

Lars Cas9-KO Strategy

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Project Overview

Project Name

Iars

Project type

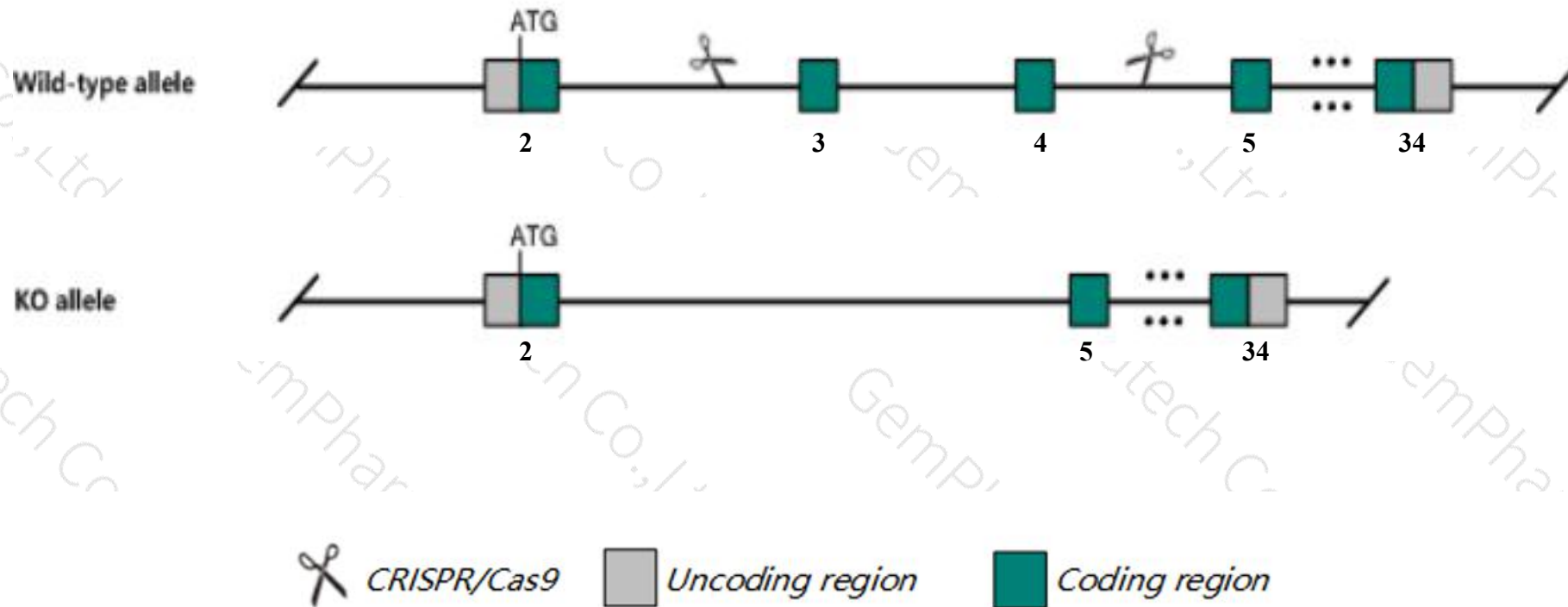
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Iars* gene has 9 transcripts. According to the structure of *Iars* gene, exon3-exon4 of *Iars*-206(ENSMUST00000165316.7) transcript is recommended as the knockout region. The region contains 277bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Iars* 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.

- The *Iars* gene is located on the Chr13. 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)

Iars isoleucine-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 105148, updated on 13-Mar-2020

Summary



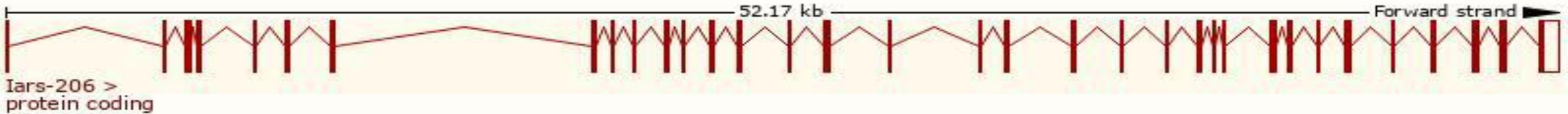
Official Symbol	Iars provided by MGI
Official Full Name	isoleucine-tRNA synthetase provided by MGI
Primary source	MGI:MGI:2145219
See related	Ensembl:ENSMUSG00000037851
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2510016L12Rik, AI327140, AU044614, E430001P04Rik, ILRS
Expression	Ubiquitous expression in liver E14 (RPKM 23.5), CNS E11.5 (RPKM 22.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

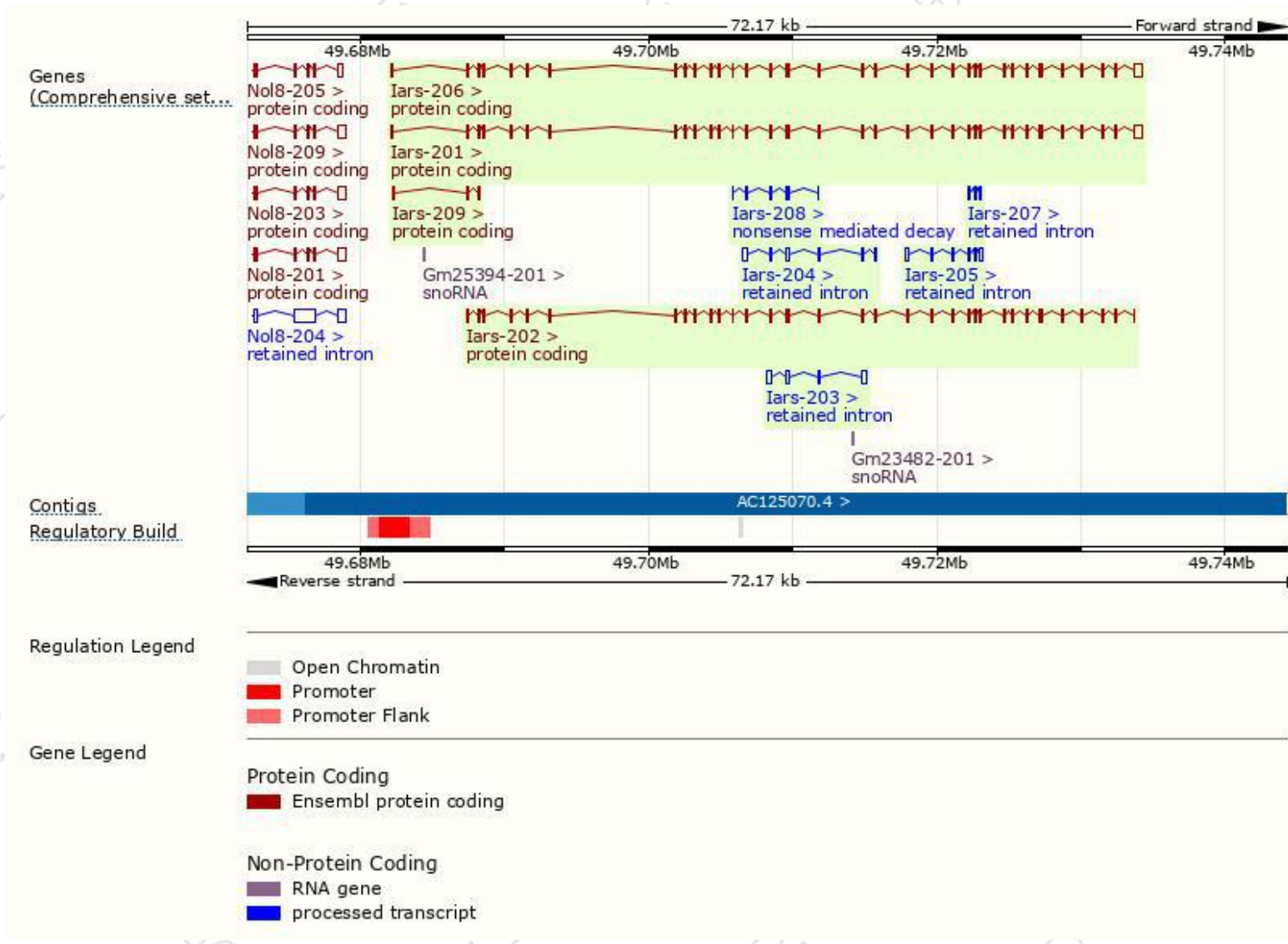
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Iars-206	ENSMUST00000165316.7	4426	1262aa	Protein coding	CCDS36659	Q8BU30	TSL:1 GENCODE basic APPRIS P1
Iars-202	ENSMUST00000164260.7	3789	1262aa	Protein coding	CCDS36659	Q8BU30	TSL:5 GENCODE basic APPRIS P1
Iars-201	ENSMUST00000047363.13	4396	1262aa	Protein coding	-	Q8BU30	TSL:5 GENCODE basic APPRIS P1
Iars-209	ENSMUST00000172254.2	401	92aa	Protein coding	-	E9Q866	CDS 3' incomplete TSL:2
Iars-208	ENSMUST00000171510.1	504	96aa	Nonsense mediated decay	-	F6Q6R1	CDS 5' incomplete TSL:3
Iars-203	ENSMUST00000164275.1	889	No protein	Retained intron	-	-	TSL:3
Iars-204	ENSMUST00000165063.7	787	No protein	Retained intron	-	-	TSL:2
Iars-205	ENSMUST00000165270.7	742	No protein	Retained intron	-	-	TSL:3
Iars-207	ENSMUST00000165656.1	356	No protein	Retained intron	-	-	TSL:2

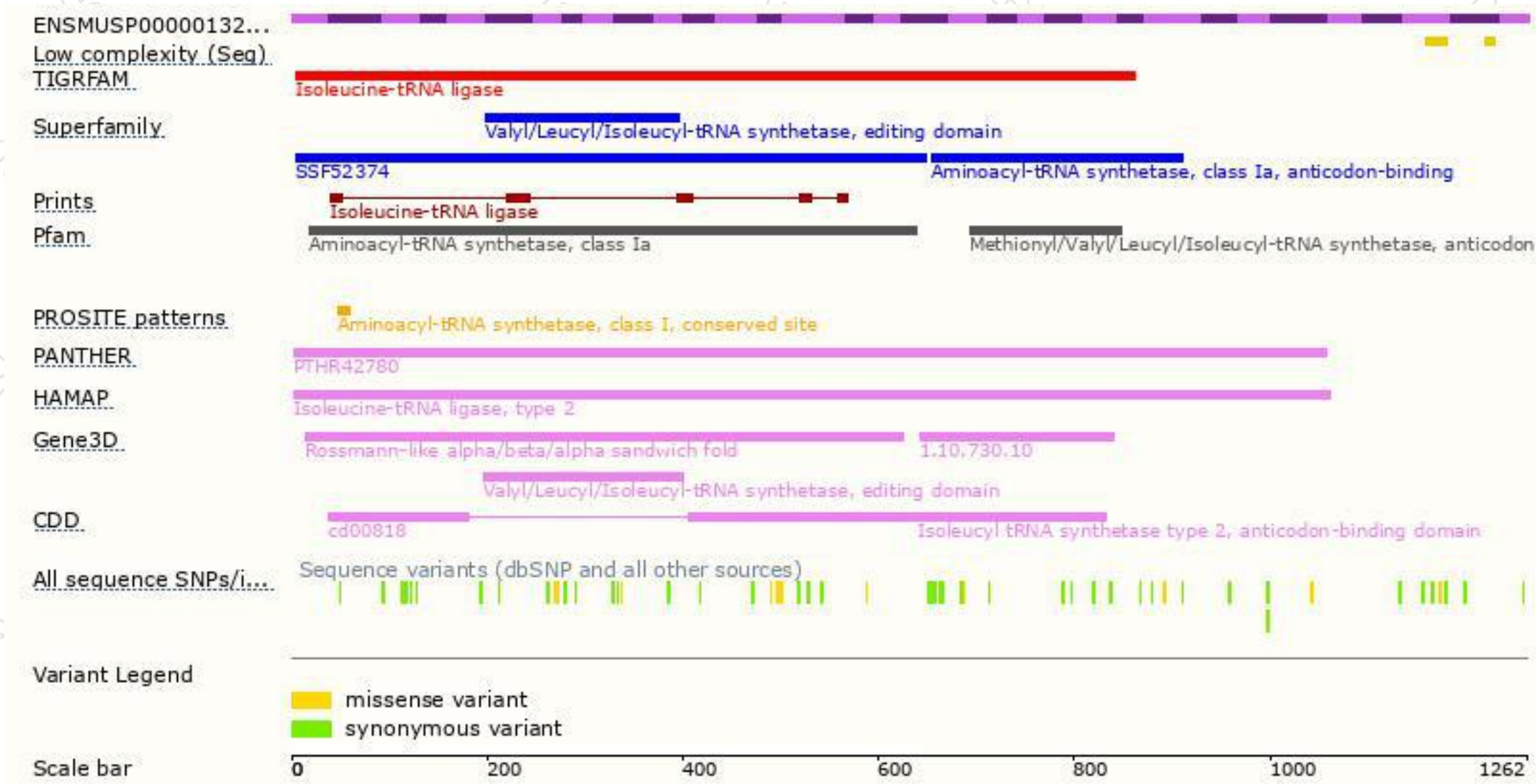
The strategy is based on the design of *Iars-206* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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