

Ppp1r12a Cas9-KO Strategy

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Design Date: **2019-9-30**

Project Overview

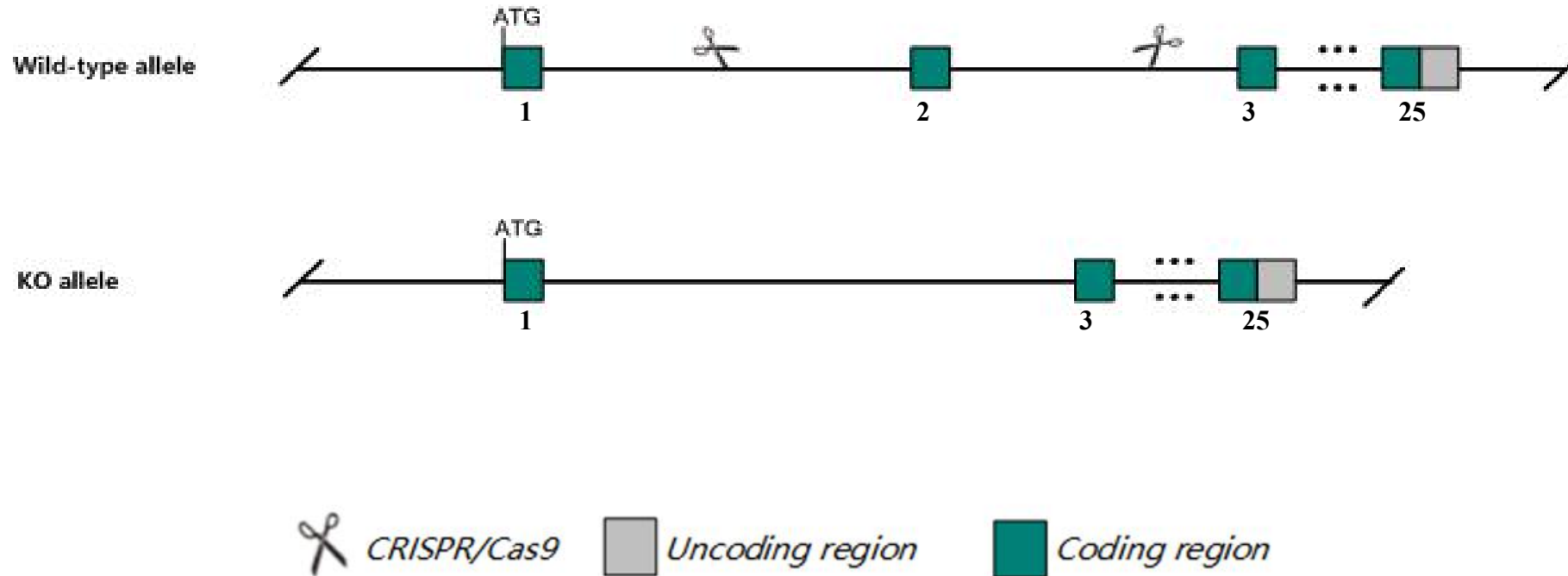
Project Name	<i>Ppp1r12a</i>
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Project type	Cas9-KO
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Strain background	C57BL/6JGpt
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Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppp1r12a* gene. The schematic diagram is as follows:



The *Ppp1r12a* gene has 8 transcripts. According to the structure of *Ppp1r12a* gene, exon2 of *Ppp1r12a-201* (ENSMUST00000070663.5) transcript is recommended as the knockout region. The region contains 131bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Ppp1r12a* gene. The brief process is as follows: CRISPR/Cas9 sys

According to the existing MGI data, Homozygous null mice die before E7.5. Mice homozygous for a floxed allele activated in smooth muscle exhibit altered intestinal smooth muscle contractility.

The *Ppp1r12a* gene is located on the Chr10. 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.

Ppp1r12a protein phosphatase 1, regulatory subunit 12A [Mus musculus (house mouse)]

Gene ID: 17931, updated on 23-Feb-2019

Summary



Official Symbol	Ppp1r12a provided by MGI
Official Full Name	protein phosphatase 1, regulatory subunit 12A provided by MGI
Primary source	MGI:MGI:1309528
See related	Ensembl:ENSMUSG00000019907
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	1200015F06Rik, 5730577I22Rik, AA792106, AV099298, D10Ert625e, Mypt1
Expression	Biased expression in bladder adult (RPKM 144.2), CNS E11.5 (RPKM 14.0) and 11 other tissues See more
Orthologs	human all

Transcript information Ensembl

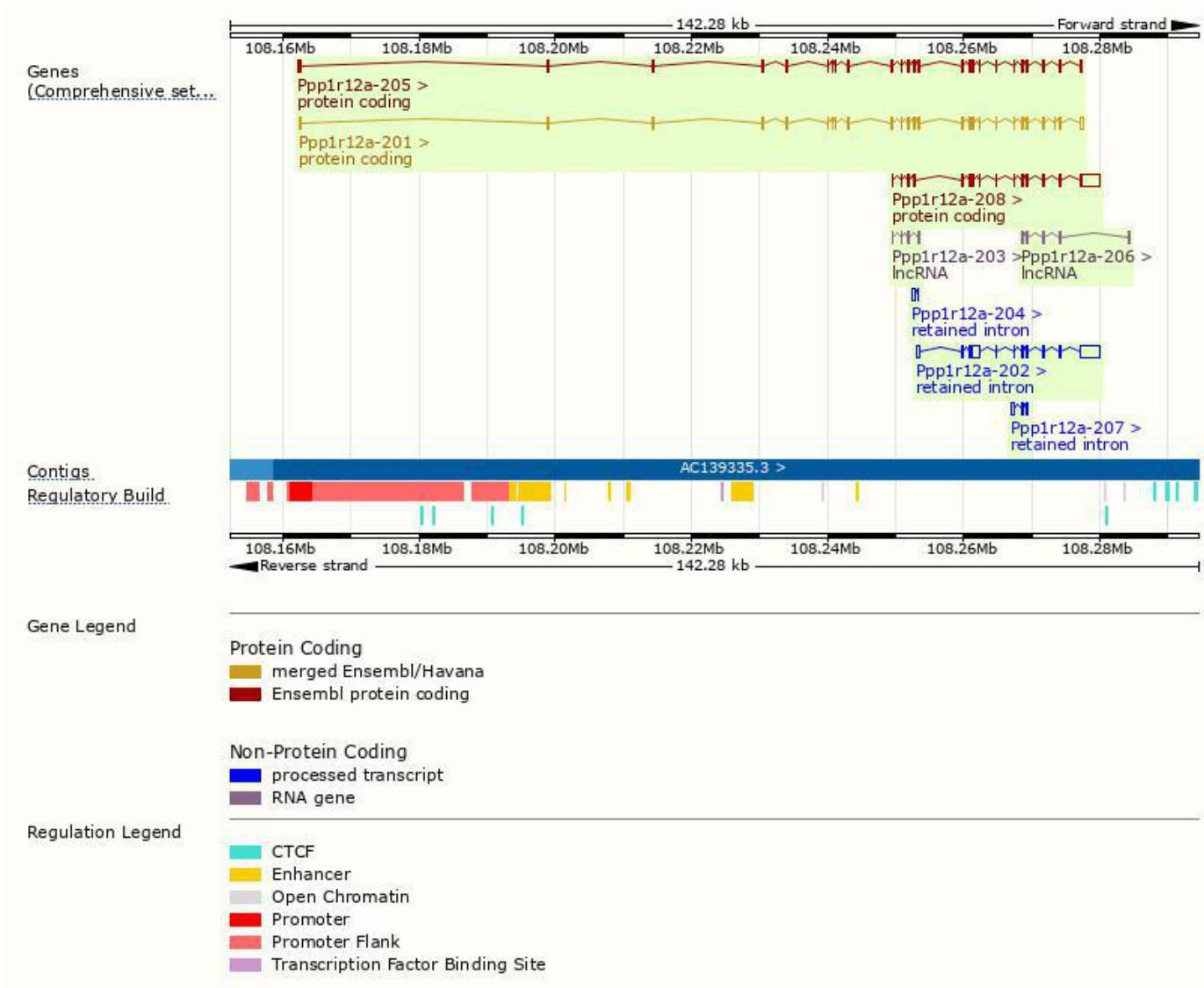
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp1r12a-201	ENSMUST00000070663.5	3403	1004aa	Protein coding	CCDS36052	Q9DBR7	TSL:1 GENCODE basic
Ppp1r12a-208	ENSMUST00000219759.1	4212	506aa	Protein coding	-	A0A1W2P750	CDS 5' incomplete TSL:1
Ppp1r12a-205	ENSMUST00000219263.1	3355	1029aa	Protein coding	-	Q9DBR7	TSL:5 GENCODE basic APPRIS P1
Ppp1r12a-202	ENSMUST00000218161.1	5066	No protein	Retained intron	-	-	TSL:2
Ppp1r12a-204	ENSMUST00000219068.1	590	No protein	Retained intron	-	-	TSL:3
Ppp1r12a-207	ENSMUST00000219653.1	563	No protein	Retained intron	-	-	TSL:3
Ppp1r12a-206	ENSMUST00000219559.1	541	No protein	lncRNA	-	-	TSL:3
Ppp1r12a-203	ENSMUST00000218773.1	386	No protein	lncRNA	-	-	TSL:2

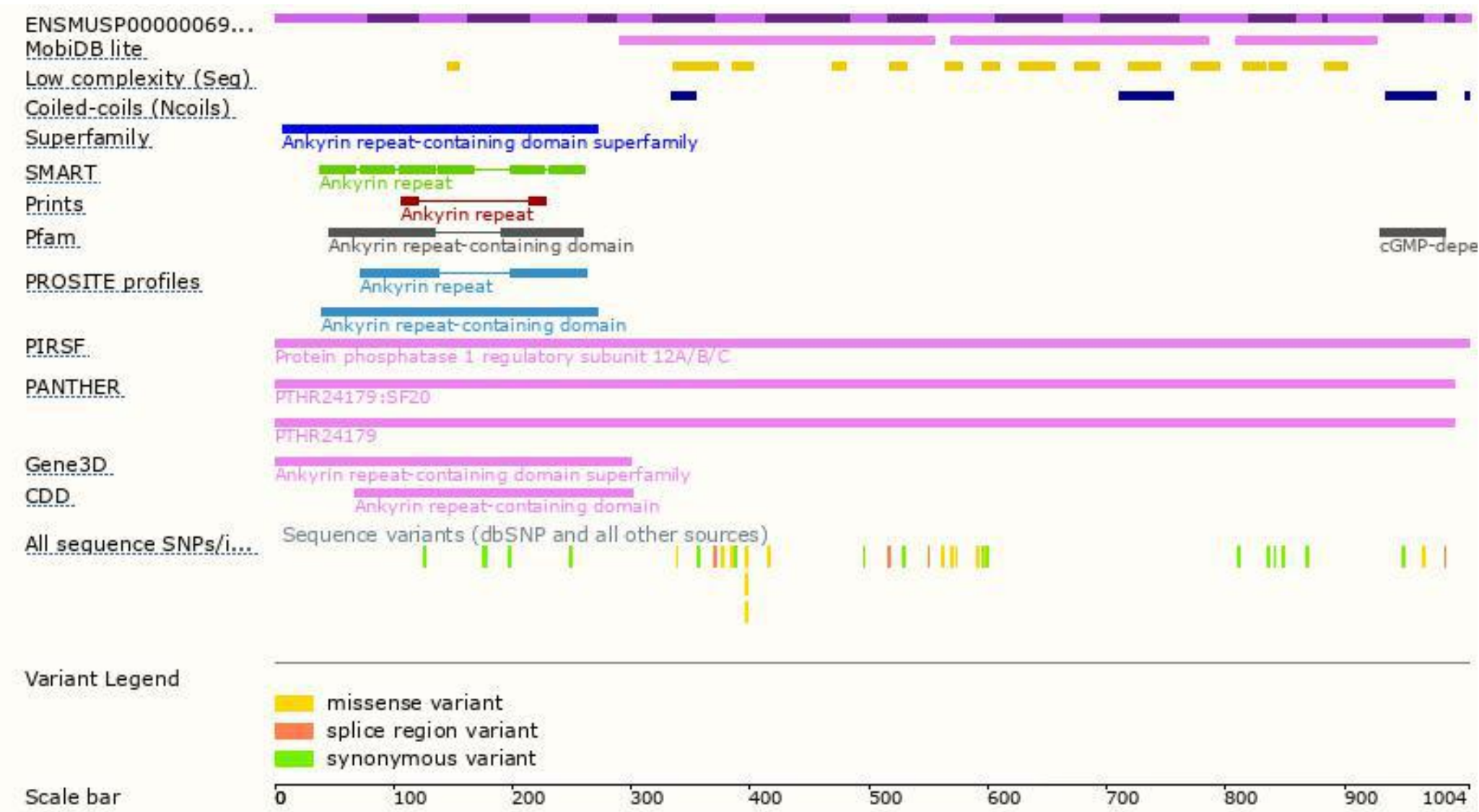
The strategy is based on the design of *Ppp1r12a-201* transcript,The transcription is shown below



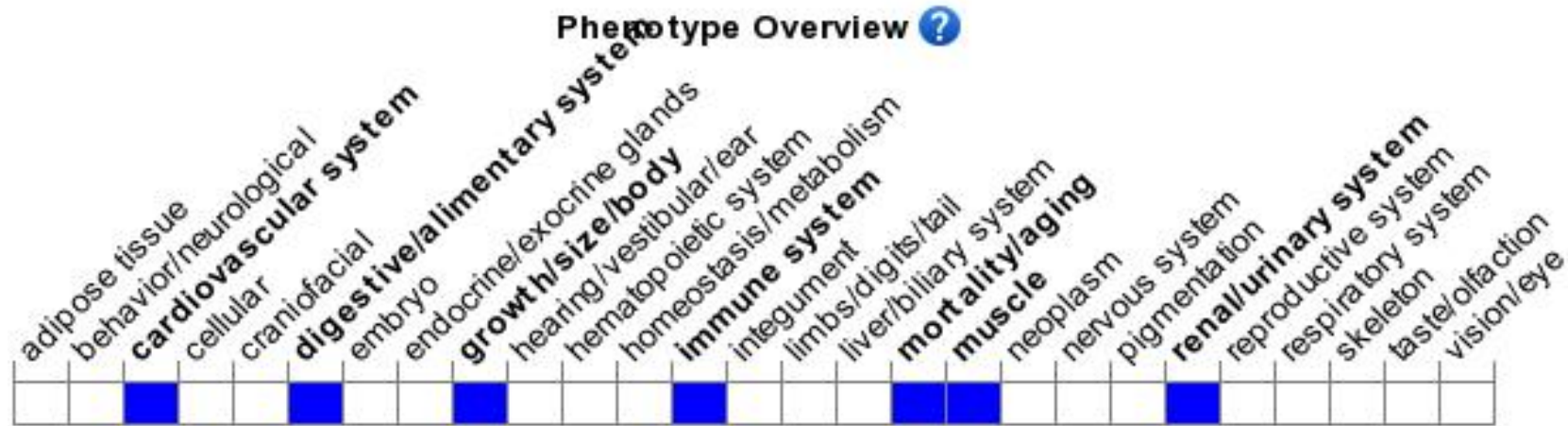
Genomic location distribution



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/>).

According to the existing MGI data, Homozygous null mice die before E7.5. Mice homozygous for a floxed allele activated in smooth muscle exhibit altered intestinal smooth muscle contractility.

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