

# ***Slc10a2* Cas9-KO Strategy**

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# Project Overview

**Project Name**

*Slc10a2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc10a2* gene. The schematic diagram is as follows:



- The *Slc10a2* gene has 1 transcript. According to the structure of *Slc10a2* gene, exon2-exon5 of *Slc10a2-201* (ENSMUST00000023835.2) transcript is recommended as the knockout region. The region contains 542bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc10a2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene are essentially indistinguishable from wild-type in terms of survival, gross appearance and behavior. However, they do have defects in lipid absorption from the intestine.
- The N-terminal of *Slc10a2* gene will remain several amino acids, it may remain the partial function of *Slc10a2* gene.
- The *Slc10a2* gene is located on the Chr8. 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)

## Slc10a2 solute carrier family 10, member 2 [ *Mus musculus* (house mouse) ]

Gene ID: 20494, updated on 22-Oct-2019

### Summary

- Official Symbol** Slc10a2 provided by [MGI](#)
- Official Full Name** solute carrier family 10, member 2 provided by [MGI](#)
- Primary source** [MGI:MGI:1201406](#)
- See related** [Ensembl:ENSMUSG00000023073](#)
- 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** ASBT; IBAT; ISBT; AI605518; 9130221J18Rik
- Expression** Biased expression in large intestine adult (RPKM 20.9), kidney adult (RPKM 7.5) and 2 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 8 A1.1; 8 2.16 cM

See Slc10a2 in [Genome Data Viewer](#)

**Exon count:** 6

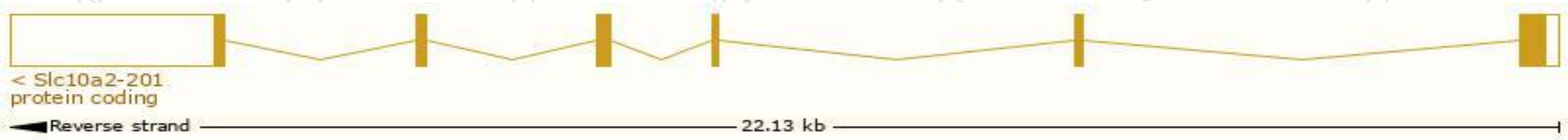
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	8	NC_000074.6 (5083219..5105287, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	8	NC_000074.5 (5085623..5105232, complement)

# Transcript information (Ensembl)

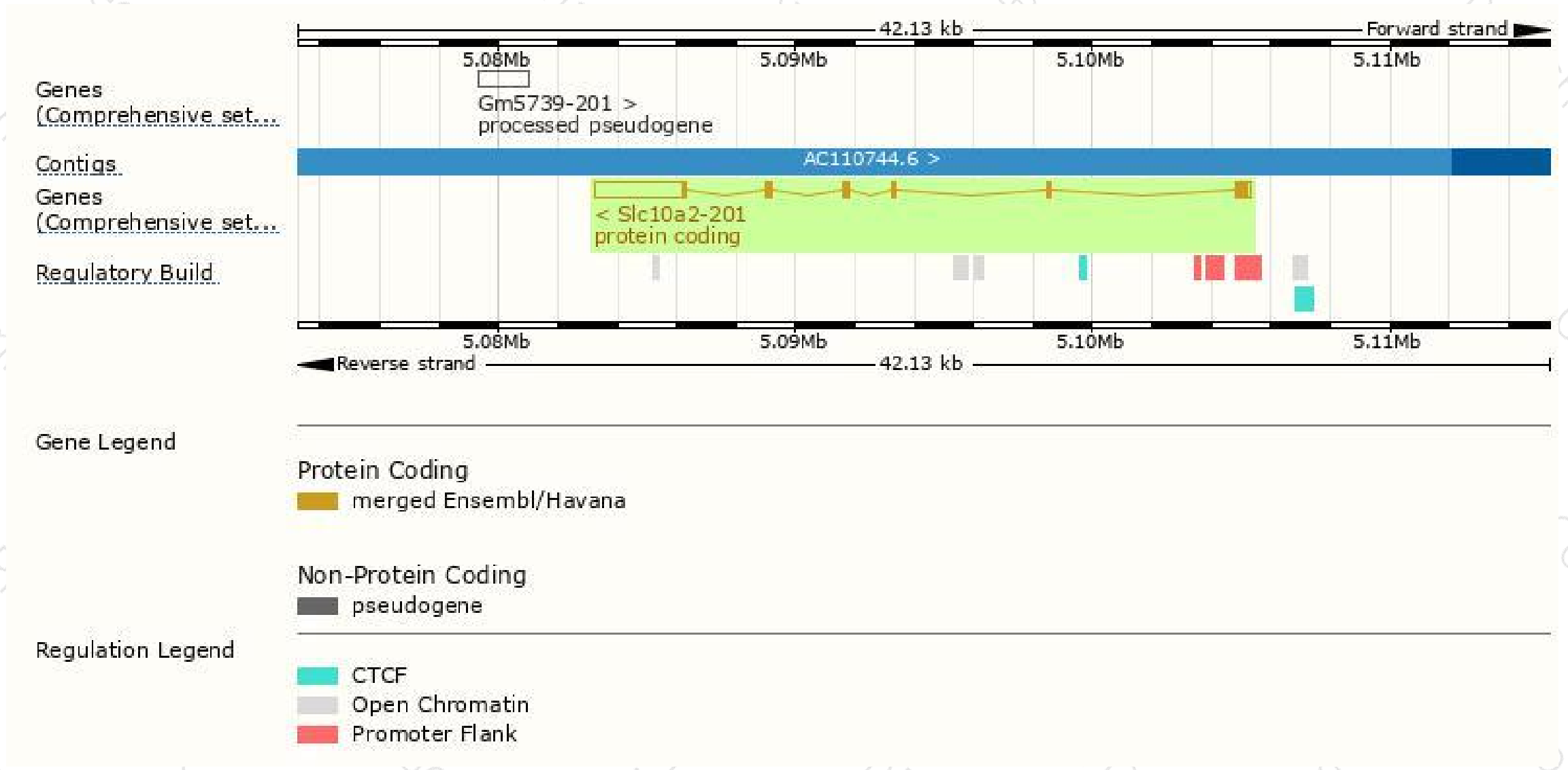
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc10a2-201	<a href="#">ENSMUST00000023835.2</a>	4152	<a href="#">348aa</a>	Protein coding	<a href="#">CCDS22089</a>	<a href="#">P70172 Q0VBB8</a>	TSL:1 GENCODE basic APPRIS P1

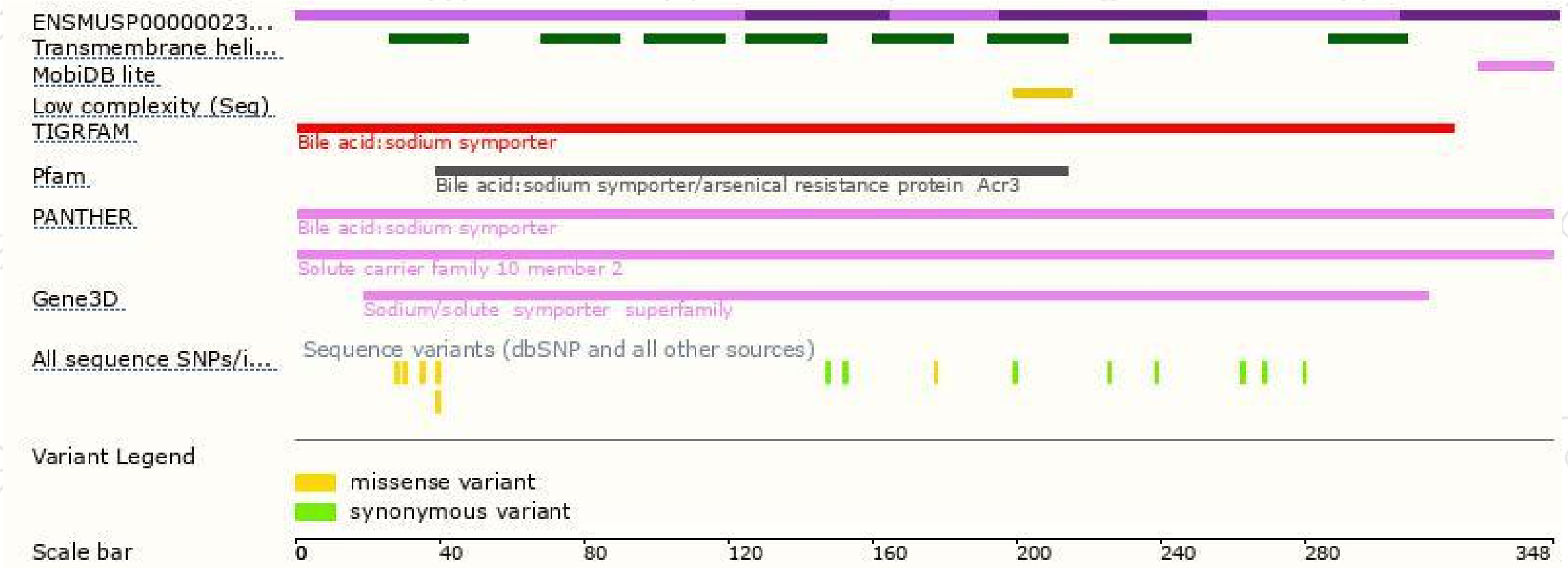
The strategy is based on the design of *Slc10a2-201* transcript, The transcription is shown below



# 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/>).*

According to the existing MGI data, Mice homozygous for disruptions in this gene are essentially indistinguishable from wild-type in terms of survival, gross appearance and behavior. However, they do have defects in lipid absorption from the intestine.

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

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