

***Slc16a7* Cas9-KO Strategy**

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Project Overview

Project Name

Slc16a7

Project type

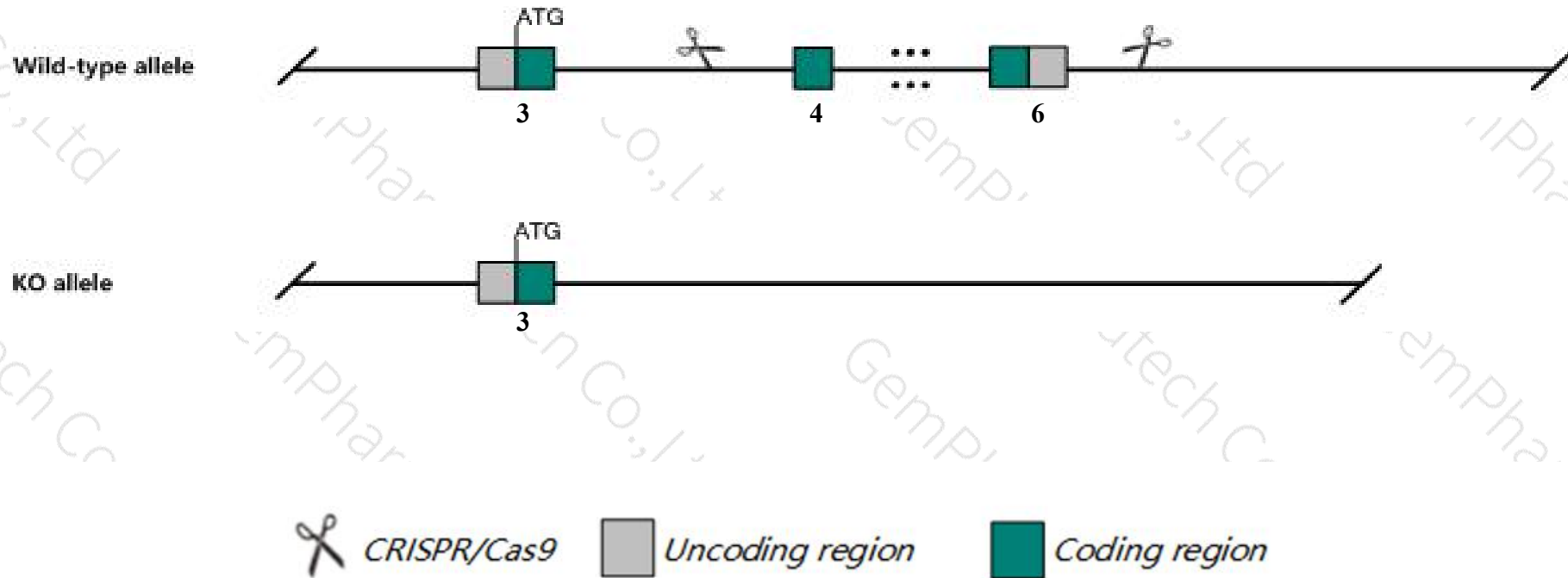
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc16a7* gene. The schematic diagram is as follows:



- The *Slc16a7* gene has 6 transcripts. According to the structure of *Slc16a7* gene, exon4-exon6 of *Slc16a7*-206 (ENSMUST00000211781.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc16a7* gene. The brief process is as follows: CRISPR/Cas9 system

- The effect on transcript *Slc16a7*-204 is unknown.
- Transcript *Slc16a7*-203 may not be affected.
- The *Slc16a7* gene is located on the Chr10. 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)

Slc16a7 solute carrier family 16 (monocarboxylic acid transporters), member 7 [*Mus musculus* (house mouse)]

Gene ID: 20503, updated on 24-Oct-2019

Summary

- Official Symbol** Slc16a7 provided by [MGI](#)
- Official Full Name** solute carrier family 16 (monocarboxylic acid transporters), member 7 provided by [MGI](#)
- Primary source** [MGI:MGI:1330284](#)
- See related** [Ensembl:ENSMUSG00000020102](#)
- 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** Mct2; 4921534N07Rik; 9030411M13Rik; D630004K10Rik
- Expression** Biased expression in testis adult (RPKM 38.6), bladder adult (RPKM 5.2) and 5 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10; 10 D3

See Slc16a7 in [Genome Data Viewer](#)

Exon count: 15

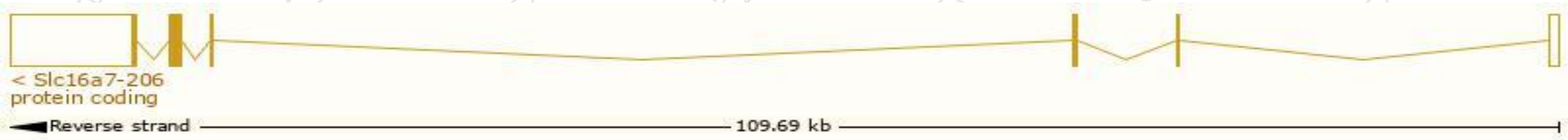
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (125219270..125389586, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (124664541..124765591, complement)

Transcript information (Ensembl)

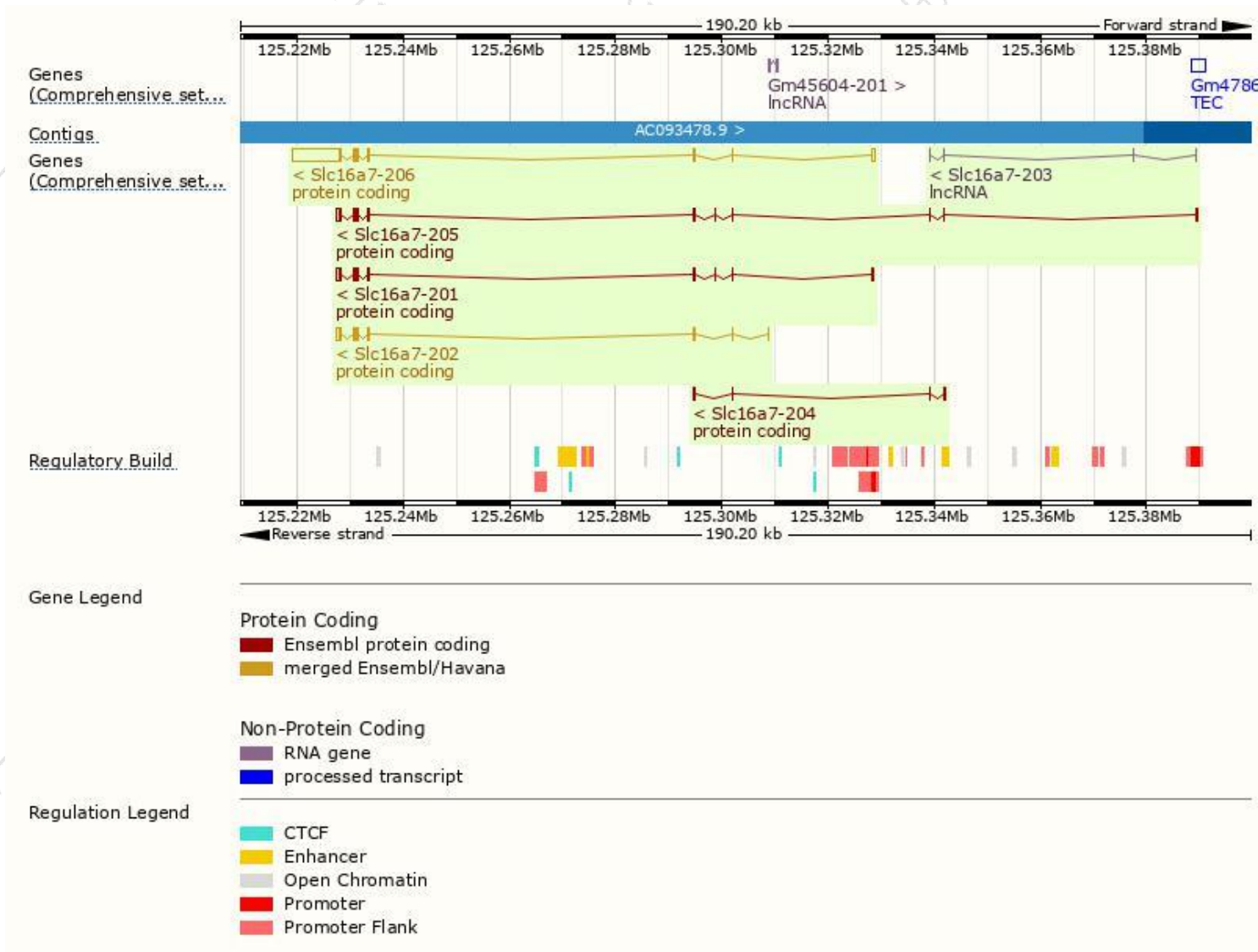
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc16a7-206	ENSMUST00000211781.1	10981	484aa	Protein coding	CCDS24218	O70451 Q149G3	TSL:1 GENCODE basic APPRIS P1
Slc16a7-205	ENSMUST00000210780.1	2562	484aa	Protein coding	CCDS24218	O70451 Q149G3	TSL:5 GENCODE basic APPRIS P1
Slc16a7-201	ENSMUST00000063318.9	2419	484aa	Protein coding	CCDS24218	O70451 Q149G3	TSL:1 GENCODE basic APPRIS P1
Slc16a7-202	ENSMUST00000105257.3	2238	484aa	Protein coding	CCDS24218	O70451 Q149G3	TSL:1 GENCODE basic APPRIS P1
Slc16a7-204	ENSMUST00000210069.1	711	55aa	Protein coding	-	A0A1B0GSA7	CDS 3' incomplete TSL:2
Slc16a7-203	ENSMUST00000209246.1	292	No protein	lncRNA	-	-	TSL:5

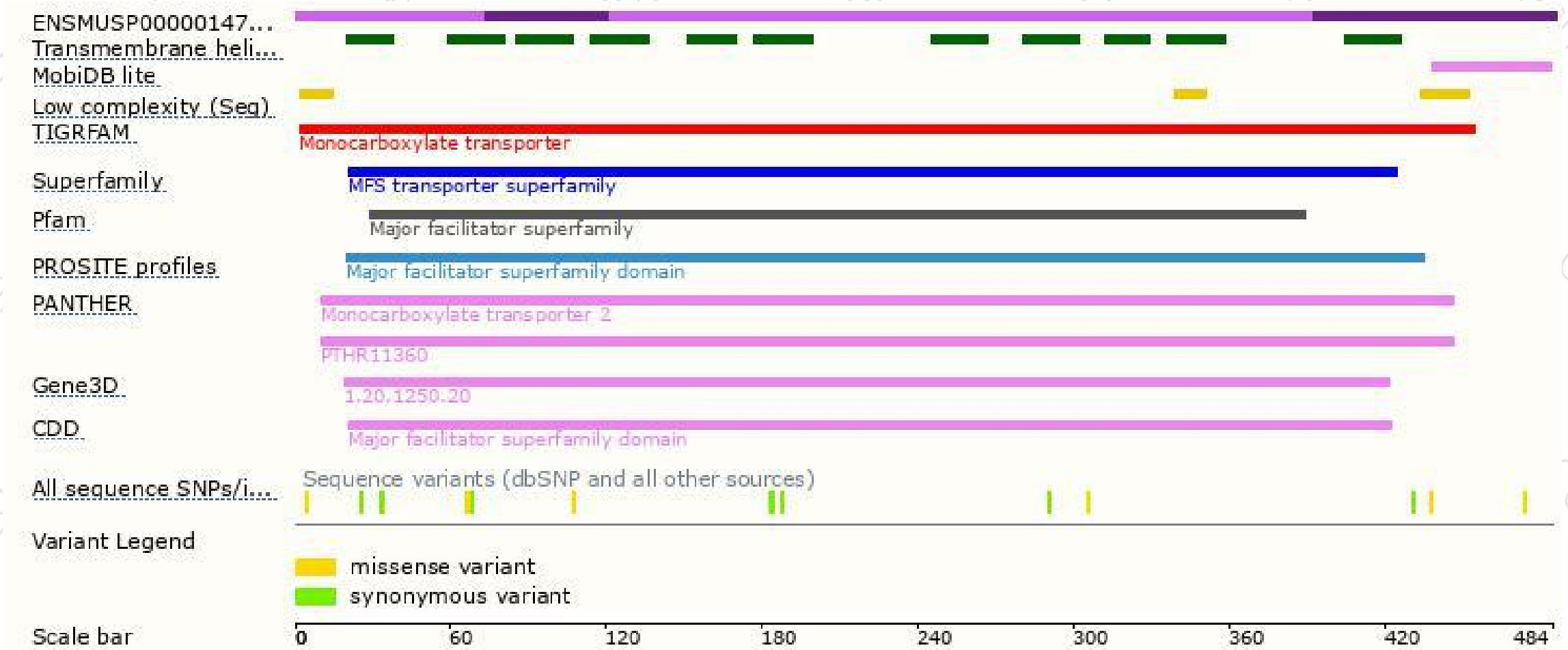
The strategy is based on the design of *Slc16a7-206* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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