

Usp21 Cas9-CKO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Usp21

Project type

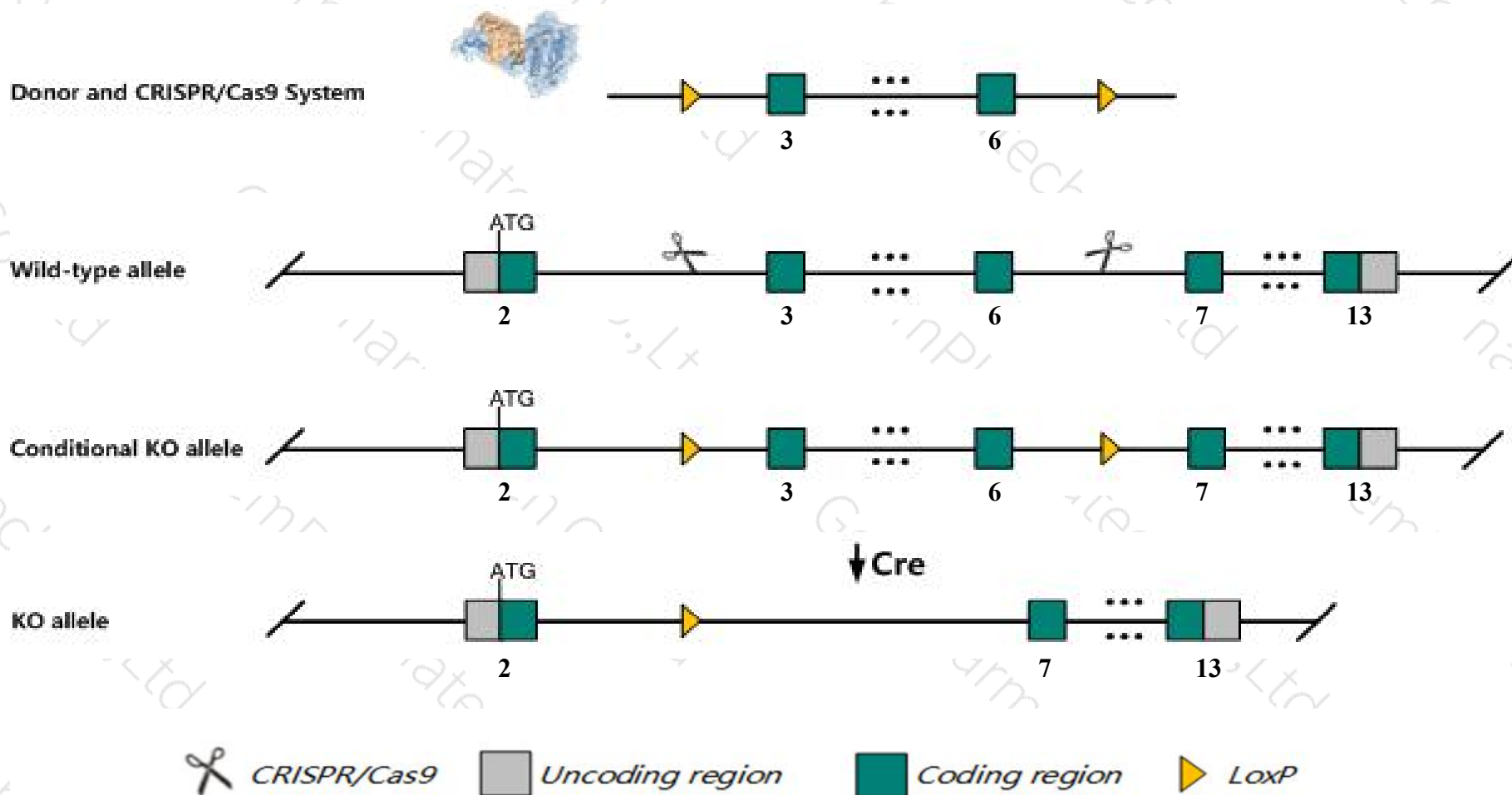
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp21* gene. The schematic diagram is as follows:



- The *Usp21* gene has 12 transcripts. According to the structure of *Usp21* gene, exon3-exon6 of *Usp21-201* (ENSMUST00000065941.11) transcript is recommended as the knockout region. The region contains 452bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp21* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

- According to the existing MGI data, Mice homozygous for a null allele are viable and fertile but develop splenomegaly, show an increased percentage of macrophages and neutrophils in spleen, and are more resistant to vesicular stomatitis virus (VSV) infection with elevated interferon production.
- The *Usp21* gene is located on the Chr1. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Usp21 ubiquitin specific peptidase 21 [Mus musculus (house mouse)]

Gene ID: 30941, updated on 7-Apr-2019

Summary



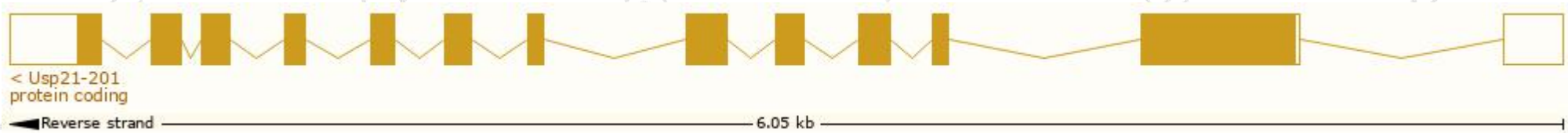
Official Symbol	Usp21 provided by MGI
Official Full Name	ubiquitin specific peptidase 21 provided by MGI
Primary source	MGI:MGI:1353665
See related	Ensembl:ENSMUSG00000053483
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ESTM28, Usp16, Usp23, W53272
Expression	Ubiquitous expression in limb E14.5 (RPKM 28.1), CNS E14 (RPKM 27.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

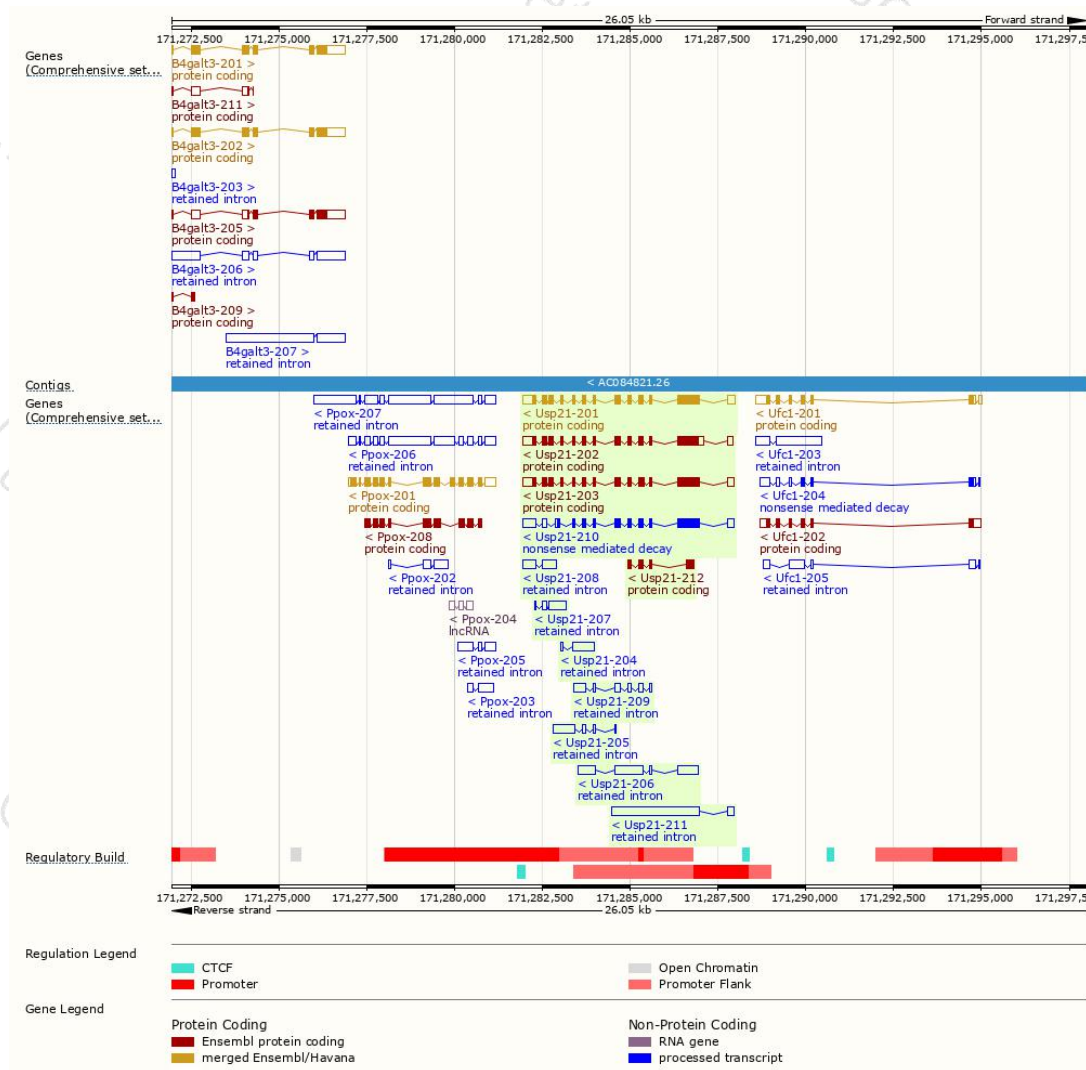
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp21-202	ENSMUST00000111305.7	2278	566aa	Protein coding	CCDS35774	E9PUE2	TSL:5 GENCODE basic APPRIS P2
Usp21-201	ENSMUST00000065941.11	2219	566aa	Protein coding	CCDS35774	E9PUE2	TSL:1 GENCODE basic APPRIS P2
Usp21-203	ENSMUST00000111306.9	2185	569aa	Protein coding	-	A0A0R4J1F5	TSL:1 GENCODE basic APPRIS ALT 1
Usp21-212	ENSMUST00000174720.1	484	162aa	Protein coding	-	G3UWN7	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
Usp21-210	ENSMUST00000149187.7	2091	451aa	Nonsense mediated decay	-	D6RJJ7	TSL:2
Usp21-211	ENSMUST00000153164.1	2706	No protein	Retained intron	-	-	TSL:1
Usp21-206	ENSMUST00000127101.1	1966	No protein	Retained intron	-	-	TSL:1
Usp21-209	ENSMUST00000147176.1	864	No protein	Retained intron	-	-	TSL:2
Usp21-205	ENSMUST00000126729.7	822	No protein	Retained intron	-	-	TSL:5
Usp21-208	ENSMUST00000144393.7	755	No protein	Retained intron	-	-	TSL:1
Usp21-204	ENSMUST00000126557.1	695	No protein	Retained intron	-	-	TSL:3
Usp21-207	ENSMUST00000142656.1	598	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Usp21-201* transcript,The transcription is shown below



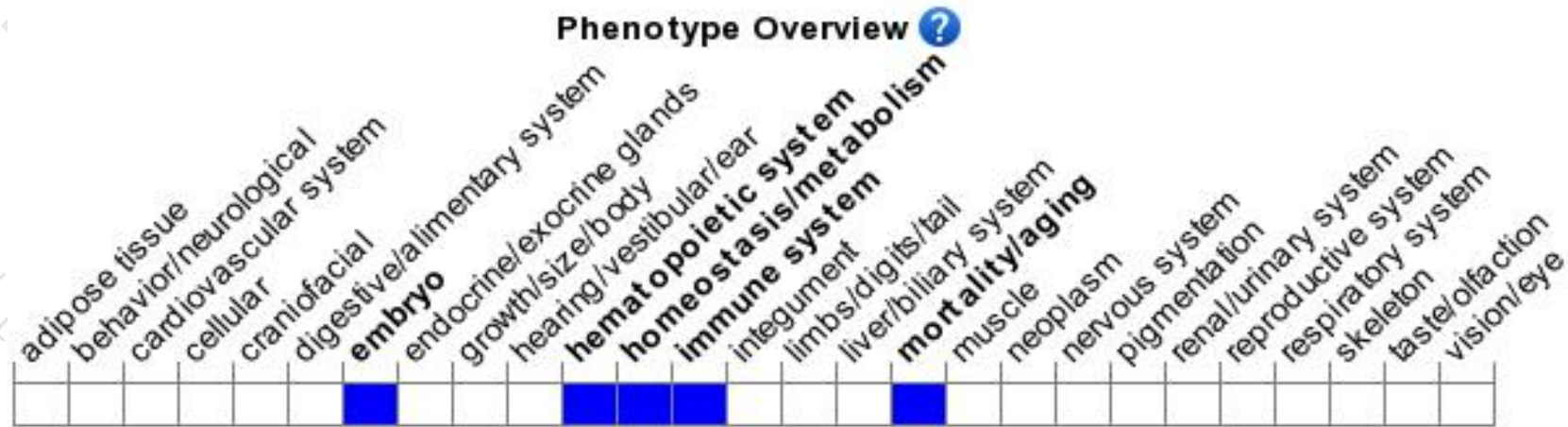
Genomic location distribution



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 are viable and fertile but develop splenomegaly, show an increased percentage of macrophages and neutrophils in spleen, and are more resistant to vesicular stomatitis virus (VSV) infection with elevated interferon production.

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

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