Usp1 Cas9-KO Strategy

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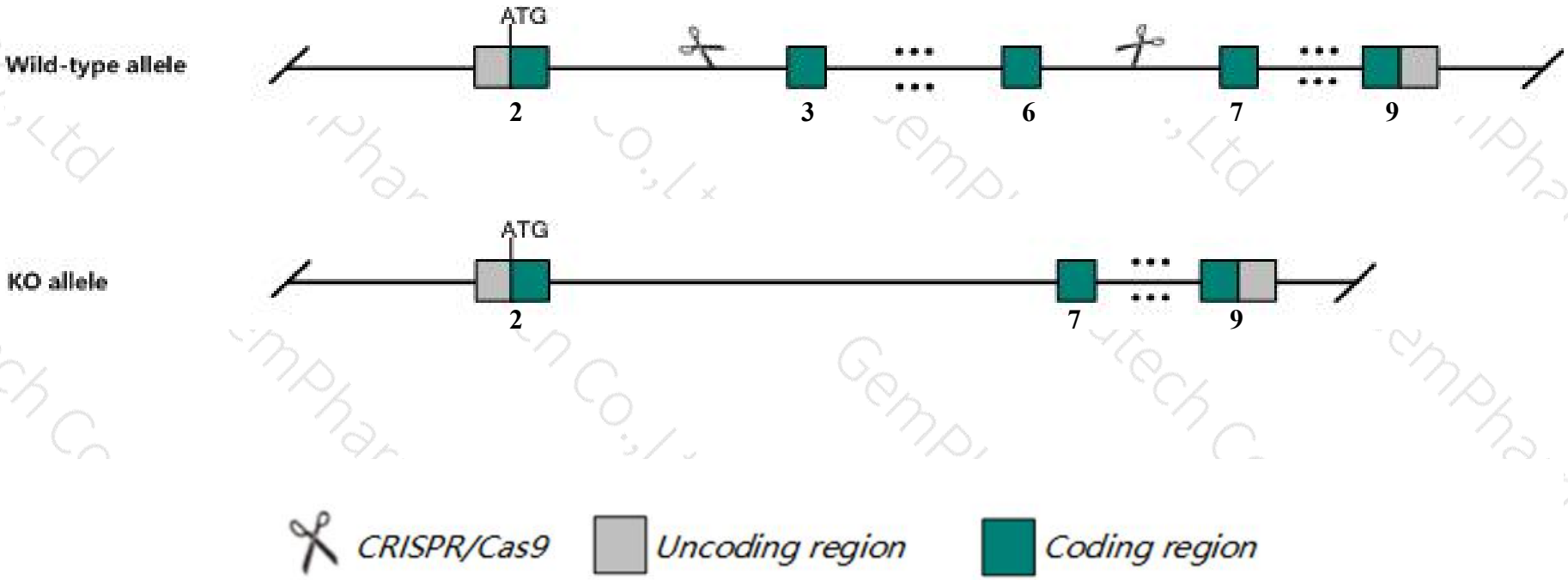
Project Overview

Project Name	***Usp1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Usp1* gene has 4 transcripts. According to the structure of *Usp1* gene, exon3-exon6 of *Usp1-201* (ENSMUST00000030289.8) transcript is recommended as the knockout region.The region contains 1076bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Usp1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous null mice have a high rate of postnatal lethality related to cyanosis. Male survivors are infertile while female survivors have reduced fertility. Both sexes have reduced number of gametes, are sensitive to ionizing radiation, and have decreased numbers of bone marrow cells.

- The *Usp1* gene is located on the Chr4. 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）

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Usp1 ubiquitin specific peptidase 1 [Mus musculus (house mouse)]

Gene ID: 230484, updated on 19-Mar-2019

Summary

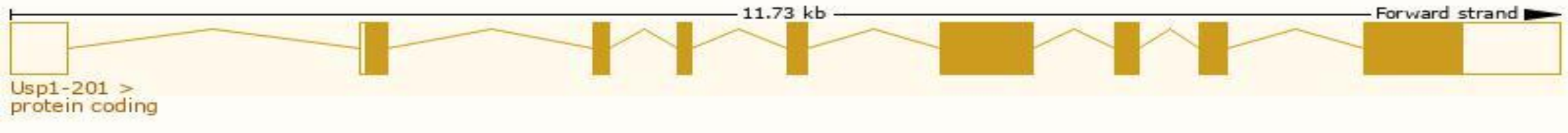
Official Symbol	Usp1 provided by MGI
Official Full Name	ubiquitin specific peptidase 1 provided by MGI
Primary source	MGI:MGI:2385198
See related	Ensembl:ENSMUSG00000028560
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes a member of the ubiquitin-specific peptidase family. The encoded protein acts as a catalytic subunit in a heterodimeric deubiquitinating enzyme complex that deubiquitinates Fanconi anemia, complementation group D2, and plays a role in homologous recombination-mediated DNA repair. Disruption of this gene is associated with a Fanconi anemia-like phenotype and genomic instability. Alternative splicing results in multiple transcript variants. Pseudogenes of this gene have been defined on chromosomes 3, 12, and 15. [provided by RefSeq, Aug 2014]
Expression	Ubiquitous expression in testis adult (RPKM 27.3), CNS E11.5 (RPKM 23.4) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

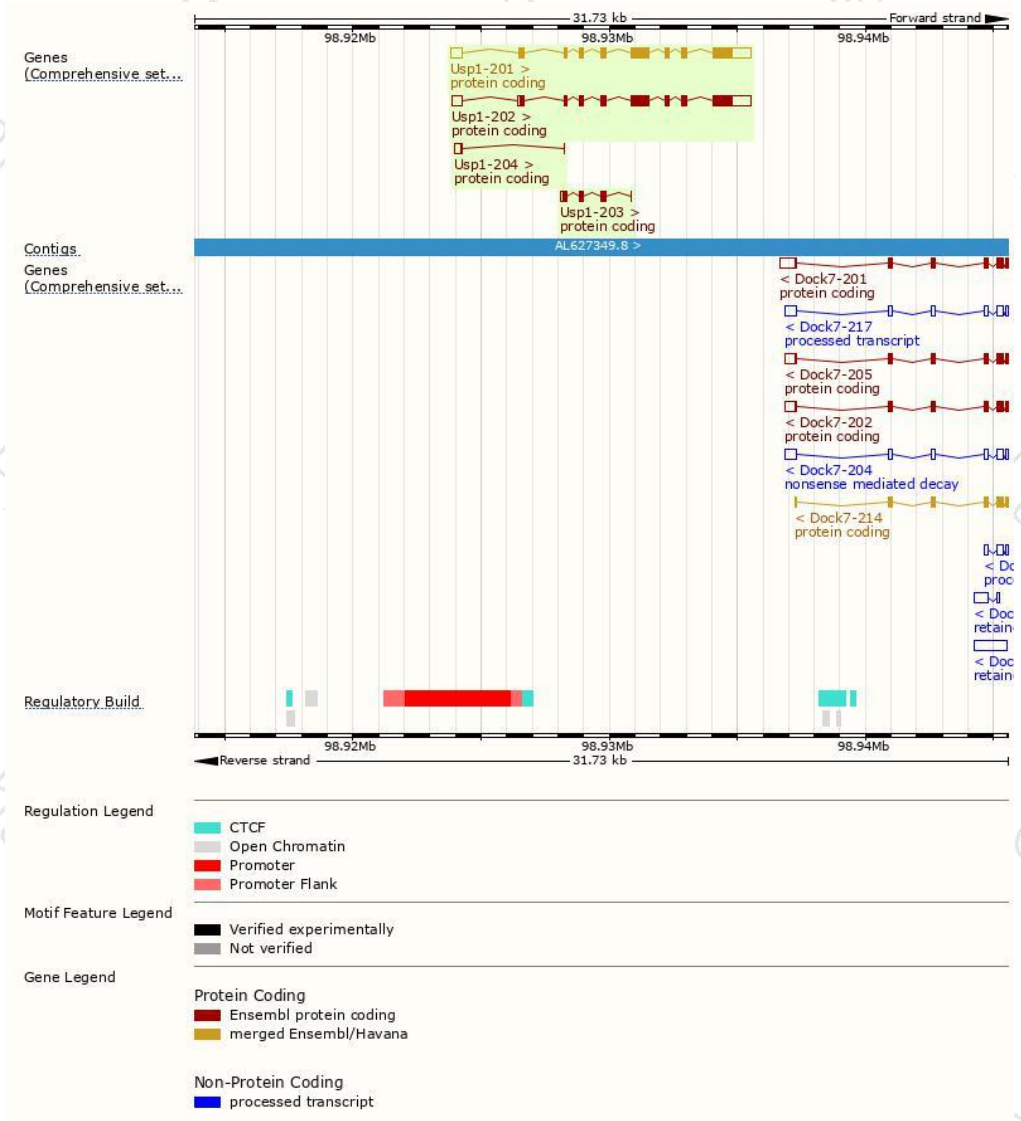
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp1-201	ENSMUST00000030289.8	3577	784aa	Protein coding	CCDS18381	Q8BJQ2	TSL:1 GENCODE basic APPRIS P1
Usp1-202	ENSMUST00000091358.10	3527	784aa	Protein coding	CCDS18381	Q8BJQ2	TSL:1 GENCODE basic APPRIS P1
Usp1-203	ENSMUST00000125104.1	546	150aa	Protein coding	-	H3BKR6	CDS 3' incomplete TSL:2
Usp1-204	ENSMUST00000169053.1	317	15aa	Protein coding	-	E9Q778	CDS 3' incomplete TSL:5

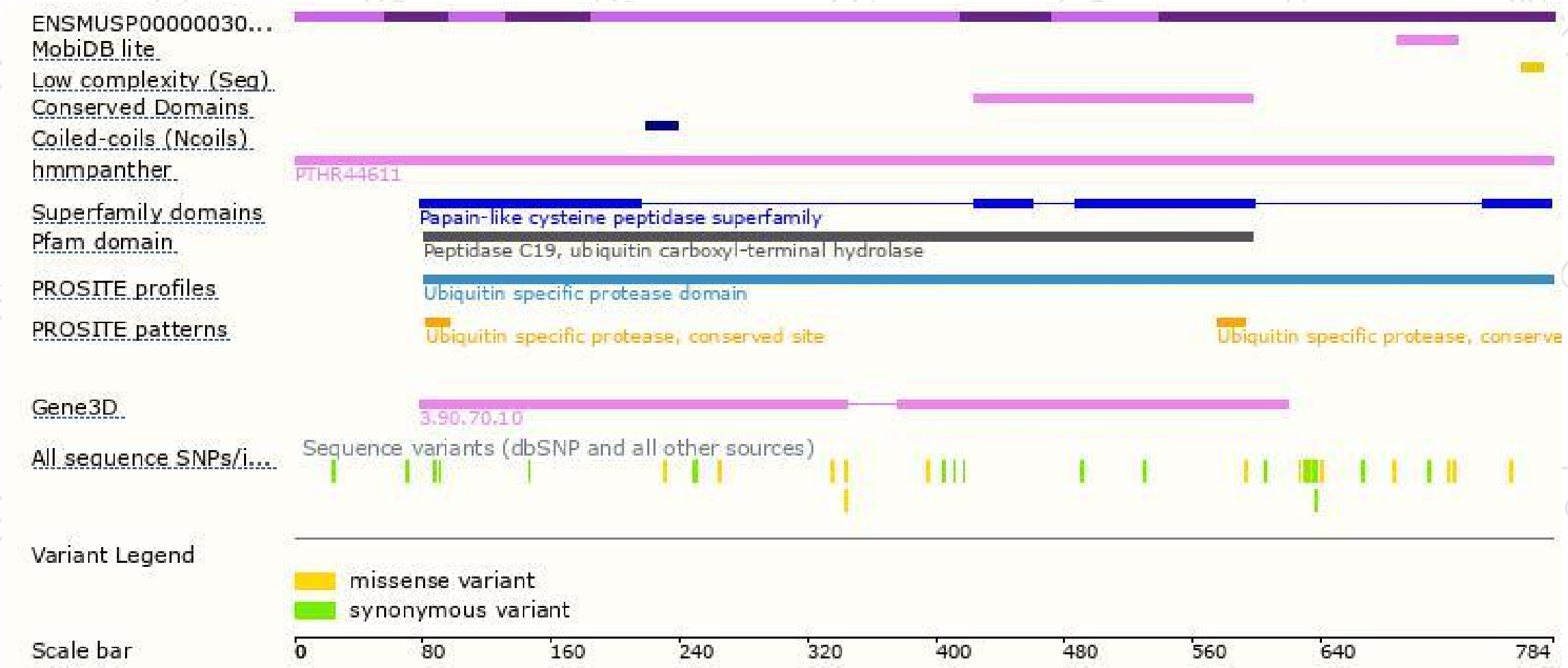
The strategy is based on the design of *Usp1-201* transcript,The transcription is shown below



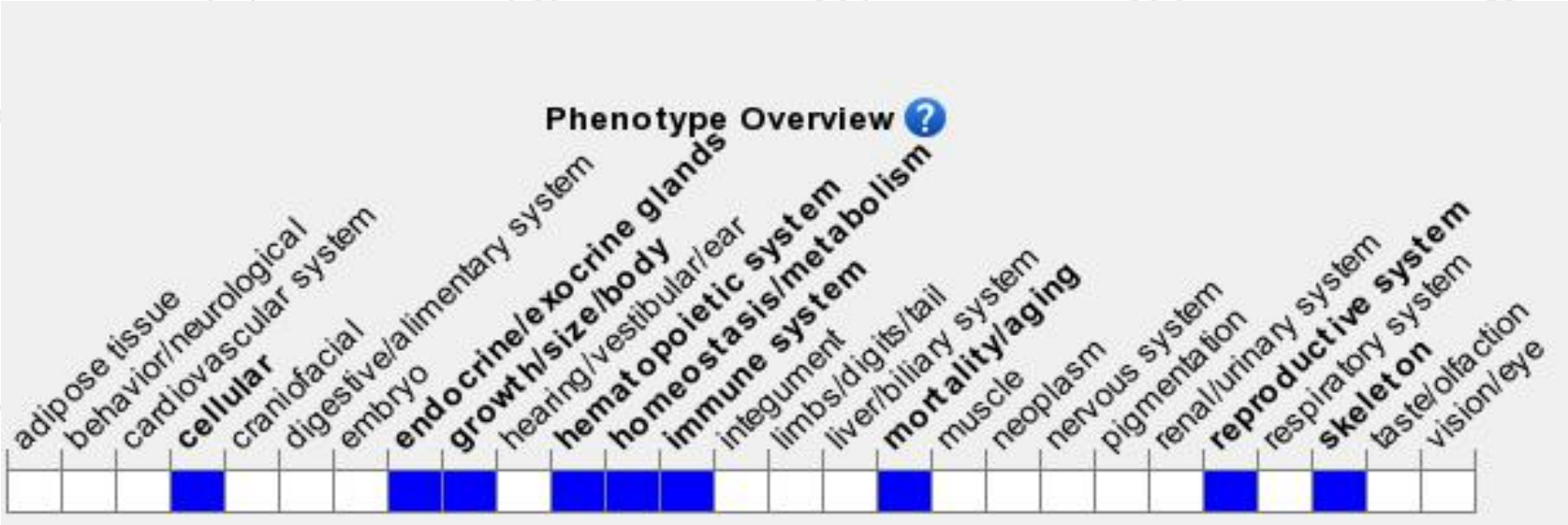
Genomic location distribution



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,Homozygous null mice have a high rate of postnatal lethality related to cyanosis. Male survivors are infertile while female survivors have reduced fertility. Both sexes have reduced number of gametes, are sensitive to ionizing radiation, and have decreased numbers of bone marrow cells.

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

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