

Ndufa5 Cas9-KO Strategy

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Project Overview

Project Name

Ndufa5

Project type

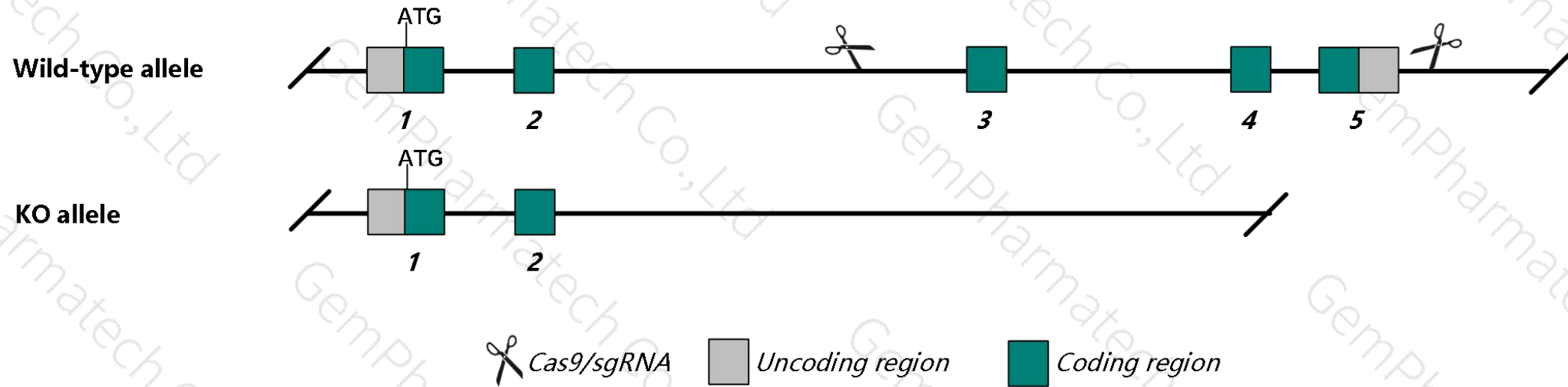
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ndufa5* gene. The schematic diagram is as follows:



- The *Ndufa5* gene has 4 transcripts. According to the structure of *Ndufa5* gene, exon3-exon5 of *Ndufa5-201* (ENSMUST00000023851.8) transcript is recommended as the knockout region. The region contains most 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 *Ndufa5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a gene trap allele exhibit embryonic lethality at E9.
- The *Ndufa5* gene is located on the Chr6. 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 knockout region is near to the N-terminal of *Iqub* gene and *Asb15* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- 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)

Ndufa5 NADH:ubiquinone oxidoreductase subunit A5 [*Mus musculus* (house mouse)]

(Gene ID: 68202, updated on 3-May-2020)

Summary

Official Symbol	Ndufa5 provided by MGI
Official Full Name	NADH:ubiquinone oxidoreductase subunit A5 provided by MGI
Primary source	MGI:MGI:1915452
See related	Ensembl:ENSMUSG00000023089
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-13kD-B; 2900002J19Rik
Expression	Broad expression in heart adult (RPKM 29.1), cerebellum adult (RPKM 24.8) and 19 other tissues See more
Orthologs	human all

Genomic context

Location: 6; 6 A3.1

See Ndufa5 in [Genome Data Viewer](#)

Exon count: 5

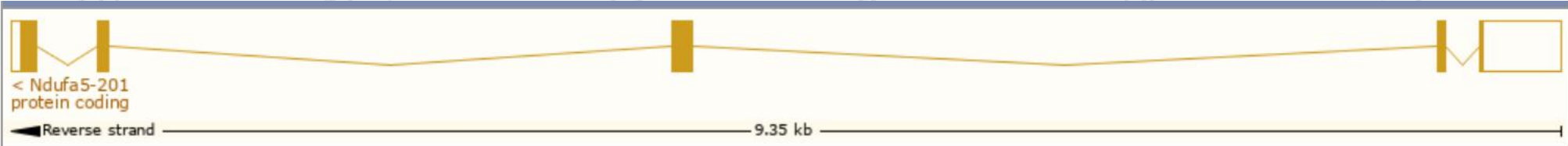
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (24518662..24527690, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (24468666..24477687, complement)

Transcript information (Ensembl)

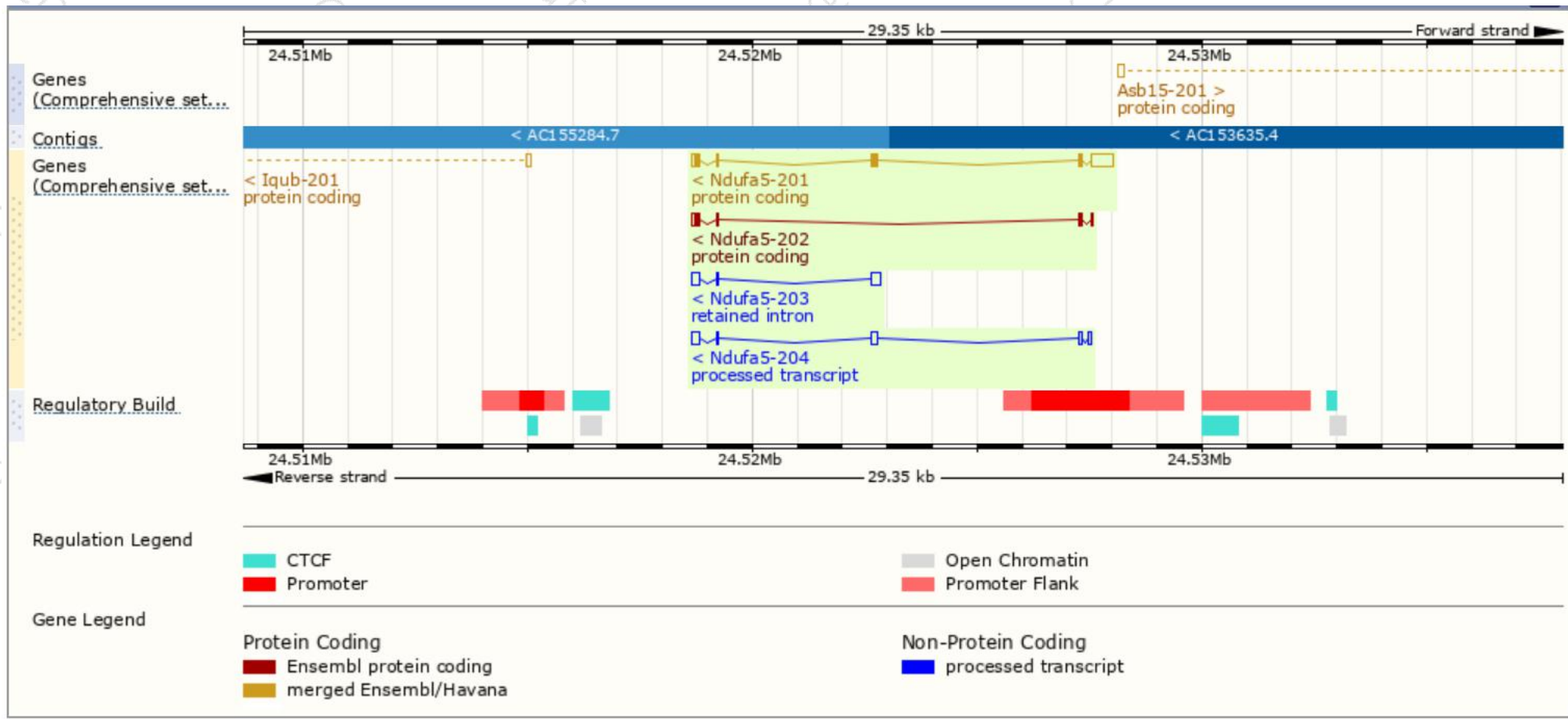
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ndufa5-201	ENSMUST00000023851.8	875	116aa	Protein coding	CCDS19942	Q9CPP6	TSL:1 GENCODE basic APPRIS P1
Ndufa5-202	ENSMUST00000118558.4	315	77aa	Protein coding	CCDS80494	D3YTQ8	TSL:2 GENCODE basic
Ndufa5-204	ENSMUST00000141274.1	453	No protein	Processed transcript	-	-	TSL:3
Ndufa5-203	ENSMUST00000132588.7	433	No protein	Retained intron	-	-	TSL:2

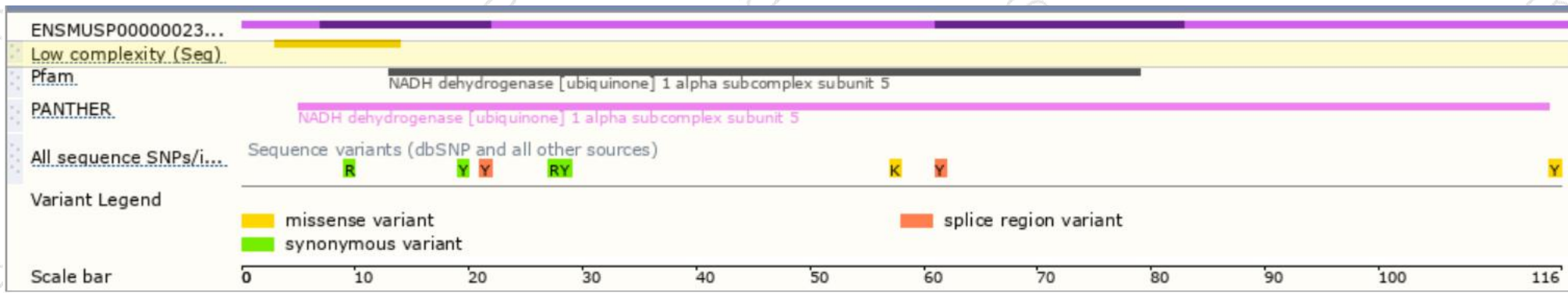
The strategy is based on the design of *Ndufa5-201* transcript,the transcription is shown below:



Genomic location distribution

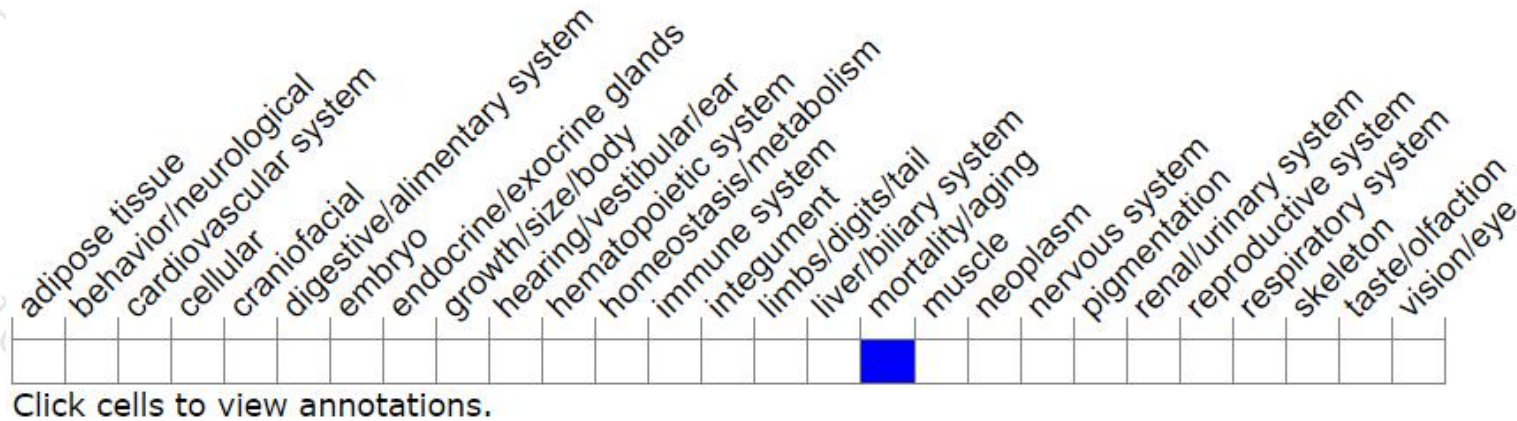


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

Mice homozygous for a gene trap allele exhibit embryonic lethality at E9.

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

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