Coq5 Cas9-CKO Strategy

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Project Overview

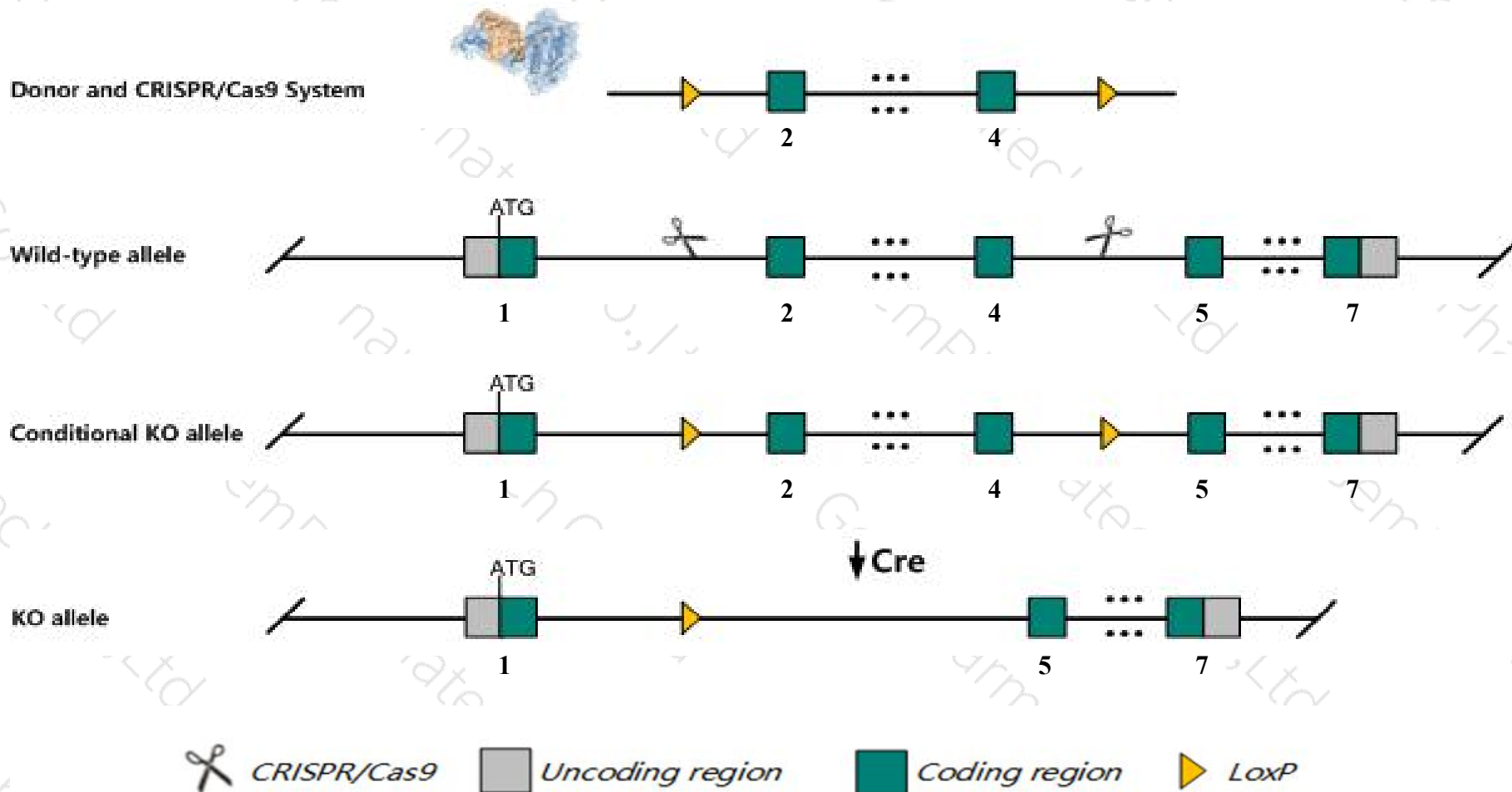|	
Project Name	*Coq5*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Coq5* gene. The schematic diagram is as follows:

Technical routes

➢ The *Coq5* gene has 3 transcripts. According to the structure of *Coq5* gene, exon2-exon4 of *Coq5-201* (ENSMUST00000040421.10) transcript is recommended as the knockout region.The region contains 479bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Coq5* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➢ 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.

Notice

➢ Transcript 203 may not be affected.

➢ *Gm13829*-201 gene may be destroyed.

➢ The *Coq5* gene is located on the Chr5. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Coq5 coenzyme Q5 methyltransferase [Mus musculus (house mouse)]
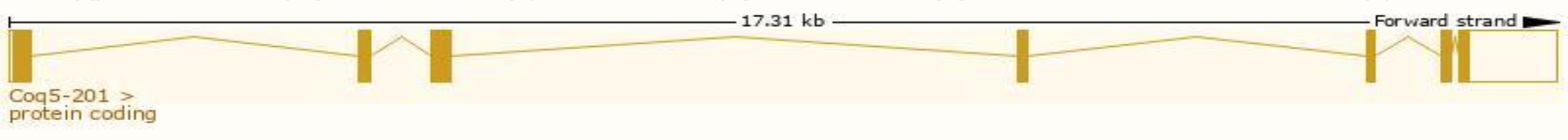
Gene ID: 52064, updated on 13-Mar-2020

Summary

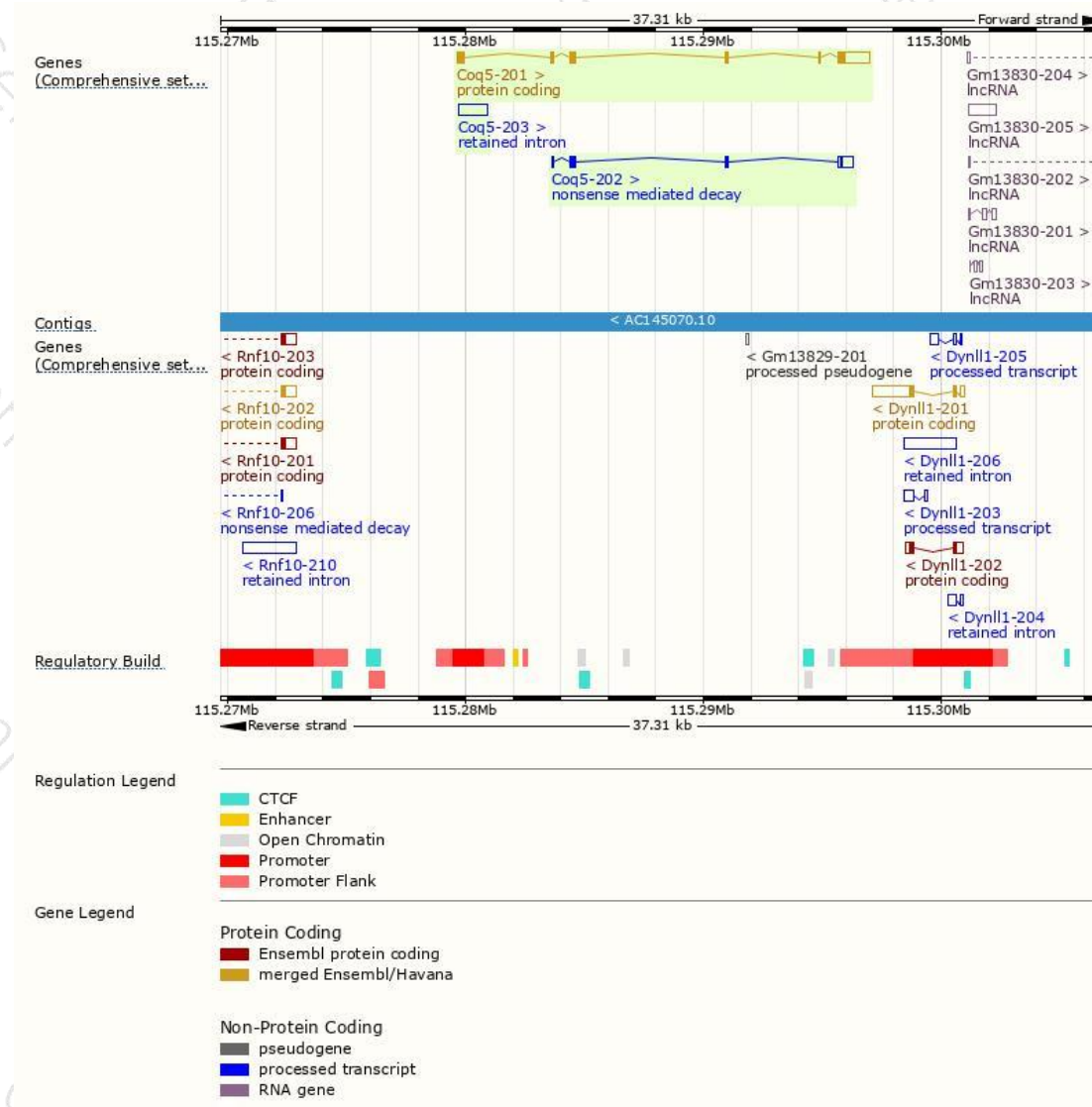|	
Official Symbol	Coq5 provided by MGI
Official Full Name	coenzyme Q5 methyltransferase provided by MGI
Primary source	MGI:MGI:1098643
See related	Ensembl:ENSMUSG00000041733
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810014G04Rik, D5Ertd33e
Expression	Ubiquitous expression in heart adult (RPKM 22.2), cerebellum adult (RPKM 9.6) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Coq5-201	ENSMUST00000040421.10	2037	327aa	Protein coding	CCDS19585	Q9CXI0	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
Coq5-202	ENSMUST00000129024.1	954	135aa	Nonsense mediated decay	-	F6X4L9	CDS 5' incomplete TSL:3
Coq5-203	ENSMUST00000201429.1	1217	No protein	Retained intron	-	-	TSL:NA

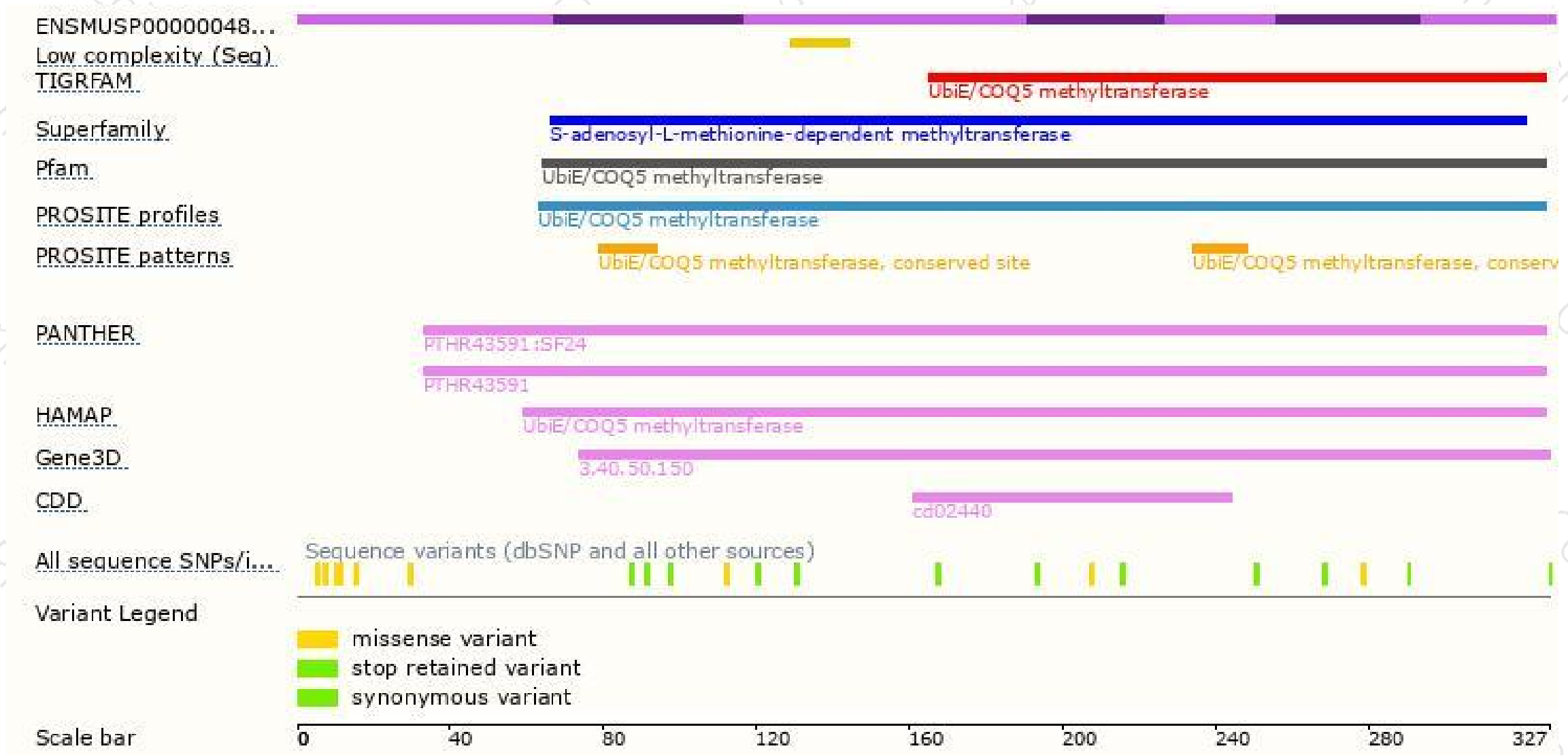The strategy is based on the design of *Coq5-201* transcript,the transcription is shown below:

Genomic location distribution

Protein domain

ENSMUSP00000048...	
Low complexity (Seg)	
TIGRFAM	UbiE/COQ5 methyltransferase
Superfamily	S-adenosyl-L-methionine-dependent methyltransferase
Pfam	UbiE/COQ5 methyltransferase
PROSITE profiles	UbiE/COQ5 methyltransferase
PROSITE patterns	UbiE/COQ5 methyltransferase, conserved site UbiE/COQ5 methyltransferase, conserv
PANTHER	PTHR43591:SF24 PTHR43591
HAMAP	UbiE/COQ5 methyltransferase
Gene3D	3.40.50.150
CDD	cd02440
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)
Variant Legend	

missense variant
stop retained variant
synonymous variant

Scale bar

0   40   80   120   160   200   240   280   327

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