

Donald Color Clock Cas9-KO Strategy To hall alto color color

Constant areas Complanna Koch Co Designer:Lixin LYU

Project Overview



Project Name

Clock

Project type

Cas9-KO

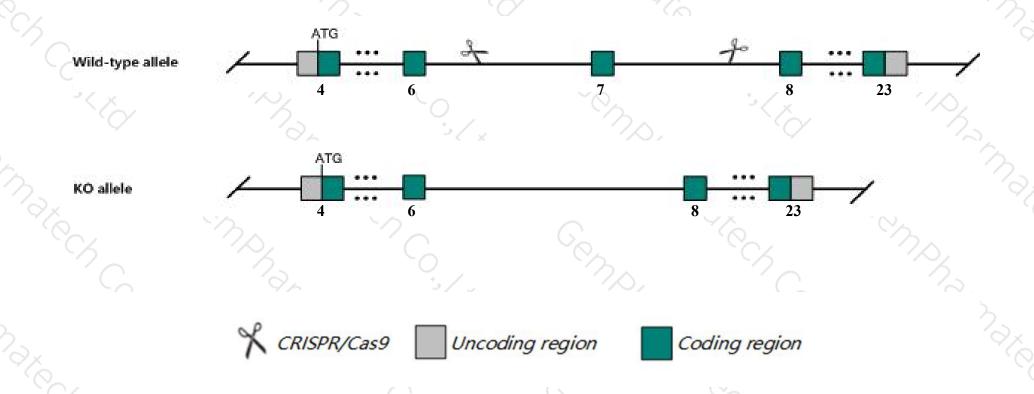
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Clock* gene has 6 transcripts. According to the structure of *Clock* gene, exon7 of *Clock-205*(ENSMUST00000202651.3) transcript is recommended as the knockout region. The region contains 92bp coding sequence.

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

Notice



- ➤ According to the existing MGI data, Mice homozygous for a knock-out allele exhibit abnormal circadian phase.

 Mice homozygous for a spontaneous mutation exhibit abnormal circadian rhythm, reproduction, behavior, hair cycle, macronutrient absorption, and metabolism.
- > The *Clock* gene is located on the Chr5. 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)



Clock circadian locomotor output cycles kaput [Mus musculus (house mouse)]

Gene ID: 12753, updated on 9-Apr-2019

Summary

☆ ?

Official Symbol Clock provided by MGI

Official Full Name circadian locomotor output cycles kaput provided by MGI

Primary source MGI:MGI:99698

See related Ensembl: ENSMUSG00000029238

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 5330400M04Rik, KAT13D

Summary The protein encoded by this gene plays a central role in the regulation of circadian rhythms. The protein encodes a transcription factor of the

basic helix-loop-helix (bHLH) family and contains DNA binding histone acetyltransferase activity. The encoded protein forms a heterodimer with Arntl (Bmal1) that binds E-box enhancer elements upstream of Period (Per1, Per2, Per3) and Cryptochrome (Cry1, Cry2) genes and activates transcription of these genes. Per and Cry proteins heterodimerize and repress their own transcription by interacting in a feedback loop with Clock/Arntl complexes. Polymorphisms in this gene may be associated with behavioral changes, obesity, and metabolic

syndrome. Two transcripts encoding the same protein have been found for this gene. [provided by RefSeq, Jan 2014]

Expression Ubiquitous expression in subcutaneous fat pad adult (RPKM 6.4), cerebellum adult (RPKM 6.2) and 28 other tissuesSee more

Orthologs human all

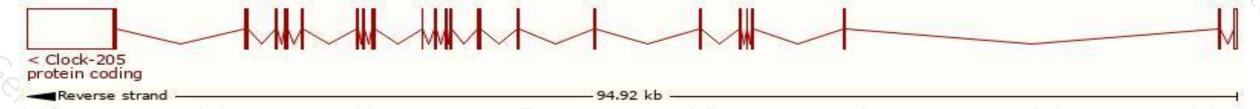
Transcript information (Ensembl)



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

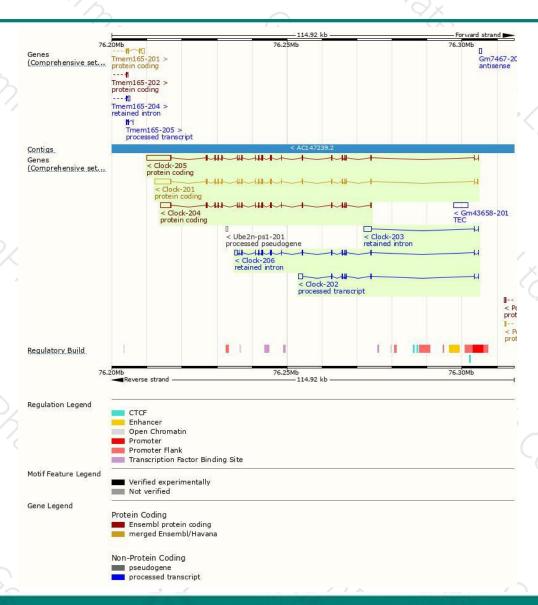
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clock-205	ENSMUST00000202651.3	9744	<u>855aa</u>	Protein coding	CCDS19360	<u>008785</u>	TSL:2 GENCODE basic APPRIS P3
Clock-201	ENSMUST00000075159.4	7478	<u>855aa</u>	Protein coding	CCDS19360	<u>008785</u>	TSL:1 GENCODE basic APPRIS P3
Clock-204	ENSMUST00000202122.1	5508	854aa	Protein coding	CCDS84889	A0A0J9YU61	TSL:1 GENCODE basic APPRIS ALT2
Clock-202	ENSMUST00000200957.3	1889	No protein	Processed transcript	2	757	TSL:2
Clock-206	ENSMUST00000202857.3	2473	No protein	Retained intron	5		TSL:2
Clock-203	ENSMUST00000201052.1	2287	No protein	Retained intron	-		TSL:1

The strategy is based on the design of Clock-205 transcript, The transcription is shown below



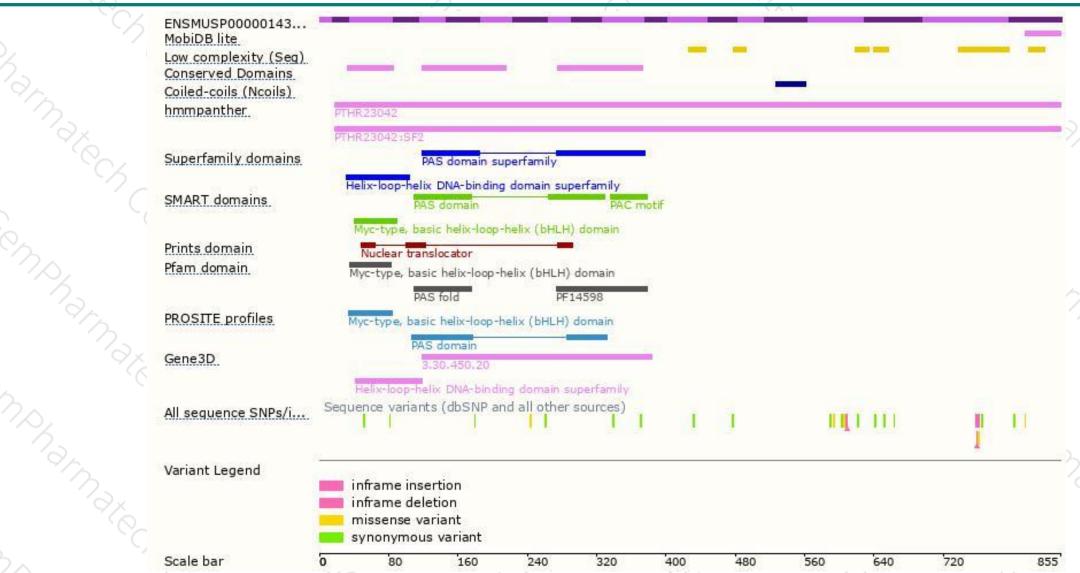
Genomic location distribution





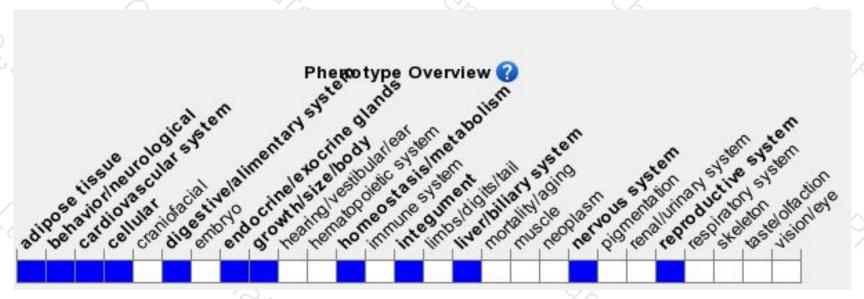
Protein domain





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 abnormal circadian phase. Mice homozygous for a spontaneous mutation exhibit abnormal circadian rhythm, reproduction, behavior, hair cycle, macronutrient absorption, and metabolism.



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





