

Slitrk5 Cas9-KO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2020-4-15

Project Overview

Project Name

Slitrk5

Project type

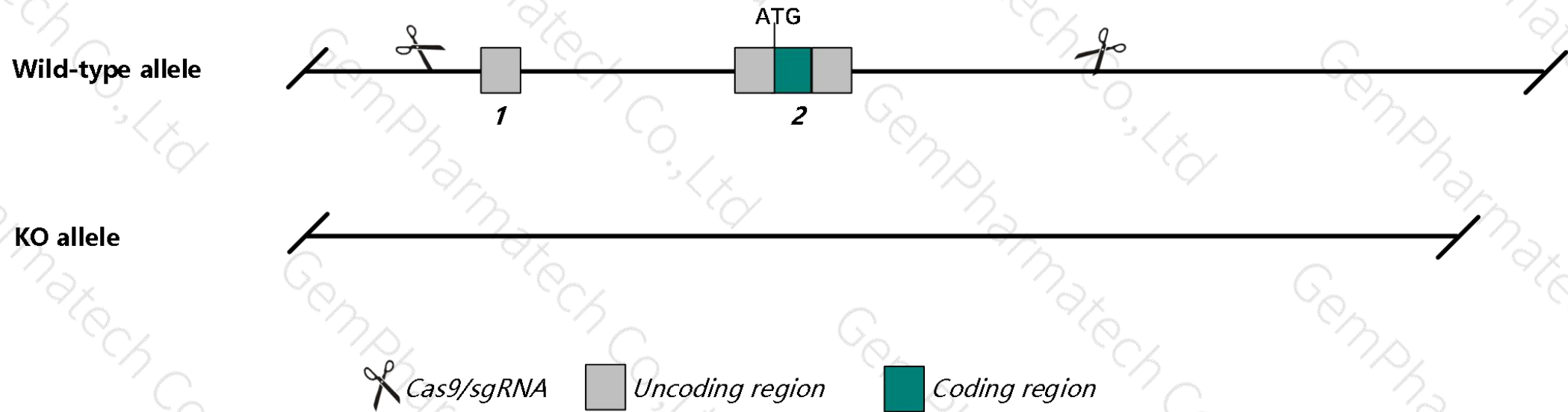
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slitrk5* gene. The schematic diagram is as follows:



- The *Slitrk5* gene has 2 transcripts. According to the structure of *Slitrk5* gene, exon1-exon2 of *Slitrk5-201* (ENSMUST00000042767.8) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slitrk5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a null allele have abnormal medium spiny neuron morphology and exhibit behavioral abnormalities.
- The *Slitrk5* gene is located on the Chr14. 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)

Slitrk5 SLIT and NTRK-like family, member 5 [Mus musculus (house mouse)]

Gene ID: 75409, updated on 13-Mar-2020

Summary



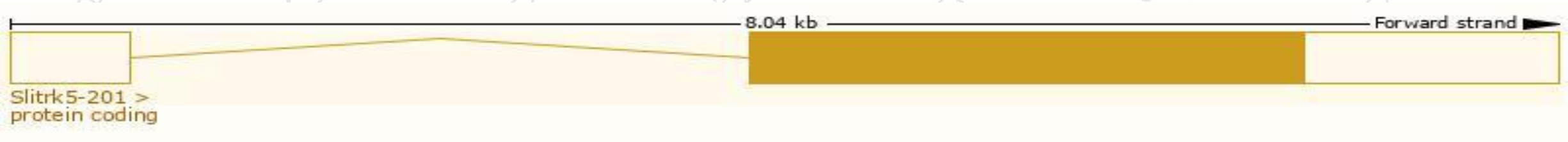
Official Symbol	Slitrk5 provided by MGI
Official Full Name	SLIT and NTRK-like family, member 5 provided by MGI
Primary source	MGI:MGI:2679448
See related	Ensembl:ENSMUSG00000033214
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610019D03Rik
Expression	Biased expression in frontal lobe adult (RPKM 6.2), CNS E18 (RPKM 6.1) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

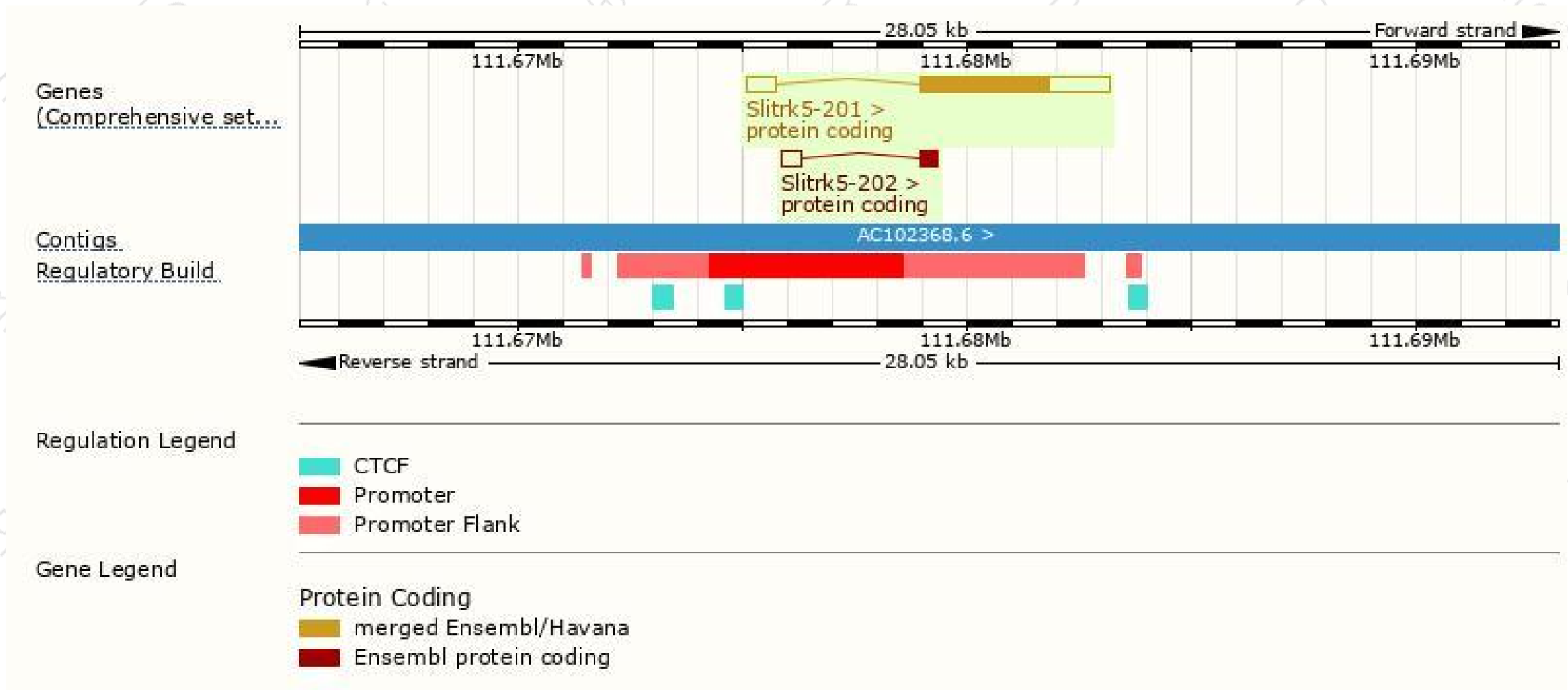
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slitrk5-201	ENSMUST00000042767.8	4831	957aa	Protein coding	CCDS27328	Q810B7	TSL:2 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
Slitrk5-202	ENSMUST00000227891.1	837	132aa	Protein coding	-	A0A2I3BQY9	CDS 3' incomplete

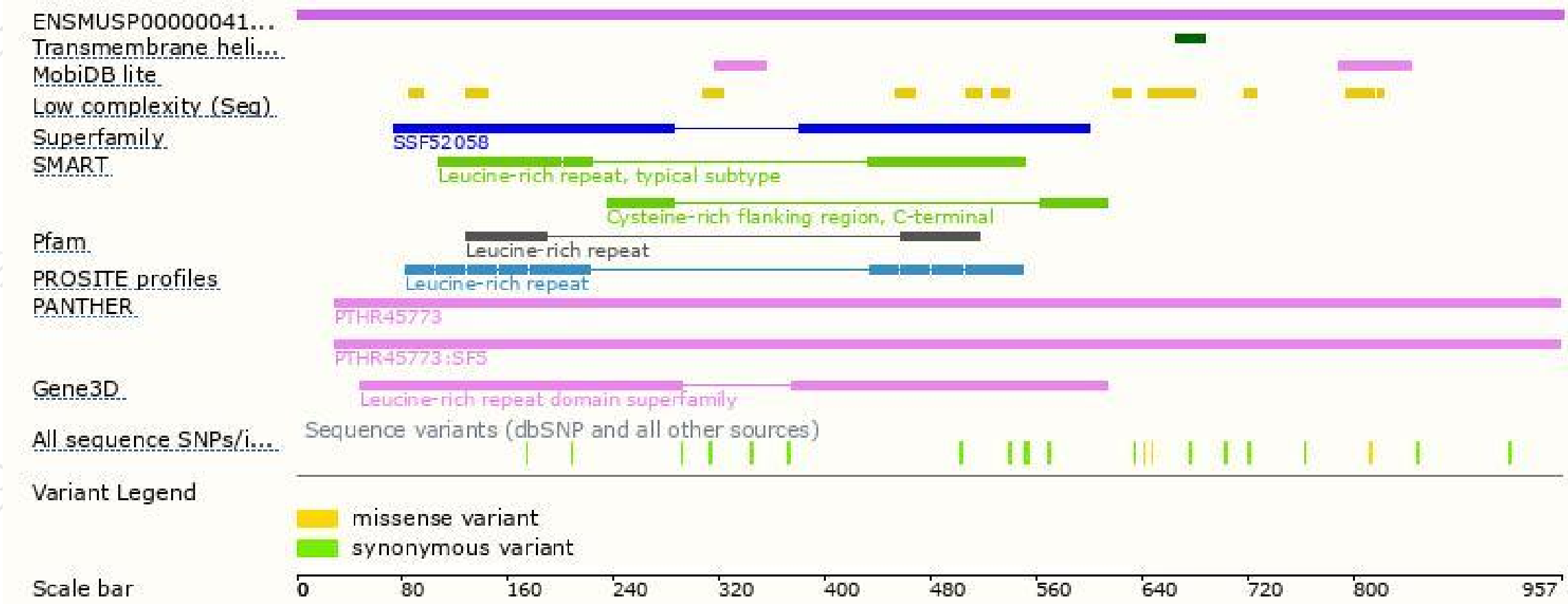
The strategy is based on the design of *Slitrk5-201* transcript,the transcription is shown below:



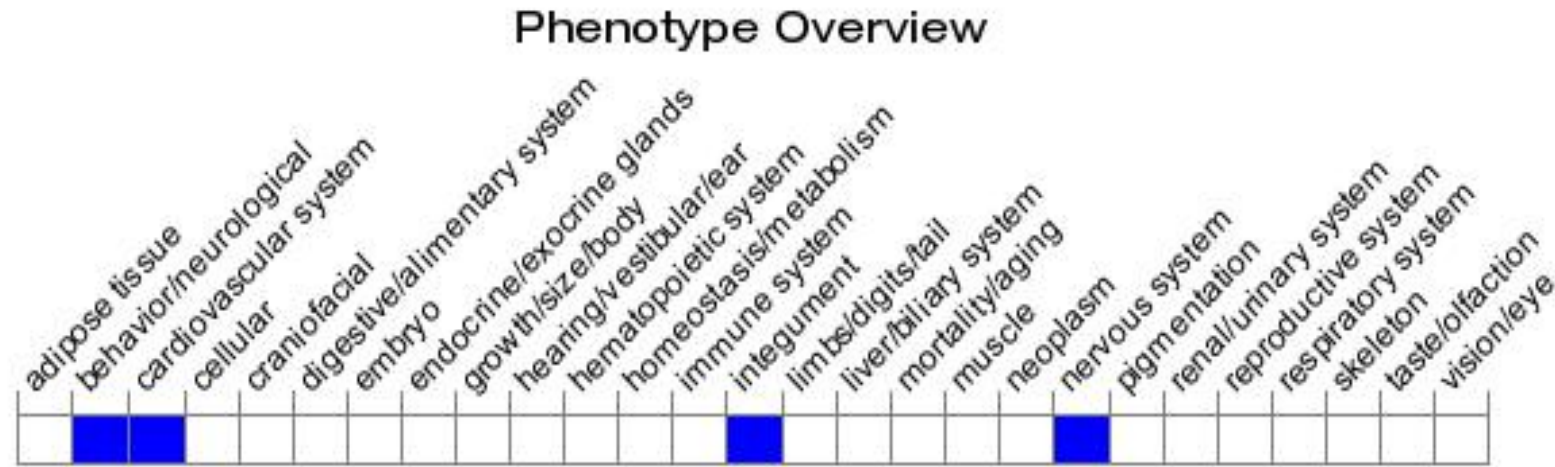
Genomic location distribution



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 null allele have abnormal medium spiny neuron morphology and exhibit behavioral abnormalities.

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

Tel: 400-9660890

