

Ndufs1 Cas9-KO Strategy

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Project Overview

Project Name

Ndufs1

Project type

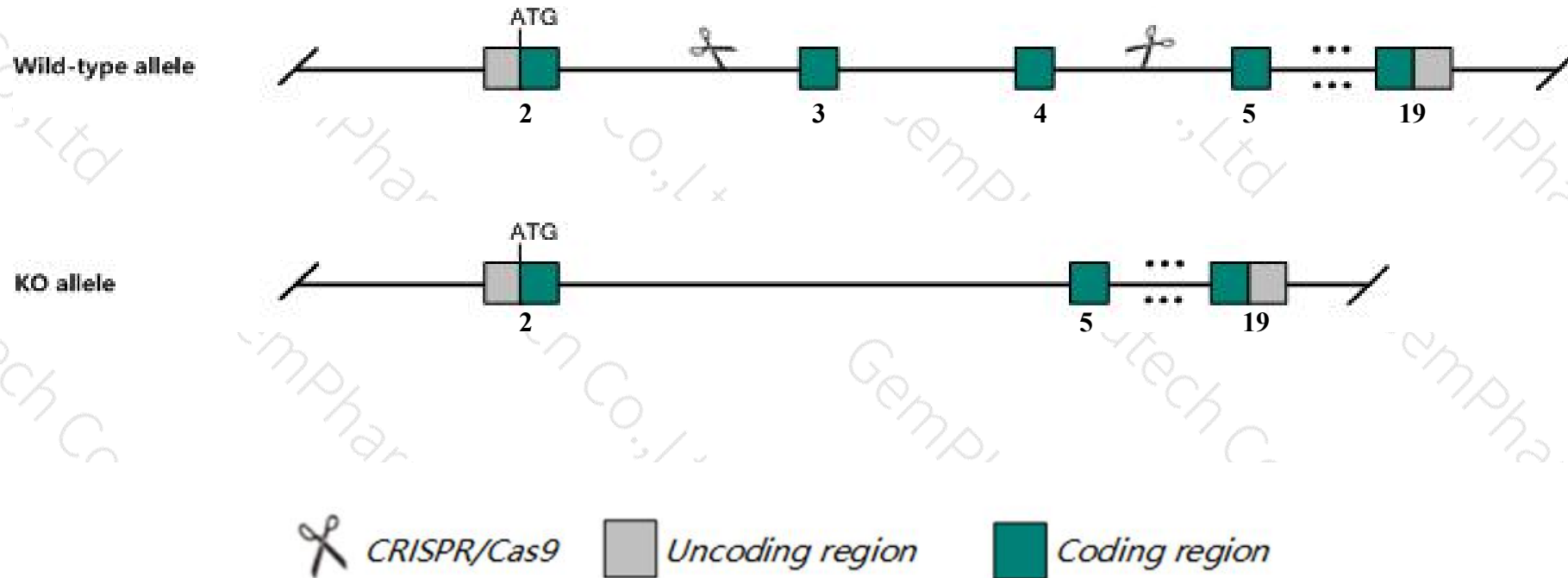
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ndufs1* gene. The schematic diagram is as follows:



- The *Ndufs1* gene has 13 transcripts. According to the structure of *Ndufs1* gene, exon3-exon4 of *Ndufs1-201* (ENSMUST00000027111.14) transcript is recommended as the knockout region. The region contains 200bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ndufs1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Ndufs1* gene is located on the Chr1. 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)

Ndufs1 NADH:ubiquinone oxidoreductase core subunit S1 [Mus musculus (house mouse)]

Gene ID: 227197, updated on 7-Apr-2019

Summary



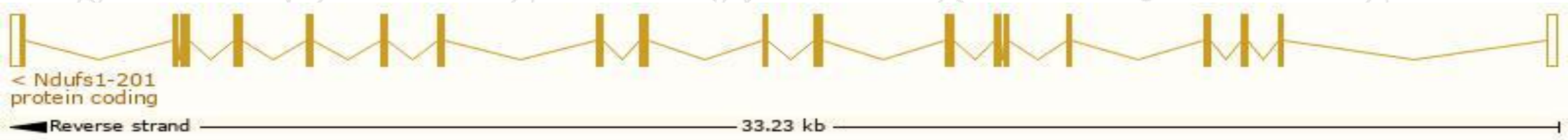
Official Symbol	Ndufs1 provided by MGI
Official Full Name	NADH:ubiquinone oxidoreductase core subunit S1 provided by MGI
Primary source	MGI:MGI:2443241
See related	Ensembl:ENSMUSG00000025968
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830412M15Rik, 9930026A05Rik
Expression	Ubiquitous expression in heart adult (RPKM 78.5), cerebellum adult (RPKM 29.7) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

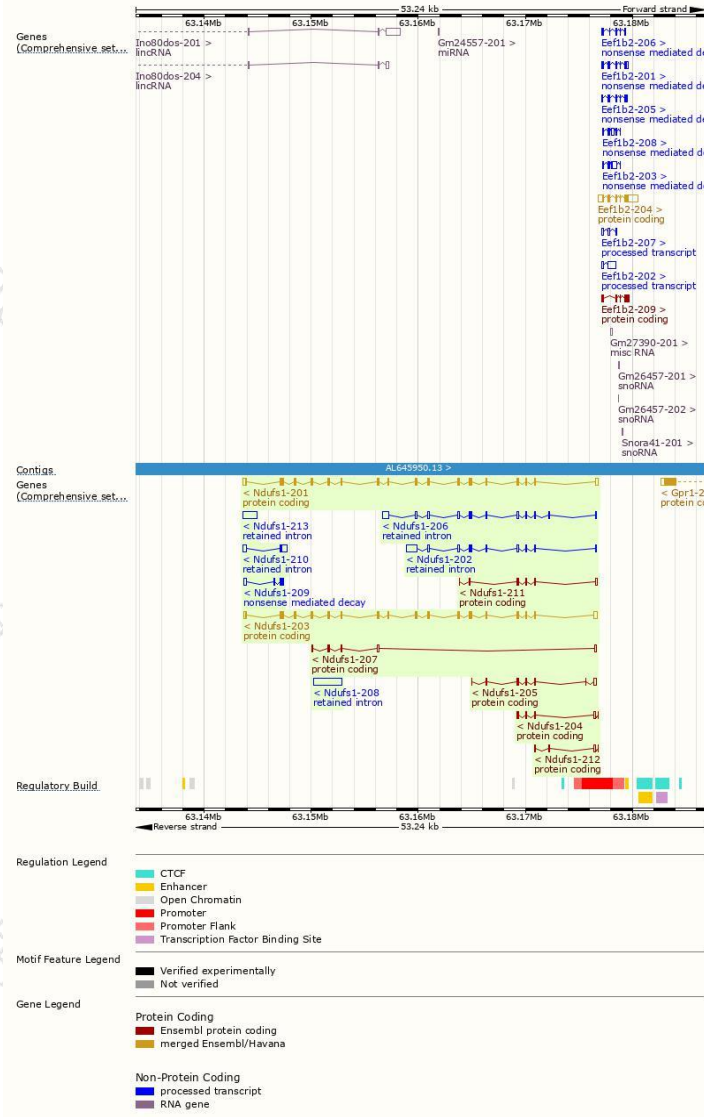
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ndufs1-201	ENSMUST00000027111.14	2661	727aa	Protein coding	CCDS14996	Q91VD9	TSL:1 GENCODE basic APPRIS P1
Ndufs1-203	ENSMUST00000168099.8	2590	727aa	Protein coding	CCDS14996	Q91VD9	TSL:1 GENCODE basic APPRIS P1
Ndufs1-207	ENSMUST00000185847.1	655	61aa	Protein coding	-	A0A087WSU3	CDS 3' incomplete TSL:5
Ndufs1-205	ENSMUST00000185732.6	651	118aa	Protein coding	-	A0A087WQR0	CDS 3' incomplete TSL:5
Ndufs1-211	ENSMUST00000188370.6	516	135aa	Protein coding	-	A0A087WP77	CDS 3' incomplete TSL:5
Ndufs1-204	ENSMUST00000185412.6	368	79aa	Protein coding	-	A0A087WR47	CDS 3' incomplete TSL:5
Ndufs1-212	ENSMUST00000189664.1	332	19aa	Protein coding	-	A0A087WRY4	CDS 3' incomplete TSL:3
Ndufs1-209	ENSMUST00000187756.6	493	62aa	Nonsense mediated decay	-	A0A087WQ77	CDS 5' incomplete TSL:3
Ndufs1-208	ENSMUST00000186569.1	2610	No protein	Retained intron	-	-	TSL:NA
Ndufs1-202	ENSMUST00000140612.1	1922	No protein	Retained intron	-	-	TSL:1
Ndufs1-206	ENSMUST00000185827.6	1775	No protein	Retained intron	-	-	TSL:1
Ndufs1-213	ENSMUST00000190095.1	1366	No protein	Retained intron	-	-	TSL:NA
Ndufs1-210	ENSMUST00000187835.1	826	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Ndufs1-201* 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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