

Prss16 Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

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Project Overview

Project Name

Prss16

Project type

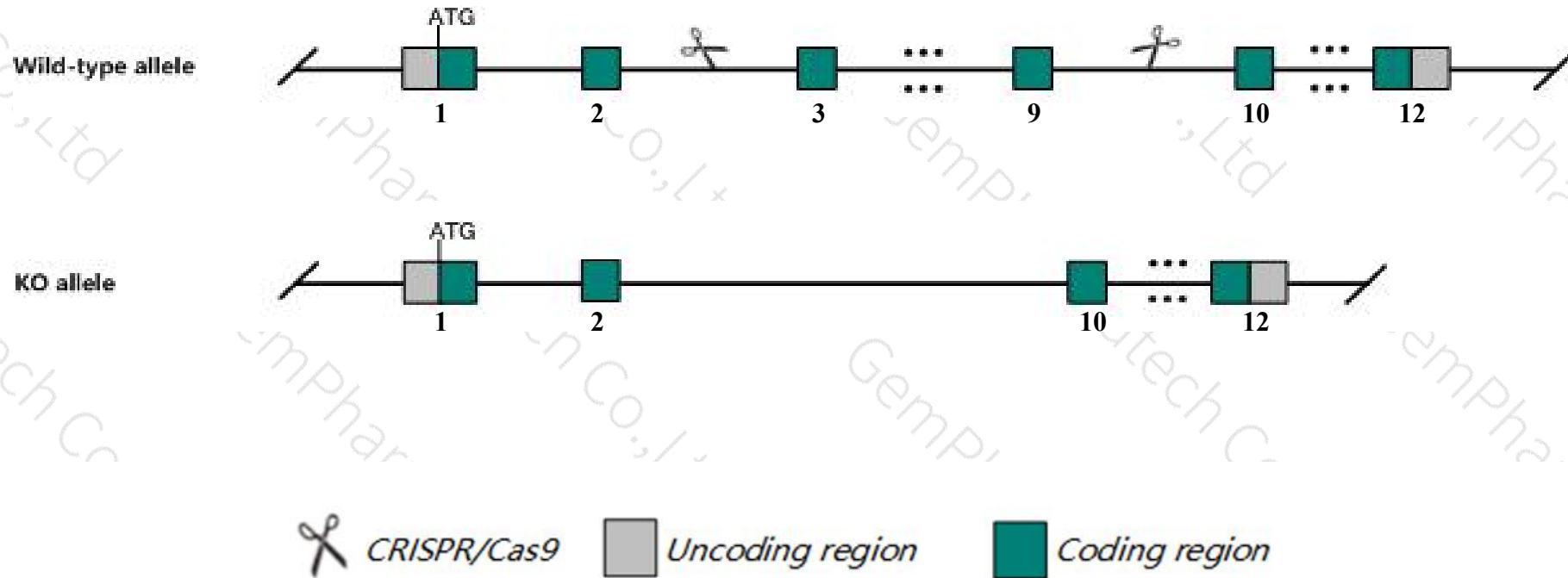
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prss16* gene. The schematic diagram is as follows:



- The *Prss16* gene has 5 transcripts. According to the structure of *Prss16* gene, exon3-exon9 of *Prss16-201* (ENSMUST00000006341.3) transcript is recommended as the knockout region. The region contains 913bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prss16* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice are viable with no gross abnormalities and normal T cell development and activation.
- The *Prss16* gene is located on the Chr13. 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)

Prss16 protease, serine 16 (thymus) [Mus musculus (house mouse)]

Gene ID: 54373, updated on 31-Jan-2019

Summary



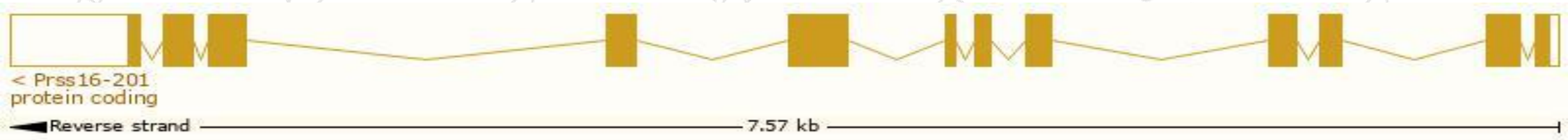
Official Symbol	Prss16 provided by MGI
Official Full Name	protease, serine 16 (thymus) provided by MGI
Primary source	MGI:MGI:1859181
See related	Ensembl:ENSMUSG00000006179
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI448615, TSSP
Expression	Restricted expression toward thymus adult (RPKM 217.8) See more
Orthologs	human all

Transcript information (Ensembl)

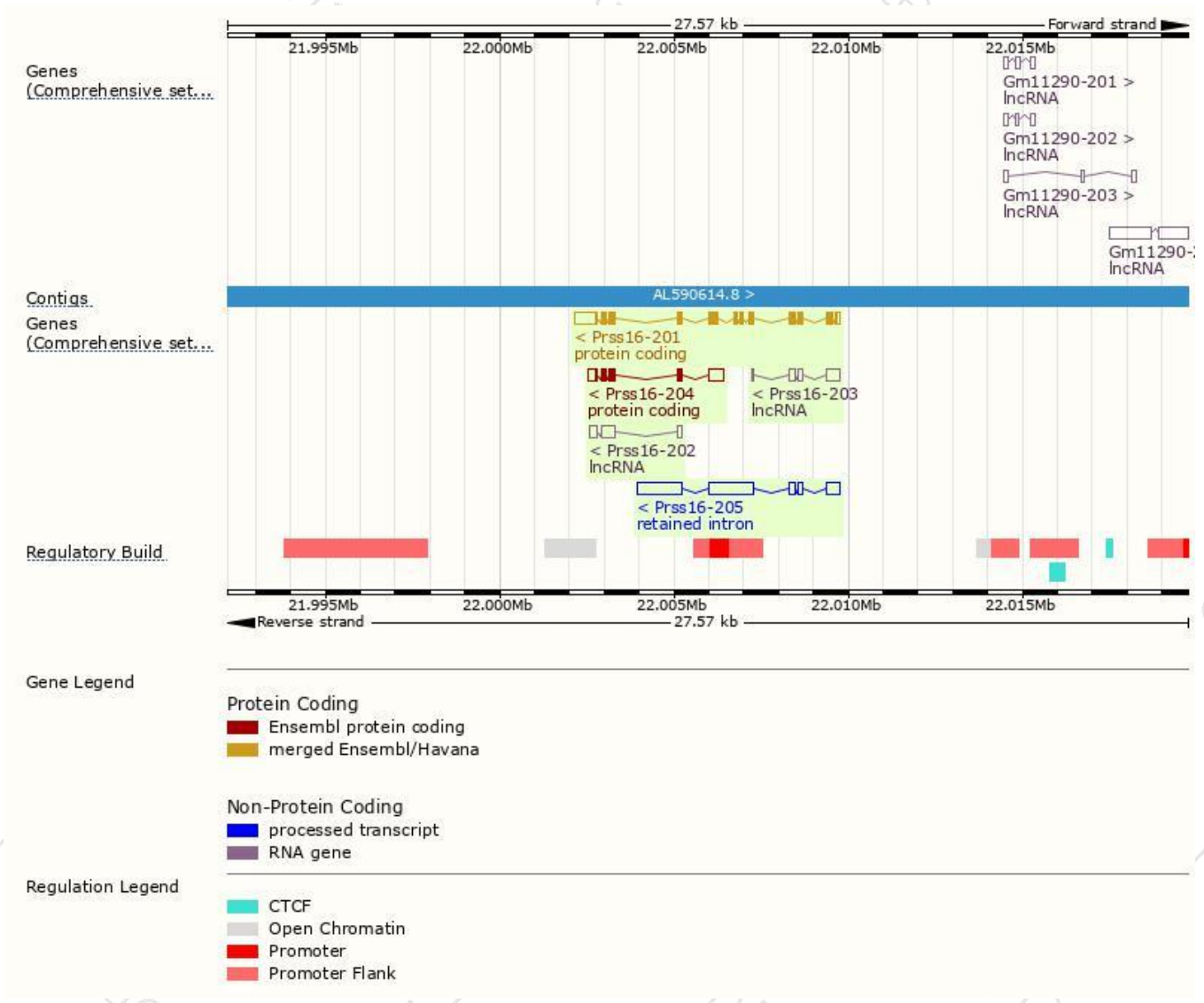
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prss16-201	ENSMUST00000006341.3	2155	509aa	Protein coding	CCDS26303	Q5SZ30 Q9QXE5	TSL:1 GENCODE basic APPRIS P1
Prss16-204	ENSMUST00000150547.2	1159	169aa	Protein coding	-	A0A286YCE6	TSL:3 GENCODE basic
Prss16-205	ENSMUST00000223857.1	3145	No protein	Retained intron	-	-	
Prss16-202	ENSMUST00000129665.7	783	No protein	lncRNA	-	-	TSL:3
Prss16-203	ENSMUST00000130585.1	618	No protein	lncRNA	-	-	TSL:3

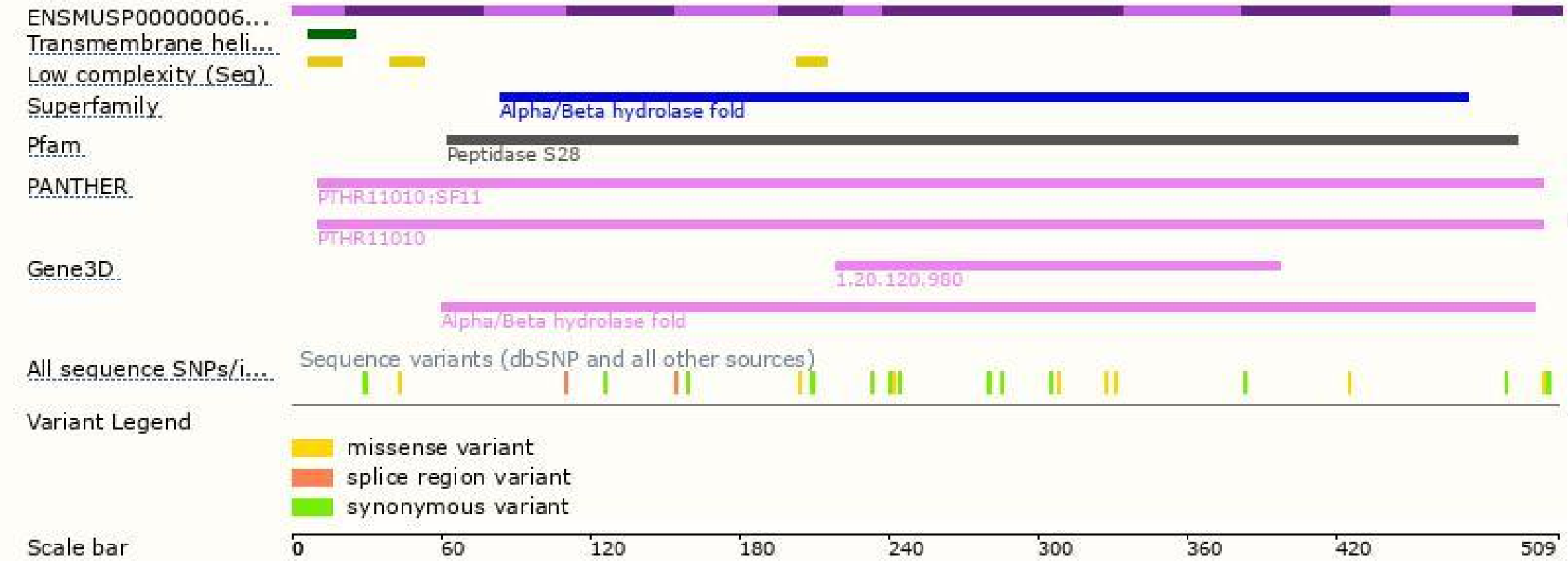
The strategy is based on the design of *Prss16-201* transcript,The transcription is shown below



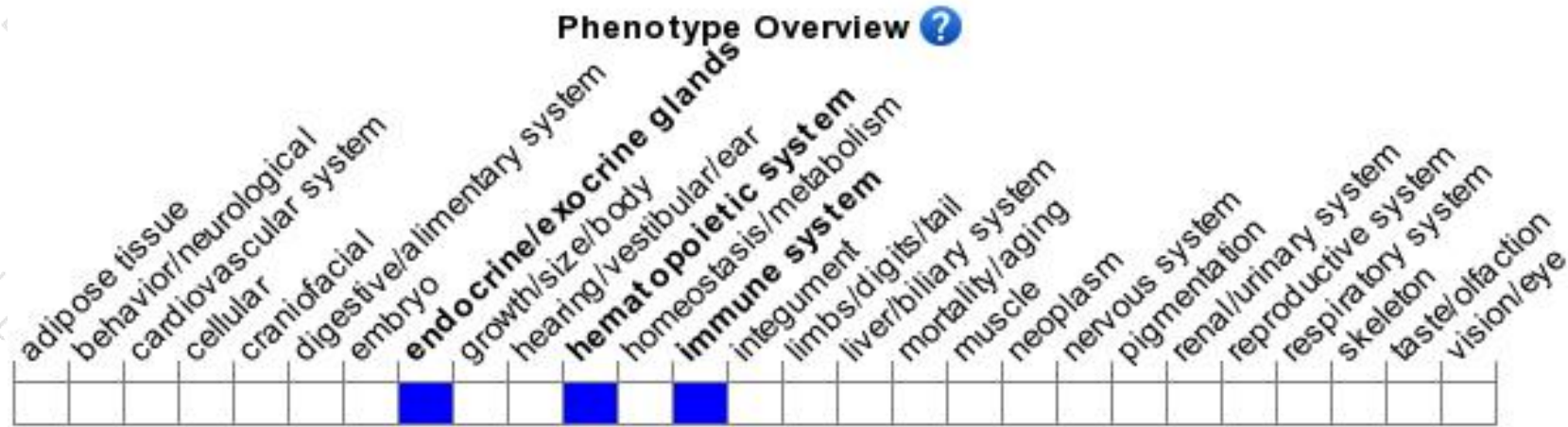
Genomic location distribution



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 are viable with no gross abnormalities and normal T cell development and activation.

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

Tel: 400-9660890

