

Sigirr Cas9-KO Strategy

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Project Overview

Project Name

Sigirr

Project type

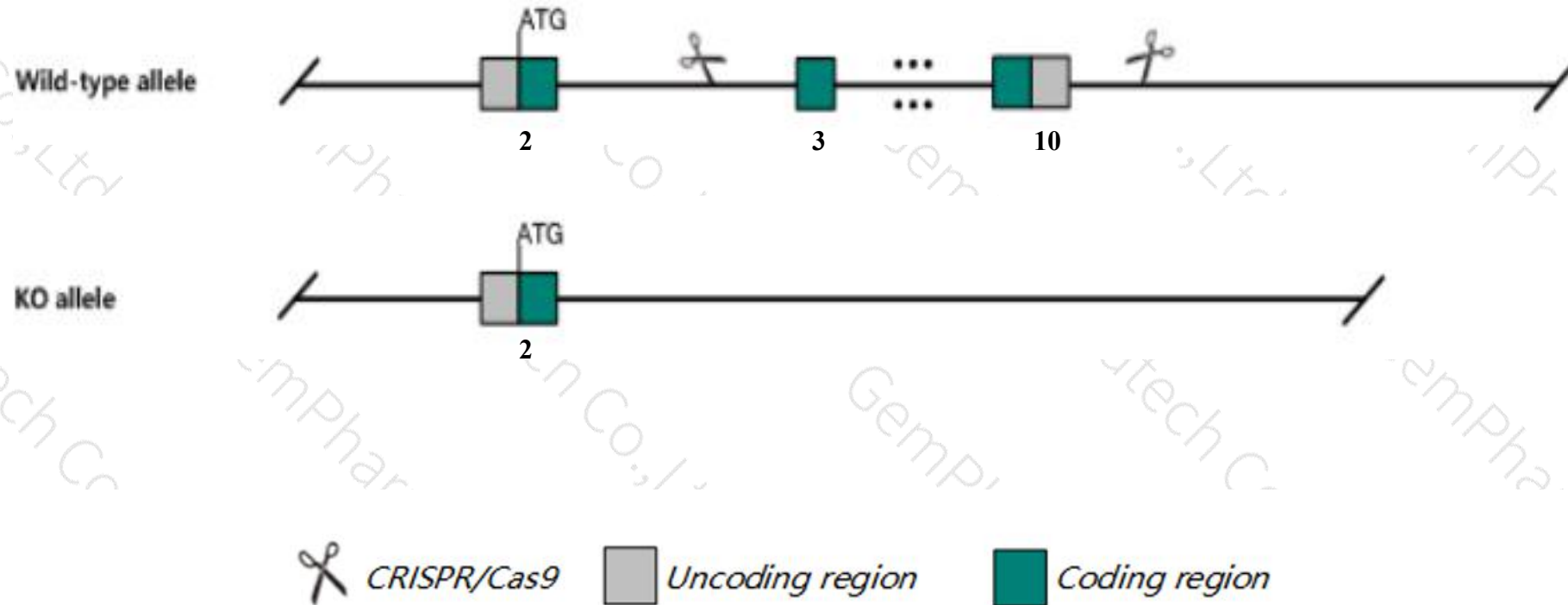
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Sigirr* gene has 8 transcripts. According to the structure of *Sigirr* gene, exon3-exon10 of *Sigirr-201* (ENSMUST00000097958.2) transcript is recommended as the knockout region. The region contains most coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sigirr* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, when challenged, homozygous mutant mice show an increased inflammatory response.
- The *Sigirr* gene is located on the Chr7. 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)

Sigirr single immunoglobulin and toll-interleukin 1 receptor (TIR) domain [Mus musculus (house mouse)]

Gene ID: 24058, updated on 13-Mar-2020

Summary



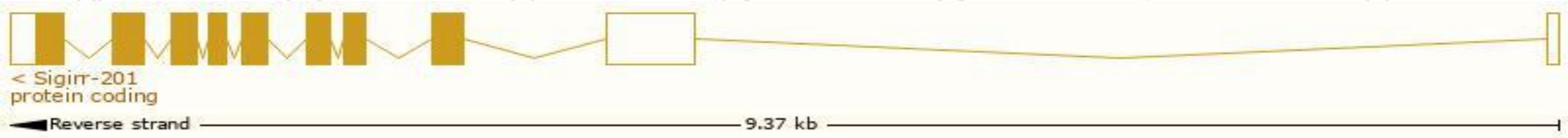
Official Symbol	Sigirr provided by MGI
Official Full Name	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain provided by MGI
Primary source	MGI:MGI:1344402
See related	Ensembl:ENSMUSG000000025494
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI256711, TIR8
Expression	Broad expression in kidney adult (RPKM 26.8), placenta adult (RPKM 18.4) and 20 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

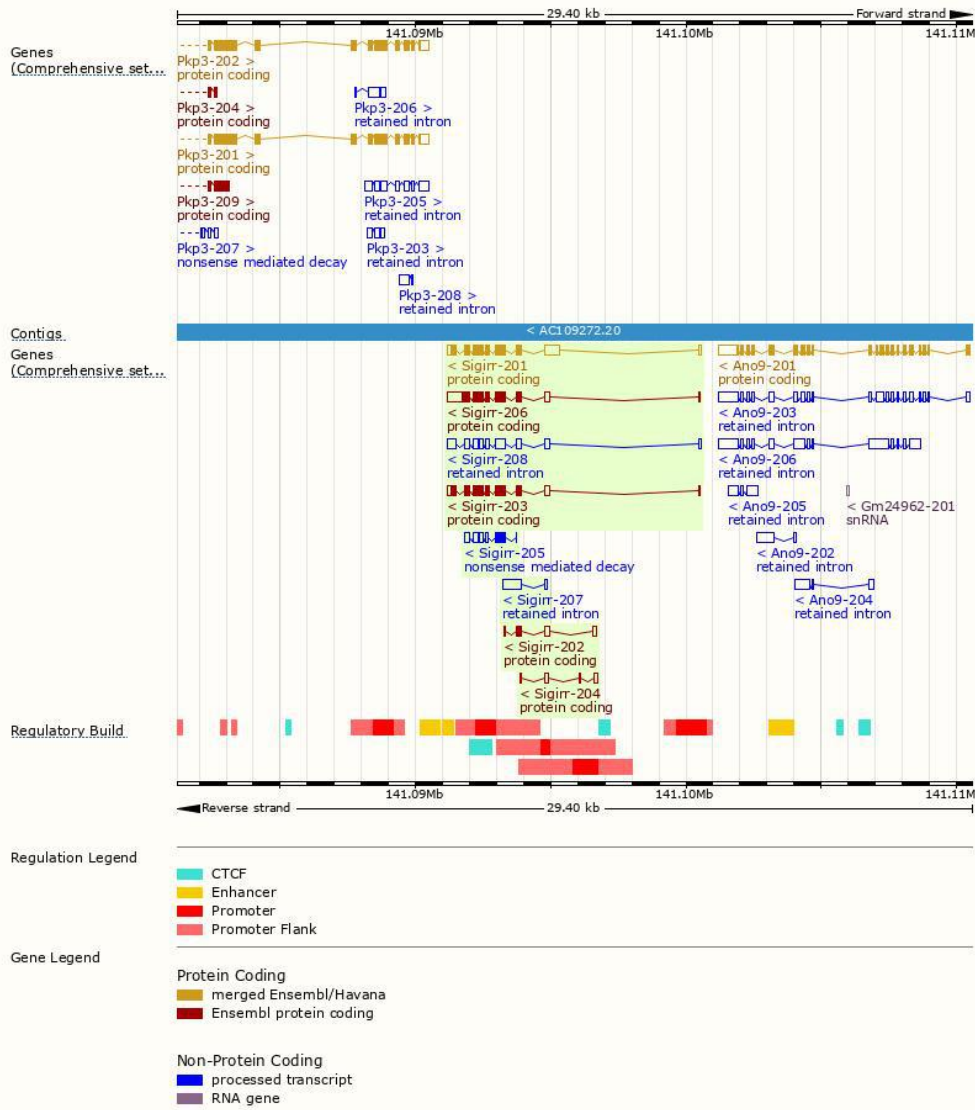
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sigirr-201	ENSMUST00000097958.2	1990	409aa	Protein coding	CCDS40179	Q3UKS3 Q9JLZ8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Sigirr-203	ENSMUST00000209294.1	1612	409aa	Protein coding	CCDS40179	Q3UKS3 Q9JLZ8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Sigirr-206	ENSMUST00000210167.1	1897	387aa	Protein coding	-	Q9JLZ8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Sigirr-202	ENSMUST00000209199.1	543	85aa	Protein coding	-	A0A1B0GRA6	CDS 3' incomplete TSL:3
Sigirr-204	ENSMUST00000209352.1	363	20aa	Protein coding	-	A0A1B0GS99	CDS 3' incomplete TSL:5
Sigirr-205	ENSMUST00000209887.1	850	108aa	Nonsense mediated decay	-	A0A1B0GRZ7	CDS 5' incomplete TSL:5
Sigirr-208	ENSMUST00000210978.1	1723	No protein	Retained intron	-	-	TSL:5
Sigirr-207	ENSMUST00000210941.1	816	No protein	Retained intron	-	-	TSL:3

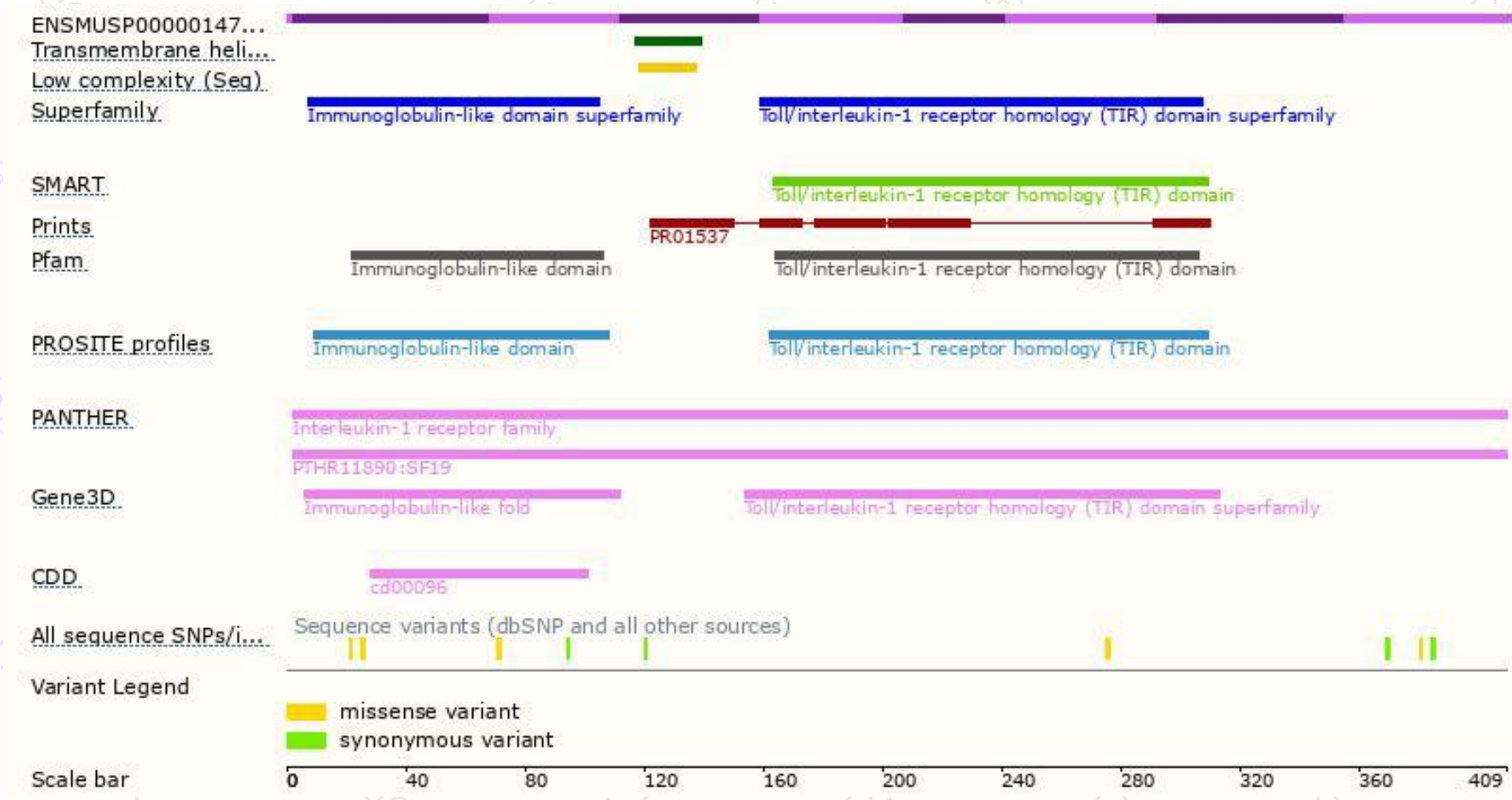
The strategy is based on the design of *Sigirr-201* transcript,the transcription is shown below:



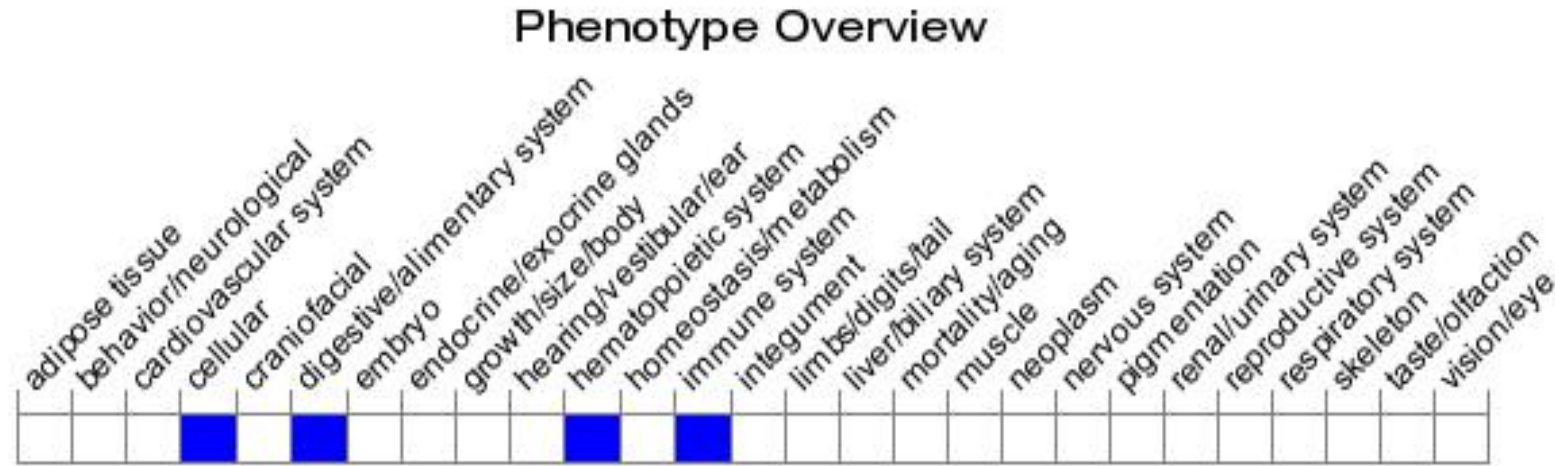
Genomic location distribution



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, when challenged, homozygous mutant mice show an increased inflammatory response.

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

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