

Vars Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Vars

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Vars* gene has 13 transcripts. According to the structure of *Vars* gene, exon3-exon8 of *Vars-201* (ENSMUST00000087315.13) transcript is recommended as the knockout region. The region contains 710bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vars* gene. The brief process is as follows: CRISPR/Cas9 system were

- The *Vars* gene is located on the Chr17. 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)

Vars valyl-tRNA synthetase [*Mus musculus* (house mouse)]

Gene ID: 22321, updated on 5-Jan-2020

Summary

Official Symbol Vars provided by [MGI](#)
Official Full Name valyl-tRNA synthetase provided by [MGI](#)
Primary source [MGI:MGI:90675](#)
See related [Ensembl:ENSMUSG00000007029](#)
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 G7a; Bat6; Vars2; D17H6S56E
Expression Ubiquitous expression in testis adult (RPKM 96.4), spleen adult (RPKM 86.9) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

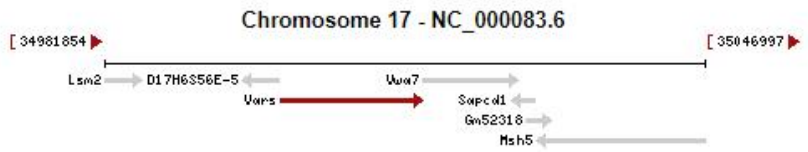
Genomic context

Location: 17 B1; 17 18.54 cM

See Vars in [Genome Data Viewer](#)

Exon count: 31

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (35000907..35016329)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (35137852..35153274)

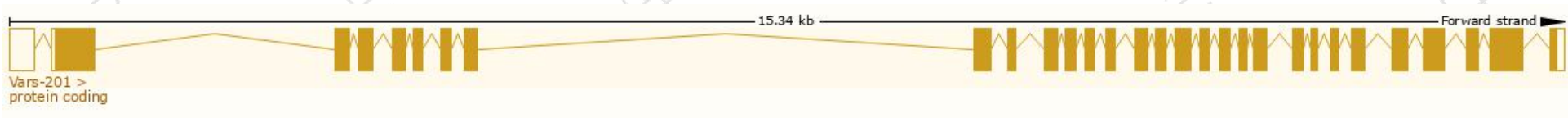


Transcript information (Ensembl)

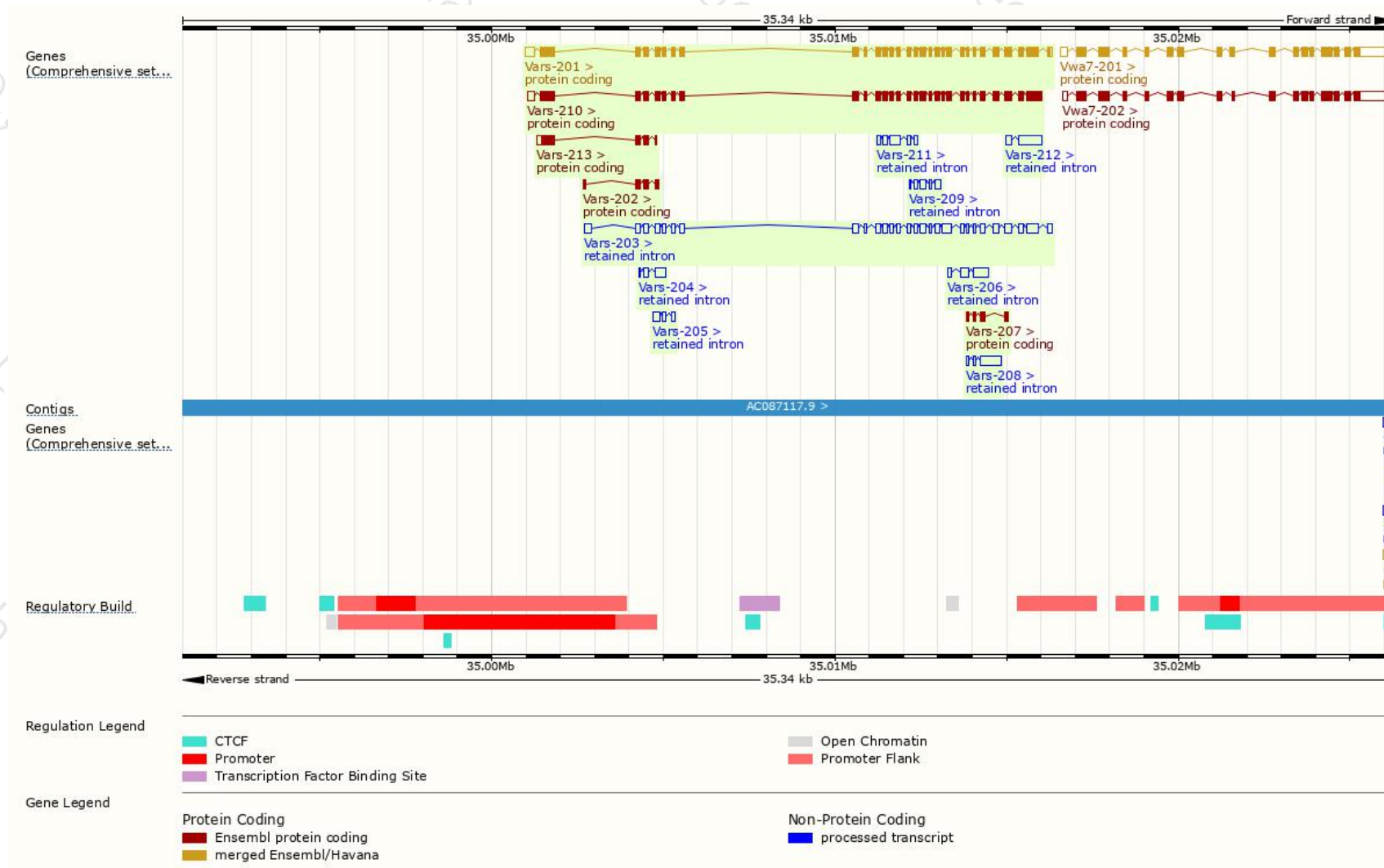
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vars-201	ENSMUST00000087315.13	4137	1263aa	Protein coding	CCDS37593	Q790I0 Q9Z1Q9	TSL:1 GENCODE basic APPRIS P1
Vars-210	ENSMUST00000173584.7	4048	1278aa	Protein coding	-	G3UY93	CDS 3' incomplete TSL:1
Vars-213	ENSMUST00000174260.7	819	230aa	Protein coding	-	G3UZ22	CDS 3' incomplete TSL:2
Vars-202	ENSMUST00000172570.1	423	125aa	Protein coding	-	G3UYW2	CDS 3' incomplete TSL:2
Vars-207	ENSMUST00000173142.1	388	130aa	Protein coding	-	G3UZX1	CDS 5' and 3' incomplete TSL:3
Vars-203	ENSMUST00000172637.7	3731	No protein	Retained intron	-	-	TSL:1
Vars-212	ENSMUST00000174084.1	826	No protein	Retained intron	-	-	TSL:3
Vars-206	ENSMUST00000172999.1	806	No protein	Retained intron	-	-	TSL:5
Vars-211	ENSMUST00000173911.1	746	No protein	Retained intron	-	-	TSL:5
Vars-208	ENSMUST00000173302.1	744	No protein	Retained intron	-	-	TSL:3
Vars-209	ENSMUST00000173336.1	557	No protein	Retained intron	-	-	TSL:2
Vars-204	ENSMUST00000172656.1	475	No protein	Retained intron	-	-	TSL:2
Vars-205	ENSMUST00000172741.1	347	No protein	Retained intron	-	-	TSL:1

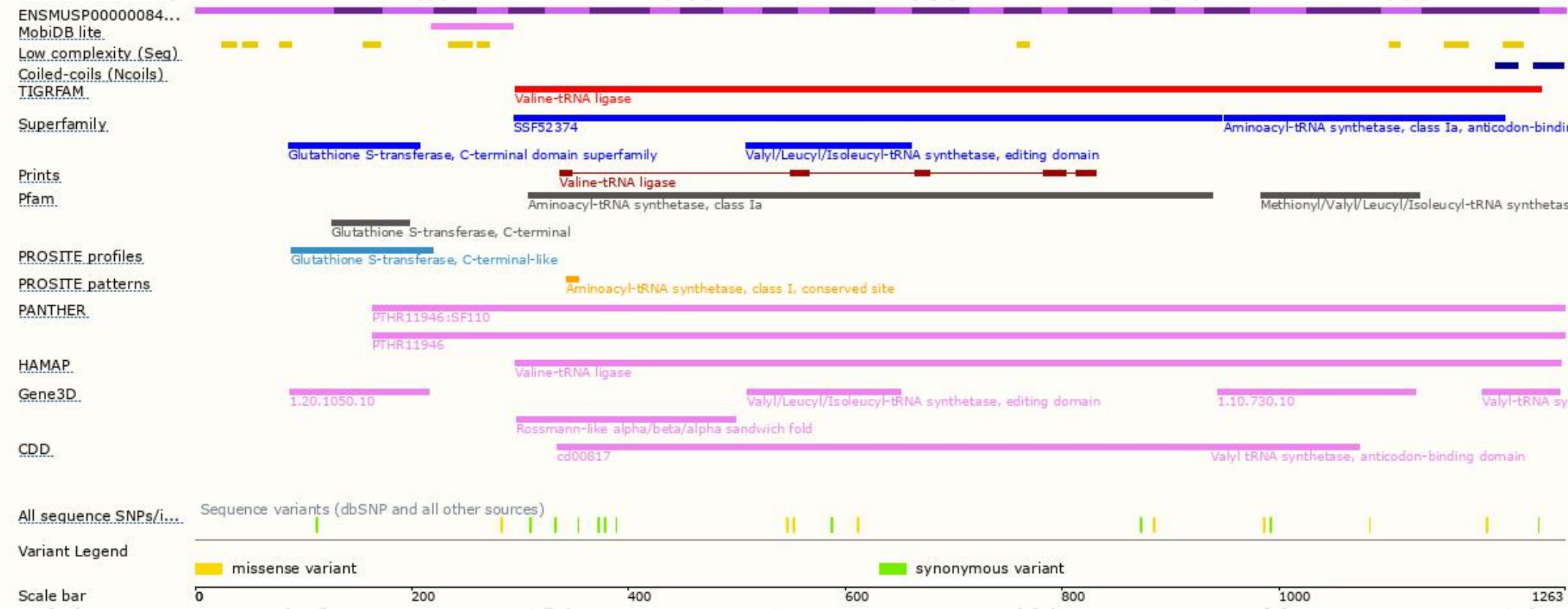
The strategy is based on the design of *Vars-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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