

Slc45a1 Cas9-CKO Strategy

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Project Overview

Project Name

Slc45a1

Project type

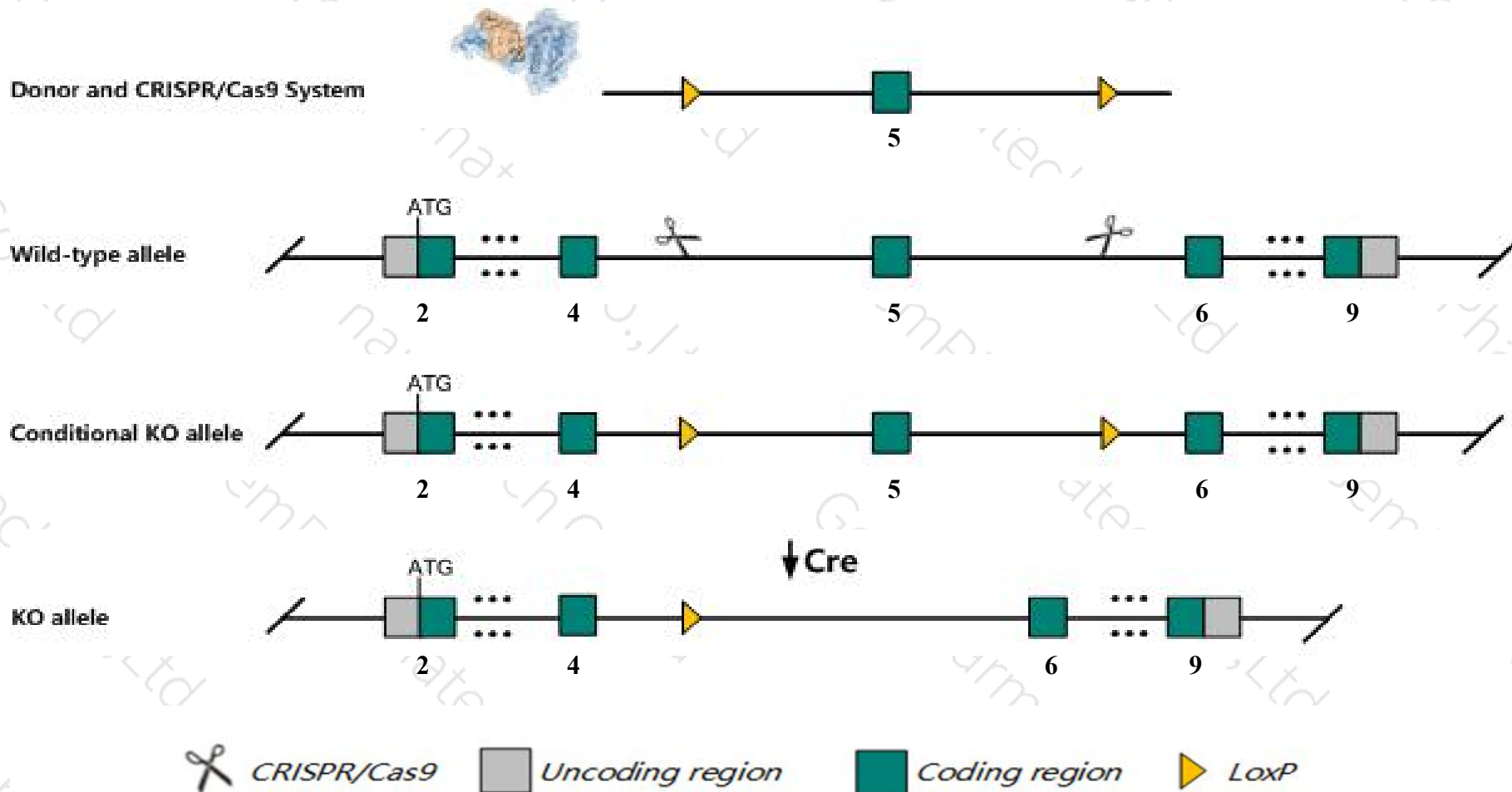
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc45a1* gene. The schematic diagram is as follows:



Technical routes

- The *Slc45a1* gene has 3 transcripts. According to the structure of *Slc45a1* gene, exon5 of *Slc45a1*-201(ENSMUST00000037827.9) transcript is recommended as the knockout region. The region contains 737bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc45a1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- The *Slc45a1* gene is located on the Chr4. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Slc45a1 solute carrier family 45, member 1 [Mus musculus (house mouse)]

Gene ID: 242773, updated on 13-Mar-2020

Summary



Official Symbol [Slc45a1](#) provided by [MGI](#)

Official Full Name [solute carrier family 45, member 1](#) provided by [MGI](#)

Primary source [MGI:MGI:2653235](#)

See related [Ensembl:ENSMUSG00000039838](#)

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 [C230078B22](#), [Dnb5](#)

Expression [Biased expression in cerebellum adult \(RPKM 14.7\), cortex adult \(RPKM 10.6\) and 5 other tissues](#)[See more](#)

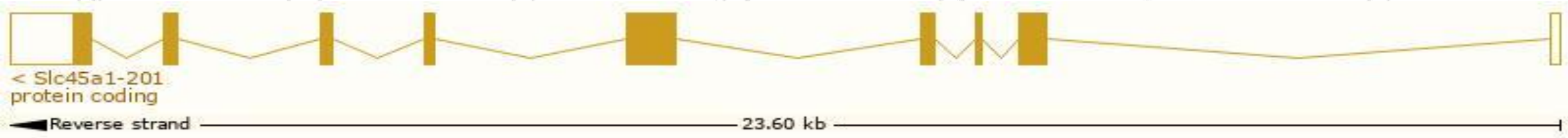
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

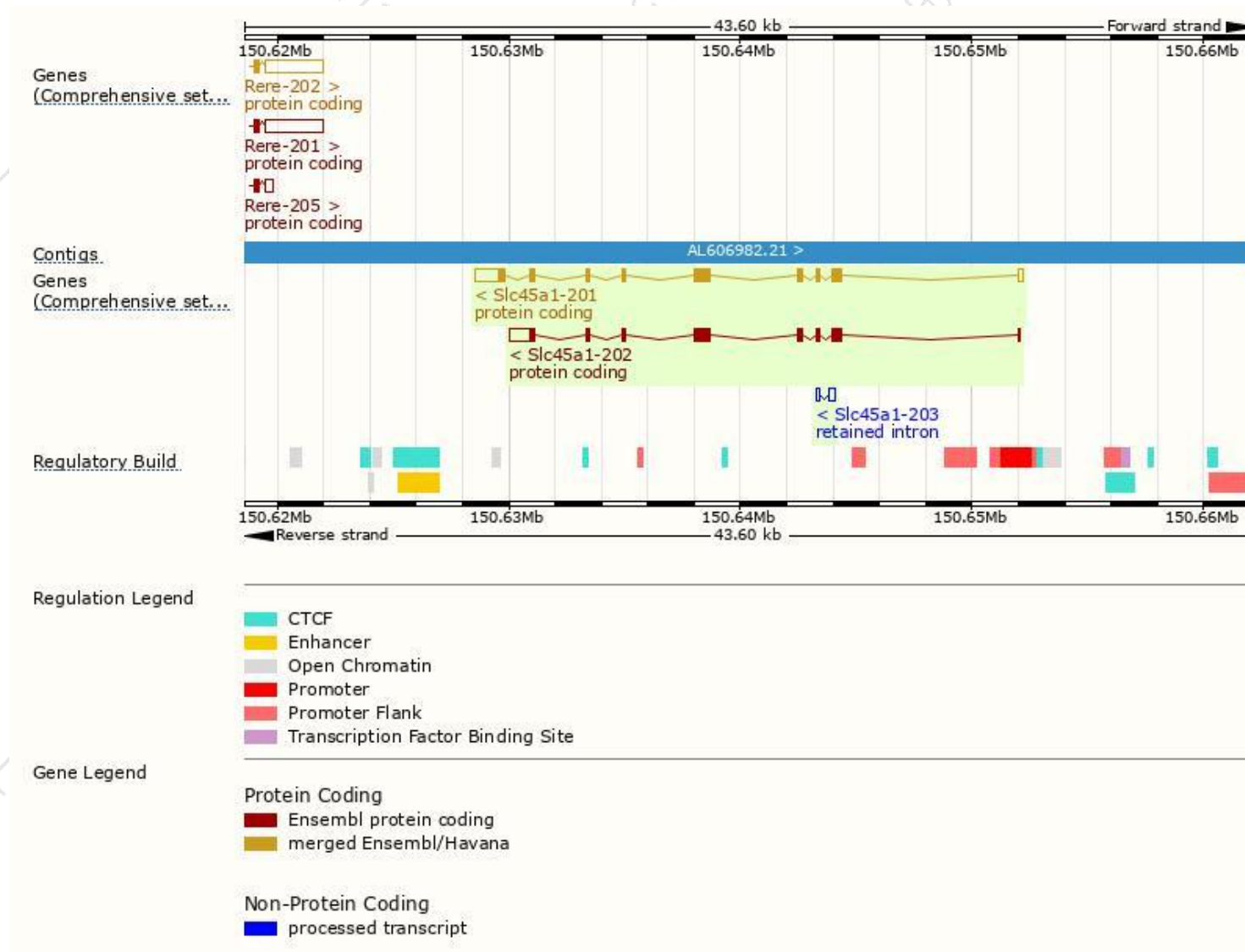
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc45a1-201	ENSMUST00000037827.9	3387	751aa	Protein coding	CCDS18973	Q8BIV7	TSL:1 GENCODE basic APPRIS P2
Slc45a1-202	ENSMUST00000117997.1	2955	675aa	Protein coding	-	B0QZL3	TSL:1 GENCODE basic APPRIS ALT2
Slc45a1-203	ENSMUST00000147706.1	372	No protein	Retained intron	-	-	TSL:3

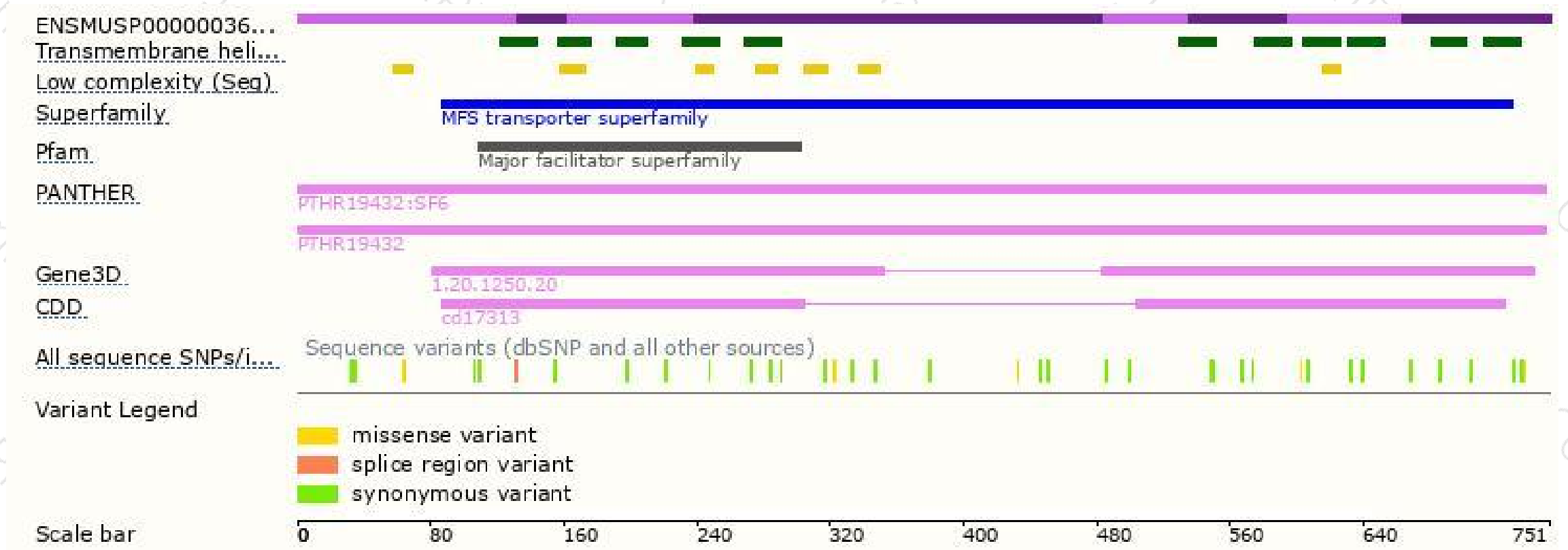
The strategy is based on the design of *Slc45a1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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