

Tnfsf10 Cas9-CKO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Tnfsf10

Project type

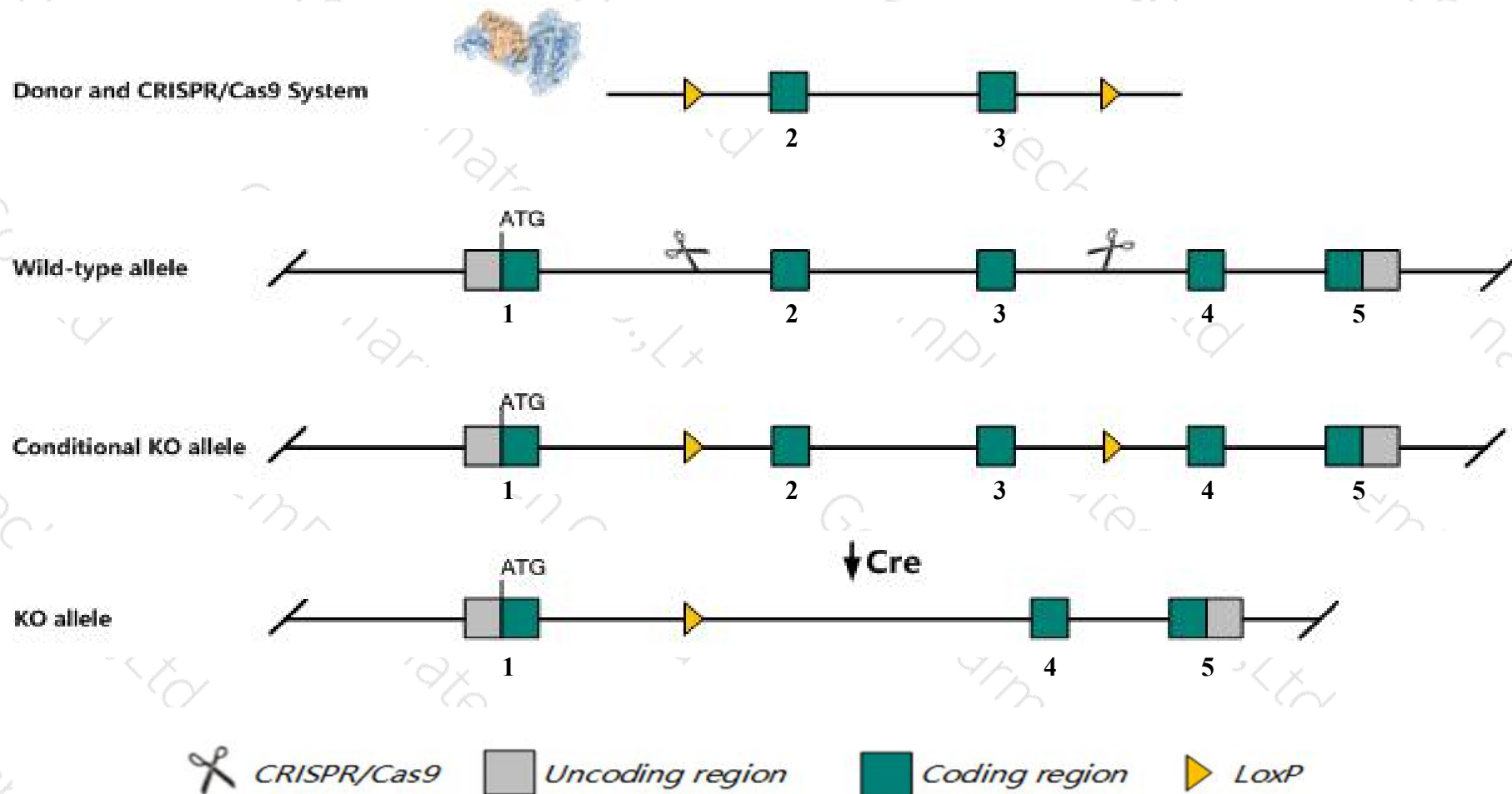
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tnfsf10* gene. The schematic diagram is as follows:



- The *Tnfsf10* gene has 2 transcripts. According to the structure of *Tnfsf10* gene, exon2-exon3 of *Tnfsf10-201* (ENSMUST00000046383.11) transcript is recommended as the knockout region. The region contains 181bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tnfsf10* 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, Homozygotes for a null allele show thymus hyperplasia, abnormal negative T cell selection, increased susceptibility to autoimmune diseases and to tumor initiation and metastasis, and resistance to induced hepatitis. Homozygotes for another null allele are unable to control A20 lymphoma progression.
- The *Tnfrsf10* gene is located on the Chr3. 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)

Tnfsf10 tumor necrosis factor (ligand) superfamily, member 10 [Mus musculus (house mouse)]

Gene ID: 22035, updated on 12-Mar-2019

Summary



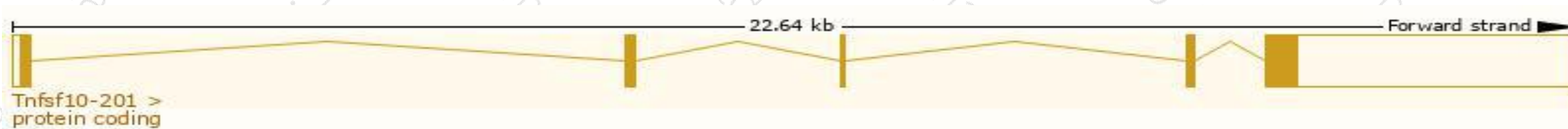
Official Symbol	Tnfsf10 provided by MGI
Official Full Name	tumor necrosis factor (ligand) superfamily, member 10 provided by MGI
Primary source	MGI:MGI:107414
See related	Ensembl:ENSMUSG00000039304
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A330042I21Rik, AI448571, APO-2L, Ly81, TL2, Tnlg6a, Trail
Expression	Biased expression in lung adult (RPKM 13.2), large intestine adult (RPKM 5.9) and 13 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

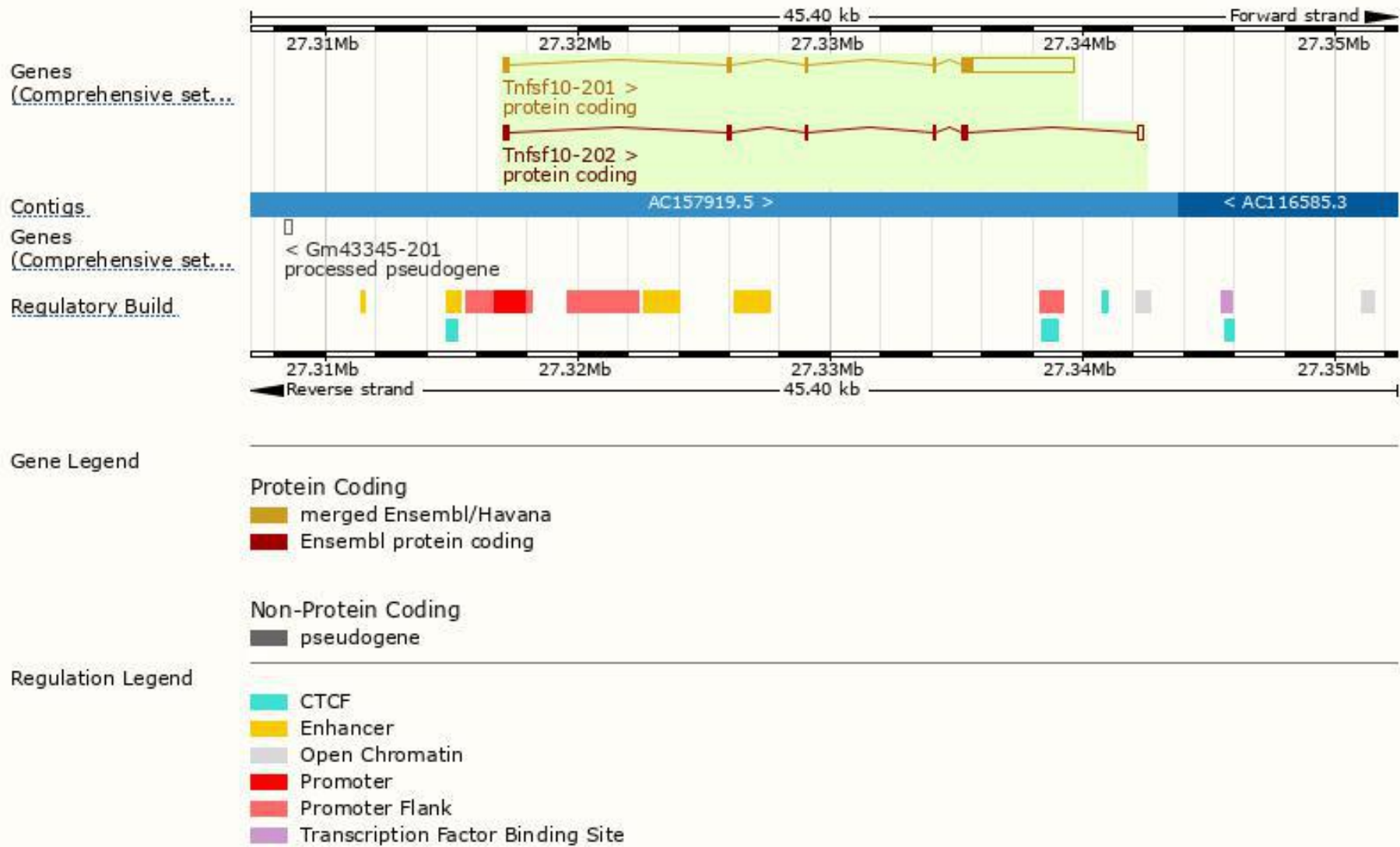
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnfsf10-201	ENSMUST00000046383.11	4993	291aa	Protein coding	CCDS17272	P50592 Q3U5H0	TSL:1 GENCODE basic APPRIS P1
Tnfsf10-202	ENSMUST00000174840.1	989	228aa	Protein coding	-	G3UY25	TSL:5 GENCODE basic

The strategy is based on the design of *Tnfsf10-201* transcript, The transcription is shown below



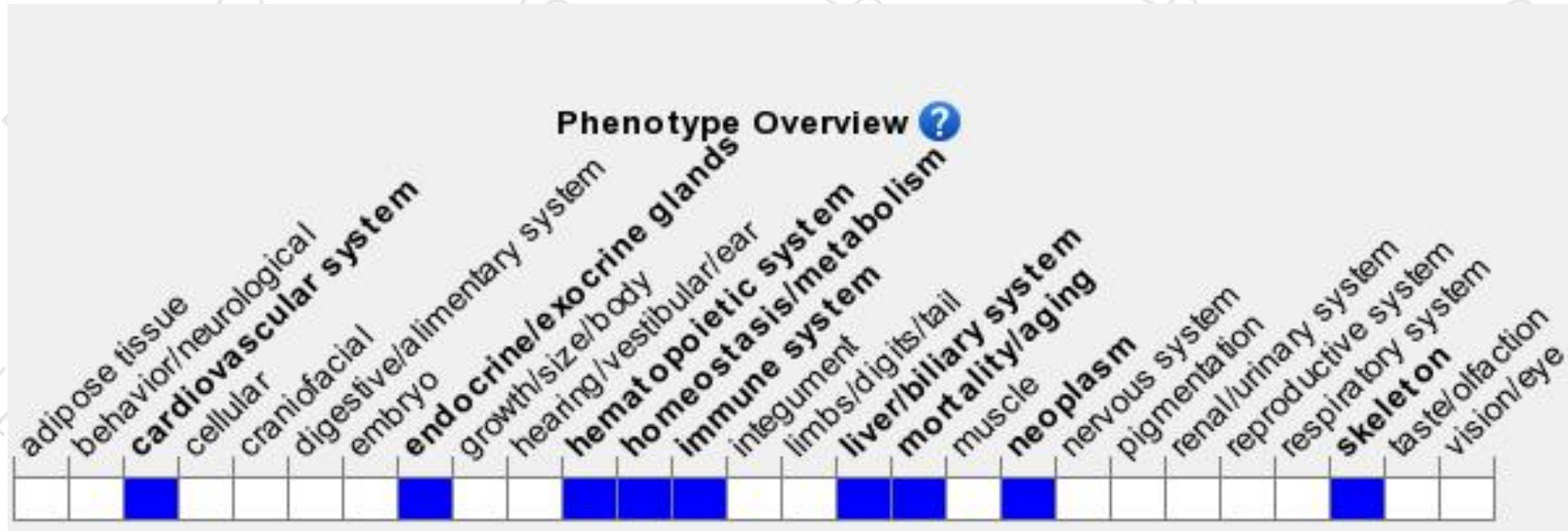
Genomic location distribution



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, Homozygotes for a null allele show thymus hyperplasia, abnormal negative T cell selection, increased susceptibility to autoimmune diseases and to tumor initiation and metastasis, and resistance to induced hepatitis. Homozygotes for another null allele are unable to control A20 lymphoma progression.

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

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