

Tars Cas9-KO Strategy

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Design Date:

2020-5-7

Project Overview

Project Name

Tars

Project type

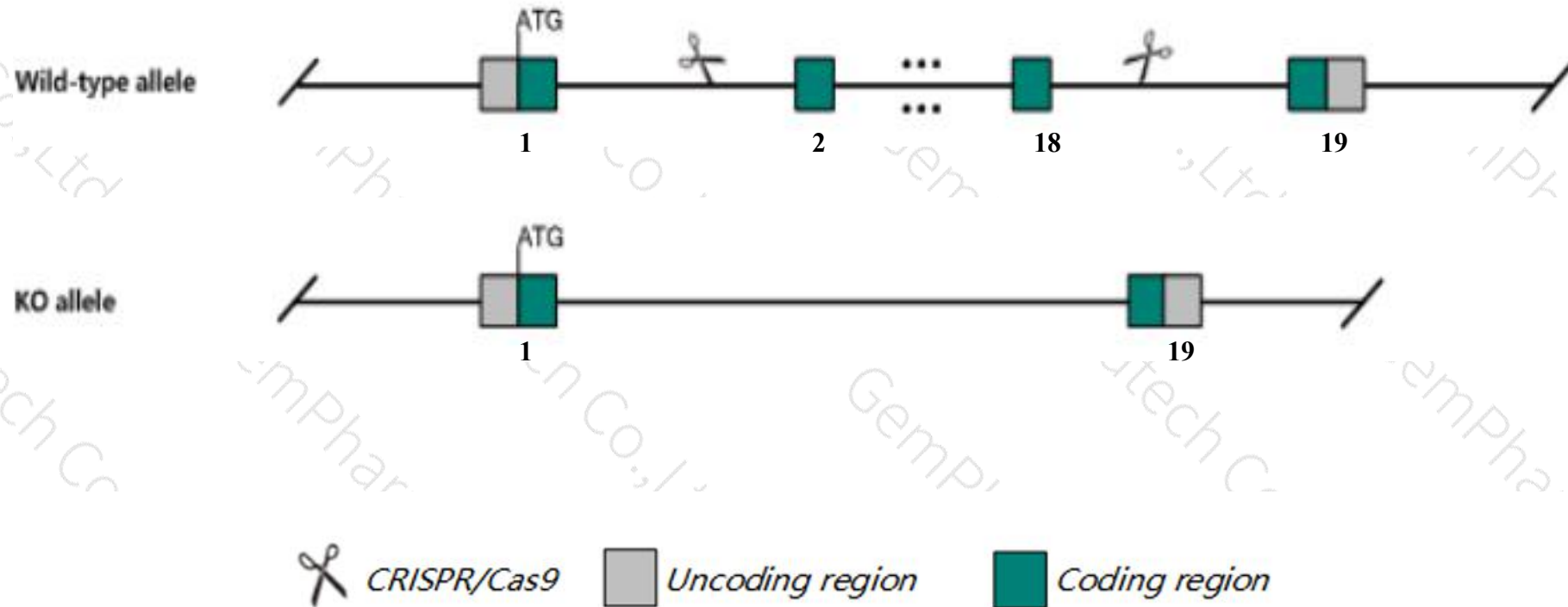
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Tars* gene has 7 transcripts. According to the structure of *Tars* gene, exon2-exon18 of *Tars-201* (ENSMUST00000022849.6) transcript is recommended as the knockout region. The region contains 1966bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tars* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Tars* gene is located on the Chr15. 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)

Tars threonyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 110960, updated on 13-Mar-2020

Summary



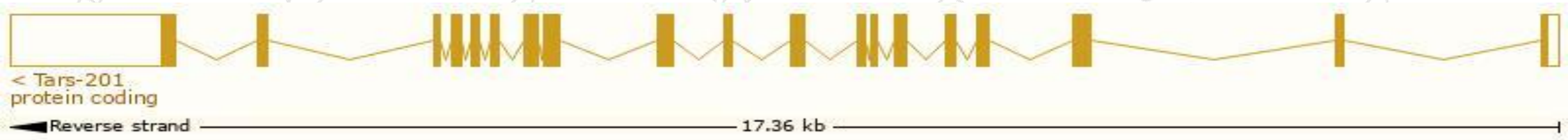
Official Symbol	Tars provided by MGI
Official Full Name	threonyl-tRNA synthetase provided by MGI
Primary source	MGI:MGI:106314
See related	Ensembl:ENSMUSG00000022241
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D15Wsu59e, Tars1, ThrRS
Expression	Ubiquitous expression in CNS E11.5 (RPKM 35.0), liver E14 (RPKM 27.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

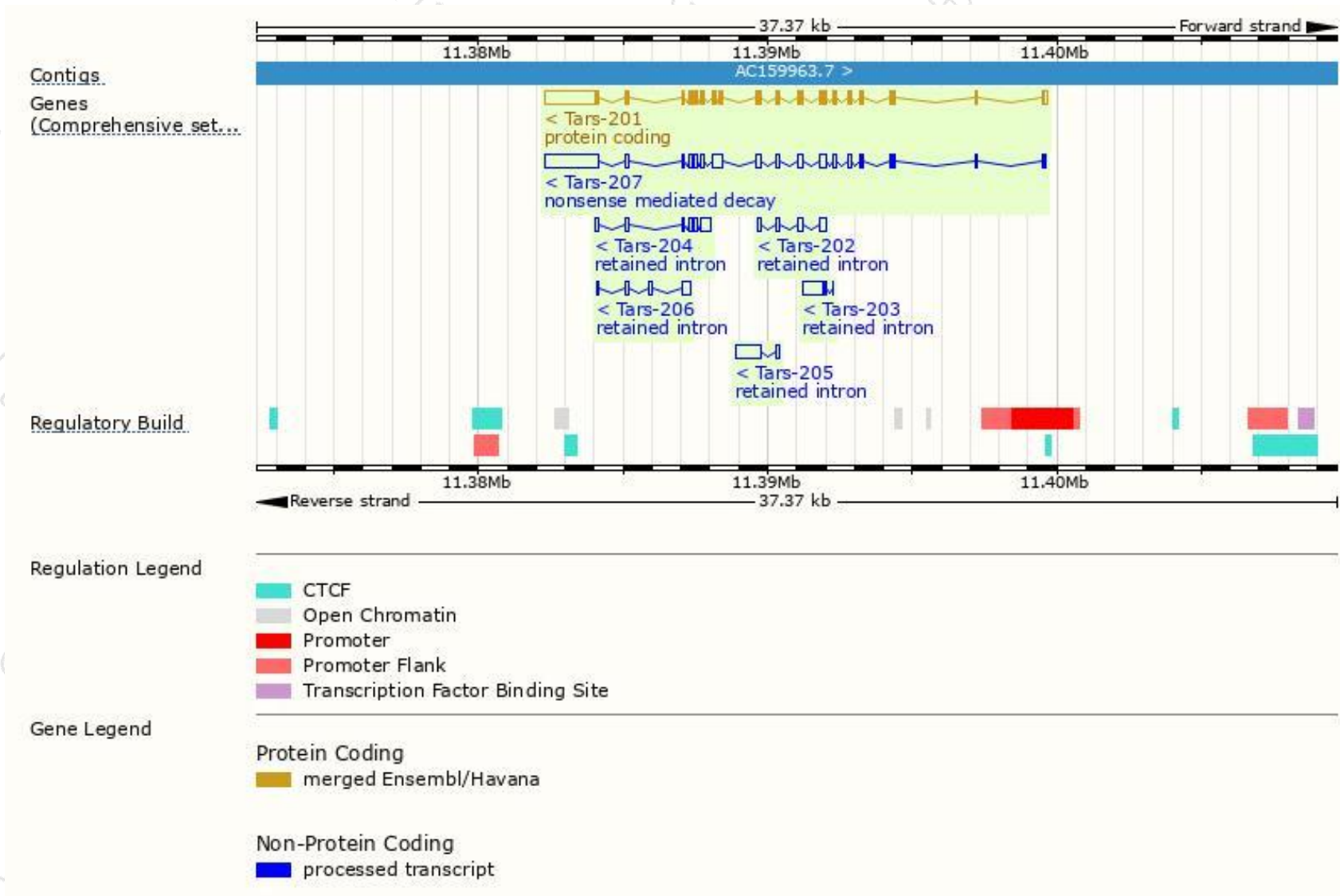
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tars-201	ENSMUST0000022849.6	4005	722aa	Protein coding	CCDS27385	Q9D0R2	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
Tars-207	ENSMUST00000228814.1	4093	119aa	Nonsense mediated decay	-	A0A2I3BPK8	
Tars-205	ENSMUST00000228207.1	916	No protein	Retained intron	-	-	
Tars-204	ENSMUST00000226944.1	859	No protein	Retained intron	-	-	
Tars-203	ENSMUST00000226904.1	785	No protein	Retained intron	-	-	
Tars-206	ENSMUST00000228710.1	617	No protein	Retained intron	-	-	
Tars-202	ENSMUST00000226597.1	539	No protein	Retained intron	-	-	

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



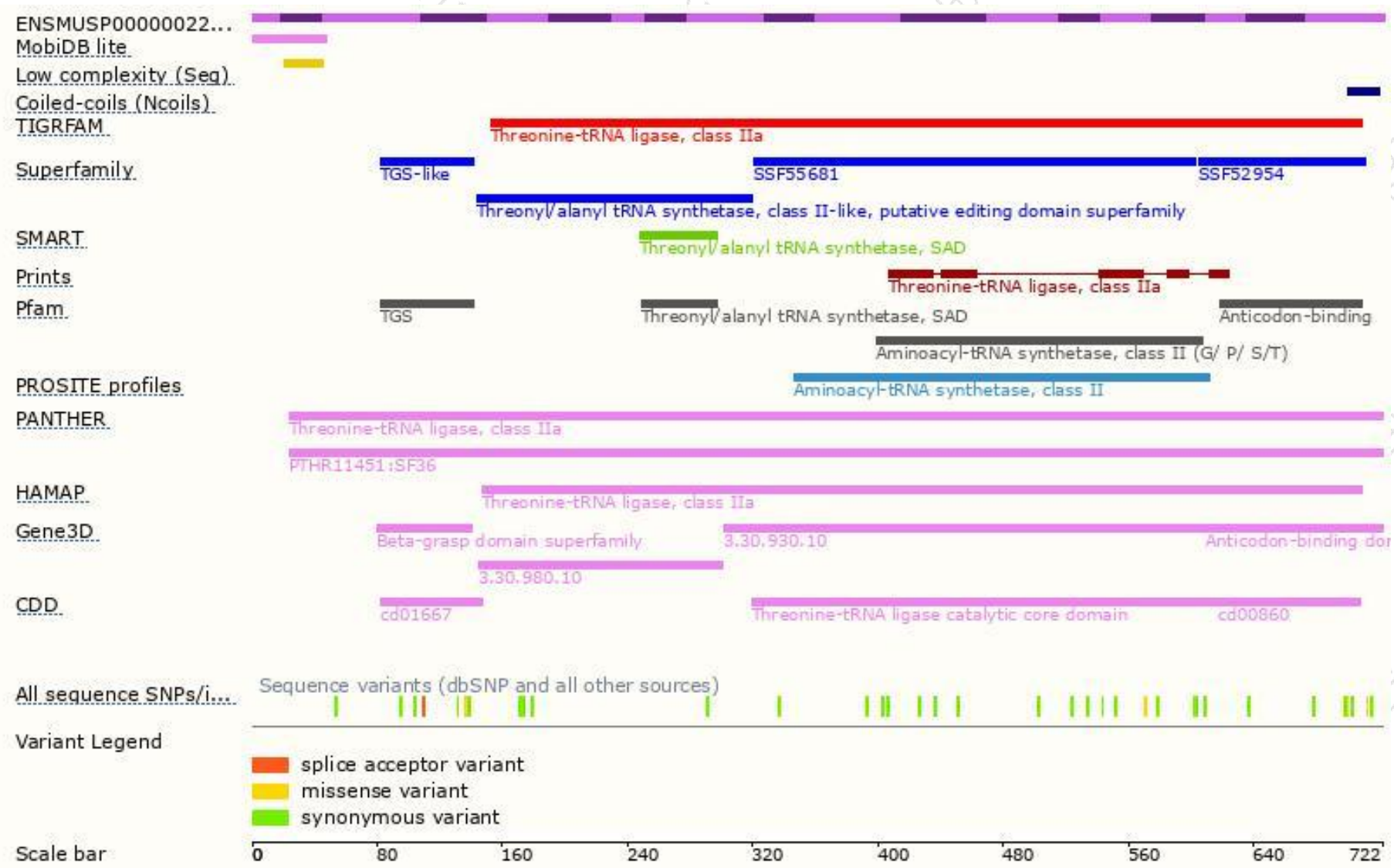
Genomic location distribution



Protein domain



集萃药康
GemPharmatech



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

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