

Ndufs2 Cas9-CKO Strategy

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Project Overview

Project Name

Ndufs2

Project type

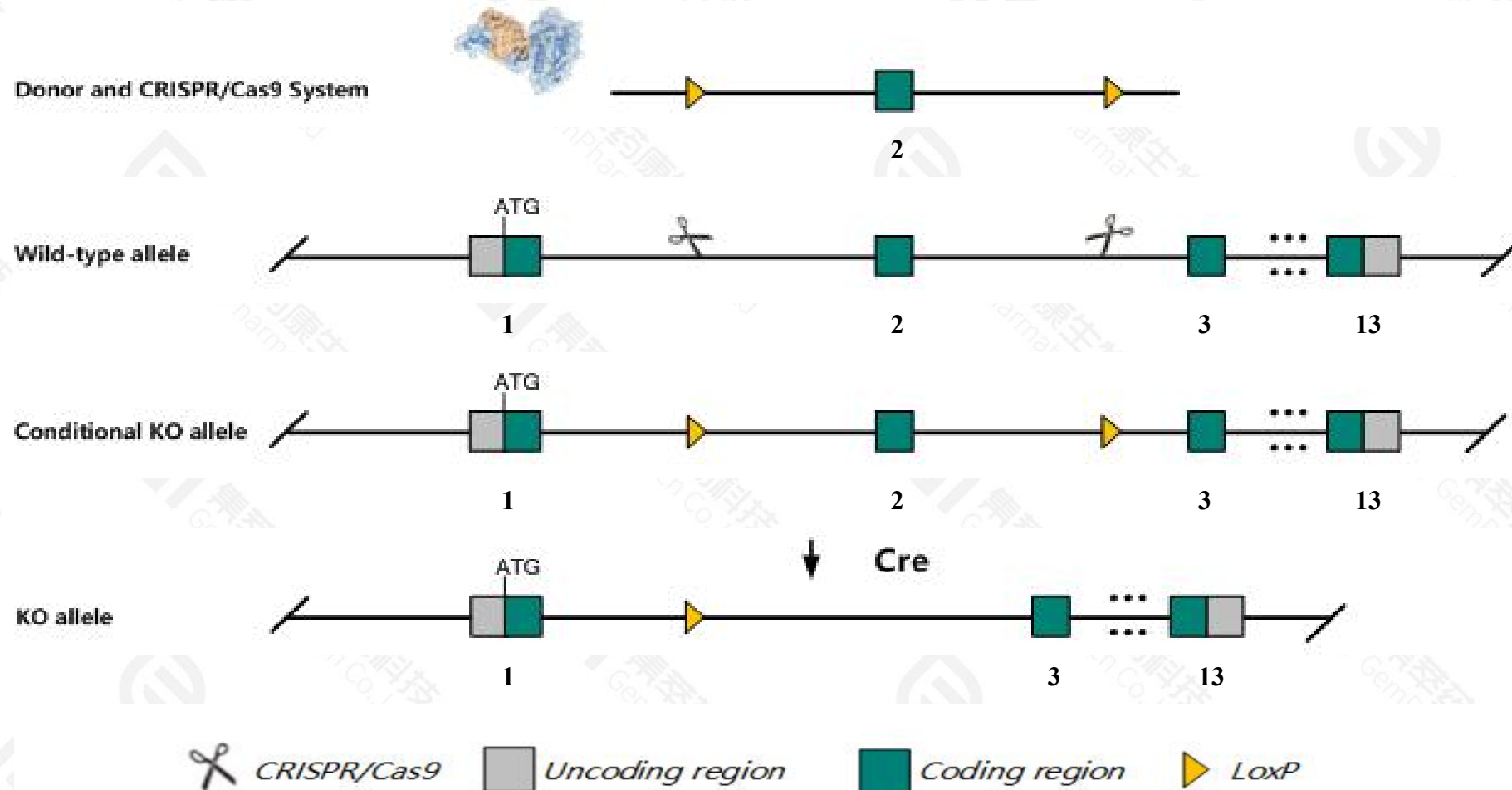
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ndufs2* gene. The schematic diagram is as follows:



Technical routes

- The *Ndufs2* gene has 8 transcripts. According to the structure of *Ndufs2* gene, exon2 of *Ndufs2-201*(ENSMUST00000013737.13) transcript is recommended as the knockout region. The region contains 107bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ndufs2* 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 *Ndufs2* 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.
- The flox region is about 4 kb away from the 5th end of the *Adamts4* gene, which may affect the regulation of this gene.
- Transcripts 207 maybe unaffected.
- 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)

Ndufs2 NADH:ubiquinone oxidoreductase core subunit S2 [Mus musculus (house mouse)]

Gene ID: 226646, updated on 3-Jan-2021

Summary



Official Symbol Ndufs2 provided by [MGI](#)

Official Full Name NADH:ubiquinone oxidoreductase core subunit S2 provided by [MGI](#)

Primary source [MGI:MGI:2385112](#)

See related [Ensembl:ENSMUSG00000013593](#)

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 CI-49kD

Expression Ubiquitous expression in heart adult (RPKM 305.9), kidney adult (RPKM 146.8) and 28 other tissues [See more](#)

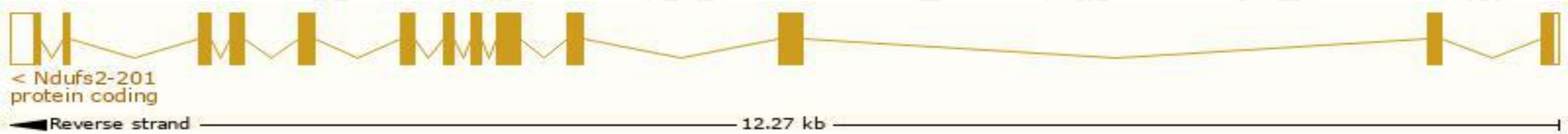
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

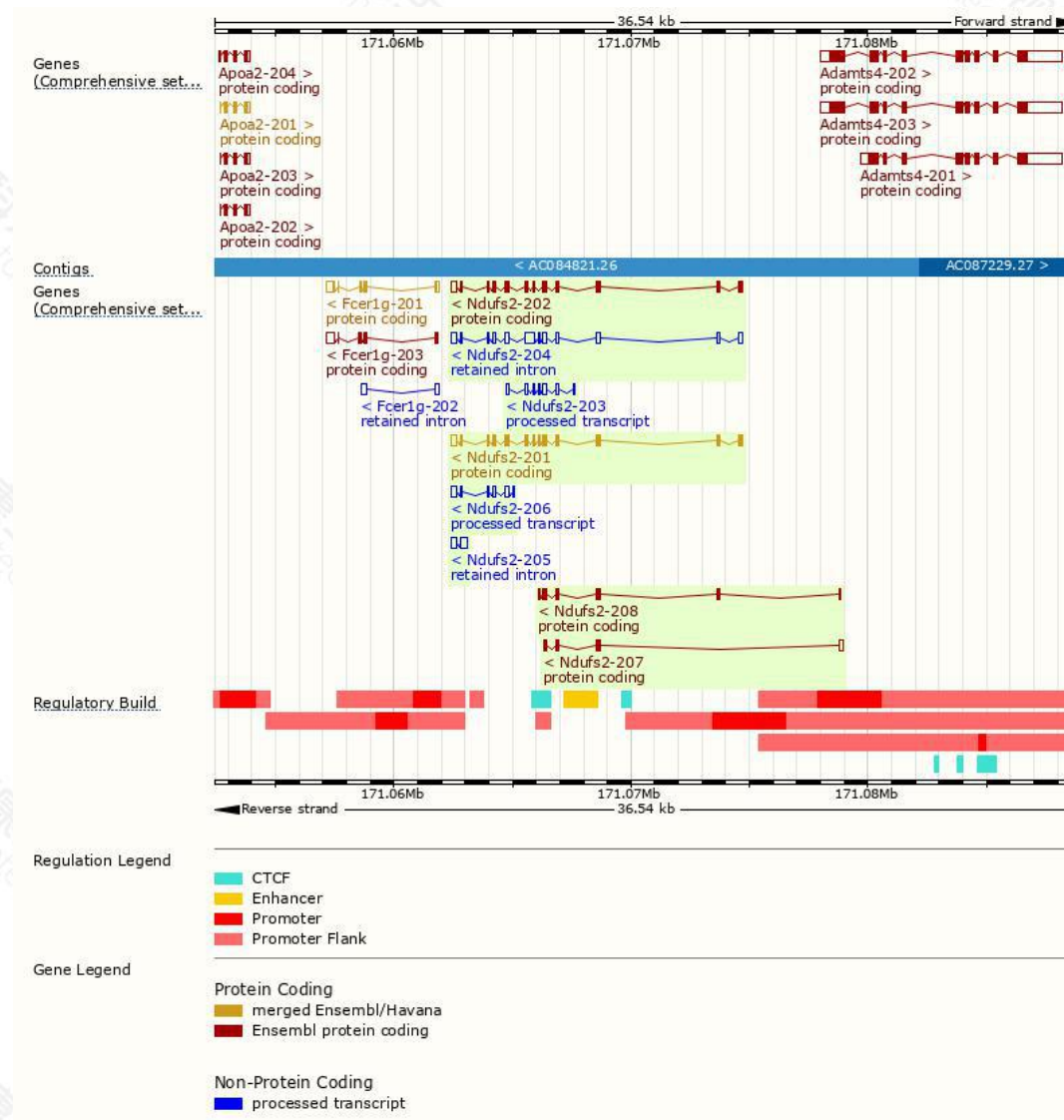
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ndufs2-201	ENSMUST00000013737.13	1623	463aa	Protein coding	CCDS15484		TSL:1 , GENCODE basic , APPRIS P1 ,
Ndufs2-202	ENSMUST00000111318.8	1545	437aa	Protein coding	-		TSL:5 , GENCODE basic ,
Ndufs2-208	ENSMUST00000194778.6	714	231aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Ndufs2-207	ENSMUST00000191871.2	643	145aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Ndufs2-203	ENSMUST00000131286.3	746	No protein	Processed transcript	-		TSL:5 ,
Ndufs2-206	ENSMUST00000150108.8	662	No protein	Processed transcript	-		TSL:2 ,
Ndufs2-204	ENSMUST00000136976.7	1845	No protein	Retained intron	-		TSL:5 ,
Ndufs2-205	ENSMUST00000138069.8	503	No protein	Retained intron	-		TSL:2 ,

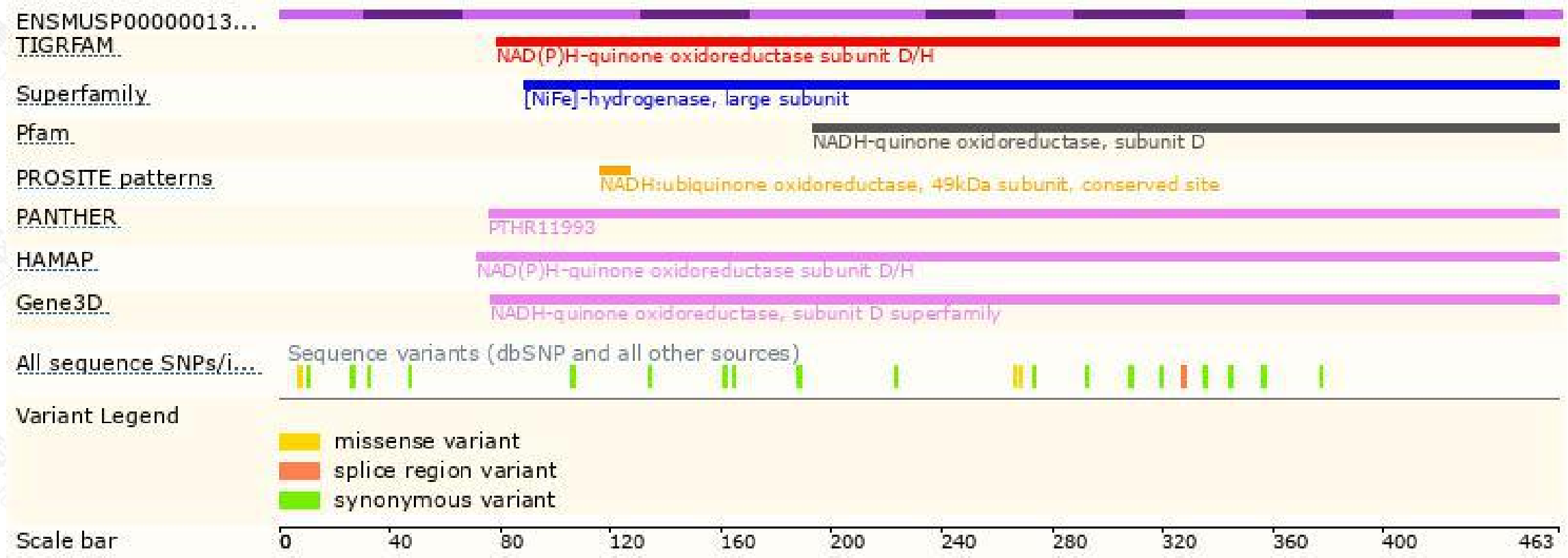
The strategy is based on the design of *Ndufs2-201* transcript,the transcription is shown below:



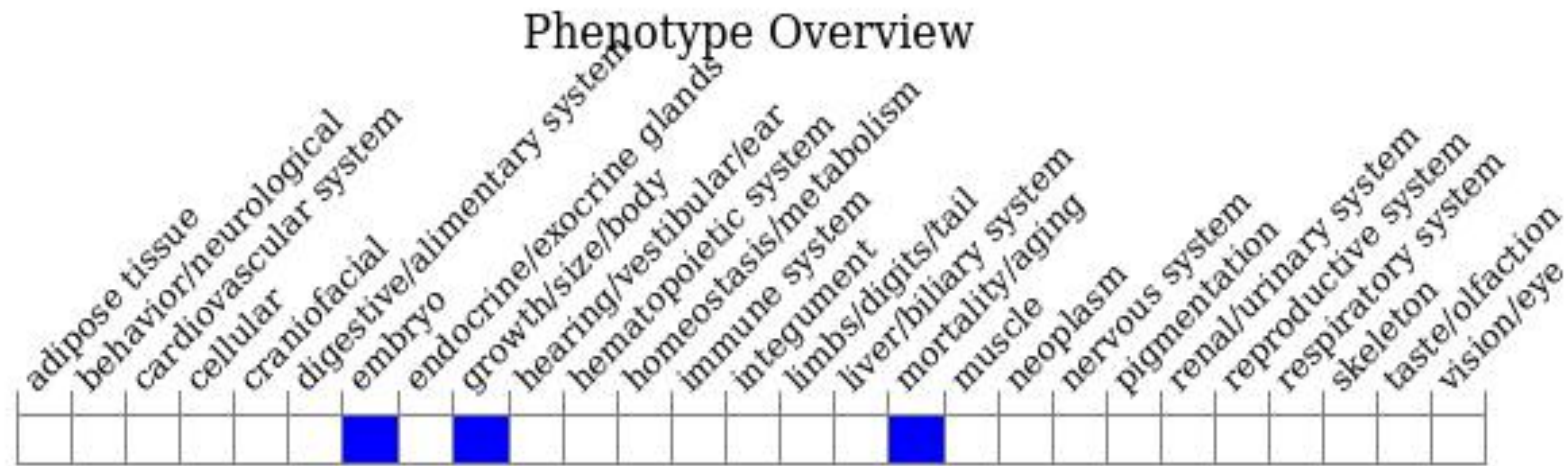
Genomic location distribution



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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