

Usp15 Cas9-KO Strategy

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Project Overview

Project Name

Usp15

Project type

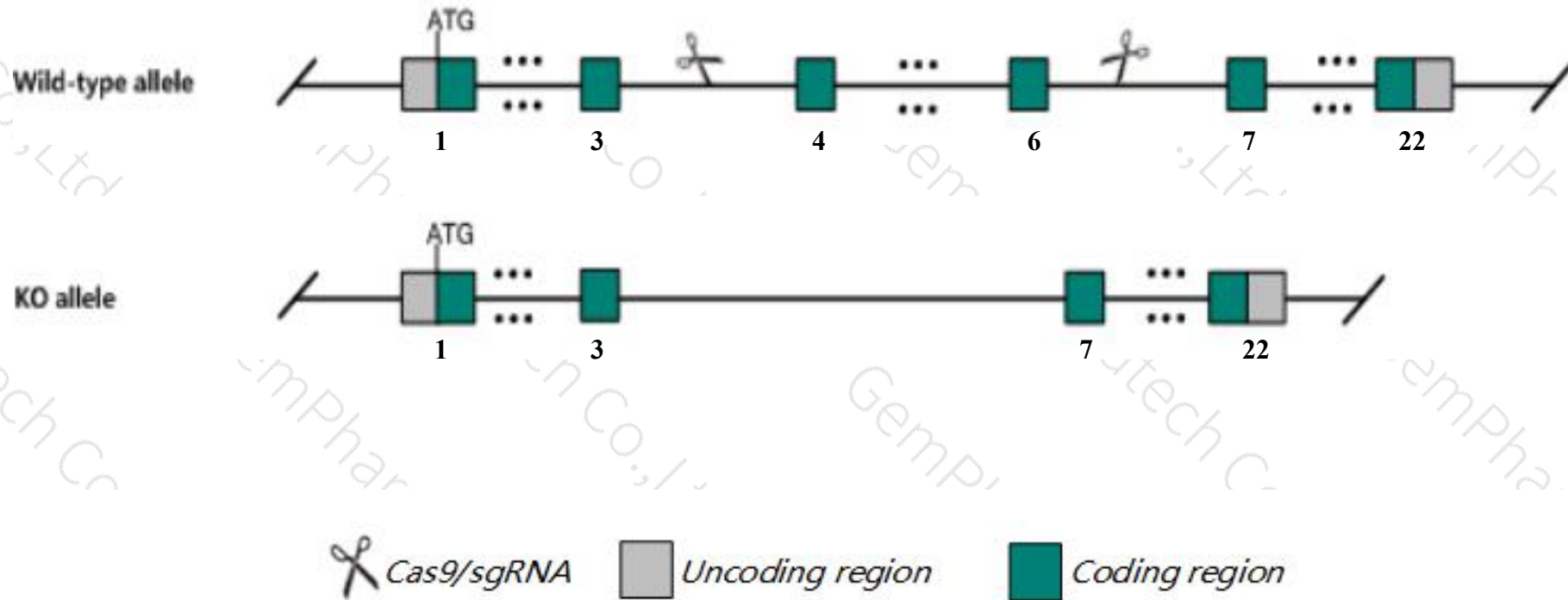
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp15* gene. The schematic diagram is as follows:



- The *Usp15* gene has 11 transcripts. According to the structure of *Usp15* gene, exon4-exon6 of *Usp15-211*(ENSMUST00000220377.1) transcript is recommended as the knockout region. The region contains 335bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp15* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele or ENU induced allele exhibit resistance to pathological neuroinflammation.
- The *Usp15* gene is located on the Chr10. 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)

Usp15 ubiquitin specific peptidase 15 [Mus musculus (house mouse)]

Gene ID: 14479, updated on 13-Mar-2020

Summary



Official Symbol Usp15 provided by [MGI](#)

Official Full Name ubiquitin specific peptidase 15 provided by [MGI](#)

Primary source [MGI:MGI:101857](#)

See related [Ensembl:ENSMUSG00000020124](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 4921514G19Rik, AI327321, E430033I05Rik, Gcap18

Summary The protein encoded by this gene is a member of the large ubiquitin specific protease (Usp) family of proteins. These proteins are known to cleave ubiquitin, and contain a conserved cysteine residue (Cys box) and two conserved histidine residues (His box) that are thought to form part of the active site of the protease. This protein has been shown to cleave both the ubiquitin-proline and the ubiquitin-methionine bonds in vitro. This protein is thought to regulate many cellular processes through its deubiquitination activity, including the transforming growth factor beta (TGF-beta) pathway. Cardiac-specific overexpression of the human ortholog of this gene in mice causes enlargement of the heart that is more pronounced in the atrium than in the ventricle. This gene has two pseudogenes on chromosome 14. Alternative splicing results in multiple transcript variants that encode multiple protein isoforms.[provided by RefSeq, Aug 2014]

Expression Ubiquitous expression in testis adult (RPKM 9.0), placenta adult (RPKM 8.8) and 26 other tissues [See more](#)

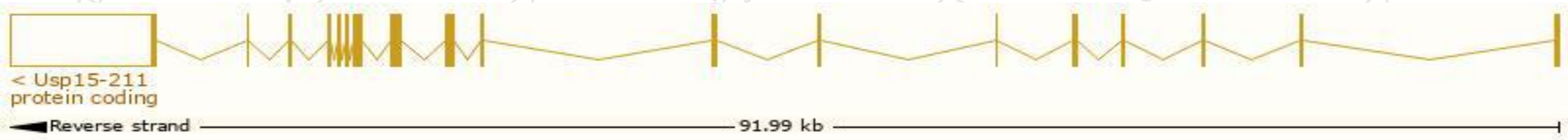
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

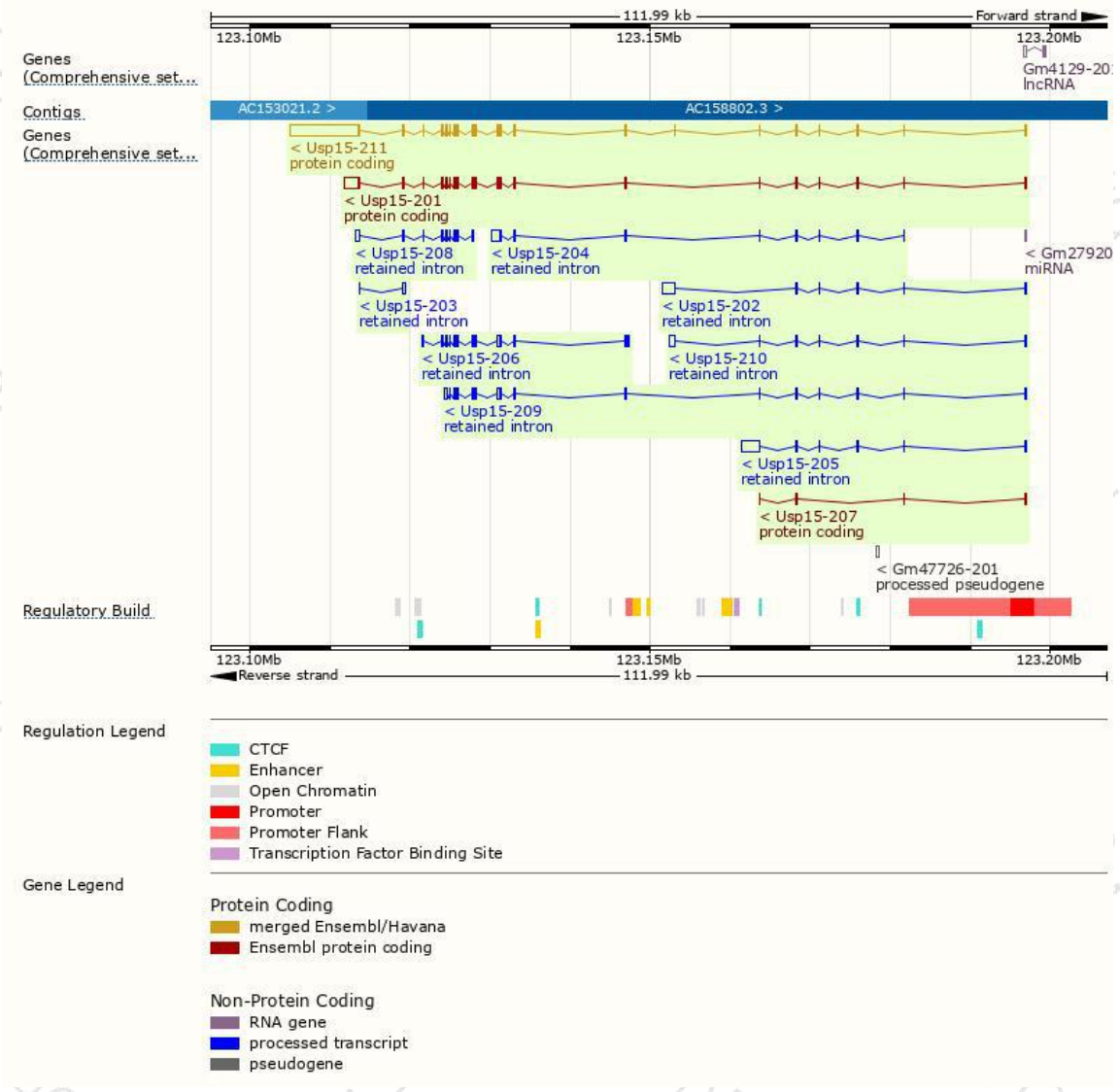
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp15-211	ENSMUST00000220377.1	11525	981aa	Protein coding	CCDS24217	Q8R5H1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Usp15-201	ENSMUST0000020334.8	4666	952aa	Protein coding	-	Q8R5H1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Usp15-207	ENSMUST00000219619.1	414	138aa	Protein coding	-	A0A1W2P8B7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Usp15-205	ENSMUST00000219010.1	2840	No protein	Retained intron	-	-	TSL:1
Usp15-209	ENSMUST00000219992.1	2603	No protein	Retained intron	-	-	TSL:2
Usp15-202	ENSMUST00000217985.1	2243	No protein	Retained intron	-	-	TSL:2
Usp15-206	ENSMUST00000219413.1	2074	No protein	Retained intron	-	-	TSL:2
Usp15-204	ENSMUST00000218079.1	2013	No protein	Retained intron	-	-	TSL:2
Usp15-208	ENSMUST00000219937.1	1587	No protein	Retained intron	-	-	TSL:2
Usp15-210	ENSMUST00000220284.1	1477	No protein	Retained intron	-	-	TSL:2
Usp15-203	ENSMUST00000218042.1	443	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Usp15-211* transcript,the transcription is shown below:



Genomic location distribution



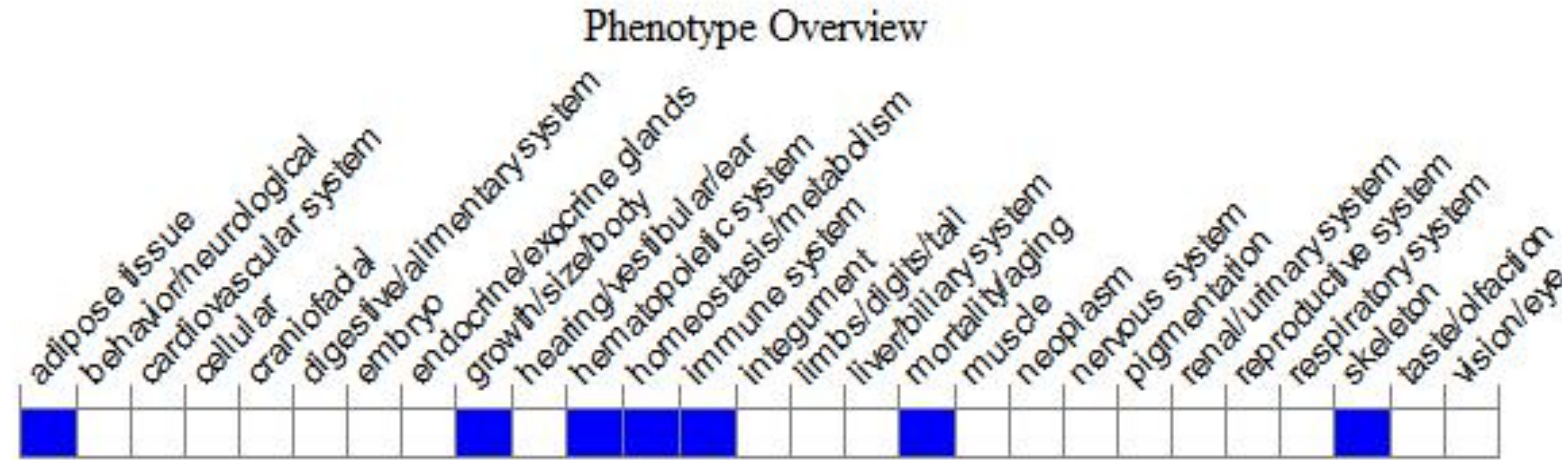
Protein domain



集萃药康
GemPharmatech



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 knock-out allele or ENU induced allele exhibit resistance to pathological neuroinflammation.

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

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