

Plekhn1 Cas9-KO Strategy

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Project Overview

Project Name

Plekhm1

Project type

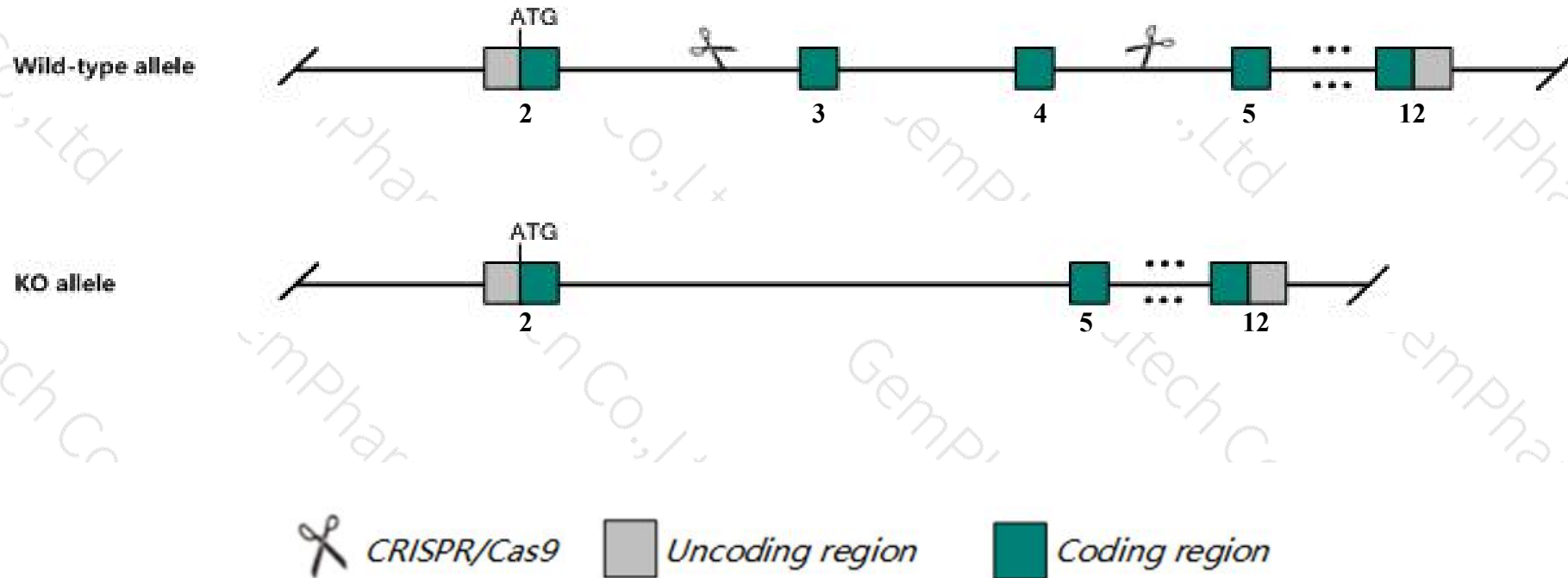
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plekhm1* gene. The schematic diagram is as follows:



- The *Plekhm1* gene has 2 transcripts. According to the structure of *Plekhm1* gene, exon3-exon4 of *Plekhm1*-201 (ENSMUST00000041272.9) transcript is recommended as the knockout region. The region contains 875bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plekhm1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased trabecular bone mass and decreased bone resorption capacity of osteoclasts caused by defects in the peripheral positioning and secretion of lysosomes. Mice homozygous for a gene trap insertion do not exhibit any detectable phenotype.
- The *Plekhl1* gene is located on the Chr11. 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)

Plekhn1 pleckstrin homology domain containing, family M (with RUN domain) member 1 [Mus musculus (house mouse)]

Gene ID: 353047, updated on 31-Jan-2019

Summary



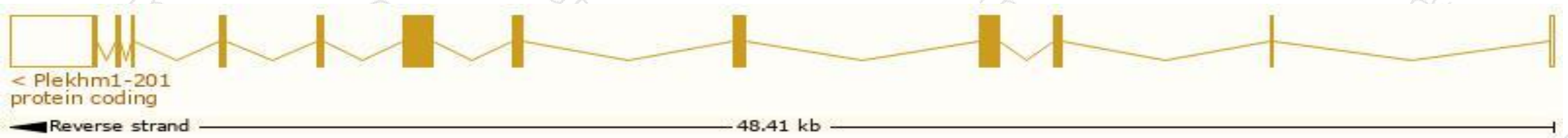
Official Symbol	Plekhn1 provided by MGI
Official Full Name	pleckstrin homology domain containing, family M (with RUN domain) member 1 provided by MGI
Primary source	MGI:MGI:2443207
See related	Ensembl:ENSMUSG00000034247
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AP162, B2, BC038943, D330036J23Rik
Expression	Ubiquitous expression in thymus adult (RPKM 17.4), mammary gland adult (RPKM 16.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

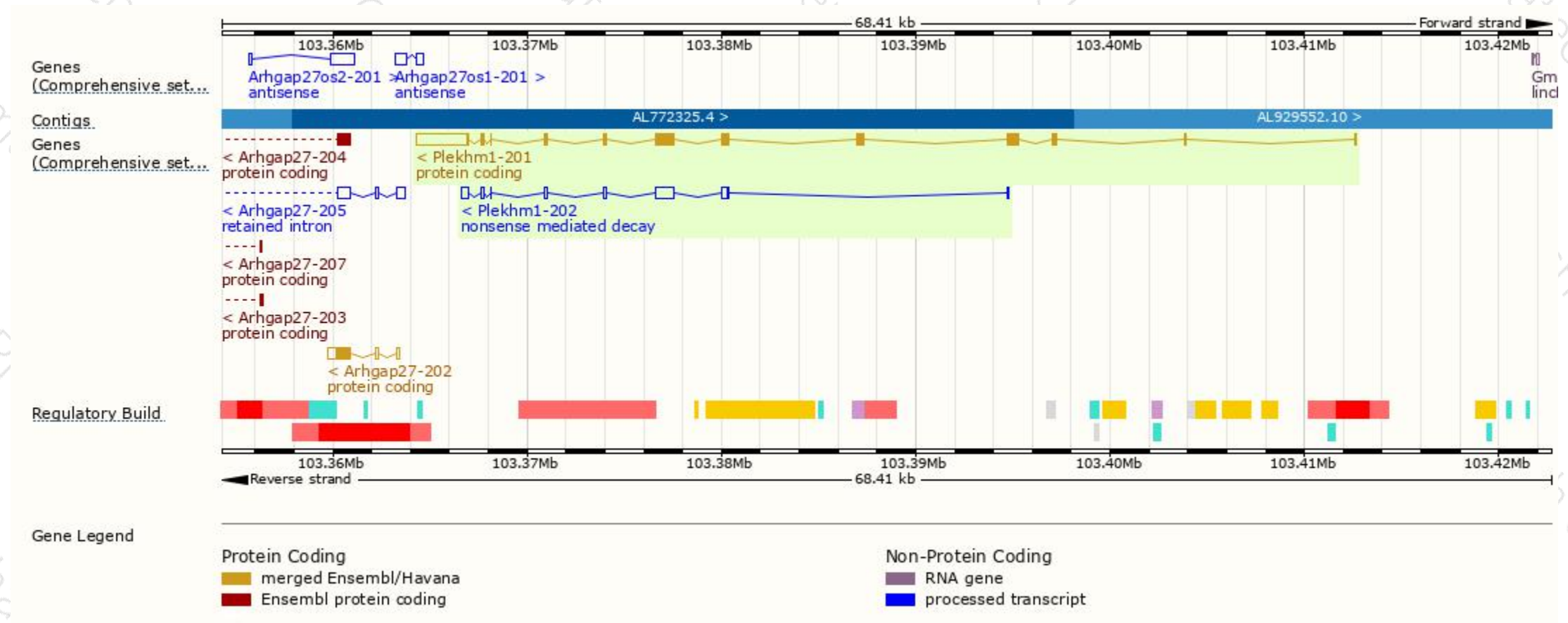
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plekhm1-201	ENSMUST00000041272.9	5968	1074aa	Protein coding	CCDS25518	Q7TSI1	TSL:1 GENCODE basic APPRIS P1
Plekhm1-202	ENSMUST00000184350.1	2260	47aa	Nonsense mediated decay	-	V9GWX7	CDS 5' incomplete TSL:5

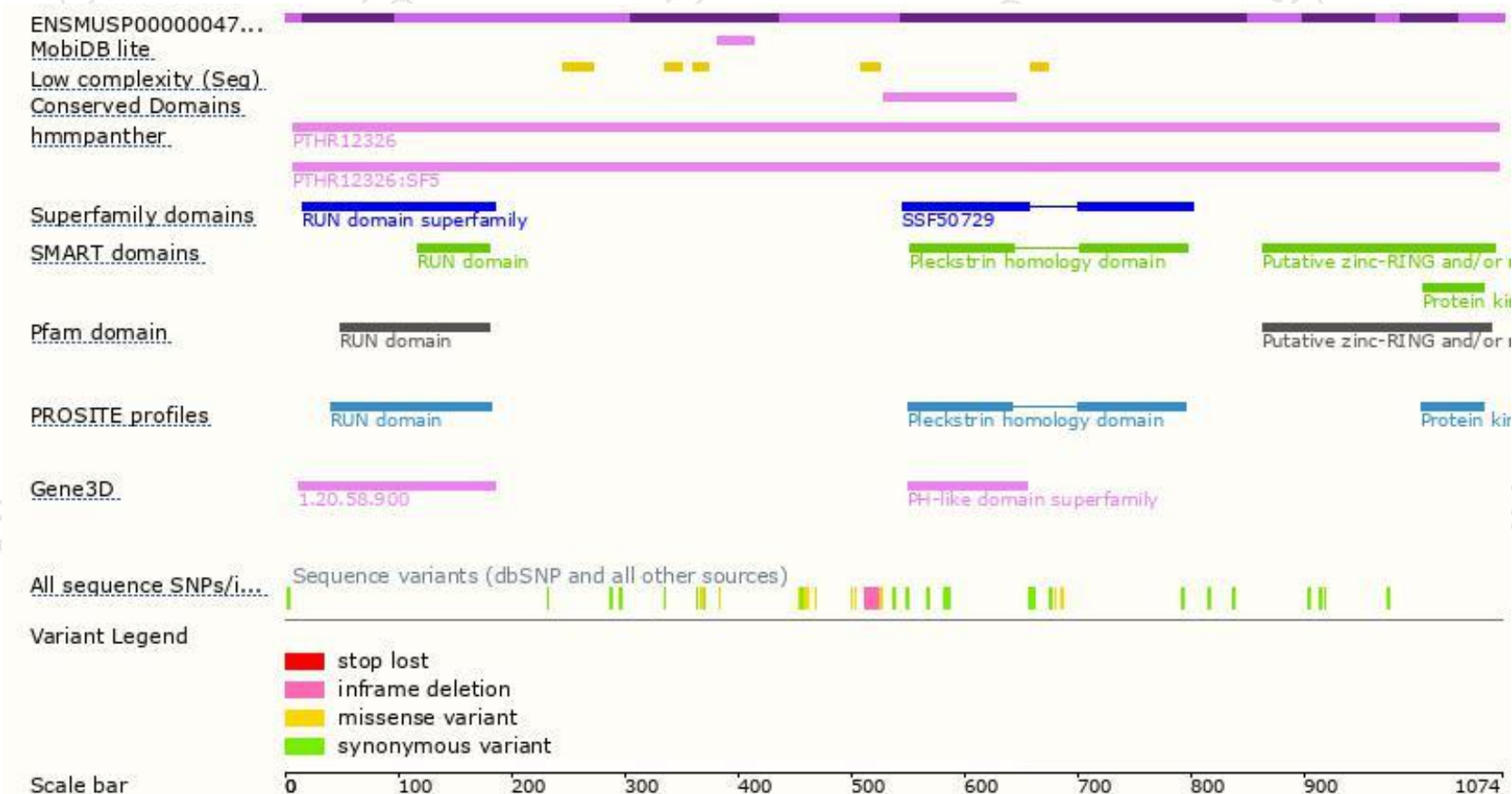
The strategy is based on the design of *Plekhm1-201* transcript,The transcription is shown below



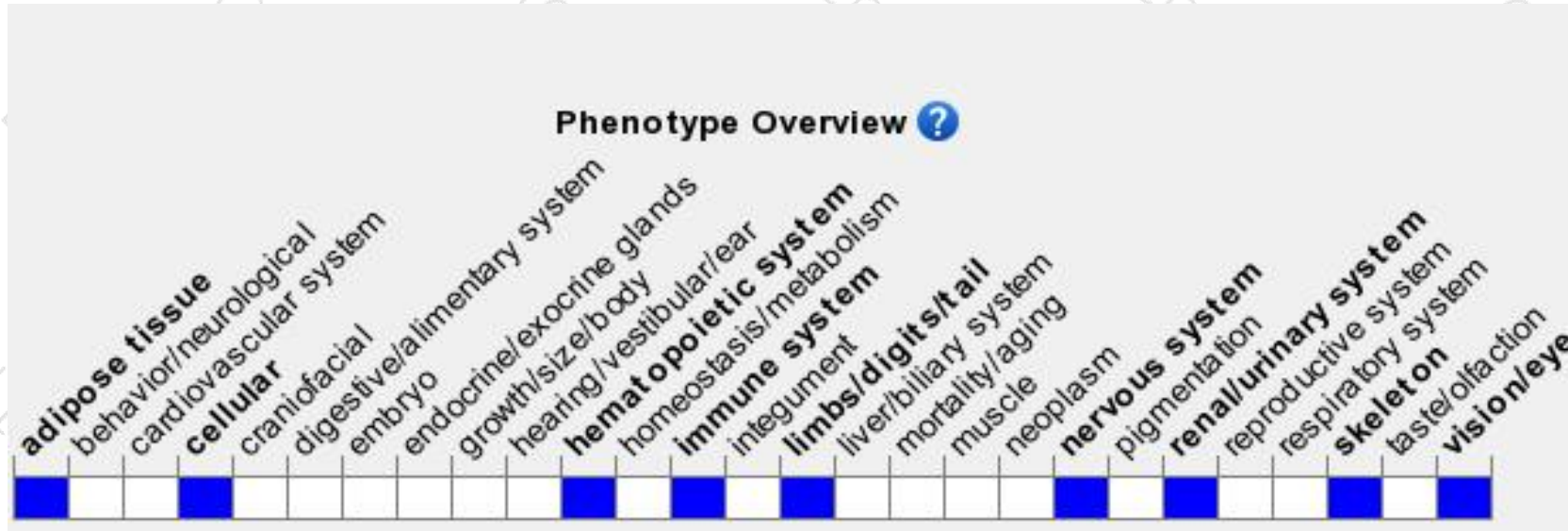
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit increased trabecular bone mass and decreased bone resorption capacity of osteoclasts caused by defects in the peripheral positioning and secretion of lysosomes. Mice homozygous for a gene trap insertion do not exhibit any detectable phenotype.

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

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