

Slc16a10 Cas9-KO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

Design Date:

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Project Overview

Project Name

Slc16a10

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc16a10* gene. The schematic diagram is as follows:



- The *Slc16a10* gene has 4 transcripts. According to the structure of *Slc16a10* gene, exon2-exon3 of *Slc16a10-201* (ENSMUST00000092566.7) transcript is recommended as the knockout region. The region contains 599bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc16a10* gene. The brief process is as follows: CRISPR/Cas9 syst

- According to the MGI data, Mice homozygous for an ENU-induced null allele exhibit altered amino acid homeostasis.
- The *Slc16a10* 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)

Slc16a10 solute carrier family 16 (monocarboxylic acid transporters), member 10 [*Mus musculus* (house mouse)]

Gene ID: 72472, updated on 24-Oct-2019

Summary

Official Symbol Slc16a10 provided by [MGI](#)
Official Full Name solute carrier family 16 (monocarboxylic acid transporters), member 10 provided by [MGI](#)
Primary source [MGI:MGI:1919722](#)
See related [Ensembl:ENSMUSG00000019838](#)
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 TAT1; Mct10; PRO0813; 9830169E08; 2610103N14Rik
Expression Broad expression in liver E14.5 (RPKM 16.2), genital fat pad adult (RPKM 15.9) and 22 other tissues [See more](#)
Orthologs [human](#) [all](#)

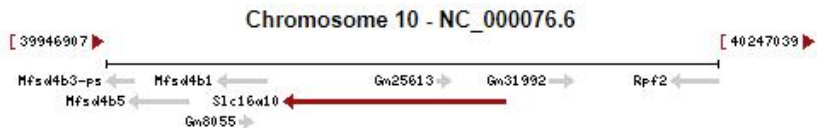
Genomic context

Location: 10; 10 B1

See Slc16a10 in [Genome Data Viewer](#)

Exon count: 9

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (40033532..40142270, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (39753341..39862060, complement)

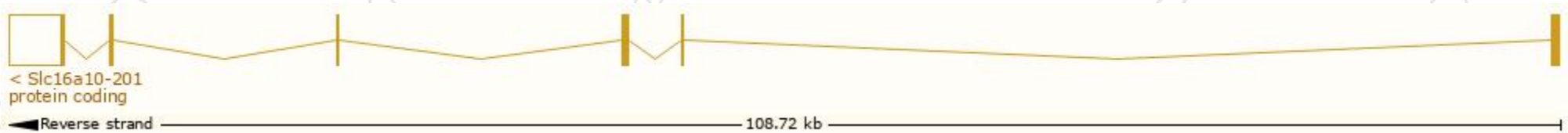


Transcript information (Ensembl)

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc16a10-201	ENSMUST00000092566.7	5397	512aa	Protein coding	CCDS48543	Q3U9N9	TSL:1 GENCODE basic APPRIS P1
Slc16a10-202	ENSMUST00000213488.1	2325	320aa	Protein coding	-	Q3U9N9	TSL:1 GENCODE basic
Slc16a10-203	ENSMUST00000213827.1	553	184aa	Protein coding	-	A0A1L1SVB8	CDS 5' and 3' incomplete TSL:3
Slc16a10-204	ENSMUST00000217252.1	1306	No protein	Processed transcript	-	-	TSL:1

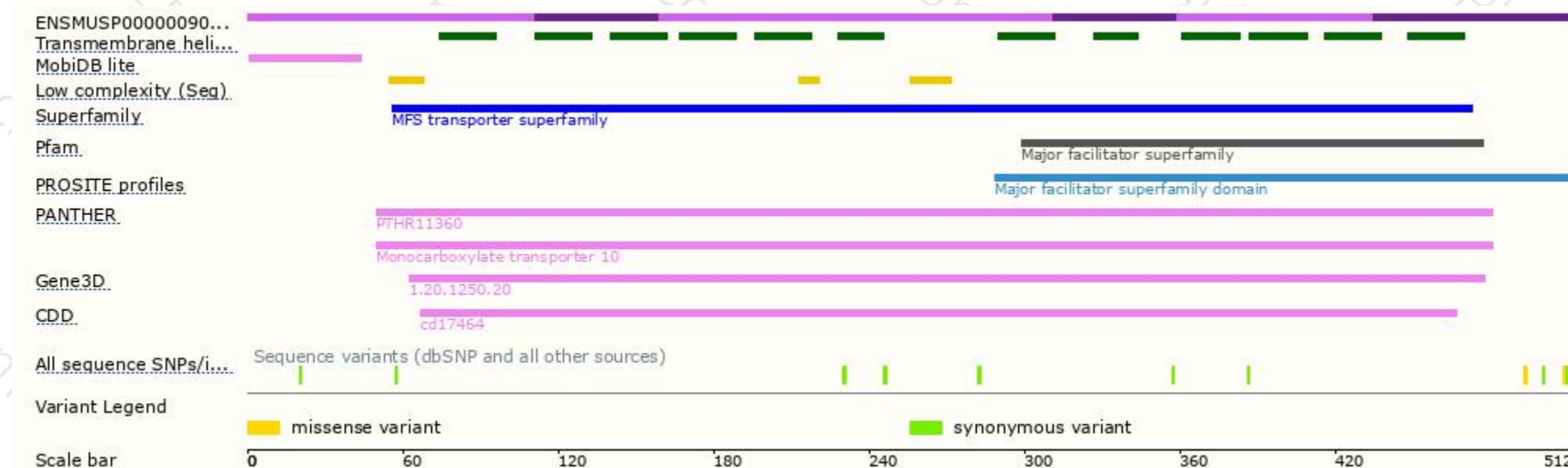
The strategy is based on the design of *Slc16a10-201* transcript,The transcription is shown below



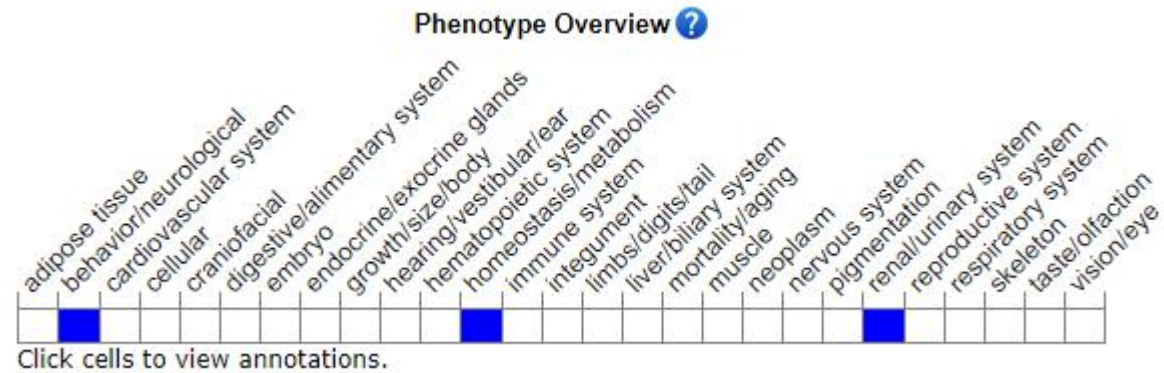
Genomic location distribution



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 an ENU-induced null allele exhibit altered amino acid homeostasis.

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

Tel: 400-9660890

