

Ppp1r35 Cas9-KO Strategy

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Project Overview

Project Name

Ppp1r35

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppp1r35* gene. The schematic diagram is as follows:



- The *Ppp1r35* gene has 4 transcripts. According to the structure of *Ppp1r35* gene, exon1-exon4 of *Ppp1r35-201* (ENSMUST00000031739.5) transcript is recommended as the knockout region. The region contains all 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 *Ppp1r35* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Ppp1r35* gene is located on the Chr5. 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 has the risk of affecting the 3-terminal regulation of *Mepce* gene.
- 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)

Ppp1r35 protein phosphatase 1, regulatory subunit 35 [*Mus musculus* (house mouse)]

Gene ID: 69871, updated on 19-Apr-2019

Summary

Official Symbol Ppp1r35 provided by [MGI](#)

Official Full Name protein phosphatase 1, regulatory subunit 35 provided by [MGI](#)

Primary source [MGI:MGI:1922853](#)

See related [Ensembl:ENSMUSG000000029725](#)

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 AL024004; 2010007H12Rik; 2010011D20Rik

Expression Ubiquitous expression in CNS E11.5 (RPKM 25.8), thymus adult (RPKM 25.4) and 28 other tissues [See more](#)

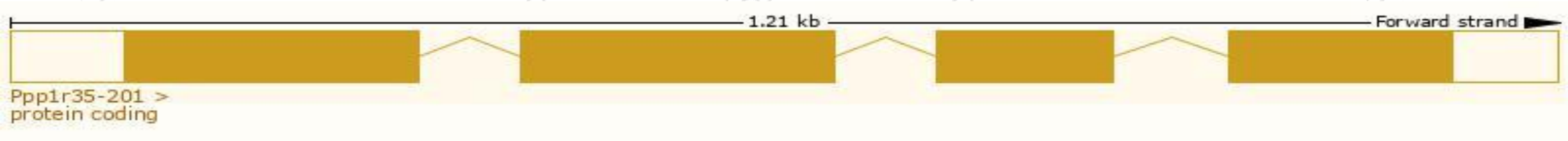
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

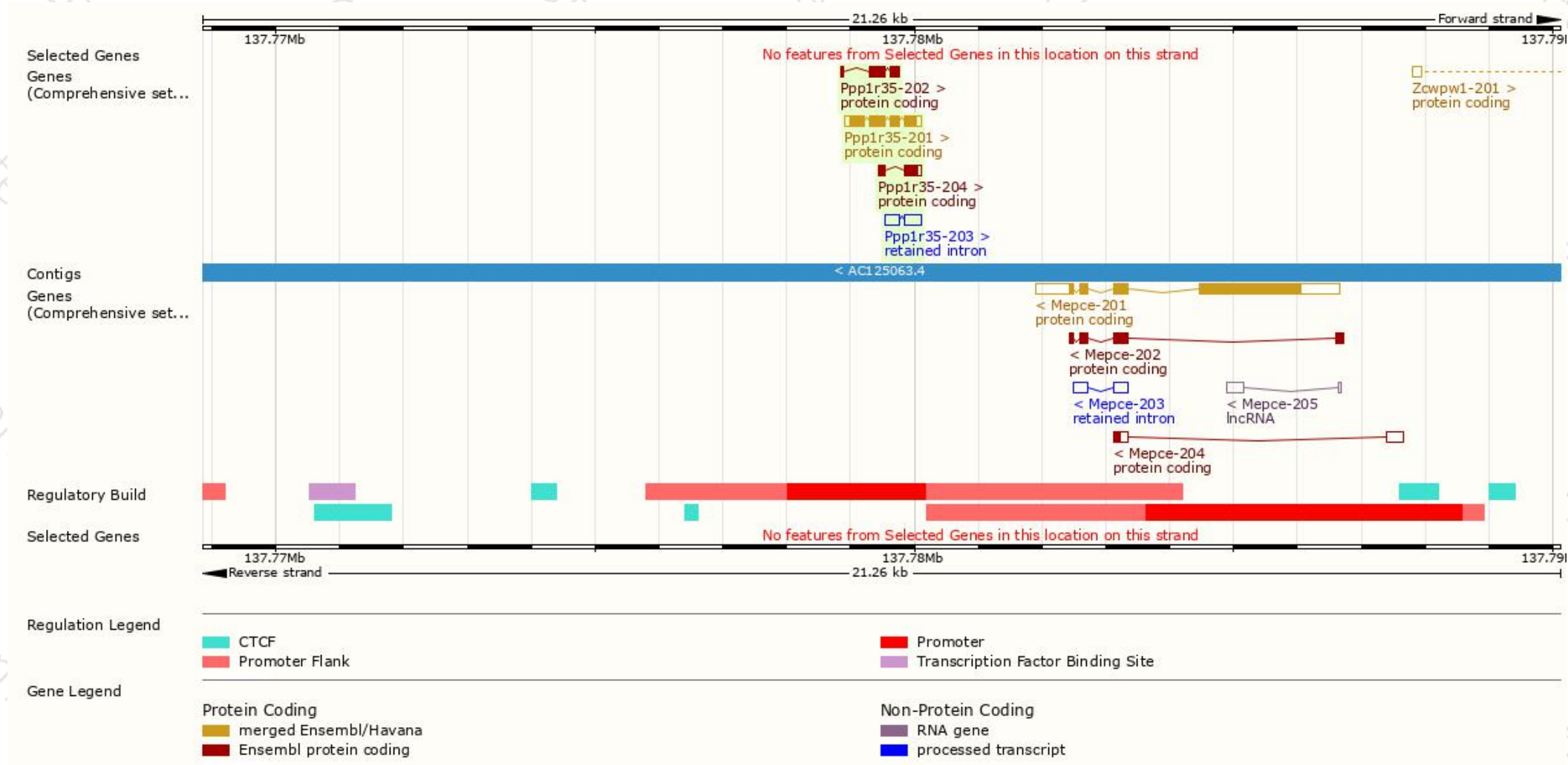
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp1r35-201	ENSMUST00000031739.5	956	260aa	Protein coding	CCDS19777	Q9D8C8	TSL:1 GENCODE basic APPRIS P1
Ppp1r35-202	ENSMUST00000126126.7	430	144aa	Protein coding	-	F6XYC5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ppp1r35-204	ENSMUST00000198929.1	362	101aa	Protein coding	-	A0A0G2JFI2	CDS 5' incomplete TSL:3
Ppp1r35-203	ENSMUST00000152298.1	476	No protein	Retained intron	-	-	TSL:2

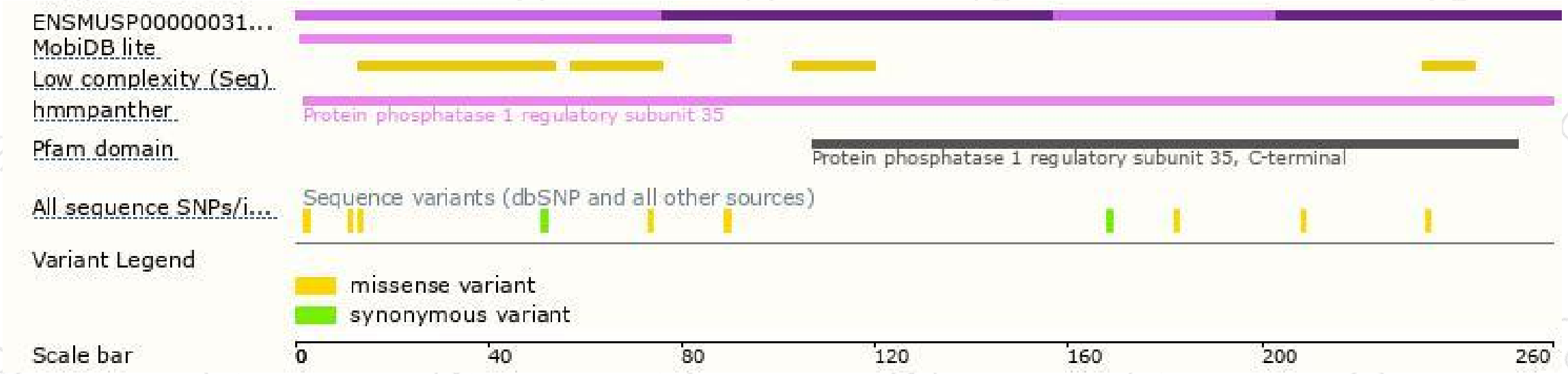
The strategy is based on the design of *Ppp1r35-201* transcript,The transcription is shown below



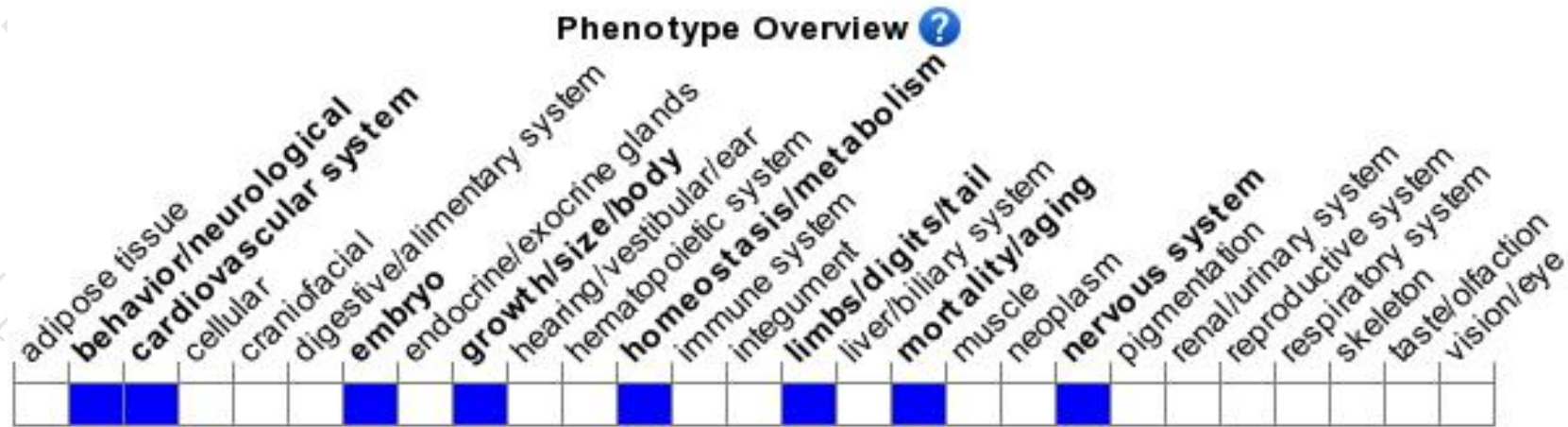
Genomic location distribution



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/>).

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

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