

Ndufs8 Cas9-CKO Strategy

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Project Overview

Project Name

Ndufs8

Project type

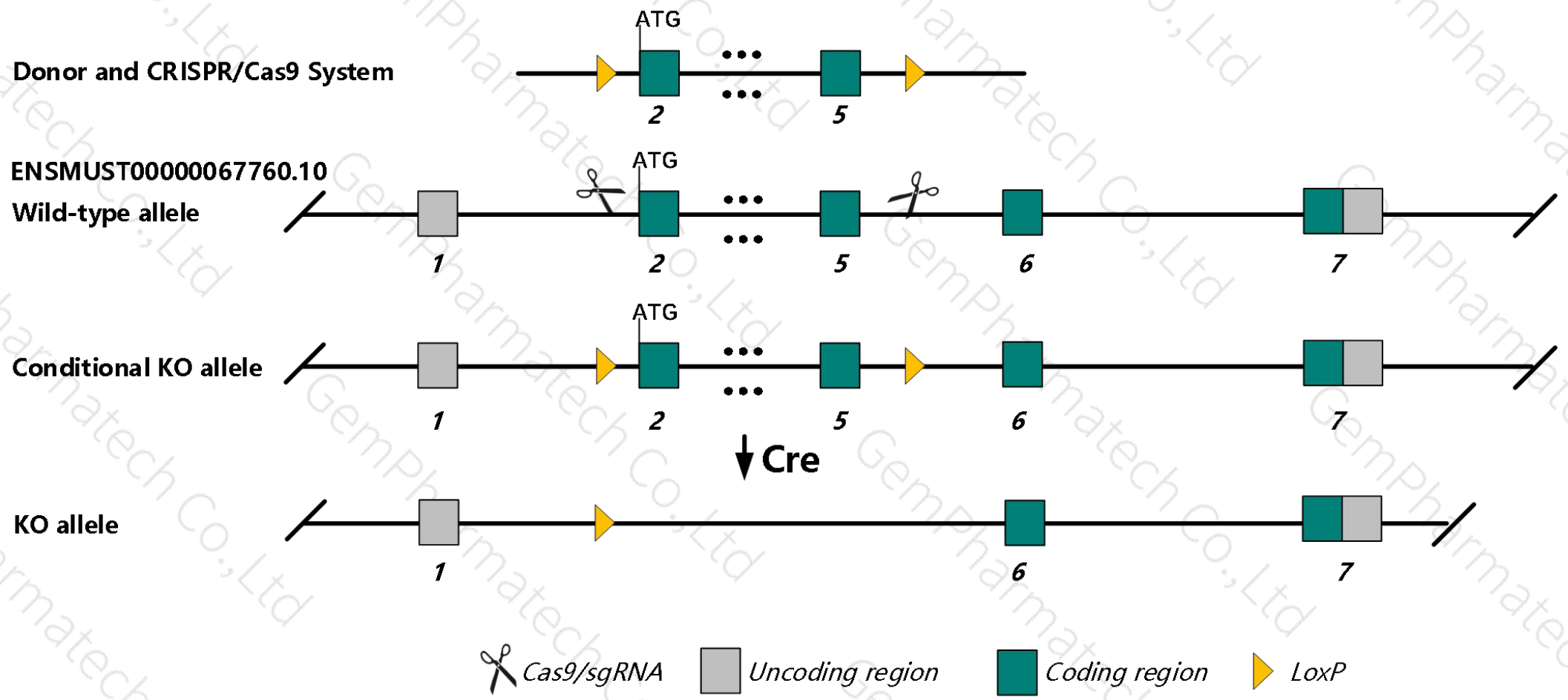
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ndufs8* gene. The schematic diagram is as follows:



Technical routes

- The *Ndufs8* gene has 5 transcripts. According to the structure of *Ndufs8* gene, exon2-exon5 of *Ndufs8-201* (ENSMUST00000075092.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ndufs8* 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.

Notice

- The *Ndufs8* gene is located on the Chr19. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ndufs8 NADH:ubiquinone oxidoreductase core subunit S8 [*Mus musculus* (house mouse)]

Gene ID: 225887, updated on 15-Apr-2019

Summary

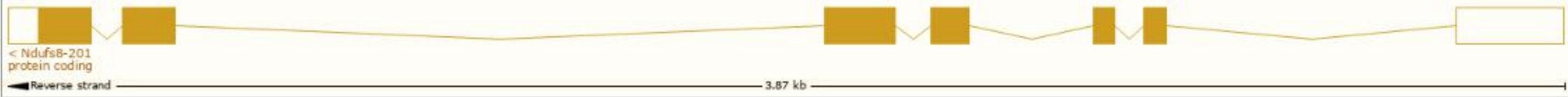
Official Symbol	Ndufs8 provided by MGI
Official Full Name	NADH:ubiquinone oxidoreductase core subunit S8 provided by MGI
Primary source	MGI:MGI:2385079
See related	Ensembl:ENSMUSG00000059734
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	TYKY; CI-23kD; BC021616
Expression	Ubiquitous expression in kidney adult (RPKM 181.5), heart adult (RPKM 175.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

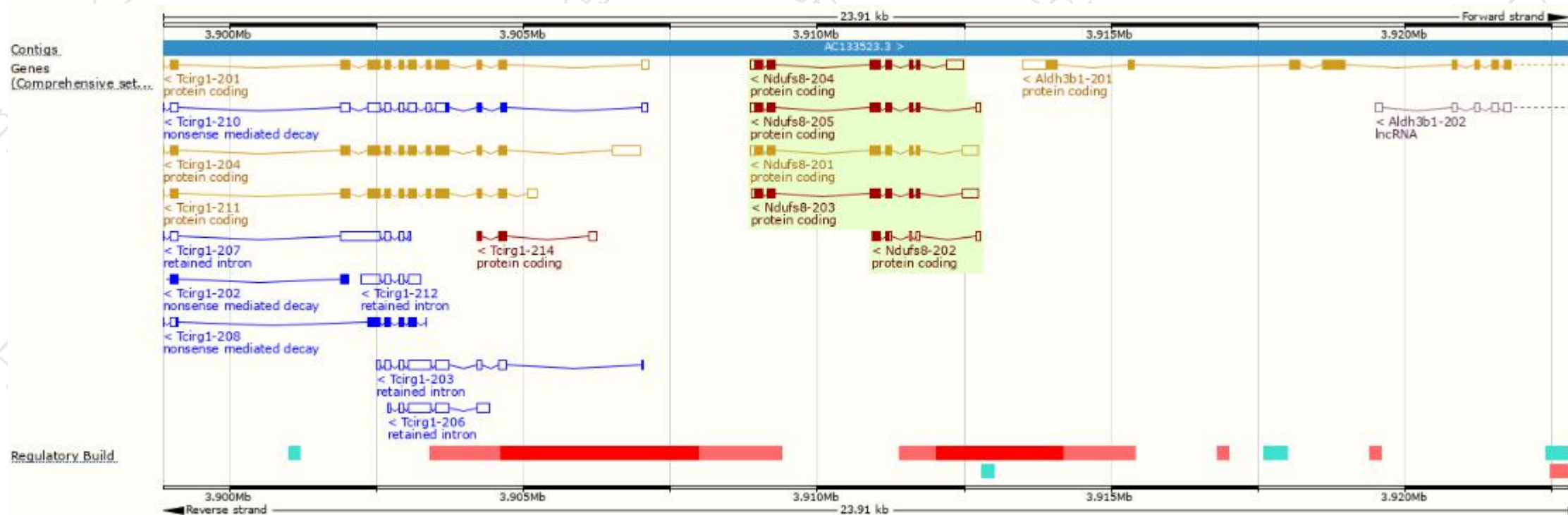
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ndufs8-204	ENSMUST00000236801.1	1005	212aa	Protein coding	CCDS29402	Q5M9P5	GENCODE basic APPRIS P1
Ndufs8-201	ENSMUST00000075092.7	983	212aa	Protein coding	CCDS29402	Q5M9P5 Q8K3J1	TSL:1 GENCODE basic APPRIS P1
Ndufs8-203	ENSMUST00000235847.1	977	212aa	Protein coding	CCDS29402	Q5M9P5	GENCODE basic APPRIS P1
Ndufs8-205	ENSMUST00000237341.1	780	212aa	Protein coding	CCDS29402	Q5M9P5	GENCODE basic APPRIS P1
Ndufs8-202	ENSMUST00000235301.1	388	67aa	Protein coding	-	-	CDS 3' incomplete

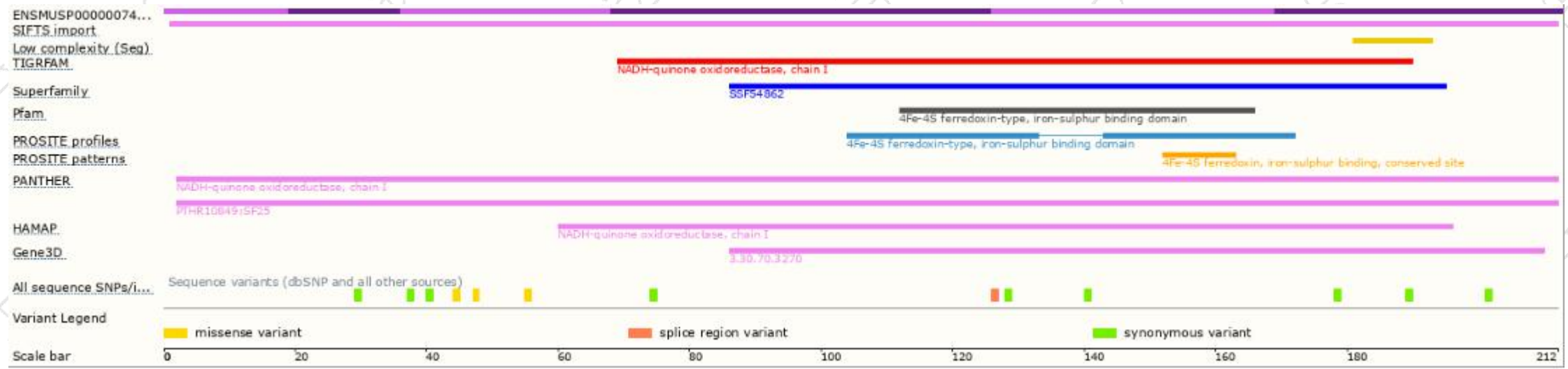
The strategy is based on the design of *Ndufs8-201* transcript,The transcription is shown below



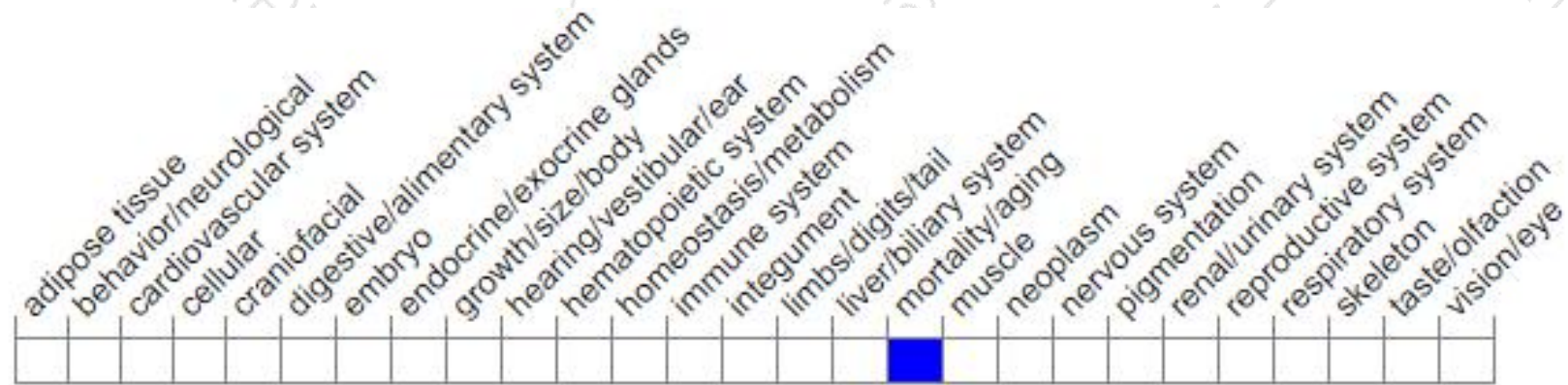
Genomic location distribution



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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