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Nop56 Cas9-CKO Strategy

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Overview

Target Gene Name

- Nop56

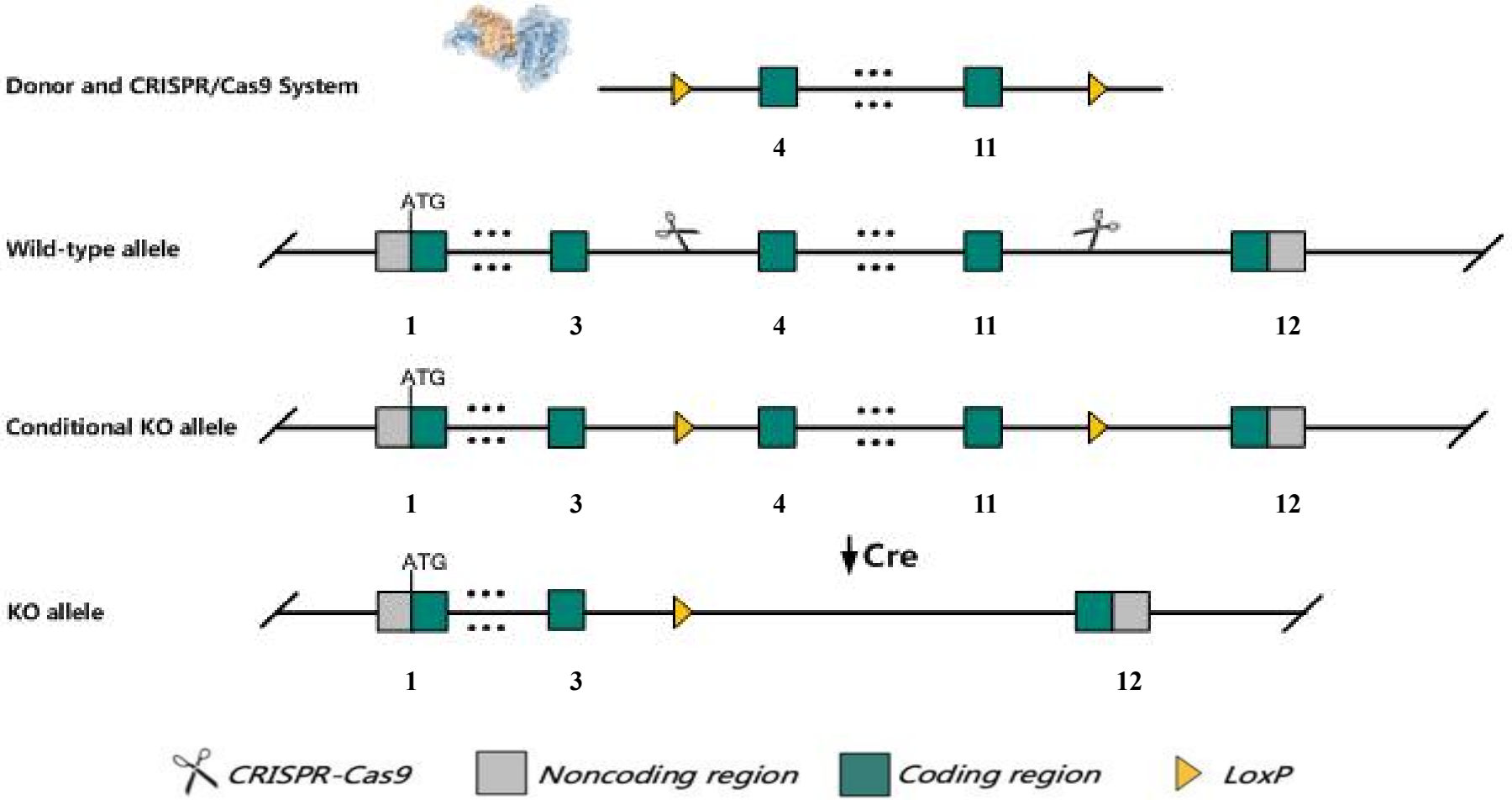
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Nop56* gene.

Technical Information

- The *Nop56* gene has 19 transcripts. According to the structure of *Nop56* gene, exon4-exon11 of *Nop56*-202 (ENSMUST00000103198.11) transcript is recommended as the knockout region. The region contains 1208bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Nop56* 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

Nop56 NOP56 ribonucleoprotein [Mus musculus (house mouse)]

Gene ID: 67134, updated on 31-May-2023

Summary

Official Symbol	Nop56 provided by MGI
Official Full Name	NOP56 ribonucleoprotein provided byMGI
Primary source	MGI:MGI:1914384
See related	Ensembl:ENSMUSG00000027405
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	2310044F10Rik, Nol5a
Summary	Enables RNA binding activity. Predicted to act upstream of or within ribosome biogenesis. Predicted to be located in fibrillar center. Predicted to be part of box C/D RNP complex; pre-snoRNP complex; and small-subunit processome. Is expressed in alimentary system; central nervous system; liver; metanephros; and retina nuclear layer. Human ortholog(s) of this gene implicated in spinocerebellar ataxia type 36. Orthologous to human NOP56 (NOP56 ribonucleoprotein). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in CNS E11.5 (RPKM 75.9), liver E14 (RPKM 61.1) and 23 other tissuesSee more
Orthologs	human all

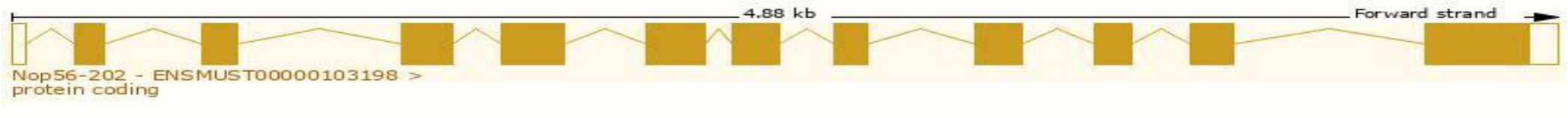
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 19 transcripts,all transcripts are shown below:

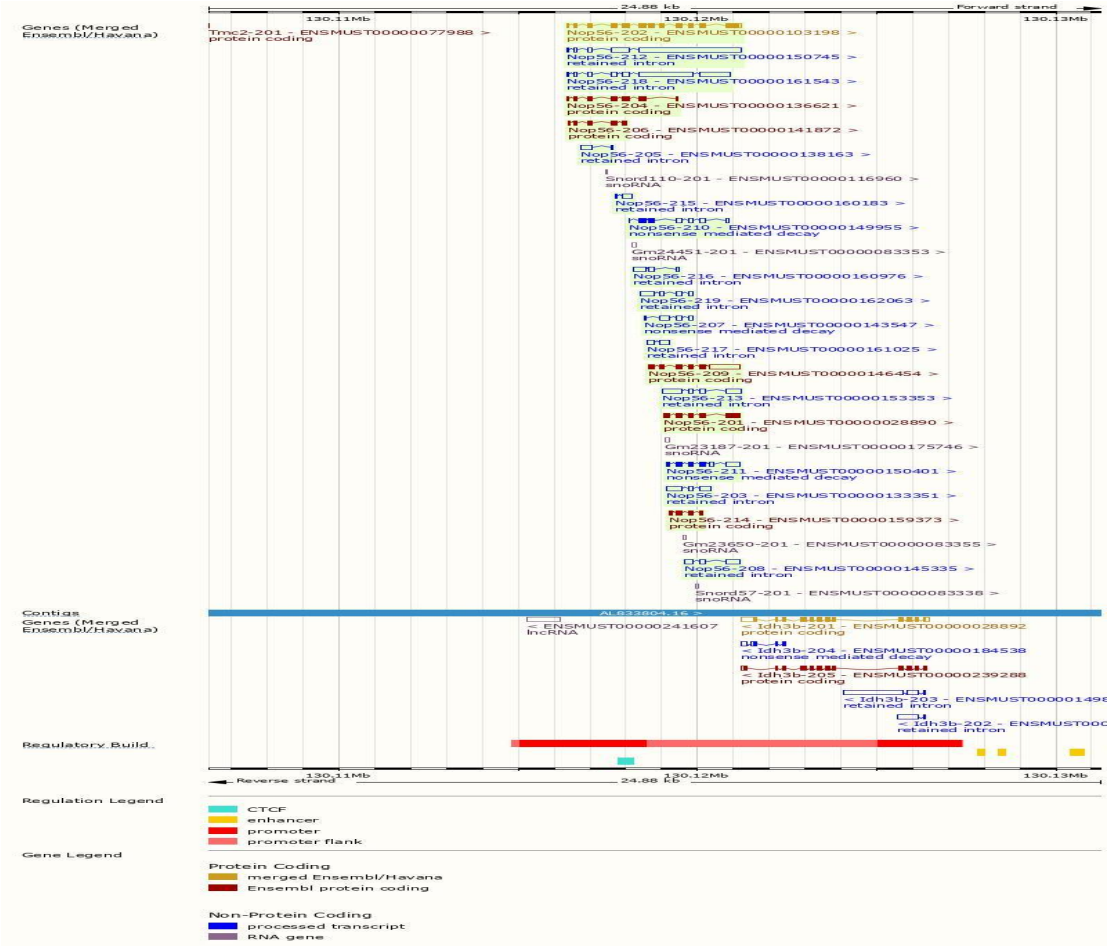
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nop56-202	ENSMUST00000103198.11	1877	580aa	Protein coding	CCDS16737		A single transcript chosen for a gene which is the most conserved, most highly expressed, has the longest coding sequence and is represented in other key resources, such as NCBI and UniProt. This is defined in detail on http://www.ensembl.org/info/genome/genebuild/canonical.html Ensembl Canonical , The GENCODE set is the gene set for human and mouse. GENCODE basic , APPRIS P1 , TSL:1 ,
Nop56-209	ENSMUST00000146454.9	1490	222aa	Protein coding			TSL:5 , CDS 5' incomplete ,
Nop56-201	ENSMUST00000028890.15	946	296aa	Protein coding			TSL:2 , CDS 5' incomplete ,
Nop56-204	ENSMUST00000136621.9	868	261aa	Protein coding			The GENCODE set is the gene set for human and mouse. GENCODE basic , TSL:5 ,
Nop56-206	ENSMUST00000141872.2	518	173aa	Protein coding			TSL:3 , CDS 5' and 3' incomplete ,
Nop56-214	ENSMUST00000159373.2	405	135aa	Protein coding			TSL:3 , CDS 5' and 3' incomplete ,
Nop56-211	ENSMUST00000150401.8	1005	173aa	Nonsense mediated decay			TSL:5 , CDS 5' incomplete ,
Nop56-210	ENSMUST00000149955.9	829	125aa	Nonsense mediated decay			TSL:3 , CDS 5' incomplete ,
Nop56-207	ENSMUST00000143547.2	600	18aa	Nonsense mediated decay			TSL:3 , CDS 5' incomplete ,
Nop56-212	ENSMUST00000150745.9	3627	No protein	Retained intron			TSL:1 ,
Nop56-218	ENSMUST00000161543.2	2960	No protein	Retained intron			TSL:2 ,
Nop56-213	ENSMUST00000153353.9	1204	No protein	Retained intron			TSL:1 ,
Nop56-203	ENSMUST00000133351.3	833	No protein	Retained intron			TSL:2 ,
Nop56-208	ENSMUST00000145335.3	779	No protein	Retained intron			TSL:2 ,
Nop56-219	ENSMUST00000162063.8	741	No protein	Retained intron			TSL:2 ,
Nop56-216	ENSMUST00000160976.2	571	No protein	Retained intron			TSL:2 ,
Nop56-217	ENSMUST00000161925.2	445	No protein	Retained intron			TSL:2 ,
Nop56-205	ENSMUST00000138163.3	350	No protein	Retained intron			TSL:3 ,
Nop56-215	ENSMUST00000160183.2	320	No protein	Retained intron			TSL:5 ,

The strategy is based on the design of *Nop56*-202 transcript, the transcription is shown below:



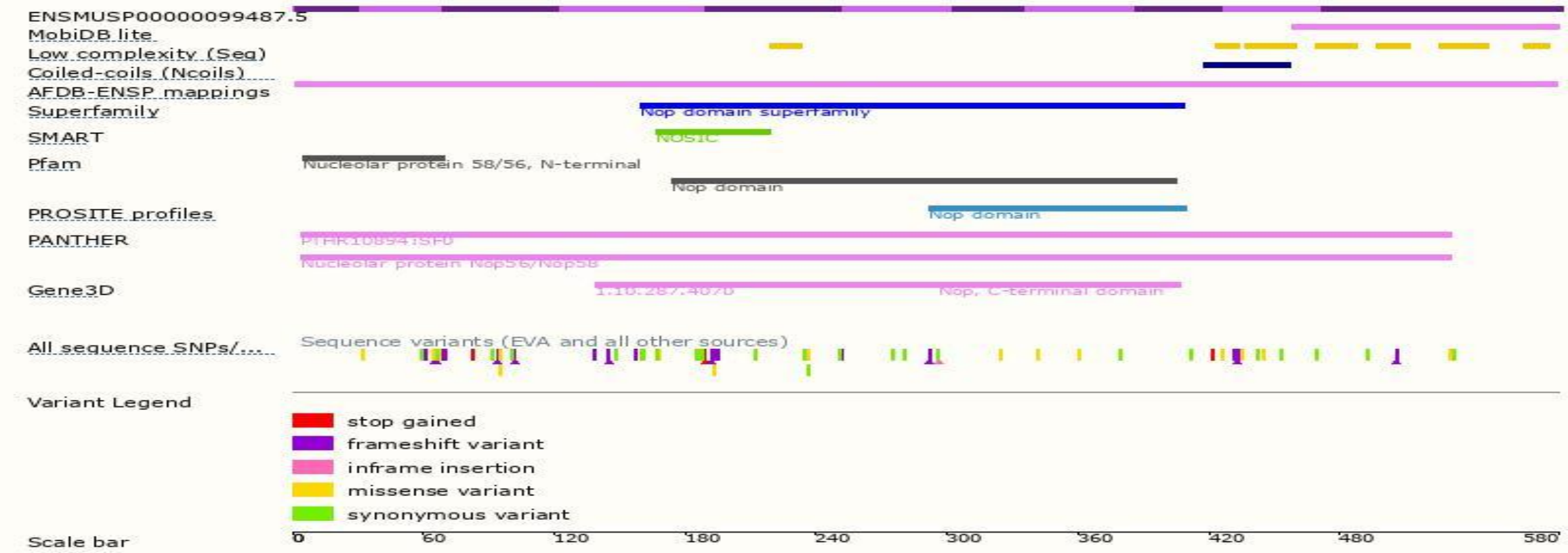
Source: https://www.ensembl.org

Genomic Information



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

Protein Information



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

Important Information

- *Nop56* is located on Chr2. 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.
- The flox region contain the Snord110,Gm24451,Gm23187,Gm23650,Snord57 genes, which may delet them after Cre.
- The flox region is about 1 kb away from the 5th end of the 2810036E18Rik gene, which may affect the regulation of this gene.