

# *Trpc4ap* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Trpc4ap***

**Project type**

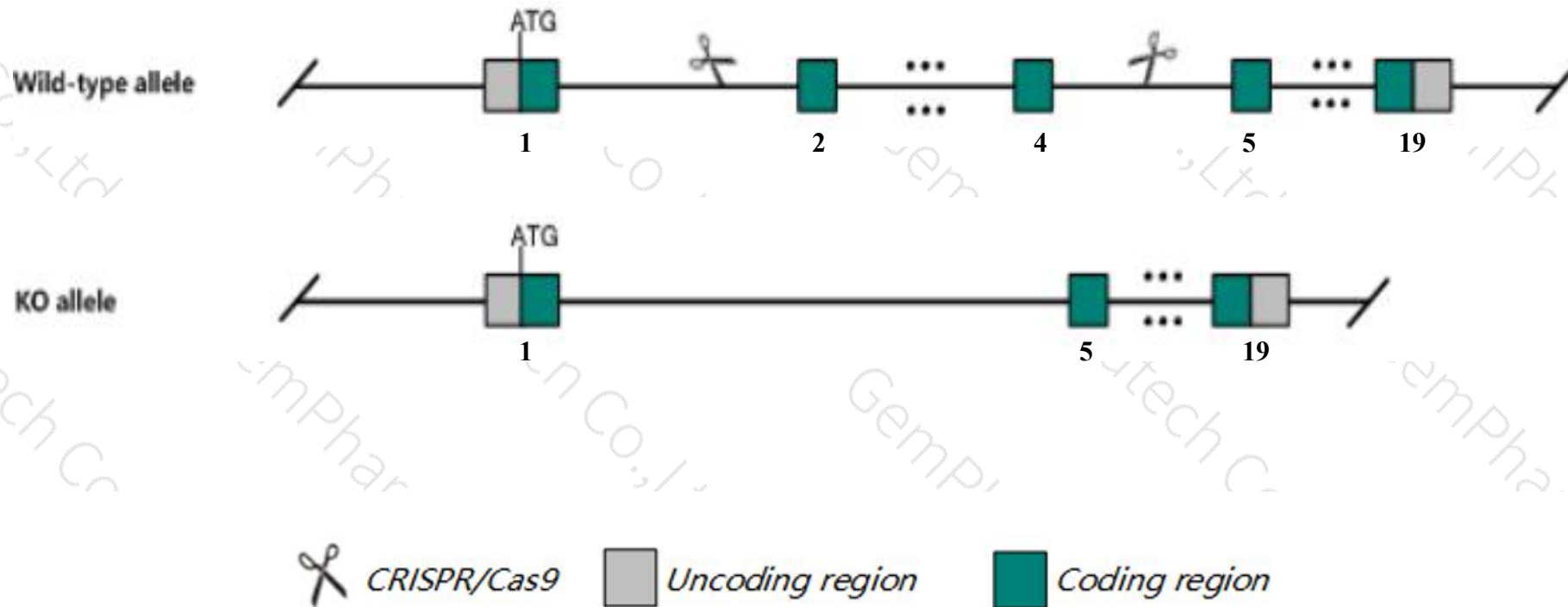
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trpc4ap* gene. The schematic diagram is as follows:



- The *Trpc4ap* gene has 10 transcripts. According to the structure of *Trpc4ap* gene, exon2-exon4 of *Trpc4ap-201*(ENSMUST00000041059.11) transcript is recommended as the knockout region. The region contains 304bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trpc4ap* gene. The brief process is as follows: CRISPR/Cas9 system 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, female mice heterozygous for a knock-out allele exhibit anomalies in the growth phase of the hair cycle (anagen).
- The *Trpc4ap* gene is located on the Chr2. 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)

## Trpc4ap transient receptor potential cation channel, subfamily C, member 4 associated protein [Mus musculus (house mouse)]

Gene ID: 56407, updated on 13-Mar-2020

### Summary



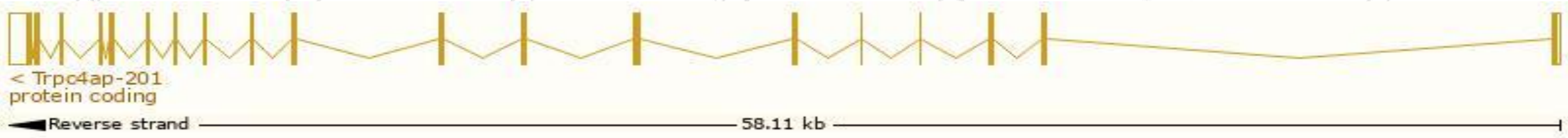
<b>Official Symbol</b>	Trpc4ap provided by <a href="#">MGI</a>
<b>Official Full Name</b>	transient receptor potential cation channel, subfamily C, member 4 associated protein provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1930751</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000038324</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	4833429F06Rik, D2Ertd113e, Trrp4ap, mFLJ00177, truss
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 93.7), ovary adult (RPKM 61.9) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

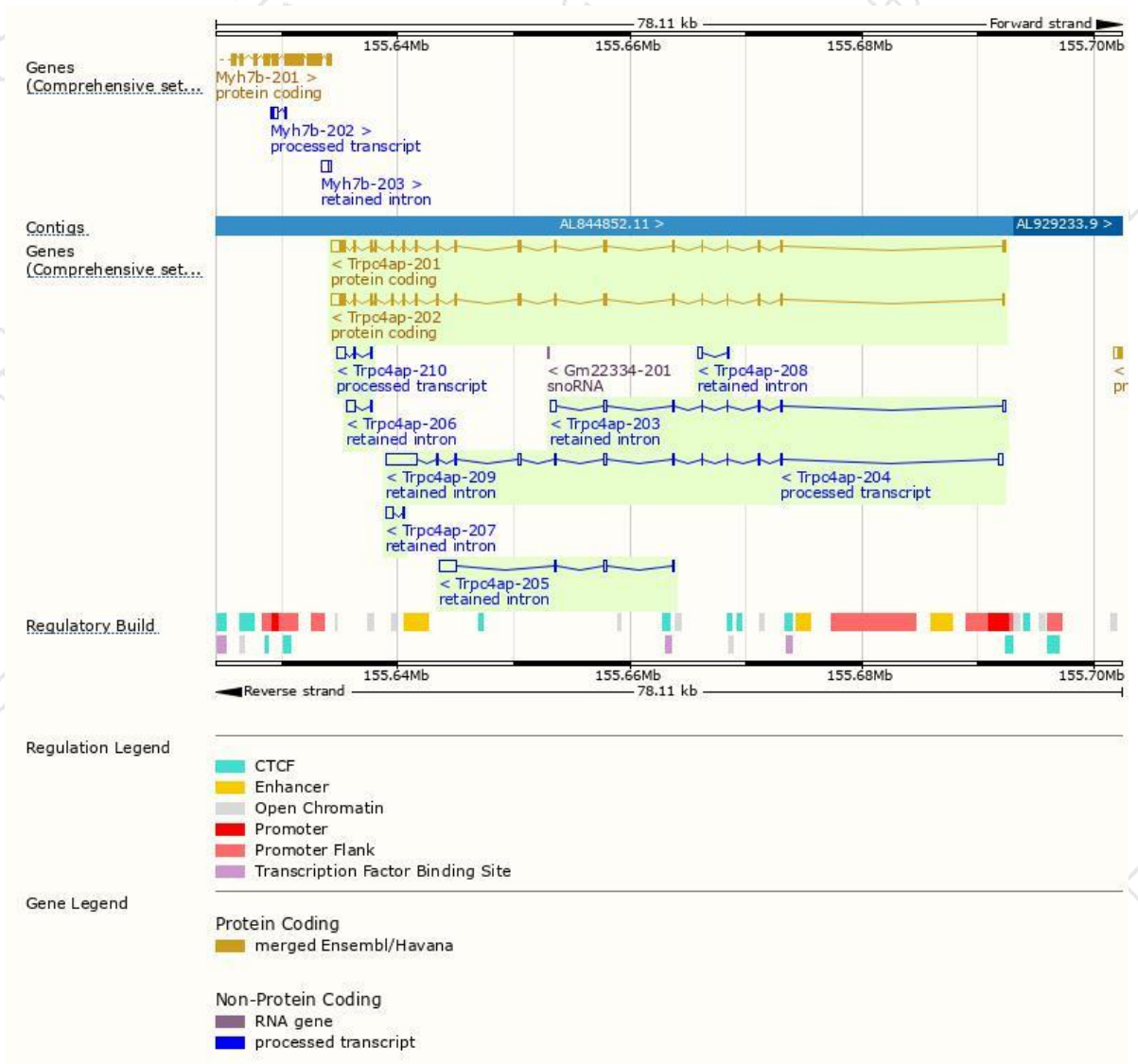
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trpc4ap-201	<a href="#">ENSMUST00000041059.11</a>	3204	<a href="#">797aa</a>	Protein coding	<a href="#">CCDS50769</a>	<a href="#">Q3TDP6</a> <a href="#">Q9JLV2</a>	TSL:1 GENCODE basic APPRIS ALT2
Trpc4ap-202	<a href="#">ENSMUST00000103140.4</a>	3091	<a href="#">789aa</a>	Protein coding	<a href="#">CCDS16952</a>	<a href="#">Q9JLV2</a>	TSL:1 GENCODE basic APPRIS P3
Trpc4ap-210	<a href="#">ENSMUST00000153246.1</a>	890	No protein	Processed transcript	-	-	TSL:2
Trpc4ap-204	<a href="#">ENSMUST00000136764.1</a>	355	No protein	Processed transcript	-	-	TSL:3
Trpc4ap-209	<a href="#">ENSMUST00000152548.7</a>	3907	No protein	Retained intron	-	-	TSL:1
Trpc4ap-205	<a href="#">ENSMUST00000140370.7</a>	2026	No protein	Retained intron	-	-	TSL:1
Trpc4ap-203	<a href="#">ENSMUST00000130755.1</a>	1516	No protein	Retained intron	-	-	TSL:1
Trpc4ap-206	<a href="#">ENSMUST00000143115.1</a>	838	No protein	Retained intron	-	-	TSL:3
Trpc4ap-207	<a href="#">ENSMUST00000146484.1</a>	648	No protein	Retained intron	-	-	TSL:3
Trpc4ap-208	<a href="#">ENSMUST00000147913.1</a>	443	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Trpc4ap-201* transcript,the transcription is shown below:

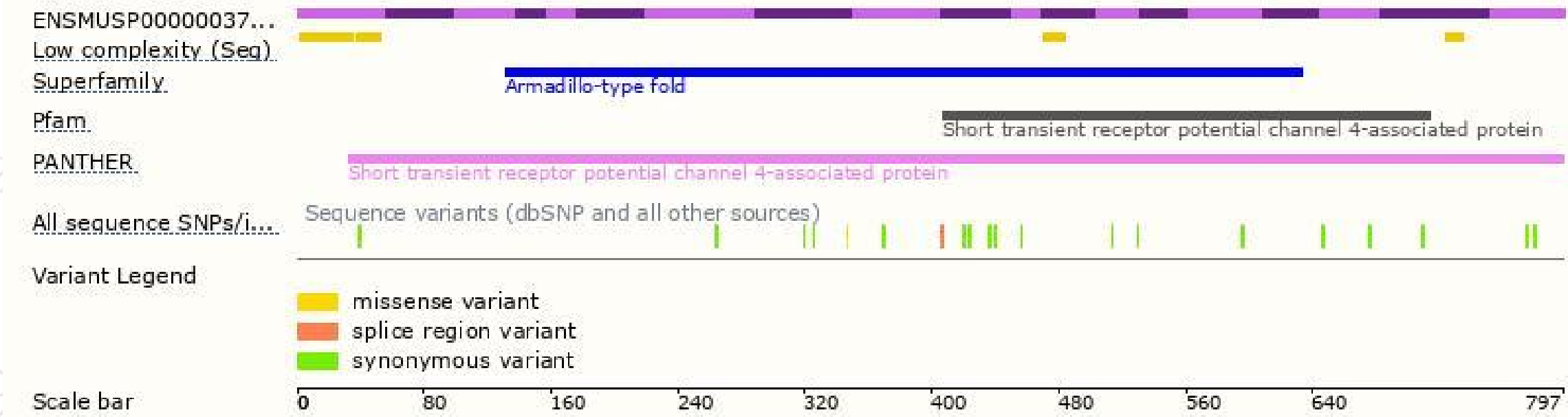


# Genomic location distribution

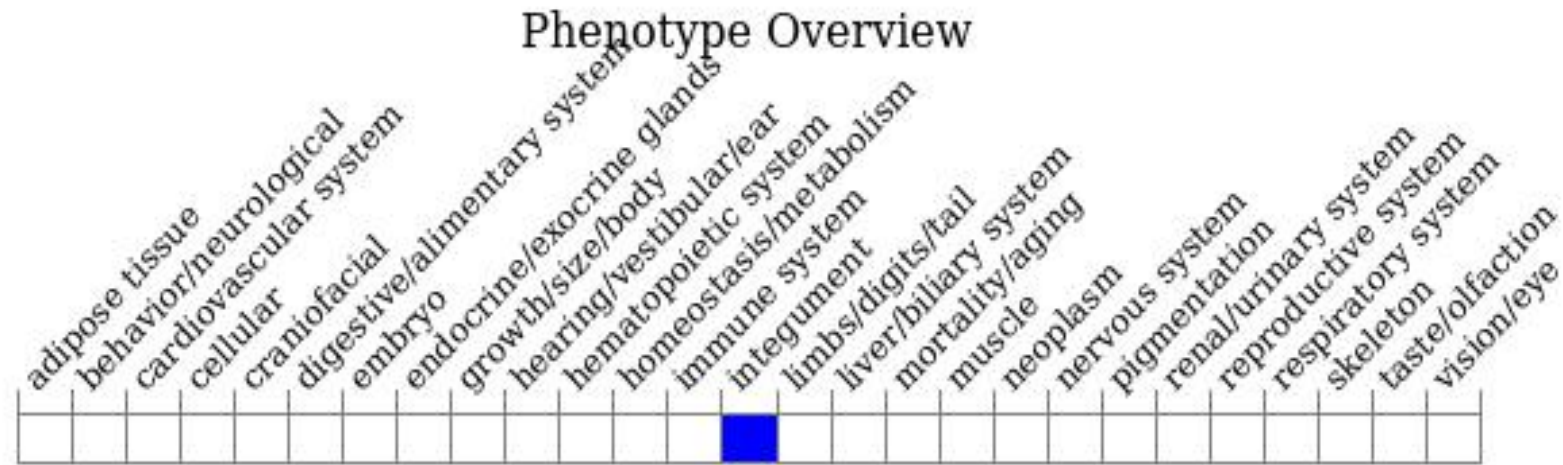




# Protein domain



# 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, female mice heterozygous for a knock-out allele exhibit anomalies in the growth phase of the hair cycle (anagen).

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

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