

Ccni Cas9-KO Strategy

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Project Overview

Project Name

Ccni

Project type

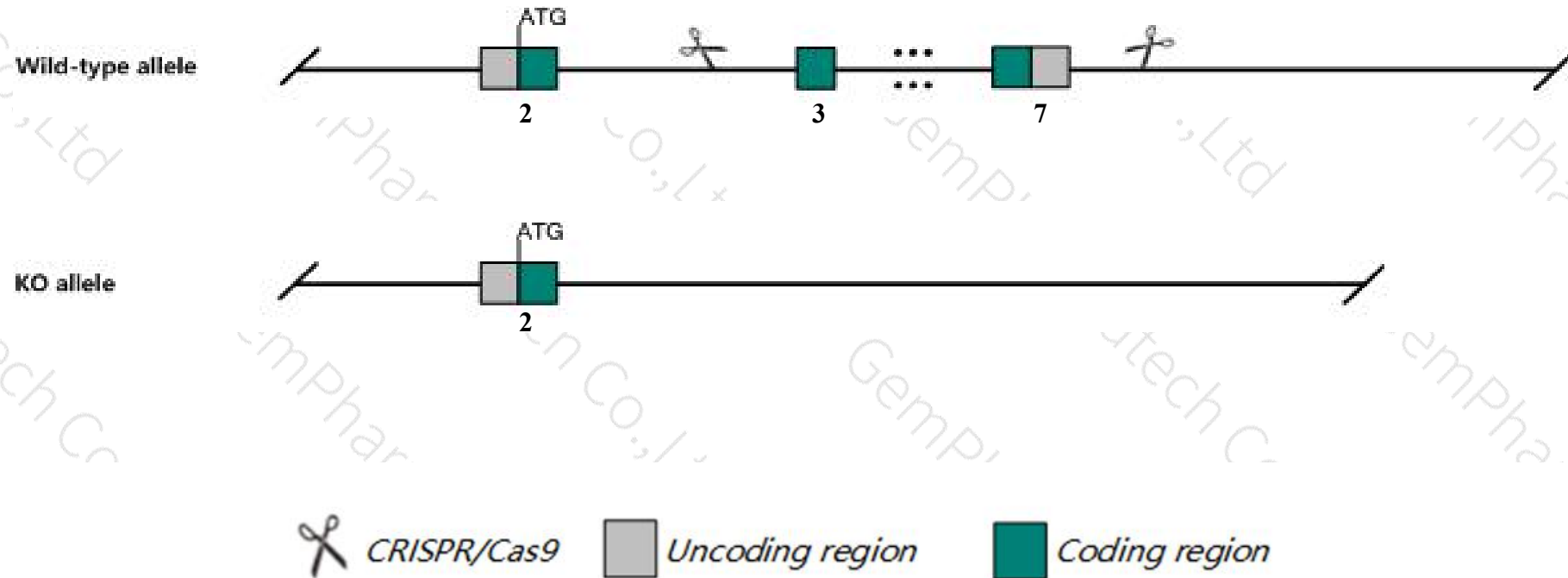
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Ccni* gene has 5 transcripts. According to the structure of *Ccni* gene, exon3-exon7 of *Ccni-201* (ENSMUST00000058550.14) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ccni* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a targeted null mutation are viable and fertile and do not display any gross physical or behavioral abnormalities.
- *Gm43681* gene will be deleted.
- The *Ccni* gene is located on the Chr5. 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)

Ccni cyclin I [*Mus musculus* (house mouse)]

Gene ID: 12453, updated on 12-Aug-2019

Summary

- Official Symbol** Ccni provided by MGI
- Official Full Name** cyclin I provided by MGI
- Primary source** MGI:MGI:1341077
- See related** Ensembl:ENSMUSG00000063015
- 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
- Expression** Ubiquitous expression in testis adult (RPKM 56.6), colon adult (RPKM 53.2) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 5; 5 E2 [See Ccni in Genome Data Viewer](#)

Exon count: 8

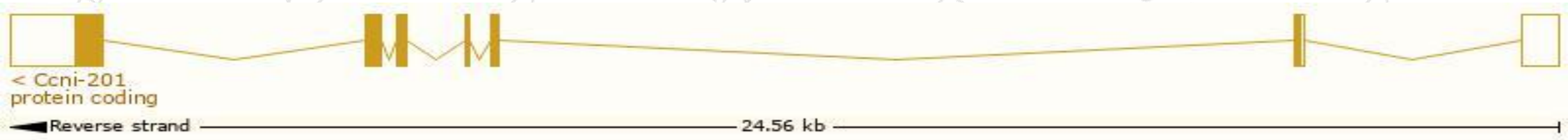
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (93181933..93206495, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (93610959..93635521, complement)

Transcript information (Ensembl)

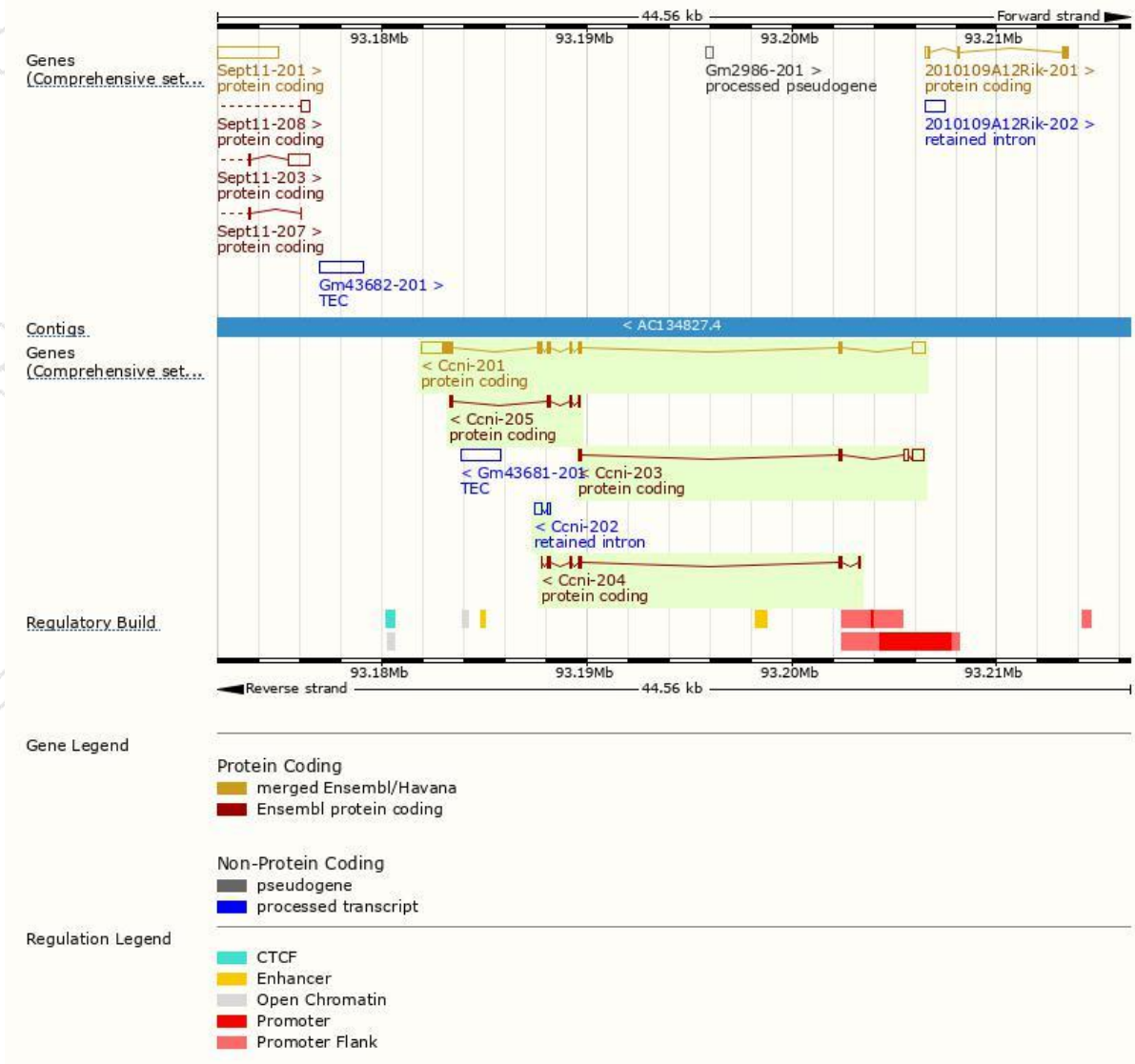
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccni-201	ENSMUST00000058550.14	2804	377aa	Protein coding	CCDS19436	Q9Z2V9	TSL:1 GENCODE basic APPRIS P1
Ccni-203	ENSMUST00000144514.2	1068	81aa	Protein coding	-	D3Z602	CDS 3' incomplete TSL:5
Ccni-204	ENSMUST00000151568.7	658	172aa	Protein coding	-	D3Z680	CDS 3' incomplete TSL:5
Ccni-205	ENSMUST00000201823.3	446	148aa	Protein coding	-	A0A0J9YU25	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Ccni-202	ENSMUST00000123033.1	507	No protein	Retained intron	-	-	TSL:2

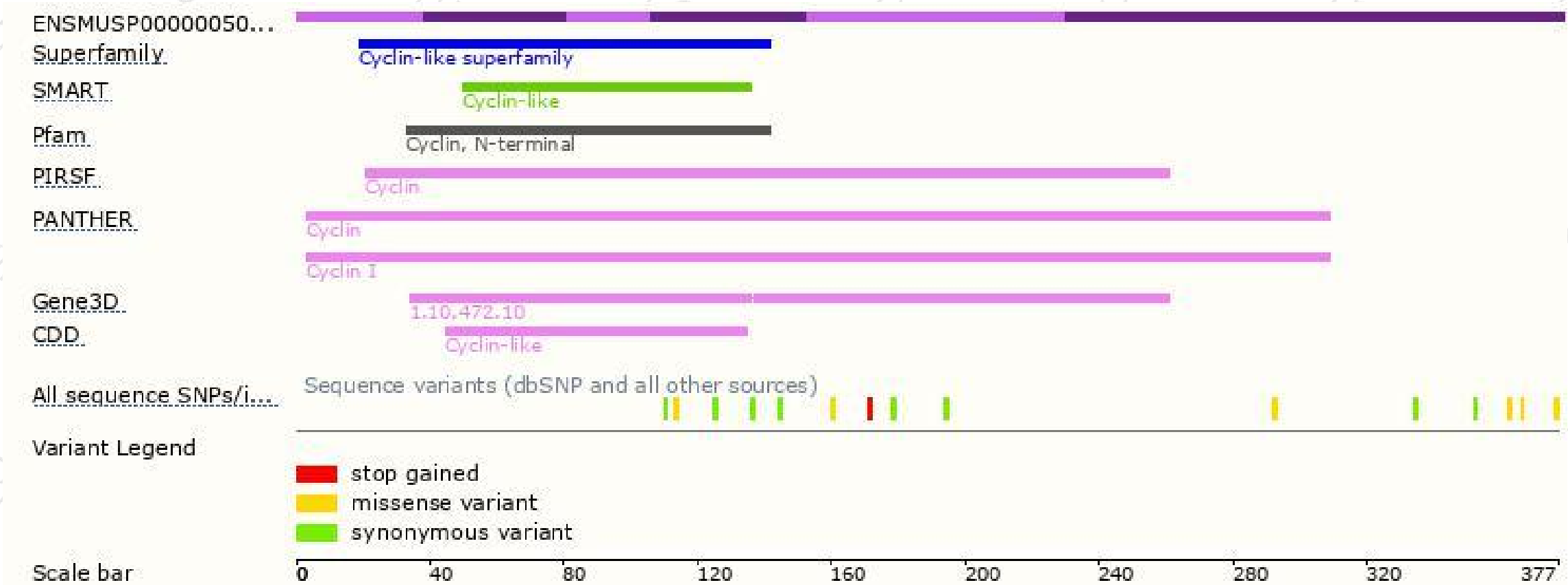
The strategy is based on the design of *Ccni-201* transcript,The transcription is shown below



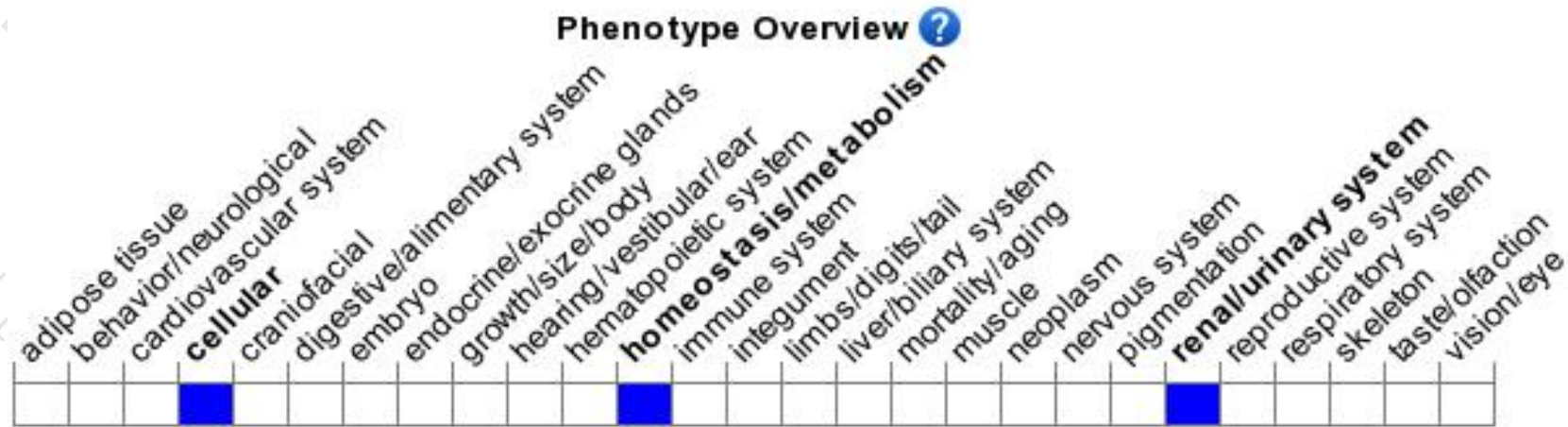
Genomic location distribution



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, Mice homozygous for a targeted null mutation are viable and fertile and do not display any gross physical or behavioral abnormalities.

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

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