

Ndufa1 Cas9-KO Strategy

Designer:

Yanhua Shen

Reviewer:

Xueting Zhang

Design Date:

2020-5-7

Project Overview

Project Name

Ndufa1

Project type

Cas9-KO

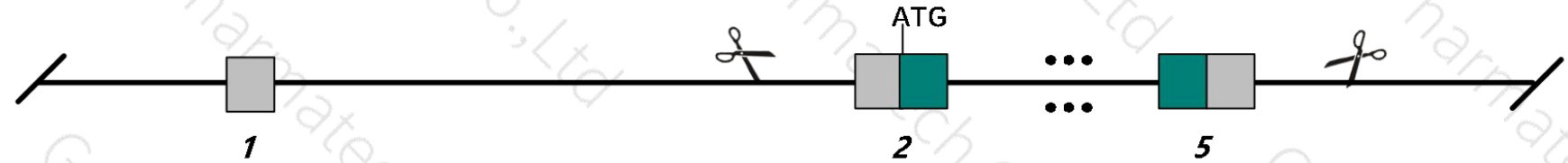
Strain background

C57BL/6JGpt

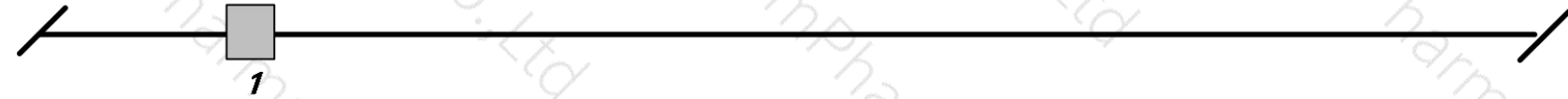
Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ndufa1* gene. The schematic diagram is as follows:

Wild-type allele



KO allele



Cas9/sgRNA



Uncoding region



Coding region

- The *Ndufa1* gene has 5 transcripts. According to the structure of *Ndufa1* gene, exon2-exon5 of *Ndufa1-201* (ENSMUST00000028768.1) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ndufa1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Ndufa1* gene is located on the Chr2. 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)

Ndutfaf1 NADH:ubiquinone oxidoreductase complex assembly factor 1 [Mus musculus (house mouse)]

Gene ID: 69702, updated on 13-Mar-2020

Summary



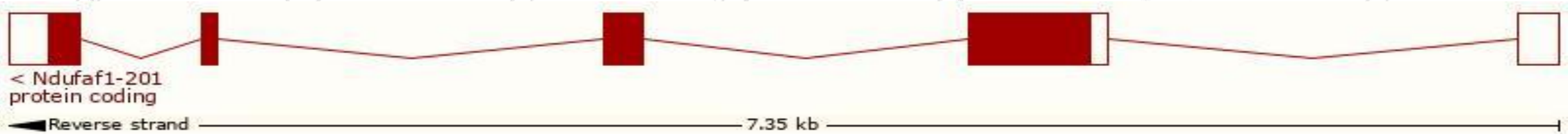
Official Symbol	Ndutfaf1 provided by MGI
Official Full Name	NADH:ubiquinone oxidoreductase complex assembly factor 1 provided by MGI
Primary source	MGI:MGI:1916952
See related	Ensembl:ENSMUSG00000027305
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410001M24Rik, CGI-65, CIA30
Expression	Ubiquitous expression in liver E14 (RPKM 7.1), heart adult (RPKM 6.2) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

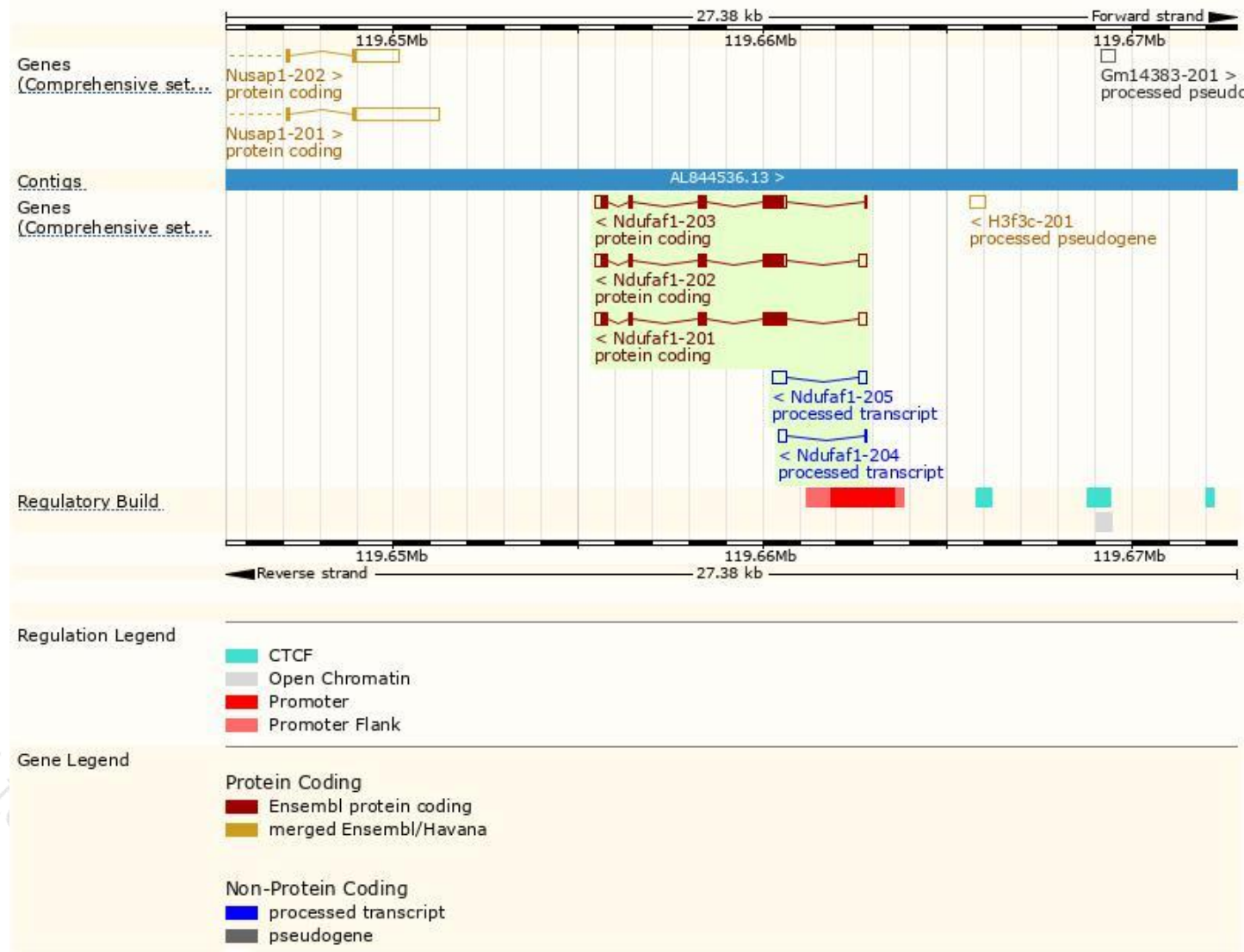
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ndufaf1-201	ENSMUST00000028768.1	1451	330aa	Protein coding	CCDS38207	A0A0R4J081	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
Ndufaf1-202	ENSMUST00000110801.7	1478	328aa	Protein coding	-	A2AQ17	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 ALT2
Ndufaf1-203	ENSMUST00000110802.7	1308	328aa	Protein coding	-	A2AQ17	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 ALT2
Ndufaf1-205	ENSMUST00000154127.1	622	No protein	Processed transcript	-	-	TSL:2
Ndufaf1-204	ENSMUST00000131596.1	291	No protein	Processed transcript	-	-	TSL:3

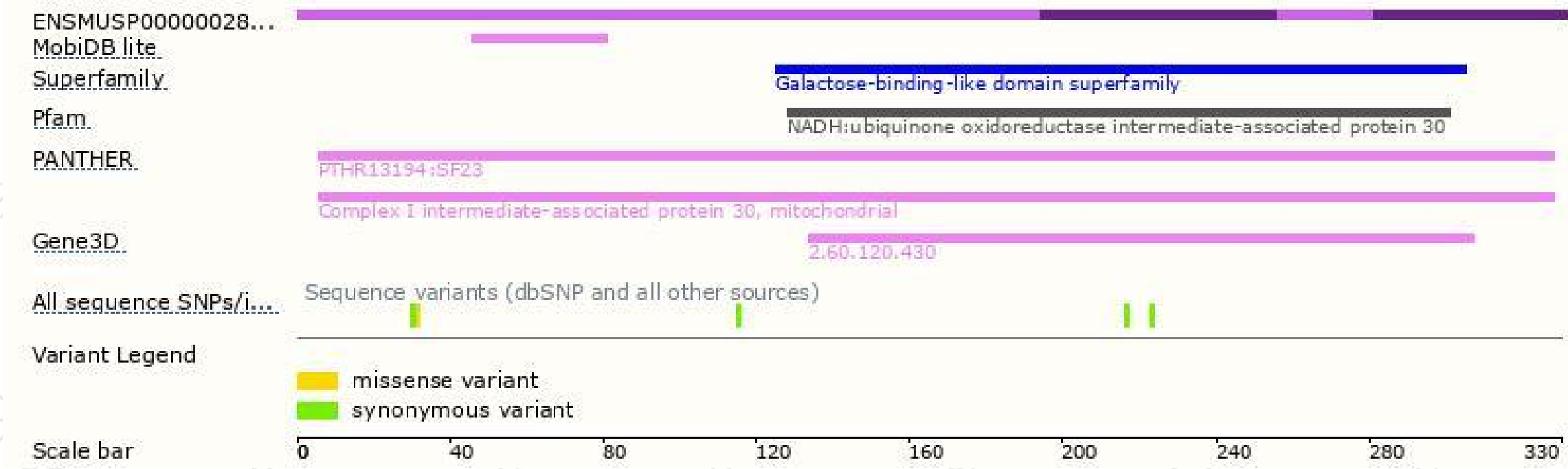
The strategy is based on the design of *Ndufaf1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

