

Ccnd1 Cas9-KO Strategy

Designer: Reviewer:

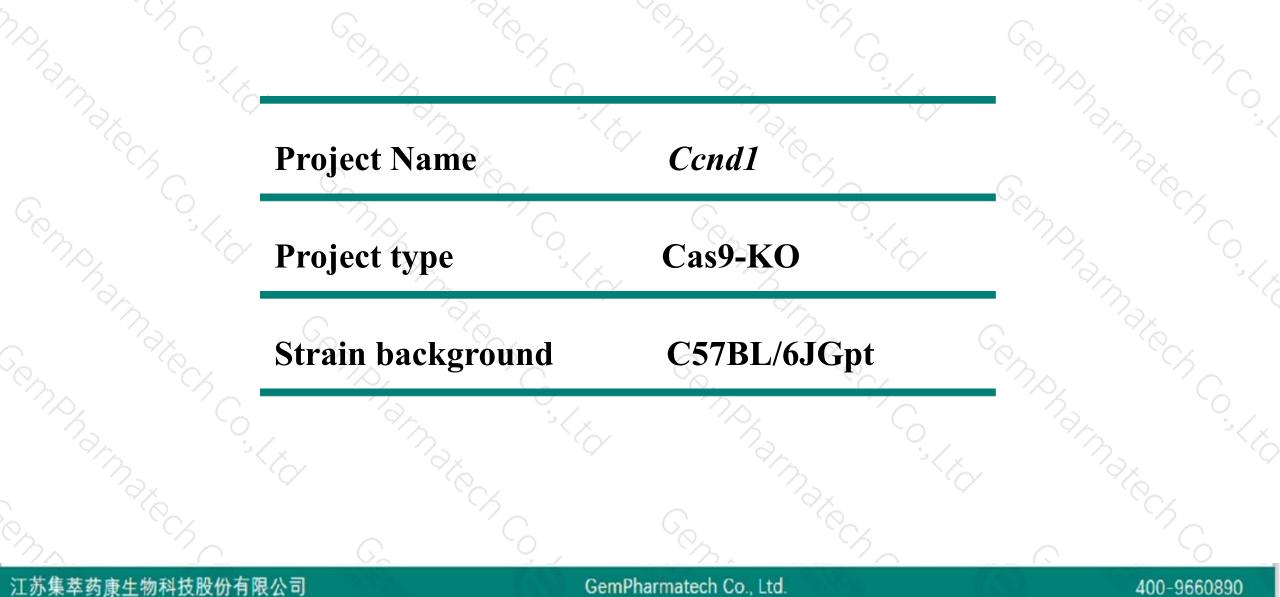
Design Date:

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2018-9-5

Project Overview

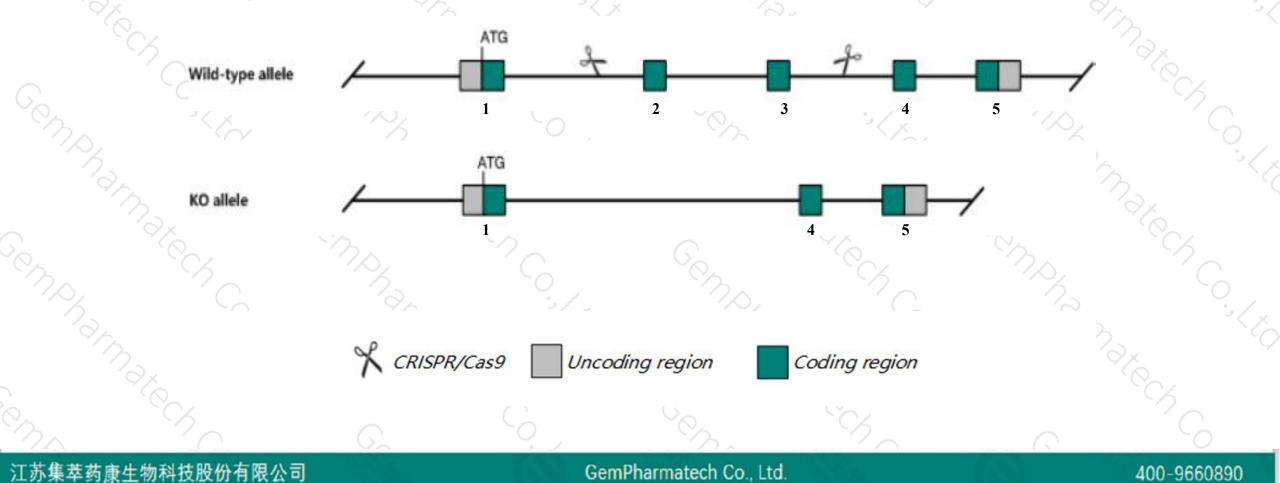




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Ccnd1 gene. The schematic diagram is as follows:





- The Ccnd1 gene has 3 transcripts. According to the structure of Ccnd1 gene, exon2-exon3 of Ccnd1-201 (ENSMUST00000093962.4) transcript is recommended as the knockout region. The region contains 376bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Ccnd1 gene. The brief process is as follows: CRISPR/Cas9 system



According to the existing MGI data,homozygotes for targeted mutations may exhibit reduced body size and viability, impaired retinal development, pregnancy-insensitive mammary glands, and modified development of mammary cancer induced by neu and ras oncogenes, depending on the specific allele or genetic background.
The *Ccnd1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



☆ ?

Ccnd1 cyclin D1 [Mus musculus (house mouse)]

Gene ID: 12443, updated on 13-Mar-2020

- Summary

Official SymbolCcnd1 provided by MGIOfficial Full Namecyclin D1 provided by MGIPrimary soureMGI:MGI:88313See relatedEnsembl:ENSMUSG0000070348Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusAlso known asAl327039, CycD1, Cyl-1, PRAD1, bcl-1, cD1ExpressionUbiquitous expression in CNS E11.5 (RPKM 58.4), adrenal adult (RPKM 54.1) and 27 other tissuesSee more
human all

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Transcript information (Ensembl)



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

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags TSL:1 GENCODE basic APPRIS P1 | | |
|-----------|----------------------|------|--------------|-----------------|-----------|---------------|--|--|--|
| Ccnd1-201 | ENSMUST0000093962.4 | 3740 | <u>295aa</u> | Protein coding | CCDS22055 | P25322 Q790L7 | | | |
| Ccnd1-203 | ENSMUST00000208193.1 | 1773 | No protein | Retained intron | - | i) | TSL:1 | | |
| Ccnd1-202 | ENSMUST00000135985.1 | 470 | No protein | Retained intron | 140 | 140 | TSL:2 | | |

The strategy is based on the design of *Ccnd1-201* transcript, the transcription is shown below:

< Cond1-201 protein coding

Reverse strand

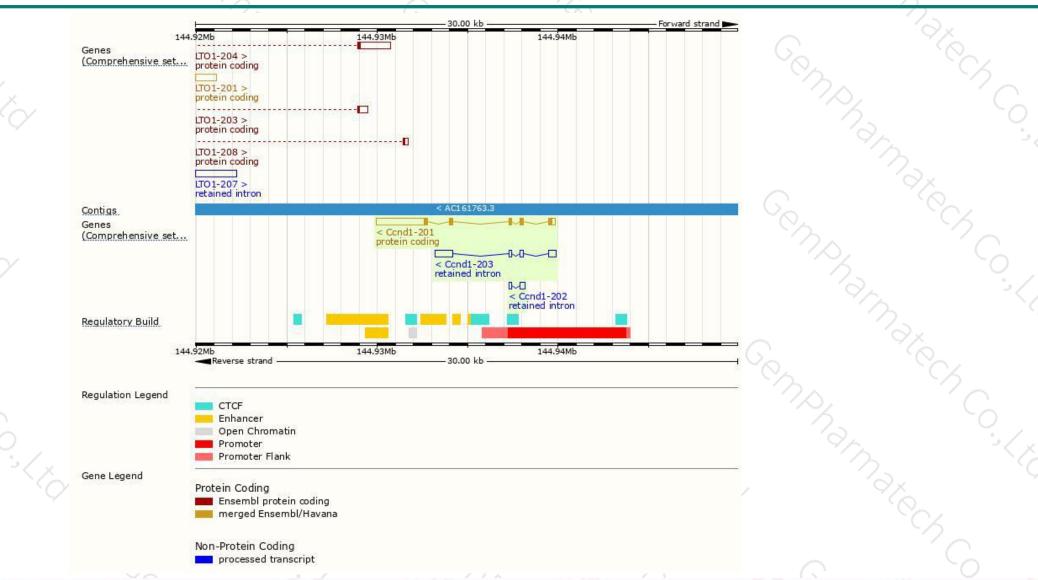
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9.94 kb

Genomic location distribution





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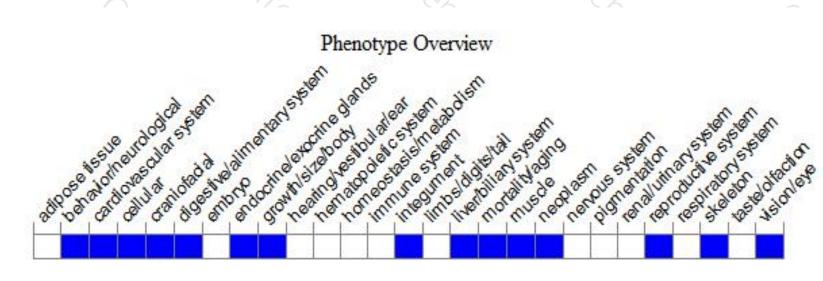
Protein domain



| | Low complexity (Seg) Superfamily SMART | Oyclin-like su | perfamily | | Cyclin, C-termi | inal domain | | 9 - ¹ - 1 | |
|-------|--|--------------------------------|-------------------------|----------|-----------------|-------------|----------|----------------------|----------------------|
| | Pfam. | Cyclin, N- | Cyclin-like terminal | | Cyclin, C-termi | 0 10000 200 | | _ | |
| Con 1 | PROSITE patterns | | Cyclin, N-terminal | | | | | | C |
| | PIRSF | Cyclin | | | | | | | - °O |
| | PANTHER | Cyclin | | | | | | | |
| | Gene3D | Cyclin D | 0 | | | | | | |
| | CDD | spin d als Style 1 at 4 mod at | Cyclin-like | | | | | | |
| | All sequence SNPs/i | Sequence variants | (dbSNP and all other | sources) | | | <u>a</u> | 1 | - <mark>1</mark> 9-2 |
| | Variant Legend | missense varia | | | | | | | |
| | Scale bar | 0 40 | 80 | 120 | 160 | 200 | 240 | | 295 |

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, homozygotes for targeted mutations may exhibit reduced body size and viability, impaired retinal development, pregnancy-insensitive mammary glands, and modified development of mammary cancer induc neu and ras oncogenes, depending on the specific allele or genetic background.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



