc18a2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc18a2* gene. The schematic diagram is as follows:



- The *Slc18a2* gene has 2 transcripts. According to the structure of *Slc18a2* gene, exon3 of *Slc18a2-201* (ENSMUST00000026084.4) transcript is recommended as the knockout region. The region contains 352bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc18a2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Nullizygous mice exhibit early postnatal death accompanied by reduced body size, hypokinesia, and reduced brain monoamine levels. Hypomorphic mutants show impaired olfaction, gastroparesis, altered sleep latency, neuron degeneration, enhanced MPTP sensitivity, anxiety- and depressive-like behavior.
- The knockout region is about 1.3 kb from the 5th end of *Gm29261*, which may affect the regulation of the 5th end of the gene.
- The *Slc18a2* gene is located on the Chr19. 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)

Slc18a2 solute carrier family 18 (vesicular monoamine), member 2 [*Mus musculus* (house mouse)]

Gene ID: 214084, updated on 10-Oct-2019

Summary

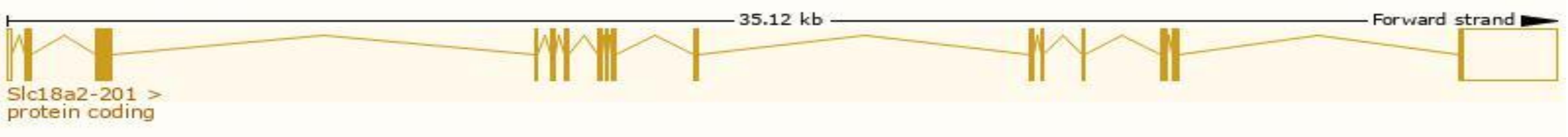
Official Symbol	Slc18a2 provided by MGI
Official Full Name	solute carrier family 18 (vesicular monoamine), member 2 provided by MGI
Primary source	MGI:MGI:106677
See related	Ensembl:ENSMUSG00000025094
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Vmat2; 9330105E13; 1110037L13Rik
Expression	Biased expression in ovary adult (RPKM 36.9), whole brain E14.5 (RPKM 10.7) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

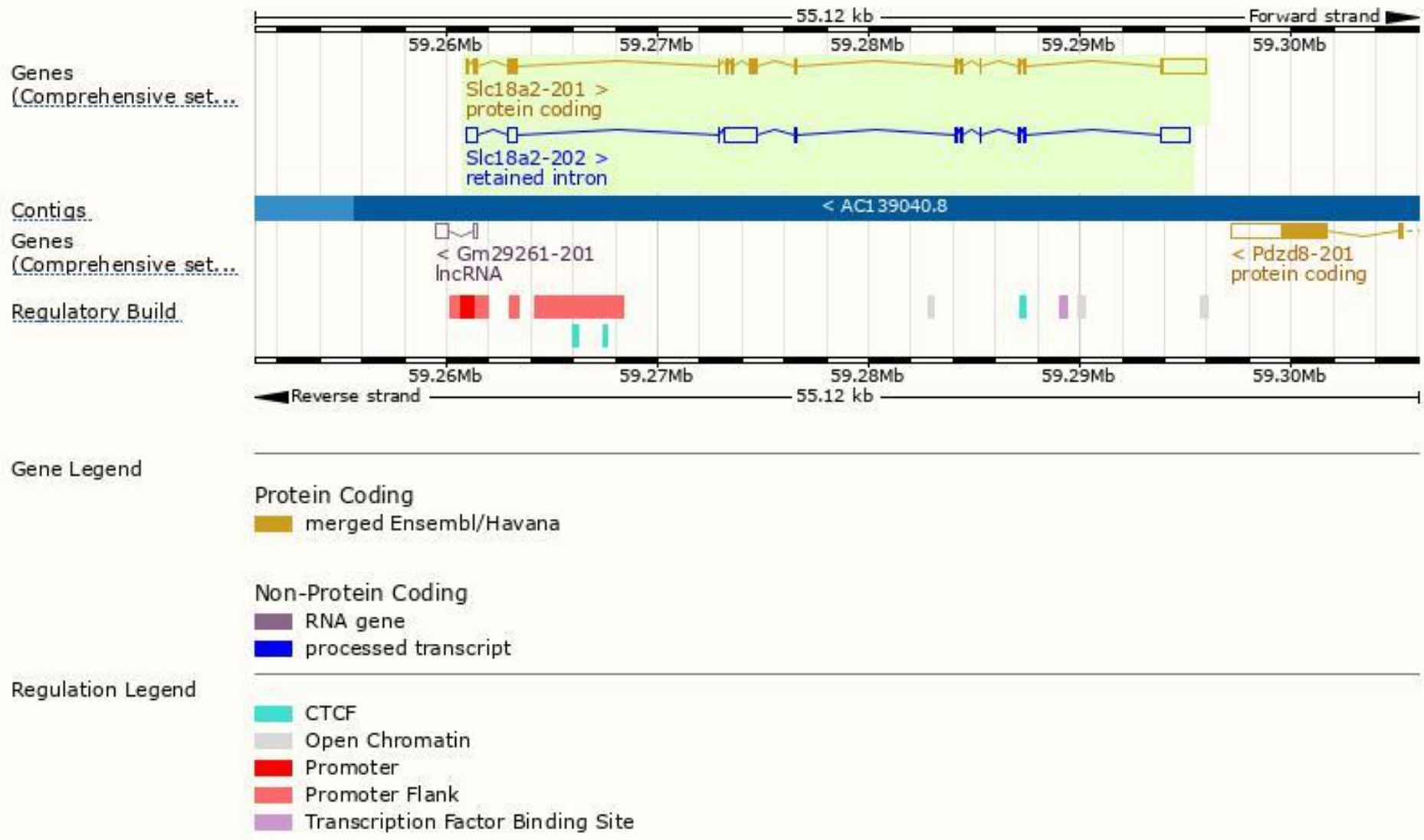
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc18a2-201	ENSMUST00000026084.4	3785	517aa	Protein coding	CCDS29935	Q8BRU6	TSL:1 GENCODE basic APPRIS P1
Slc18a2-202	ENSMUST00000236270.1	4393	No protein	Retained intron	-	-	

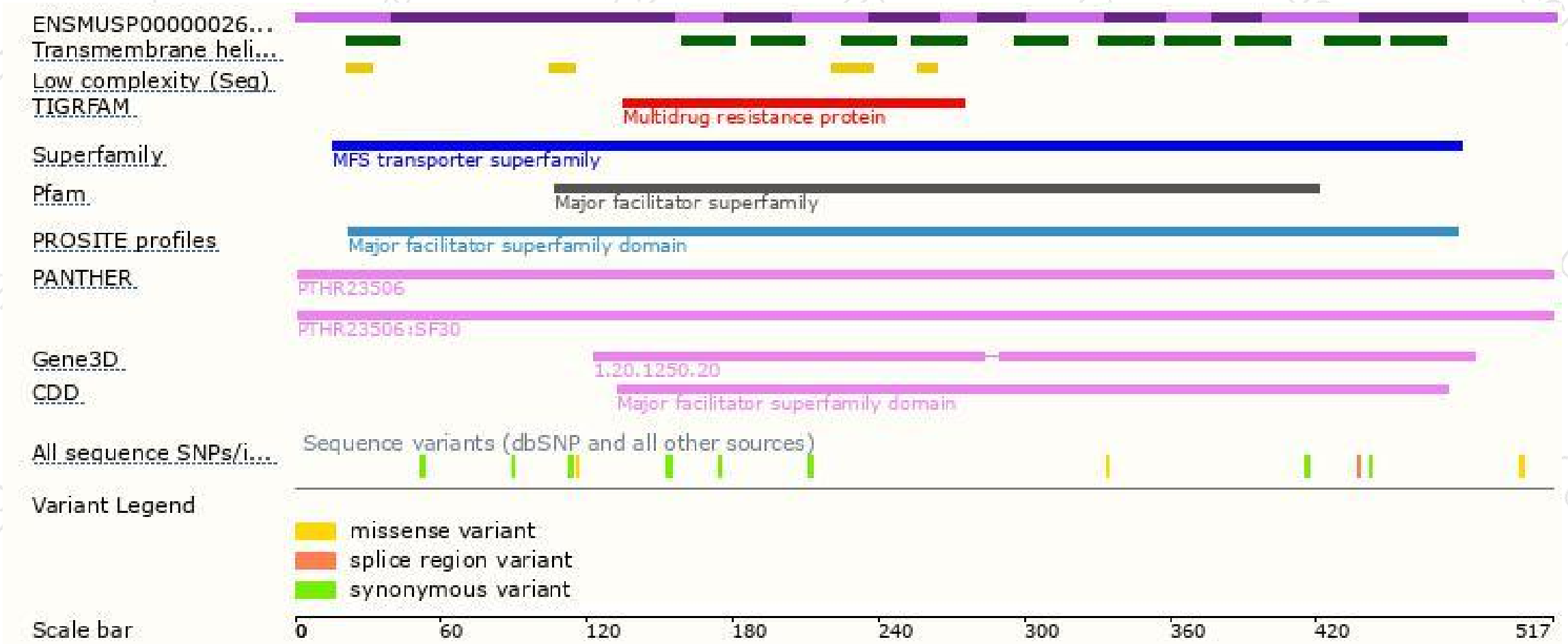
The strategy is based on the design of *Slc18a2-201* transcript,The transcription is shown below



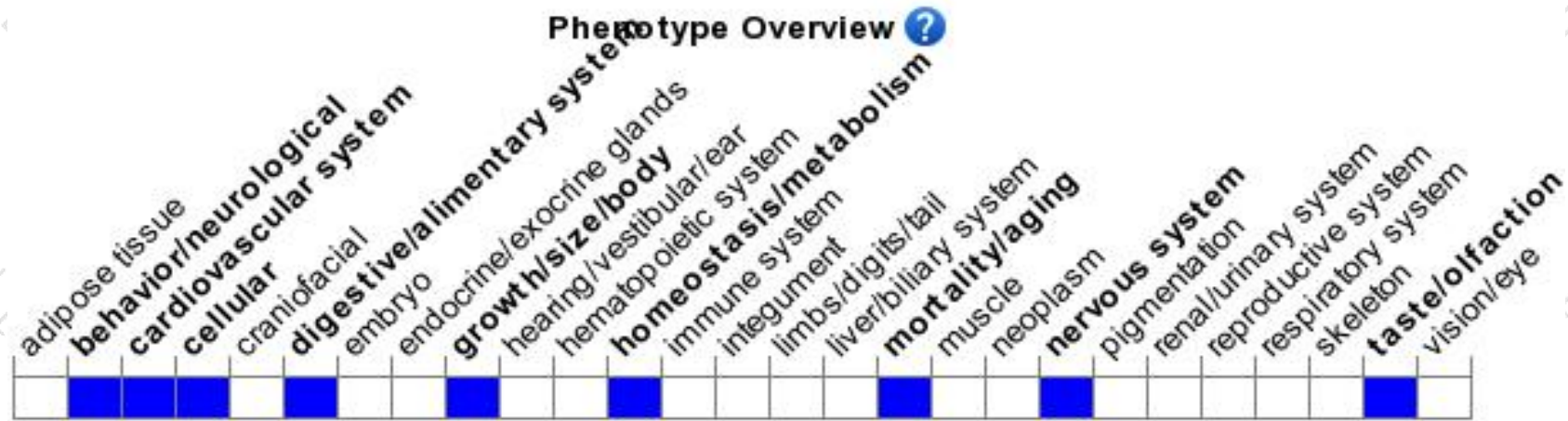
Genomic location distribution



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, Nullizygous mice exhibit early postnatal death accompanied by reduced body size, hypokinesia, and reduced brain monoamine levels. Hypomorphic mutants show impaired olfaction, gastroparesis, altered sleep latency, neuron degeneration, enhanced MPTP sensitivity, anxiety- and depressive-like behavior.

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

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