Pkp1 Cas9-KO Strategy

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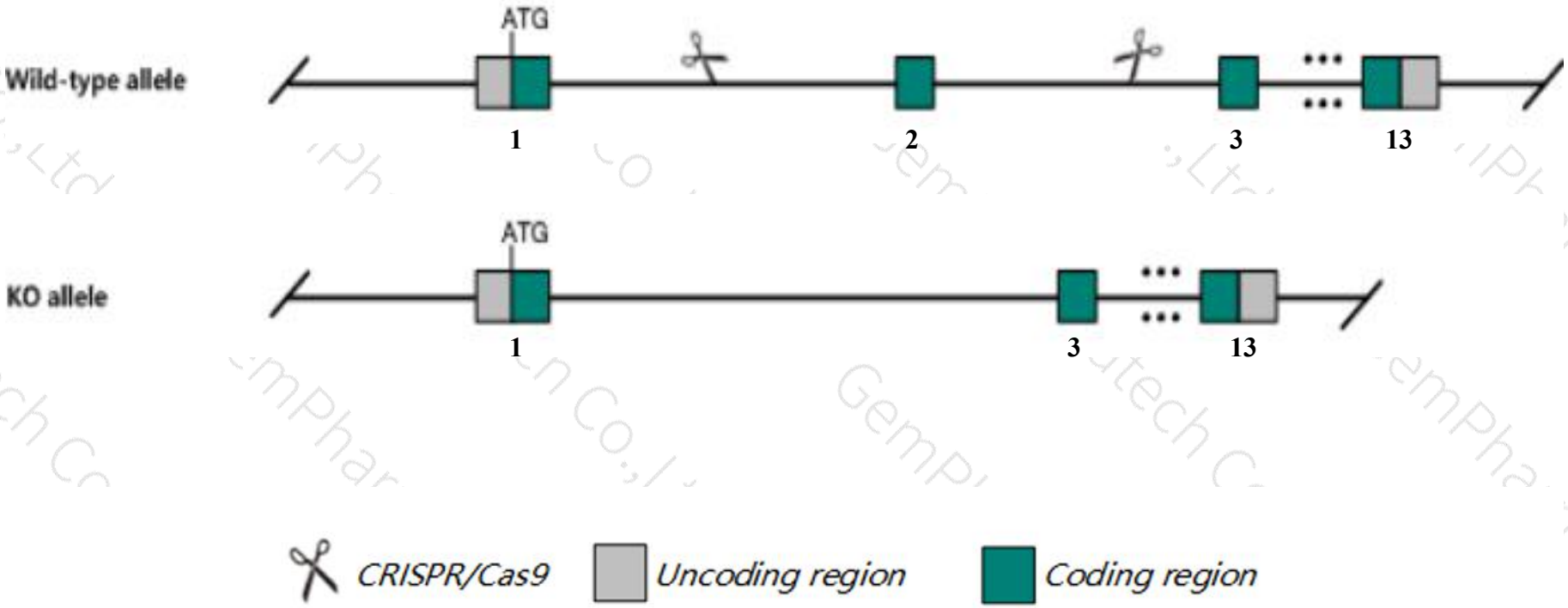
Design Date: 2020-4-7

Project Overview

Project Name	***Pkp1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pkp1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Pkp1* gene has 4 transcripts. According to the structure of *Pkp1* gene, exon2 of *Pkp1-201* (ENSMUST00000027667.12) transcript is recommended as the knockout region.The region contains 107bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Pkp1* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit reduced birth weight, absent whiskers, and neonatal lethality associated with skin fragility, skin lesions, loss of desmosomal adhesion, and impaired skin barrier function due to abnormal tight junction formation.
- The *Pkp1* 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.
- 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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Pkp1 plakophilin 1 [Mus musculus (house mouse)]

Gene ID: 18772, updated on 13-Mar-2020

Summary

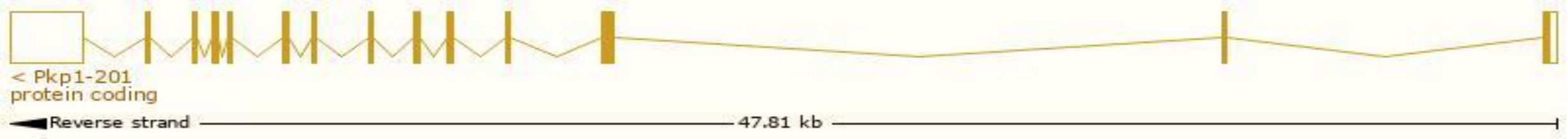
Official Symbol	Pkp1 provided by MGI
Official Full Name	plakophilin 1 provided byMGI
Primary source	MGI:MGI:1328359
See related	Ensembl:ENSMUSG00000026413
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in stomach adult (RPKM 26.4), limb E14.5 (RPKM 12.9) and 9 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

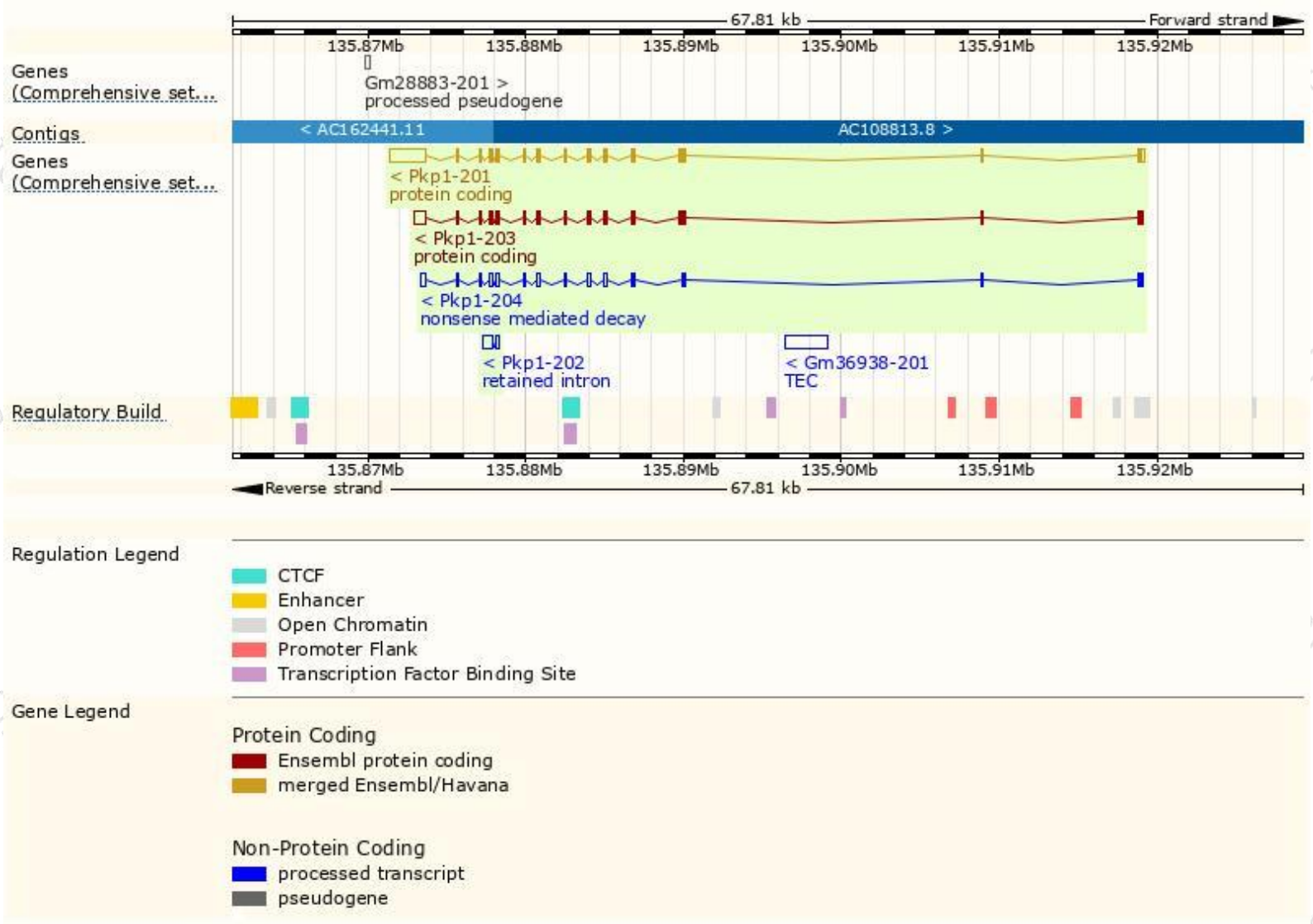
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pkp1-201	ENSMUST00000027667.12	4669	728aa	Protein coding	CCDS15322	P97350	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
Pkp1-203	ENSMUST00000163260.7	3023	728aa	Protein coding	CCDS15322	P97350	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
Pkp1-204	ENSMUST00000189805.6	2395	166aa	Nonsense mediated decay	-	A0A087WS37	TSL:5
Pkp1-202	ENSMUST00000132793.1	696	No protein	Retained intron	-	-	TSL:3

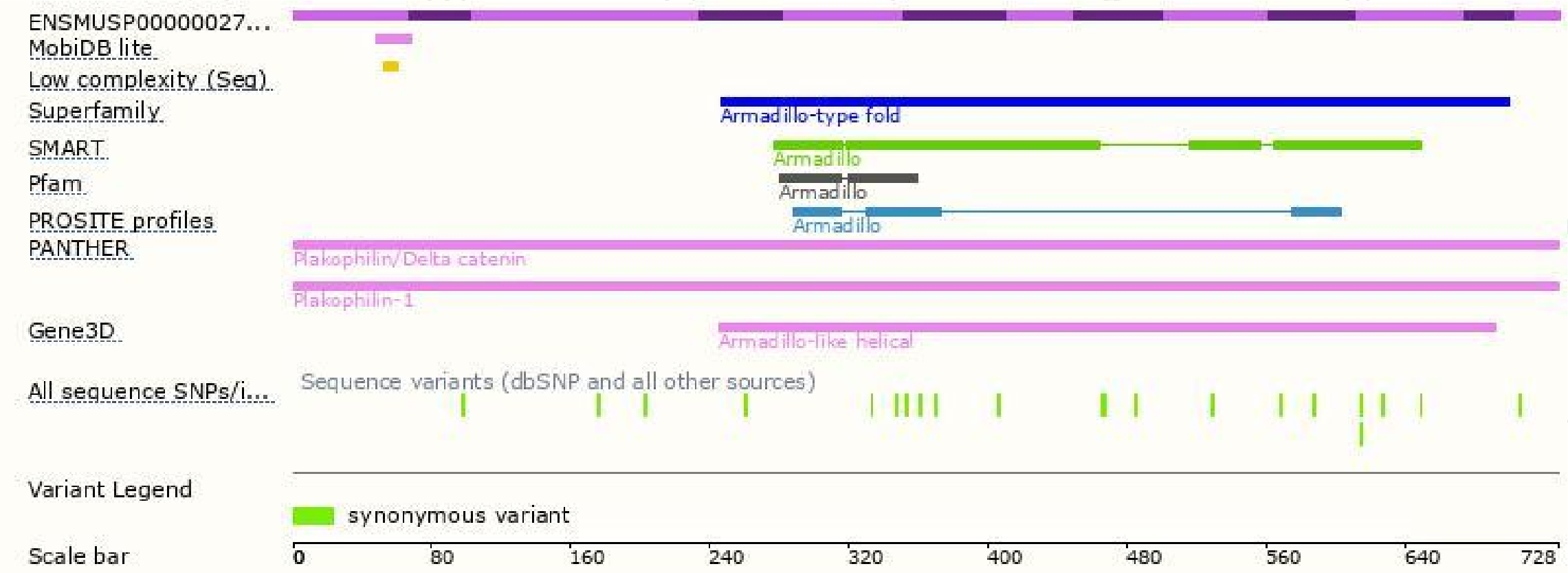
The strategy is based on the design of *Pkp1-201* transcript,The transcription is shown below



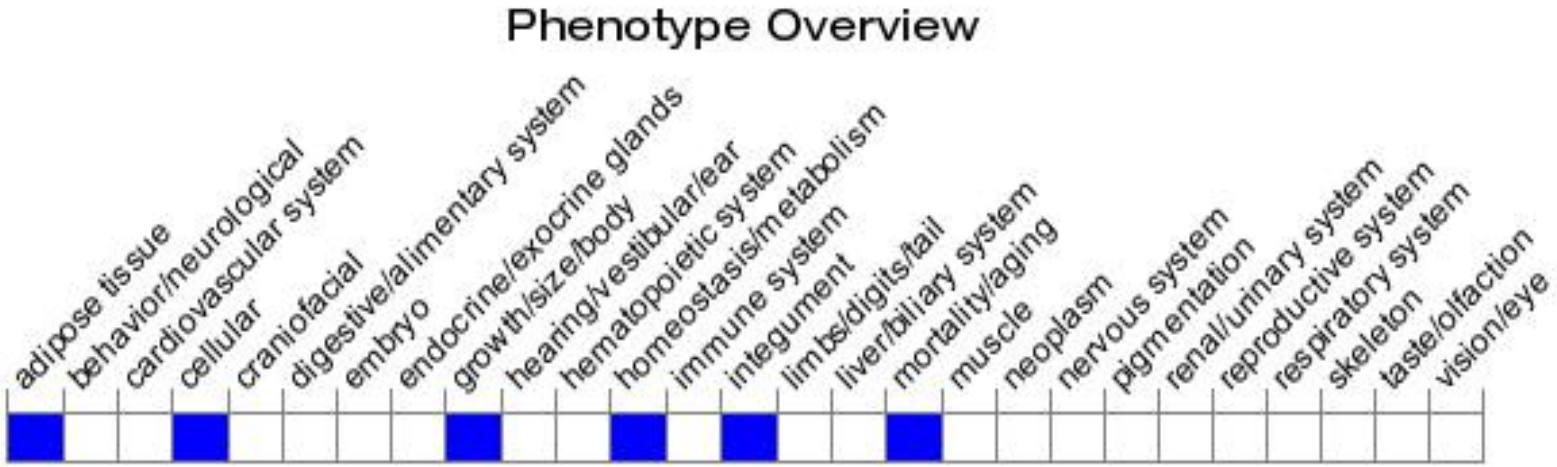
Genomic location distribution



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.

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