

Ndufs7 Cas9-KO Strategy

Designer: Huan Fan

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Project Overview



Project Name

Ndufs7

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Ndufs7* gene. The schematic diagram is as follows:

Technical routes



The Ndufs7 gene has 6 transcripts. According to the structure of Ndufs7 gene, exon2-4 of Ndufs7-201

(ENSMUST00000020361.6) transcript is recommended as the knockout region. The region contains 245bp coding sequence.

Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify Ndufs7 gene. The brief process is as follows: CRISPR/Cas9 system

Notice



The *Ndufs7* gene is located on the Chr10. 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



Ndufs7 NADH:ubiquinone oxidoreductase core subunit S7 [Mus musculus (house mouse)]

Gene ID: 75406, updated on 7-Apr-2019

Summary

☆ ?

Official Symbol Ndufs7 provided by MGI

Official Full Name NADH:ubiquinone oxidoreductase core subunit S7 provided by MGI

Primary source MGI:MGI:1922656

See related Ensembl:ENSMUSG00000020153

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 1010001M04Rik, CI-20kD

Expression Ubiquitous expression in heart adult (RPKM 322.2), duodenum adult (RPKM 296.5) and 28 other tissuesSee more

Orthologs <u>human all</u>

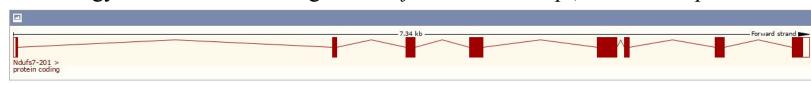
Transcript information Ensembl



The gene has 6 transcripts, all transcripts are shown below:

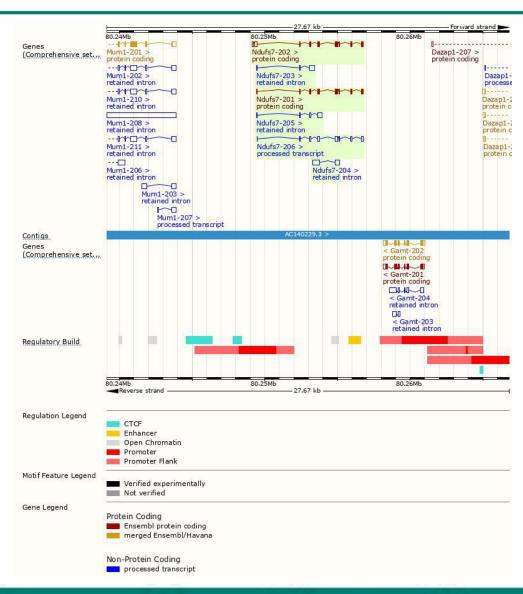
Name	Transcript ID	bp	Protein	Biotype	ccds	UniProt	Flags
Ndufs7-202	ENSMUST00000105364.7	983	224aa	Protein coding	CCDS24015	Q9DC70	TSL:5 GENCODE basic APPRIS P1
Ndufs7-201	ENSMUST00000020361.6	758	224aa	Protein coding	CCDS24015	Q9DC70	TSL:1 GENCODE basic APPRIS P1
Ndufs7-206	ENSMUST00000157063.1	722	No protein	Processed transcript	-	-	TSL:5
Ndufs7-204	ENSMUST00000155336.1	770	No protein	Retained intron	24	-	TSL:2
Ndufs7-205	ENSMUST00000155523.7	435	No protein	Retained intron	-		TSL:2
Ndufs7-203	ENSMUST00000152939.7	420	No protein	Retained intron	-8	-	TSL:2

The strategy is based on the design of *Ndufs7-201* transcript, The transcription is shown below



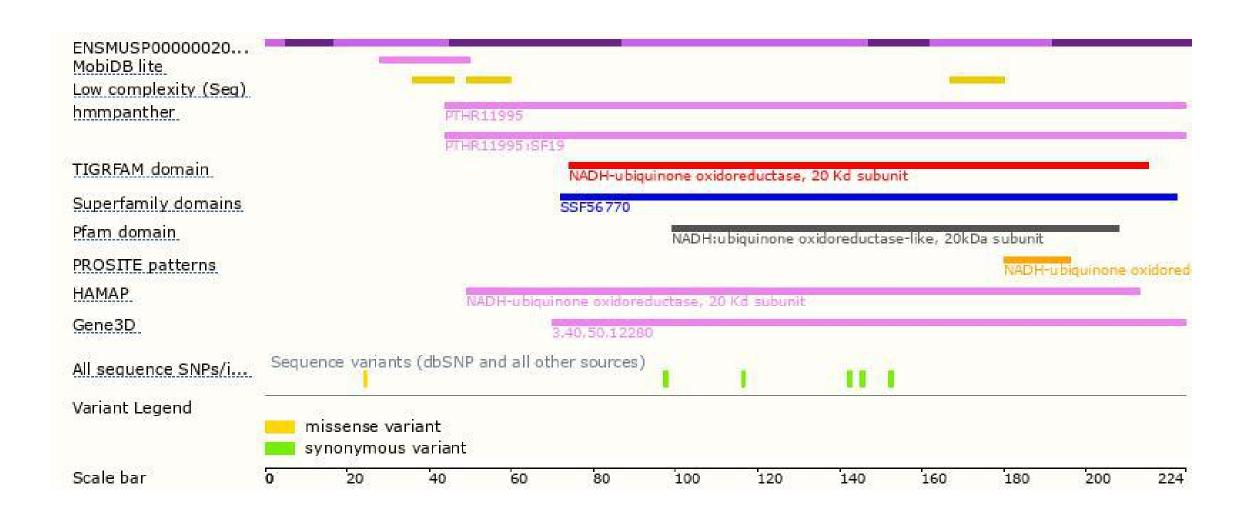
Genomic location distribution





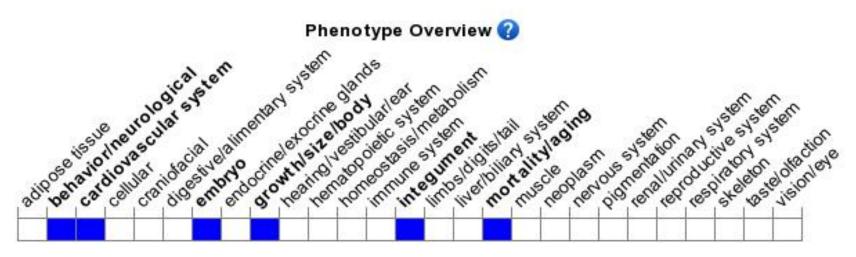
Protein domain





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. Tel: 400-9660890





