

Coq3 Cas9-KO Strategy

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Project Overview

Project Name

Coq3

Project type

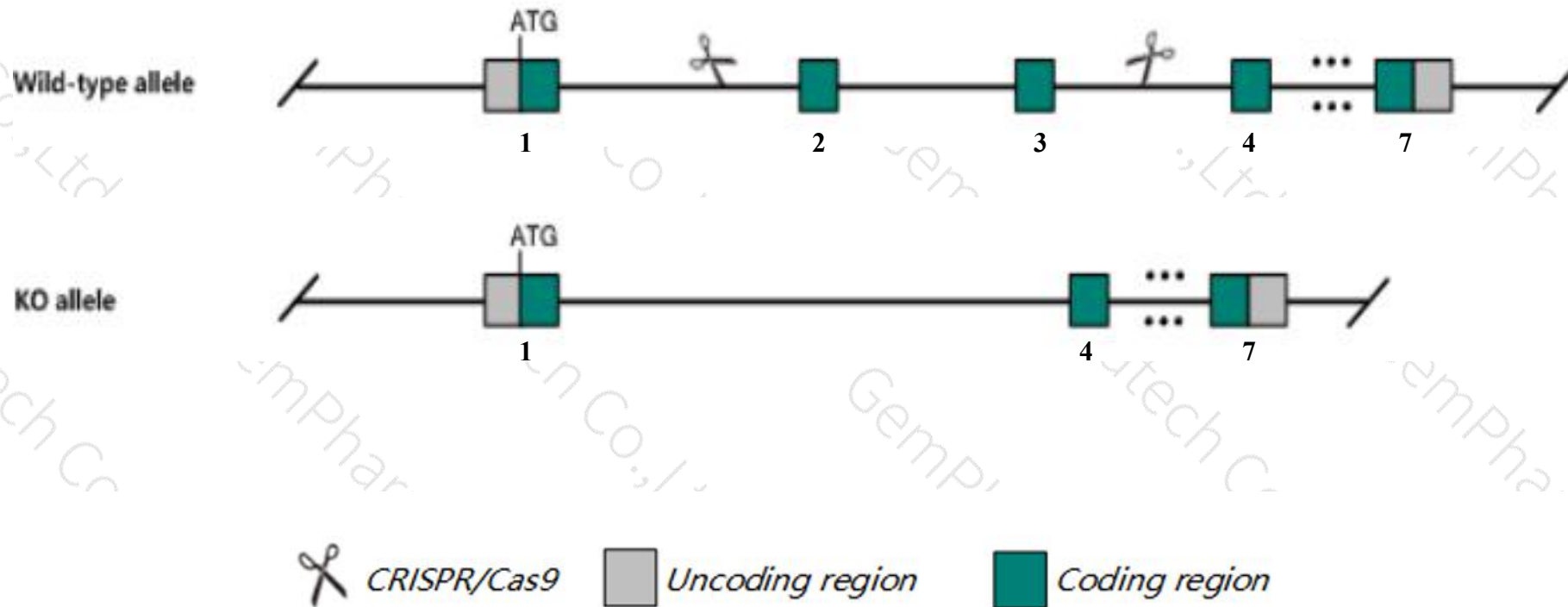
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Coq3* gene. The schematic diagram is as follows:



- The *Coq3* gene has 2 transcripts. According to the structure of *Coq3* gene, exon2-exon3 of *Coq3-201* (ENSMUST00000029909.2) transcript is recommended as the knockout region. The region contains 280bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Coq3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a null allele die in utero.
- The *Coq3* gene is located on the Chr4. 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)

Coq3 coenzyme Q3 methyltransferase [Mus musculus (house mouse)]

Gene ID: 230027, updated on 13-Mar-2020

Summary



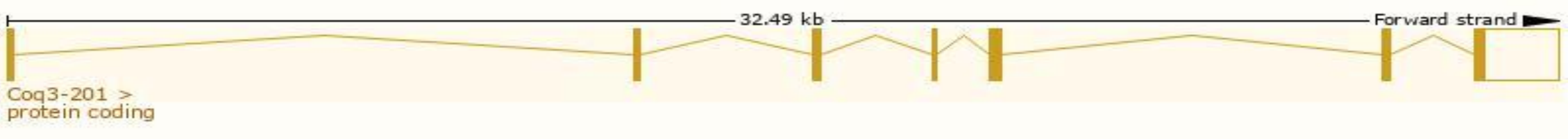
Official Symbol	Coq3 provided by MGI
Official Full Name	coenzyme Q3 methyltransferase provided by MGI
Primary source	MGI:MGI:101813
See related	Ensembl:ENSMUSG00000028247
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4732433J24, C77934
Expression	Ubiquitous expression in heart adult (RPKM 5.7), placenta adult (RPKM 4.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

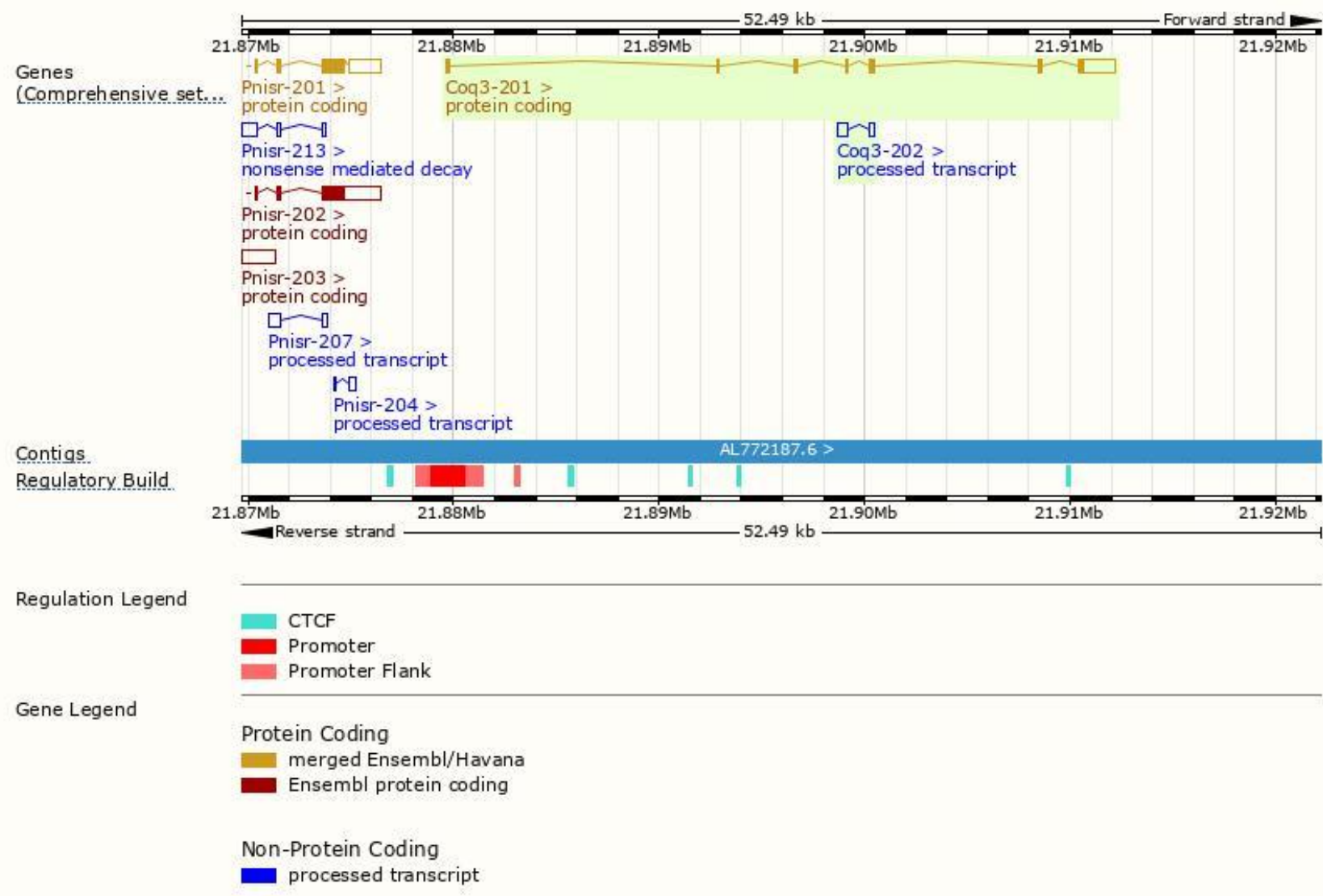
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Coq3-201	ENSMUST00000029909.2	2651	370aa	Protein coding	CCDS18003	Q8BMS4	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
Coq3-202	ENSMUST00000142244.1	628	No protein	Processed transcript	-	-	TSL:3

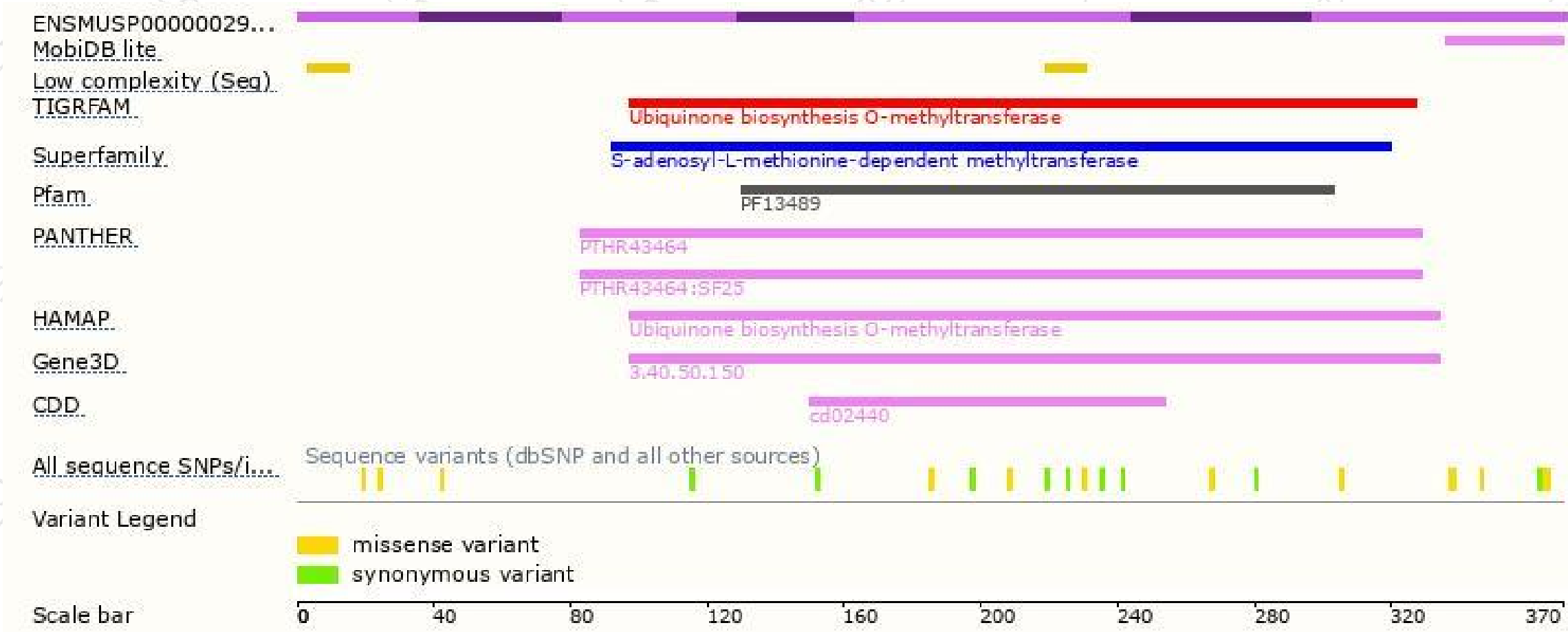
The strategy is based on the design of *Coq3-201* transcript,The transcription is shown below



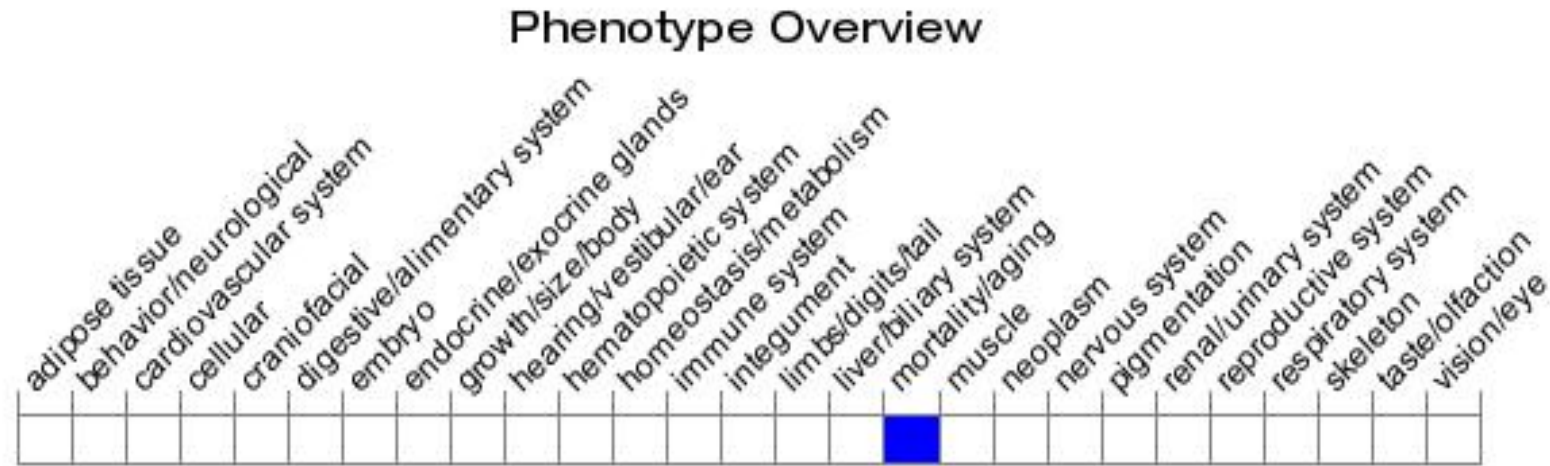
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice homozygous for a null allele die in utero.

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

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