

Mtch1 Cas9-KO Strategy

Designer:

Yanhua Shen

Reviewer:

Xueting Zhang

Design Date:

2019-10-11

Project Overview

Project Name

Mtch1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mtch1* gene. The schematic diagram is as follows:



- The *Mtch1* gene has 19 transcripts. According to the structure of *Mtch1* gene, exon2-exon7 of *Mtch1-201* (ENSMUST00000095427.11) transcript is recommended as the knockout region. The region contains 440bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mtch1* gene. The brief process is as follows: CRISPR/Cas9 system w

- Transcript 205,218,219 is unaffected.
- The *Mtchl* gene is located on the Chr17. 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)

Mtch1 mitochondrial carrier 1 [*Mus musculus* (house mouse)]

Gene ID: 56462, updated on 12-Aug-2019

Summary

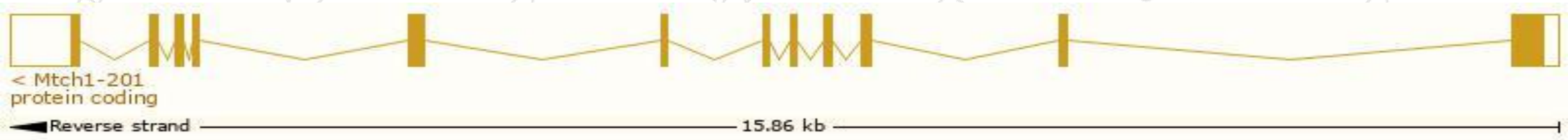
Official Symbol	Mtch1 provided by MGI
Official Full Name	mitochondrial carrier 1 provided by MGI
Primary source	MGI:MGI:1929261
See related	Ensembl:ENSMUSG00000024012
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PSAP; C77849; AI255158; AU018396; 2310034O17Rik
Expression	Ubiquitous expression in colon adult (RPKM 154.2), genital fat pad adult (RPKM 153.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

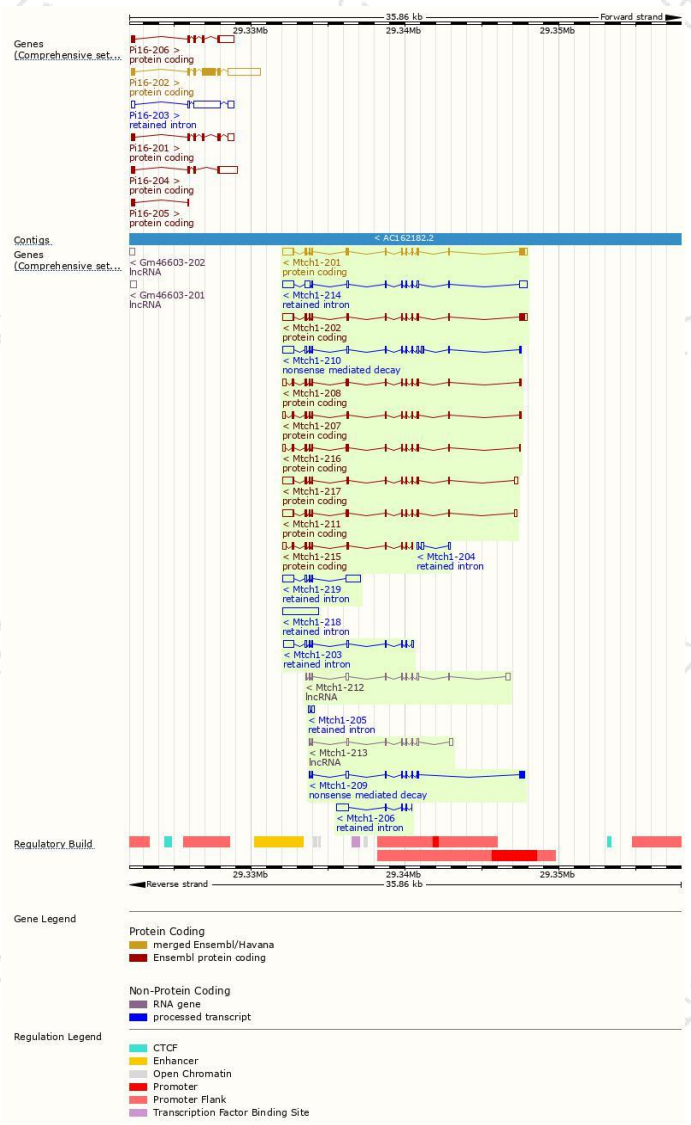
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mtch1-201	ENSMUST00000095427.11	1952	389aa	Protein coding	CCDS28596	Q791T5	TSL:1 GENCODE basic APPRIS P3
Mtch1-202	ENSMUST00000118366.8	1897	372aa	Protein coding	CCDS84288	Q791T5	TSL:1 GENCODE basic APPRIS ALT 1
Mtch1-217	ENSMUST00000235088.1	1660	260aa	Protein coding	-	-	GENCODE basic
Mtch1-211	ENSMUST00000234507.1	1653	277aa	Protein coding	-	-	GENCODE basic
Mtch1-208	ENSMUST00000234129.1	1185	311aa	Protein coding	-	-	CDS 5' incomplete
Mtch1-216	ENSMUST00000235021.1	1108	299aa	Protein coding	-	-	CDS 5' incomplete
Mtch1-207	ENSMUST00000153658.2	1093	294aa	Protein coding	-	D3YXC2	CDS 5' incomplete TSL:3
Mtch1-215	ENSMUST00000234970.1	826	199aa	Protein coding	-	-	CDS 5' incomplete
Mtch1-210	ENSMUST00000234416.1	1652	63aa	Nonsense mediated decay	-	-	CDS 5' incomplete
Mtch1-209	ENSMUST00000234180.1	894	112aa	Nonsense mediated decay	-	-	CDS 5' incomplete
Mtch1-218	ENSMUST00000235097.1	2292	No protein	Retained intron	-	-	
Mtch1-214	ENSMUST00000234948.1	2082	No protein	Retained intron	-	-	
Mtch1-219	ENSMUST00000235118.1	1867	No protein	Retained intron	-	-	
Mtch1-203	ENSMUST00000127423.2	1267	No protein	Retained intron	-	-	TSL:2
Mtch1-206	ENSMUST00000151739.2	935	No protein	Retained intron	-	-	TSL:2
Mtch1-204	ENSMUST00000132753.1	351	No protein	Retained intron	-	-	TSL:3
Mtch1-205	ENSMUST00000141319.1	274	No protein	Retained intron	-	-	TSL:2
Mtch1-212	ENSMUST00000234856.1	959	No protein	lncRNA	-	-	
Mtch1-213	ENSMUST00000234868.1	743	No protein	lncRNA	-	-	

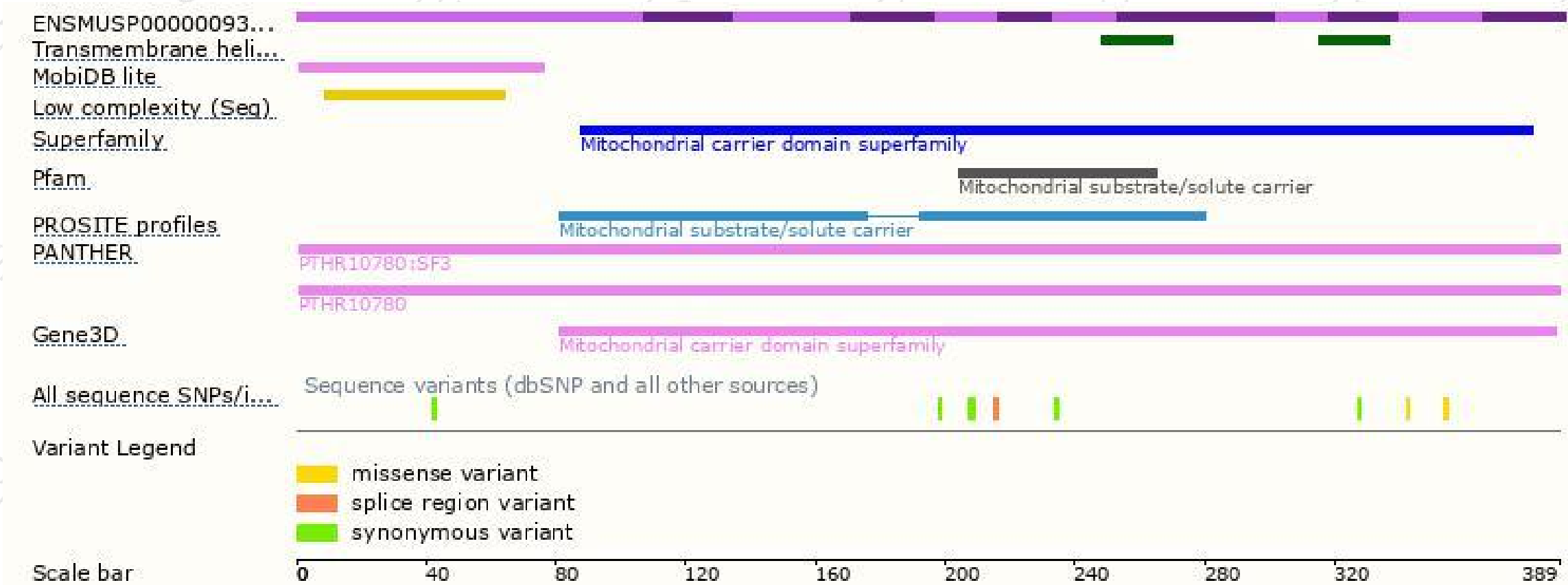
The strategy is based on the design of *Mtch1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

