

Usp42 Cas9-KO Strategy

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Project Overview



Project Name

Usp42

Project type

Cas9-KO

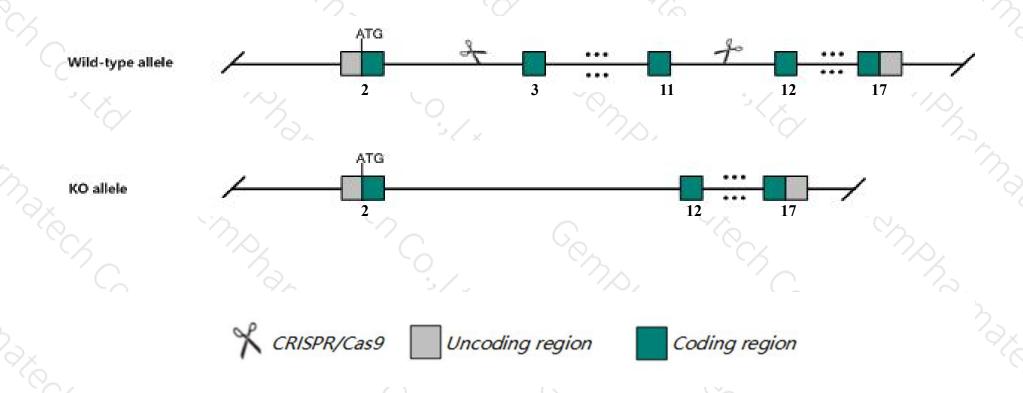
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Usp42* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Usp42* gene has 5 transcripts. According to the structure of *Usp42* gene, exon3-exon11 of *Usp42-201*(ENSMUST0000053287.5) transcript is recommended as the knockout region. The region contains 991bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Usp42* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for a null allele exhibit fecundity and behavioral abnormalities, hyperactivity, increased T cell number, abnormal lens morphology, and cataracts. Males display oligozoospermia and testis degeneration.
- > The *Usp42* gene is located on the Chr5. 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)



Usp42 ubiquitin specific peptidase 42 [Mus musculus (house mouse)]

Gene ID: 76800, updated on 19-Mar-2019

Summary

☆ ?

Official Symbol Usp42 provided by MGI

Official Full Name ubiquitin specific peptidase 42 provided by MGI

Primary source MGI:MGI:1924050

See related Ensembl: ENSMUSG00000051306

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 2410140K03Rik, 3110031A07Rik, A630018G05Rik, D5Ertd591e

Expression Broad expression in testis adult (RPKM 13.7), CNS E11.5 (RPKM 4.9) and 25 other tissuesSee more

Orthologs <u>human</u> all

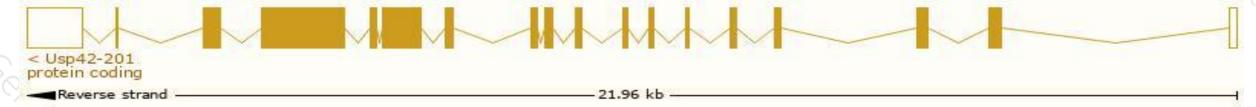
Transcript information (Ensembl)



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

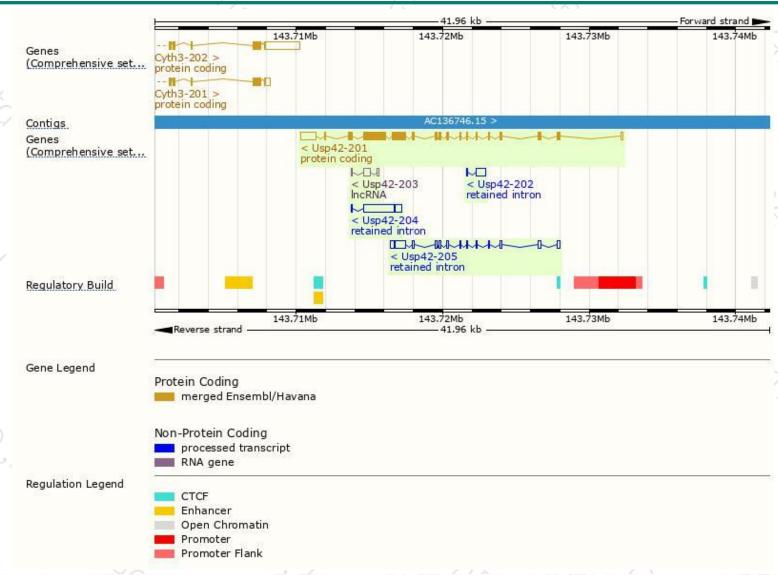
| Name | Transcript ID | bp | Protein | Biotype | ccds | UniProt | Flags |
|-----------|----------------------|------|---------------|-----------------|-----------|---------|-------------------------------|
| Usp42-201 | ENSMUST00000053287.5 | 5151 | <u>1324aa</u> | Protein coding | CCDS39372 | B2RQC2 | TSL:5 GENCODE basic APPRIS P1 |
| Usp42-204 | ENSMUST00000141396.1 | 2554 | No protein | Retained intron | - | -8 | TSL:1 |
| Usp42-205 | ENSMUST00000155408.1 | 2359 | No protein | Retained intron | | - | TSL:1 |
| Usp42-202 | ENSMUST00000129606.1 | 710 | No protein | Retained intron | - | 20 | TSL:3 |
| Usp42-203 | ENSMUST00000141225.1 | 654 | No protein | IncRNA | 5 | - | TSL:3 |

The strategy is based on the design of *Usp42-201* transcript, The transcription is shown below



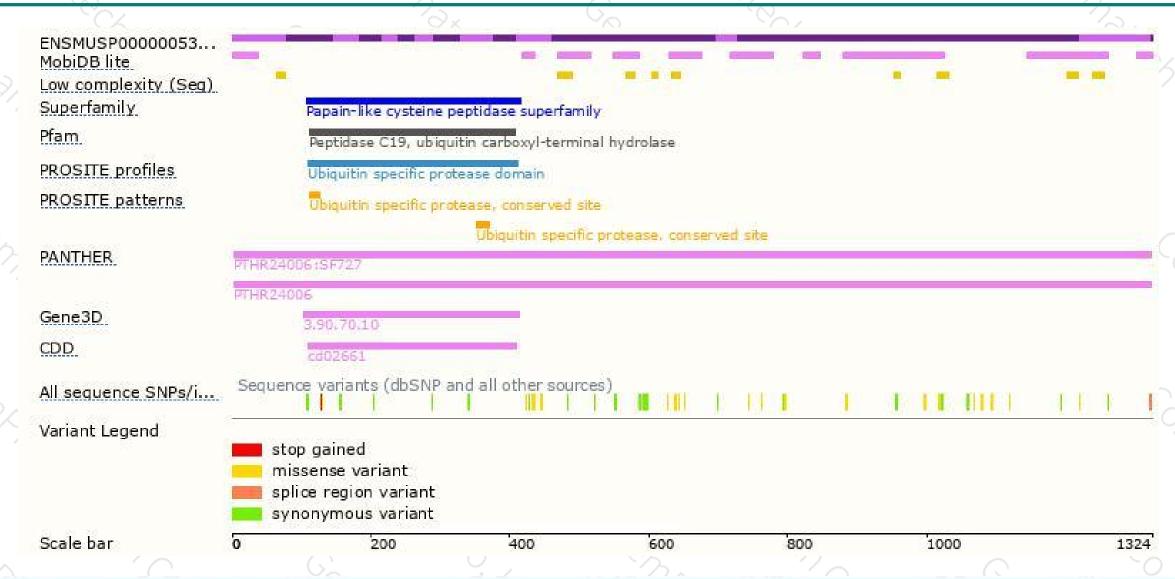
Genomic location distribution





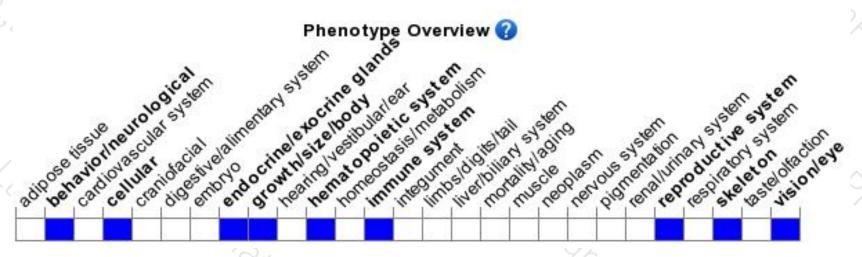
Protein domain





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 null allele exhibit fecundity and behavioral abnormalities, hyperactivity, increased T cell number, abnormal lens morphology, and cataracts. Males display oligozoospermia and testis degeneration.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





