

Ccne2 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Design Date: 2020-4-15

Project Overview

Project Name

Ccne2

Project type

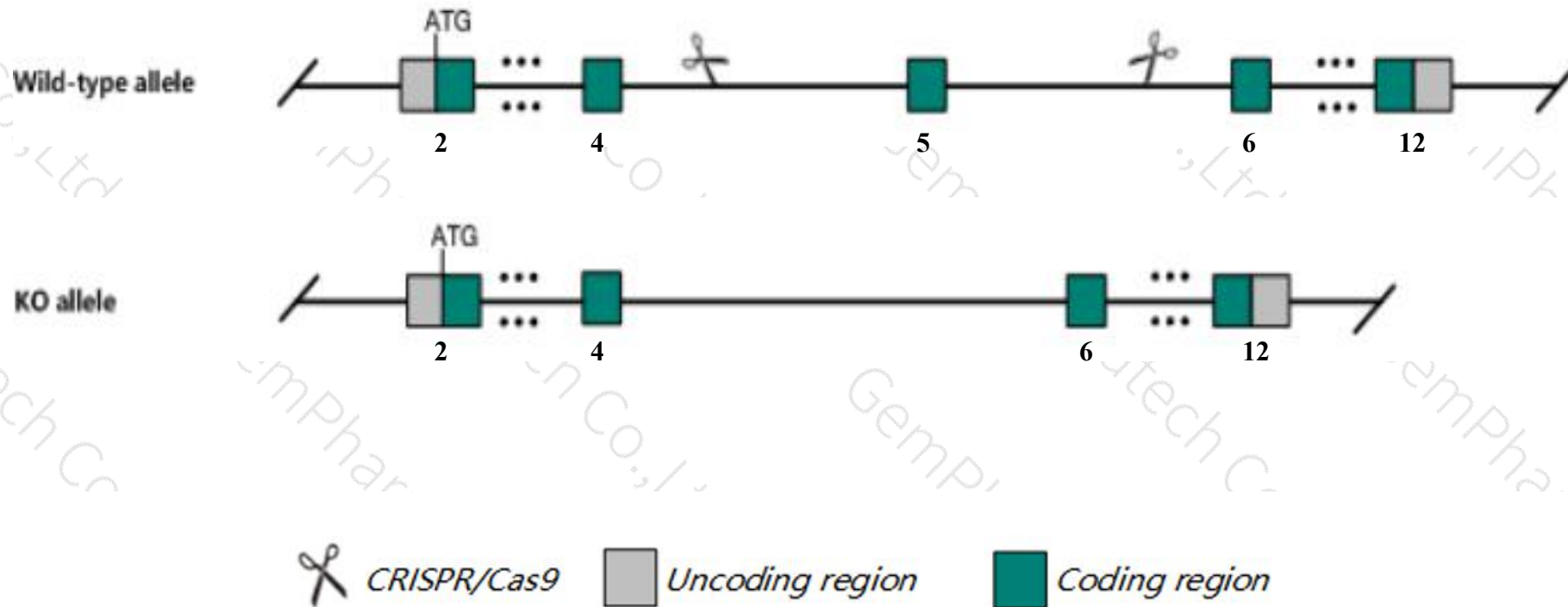
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccne2* gene. The schematic diagram is as follows:



- The *Ccne2* gene has 7 transcripts. According to the structure of *Ccne2* gene, exon5 of *Ccne2-207* (ENSMUST00000170901.7) transcript is recommended as the knockout region. The region contains 152bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ccne2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, female mice homozygous for disruptions in this gene are phenotypically normal. Male mice show reduced fertility but are otherwise normal.
- Transcript *Ccne2*-206 may not be affected.
- The *Ccne2* gene is located on the Chr4. 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)

Ccne2 cyclin E2 [Mus musculus (house mouse)]

Gene ID: 12448, updated on 13-Mar-2020

Summary

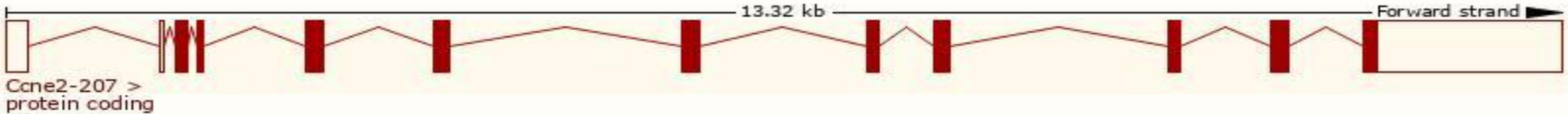
Official Symbol	Ccne2 provided by MGI
Official Full Name	cyclin E2 provided by MGI
Primary source	MGI:MGI:1329034
See related	Ensembl:ENSMUSG00000028212
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in liver E14 (RPKM 11.2), liver E14.5 (RPKM 8.4) and 13 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

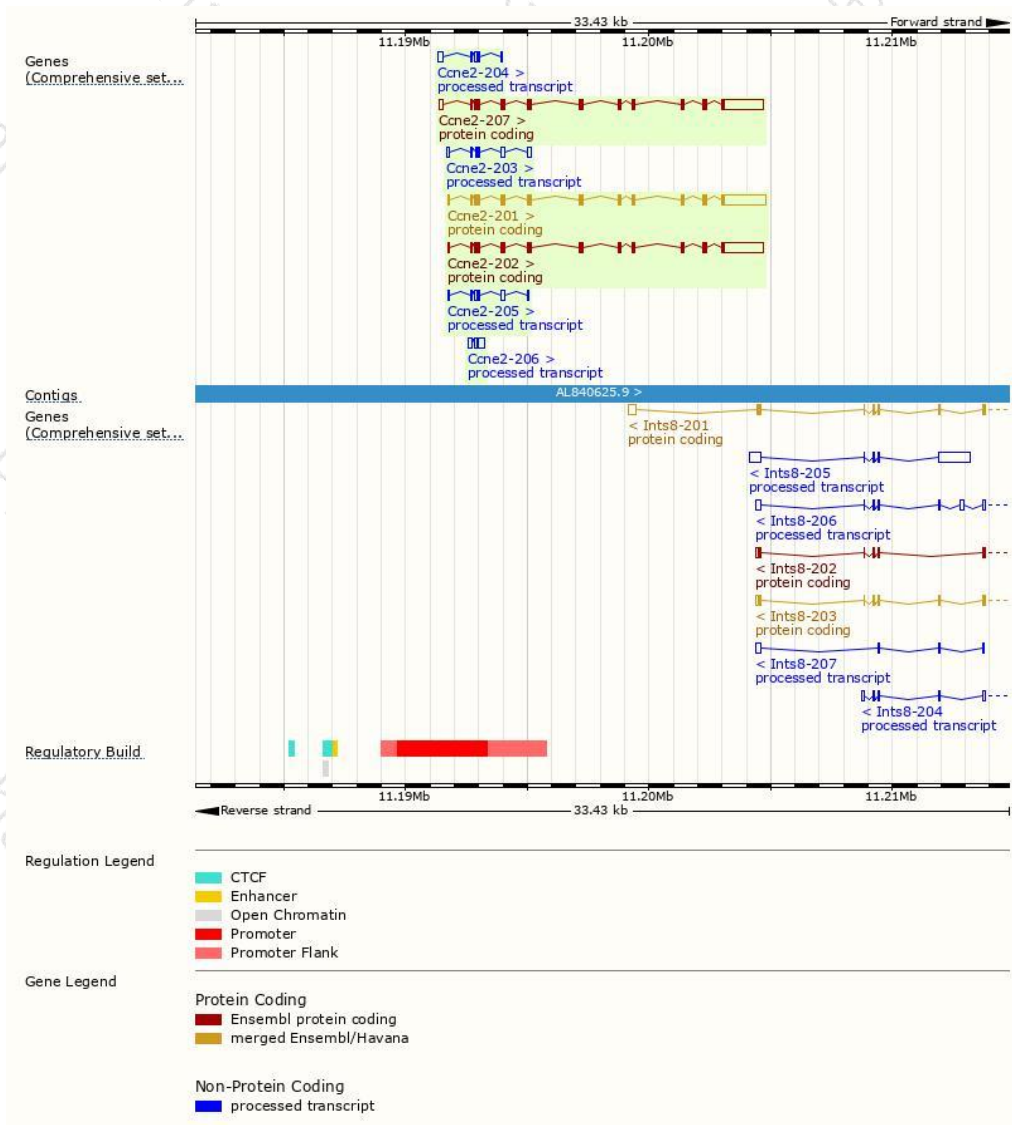
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccne2-201	ENSMUST00000029866.15	3006	403aa	Protein coding	CCDS17966	A2API1	TSL:1 GENCODE basic APPRIS ALT1
Ccne2-207	ENSMUST00000170901.7	3006	404aa	Protein coding	CCDS17965	Q544H6 Q9Z238	TSL:1 GENCODE basic APPRIS P4
Ccne2-202	ENSMUST00000108324.3	2908	404aa	Protein coding	CCDS17965	Q544H6 Q9Z238	TSL:1 GENCODE basic APPRIS P4
Ccne2-203	ENSMUST00000144438.7	535	No protein	Processed transcript	-	-	TSL:2
Ccne2-206	ENSMUST00000149075.1	461	No protein	Processed transcript	-	-	TSL:3
Ccne2-205	ENSMUST00000147725.7	432	No protein	Processed transcript	-	-	TSL:5
Ccne2-204	ENSMUST00000145430.7	418	No protein	Processed transcript	-	-	TSL:5

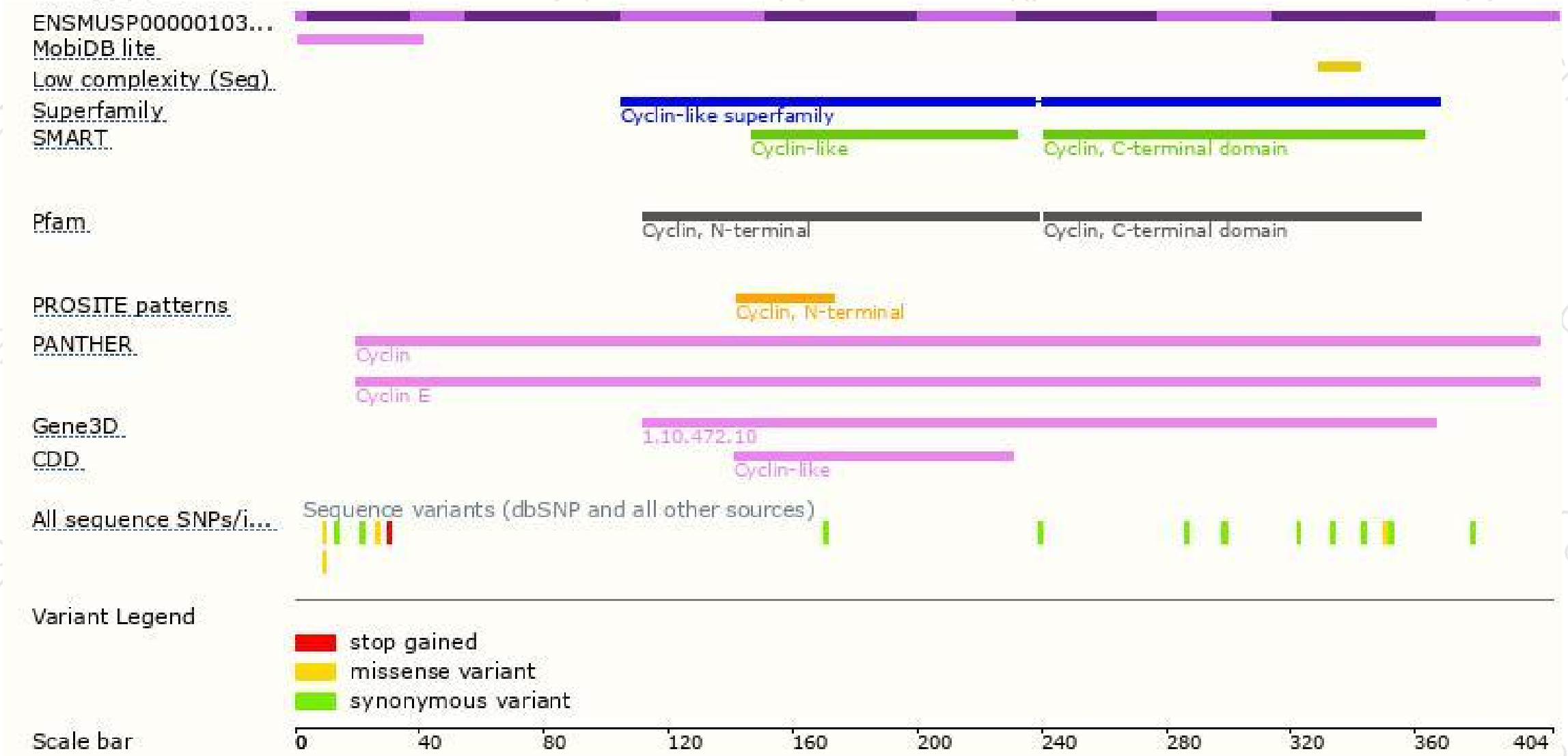
The strategy is based on the design of *Ccne2-207* transcript,the transcription is shown below



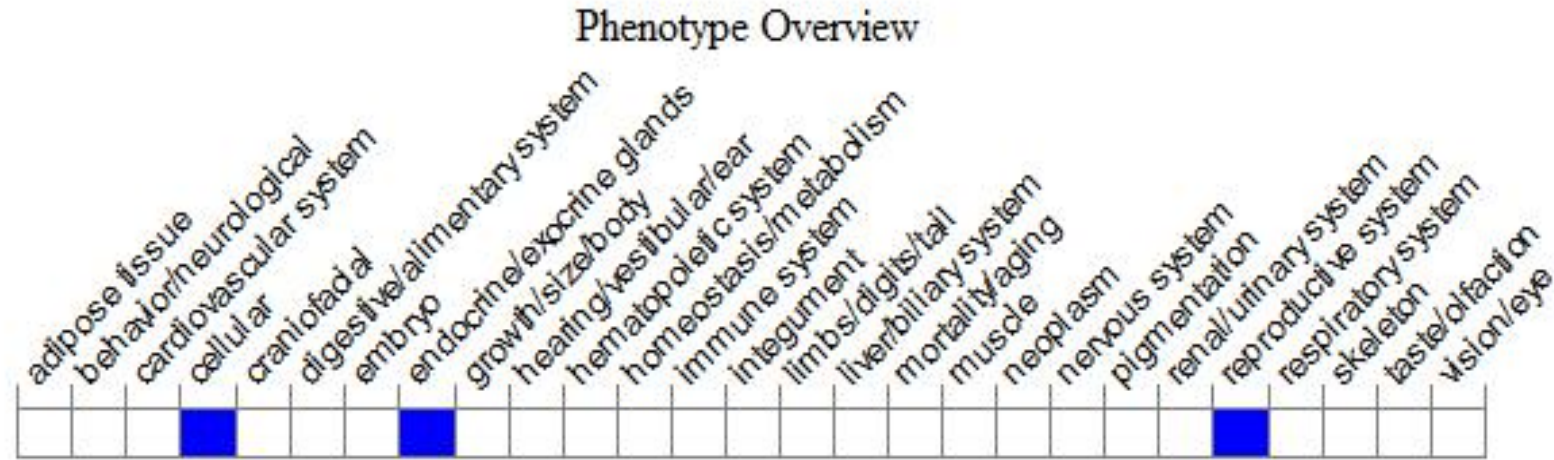
Genomic location distribution



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, female mice homozygous for disruptions in this gene are phenotypically normal.

Male mice show reduced fertility but are otherwise normal.

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

Tel: 400-9660890

