

Slc6a3 Cas9-KO Strategy

Designer:	Huan Wang
Reviewer:	Huan Fan
Design Date:	2020-5-22

Project Overview

Project Name

Slc6a3

Project type

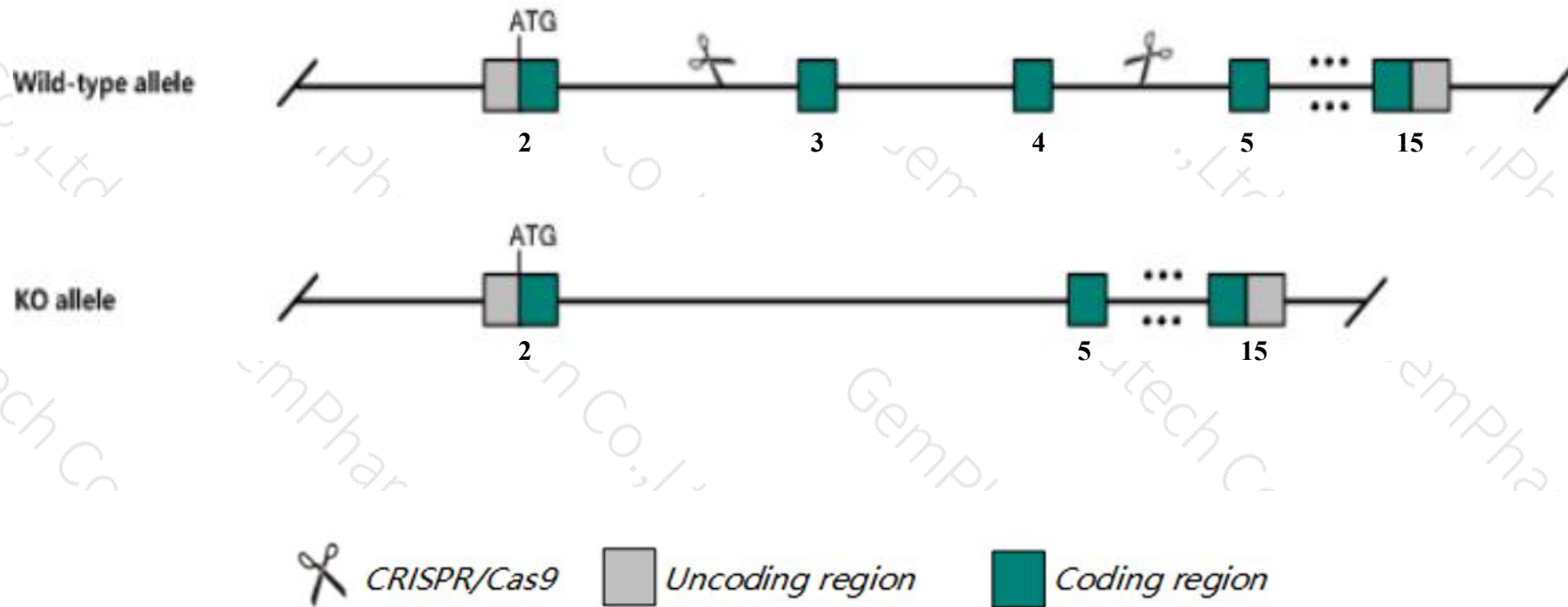
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc6a3* gene. The schematic diagram is as follows:



- The *Slc6a3* gene has 1 transcript. According to the structure of *Slc6a3* gene, exon3-exon4 of *Slc6a3-201* (ENSMUST00000022100.6) transcript is recommended as the knockout region. The region contains 364bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc6a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygotes for targeted null mutations exhibit dwarfism, hyperactivity (especially in a novel environment), 5-fold higher extracellular dopamine levels, impaired spatial cognitive function, anterior pituitary hypoplasia, and failure to lactate.
- The *Slc6a3* gene is located on the Chr13. 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)

Slc6a3 solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 [Mus musculus (house mouse)]

Gene ID: 13162, updated on 13-Mar-2020

Summary

Official Symbol Slc6a3 provided by [MGI](#)

Official Full Name solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 provided by [MGI](#)

Primary source [MGI:MGI:94862](#)

See related [Ensembl:ENSMUSG00000021609](#)

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 DAT, Dat1

Expression Low expression observed in reference dataset [See more](#)

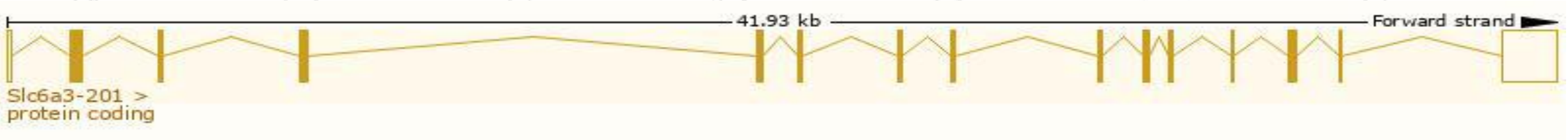
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

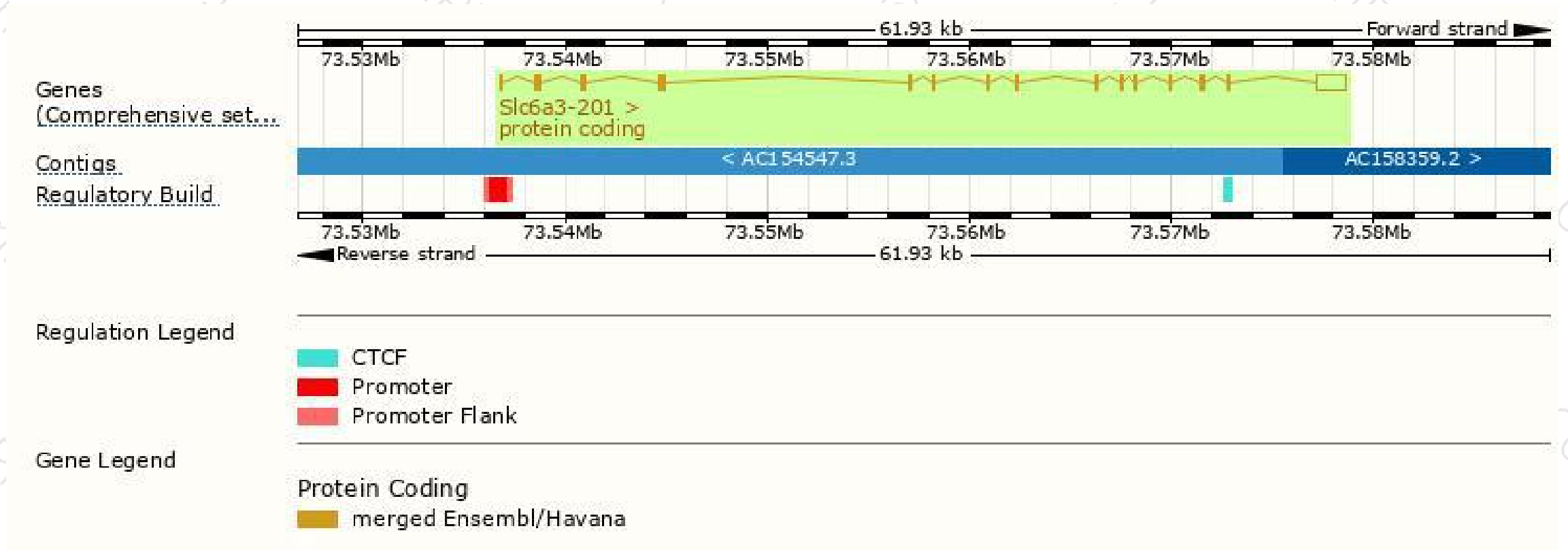
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc6a3-201	ENSMUST00000022100.6	3456	619aa	Protein coding	CCDS26632	Q61327	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

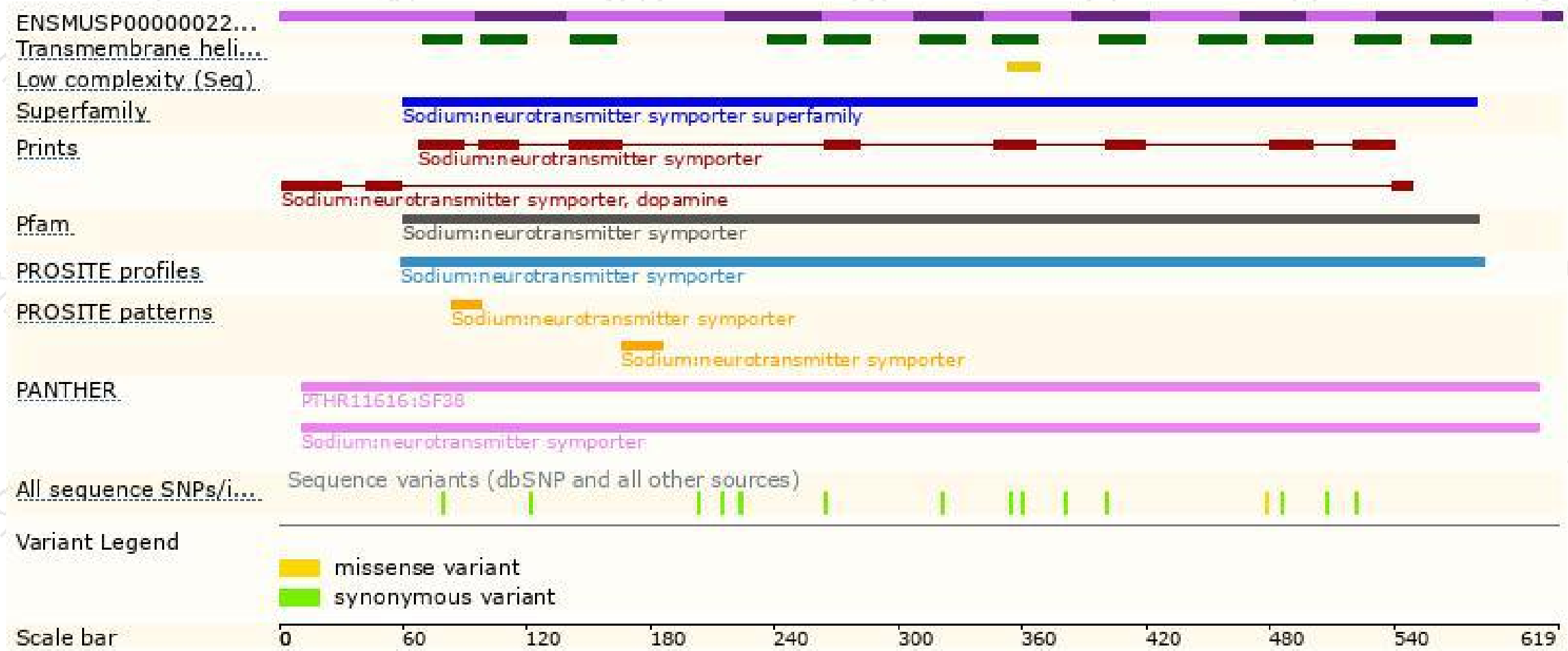
The strategy is based on the design of *Slc6a3-201* transcript, the transcription is shown below:



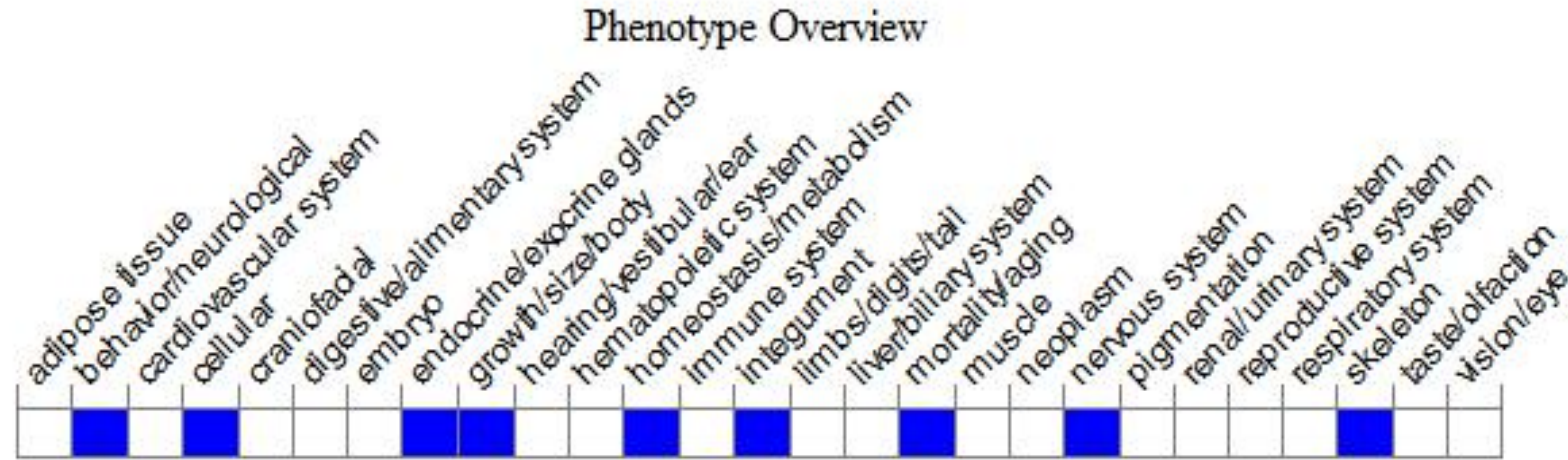
Genomic location distribution



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, homozygotes for targeted null mutations exhibit dwarfism, hyperactivity (especially in a novel environment), 5-fold higher extracellular dopamine levels, impaired spatial cognitive function, anterior pituitary hypoplasia, and failure to lactate.

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

Tel: 400-9660890

