

Skap1 Cas9-KO Strategy

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Project Overview

Project Name

Skap1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Skap1* gene. The schematic diagram is as follows:



- The *Skap1* gene has 10 transcripts. According to the structure of *Skap1* gene, exon2 of *Skap1-203* (ENSMUST00000100521.9) transcript is recommended as the knockout region. The region contains 106bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Skap1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene trapped allele exhibit decreased T cell aggregation, adhesion and proliferation following stimulation.
- The *Skap1* gene is located on the Chr11. 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)

Skap1 src family associated phosphoprotein 1 [Mus musculus (house mouse)]

Gene ID: 78473, updated on 31-Jan-2019

Summary



Official Symbol	Skap1 provided by MGI
Official Full Name	src family associated phosphoprotein 1 provided by MGI
Primary source	MGI:MGI:1925723
See related	Ensembl:ENSMUSG00000057058
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	1700091G21Rik, Scap1, Skap-55
Expression	Biased expression in thymus adult (RPKM 30.5), spleen adult (RPKM 5.2) and 2 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

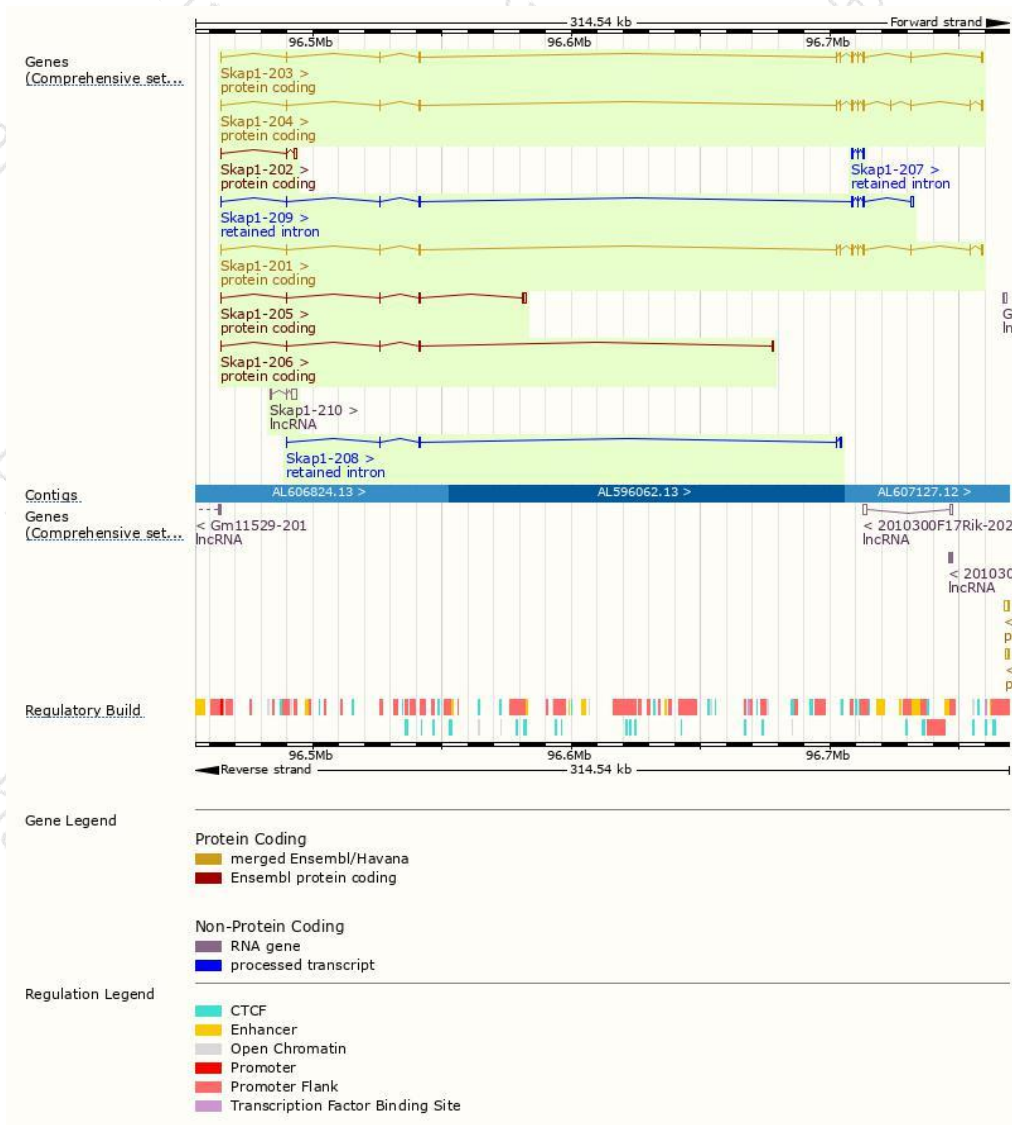
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Skap1-203	ENSMUST00000100521.9	1539	345aa	Protein coding	CCDS48892	Q3UUV5	TSL:1 GENCODE basic
Skap1-204	ENSMUST00000103154.10	1507	355aa	Protein coding	CCDS25301	Q3UUV5	TSL:1 GENCODE basic APPRIS P3
Skap1-201	ENSMUST00000071510.13	1425	339aa	Protein coding	CCDS48891	Q3UUV5	TSL:1 GENCODE basic APPRIS ALT2
Skap1-205	ENSMUST00000107662.8	1861	165aa	Protein coding	-	B1AQX1	TSL:1 GENCODE basic
Skap1-202	ENSMUST00000100519.10	1100	78aa	Protein coding	-	Q3U5H2	TSL:1 GENCODE basic
Skap1-206	ENSMUST00000107663.3	742	126aa	Protein coding	-	B1AQX5	TSL:3 GENCODE basic
Skap1-209	ENSMUST00000136836.7	2051	No protein	Retained intron	-	-	TSL:1
Skap1-207	ENSMUST00000123814.1	706	No protein	Retained intron	-	-	TSL:2
Skap1-208	ENSMUST00000127639.1	643	No protein	Retained intron	-	-	TSL:3
Skap1-210	ENSMUST00000149988.1	2095	No protein	lncRNA	-	-	TSL:1

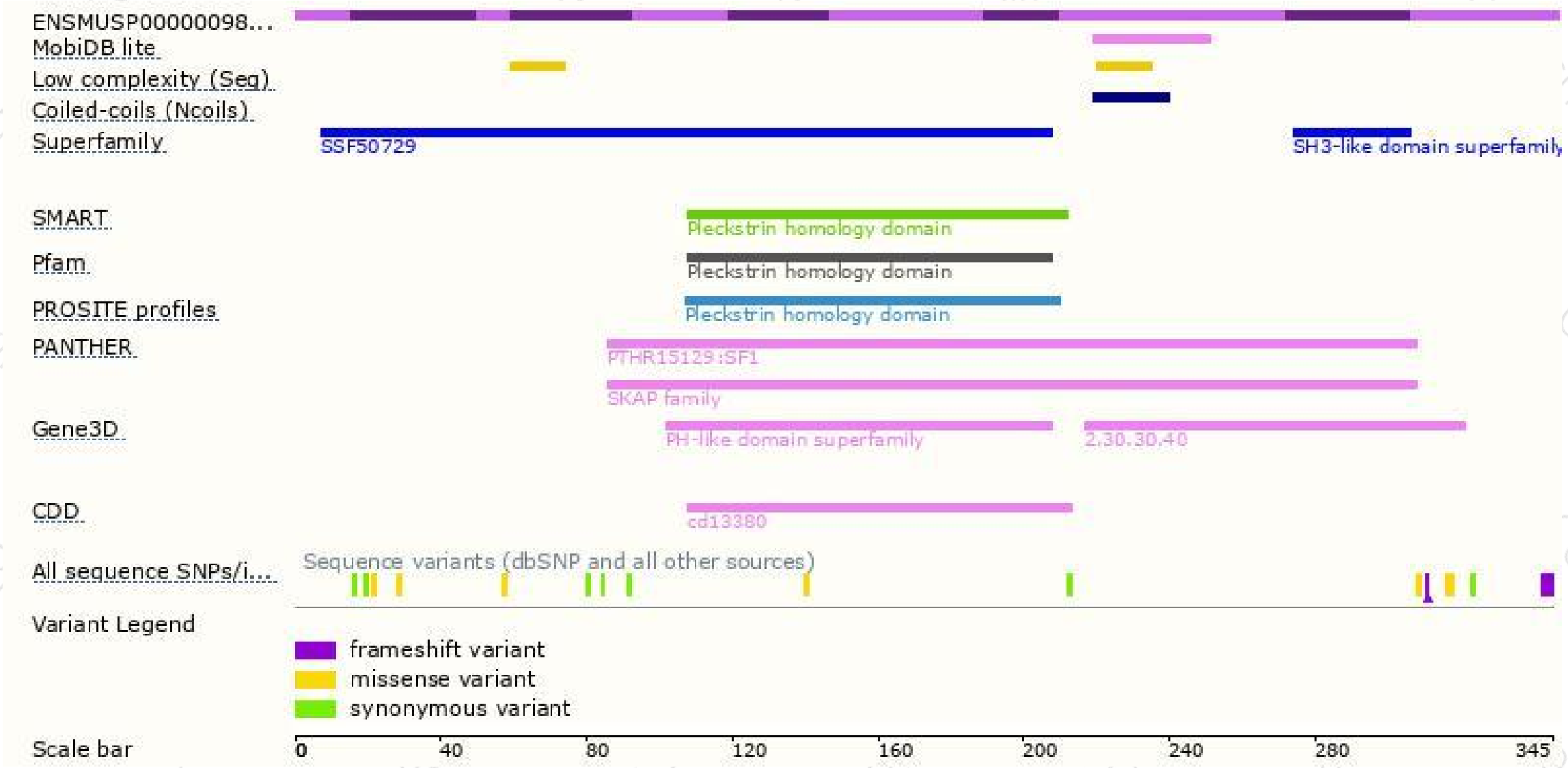
The strategy is based on the design of *Skap1-203* transcript,The transcription is shown below



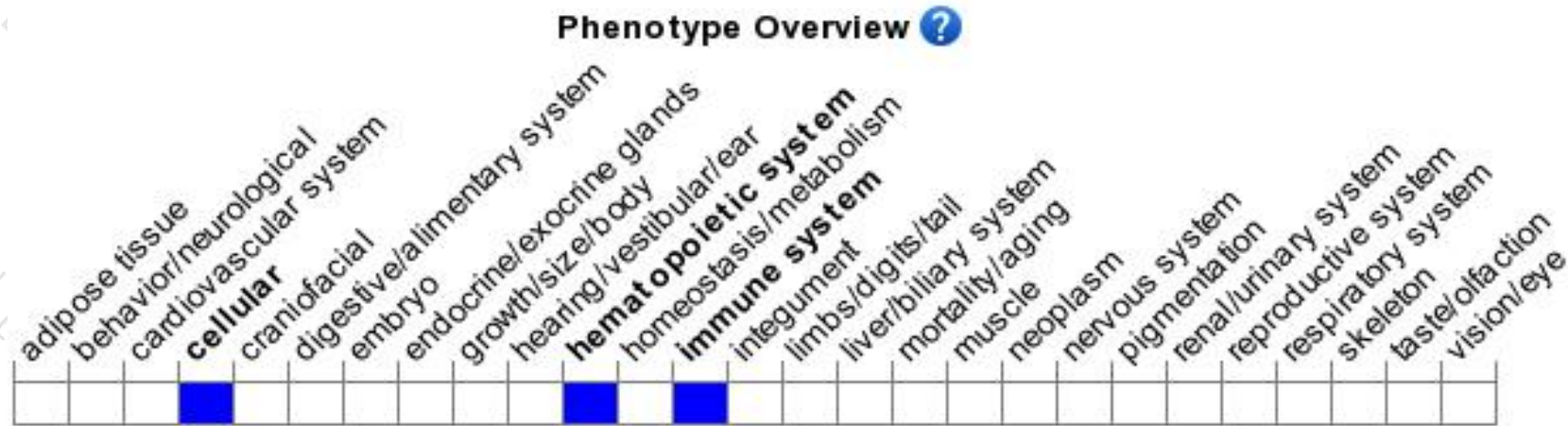
Genomic location distribution



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, Mice homozygous for a gene trapped allele exhibit decreased T cell aggregation, adhesion and proliferation following stimulation.

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

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