

# ***Slc19a3*** Cas9-KO Strategy

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# Project Overview

**Project Name**

*Slc19a3*

**Project type**

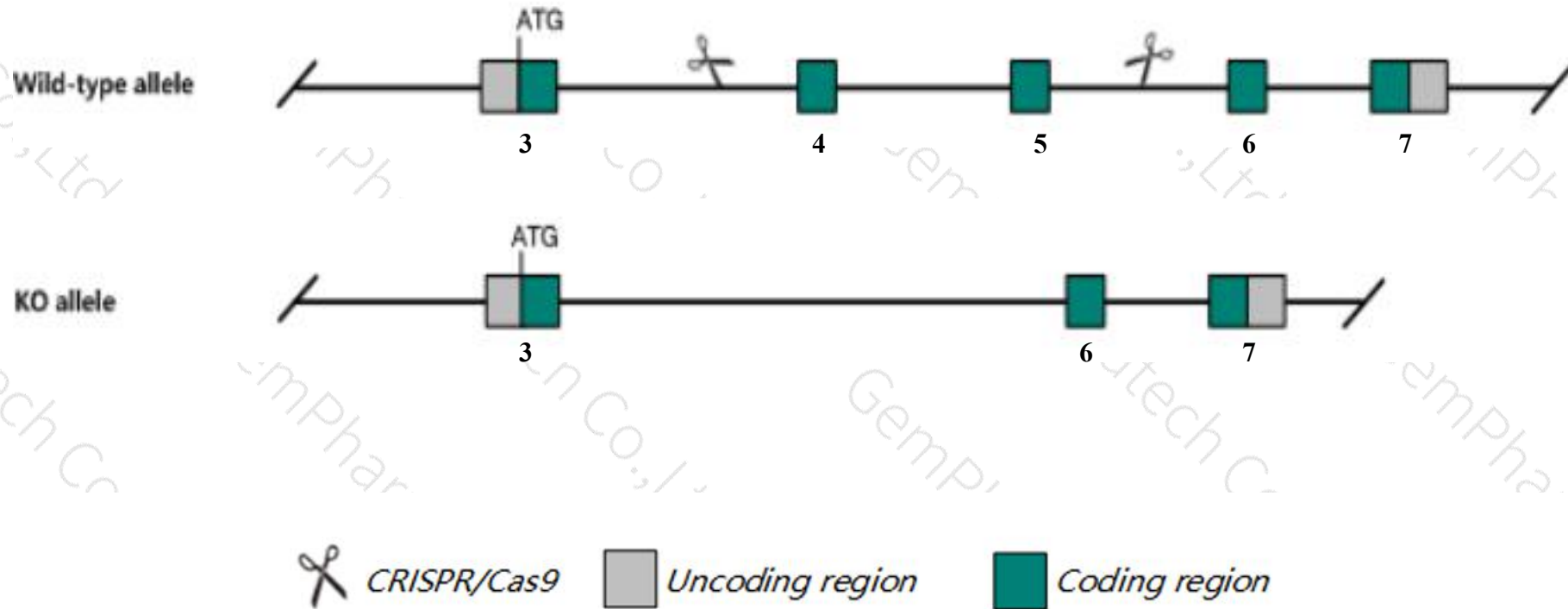
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc19a3* gene. The schematic diagram is as follows:



- The *Slc19a3* gene has 3 transcripts. According to the structure of *Slc19a3* gene, exon4-exon5 of *Slc19a3-201* (ENSMUST00000045560.14) transcript is recommended as the knockout region. The region contains 1001bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc19a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit premature death within a year of age, impaired thiamin uptake, lethargy, cachexia, injured liver parenchyma, hepatic necrosis, liver and kidney inflammation, and nephrosclerosis.
- The *Slc19a3* gene is located on the Chr1. 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)

## Slc19a3 solute carrier family 19, member 3 [Mus musculus (house mouse)]

Gene ID: 80721, updated on 13-Mar-2020

### Summary



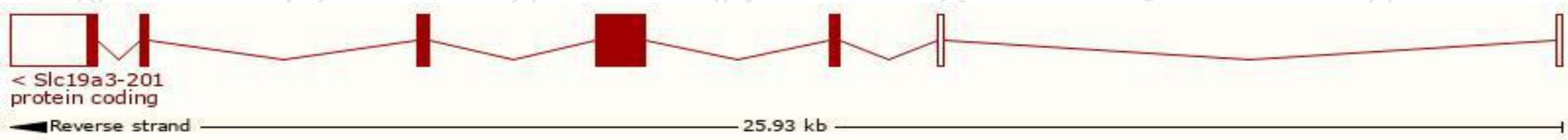
<b>Official Symbol</b>	Slc19a3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	solute carrier family 19, member 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1931307</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000038496</a>
<b>Gene type</b>	protein coding
<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>	A230084E24Rik, AI788884, ThTr2
<b>Expression</b>	Biased expression in kidney adult (RPKM 6.0), duodenum adult (RPKM 1.7) and 10 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

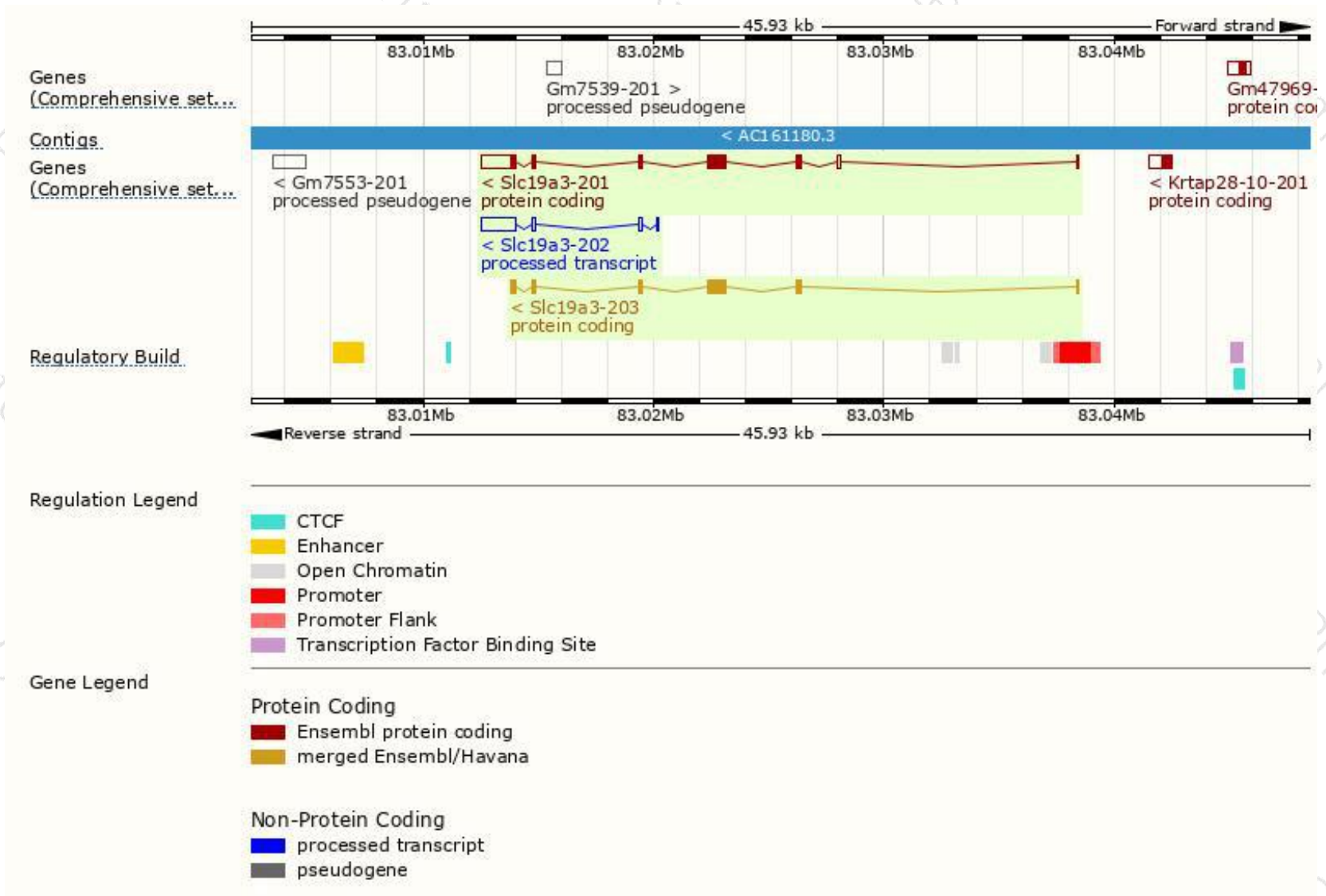
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc19a3-201	<a href="#">ENSMUST00000045560.14</a>	2974	<a href="#">488aa</a>	Protein coding	<a href="#">CCDS15101</a>	<a href="#">Q99PL8</a>	TSL:1 GENCODE basic APPRIS P1
Slc19a3-203	<a href="#">ENSMUST00000164473.1</a>	1550	<a href="#">488aa</a>	Protein coding	<a href="#">CCDS15101</a>	<a href="#">Q99PL8</a>	TSL:1 GENCODE basic APPRIS P1
Slc19a3-202	<a href="#">ENSMUST00000142805.1</a>	1892	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Slc19a3-201* transcript,the transcription is shown below:



# Genomic location distribution

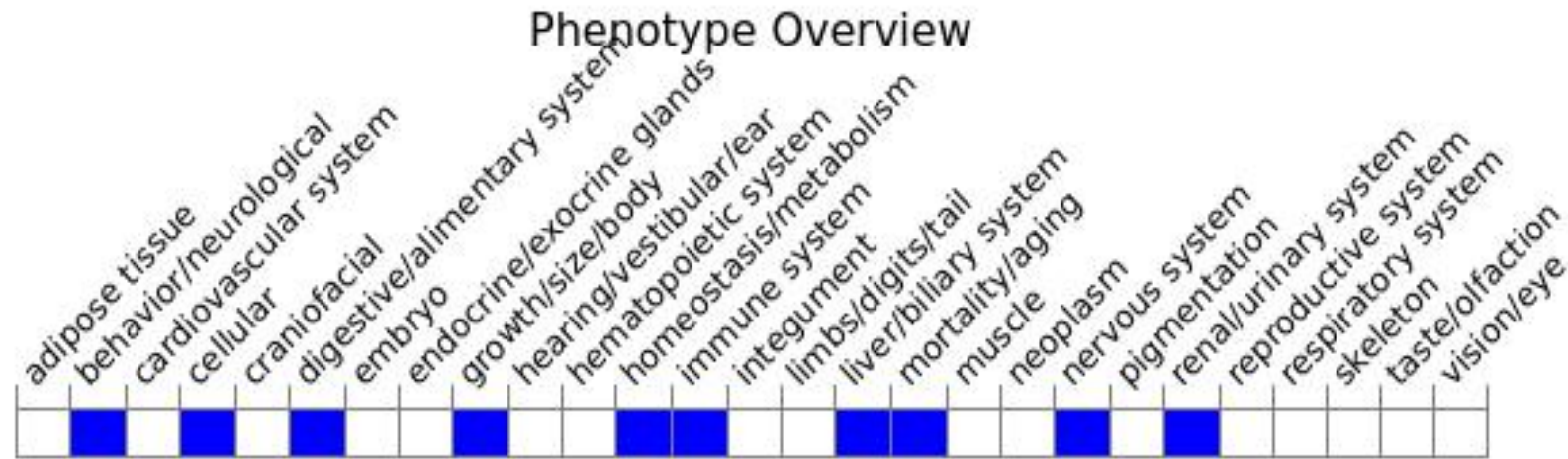




# Protein domain



# 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 a knock-out allele exhibit premature death within a year of age, impaired thiamin uptake, lethargy, cachexia, injured liver parenchyma, hepatic necrosis, liver and kidney inflammation, and nephrosclerosis.

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

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