

***Commd1* Cas9-KO Strategy**

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Project Overview

Project Name

Commd1

Project type

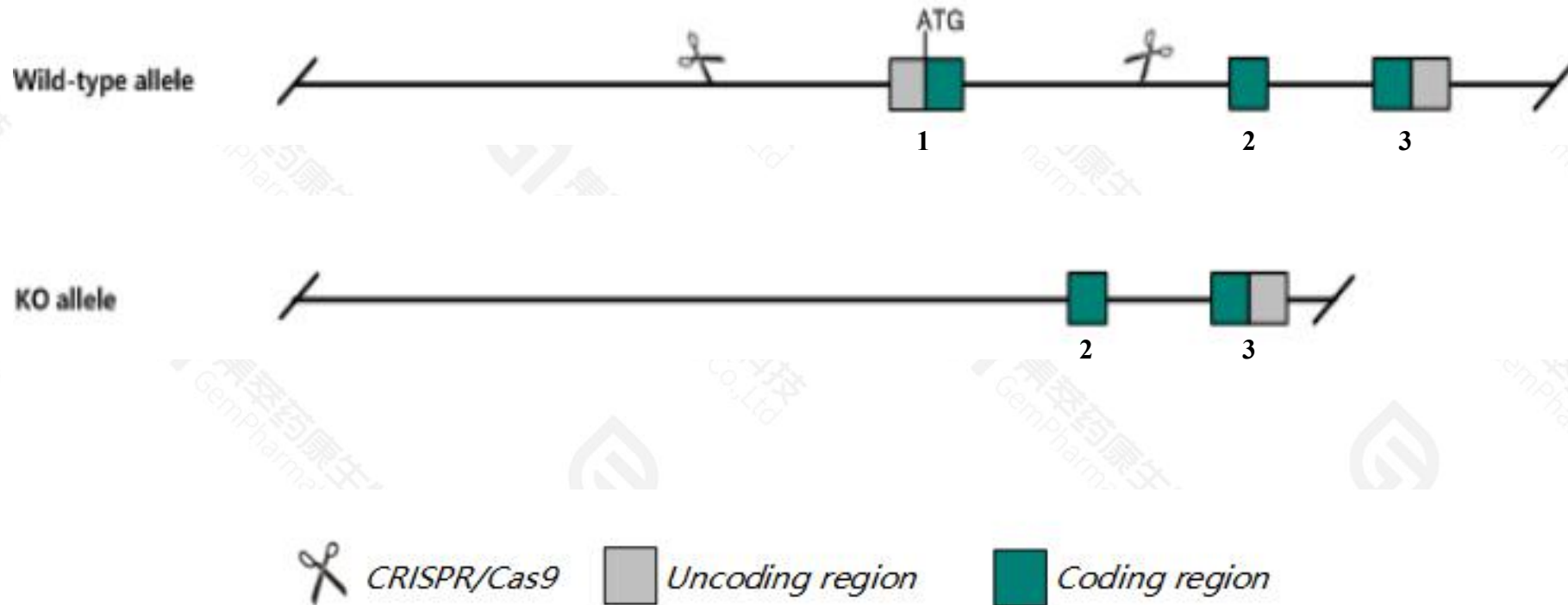
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Commd1* gene. The schematic diagram is as follows:



- The *Commd1* gene has 6 transcripts. According to the structure of *Commd1* gene, exon1 of *Commd1*-204(ENSMUST00000159081.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Commd1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a null allele are embryonic lethal with growth retardation, failure to turn, increased apoptosis in brain mesenchyme and defects in extraembryonic tissue development.
- *Commd1b* gene will be destroyed.
- The *Commd1* 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)

Commd1 COMM domain containing 1 [Mus musculus (house mouse)]

Gene ID: 17846, updated on 13-Mar-2020

Summary

Official Symbol Commd1 provided by [MGI](#)

Official Full Name COMM domain containing 1 provided by [MGI](#)

Primary source [MGI:MGI:109474](#)

See related [Ensembl:ENSMUSG00000051355](#)

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 AI256843, Murr1, U2/Mu

Expression Ubiquitous expression in testis adult (RPKM 10.4), CNS E11.5 (RPKM 10.2) and 28 other tissues [See more](#)

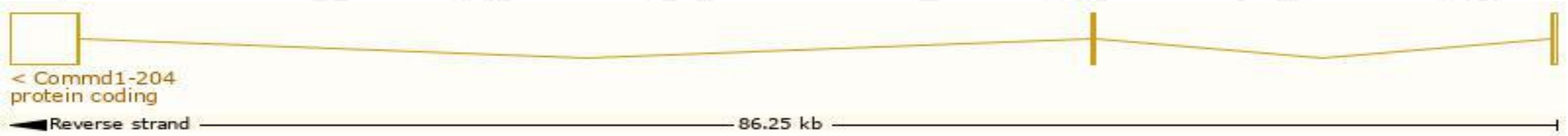
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

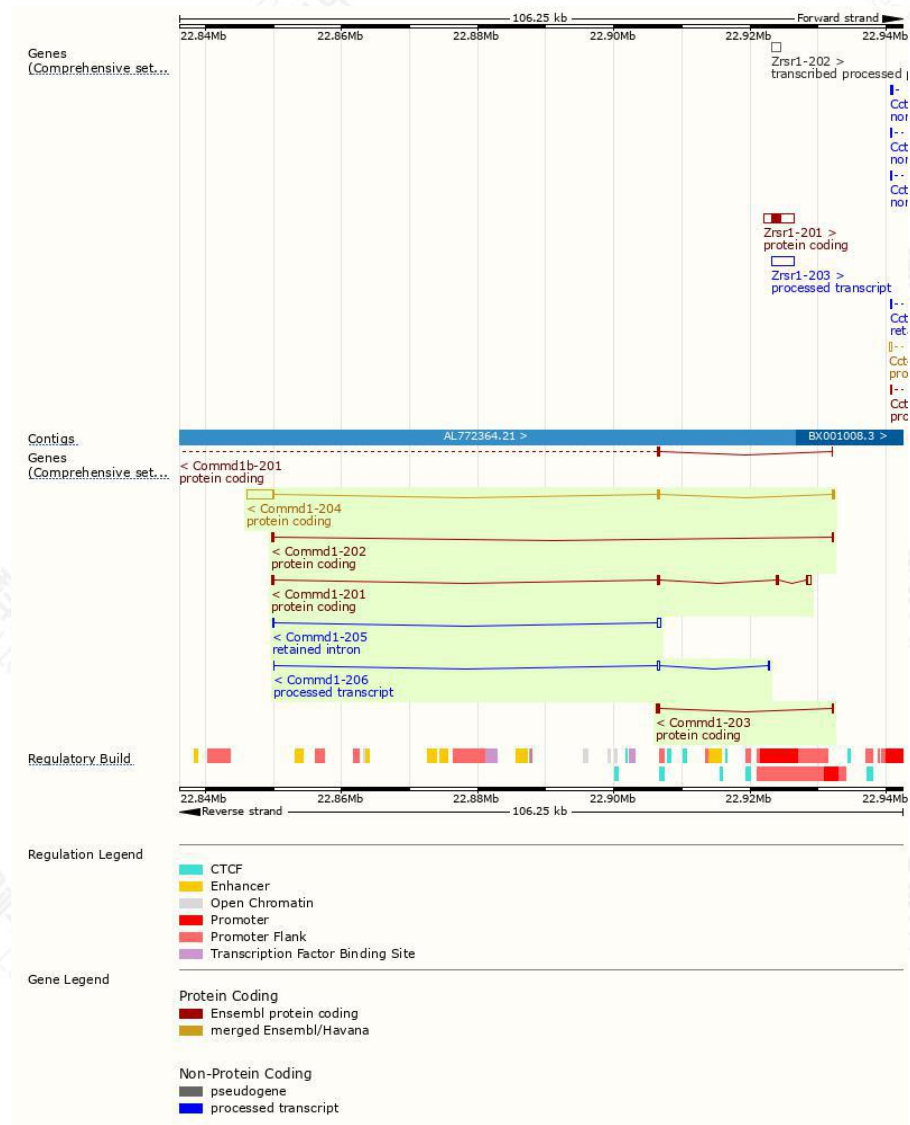
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Commd1-204	ENSMUST00000159081.7	4508	188aa	Protein coding	CCDS24472	A2RSF1 Q8K4M5	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
Commd1-201	ENSMUST00000057843.11	1459	243aa	Protein coding	-	Q8VI86	TSL:1 GENCODE basic
Commd1-202	ENSMUST00000071068.8	473	93aa	Protein coding	-	G8JL54	CDS 5' incomplete TSL:2
Commd1-203	ENSMUST00000093270.5	469	140aa	Protein coding	-	F7BZY0	CDS 5' incomplete TSL:3
Commd1-206	ENSMUST00000162924.1	526	No protein	Processed transcript	-	-	TSL:3
Commd1-205	ENSMUST00000161944.1	760	No protein	Retained intron	-	-	TSL:2

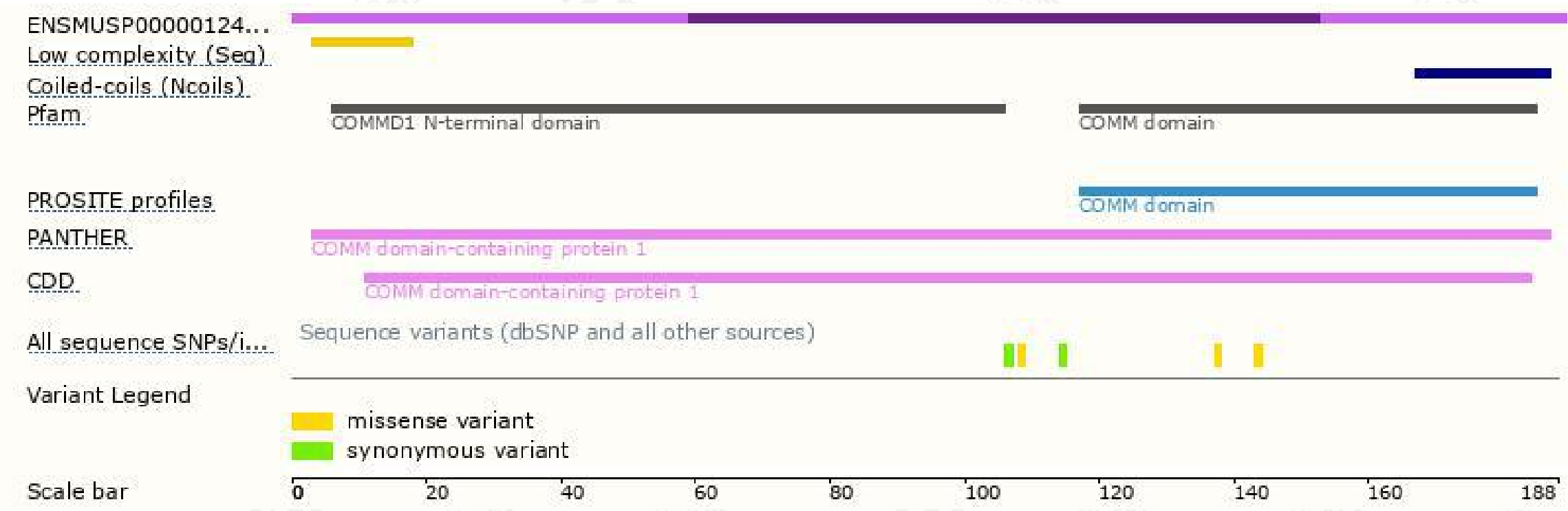
The strategy is based on the design of *Commd1-204* transcript,the transcription is shown below:



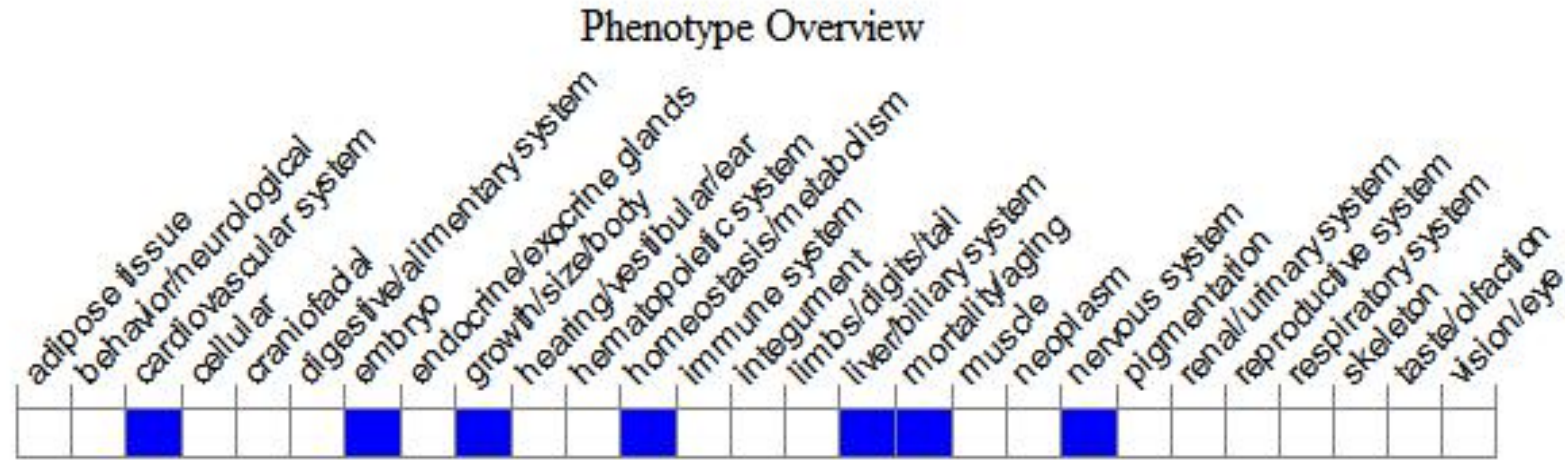
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a null allele are embryonic lethal with growth retardation, failure to turn, increased apoptosis in brain mesenchyme and defects in extraembryonic tissue development.

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