

# ***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

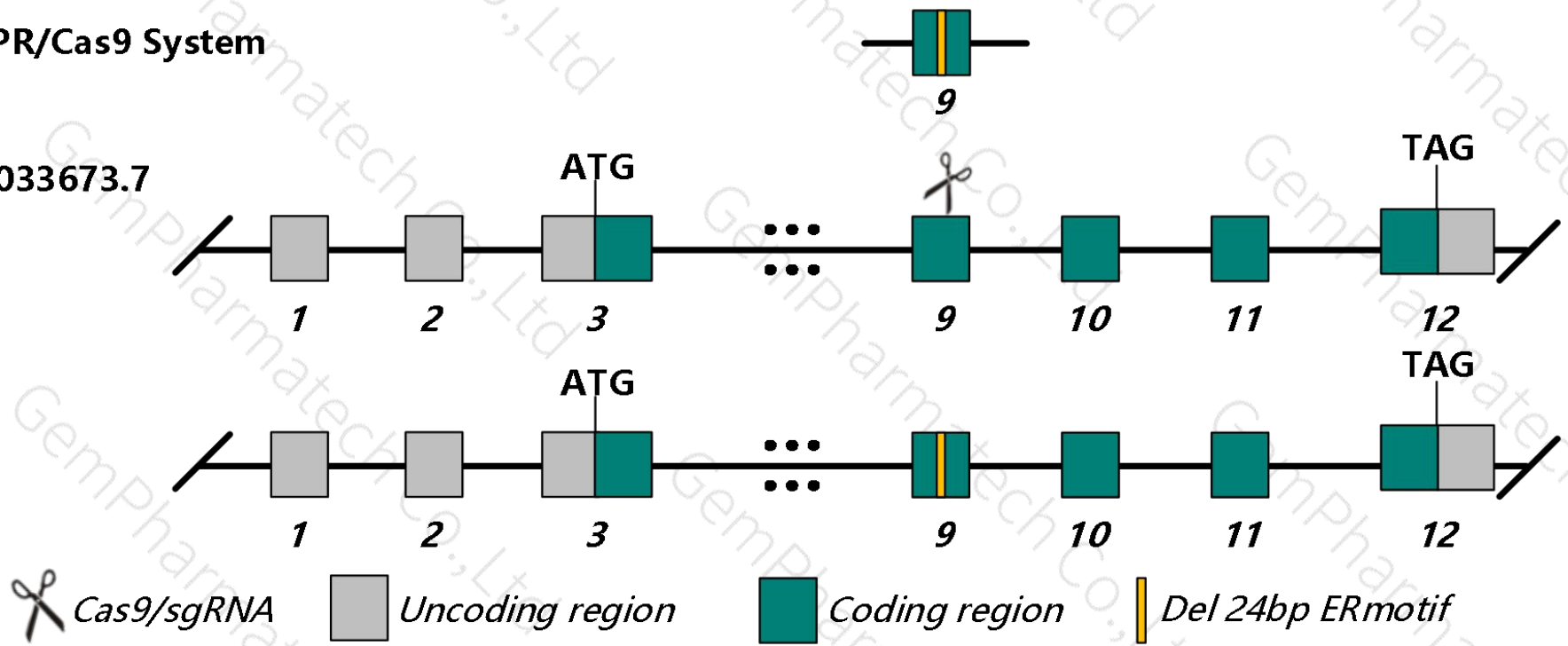
This model will use CRISPR/Cas9 technology to edit the *Nono* gene. The schematic diagram is as follows:

### 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 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.

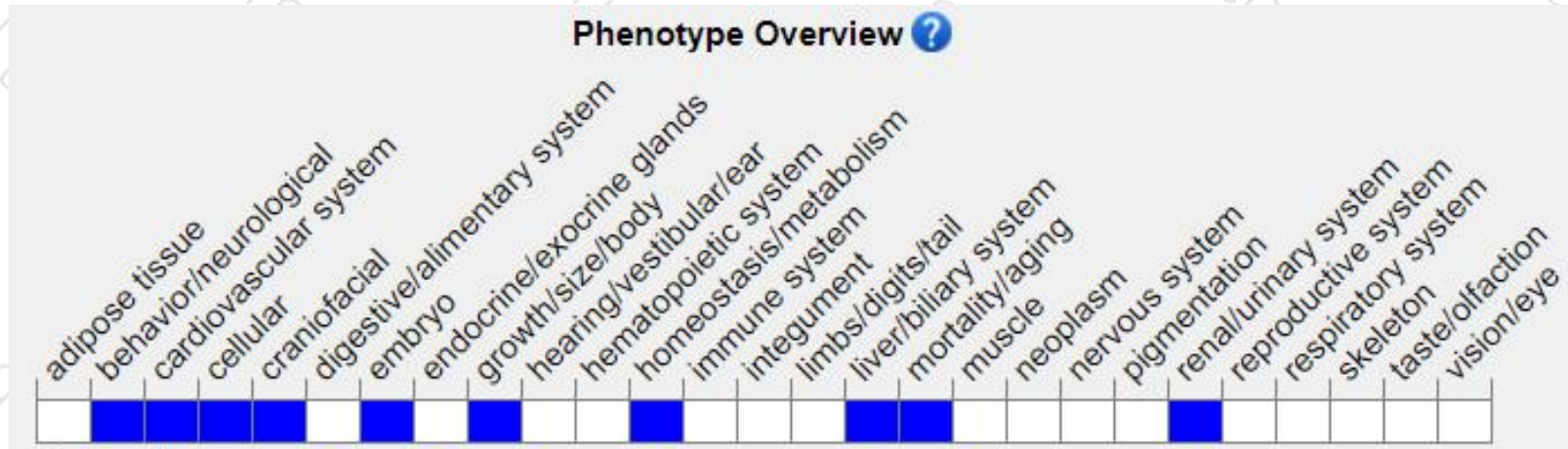
# Exon9 of *Nono*-201 sequence

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)

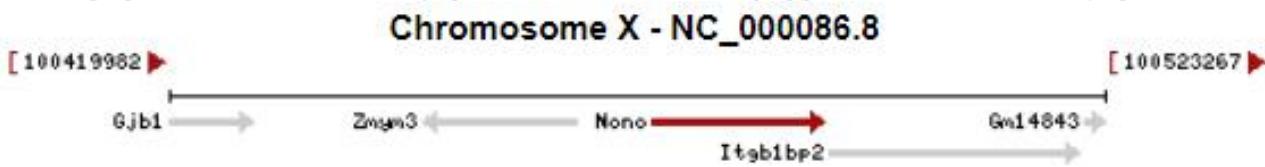
**Nono** non-POU-domain-containing, octamer binding protein [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

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

**Summary**

Official Symbol	Nono provided by <a href="#">MGI</a>
Official Full Name	non-POU-domain-containing, octamer binding protein provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1855692</a>
See related	<a href="#">Ensembl:ENSMUSG00000031311</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
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 <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a>
	Try the new <a href="#">Transcript table</a>



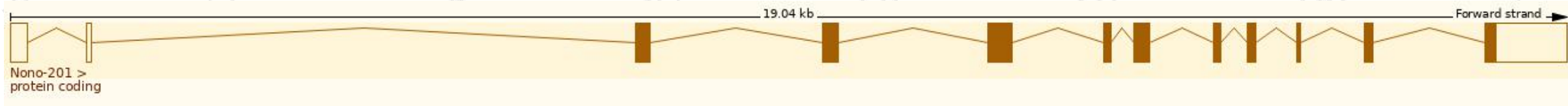


# Transcript information (Ensembl)

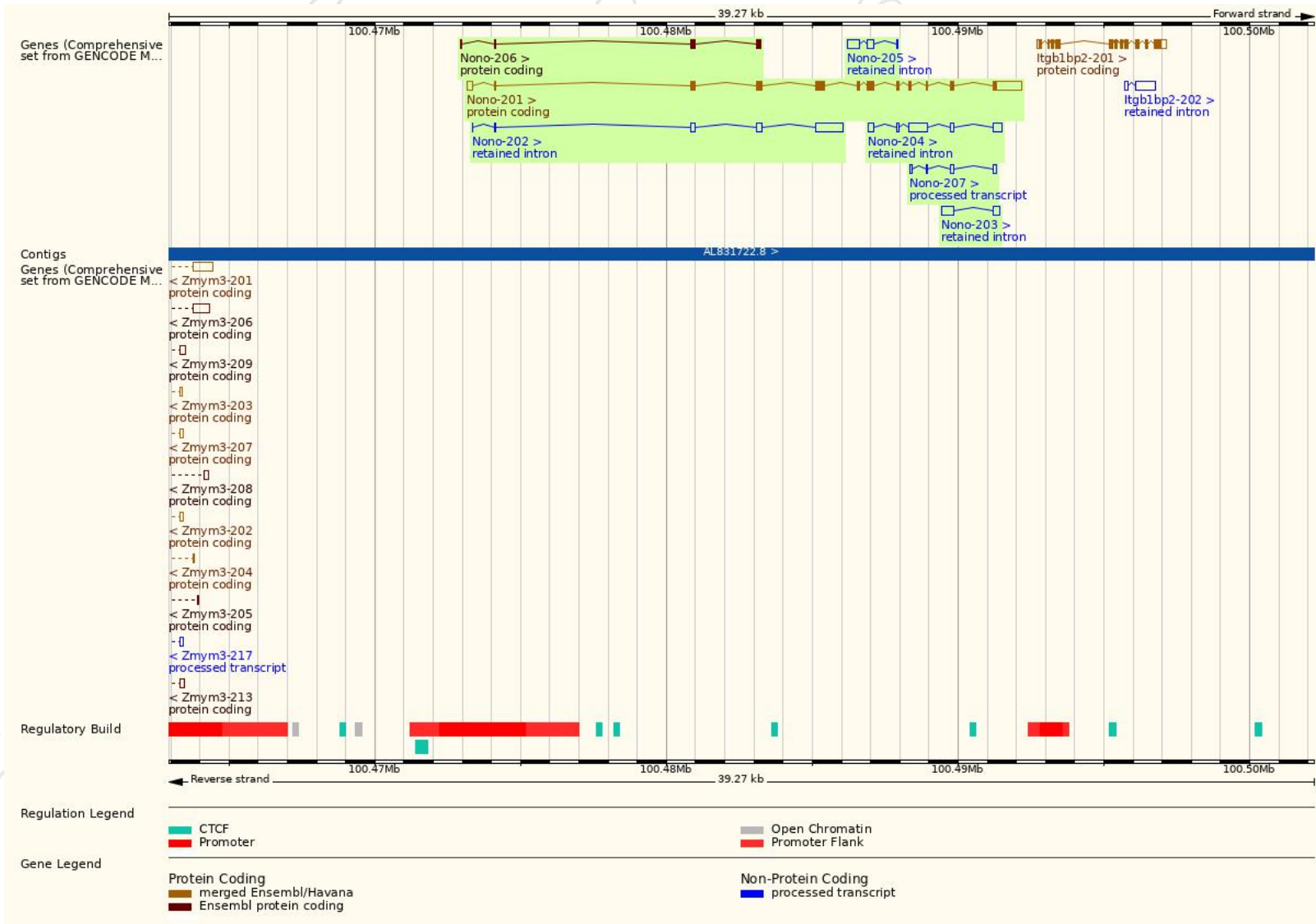
The gene has 7 transcripts, and all transcripts are shown below :

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

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

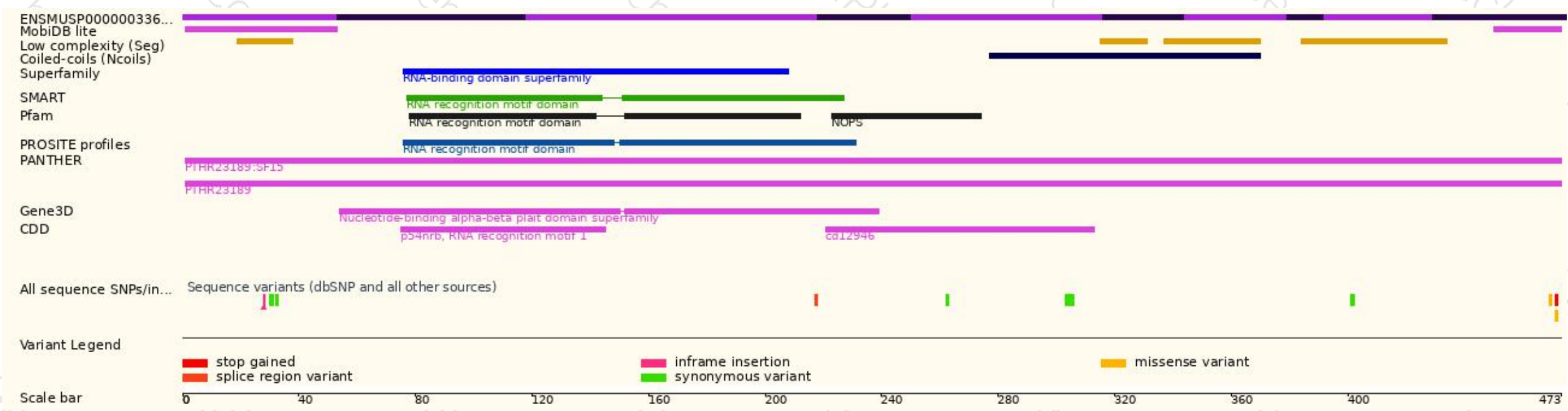


# Genomic location distribution



# Protein domain

## Protein domains for ENSMUSP00000033673.7



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