

Nono-del ERmotif cas9-ki Strategy

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Reviewer

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Project Overview

Project Name

Nono-del ERmotif

Project type

cas9-ki

Strain background

C57BL/6JGpt

Knockin strategy

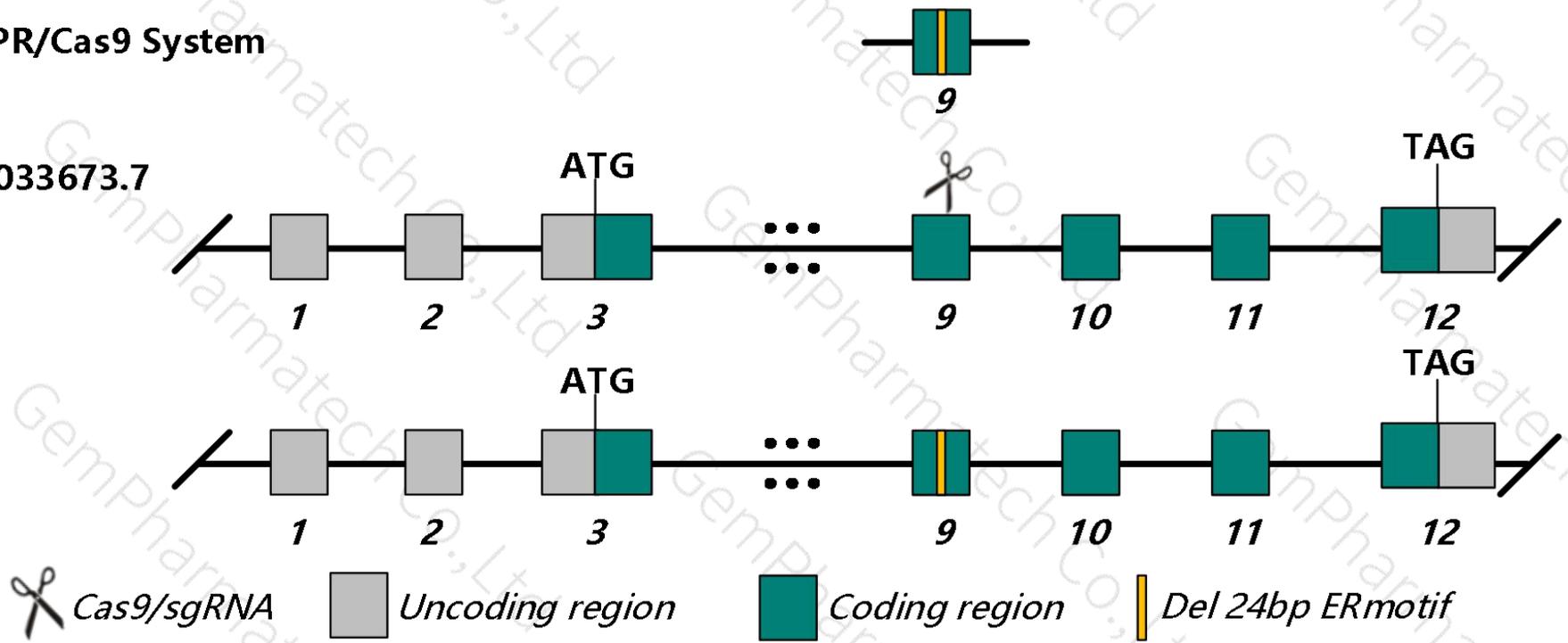
This model will use CRISPR/Cas9 technology to edit the *Nono* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

ENSMUST00000033673.7

Wild-type allele

Targeted allele



- The *Nono* gene has 7 transcripts. According to the structure of *Nono* gene, *Nono*-201(ENSMUST00000033673.7) is selected is selected for this strategy. 24bp of ERmotif in exon9 of *Nono*-201 will be deleted in this strategy.
- *Nono*-201 gene has 12 exons, with the ATG start codon in exon3 and TAG stop codon in exon12.
- In this project, *Nono* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: In vitro, sgRNA and donor vectors were constructed. Cas9, sgRNA and donor were injected into the fertilized eggs of C57BL/6JGpt mice for homologous recombination, and obtained positive F0 mice identified by PCR and sequencing analysis. The stable inheritable positive F1 mice model was obtained by mating F0 mice with C57BL/6JGpt mice.

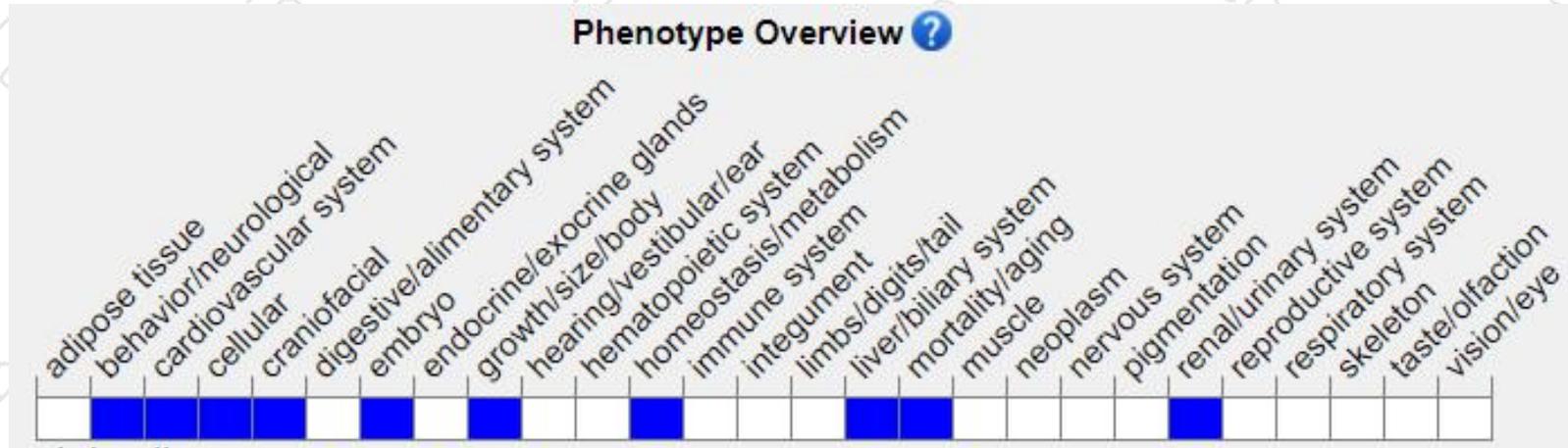
- According to the existing MGI data, mice carrying a gene trap allele show shortening of the circadian period under constant dark conditions. Chimeras for some other gene trap alleles may display gastrulation defects. Hemizygous KO in males causes cardiac fibrosis and results in decreased body weight and increased mortality.
- One or two synonymous mutations of amino acids may be introduced on exon9 of *Nono*-201.
- The KO region is close to the 5' of *Itgb1bp2* gene, and this strategy may affect the regulation of the 5' of *Itgb1bp2* gene.
- In this strategy, the effect of *Nono*-206 transcript is unknown, and *Nono*-202/203/205 may not be affected.
- The *Nono* gene is located on the ChrX. If the 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Exon9 of *Nono-201* sequence

GCAG**GAAGAGGAACGCAGGCGCCGTGAG**GAAGAGATGCGGCGACAGCAAGAGGAAATGATGCGCCGACAGCA
GGAAGGATTCAAGGGAACCTTCCCTGATGCG

The red letters are 24bp ERmotif which to be deleted.

Mouse phenotype description(MGI)



Mice carrying a gene trap allele show shortening of the circadian period under constant dark conditions. Chimeras for some other gene trap alleles may display gastrulation defects. Hemizygous KO in males causes cardiac fibrosis and results in decreased body weight and increased mortality.

<http://www.informatics.jax.org/marker/MGI:1855692>

Gene information (NCBI)

Nono non-POU-domain-containing, octamer binding protein [*Mus musculus* (house mouse)]

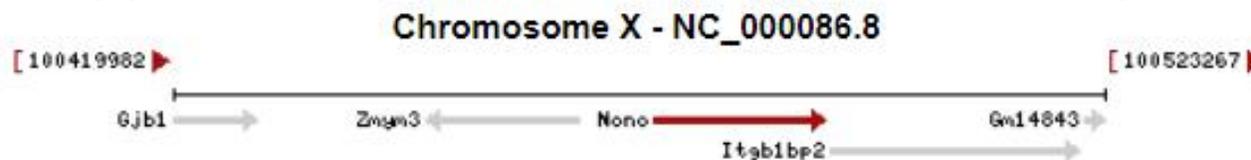
[Download Datasets](#)

Gene ID: 53610, updated on 23-Jun-2021

Summary

Official Symbol	Nono provided by MGI
Official Full Name	non-POU-domain-containing, octamer binding protein provided by MGI
Primary source	MGI:MGI:1855692
See related	Ensembl:ENSMUSG00000031311
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	P54; nonA; NRB54; P54NRB; AA407051; AV149256
Expression	Broad expression in CNS E11.5 (RPKM 221.3), CNS E14 (RPKM 143.5) and 22 other tissues See more
Orthologs	human all

NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

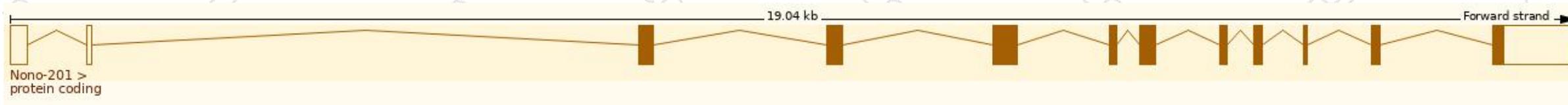


Transcript information (Ensembl)

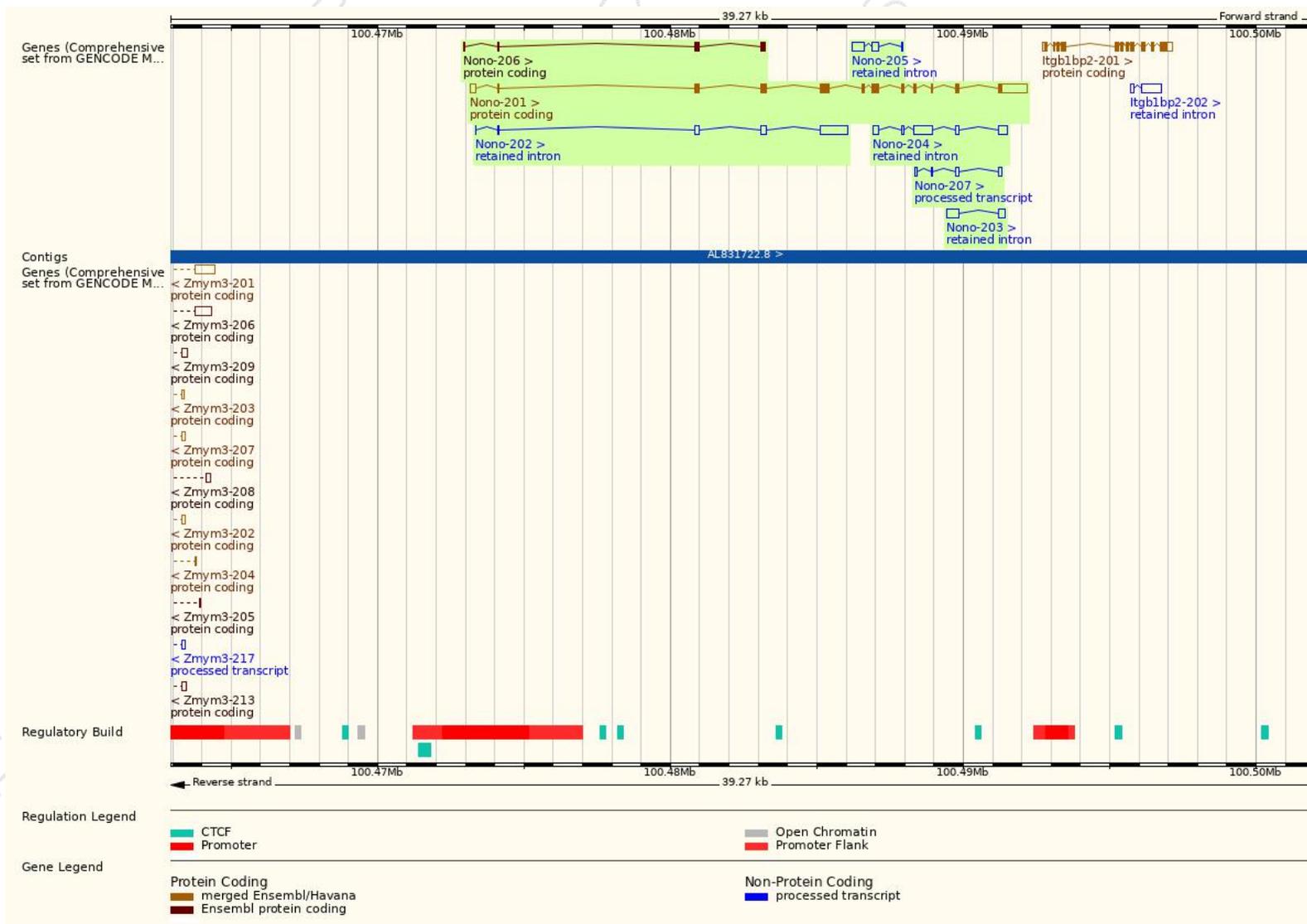
The gene has 7 transcripts, and all transcripts are shown below :

Name ▲	Transcript ID	bp	Protein	Biotype	CCDS	UniProt Match	Flags
Nono-201	ENSMUST00000033673.7	2562	473aa	Protein coding	CCDS30316	Q99K48-1	GENCODE basic APPRIS P1 TSL:1
Nono-202	ENSMUST00000126019.2	1364	No protein	Retained intron	-	-	TSL:2
Nono-203	ENSMUST00000134783.2	631	No protein	Retained intron	-	-	TSL:2
Nono-204	ENSMUST00000136251.8	1337	No protein	Retained intron	-	-	TSL:5
Nono-205	ENSMUST00000147498.2	687	No protein	Retained intron	-	-	TSL:3
Nono-206	ENSMUST00000147708.8	424	98aa	Protein coding	-	B1AXT0	TSL:5 CDS 3' incomplete
Nono-207	ENSMUST00000148312.2	345	No protein	Processed transcript	-	-	TSL:2

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

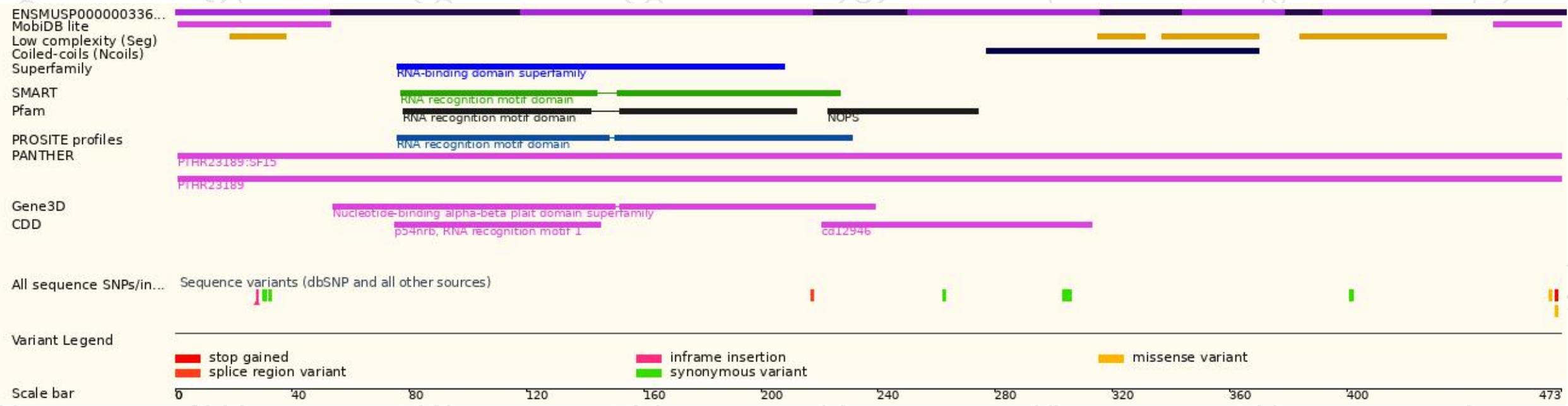


Genomic location distribution



Protein domain

Protein domains for ENSMUSP00000033673.7



If you have any questions, you are welcome to inquire.

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