

***Cnnm4* Cas9-KO Strategy**

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Project Overview

Project Name

Cnnm4

Project type

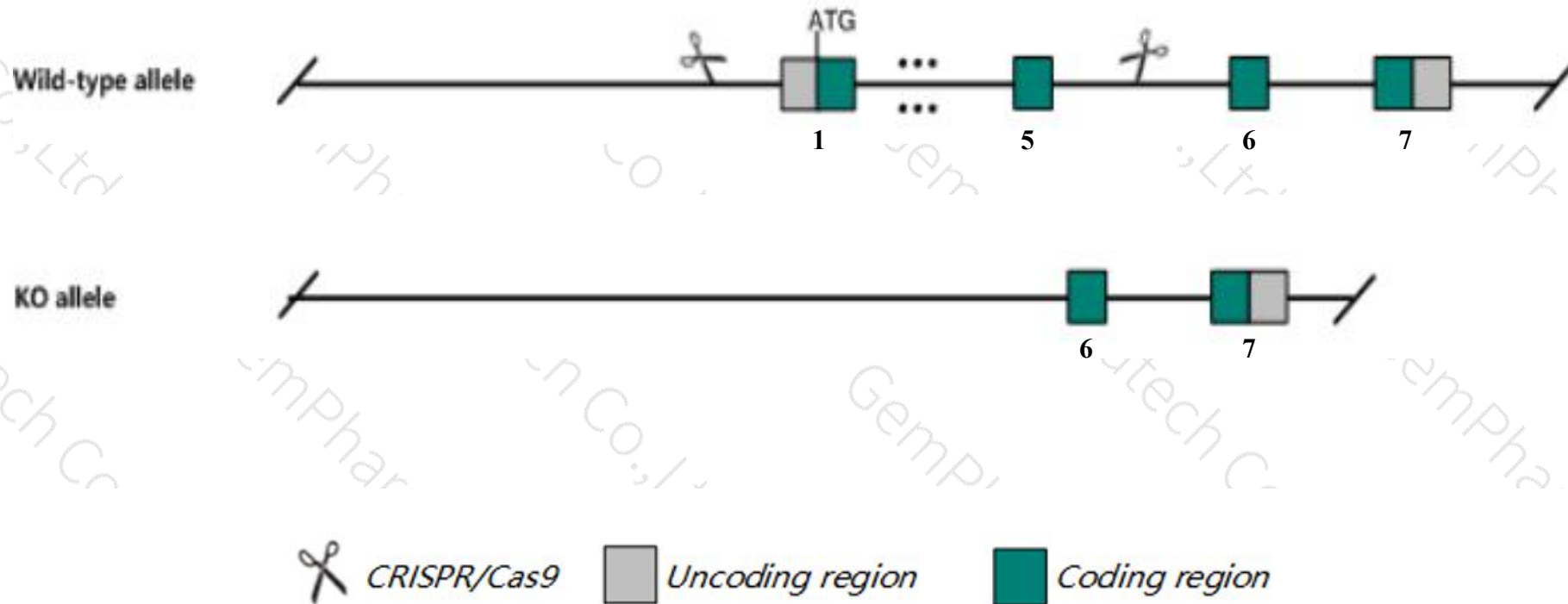
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cnnm4* gene. The schematic diagram is as follows:



- The *Cnnm4* gene has 2 transcripts. According to the structure of *Cnnm4* gene, exon1-exon5 of *Cnnm4-201* (ENSMUST00000153128.1) 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 *Cnnm4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutants exhibit hypomagnesemia and defective amelogenesis.
- *Gm37909* gene will be deleted.
- The knockout region is near to the N-terminal of *Gm47280* gene, this strategy may influence the regulatory function of the N-terminal of *Gm47280* gene.
- The *Cnnm4* gene is located on the Chr1. 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)

Cnnm4 cyclin M4 [*Mus musculus* (house mouse)]

Gene ID: 94220, updated on 14-Dec-2019

Summary

- Official Symbol** Cnnm4 provided by [MGI](#)
- Official Full Name** cyclin M4 provided by [MGI](#)
- Primary source** [MGI:MGI:2151060](#)
- See related** [Ensembl:ENSMUSG00000037408](#)
- 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** Acdp4; 5430430O18Rik
- Expression** Biased expression in colon adult (RPKM 97.1), large intestine adult (RPKM 49.6) and 6 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 1 B; 1 15.28 cM See Cnnm4 in [Genome Data Viewer](#)

Exon count: 7

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (36471597..36508776)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (36528442..36565621)

Transcript information (Ensembl)

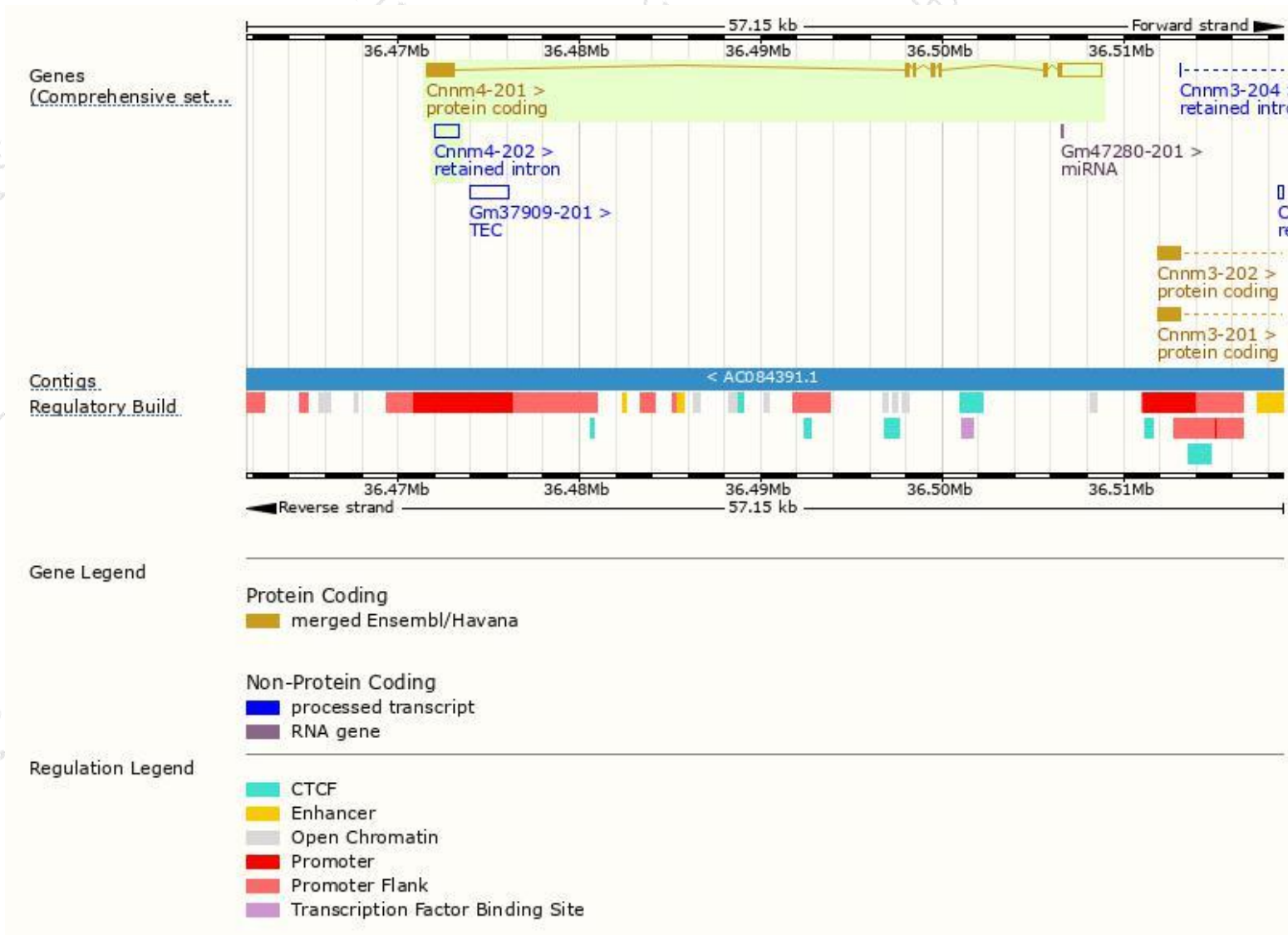
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnnm4-201	ENSMUST00000153128.1	4547	771aa	Protein coding	CCDS14879	Q69ZF7	TSL:1 GENCODE basic APPRIS P1
Cnnm4-202	ENSMUST00000192530.1	1372	No protein	Retained intron	-	-	TSL:NA

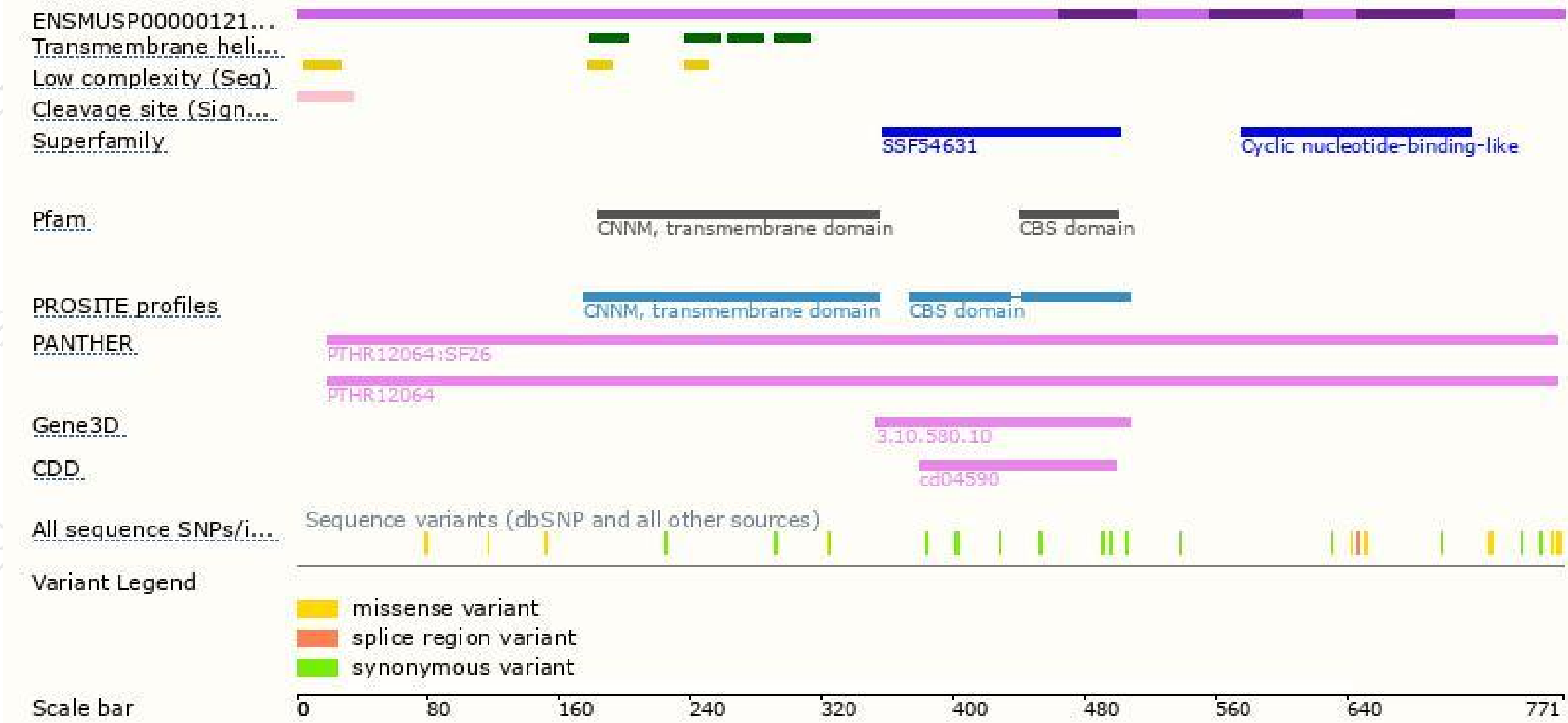
The strategy is based on the design of *Cnnm4-201* transcript,The transcription is shown below



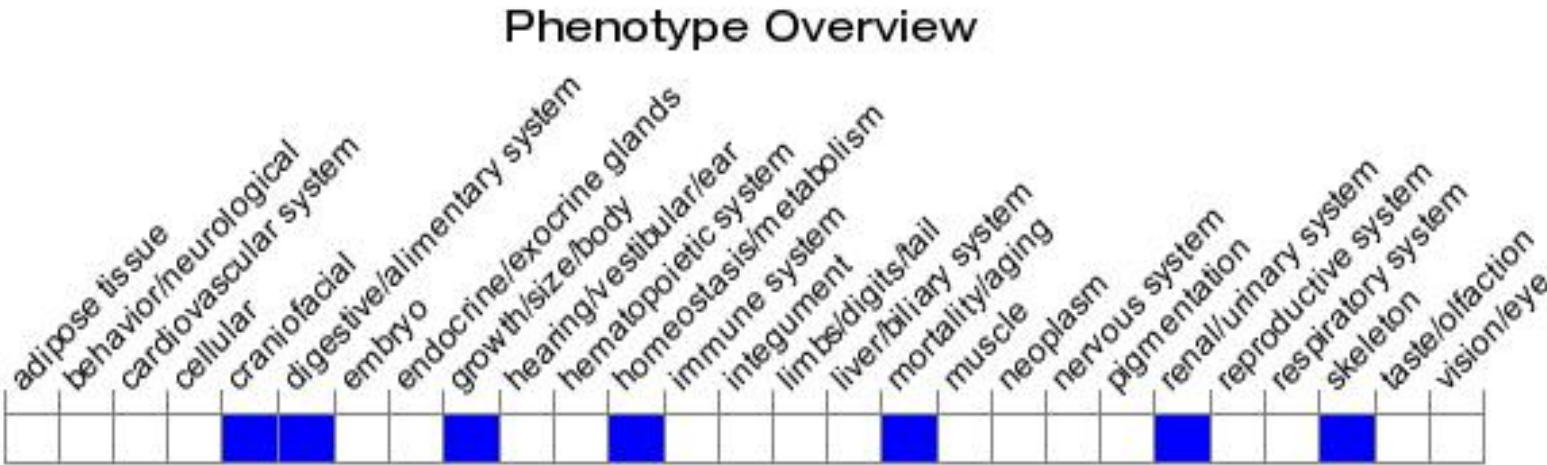
Genomic location distribution



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, Homozygous mutants exhibit hypomagnesemia and defective amelogenesis.

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

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