

# *Usp8* Cas9-KO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Usp8*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp8* gene. The schematic diagram is as follows:



- The *Usp8* gene has 3 transcripts. According to the structure of *Usp8* gene, exon3-exon5 of *Usp8-202* (ENSMUST00000110416.2) transcript is recommended as the knockout region. The region contains 427bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp8* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Embryos homozygous for a knock-out allele appear severely growth retarded and disorganized at E9.5 and die in utero due to ventral-folding defects.
- The knockout region is located in the intron 7-8 of *Usp50-203*, and the effect on *Usp50-203* is unknown.
- The *Usp8* gene is located on the Chr2. 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)

## Usp8 ubiquitin specific peptidase 8 [Mus musculus (house mouse)]

Gene ID: 84092, updated on 5-Mar-2019

### Summary



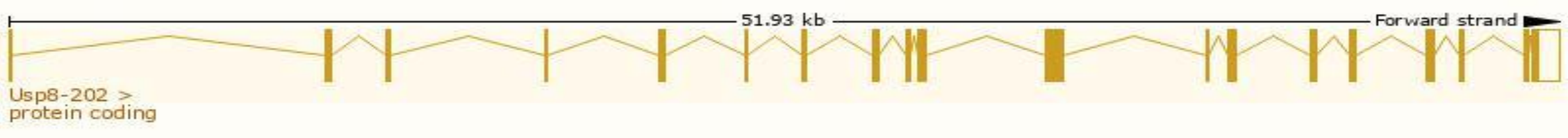
<b>Official Symbol</b>	Usp8 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ubiquitin specific peptidase 8 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1934029</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000027363</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AI574262, AW557536, Ubpy, mKIAA0055
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 45.2), bladder adult (RPKM 14.4) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

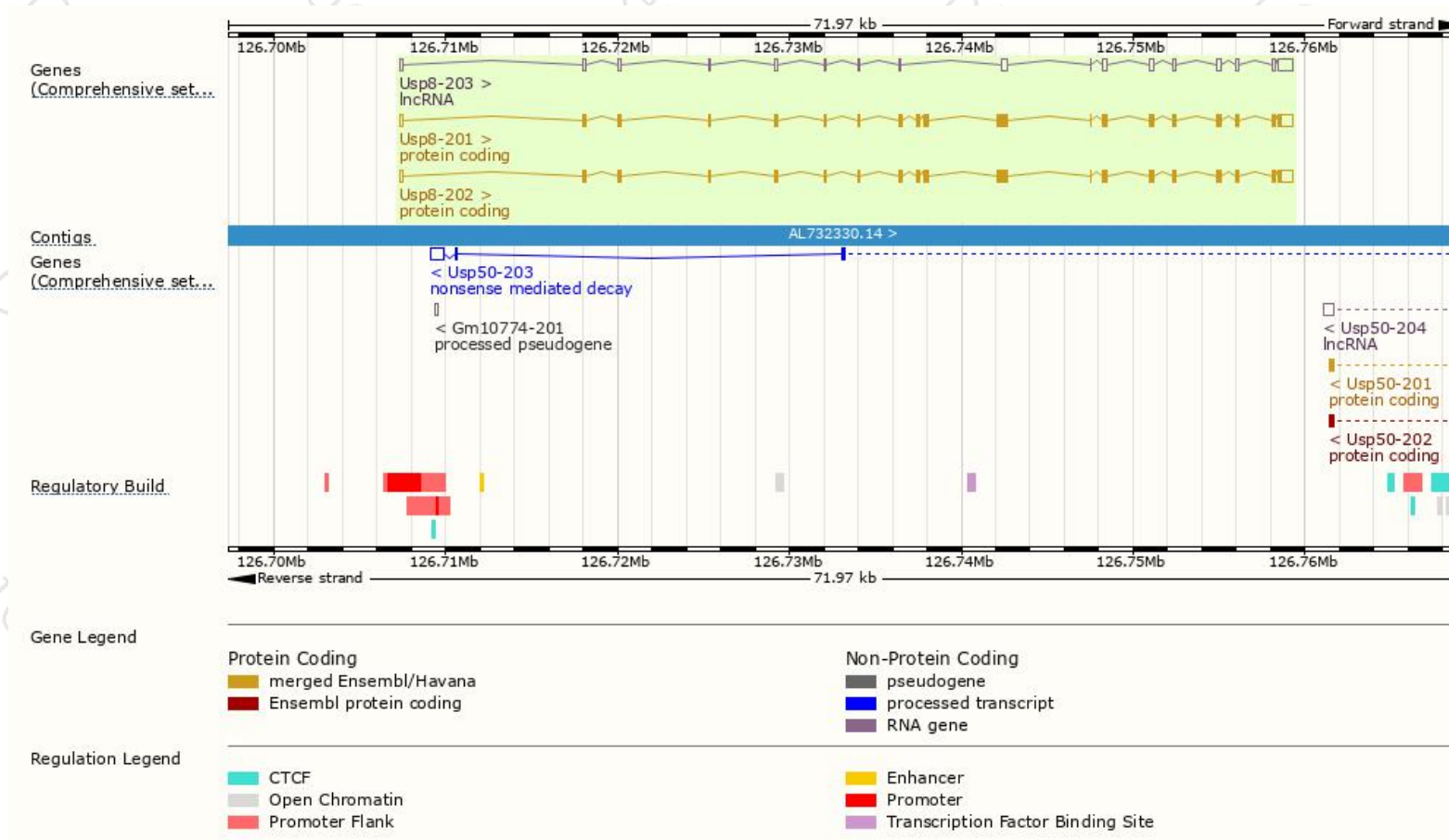
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp8-202	<a href="#">ENSMUST00000110416.2</a>	4154	<a href="#">1091aa</a>	Protein coding	<a href="#">CCDS57185</a>	<a href="#">A2AI52</a>	TSL:1 GENCODE basic APPRIS ALT2
Usp8-201	<a href="#">ENSMUST00000028841.13</a>	4145	<a href="#">1080aa</a>	Protein coding	<a href="#">CCDS16687</a>	<a href="#">Q80U87</a>	TSL:1 GENCODE basic APPRIS P3
Usp8-203	<a href="#">ENSMUST00000138859.1</a>	3463	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Usp8-202* transcript,The transcription is shown below

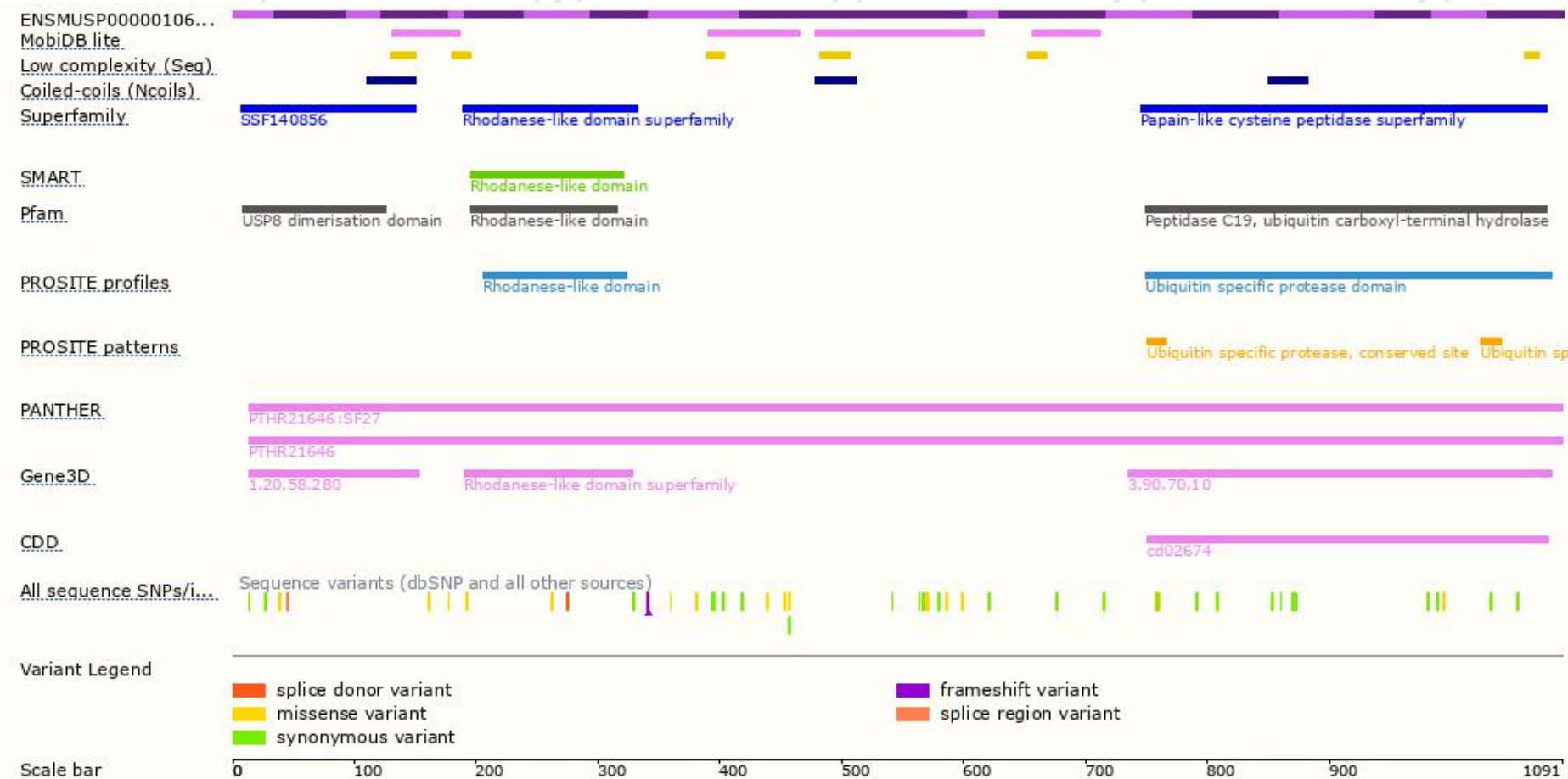


# Genomic location distribution

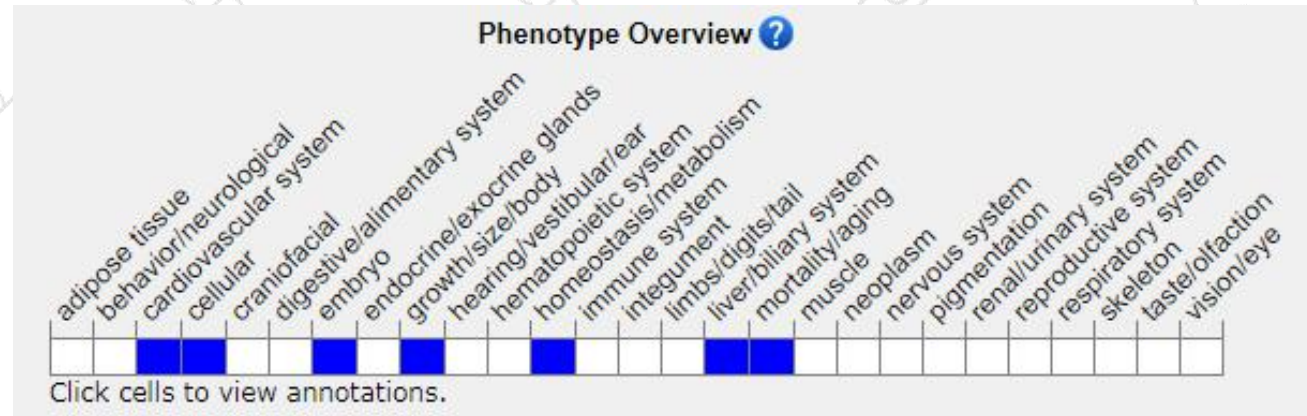




# Protein domain



# 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, Embryos homozygous for a knock-out allele appear severely growth retarded and disorganized at E9.5 and die in utero due to ventral-folding defects.

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

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