

Tcf19 Cas9-KO Strategy

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Overview

Target Gene Name

- *Tcf19*

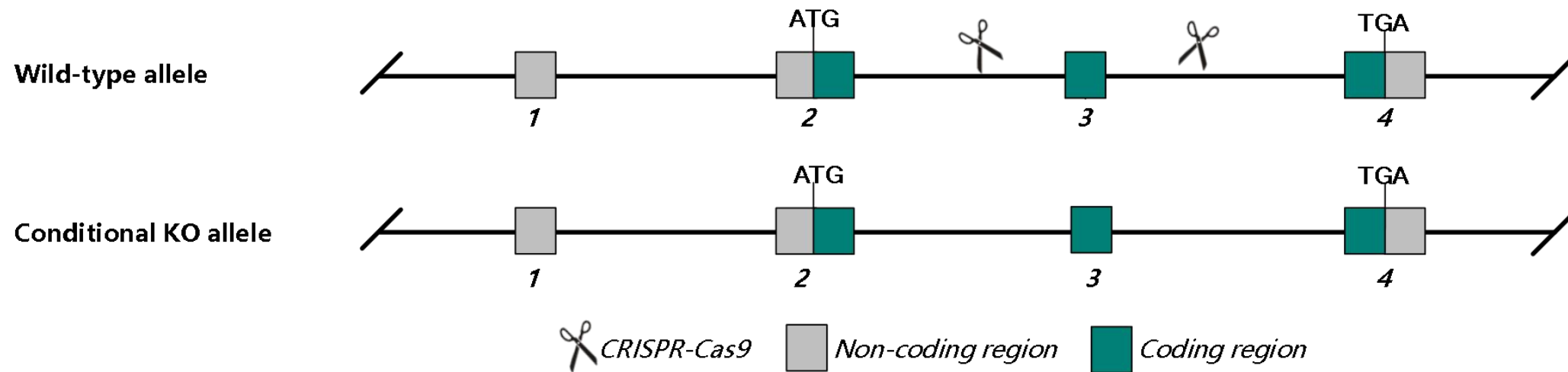
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Tcf19* gene.

Technical Information

- The *Tcf19* gene has 4 transcripts. According to the structure of *Tcf19* gene, exon 3 of *Tcf19*-202 (ENSMUST00000160885.2) is recommended as the knockout region. The region contains 547 bp of coding sequences. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Tcf19* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

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Tcf19 transcription factor 19 [*Mus musculus* (house mouse)]

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Gene ID: 106795, updated on 26-Sep-2022

Summary



Official Symbol	Tcf19 provided by MGI
Official Full Name	transcription factor 19 provided by MGI
Primary source	MGI:MGI:103180
See related	Ensembl:ENSMUSG00000050410 AllianceGenome:MGI:103180
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	5730403J10Rik
Summary	Acts upstream of or within G1/S transition of mitotic cell cycle; regulation of gene expression; and type B pancreatic cell proliferation. Located in nucleus. Is expressed in forebrain; genitourinary system; and limb. Orthologous to human TCF19 (transcription factor 19). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in limb E14.5 (RPKM 21.9), thymus adult (RPKM 20.3) and 25 other tissues See more
Orthologs	human all
<div>NEW</div>	Try the new Gene table
	Try the new Transcript table

Genomic context



Location: 17; 17 B1

See Tcf19 in [Genome Data Viewer](#)

Exon count: 4

Source: <https://www.ncbi.nlm.nih.gov/gene/106795>

Transcript Information

The gene has 4 transcripts, all transcripts are shown below:

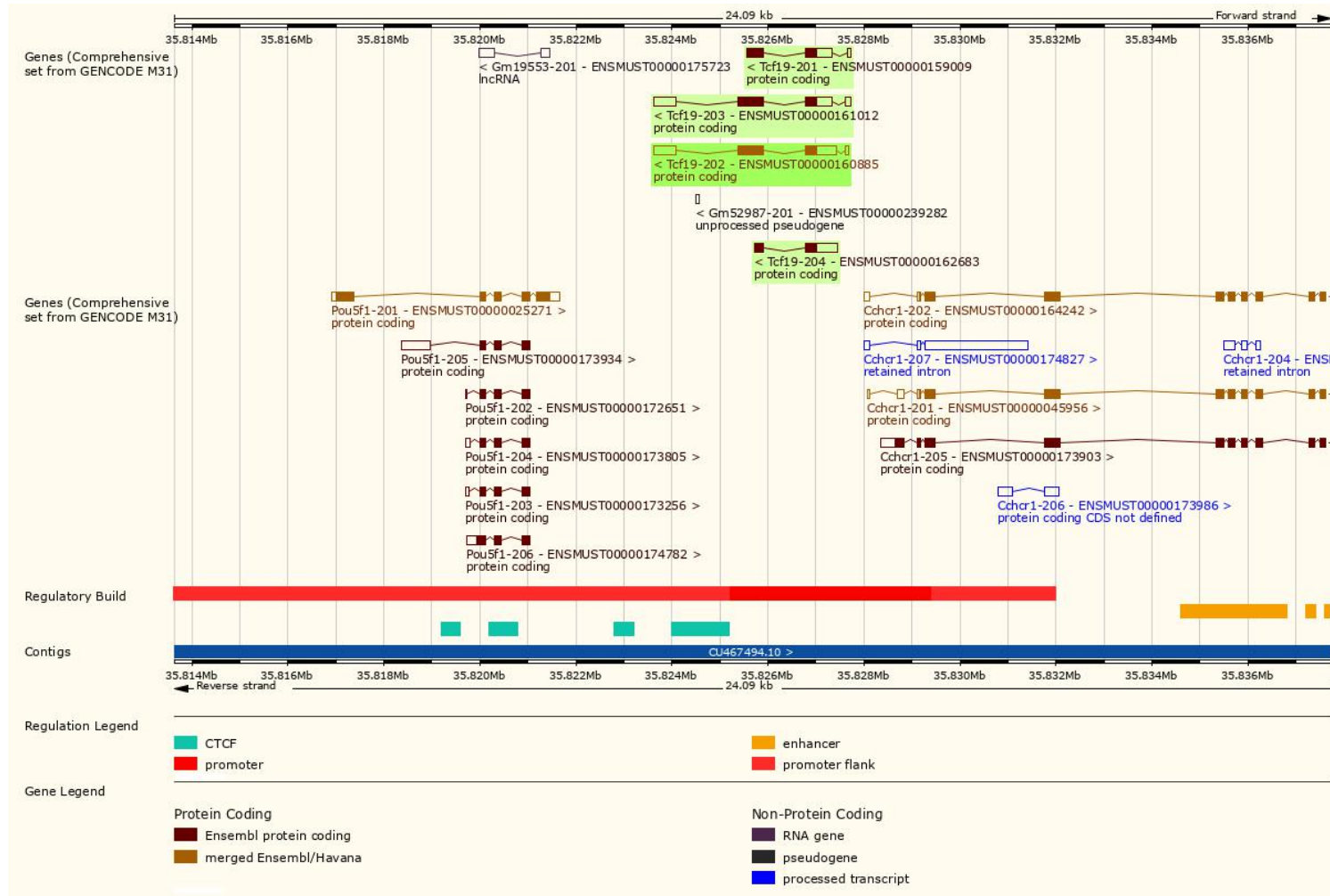
Transcript ID ▼	Name ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt Match ▲	Flags ▲
ENSMUST00000162683.2	Tcf19-204	873	147aa	Protein coding		E0CZ64	TSL:1 CDS 3' incomplete
ENSMUST00000161012.8	Tcf19-203	1665	263aa	Protein coding	CCDS50089	G3XA31	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000160885.2	Tcf19-202	1732	263aa	Protein coding	CCDS50089	G3XA31	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000159009.2	Tcf19-201	982	201aa	Protein coding		E0CY69	TSL:2 CDS 3' incomplete

The strategy is based on the design of *Tcf19-202* transcript, the transcription is shown below:



Source: <http://asia.ensembl.org/>

Genomic Information



Source: <http://asia.ensembl.org/>

Important Information

- The knockout region is about 1.8 kb away from the 5th end of the *Cchcr1* gene, which may affect the regulation of these gene.
- The knockout region is about 500 bp away from the 5th end of the *Gm52987* gene, which may affect the regulation of this gene.
- The knockout region is about 3.5 kb away from the 5th end of the *Gm19553* gene, which may affect the regulation of this gene.
- A part of amino acid sequence will still remain at the N-terminal of the *Tcf19* gene.
- *Tcf19* is located on Chr 17. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.