

Nosip Cas9-KO Strategy

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Project Overview



Project Name

Nosip

Project type

Cas9-KO

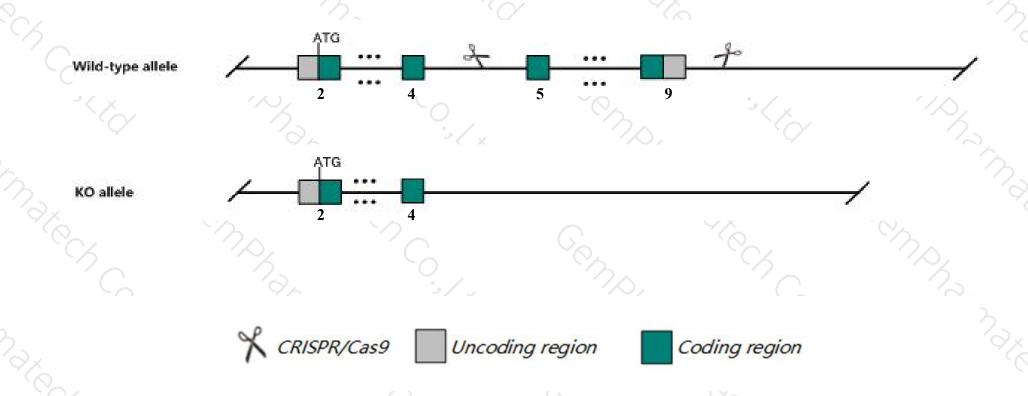
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Nosip* gene has 10 transcripts. According to the structure of *Nosip* gene, exon5-exon9 of *Nosip-201* (ENSMUST00000003513.10) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Nosip* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > The *Nosip* gene is located on the Chr7. 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)



Nosip nitric oxide synthase interacting protein [Mus musculus (house mouse)]

Gene ID: 66394, updated on 31-Jan-2019

Summary

☆ ?

Official Symbol Nosip provided by MGI

Official Full Name nitric oxide synthase interacting protein provided by MGI

Primary source MGI:MGI:1913644

See related Ensembl:ENSMUSG00000003421

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 2310061K06Rik, CGI-25

Expression Ubiquitous expression in ovary adult (RPKM 33.0), thymus adult (RPKM 26.0) and 28 other tissuesSee more

Orthologs human all

Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

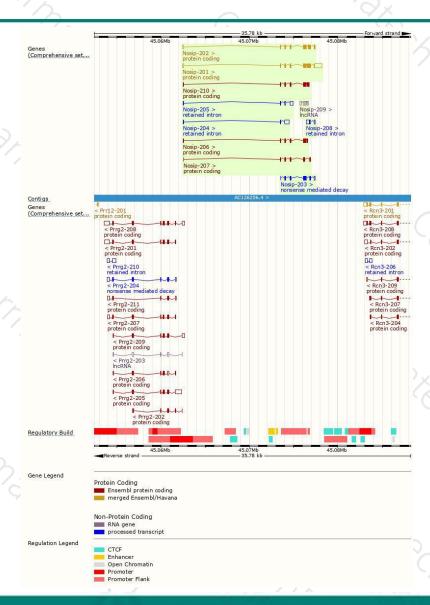
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000003513.10	1814	301aa	Protein coding	CCDS21228	Q9D6T0	TSL:1 GENCODE basic APPRIS P3
ENSMUST00000107829.8	972	276aa	Protein coding	CCDS52242	Q9D6T0	TSL:1 GENCODE basic APPRIS ALT2
ENSMUST00000211465.1	777	237aa	Protein coding	-	A0A1B0GT07	CDS 3' incomplete TSL:2
ENSMUST00000210088.1	696	221aa	Protein coding	14	A0A1B0GSR8	CDS 3' incomplete TSL:3
ENSMUST00000210520.1	534	<u>151aa</u>	Protein coding		A0A1B0GS52	TSL:5 GENCODE basic APPRIS ALT2
ENSMUST00000209243.1	679	<u>167aa</u>	Nonsense mediated decay	8 7	A0A1B0GS48	CDS 5' incomplete TSL:5
ENSMUST00000209308.1	598	No protein	Retained intron	84	ų.	TSL:2
ENSMUST00000209901.1	549	No protein	Retained intron	- 62		TSL:2
ENSMUST00000210668.1	542	No protein	Retained intron	15		TSL:2
ENSMUST00000210998.1	488	No protein	IncRNA	-		TSL:5
	ENSMUST00000003513.10 ENSMUST00000107829.8 ENSMUST00000211465.1 ENSMUST00000210088.1 ENSMUST00000210520.1 ENSMUST00000209243.1 ENSMUST00000209308.1 ENSMUST00000209901.1 ENSMUST00000210668.1	ENSMUST000000003513.10 1814 ENSMUST00000107829.8 972 ENSMUST00000211465.1 777 ENSMUST00000210088.1 696 ENSMUST00000210520.1 534 ENSMUST00000209243.1 679 ENSMUST00000209308.1 598 ENSMUST00000209901.1 549 ENSMUST00000210668.1 542	ENSMUST00000003513.10 1814 301aa ENSMUST00000107829.8 972 276aa ENSMUST00000211465.1 777 237aa ENSMUST00000210088.1 696 221aa ENSMUST00000210520.1 534 151aa ENSMUST00000209243.1 679 167aa ENSMUST00000209308.1 598 No protein ENSMUST00000209901.1 549 No protein ENSMUST00000210668.1 542 No protein	ENSMUST000000003513.10 1814 301aa Protein coding ENSMUST00000107829.8 972 276aa Protein coding ENSMUST00000211465.1 777 237aa Protein coding ENSMUST00000210088.1 696 221aa Protein coding ENSMUST00000210520.1 534 151aa Protein coding ENSMUST00000209243.1 679 167aa Nonsense mediated decay ENSMUST00000209308.1 598 No protein Retained intron ENSMUST00000209901.1 549 No protein Retained intron ENSMUST00000210668.1 542 No protein Retained intron	ENSMUST00000003513.10 1814 301aa Protein coding CCDS21228 ENSMUST00000107829.8 972 276aa Protein coding CCDS52242 ENSMUST00000211465.1 777 237aa Protein coding - ENSMUST00000210088.1 696 221aa Protein coding - ENSMUST00000210520.1 534 151aa Protein coding - ENSMUST00000209243.1 679 167aa Nonsense mediated decay - ENSMUST00000209308.1 598 No protein Retained intron - ENSMUST00000209901.1 549 No protein Retained intron - ENSMUST00000210668.1 542 No protein Retained intron -	ENSMUST00000003513.10 1814 301aa Protein coding CCDS21228 Q9D6T0 ENSMUST00000107829.8 972 276aa Protein coding CCDS52242 Q9D6T0 ENSMUST00000211465.1 777 237aa Protein coding - A0A1B0GT07 ENSMUST00000210088.1 696 221aa Protein coding - A0A1B0GSR8 ENSMUST00000210520.1 534 151aa Protein coding - A0A1B0GS52 ENSMUST00000209243.1 679 167aa Nonsense mediated decay - A0A1B0GS48 ENSMUST00000209308.1 598 No protein Retained intron - - ENSMUST00000209901.1 549 No protein Retained intron - - ENSMUST00000210668.1 542 No protein Retained intron - -

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

Nosip-201 > protein coding

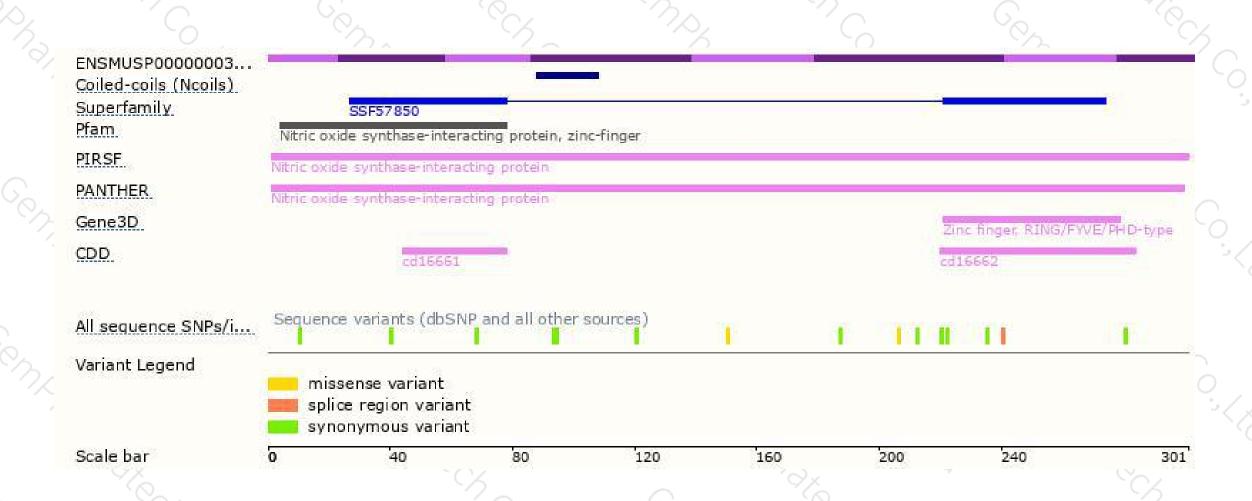
Genomic location distribution





Protein domain







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





