

# Usp10 Cas9-CKO Strategy

Designer: Jiaojiao Yan

Reviewer: Xiangli Bian

Design Date: 2023.11.17

# Overview

### Target Gene Name

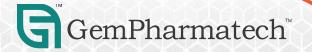
• Usp10

## Project Type

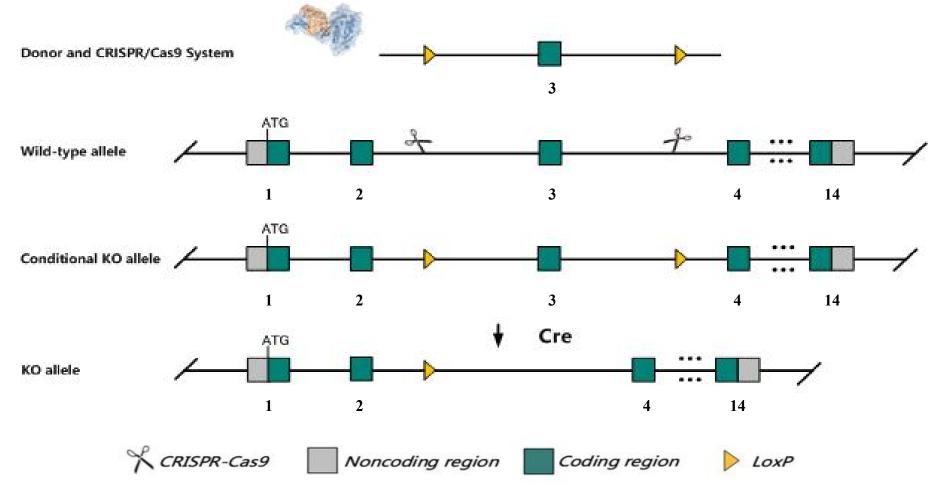
• Cas9-CKO

### Genetic Background

• C57BL/6JGpt



# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Usp10* gene.



### **Technical Information**

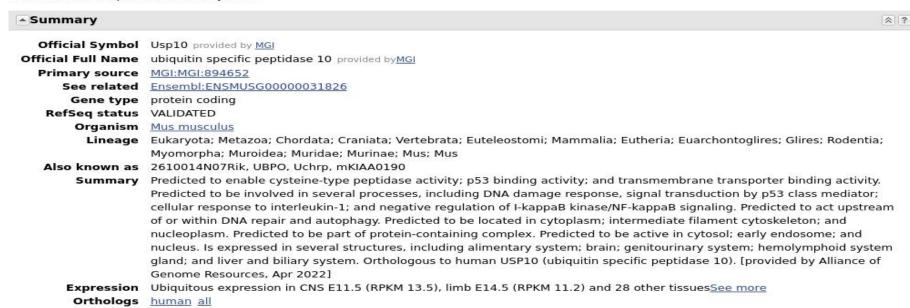
- The *Usp10* gene has 13 transcripts. According to the structure of *Usp10* gene, exon3 of *Usp10*-210 (ENSMUST00000144458.8) transcript is recommended as the knockout region. The region contains 58bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Usp10* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



### Gene Information

#### Usp10 ubiquitin specific peptidase 10 [Mus musculus (house mouse)]

Gene ID: 22224, updated on 21-May-2023



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



# Transcript Information

The gene has 13 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp10-210	ENSMUST000001444	58.8 3726	<u>793aa</u>	Protein coding	CCDS40495	5	A single transcript chosen for a gene which is the most conserved, most highly expressed, has the longest coding sequence and is represented in other key resources, such as NCBI and UniProt. This is defined in detail on http://www.ensembl.org/info/genome/genebuild/canonical.html Ensembl Canonical, The GENCODE set is the gene set for human and mouse. GENCODE basic , APPRIS P4 , TSL1.,
Usp10-202	ENSMUST000001089	88.9 3274	<u>792aa</u>	Protein coding	CCDS80938	<u>B</u>	The GENCODE set is the gene set for human and mouse. GENCODE basic , APPRIS ALT2 , TSL:1 ,
Usp10-201	ENSMUST000001089	<u>32.11</u> 559	114aa	Protein coding			TSL5 , CDS 31 incomplete ,
Usp10-204	ENSMUST000001347	29.2 424	88aa	Protein coding			TSL3 , CD5 3' incomplete ,
Usp10-209	ENSMUST000001436	<u>15.8</u> 2129	No protein	Protein coding CDS not defined			TSL1,
Usp10-205	ENSMUST000001352	10.2 467	No protein	Protein coding CDS not defined			TSL5,
Usp10-207	ENSMUST000001396	48.2 459	No protein	Protein coding CDS not defined			TSL5 ,
Usp10-212	ENSMUST000002119	<u>35.2</u> 3723	No protein	Retained intron			TSLNA,
Usp10-206	ENSMUST000001373	10.2 831	No protein	Retained intron			TSL2,
Usp10-213	ENSMUST000002126	12.2 761	No protein	Retained intron			TSLNA,
Usp10-203	ENSMUST000001250	66.2 747	No protein	Retained intron			TSL3,
Usp10-211	ENSMUST000001487	67.2 717	No protein	Retained intron			TSL3,
Usp10-208	ENSMUST000001424	32.8 665	No protein	Retained intron			TSL2,

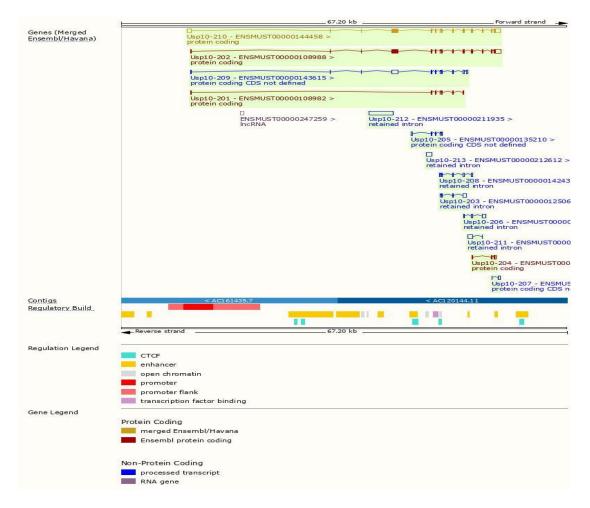
The strategy is based on the design of *Usp10*-210 transcript, the transcription is shown below:



Source: https://www.ensembl.org

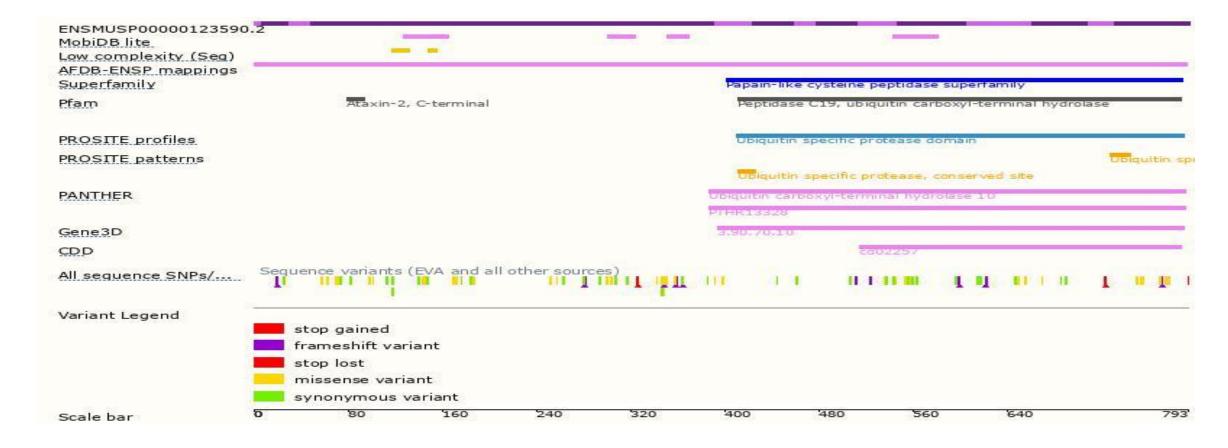


# Genomic Information





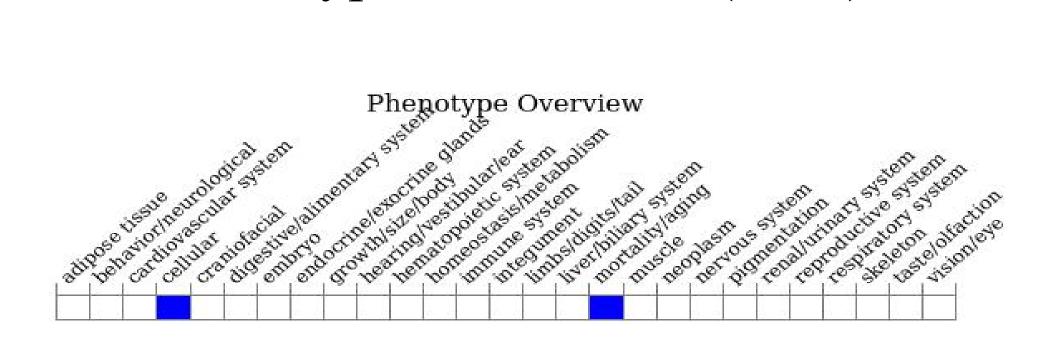
### Protein Information





Source: https://www.ensembl.org

# Mouse Phenotype Information (MGI)



• Homozygous inactivation of this gene leads to alterations in arsenite-induced stress granule formation, reactive oxygen species (ROS) production, and ROS-dependent apoptosis in mouse embryonic fibroblasts.



Source: https://www.informatics.jax.org

# Important Information

- According to MGI, homozygous mice that knock out this gene completely die before weaning.
- This stratergy may not affect *Usp10*-203~208 and *Usp10*-211~*Usp10*-213 transcript.
- *Usp10* is located on Chr8. 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



### Reference

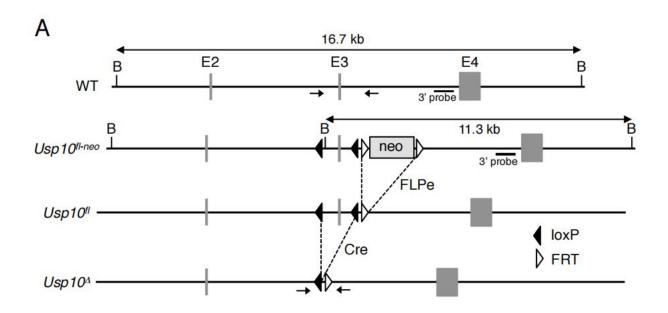


Figure S1 related to figure 1. Generation of USP10-KO mice. (A) Genomic structure of mouse *Usp10*. Grey rectangles (E2, E3, E4) represent *Usp10* exons. Neo indicates the Neomycin selection cassette flanked by FRT recombination sites (white triangles), inserted between exon 3 and 4. Black triangles represent the loxP sites, flanking exon 3. Removal of the Neomycin cassette by crossing with *CAG-FLPe* mice resulted in the generation of the conditional *Usp10*<sup>¶</sup> allele. The conditional *Usp10*<sup>¶</sup> allele was converted to the recombined *Usp10*<sup>A</sup> allele by crossing with *TLCN-Cre* mice. Positions of primers used for genotyping are indicated as small arrows. The Bgl II recognition sites were indicated as B. (B) Southern blot analysis of the tail DNA derived from *Usp10*<sup>¶-neol+</sup> heterozygous mice. (C) PCR genotyping of USP10-KO mice. The primer sequences are 5'-GGTGTTTGGGGCTCGGTTCTGTCA-3' and 5'-TGGCAGTTGTGGTGGTTTGAGTATG-3'. (D) USP10 protein expression in USP10-WT and KO MEFs. Total cell lysates were prepared from USP10-WT and KO MEFs and probed with anti-USP10 or anti-eIF4E antibody.

Higuchi M, Kawamura H, Matsuki H, Hara T, Takahashi M, Saito S, Saito K, Jiang S, Naito M, Kiyonari H, Fujii M. USP10 Is an Essential Deubiquitinase for Hematopoiesis and Inhibits Apoptosis of Long-Term Hematopoietic Stem Cells. Stem Cell Reports. 2016 Dec 13;7(6):1116-1129.

