

Usp7 Cas9-KO Strategy

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Design Date: 2018/5/31

Project Overview



Project Name Usp7

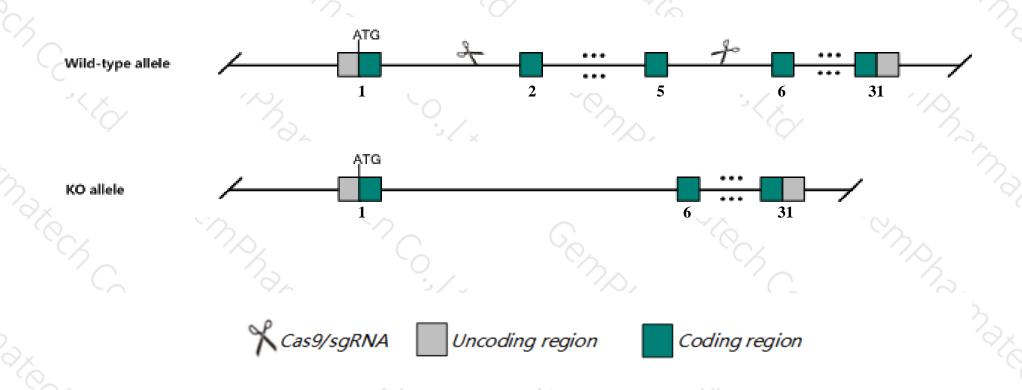
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Usp7* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Usp7* gene has 13 transcripts. According to the structure of *Usp7* gene, exon2-exon5 of *Usp7-208*(ENSMUST00000161046.8) transcript is recommended as the knockout region. The region contains 532bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Usp7* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice



- ➤ According to the existing MGI data, Mice homozygous for a null allele show embryonic growth arrest and die between E6.5 and E7.5. Mice homozygous for a conditional allele activated in neural cells exhibit complete neonatal lethality, absent gastric milk, uncoordinated movement and abnormalforebrain morphology.
- ➤ The *Usp7* gene is located on the Chr16. 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)



Usp7 ubiquitin specific peptidase 7 [Mus musculus (house mouse)]

Gene ID: 252870, updated on 12-Aug-2019

Summary

| ↑ | ?

Official Symbol Usp7 provided by MGI

Official Full Name ubiquitin specific peptidase 7 provided by MGI

Primary source MGI:MGI:2182061

See related Ensembl:ENSMUSG00000022710

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 Hausp; C80752; AA409944; AA617399; AU019296; AW548146; 2210010009Rik

Expression Ubiquitous expression in CNS E11.5 (RPKM 25.2), liver E14 (RPKM 24.8) and 28 other tissues See more

Orthologs human all

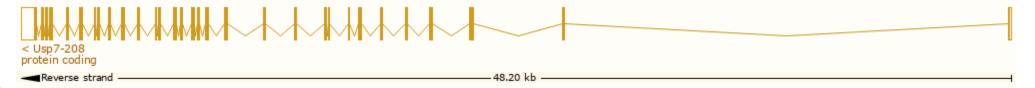
Transcript information (Ensembl)



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

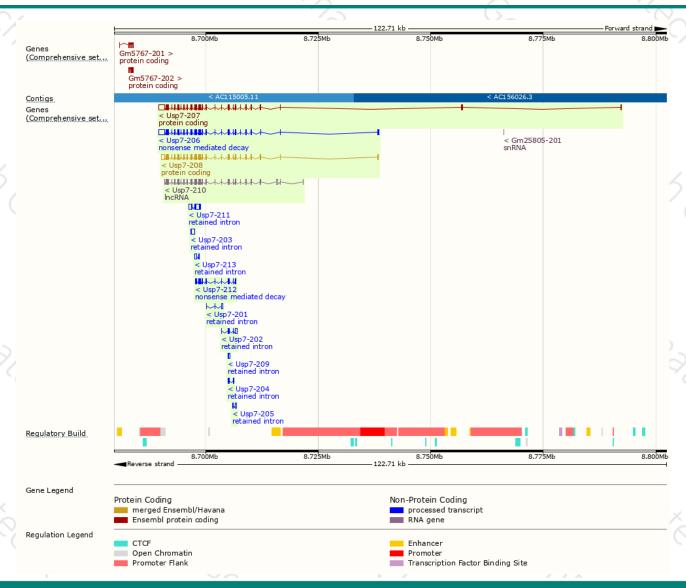
Name 🍦	Transcript ID	bp 🍦	Protein 🍦	Biotype	CCDS 🍦	UniProt 🍦	Flags
Usp7-208	ENSMUST00000161046.8	4003	<u>1103aa</u>	Protein coding	CCDS49755 ₽	F8VPX1₽	TSL:1 GENCODE basic APPRIS P2
Usp7-207	ENSMUST00000160405.7	4745	<u>1143aa</u>	Protein coding	-	E9PXY8 ₽	TSL:5 GENCODE basic APPRIS ALT2
Usp7-206	ENSMUST00000160326.7	4488	<u>92aa</u>	Nonsense mediated decay	-	E0CY04@	TSL:1
Usp7-212	ENSMUST00000172505.1	1225	<u>327aa</u>	Nonsense mediated decay	-	G3UWR8₽	CDS 5' incomplete TSL:5
Usp7-211	ENSMUST00000162929.1	1572	No protein	Retained intron	-	-	TSL:1
Usp7-203	ENSMUST00000159387.1	823	No protein	Retained intron	-	-	TSL:3
Usp7-202	ENSMUST00000159287.7	637	No protein	Retained intron	-	-	TSL:3
Usp7-213	ENSMUST00000173939.1	600	No protein	Retained intron	-	-	TSL:3
Usp7-201	ENSMUST00000159281.1	474	No protein	Retained intron	-	-	TSL:3
Usp7-205	ENSMUST00000159509.1	411	No protein	Retained intron	-	-	TSL:3
Usp7-204	ENSMUST00000159503.1	280	No protein	Retained intron	-	-	TSL:5
Usp7-209	ENSMUST00000162141.1	280	No protein	Retained intron	-	-	TSL:3
Usp7-210	ENSMUST00000162445.8	3447	No protein	IncRNA	-	-	TSL:5

The strategy is based on the design of *Usp7-208* transcript, The transcription is shown below



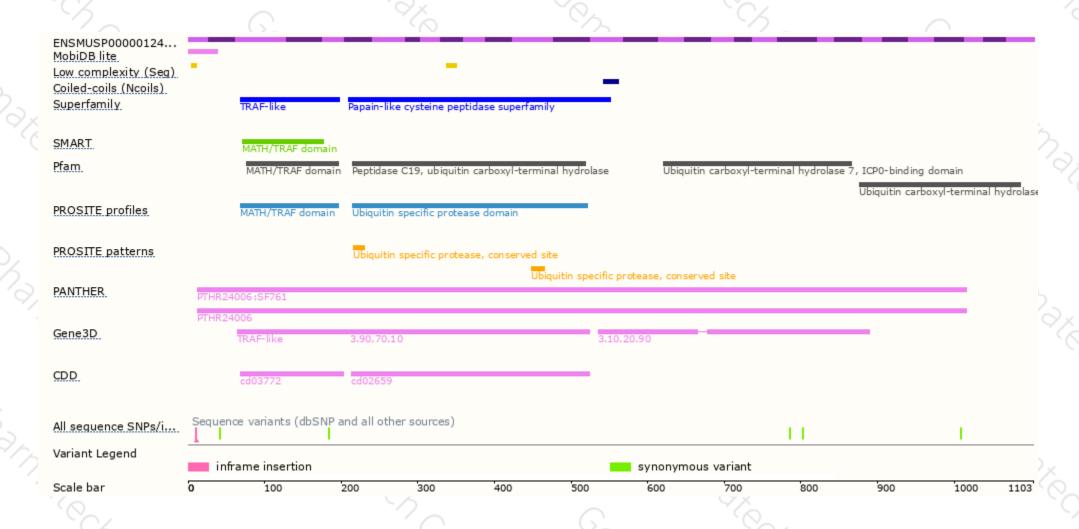
Genomic location distribution





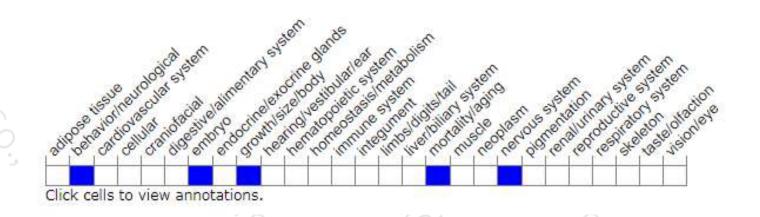
Protein domain





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 show embryonic growth arrest and die between E6.5 and E7.5. Mice homozygous for a conditional allele activated in neural cells exhibit complete neonatal lethality, absent gastric milk, uncoordinated movement and abnormal forebrain morphology.



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

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