Cadm1 Cas9-CKO Strategy

Designer: Jing Chen

Reviewer: Xingkai Xiao

Design Date:2025-1-8

Overview

Target Gene Name

- Cadm1

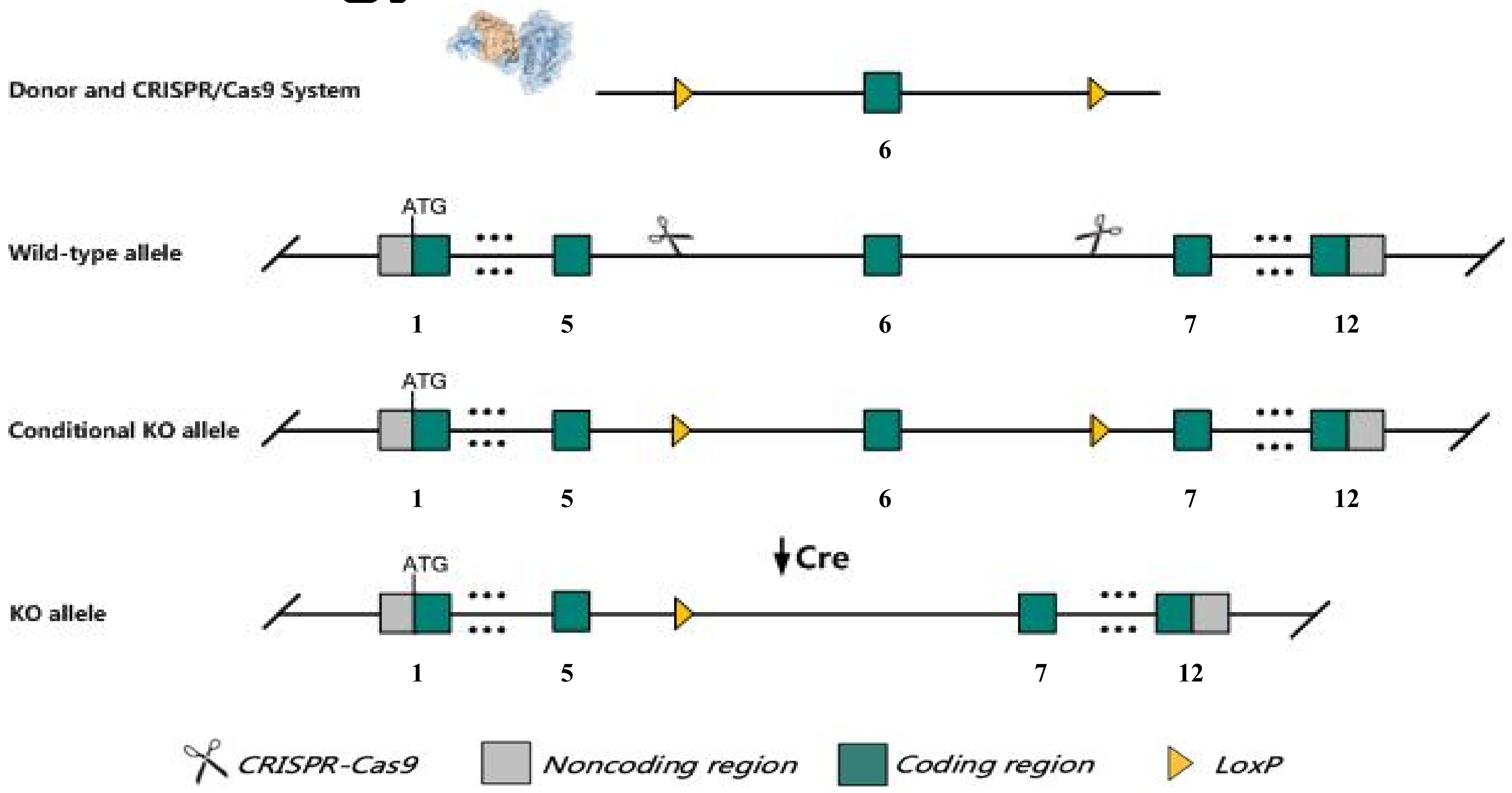
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Cadm1* gene.

Technical Information

- The *Cadm1* gene has 11 transcripts. According to the structure of *Cadm1* gene, exon 6 of *Cadm1*-209 (ENSMUST00000152459.8) transcript is recommended as the knockout region. The region contains 100 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Cadm1* 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 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.

Gene Information

Cadm1 cell adhesion molecule 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 54725, updated on 4-Jan-2025

Summary

Official Symbol	Cadm1 provided by MGI
Official Full Name	cell adhesion molecule 1 provided by MGI
Primary source	MGI:MGI:1889272
See related	Ensembl:ENSMUSG00000032076 AllianceGenome:MGI:1889272
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	Bl2; ST17; Igsf4; Necl2; RA175; Tslc1; Igsf4a; RA175A; RA175B; RA175C; RA175N; SgIGSF; SynCam; 2900073G06Rik; 3100001I08Rik
Summary	Enables PDZ domain binding activity; protein homodimerization activity; and signaling receptor binding activity. Involved in several processes, including heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules; homophilic cell adhesion via plasma membrane adhesion molecules; and synapse organization. Acts upstream of or within bone development; calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules; and unidimensional cell growth. Located in several cellular components, including basolateral plasma membrane; dendrite; and synaptic vesicle. Is active in Schaffer collateral - CA1 synapse; glutamatergic synapse; and synaptic membrane. Is expressed in several structures, including central nervous system; metanephros; peripheral nervous system; sensory organ; and tooth. Human ortholog(s) of this gene implicated in breast carcinoma and prostate cancer. Orthologous to human CADM1 (cell adhesion molecule 1). [provided by Alliance of Genome Resources, Jan 2025]
Expression	Broad expression in CNS E18 (RPKM 13.0), CNS E14 (RPKM 8.1) and 15 other tissues See more
Orthologs	human all
NEW	**Try the new Gene table** **Try the new Transcript table**

Genomic context

Location: 9 A5.3; 9 25.83 cM

See Cadm1 in Genome Data Viewer

Exon count: 19

Annotation release	Status	Assembly	Chr	Location
RS_2024_02	current	GRCm39 (GCF_000001635.27)	9	NC_000075.7 (47441468..47773578)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (47530170..47862280)

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

Transcript Information

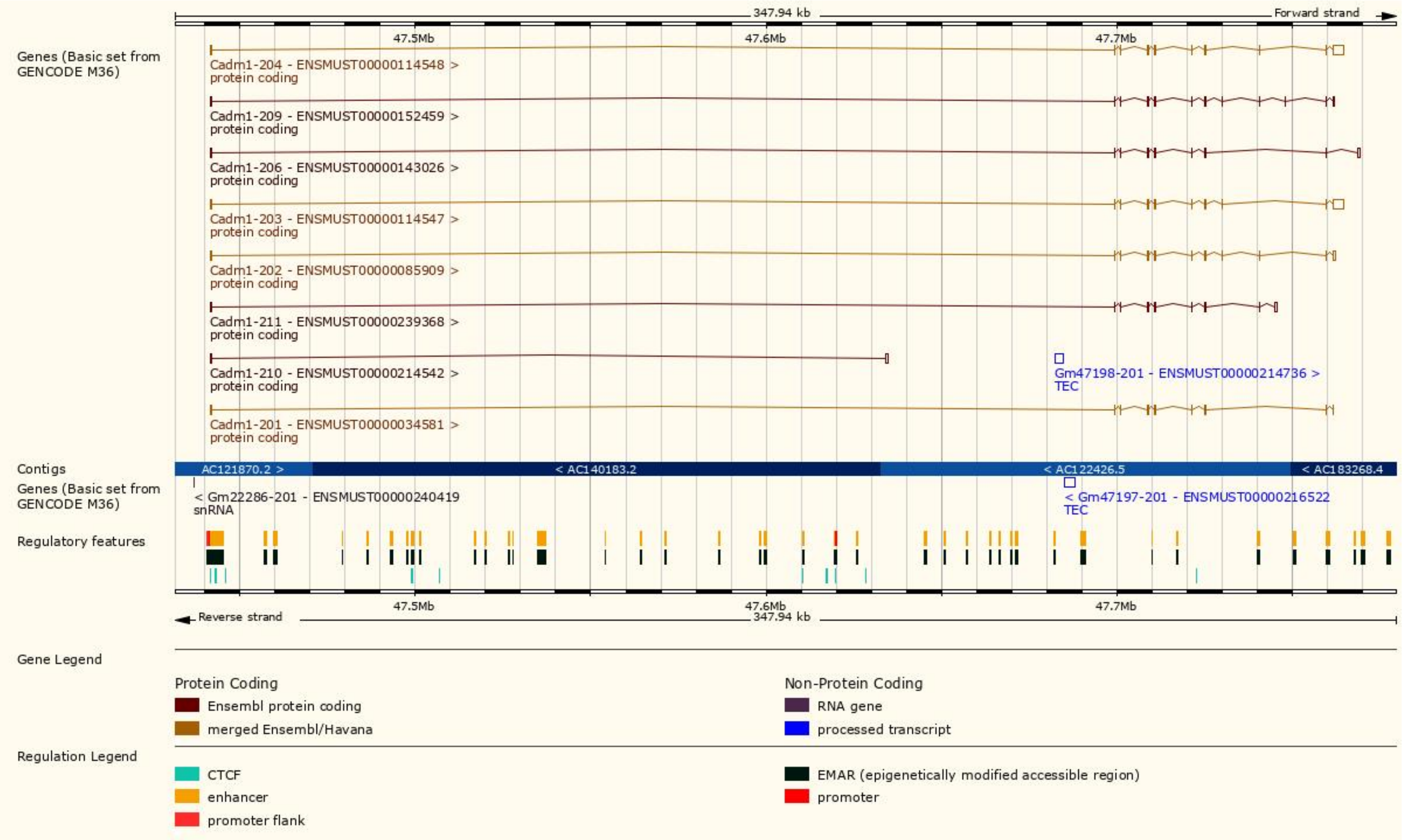
The gene has 11 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000143026.9	Cadm1-206	2121	390aa	Protein coding		E0CY16	GENCODE Basic TSL:5
ENSMUST00000239368.2	Cadm1-211	1937	361aa	Protein coding		A0A668KLV1	GENCODE Basic
ENSMUST00000214542.2	Cadm1-210	899	63aa	Protein coding		A0A1L1SS08	GENCODE Basic TSL:1
ENSMUST00000151624.2	Cadm1-208	1112	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000148925.2	Cadm1-207	4767	No protein	Retained intron		-	TSL:1
ENSMUST00000124073.8	Cadm1-205	1371	No protein	Retained intron		-	TSL:1
ENSMUST00000034581.4	Cadm1-201	1254	417aa	Protein coding	CCDS23147	Q8R5M8-4	GENCODE Basic TSL:1
ENSMUST00000114547.8	Cadm1-203	4444	445aa	Protein coding	CCDS23148	Q8R5M8-2	GENCODE Basic APPRIS ALT1 TSL:1
ENSMUST00000085909.9	Cadm1-202	2126	456aa	Protein coding	CCDS23149	Q8R5M8-1	GENCODE Basic APPRIS ALT1 TSL:1
ENSMUST00000114548.8	Cadm1-204	4482	428aa	Protein coding	CCDS23150	Q8R5M8-3	GENCODE Basic TSL:1
ENSMUST00000152459.8	Cadm1-209	1784	474aa	Protein coding	CCDS80990	E9PYN1	Ensembl Canonical GENCODE Basic APPRIS P4 TSL:1

The strategy is based on the design of *Cadm1*-209 transcript, the transcription is shown below:

Source: https://www.ensembl.org

Genomic Information

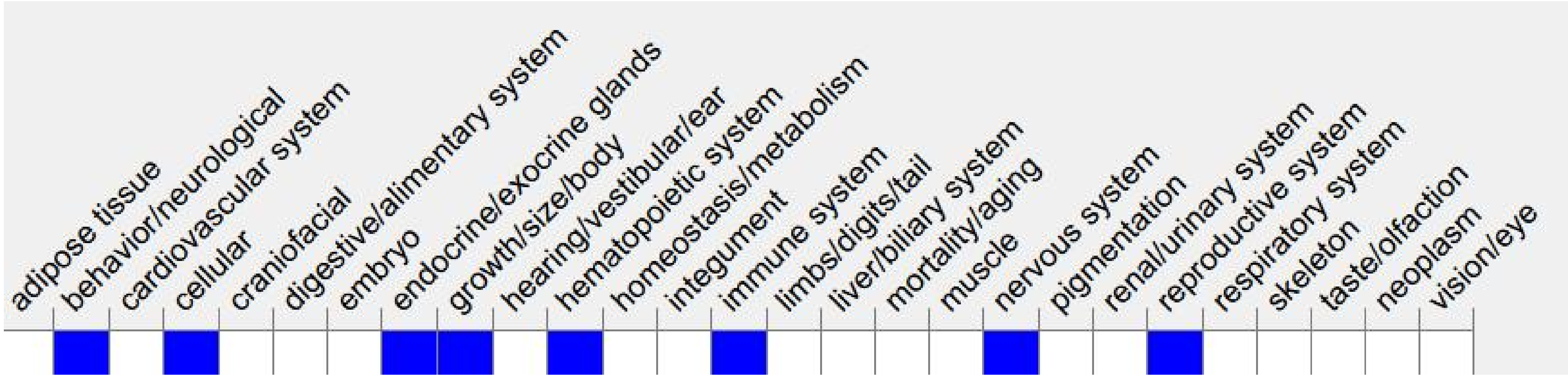


Source: : https://www.ensembl.org

Protein Information

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

Mouse Phenotype Information (MGI)



- Homozygous mutant male mice show infertility due to block in maturation of spermatogenesis. Mice homozygous for a gene trap allele exhibit decreased body size, impaired T cell development, and impaired T cell response to anti-CD3/CD28 antibody stimulation.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data， Homozygous mutant male mice show infertility due to block in maturation of spermatogenesis. Mice homozygous for a gene trap allele exhibit decreased body size, impaired T cell development, and impaired T cell response to anti-CD3/CD28 antibody stimulation.
- The influence of the transcript *Cadm1*-210 is unknown.
- *Cadm1* is located on Chr 9. 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.