# *Slc16a10* Cas9-CKO Strategy

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| **Reviewer:** | **Ruirui Zhang** |
| **Design Date:** | **2020/2/14** |

# Project Overview

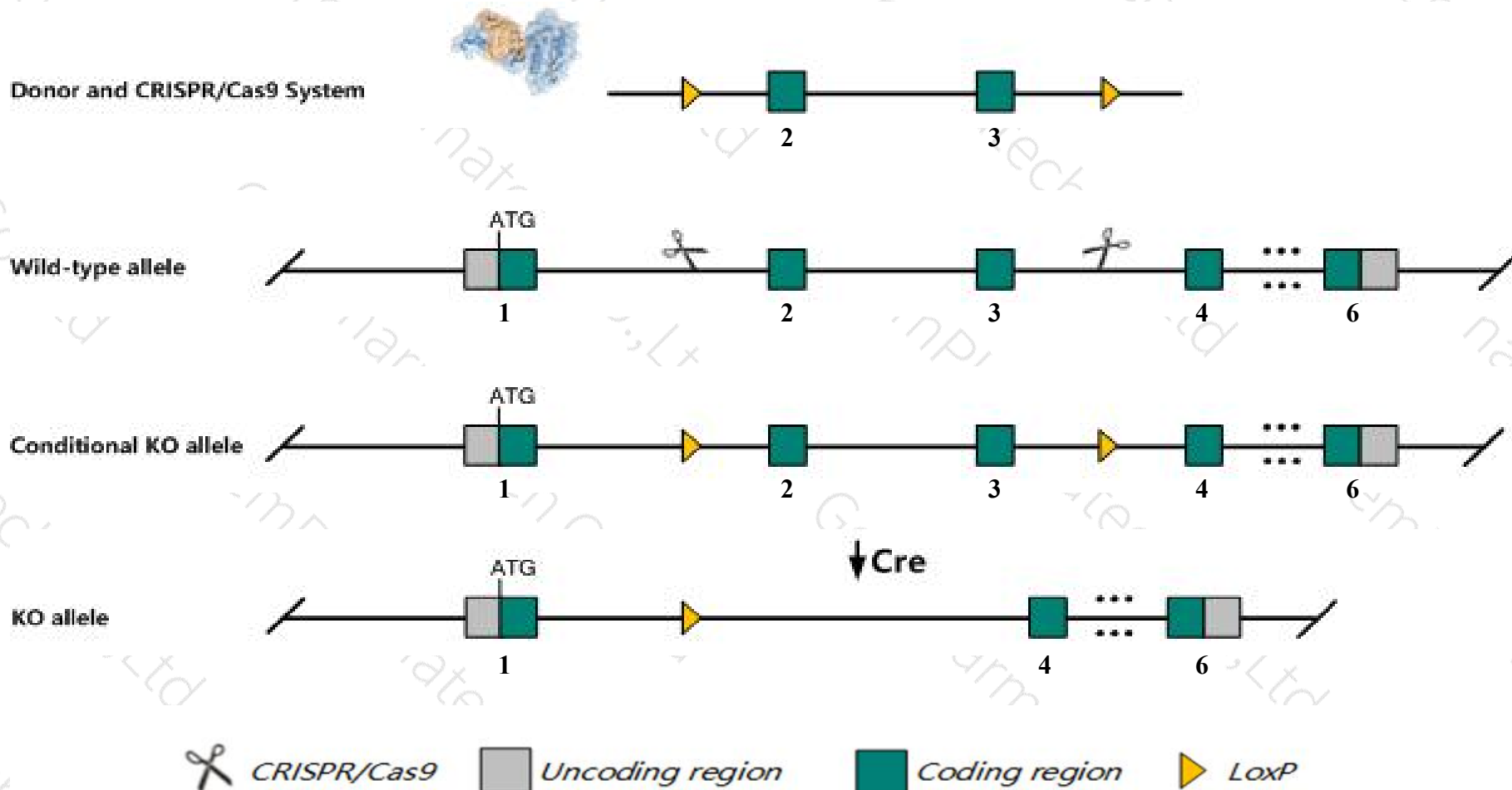| | |
|---|---|
| **Project Name** | *Slc16a10* |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

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



Donor and CRISPR/Cas9 System

Wild-type allele

Conditional KO allele

KO allele

ATG

Cre

CRISPR/Cas9    Uncoding region    Coding region    LoxP

# Technical routes

➤ 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 Ens 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 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.

➤ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Notice

➤ According to the MGI date, 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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 |

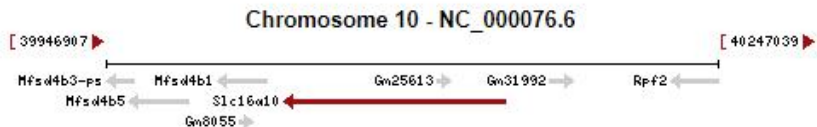### Genomic context

Location:　10; 10 B1

Exon count:　9

See Slc16a10 in Genome Data Viewer

| 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) |

Chromosome 10 - NC_000076.6

[39946907     [40247039

Mfsd4b3-ps   Mfsd4b1    Gm25613   Gm31992   Rpf2
Mfsd4b5    Slc16a10
Gm8055

# 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



< Slc16a10-201
protein coding
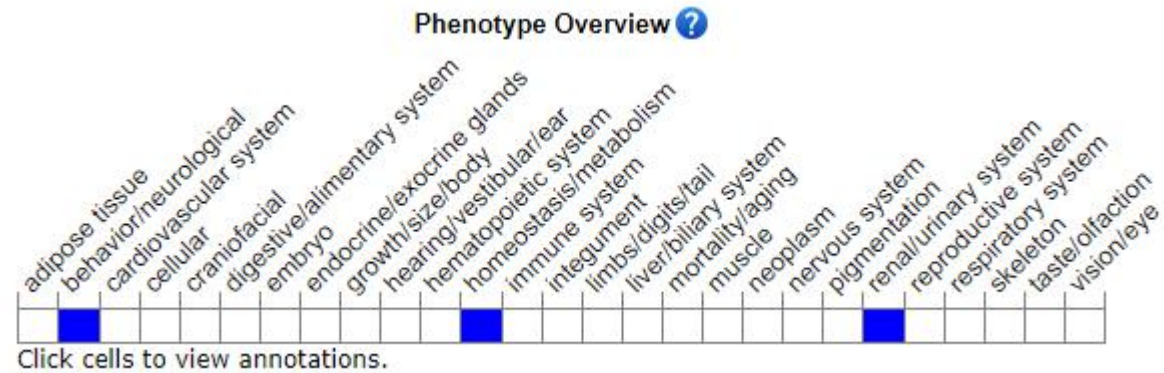◄ Reverse strand

108.72 kb
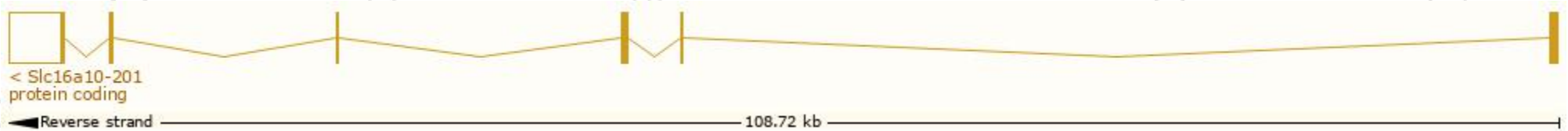
# Genomic location distribution
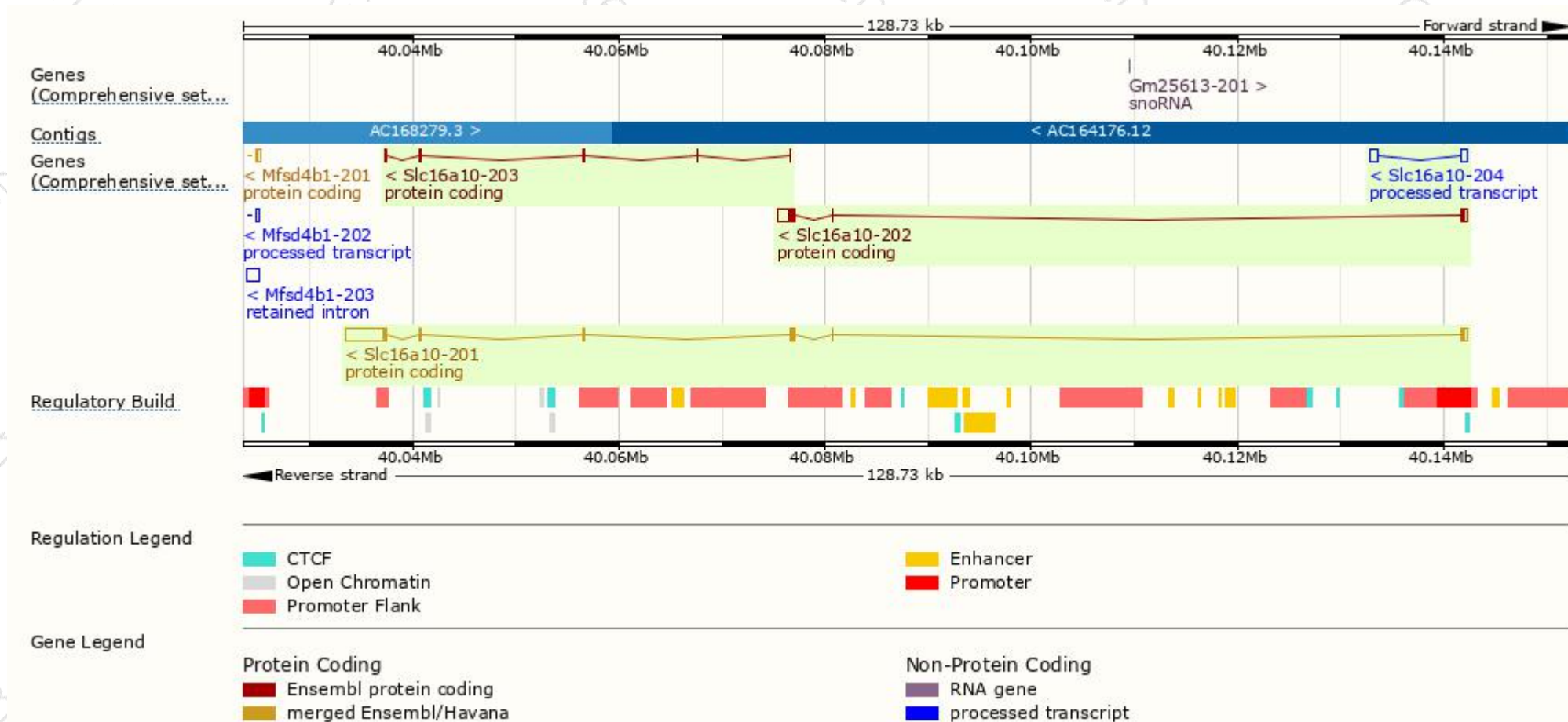
# Protein domain
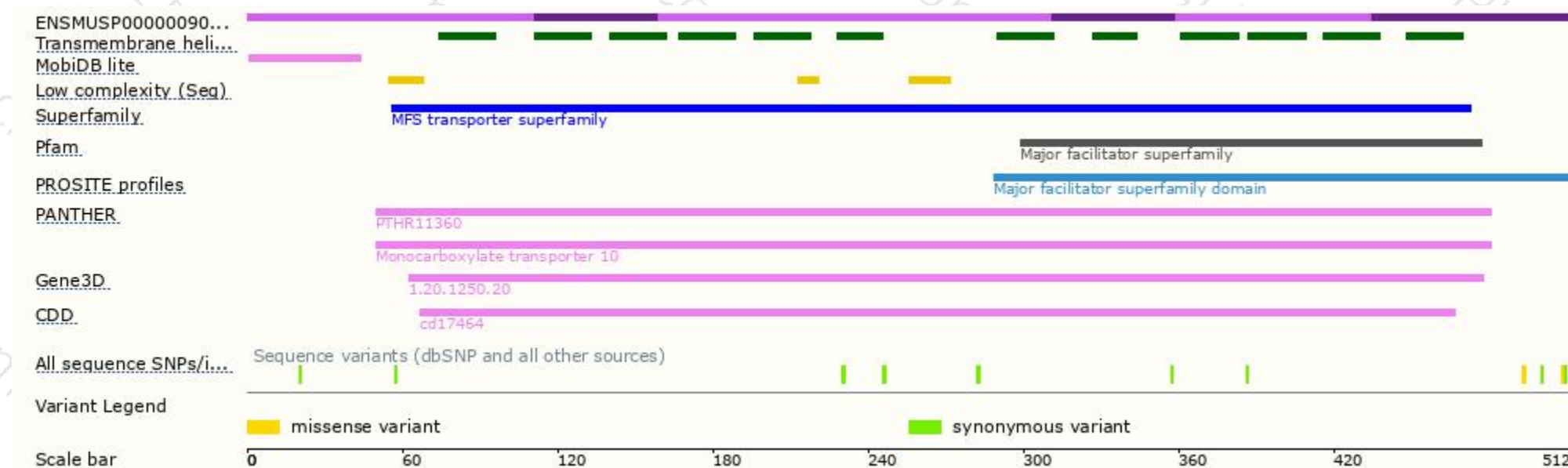
# Mouse phenotype description(MGI )



*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.
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