

Sema7a Cas9-KO Strategy

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Reviewer:

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Project Overview



Project Name

Sema7a

Project type

Cas9-KO

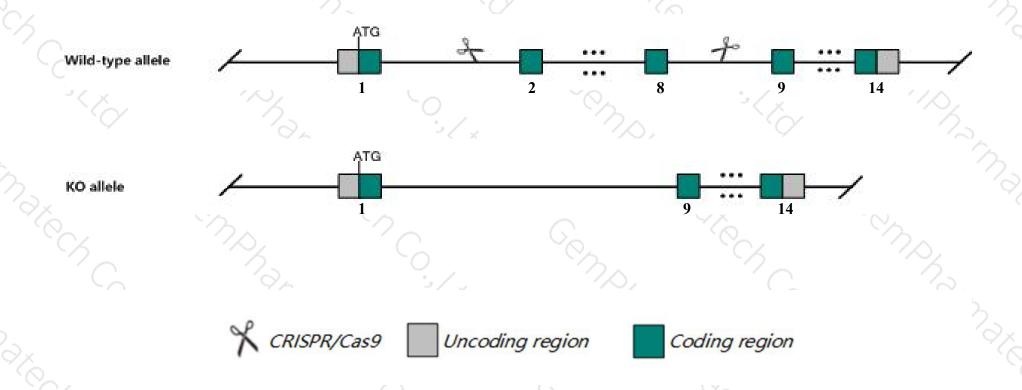
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Sema7a gene. The schematic diagram is as follows:



Technical routes



- ➤ The Sema7a gene has 2 transcripts. According to the structure of Sema7a gene, exon2-exon8 of Sema7a-201 (ENSMUST00000043059.8) transcript is recommended as the knockout region. The region contains 802bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify Sema7a gene. The brief process is as follows: CRISPR/Cas9 syste

Notice



- ➤ According to the existing MGI data, The development of the olfactory tract is impaired in homozygous null mice.
- > The Sema7a 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



Sema7a sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A [Mus musculus (house mouse)]

Gene ID: 20361, updated on 31-Jan-2019

Summary

↑ ?

Official Symbol Sema7a provided by MGI

Official Full Name sema domain, immunoglobulin domain (lg), and GPI membrane anchor, (semaphorin) 7A provided by MGI

Primary source MGI:MGI:1306826

See related Ensembl:ENSMUSG00000038264

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 2900057C09Rik, CDw108, H-Sema K1, H-Sema-L, M-Sema-L, Semal, sema K1, sema L

Expression Broad expression in ovary adult (RPKM 69.7), cerebellum adult (RPKM 47.2) and 22 other tissuesSee more

Orthologs <u>human</u> all

Transcript information (Ensembl)



The gene has 2 transcripts, all transcripts are shown below:

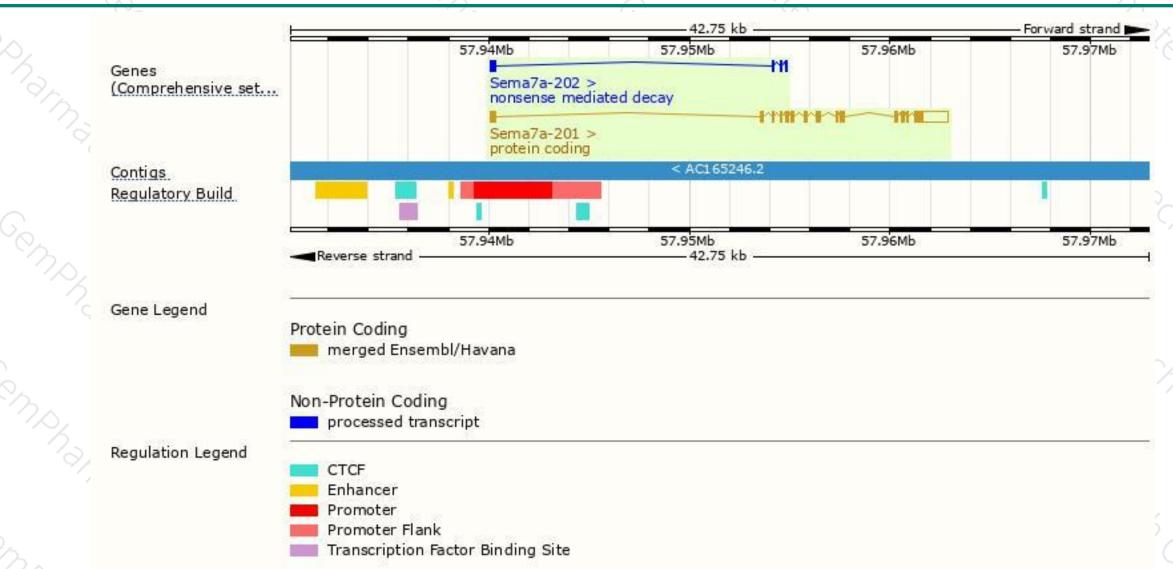
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sema7a-201	ENSMUST00000043059.8	3297	664aa	Protein coding	CCDS23235	Q9QUR8	TSL:1 GENCODE basic APPRIS P1
Sema7a-202	ENSMUST00000214314.1	417	86aa	Nonsense mediated decay	-	A0A1L1SQ43	TSL:3

The strategy is based on the design of Sema7a-201 transcript, The transcription is shown below



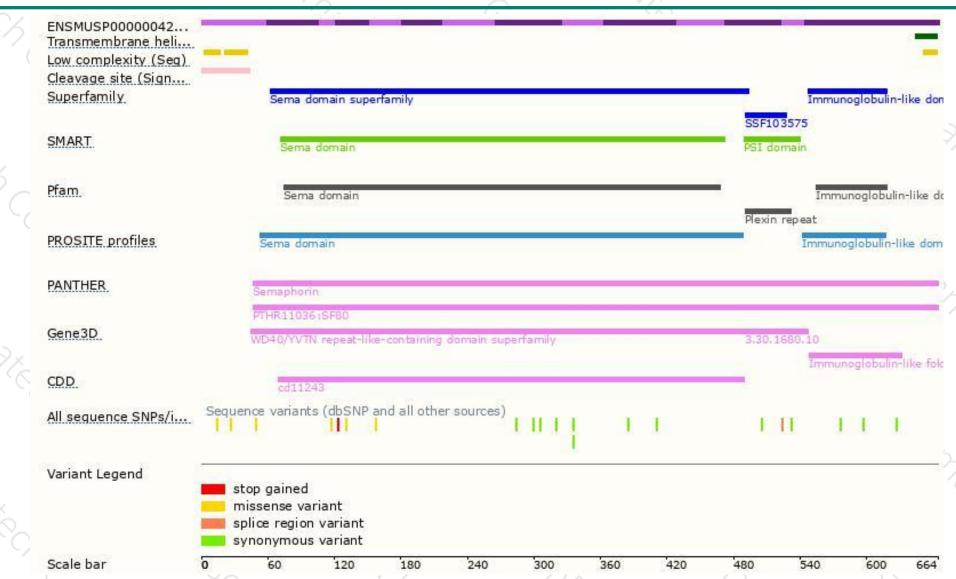
Genomic location distribution





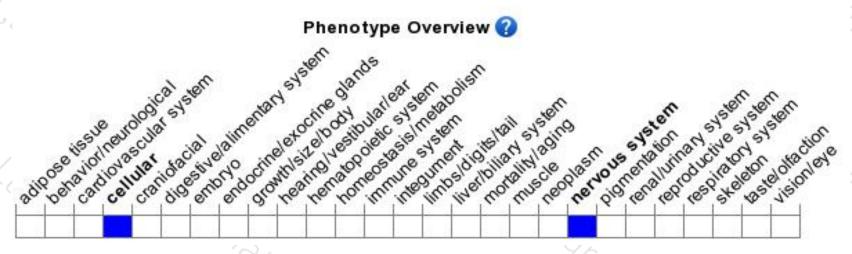
Protein domain





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, The development of the olfactory tract is impaired in homozygous null mice.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





