

# *Ccnk* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Ccnk*

**Project type**

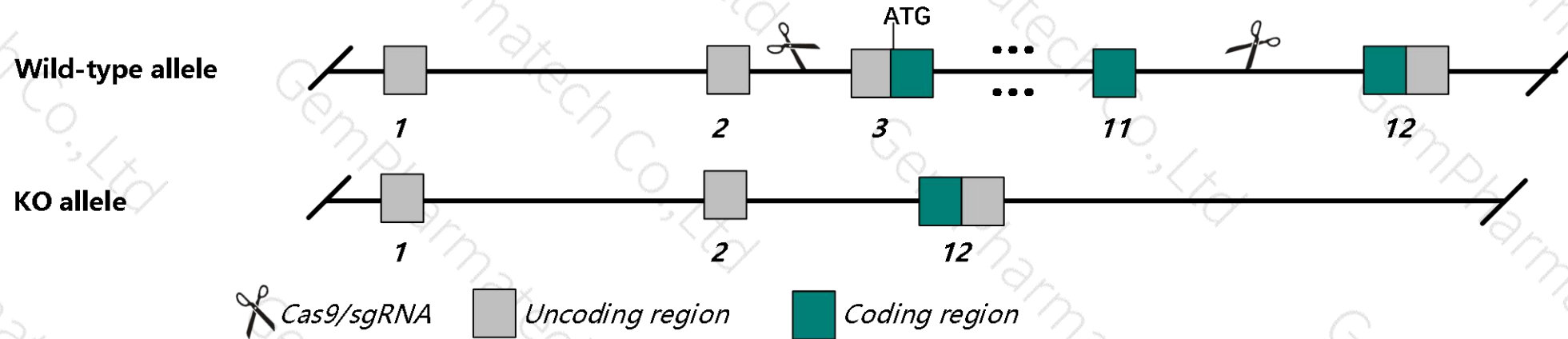
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Ccnk* gene has 3 transcripts. According to the structure of *Ccnk* gene, exon3-exon11 of *Ccnk*-202 (ENSMUST00000221167.1) 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 *Ccnk* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a gene trap allele display complete embryonic lethality before implantation.
- The knockout region is near to the N-terminal of *Setd3* gene, this strategy may influence the regulatory function of the N-terminal of *Setd3* gene.
- The *Ccnk* gene is located on the Chr12. 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)

## Ccnk cyclin K [Mus musculus (house mouse)]

Gene ID: 12454, updated on 13-Mar-2020

### Summary



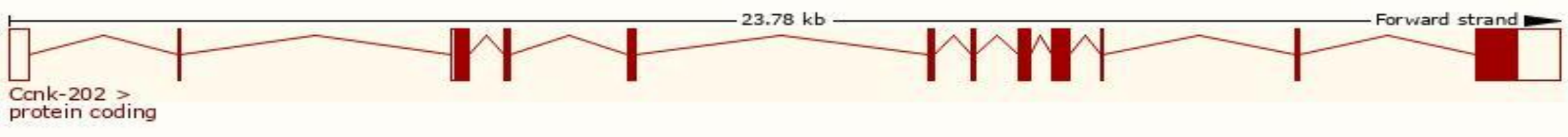
Official Symbol	Ccnk provided by <a href="#">MGI</a>
Official Full Name	cyclin K provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1276106</a>
See related	<a href="#">Ensembl:ENSMUSG000000021258</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW123198, AW413594, CPR4, CycK
Expression	Biased expression in testis adult (RPKM 101.3), limb E14.5 (RPKM 9.5) and 7 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

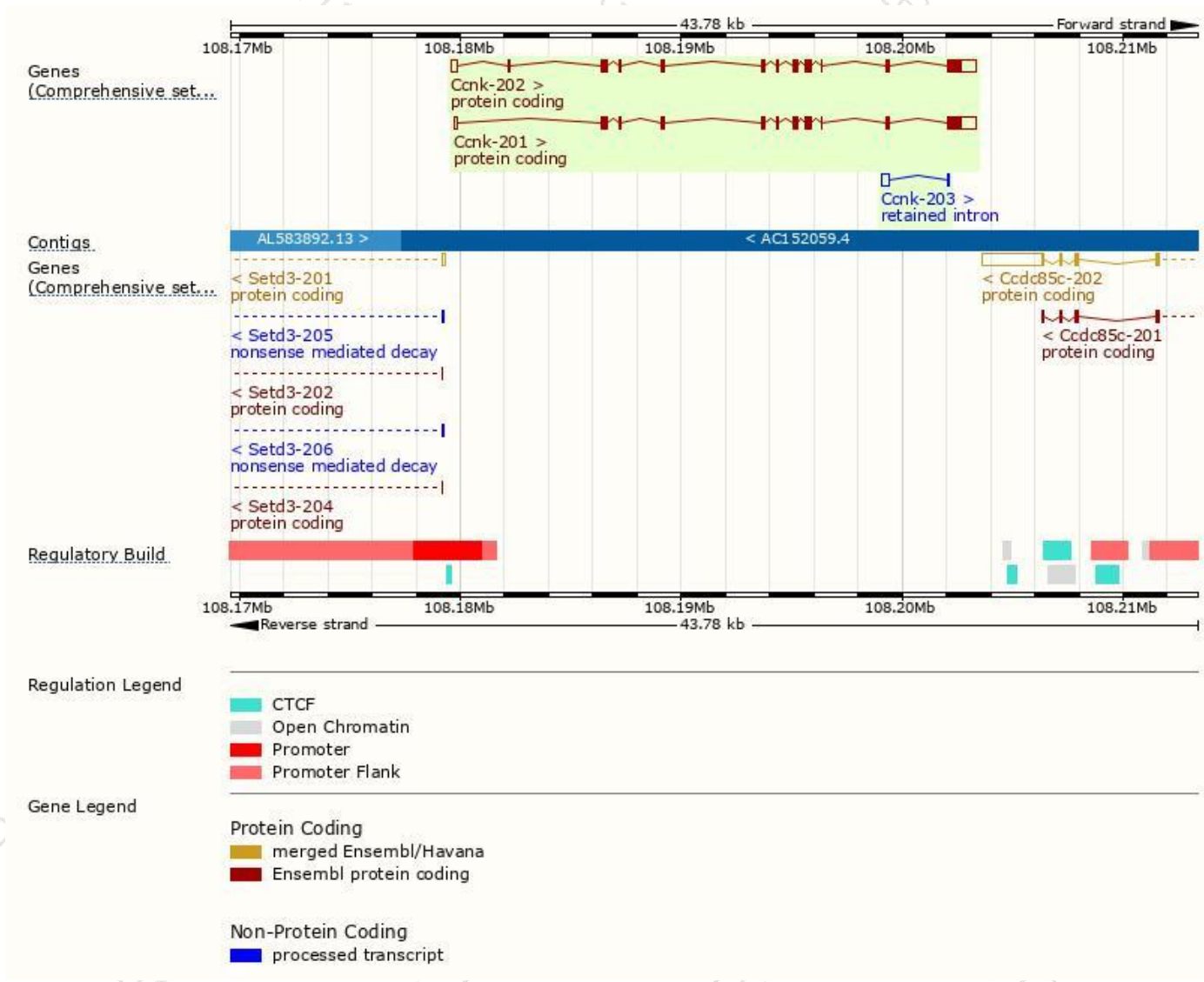
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccnk-202	<a href="#">ENSMUST00000221167.1</a>	2789	<a href="#">582aa</a>	Protein coding	<a href="#">CCDS49165</a>	<a href="#">Q3U3M5</a>	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
Ccnk-201	<a href="#">ENSMUST00000101055.4</a>	2627	<a href="#">582aa</a>	Protein coding	<a href="#">CCDS49165</a>	<a href="#">Q3U3M5</a>	TSL:5 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
Ccnk-203	<a href="#">ENSMUST00000223363.1</a>	370	No protein	Retained intron	-	-	TSL:2

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

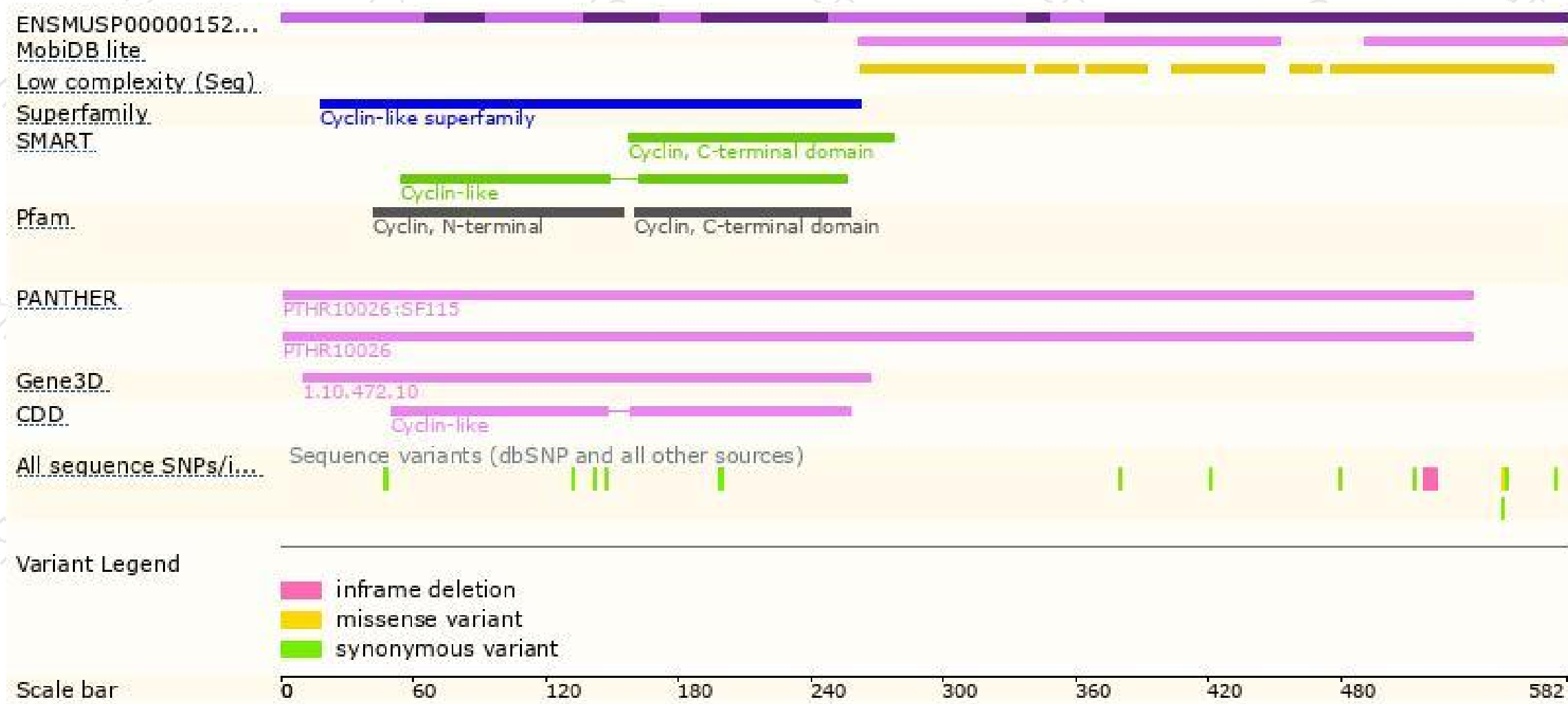


# Genomic location distribution

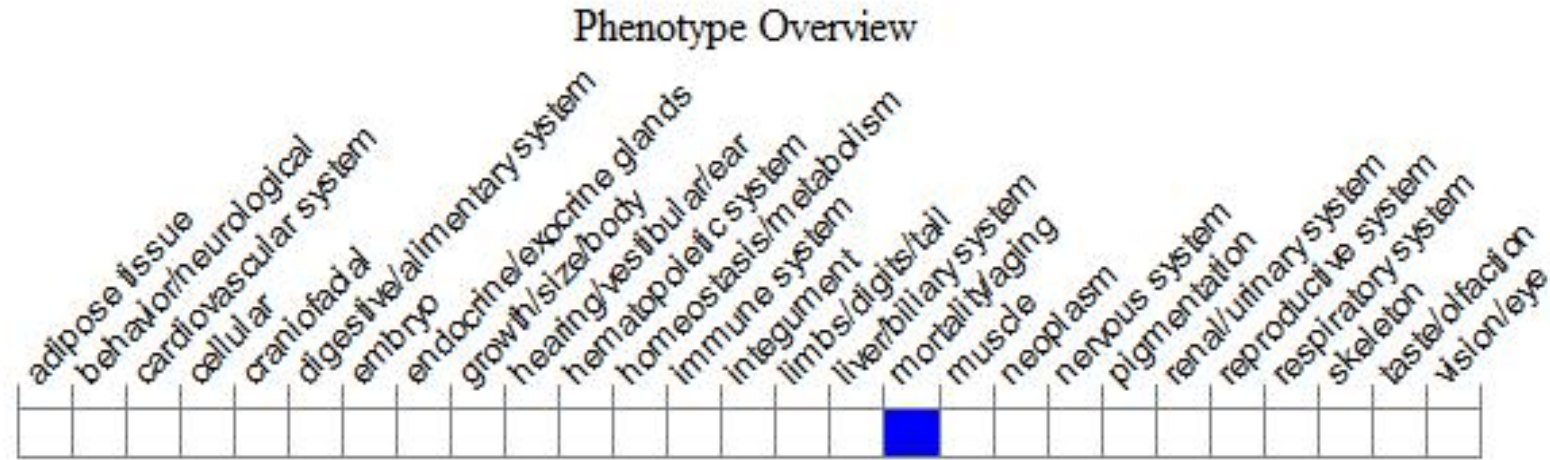




# Protein domain



# 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 gene trap allele display complete embryonic lethality before implantation.

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

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