Ccnl1 Cas9-KO Strategy

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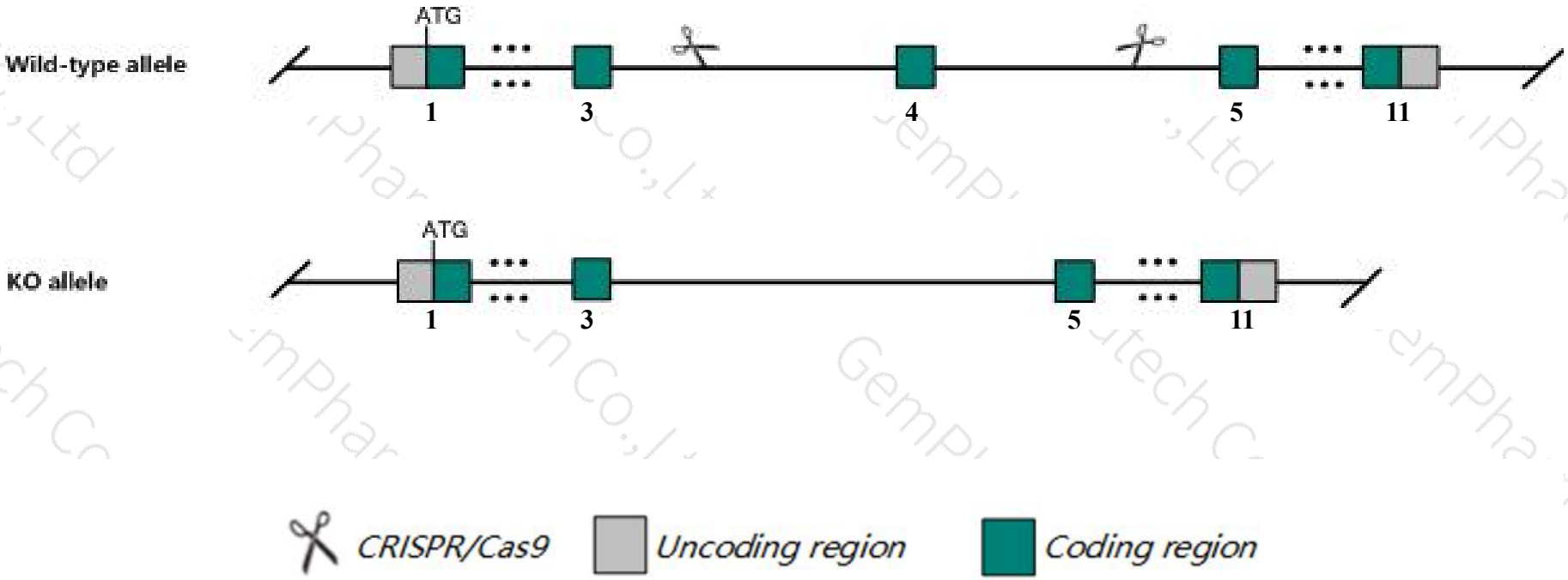
Project Overview

Project Name	***Ccnl1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccnl1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ccnl1* gene has 14 transcripts. According to the structure of *Ccnl1* gene, exon4 of *Ccnl1-201* (ENSMUST00000029416.13) transcript is recommended as the knockout region.The region contains 121bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ccnl1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- The *Ccnl1* gene is located on the Chr3. 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.

- Some amino acids will remain at the N-terminus and some functions may be retained.

- 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）

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Ccnl1 cyclin L1 [Mus musculus (house mouse)]

Gene ID: 56706, updated on 19-Mar-2019

Summary

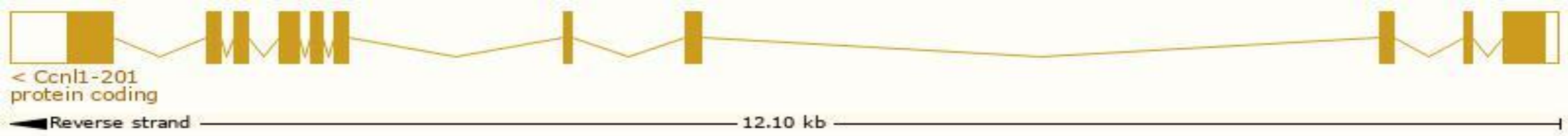
Official Symbol	Ccnl1 provided by MGI
Official Full Name	cyclin L1 provided by MGI
Primary source	MGI:MGI:1922664
See related	Ensembl:ENSMUSG00000027829
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610030E23Rik, AU018493, Ccnl, ania-6a
Expression	Ubiquitous expression in ovary adult (RPKM 21.2), thymus adult (RPKM 20.1) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

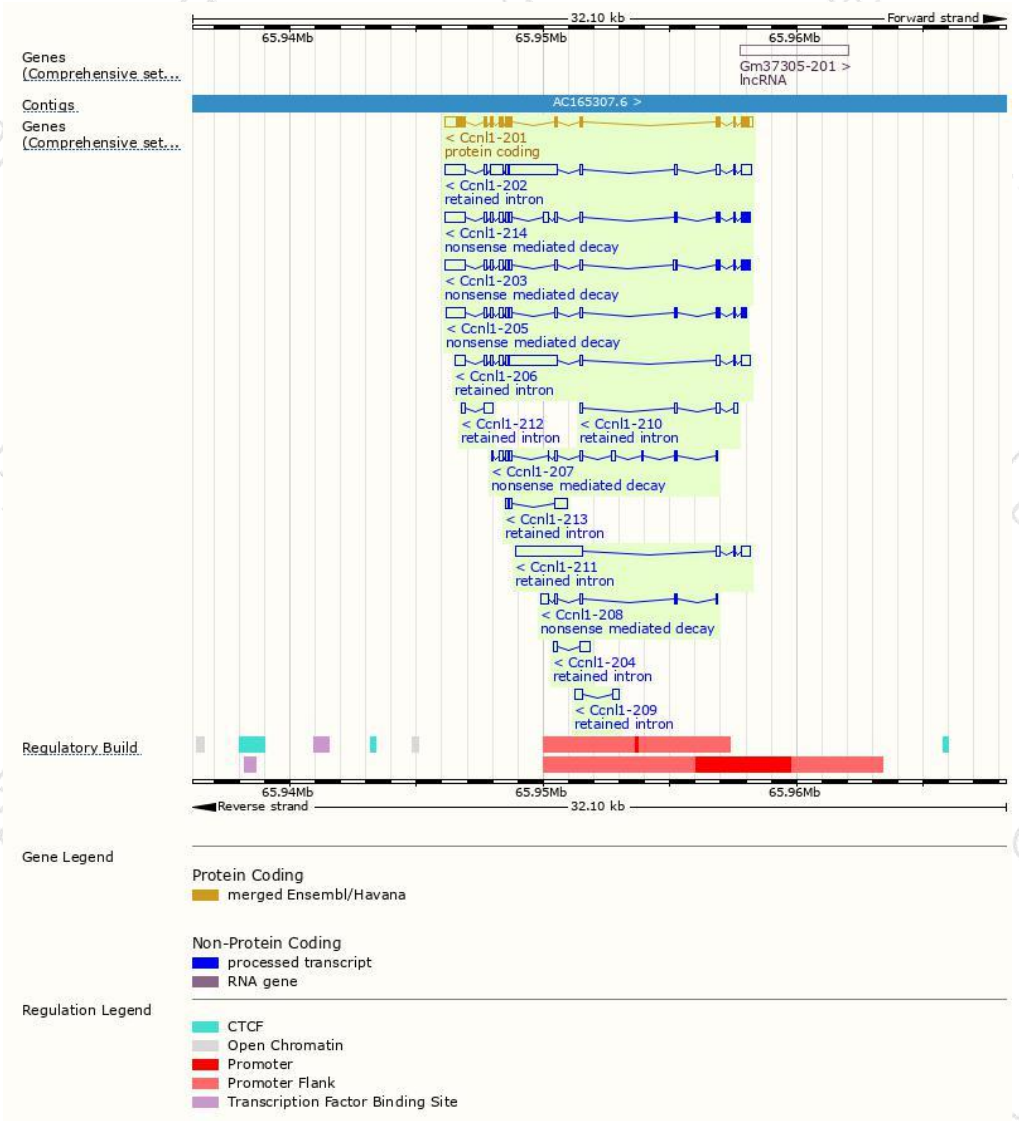
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccnl1-201	ENSMUST00000029416.13	2169	532aa	Protein coding	CCDS17390	Q52KE7	TSL:1 GENCODE basic APPRIS P1
Ccnl1-214	ENSMUST00000154585.7	2364	178aa	Nonsense mediated decay	-	F6WYR6	TSL:5
Ccnl1-203	ENSMUST00000129002.7	2229	178aa	Nonsense mediated decay	-	F6WYR6	TSL:1
Ccnl1-205	ENSMUST00000135719.7	1981	146aa	Nonsense mediated decay	-	F6WST0	CDS 5' incomplete TSL:5
Ccnl1-207	ENSMUST00000144810.7	896	11aa	Nonsense mediated decay	-	F7BER3	CDS 5' incomplete TSL:5
Ccnl1-208	ENSMUST00000145186.7	622	22aa	Nonsense mediated decay	-	F7BI63	CDS 5' incomplete TSL:3
Ccnl1-202	ENSMUST00000122919.7	4134	No protein	Retained intron	-	-	TSL:1
Ccnl1-206	ENSMUST00000142153.7	3414	No protein	Retained intron	-	-	TSL:1
Ccnl1-211	ENSMUST00000149160.7	3222	No protein	Retained intron	-	-	TSL:1
Ccnl1-213	ENSMUST00000150304.1	692	No protein	Retained intron	-	-	TSL:5
Ccnl1-204	ENSMUST00000132998.1	573	No protein	Retained intron	-	-	TSL:2
Ccnl1-209	ENSMUST00000146284.1	563	No protein	Retained intron	-	-	TSL:2
Ccnl1-212	ENSMUST00000149729.1	475	No protein	Retained intron	-	-	TSL:1
Ccnl1-210	ENSMUST00000148623.1	457	No protein	Retained intron	-	-	TSL:3

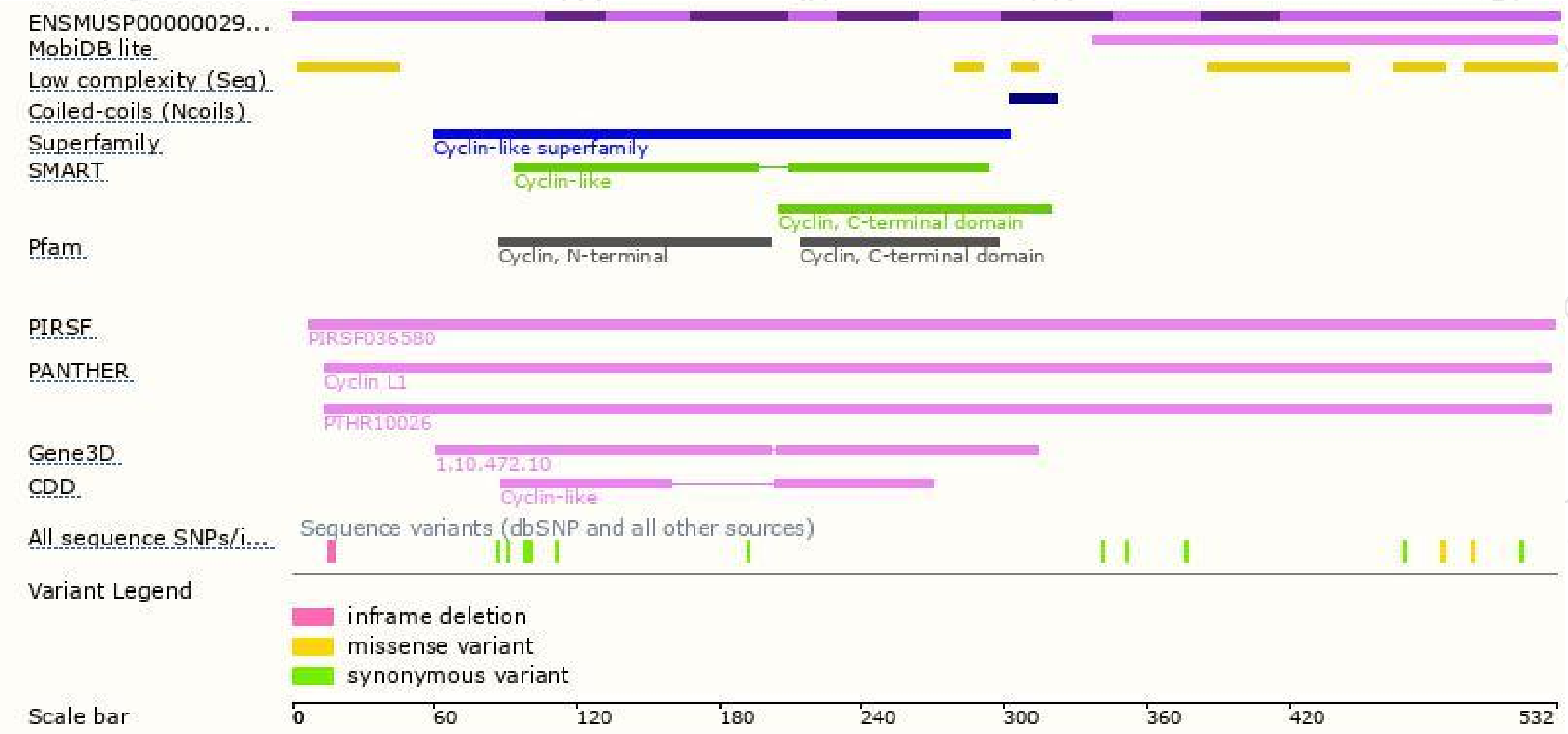
The strategy is based on the design of *Ccnl1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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