

Copz2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Copz2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Copz2* gene. The schematic diagram is as follows:



- The *Copz2* gene has 5 transcripts. According to the structure of *Copz2* gene, exon3-exon6 of *Copz2-201* (ENSMUST00000018816.13) transcript is recommended as the knockout region. The region contains 308bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Copz2* gene. The brief process is as follows: CRISPR/Cas9 system will

- The *Copz2* gene is located on the Chr11. 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)

Copz2 coatomer protein complex, subunit zeta 2 [*Mus musculus* (house mouse)]

Gene ID: 56358, updated on 13-Mar-2020

Summary

Official Symbol Copz2 provided by [MGI](#)
Official Full Name coatomer protein complex, subunit zeta 2 provided by [MGI](#)
Primary source [MGI:MG1:1929008](#)
See related [Ensembl:ENSMUSG00000018672](#)
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 zeta2-COP; 1110012D12Rik
Expression Ubiquitous expression in bladder adult (RPKM 34.8), limb E14.5 (RPKM 33.8) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

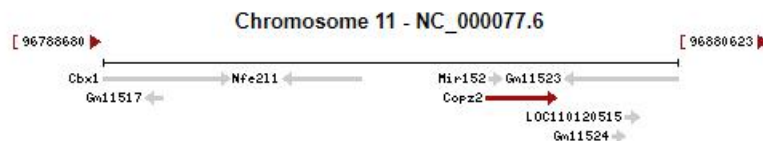
Genomic context

Location: 11; 11 D

See Copz2 in [Genome Data Viewer](#)

Exon count: 9

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (96849876..96861203)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (96711190..96722517)

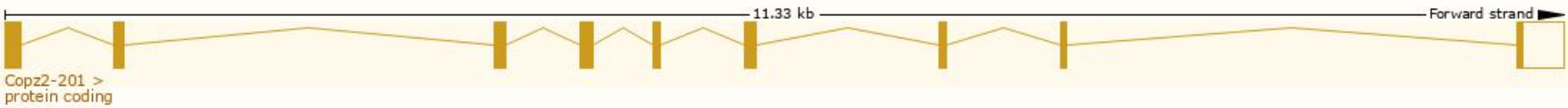


Transcript information (Ensembl)

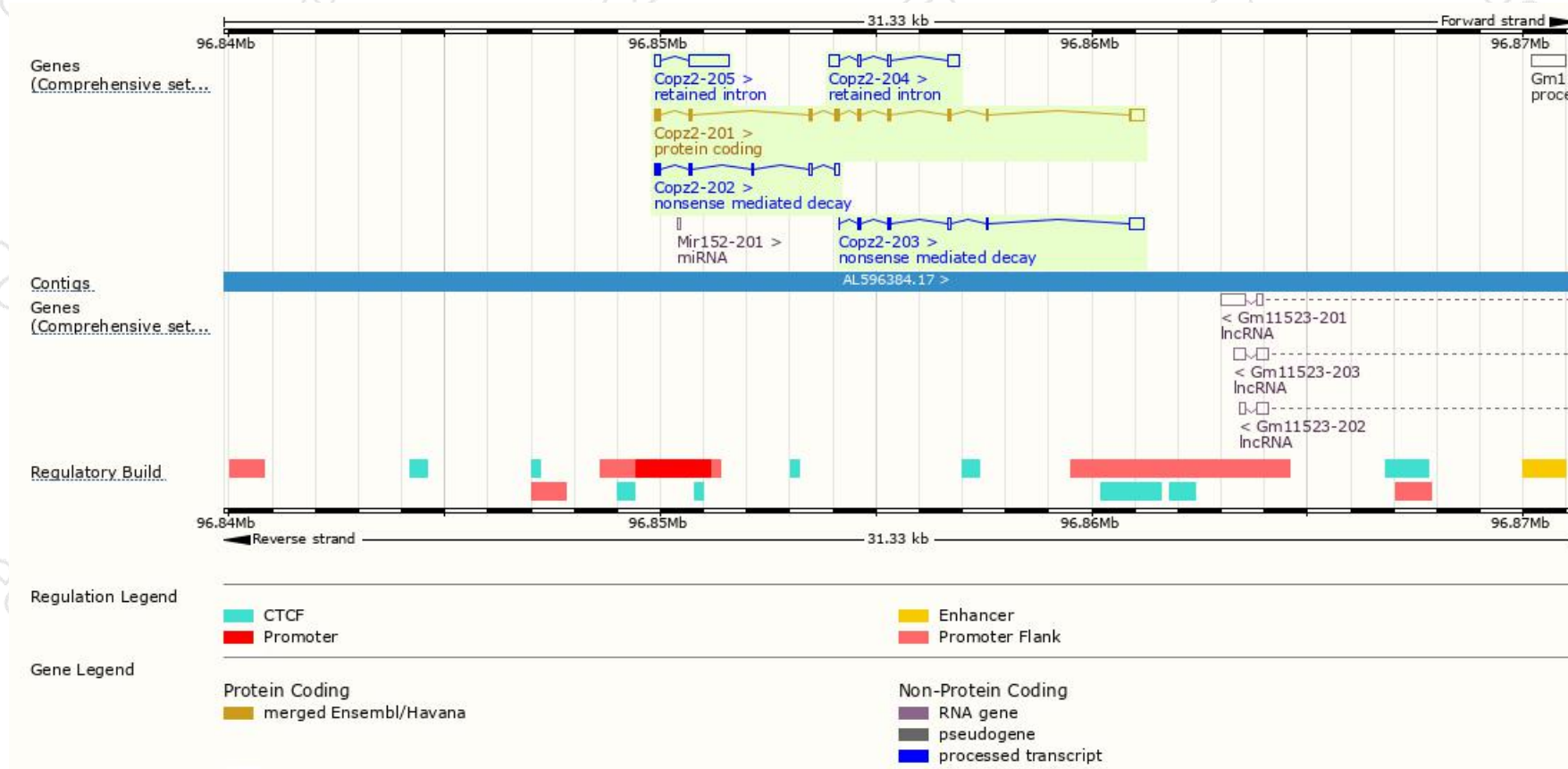
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Copz2-201	ENSMUST00000018816.13	930	205aa	Protein coding	CCDS25305	Q9JHH9	TSL:1 GENCODE basic APPRIS P1
Copz2-203	ENSMUST00000147710.1	581	51aa	Nonsense mediated decay	-	F6WZN3	CDS 5' incomplete TSL:3
Copz2-202	ENSMUST00000145633.1	407	68aa	Nonsense mediated decay	-	F2Z4A2	TSL:5
Copz2-205	ENSMUST00000155696.1	1045	No protein	Retained intron	-	-	TSL:1
Copz2-204	ENSMUST00000154191.1	653	No protein	Retained intron	-	-	TSL:5

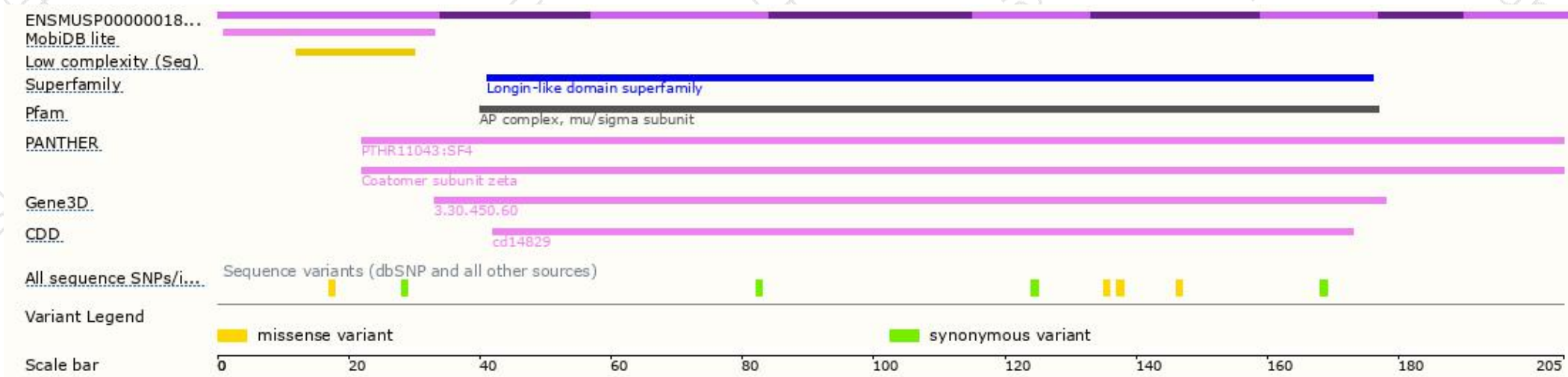
The strategy is based on the design of *Copz2-201* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

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