

Nars2 Cas9-CKO Strategy

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Project Overview

Project Name

Nars2

Project type

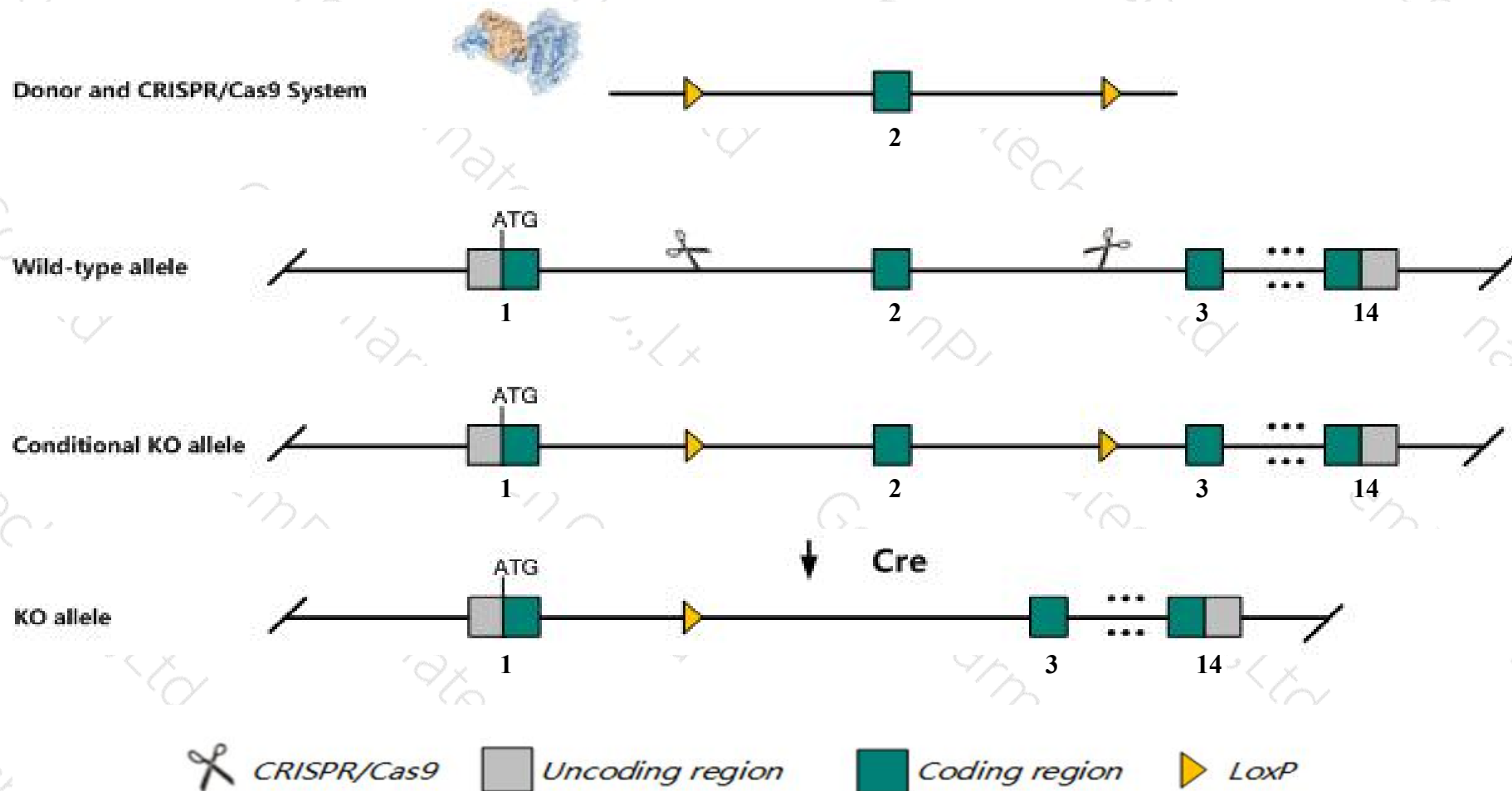
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nars2* gene. The schematic diagram is as follows:



Technical routes

- The *Nars2* gene has 6 transcripts. According to the structure of *Nars2* gene, exon2 of *Nars2-201* (ENSMUST00000044466.11) transcript is recommended as the knockout region. The region contains 110bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nars2* 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 *Nars2* gene is located on the Chr7. 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)

Nars2 asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) [Mus musculus (house mouse)]

Gene ID: 244141, updated on 31-Jan-2019

Summary



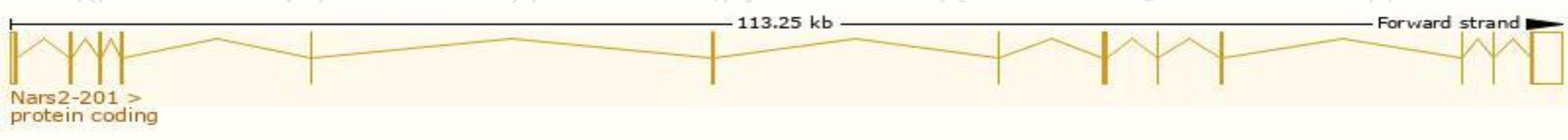
Official Symbol	Nars2 provided by MGI
Official Full Name	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) provided by MGI
Primary source	MGI:MGI:2142075
See related	Ensembl:ENSMUSG00000018995
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI875199
Expression	Ubiquitous expression in liver E14 (RPKM 2.7), CNS E11.5 (RPKM 2.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

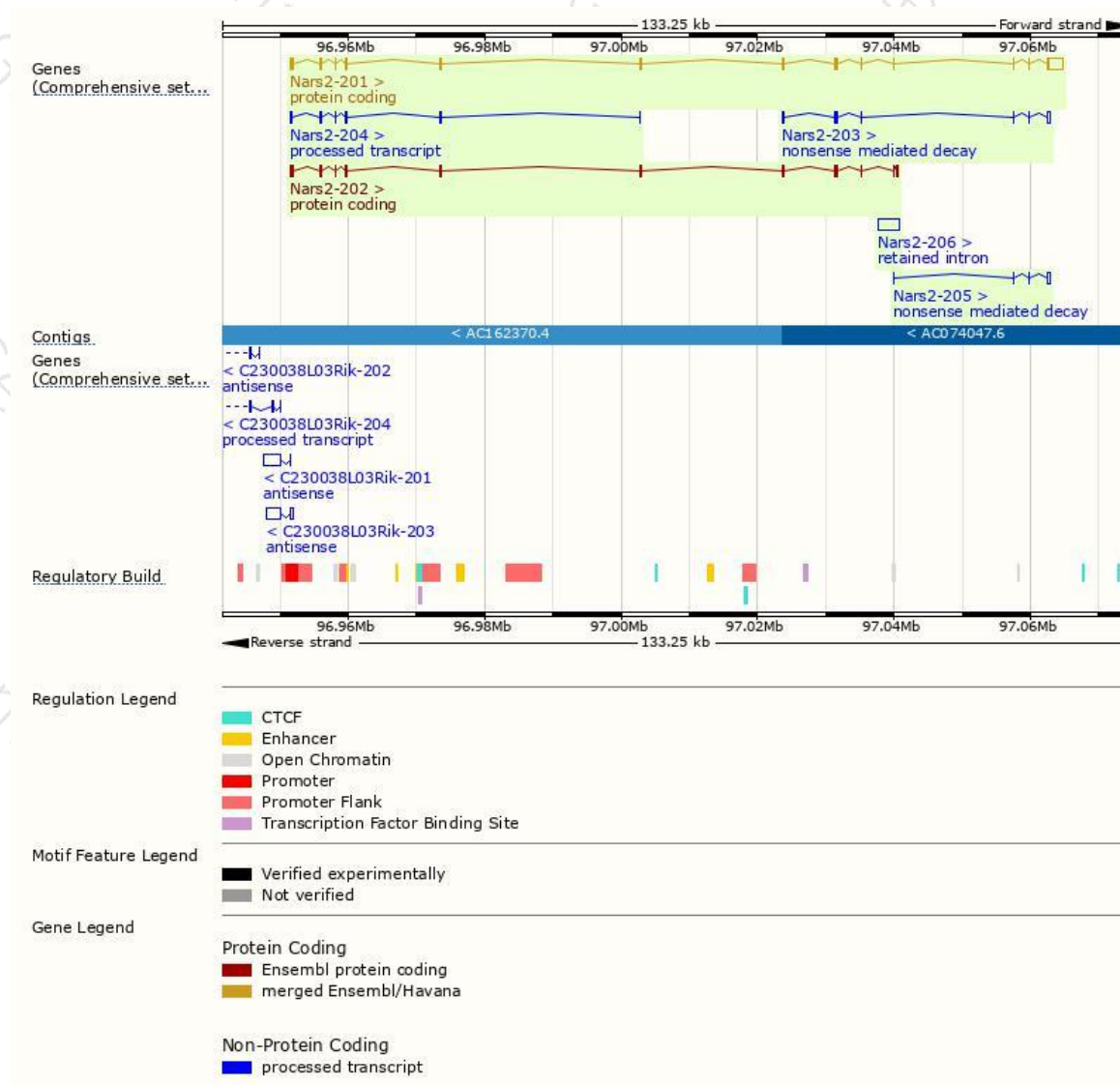
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nars2-201	ENSMUST00000044466.11	3778	477aa	Protein coding	CCDS21454	Q8BGV0	TSL:1 GENCODE basic APPRIS P1
Nars2-202	ENSMUST00000107159.2	1777	391aa	Protein coding	-	D3YV21	TSL:5 GENCODE basic
Nars2-203	ENSMUST00000122835.7	780	79aa	Nonsense mediated decay	-	A0A0U1RPL7	CDS 5' incomplete TSL:3
Nars2-205	ENSMUST00000150681.2	623	53aa	Nonsense mediated decay	-	A0A0U1RPY0	TSL:5
Nars2-206	ENSMUST00000206109.1	3266	No protein	Retained intron	-	-	TSL:NA
Nars2-204	ENSMUST00000149204.2	606	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Nars2-201* transcript,The transcription is shown below



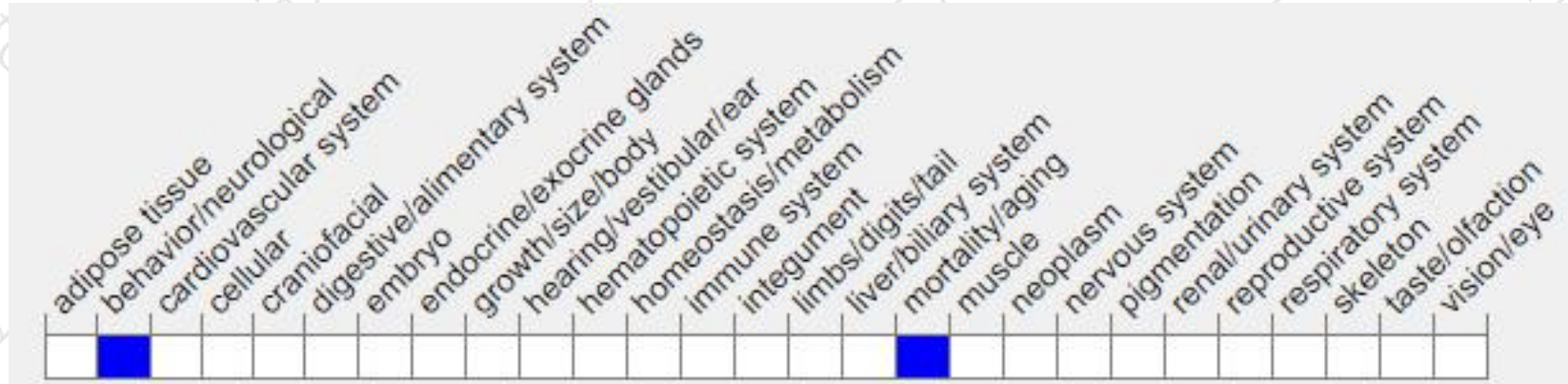
Genomic location distribution



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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