

Cope Cas9-CKO Strategy

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Project Overview

Project Name

Cope

Project type

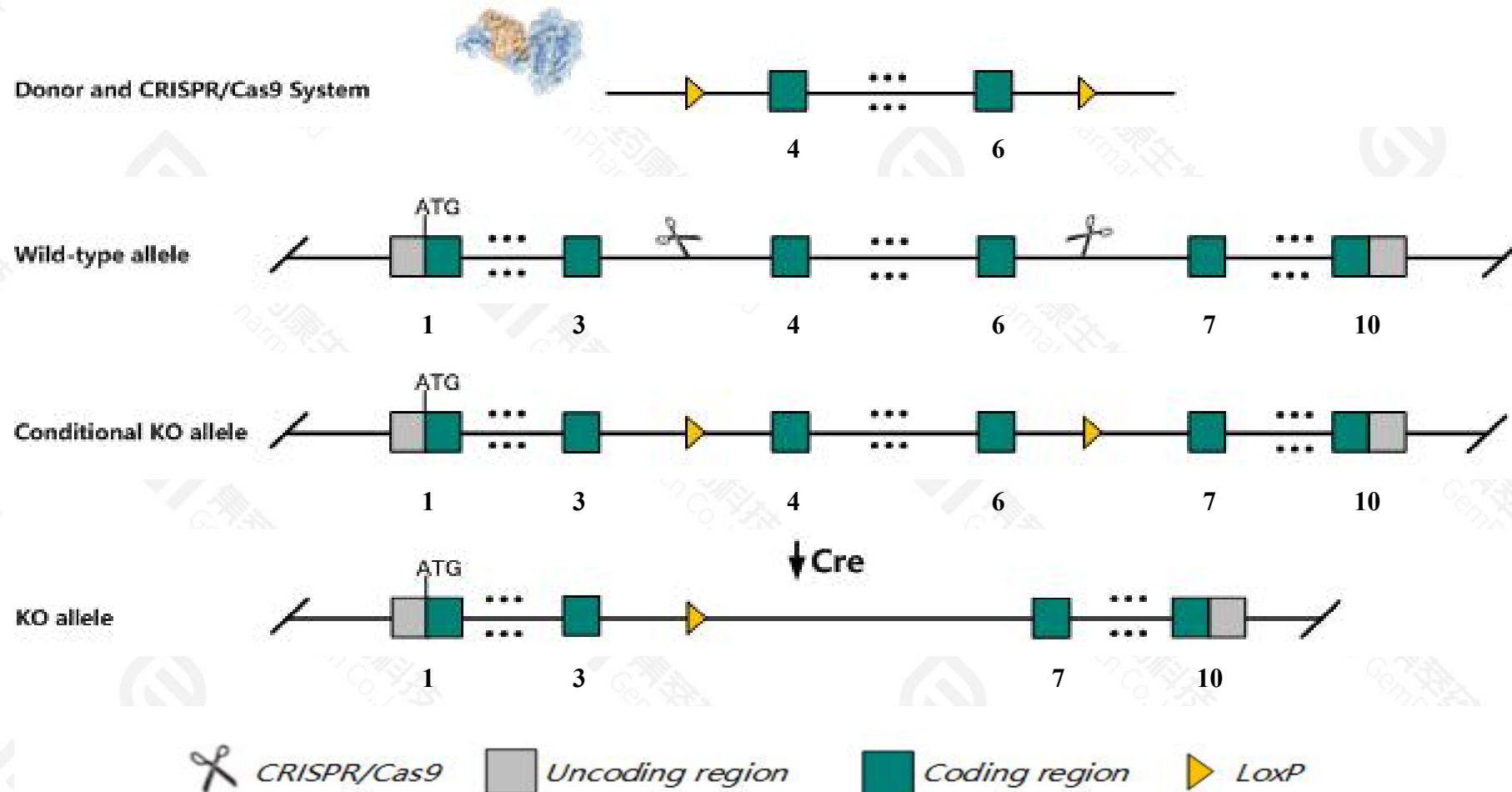
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Cope* gene has 8 transcripts. According to the structure of *Cope* gene, exon4-exon6 of *Cope-201*(ENSMUST00000066469.14) transcript is recommended as the knockout region. The region contains 289bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cope* 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.

- The *Cope* gene is located on the Chr8. 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)

Cope coatomer protein complex, subunit epsilon [Mus musculus (house mouse)]

Gene ID: 59042, updated on 12-Feb-2021

Summary



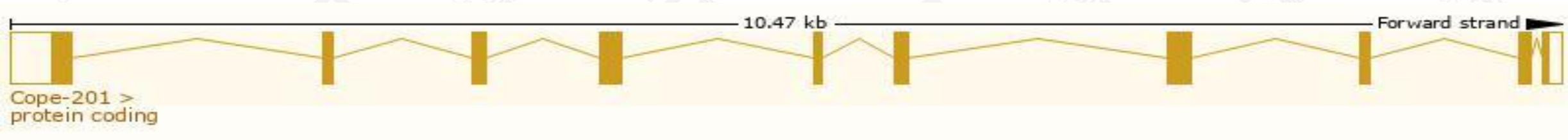
Official Symbol	Cope provided by MGI
Official Full Name	coatomer protein complex, subunit epsilon provided by MGI
Primary source	MGI:MGI:1891702
See related	Ensembl:ENSMUSG00000055681
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110005D17Rik, Cop, Cope1
Expression	Ubiquitous expression in duodenum adult (RPKM 240.8), ovary adult (RPKM 233.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

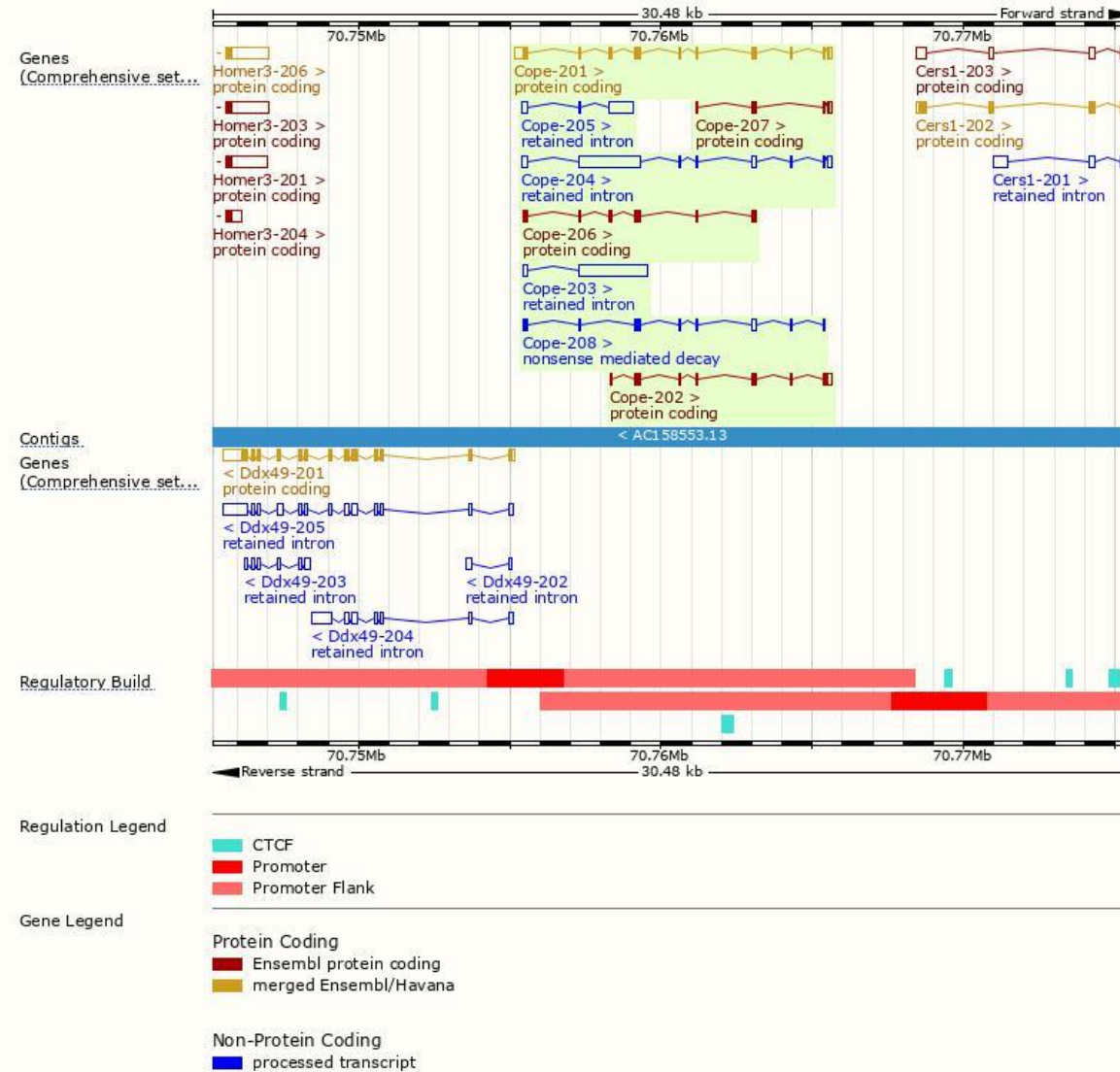
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cope-201	ENSMUST00000066469.14	1300	308aa	Protein coding	CCDS22365		TSL:1 , GENCODE basic , APPRIS P1 ,
Cope-202	ENSMUST00000128003.8	837	234aa	Protein coding	-		CDS 5' incomplete , TSL:3 ,
Cope-206	ENSMUST00000150968.8	715	227aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Cope-207	ENSMUST00000167850.3	433	116aa	Protein coding	-		CDS 5' incomplete , TSL:2 ,
Cope-208	ENSMUST00000168018.2	781	112aa	Nonsense mediated decay	-		TSL:5 ,
Cope-204	ENSMUST00000134822.8	2753	No protein	Retained intron	-		TSL:1 ,
Cope-203	ENSMUST00000128822.2	2429	No protein	Retained intron	-		TSL:1 ,
Cope-205	ENSMUST00000140363.2	1038	No protein	Retained intron	-		TSL:2 ,

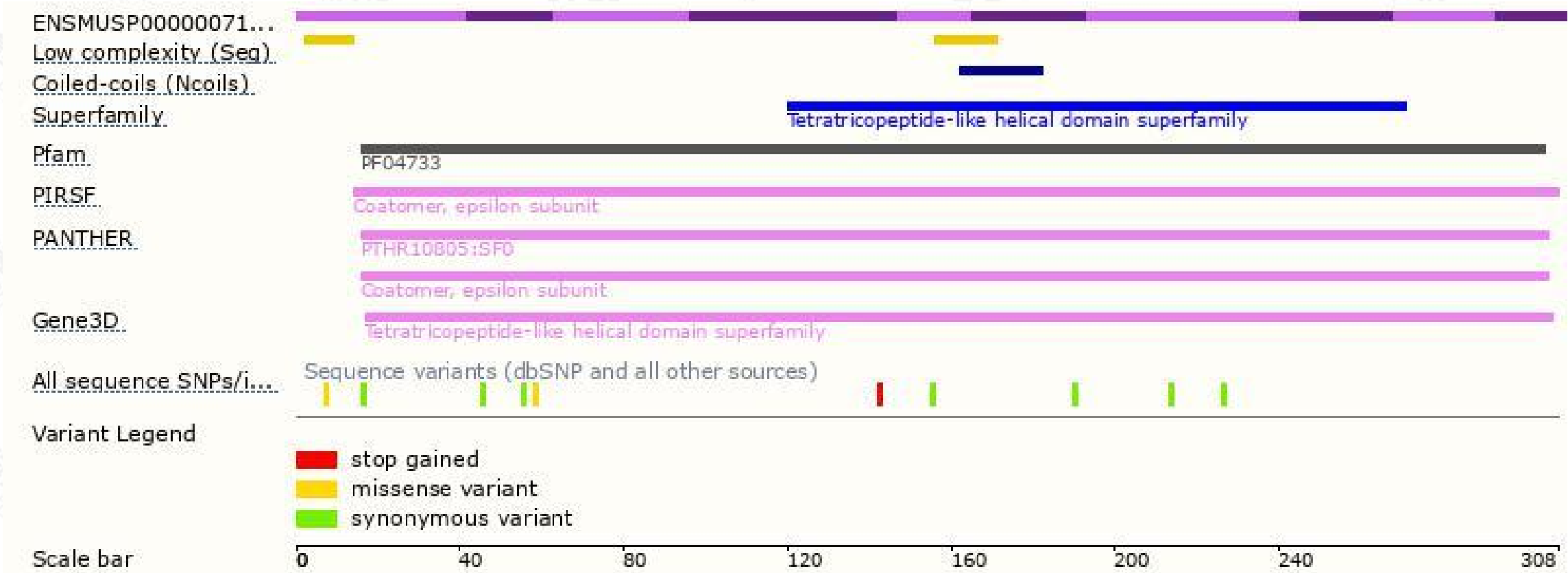
The strategy is based on the design of *Cope-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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