

***Slc18b1* Cas9-KO Strategy**

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Project Overview

Project Name

Slc18b1

Project type

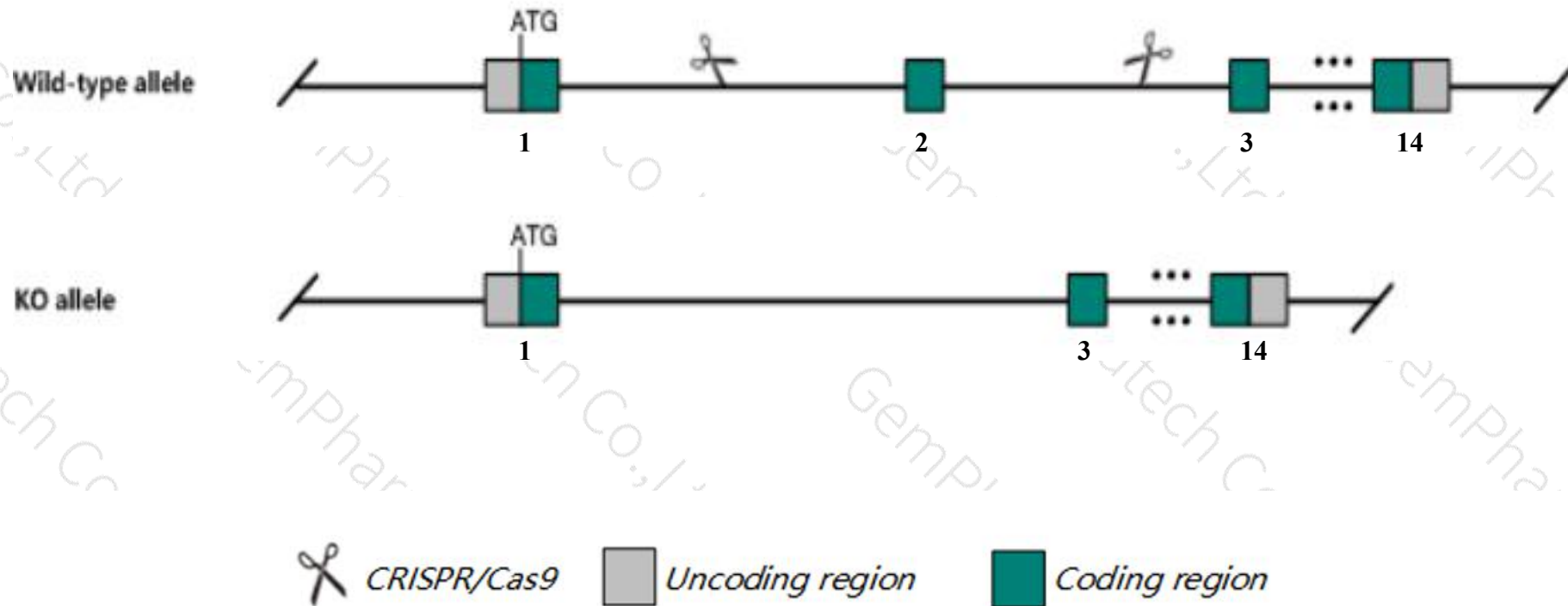
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc18b1* gene. The schematic diagram is as follows:



- The *Slc18b1* gene has 6 transcripts. According to the structure of *Slc18b1* gene, exon2 of *Slc18b1*-201(ENSMUST00000119597.7) transcript is recommended as the knockout region. The region contains 140bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc18b1* gene. The brief process is as follows: CRISPR/Cas9 system 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, mice homozygous for a conditional allele ubiquitously activated exhibit reduced brain polyamine levels, impaired memory and altered response to addictive substances.
- Transcript *Slc18b1*-205 may not be affected.
- The *Slc18b1* gene is located on the Chr10. 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)

Slc18b1 solute carrier family 18, subfamily B, member 1 [Mus musculus (house mouse)]

Gene ID: 76306, updated on 13-Mar-2020

Summary



Official Symbol Slc18b1 provided by [MGI](#)

Official Full Name solute carrier family 18, subfamily B, member 1 provided by [MGI](#)

Primary source [MGI:MGI:1923556](#)

See related [Ensembl:ENSMUSG00000037455](#)

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 1110021L09Rik

Expression Ubiquitous expression in subcutaneous fat pad adult (RPKM 9.6), large intestine adult (RPKM 9.6) and 26 other tissues [See more](#)

Orthologs [human](#) [all](#)

Transcript information (Ensembl)

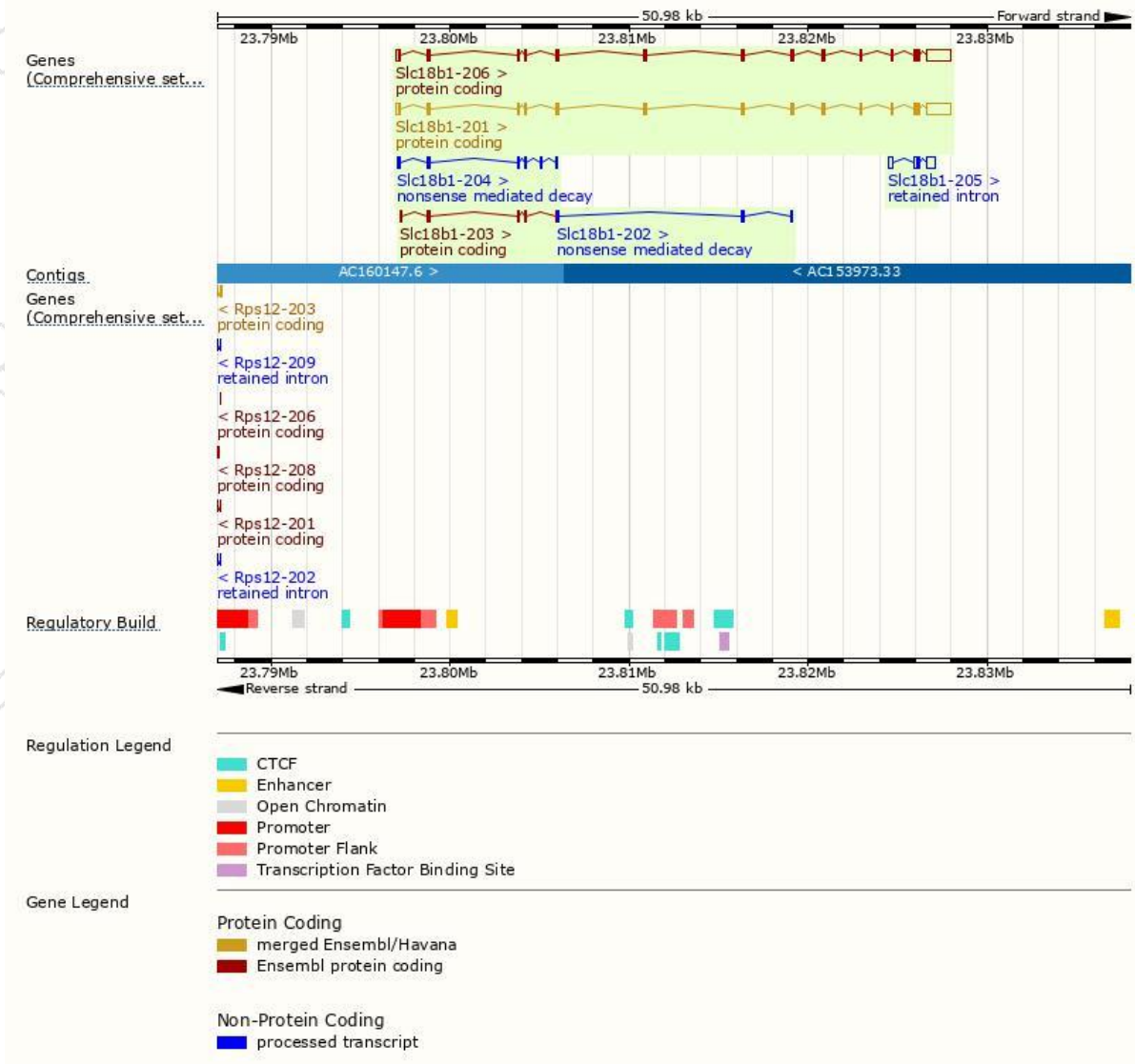
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc18b1-201	ENSMUST00000119597.7	2837	457aa	Protein coding	CCDS48521	E9PU92	TSL:5 GENCODE basic APPRIS P1
Slc18b1-206	ENSMUST00000179321.7	2843	459aa	Protein coding	-	D3Z5L6	TSL:5 GENCODE basic
Slc18b1-203	ENSMUST00000133289.1	437	142aa	Protein coding	-	D3Z2W5	CDS 3' incomplete TSL:1
Slc18b1-204	ENSMUST00000134170.7	617	130aa	Nonsense mediated decay	-	D6RGT8	TSL:3
Slc18b1-202	ENSMUST00000127841.1	224	42aa	Nonsense mediated decay	-	F6WI82	CDS 5' incomplete TSL:1
Slc18b1-205	ENSMUST00000143931.1	916	No protein	Retained intron	-	-	TSL:3

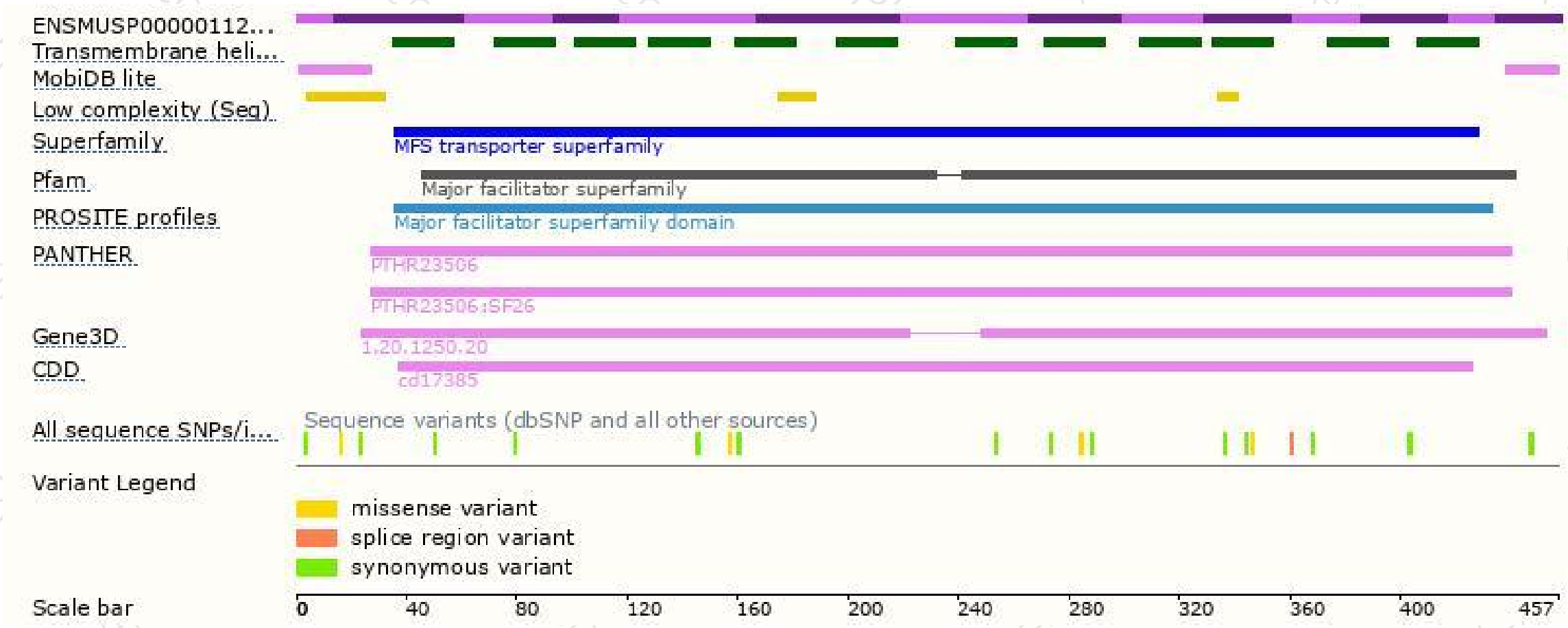
The strategy is based on the design of *Slc18b1-201* transcript,the transcription is shown below:



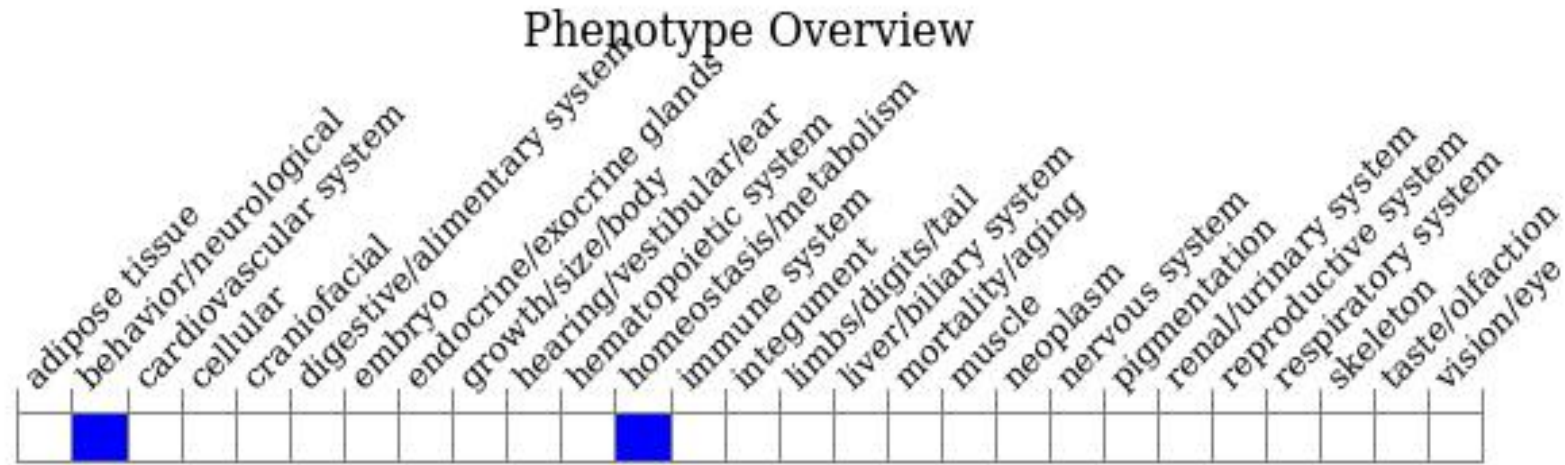
Genomic location distribution



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 conditional allele ubiquitously activated exhibit reduced brain polyamine levels, impaired memory and altered response to addictive substances.

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

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