

Trap1 Cas9-KO Strategy

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Project Overview

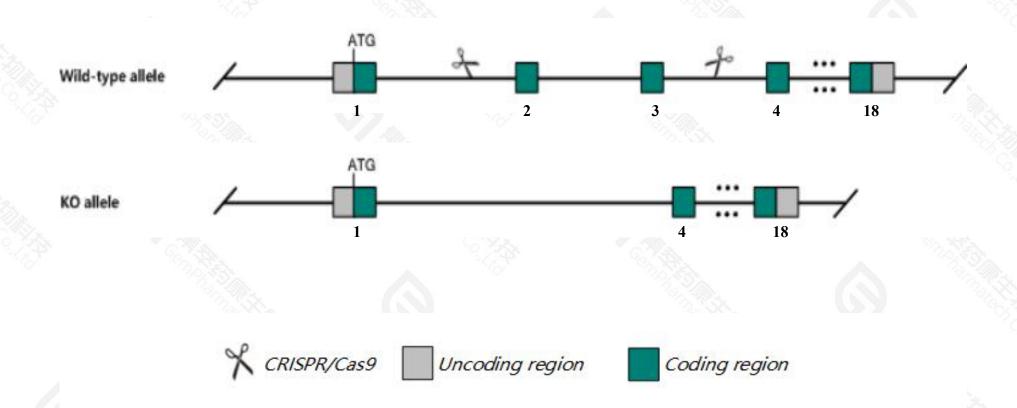


Project Name	Trap1
Project type	Cas9-KO
Strain background	C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Trap1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Trap1* gene has 4 transcripts. According to the structure of *Trap1* gene, exon2-exon3 of *Trap1*201(ENSMUST00000006137.9) transcript is recommended as the knockout region. The region contains 248bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Trap1* 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.

Notice



- > According to the existing MGI data, mice homozygous for a gene trap allele exhibit reduced body weight; liver and spleen hyperplasia; decreased chronic inflammation and tumor incidents; deregulated mitochondrial respiration; and increased oxidative stress.
- > The *Trap1* gene is located on the Chr16. 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)



Trap1 TNF receptor-associated protein 1 [Mus musculus (house mouse)]

Gene ID: 68015, updated on 17-Nov-2020

Summary

☆ ?

Official Symbol Trap1 provided by MGI

Official Full Name TNF receptor-associated protein 1 provided by MGI

Primary source MGI:MGI:1915265

See related Ensembl: ENSMUSG00000005981

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 2410002K23Rik, HSP, HSP75

Expression Ubiquitous expression in kidney adult (RPKM 74.7), adrenal adult (RPKM 61.5) and 28 other tissuesSee more

Orthologs <u>human all</u>

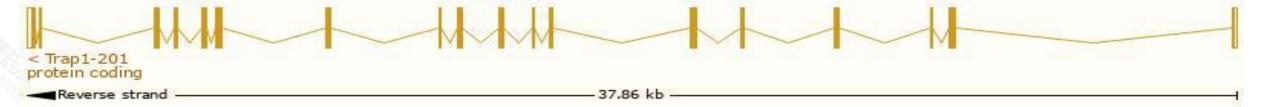
Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

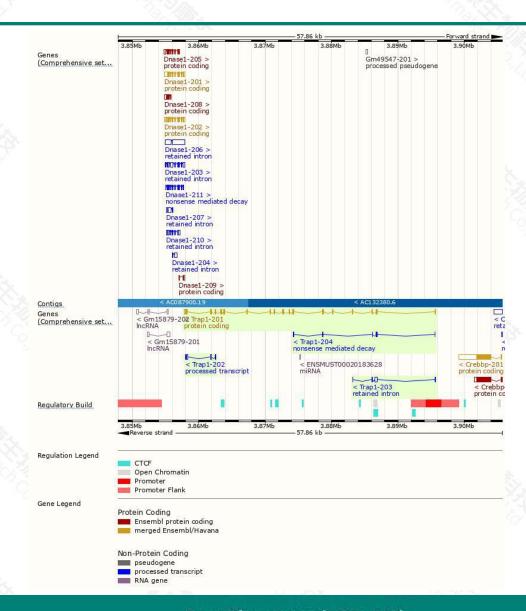
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trap1-201	ENSMUST00000006137.9	2320	<u>706aa</u>	Protein coding	CCDS27914		TSL:1 , GENCODE basic , APPRIS P1 ,
Trap1-204	ENSMUST00000150354.3	431	<u>113aa</u>	Nonsense mediated decay			CDS 5' incomplete , TSL:5 ,
Trap1-202	ENSMUST00000137945.2	449	No protein	Processed transcript	857		TSL:3,
Trap1-203	ENSMUST00000138594.2	621	No protein	Retained intron	100		TSL:5,

The strategy is based on the design of *Trap1-201* transcript, the transcription is shown below:



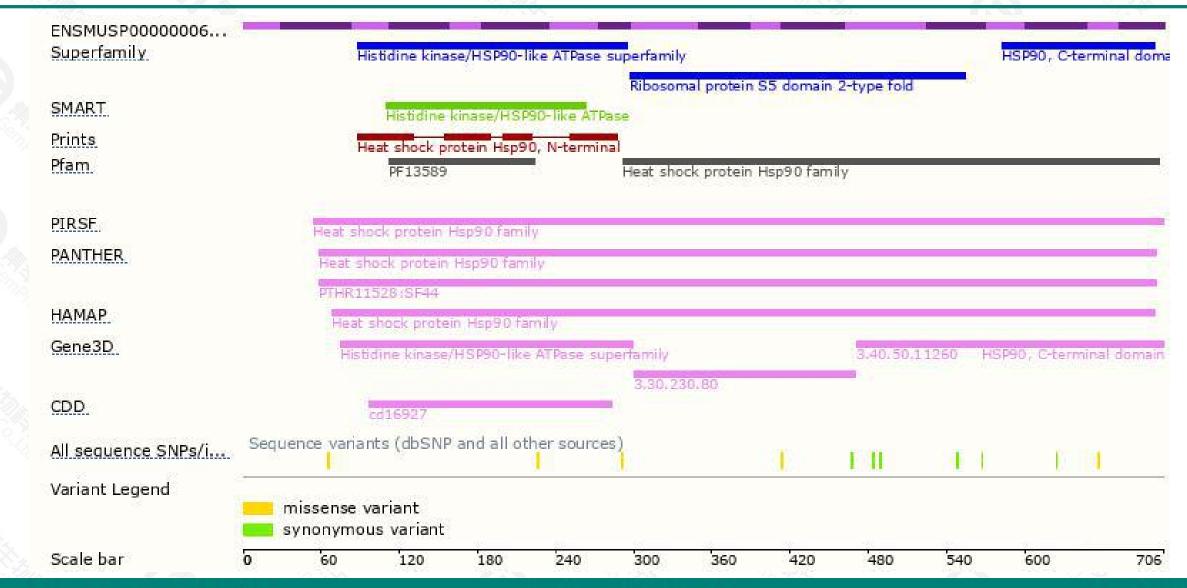
Genomic location distribution





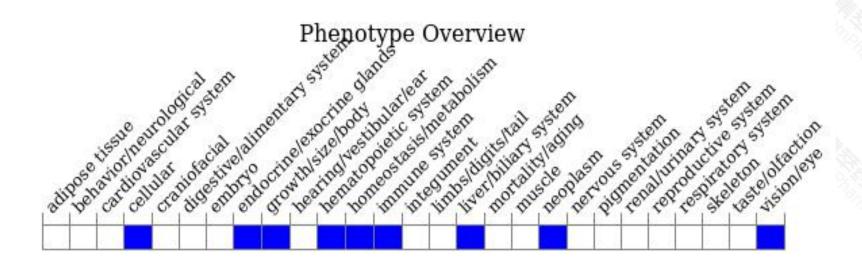
Protein domain





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,mice homozygous for a gene trap allele exhibit reduced body weight; liver and spleen hyperplasia; decreased chronic inflammation and tumor incidents; deregulated mitochondrial respiration; and increased oxidative stress.



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

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