

Ccng1 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Date: 2019-12-23

Project Overview

Project Name

Ccng1

Project type

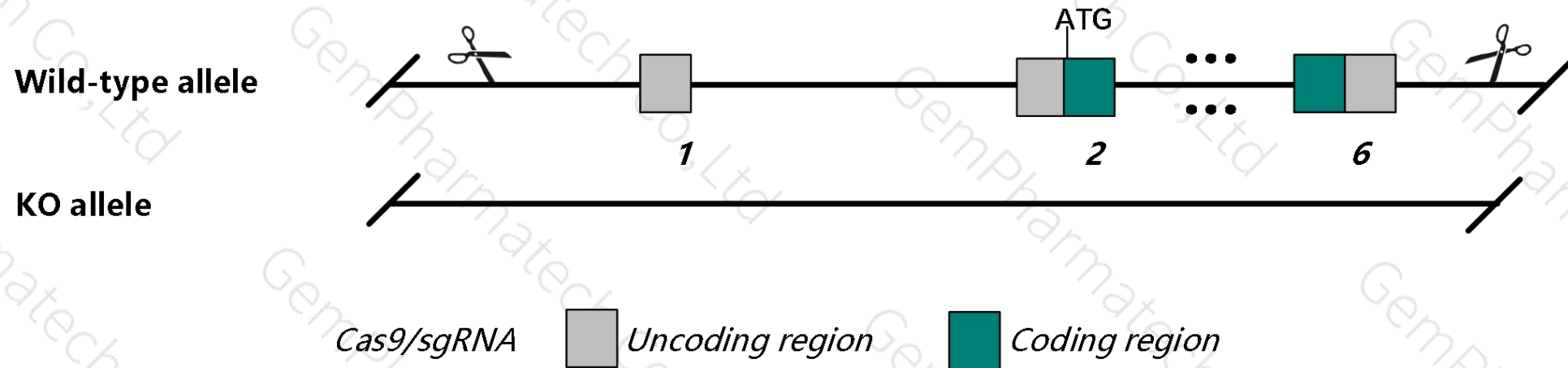
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccng1* gene. The schematic diagram is as follows:



- The *Ccng1* gene has 2 transcripts. According to the structure of *Ccng1* gene, exon1-exon6 of *Ccng1-201* (ENSMUST00000020576.7) 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 *Ccng1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Depending on the allele, homozygous mutants exhibit increased cellular sensitivity to gamma-irradiation or decreased incidence of induced hepatic tumors.
- The *Ccng1* gene is located on the Chr11. 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)

Ccng1 cyclin G1 [*Mus musculus* (house mouse)]

Gene ID: 12450, updated on 12-Nov-2019

Summary

- Official Symbol Ccng1 provided by MGI
- Official Full Name cyclin G1 provided by MGI
- Primary source MGI:MGI:102890
- See related Ensembl:ENSMUSG00000020326
- 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 AI314029
- Expression Broad expression in heart adult (RPKM 67.7), bladder adult (RPKM 21.1) and 22 other tissues [See more](#)
- Orthologs [human](#) [all](#)

Genomic context

Location: 11; 11 A5 [See Ccng1 in Genome Data Viewer](#)

Exon count: 6

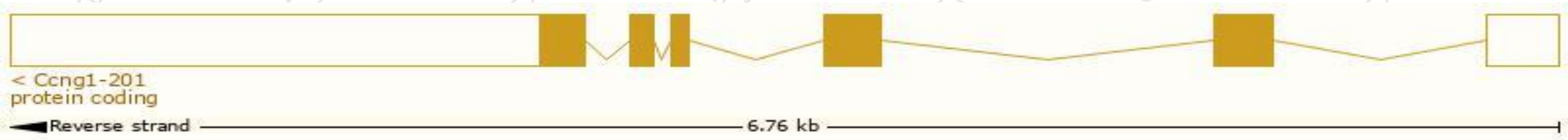
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (40748552..40755309, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (40562054..40568788, complement)

Transcript information (Ensembl)

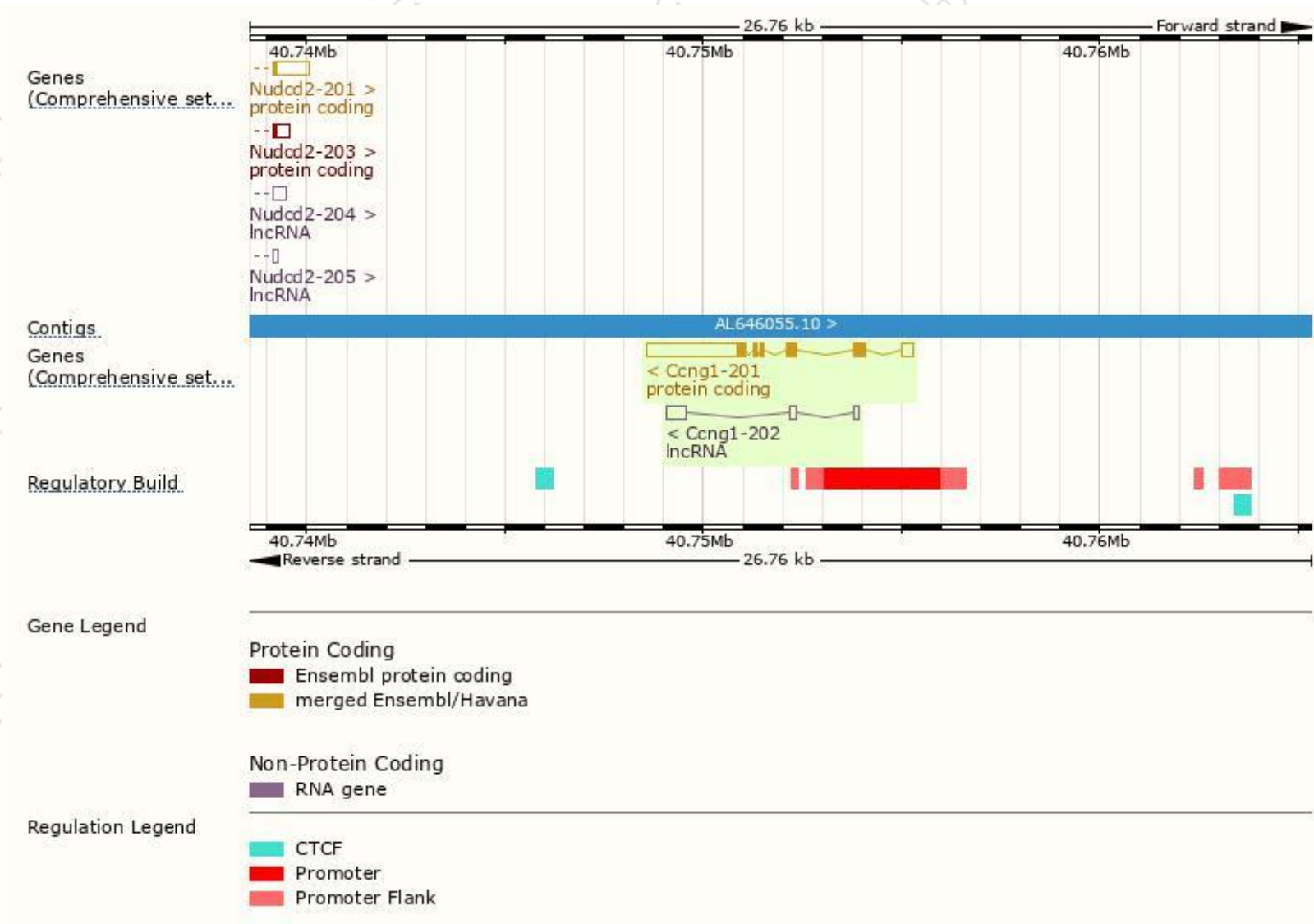
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccng1-201	ENSMUST00000020576.7	3512	294aa	Protein coding	CCDS24550	P51945 Q5NC86	TSL:1 GENCODE basic APPRIS P1
Ccng1-202	ENSMUST00000151359.1	804	No protein	lncRNA	-	-	TSL:5

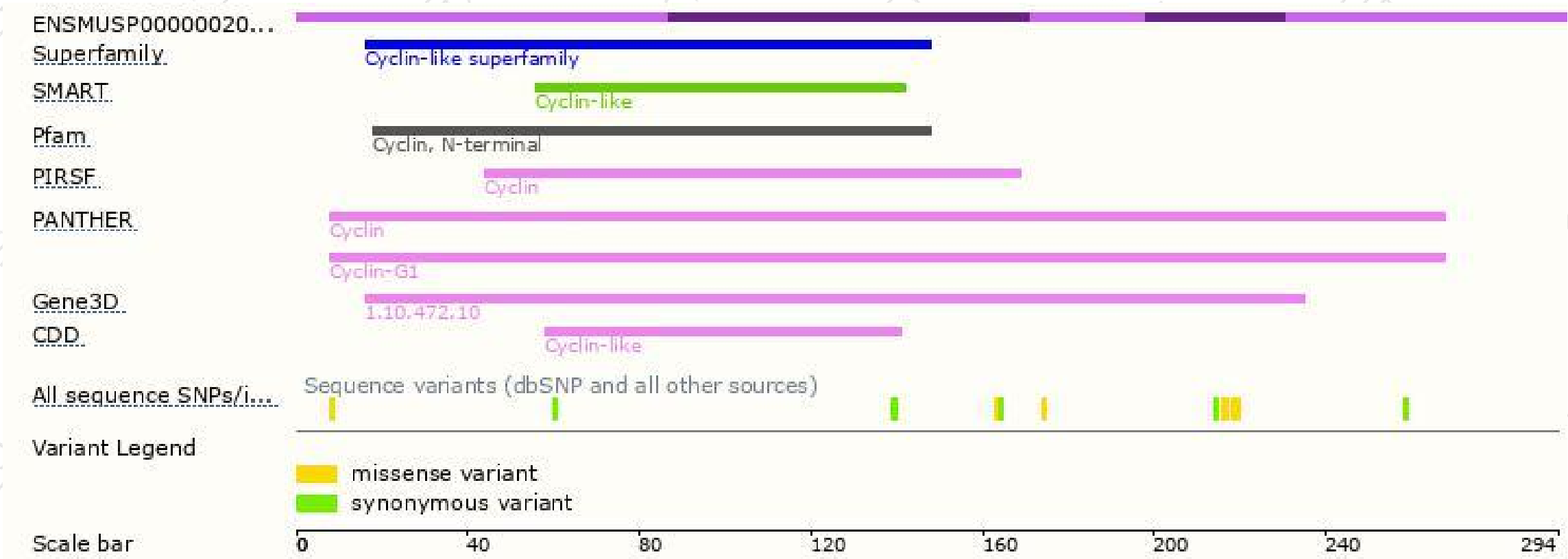
The strategy is based on the design of *Ccng1-201* transcript,The transcription is shown below



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, Depending on the allele, homozygous mutants exhibit increased cellular sensitivity to gamma-irradiation or decreased incidence of induced hepatic tumors.

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

Tel: 400-9660890

