

Cnmd Cas9-KO Strategy

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Project Overview

Project Name

Cnmd

Project type

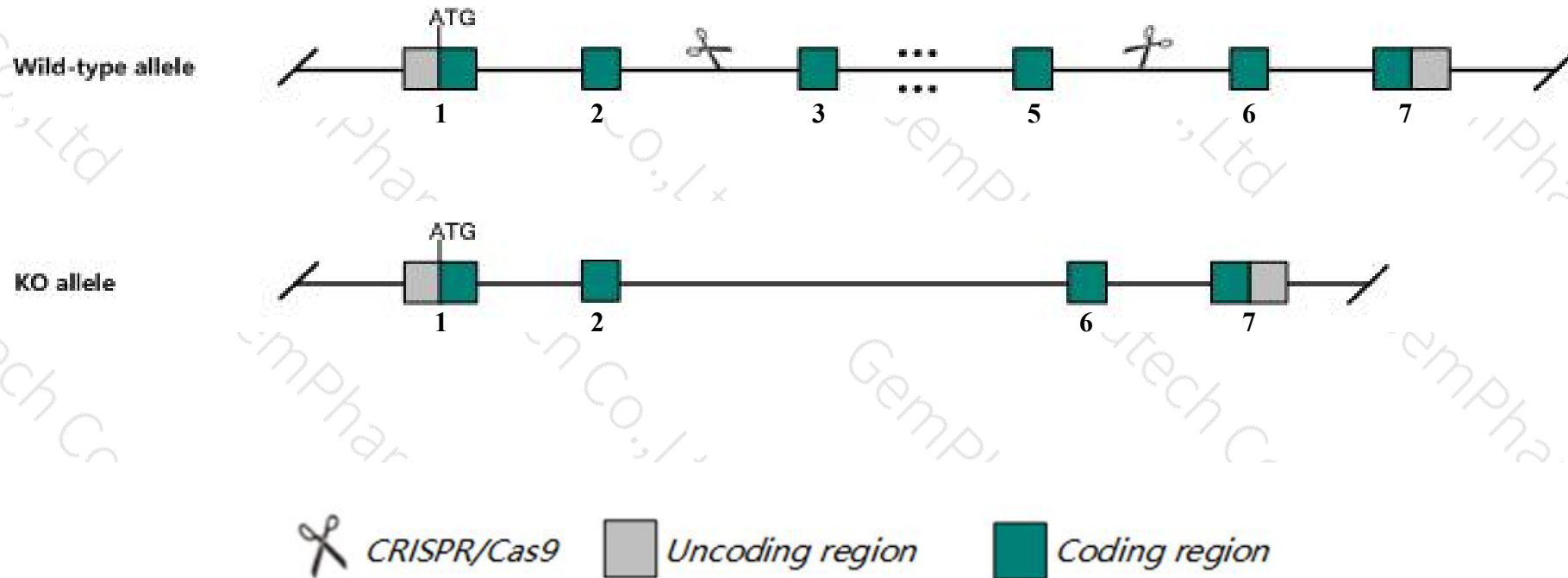
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Cnmd* gene has 5 transcripts. According to the structure of *Cnmd* gene, exon3-exon5 of *Cnmd-201* (ENSMUST00000022603.7) transcript is recommended as the knockout region. The region contains 406bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cnmd* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice are viable and show no gross morphologic defects. While cartilage development and embryonic endochondral bone formation were found to be normal in mutant mice, one line of targeted mutants showed increased bone density and impaired bone resorption.
- Transcript *Cnmd*-202 may not be affected.
- The *Cnmd* gene is located on the Chr14. 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)

Cnmd chondromodulin [*Mus musculus* (house mouse)]

Gene ID: 16840, updated on 12-Aug-2019

Summary

- Official Symbol** Cnmd provided by [MGI](#)
- Official Full Name** chondromodulin provided by [MGI](#)
- Primary source** [MGI:MGI:1341171](#)
- See related** [Ensembl:ENSMUSG00000022025](#)
- 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** Chmd; ChM-I; Lect1; Bricd3
- Expression** Biased expression in limb E14.5 (RPKM 98.5), ovary adult (RPKM 23.0) and 1 other tissue [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 14; 14 D3

See Cnmd in [Genome Data Viewer](#)

Exon count: 7

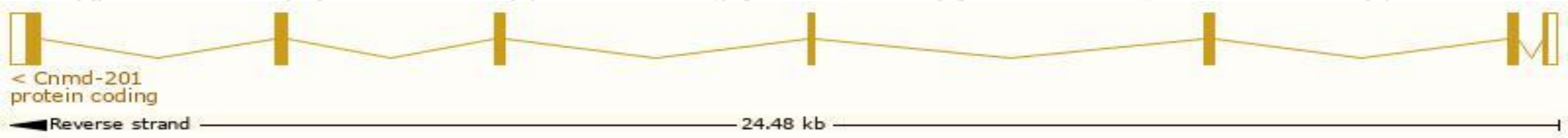
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	14	NC_000080.6 (79637682..79662194, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	14	NC_000080.5 (80037497..80061977, complement)

Transcript information (Ensembl)

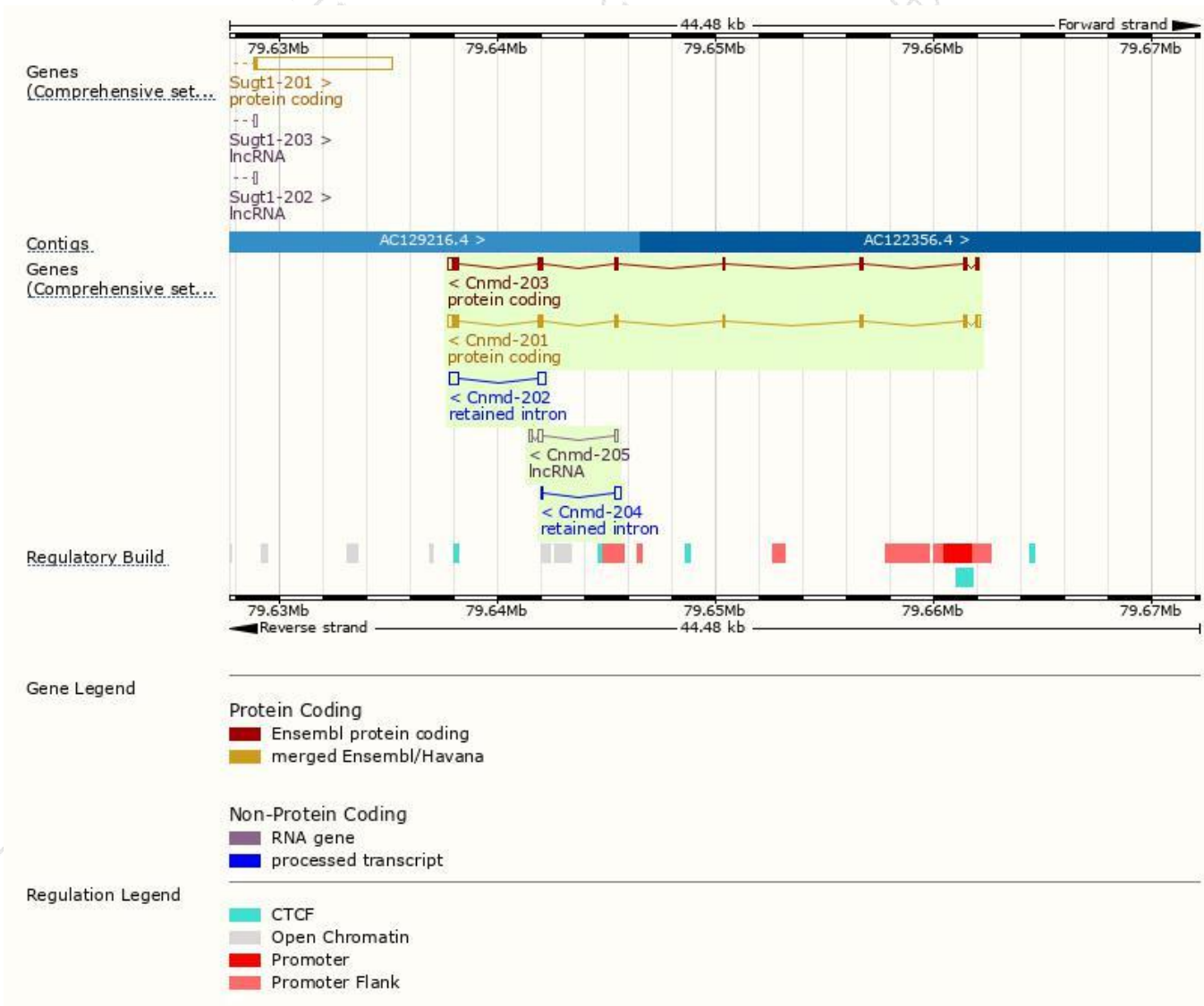
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnmd-201	ENSMUST00000022603.7	1433	334aa	Protein coding	CCDS27302	Q9Z1F6	TSL:1 GENCODE basic APPRIS P3
Cnmd-203	ENSMUST00000165835.7	1362	338aa	Protein coding	CCDS79348	G5E8Z6	TSL:1 GENCODE basic APPRIS ALT2
Cnmd-202	ENSMUST00000165204.1	659	No protein	Retained intron	-	-	TSL:2
Cnmd-204	ENSMUST00000167524.1	372	No protein	Retained intron	-	-	TSL:3
Cnmd-205	ENSMUST00000172331.1	459	No protein	lncRNA	-	-	TSL:3

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



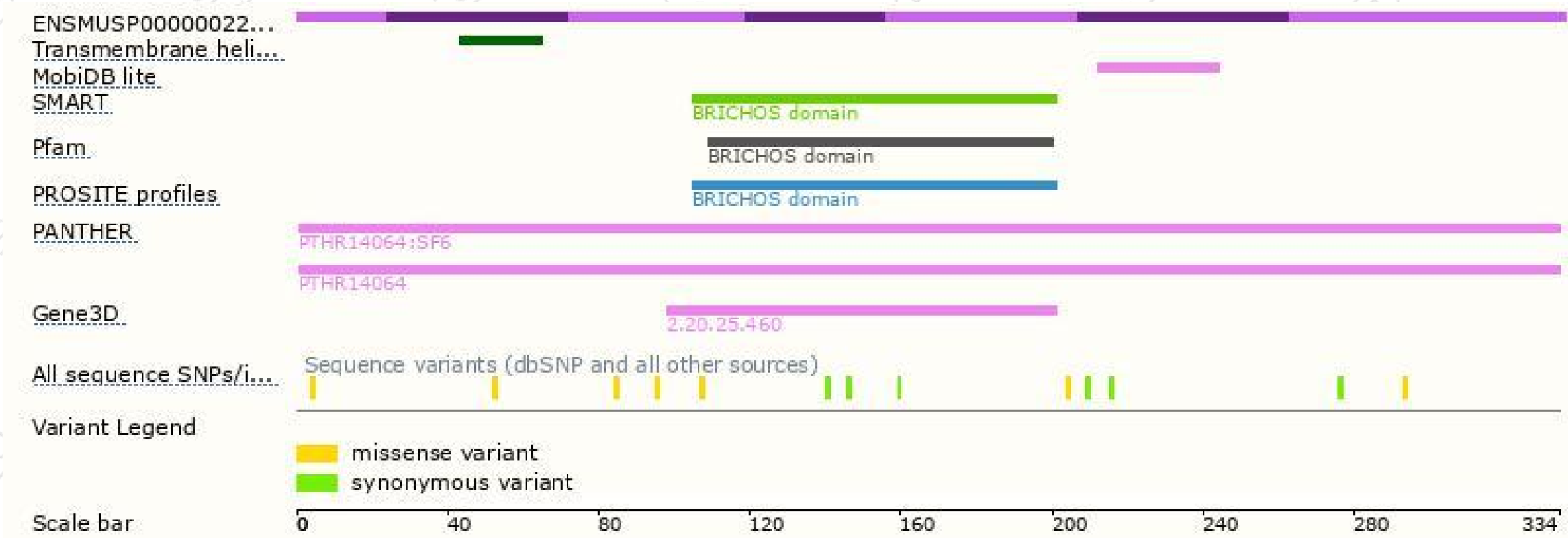
Genomic location distribution



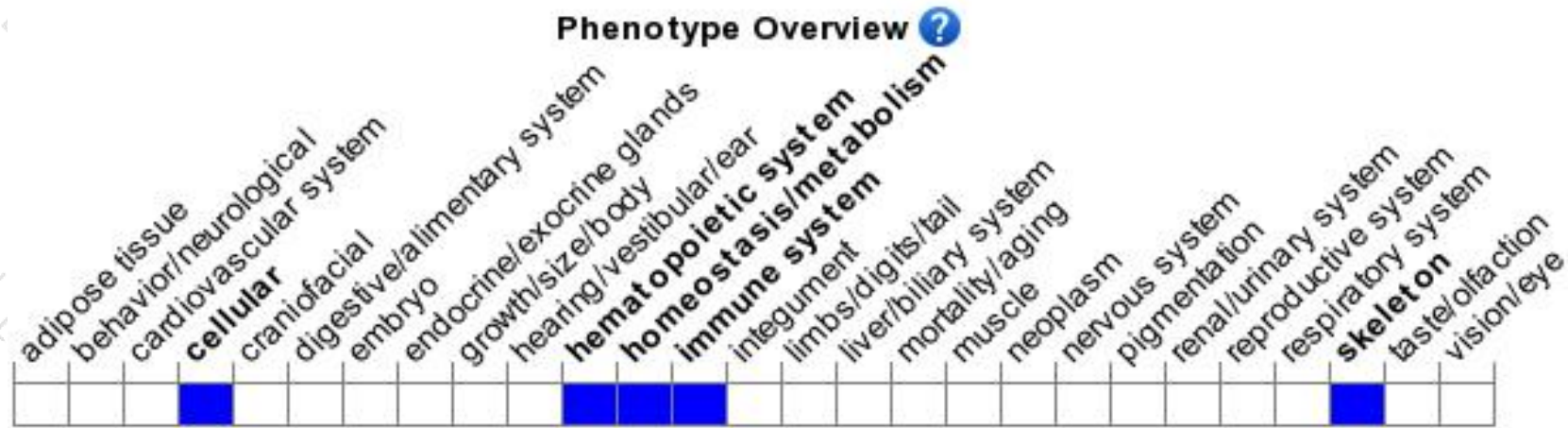
Protein domain



集萃药康
GemPharmatech



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 mutant mice are viable and show no gross morphologic defects. While cartilage development and embryonic endochondral bone formation were found to be normal in mutant mice, one line of target mutants showed increased bone density and impaired bone resorption.

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

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