

Farsb Cas9-KO Strategy

Designer: Longyun Hu

Reviewer: Rui Xiong

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Project Overview

Project Name

Farsb

Project type

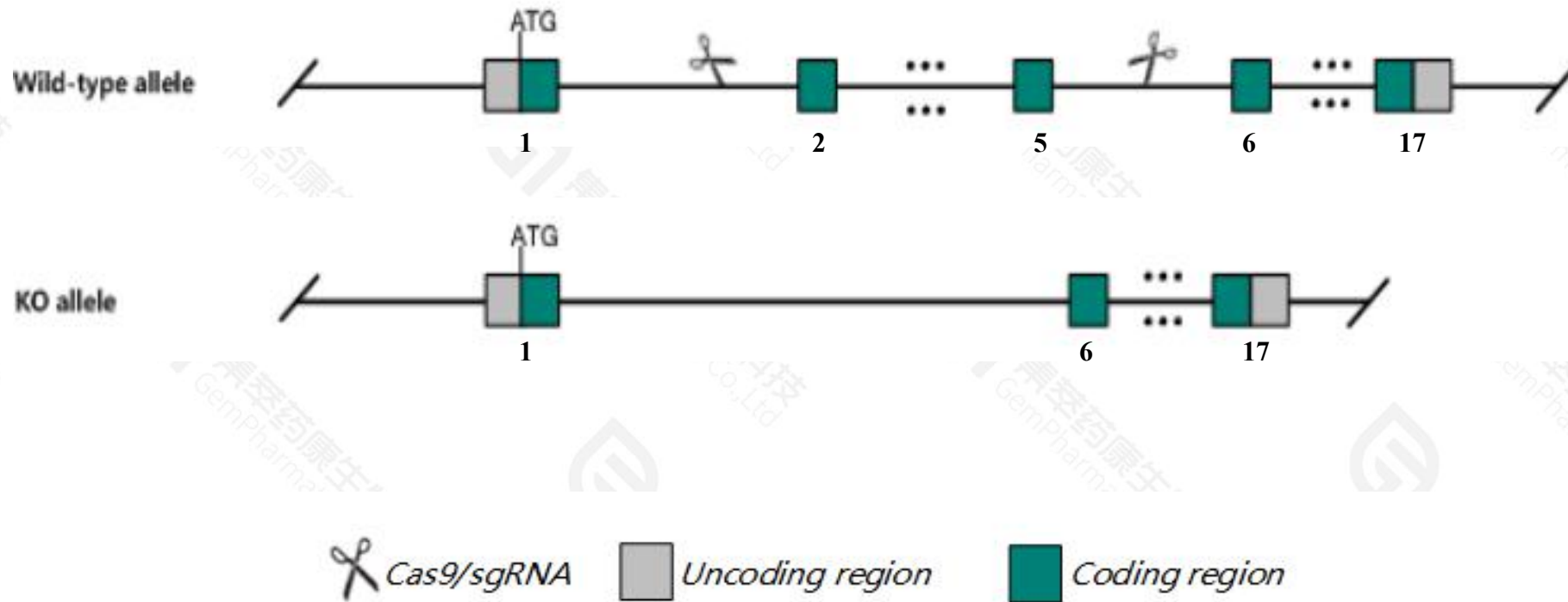
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Farsb* gene has 7 transcripts. According to the structure of *Farsb* gene, exon2-exon5 of *Farsb*-202(ENSMUST00000170217.7) transcript is recommended as the knockout region. The region contains 397bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Farsb* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 *Farsb* gene is located on the Chr1. 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.

Farsb phenylalanyl-tRNA synthetase, beta subunit [Mus musculus (house mouse)]

Gene ID: 23874, updated on 13-Mar-2020

Summary



Official Symbol Farsb provided by [MGI](#)

Official Full Name phenylalanyl-tRNA synthetase, beta subunit provided by [MGI](#)

Primary source [MGI:MGI:1346035](#)

See related [Ensembl:ENSMUSG00000026245](#)

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 C76708, Farsa, Farsl, Farslb, Frsb

Expression Ubiquitous expression in placenta adult (RPKM 23.6), liver E14 (RPKM 19.9) and 27 other tissues [See more](#)

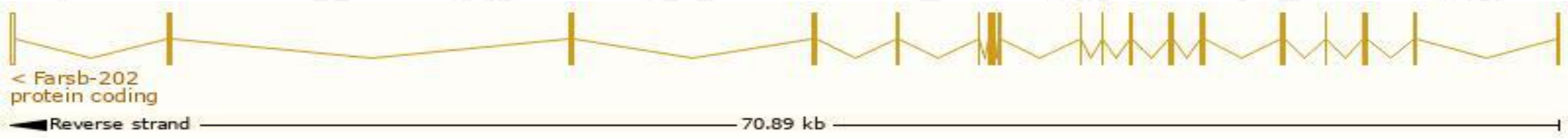
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

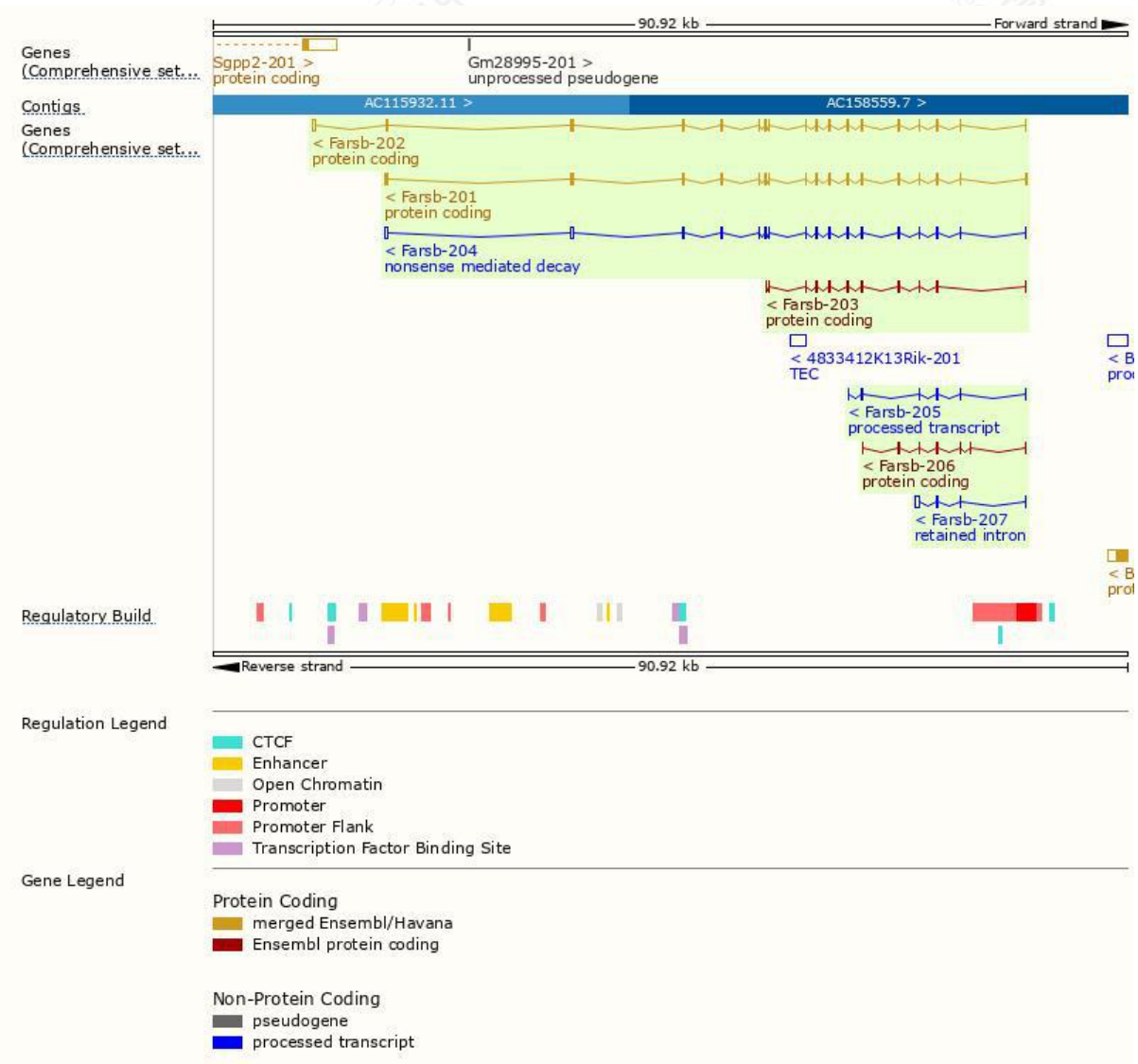
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Farsb-202	ENSMUST00000170217.7	2036	589aa	Protein coding	CCDS15084	Q9WUA2	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
Farsb-201	ENSMUST00000068333.13	1951	589aa	Protein coding	CCDS15084	Q9WUA2	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
Farsb-203	ENSMUST00000188247.6	970	237aa	Protein coding	-	A0A087WPV4	CDS 3' incomplete TSL:5
Farsb-206	ENSMUST00000190441.1	619	206aa	Protein coding	-	A0A087WS80	CDS 3' incomplete TSL:3
Farsb-204	ENSMUST00000189529.6	1801	63aa	Nonsense mediated decay	-	A0A087WQ15	TSL:1
Farsb-205	ENSMUST00000189931.6	449	No protein	Processed transcript	-	-	TSL:5
Farsb-207	ENSMUST00000191021.1	656	No protein	Retained intron	-	-	TSL:2

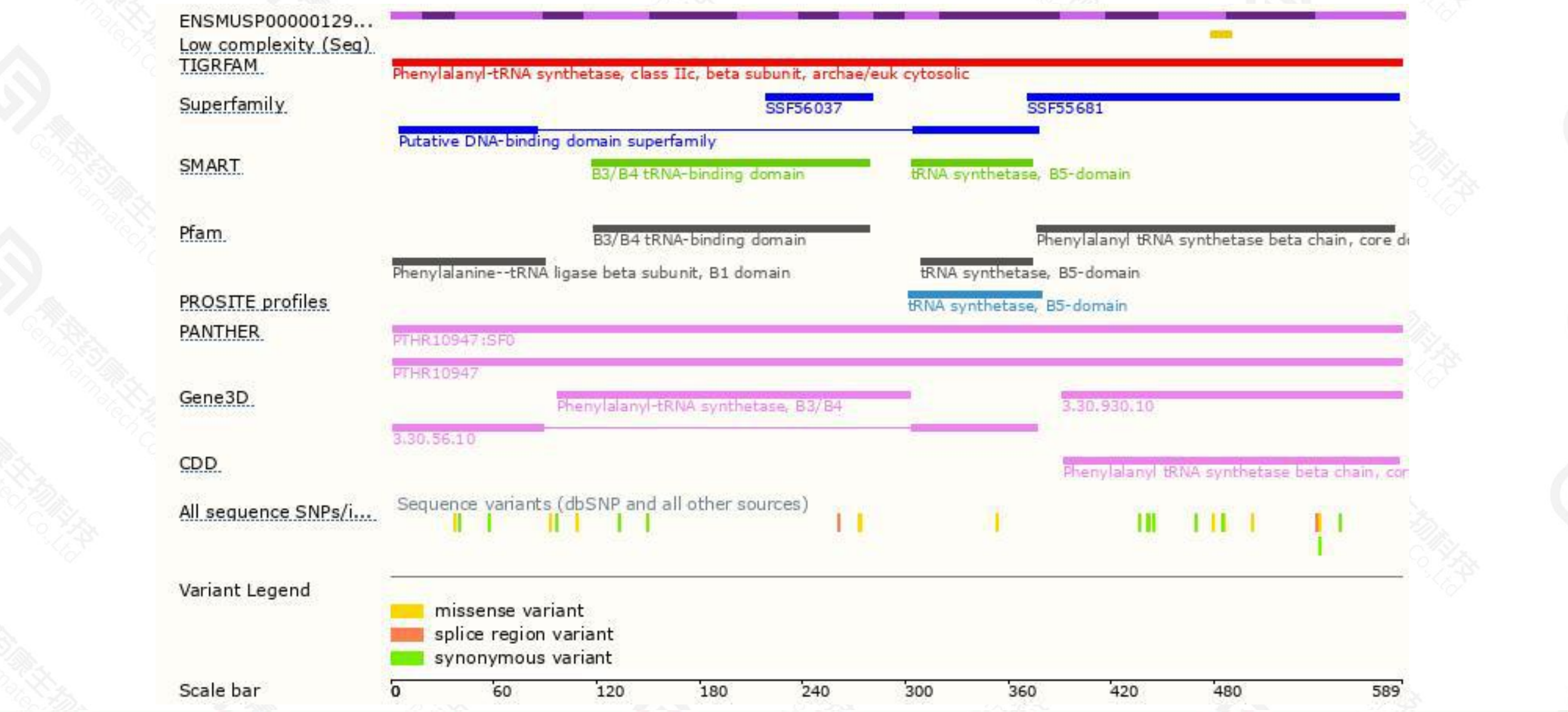
The strategy is based on the design of *Farsb-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 025-5864 1534

