

Slc39a7 Cas9-KO Strategy

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Project Overview

Project Name

Slc39a7

Project type

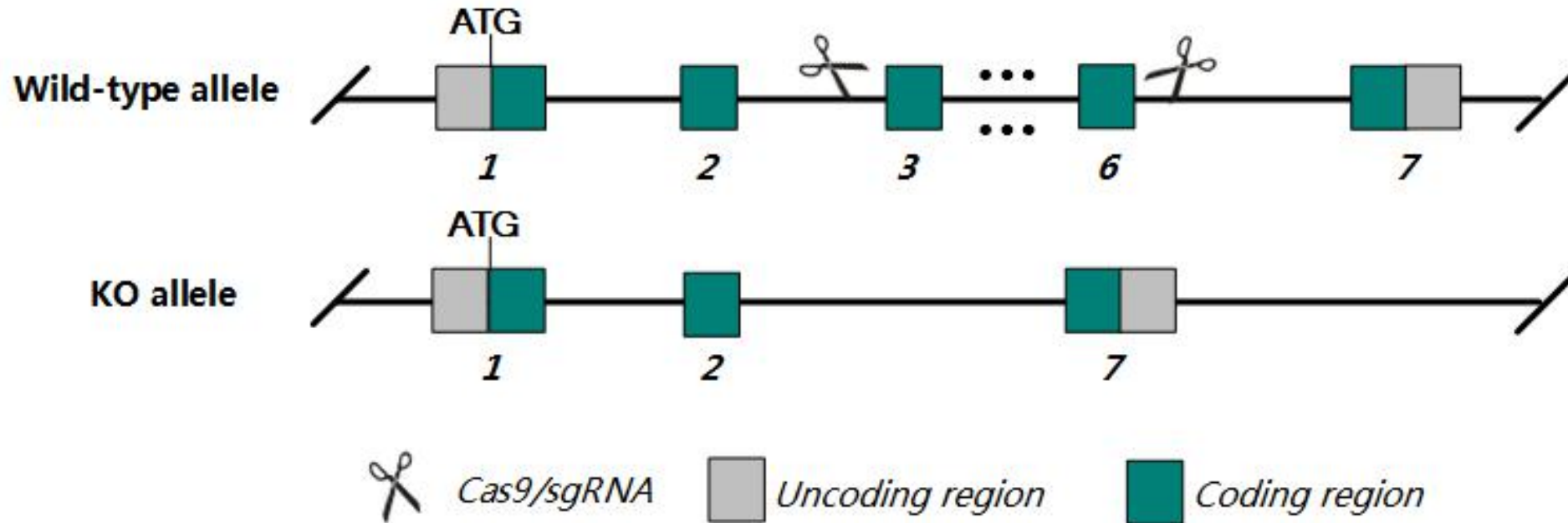
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc39a7* gene. The schematic diagram is as follows:



- The *Slc39a7* gene has 6 transcripts. According to the structure of *Slc39a7* gene, exon3-exon6 of *Slc39a7-201* (ENSMUST00000025186.15) transcript is recommended as the knockout region. The region contains 617bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc39a7* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mice homozygous for a conditional allele activated in intestinal epithelial cells exhibit premature death, loss of epithelial integrity, reduced enterocyte proliferation and increased enterocyte apoptosis.
- The knpckout region is near to the N-terminal of *Rxrb\Col11a2\H2-ke6\Mir219a\Gm26940\Ring1* gene, this strategy may influence the regulatory function of the N-terminal of these gene.
- The *Gm20427* gene will be deleted together in this strategy.
- The *Slc39a7* gene is located on the Chr11. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Slc39a7 solute carrier family 39 (zinc transporter), member 7 [*Mus musculus* (house mouse)]

Gene ID: 14977, updated on 15-Apr-2019

Summary

- Official Symbol** Slc39a7 provided by [MGI](#)
- Official Full Name** solute carrier family 39 (zinc transporter), member 7 provided by [MGI](#)
- Primary source** [MGI:MGI:95909](#)
- See related** [Ensembl:ENSMUSG00000024327](#)
- 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** Ke4; Ke-4; Zip7; Ring5; H-2Ke4; H2-Ke4; AA408174; AI117660; AL024048
- Expression** Ubiquitous expression in ovary adult (RPKM 99.5), adrenal adult (RPKM 66.7) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 17 B1; 17 17.98 cM [See Slc39a7 in Genome Data Viewer](#)

Exon count: 7

| Annotation release | Status | Assembly | Chr | Location |
|---------------------|-------------------|--|-----|--|
| 106 | current | GRCm38.p4 (GCF_000001635.24) | 17 | NC_000083.6 (34028266..34031690, complement) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 17 | NC_000083.5 (34165211..34168635, complement) |

Transcript information (Ensembl)

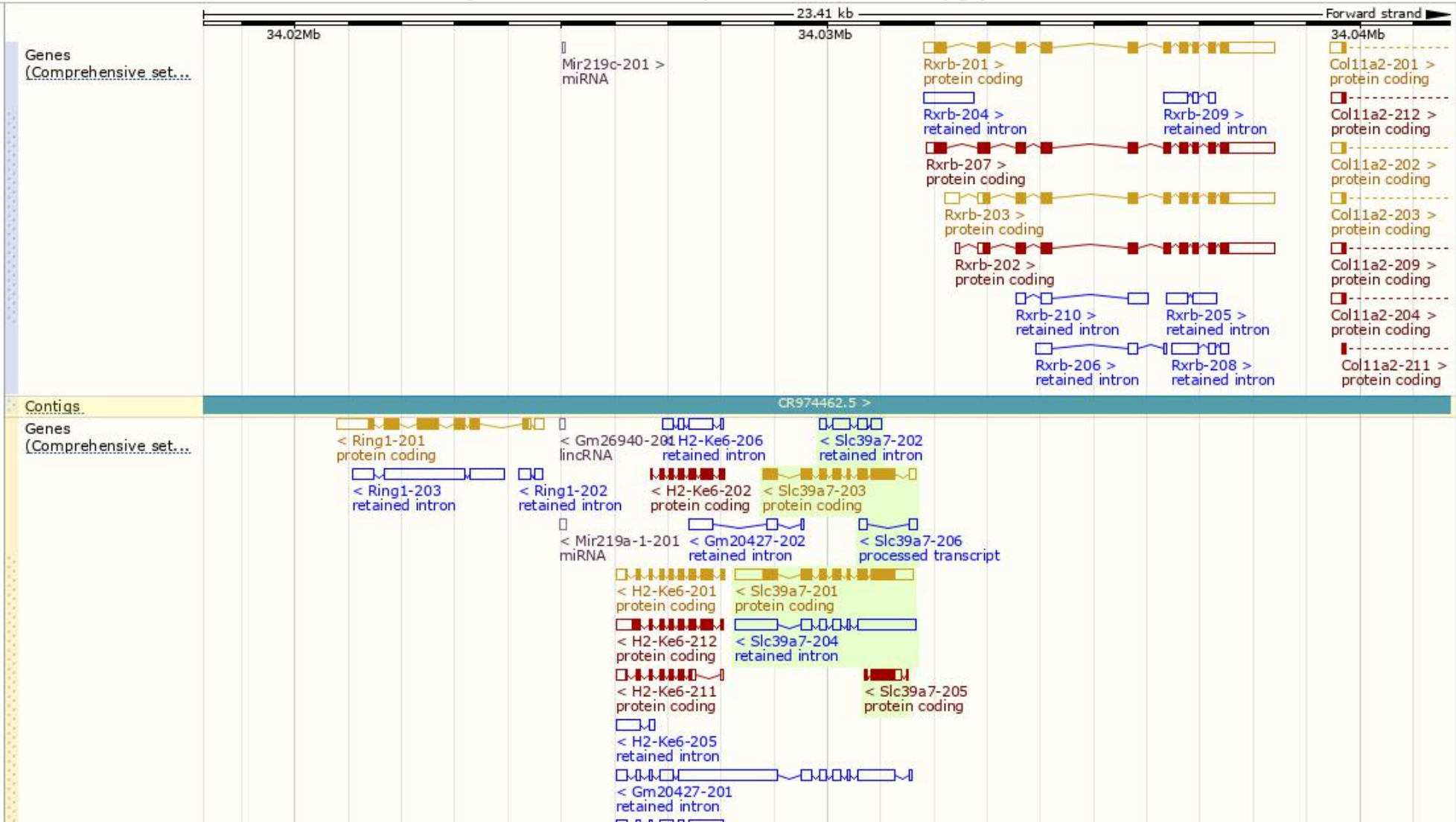
The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-------------|---------------------------------------|------|-----------------------|----------------------|---------------------------|---|-------------------------------|
| Slc39a7-201 | ENSMUST00000025186.15 | 2320 | 476aa | Protein coding | CCDS37576 | A0A068BIT0 Q31125 | TSL:1 GENCODE basic APPRIS P1 |
| Slc39a7-202 | ENSMUST00000167145.1 | 844 | No protein | Retained intron | - | - | TSL:5 |
| Slc39a7-203 | ENSMUST00000169397.8 | 1550 | 476aa | Protein coding | CCDS37576 | A0A068BIT0 Q31125 | TSL:5 GENCODE basic APPRIS P1 |
| Slc39a7-204 | ENSMUST00000170491.7 | 2433 | No protein | Retained intron | - | - | TSL:1 |
| Slc39a7-205 | ENSMUST00000171872.2 | 620 | 161aa | Protein coding | - | E9PV10 | CDS 3' incomplete TSL:5 |
| Slc39a7-206 | ENSMUST00000173810.1 | 277 | No protein | Processed transcript | - | - | TSL:5 |

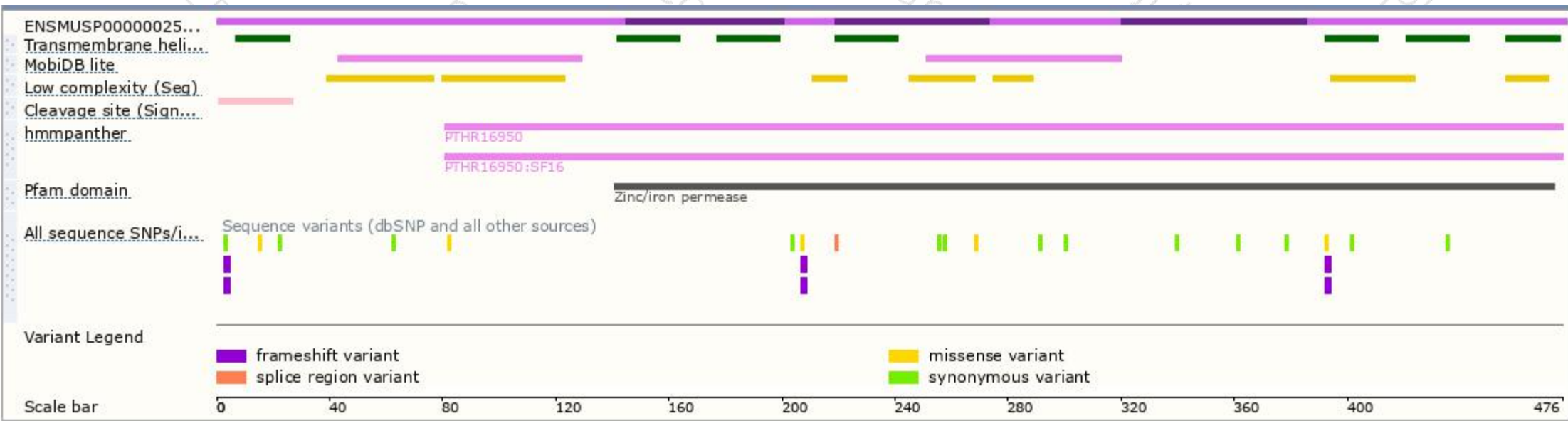
The strategy is based on the design of *Slc39a7-201* transcript,The transcription is shown below



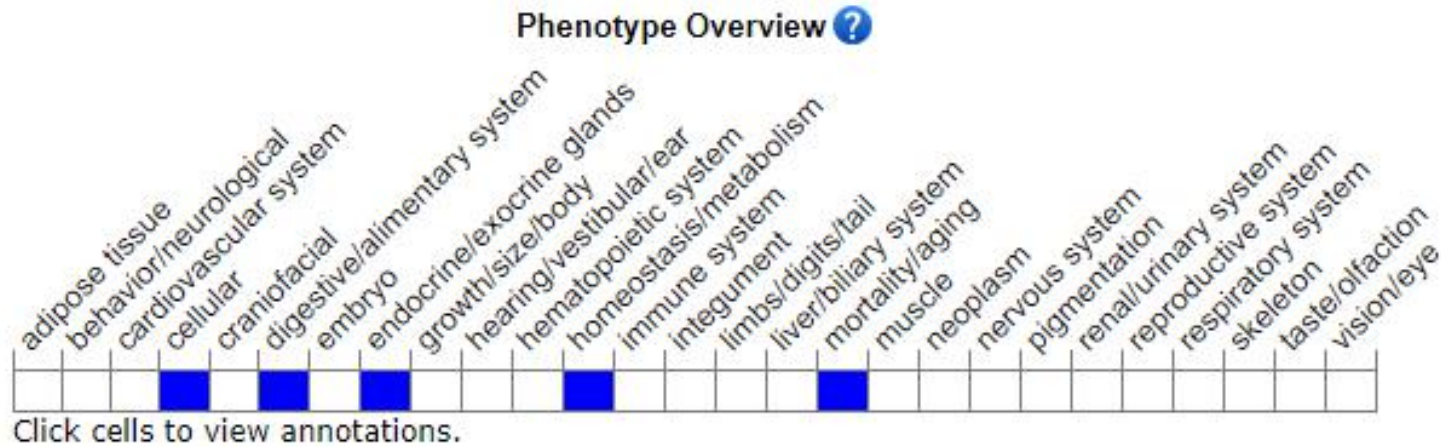
Genomic location distribution



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/>).

Mice homozygous for a conditional allele activated in intestinal epithelial cells exhibit premature death, loss of epithelial integrity, reduced enterocyte proliferation and increased enterocyte apoptosis.

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

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