Ptpn20 Cas9-CKO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

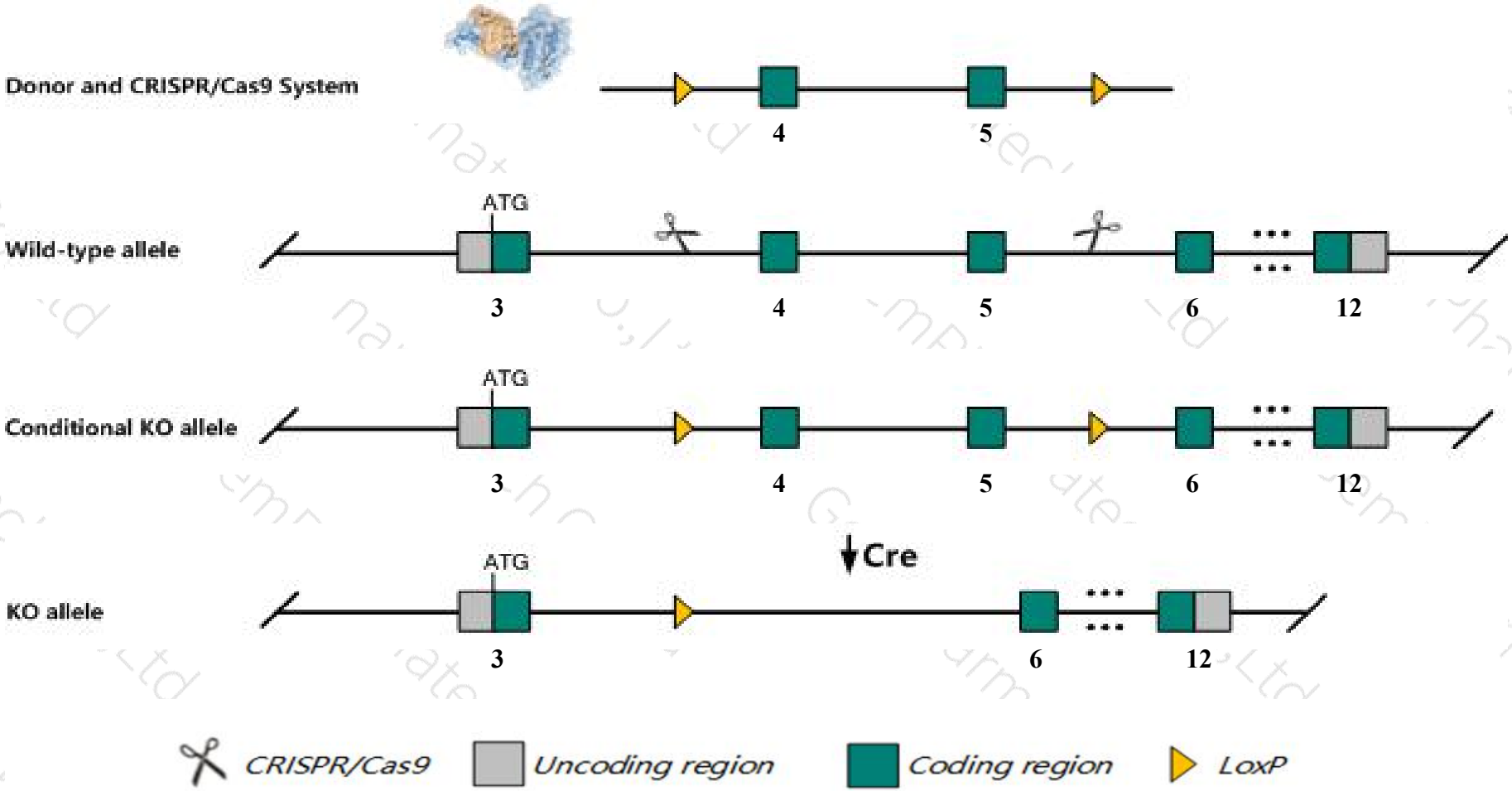
Design Date: 2020-5-9

Project Overview

Project Name	***Ptpn20***
Project type	**Cas9-CKO**
Strain background	**C57BL/6J**

Conditional Knockout strategy

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



Technical routes

- 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 and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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

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

Summary

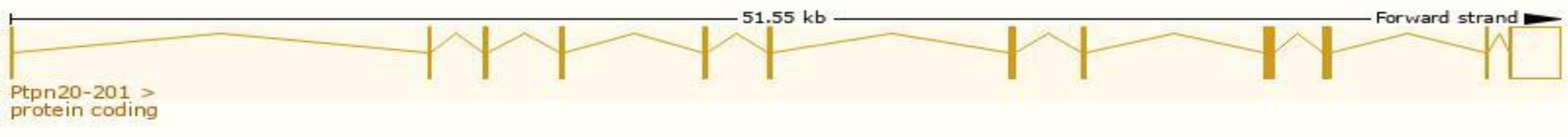
Official Symbol	Ptpn20 provided by MGI
Official Full Name	protein tyrosine phosphatase, non-receptor type 20 provided byMGI
Primary source	MGI:MGI:1196295
See related	Ensembl:ENSMUSG00000021940
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; 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）

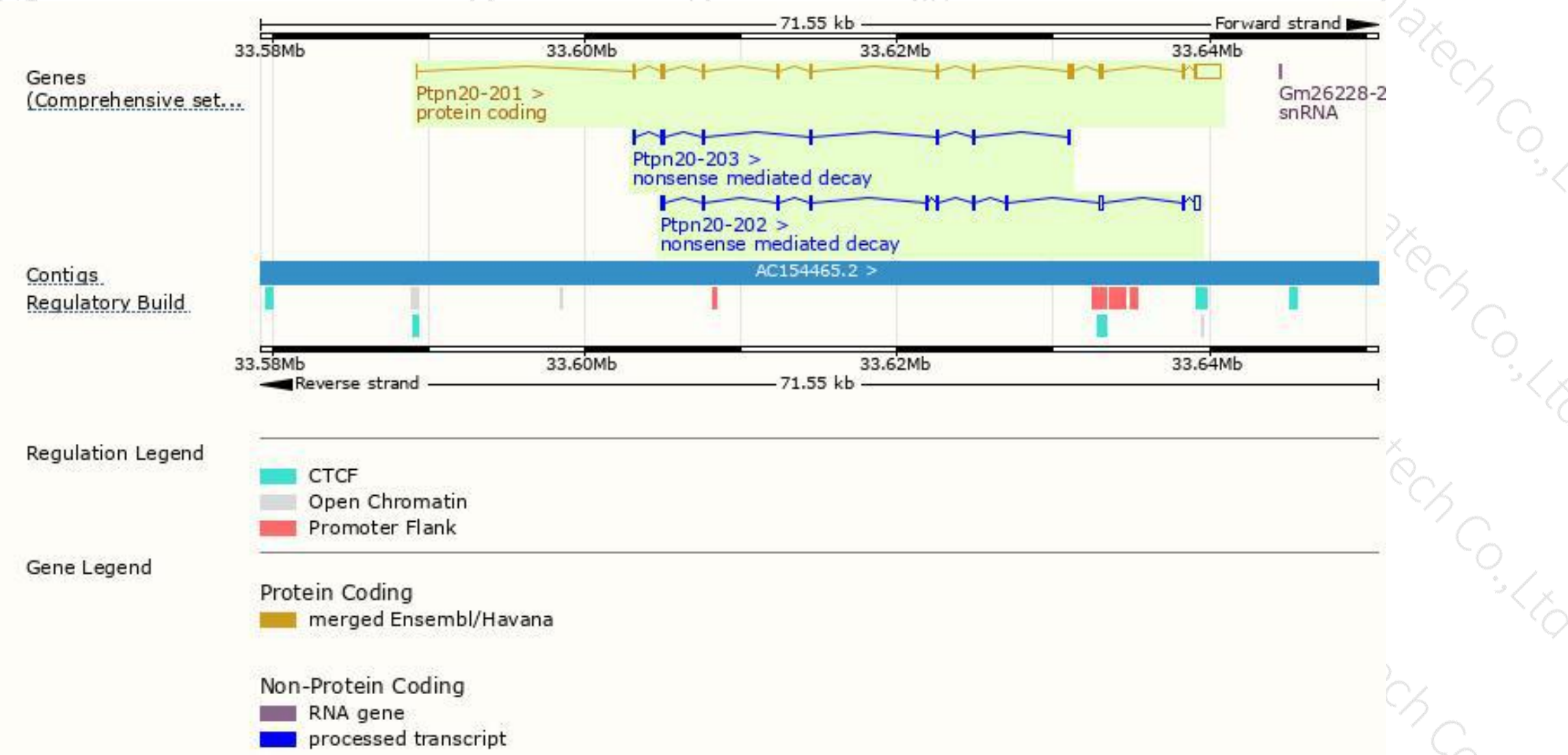
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptpn20-201	ENSMUST00000022508.7	3153	426aa	Protein coding	CCDS36870	O55082	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	ENSMUST00000226512.1	1467	133aa	Nonsense mediated decay	-	O55082	
Ptpn20-203	ENSMUST00000227887.1	792	43aa	Nonsense mediated decay	-	A0A2I3BQP0	

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

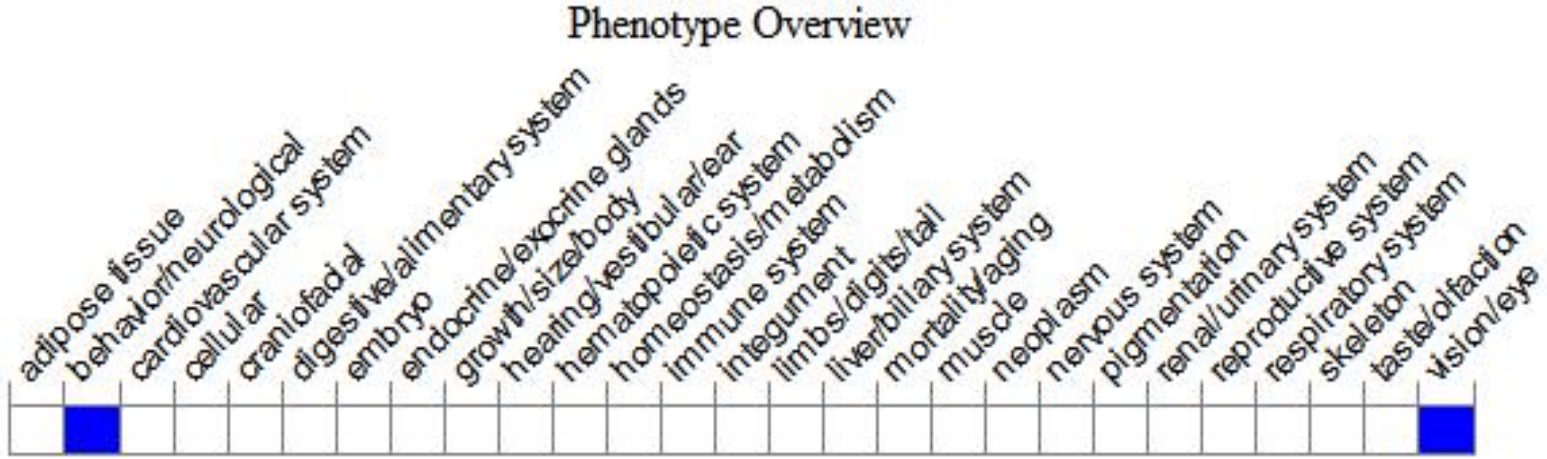


Genomic location distribution



Protein domain

Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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

Tel: 400-9660890

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