

***Ptpn20* Cas9-KO Strategy**

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Project Overview

Project Name

Ptpn20

Project type

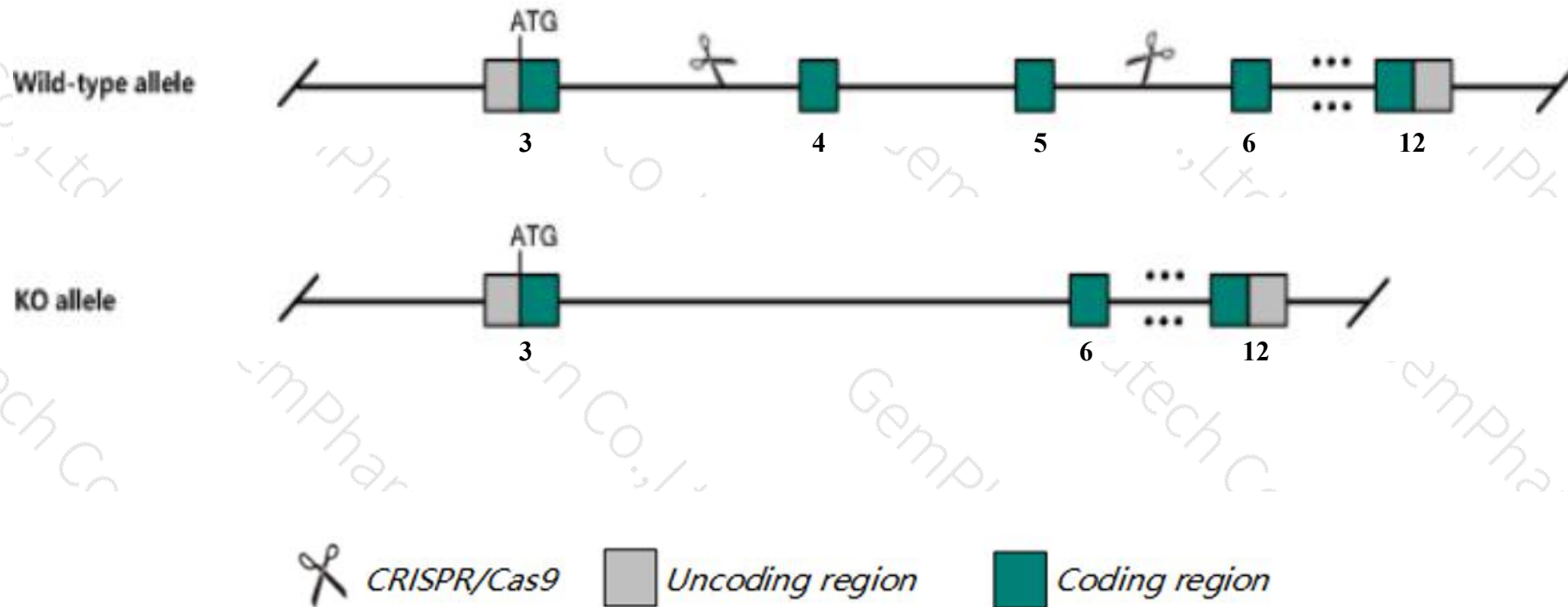
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptpn20* gene. The schematic diagram is as follows:



- The *Ptpn20* gene has 3 transcripts. According to the structure of *Ptpn20* gene, exon4-exon5 of *Ptpn20-201* (ENSMUST00000022508.7) transcript is recommended as the knockout region. The region contains 193bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ptpn20* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Ptpn20* gene is located on the Chr14. 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)

Ptpn20 protein tyrosine phosphatase, non-receptor type 20 [Mus musculus (house mouse)]

Gene ID: 19256, updated on 13-Mar-2020

Summary



Official Symbol Ptpn20 provided by [MGI](#)

Official Full Name protein tyrosine phosphatase, non-receptor type 20 provided by [MGI](#)

Primary source [MGI:MGI:1196295](#)

See related [Ensembl:ENSMUSG000000021940](#)

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 typ

Expression Restricted expression toward testis adult (RPKM 17.2)[See more](#)

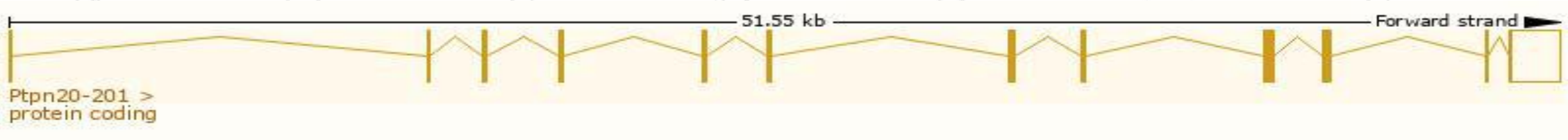
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

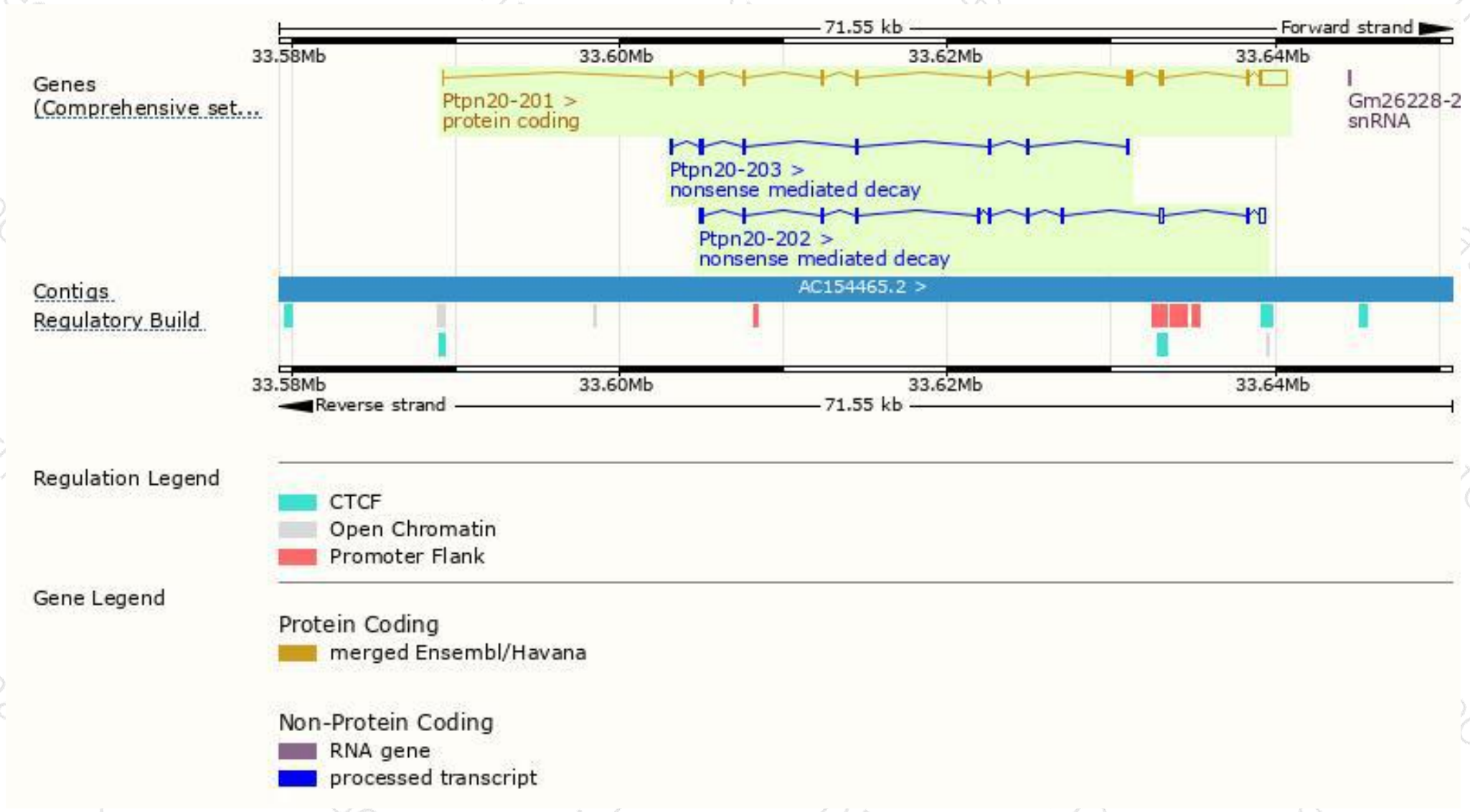
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptpn20-201	ENSMUST00000022508.7	3153	426aa	Protein coding	CCDS36870	Q55082	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
Ptpn20-202	ENSMUST000000226512.1	1467	133aa	Nonsense mediated decay	-	Q55082	
Ptpn20-203	ENSMUST000000227887.1	792	43aa	Nonsense mediated decay	-	A0A2I3BQP0	

The strategy is based on the design of *Ptpn20-201* transcript,the transcription is shown below:



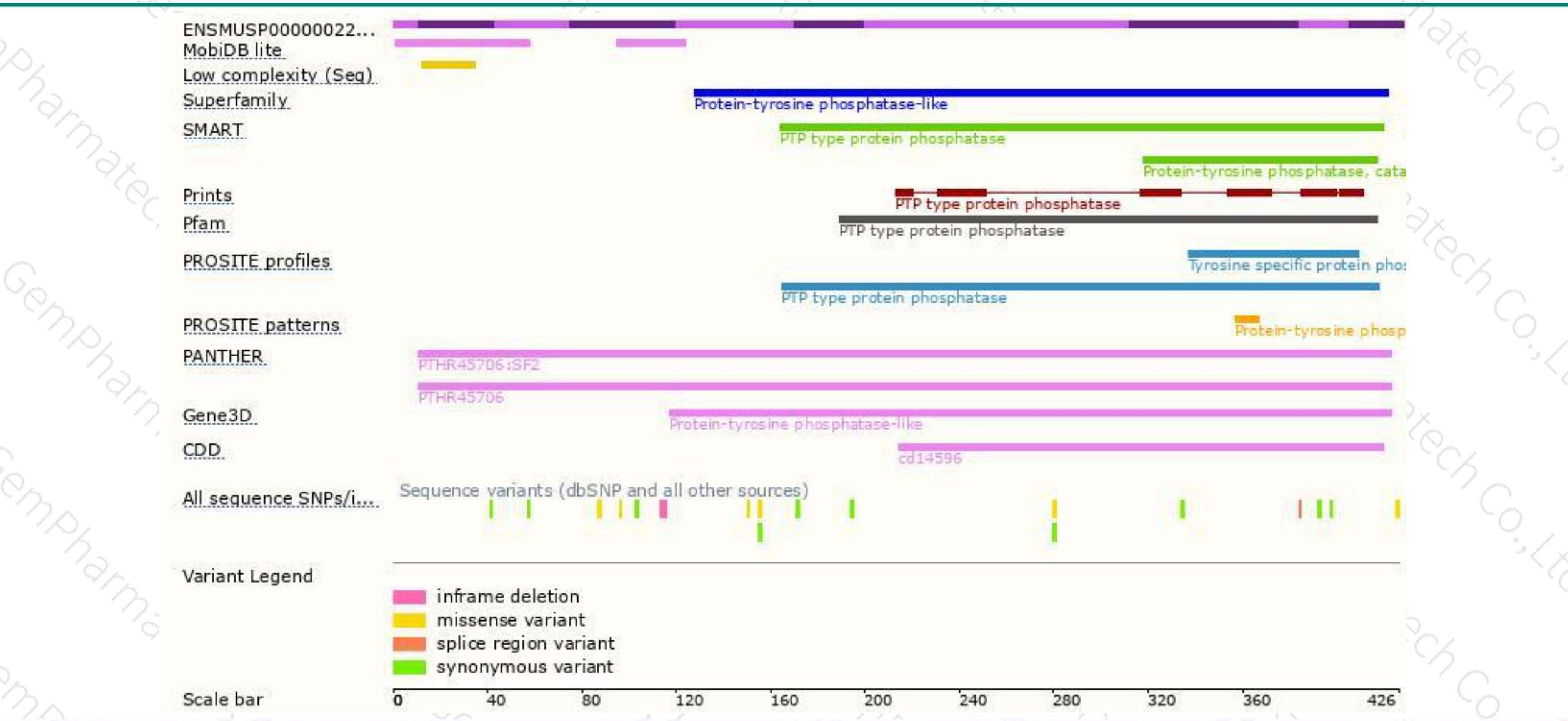
Genomic location distribution



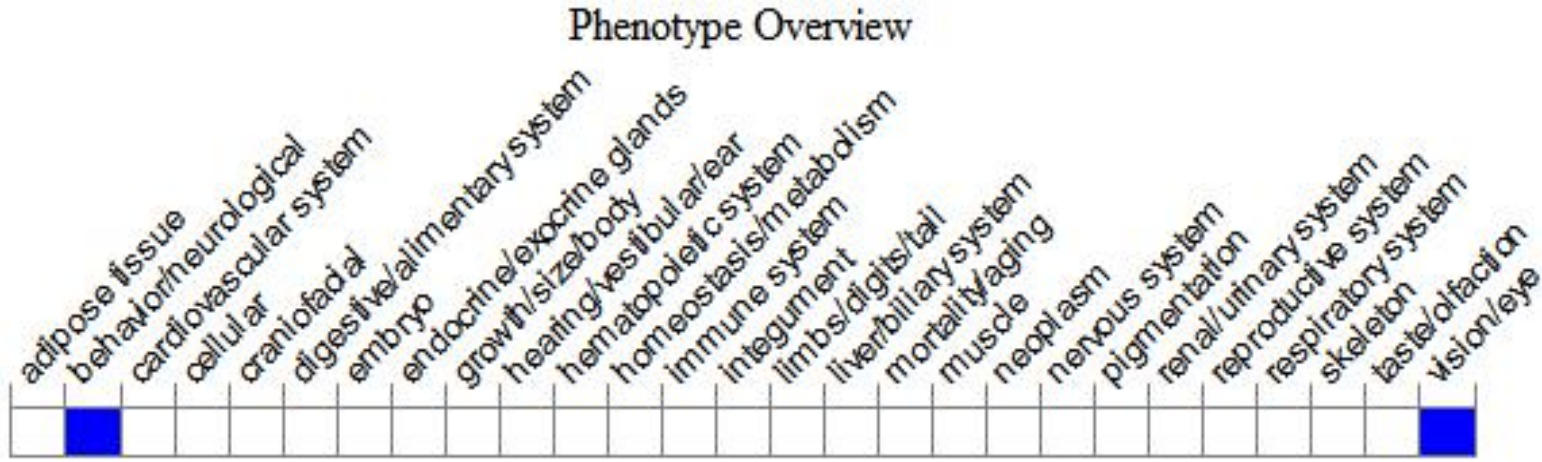
Protein domain



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/>).

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

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