

Tnfsf13 Cas9-CKO Strategy

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Overview

Target Gene Name

- Tnfsf13

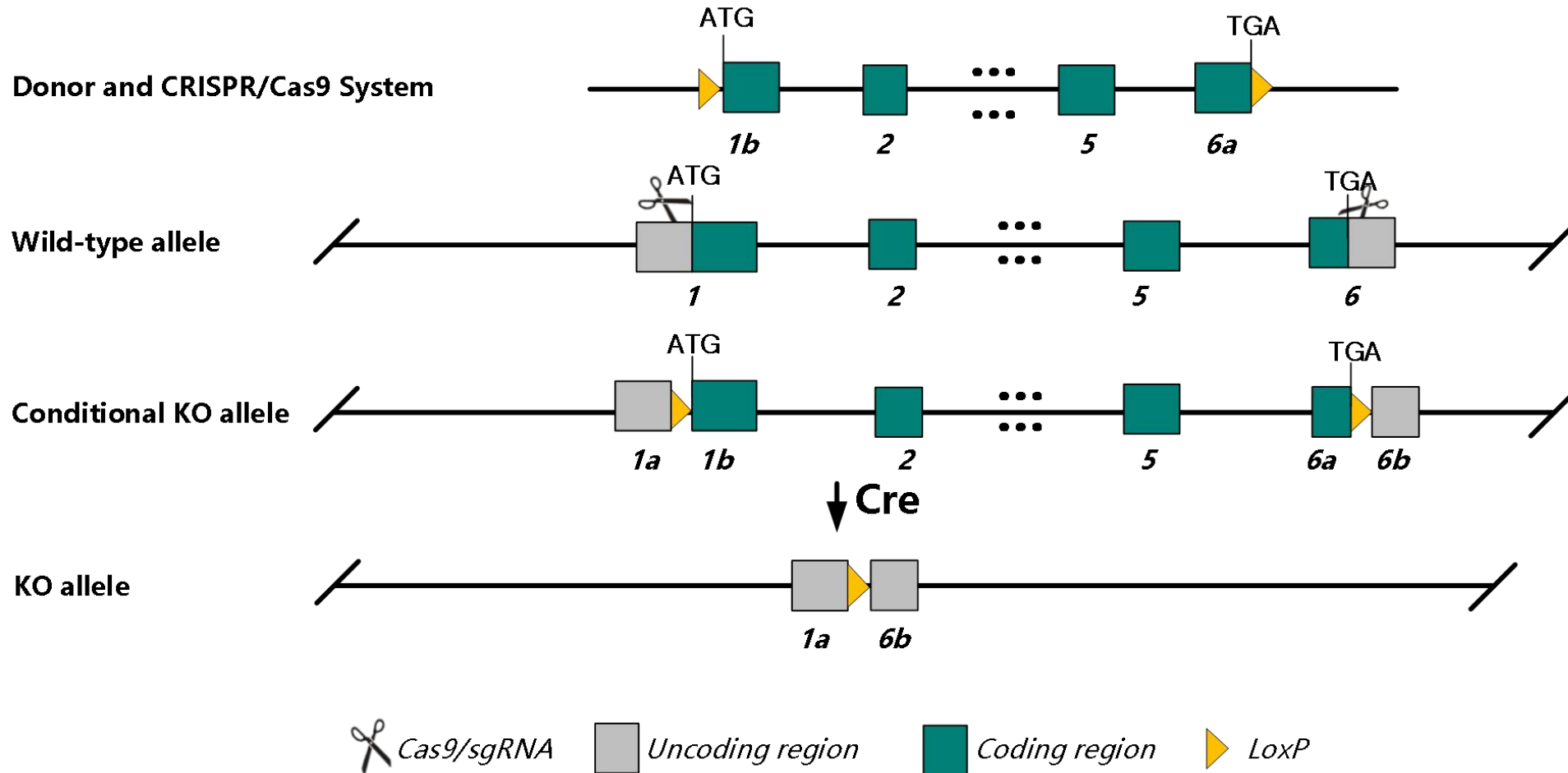
Project Type

- Cas9-CKO

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: 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

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

[Download Datasets](#)

Gene ID: 69583, updated on 18-Sep-2024

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 central nervous system; renal vasculature; retina outer nuclear layer; and superior cervical ganglion. 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 2022]

Expression Broad expression in lung adult (RPKM 9.6), colon adult (RPKM 8.2) and 24 other tissues [See more](#)

Orthologs [human](#) [all](#)

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

Transcript Information

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

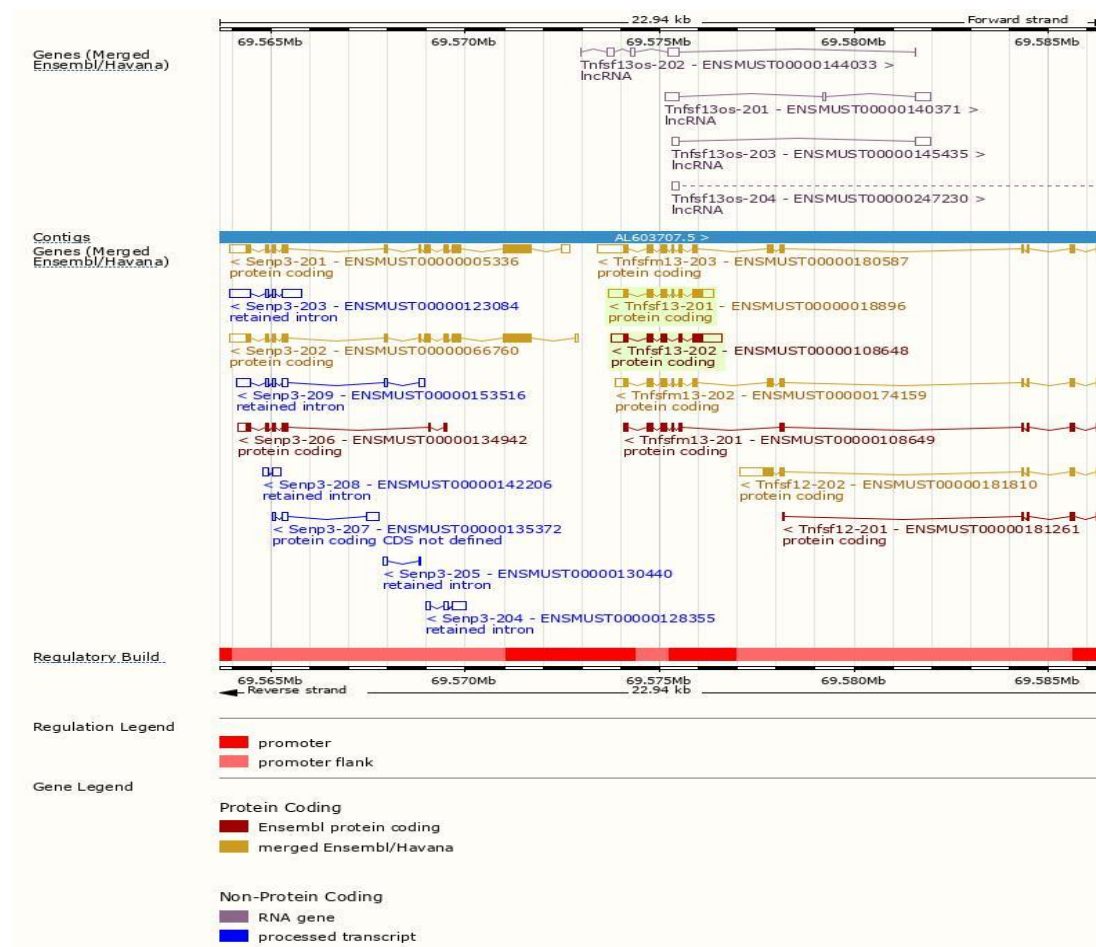
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000018896.14	Tnfsf13-201	1407	240aa	Protein coding	CCDS48827	Q5F2A4	Ensembl Canonical Gencode basic APPRIS P2 TSL:1
ENSMUST00000108648.3	Tnfsf13-202	1503	224aa	Protein coding		Q5F2A3	Gencode basic APPRIS ALT2 TSL:5

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

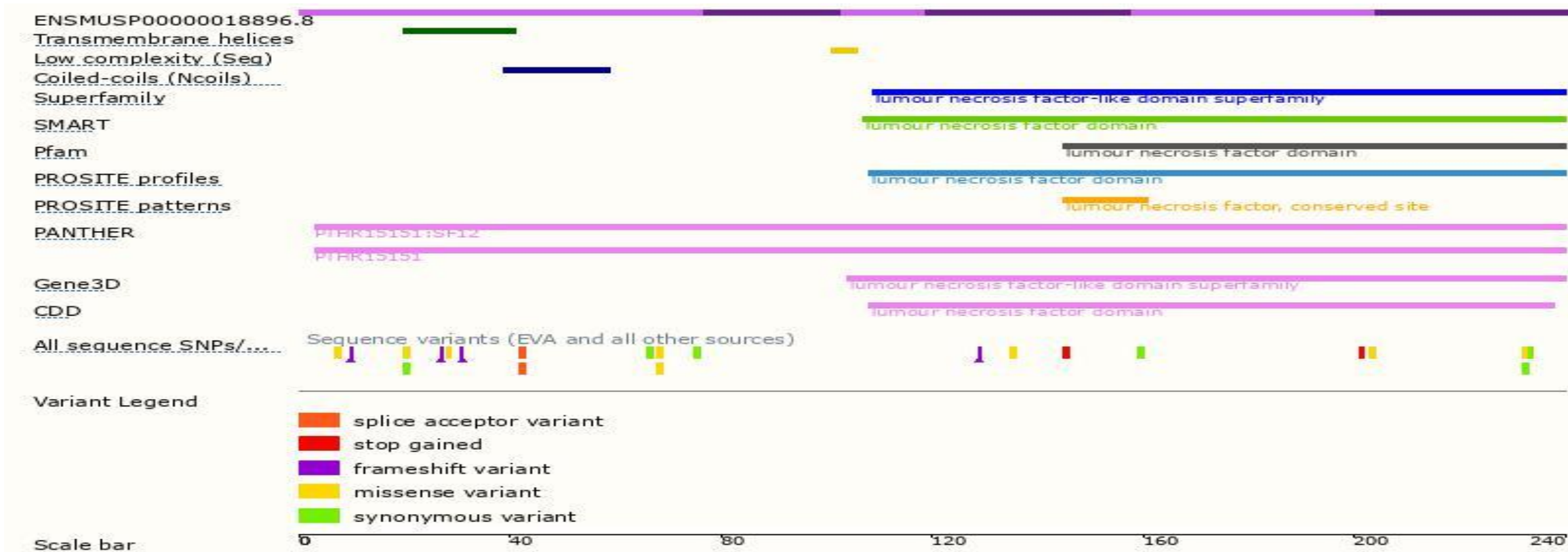


Source: <https://www.ensembl.org>

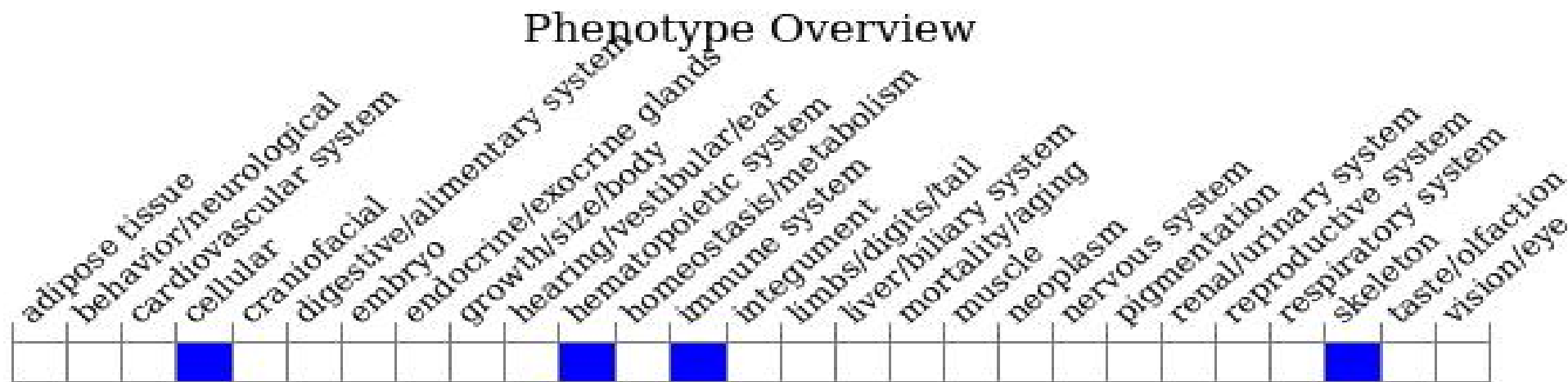
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)

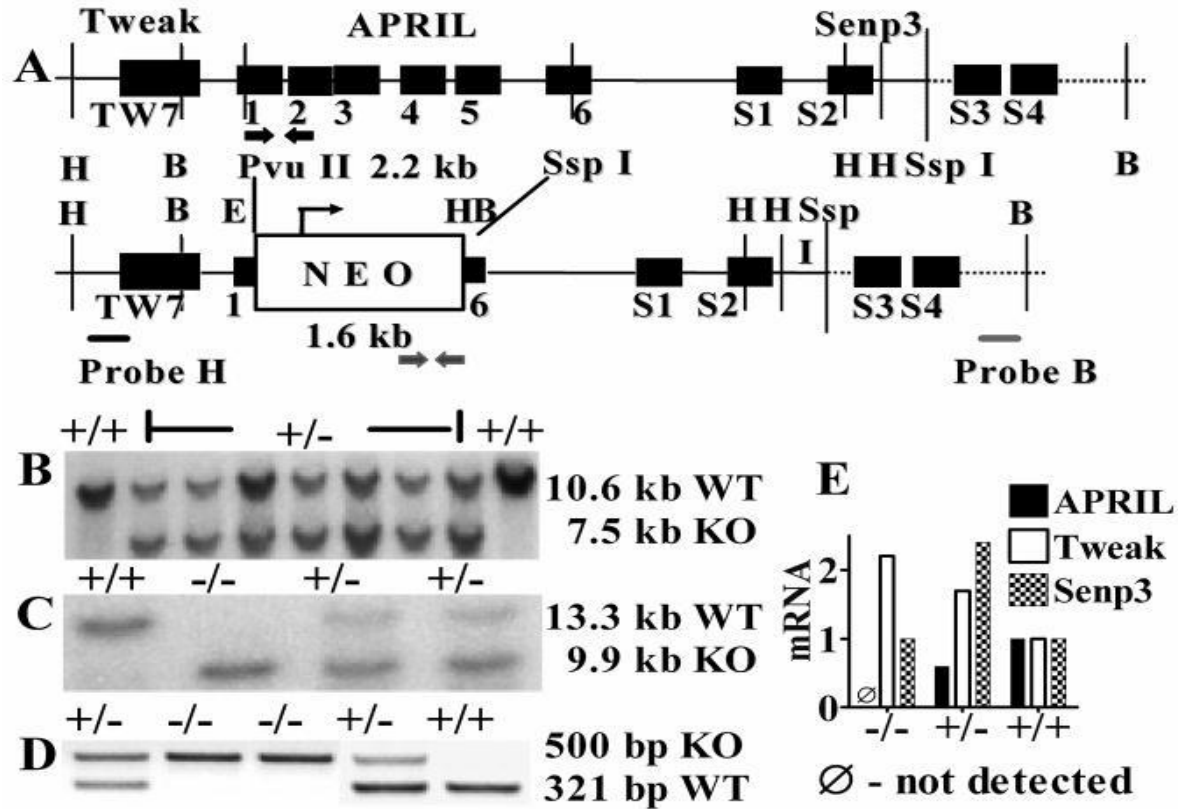


- Homozygous null mice are viable and fertile. No apparent defects of the immune system have been reported.

Important Information

- According to MGI information, homozygous null mice are viable and fertile. No apparent defects of the immune system have been reported.
- The floxed region overlap with *Tnfsfm13* and *Tnfsf13os* genes, these genes will be destroyed directly.
- The floxed 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 floxed 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.
- The insertion of Loxp may influence the regulatory function of the *Tnfsf13* 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

References



APRIL deficient mice were created by replacing exons 2-5 and the majority of exon 1 and 6 of the APRIL gene with a neomycin cassette (Fig 1A) by homologous recombination in embryonal stem cells and blastocyst injection. Homozygous APRIL^{-/-} mice showed complete absence of APRIL mRNA in splenocytes (Fig. 1E) while mRNA for TNF-related weak inducer of apoptosis (Tweak, or TNFSF12) and Sentrin specific peptidase 3 (Senp3), two genes located 794 bp and 731 bp up- and down-stream, respectively, of APRIL were expressed normally.

Xiao Y, Motomura S, Podack ER. APRIL (TNFSF13) regulates collagen-induced arthritis, IL-17 production and Th2 response. *Eur J Immunol.* 2008 Dec;38(12):3450-8. doi: 10.1002/eji.200838640. PMID: 19016524; PMCID: PMC2755626.