

Slamf6 Cas9-CKO Strategy

Designer: Xingkai Xiao

Reviewer: Xiangli Bian

Design Date: 2024-2-28

Overview

Target Gene Name

- *Slamf6*

Project Type

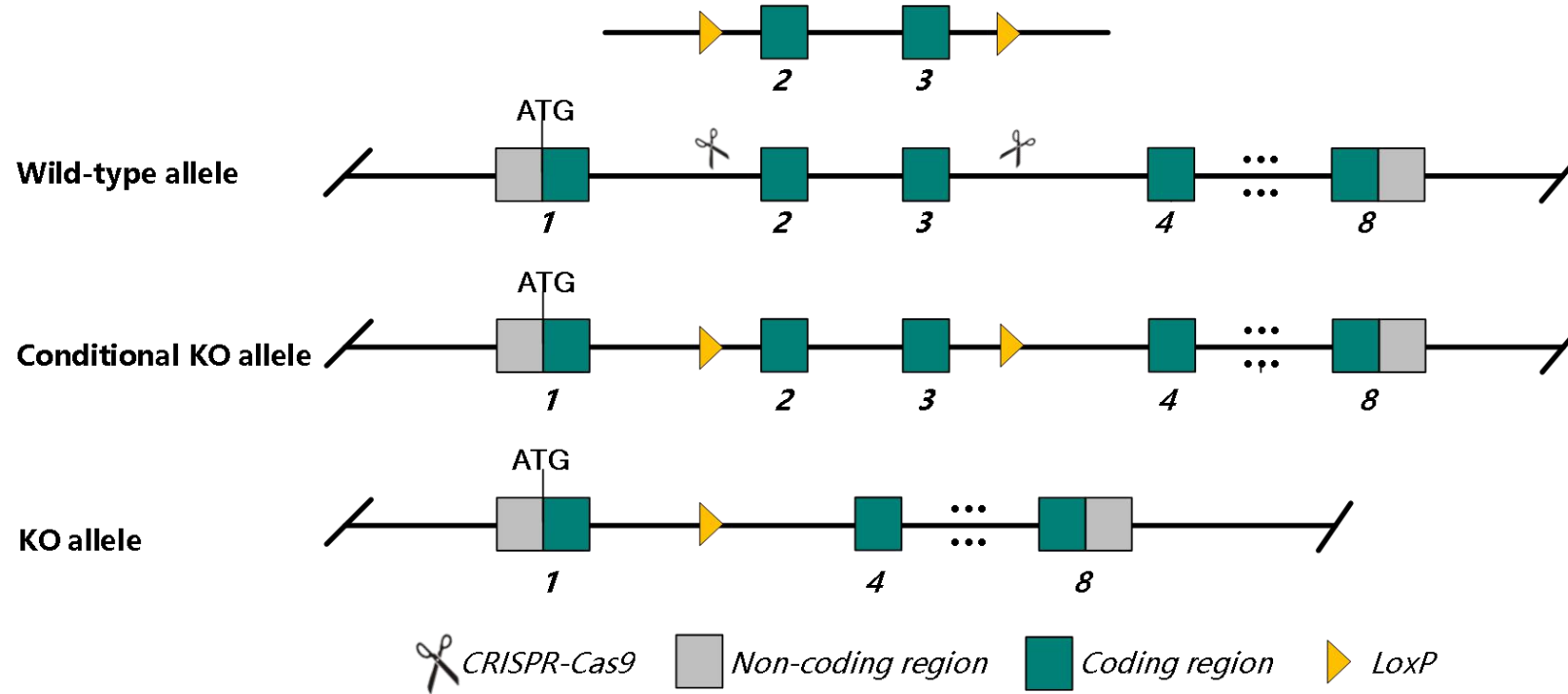
- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Slamf6* gene.

Technical Information

- The *Slamf6* gene has 7 transcripts. According to the structure of *Slamf6* gene, exon 2-3 of *Slamf6*-201 (ENSMUST00000171330.7) is recommended as the knockout region. The region contains 606 bp of coding sequence. Knocking out the region will delete the most coding region of *Slamf6* and may result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Slamf6* 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

Slamf6 SLAM family member 6 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 30925, updated on 8-Feb-2024

Summary

Official Symbol	Slamf6 provided by MGI
Official Full Name	SLAM family member 6 provided by MGI
Primary source	MGI:MGI:1353620
See related	Ensembl:ENSMUSG00000015314 AllianceGenome:MGI:1353620
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	KAL1; NTBA; KAL1b; Ly108; NTB-A; SF2000
Summary	Involved in natural killer cell differentiation and natural killer cell proliferation. Predicted to be located in plasma membrane. Predicted to be integral component of plasma membrane. Predicted to be active in external side of plasma membrane. Orthologous to human SLAMF6 (SLAM family member 6). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in thymus adult (RPKM 5.3), spleen adult (RPKM 3.2) and 4 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

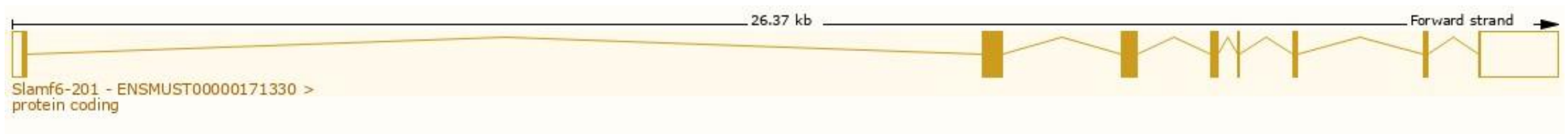
<https://www.ncbi.nlm.nih.gov/gene/30925>

Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

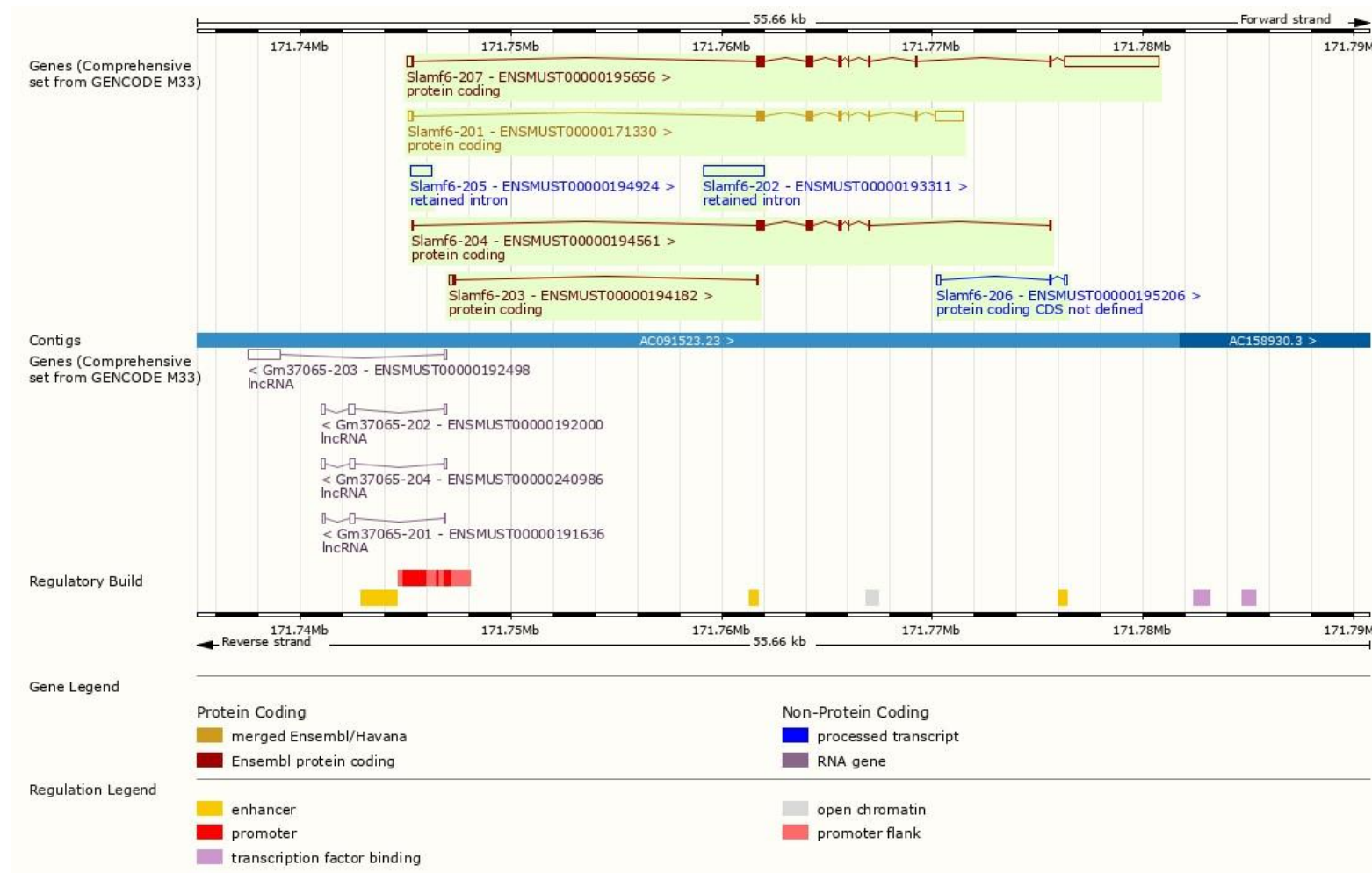
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000195656.6	Slamf6-207	5729	351aa	Protein coding	CCDS83638	Q18PJ0 Q9ET39	Ensembl Canonical	GENCODE basic APPRIS ALT2 TSL:1
ENSMUST00000171330.7	Slamf6-201	2485	331aa	Protein coding	CCDS15504	Q9ET39-2	GENCODE basic	APPRIS P2 TSL:1
ENSMUST00000194561.2	Slamf6-204	984	327aa	Protein coding	CCDS83639	Q9ET39-3	GENCODE basic	APPRIS ALT2 TSL:1
ENSMUST00000194182.2	Slamf6-203	346	55aa	Protein coding		A0A0A6YY21	TSL:3	CDS 3' incomplete
ENSMUST00000195206.2	Slamf6-206	444	No protein	Protein coding CDS not defined		-	TSL:3	
ENSMUST00000193311.2	Slamf6-202	2920	No protein	Retained intron		-	TSL:NA	
ENSMUST00000194924.2	Slamf6-205	998	No protein	Retained intron		-	TSL:NA	

The strategy is based on the design of *Slamf6-201* transcript, the transcription is shown below:

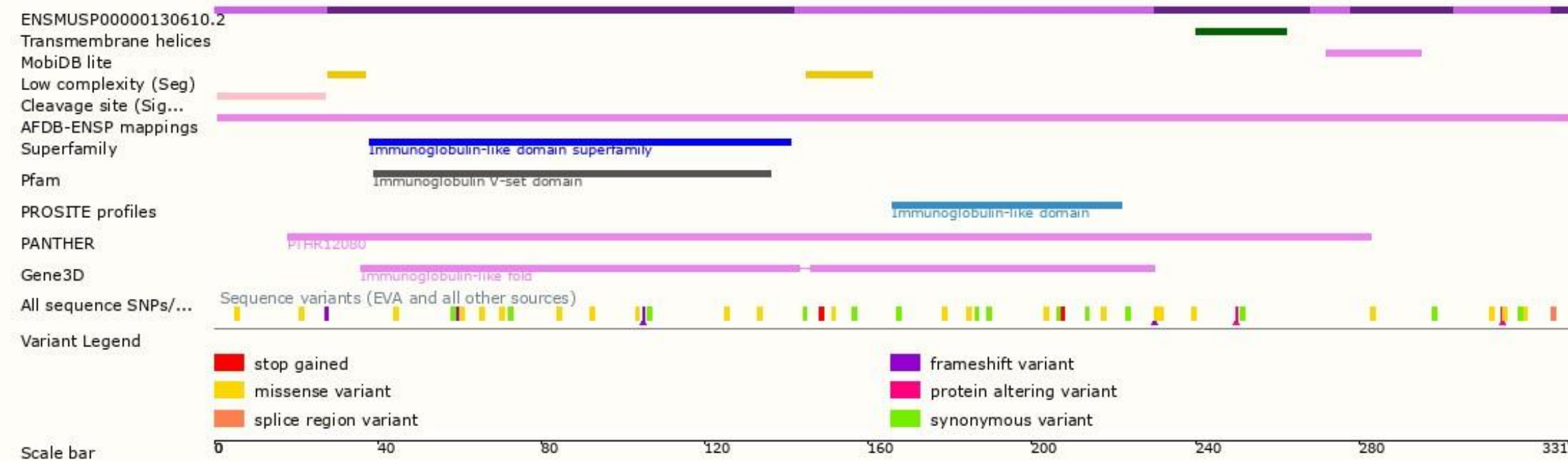


Source: <http://asia.ensembl.org/>

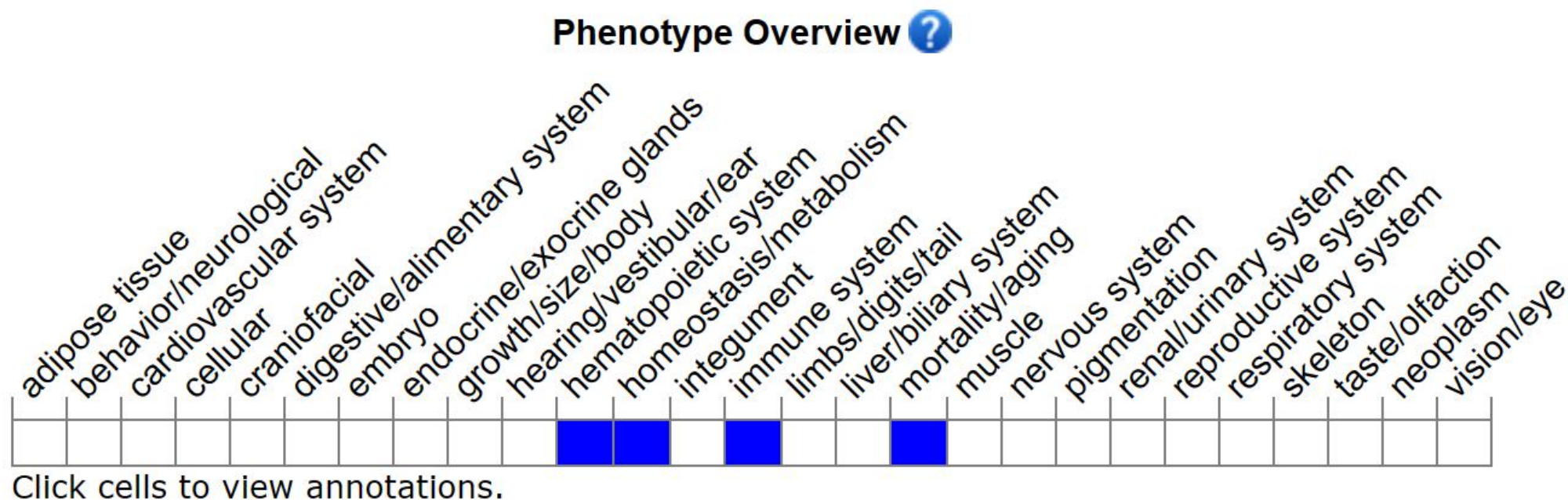
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)

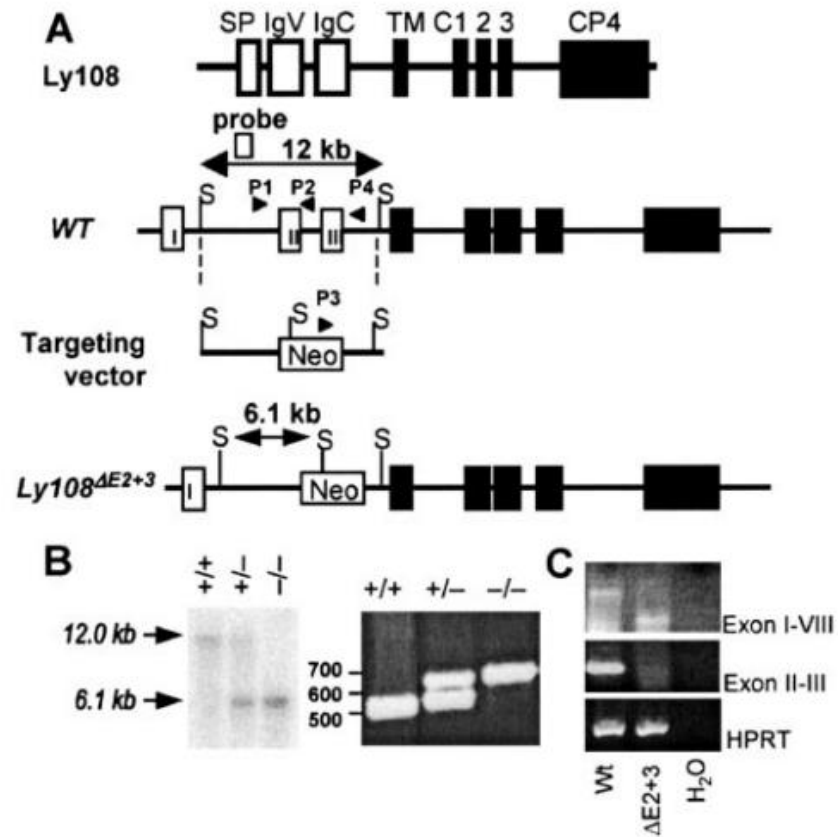


Mice homozygous for one null allele show no overt phenotype. Mice homozygous for another null allele show impaired IL-4 production by CD4⁺ T cells, reduced inflammatory response to *L. mexicana* infection, high susceptibility to *S. typhimurium* infection, and defective neutrophil bactericidal activity.

Important Information

- Mice homozygous show impaired IL-4 production by CD4+ T cells, reduced inflammatory response to *L. mexicana* infection, high susceptibility to *S. typhimurium* infection, and defective neutrophil bactericidal activity.
- The 3' incomplete of transcript *Slamf6*-203, the effect is unknown.
- This strategy do not affect the transcript *Slamf6*-205 and 206.
- In this strategy, 3' of *Slamf6* will retain 100 aa, the risk is unknown.
- *Slamf6* is located on Chr 1. 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.

Reference



[1] Cutting Edge: The SLAM Family Receptor Ly108 Controls T Cell and Neutrophil Functions. *J Immunol.* 2005 May 15;174(10):5931-5. Doi:10.4049/jimmunol.174.10.5931.