

Plxna1 Cas9-CKO Strategy

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Project Overview



Project Name

Plxna1

Project type

Cas9-CKO

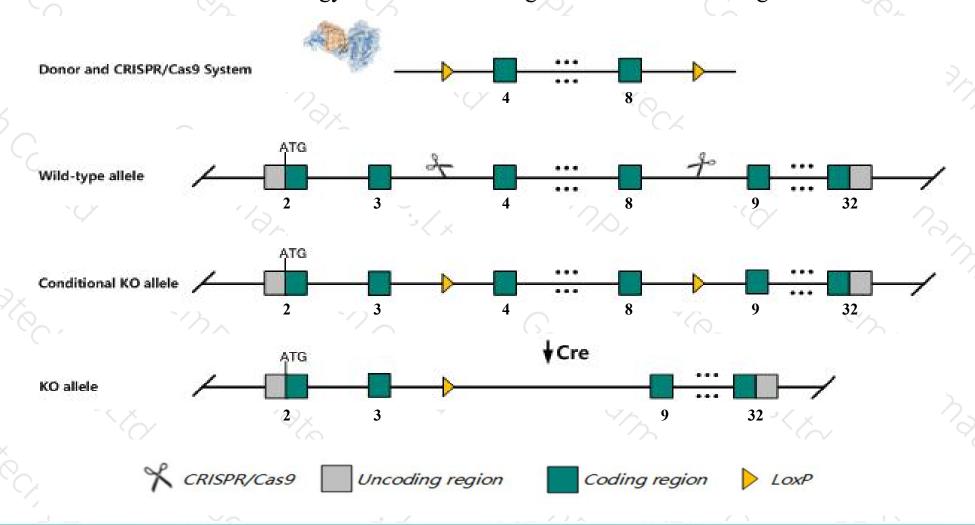
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Plxna1* gene. The schematic diagram is as follows:



Technical routes



- The *Plxna1* gene has 6 transcripts. According to the structure of *Plxna1* gene, exon4-exon8 of *Plxna1-202* (ENSMUST00000163139.7) transcript is recommended as the knockout region. The region contains 620bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plxna1* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

Notice



- > According to the existing MGI data, Mice homozygous for a null allele exhibit bone cellularity abnormalities, altered dendritic cell physiology, abnormal proprioceptive and oligodendrocyte morphology, and increased lymphatic branching complexity and LEC numbers.
- \succ The distance between Gm44207 and exon4 of Plxna1 is about 1kb, so the 5-terminal regulation of Gm44207 may be affected.
- The *Plxna1* gene is located on the Chr6. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Plxna1 plexin A1 [Mus musculus (house mouse)]

Gene ID: 18844, updated on 29-Oct-2019

Summary



Official Symbol Plxna1 provided by MGI

Official Full Name plexin A1 provided by MGI

Primary source MGI:MGI:107685

See related Ensembl: ENSMUSG00000030084

Gene type protein coding
RefSeq status VALIDATED

Organism Mus musculus

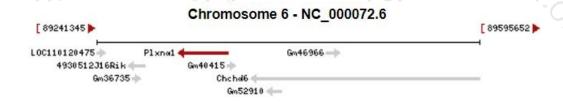
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as NOV; Plxn1; PlexA1; mKIAA4053; 2600013D04Rik

Expression Broad expression in lung adult (RPKM 77.1), ovary adult (RPKM 54.3) and 24 other tissues See more

Orthologs human all



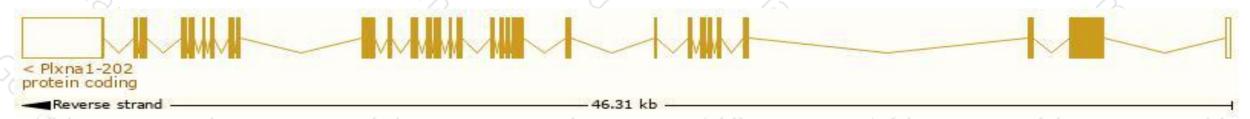
Transcript information (Ensembl)



The gene has 6 transcripts, all transcripts are shown below:

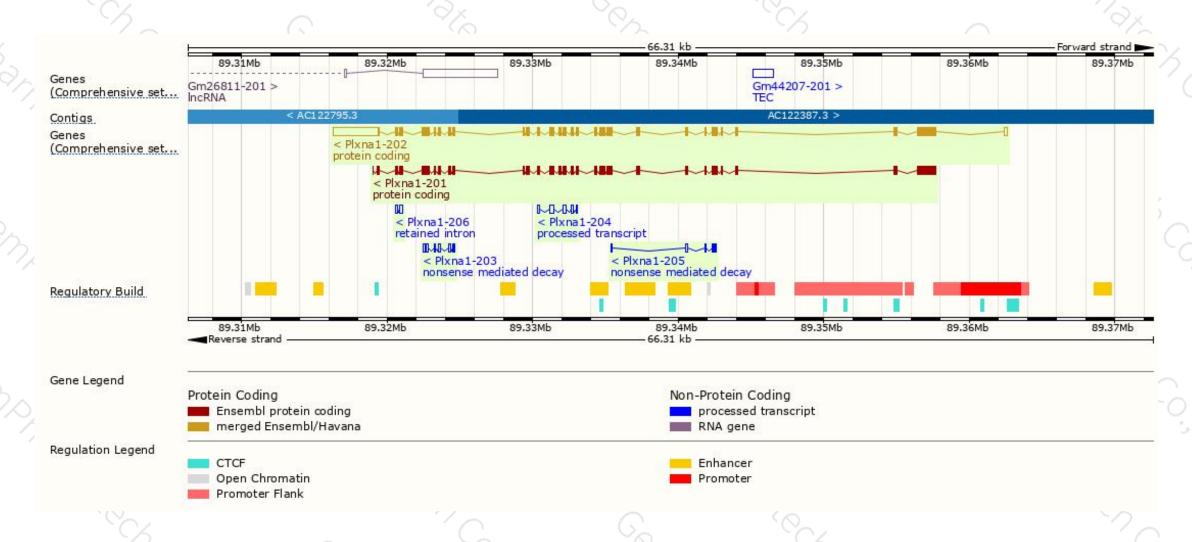
Name	Transcript ID #	bp 🌲	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Plxna1-202	ENSMUST00000163139.7	9034	1894aa	ENSMUSP00000131840.1	Protein coding	CCDS20344@	P70206 _€	TSL:1 GENCODE basic APPRIS P1
Plxna1-201	ENSMUST00000049845.5	5810	1894aa	ENSMUSP00000063066.5	Protein coding	CCDS20344@	P70206₽	TSL:1 GENCODE basic APPRIS P1
Plxna1-203	ENSMUST00000204468.1	678	<u>16aa</u>	ENSMUSP00000144822.1	Nonsense mediated decay	20	A0A0N4SUU1@	CDS 5' incomplete TSL:3
Plxna1-205	ENSMUST00000205121.1	459	<u>59aa</u>	ENSMUSP00000145403.1	Nonsense mediated decay	50	A0A0N4SW74@	CDS 5' incomplete TSL:5
Plxna1-206	ENSMUST00000205230.1	372	No protein	120	Retained intron	1.24	2	TSL:3
Plxna1-204	ENSMUST00000204997.1	735	No protein	99	IncRNA	- 6	+	TSL:3

The strategy is based on the design of *Plxna1-202* transcript, The transcription is shown below



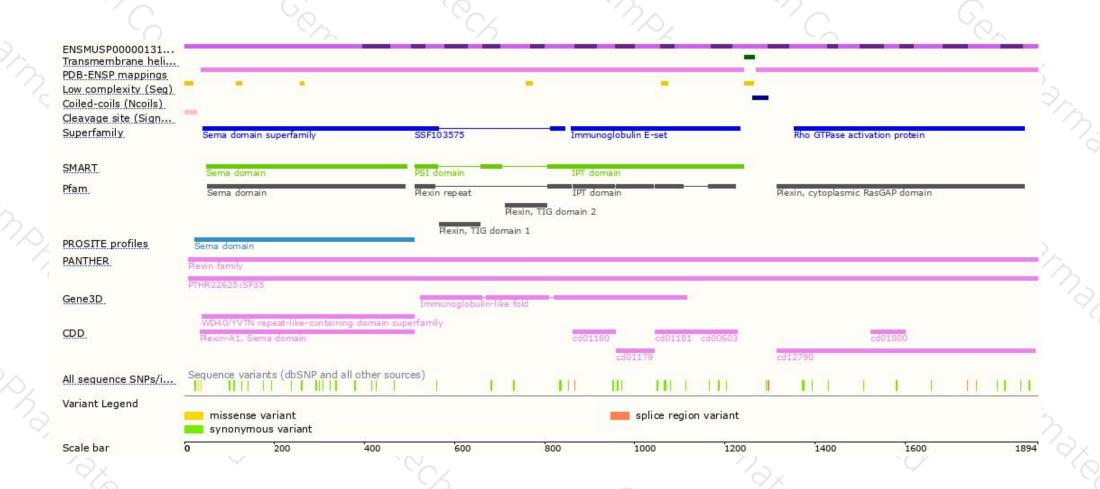
Genomic location distribution





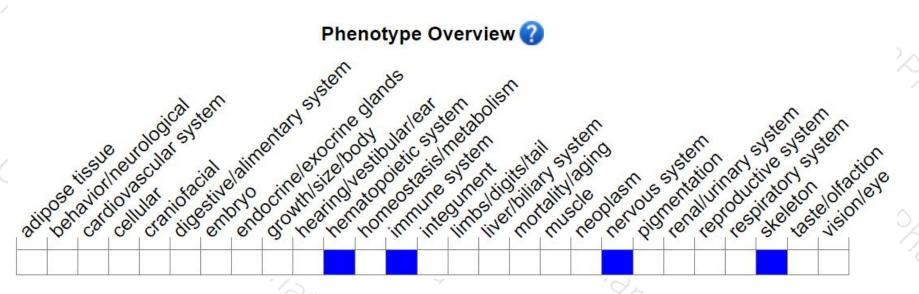
Protein domain





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, Mice homozygous for a null allele exhibit bone cellularity abnormalities, altered dendritic cell physiology, abnormal proprioceptive and oligodendrocyte morphology, and increased lymphatic branching complexity and LEC numbers.



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





