

Nol8 Cas9-KO Strategy

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Project Overview

Project Name

Nol8

Project type

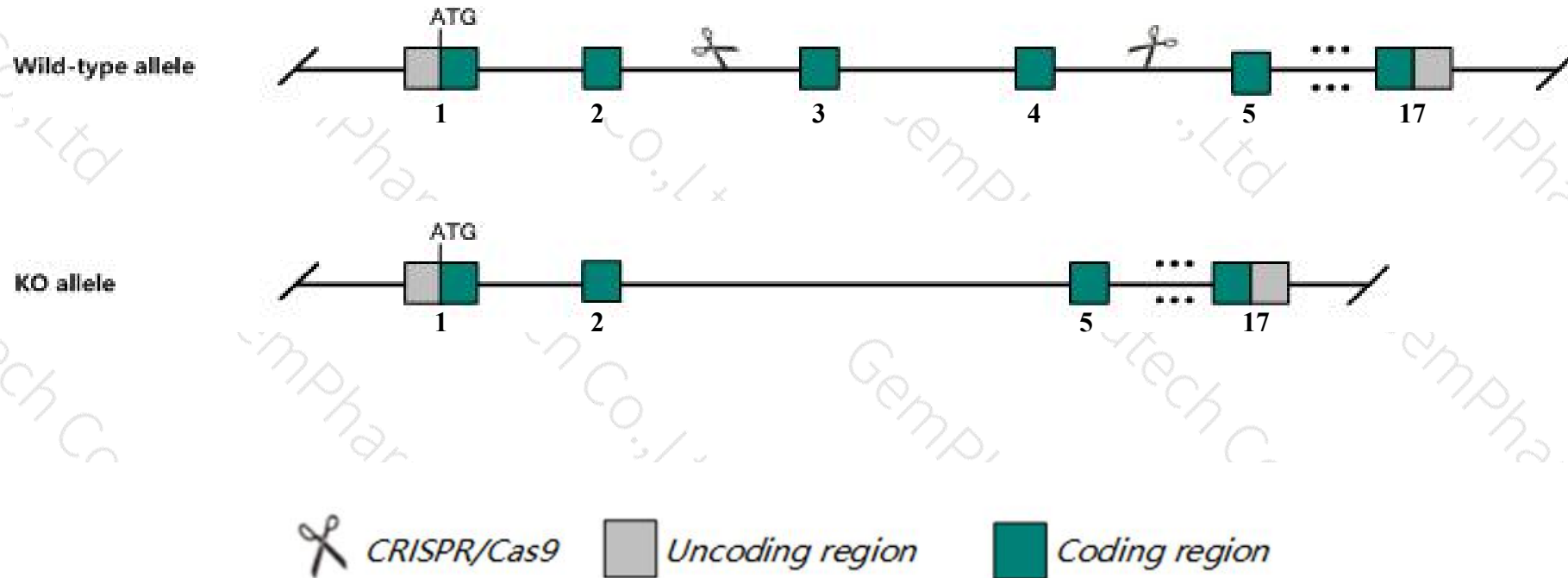
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *No18* gene. The schematic diagram is as follows:



- The *Nol8* gene has 9 transcripts. According to the structure of *Nol8* gene, exon3-exon4 of *Nol8-205* (ENSMUST00000222197.1) transcript is recommended as the knockout region. The region contains 142bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nol8* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Nol8* gene is located on the Chr13. 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)

Nol8 nucleolar protein 8 [Mus musculus (house mouse)]

Gene ID: 70930, updated on 31-Jan-2019

Summary



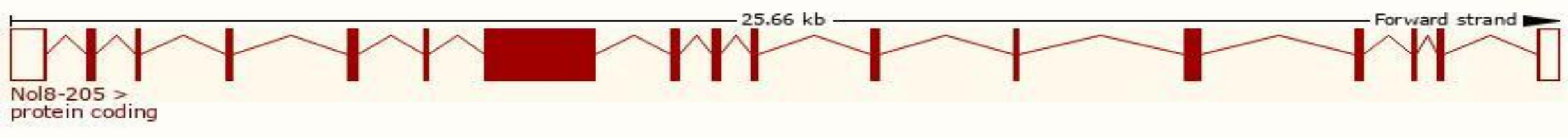
Official Symbol	Nol8 provided by MGI
Official Full Name	nucleolar protein 8 provided by MGI
Primary source	MGI:MGI:1918180
See related	Ensembl:ENSMUSG000000021392
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4921532D18Rik, 5730412B09Rik
Expression	Broad expression in testis adult (RPKM 7.6), CNS E11.5 (RPKM 5.9) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

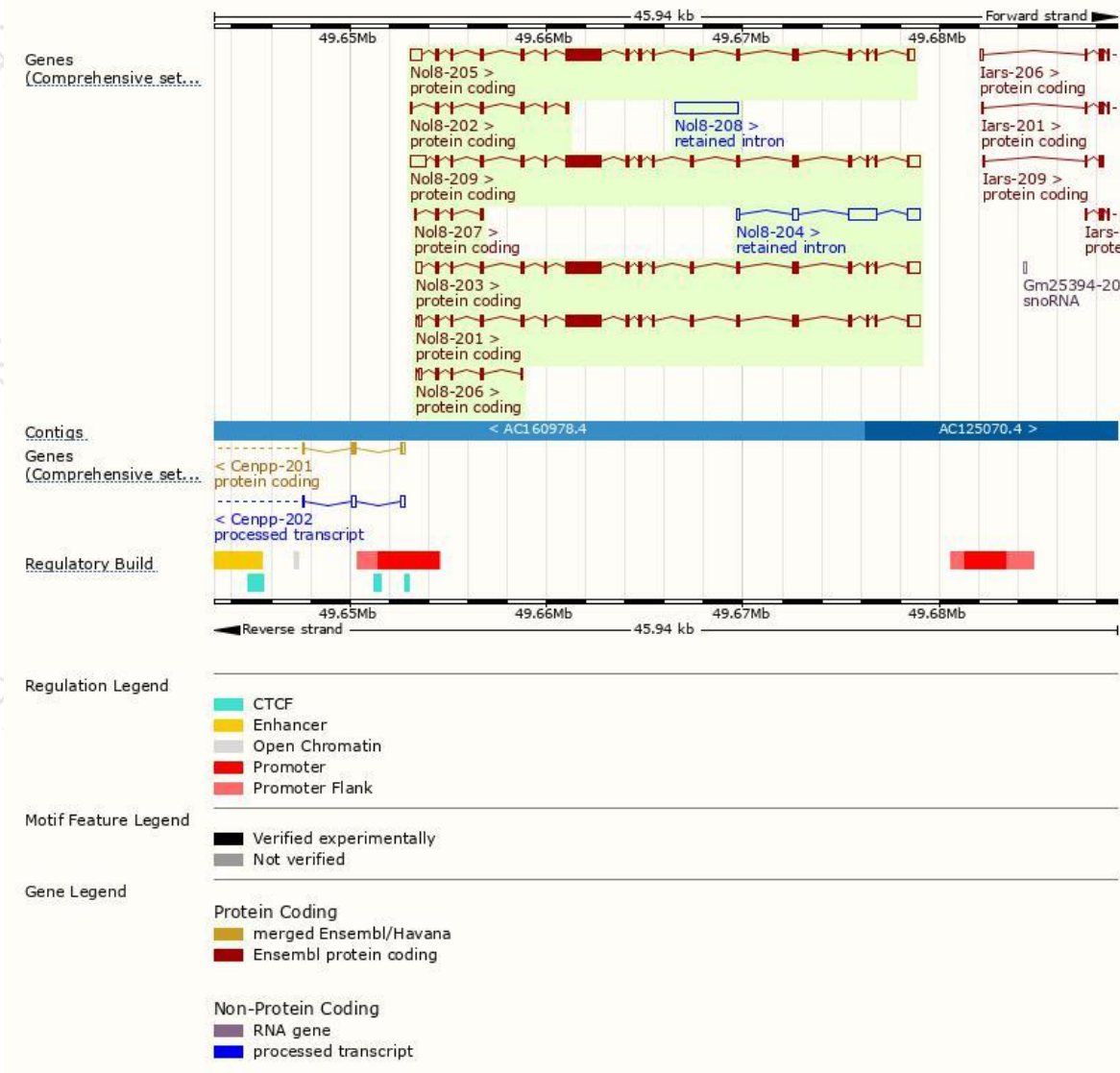
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
NoI8-205	ENSMUST00000222197.1	4368	1165aa	Protein coding	CCDS36658	E9QKD1	TSL:1 GENCODE basic APPRIS P2
NoI8-201	ENSMUST00000021824.7	4242	1165aa	Protein coding	CCDS36658	E9QKD1	TSL:5 GENCODE basic APPRIS P2
NoI8-209	ENSMUST00000223467.1	4765	1147aa	Protein coding	-	Q3UHX0	TSL:1 GENCODE basic APPRIS ALT2
NoI8-203	ENSMUST00000221142.1	4381	1147aa	Protein coding	-	Q3UHX0	TSL:1 GENCODE basic APPRIS ALT2
NoI8-202	ENSMUST00000221083.1	745	225aa	Protein coding	-	A0A1Y7VN09	CDS 3' incomplete TSL:3
NoI8-206	ENSMUST00000222333.1	600	145aa	Protein coding	-	A0A1Y7VNA8	CDS 3' incomplete TSL:3
NoI8-207	ENSMUST00000223264.1	363	93aa	Protein coding	-	A0A1Y7VJP6	CDS 3' incomplete TSL:2
NoI8-208	ENSMUST00000223346.1	3239	No protein	Retained intron	-	-	TSL:NA
NoI8-204	ENSMUST00000221328.1	2424	No protein	Retained intron	-	-	TSL:2

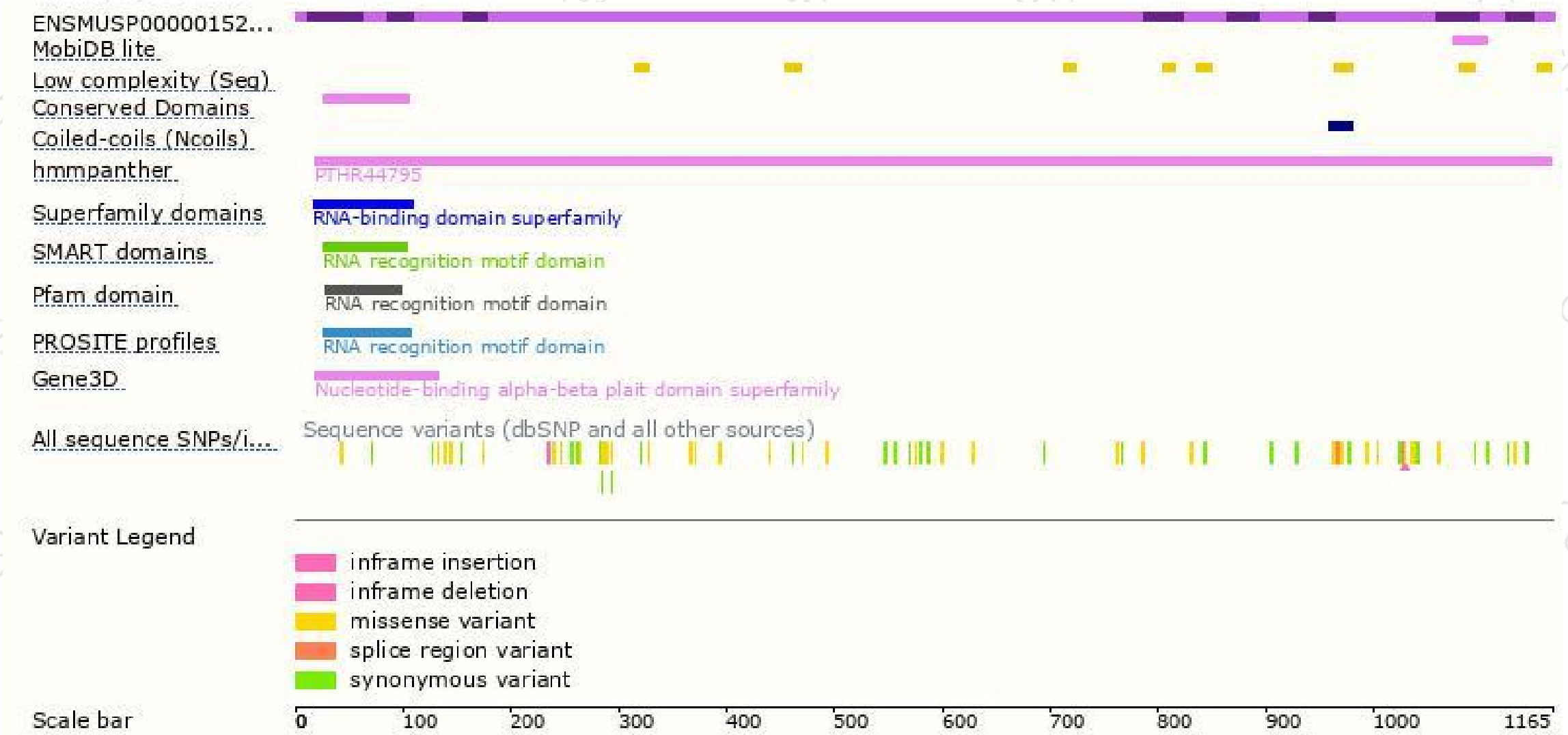
The strategy is based on the design of *NoI8-205* transcript,The transcription is shown below



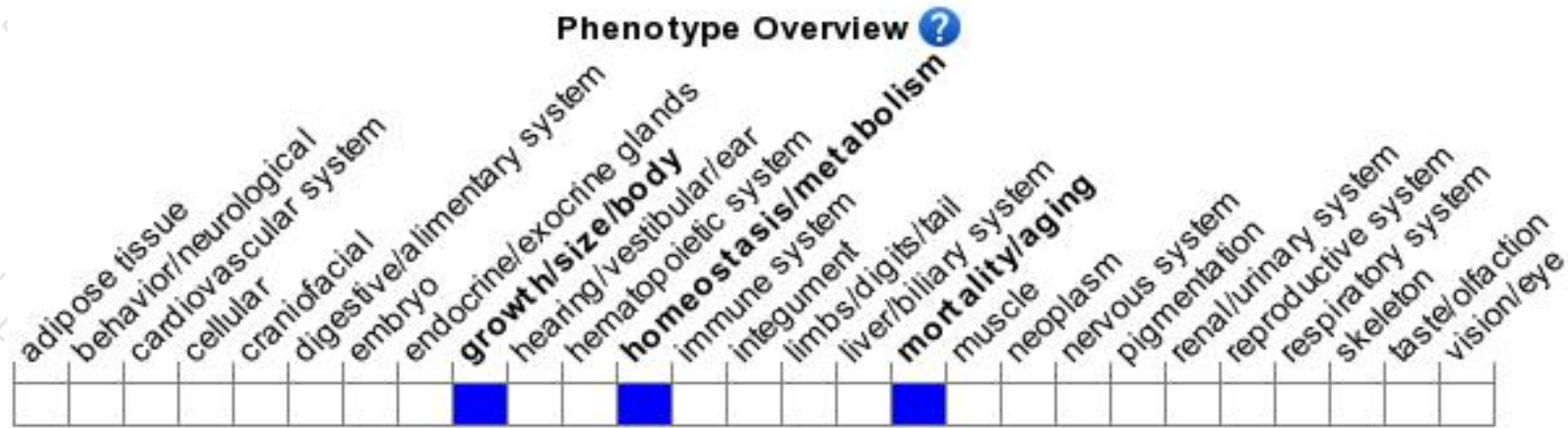
Genomic location distribution



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/>).

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

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