

Slamf6 Cas9-KO Strategy

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Project Overview

Project Name

Slamf6

Project type

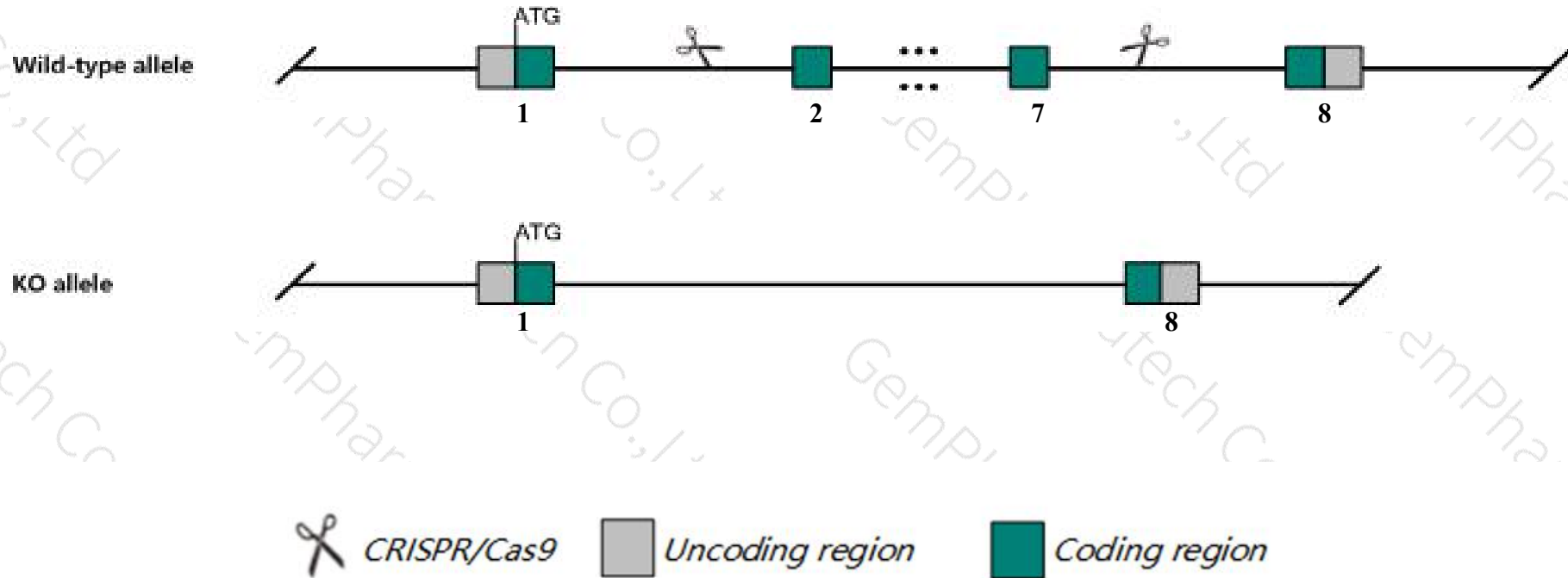
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slamf6* gene. The schematic diagram is as follows:



- The *Slamf6* gene has 7 transcripts. According to the structure of *Slamf6* gene, exon2-exon7 of *Slamf6*-207 (ENSMUST00000195656.5) transcript is recommended as the knockout region. The region contains 896bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slamf6* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, 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.
- The *Slamf6* 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)

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

Gene ID: 30925, updated on 19-Mar-2019

Summary



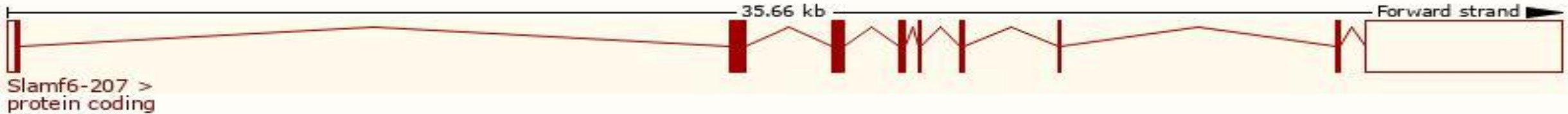
Official Symbol	Slamf6 provided by MGI
Official Full Name	SLAM family member 6 provided by MGI
Primary source	MGI:MGI:1353620
See related	Ensembl:ENSMUSG00000015314
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	KAL1, KAL1b, Ly108, NTB-A, NTBA, SF2000
Expression	Biased expression in thymus adult (RPKM 5.3), spleen adult (RPKM 3.2) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

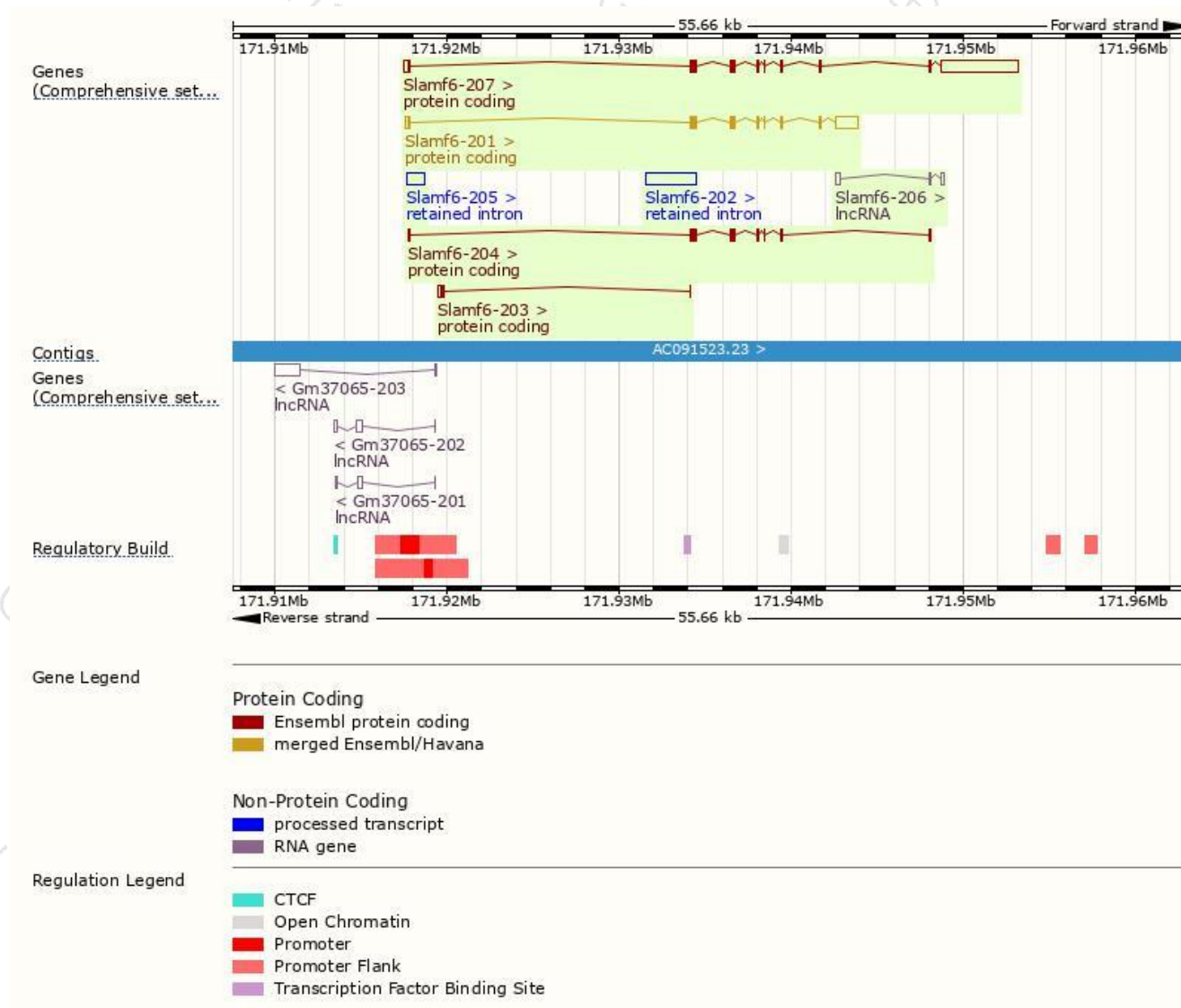
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slamf6-207	ENSMUST00000195656.5	5729	351aa	Protein coding	CCDS83638	Q18PJ0 Q9ET39	TSL:1 GENCODE basic APPRIS ALT2
Slamf6-201	ENSMUST00000171330.6	2485	331aa	Protein coding	CCDS15504	Q18PG5 Q9ET39	TSL:1 GENCODE basic APPRIS P3
Slamf6-204	ENSMUST00000194561.1	984	327aa	Protein coding	CCDS83639	Q9ET39	TSL:1 GENCODE basic APPRIS ALT2
Slamf6-203	ENSMUST00000194182.1	346	55aa	Protein coding	-	A0A0A6YY21	CDS 3' incomplete TSL:3
Slamf6-202	ENSMUST00000193311.1	2920	No protein	Retained intron	-	-	TSL:NA
Slamf6-205	ENSMUST00000194924.1	998	No protein	Retained intron	-	-	TSL:NA
Slamf6-206	ENSMUST00000195206.1	444	No protein	lncRNA	-	-	TSL:3

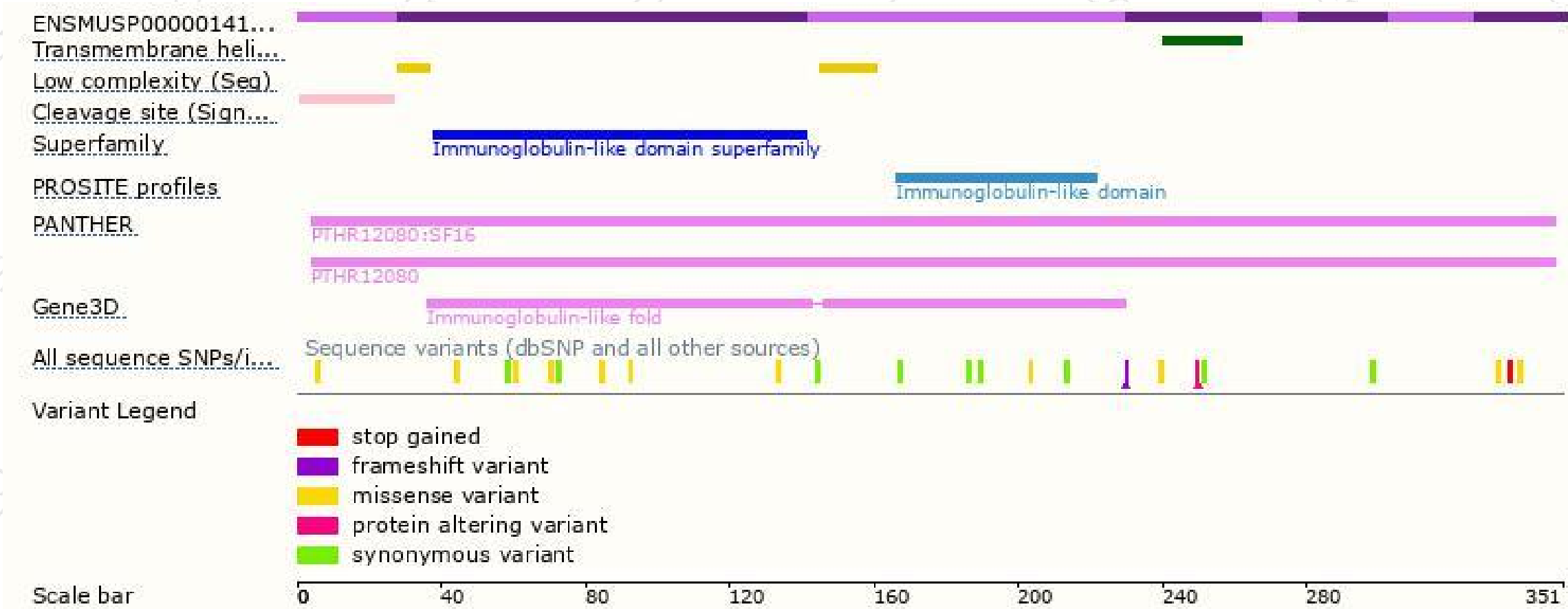
The strategy is based on the design of *Slamf6-207* transcript,The transcription is shown below



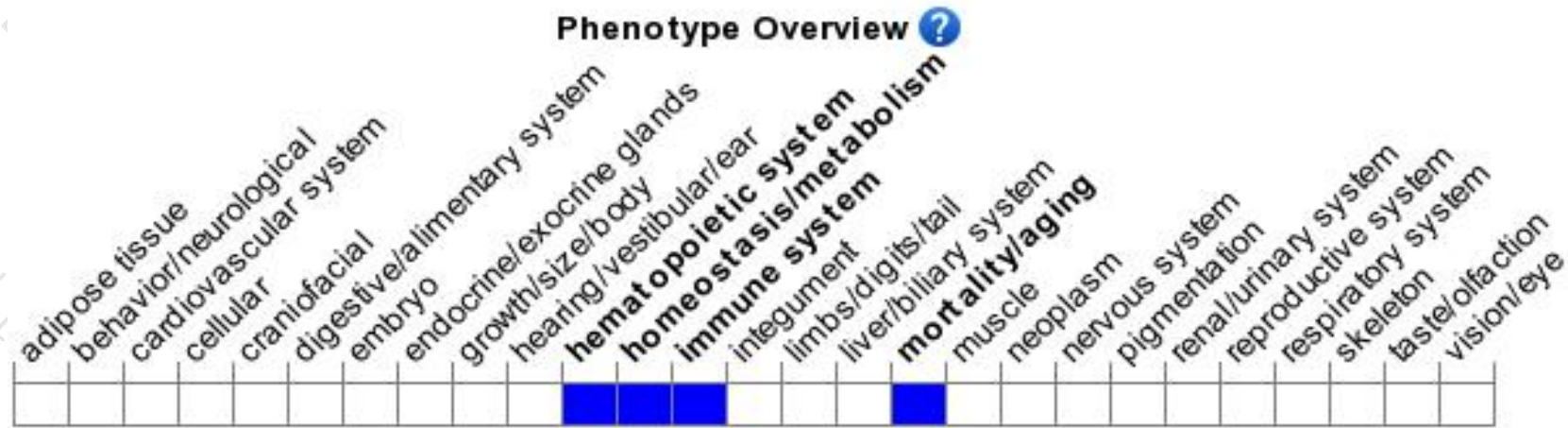
Genomic location distribution



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/>).

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

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