Ccne1 Cas9-CKO Strategy

Designer: Ruirui Zhang
Reviewer. Huimin Su

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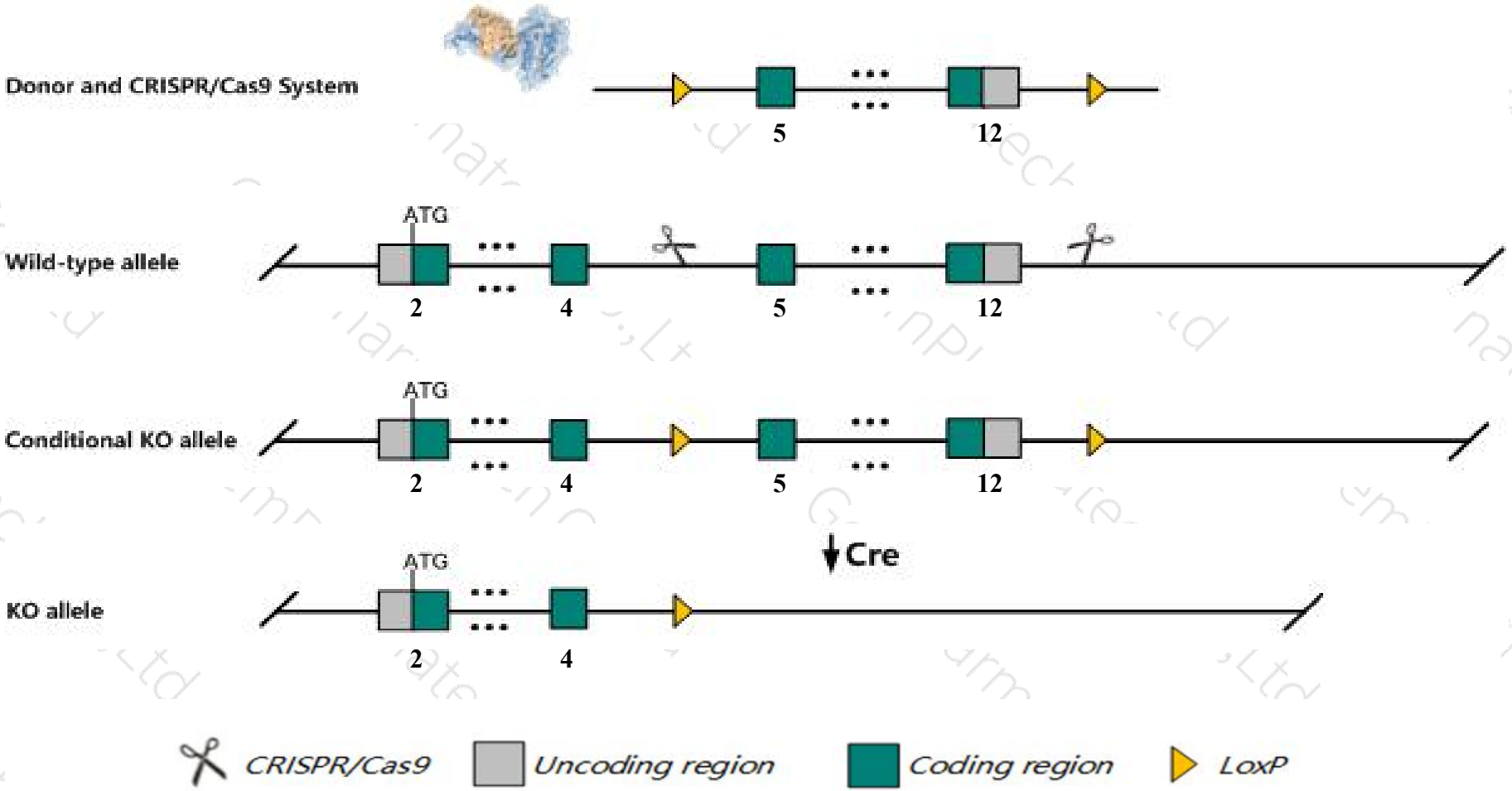
GemPharmatech Co.,Ltd

Project Overview

Project Name	***Ccne1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccne1* gene. The schematic diagram is as follows:



Technical routes

- The *Ccne1* gene has 5 transcripts. According to the structure of *Ccne1* gene, exon5-exon12 of *Ccne1-201* (ENSMUST00000108023.9) 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 *Ccne1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,mice homozygous for disruptions in this gene display no abnormal phenotype.

- The *Ccne1* gene is located on the Chr7. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Ccne1 cyclin E1 [*Mus musculus* (house mouse)]

Gene ID: 12447, updated on 13-Aug-2019

Summary

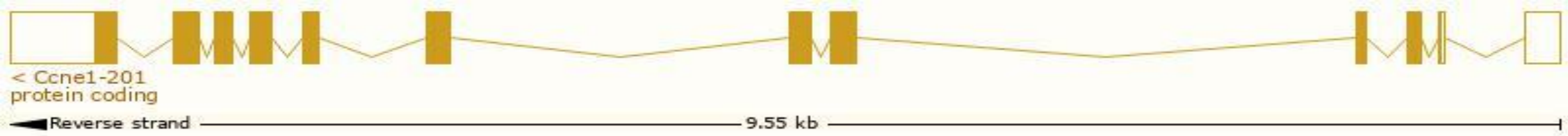
Official Symbol	Ccne1 provided by MGI
Official Full Name	cyclin E1 provided by MGI
Primary source	MGI:MGI:88316
See related	Ensembl:ENSMUSG00000002068
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CycE1; AW538188
Expression	Broad expression in liver E14 (RPKM 46.5), liver E14.5 (RPKM 42.0) and 16 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

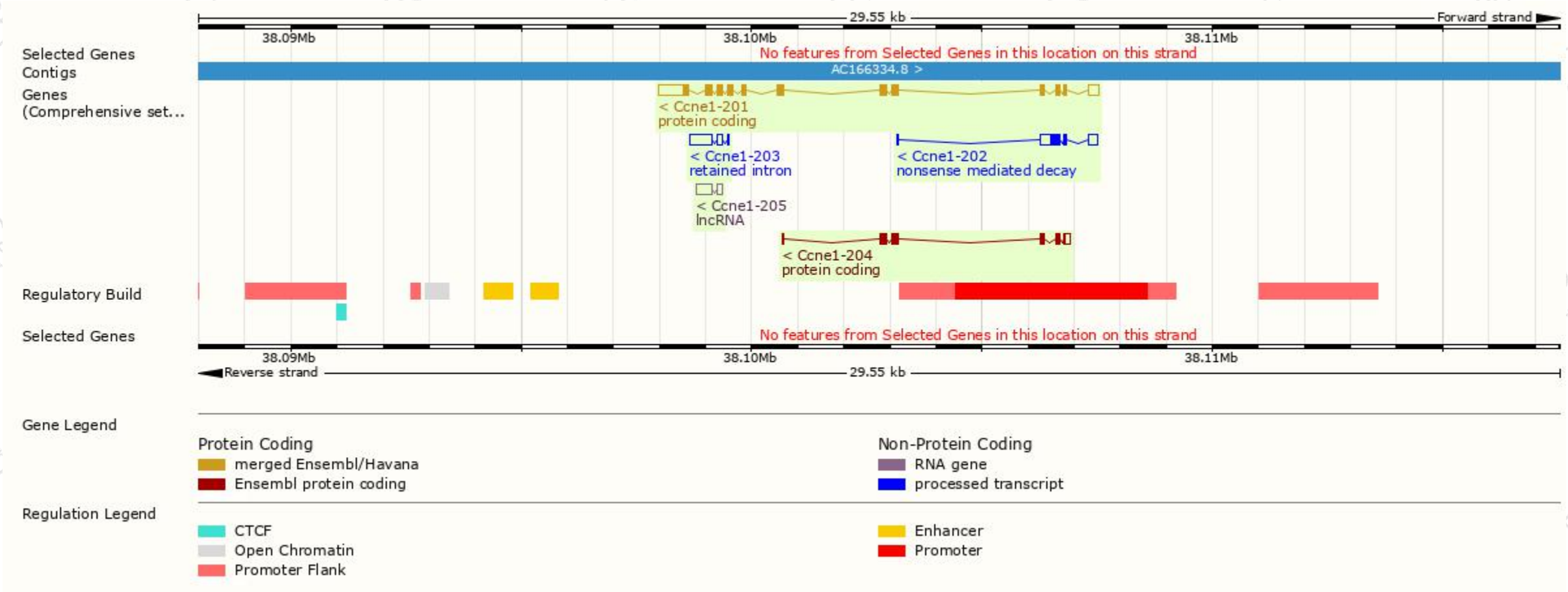
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccne1-201	ENSMUST00000108023.9	2000	408aa	Protein coding	CCDS39914	Q61457	TSL:1 GENCODE basic APPRIS P1
Ccne1-204	ENSMUST00000130329.1	608	166aa	Protein coding	-	D3Z3N8	CDS 3' incomplete TSL:3
Ccne1-202	ENSMUST00000124979.2	656	69aa	Nonsense mediated decay	-	A0A0U1RNE6	TSL:5
Ccne1-203	ENSMUST00000128785.1	628	No protein	Retained intron	-	-	TSL:2
Ccne1-205	ENSMUST00000137097.1	462	No protein	lncRNA	-	-	TSL:5

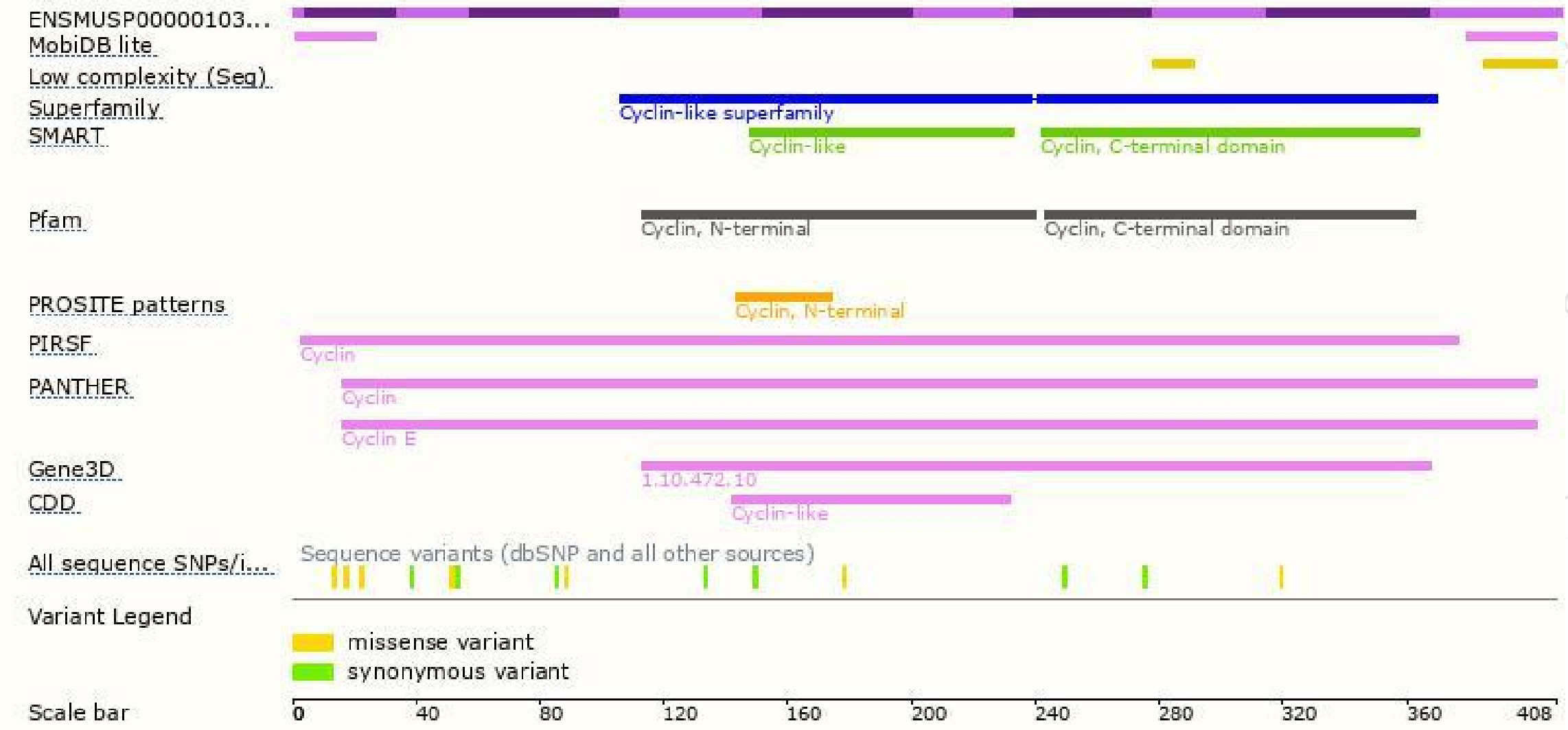
The strategy is based on the design of *Ccne1-201* transcript, The transcription is shown below



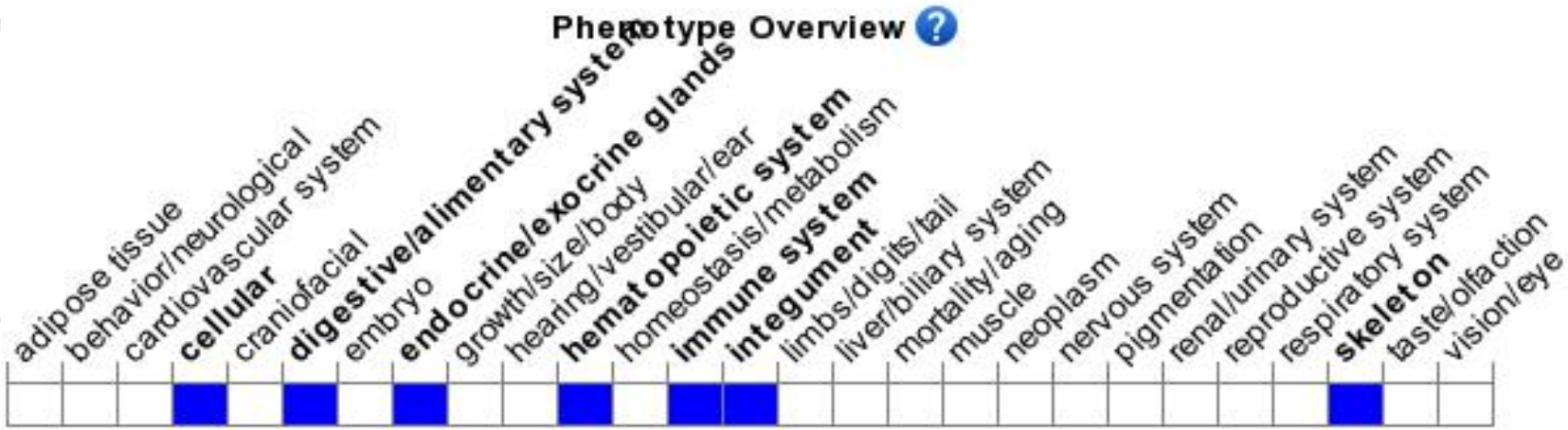
Genomic location distribution



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,Mice homozygous for disruptions in this gene display no abnormal phenotype.

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GemPharmatech

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

Tel: 400-9660890

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