

Copg1 Cas9-KO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

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Project Overview

Project Name

Copg1

Project type

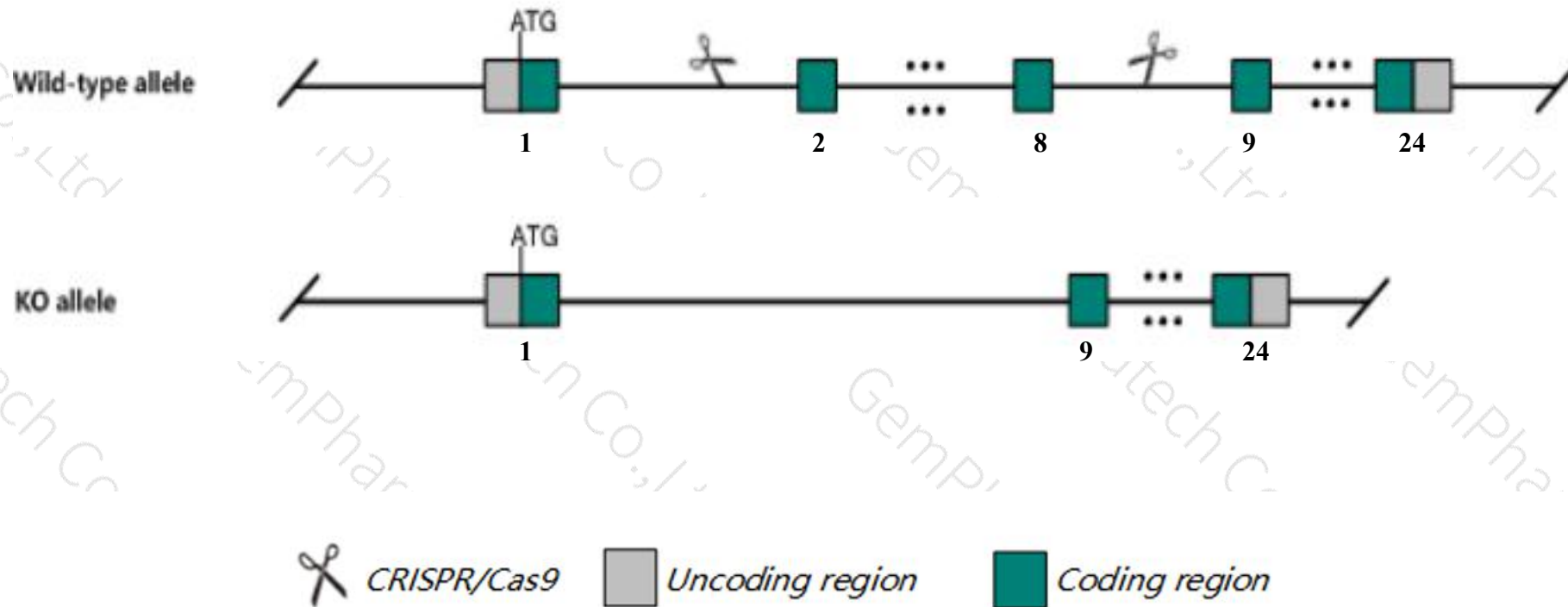
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Copg1* gene. The schematic diagram is as follows:



- The *Copg1* gene has 10 transcripts. According to the structure of *Copg1* gene, exon2-exon8 of *Copg1-202* (ENSMUST00000113607.9) transcript is recommended as the knockout region. The region contains 542bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Copg1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Copgl* 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)

Copg1 coatomer protein complex, subunit gamma 1 [Mus musculus (house mouse)]

Gene ID: 54161, updated on 13-Mar-2020

Summary



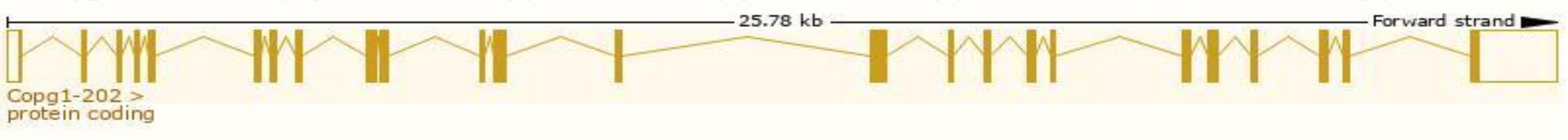
Official Symbol	Copg1 provided by MGI
Official Full Name	coatomer protein complex, subunit gamma 1 provided by MGI
Primary source	MGI:MGI:1858696
See related	Ensembl:ENSMUSG00000030058
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU019265, BC056168, Copg, D6Ert71e, D6Wsu16e
Expression	Ubiquitous expression in cerebellum adult (RPKM 31.9), limb E14.5 (RPKM 28.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

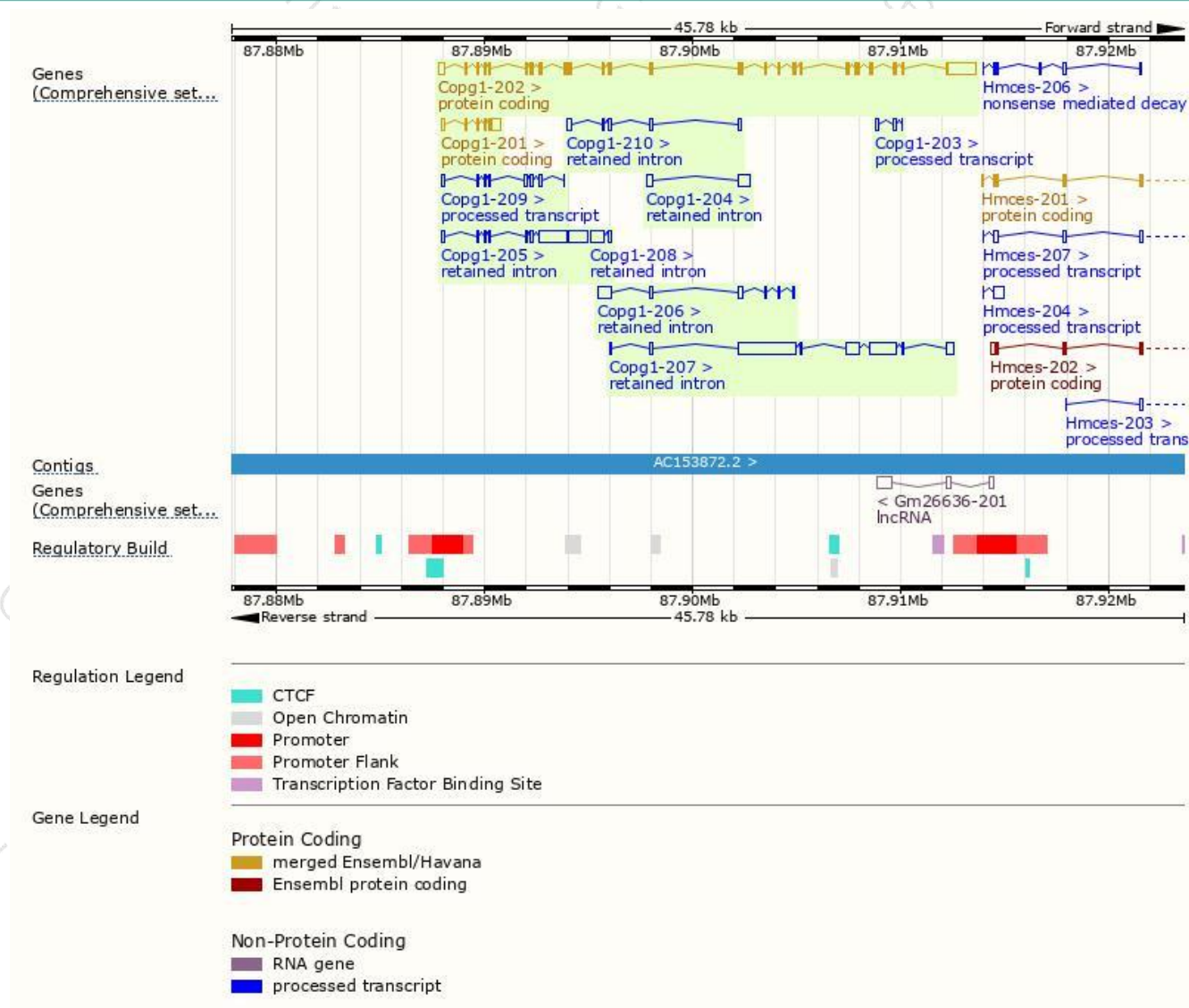
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Copg1-202	ENSMUST00000113607.9	4140	874aa	Protein coding	CCDS39549	Q9QZE5	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 TSL:1 GENCODE basic TSL:5 TSL:3 TSL:1 TSL:1 TSL:2 TSL:3 TSL:1 TSL:2
Copg1-201	ENSMUST00000049966.5	921	121aa	Protein coding	CCDS39550	Q7TNQ1	
Copg1-209	ENSMUST00000203240.2	633	No protein	Processed transcript	-	-	
Copg1-203	ENSMUST00000127614.1	332	No protein	Processed transcript	-	-	
Copg1-207	ENSMUST00000149907.2	5357	No protein	Retained intron	-	-	
Copg1-205	ENSMUST00000137717.1	2761	No protein	Retained intron	-	-	
Copg1-206	ENSMUST00000149409.7	1232	No protein	Retained intron	-	-	
Copg1-208	ENSMUST00000152175.1	822	No protein	Retained intron	-	-	
Copg1-204	ENSMUST00000132938.1	815	No protein	Retained intron	-	-	
Copg1-210	ENSMUST00000205234.2	742	No protein	Retained intron	-	-	

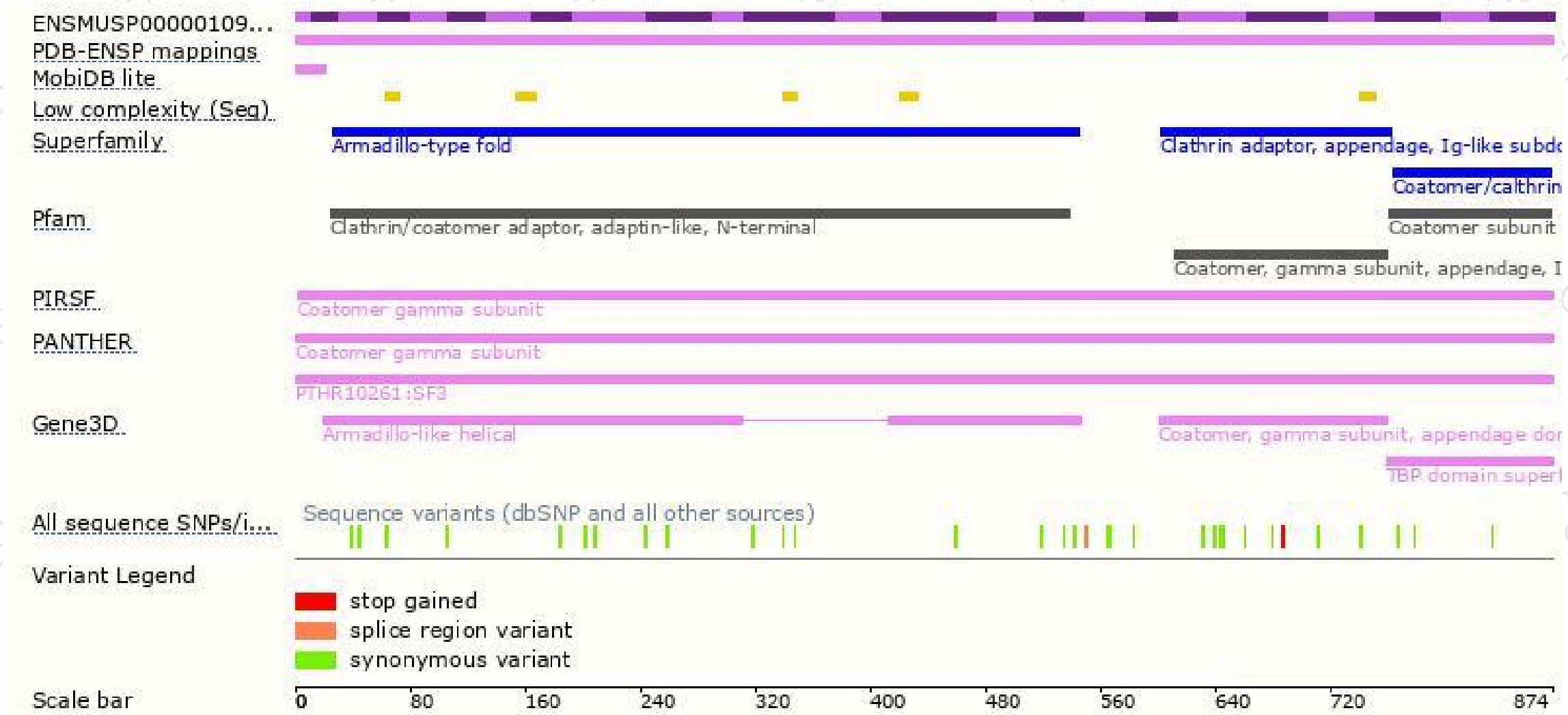
The strategy is based on the design of *Copg1-202* transcript,the transcription is shown below:



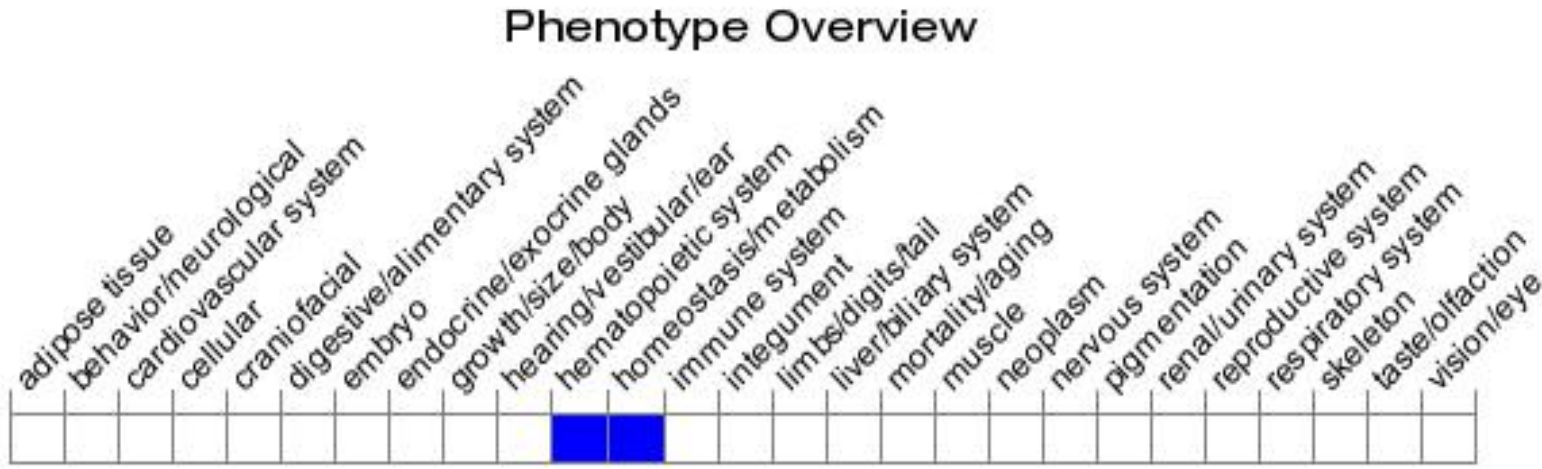
Genomic location distribution



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/>).

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

Tel: 400-9660890

