

Usp13 Cas9-KO Strategy

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Overview

Target Gene Name

- Usp13

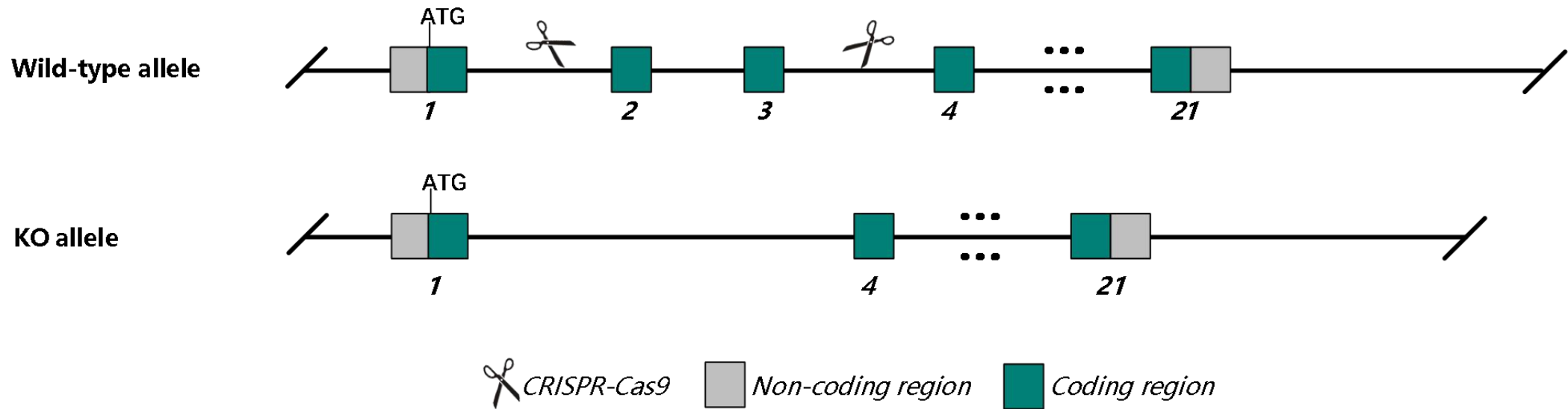
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Usp13* gene.

Technical Information

- The *Usp13* gene has 4 transcripts. According to the structure of *Usp13* gene, exon2-exon3 of *Usp13*-201 (ENSMUST00000072312.12) transcript is recommended as the knockout region. The region contains 187bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Usp13* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Usp13 ubiquitin specific peptidase 13 (isopeptidase T-3) [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 72607, updated on 12-Apr-2023

Summary

Official Symbol	Usp13 provided by MGI
Official Full Name	ubiquitin specific peptidase 13 (isopeptidase T-3) provided by MGI
Primary source	MGI:MGI:1919857
See related	Ensembl:ENSMUSG00000056900 AllianceGenome:MGI:1919857
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ISOT3; IsoT-3; 2700071E21Rik
Summary	Predicted to enable several functions, including BAT3 complex binding activity; chaperone binding activity; and cysteine-type peptidase activity. Predicted to be involved in several processes, including proteolysis; regulation of cellular catabolic process; and regulation of transcription, DNA-templated. Predicted to act upstream of or within protein K29-linked deubiquitination; protein K6-linked deubiquitination; and protein stabilization. Predicted to be active in cytosol and nucleus. Orthologous to human USP13 (ubiquitin specific peptidase 13). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in heart adult (RPKM 18.6), frontal lobe adult (RPKM 2.9) and 10 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

Location: 3; 3 A3

See Usp13 in [Genome Data Viewer](#)

Exon count: 21

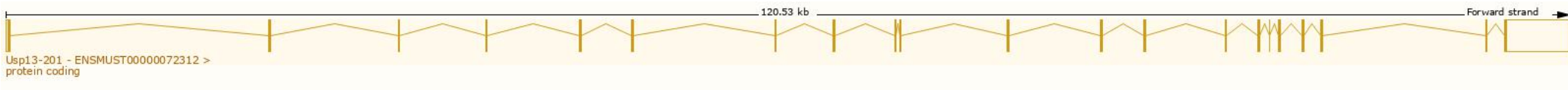
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

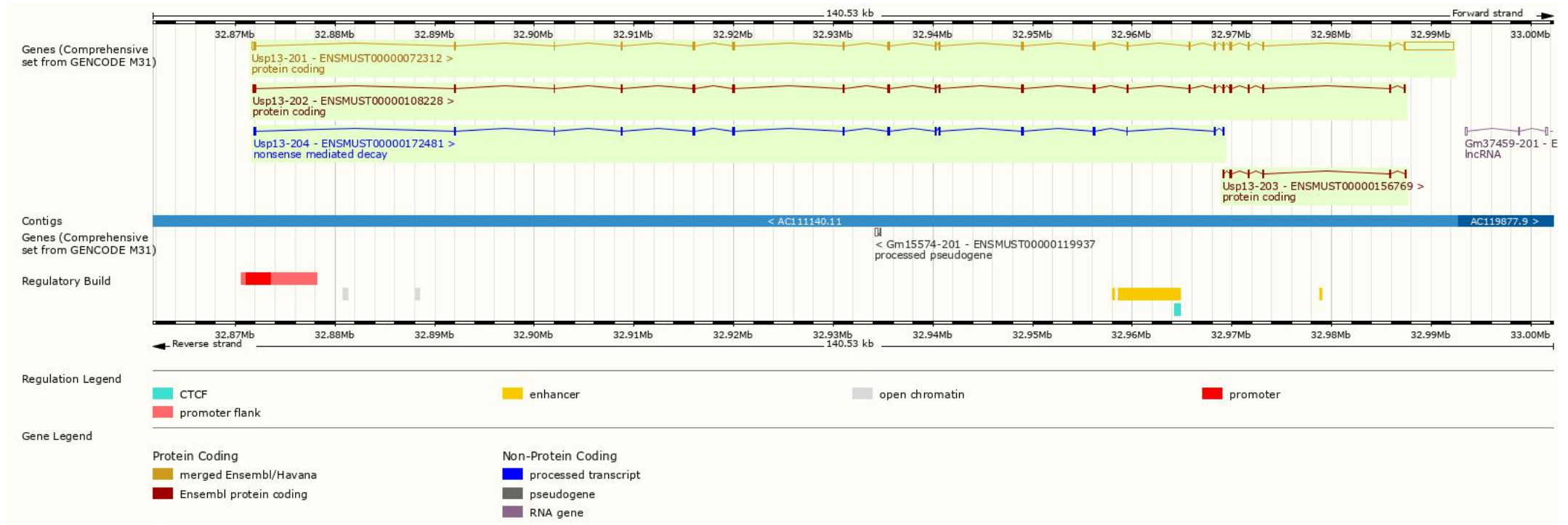
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000072312.12	Usp13-201	7580	858aa	Protein coding	CCDS17301	Q5BKP2	Ensembl Canonical Gencode basic APPRIS P4 TSL:1
ENSMUST00000108228.8	Usp13-202	2767	857aa	Protein coding		J3QSN2	Gencode basic APPRIS ALT1 TSL:1
ENSMUST00000156769.2	Usp13-203	627	188aa	Protein coding		F6ZE47	TSL:5 CDS 5' incomplete
ENSMUST00000172481.2	Usp13-204	1744	534aa	Nonsense mediated decay		G3UXT9	TSL:5

The strategy is based on the design of *Usp13-201* transcript, the transcription is shown below:

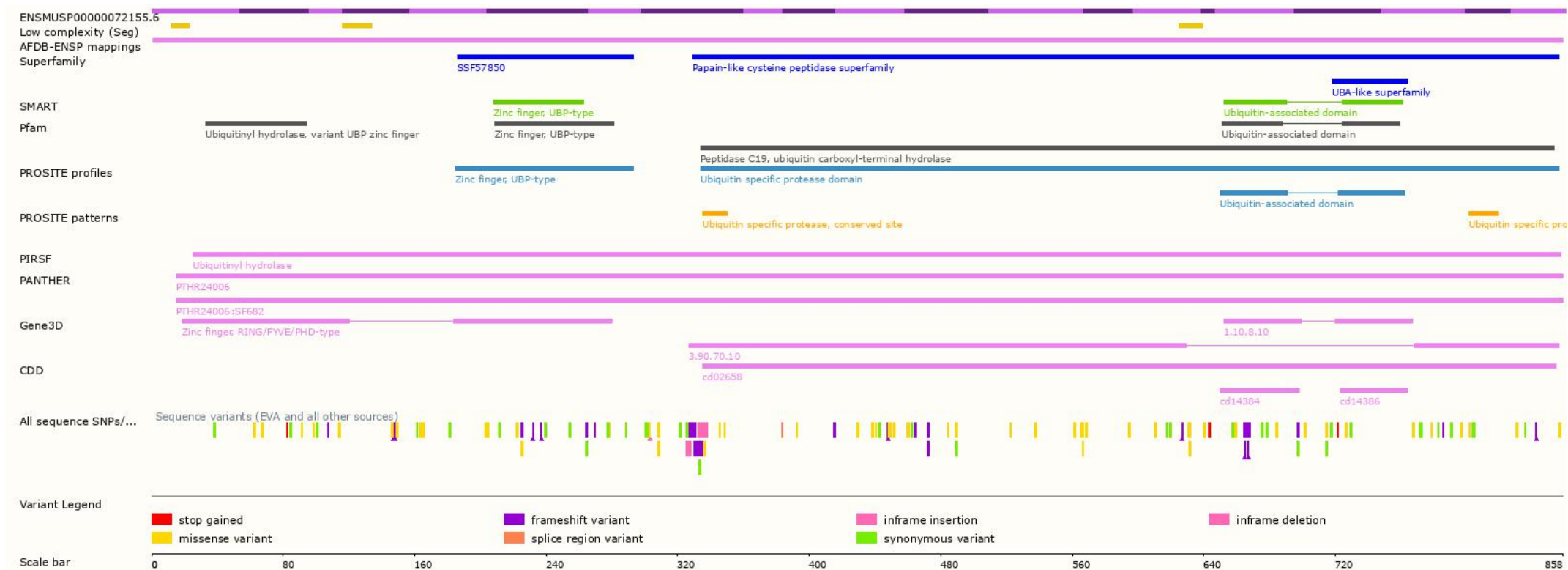


Source: <https://www.ensembl.org>

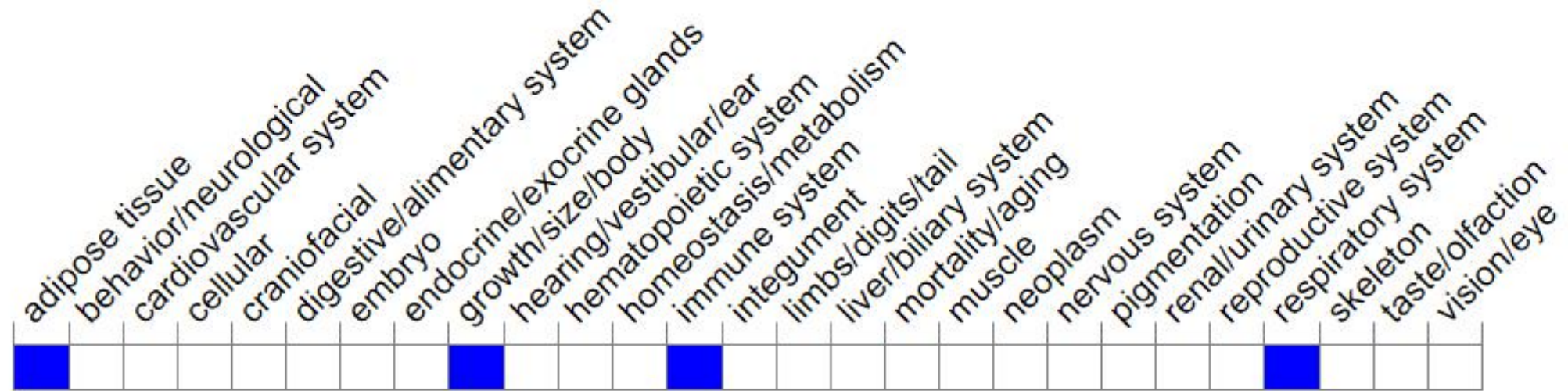
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Usp13* gene are marked in blue. Mice homozygous for a null allele exhibit increased susceptibility to LPS- or *Pseudomonas aeruginosa* (strain PA103)- induced lung inflammation and injury.

Important Information

- The effect of *Usp13*-203 transcript is unknown.
- *Usp13* is located on Chr3. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.