

Ccnf Cas9-KO Strategy

Designer: Xueting Zhang

Design Date: 2019-8-2

Project Overview



Project Name

Project type

Strain background

Cenf

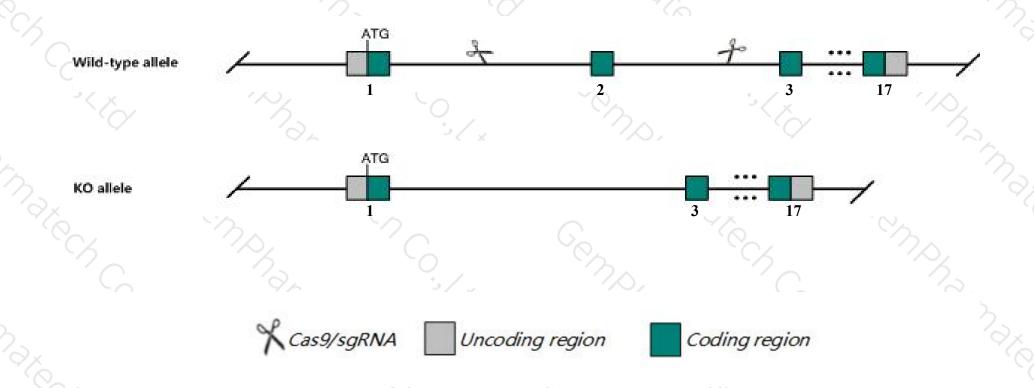
Cas9-KO

C57BL/6JGpt

Knockout strategy



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



Technical routes



- The *Ccnf* gene has 10 transcripts. According to the structure of *Ccnf* gene, exon2 of *Ccnf-201*(ENSMUST00000115390.4) transcript is recommended as the knockout region. The region contains 155bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ccnf* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice



- ➤ According to the existing MGI data, Homozygous mutation of this gene results in embryonic lethality between E9.5 and E10.5 due to defects in yolk sac and chorioallantoic placenta maturation. Embryos show incomplete turning, underdeveloped posterior structures, neural tube closure and braindefects. MEFs have cell cycle defects.
- > Transcript *Ccnf*-202&205&209 may not be affected.
- > The *Ccnf* gene is located on the Chr17. 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)



Ccnf cyclin F [Mus musculus (house mouse)]

Gene ID: 12449, updated on 3-Feb-2019

Summary

☆ ?

Official Symbol Conf provided by MGI

Official Full Name cyclin F provided by MGI

Primary source MGI:MGI:102551

See related Ensembl: ENSMUSG00000072082

Gene type protein coding
RefSeq status PROVISIONAL
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as CycF, Fbxo1

Expression Broad expression in liver E14.5 (RPKM 29.9), thymus adult (RPKM 27.8) and 18 other tissuesSee more

Orthologs <u>human</u> all

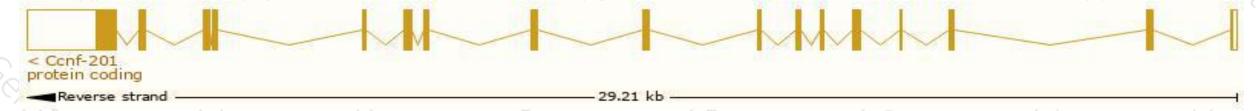
Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

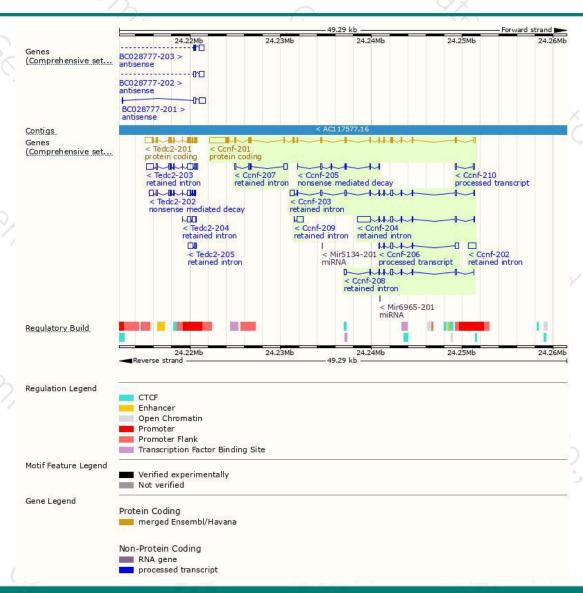
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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccnf-201	ENSMUST00000115390.4	4133	<u>777aa</u>	Protein coding	CCDS37484	P51944	TSL:1 GENCODE basic APPRIS P1
Ccnf-205	ENSMUST00000234541.1	675	<u>124aa</u>	Nonsense mediated decay		-	CDS 5' incomplete
Ccnf-206	ENSMUST00000234708.1	825	No protein	Processed transcript	20	0.20	
Ccnf-210	ENSMUST00000235059.1	317	No protein	Processed transcript	29	3523	
Ccnf-204	ENSMUST00000234491.1	2222	No protein	Retained intron	56	187	
Ccnf-203	ENSMUST00000234381.1	1721	No protein	Retained intron		-	
Ccnf-208	ENSMUST00000234916.1	1045	No protein	Retained intron	20	0.20	
Ccnf-202	ENSMUST00000234096.1	777	No protein	Retained intron	29	N28	
Ccnf-207	ENSMUST00000234837.1	756	No protein	Retained intron	-	187	
Ccnf-209	ENSMUST00000234949.1	756	No protein	Retained intron			
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The strategy is based on the design of *Ccnf-201* transcript, The transcription is shown below



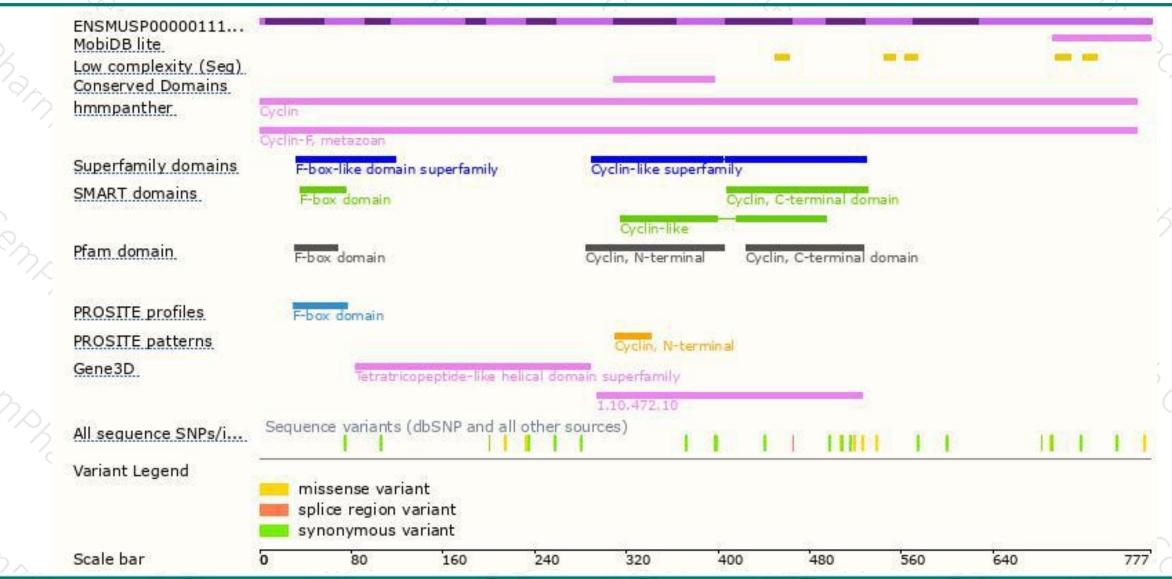
Genomic location distribution





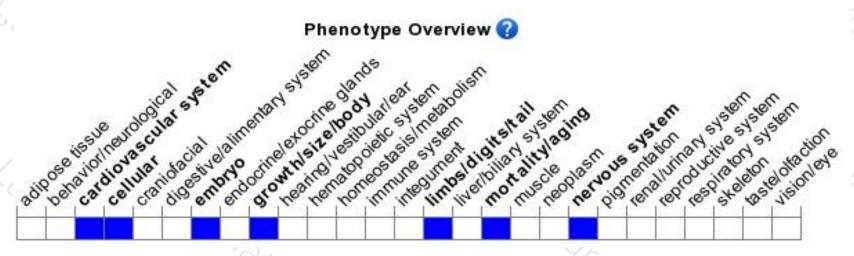
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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

Tel: 025-5864 1534





