

Ndufa13 Cas9-KO Strategy

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Design Date: 2021-3-22

Project Overview

Project Name

Ndufa13

Project type

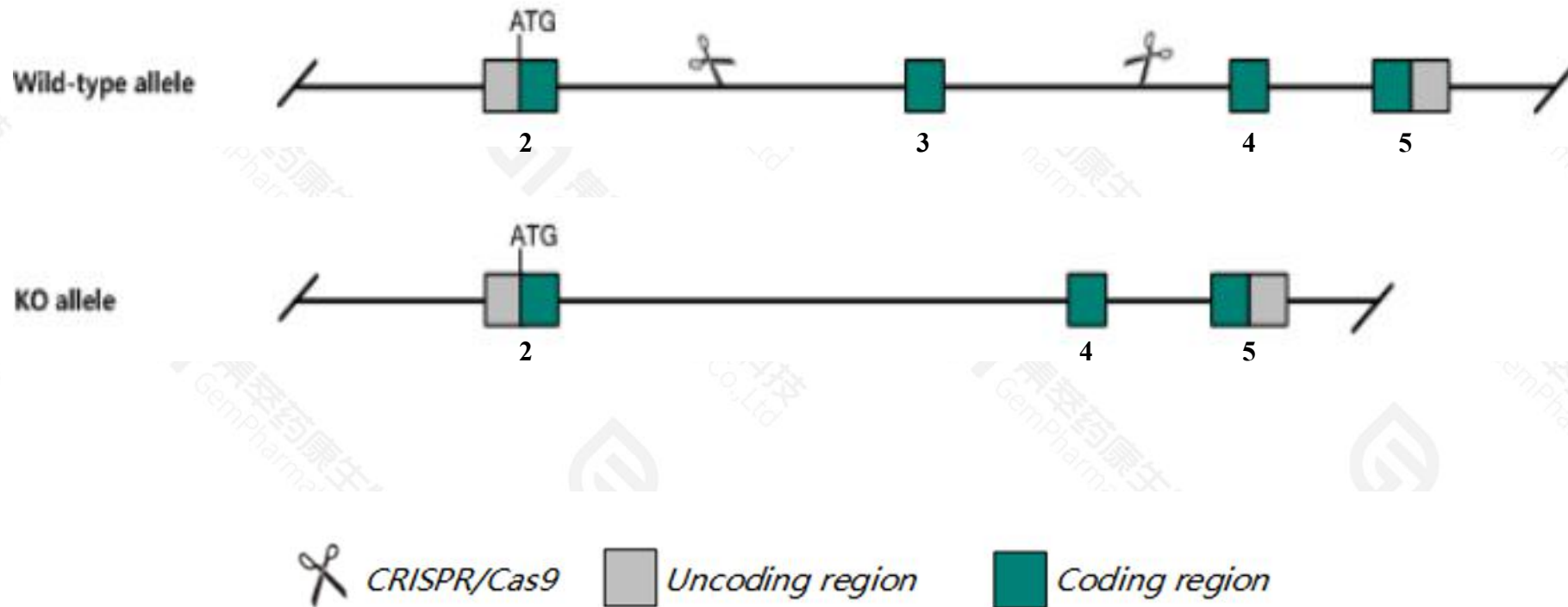
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ndufa13* gene. The schematic diagram is as follows:



- The *Ndufa13* gene has 1 transcript. According to the structure of *Ndufa13* gene, exon3 of *Ndufa13*-201(ENSMUST00000110167.5) transcript is recommended as the knockout region. The region contains 79bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ndufa13* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous null mice display embryonic lethality, failed gastrulation, absent organogenesis, small and abnormal inner cell mass and trophoblast, and abnormal mitochondria.
- The KO region contains functional region of the *Yjefn3* gene. Knockout the region may affect the function of *Yjefn3* gene.
- The *Ndufa13* gene is located on the Chr8. 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.

Ndufa13 NADH:ubiquinone oxidoreductase subunit A13 [Mus musculus (house mouse)]

Gene ID: 67184, updated on 12-Feb-2021

Summary



Official Symbol Ndufa13 provided by [MGI](#)

Official Full Name NADH:ubiquinone oxidoreductase subunit A13 provided by [MGI](#)

Primary source [MGI:MGI:1914434](#)

See related [Ensembl:ENSMUSG00000036199](#)

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 2700054G14Rik, AU022060, CDA01, CDA016, CGI-3, CGI-39, CI-B16.6, GRIM-, GRIM-19, Grim, Grim19

Expression Ubiquitous expression in heart adult (RPKM 81.9), testis adult (RPKM 75.3) and 28 other tissues [See more](#)

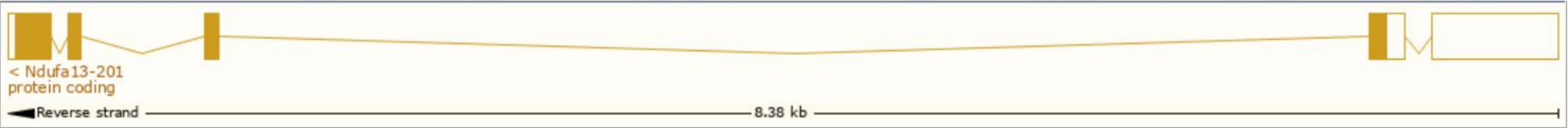
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

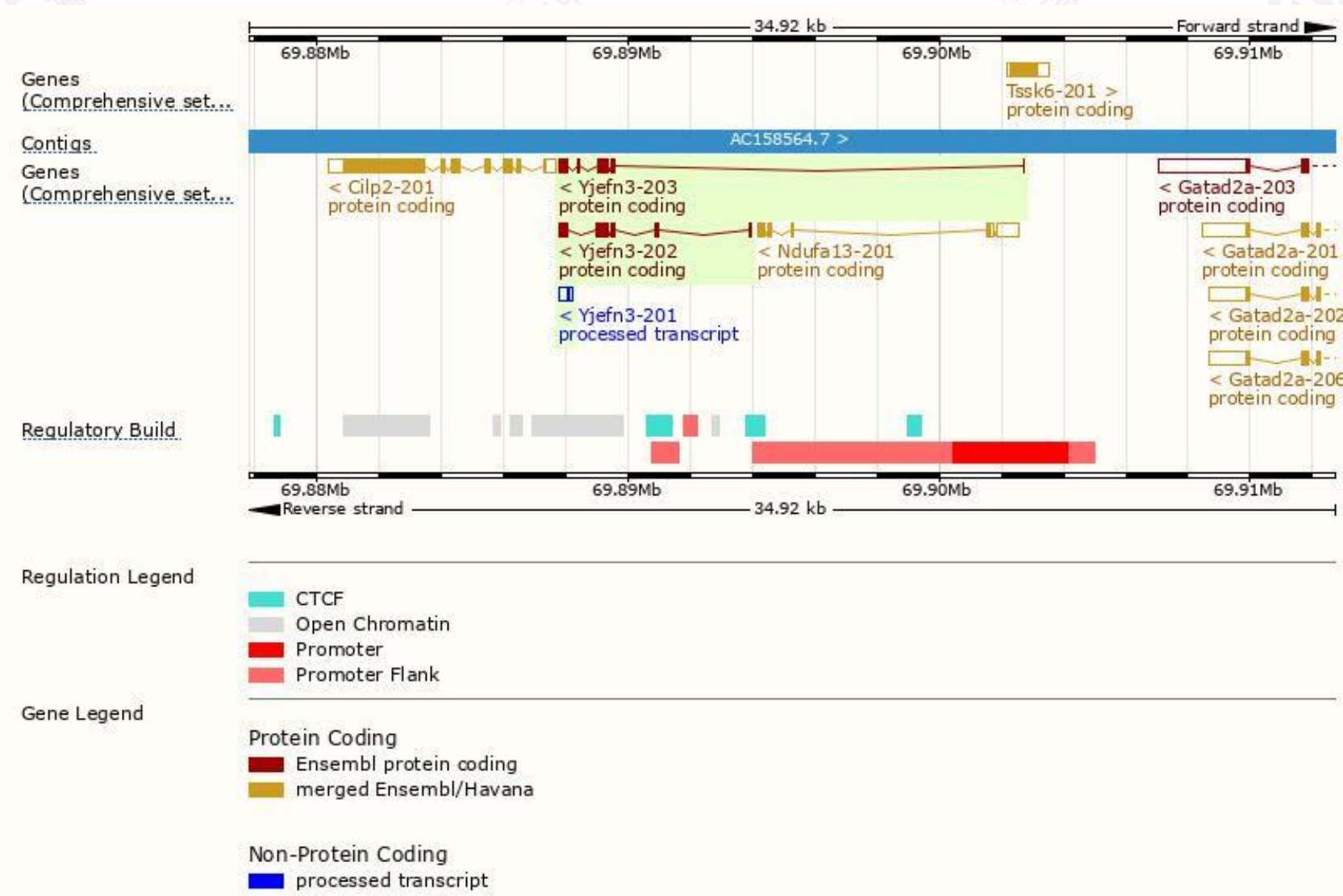
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ndufa13-201	ENSMUST00000110167.5	1251	144aa	Protein coding	CCDS22353		TSL:1 , GENCODE basic , APPRIS P1 ,

The strategy is based on the design of *Ndufa13-201* transcript,the transcription is shown below:



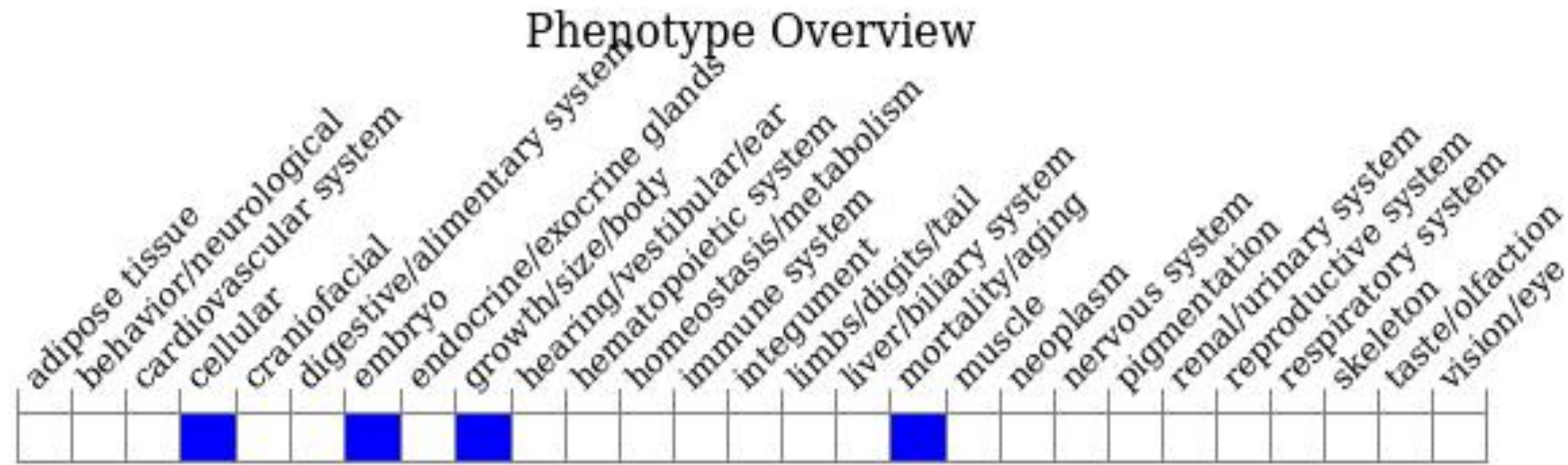
Genomic location distribution



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/>).

According to the existing MGI data, homozygous null mice display embryonic lethality, failed gastrulation, absent organogenesis, small and abnormal inner cell mass and trophoblast, and abnormal mitochondria.

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