

***Tap1* Cas9-CKO Strategy**

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Project Overview

Project Name

Tap1

Project type

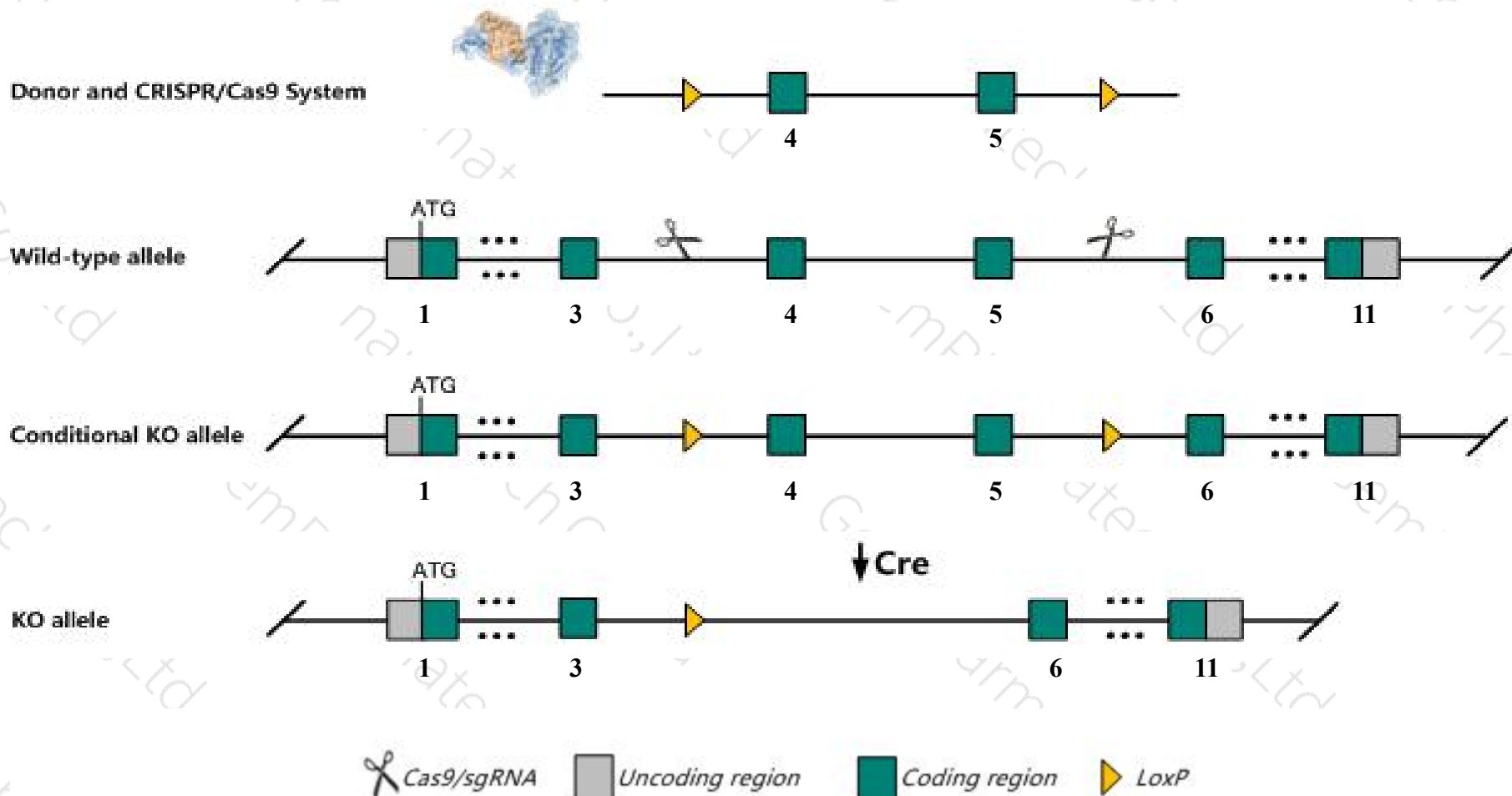
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tap1* gene. The schematic diagram is as follows:



Technical routes

- The *Tap1* gene has 7 transcripts. According to the structure of *Tap1* gene, exon4-exon5 of *Tap1*-206(ENSMUST00000170086.7) transcript is recommended as the knockout region. The region contains 404bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tap1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor 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.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, mice homozygous for targeted mutations that inactivate the gene are deficient in antigen presentation, surface class I antigens, and CD4-8⁺ T cells.
- The flox region is near the gene *Psmb9*, this strategy may destroy the function of gene *Psmb9*.
- This strategy directly destroy the transcript 202, 204 and 205.
- The *Tap1* gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Tap1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Mus musculus (house mouse)]

Gene ID: 21354, updated on 13-Mar-2020

Summary

Official Symbol Tap1 provided by MGI

Official Full Name transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) provided by MGI

Primary source [MGI:MGI:98483](#)

See related [Ensembl:ENSMUSG00000037321](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as ABC17, APT1, Abcb, Abcb2, Ham, Ham-, Ham-1, Ham1, MTP, MTP1, PSF, PSF1, RI, RING4, T, TAP, Tap-1, Y3

Summary The membrane-associated protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This protein is a member of the MDR/TAP subfamily. Members of the MDR/TAP subfamily are involved in multidrug resistance. This protein forms a heterodimer with Tap2 that transports short peptides from the cytosol into the endoplasmic reticulum lumen. Mutations in the human gene may be associated with ankylosing spondylitis, insulin-dependent diabetes mellitus, and celiac disease. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jun 2009]

Expression Broad expression in spleen adult (RPKM 66.8), thymus adult (RPKM 59.4) and 17 other tissues [See more](#)

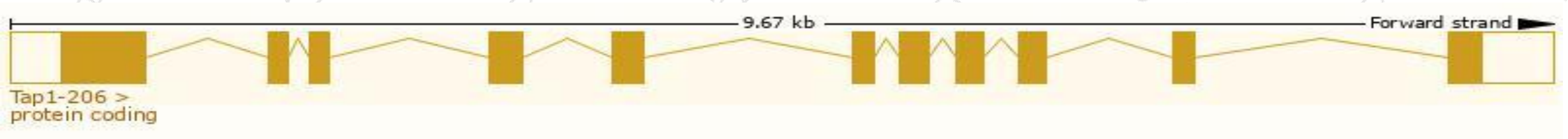
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

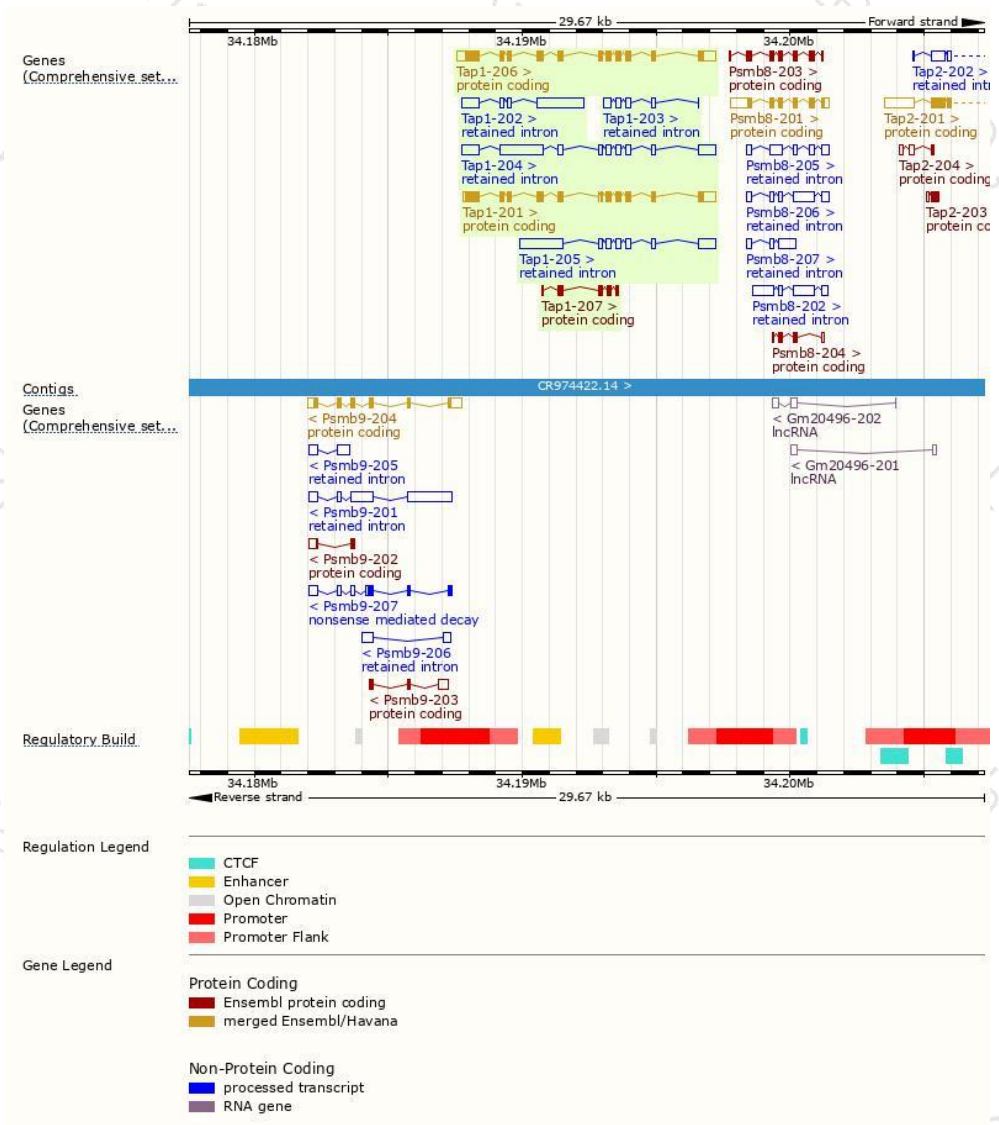
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tap1-206	ENSMUST00000170086.7	2953	724aa	Protein coding	CCDS28643	P21958	TSL:1 GENCODE basic APPRIS P3
Tap1-201	ENSMUST00000041633.14	2614	696aa	Protein coding	CCDS50072	Q3TBA3	TSL:1 GENCODE basic APPRIS ALT 2
Tap1-207	ENSMUST00000171148.1	587	196aa	Protein coding	-	F6QHF1	CDS 5' and 3' incomplete TSL:5
Tap1-204	ENSMUST00000166853.7	3911	No protein	Retained intron	-	-	TSL:1
Tap1-205	ENSMUST00000168351.7	3081	No protein	Retained intron	-	-	TSL:1
Tap1-202	ENSMUST00000166287.1	2638	No protein	Retained intron	-	-	TSL:1
Tap1-203	ENSMUST00000166582.1	757	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Tap1-206* transcript,the transcription is shown below:



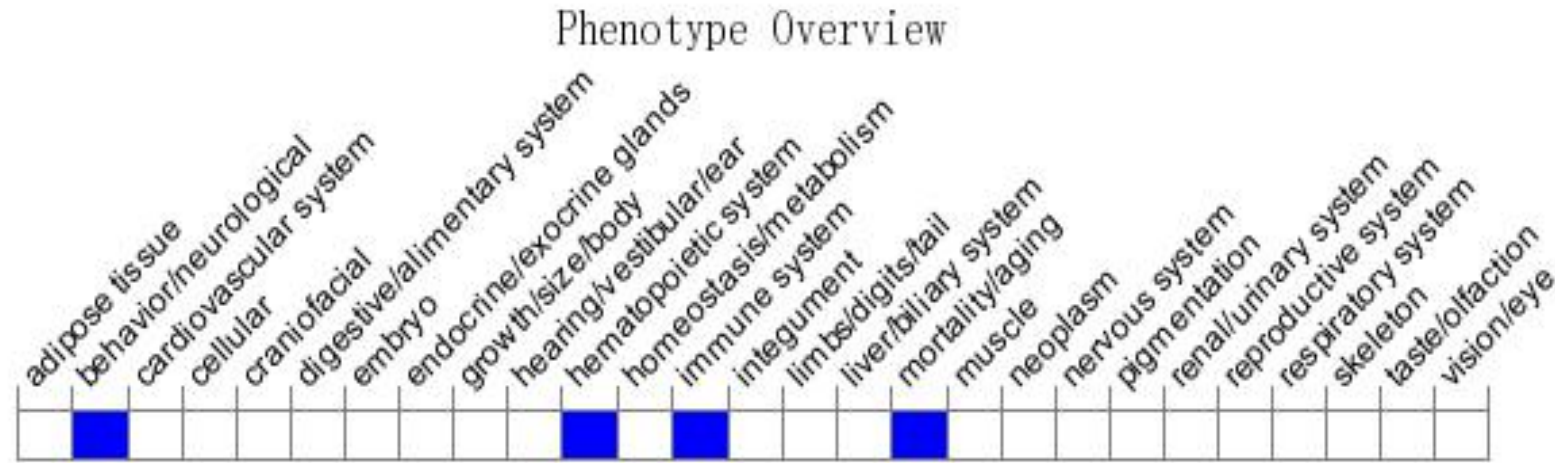
Genomic location distribution



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 targeted mutations that inactivate the gene are deficient in antigen presentation, surface class I antigens, and CD4-8⁺ T cells.

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

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