

Slc39a6 Cas9-CKO Strategy

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Project Overview

Project Name

Slc39a6

Project type

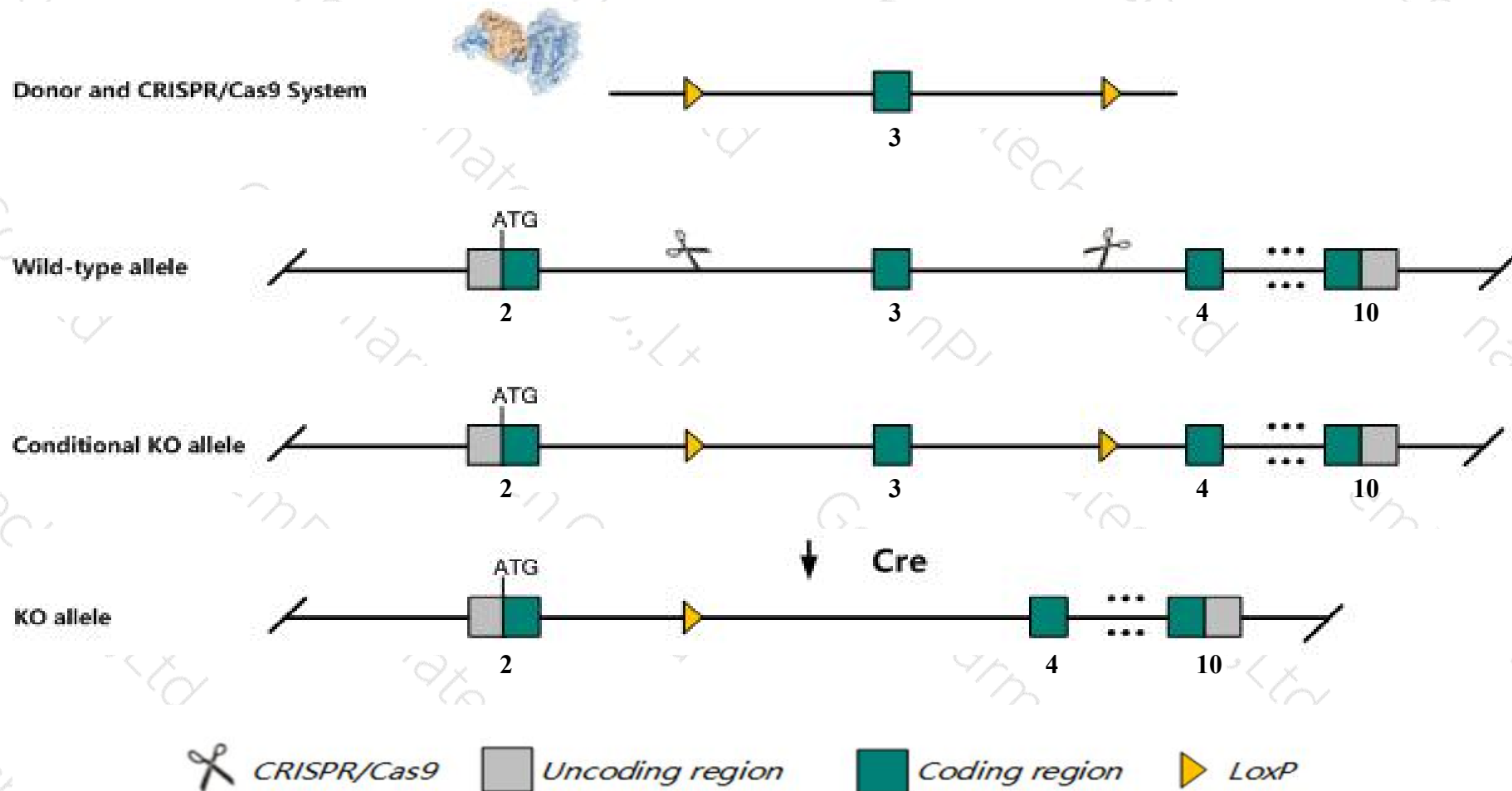
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc39a6* gene. The schematic diagram is as follows:



Technical routes

- The *Slc39a6* gene has 4 transcripts. According to the structure of *Slc39a6* gene, exon3 of *Slc39a6-201* (ENSMUST00000070726.9) transcript is recommended as the knockout region. The region contains 184bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc39a6* 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.

- According to the existing MGI data, Mice homozygous for a null allele do not display any gross skin abnormalities.
- The floxed region is near to the N-terminal of *Elp2* gene, this strategy may influence the regulatory function of the N-terminal of *Elp2* gene.
- The effect on transcript *Slc39a6*-203 is unknown.
- The N-terminal of *Slc39a6* gene will remain several amino acids, it may remain the partial function of *Slc39a6* gene.
- The *Slc39a6* gene is located on the Chr18. 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)

Slc39a6 solute carrier family 39 (metal ion transporter), member 6 [*Mus musculus* (house mouse)]

Gene ID: 106957, updated on 12-Aug-2019

Summary

- Official Symbol** Slc39a6 provided by [MGI](#)
- Official Full Name** solute carrier family 39 (metal ion transporter), member 6 provided by [MGI](#)
- Primary source** [MGI:MGI:2147279](#)
- See related** [Ensembl:ENSMUSG00000024270](#)
- 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** Zip6; Ermelin
- Expression** Broad expression in whole brain E14.5 (RPKM 19.9), CNS E14 (RPKM 19.7) and 24 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 18; 18 A2 See Slc39a6 in [Genome Data Viewer](#)

Exon count: 10

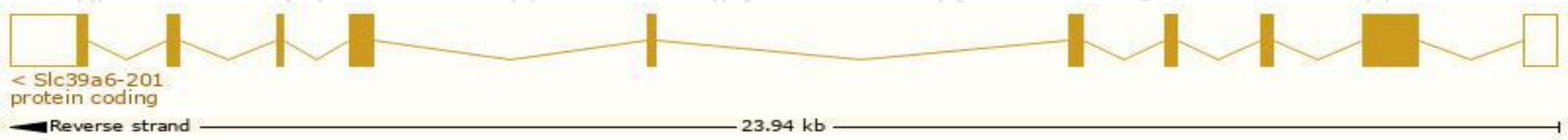
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (24579881..24603817, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (24738382..24762318, complement)

Transcript information (Ensembl)

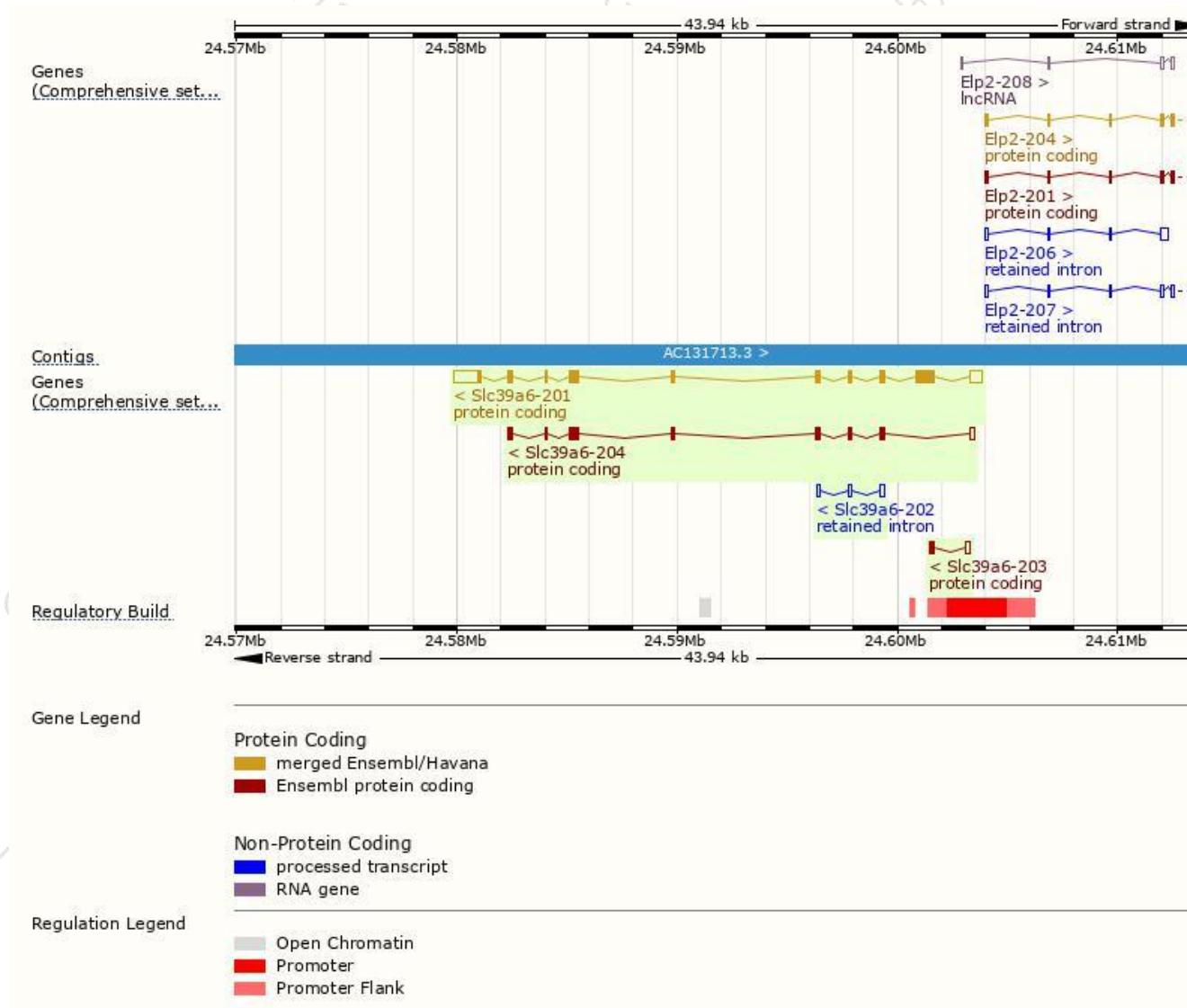
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc39a6-201	ENSMUST00000070726.9	3882	765aa	Protein coding	CCDS50239	Q8C145	TSL:1 GENCODE basic APPRIS P1
Slc39a6-204	ENSMUST00000154205.1	1567	434aa	Protein coding	-	D3Z7N4	CDS 3' incomplete TSL:5
Slc39a6-203	ENSMUST00000152504.1	337	48aa	Protein coding	-	D3Z0J4	CDS 3' incomplete TSL:3
Slc39a6-202	ENSMUST00000128106.1	529	No protein	Retained intron	-	-	TSL:2

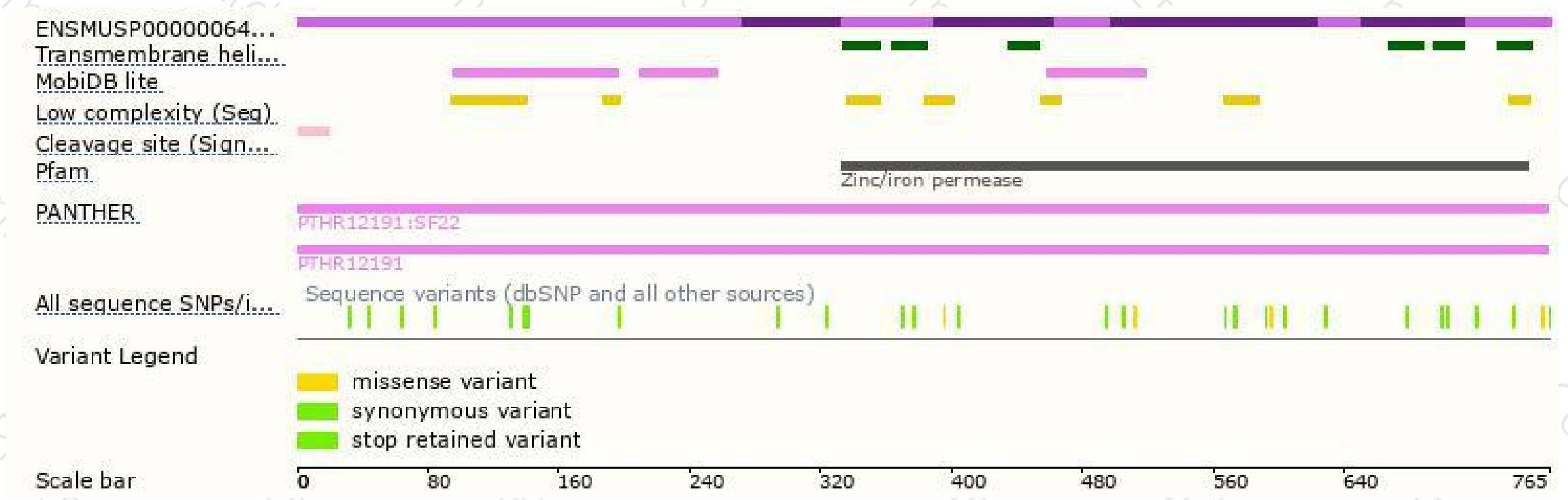
The strategy is based on the design of *Slc39a6-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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