

Pstpip1 Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

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Project Overview

Project Name

Pstpip1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pstpip1* gene. The schematic diagram is as follows:



- The *Pstpip1* gene has 7 transcripts. According to the structure of *Pstpip1* gene, exon2-exon3 of *Pstpip1-201* (ENSMUST00000059206.7) transcript is recommended as the knockout region. The region contains 176bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pstpip1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit defects in immune cells with T cell hyperresponsive to antigen receptor stimulation.
- The *Pstpip1* gene is located on the Chr9. 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)

Pstpip1 proline-serine-threonine phosphatase-interacting protein 1 [Mus musculus (house mouse)]

Gene ID: 19200, updated on 19-Mar-2019

Summary



Official Symbol	Pstpip1 provided by MGI
Official Full Name	proline-serine-threonine phosphatase-interacting protein 1 provided by MGI
Primary source	MGI:MGI:1321396
See related	Ensembl:ENSMUSG00000032322
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	CD2BP1, def-2
Expression	Biased expression in thymus adult (RPKM 36.1), spleen adult (RPKM 16.1) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

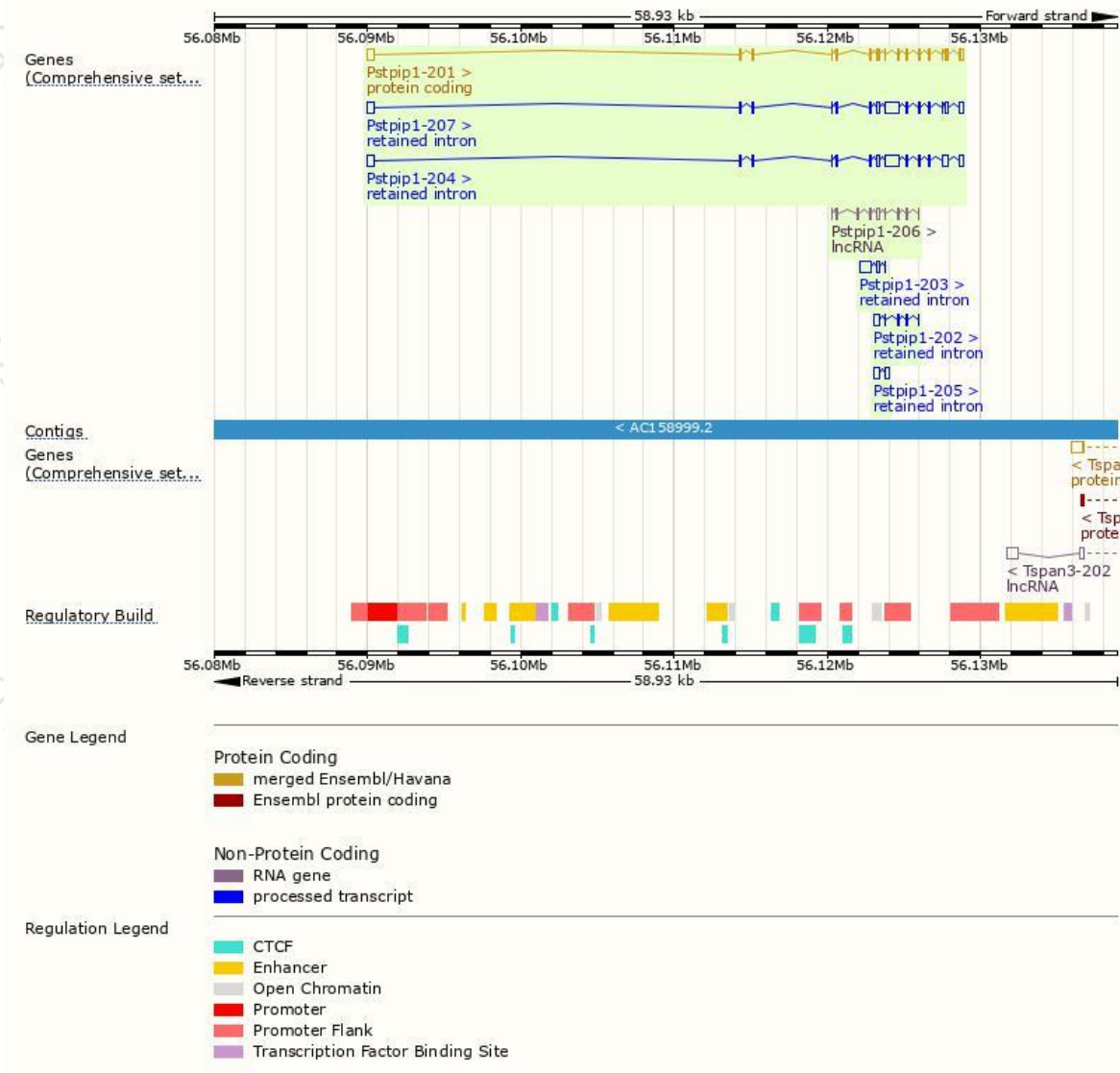
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pstpip1-201	ENSMUST00000059206.7	1863	415aa	Protein coding	CCDS40645	A0A0R4J0P5	TSL:1 GENCODE basic APPRIS P1
Pstpip1-204	ENSMUST00000138646.7	2822	No protein	Retained intron	-	-	TSL:2
Pstpip1-207	ENSMUST00000147360.7	2637	No protein	Retained intron	-	-	TSL:1
Pstpip1-203	ENSMUST00000135103.1	841	No protein	Retained intron	-	-	TSL:3
Pstpip1-205	ENSMUST00000142894.7	606	No protein	Retained intron	-	-	TSL:2
Pstpip1-202	ENSMUST00000132800.1	597	No protein	Retained intron	-	-	TSL:3
Pstpip1-206	ENSMUST00000144638.7	638	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Pstpip1-201* transcript,The transcription is shown below



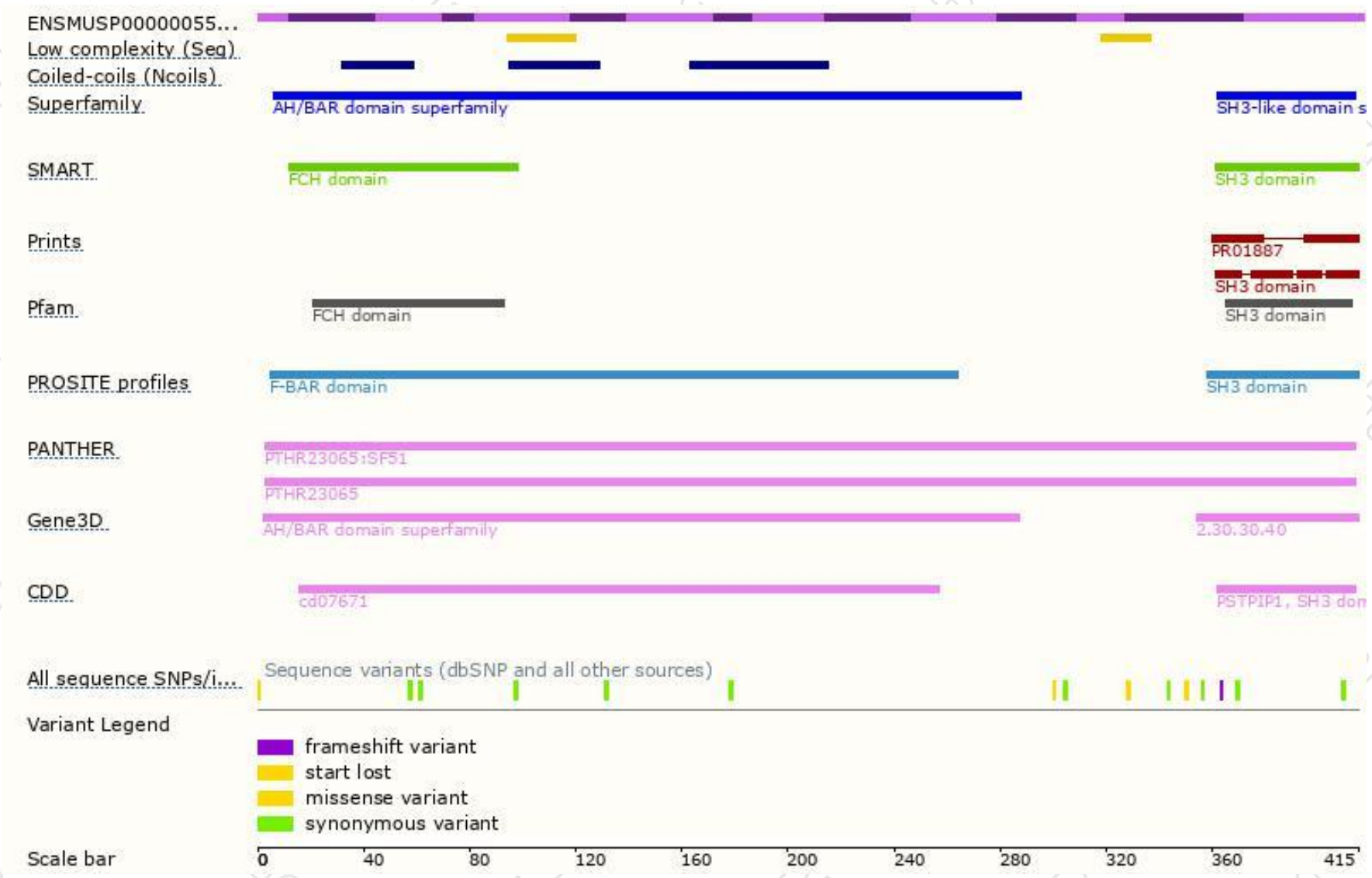
Genomic location distribution



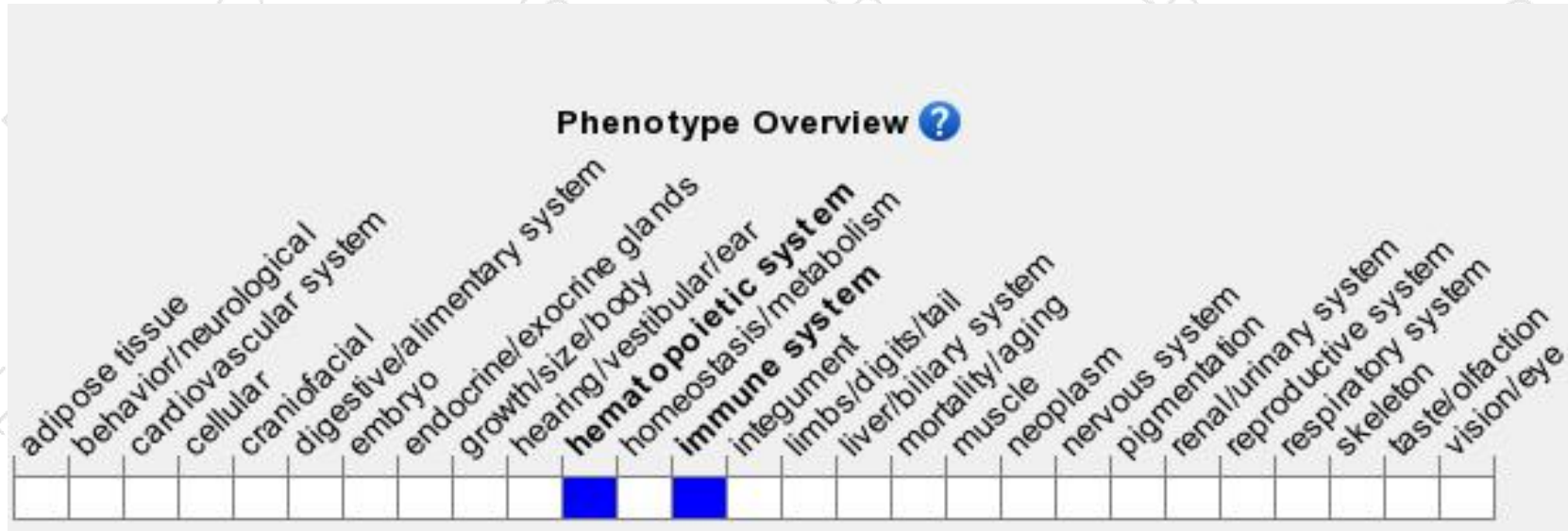
Protein domain



集萃药康
GemPharmatech



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 knock-out allele exhibit defects in immune cells with T cell hyperresponsive to antigen receptor stimulation.

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

Tel: 400-9660890

