

Yars2 Cas9-CKO Strategy

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Design Date: 2023-10-24

Overview

Target Gene Name

- Yars2

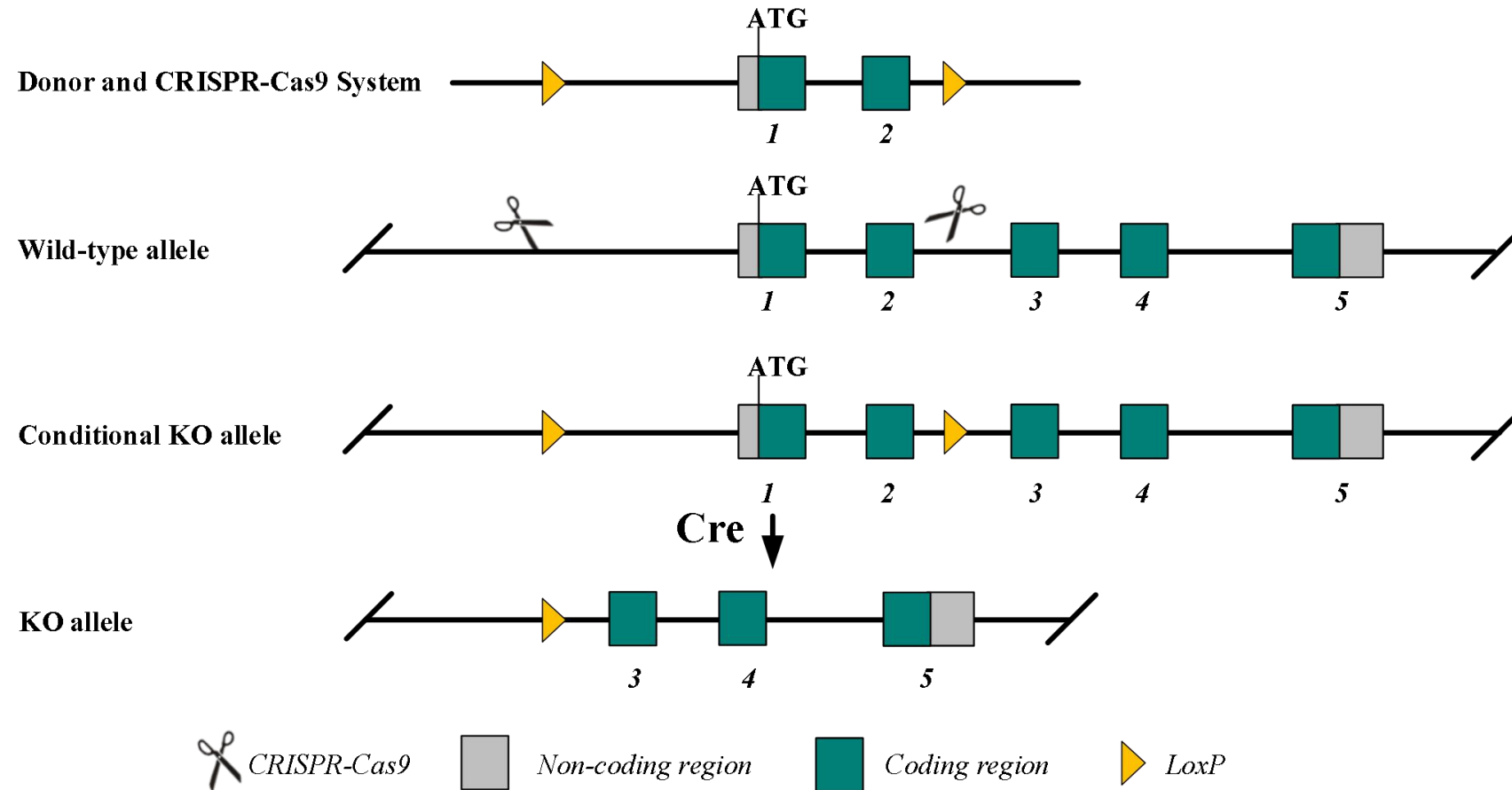
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Yars2* gene.

Technical Information

- The *Yars2* gene has 6 transcripts. According to the structure of *Yars2* gene, exon1-2 of *Yars2*-201 (ENSMUST00000059955.15) transcript is recommended as the knockout region. The region contains ATG and most of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Yars2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

Yars2 tyrosyl-tRNA synthetase 2 (mitochondrial) [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 70120, updated on 15-Oct-2023

Summary

Official Symbol	Yars2 provided by MGI
Official Full Name	tyrosyl-tRNA synthetase 2 (mitochondrial) provided by MGI
Primary source	MGI:MGI:1917370
See related	Ensembl:ENSMUSG00000022792 AllianceGenome:MGI:1917370
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	tyrRS; 2210023C10Rik
Summary	Predicted to enable several functions, including protein homodimerization activity; tyrosine binding activity; and tyrosine-tRNA ligase activity. Predicted to be involved in mitochondrial tyrosyl-tRNA aminoacylation. Predicted to act upstream of or within translation. Located in mitochondrion. Is expressed in several structures, including alimentary system; central nervous system; genitourinary system; integumental system; and respiratory system. Human ortholog(s) of this gene implicated in myopathy, lactic acidosis, and sideroblastic anemia 2. Orthologous to human YARS2 (tyrosyl-tRNA synthetase 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 30.6), ovary adult (RPKM 17.1) and 28 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

Location: 16 A2; 16 10.11 cM

See Yars2 in [Genome Data Viewer](#)

Exon count: 5

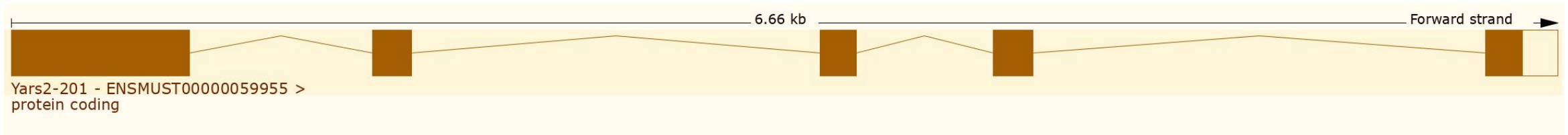
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 6 transcripts, all transcript are shown below:

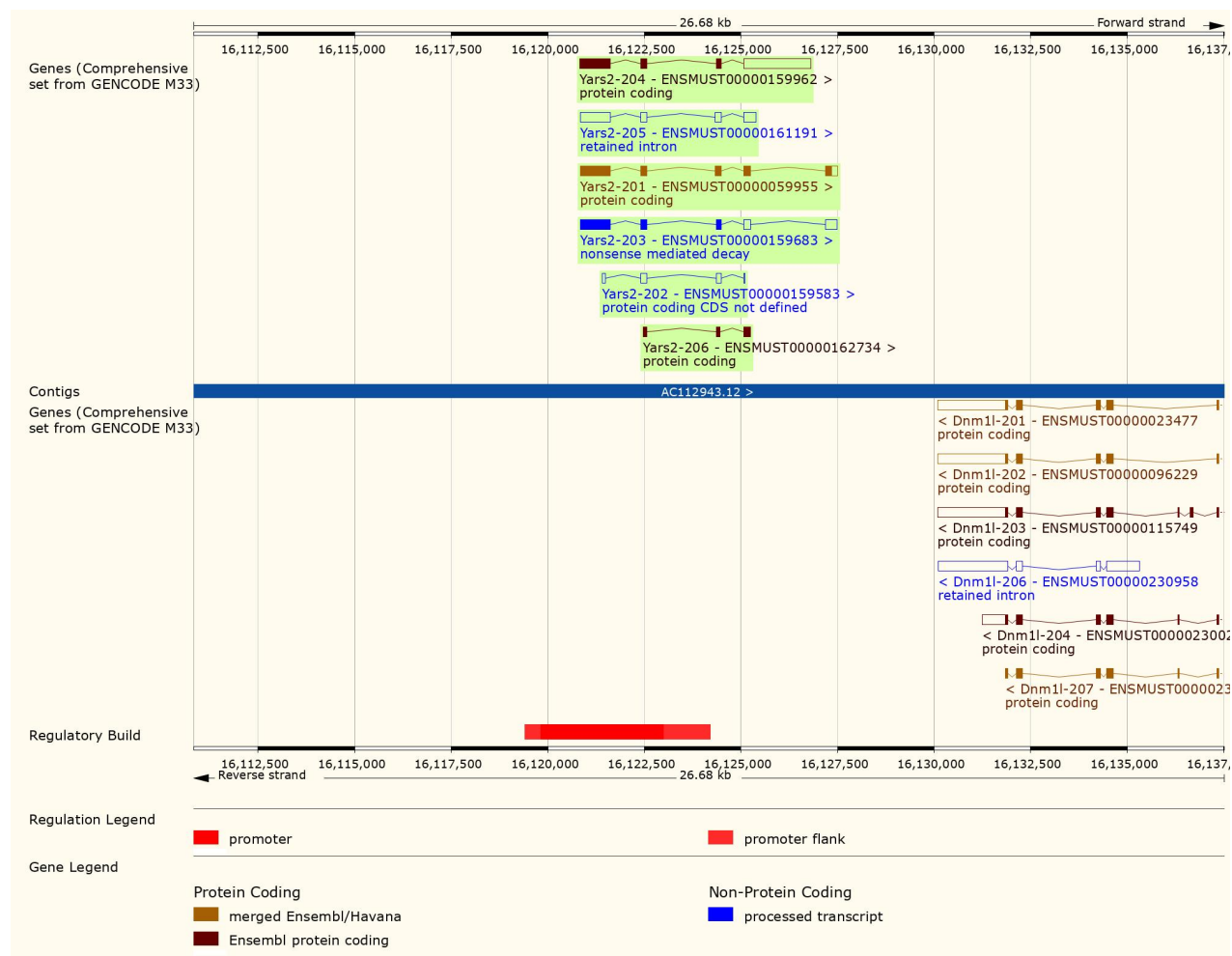
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000059955.15	Yars2-201	1574	472aa	Protein coding	CCDS27983	Q8BYL4	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000159962.8	Yars2-204	2805	349aa	Protein coding		E9PX65	GENCODE basic TSL:2
ENSMUST00000162734.3	Yars2-206	377	125aa	Protein coding		F7BWC1	TSL:5 CDS 5' and 3' incomplete
ENSMUST00000159683.2	Yars2-203	1528	349aa	Nonsense mediated decay		E9PX65	TSL:1
ENSMUST00000159583.2	Yars2-202	403	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000161191.8	Yars2-205	1412	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Yars2-201* transcript, the transcription is shown below:



Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Important Information

- *Yars2* is located on Chr16. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.