

Slc25a37 Cas9-KO Strategy

Designer:

Jinling Wang

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Project Overview

Project Name

Slc25a37

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc25a37* gene. The schematic diagram is as follows:



- The *Slc25a37* gene has 4 transcripts. According to the structure of *Slc25a37* gene, exon2-exon3 of *Slc25a37-201* (ENSMUST00000037064.4) transcript is recommended as the knockout region. The region contains 286bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc25a37* gene. The brief process is as follows: CRISPR/Cas9 syst

- According to the existing MGI data, Embryos homozygous for a knock-out allele are pale, exhibit no hemoglobinization in the yolk sac and heart, and die during organogenesis.
- The *Slc25a37* gene is located on the Chr14. 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)

Slc25a37 solute carrier family 25, member 37 [Mus musculus (house mouse)]

Gene ID: 67712, updated on 3-Feb-2019

Summary



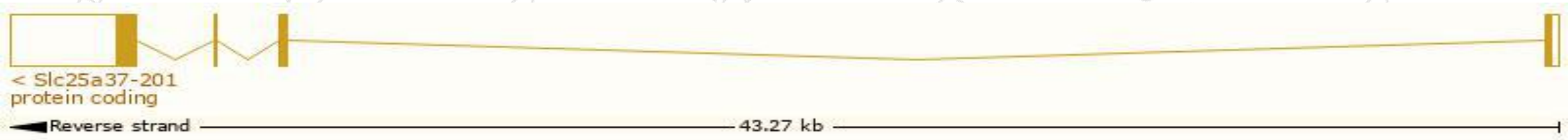
Official Symbol	Slc25a37 provided by MGI
Official Full Name	solute carrier family 25, member 37 provided by MGI
Primary source	MGI:MGI:1914962
See related	Ensembl:ENSMUSG00000034248
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700020E22Rik, 4930513O14Rik, 4930526G11Rik, AI848481, C330015G08Rik, Mfrn, Mfrn1, Mscp, frascati, mitoferrin
Expression	Biased expression in liver E14.5 (RPKM 331.9), liver E14 (RPKM 297.3) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

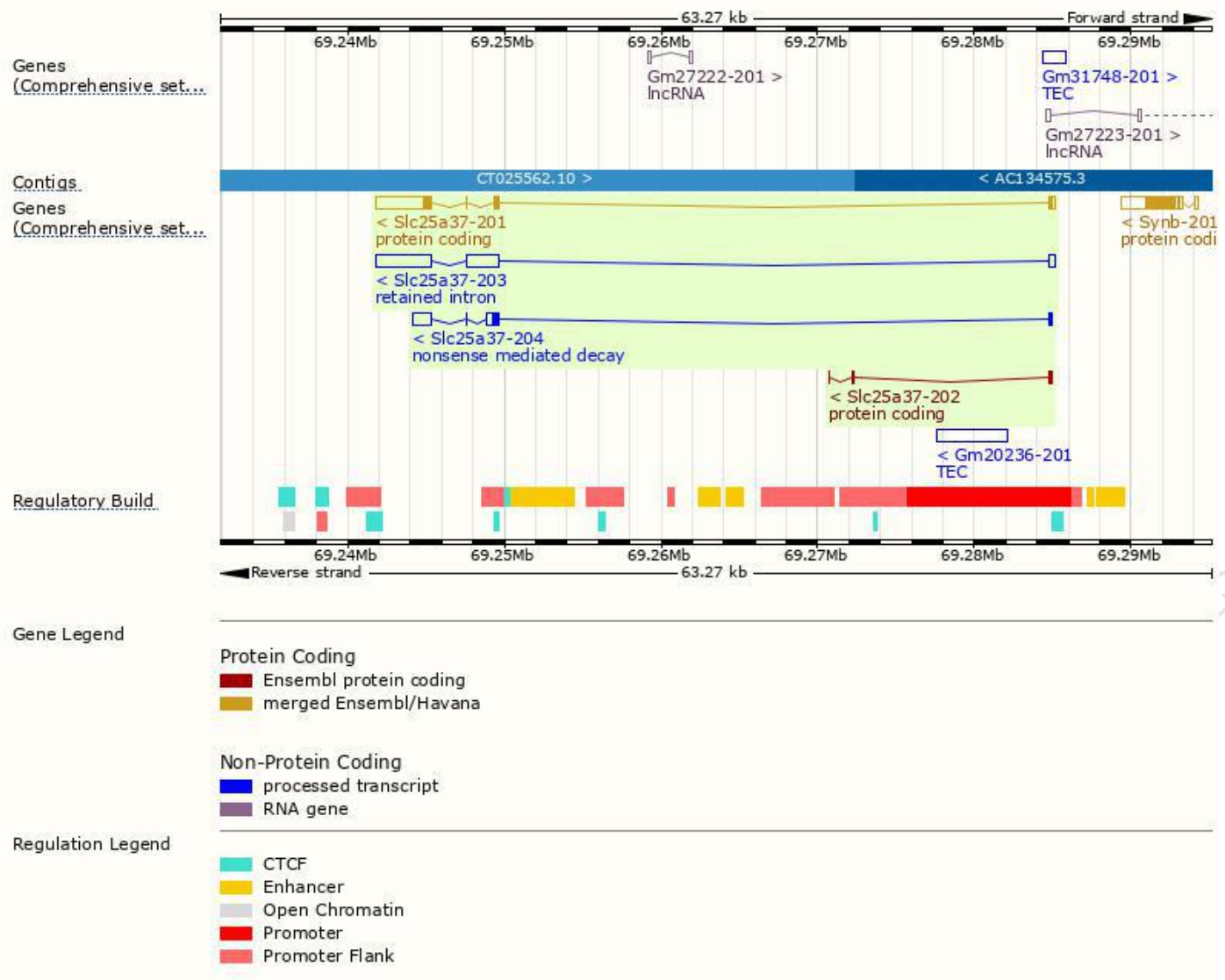
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a37-201	ENSMUST00000037064.4	4174	338aa	Protein coding	CCDS27238	Q920G8	TSL:1 GENCODE basic APPRIS P1
Slc25a37-202	ENSMUST00000183882.1	342	100aa	Protein coding	-	J3QPY4	CDS 3' incomplete TSL:3
Slc25a37-204	ENSMUST00000184914.1	2212	182aa	Nonsense mediated decay	-	Q920G8	TSL:1
Slc25a37-203	ENSMUST00000184497.1	5927	No protein	Retained intron	-	-	TSL:1

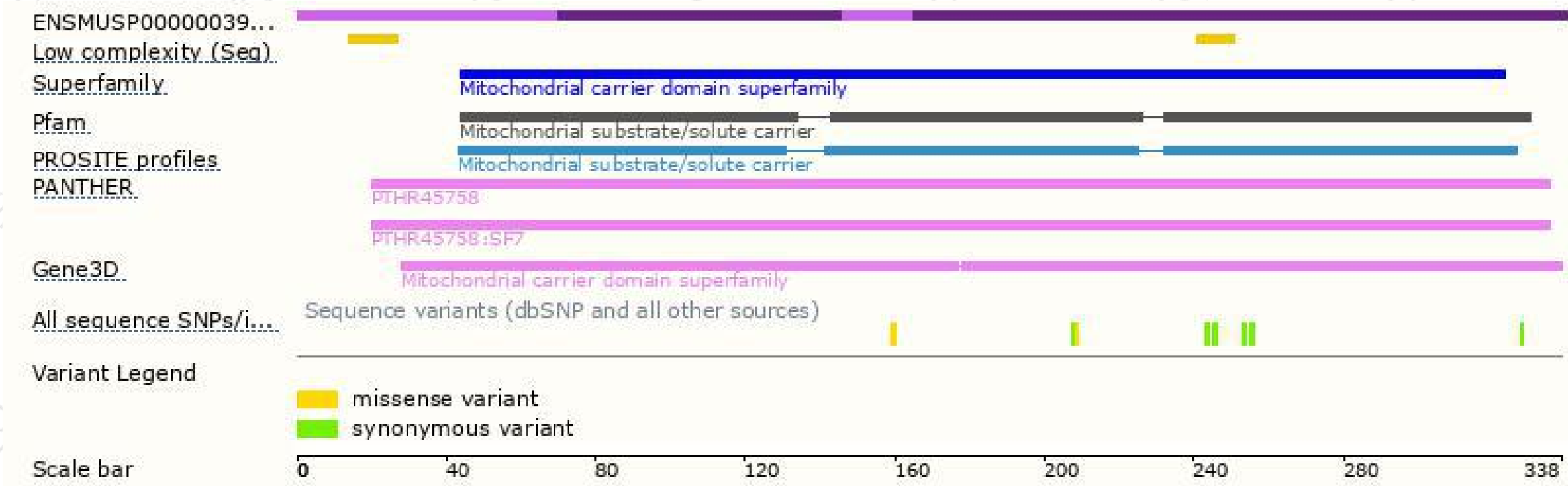
The strategy is based on the design of *Slc25a37-201* transcript,The transcription is shown below



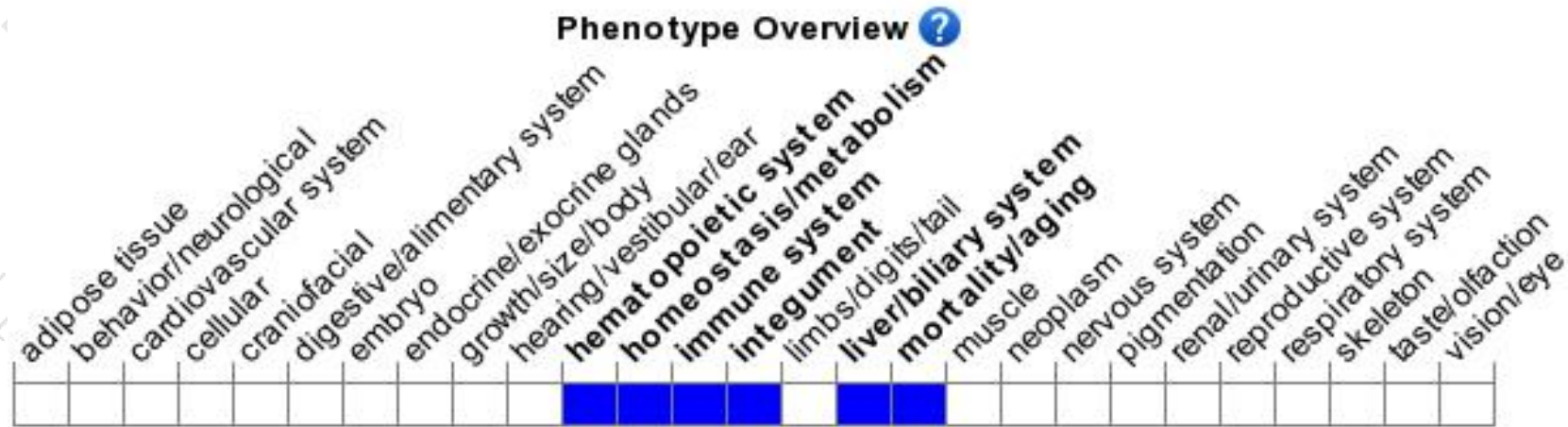
Genomic location distribution



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/>).

According to the existing MGI data, Embryos homozygous for a knock-out allele are pale, exhibit no hemoglobinization in the yolk sac and heart, and die during organogenesis.

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

Tel: 400-9660890

