

Tap2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Tap2

Project type

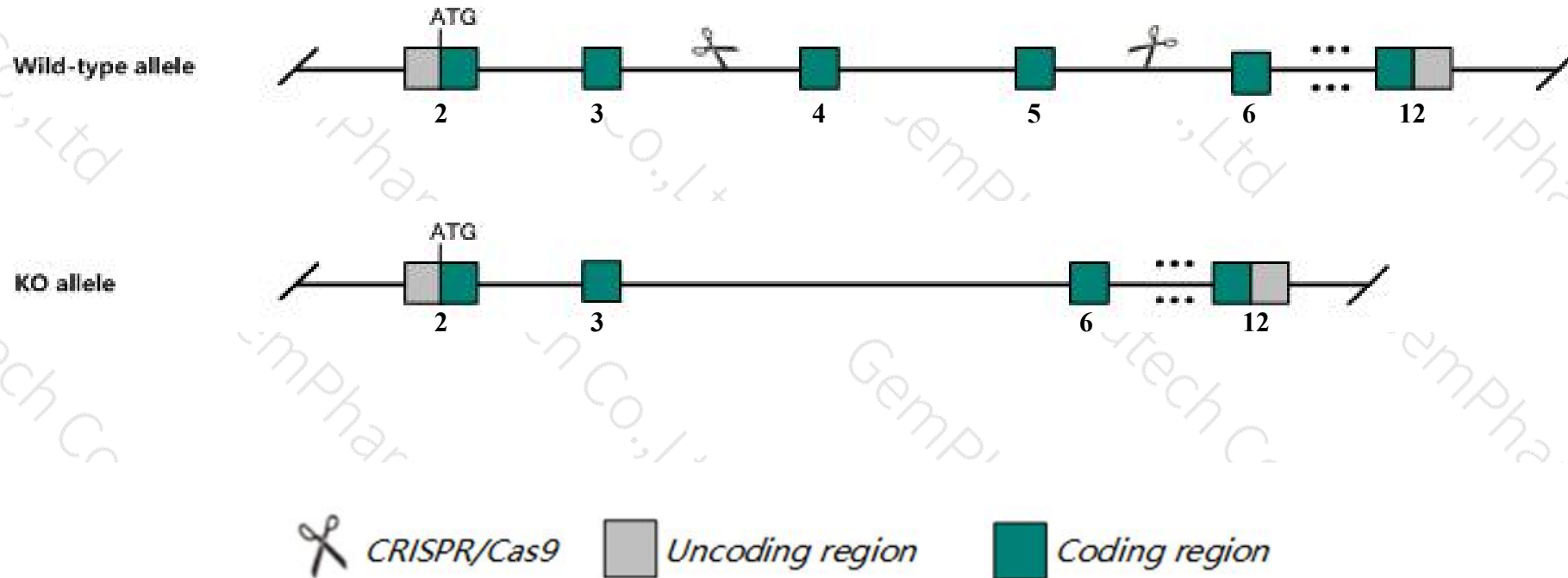
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tap2* gene. The schematic diagram is as follows:



- The *Tap2* gene has 5 transcripts. According to the structure of *Tap2* gene, exon4-exon5 of *Tap2-201* (ENSMUST00000025197.5) transcript is recommended as the knockout region. The region contains 337bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tap2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mutant mice have no CD8+ T cells, although their numbers of CD4+ T cells and B cells are normal.
- The *Tap2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Tap2 transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) [*Mus musculus* (house mouse)]

Gene ID: 21355, updated on 12-Aug-2019

Summary

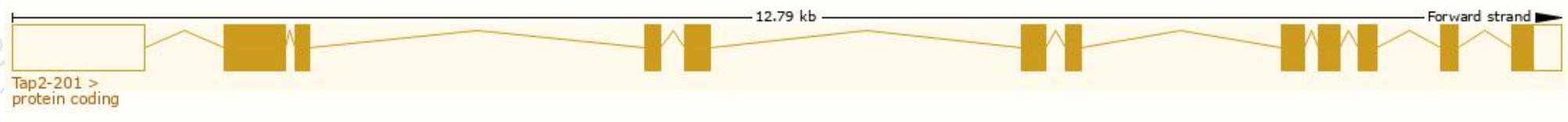
Official Symbol	Tap2 provided by MGI
Official Full Name	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) provided by MGI
Primary source	MGI:MGI:98484
See related	Ensembl:ENSMUSG00000024339
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Y1; jas; APT2; Ham2; MTP2; PSF2; ABC18; Abcb3; Ham-2; Tap-2; RING11; A1462429
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. The protein encoded by this gene is involved in antigen presentation. This protein forms a heterodimer with Tap1 in order to transport peptides from the cytoplasm to the endoplasmic reticulum. Mutations in the human gene may be associated with ankylosing spondylitis, insulin-dependent diabetes mellitus, and celiac disease. [provided by RefSeq, Jul 2008]
Expression	Broad expression in thymus adult (RPKM 79.3), spleen adult (RPKM 48.3) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

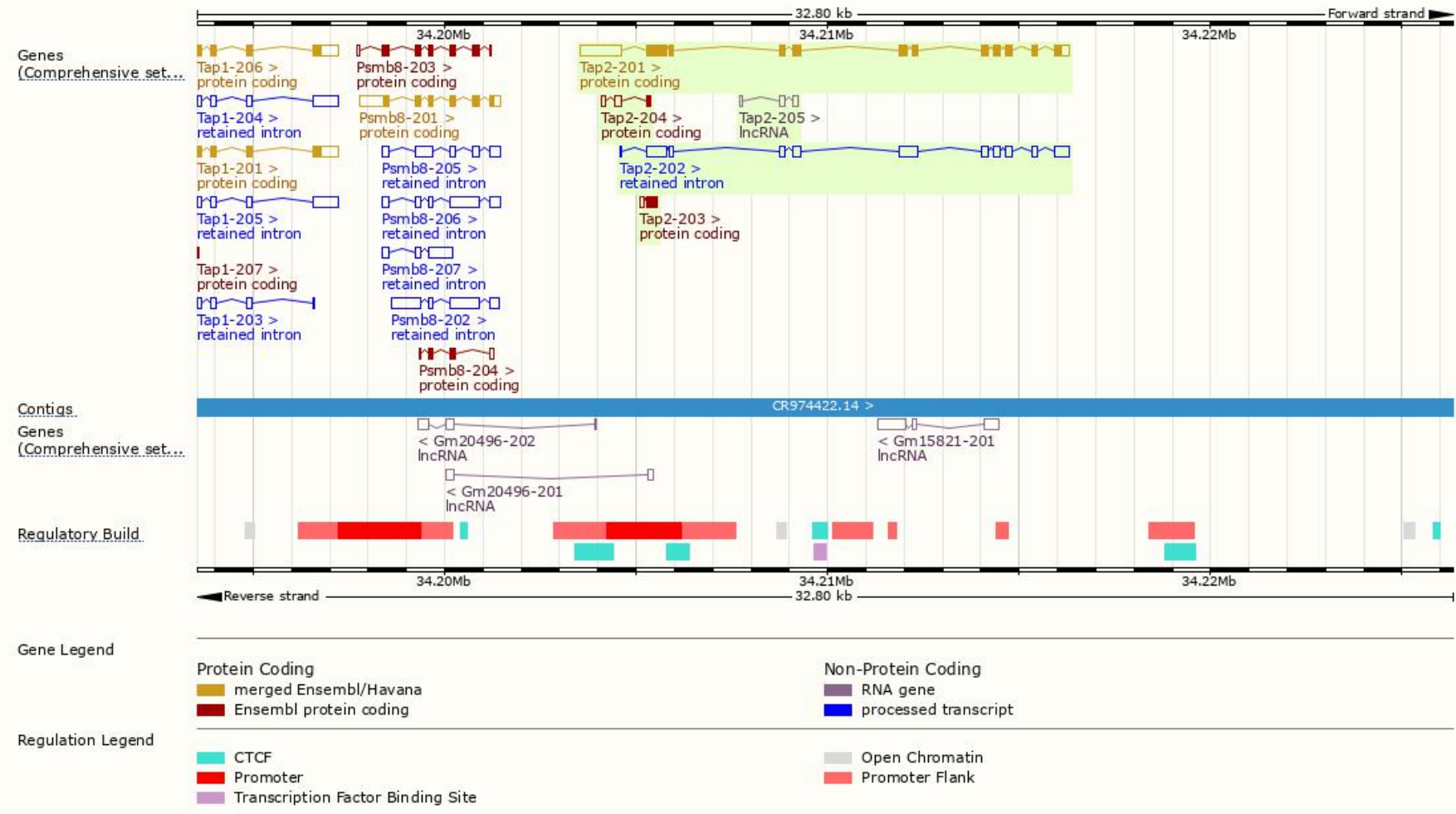
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tap2-201	ENSMUST00000025197.5	3442	702aa	Protein coding	CCDS28644	P36371 Q792S7	TSL:1 GENCODE basic APPRIS P1
Tap2-204	ENSMUST00000138491.1	378	24aa	Protein coding	-	A0A1B0GXB3	CDS 3' incomplete TSL:3
Tap2-203	ENSMUST00000131105.1	376	91aa	Protein coding	-	A6X8J6	CDS 3' incomplete TSL:5
Tap2-202	ENSMUST00000127543.7	2561	No protein	Retained intron	-	-	TSL:2
Tap2-205	ENSMUST00000145528.1	344	No protein	lncRNA	-	-	TSL:3

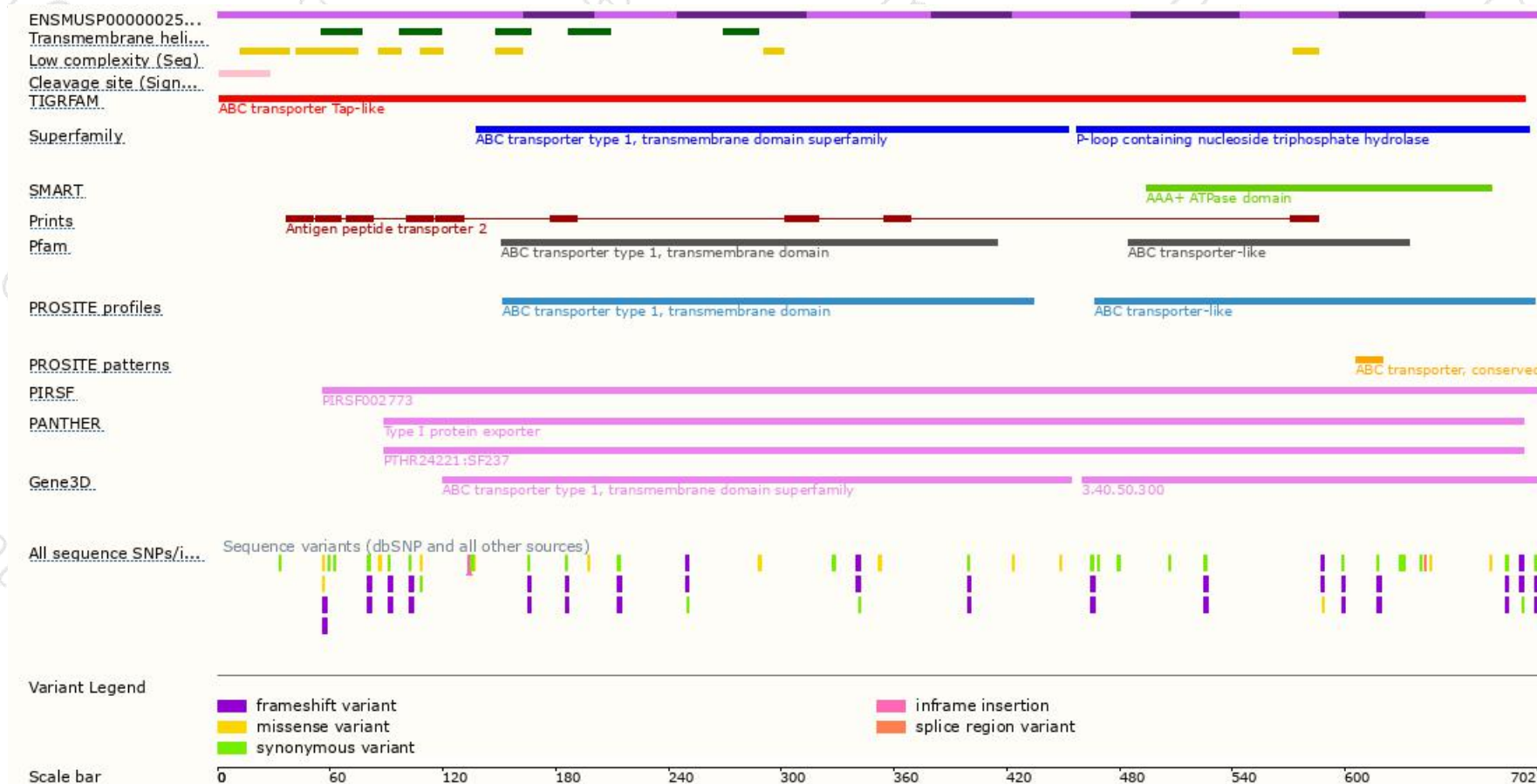
The strategy is based on the design of *Tap2-201* transcript,The transcription is shown below



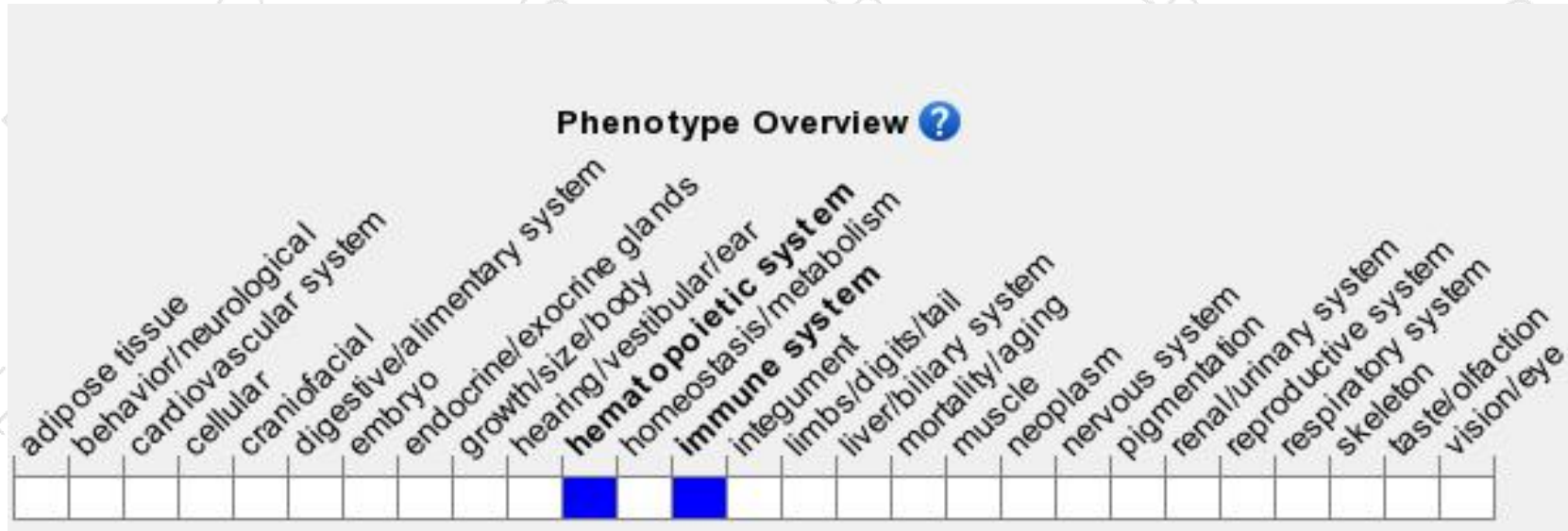
Genomic location distribution



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 mutant mice have no CD8⁺ T cells, although their numbers of CD4⁺ T cells and B cells are normal.

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

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