

# Slc25a3 Cas9-KO Strategy

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# Overview

## Target Gene Name

- Slc25a3

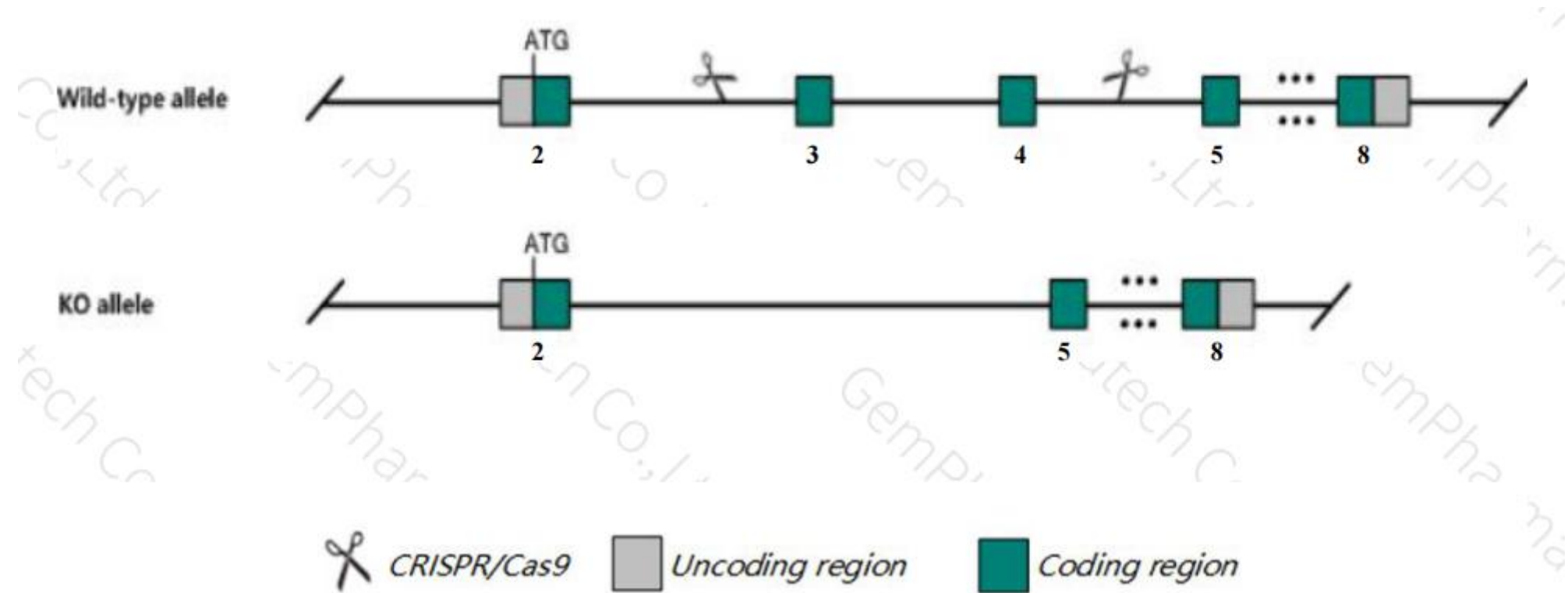
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Slc25a3* gene.

# Technical Information

- The *Slc25a3* gene has 8 transcripts. According to the structure of *Slc25a3* gene, exon3-exon4 of *Slc25a3-201* (ENSMUST00000076694.12) transcript is recommended as the knockout region. The region contains 302bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Slc25a3* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

# Gene Information

## Slc25a3 solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus (house mouse)]

Gene ID: 18674, updated on 13-Mar-2020

### Summary

<b>Official Symbol</b>	Slc25a3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1353498</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000061904</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>	5730556H19Rik, PTP, Phc
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 904.7), duodenum adult (RPKM 787.5) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

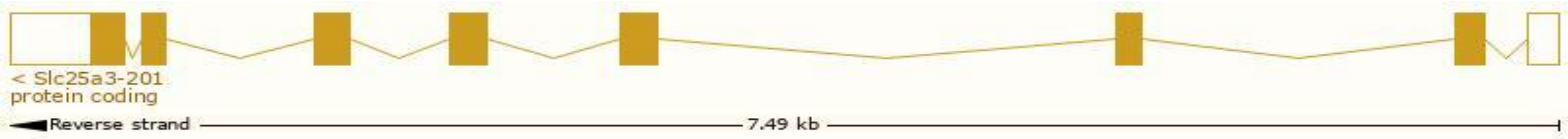
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 8 transcripts, all transcripts are shown below:

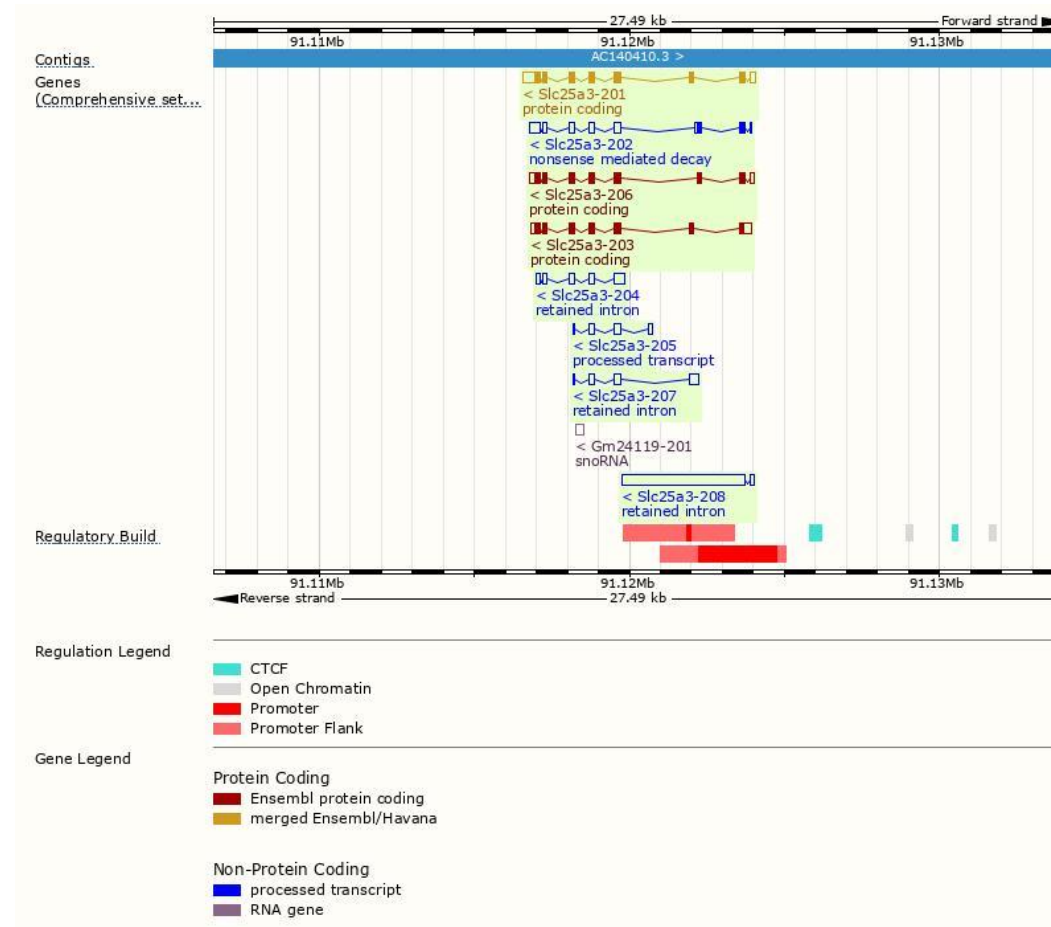
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a3-201	<a href="#">ENSMUST00000076694.12</a>	1612	<a href="#">357aa</a>	Protein coding	<a href="#">CCDS24121</a>	<a href="#">Q8VEM8</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Slc25a3-203	<a href="#">ENSMUST00000164505.1</a>	1483	<a href="#">357aa</a>	Protein coding	<a href="#">CCDS24121</a>	<a href="#">Q8VEM8</a>	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Slc25a3-206	<a href="#">ENSMUST00000170810.7</a>	1341	<a href="#">358aa</a>	Protein coding	-	<a href="#">G5E902</a>	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Slc25a3-202	<a href="#">ENSMUST00000163246.7</a>	1395	<a href="#">101aa</a>	Nonsense mediated decay	-	<a href="#">E9PX16</a>	TSL:5
Slc25a3-205	<a href="#">ENSMUST00000169339.7</a>	507	No protein	Processed transcript	-	-	TSL:3
Slc25a3-208	<a href="#">ENSMUST00000172442.1</a>	4039	No protein	Retained intron	-	-	TSL:1
Slc25a3-204	<a href="#">ENSMUST00000167455.7</a>	891	No protein	Retained intron	-	-	TSL:2
Slc25a3-207	<a href="#">ENSMUST00000171960.1</a>	682	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Slc25a3*-201 transcript, the transcription is shown below:



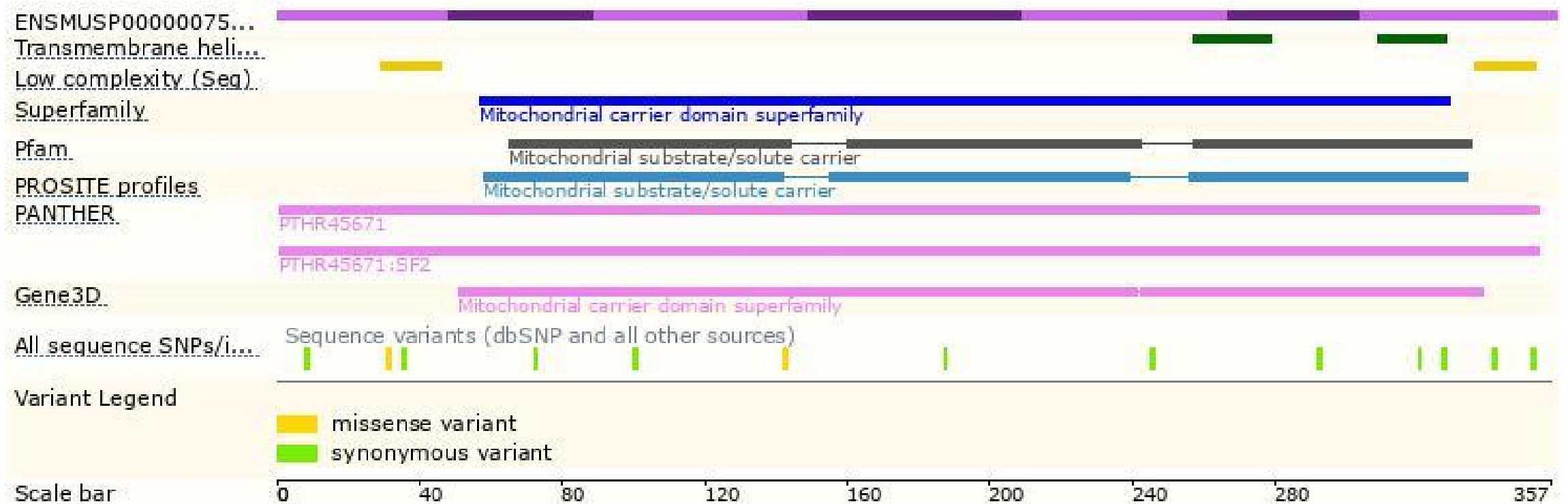
Source: <https://www.ensembl.org>

# Genomic Information



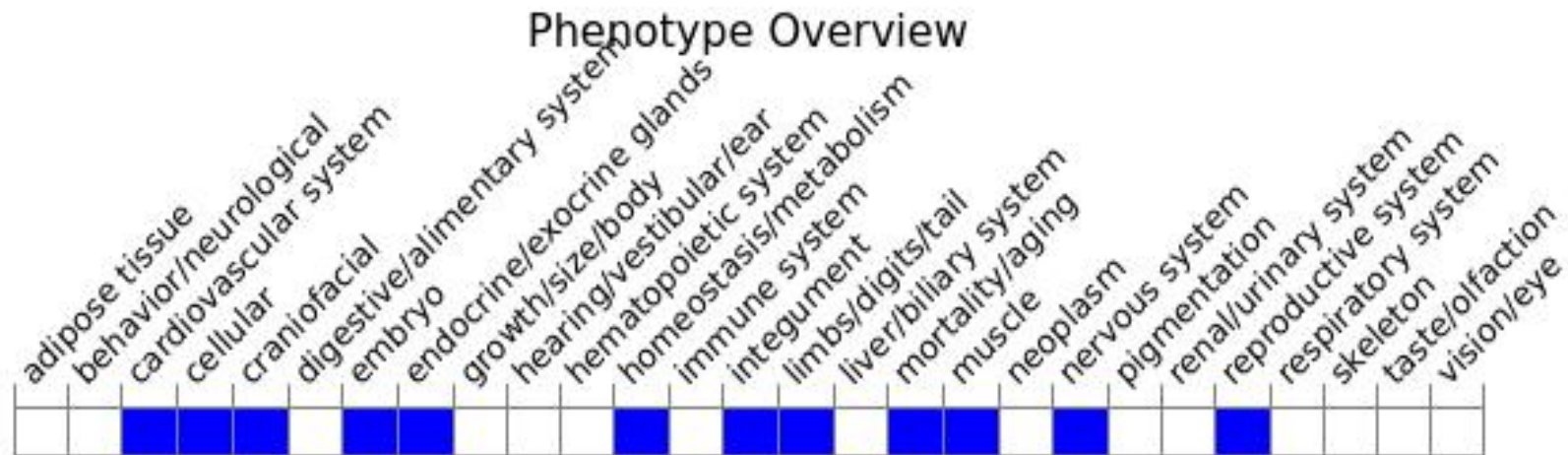


# Protein Information





# Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Slc25a3* gene are marked in blue. Death prior to the completion of embryo turning, death of all organisms of a given genotype in a population between fertilization and weaning age.

# Important Information

- The Slc25a3 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.