

Tnfsf13 Cas9-KO Strategy

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Overview

Target Gene Name

- Tnfsf13

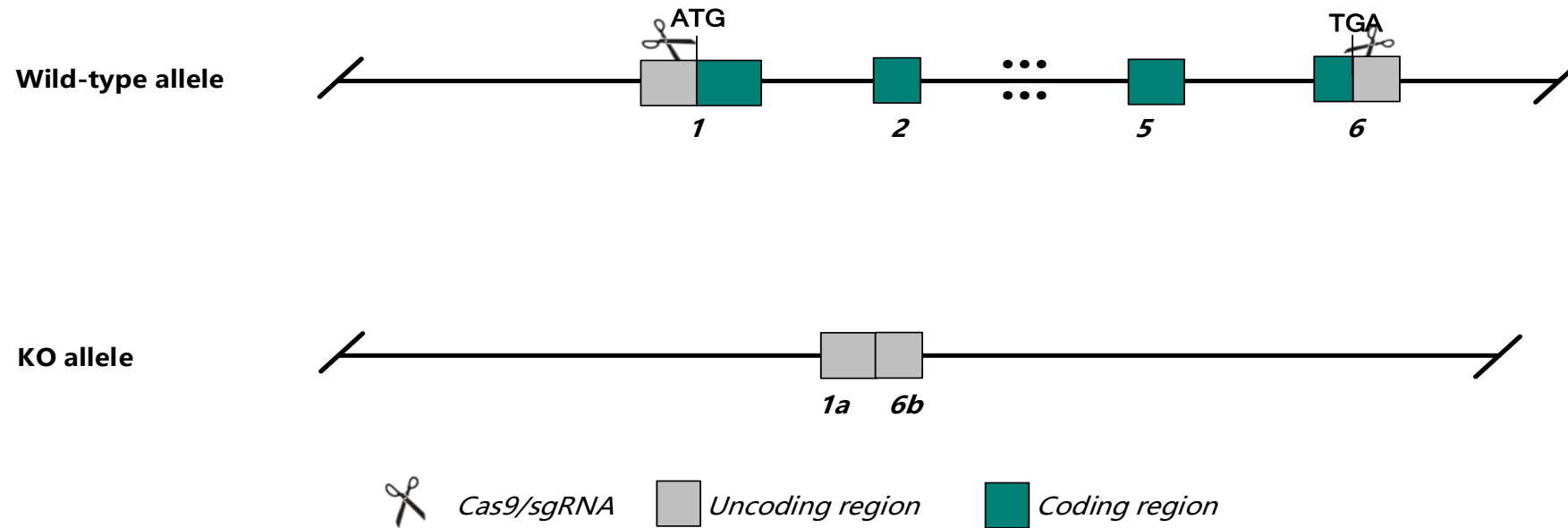
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Tnfsf13* gene.

Technical Information

- The *Tnfsf13* gene has 2 transcripts. According to the structure of *Tnfsf13* gene, exon1-exon6 of *Tnfsf13*-201 (ENSMUST00000018896.14) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Tnfsf13* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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

Tnfsf13 tumor necrosis factor (ligand) superfamily, member 13 [*Mus musculus* (house mouse)]

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Gene ID: 69583, updated on 30-Jul-2025

Summary

Official Symbol	Tnfsf13 provided by MGI
Official Full Name	tumor necrosis factor (ligand) superfamily, member 13 provided by MGI
Primary source	MGI:MGI:1916833
See related	Ensembl:ENSMUSG00000089669 AllianceGenome:MGI:1916833
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	April; Tall2; Trdl1; Tnlg7b; 2310026N09Rik
Summary	Predicted to enable receptor ligand activity. Acts upstream of or within immunoglobulin mediated immune response; positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains; and positive regulation of cell population proliferation. Located in external side of plasma membrane. Is expressed in future midbrain; nervous system; renal vasculature; retina outer nuclear layer; and spleen. Human ortholog(s) of this gene implicated in B-lymphoblastic leukemia/lymphoma. Orthologous to human TNFSF13 (TNF superfamily member 13). [provided by Alliance of Genome Resources, Apr 2025]
Expression	Broad expression in lung adult (RPKM 9.6), colon adult (RPKM 8.2) and 24 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 2 transcripts, all transcripts are shown below:

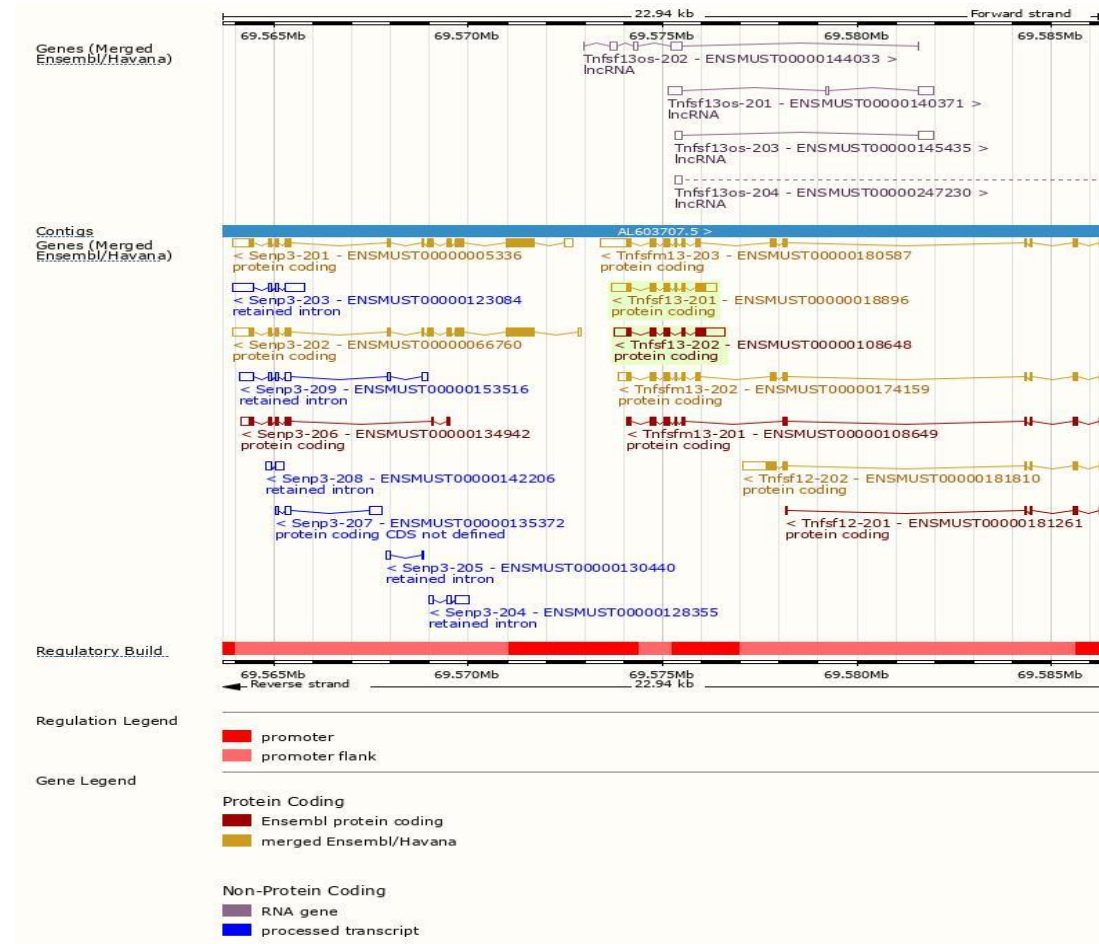
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000018896.14	Tnfsf13-201	1407	240aa	Protein coding	CCDS48827	Q5F2A4	Ensembl Canonical GENCODE basic APPRIS P2 TSL:1
ENSMUST000000108648.3	Tnfsf13-202	1503	224aa	Protein coding		Q5F2A3	GENCODE basic APPRIS ALT2 TSL:5

The strategy is based on the design of *Tnfsf13-201* transcript, the transcription is shown below:

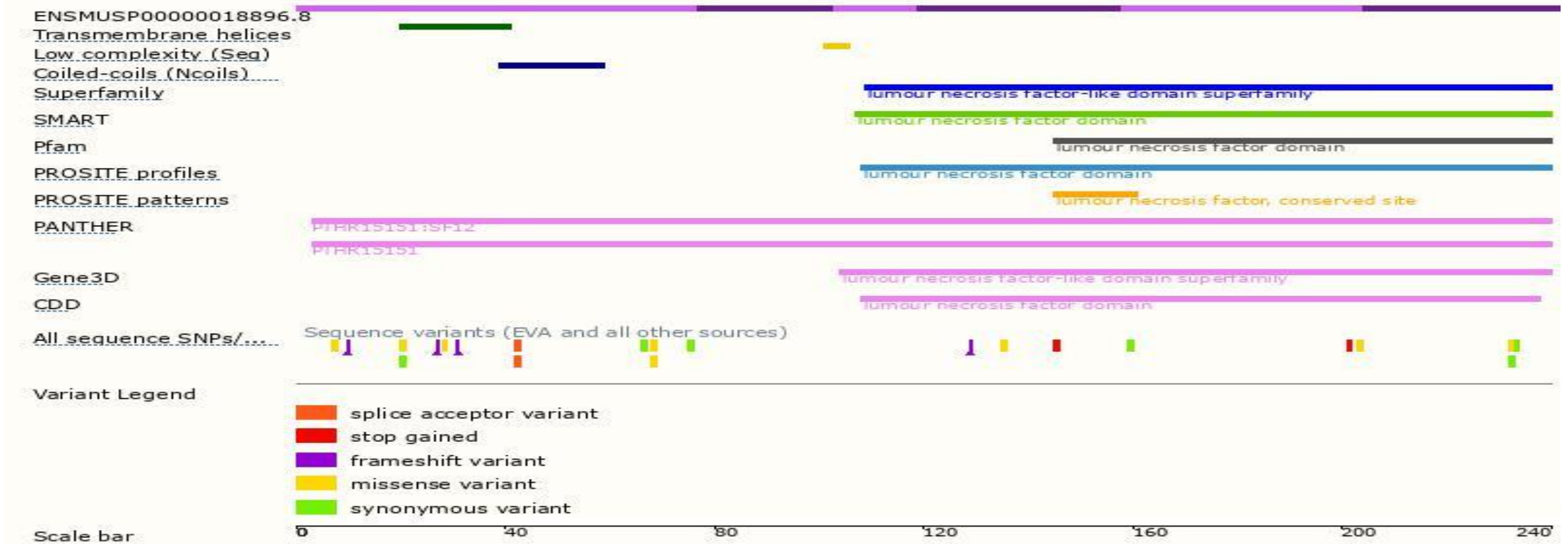


Source: <https://www.ensembl.org>

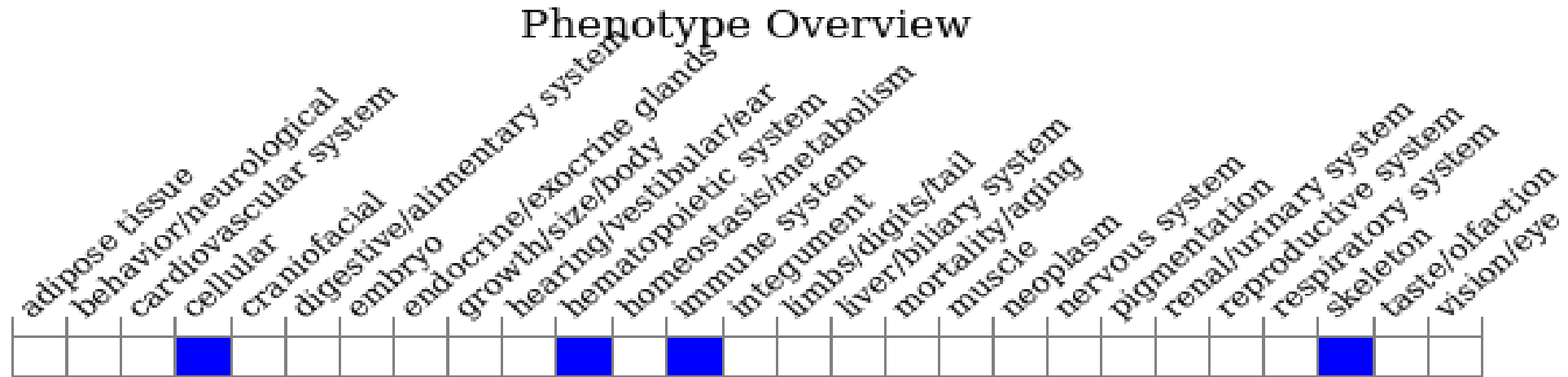
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Homozygous null mice are viable and fertile. No apparent defects of the immune system have been reported.

Important Information

- According to MGI information, homozygous null mice are viable and fertile. No apparent defects of the immune system have been reported.
- The KO region overlap with *Tnfsfm13* and *Tnfsf13os* genes, these genes will be destroyed directly.
- The KO region is about ~1.1kb away from the N-terminal of *Senp3* gene, this strategy may influence the regulatory function of the N-terminal of *Senp3* gene.
- The KO region is about ~0.9kb away from the C-terminal of *Tnfsf12* gene, this strategy may influence the regulatory function of the C-terminal of *Tnfsf12* gene.
- *Tnfsf13* is located on Chr11. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.