

Tnfrsf8 Cas9-KO Strategy

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Project Overview

Project Name

Tnfrsf8

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tnfrsf8* gene. The schematic diagram is as follows:



- The *Tnfrsf8* gene has 2 transcripts. According to the structure of *Tnfrsf8* gene, exon2 of *Tnfrsf8-201* (ENSMUST00000030339.12) transcript is recommended as the knockout region. The region contains 88bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tnfrsf8* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele display an enlarged thymus, impaired activation-induced death of double-positive thymocytes after CD3 cross-linking, and decreased susceptibility to graft versus host disease.
- The *Tnfrsf8* gene is located on the Chr4. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Tnfrsf8 tumor necrosis factor receptor superfamily, member 8 [Mus musculus (house mouse)]

Gene ID: 21941, updated on 31-Jan-2019

Summary



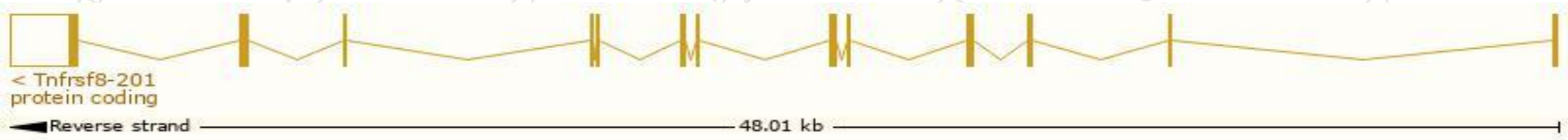
Official Symbol	Tnfrsf8 provided by MGI
Official Full Name	tumor necrosis factor receptor superfamily, member 8 provided by MGI
Primary source	MGI:MGI:99908
See related	Ensembl:ENSMUSG00000028602
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cd30, D1S166E, Ki, Ki-1
Expression	Biased expression in thymus adult (RPKM 4.6), testis adult (RPKM 0.6) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

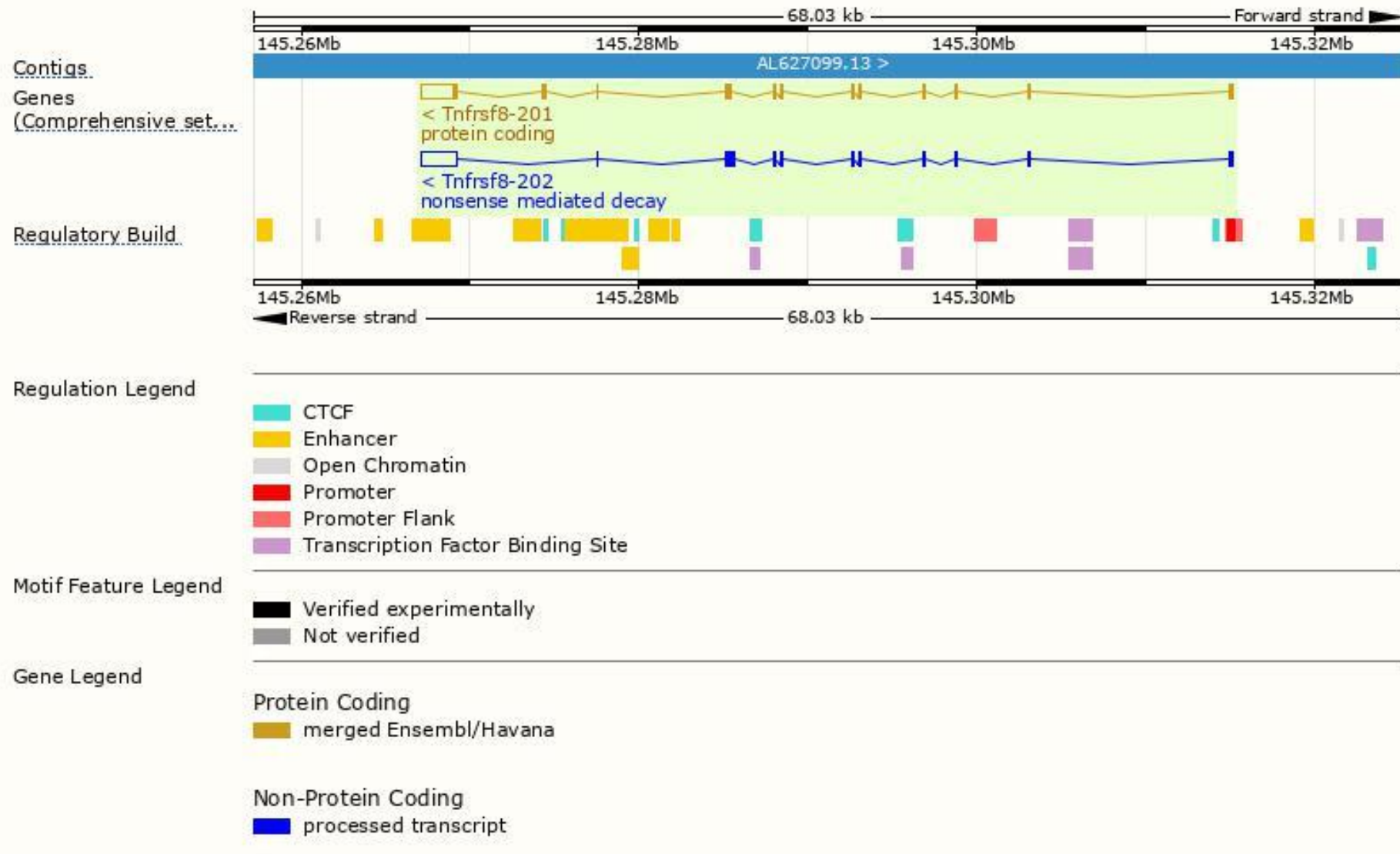
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnfrsf8-201	ENSMUST00000030339.12	3414	498aa	Protein coding	CCDS18915	A1L3C9 Q60846	TSL:1 GENCODE basic APPRIS P1
Tnfrsf8-202	ENSMUST00000123027.1	3243	322aa	Nonsense mediated decay	-	D6RHK4	TSL:1

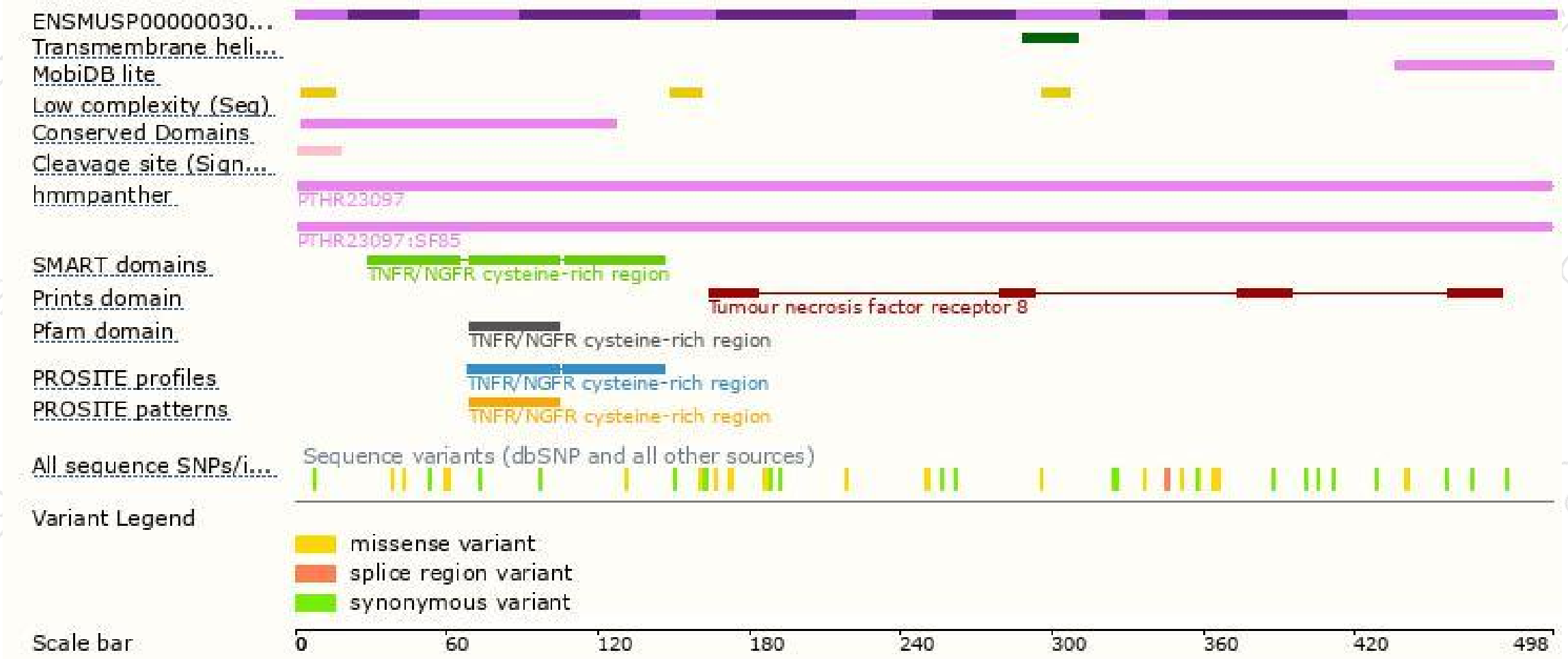
The strategy is based on the design of *Tnfrsf8-201* transcript,The transcription is shown below



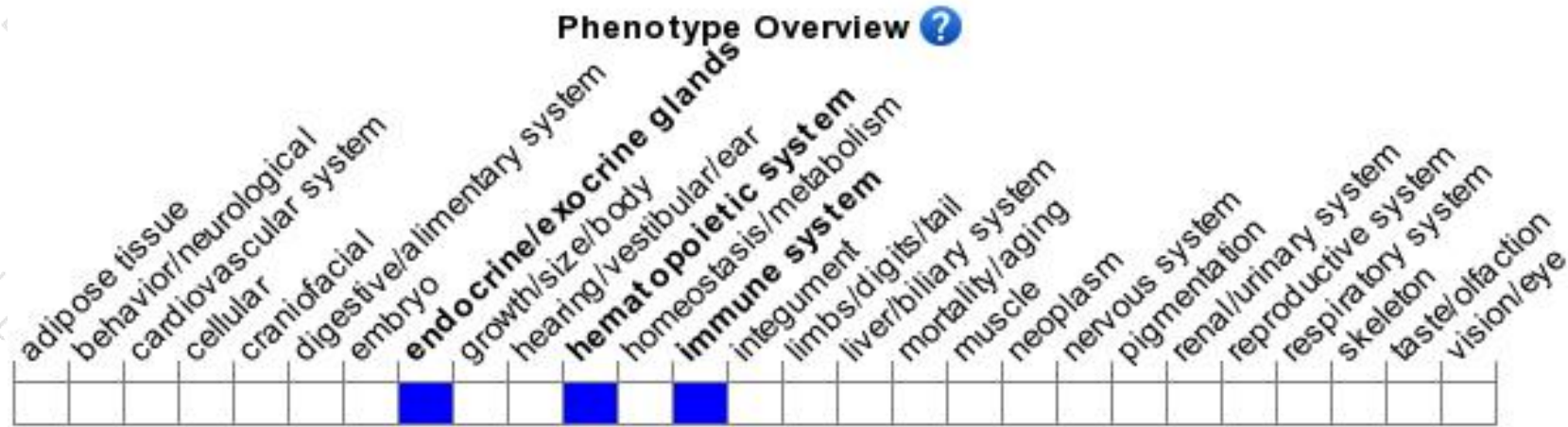
Genomic location distribution



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, Mice homozygous for a knock-out allele display an enlarged thymus, impaired activation-induced death of double-positive thymocytes after CD3 cross-linking, and decreased susceptibility to graft versus host disease.

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

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