

# *Slc16a5* Cas9-KO Strategy

**Designer: Lingyan Wu**

**Reviewer: Miaomiao Cui**

**Design Date: 2021-9-22**

# Project Overview

---

**Project Name**

*Slc16a5*

---

**Project type**

**Cas9-KO**

---

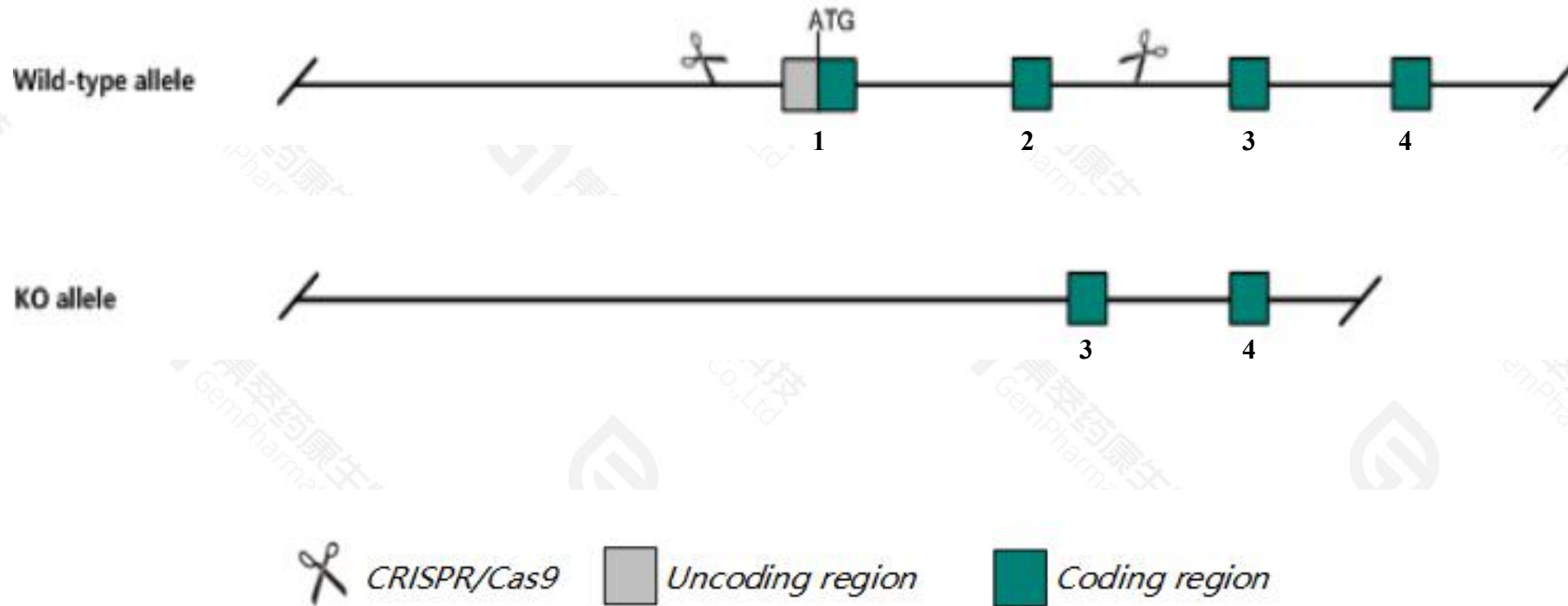
**Strain background**

**C57BL/6JGpt**

---

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc16a5* gene. The schematic diagram is as follows:



- The *Slc16a5* gene has 9 transcripts. According to the structure of *Slc16a5* gene, exon1-exon2 of *Slc16a5*-201(ENSMUST00000092445.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc16a5* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- *Gm11695* gene will be deleted.
- The *Slc16a5* 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 biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



## Slc16a5 solute carrier family 16 (monocarboxylic acid transporters), member 5 [Mus musculus (house mouse)]

Gene ID: 217316, updated on 17-Dec-2020

### Summary



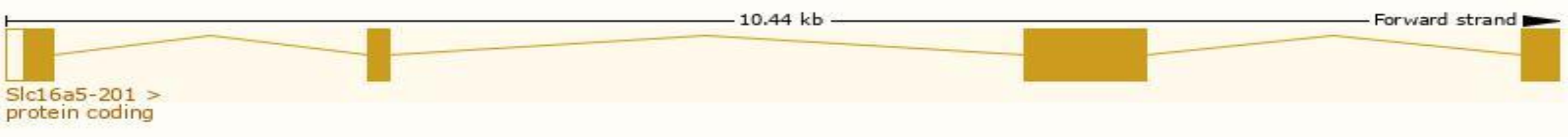
<b>Official Symbol</b>	Slc16a5 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	solute carrier family 16 (monocarboxylic acid transporters), member 5 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2443515</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000045775</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	A130015N09Rik, MCT 5, MCT 6, MCT5
<b>Expression</b>	Biased expression in thymus adult (RPKM 51.1), duodenum adult (RPKM 26.1) and 6 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

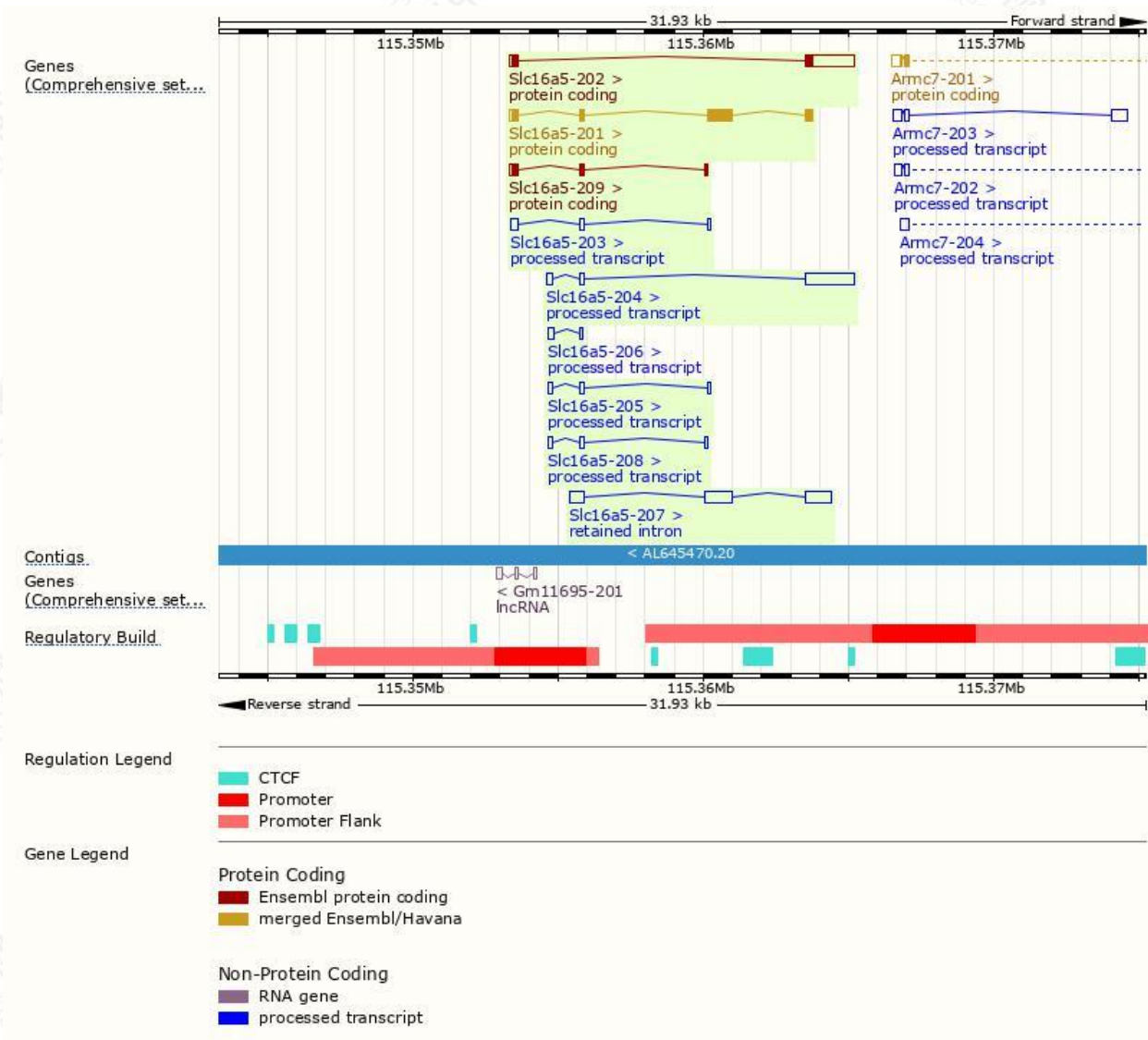
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc16a5-201	<a href="#">ENSMUST00000092445.12</a>	1538	<a href="#">468aa</a>	Protein coding	<a href="#">CCDS36373</a>		CDS 3' incomplete , TSL:5 ,
Slc16a5-202	<a href="#">ENSMUST00000106532.4</a>	2062	<a href="#">149aa</a>	Protein coding	-		TSL:1 , GENCODE basic , APPRIS P1 ,
Slc16a5-209	<a href="#">ENSMUST00000153466.2</a>	516	<a href="#">137aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Slc16a5-204	<a href="#">ENSMUST00000133636.8</a>	2044	No protein	Processed transcript	-		TSL:1 ,
Slc16a5-203	<a href="#">ENSMUST00000125251.8</a>	460	No protein	Processed transcript	-		TSL:2 ,
Slc16a5-208	<a href="#">ENSMUST00000146500.2</a>	411	No protein	Processed transcript	-		TSL:3 ,
Slc16a5-205	<a href="#">ENSMUST00000139318.8</a>	370	No protein	Processed transcript	-		TSL:2 ,
Slc16a5-206	<a href="#">ENSMUST00000140567.2</a>	323	No protein	Processed transcript	-		TSL:3 ,
Slc16a5-207	<a href="#">ENSMUST00000140739.2</a>	2340	No protein	Retained intron	-		TSL:1 ,

The strategy is based on the design of *Slc16a5-201* transcript,the transcription is shown below:

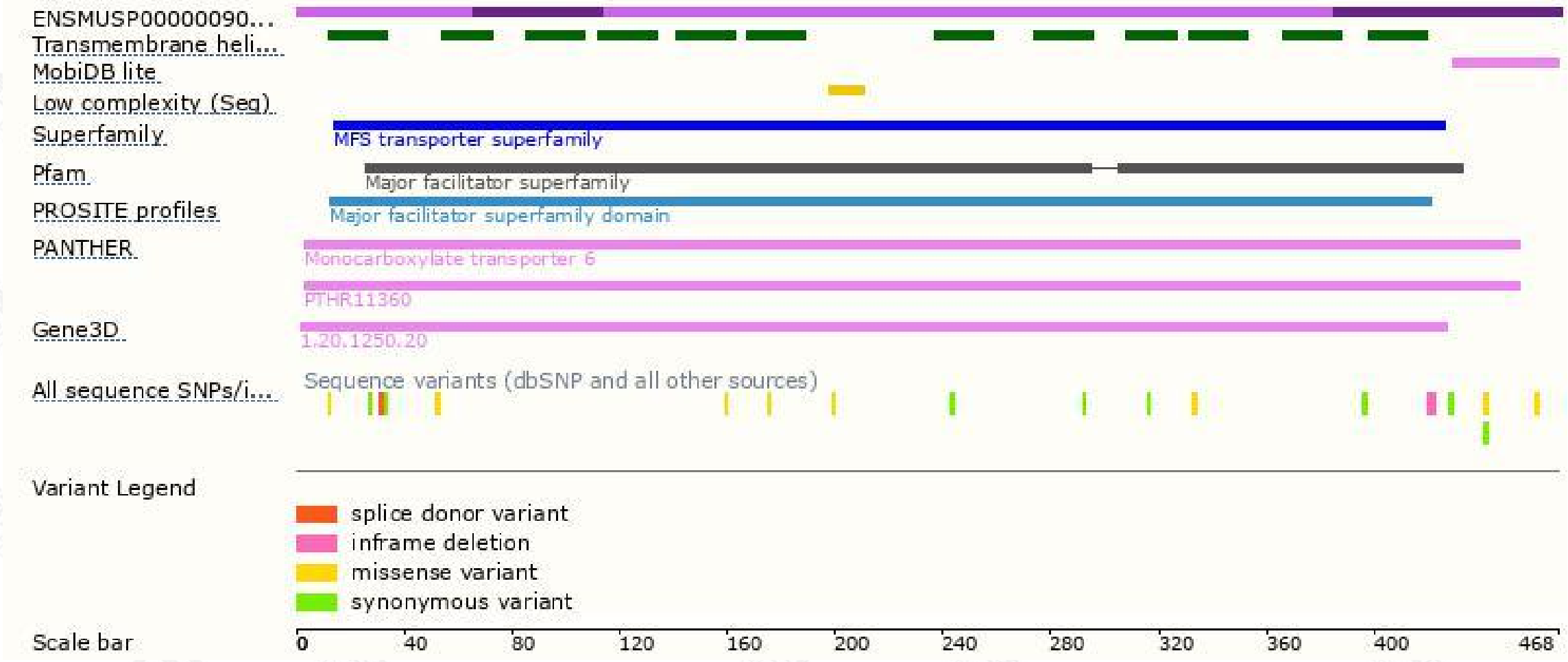


# Genomic location distribution





# Protein domain



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

