

Slc38a11 Cas9-CKO Strategy

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Project Overview

Project Name

Slc38a11

Project type

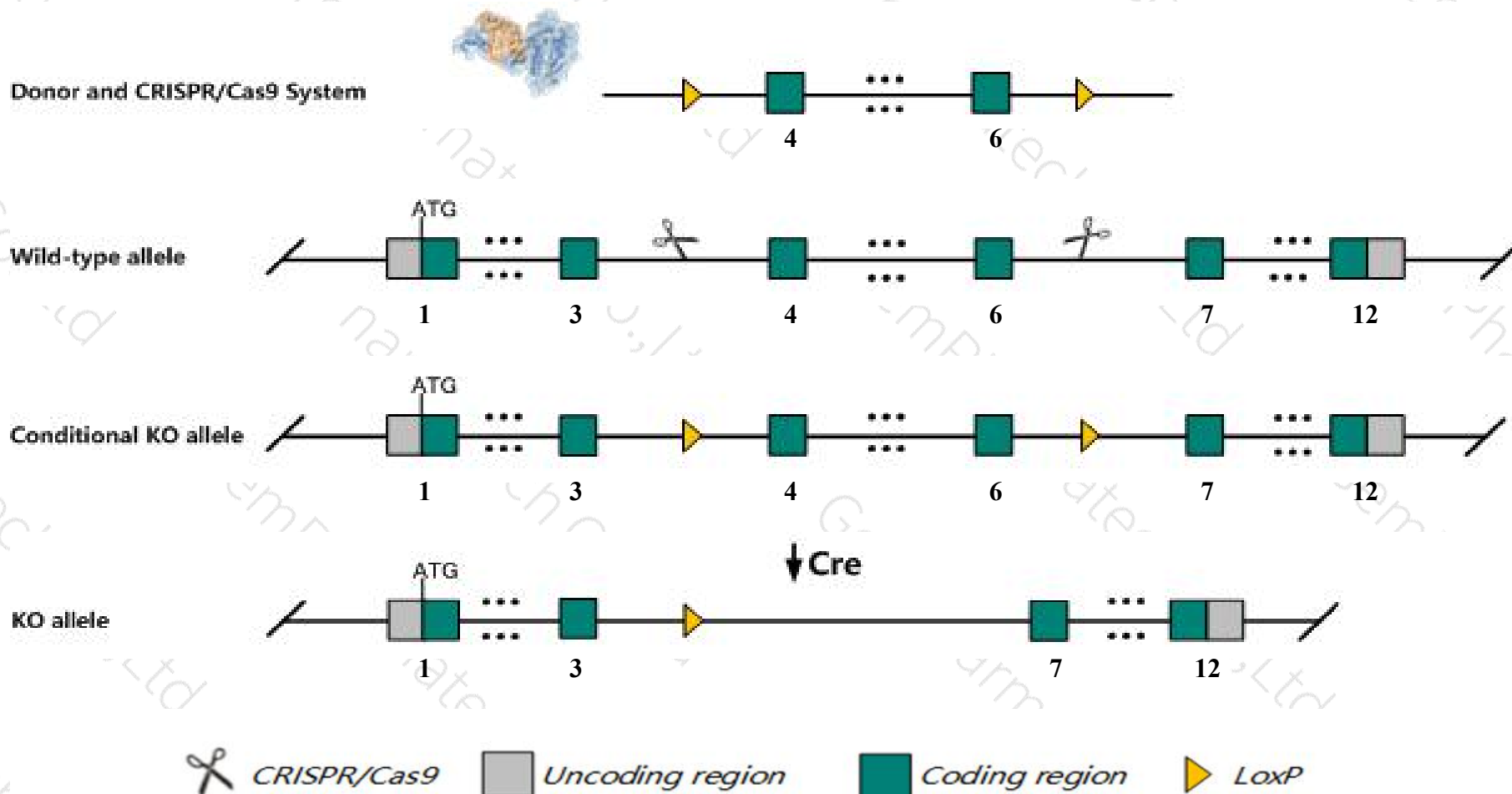
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc38a11* gene. The schematic diagram is as follows:



Technical routes

- The *Slc38a11* gene has 8 transcripts. According to the structure of *Slc38a11* gene, exon4-exon6 of *Slc38a11-201* (ENSMUST00000112420.7) transcript is recommended as the knockout region. The region contains 308bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc38a11* 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.

Notice

- The *Slc38a11* gene is located on the Chr2. 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)

Slc38a11 solute carrier family 38, member 11 [*Mus musculus* (house mouse)]

Gene ID: 320106, updated on 13-Mar-2020

Summary

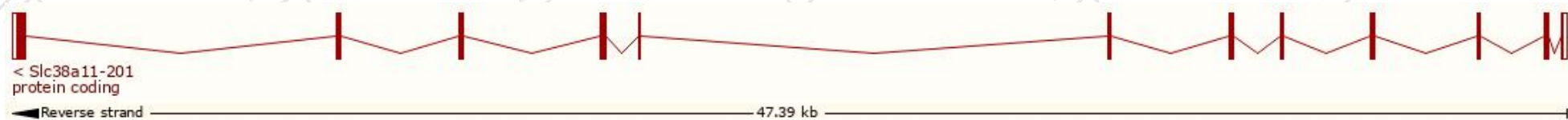
Official Symbol	Slc38a11 provided by MGI
Official Full Name	solute carrier family 38, member 11 provided by MGI
Primary source	MGI:MGI:2443383
See related	Ensembl:ENSMUSG000000061171
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9330158F14Rik
Expression	Broad expression in adrenal adult (RPKM 1.8), bladder adult (RPKM 0.8) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

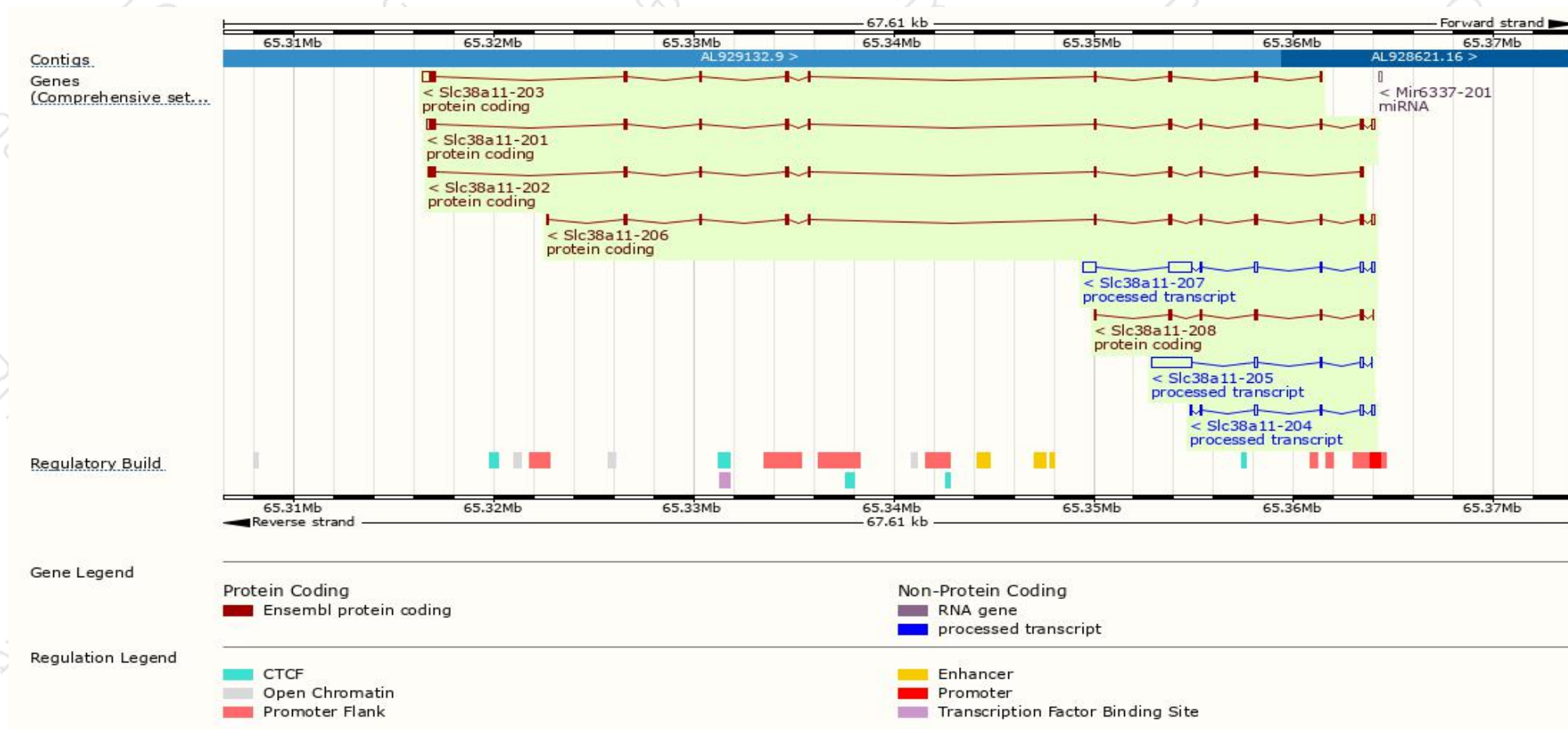
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc38a11-201	ENSMUST00000112420.7	1606	453aa	Protein coding	CCDS38129	Q3USY0	TSL:1 GENCODE basic APPRIS P1
Slc38a11-203	ENSMUST00000127623.7	1476	378aa	Protein coding	-	F6WJL8	CDS 5' incomplete TSL:5
Slc38a11-202	ENSMUST00000124918.7	1299	414aa	Protein coding	-	F6X0X3	CDS 5' incomplete TSL:5
Slc38a11-206	ENSMUST00000152324.7	1241	375aa	Protein coding	-	A2ASI2	CDS 3' incomplete TSL:1
Slc38a11-208	ENSMUST00000155962.2	615	205aa	Protein coding	-	F6WP73	CDS 5' and 3' incomplete TSL:5
Slc38a11-205	ENSMUST00000145583.7	2394	No protein	Processed transcript	-	-	TSL:1
Slc38a11-207	ENSMUST00000155422.7	2339	No protein	Processed transcript	-	-	TSL:1
Slc38a11-204	ENSMUST00000141690.1	658	No protein	Processed transcript	-	-	TSL:3

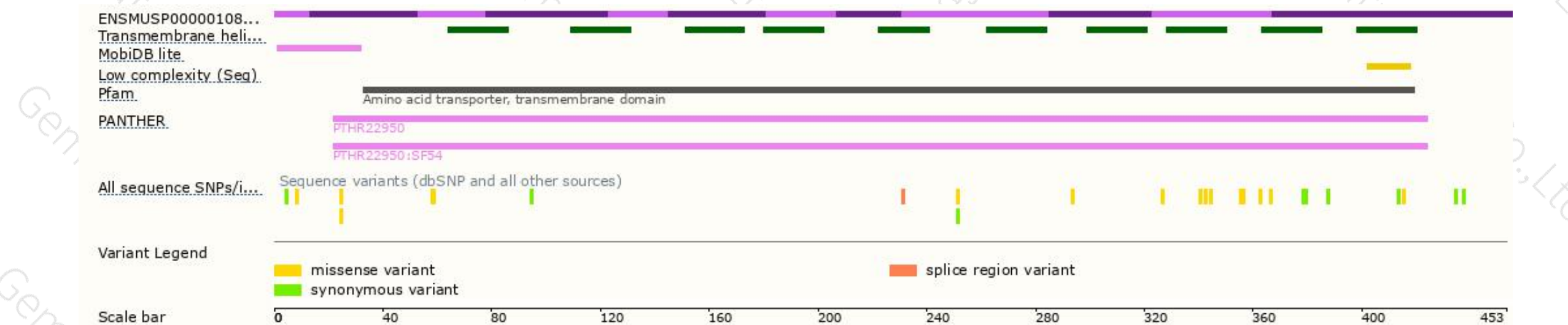
The strategy is based on the design of *Slc38a11-201* transcript, the transcription is shown below



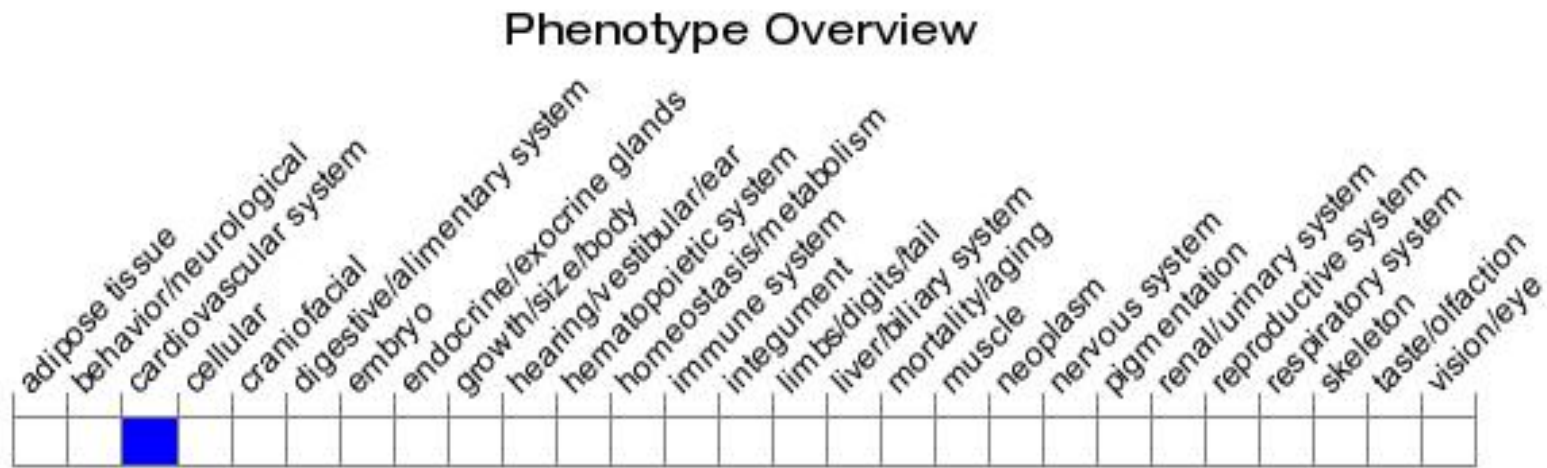
Genomic location distribution



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/>).

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

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