Ticam2 Cas9-KO Strategy

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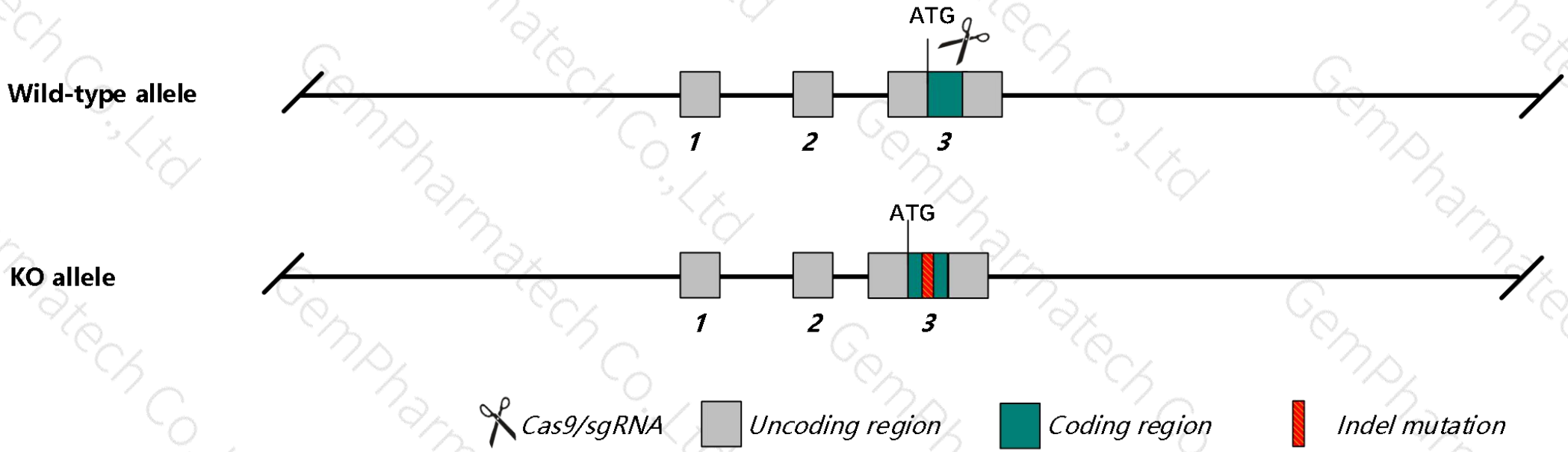
Project Overview

Project Name	***Ticam2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ticam2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ticam2* gene has 2 transcripts. According to the structure of *Ticam2* gene, partial exon3 of *Ticam2-201* (ENSMUST00000070084.10) transcript is recommended as the knockout region.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ticam2* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

➢ According to the existing MGI data,homozygous inactivation of this gene affects tlr4-mediated immune responses.

➢The KO region contains 3'UTR region of the *Tmed7* gene.Knockout the region may affect the function of *Tmed7* gene.

➢ The *Ticam2* gene is located on the Chr18. 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）

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Ticam2 toll-like receptor adaptor molecule 2 [Mus musculus (house mouse)]

Gene ID: 225471, updated on 13-Mar-2020

Summary

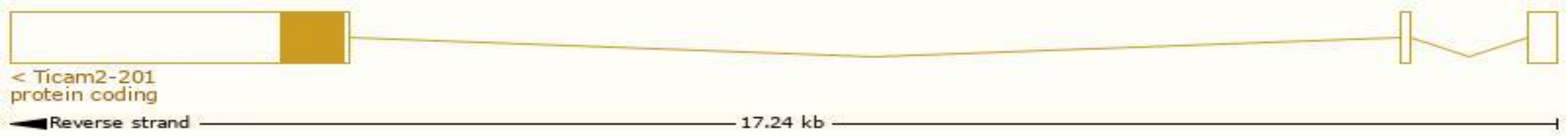
Official Symbol	Ticam2 provided by MGI
Official Full Name	toll-like receptor adaptor molecule 2 provided by MGI
Primary source	MGI:MGI:3040056
See related	Ensembl:ENSMUSG00000056130
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B430113A10, TICAM-2, TRAM, Tirp, Trif
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information（Ensembl）

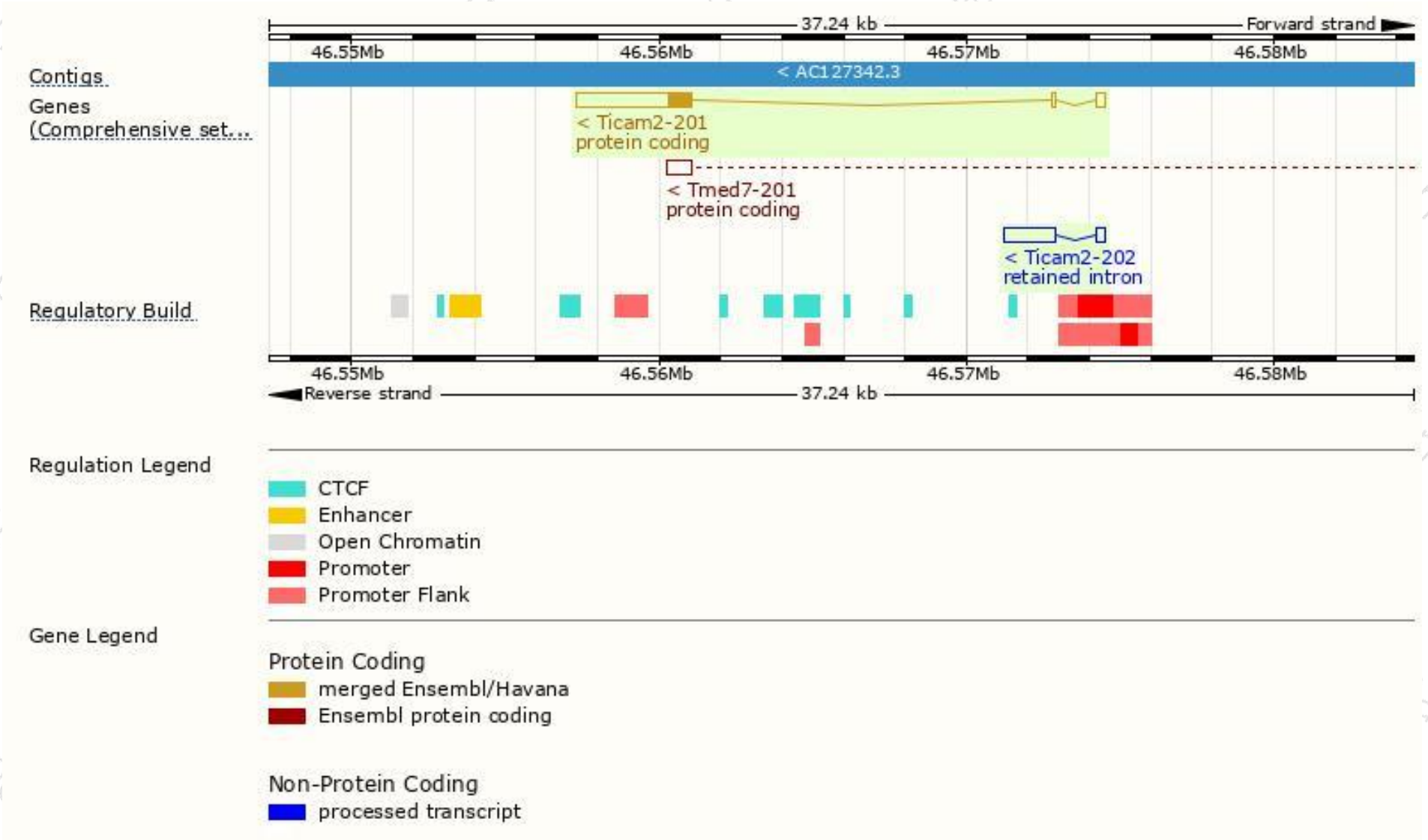
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ticam2-201	ENSMUST00000070084.10	4204	232aa	Protein coding	CCDS29232	Q8BJQ4	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 P1
Ticam2-202	ENSMUST00000149929.1	2010	No protein	Retained intron	-	-	TSL:1

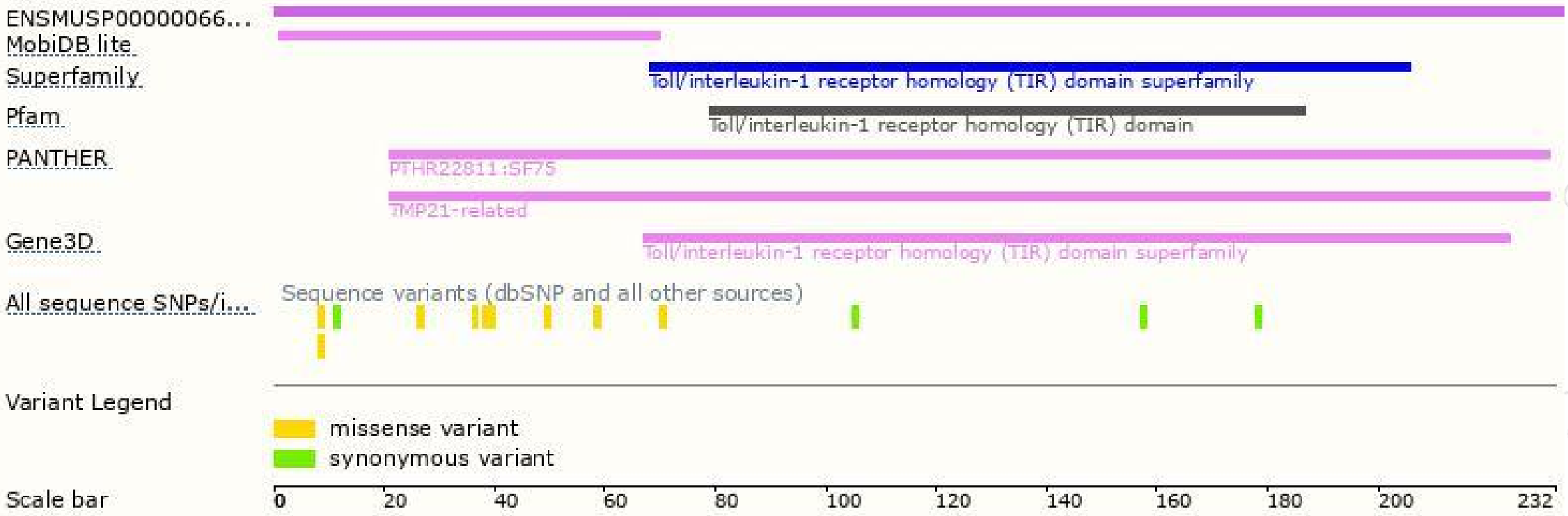
The strategy is based on the design of *Ticam2-201* transcript,the transcription is shown below:



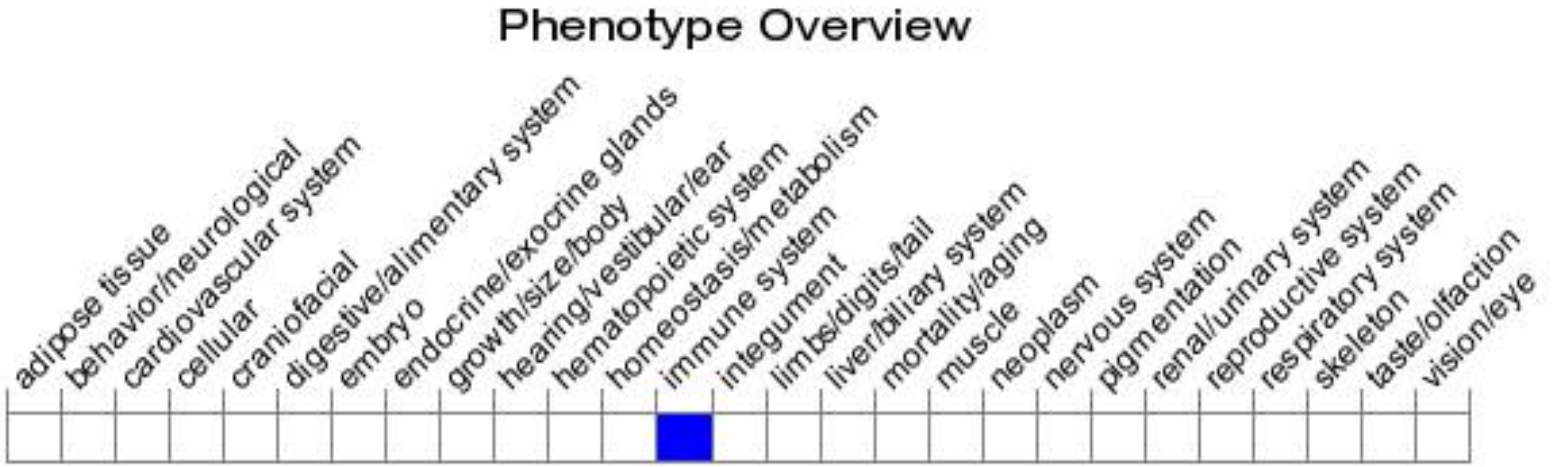
Genomic location distribution



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,homozygous inactivation of this gene affects TLR4-mediated immune responses.

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

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