

# *Usp28* Cas9-KO Strategy

**Designer:**

**Baocheng Zhuang**

**Reviewer:**

**Yang Zeng**

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# Project Overview

**Project Name**

*Usp28*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp28* gene. The schematic diagram is as follows:



- The *Usp28* gene has 10 transcripts. According to the structure of *Usp28* gene, exon2-exon12 of *Usp28-201* (ENSMUST00000047349.7) transcript is recommended as the knockout region. The region contains 1229bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp28* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable and fertile and exhibit slightly decreased spleen weight and splenocyte number but show neither major signaling defects in DNA damage response nor developmental defects indicative of impaired double-strand break metabolism.
- Transcript *Usp28-202/204/207/210* may not be affected.
- The *Usp28* gene is located on the Chr9. 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)

## Usp28 ubiquitin specific peptidase 28 [ *Mus musculus* (house mouse) ]

Gene ID: 235323, updated on 12-Aug-2019

### Summary



Official Symbol	Usp28 provided by <a href="#">MGI</a>
Official Full Name	ubiquitin specific peptidase 28 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2442293</a>
See related	<a href="#">Ensembl:ENSMUSG00000032267</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU022237; mKIAA1515; 9830148O20Rik
Expression	Broad expression in heart adult (RPKM 15.4), CNS E11.5 (RPKM 7.7) and 23 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

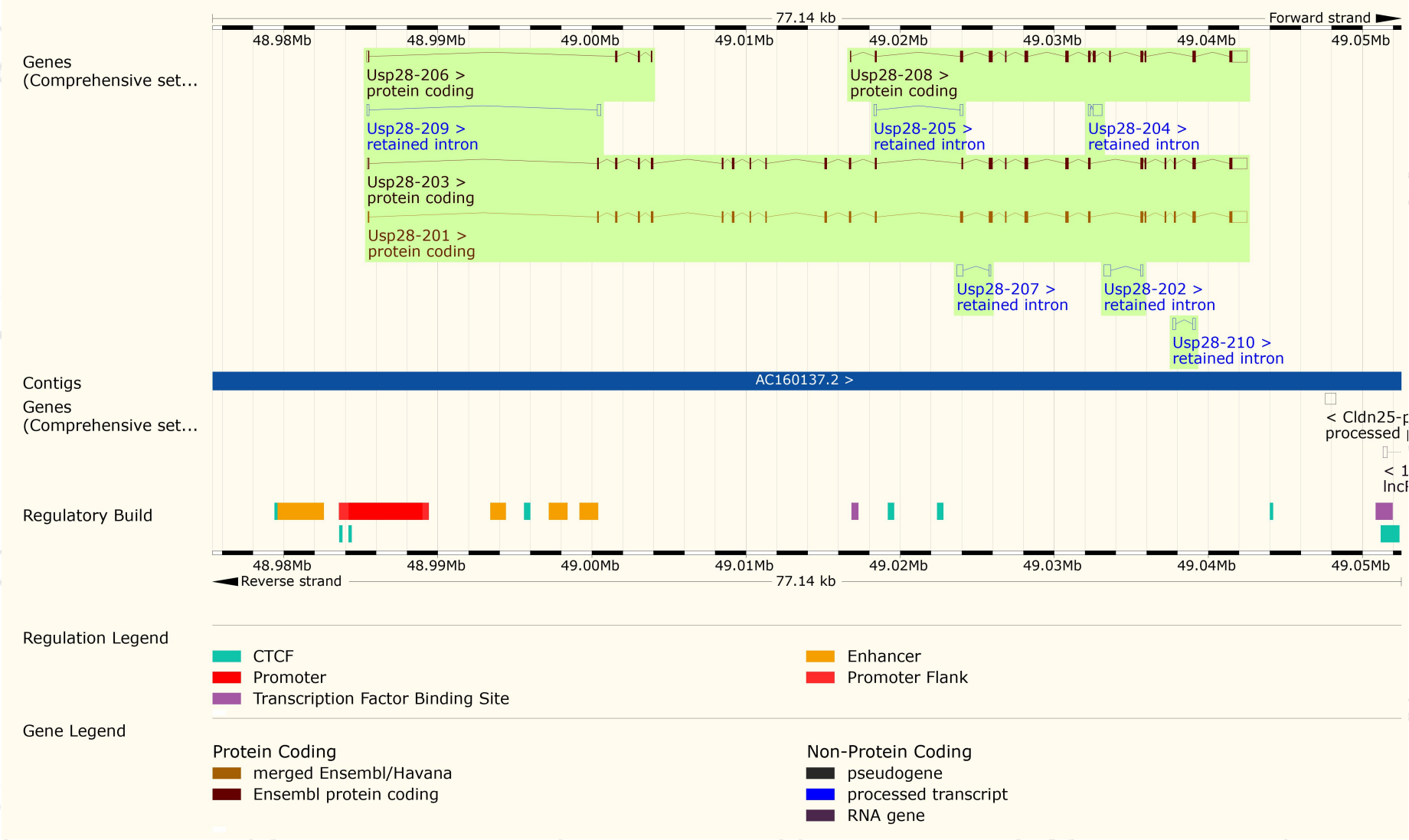
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp28-201	<a href="#">ENSMUST00000047349.7</a>	4133	<a href="#">1051aa</a>	Protein coding	<a href="#">CCDS40613</a>	<a href="#">Q5I043</a>	TSL:1 GENCODE basic APPRIS P2
Usp28-203	<a href="#">ENSMUST00000213874.1</a>	4109	<a href="#">1026aa</a>	Protein coding	-	<a href="#">Q5I043</a>	TSL:1 GENCODE basic APPRIS ALT2
Usp28-208	<a href="#">ENSMUST00000215856.1</a>	3065	<a href="#">698aa</a>	Protein coding	-	<a href="#">A0A1L1SUC4</a>	CDS 5' incomplete TSL:1
Usp28-206	<a href="#">ENSMUST00000215788.1</a>	489	<a href="#">127aa</a>	Protein coding	-	<a href="#">A0A1L1SSQ8</a>	CDS 3' incomplete TSL:2
Usp28-204	<a href="#">ENSMUST00000215118.1</a>	732	No protein	Retained intron	-	-	TSL:3
Usp28-202	<a href="#">ENSMUST00000213457.1</a>	634	No protein	Retained intron	-	-	TSL:5
Usp28-207	<a href="#">ENSMUST00000215850.1</a>	535	No protein	Retained intron	-	-	TSL:3
Usp28-210	<a href="#">ENSMUST00000216657.1</a>	392	No protein	Retained intron	-	-	TSL:2
Usp28-209	<a href="#">ENSMUST00000216607.1</a>	379	No protein	Retained intron	-	-	TSL:3
Usp28-205	<a href="#">ENSMUST00000215378.1</a>	363	No protein	Retained intron	-	-	TSL:2

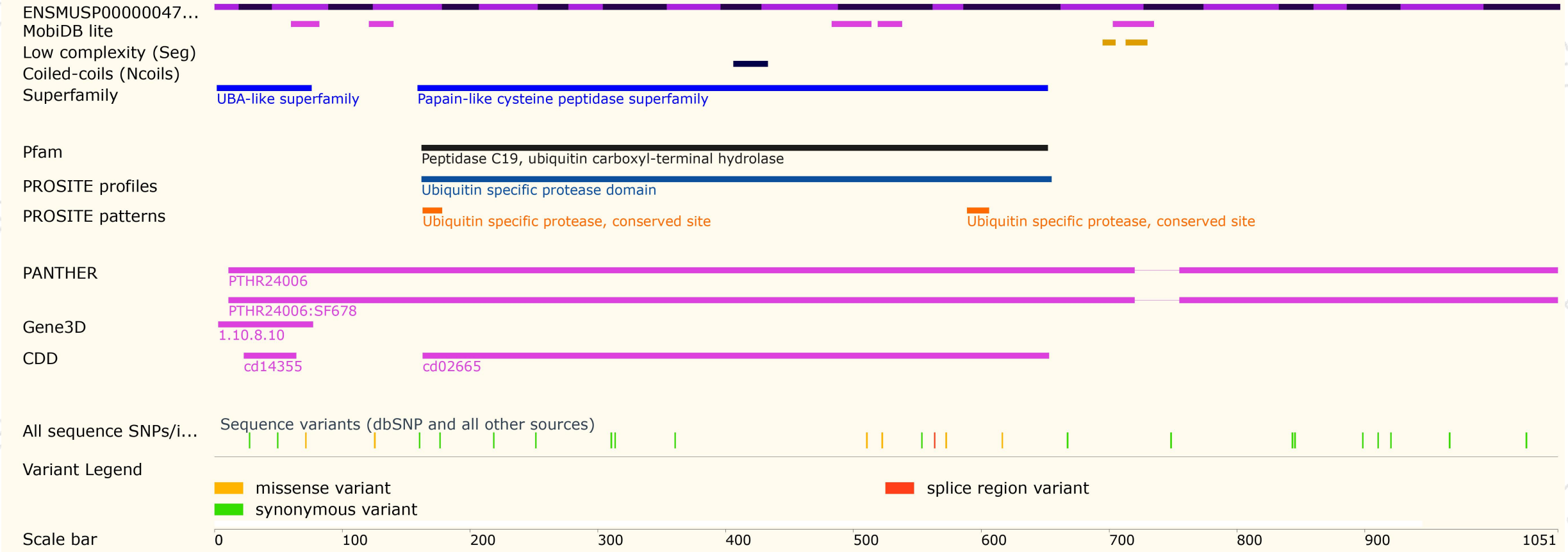
The strategy is based on the design of *Usp28-201* transcript,The transcription is shown below



# Genomic location distribution

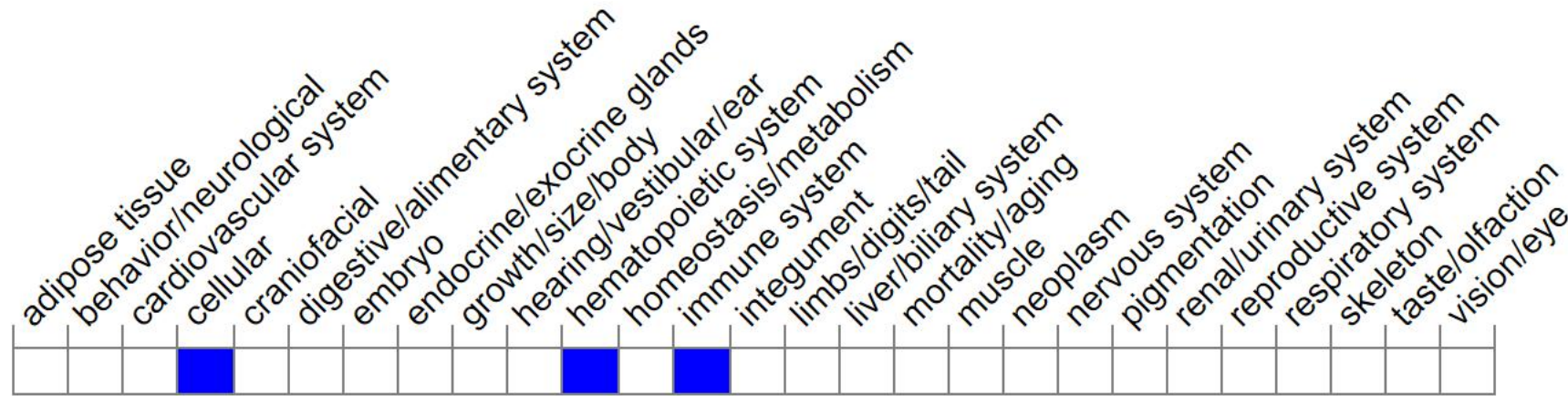


# Protein domain



# Mouse phenotype description(MGI )

## Phenotype Overview ?



*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 knock-out allele are viable and fertile and exhibit slightly decreased spleen weight and splenocyte number but show neither major signaling defects in DNA damage response nor developmental defects indicative of impaired double-strand break metabolism.

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

Tel: 400-9660890

