# *Slc25a22* Cas9-CKO Strategy

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**Reviewer: Yanhua Shen**

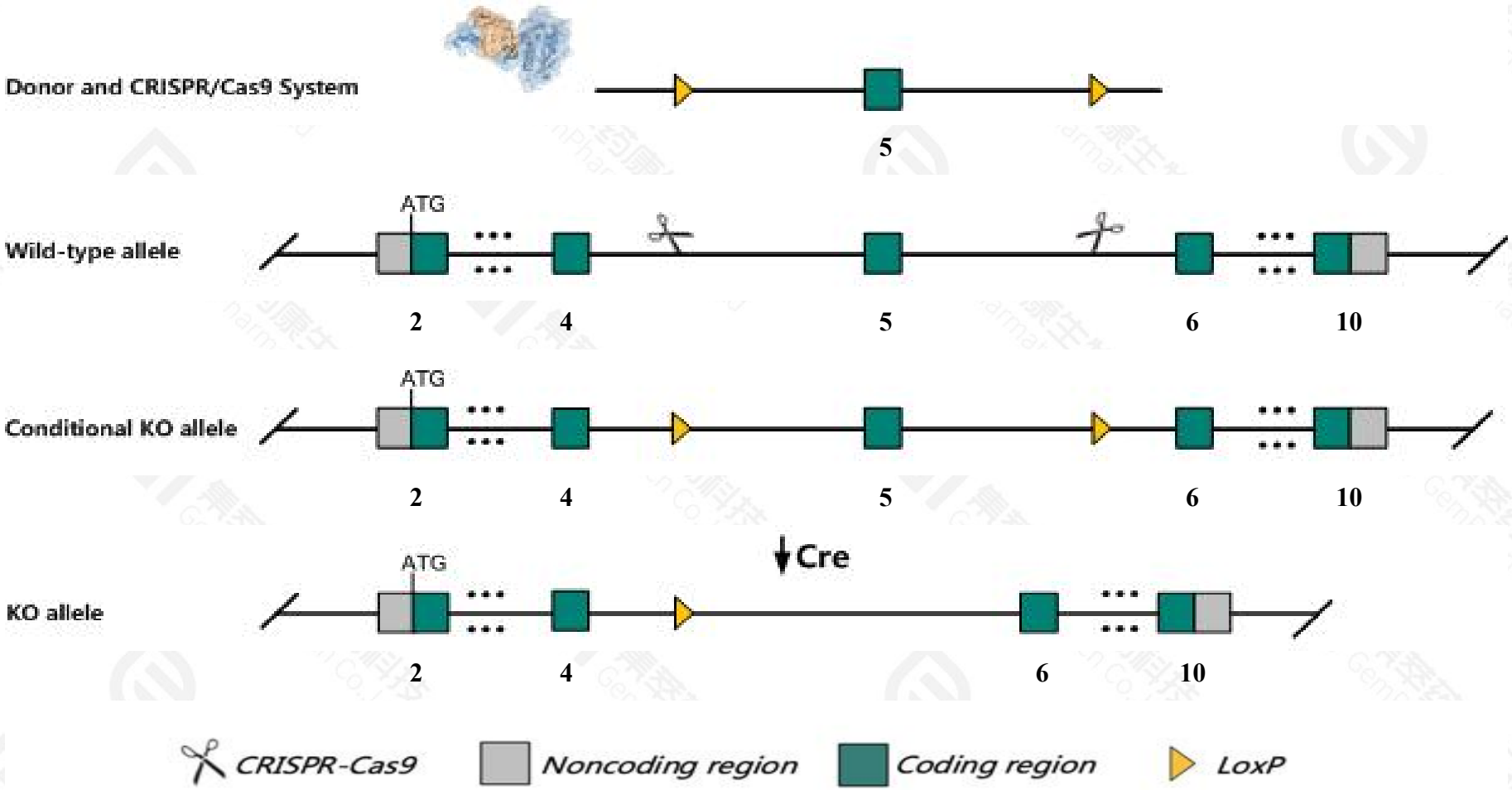
**Design Date: 2022-5-30**

# Project Overview

| | |
|---|---|
| **Project Name** | ***Slc25a22*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Slc25a22* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Slc25a22* gene has 25 transcripts. According to the structure of *Slc25a22* gene, exon5 of *Slc25a22-201*(ENSMUST00000019226.14) transcript is recommended as the knockout region.The region contains 91bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Slc25a22* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➢ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

# Notice

➢ The Intron5 is only 523bp,loxp insertion may affect mRNA splicing.

➢ The insertion position of loxp is about 3.1 kb from the 5-terminal of *Cend1* gene, which may affect the regulation of the 5-terminal of *Cend1* gene.

➢ The *Slc25a22* gene is located on the Chr7. 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.

# Gene information（NCBI）

**Slc25a22 solute carrier family 25 (mitochondrial carrier, glutamate), member 22 [ *Mus musculus* (house mouse) ]**

Download Datasets

Gene ID: 68267, updated on 24-Apr-2022

## Summary

| | |
|---|---|
| **Official Symbol** | Slc25a22 provided by MGI |
| **Official Full Name** | solute carrier family 25 (mitochondrial carrier, glutamate), member 22 provided by MGI |
| **Primary source** | MGI:MGI:1915517 |
| **See related** | Ensembl:ENSMUSG00000019082 AllianceGenome:MGI:1915517 |
| **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** | Gc1; AI060884; 1300006L01Rik |
| **Summary** | Predicted to enable L-aspartate transmembrane transporter activity and L-glutamate transmembrane transporter activity. Predicted to be involved in L-glutamate transmembrane transport; aspartate transmembrane transport; and malate-aspartate shuttle. Located in mitochondrion. Is expressed in alimentary system; eye; liver; and nervous system. Human ortholog(s) of this gene implicated in developmental and epileptic encephalopathy 3. Orthologous to human SLC25A22 (solute carrier family 25 member 22). [provided by Alliance of Genome Resources, Apr 2022] |
| **Expression** | Ubiquitous expression in liver adult (RPKM 89.8), duodenum adult (RPKM 85.7) and 27 other tissues See more |
| **Orthologs** | human all |

NEW Try the new Gene table
Try the new Transcript table

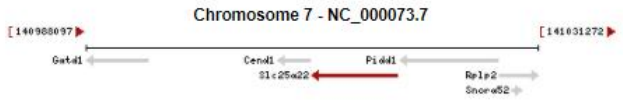
## Genomic context

**Location:** 7; 7 F5

See Slc25a22 in Genome Data Viewer

**Exon count:** 13

| Annotation release | Status | Assembly | Chr | Location |
|---|---|---|---|---|
| 109 | current | GRCm39 (GCF_000001635.27) | 7 | NC_000073.7 (141009662..141017787, complement) |
| 108.20200622 | previous assembly | GRCm38.p6 (GCF_000001635.26) | 7 | NC_000073.6 (141429749..141437874, complement) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 7 | NC_000073.5 (148615648..148623773, complement) |

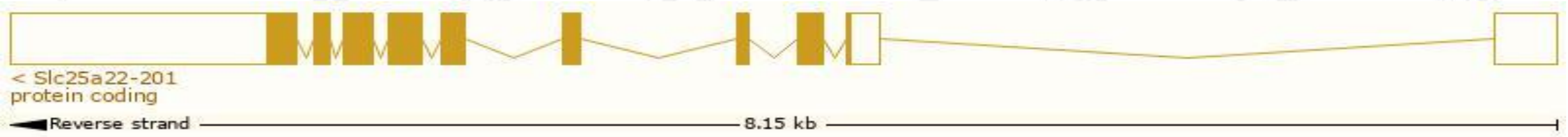


# Transcript information（Ensembl）

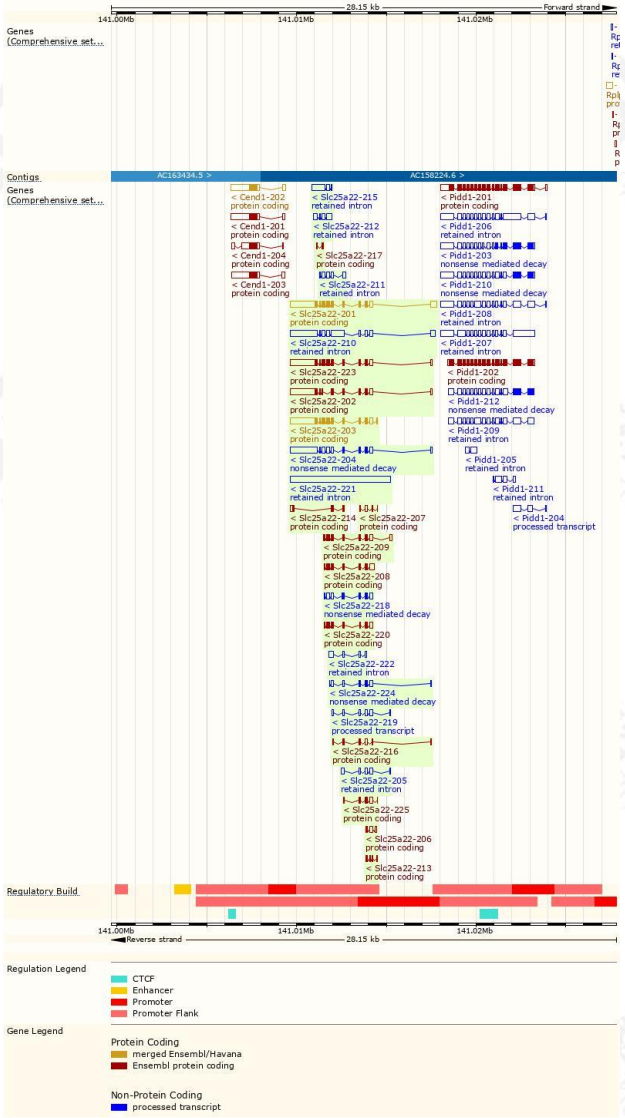
The gene has 25 transcripts,all transcripts are shown below:

| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
|---|---|---|---|---|---|---|---|
| ENSMUST00000019226.14 | Slc25a22-201 | 2811 | 323aa | Protein coding | CCDS22013 | Q9D6M3 | Ensembl Canonical GENCODE basic APPRIS P1 TSL:1 |
| ENSMUST00000201710.4 | Slc25a22-223 | 2565 | 323aa | Protein coding | CCDS22013 | Q9D6M3 | GENCODE basic APPRIS P1 TSL:5 |
| ENSMUST00000106007.10 | Slc25a22-203 | 2546 | 323aa | Protein coding | CCDS22013 | Q9D6M3 | GENCODE basic APPRIS P1 TSL:1 |
| ENSMUST00000106006.8 | Slc25a22-202 | 2277 | 229aa | Protein coding | | E9Q6M6 | GENCODE basic TSL:5 |
| ENSMUST00000138865.8 | Slc25a22-209 | 932 | 222aa | Protein coding | | E9PY45 | TSL:5 CDS 3' incomplete |
| ENSMUST00000136354.8 | Slc25a22-208 | 866 | 206aa | Protein coding | | E9PV90 | TSL:2 CDS 3' incomplete |
| ENSMUST00000201127.5 | Slc25a22-220 | 743 | 196aa | Protein coding | | A0A0J9YTY6 | TSL:5 CDS 3' incomplete |
| ENSMUST00000202840.4 | Slc25a22-225 | 423 | 85aa | Protein coding | | A0A0J9YUX4 | TSL:3 CDS 3' incomplete |
| ENSMUST00000153190.5 | Slc25a22-214 | 402 | 99aa | Protein coding | | A0A0J9YVJ3 | TSL:3 CDS 5' incomplete |
| ENSMUST00000172654.8 | Slc25a22-216 | 355 | 63aa | Protein coding | | V9GWS2 | TSL:5 CDS 3' incomplete |
| ENSMUST00000133021.2 | Slc25a22-206 | 345 | 38aa | Protein coding | | G3UX09 | TSL:5 CDS 3' incomplete |
| ENSMUST00000150026.2 | Slc25a22-213 | 225 | 28aa | Protein coding | | G3UY41 | TSL:3 CDS 3' incomplete |
| ENSMUST00000133206.9 | Slc25a22-207 | 213 | 18aa | Protein coding | | V9GWV4 | TSL:5 CDS 3' incomplete |
| ENSMUST00000174095.2 | Slc25a22-217 | 170 | 44aa | Protein coding | | G3UZ58 | TSL:1 CDS 5' incomplete |
| ENSMUST00000124266.8 | Slc25a22-204 | 2568 | 103aa | Nonsense mediated decay | | E9Q579 | TSL:1 |
| ENSMUST00000184518.8 | Slc25a22-218 | 794 | 98aa | Nonsense mediated decay | | Q80X52 | TSL:5 |
| ENSMUST00000201822.4 | Slc25a22-224 | 617 | 72aa | Nonsense mediated decay | | A0A0J9YUJ4 | TSL:5 |
| ENSMUST00000201072.4 | Slc25a22-219 | 574 | No protein | Processed transcript | | - | TSL:5 |
| ENSMUST00000201558.2 | Slc25a22-221 | 5590 | No protein | Retained intron | | - | TSL:NA |
| ENSMUST00000140602.8 | Slc25a22-210 | 3264 | No protein | Retained intron | | - | TSL:2 |
| ENSMUST00000156002.8 | Slc25a22-215 | 896 | No protein | Retained intron | | - | TSL:2 |
| ENSMUST00000148100.8 | Slc25a22-212 | 791 | No protein | Retained intron | | - | TSL:1 |
| ENSMUST00000144174.8 | Slc25a22-211 | 693 | No protein | Retained intron | | - | TSL:3 |
| ENSMUST00000132635.2 | Slc25a22-205 | 562 | No protein | Retained intron | | - | TSL:3 |
| ENSMUST00000201708.4 | Slc25a22-222 | 465 | No protein | Retained intron | | - | TSL:3 |

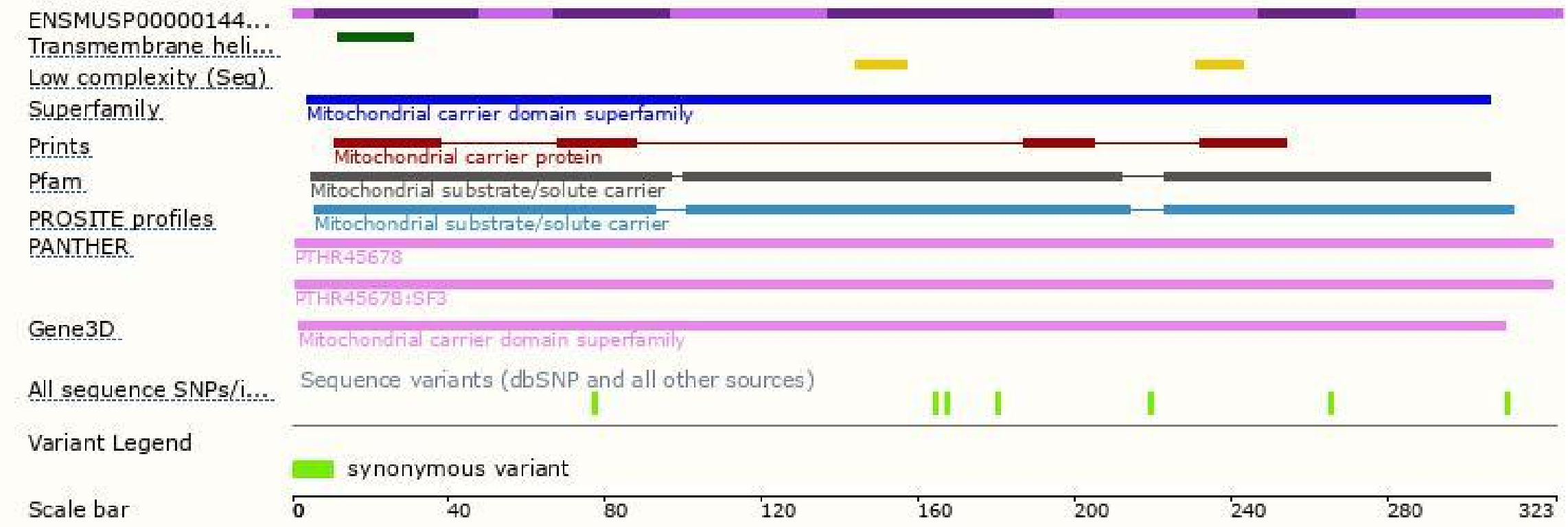
The strategy is based on the design of *Slc25a22-201* transcript,the transcription is shown below:



# Genomic location distribution



# Protein domain



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