Slc25a22 Cas9-KO *Strategy*

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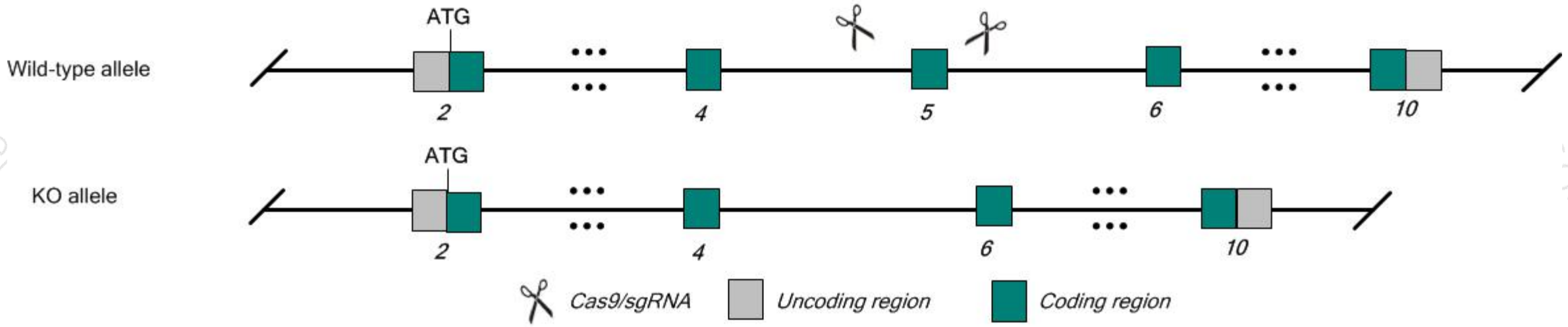
Project Overview

Project Name	***Slc25a22***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

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 (ENSMUST00000019226.13)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: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

- The impact on Transcript *Slc25a22*-206 , *Slc25a22*-207, *Slc25a22*-213, *Slc25a22*-217 is unknown.
- The position of *Slc25a22* gene and *Cend1* gene is adjacent. Knockout the region may affect the function 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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

Gene ID: 68267, updated on 7-Apr-2019

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
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
Expression	Ubiquitous expression in liver adult (RPKM 89.8), duodenum adult (RPKM 85.7) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

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

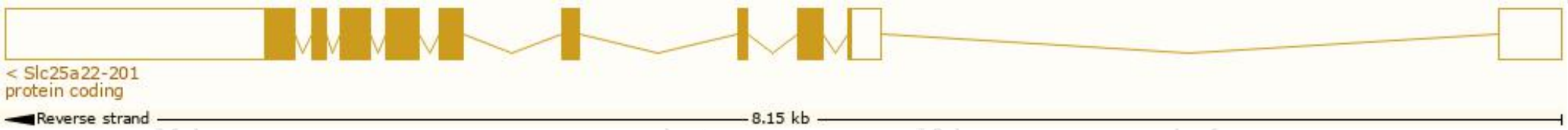
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a22-201	ENSMUST00000019226.13	2811	323aa	Protein coding	CCDS22013	Q9D6M3	TSL:1 GENCODE basic APPRIS P1
Slc25a22-223	ENSMUST00000201710.3	2565	323aa	Protein coding	CCDS22013	Q9D6M3	TSL:5 GENCODE basic APPRIS P1
Slc25a22-203	ENSMUST00000106007.9	2546	323aa	Protein coding	CCDS22013	Q9D6M3	TSL:1 GENCODE basic APPRIS P1
Slc25a22-202	ENSMUST00000106006.7	2277	229aa	Protein coding	-	E9Q6M6	TSL:5 GENCODE basic
Slc25a22-209	ENSMUST00000138865.7	932	222aa	Protein coding	-	E9PY45	CDS 3' incomplete TSL:5
Slc25a22-208	ENSMUST00000136354.7	866	206aa	Protein coding	-	E9PV90	CDS 3' incomplete TSL:2
Slc25a22-220	ENSMUST00000201127.4	743	196aa	Protein coding	-	A0A0J9YTY6	CDS 3' incomplete TSL:5
Slc25a22-225	ENSMUST00000202840.3	423	85aa	Protein coding	-	A0A0J9YUX4	CDS 3' incomplete TSL:3
Slc25a22-214	ENSMUST00000153190.4	402	99aa	Protein coding	-	A0A0J9YVJ3	CDS 5' incomplete TSL:3
Slc25a22-216	ENSMUST00000172654.7	355	63aa	Protein coding	-	V9GWS2	CDS 3' incomplete TSL:5
Slc25a22-206	ENSMUST00000133021.1	345	38aa	Protein coding	-	G3UX09	CDS 3' incomplete TSL:5
Slc25a22-213	ENSMUST00000150026.1	225	28aa	Protein coding	-	G3UY41	CDS 3' incomplete TSL:3
Slc25a22-207	ENSMUST00000133206.8	213	18aa	Protein coding	-	V9GWV4	CDS 3' incomplete TSL:5
Slc25a22-217	ENSMUST00000174095.1	170	44aa	Protein coding	-	G3UZ58	CDS 5' incomplete TSL:1
Slc25a22-204	ENSMUST00000124266.7	2568	103aa	Nonsense mediated decay	-	E9Q579	TSL:1
Slc25a22-218	ENSMUST00000184518.7	794	98aa	Nonsense mediated decay	-	Q80X52	TSL:5
Slc25a22-224	ENSMUST00000201822.3	617	72aa	Nonsense mediated decay	-	A0A0J9YUJ4	TSL:5
Slc25a22-219	ENSMUST00000201072.3	574	No protein	Processed transcript	-	-	TSL:5
Slc25a22-221	ENSMUST00000201558.1	5590	No protein	Retained intron	-	-	TSL:NA

Transcript information（Ensembl）

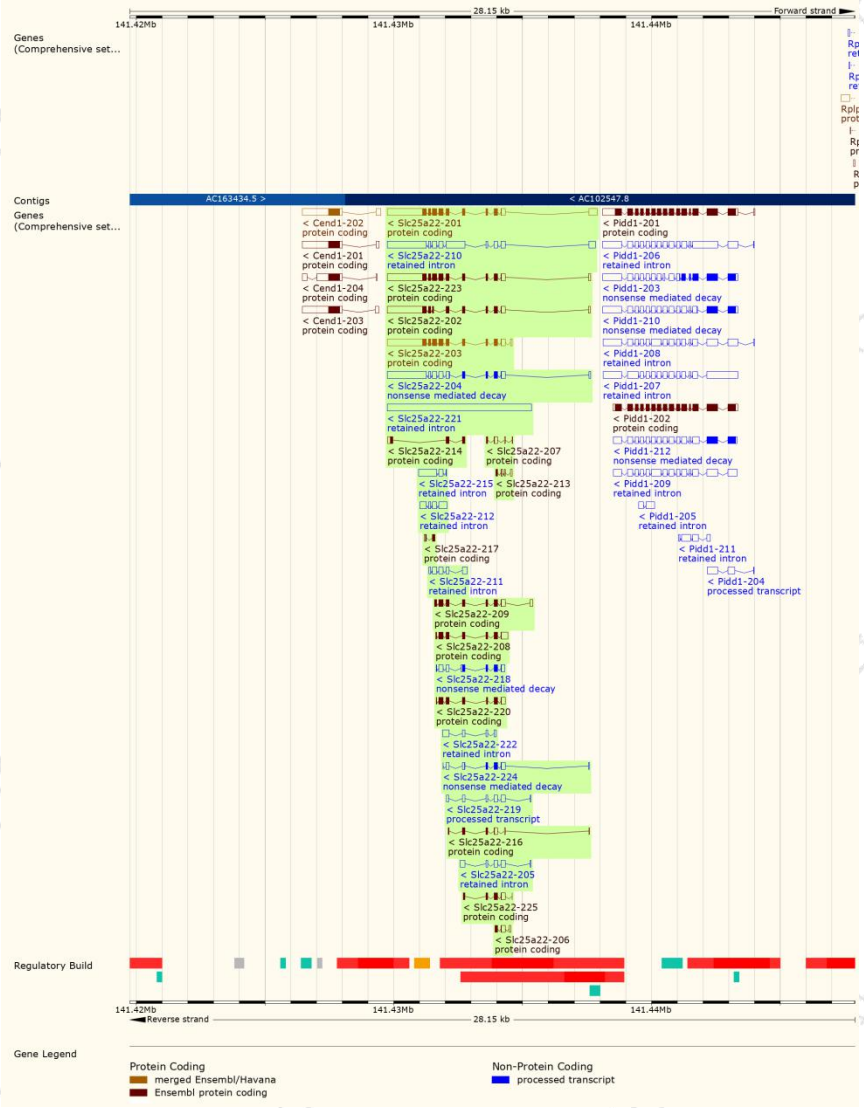
The gene has 25 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a22-210	ENSMUST00000140602.7	3264	No protein	Retained intron	-	-	TSL:2
Slc25a22-215	ENSMUST00000156002.7	896	No protein	Retained intron	-	-	TSL:2
Slc25a22-212	ENSMUST00000148100.7	791	No protein	Retained intron	-	-	TSL:1
Slc25a22-211	ENSMUST00000144174.7	693	No protein	Retained intron	-	-	TSL:3
Slc25a22-205	ENSMUST00000132635.1	562	No protein	Retained intron	-	-	TSL:3
Slc25a22-222	ENSMUST00000201708.3	465	No protein	Retained intron	-	-	TSL:3

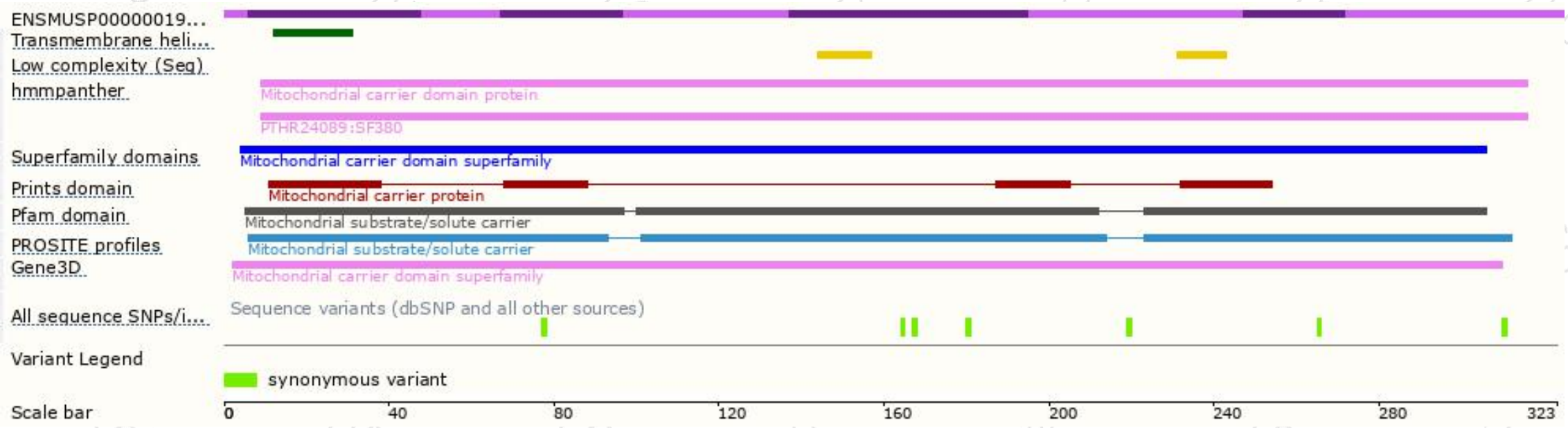
The strategy is based on the design of *Slc25a22-201* transcript,The transcription is shown below



Genomic location (Ensembl)



Protein domain (Ensembl)



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

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