

Pecam1 CKO Strategy

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Reviewer: Yanhua Shen

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Overview

Target Gene Name

- *Pecam1*

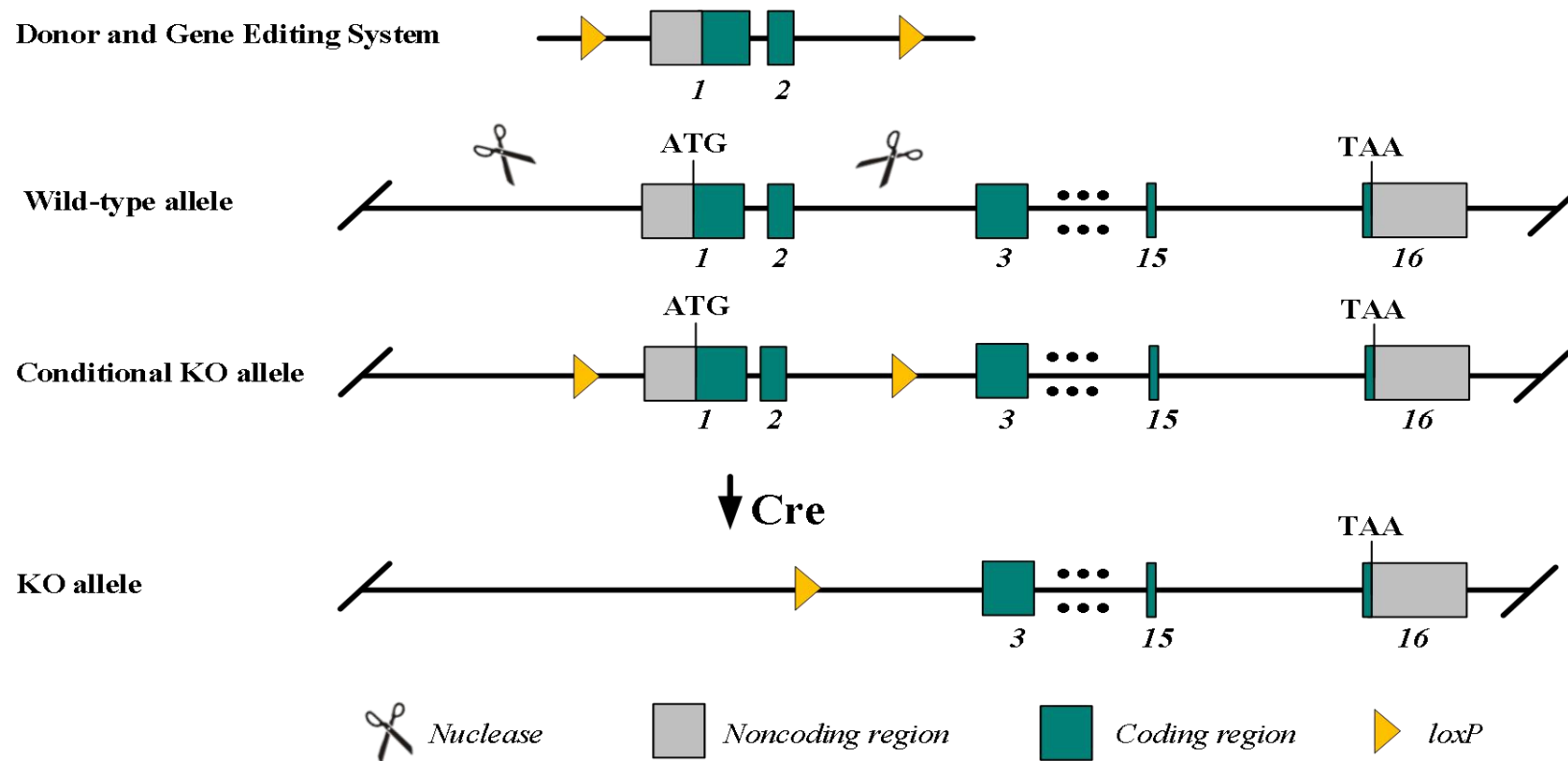
Project Type

- CKO

Genetic Background

- *C57BL/6JGpt*

Strain Strategy



Schematic representation of nuclease system used to edit the *Pecam1* gene.

Technical Information

- The *Pecam1* gene has 8 transcripts. According to the structure of *Pecam1* gene, exon 1-exon 2 of *Pecam1*-204 (ENSMUST00000106796.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knocking out the region will result in disruption of protein function.
- In this project we use gene editing technology to modify *Pecam1* gene. The brief process is as follows: nuclease system and donor were constructed in vitro, and microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

5'-end loxP insertion site

AGGACTGCATATTGTCGGAGAAGCTGGCCAGTGCAGGATAGGAGGCCCA
GATTACACTCTATGGATACAGCCCCCATAGGGAGCCCACAGGAAAGGCA
AACAGGTCTTGCTAGGTATCCCACAAAAGCACTTTTGAGTGGAAATAAAA
CCTCCTTGTCCTGTCAGGA

Reference:10.1002/dvg.23346

3'-end loxP insertion site

TTTAAAAAAATTCCTTATATGTATATATGTATATATATGATTCCTTATATGTT
TGTGGTCTTTCTGTCATAAGCTATTTCTTTTTTACATCATACTATGCCTCTAAT
TGTTTACTTTCAAACCTTCTCTTTTATTTCGCTTGGATTAGAGTCTGTAATC
CCAGTACTTGGAAAACAGACACAGAAAGATCAGTAGTGAAGTCCAGCTT
CGGCTCCATAGGAGTTTGAGGGAGGCCTGAGCTACTACGTGAAACAGTA
CAAAACCGACTCCCAAAAAAATAAAAAACTTAAAAAAGTATTTTTTTTTTCCT
TTCACTTGTTTTAATTTACAAATGAGACTCAGTTGACTTGACAGACTATGG
AGGCTGAAGGAGCAGACAGTAAATGGGTGTCAGGACTCCCTCTGTCCTA
AGAGAGTAACAAAAAGGACCAGCCAGATCCCCTTTCCCTCCCACCGGGG
AGGCTCCGCTCCTATCTGAGCTTGCTTGTGGGGAAGGGTTCTGCCTGTCT
TTAAAGTCAGACCTATCATCCACTCG

Reference:10.1002/dvg.23346

Gene Information

Pecam1 platelet/endothelial cell adhesion molecule 1 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 18613, updated on 29-Jan-2026

Summary

Official Symbol	Pecam1 provided by MGI
Official Full Name	platelet/endothelial cell adhesion molecule 1 provided by MGI
Primary source	MGI:MGI:97537
See related	Ensembl:ENSMUSG00000020717 AllianceGenome:MGI:97537
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	Cd31; Pecam; PECAM-1
Summary	Predicted to enable protein homodimerization activity; protein phosphatase binding activity; and transmembrane signaling receptor activity. Acts upstream of or within several processes, including Rho protein signal transduction; endothelial cell morphogenesis; and positive regulation of tyrosine phosphorylation of STAT protein. Located in several cellular components, including cell-cell contact zone; external side of plasma membrane; and smooth muscle contractile fiber. Is expressed in several structures, including alimentary system; cardiovascular system; central nervous system; extraembryonic component; and genitourinary system. Human ortholog(s) of this gene implicated in coronary artery disease; coronary stenosis; myocardial infarction; neuroblastoma; and psoriatic arthritis. Orthologous to human PECAM1 (platelet and endothelial cell adhesion molecule 1). [provided by Alliance of Genome Resources, Jul 2025]
Expression	Broad expression in lung adult (RPKM 94.3), subcutaneous fat pad adult (RPKM 41.1) and 17 other tissues See more
Orthologs	human all

Try the new [Gene page](#)
Try the new [Transcripts and proteins table](#)

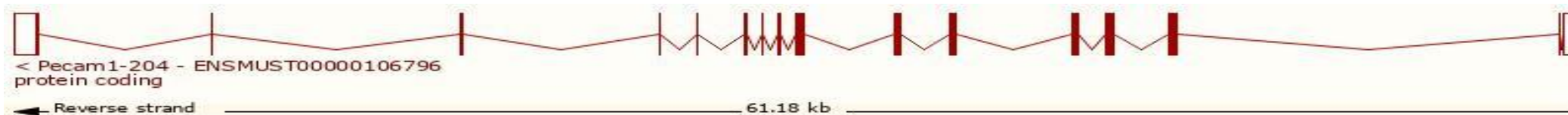
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

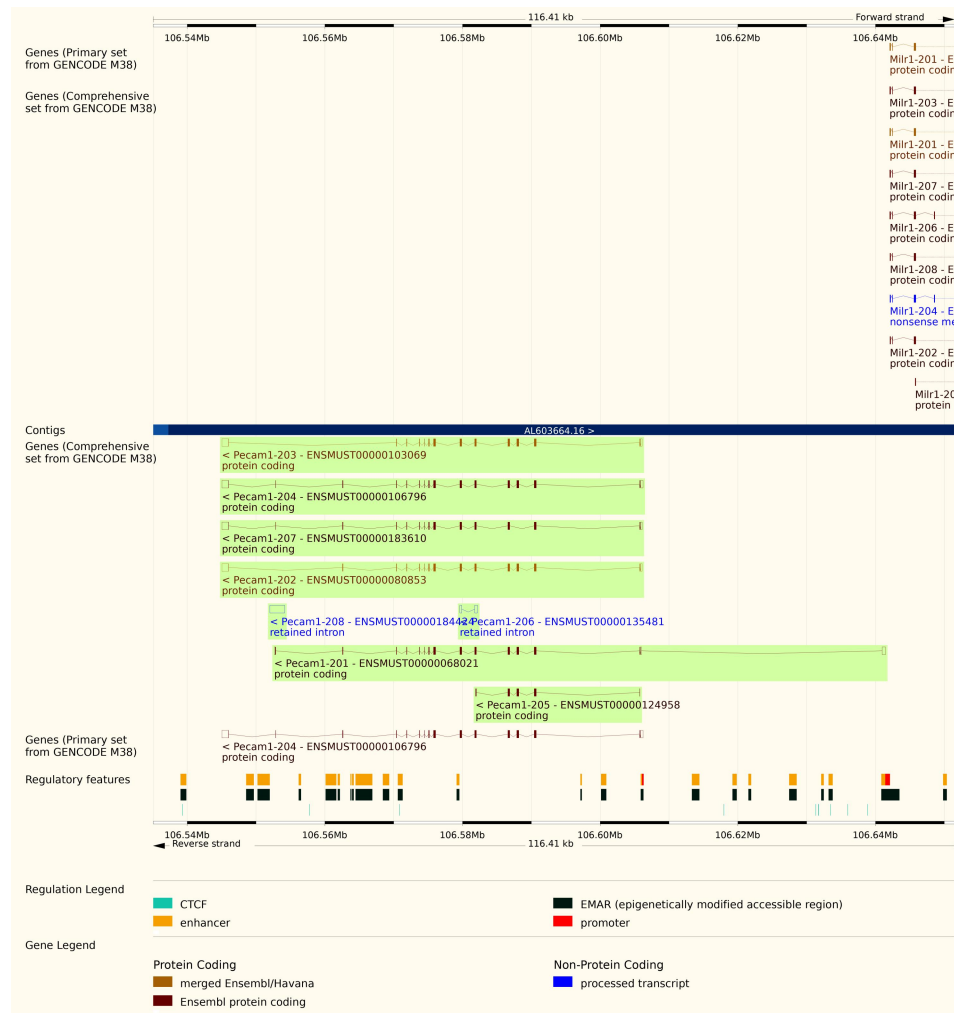
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000106796.9	Pecam1-204	3441	727aa	Protein coding	CCDS79069	Q08481-1	Ensembl Canonical Gencode Primary Gencode Basic APPRIS P1 TSL:1
ENSMUST00000080853.11	Pecam1-202	3283	716aa	Protein coding	CCDS25559	Q08481-3	Gencode Basic TSL:1
ENSMUST00000103069.10	Pecam1-203	3233	697aa	Protein coding	CCDS25558	Q08481-2	Gencode Basic TSL:1
ENSMUST00000183610.8	Pecam1-207	3006	626aa	Protein coding	CCDS79068	Q08481-4	Gencode Basic TSL:1
ENSMUST00000068021.9	Pecam1-201	2977	732aa	Protein coding		B1ARB3	Gencode Basic TSL:2
ENSMUST00000124958.3	Pecam1-205	1020	317aa	Protein coding		B1ARA9	TSL:5 CDS 3' incomplete
ENSMUST00000184424.2	Pecam1-208	2142	No protein	Retained intron		-	TSL:NA
ENSMUST00000135481.2	Pecam1-206	681	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Pecam1-204* transcript, the transcription is shown below:

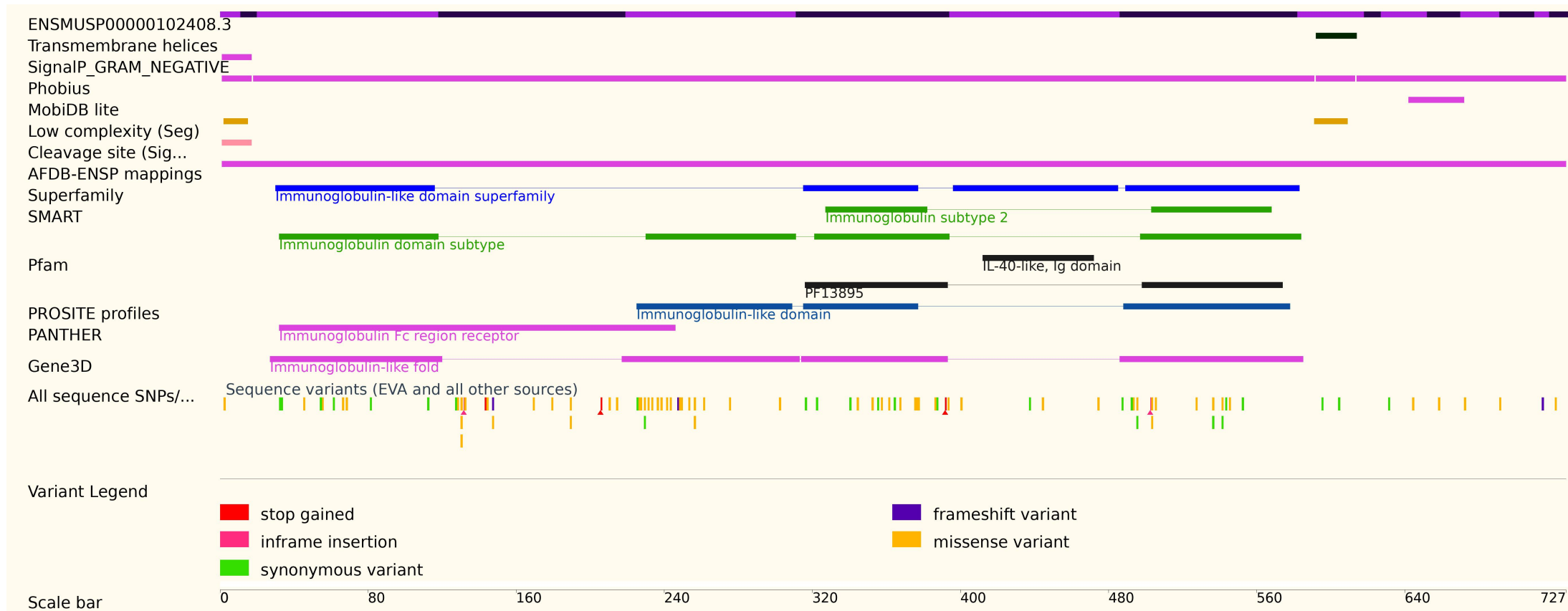


Source: <https://www.ensembl.org>

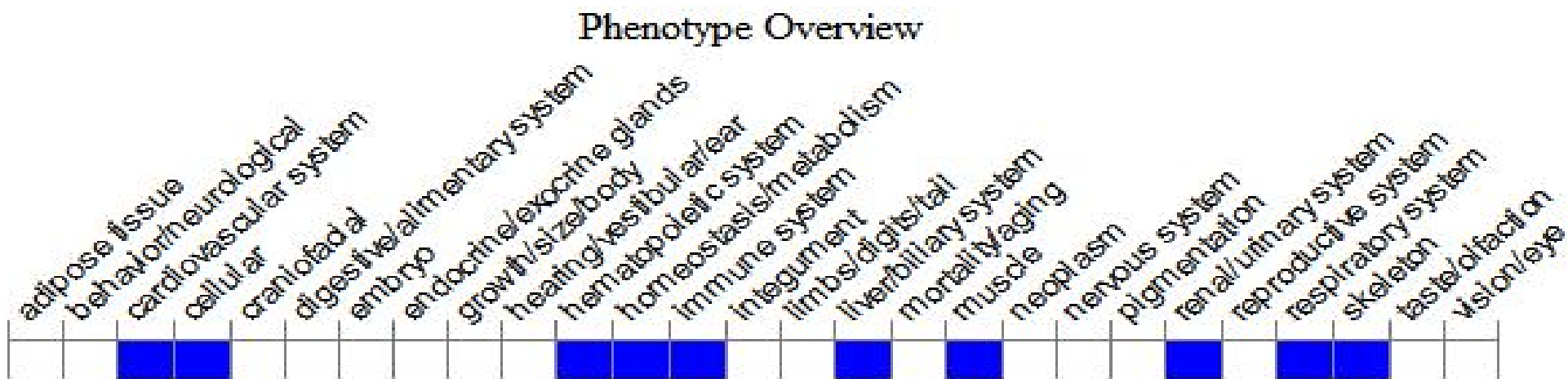
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)

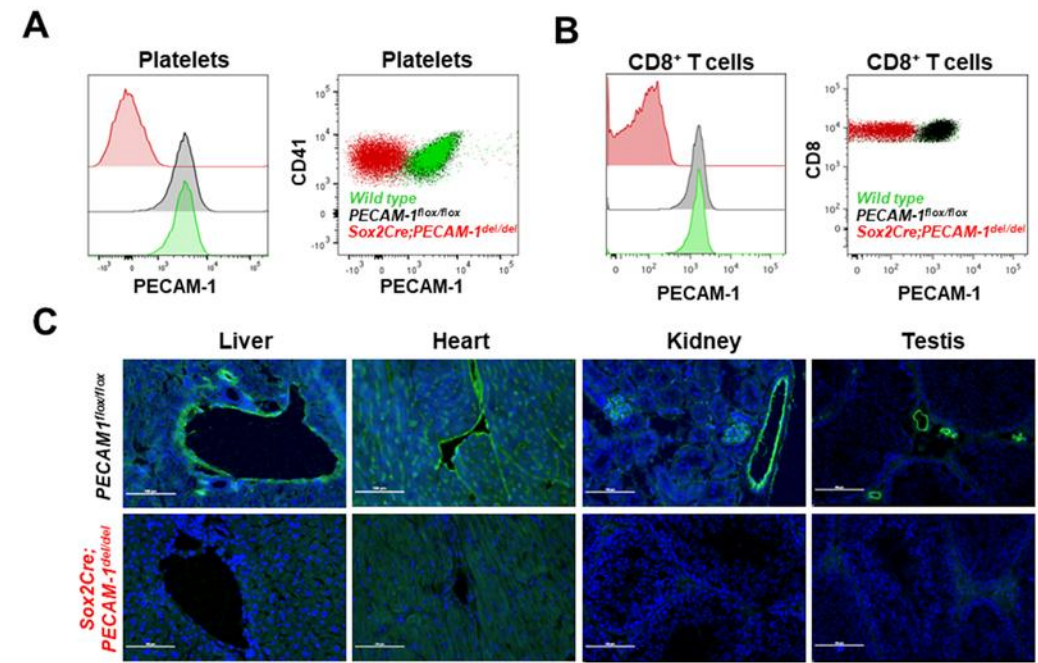
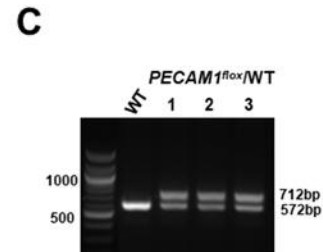
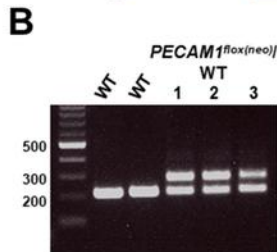
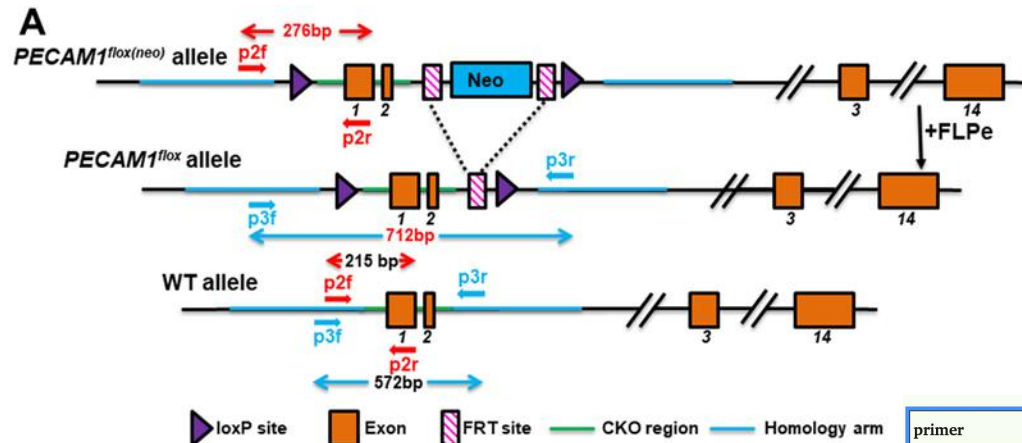


- Mice homozygous for a knock-out allele show increased susceptibility to collagen-induced arthritis, impaired lung alveolarization, and enhanced susceptibility to endotoxic shock. Mice homozygous for a gene-trapped allele show altered vasodilation and nitric oxide homeostasis.

Important Information

- According to the existing MGI data, mice homozygous for a knock-out allele show increased susceptibility to collagen-induced arthritis, impaired lung alveolarization, and enhanced susceptibility to endotoxic shock. Mice homozygous for a gene-trapped allele show altered vasodilation and nitric oxide homeostasis.
- *Pecam1* is located on Chr11. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.
- This model was developed based on existing reference, and we cannot guarantee that the phenotype (generated by the model) is consistent with what is reported in the reference.
- This model has deleted the ATG site, and the retained coding region structure at the 3' end may re-translate into an unknown protein with unpredictable function.

Reference



primer	Orientation	Primer sequence
Primer 1	Forward	5'-gctgaccctctctctgtcttta-3'
	Reverse	5'-cctctctccccctctttttgag-3'
Primer 2	Forward	5'-agccaccagtagcgttctctcaca-3'
	Reverse	5'-tcattctgggtttgggactcttc-3'
Primer 3	Forward	5'-ggaatgggagatgggttt-3'
	Reverse	5'-ggaggtccgaatcagctct-3'
Primer 4	Forward	5'-caccagtagcgttctctcaca-3'
	Reverse	5'-tgctcctcagcctccatag-3'
5'Probe	Forward	5'-taactgcagaagcatctctccagc-3'
	Reverse	5'-gcagaggtactgggtgatacaaatg-3'
3'Probe	Forward	5'-gctgaccctctgactcctctat-3'
	Reverse	5'-aggcttggcatcaggtggtcttt-3'
Neo probe	Forward	5'- cctgaatgaactgcaggacgag-3'
	Reverse	5'- agctcttcagcaatatacgggtagc-3'

Reference: 10.1002/dvg.23346