Ptpn18 Cas9-KO Strategy

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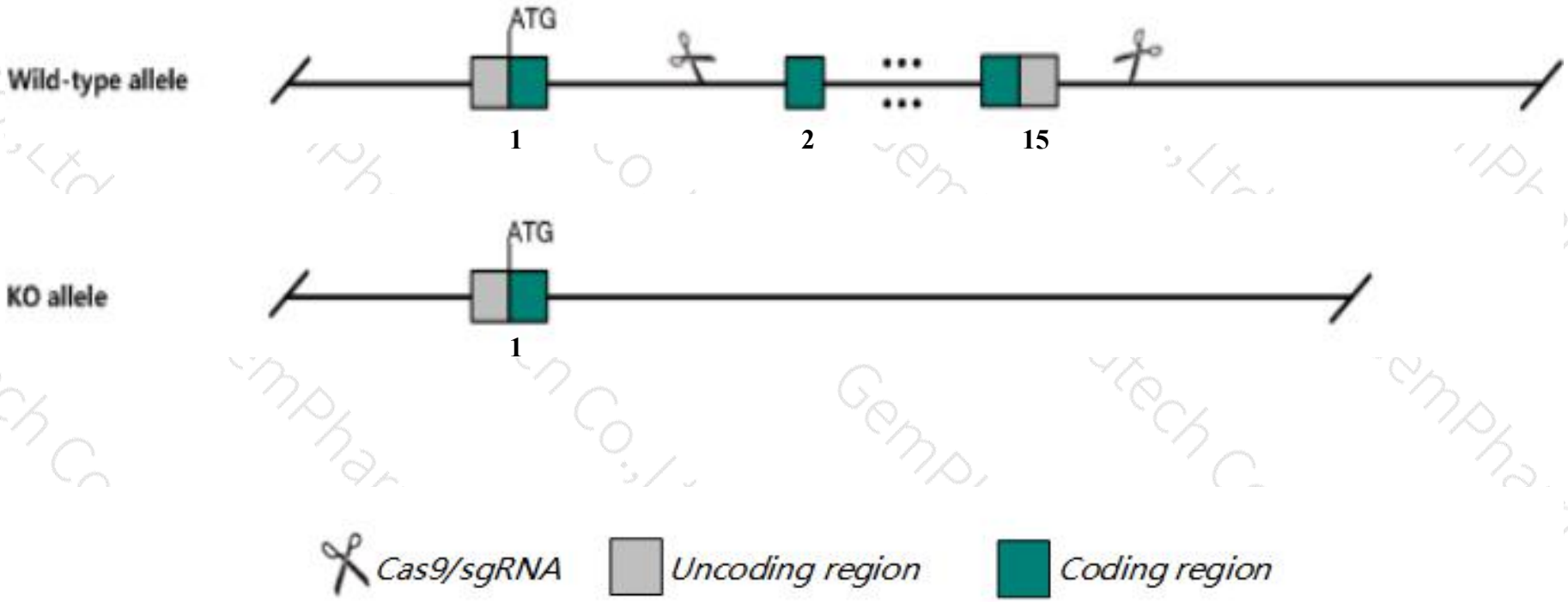
Project Overview

Project Name	***Ptpn18***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptpn18* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ptpn18* gene has 7 transcripts. According to the structure of *Ptpn18* gene, exon2-exon15 of *Ptpn18-201*(ENSMUST00000027302.13) transcript is recommended as the knockout region.The region contains most 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 *Ptpn18* 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.

Notice

➢ The *Ptpn18* gene is located on the Chr1. 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.

➢The Gm28417 gene will be deleted.

➢ 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）

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Ptpn18 protein tyrosine phosphatase, non-receptor type 18 [Mus musculus (house mouse)]

Gene ID: 19253, updated on 13-Mar-2020

Summary

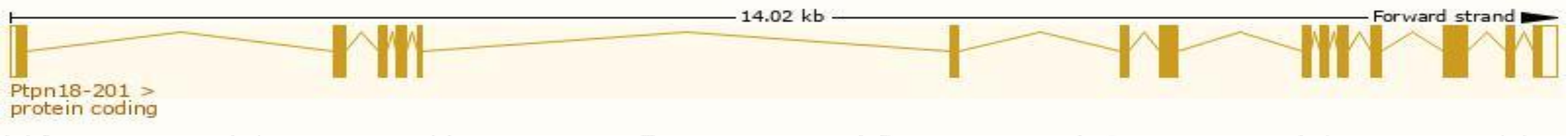
Official Symbol	Ptpn18 provided by MGI
Official Full Name	protein tyrosine phosphatase, non-receptor type 18 provided byMGI
Primary source	MGI:MGI:108410
See related	Ensembl:ENSMUSG00000026126
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FLP1, HSCF, PTP-HSCF, PTP-K1, Ptpk1
Expression	Biased expression in colon adult (RPKM 76.4), duodenum adult (RPKM 74.3) and 13 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

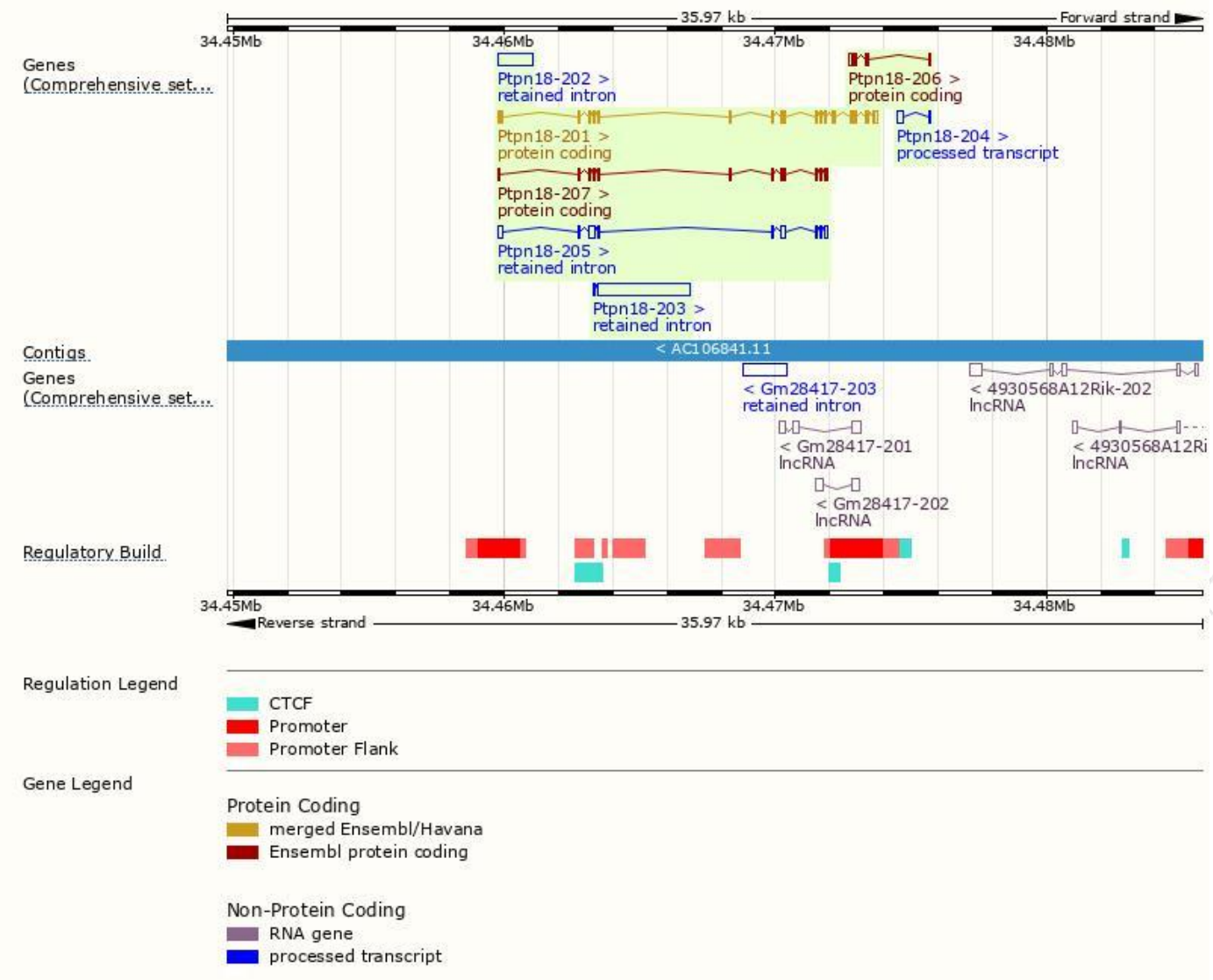
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptpn18-201	ENSMUST00000027302.13	1559	453aa	Protein coding	CCDS14867	Q61152	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
Ptpn18-207	ENSMUST00000190122.1	915	289aa	Protein coding	-	A0A087WPR5	CDS 3' incomplete TSL:5
Ptpn18-206	ENSMUST00000188972.2	414	85aa	Protein coding	-	Q3V441	TSL:1 GENCODE basic
Ptpn18-204	ENSMUST00000188019.1	284	No protein	Processed transcript	-	-	TSL:3
Ptpn18-203	ENSMUST00000186252.1	3495	No protein	Retained intron	-	-	TSL:3
Ptpn18-202	ENSMUST00000185610.1	1295	No protein	Retained intron	-	-	TSL:NA
Ptpn18-205	ENSMUST00000188884.2	987	No protein	Retained intron	-	-	TSL:5

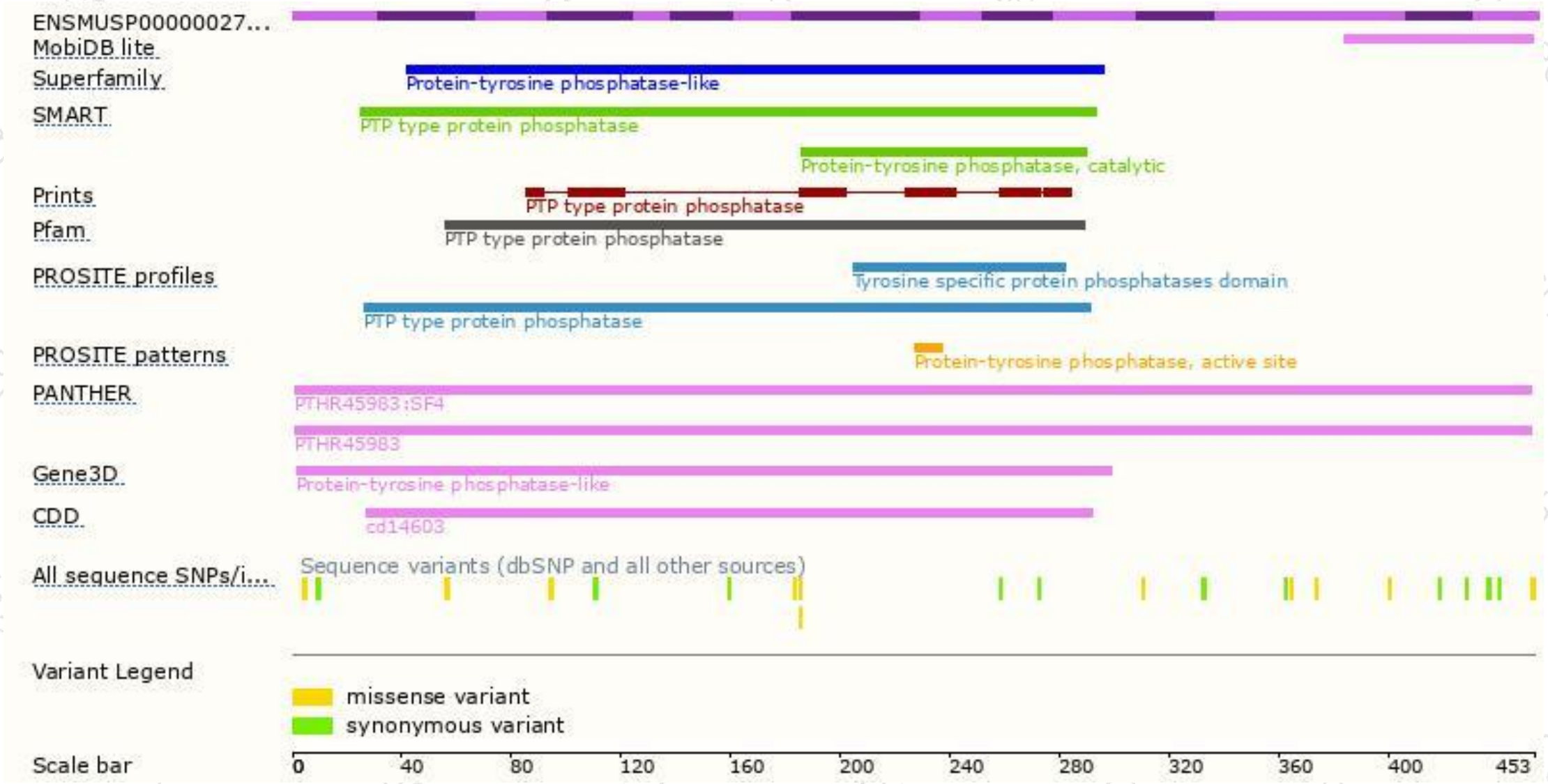
The strategy is based on the design of *Ptpn18-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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