

Slamf1 Cas9-KO Strategy

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Project Overview



Project Name

Slamf1

Project type

Cas9-KO

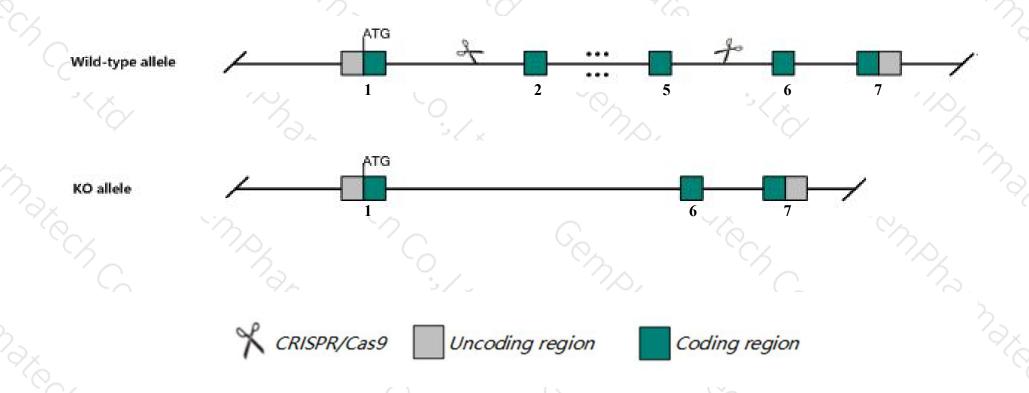
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Slamf1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Slamf1* gene has 2 transcripts. According to the structure of *Slamf1* gene, exon2-exon5 of *Slamf1-201* (ENSMUST00000015460.4) transcript is recommended as the knockout region. The region contains 809bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Slamf1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Homozygous null mice are fertile and display impaired T cell and macrophage cytokine production.
- > The *Slamf1* gene is located on the Chr1. 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)



Slamf1 signaling lymphocytic activation molecule family member 1 [Mus musculus (house mouse)]

Gene ID: 27218, updated on 31-Jan-2019

Summary

☆ ?

Official Symbol Slamf1 provided by MGI

Official Full Name signaling lymphocytic activation molecule family member 1 provided by MGI

Primary source MGI:MGI:1351314

See related Ensembl: ENSMUSG00000015316

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 4933415F16, AA177906, CD150, CDw150, ESTM51, IPO-3, Slam

Expression Biased expression in thymus adult (RPKM 5.3), spleen adult (RPKM 1.6) and 5 other tissuesSee more

Orthologs <u>human all</u>

Transcript information (Ensembl)



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

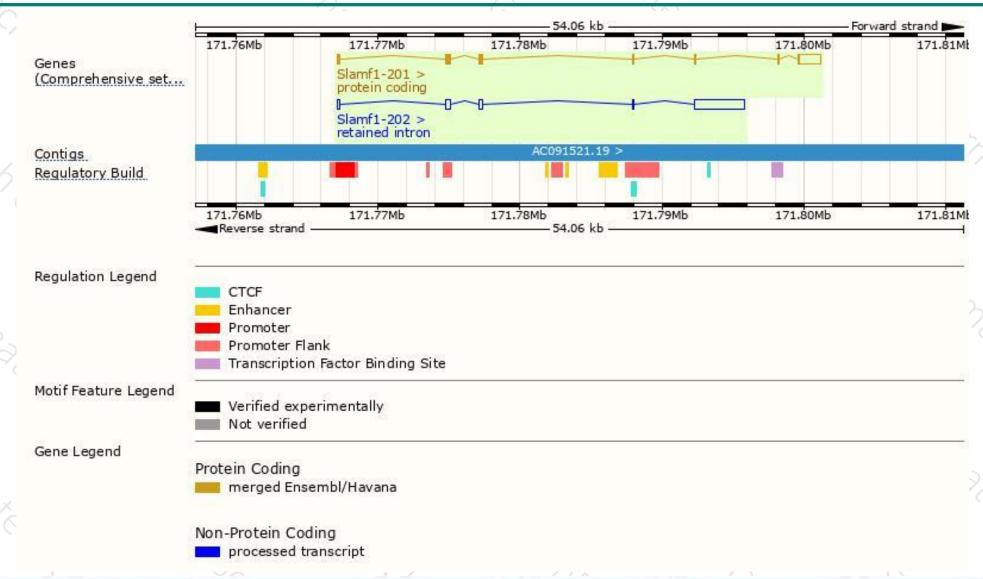
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slamf1-201	ENSMUST00000015460.4	2693	<u>343aa</u>	Protein coding	CCDS15502	Q544K1 Q9QUM4	TSL:1 GENCODE basic APPRIS P1
Slamf1-202	ENSMUST00000163992.2	4420	No protein	Retained intron		19-	TSL:1

The strategy is based on the design of Slamf1-201 transcript, The transcription is shown below



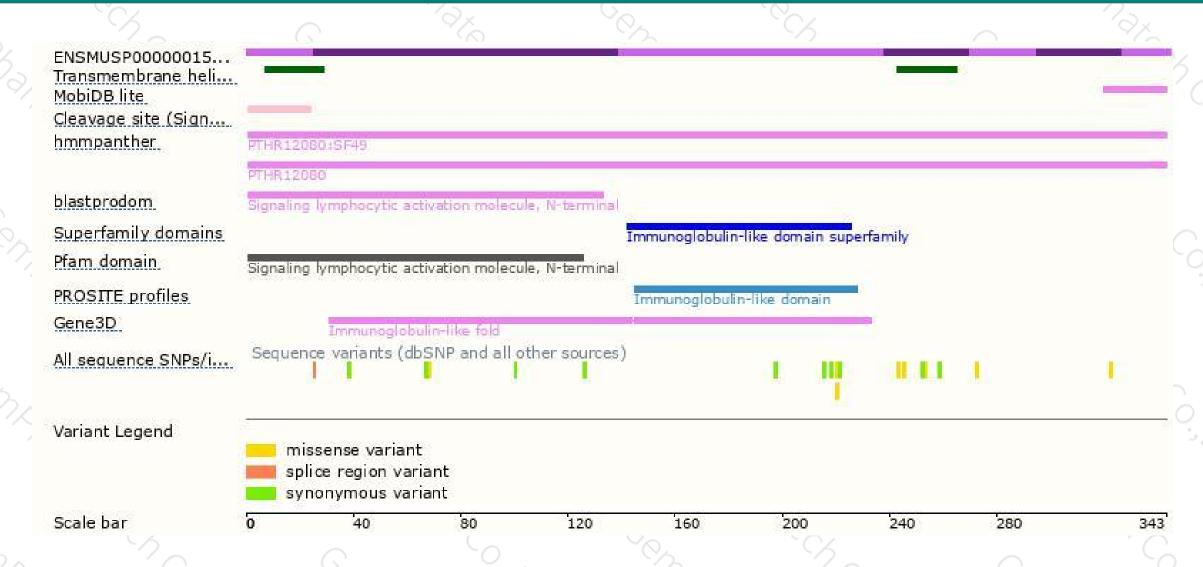
Genomic location distribution





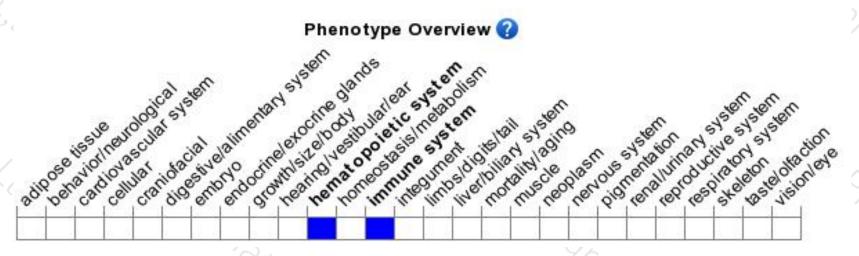
Protein domain





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, Homozygous null mice are fertile and display impaired T cell and macrophage cytokine production.



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





