

Ccny Cas9-CKO Strategy

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Design Date: 2019-8-8

Project Overview



Project Name Ccny

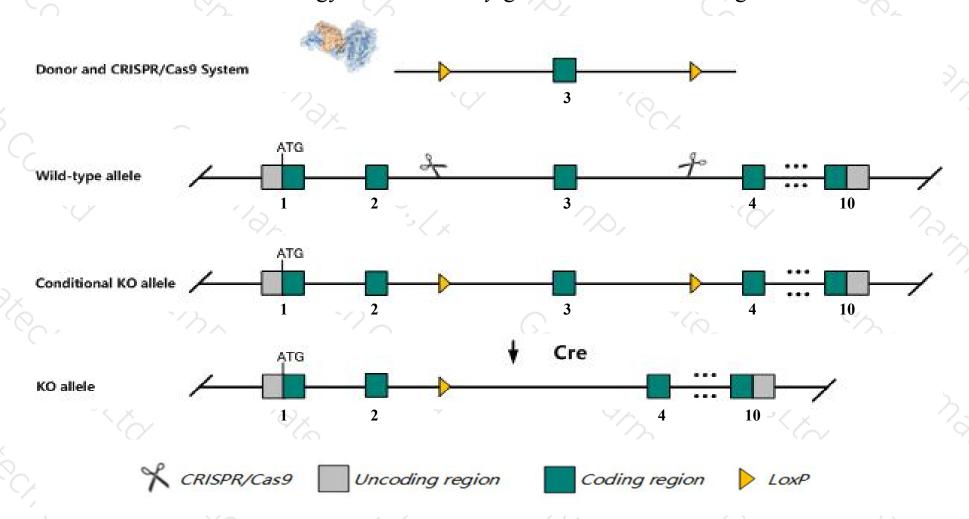
Project type Cas9-CKO

Strain background C57BL/6JGpt

Conditional Knockout strategy



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



Technical routes



- The *Ccny* gene has 5 transcripts. According to the structure of *Ccny* gene, exon3 of *Ccny-201* (ENSMUST0000053917.5) transcript is recommended as the knockout region. The region contains 35bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ccny* 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 a knock-out allele exhibit impaired adipogenesis and lipid production.
- The *Ccny* gene is located on the Chr18. 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)



Ccny cyclin Y [Mus musculus (house mouse)]

Gene ID: 67974, updated on 19-Mar-2019

Summary

☆ ?

Official Symbol Cony provided by MGI

Official Full Name cyclin Y provided by MGI

Primary source MGI:MGI:1915224

See related Ensembl:ENSMUSG00000024286

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 1700025H17Rik, 3110050L10Rik, 4631402G10Rik, 5730405l09Rik

Expression Ubiquitous expression in adrenal adult (RPKM 25.9), ovary adult (RPKM 20.4) and 28 other tissuesSee more

Orthologs <u>human</u> all

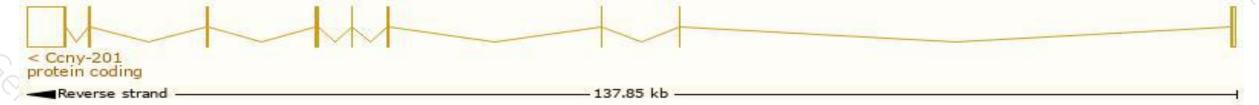
Transcript information (Ensembl)



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

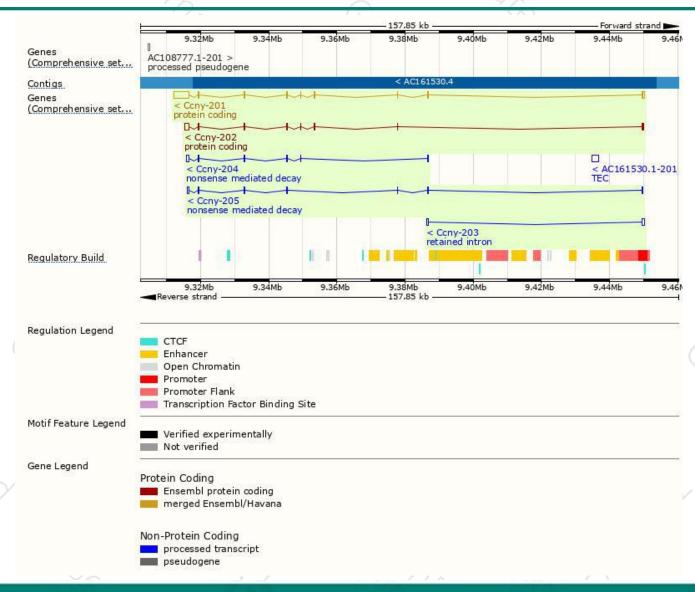
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccny-201	ENSMUST00000053917.5	5757	<u>341aa</u>	Protein coding	CCDS29050	Q8BGU5	TSL:1 GENCODE basic APPRIS P1
Ccny-202	ENSMUST00000234102.1	2505	<u>316aa</u>	Protein coding	688	6.5%	GENCODE basic
Ccny-205	ENSMUST00000234844.1	1354	99aa	Nonsense mediated decay	1940	1340	
Ccny-204	ENSMUST00000234779.1	1341	<u>26aa</u>	Nonsense mediated decay	323	100	CDS 5' incomplete
Ccny-203	ENSMUST00000234382.1	1046	No protein	Retained intron	(5)	1783	

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



Genomic location distribution





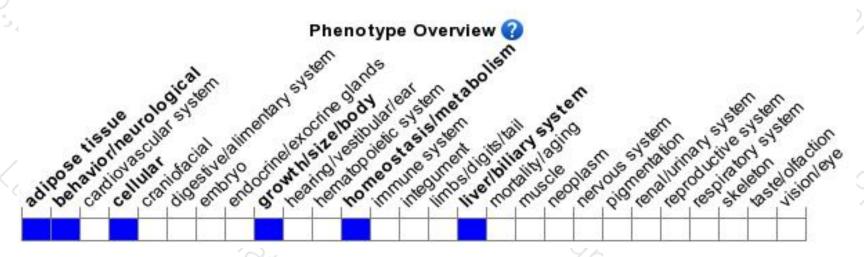
Protein domain





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 a knock-out allele exhibit impaired adipogenesis and lipid production.



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





