

Pls1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Pls1

Project type

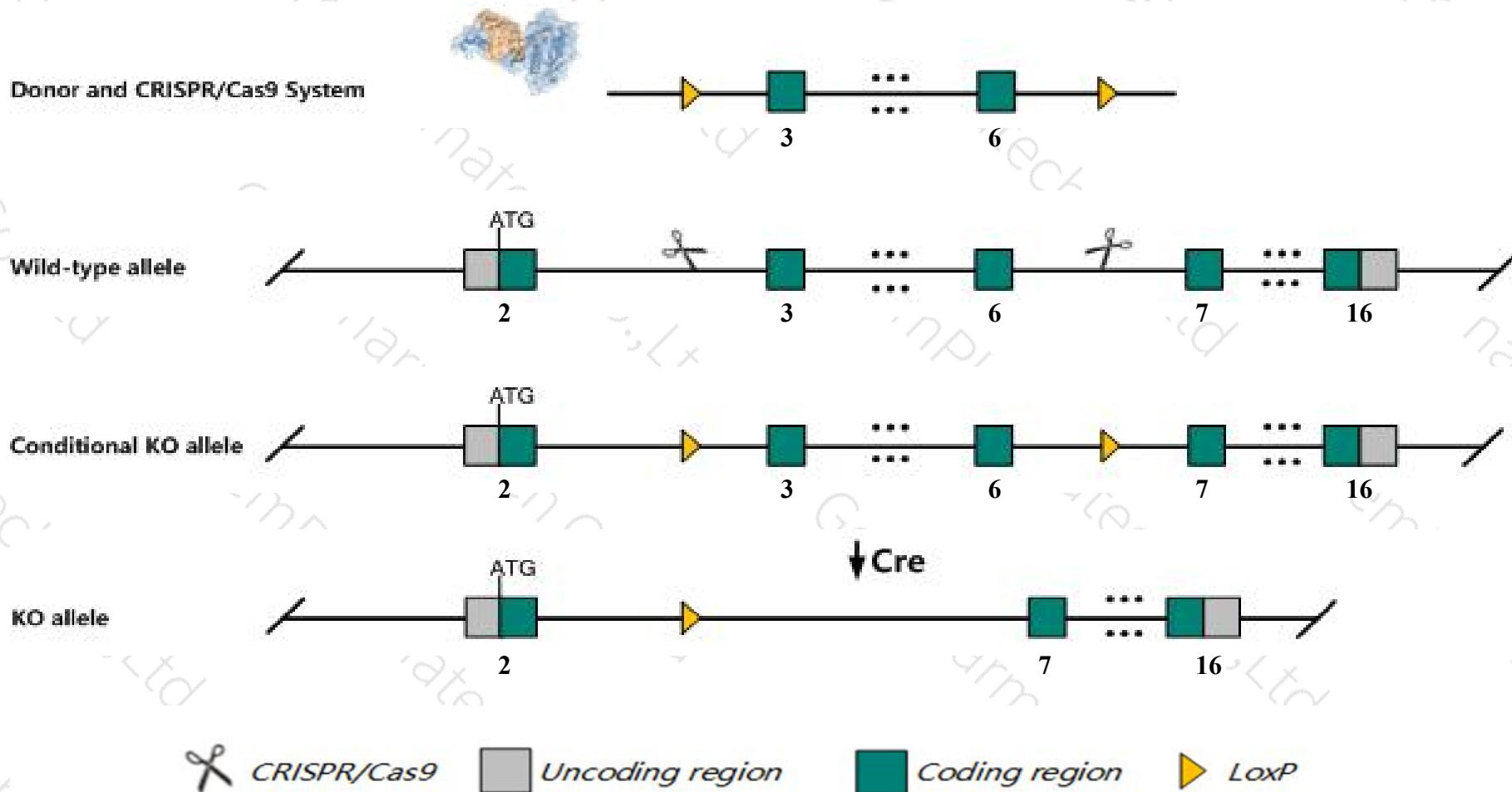
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pls1* gene. The schematic diagram is as follows:



Technical routes

- The *Pls1* gene has 3 transcripts. According to the structure of *Pls1* gene, exon3-exon6 of *Pls1-201* (ENSMUST00000093800.8) transcript is recommended as the knockout region. The region contains 509bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pls1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous inactivation for this gene leads to altered intestinal morphology and physiology, increased brush border fragility and susceptibility to induced colitis, as well as a moderate and progressive form of hearing loss associated with defects in stereocilia morphology.
- The *Pls1* gene is located on the Chr9. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Pls1 plastin 1 (I-isoform) [Mus musculus (house mouse)]

Gene ID: 102502, updated on 31-Jan-2019

Summary



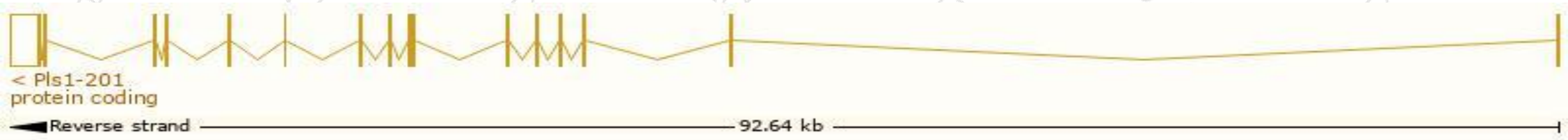
Official Symbol	Pls1 provided by MGI
Official Full Name	plastin 1 (I-isoform) provided by MGI
Primary source	MGI:MGI:104809
See related	Ensembl:ENSMUSG00000049493
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI427122
Expression	Biased expression in large intestine adult (RPKM 58.4), small intestine adult (RPKM 19.6) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

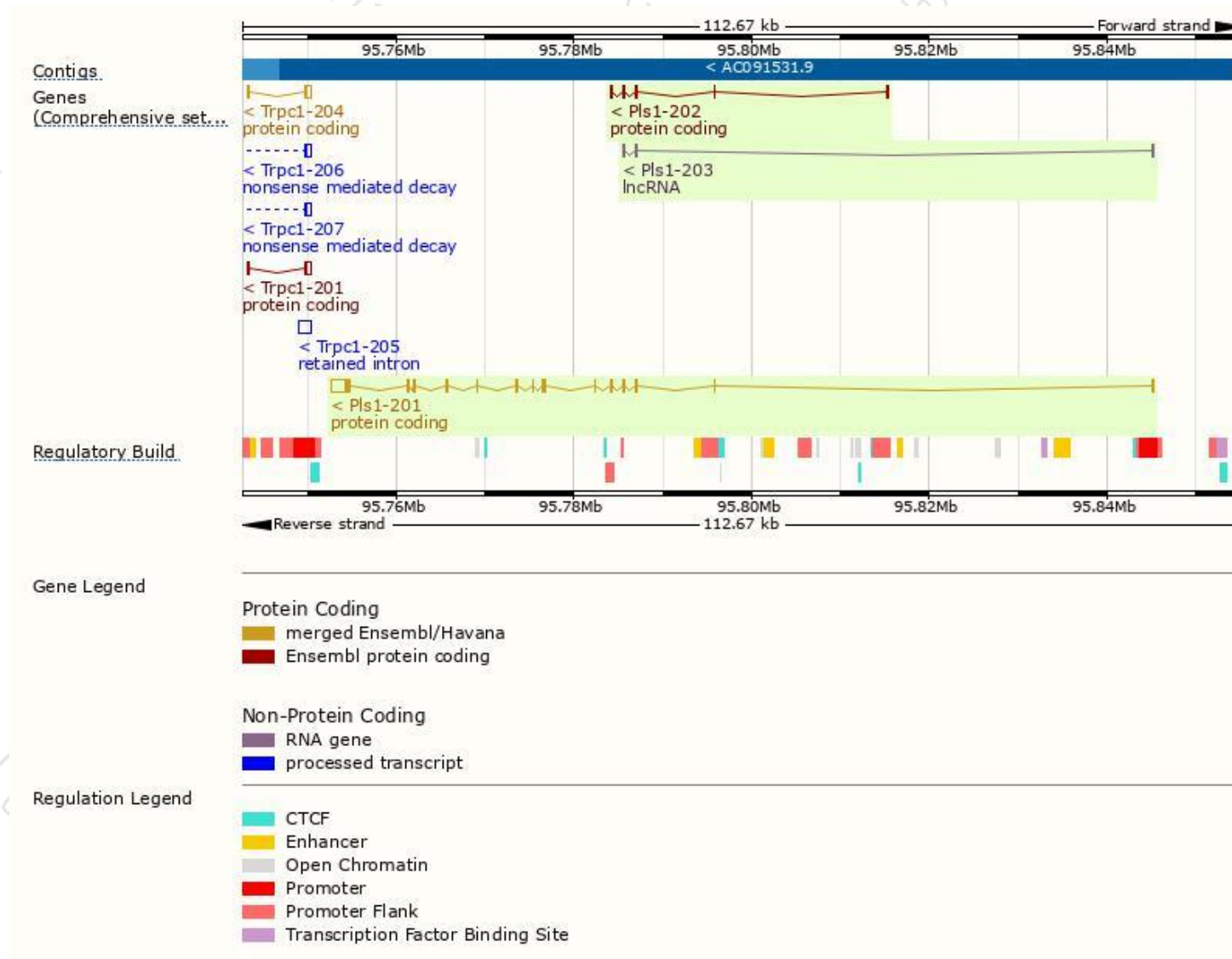
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pls1-201	ENSMUST00000093800.8	3704	630aa	Protein coding	CCDS23412	Q3V0K9	TSL:1 GENCODE basic APPRIS P1
Pls1-202	ENSMUST00000119760.1	612	138aa	Protein coding	-	D3Z6J7	CDS 3' incomplete TSL:3
Pls1-203	ENSMUST00000135816.1	371	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Pls1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000091...

Low complexity (Seq)

Superfamily

EF-hand domain pair

CH domain superfamily

SMART

Pfam

EF-hand domain

Calponin homology domain

EF-hand domain

Calponin homology domain

PROSITE profiles

PROSITE patterns

EF-hand domain

Calponin homology domain

EF-Hand 1, calcium-binding site

Actinin-type actin-binding domain, conserved site

Actinin-type actin-binding domain, conserved site

PANTHER

Fimbrin/Plastin

Plastin-1

Gene3D

1.10.238.10

CH domain superfamily

CDD

EF-hand domain

Calponin homology domain

All sequence SNPs/i....

Sequence variants (dbSNP and all other sources)

Variant Legend

missense variant

splice region variant

synonymous variant

Scale bar

0 60 120 180 240 300 360 420 480 540 630

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 inactivation for this gene leads to altered intestinal morphology and physiology, increased brush border fragility and susceptibility to induced colitis, as well as a moderate and progressive form of hearing loss associated with defects in stereocilia morphology.

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

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