

Slc25a3 Cas9-CKO Strategy

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Project Overview

Project Name

Slc25a3

Project type

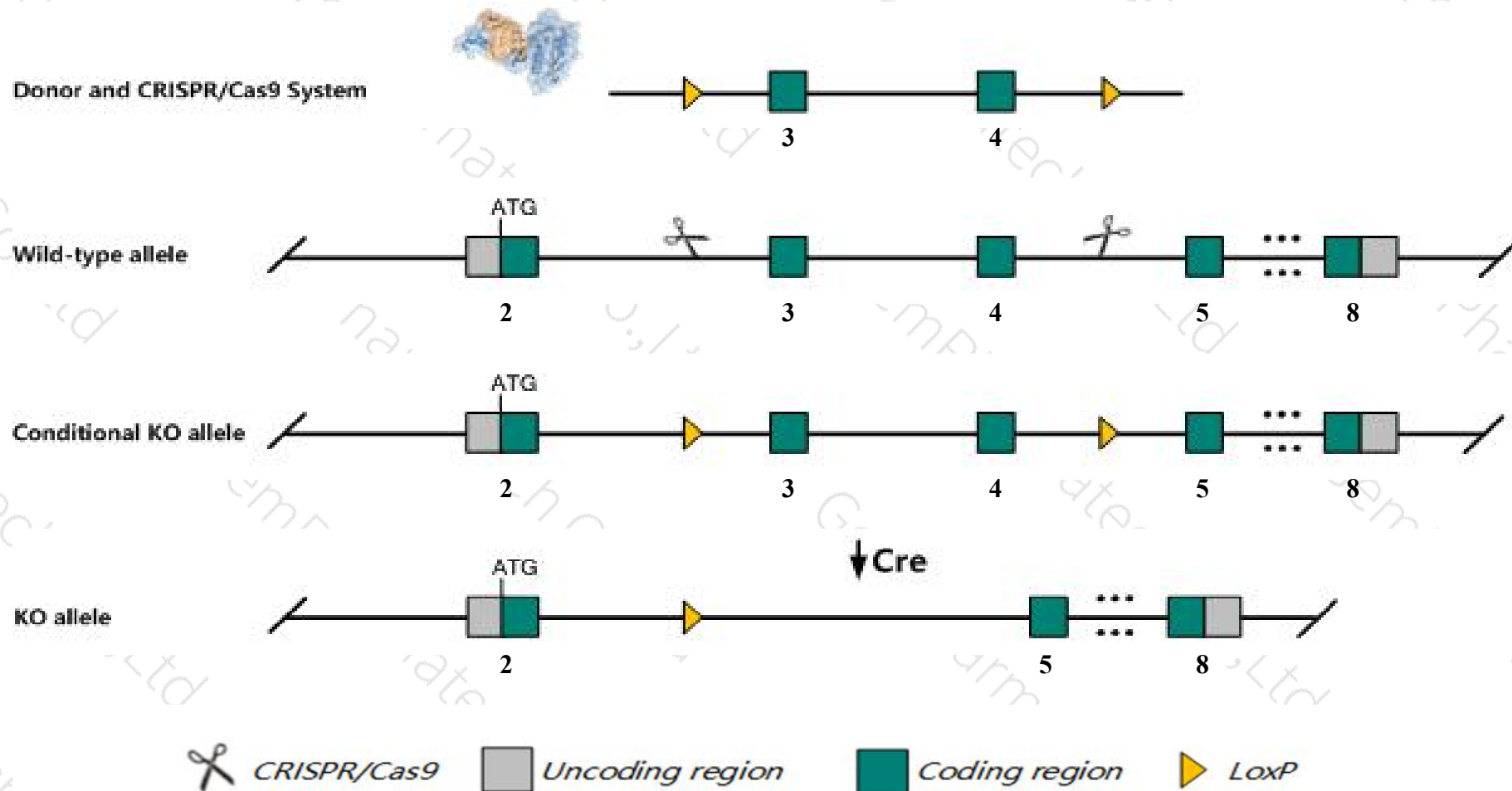
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc25a3* gene. The schematic diagram is as follows:



Technical routes

- 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: 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.

- 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.

Gene information (NCBI)

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

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

Summary



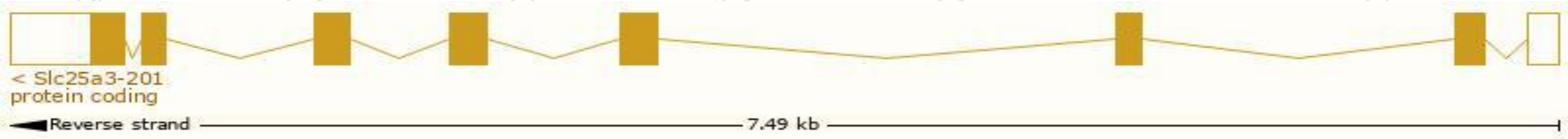
Official Symbol	Slc25a3 provided by MGI
Official Full Name	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 provided by MGI
Primary source	MGI:MGI:1353498
See related	Ensembl:ENSMUSG000000061904
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730556H19Rik, PTP, Phc
Expression	Ubiquitous expression in adrenal adult (RPKM 904.7), duodenum adult (RPKM 787.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

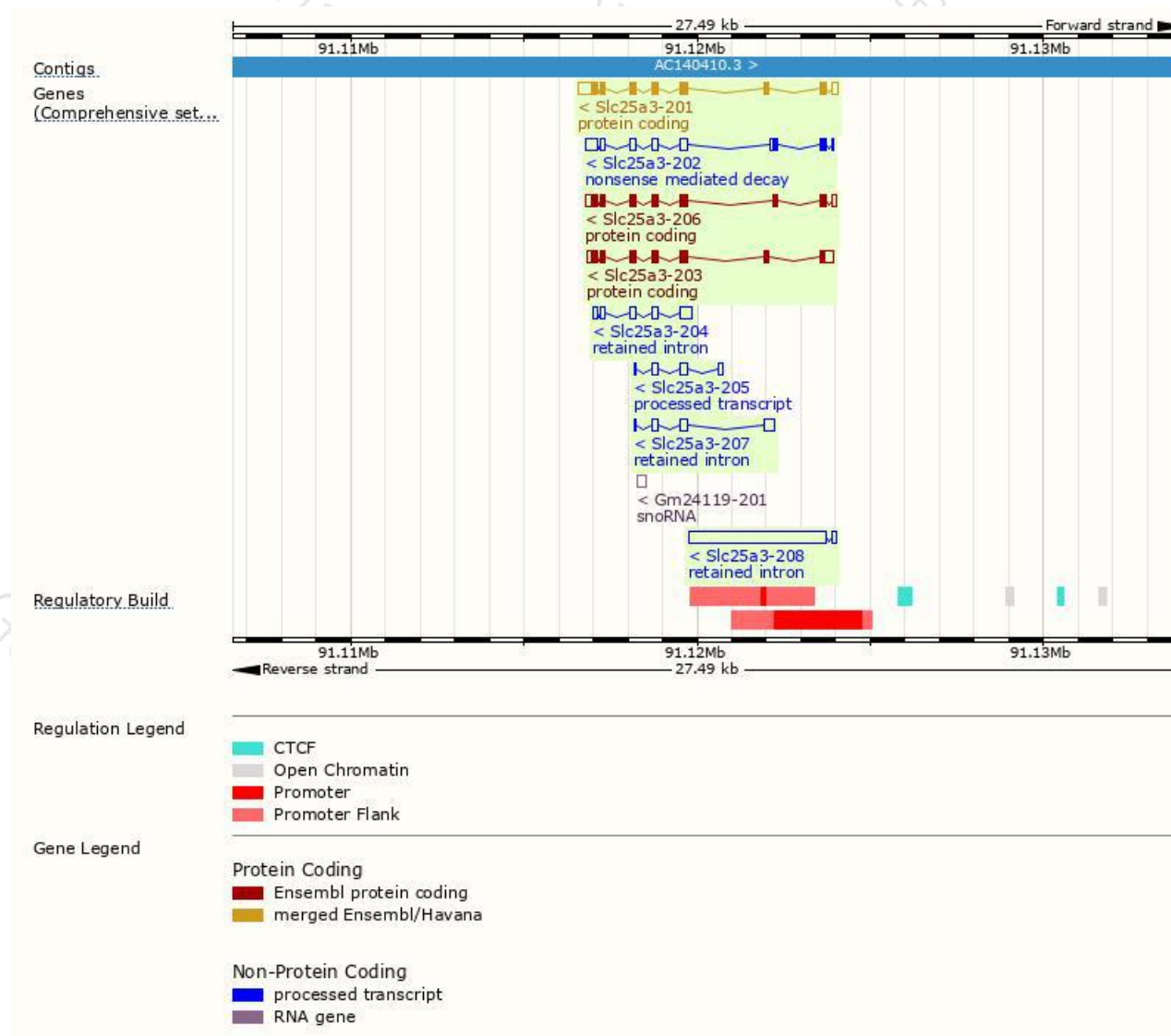
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a3-201	ENSMUST00000076694.12	1612	357aa	Protein coding	CCDS24121	Q8VEM8	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	ENSMUST00000164505.1	1483	357aa	Protein coding	CCDS24121	Q8VEM8	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	ENSMUST00000170810.7	1341	358aa	Protein coding	-	G5E902	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	ENSMUST00000163246.7	1395	101aa	Nonsense mediated decay	-	E9PX16	TSL:5
Slc25a3-205	ENSMUST00000169339.7	507	No protein	Processed transcript	-	-	TSL:3
Slc25a3-208	ENSMUST00000172442.1	4039	No protein	Retained intron	-	-	TSL:1
Slc25a3-204	ENSMUST00000167455.7	891	No protein	Retained intron	-	-	TSL:2
Slc25a3-207	ENSMUST00000171960.1	682	No protein	Retained intron	-	-	TSL:2

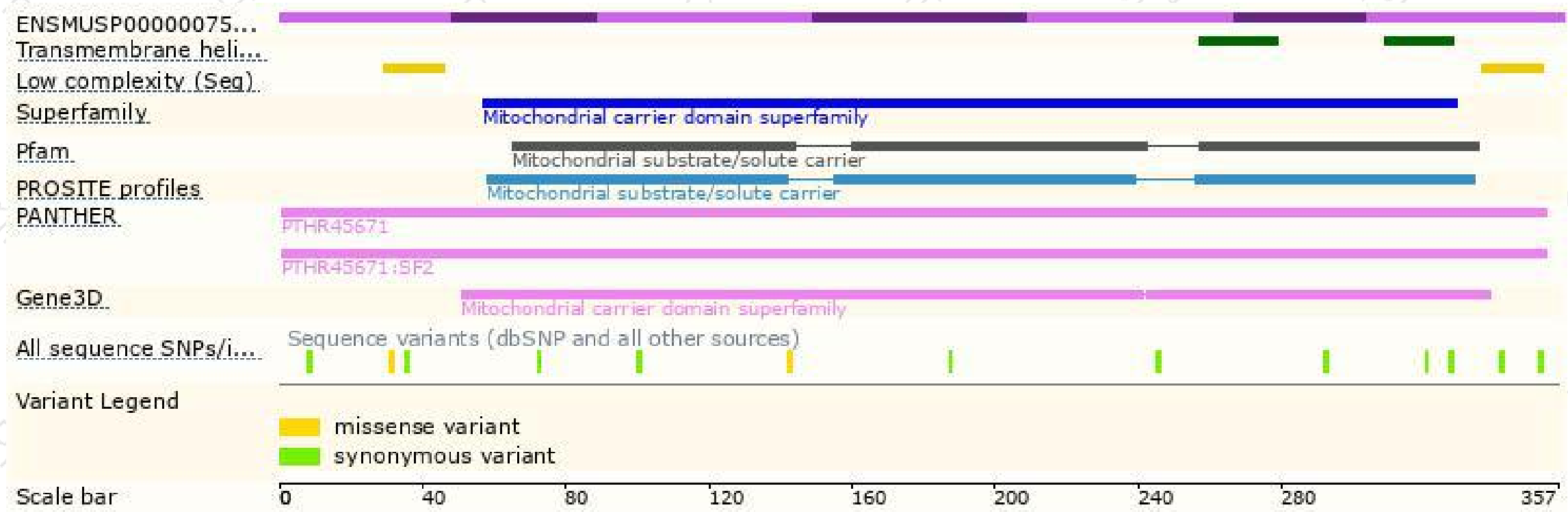
The strategy is based on the design of *Slc25a3-201* transcript,The transcription is shown below



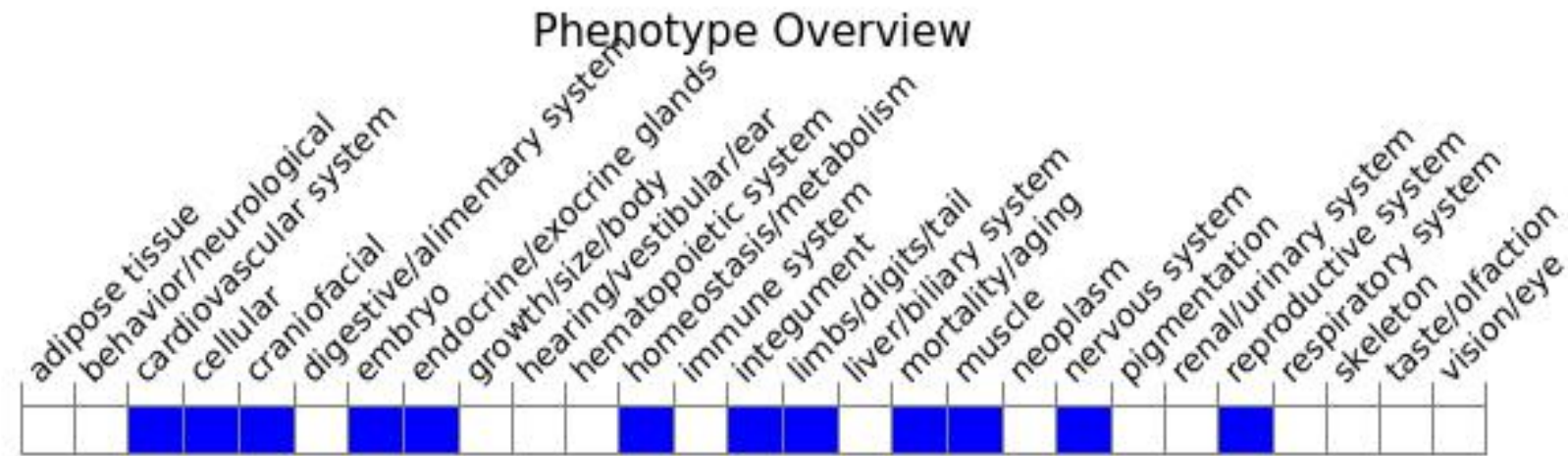
Genomic location distribution



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/>).

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

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