

Slamf7 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Slamf7

Project type

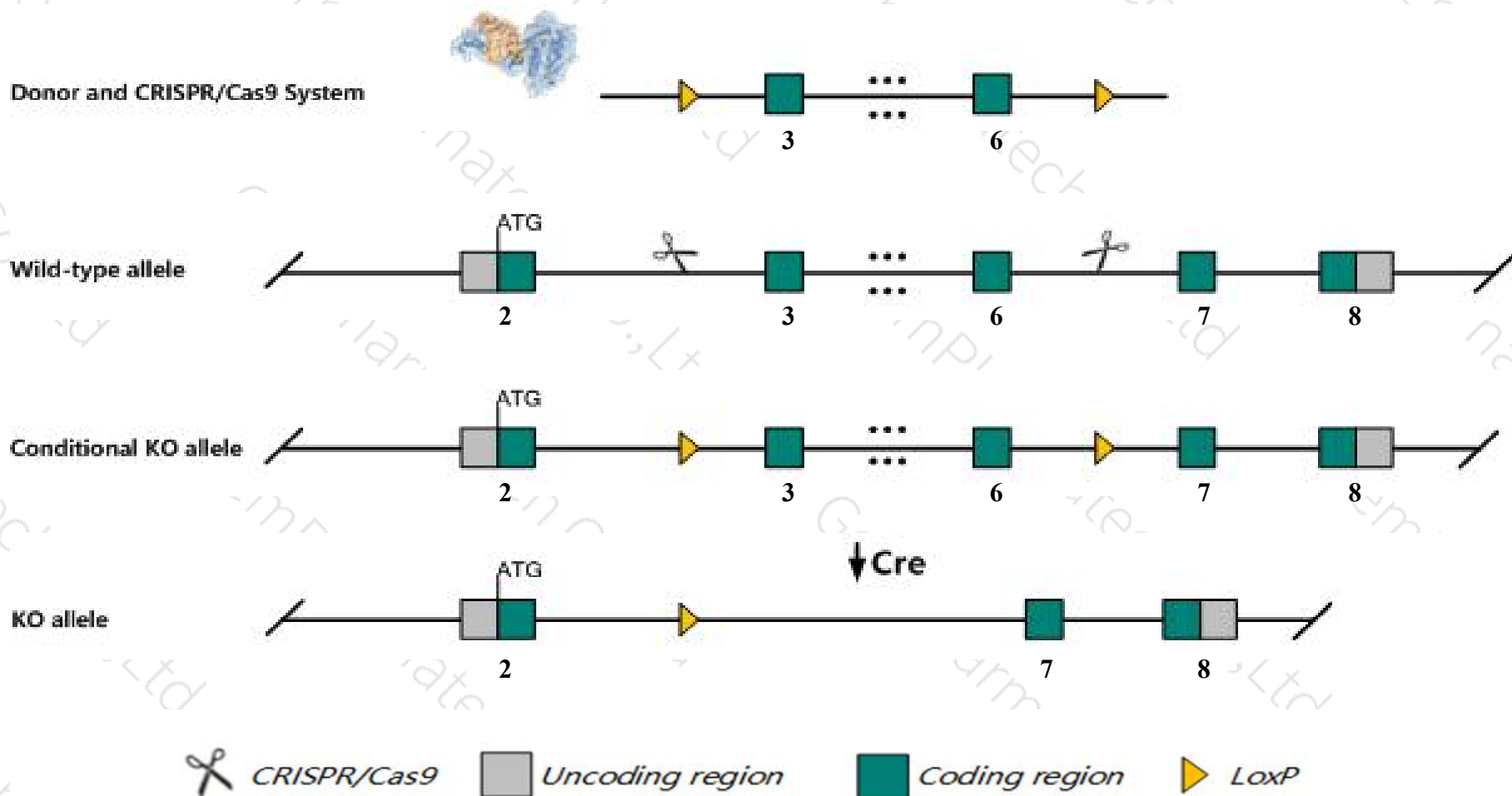
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slamf7* gene. The schematic diagram is as follows:



- The *Slamf7* gene has 5 transcripts. According to the structure of *Slamf7* gene, exon3-exon6 of *Slamf7*-203 (ENSMUST00000192195.5) transcript is recommended as the knockout region. The region contains 812bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slamf7* 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.

- According to the existing MGI data, Natural Killer cells from null homozygotes display impaired cytolysis of certain target cells.
- The *Slamf7* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Slamf7 SLAM family member 7 [Mus musculus (house mouse)]

Gene ID: 75345, updated on 31-Jan-2019

Summary



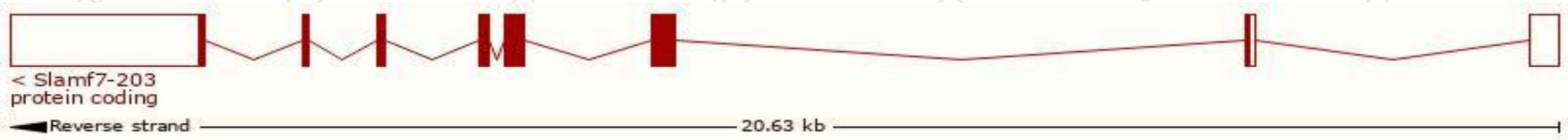
Official Symbol	Slamf7 provided by MGI
Official Full Name	SLAM family member 7 provided by MGI
Primary source	MGI:MGI:1922595
See related	Ensembl:ENSMUSG00000038179
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	19A, 19A24, 4930560D03Rik, CRACC, CS1
Expression	Biased expression in testis adult (RPKM 3.6), spleen adult (RPKM 2.3) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

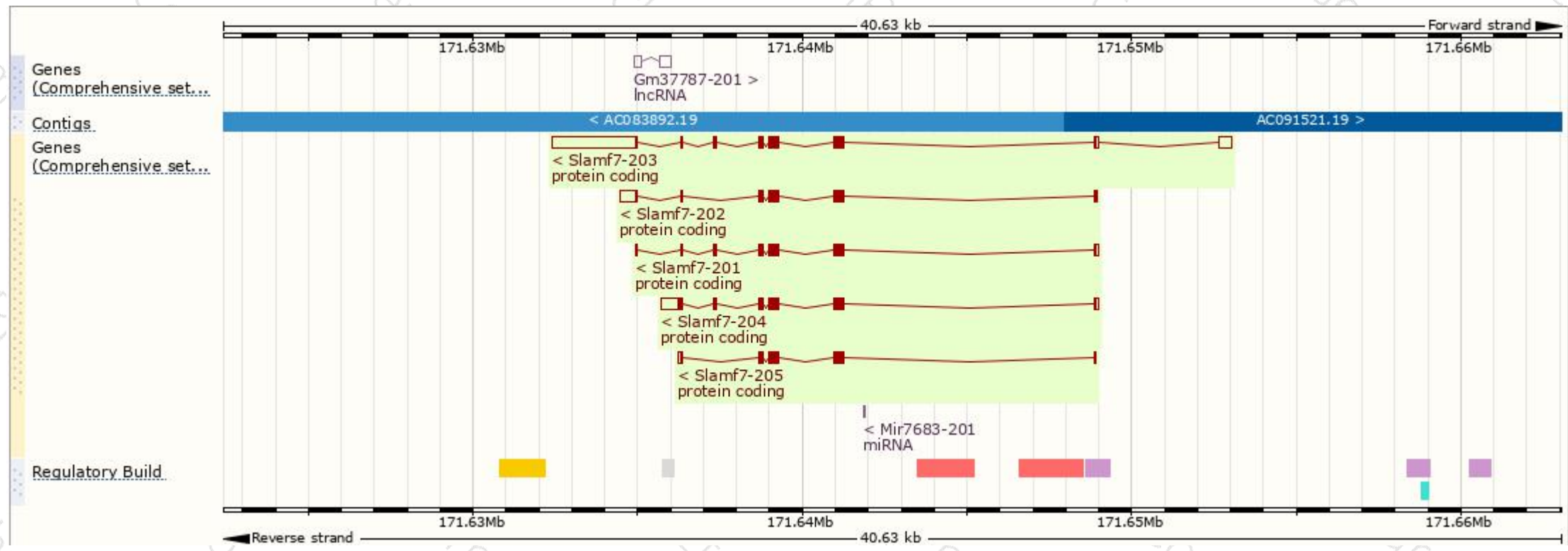
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slamf7-203	ENSMUST00000192195.5	3975	333aa	Protein coding	CCDS15500	A0A0R4J2D8	TSL:1 GENCODE basic APPRIS P3
Slamf7-202	ENSMUST00000192024.5	1361	294aa	Protein coding	CCDS83636	A0A0A6YW73	TSL:1 GENCODE basic APPRIS ALT2
Slamf7-201	ENSMUST00000111276.8	1082	333aa	Protein coding	CCDS15500	A0A0R4J2D8	TSL:1 GENCODE basic APPRIS P3
Slamf7-204	ENSMUST00000194531.5	1604	335aa	Protein coding	-	A0A0R4J2D6	TSL:1 GENCODE basic APPRIS ALT2
Slamf7-205	ENSMUST00000194791.1	909	281aa	Protein coding	-	A0A0A6YWL9	TSL:1 GENCODE basic APPRIS ALT2

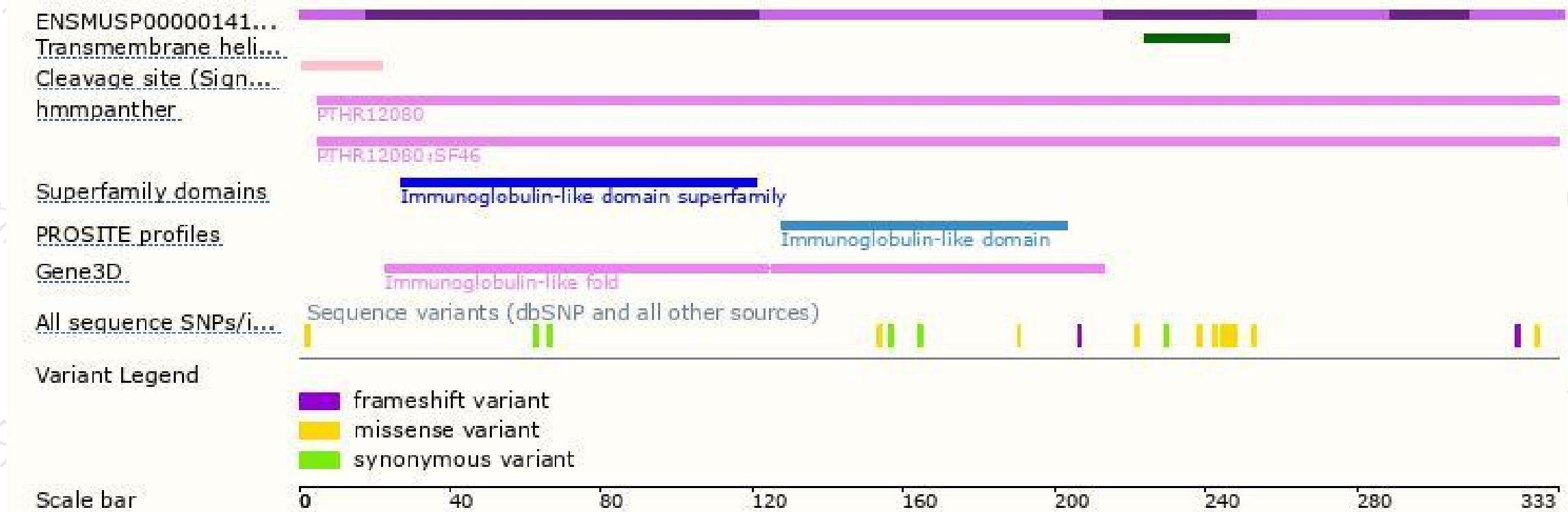
The strategy is based on the design of *Slamf7-203* transcript,The transcription is shown below



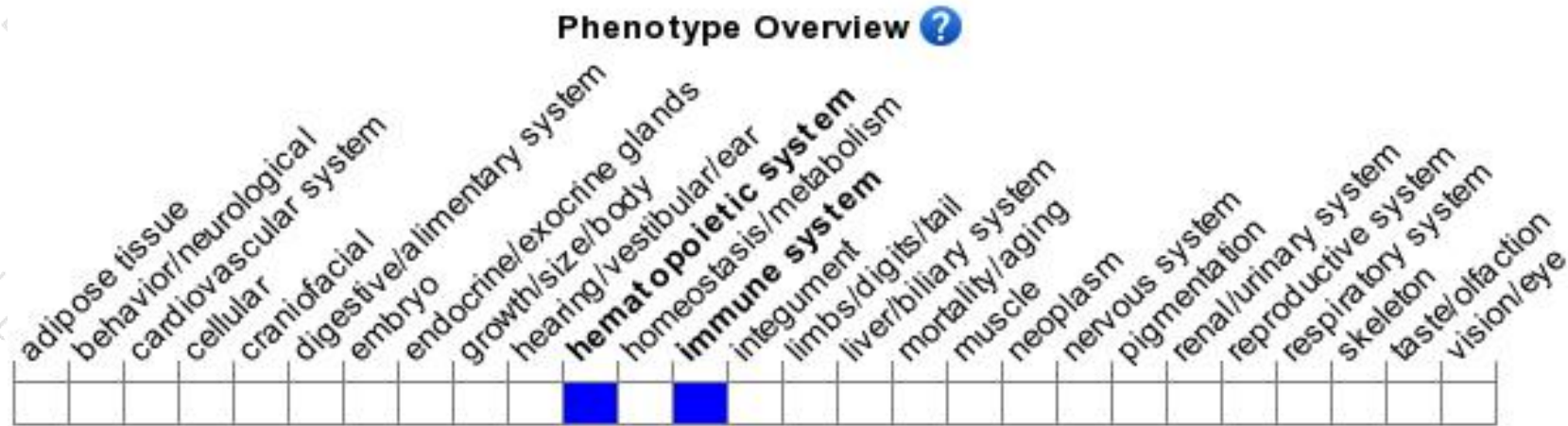
Genomic location distribution



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, Natural Killer cells from null homozygotes display impaired cytolysis of certain target cells.

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

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