

Sema3e Cas9-CKO Strategy

Designer: Ruirui Zhang

Reviewer: Xueting Zhang

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Overview

Target Gene Name

- Sema3e

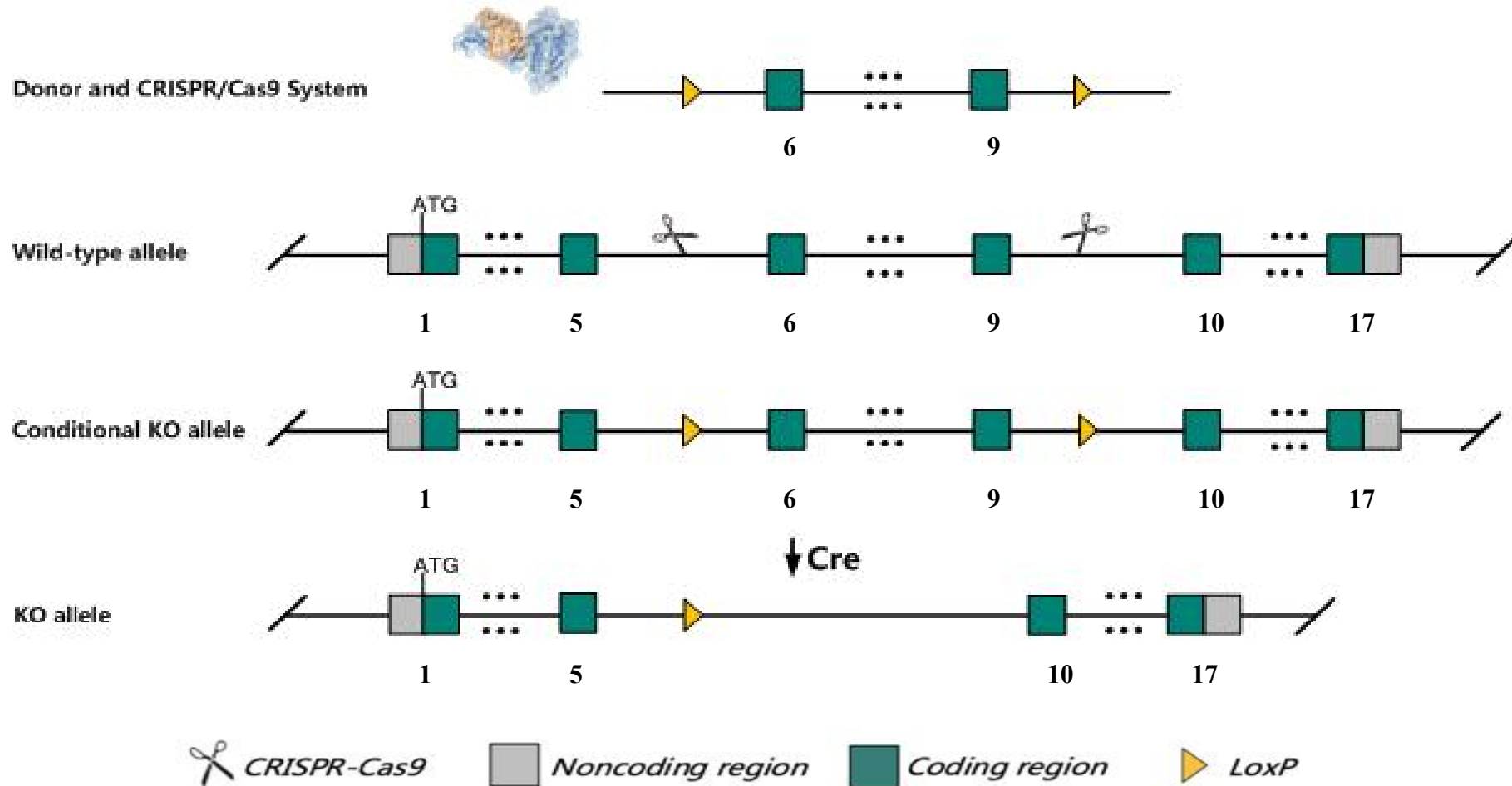
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Sema3e* gene.

Technical Information

- The *Sema3e* gene has 3 transcripts. According to the structure of *Sema3e* gene, exon6-exon9 of *Sema3e*-201 (ENSMUST00000073957.8) transcript is recommended as the knockout region. The region contains 448bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Sema3e* 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

Sema3e sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E [Mus musculus (house mouse)]

Gene ID: 20349, updated on 12-Apr-2023

Summary

Official Symbol	Sema3e provided by MGI
Official Full Name	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E provided by MGI
Primary source	MGI:MGI:1340034
See related	Ensembl:ENSMUSG00000063531
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	6430702L12, Semah, mKIAA0331
Summary	Enables semaphorin receptor binding activity. Involved in several processes, including angiogenesis; negative regulation of angiogenesis; and regulation of actin cytoskeleton reorganization. Located in extracellular space. Is expressed in several structures, including hemolymphoid system gland; nervous system; nose; palatal shelf mesenchyme; and trunk mesenchyme. Human ortholog(s) of this gene implicated in CHARGE syndrome. Orthologous to human SEMA3E (semaphorin 3E). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in lung adult (RPKM 7.6), placenta adult (RPKM 3.8) and 10 other tissues See more
Orthologs	human all

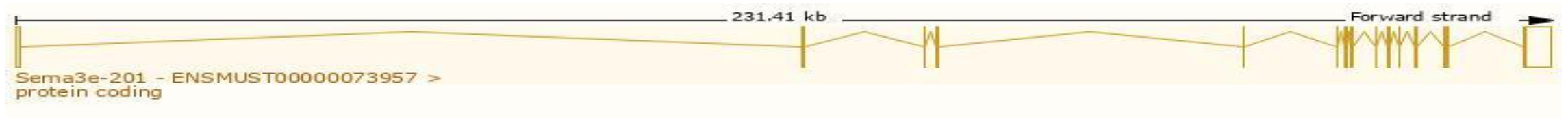
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

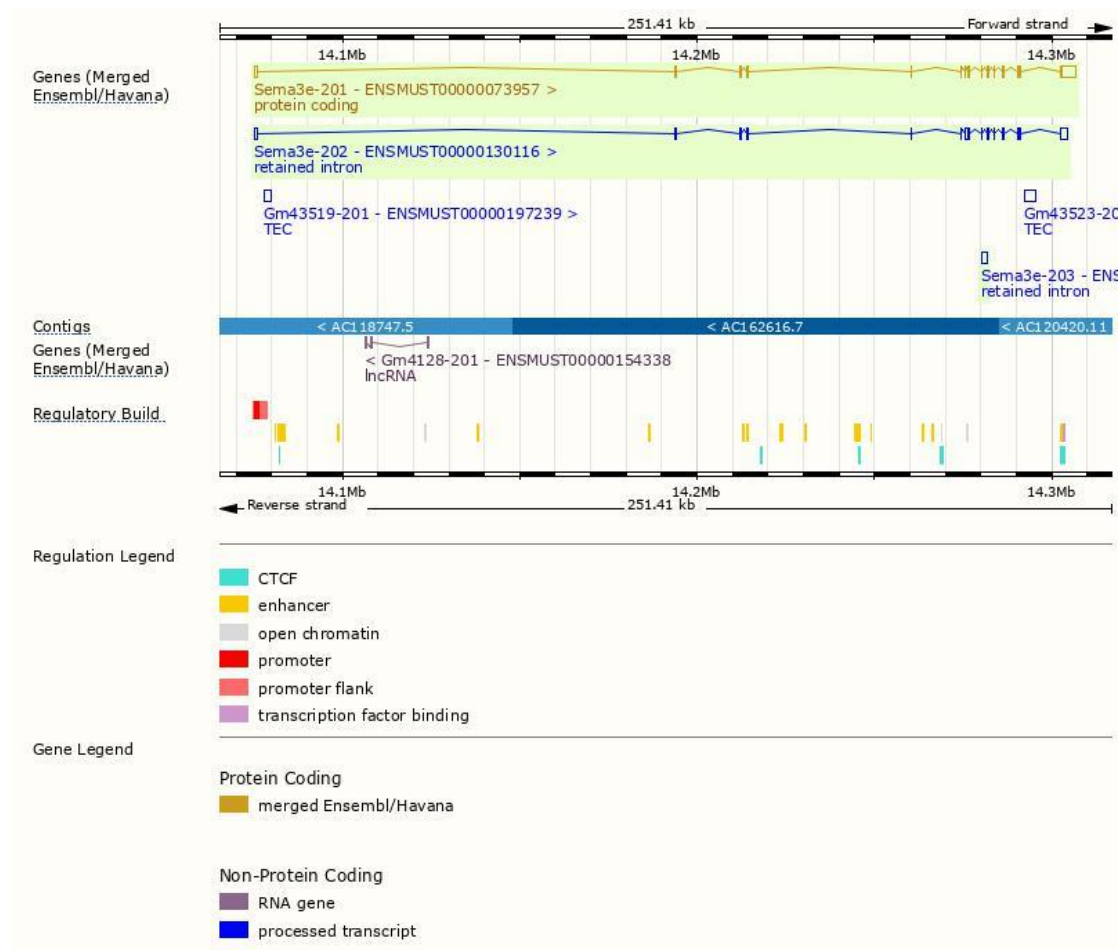
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags			
ENSMUST00000073957.8	Sema3e-201	6861	775aa	Protein coding	CCDS19093	P70275	Ensembl Canonical	GENCODE basic	APPRIS P1	TSL:1
ENSMUST00000130116.2	Sema3e-202	5206	No protein	Retained intron		-		TSL:2		
ENSMUST00000199698.2	Sema3e-203	1849	No protein	Retained intron		-		TSL:NA		

The strategy is based on the design of *Sema3e-201* transcript, the transcription is shown below:

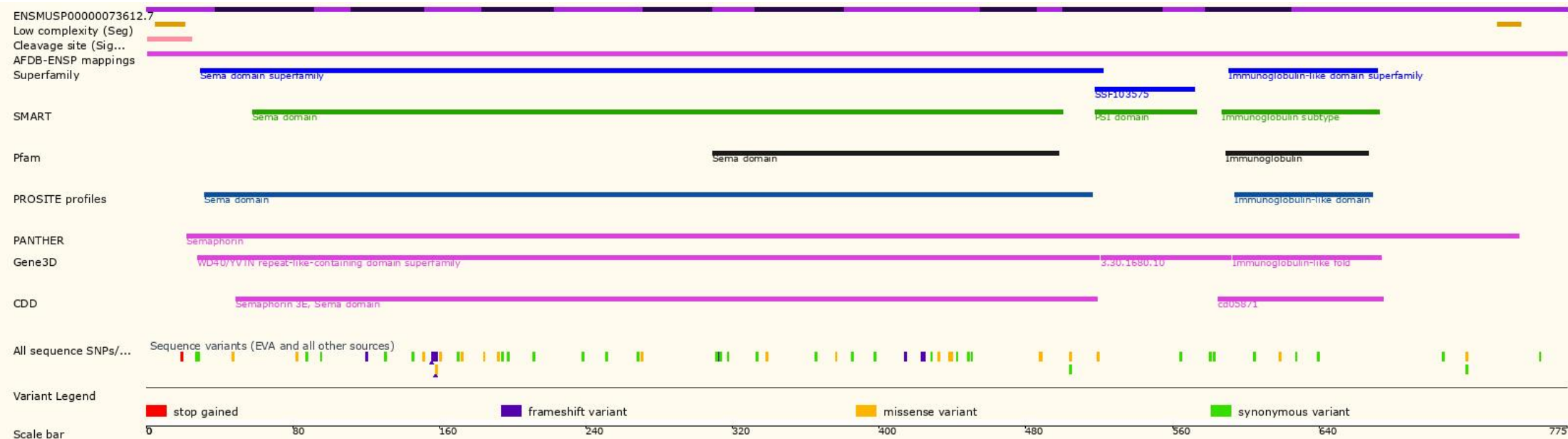


Source: <https://www.ensembl.org>

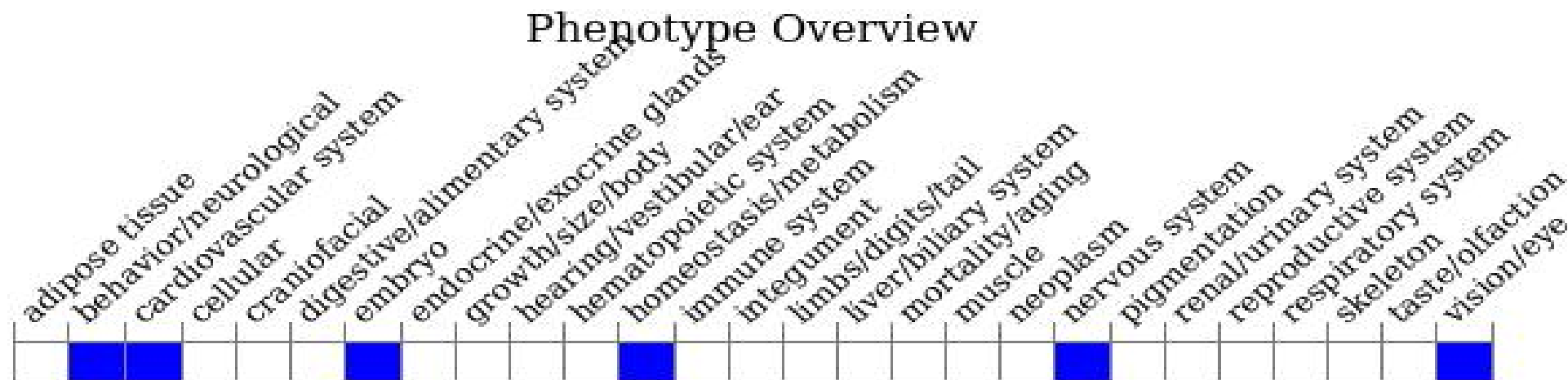
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Homozygous null mice display abnormal intersomitic vacular development and loss of the normal segmented somite pattern. Homozygous mutants for another allele have Bergmeister papillae on the surface of the optic disc.

Important Information

- *Sema3e* is located on Chr5. 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.