

# *Usp25* Cas9-KO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Usp25*

**Project type**

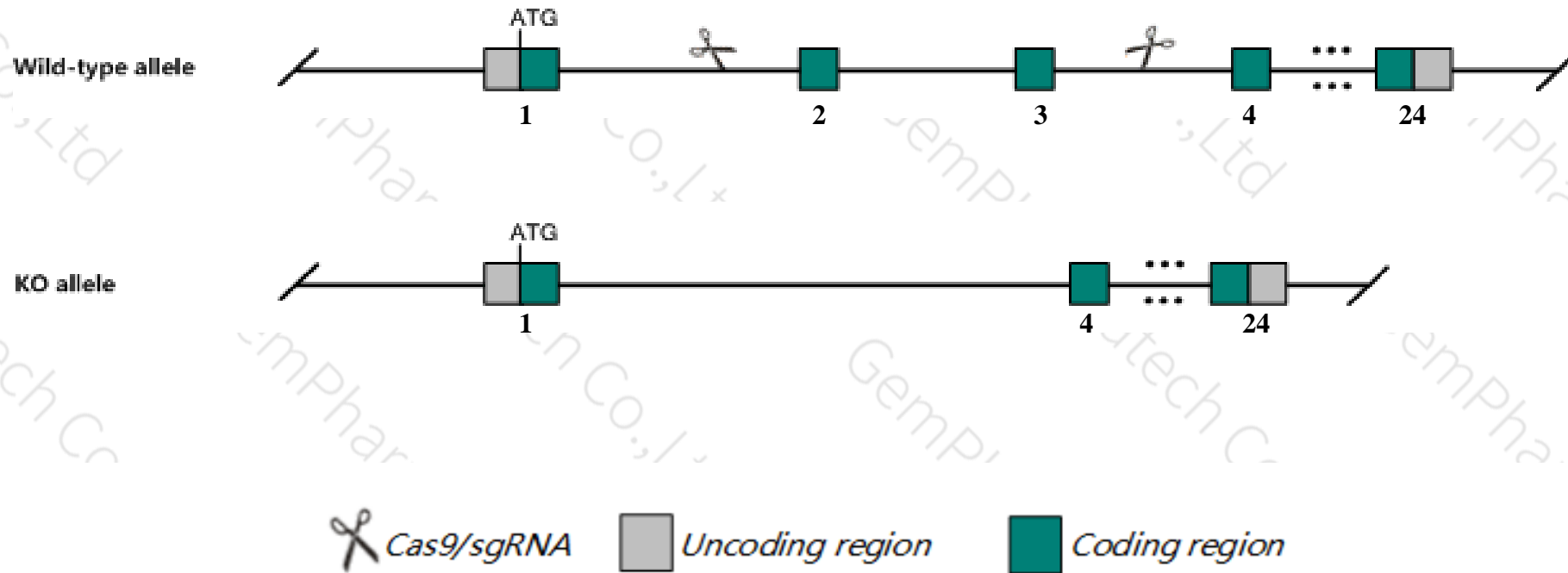
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp25* gene. The schematic diagram is as follows:



- The *Usp25* gene has 4 transcripts. According to the structure of *Usp25* gene, exon2-exon3 of *Usp25-201* (ENSMUST00000023580.7) transcript is recommended as the knockout region. The region contains 223bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp25* 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 gene trap allele exhibit increased severity of IL17-induced pulmonary inflammation and MOG-induced experimental autoimmune encephalomyelitis.
- The *Usp25* 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)

## Usp25 ubiquitin specific peptidase 25 [ *Mus musculus* (house mouse) ]

Gene ID: 30940, updated on 21-Aug-2019

### Summary

Official Symbol	Usp25 provided by <a href="#">MGI</a>
Official Full Name	ubiquitin specific peptidase 25 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1353655</a>
See related	<a href="#">Ensembl:ENSMUSG00000022867</a>
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in liver E14 (RPKM 19.3), liver E14.5 (RPKM 16.8) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

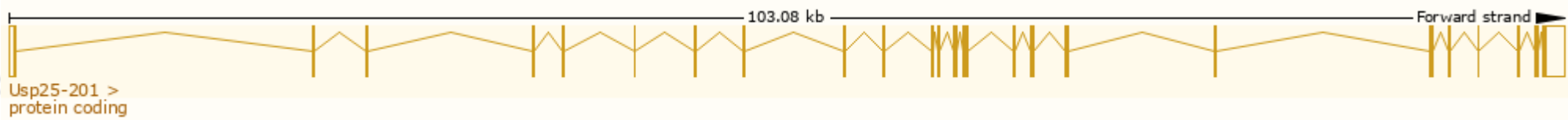


# Transcript information (Ensembl)

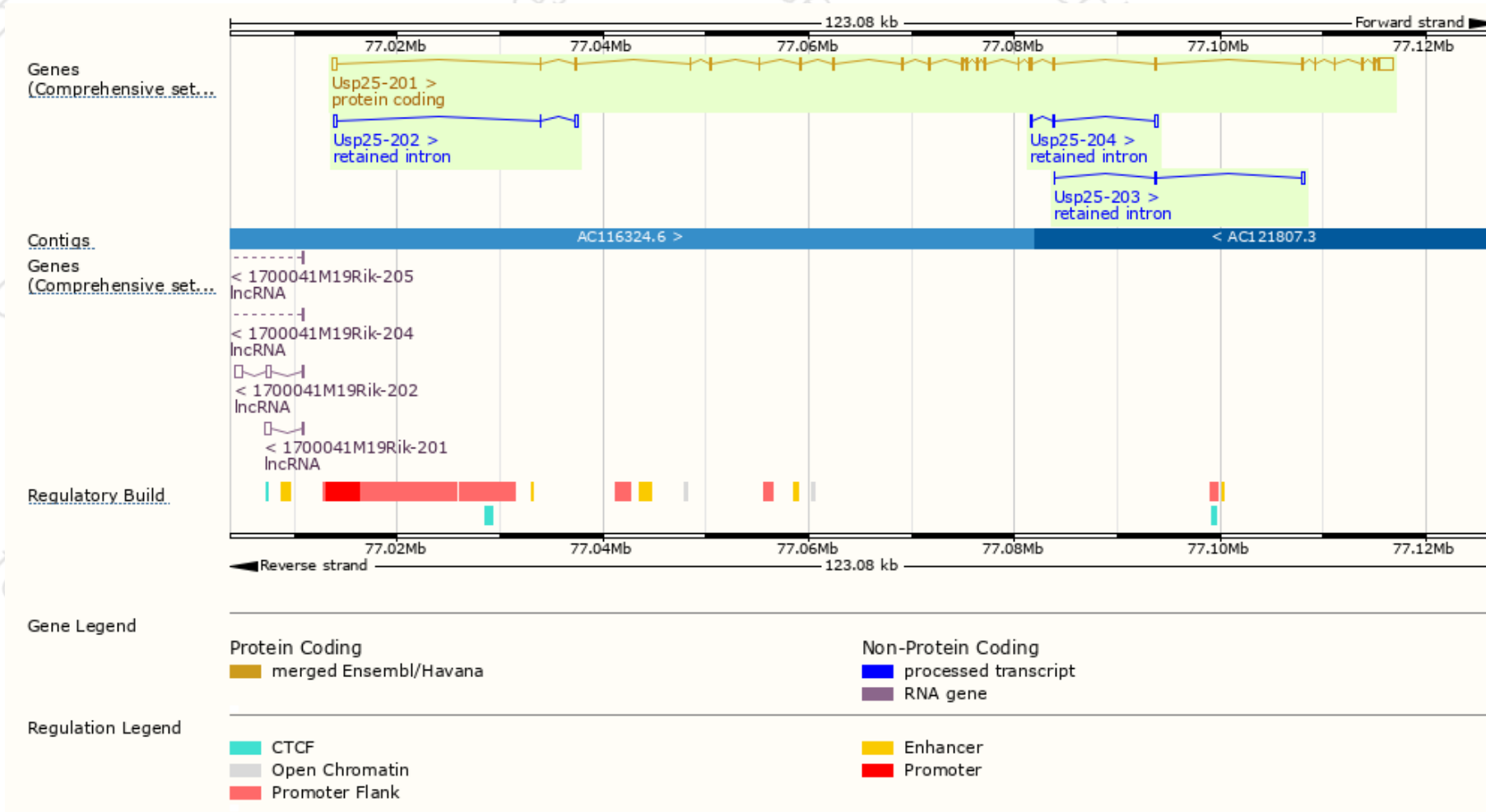
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp25-201	<a href="#">ENSMUST00000023580.7</a>	4776	<a href="#">1055aa</a>	Protein coding	<a href="#">CCDS28275</a>	<a href="#">P57080</a>	TSL:1 GENCODE basic APPRIS P1
Usp25-204	<a href="#">ENSMUST00000232538.1</a>	711	No protein	Retained intron	-	-	-
Usp25-202	<a href="#">ENSMUST00000232047.1</a>	674	No protein	Retained intron	-	-	-
Usp25-203	<a href="#">ENSMUST00000232351.1</a>	511	No protein	Retained intron	-	-	-

The strategy is based on the design of *Usp25-201* transcript,The transcription is shown below

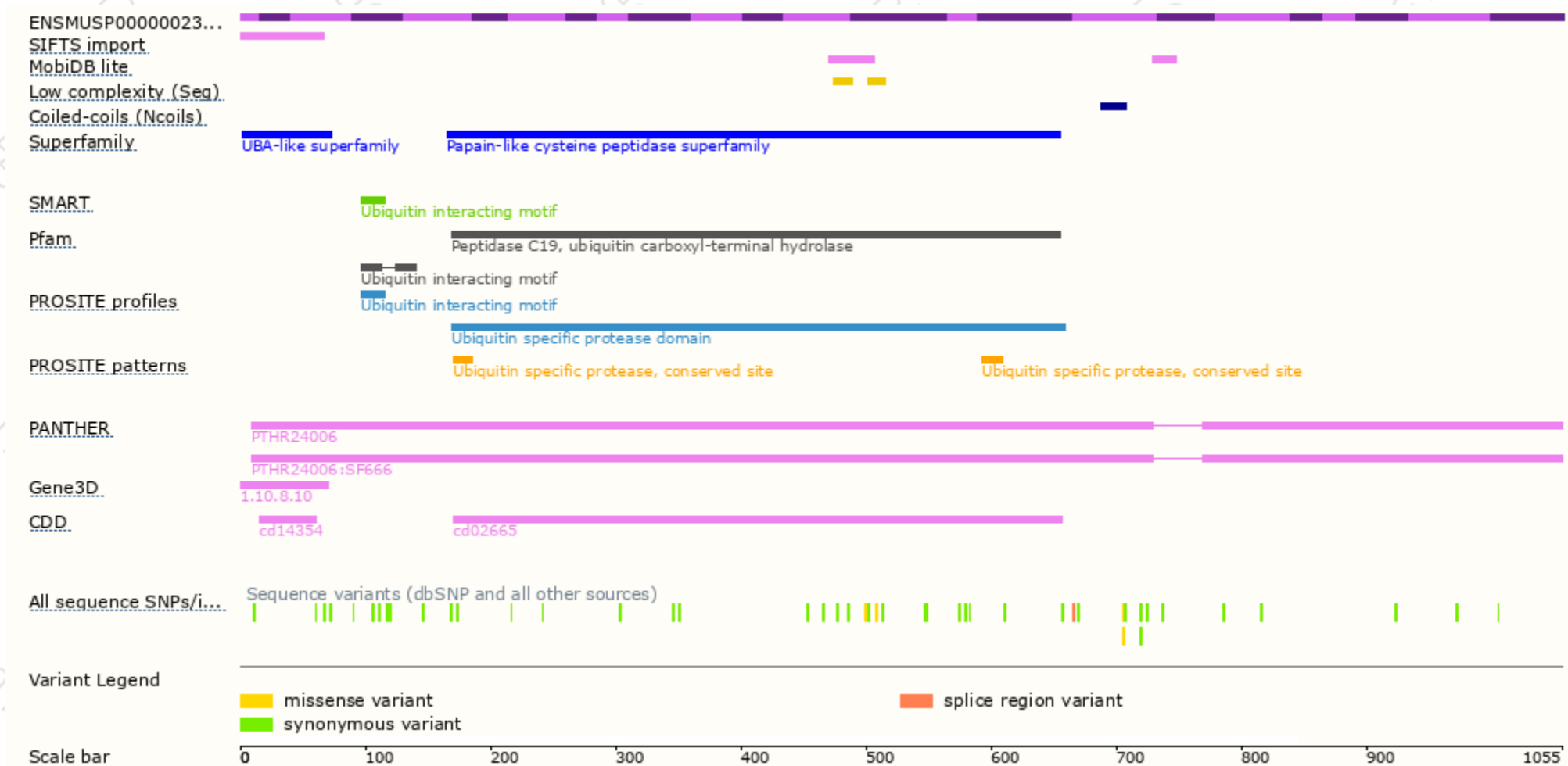


# Genomic location distribution

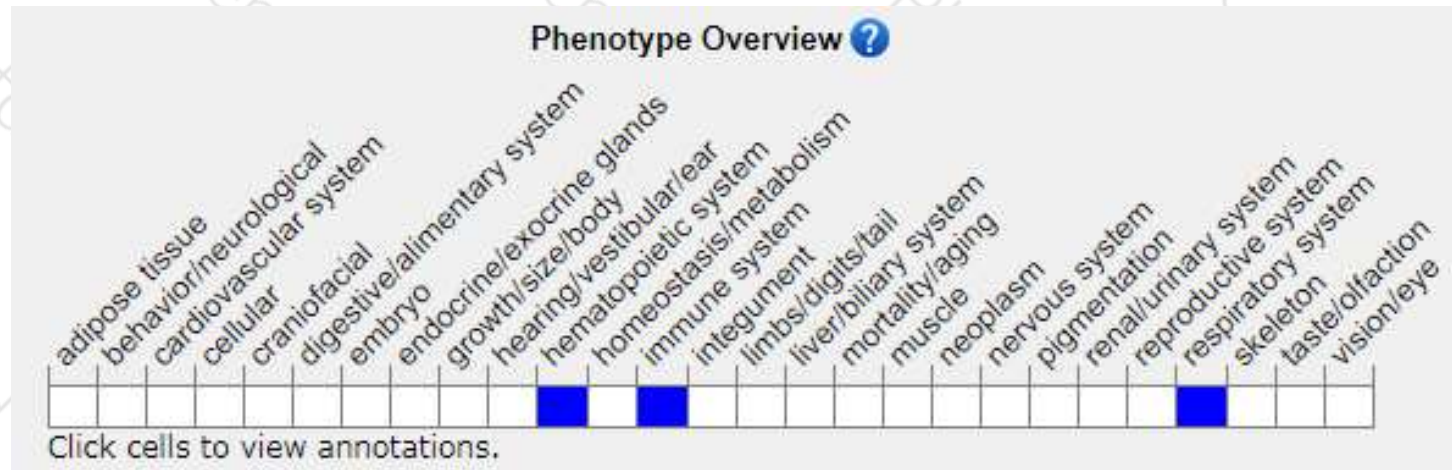




# Protein domain



# 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 gene trap allele exhibit increased severity of IL17-induced pulmonary inflammation and MOG-induced experimental autoimmune encephalomyelitis.

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

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