

Ctcf Cas9-KO Strategy

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Project Overview



Project Name

Ctcf

Project type

Cas9-KO

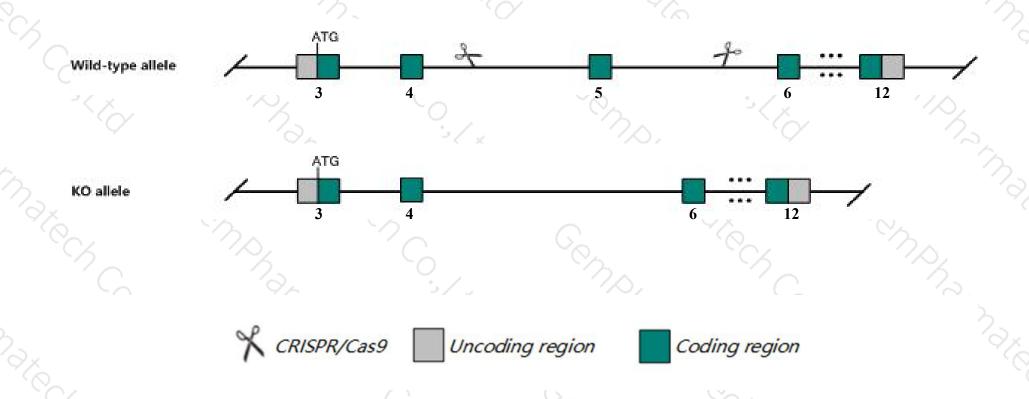
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- > The *Ctcf* gene has 6 transcripts. According to the structure of *Ctcf* gene, exon5 of *Ctcf-201*(ENSMUST0000005841.15) transcript is recommended as the knockout region. The region contains 134bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ctcf* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice



- ➤ According to the existing MGI data, Mice homozygous for a null allele die prior at implantation. Mice homozygous for a conditional allele activated in T cells exhibit a defect in the transition from immature single positive T cells to double positive T cells.
- > The *Ctcf* gene is located on the Chr8. 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)



Ctcf CCCTC-binding factor [Mus musculus (house mouse)]

Gene ID: 13018, updated on 26-Mar-2019

Summary

↑ ?

Official Symbol Ctcf provided by MGI

Official Full Name CCCTC-binding factor provided by MGI

Primary source MGI:MGI:109447

See related Ensembl:ENSMUSG00000005698

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 AW108038

Expression Ubiquitous expression in CNS E11.5 (RPKM 18.2), thymus adult (RPKM 13.4) and 27 other tissuesSee more

Orthologs <u>human all</u>

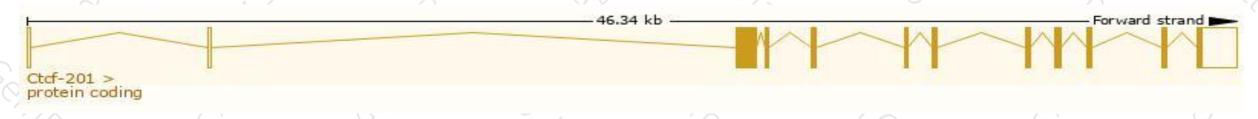
Transcript information (Ensembl)



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

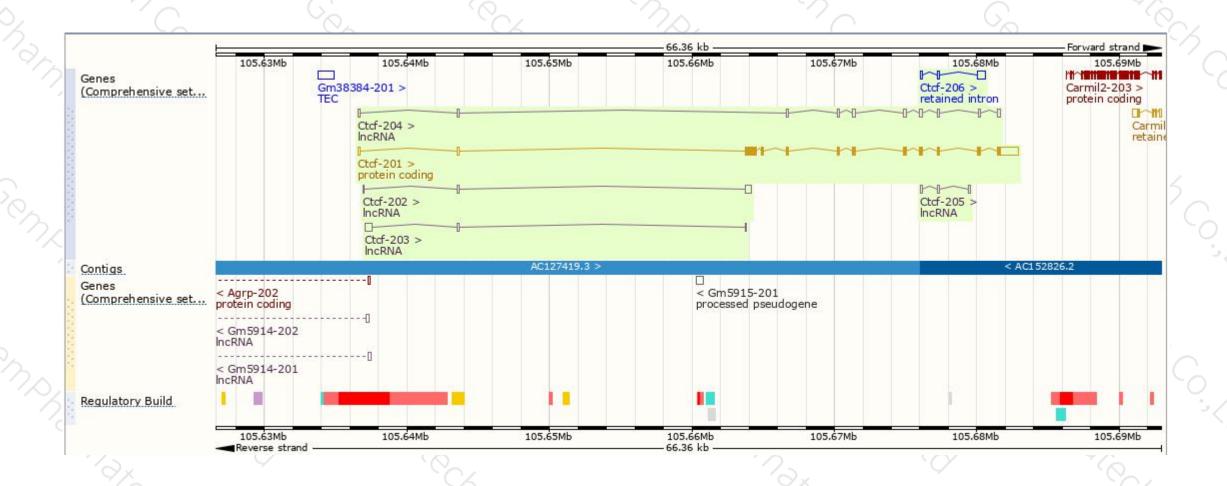
Name 🍦	Transcript ID 👙	bp 🌲	Protein 👙	Biotype 🍦	CCDS	UniProt #	Flags
Ctcf-201	ENSMUST00000005841.15	3782	<u>736aa</u>	Protein coding	<u>CCDS22606</u> ₽	<u>Q61164</u> ₺	TSL:1 GENCODE basic APPRIS P1
Ctcf-206	ENSMUST00000156436.1	851	No protein	Retained intron	=	1-8	TSL:3
Ctcf-204	ENSMUST00000132679.7	1554	No protein	IncRNA) .	11 - 11	TSL:5
Ctcf-203	ENSMUST00000129388.1	729	No protein	IncRNA	3 2	2.2	TSL:3
Ctcf-202	ENSMUST00000128510.7	528	No protein	IncRNA	8	148	TSL:3
Ctcf-205	ENSMUST00000137735.7	469	No protein	IncRNA	-	(4)	TSL:3

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



Genomic location distribution





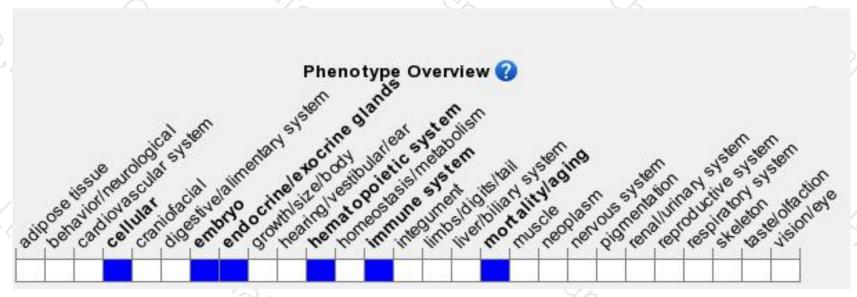
Protein domain





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 null allele die prior at implantation. Mice homozygous for a conditional allele activated in T cells exhibit a defect in the transition from immature single positive T cells to double positive T cells.



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





