

# *Slc39a5* Cas9-KO Strategy

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**Reviewer:**

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**Design Date:**

**2020-2-19**

# Project Overview

**Project Name**

*Slc39a5*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc39a5* gene. The schematic diagram is as follows:



- The *Slc39a5* gene has 5 transcripts. According to the structure of *Slc39a5* gene, exon4-exon11 of *Slc39a5-202* (ENSMUST00000167859.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc39a5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit altered zinc homeostasis and increased susceptibility to zinc-induced pancreatitis.
- The function of *Gm17201* may be affected.
- The *Slc39a5* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Slc39a5 solute carrier family 39 (metal ion transporter), member 5 [ *Mus musculus* (house mouse) ]

Gene ID: 72002, updated on 12-Aug-2019

### Summary

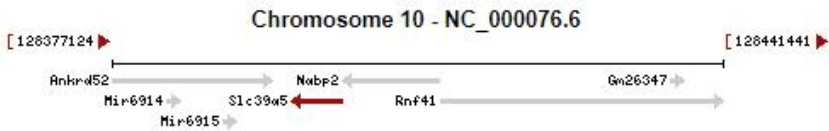
- Official Symbol** Slc39a5 provided by [MGI](#)
- Official Full Name** solute carrier family 39 (metal ion transporter), member 5 provided by [MGI](#)
- Primary source** [MGI: MGI:1919336](#)
- See related** [Ensembl: ENSMUSG00000039878](#)
- Gene type** protein coding
- RefSeq status** VALIDATED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** Zip5; 1810013D05Rik; 2010205A06Rik
- Expression** Biased expression in duodenum adult (RPKM 158.7), large intestine adult (RPKM 83.5) and 7 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 10; 10 D3 See Slc39a5 in [Genome Data Viewer](#)

**Exon count:** 12

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	10	NC_000076.6 (128395927..128401276, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	10	NC_000076.5 (127832987..127838280, complement)

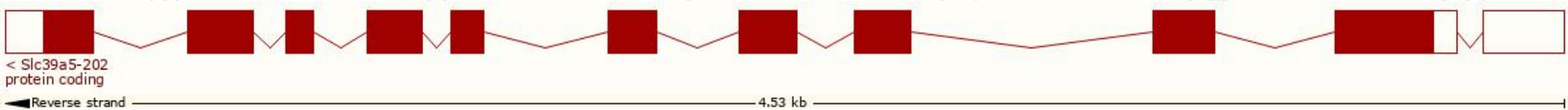


# Transcript information (Ensembl)

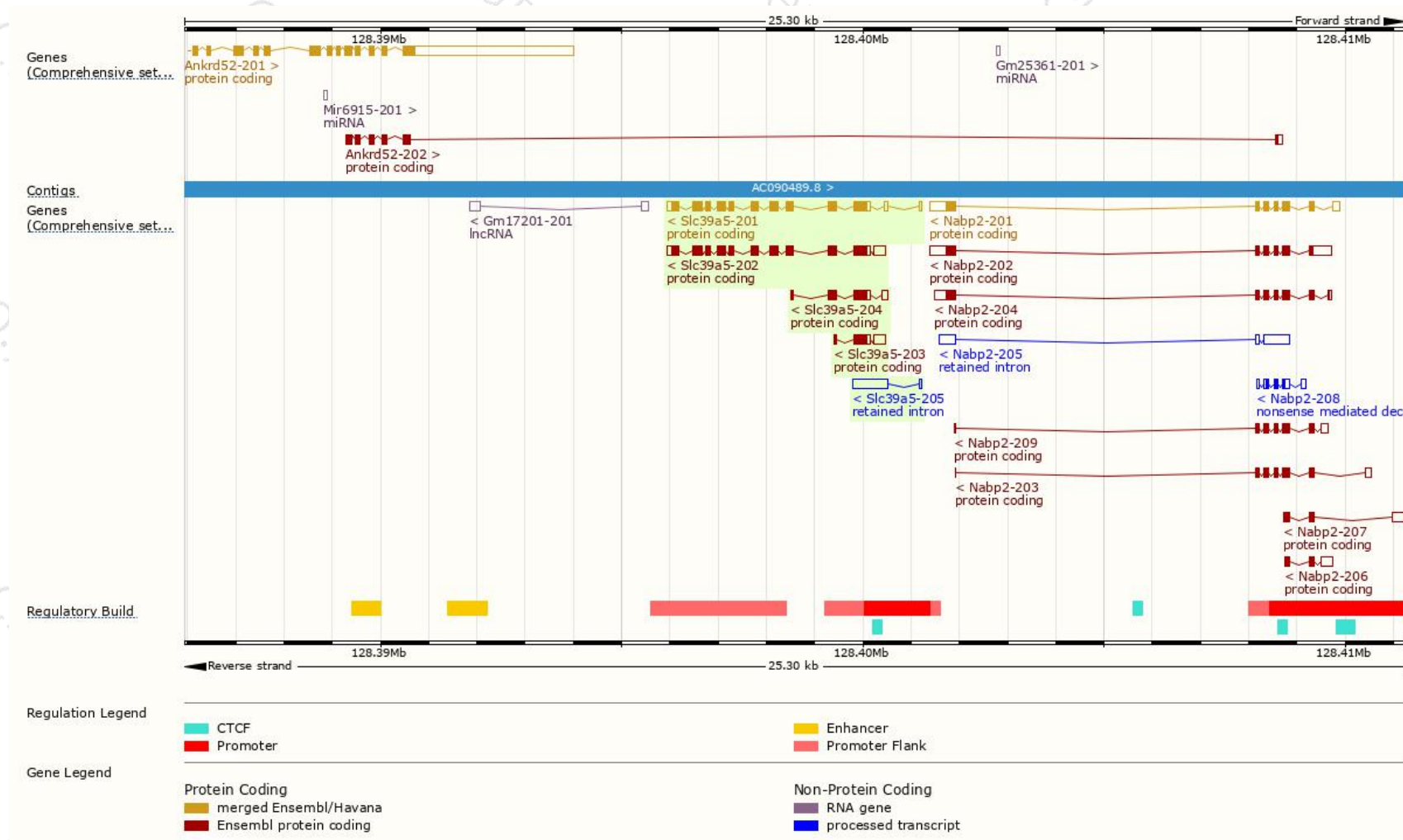
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc39a5-202	<a href="#">ENSMUST00000167859.1</a>	2025	<a href="#">535aa</a>	Protein coding	<a href="#">CCDS24275</a>	<a href="#">Q9D856</a>	TSL:1 GENCODE basic APPRIS P1
Slc39a5-201	<a href="#">ENSMUST00000042666.12</a>	1947	<a href="#">535aa</a>	Protein coding	<a href="#">CCDS24275</a>	<a href="#">Q9D856</a>	TSL:1 GENCODE basic APPRIS P1
Slc39a5-204	<a href="#">ENSMUST00000219131.1</a>	709	<a href="#">176aa</a>	Protein coding	-	<a href="#">A0A1W2P7R0</a>	CDS 3' incomplete TSL:5
Slc39a5-203	<a href="#">ENSMUST00000218858.1</a>	648	<a href="#">114aa</a>	Protein coding	-	<a href="#">A0A1W2P7Q2</a>	CDS 3' incomplete TSL:5
Slc39a5-205	<a href="#">ENSMUST00000219222.1</a>	766	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Slc39a5-202* transcript,The transcription is shown below

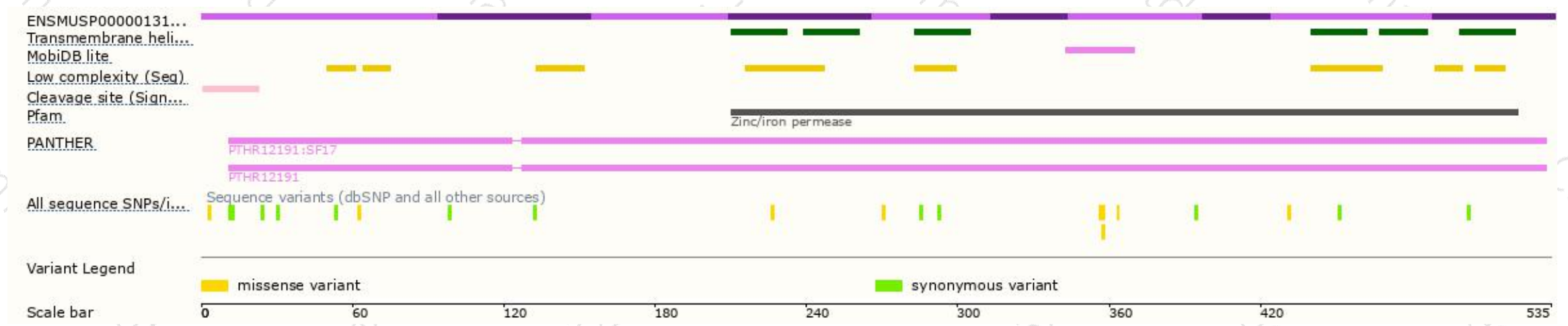


# Genomic location distribution

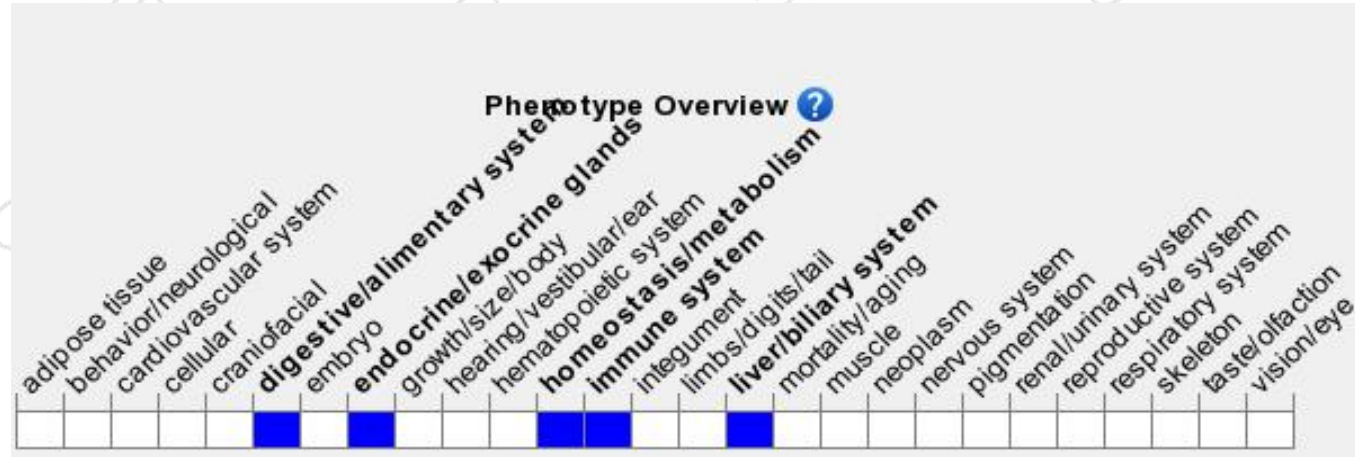




# Protein domain



# 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 altered zinc homeostasis and increased susceptibility to zinc-induced pancreatitis.

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

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