GemPharmatech™

Tnfrsf13b Cas9-CKO Strategy

Designer: Yunpeng Zhang

Reviewer: Ruirui Zhang

Design Date: 2024-7-8

Overview

Target Gene Name

- Tnfrsf13b

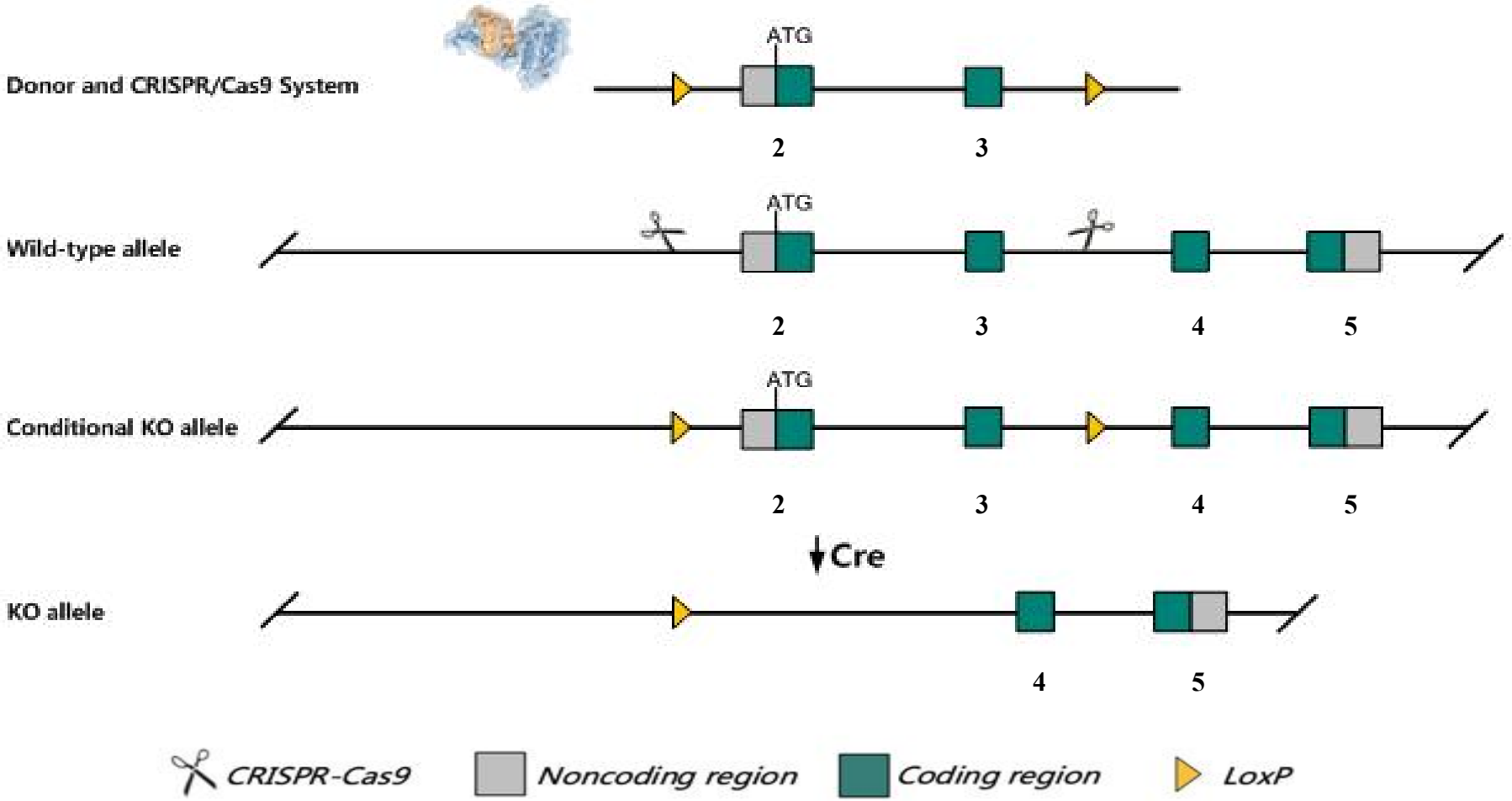
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Tnfrsf13b* gene.

Technical Information

- The *Tnfrsf13b* gene has 7 transcripts. According to the structure of *Tnfrsf13b* gene, exon2-exon3 of *Tnfrsf13b*-201 (ENSMUST00000010286.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Tnfrsf13b* 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.
- 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.

Gene Information

Tnfrsf13b tumor necrosis factor receptor superfamily, member 13b [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 57916, updated on 12-May-2024

Summary

Official Symbol	Tnfrsf13b provided by MGI
Official Full Name	tumor necrosis factor receptor superfamily, member 13b provided by MGI
Primary source	MGI:MGI:1889411
See related	Ensembl:ENSMUSG00000010142 AllianceGenome:MGI:1889411
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	Taci; 1200009E08Rik
Summary	Acts upstream of or within B cell homeostasis; hematopoietic progenitor cell differentiation; and negative regulation of B cell proliferation. Located in external side of plasma membrane. Is integral component of plasma membrane. Is expressed in renal vasculature. Used to study systemic lupus erythematosus. Human ortholog(s) of this gene implicated in common variable immunodeficiency. Orthologous to human TNFRSF13B (TNF receptor superfamily member 13B). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in spleen adult (RPKM 32.7), thymus adult (RPKM 12.2) and 6 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

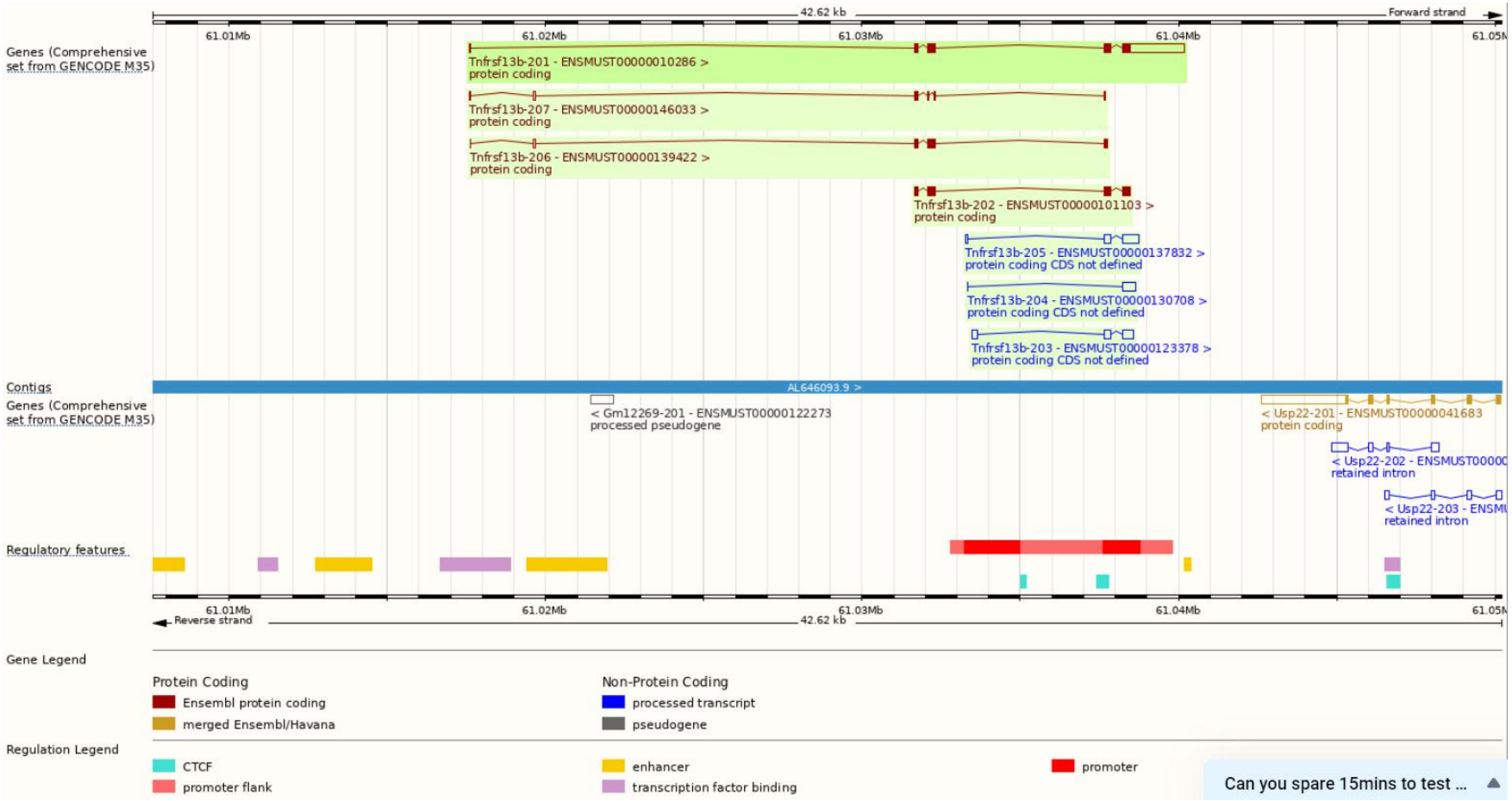
The gene has 7 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000146033.8	Tnfrsf13b-207	364	73aa	Protein coding		B1ATI3	TSL:5 CDS 3' incomplete
ENSMUST00000139422.8	Tnfrsf13b-206	532	140aa	Protein coding		B1ATI4	TSL:5 CDS 3' incomplete
ENSMUST00000137832.8	Tnfrsf13b-205	764	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000130708.2	Tnfrsf13b-204	422	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000123378.2	Tnfrsf13b-203	662	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000101103.4	Tnfrsf13b-202	750	249aa	Protein coding	CCDS24806	A5D8Y6 Q9ET35	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000010286.8	Tnfrsf13b-201	2556	249aa	Protein coding	CCDS24806	A5D8Y6 Q9ET35	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1

The strategy is based on the design of *Tnfrsf13b*-201 transcript, the transcription is shown below:

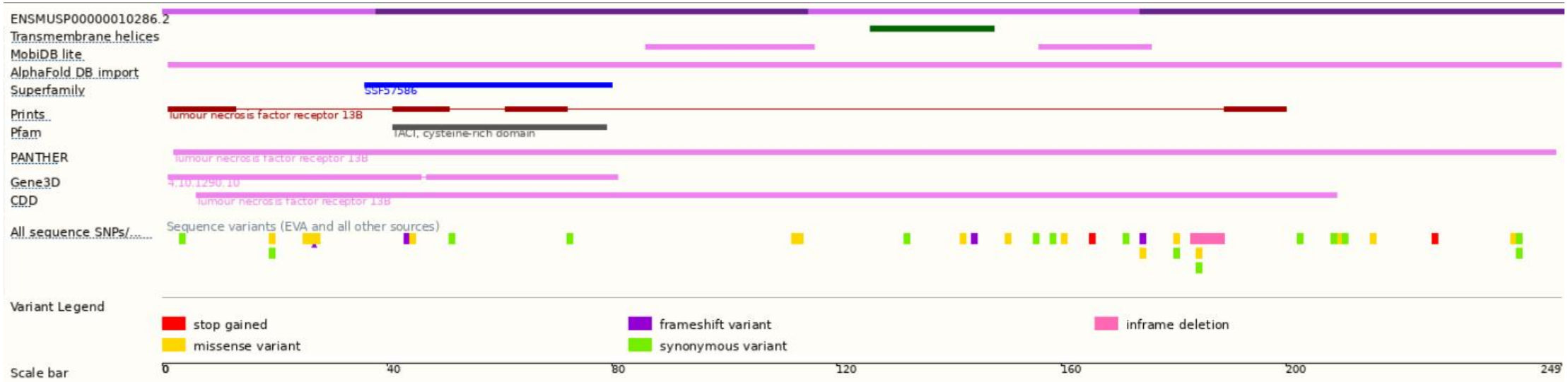
Source: https://www.ensembl.org

Genomic Information



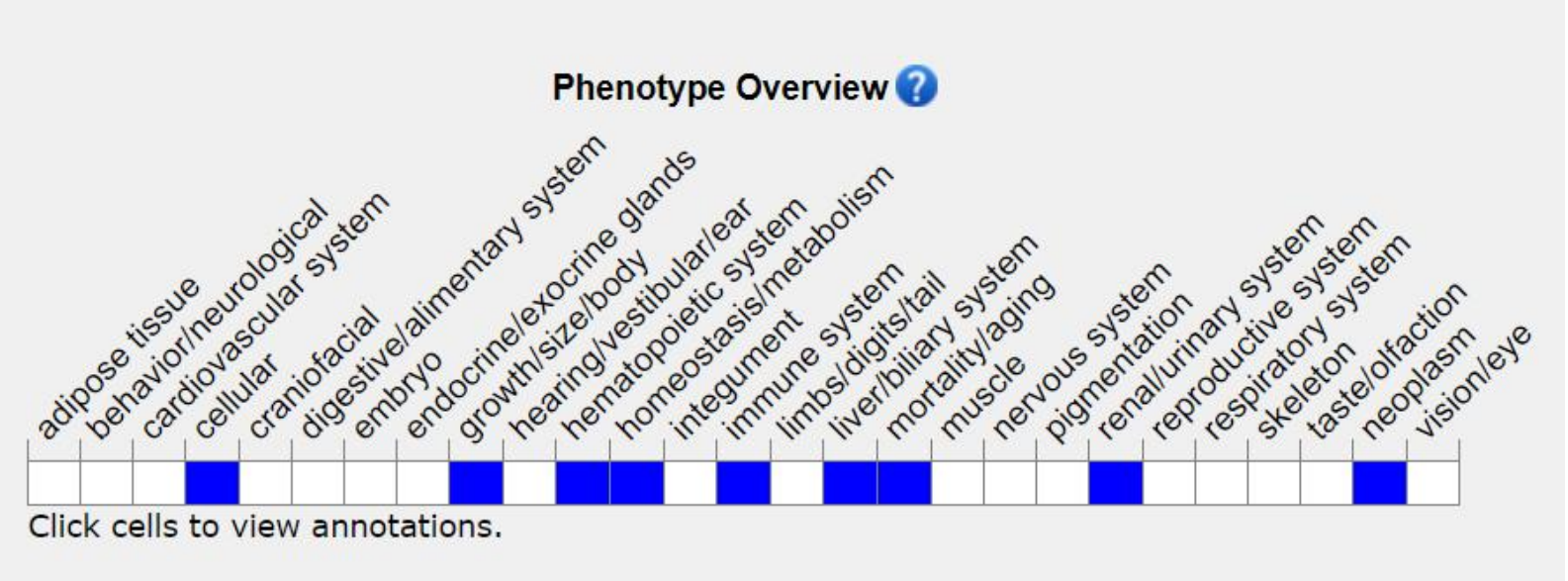
Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Nullizygous mice show increased B cell numbers and splenomegaly. Homozygotes for a null allele show impaired T cell-independent immune responses and isotype switching. Homozygotes for another null allele develop lymphoproliferation and fatal autoimmune nephritis with high titers of autoantibodies.

Source: https://www.informatics.jax.org

Important Information

- The knockout region contains the start codon ATG, which may be followed by the generation of new ATG. It may generate a new protein and the fuction is unknow.
- *Tnfrsf13b* is located on Chr 11. 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.