

***Copg2* Cas9-KO Strategy**

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Project Overview

Project Name

Copg2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Copg2* gene. The schematic diagram is as follows:



- The *Copg2* gene has 8 transcripts. According to the structure of *Copg2* gene, exon4-exon5 of *Copg2-201* (ENSMUST00000048774.12) transcript is recommended as the knockout region. The region contains 152bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Copg2* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Copg2*-205&207 may not be affected.
- The knockout region is near to the N-terminal of *4930412F09Rik* gene, this strategy may influence the regulatory function of the N-terminal of *4930412F09Rik* gene.
- The *Copg2* gene is located on the Chr6. 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)

Copg2 coatomer protein complex, subunit gamma 2 [*Mus musculus* (house mouse)]

Gene ID: 54160, updated on 27-Feb-2020

Summary

Official Symbol	Copg2 provided by MGI
Official Full Name	coatomer protein complex, subunit gamma 2 provided by MGI
Primary source	MGI:MGI:1858683
See related	Ensembl:ENSMUSG00000025607
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW227625; gamma-2-COP
Annotation information	Annotation category: suggests misassembly
Expression	Broad expression in limb E14.5 (RPKM 91.4), CNS E11.5 (RPKM 47.5) and 15 other tissues See more
Orthologs	human all

Genomic context

Location: 6; 6 A3.3 [See Copg2 in Genome Data Viewer](#)

Exon count: 25

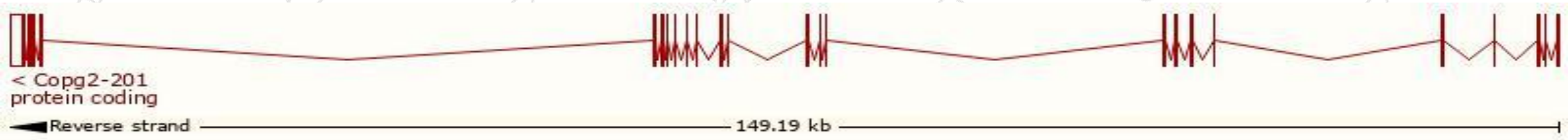
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (30747554..30896815, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (30759559..30846760, complement) , (30698411..30700638, complement)

Transcript information (Ensembl)

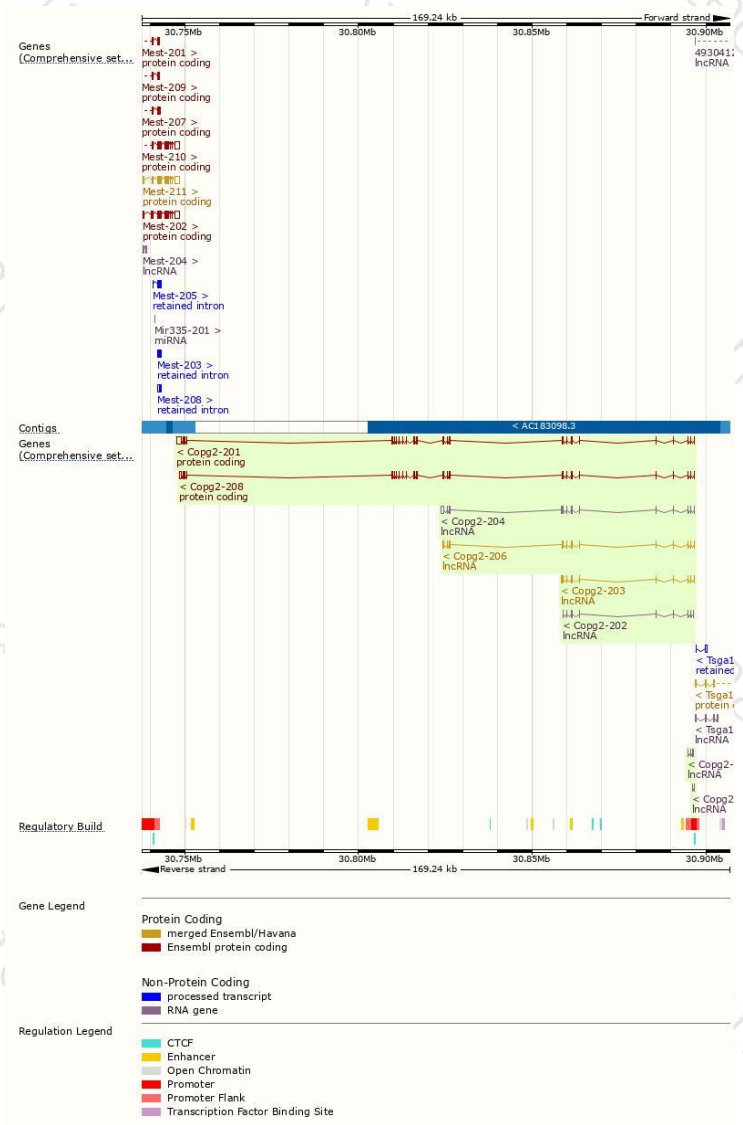
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Copg2-201	ENSMUST00000048774.12	3961	871aa	Protein coding	CCDS85027	Q9QXK3	TSL:1 GENCODE basic APPRIS P2
Copg2-208	ENSMUST00000166192.6	3155	870aa	Protein coding	-	Q9QXK3	TSL:1 APPRIS ALT 1
Copg2-204	ENSMUST00000133916.4	1915	No protein	lncRNA	-	-	TSL:2
Copg2-206	ENSMUST00000135230.7	1261	No protein	lncRNA	-	-	TSL:1
Copg2-203	ENSMUST00000131256.7	961	No protein	lncRNA	-	-	TSL:2
Copg2-202	ENSMUST00000122833.7	695	No protein	lncRNA	-	-	TSL:3
Copg2-207	ENSMUST00000151973.1	333	No protein	lncRNA	-	-	TSL:5
Copg2-205	ENSMUST00000134137.1	215	No protein	lncRNA	-	-	TSL:3

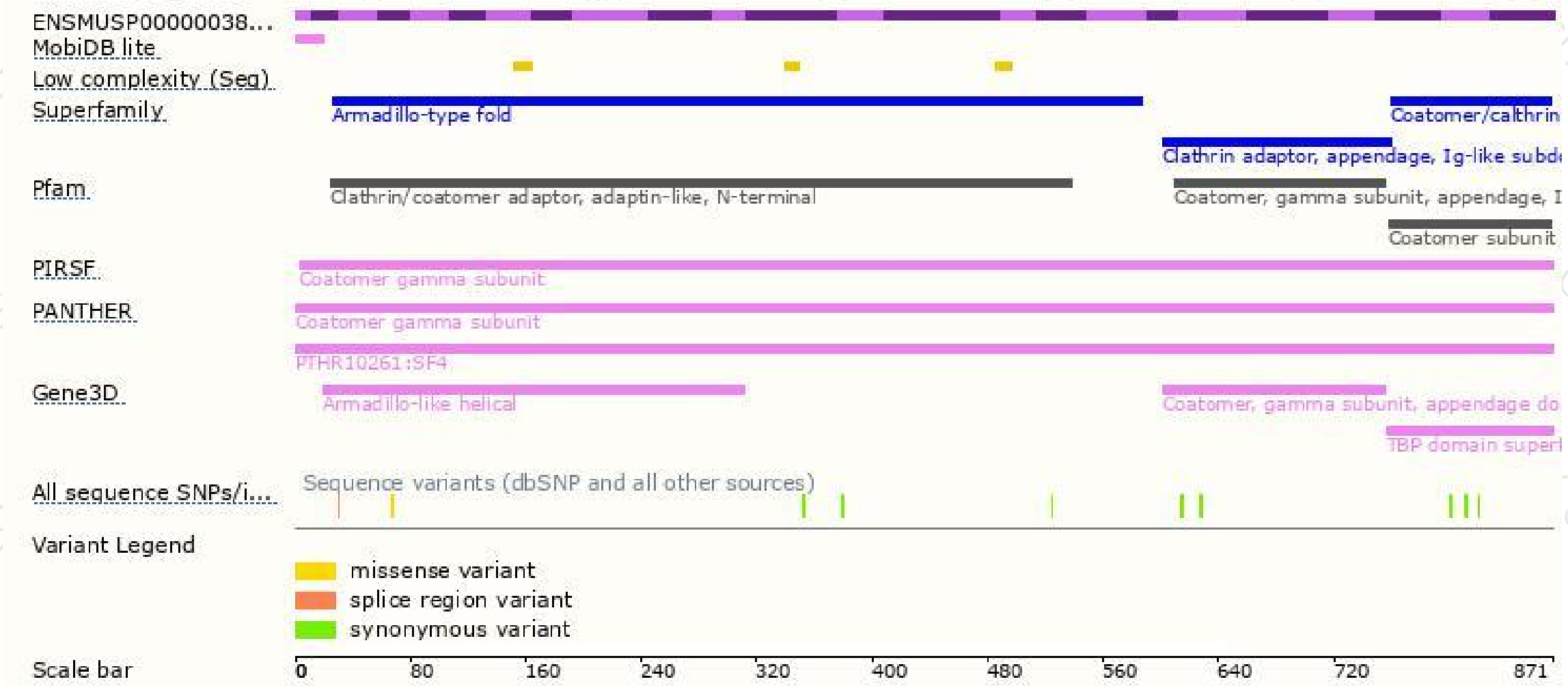
The strategy is based on the design of *Copg2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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