

Sema3e Cas9-KO Strategy

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Reviewer: Shilei Zhu

Design Date: 2018-11-28

Overview

Target Gene Name

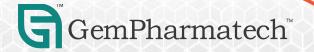
• Sema3e

Project Type

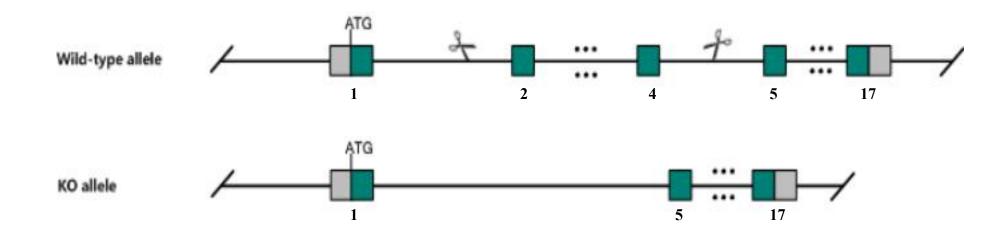
• Cas9-KO

Genetic Background

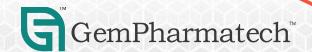
• C57BL/6JGpt



Strain Strategy







Technical Information

- The *Sema3e* gene has 3 transcripts. According to the structure of *Sema3e* gene, exon2-exon4 of *Sema3e*-201 (ENSMUST00000073957.8) transcript is recommended as the knockout region. The region contains 341bp 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: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 ontarget 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.



Gene Information

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

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Gene ID: 20349, updated on 31-Oct-2023



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 AllianceGenome:MGI:1340034

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 Semah; mKIAA0331; 6430702L12

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

Try the new Gene table

Try the new Transcript table

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

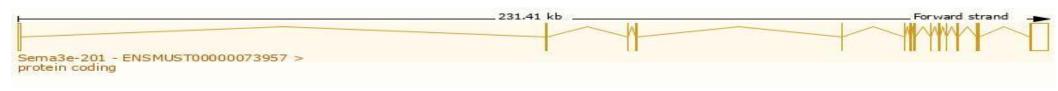


Transcript Information

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	<u>775aa</u>	Protein coding	CCDS19093₽	P70275 ₺	Ensembl Canonical	GENCODE basic	APPRIS P1	TSL:1
ENSMUST00000130116.2	Sema3e-202	5206	No protein	Retained intron		22%		TSL:2		
ENSMUST00000199698.2	Sema3e-203	1849	No protein	Retained intron		8277		TSL:NA		

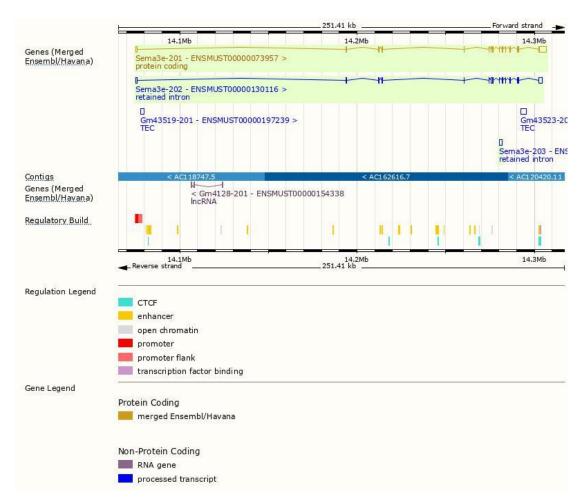
The strategy is based on the design of *Sema3e*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



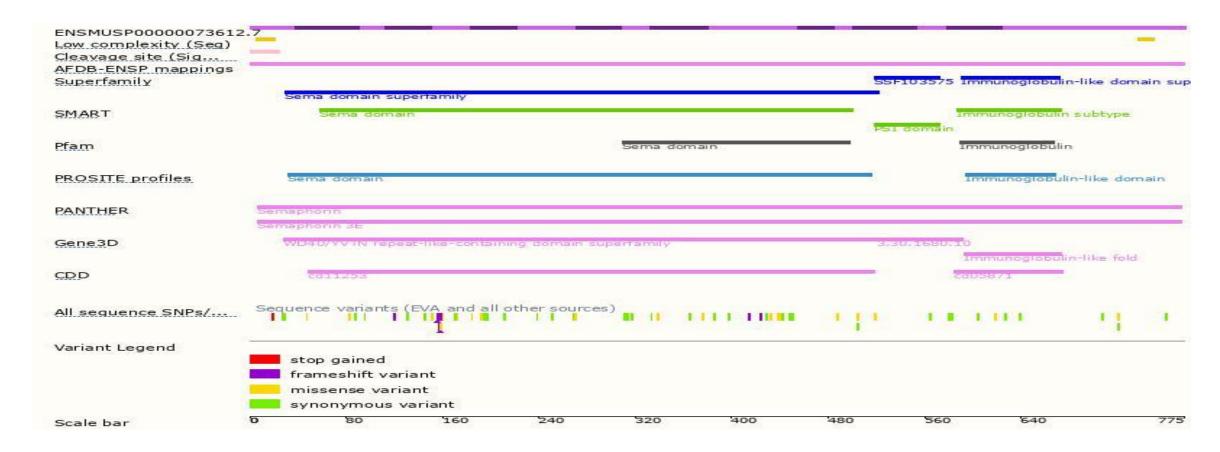
Genomic Information

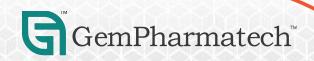




Source: : https://www.ensembl.org

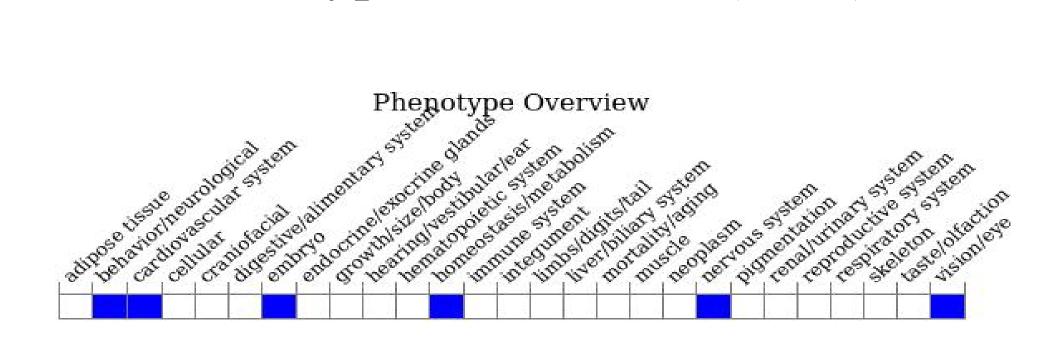
Protein Information





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

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.



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

Important Information

- According to MGI information, 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.
- *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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

