

Traf3 Cas9-CKO Strategy

Designer: Huan Fan

Reviewer: Huan Wang

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Project Overview

Project Name

Traf3

Project type

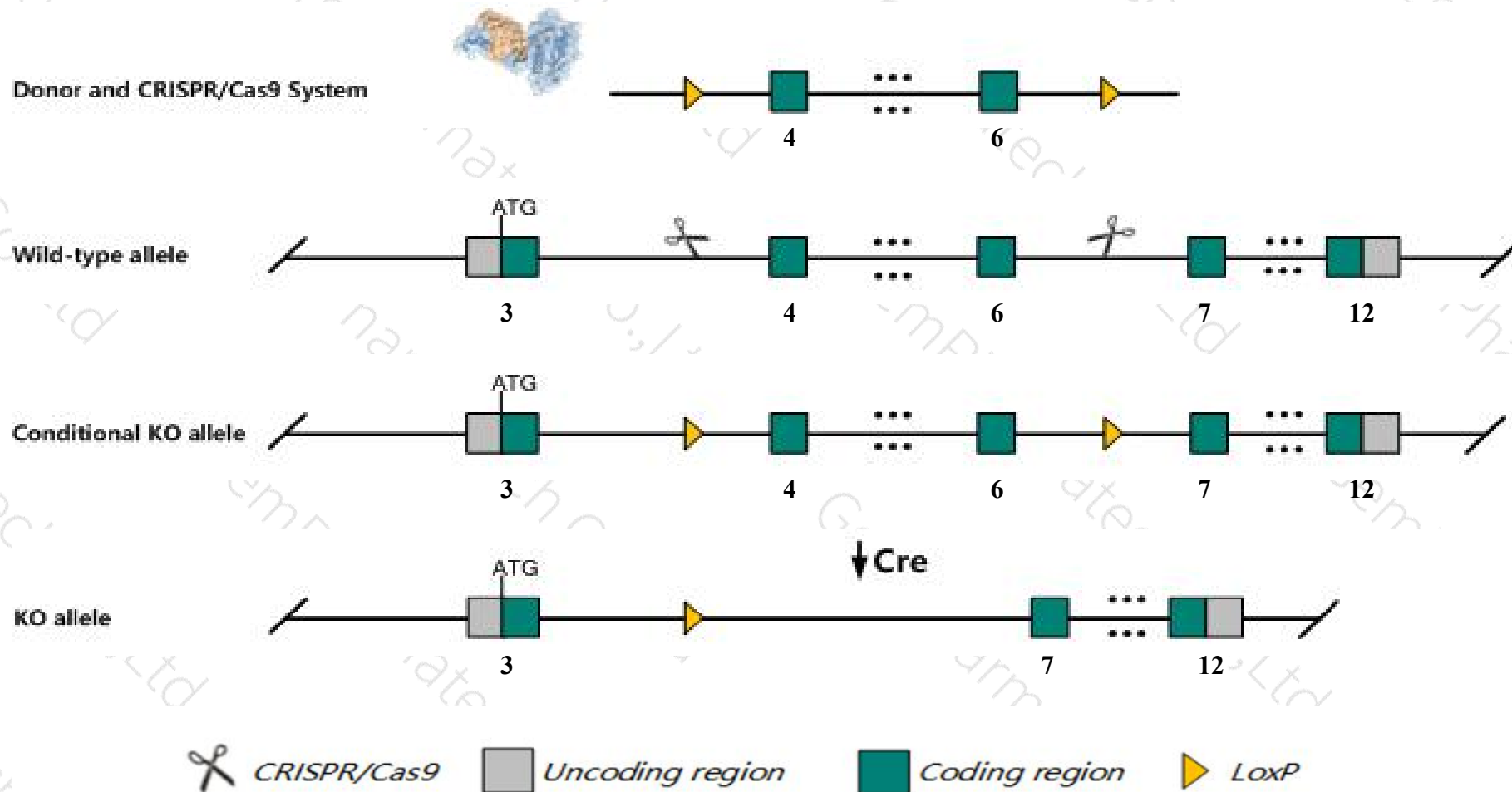
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Traf3* gene. The schematic diagram is as follows:



Technical routes

- The *Traf3* gene has 5 transcripts. According to the structure of *Traf3* gene, exon4-exon6 of *Traf3-201* (ENSMUST00000021706.10) transcript is recommended as the knockout region. The region contains 325bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Traf3* 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 mutation of this gene results in progressive runting, hypoglycemia, and depletion of peripheral white blood cells, leading to death by 10 days of age. immune responses to t-dependent antigen are impaired in lethally irradiated mice reconstituted with mutant cells.
- The *Traf3* gene is located on the Chr12. 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)

Traf3 TNF receptor-associated factor 3 [Mus musculus (house mouse)]

Gene ID: 22031, updated on 13-Mar-2020

Summary



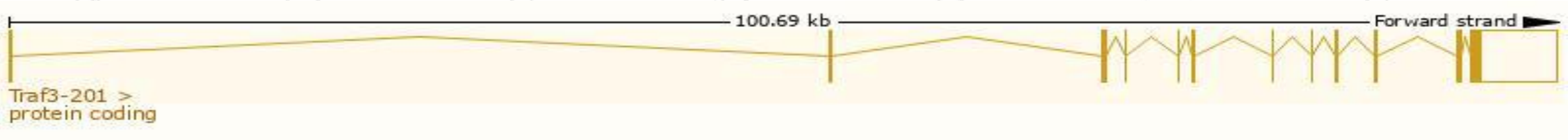
Official Symbol	Traf3 provided by MGI
Official Full Name	TNF receptor-associated factor 3 provided by MGI
Primary source	MGI:MGI:108041
See related	Ensembl:ENSMUSG000000021277
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI528849, CAP-1, CD40bp, CRAF1, LAP1, T-BAM, TRAFAMN, amn
Expression	Ubiquitous expression in spleen adult (RPKM 14.4), thymus adult (RPKM 12.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

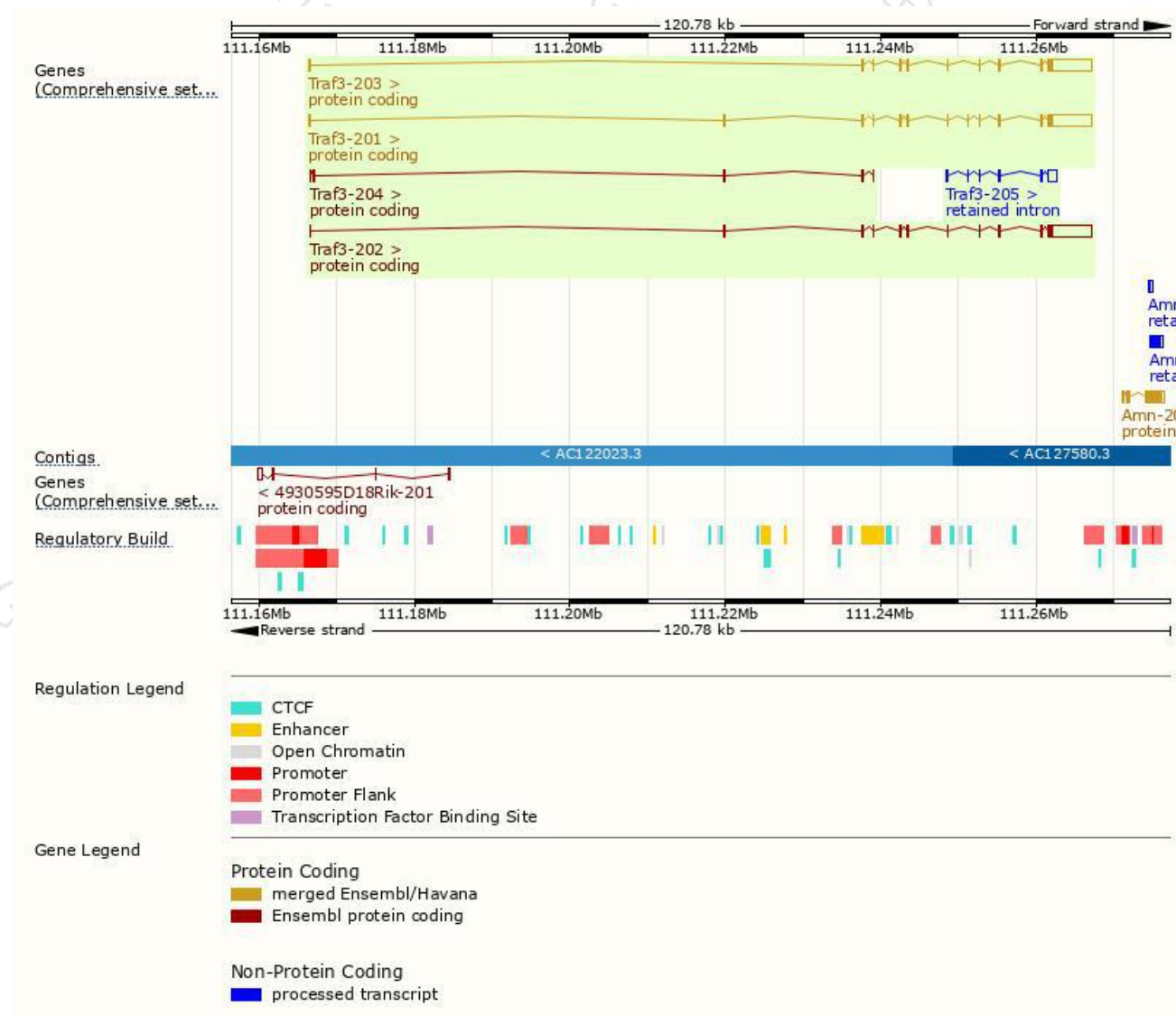
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Traf3-201	ENSMUST00000021706.10	7060	567aa	Protein coding	CCDS26175	Q60803	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Traf3-203	ENSMUST00000117269.7	6972	542aa	Protein coding	CCDS36563	Q3UHV1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT 1
Traf3-202	ENSMUST00000060274.6	6896	542aa	Protein coding	CCDS36563	Q3UHV1	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT 1
Traf3-204	ENSMUST00000139162.7	645	97aa	Protein coding	-	D3Z343	CDS 3' incomplete TSL:3
Traf3-205	ENSMUST00000143395.1	1720	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Traf3-201* transcript,the transcription is shown below



Genomic location distribution

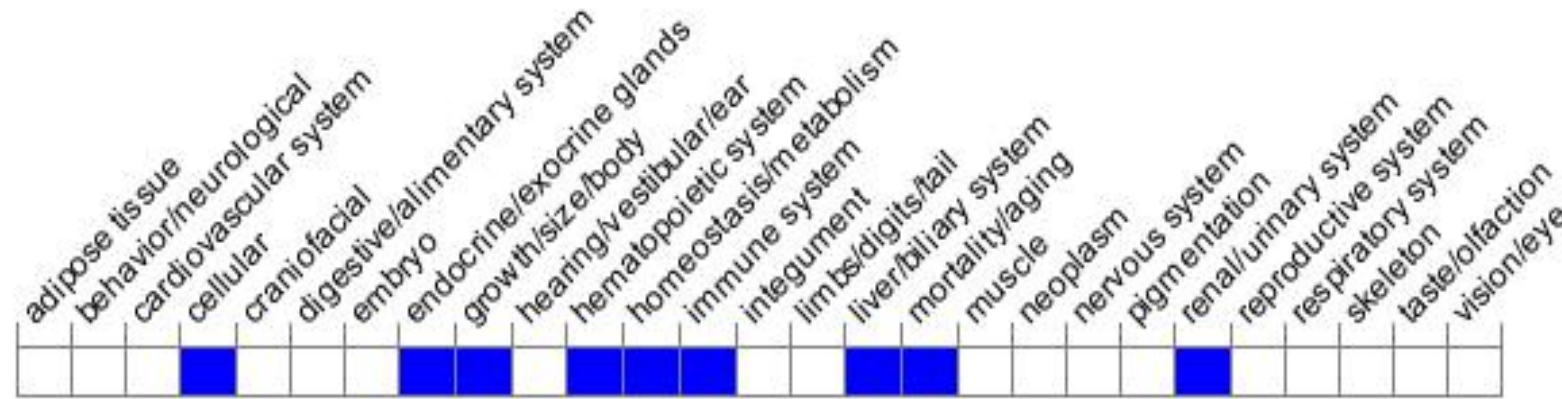


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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 mutation of this gene results in progressive runting, hypoglycemia, and depletion of peripheral white blood cells, leading to death by 10 days of age. Immune responses to T-dependent antigen are impaired in lethally irradiated mice reconstituted with mutant cells.

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

Tel: 400-9660890

