Prss23 Cas9-KO Strategy

Designer: **Daohua Xu**

Reviewer: **Huimin Su**

Design Date: **2020-4-15**

Project Name	***Prss23***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prss23* gene. The schematic diagram is as follows:

Technical routes

➤ The *Prss23* gene has 8 transcripts. According to the structure of *Prss23* gene, exon2 of *Prss23-201* (ENSMUST00000041761.6) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Prss23* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The KO region contains functional region of the *Prss23os* gene.Knockout the region may affect the function of *Prss23os* gene.

➢ The *Prss23* gene is located on the Chr7. 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）

Prss23 protease, serine 23 [Mus musculus (house mouse)]

Gene ID: 76453, updated on 13-Mar-2020

▲ Summary

Official Symbol	Prss23 provided by MGI
Official Full Name	protease, serine 23 provided by MGI
Primary source	MGI:MGI:1923703
See related	Ensembl:ENSMUSG00000039405
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	2310046G15Rik, 4930479H08Rik, AI790574, Spuve
Expression	Broad expression in bladder adult (RPKM 53.0), ovary adult (RPKM 40.2) and 18 other tissuesSee more
Orthologs	human all

The gene has 8 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prss23-201	ENSMUST00000041761.6	3228	382aa	Protein coding	CCDS21442	Q9D6X6	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 P1
Prss23-204	ENSMUST00000207932.1	1937	382aa	Protein coding	CCDS21442	Q9D6X6	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 P1
Prss23-205	ENSMUST00000208402.1	682	167aa	Protein coding	-	A0A140LJH8	CDS 3' incomplete TSL:2
Prss23-203	ENSMUST00000207636.1	507	140aa	Protein coding	-	A0A140LHE7	CDS 3' incomplete TSL:3
Prss23-206	ENSMUST00000208888.1	494	138aa	Protein coding	-	A0A140LHF1	CDS 3' incomplete TSL:2
Prss23-202	ENSMUST00000207538.1	361	86aa	Protein coding	-	A0A140LIL0	CDS 3' incomplete TSL:3
Prss23-207	ENSMUST00000208903.1	355	78aa	Protein coding	-	A0A140LIH7	CDS 3' incomplete TSL:3
Prss23-208	ENSMUST00000209118.1	633	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Prss23-201* transcript,the transcription is shown below:

< Prss23-201
protein coding

◀ Reverse strand   9.80 kb
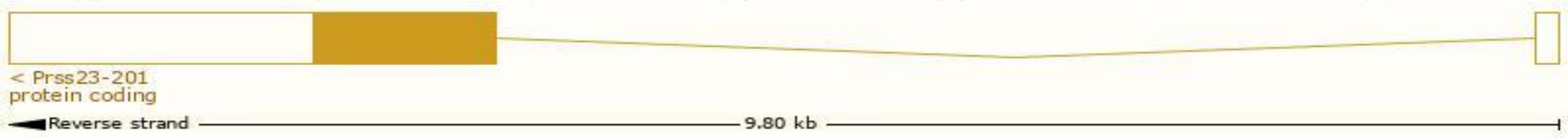
Genomic location distribution
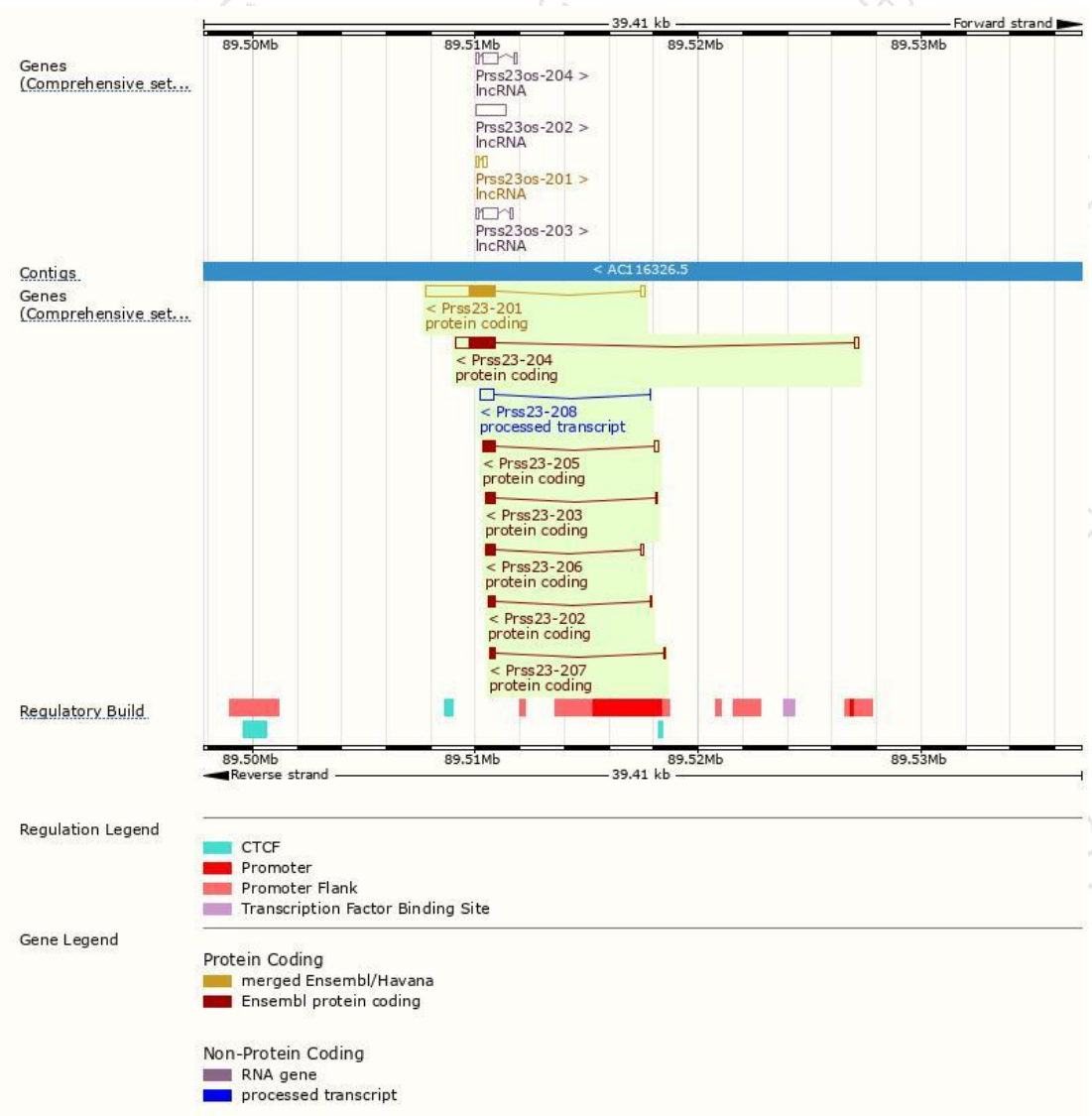
Protein domain
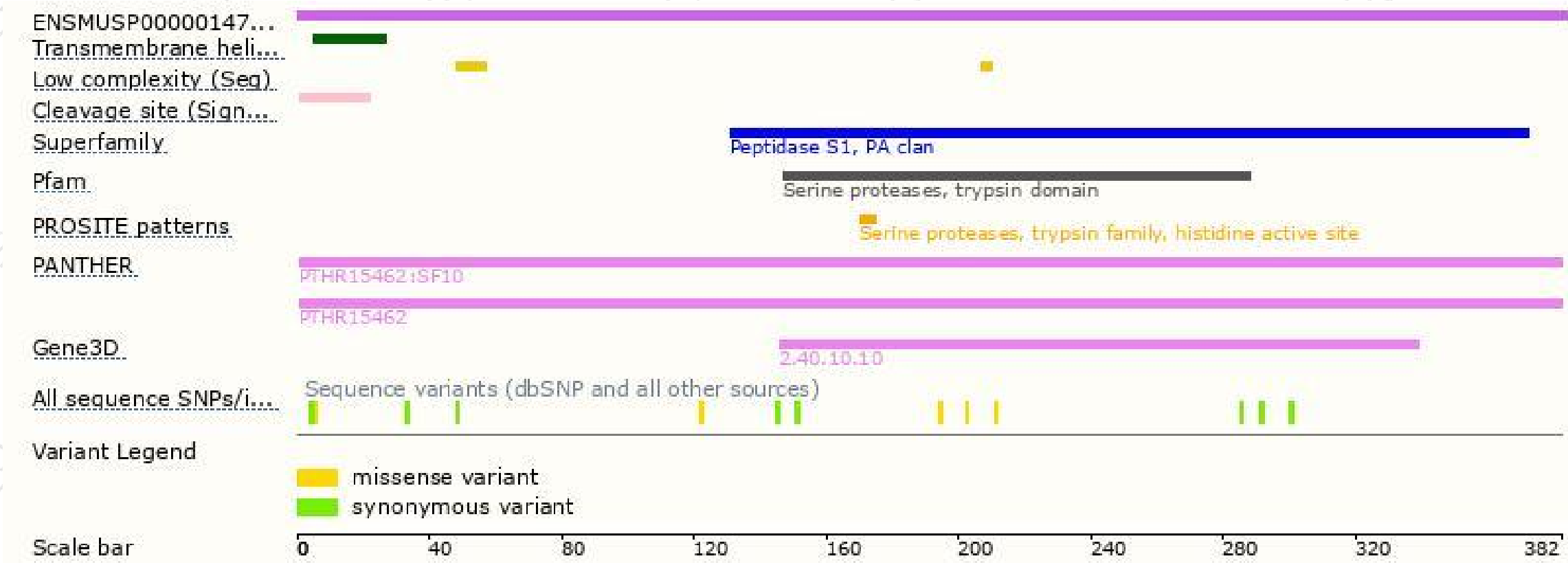
If you have any questions, you are welcome to inquire.
Tel: 400-9660890