

# *Slc31a2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Slc31a2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc31a2* gene. The schematic diagram is as follows:



- The *Slc31a2* gene has 3 transcripts. According to the structure of *Slc31a2* gene, exon2-exon3 of *Slc31a2-201* (ENSMUST00000084530.8) transcript is recommended as the knockout region. The region contains 257bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc31a2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Slc31a2* gene is located on the Chr4. 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)

## Slc31a2 solute carrier family 31, member 2 [Mus musculus (house mouse)]

Gene ID: 20530, updated on 31-Jan-2019

### Summary



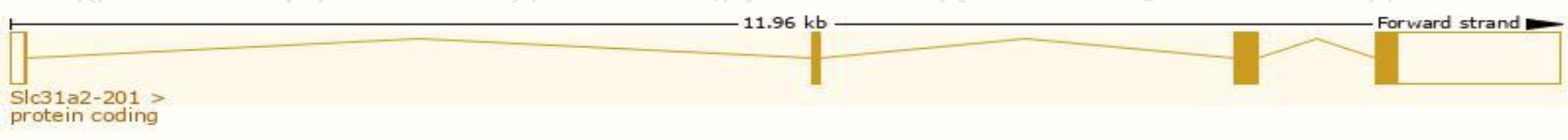
<b>Official Symbol</b>	Slc31a2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	solute carrier family 31, member 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1333844</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000066152</a>
<b>Gene type</b>	protein coding
<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>	AI604396, CTR2
<b>Expression</b>	Ubiquitous expression in genital fat pad adult (RPKM 27.9), adrenal adult (RPKM 15.7) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

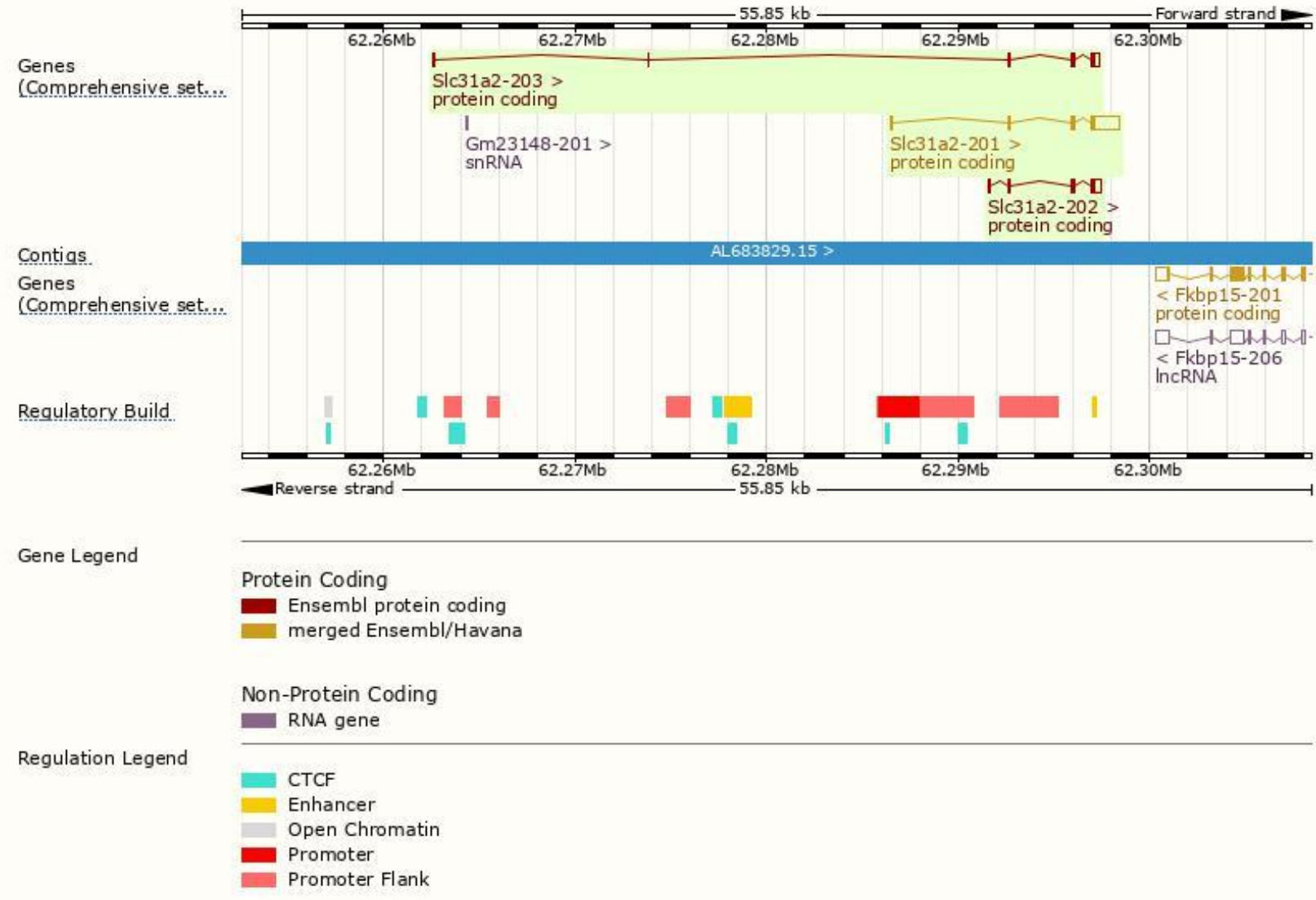
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc31a2-201	<a href="#">ENSMUST00000084530.8</a>	1820	<a href="#">143aa</a>	Protein coding	<a href="#">CCDS18236</a>	<a href="#">Q4KL43</a> <a href="#">Q9CPU9</a>	TSL:1 GENCODE basic APPRIS P3
Slc31a2-202	<a href="#">ENSMUST00000107467.2</a>	868	<a href="#">141aa</a>	Protein coding	<a href="#">CCDS71401</a>	<a href="#">Q9D524</a>	TSL:1 GENCODE basic APPRIS ALT1
Slc31a2-203	<a href="#">ENSMUST00000107468.7</a>	743	<a href="#">141aa</a>	Protein coding	<a href="#">CCDS71401</a>	<a href="#">Q9D524</a>	TSL:5 GENCODE basic APPRIS ALT1

The strategy is based on the design of *Slc31a2-201* transcript,The transcription is shown below

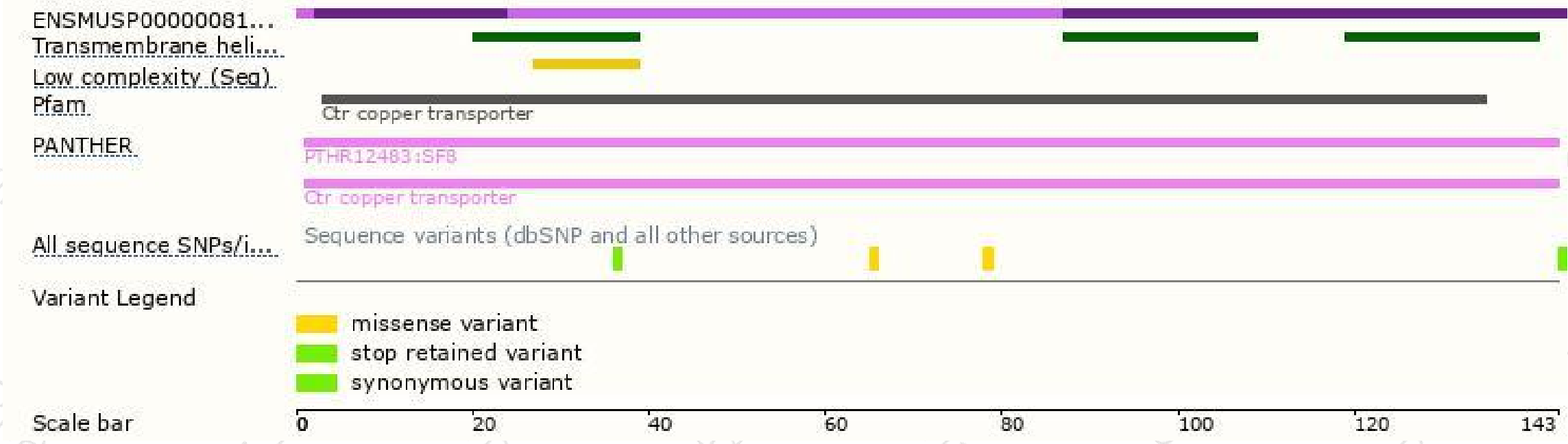


# Genomic location distribution





# Protein domain



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

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