

Lars2 Cas9-KO Strategy

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Project Overview

Project Name

Lars2

Project type

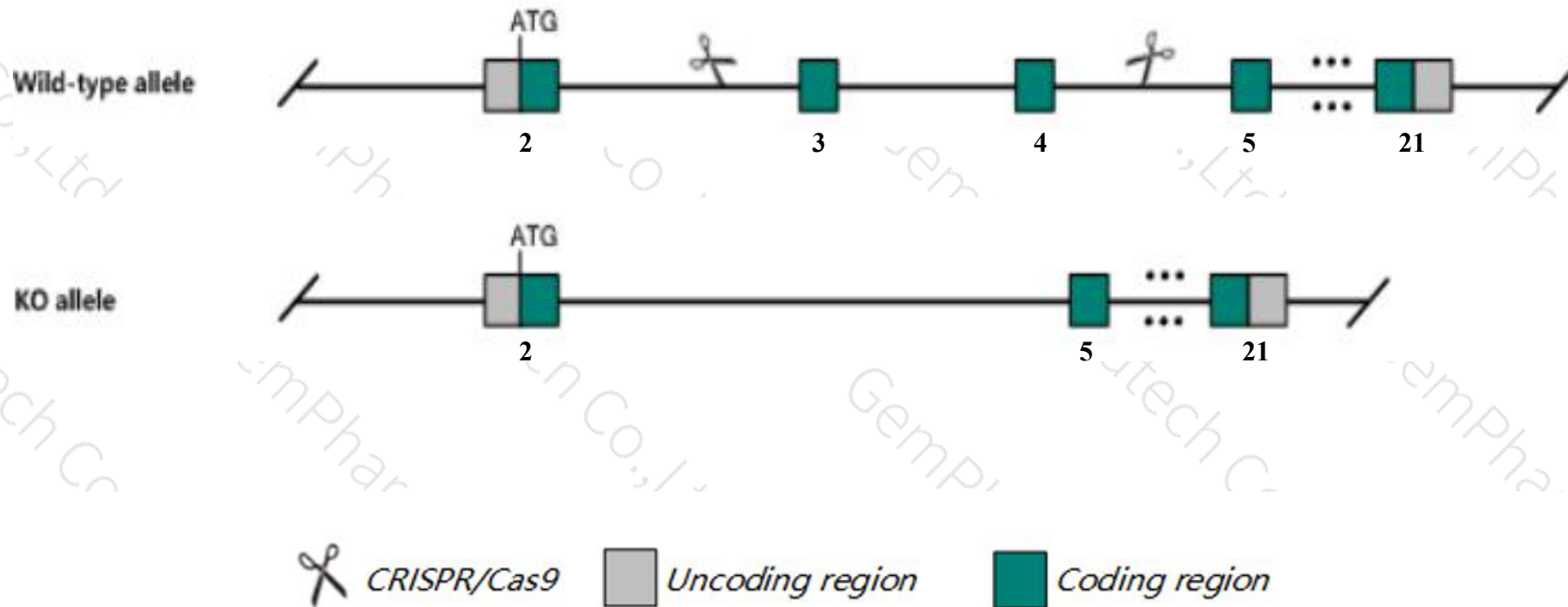
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lars2* gene. The schematic diagram is as follows:



- The *Lars2* gene has 9 transcripts. According to the structure of *Lars2* gene, exon3-exon4 of *Lars2-201* (ENSMUST00000038863.8) transcript is recommended as the knockout region. The region contains 221bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lars2* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcripts 202,203,204,205,207 may not be affected. The effect of transcripts 206,208 is unknown.
- The *Lars2* gene is located on the Chr9. 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)

Lars2 leucyl-tRNA synthetase, mitochondrial [Mus musculus (house mouse)]

Gene ID: 102436, updated on 13-Mar-2020

Summary



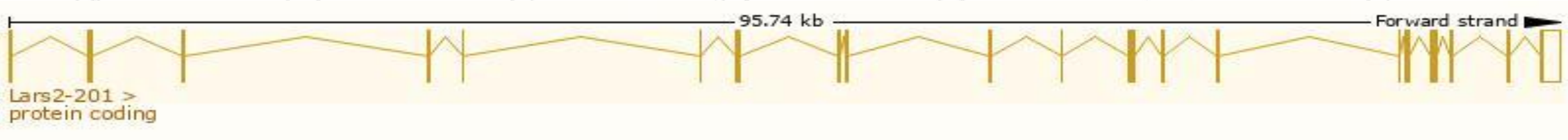
Official Symbol	Lars2 provided by MGI
Official Full Name	leucyl-tRNA synthetase, mitochondrial provided by MGI
Primary source	MGI:MGI:2142973
See related	Ensembl:ENSMUSG00000035202
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI035546, Kiaa0028, LEURS
Expression	Ubiquitous expression in cortex adult (RPKM 1105.1), placenta adult (RPKM 827.6) and 25 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

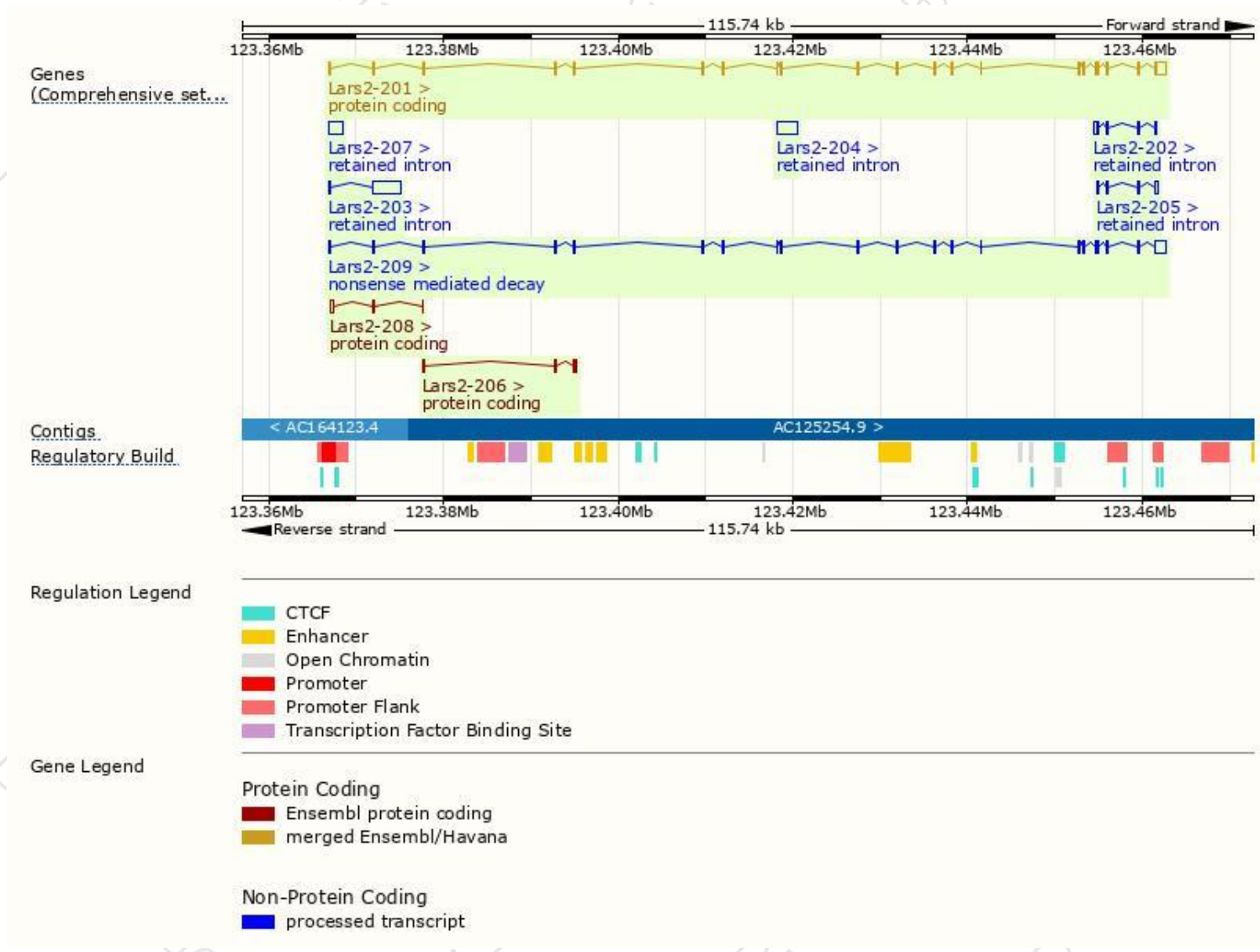
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lars2-201	ENSMUST00000038863.8	3894	902aa	Protein coding	CCDS23659	Q8VDC0	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 P1
Lars2-208	ENSMUST00000216843.1	720	88aa	Protein coding	-	A0A1L1SUS6	CDS 3' incomplete TSL:5
Lars2-206	ENSMUST00000215464.1	554	121aa	Protein coding	-	A0A1L1SQK2	CDS 5' incomplete TSL:3
Lars2-209	ENSMUST00000217116.1	3756	495aa	Nonsense mediated decay	-	A0A1L1SSW1	TSL:5
Lars2-203	ENSMUST00000214074.1	3415	No protein	Retained intron	-	-	TSL:1
Lars2-204	ENSMUST00000214557.1	2441	No protein	Retained intron	-	-	TSL:NA
Lars2-207	ENSMUST00000215674.1	1598	No protein	Retained intron	-	-	TSL:NA
Lars2-205	ENSMUST00000215087.1	889	No protein	Retained intron	-	-	TSL:3
Lars2-202	ENSMUST00000213711.1	787	No protein	Retained intron	-	-	TSL:5

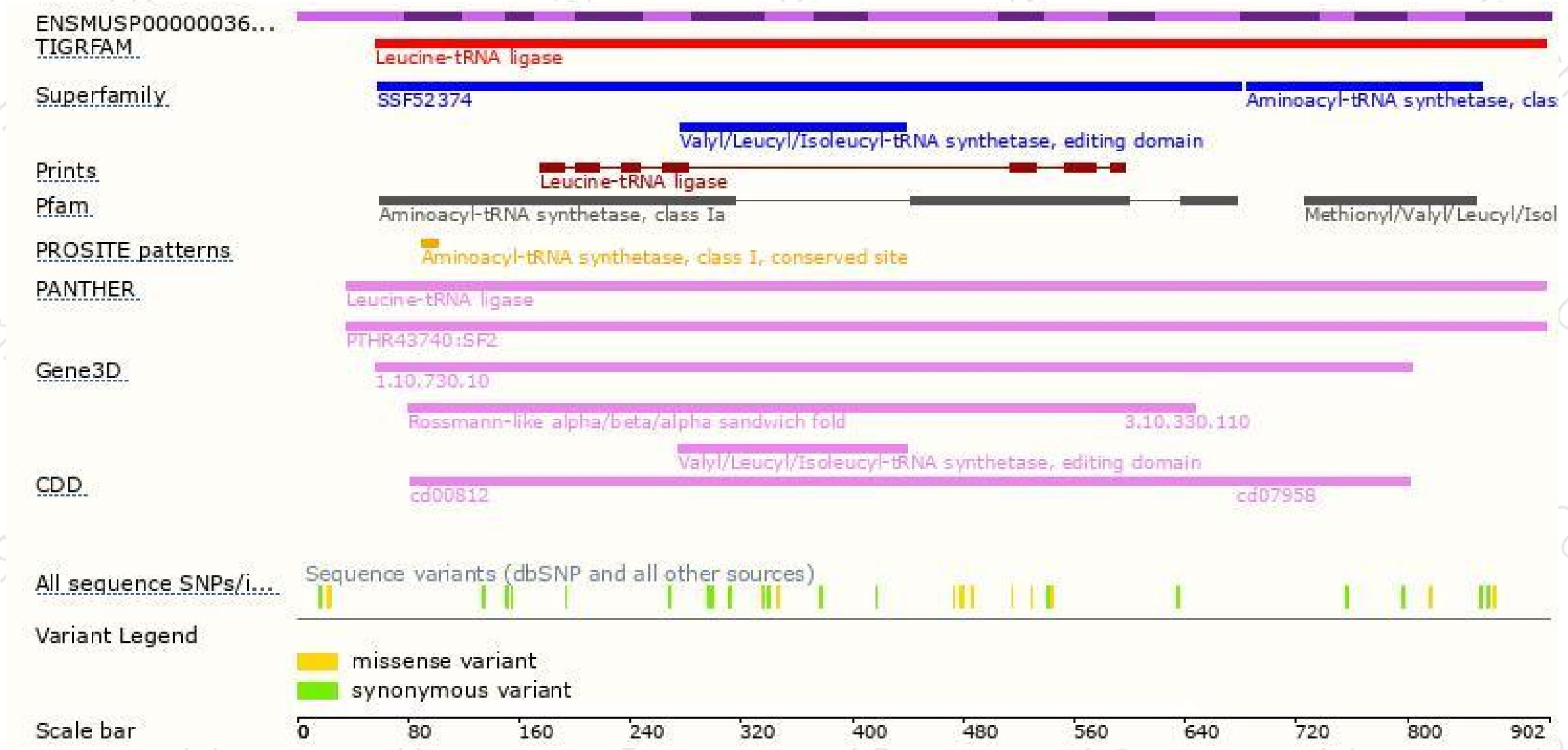
The strategy is based on the design of *Lars2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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