

Tnfrsf1b Cas9-CKO Strategy

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Design Date: 2019-9-23

Project Overview



Project Name

Tnfrsf1b

Project type

Cas9-CKO

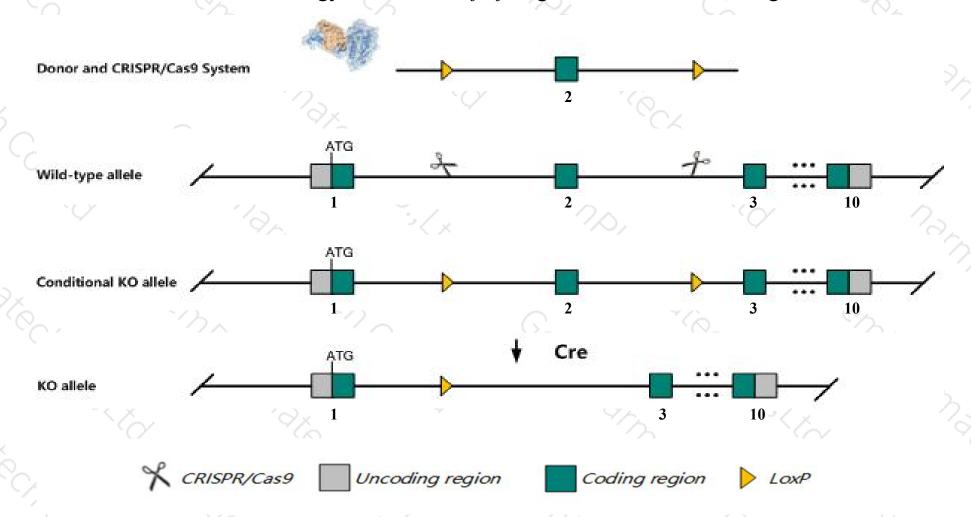
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Tnfrsf1b* gene. The schematic diagram is as follows:



Technical routes



- The *Tnfrsf1b* gene has 2 transcripts. According to the structure of *Tnfrsf1b* gene, exon2 of *Tnfrsf1b-201* (ENSMUST00000030336.10) transcript is recommended as the knockout region. The region contains 103bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tnfrsf1b* 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.

Notice



- ➤ According to the existing MGI data, Homozygotes for targeted null mutations exhibit altered inflammatory responses in a variety of experimental conditions, impaired recovery from spinal cord injury, enhanced ischemia-reperfusion-induced retinal damage, and resistance to cerebral malaria.
- The *Tnfrsf1b* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Tnfrsf1b tumor necrosis factor receptor superfamily, member 1b [Mus musculus (house mouse)]

Gene ID: 21938, updated on 9-Apr-2019

Summary

☆ ?

Official Symbol Tnfrsf1b provided by MGI

Official Full Name tumor necrosis factor receptor superfamily, member 1b provided by MGI

Primary source MGI:MGI:1314883

See related Ensembl: ENSMUSG00000028599

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 CD120b, TNF-R-II, TNF-R2, TNF-R75, TNF-alphaR2, TNFBR, TNFR80, TNFRII, TNFalpha-R2, Tnfr-1, Tnfr2, p75

Expression Broad expression in spleen adult (RPKM 20.1), mammary gland adult (RPKM 14.7) and 20 other tissuesSee more

Orthologs <u>human</u> all

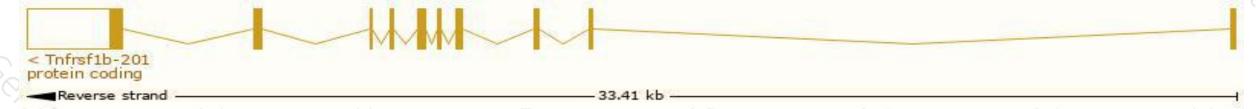
Transcript information (Ensembl)



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

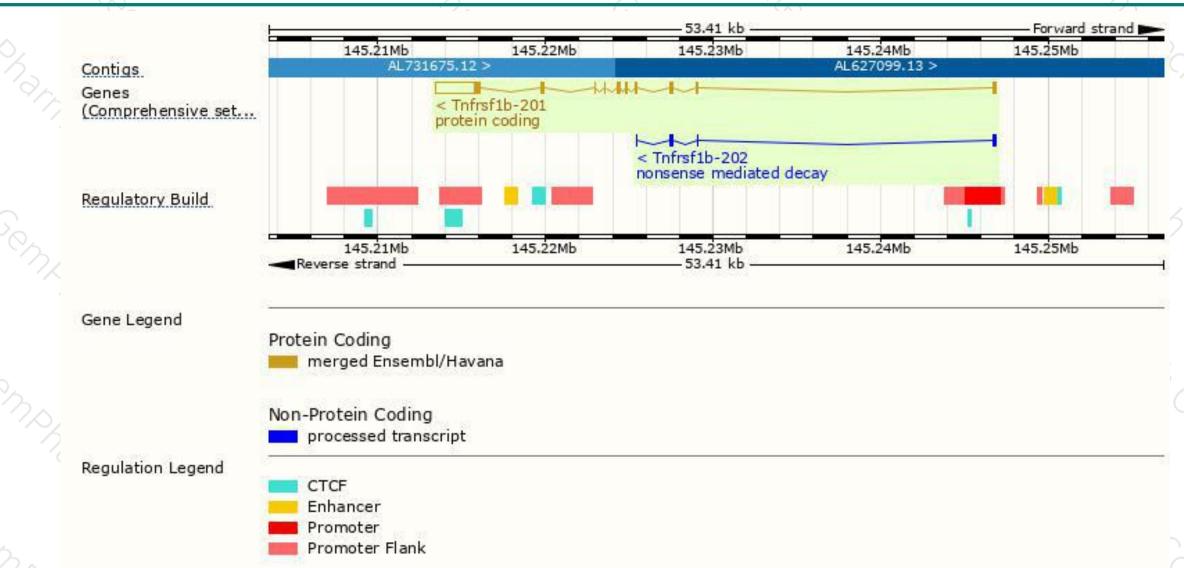
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnfrsf1b-201	ENSMUST00000030336.10	3818	<u>474aa</u>	Protein coding	CCDS18914	P25119 Q545P4	TSL:1 GENCODE basic APPRIS P1
Tnfrsf1b-202	ENSMUST00000143055.1	375	<u>55aa</u>	Nonsense mediated decay	6.00	D6RG55	TSL:3

The strategy is based on the design of *Tnfrsf1b-201* transcript, The transcription is shown below



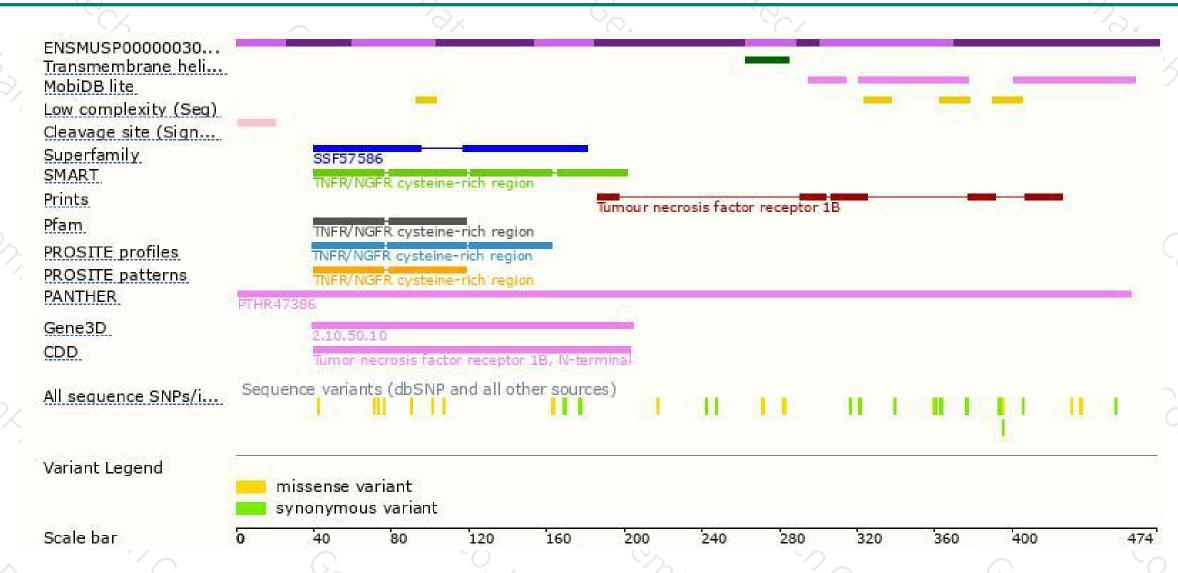
Genomic location distribution





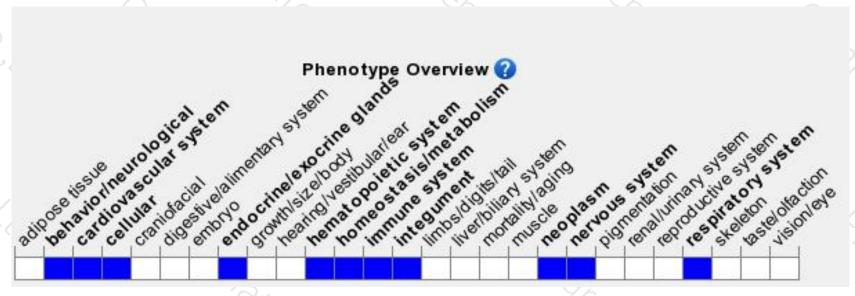
Protein domain





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 targeted null mutations exhibit altered inflammatory responses in a variety of experimental conditions, impaired recovery from spinal cord injury, enhanced ischemia-reperfusion-induced retinal damage, and resistance to cerebral malaria.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





