

Nars Cas9-KO Strategy

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Project Overview

Project Name

Nars

Project type

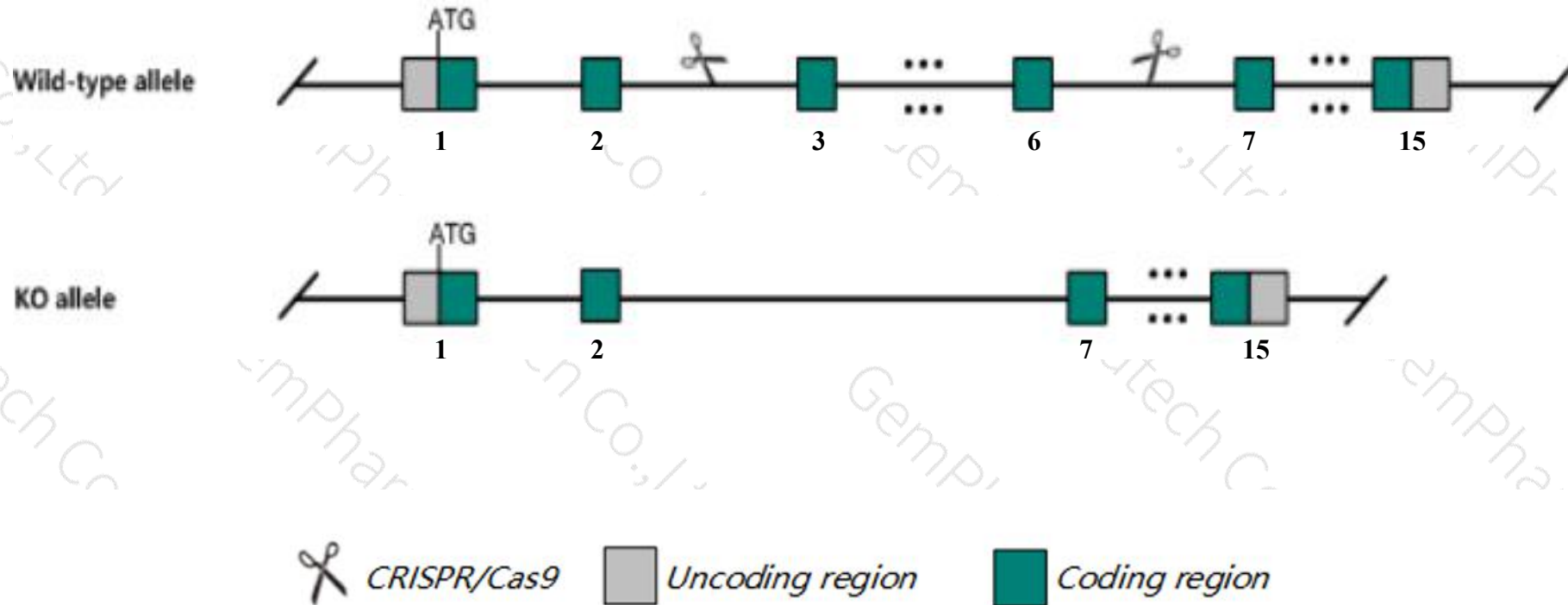
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Nars* gene has 16 transcripts. According to the structure of *Nars* gene, exon3-exon6 of *Nars-213* (ENSMUST00000237400.1) transcript is recommended as the knockout region. The region contains 328bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nars* gene. The brief process is as follows: CRISPR/Cas9 system v

- Transcripts 204,210,214 may not be affected.
- The *Nars* gene is located on the Chr18. 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)

Nars asparaginyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 70223, updated on 13-Mar-2020

Summary



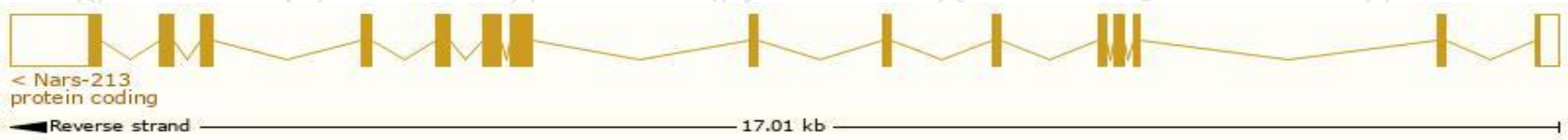
Official Symbol	Nars provided by MGI
Official Full Name	asparaginyl-tRNA synthetase provided by MGI
Primary source	MGI:MGI:1917473
See related	Ensembl:ENSMUSG00000024587
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3010001M15Rik, AA960128, ASNRS, C78150, NARS1
Expression	Ubiquitous expression in liver E14 (RPKM 51.7), placenta adult (RPKM 44.5) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

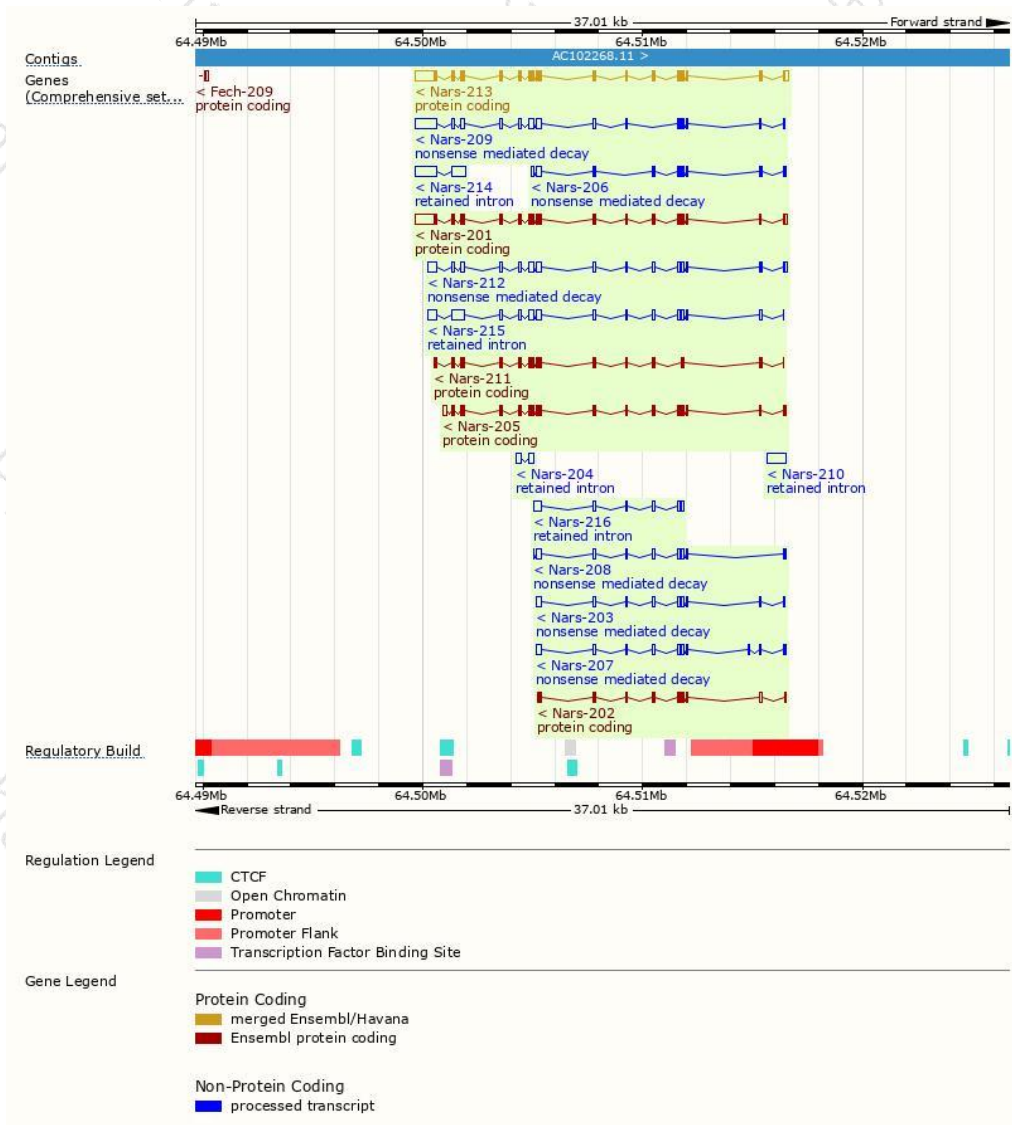
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nars-213	ENSMUST00000237400.1	2745	559aa	Protein coding	CCDS50308	Q8BP47	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Nars-201	ENSMUST0000025483.10	2687	558aa	Protein coding	-	A0A498WGK2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Nars-205	ENSMUST00000236186.1	1784	517aa	Protein coding	-	A0A494BB89	GENCODE basic
Nars-211	ENSMUST00000237351.1	1492	497aa	Protein coding	-	A0A494BAX5	CDS 5' incomplete
Nars-202	ENSMUST00000235325.1	761	210aa	Protein coding	-	A0A494B927	CDS 3' incomplete
Nars-209	ENSMUST00000236873.1	2482	127aa	Nonsense mediated decay	-	A0A494B996	
Nars-212	ENSMUST00000237369.1	2103	70aa	Nonsense mediated decay	-	A0A494B949	
Nars-206	ENSMUST00000236392.1	935	164aa	Nonsense mediated decay	-	A0A494BAW6	
Nars-207	ENSMUST00000236463.1	894	43aa	Nonsense mediated decay	-	A0A494BB92	
Nars-203	ENSMUST00000235647.1	874	69aa	Nonsense mediated decay	-	A0A494B9G0	
Nars-208	ENSMUST00000236583.1	845	35aa	Nonsense mediated decay	-	A0A494BB81	
Nars-215	ENSMUST00000237585.1	2268	No protein	Retained intron	-	-	
Nars-214	ENSMUST00000237503.1	1648	No protein	Retained intron	-	-	
Nars-210	ENSMUST00000237027.1	848	No protein	Retained intron	-	-	
Nars-216	ENSMUST00000237831.1	774	No protein	Retained intron	-	-	
Nars-204	ENSMUST00000235887.1	434	No protein	Retained intron	-	-	

The strategy is based on the design of *Nars-213* transcript,the transcription is shown below:



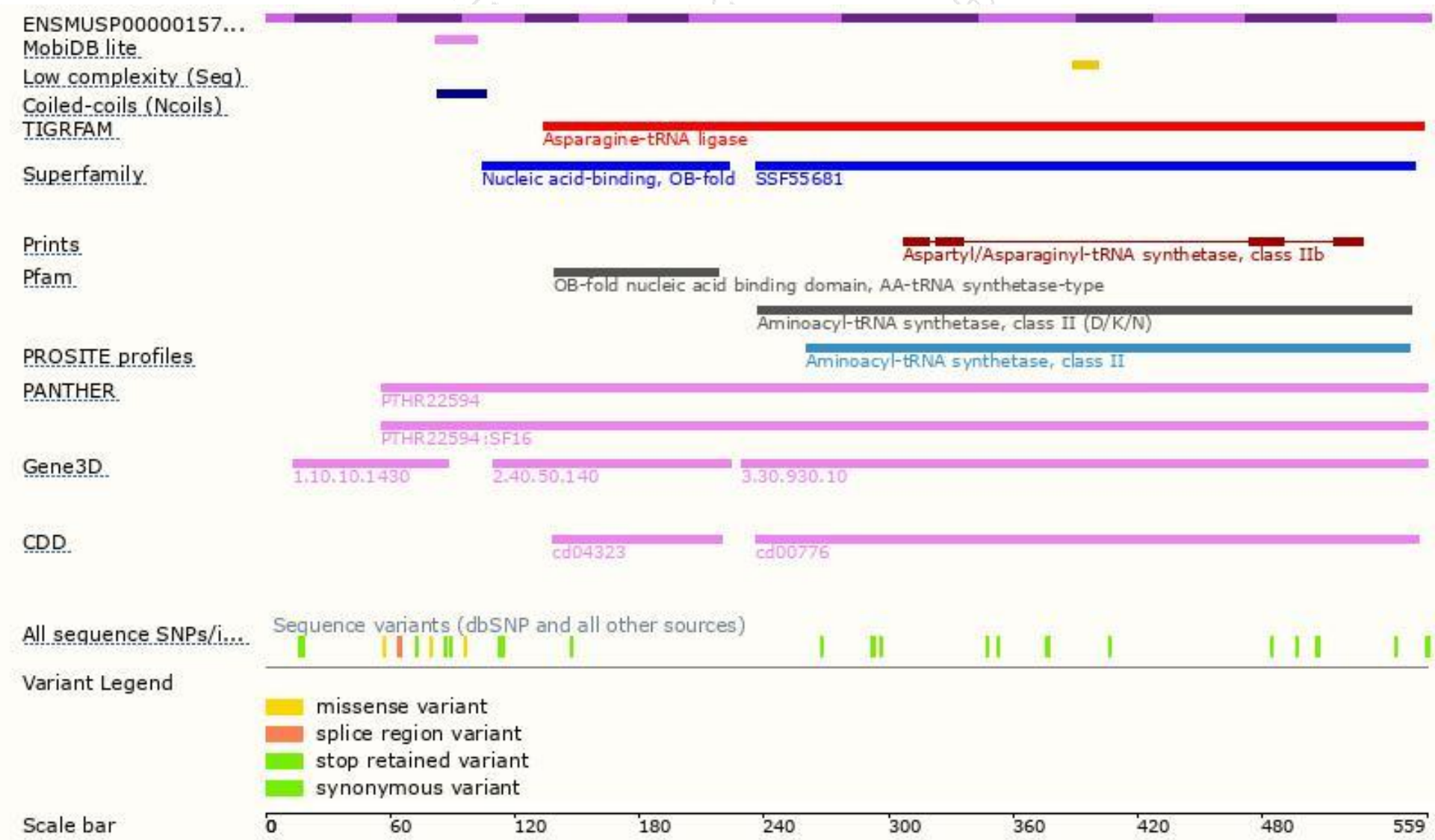
Genomic location distribution



Protein domain



集萃药康
GemPharmatech



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

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