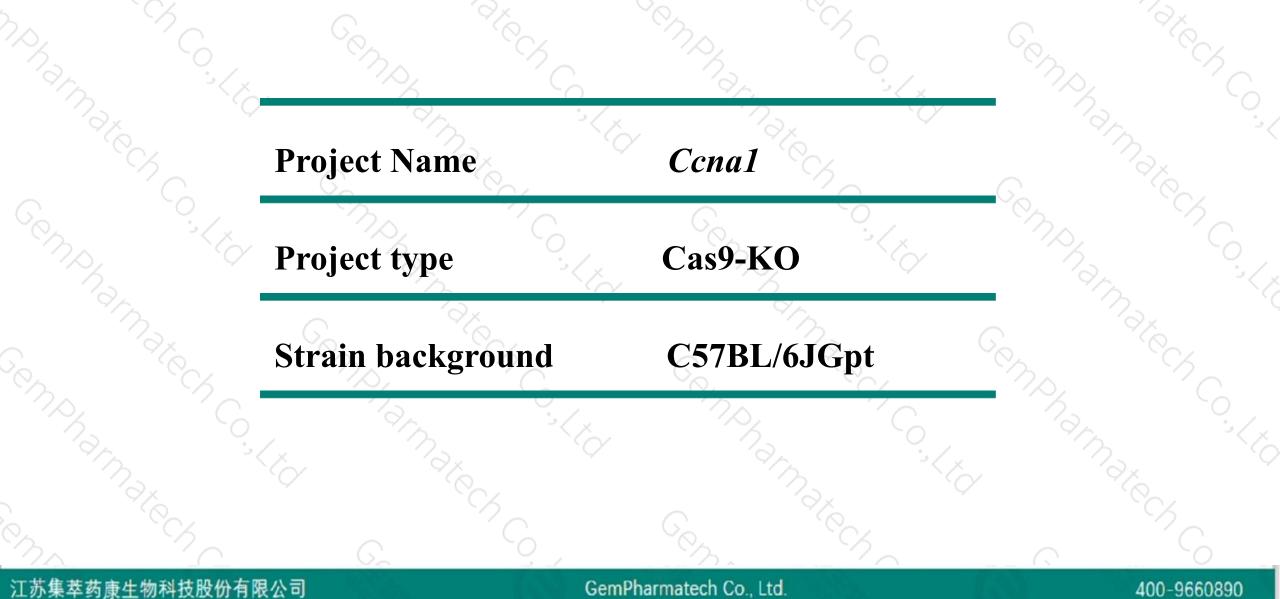


Ccnal Cas9-KO Strategy

Designer: Reviewer.gz Design Date: Ruirui Zhang Huimin Su 2019-8-30

Project Overview

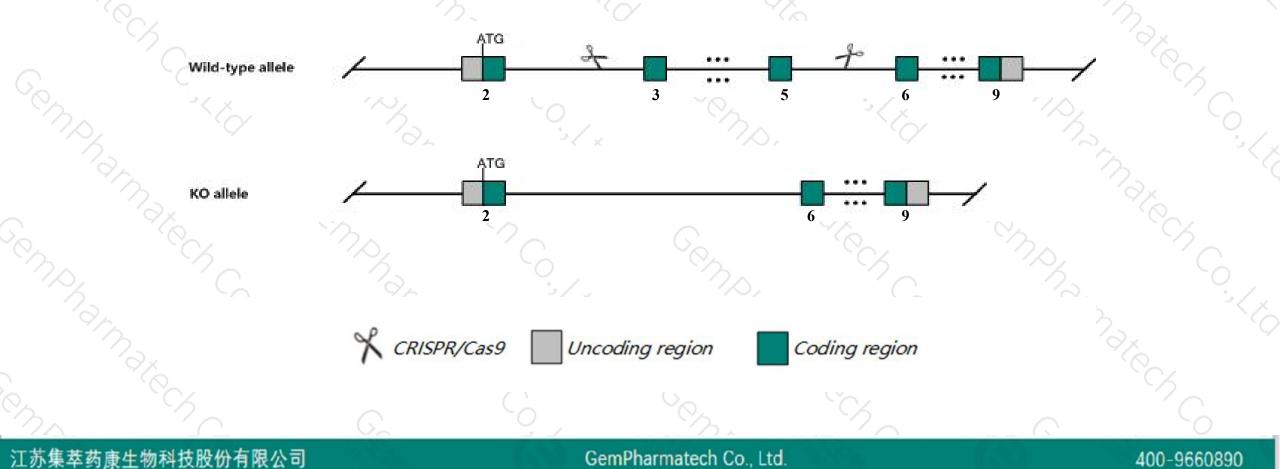




Knockout strategy



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





- The Ccnal gene has 6 transcripts. According to the structure of Ccnal gene, exon3-exon5 of Ccnal-202 (ENSMUST00000197238.4) transcript is recommended as the knockout region. The region contains 596bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Ccnal gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, homozygous null males are infertile due to the arrest of spermatogenesis prior to the first meiotic division. Female mutant mice are fertile.
- > This strategy may affect the 5 terminal regulatory function of *4931419H13Rik* gene.
- The Ccnal 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.
- 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.

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Gene information (NCBI)



Ccna1 cyclin A1 [Mus musculus (house mouse)]

Gene ID: 12427, updated on 14-Aug-2019

- Summary

Official Symbol	Ccna1 provided by MGI
Official Full Name	cyclin A1 provided by MGI
Primary source	MGI:MGI:108042
See related	Ensembl:ENSMUSG0000027793
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 testis adult (RPKM 38.8) and limb E14.5 (RPKM 0.7) See more
Orthologs	human all

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400-9660890

☆ ?

Transcript information (Ensembl)



The gene has 6 transcripts, all transcripts are shown below:

Name 🍦	Transcript ID 🍦	bp 🖕	Protein 🖕	Biotype 🍦	CCDS 🖕	UniProt 🔻	Flags
Ccna1-202	ENSMUST00000197238.4	1719	<u>421aa</u>	Protein coding	CCDS17356	<u>Q61456</u> &	TSL:5 GENCODE basic APPRIS P1
Ccna1-204	ENSMUST00000198320.4	1564	<u>421aa</u>	Protein coding	<u>CCDS17356</u>	<u>Q61456</u> &	TSL:1 GENCODE basic APPRIS P1
Ccna1-201	ENSMUST0000029368.6	1560	<u>421aa</u>	Protein coding	CCDS17356	<u>Q61456</u> &	TSL:1 GENCODE basic APPRIS P1
Ccna1-206	ENSMUST00000199352.1	391	<u>93aa</u>	Protein coding		<u>A0A0G2JGG4</u> &	CDS 3' incomplete TSL:5
Ccna1-205	ENSMUST00000199144.4	749	<u>165aa</u>	Protein coding	979	A0A0G2JFR4	CDS 3' incomplete TSL:5
Ccna1-203	ENSMUST00000198102.4	876	<u>250aa</u>	Protein coding		A0A0G2JEB5	CDS 5' incomplete TSL:3

The strategy is based on the design of *Ccna1-202* transcript, The transcription is shown below

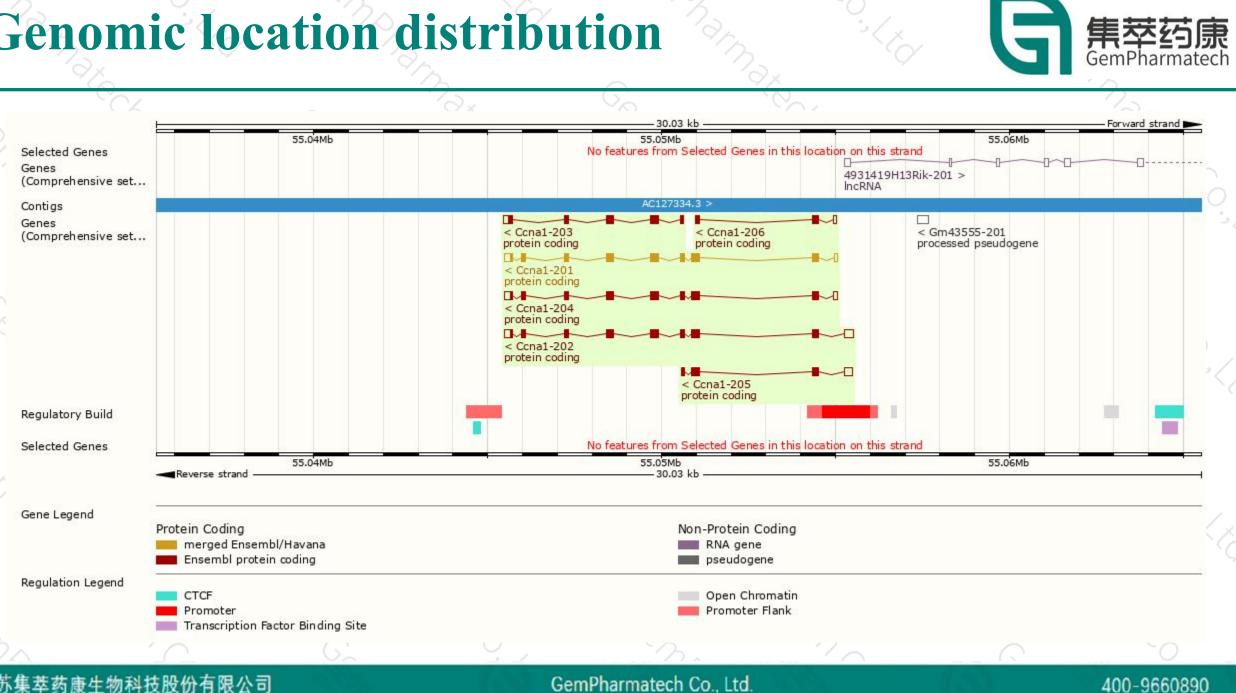
< Ccna1-202 protein coding

- 10.02 kb

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Genomic location distribution



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Protein domain



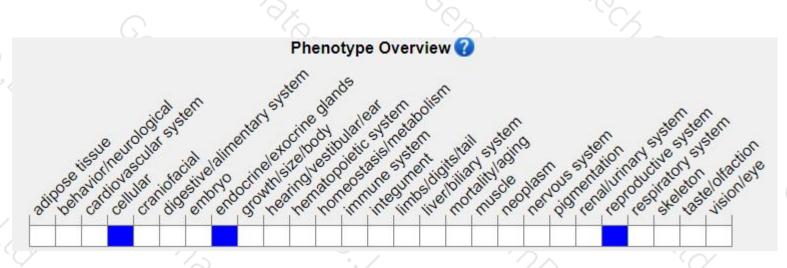
	10		(Co)							
2	ENSMUSP00000142 Superfamily SMART			Cyclin-lik	e superfamily <mark>Oyclin-lil</mark>			-		S.
	<u>Pfam</u>			Cyclin	, N-terminal	-	Cyclin, C-termi Cyclin, C-termi	NG/SA		
	PROSITE patterns				Cyclin, N-1	termin al				
	PANTHER		Dyclin							0
		F	THR10177:SF254							
	Gene3D CDD			1,10,	472.10 Cyclin-like					
	All sequence SNPs/i	Sequence variants	(dbSNP and all of	ther sources)		Ш	DC D	T.		
	Variant Legend	frameshift va missense var synonymous	iant							
	Scale bar	o 40	80 120	160	200	240	280 320	360	421	
	~~~	G,	í G	5		^c S _c			6	

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### 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, homozygous null males are infertile due to the arrest of spermatogenesis prior to the first meiotic division. Female mutant mice are fertile.

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



