Ppp2r5b Cas9-KO Strategy

Designer: **Daohua Xu**

Reviewer: **Huimin Su**

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Project Overview

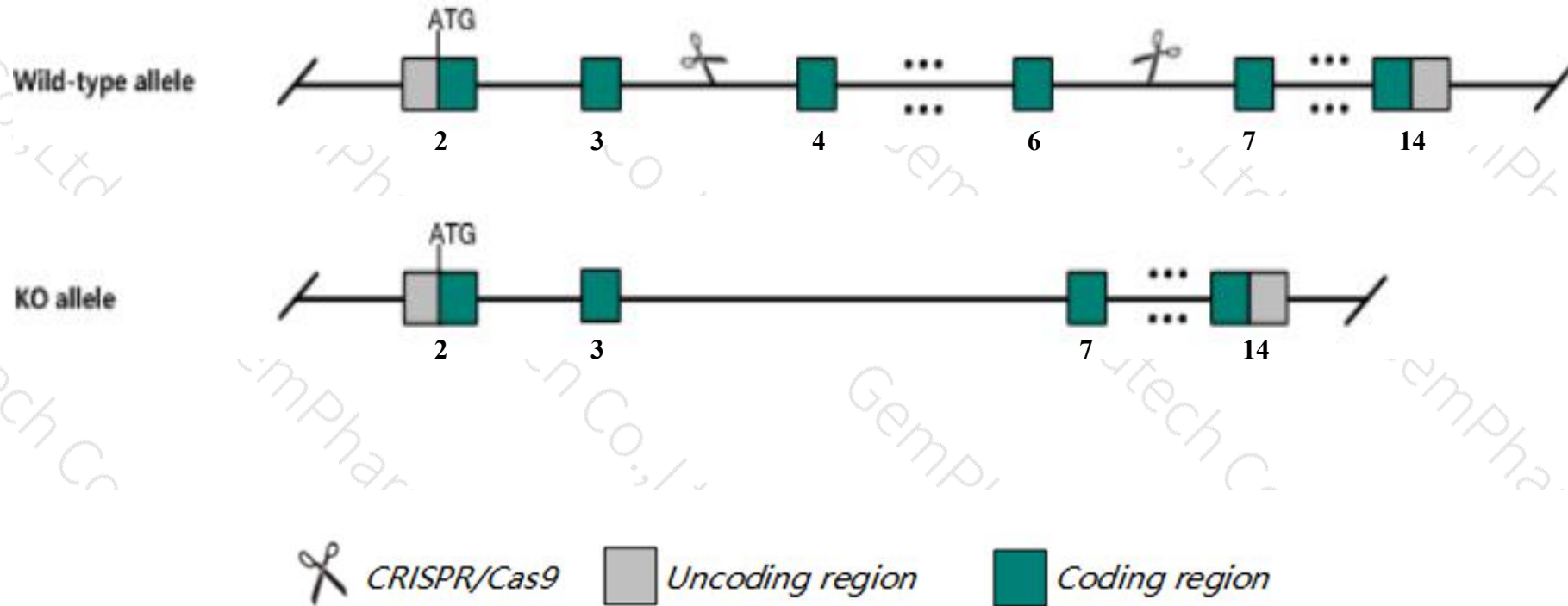|	
Project Name	***Ppp2r5b***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppp2r5b* gene. The schematic diagram is as follows:

Technical routes

➢ The *Ppp2r5b* gene has 4 transcripts. According to the structure of *Ppp2r5b* gene, exon4-exon6 of *Ppp2r5b-201* (ENSMUST00000025695.9) transcript is recommended as the knockout region.The region contains 326bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ppp2r5b* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ The *Ppp2r5b* gene is located on the Chr19. 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）

Ppp2r5b protein phosphatase 2, regulatory subunit B', beta [Mus musculus (house mouse)]
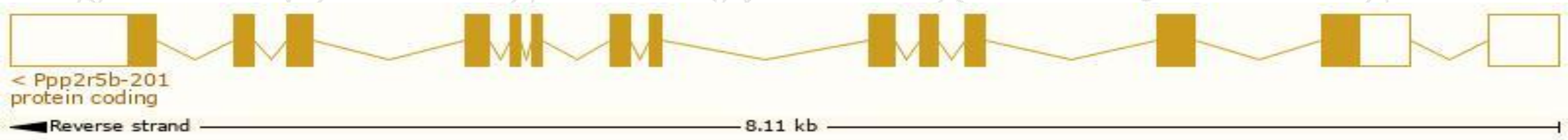
Gene ID: 225849, updated on 13-Mar-2020

Summary

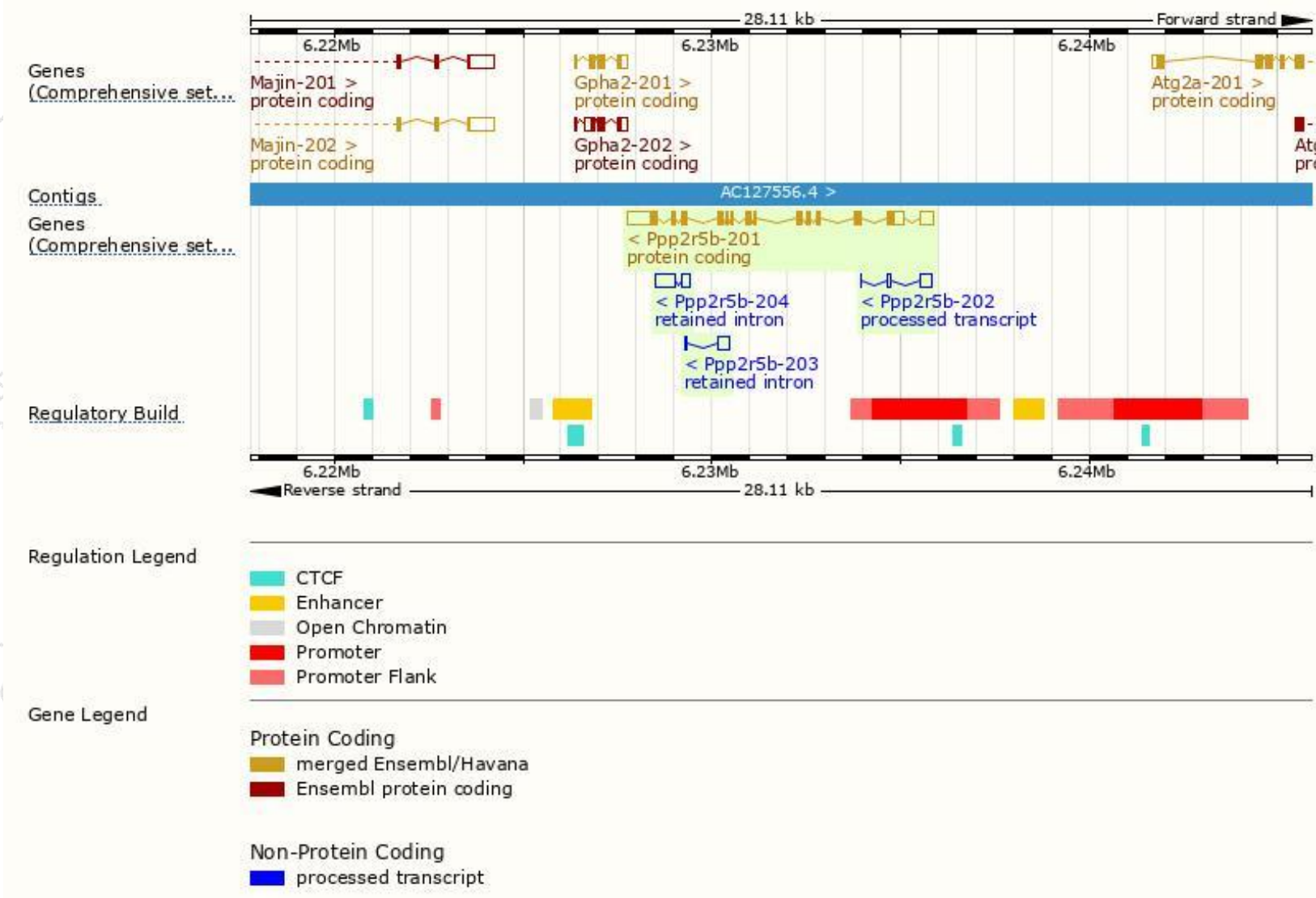|	
Official Symbol	Ppp2r5b provided by MGI
Official Full Name	protein phosphatase 2, regulatory subunit B', beta provided by MGI
Primary source	MGI:MGI:2388480
See related	Ensembl:ENSMUSG00000024777
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B'beta, BC026670
Expression	Ubiquitous expression in adrenal adult (RPKM 89.9), cerebellum adult (RPKM 51.2) and 23 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

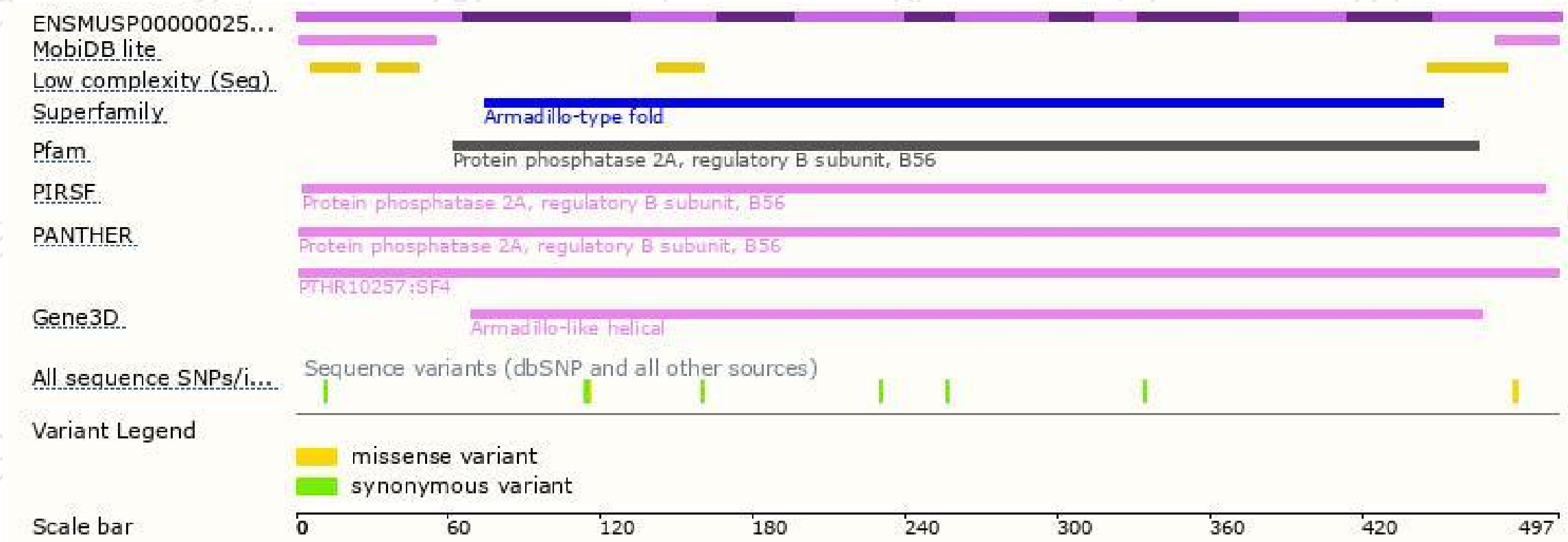| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp2r5b-201	ENSMUST00000025695.9	2742	497aa	Protein coding	CCDS29499	Q6PD28	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Ppp2r5b-202	ENSMUST00000148693.1	467	No protein	Processed transcript	-	-	TSL:5
Ppp2r5b-204	ENSMUST00000236699.1	740	No protein	Retained intron	-	-	
Ppp2r5b-203	ENSMUST00000153155.1	389	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Ppp2r5b-201* transcript,The transcription is shown below

< Ppp2r5b-201
protein coding

Reverse strand

8.11 kb

Genomic location distribution

Protein domain

ENSMUSP00000025...								
MobiDB lite								
Low complexity (Seg)								
Superfamily	Armadillo-type fold							
Pfam	Protein phosphatase 2A, regulatory B subunit, B56							
PIRSF	Protein phosphatase 2A, regulatory B subunit, B56							
PANTHER	Protein phosphatase 2A, regulatory B subunit, B56							
	PTHR10257:SF4							
Gene3D	Armadillo-like helical							
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)							
Variant Legend	missense variant							
	synonymous variant							
Scale bar	0	60	120	180	240	300	360	420	497

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd