

Trim21 Cas9-KO Strategy

Designer:

Project Overview



Project Name

Trim21

Project type

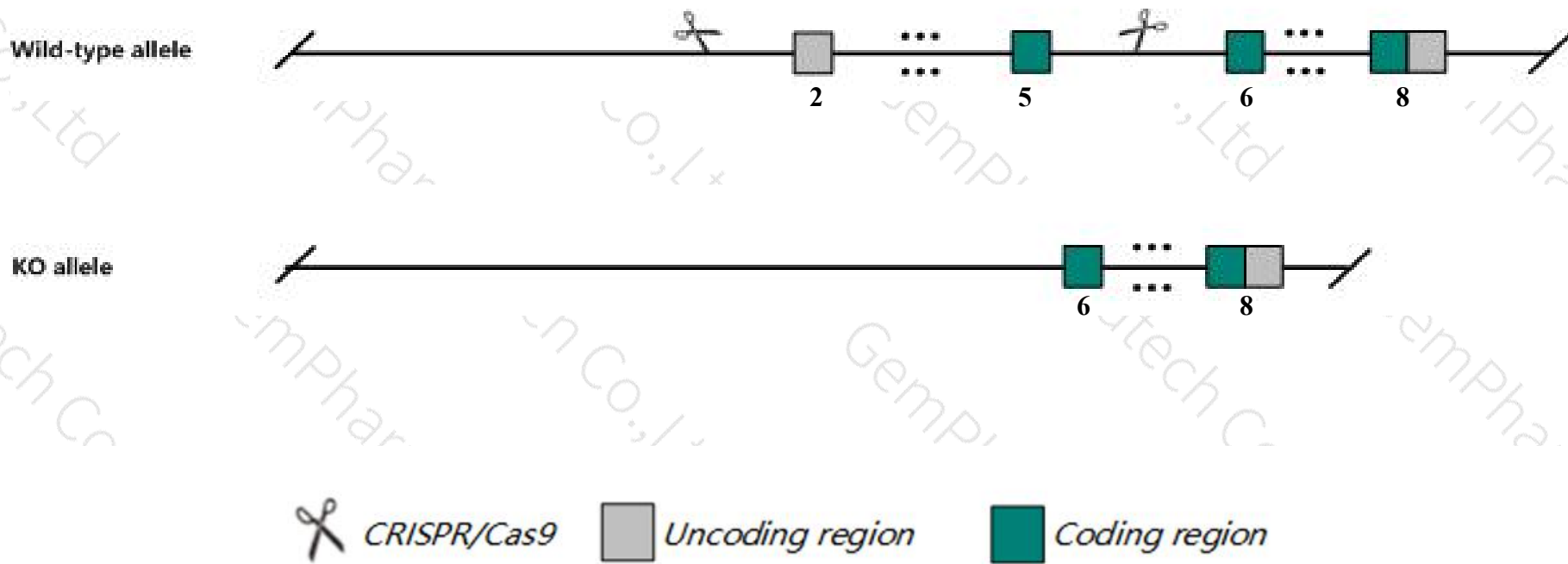
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trim21* gene. The schematic diagram is as follows:



➤ The *Trim21* gene has 5 transcripts. According to the structure of *Trim21* gene, exon2-exon5 of *Trim21-201* (ENSMUST00000033264.11) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Trim21* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Unmanipulated homozygous mice are normal, but leads to tissue inflammation and systemic autoimmunity in vivo and reduced number of CD11c+ dendritic cells from mutant bone marrow in vitro.
- The *Trim21* 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)

Trim21 tripartite motif-containing 21 [Mus musculus (house mouse)]

Gene ID: 20821, updated on 7-Apr-2019

Summary



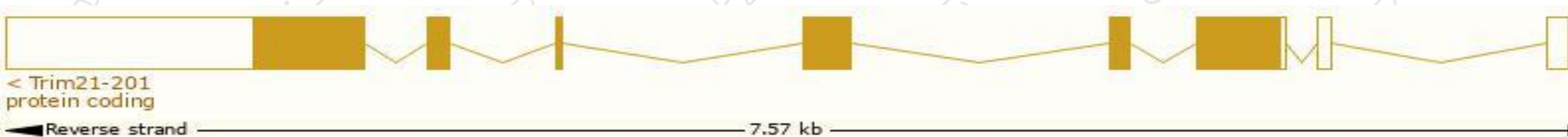
Official Symbol	Trim21 provided by MGI
Official Full Name	tripartite motif-containing 21 provided by MGI
Primary source	MGI:MGI:106657
See related	Ensembl:ENSMUSG00000030966
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ro52, Ssa1
Expression	Ubiquitous expression in thymus adult (RPKM 5.4), bladder adult (RPKM 4.4) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

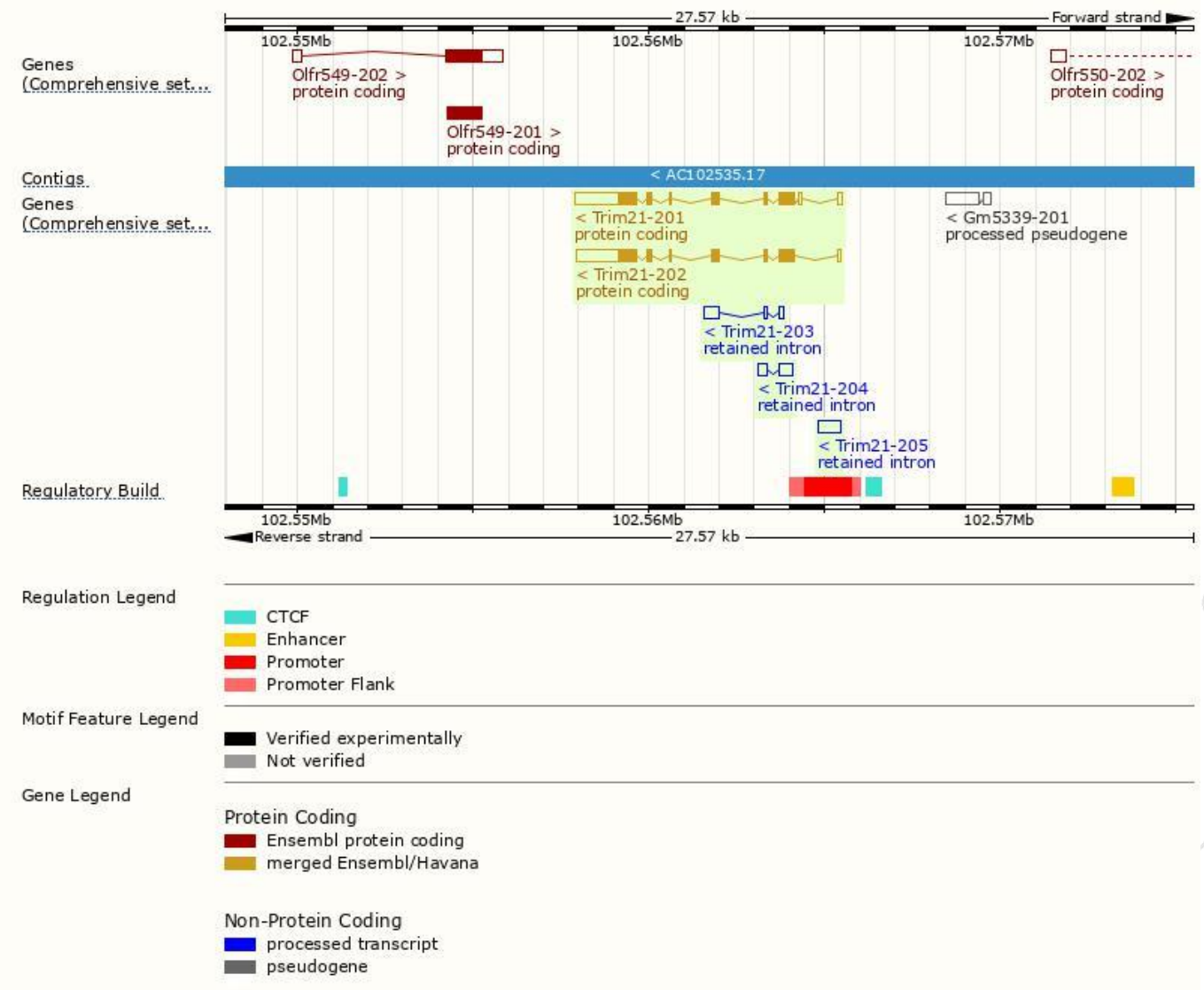
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trim21-201	ENSMUST00000033264.11	2793	462aa	Protein coding	CCDS40051	Q3U7K7	TSL:1 GENCODE basic APPRIS P1
Trim21-202	ENSMUST00000106913.2	2682	462aa	Protein coding	CCDS40051	Q3U7K7	TSL:1 GENCODE basic APPRIS P1
Trim21-203	ENSMUST00000209679.1	666	No protein	Retained intron	-	-	TSL:2
Trim21-204	ENSMUST00000209907.1	642	No protein	Retained intron	-	-	TSL:2
Trim21-205	ENSMUST00000210261.1	634	No protein	Retained intron	-	-	TSL:NA

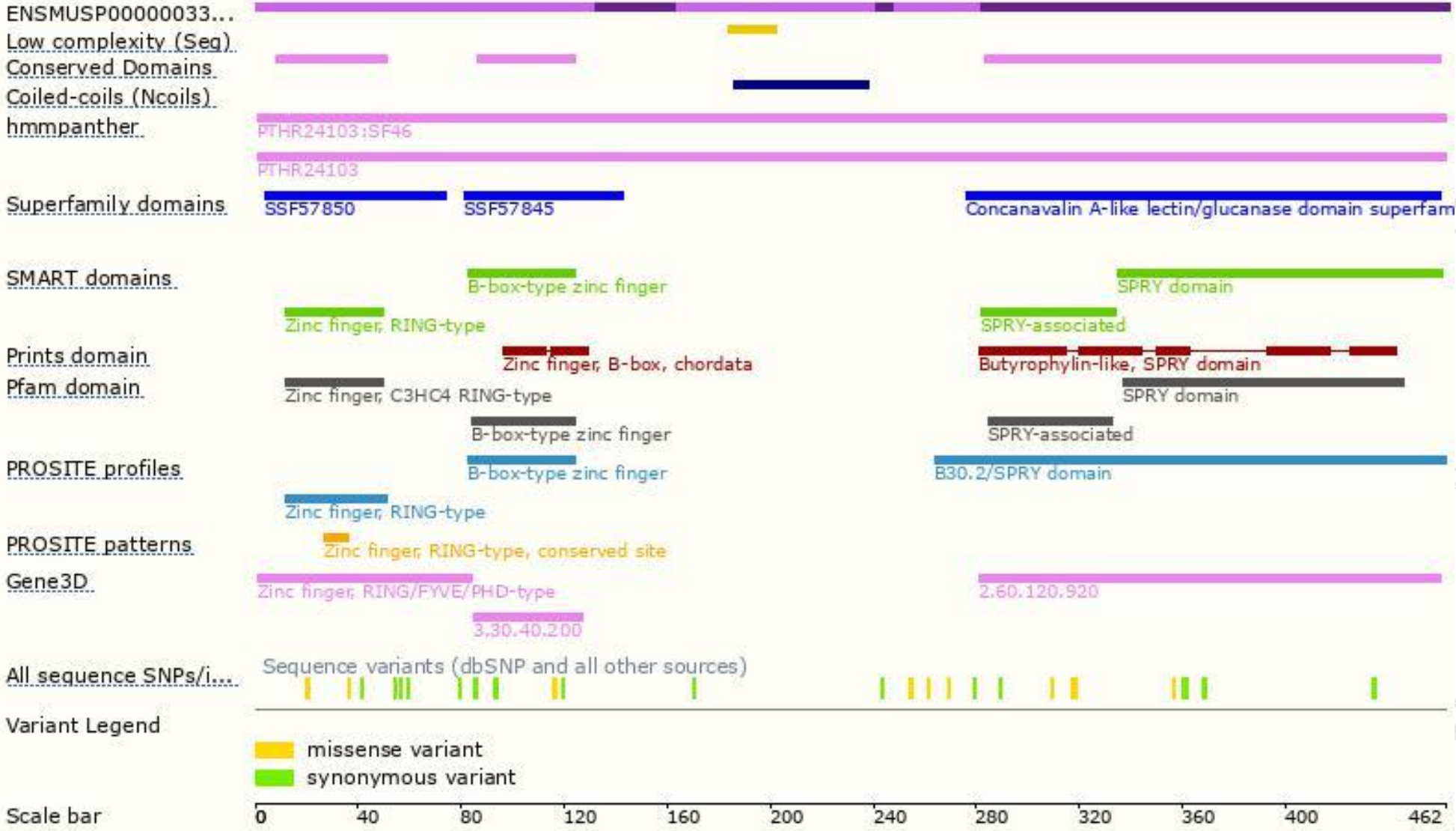
The strategy is based on the design of *Trim21-201* transcript, The transcription is shown below



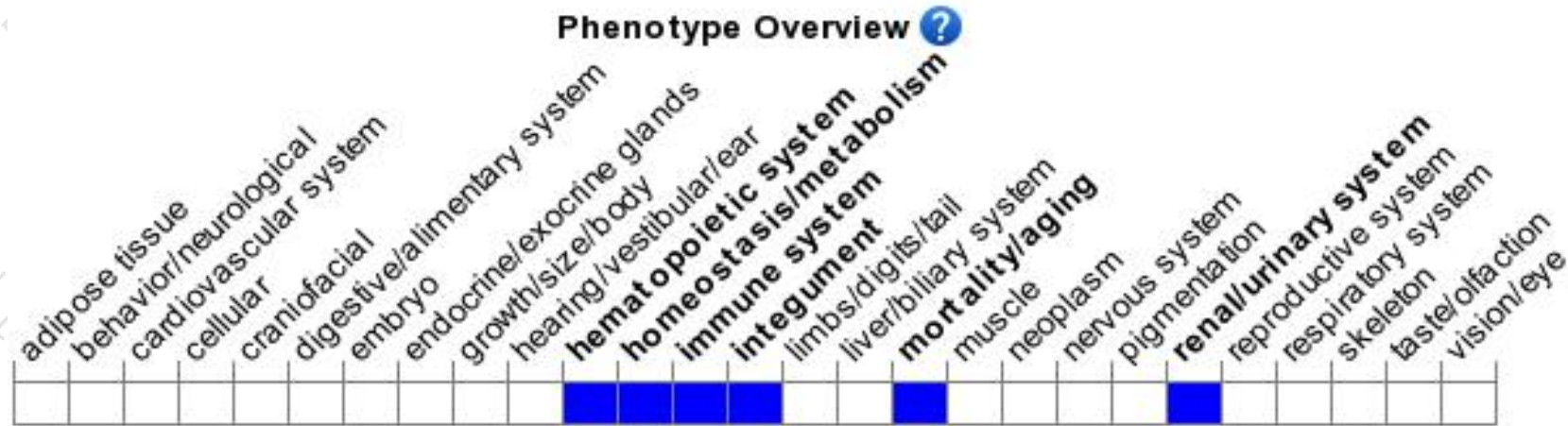
Genomic location distribution



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, Unmanipulated homozygous mice are normal, but leads to tissue inflammation and systemic autoimmunity in vivo and reduced number of CD11c⁺ dendritic cells from mutant bone marrow in vitro.

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

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