

Vtcn1 Cas9-KO Strategy

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Project Overview



Project Name

Vtcn1

Project type

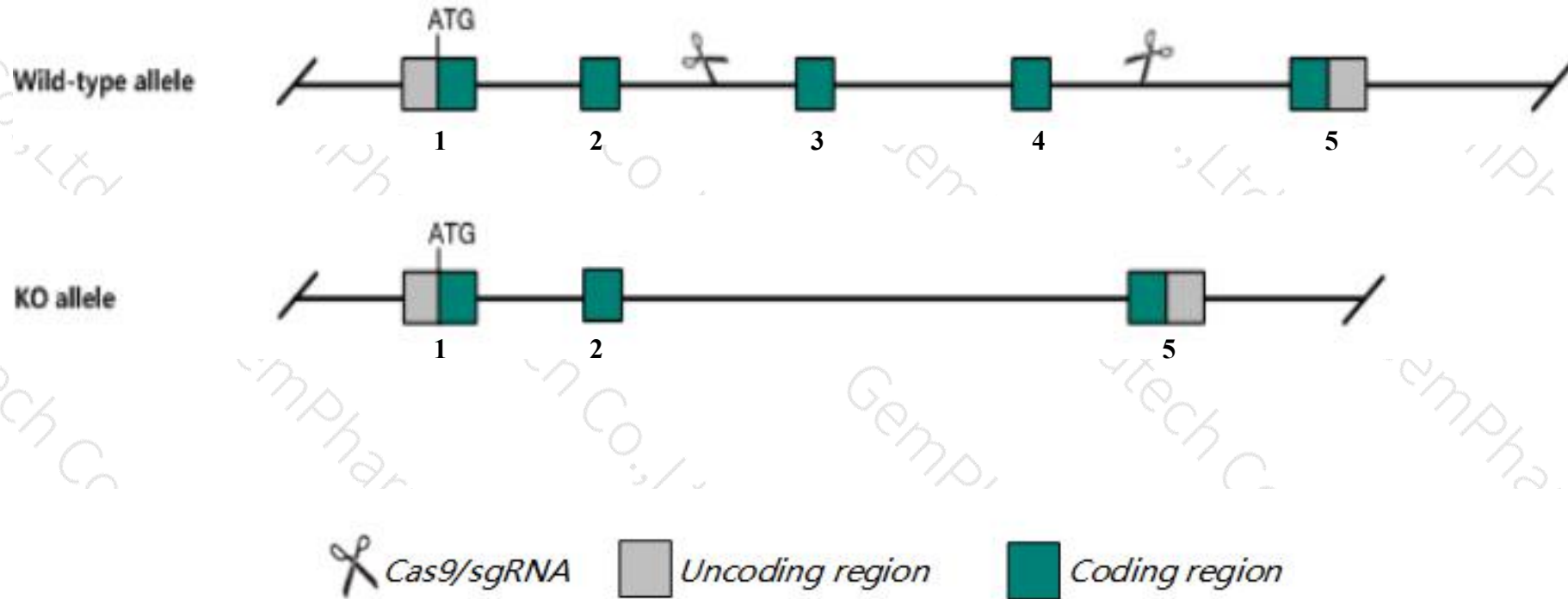
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Vtcn1* gene. The schematic diagram is as follows:



- The *Vtcn1* gene has 1 transcript. According to the structure of *Vtcn1* gene, exon3-exon4 of *Vtcn1-201*(ENSMUST00000054791.8) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vtcn1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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, mice homozygous for this mutation display stronger Th1 responses upon parasitic infection by *L. major* including reduced footpad swelling and lower parasite burden compared to controls. Responses to other Th1-driven immune responses are normal.
- The *Vtcn1* gene is located on the Chr3. 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)

Vtcn1 V-set domain containing T cell activation inhibitor 1 [Mus musculus (house mouse)]

Gene ID: 242122, updated on 13-Mar-2020

Summary



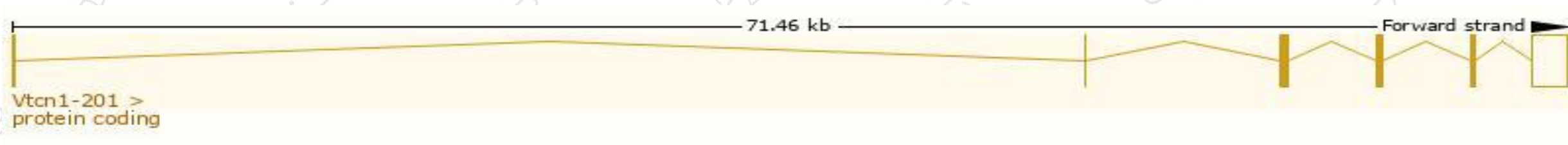
Official Symbol	Vtcn1 provided by MGI
Official Full Name	V-set domain containing T cell activation inhibitor 1 provided by MGI
Primary source	MGI:MGI:3039619
See related	Ensembl:ENSMUSG00000051076
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B7h4, B7s1, B7x, BC032925
Expression	Biased expression in subcutaneous fat pad adult (RPKM 4.1), mammary gland adult (RPKM 2.4) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

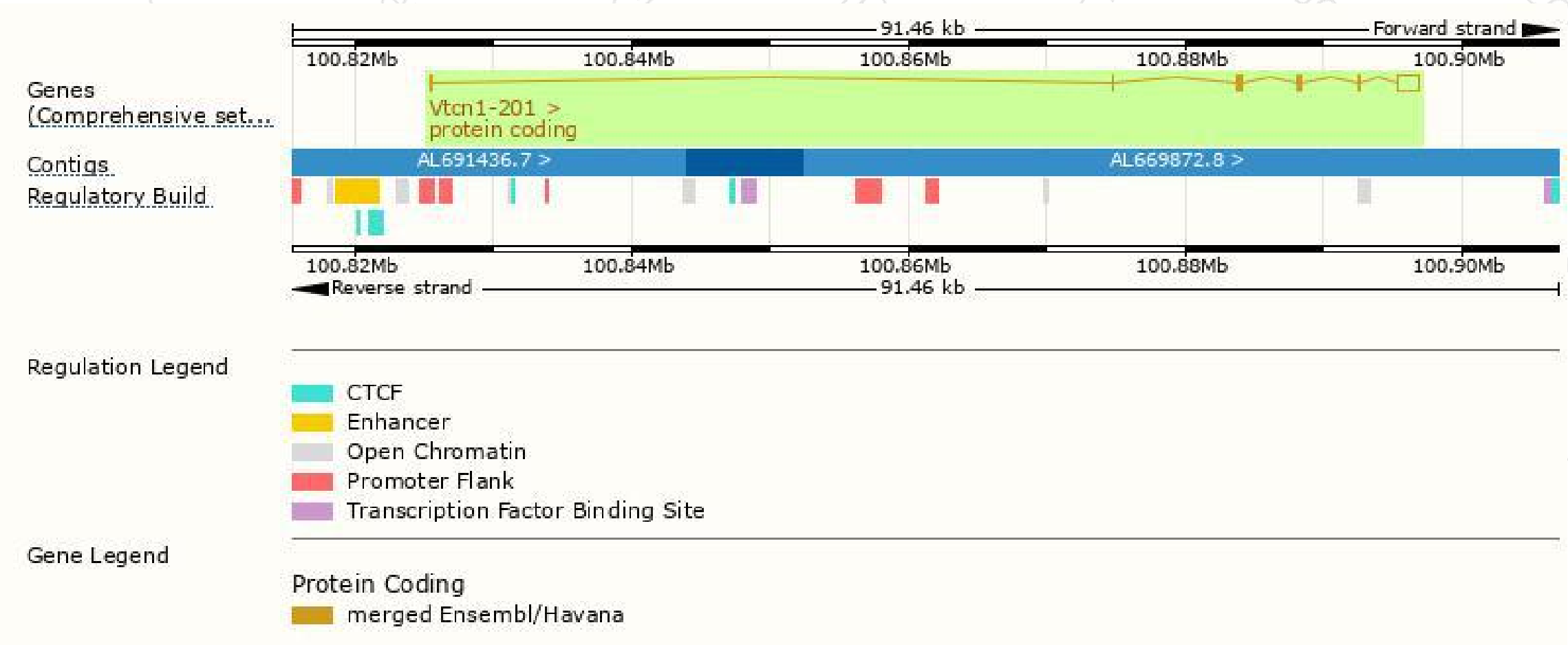
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vtcn1-201	ENSMUST00000054791.8	2622	283aa	Protein coding	CCDS17677	Q7TSP5	TSL:1 GENCODE basic APPRIS P1

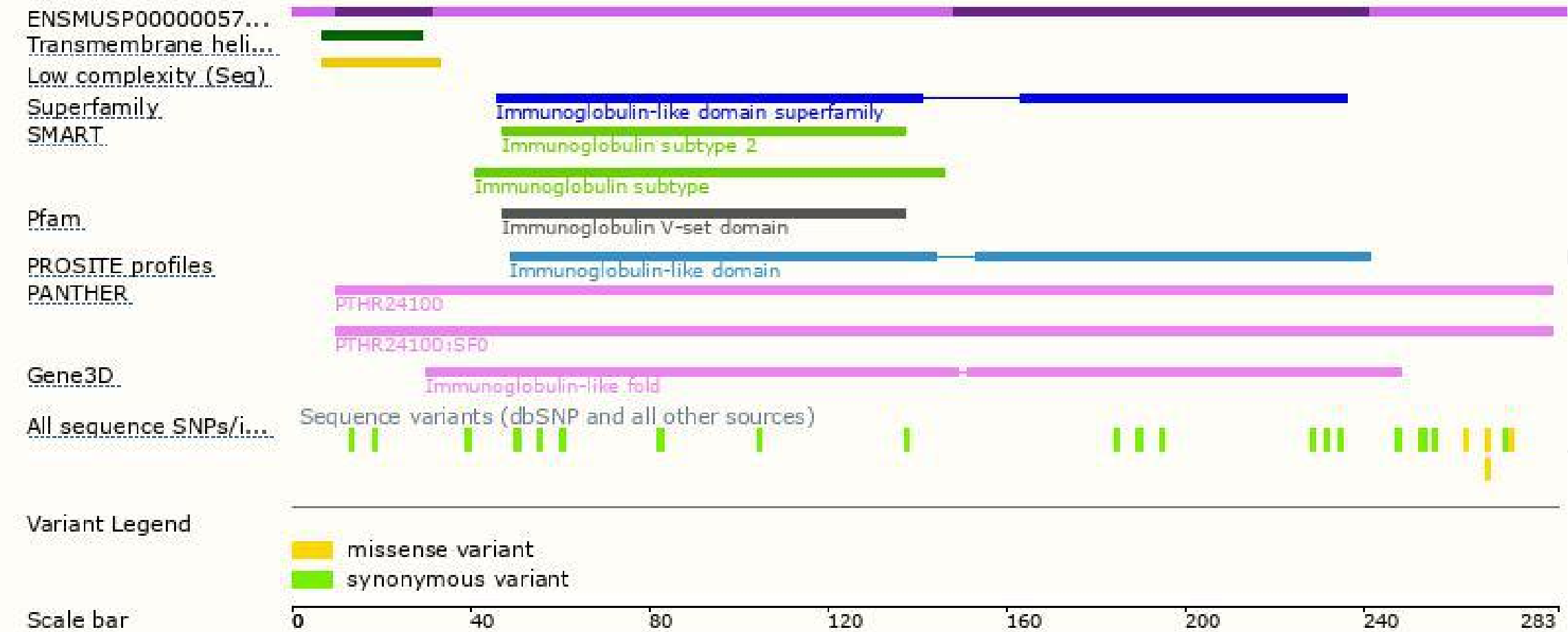
The strategy is based on the design of *Vtcn1-201* transcript, the transcription is shown below:



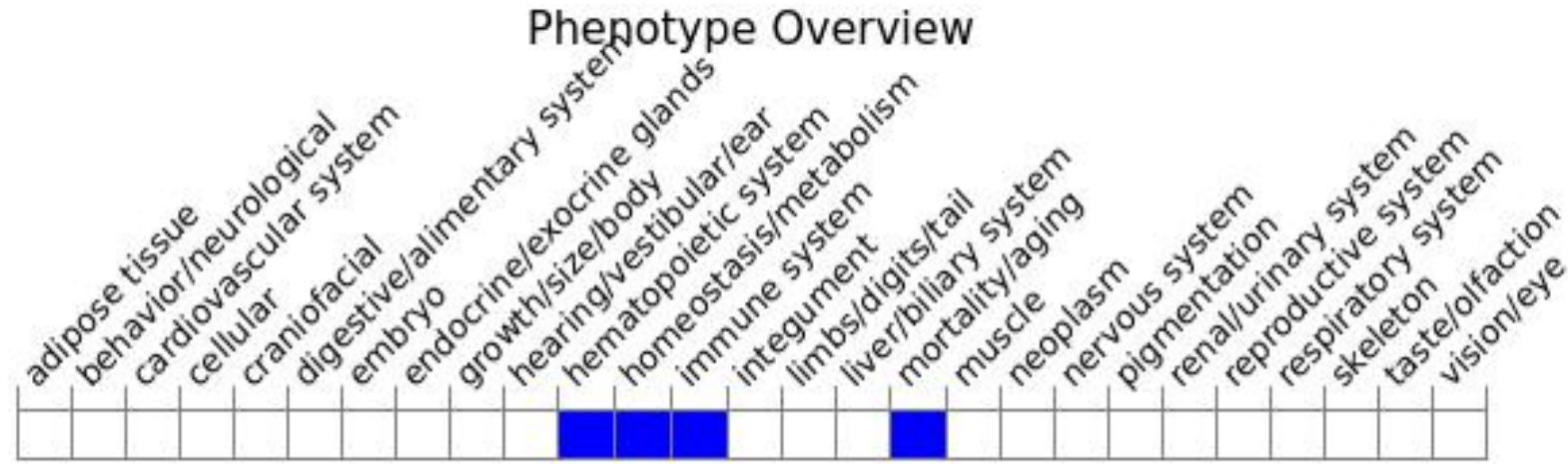
Genomic location distribution



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, mice homozygous for this mutation display stronger Th1 responses upon parasitic infection by *L. major* including reduced footpad swelling and lower parasite burden compared to controls.

Responses to other Th1-driven immune responses are normal.

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

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