

Slc7a14 Cas9-KO Strategy

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Project Overview

Project Name

Slc7a14

Project type

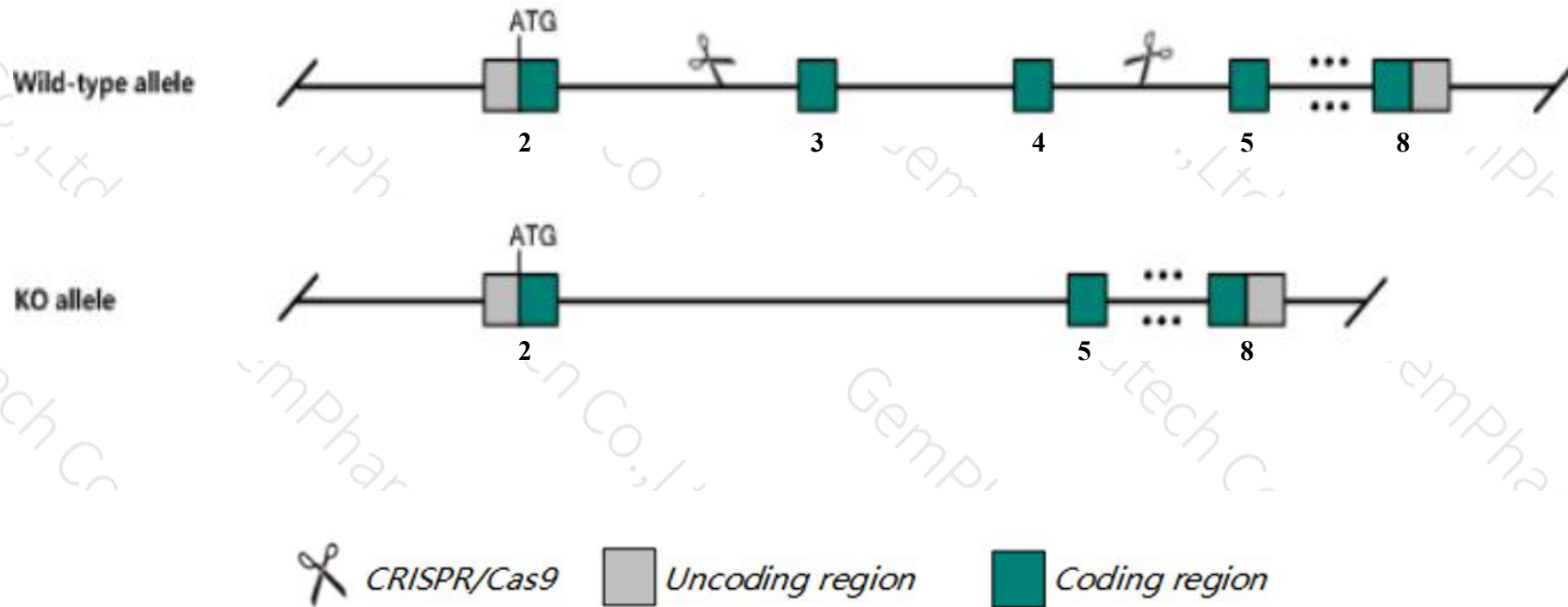
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a14* gene. The schematic diagram is as follows:



- The *Slc7a14* gene has 2 transcripts. According to the structure of *Slc7a14* gene, exon3-exon4 of *Slc7a14-201* (ENSMUST00000091259.8) transcript is recommended as the knockout region. The region contains 455bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc7a14* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit abnormal eye electrophysiology, thin retinal outer nuclear and decreased total retinal thickness.
- The *Slc7a14* gene is located on the Chr3. 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)

Slc7a14 solute carrier family 7 (cationic amino acid transporter, y+ system), member 14 [*Mus musculus* (house mouse)]

Gene ID: 241919, updated on 14-Apr-2020

Summary

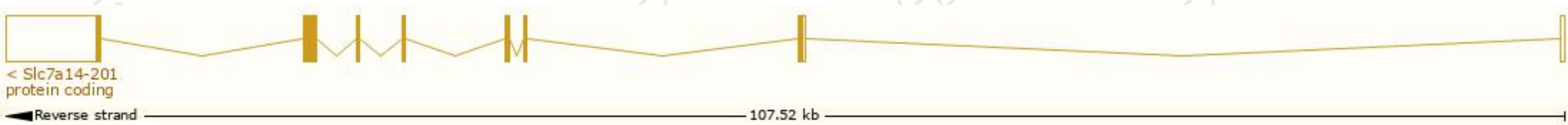
Official Symbol	Slc7a14 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14 provided by MGI
Primary source	MGI:MGI:3040688
See related	Ensembl:ENSMUSG00000069072
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC061928; A930013N06
Expression	Biased expression in cerebellum adult (RPKM 7.7), cortex adult (RPKM 5.2) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

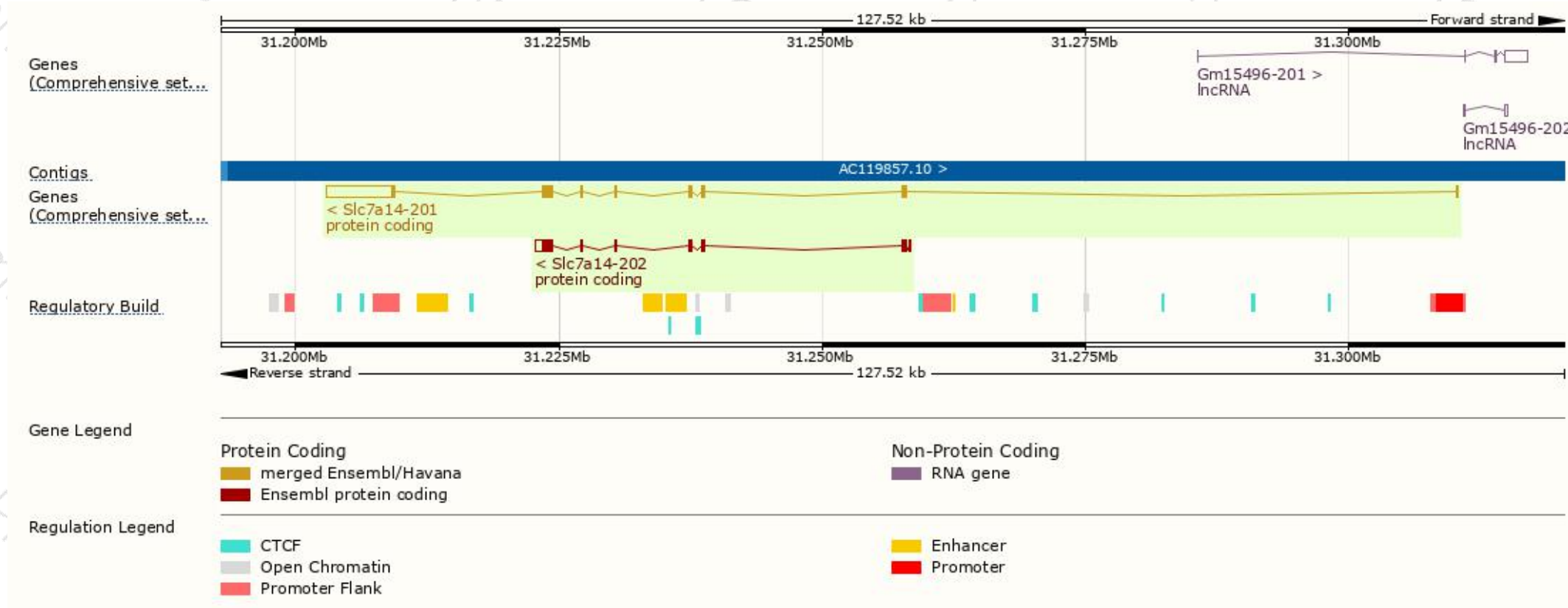
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a14-201	ENSMUST00000091259.8	8897	771aa	Protein coding	CCDS17291	Q8BXR1	TSL:1 GENCODE basic APPRIS P1
Slc7a14-202	ENSMUST00000108245.1	3080	677aa	Protein coding	-	D3YY38	TSL:1 GENCODE basic

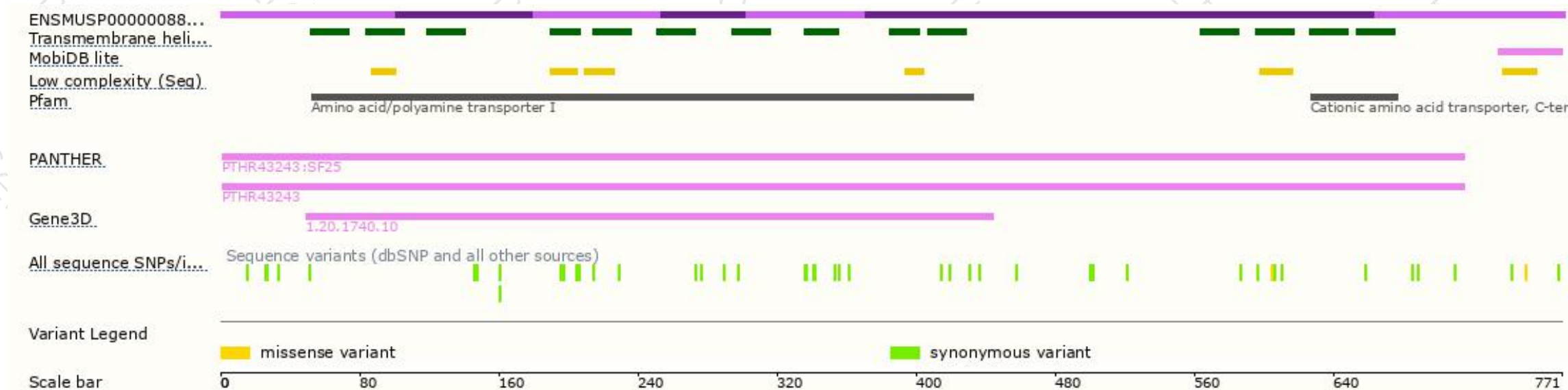
The strategy is based on the design of *Slc7a14-201* transcript, the transcription is shown below



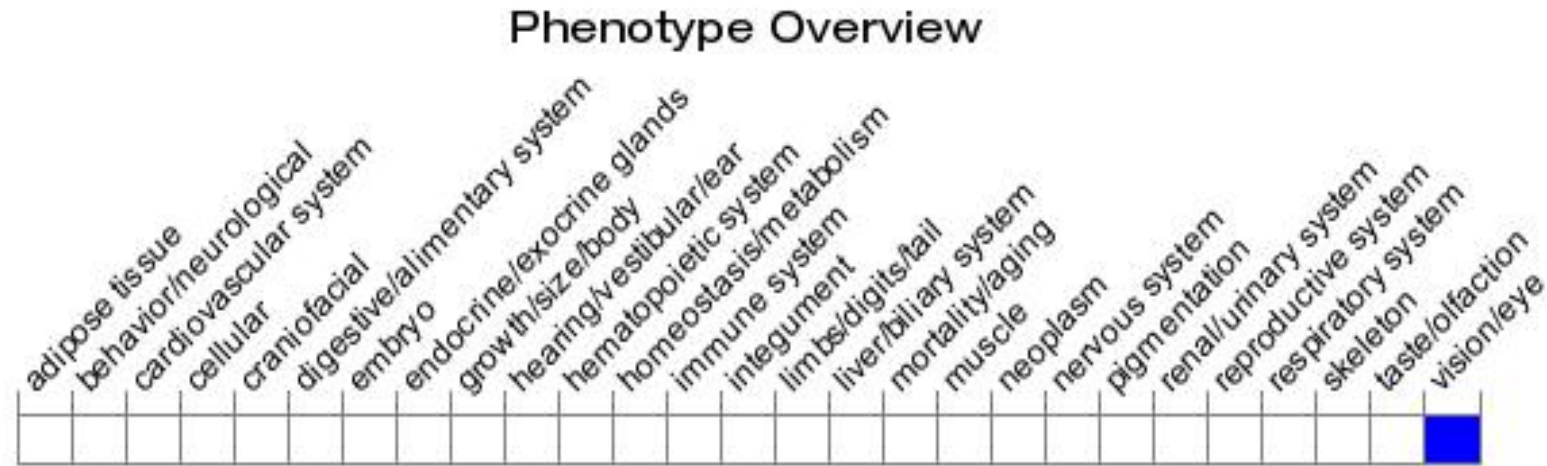
Genomic location distribution



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 knock-out allele exhibit abnormal eye electrophysiology, thin retinal outer nuclear and decreased total retinal thickness.

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

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