

Tcf7 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Tcf7

Project type

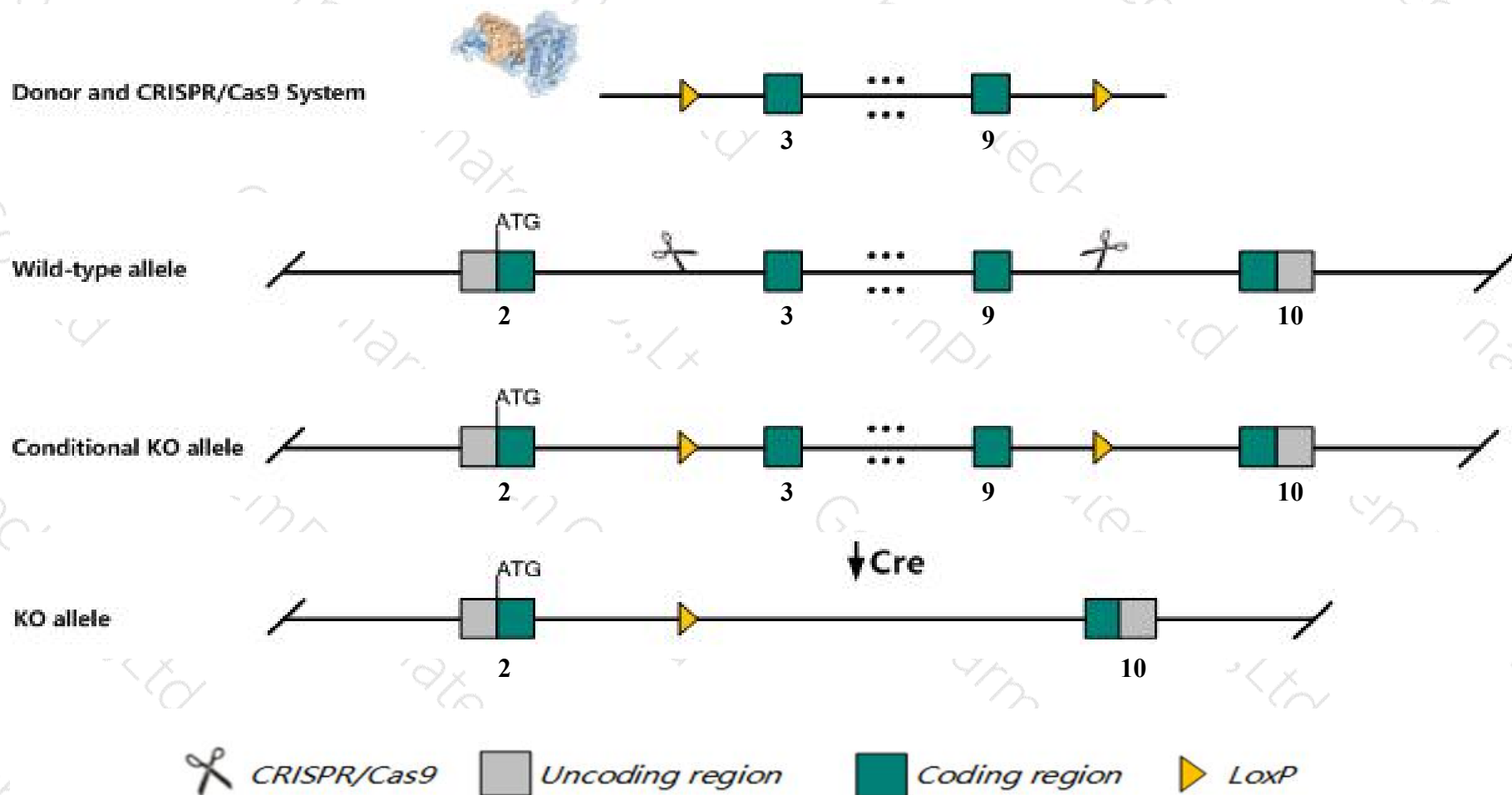
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tcf7* gene. The schematic diagram is as follows:



- The *Tcf7* gene has 2 transcripts. According to the structure of *Tcf7* gene, exon3-exon9 of *Tcf7-201* (ENSMUST00000086844.9) transcript is recommended as the knockout region. The region contains 736bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tcf7* 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.

- According to the existing MGI data, Homozygous null mice have defects in T cell development leading to decreased numbers of T cells in the periphery.
- The *Tcf7* gene is located on the Chr11. 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)

Tcf7 transcription factor 7, T cell specific [*Mus musculus* (house mouse)]

Gene ID: 21414, updated on 21-Jan-2020

Summary

Official Symbol

Tcf7 provided by MGI

Official Full Name

transcription factor 7, T cell specific provided by MGI

Primary source

MGI:MGI:98507

See related

Ensembl:ENSMUSG00000000782

Gene type

protein coding

RefSeq status

REVIEWED

Organism

Mus musculus

Lineage

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as

Tcf1; TCF-1; AI465550

Summary

This gene encodes a transcription factor which is a member of the T-cell specific transcription factor family. The encoded protein is distinct from the hepatic transcription factor, transcription factor 1, which is also referred to by the symbol Tcf1. Several alternatively spliced transcript variants of this gene have been described, but the full-length nature of some of these variants has not been determined. [provided by RefSeq, Sep 2015]

Expression

Biased expression in thymus adult (RPKM 829.6) and spleen adult (RPKM 56.0) See more

Orthologs

human all

Genomic context

Location:

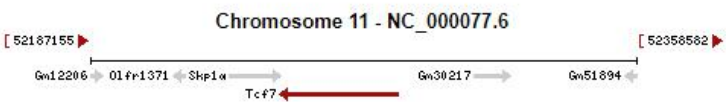
11 B1.3; 11 31.86 cM

Exon count:

16

See Tcf7 in [Genome Data Viewer](#)

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (52246527..52283383, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (52066106..52096073, complement)

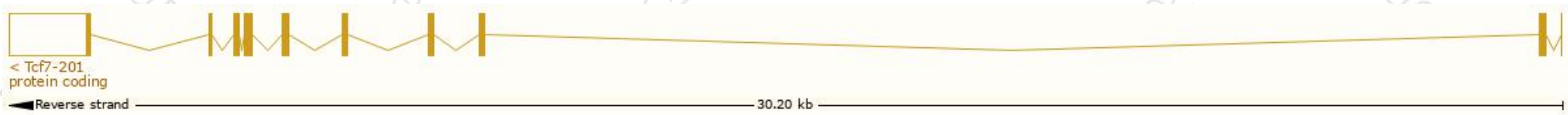


Transcript information (Ensembl)

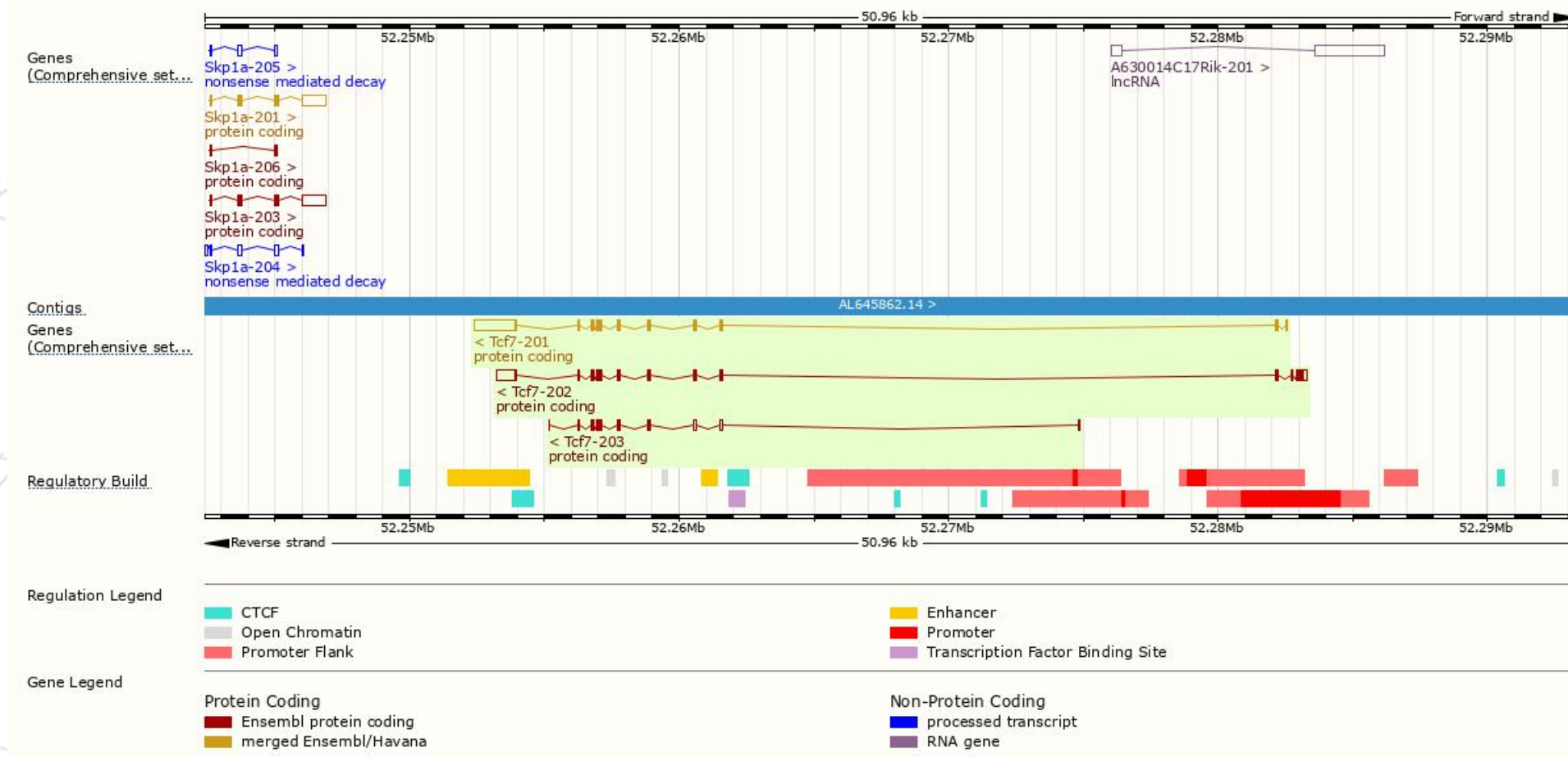
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tcf7-201	ENSMUST00000086844.9	2471	303aa	Protein coding	CCDS24670	Q00417 Q80UF1	TSL:1 GENCODE basic
Tcf7-202	ENSMUST00000109071.2	2059	419aa	Protein coding	-	Q00417	TSL:1 GENCODE basic APPRIS P1
Tcf7-203	ENSMUST00000238914.1	813	192aa	Protein coding	-	-	CDS 3' incomplete

The strategy is based on the design of *Tcf7-201* transcript,The transcription is shown below



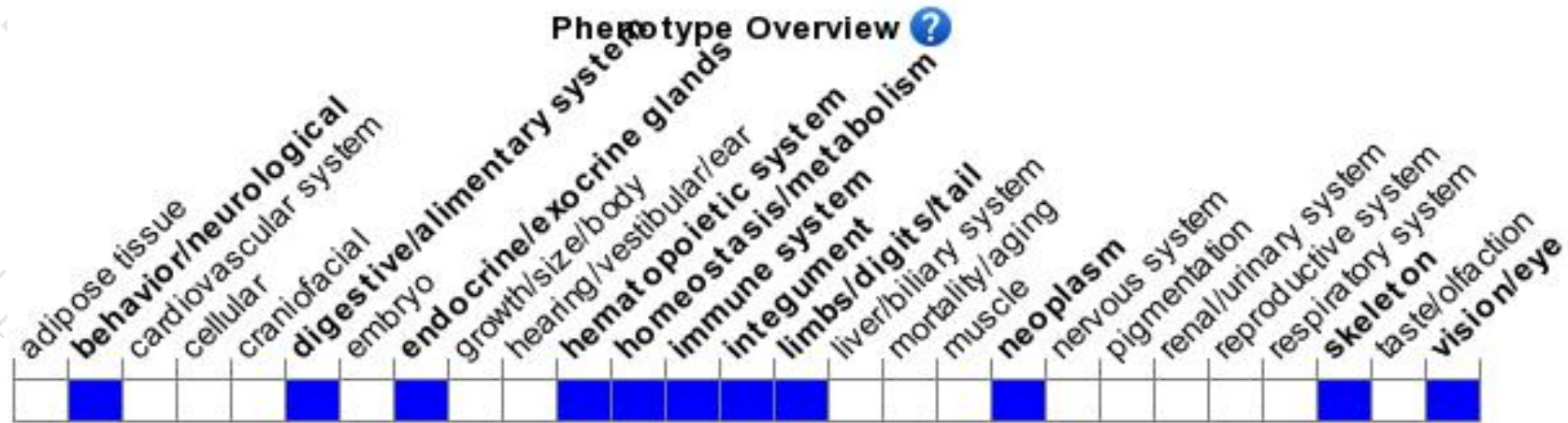
Genomic location distribution



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, Homozygous null mice have defects in T cell development leading to decreased numbers of T cells in the periphery.

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

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