

# *Ccnd3* Cas9-KO Strategy

**Designer:**

**Ruirui Zhang**

**Reviewer:**

**Huimin Su**

**Design Date:**

**2020-1-7**

# Project Overview

**Project Name**

***Ccnd3***

**Project type**

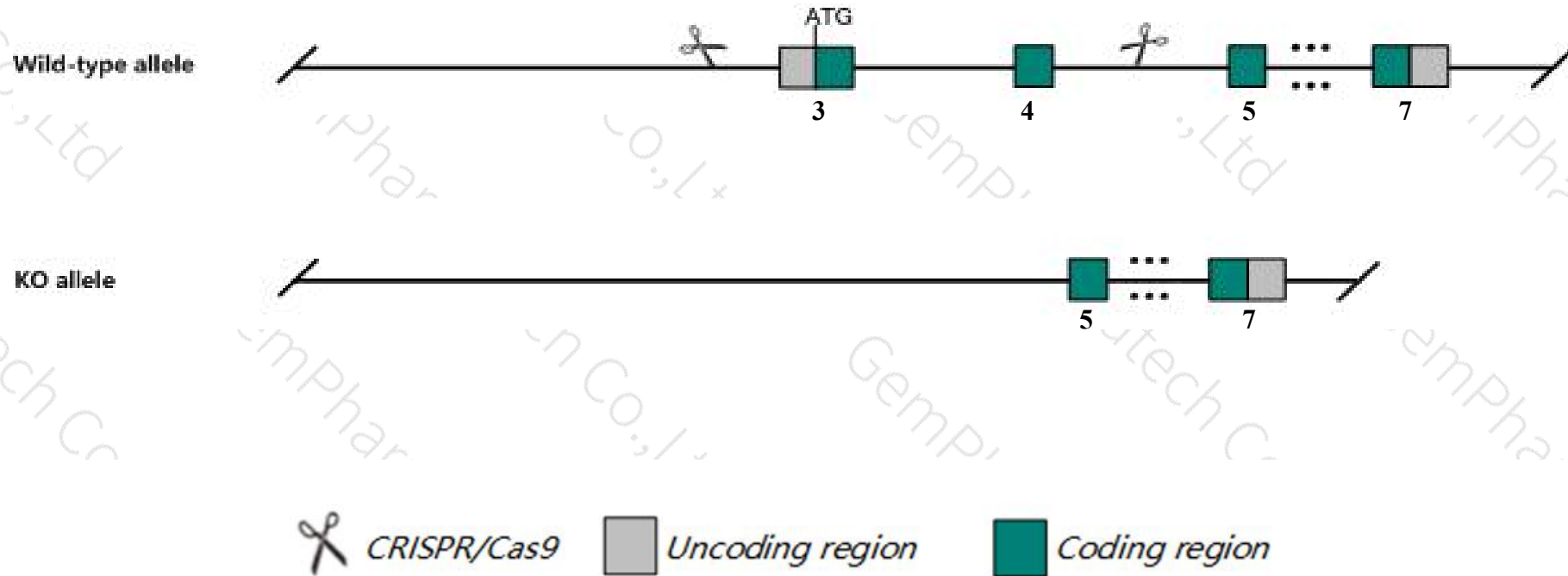
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccnd3* gene. The schematic diagram is as follows:



- The *Ccnd3* gene has 21 transcripts. According to the structure of *Ccnd3* gene, exon3-exon4 of *Ccnd3-202* (ENSMUST00000171031.7) 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 *Ccnd3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit severe thymus hypoplasia, abnormal thymocyte development, and impaired expansion of immature T lymphocytes.
- Transcripts *Ccnd3*-209, *Ccnd3*-219, *Ccnd3*-221 may not be affected.
- The *Ccnd3* gene is located on the Chr17. 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)

## Ccnd3 cyclin D3 [ *Mus musculus* (house mouse) ]

Gene ID: 12445, updated on 5-Nov-2019

### Summary

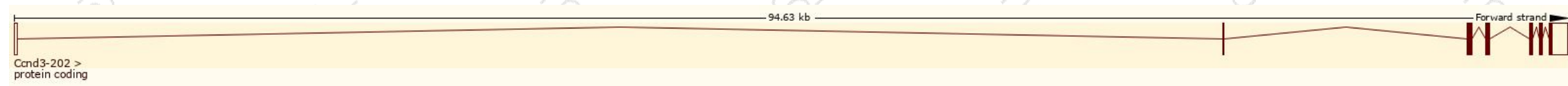
Official Symbol	Ccnd3 provided by MGI
Official Full Name	cyclin D3 provided by MGI
Primary source	<a href="#">MGI:MGI:88315</a>
See related	<a href="#">Ensembl:ENSMUSG000000034165</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C78795; AA682053; AL024085; AW146355; 9230106B05Rik
Expression	Broad expression in thymus adult (RPKM 402.8), adrenal adult (RPKM 319.1) and 18 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

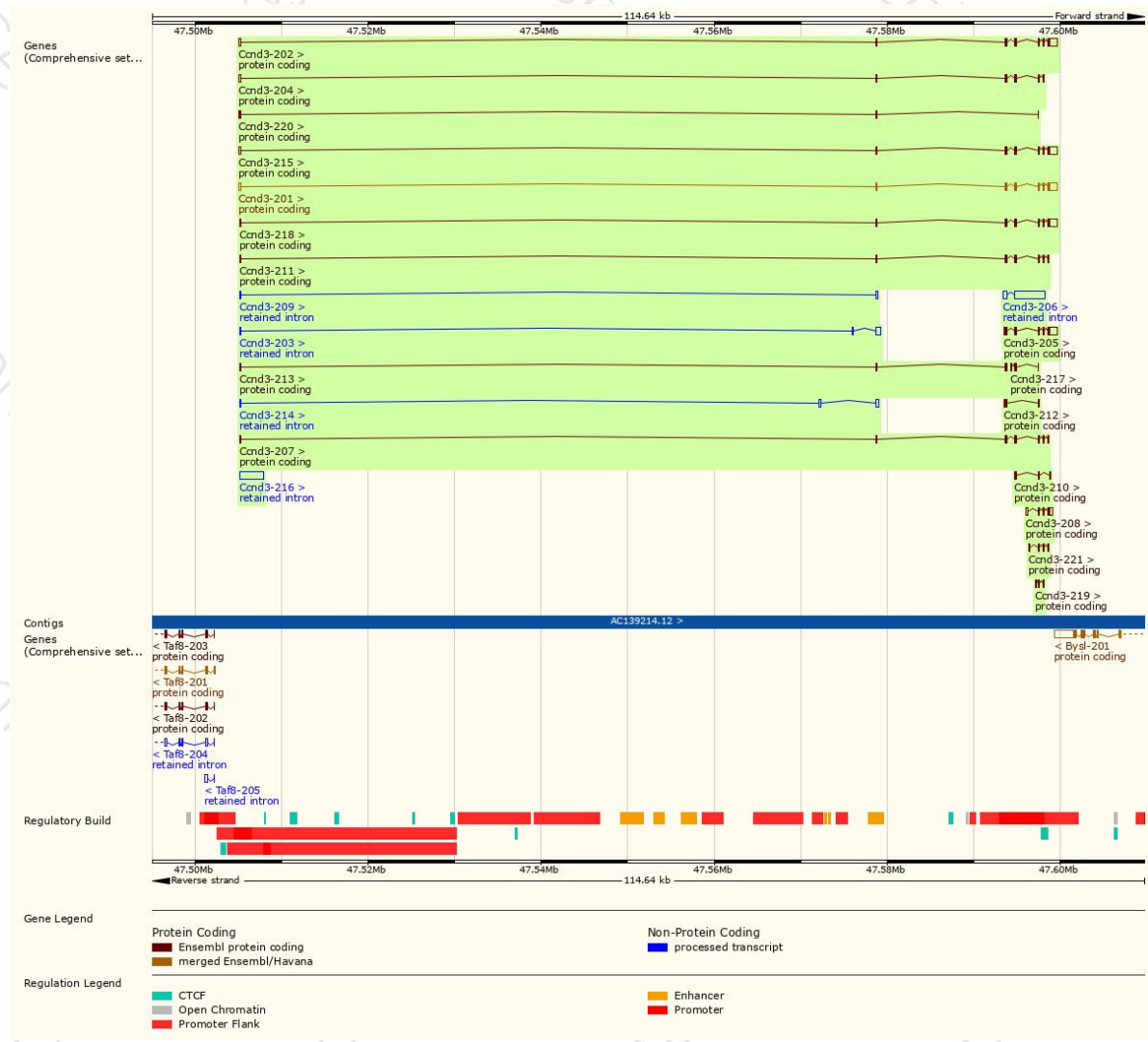
The gene has 21 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccnd3-202	<a href="#">ENSMUST00000171031.7</a>	2113	<a href="#">292aa</a>	Protein coding	<a href="#">CCDS28850</a>	<a href="#">P30282</a> <a href="#">Q3TSW4</a>	TSL:5 GENCODE basic APPRIS P1
Ccnd3-215	<a href="#">ENSMUST00000183044.7</a>	2064	<a href="#">292aa</a>	Protein coding	<a href="#">CCDS28850</a>	<a href="#">P30282</a> <a href="#">Q3TSW4</a>	TSL:1 GENCODE basic APPRIS P1
Ccnd3-218	<a href="#">ENSMUST00000183177.7</a>	2060	<a href="#">292aa</a>	Protein coding	<a href="#">CCDS28850</a>	<a href="#">P30282</a> <a href="#">Q3TSW4</a>	TSL:5 GENCODE basic APPRIS P1
Ccnd3-201	<a href="#">ENSMUST00000037333.16</a>	1999	<a href="#">292aa</a>	Protein coding	<a href="#">CCDS28850</a>	<a href="#">P30282</a> <a href="#">Q3TSW4</a>	TSL:1 GENCODE basic APPRIS P1
Ccnd3-205	<a href="#">ENSMUST00000182209.7</a>	1977	<a href="#">292aa</a>	Protein coding	<a href="#">CCDS28850</a>	<a href="#">P30282</a> <a href="#">Q3TSW4</a>	TSL:1 GENCODE basic APPRIS P1
Ccnd3-204	<a href="#">ENSMUST00000182129.7</a>	952	<a href="#">214aa</a>	Protein coding	-	<a href="#">S4R240</a>	CDS 3' incomplete TSL:5
Ccnd3-208	<a href="#">ENSMUST00000182539.7</a>	931	<a href="#">96aa</a>	Protein coding	-	<a href="#">S4R216</a>	TSL:2 GENCODE basic
Ccnd3-211	<a href="#">ENSMUST00000182848.7</a>	926	<a href="#">243aa</a>	Protein coding	-	<a href="#">S4R2N5</a>	CDS 3' incomplete TSL:5
Ccnd3-207	<a href="#">ENSMUST00000182506.7</a>	853	<a href="#">250aa</a>	Protein coding	-	<a href="#">S4R1D9</a>	CDS 3' incomplete TSL:5
Ccnd3-221	<a href="#">ENSMUST00000183256.7</a>	560	<a href="#">75aa</a>	Protein coding	-	<a href="#">S4R275</a>	CDS 3' incomplete TSL:5
Ccnd3-212	<a href="#">ENSMUST00000182874.2</a>	484	<a href="#">119aa</a>	Protein coding	-	<a href="#">S4R2N1</a>	CDS 3' incomplete TSL:5
Ccnd3-210	<a href="#">ENSMUST00000182846.2</a>	464	<a href="#">125aa</a>	Protein coding	-	<a href="#">S4R1R1</a>	CDS 5' incomplete TSL:3
Ccnd3-217	<a href="#">ENSMUST00000183158.1</a>	385	<a href="#">99aa</a>	Protein coding	-	<a href="#">S4R1C8</a>	CDS 3' incomplete TSL:2
Ccnd3-219	<a href="#">ENSMUST00000183206.1</a>	336	<a href="#">29aa</a>	Protein coding	-	<a href="#">S4R2Q7</a>	CDS 3' incomplete TSL:3
Ccnd3-220	<a href="#">ENSMUST00000183210.1</a>	299	<a href="#">52aa</a>	Protein coding	-	<a href="#">S4R2I5</a>	CDS 3' incomplete TSL:5
Ccnd3-213	<a href="#">ENSMUST00000182935.7</a>	277	<a href="#">43aa</a>	Protein coding	-	<a href="#">S4R1L8</a>	CDS 3' incomplete TSL:3
Ccnd3-206	<a href="#">ENSMUST00000182281.1</a>	3858	No protein	Retained intron	-	-	TSL:1
Ccnd3-216	<a href="#">ENSMUST00000183061.1</a>	2670	No protein	Retained intron	-	-	TSL:NA
Ccnd3-203	<a href="#">ENSMUST00000182060.1</a>	754	No protein	Retained intron	-	-	TSL:1
Ccnd3-214	<a href="#">ENSMUST00000183014.1</a>	552	No protein	Retained intron	-	-	TSL:3
Ccnd3-209	<a href="#">ENSMUST00000182591.1</a>	283	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Ccnd3-202* transcript, the transcription is shown below:

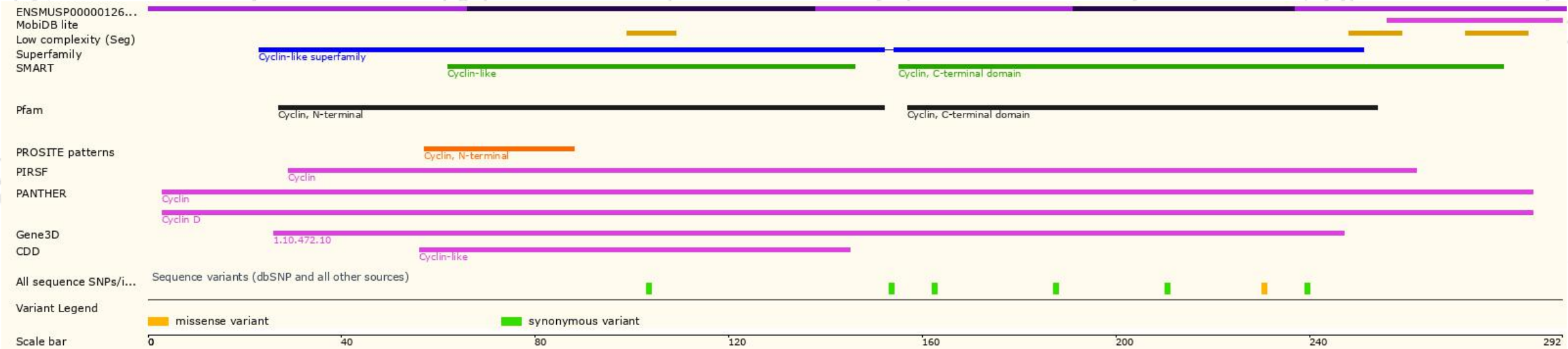


# Genomic location distribution

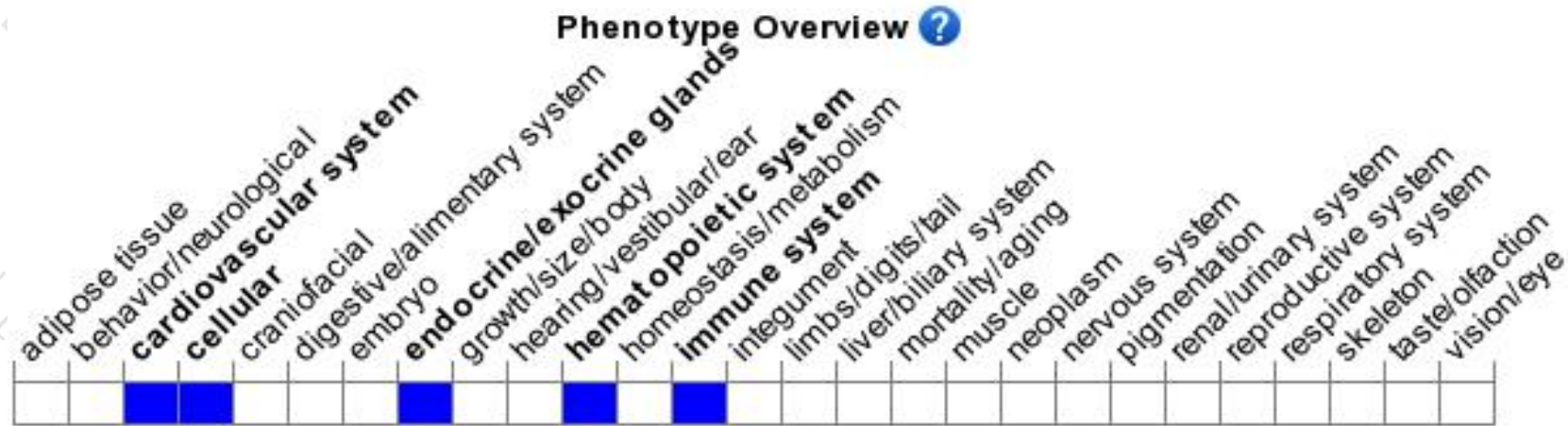




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit severe thymus hypoplasia, abnormal thymocyte development, and impaired expansion of immature T lymphocytes.

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

Tel: 400-9660890

