

Slc17a1 Cas9-KO Strategy

Designer:Xiaojing Li

Reviewer:JiaYu

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Project Overview



Project Name

Slc17a1

Project type

Cas9-KO

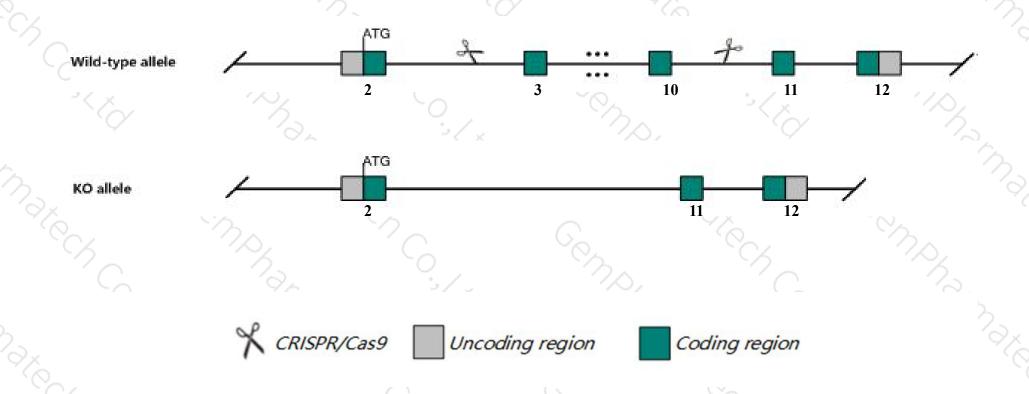
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Slc17a1 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Slc17a1* gene has 4 transcripts. According to the structure of *Slc17a1* gene, exon3-exon10 of *Slc17a1-201* (ENSMUST00000006785.7) transcript is recommended as the knockout region. The region contains 1144bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Slc17a1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice



- ➤ The *Slc17a1* gene is located on the Chr13. 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)



SIc17a1 solute carrier family 17 (sodium phosphate), member 1 [Mus musculus (house mouse)]

Gene ID: 20504, updated on 28-Jan-2020

Summary

Official Symbol Slc17a1 provided by MGI

Official Full Name solute carrier family 17 (sodium phosphate), member 1 provided by MGI

Primary source MGI:MGI:103209

See related Ensembl: ENSMUSG00000021335

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 Npt1; Napi1; NAPI-1

Expression Restricted expression toward kidney adult (RPKM 67.9) See more

Orthologs human all

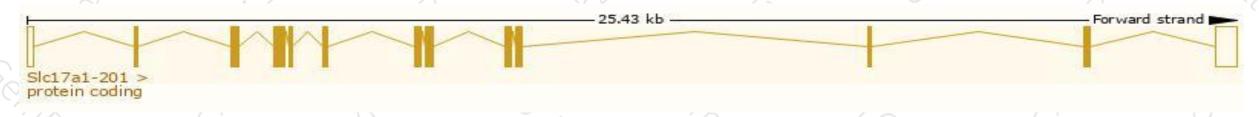
Transcript information (Ensembl)



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

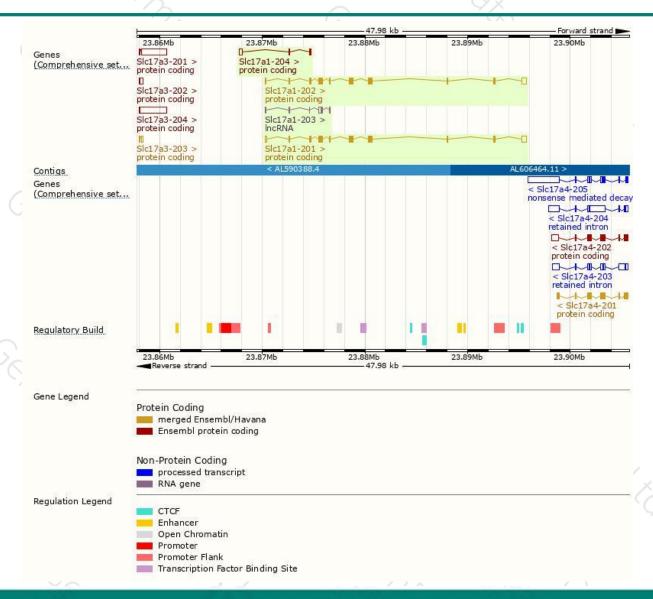
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-------------|----------------------|------|--------------|----------------|-----------|---------|-------------------------------|
| SIc17a1-201 | ENSMUST00000006785.7 | 2026 | 465aa | Protein coding | CCDS26372 | Q61983 | TSL:1 GENCODE basic APPRIS P1 |
| SIc17a1-202 | ENSMUST00000110413.7 | 1965 | <u>465aa</u> | Protein coding | CCDS26372 | Q61983 | TSL:1 GENCODE basic APPRIS P1 |
| SIc17a1-204 | ENSMUST00000130211.7 | 551 | <u>65aa</u> | Protein coding | 1/4/ | Q5SZ94 | CDS 3' incomplete TSL:3 |
| SIc17a1-203 | ENSMUST00000129042.1 | 503 | No protein | IncRNA | 127 | - | TSL:3 |

The strategy is based on the design of Slc17a1-201 transcript, The transcription is shown below



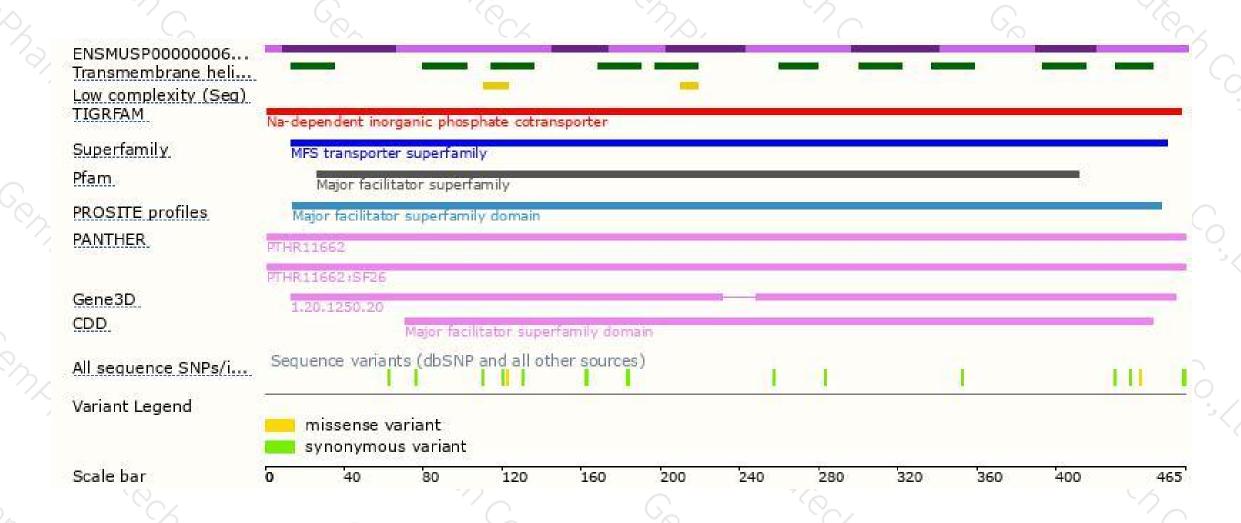
Genomic location distribution





Protein domain







If you have any questions, you are welcome to inquire. Tel: 400-9660890





