Nol9 Cas9-KO Strategy

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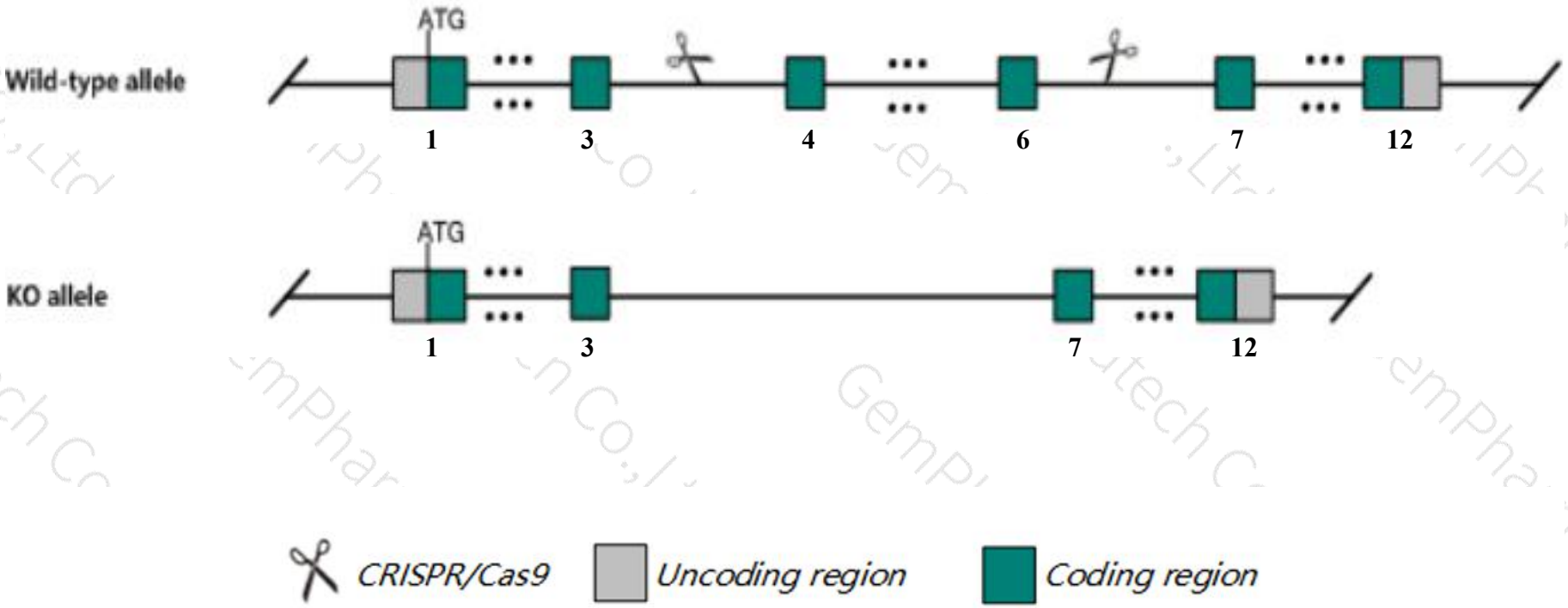
Project Overview

Project Name	***Nol9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nol9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Nol9* gene has 5 transcripts. According to the structure of *Nol9* gene, exon4-exon6 of *Nol9-201* (ENSMUST00000084116.12) transcript is recommended as the knockout region.The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nol9* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- The N-terminal of *Nol9* gene will remain several amino acids ,it may remain the partial function of *Nol9* gene.
- The knockout region is near to the N-terminal of *Tas1r1* gene,this strategy may influence the regulatory function of the N-terminal of *Tas1r1* gene.
- The *Nol9* gene is located on the Chr4. 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）

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Nol9 nucleolar protein 9 [Mus musculus (house mouse)]

Gene ID: 74035, updated on 13-Mar-2020

Summary

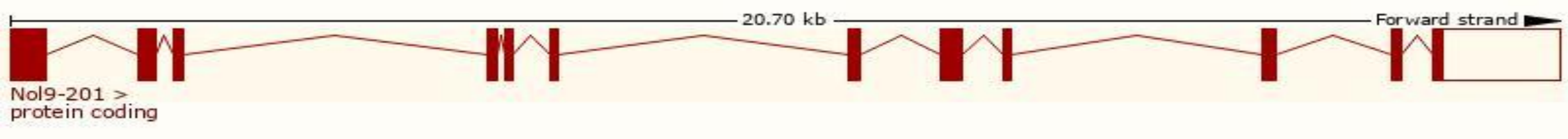
Official Symbol	Nol9 provided by MGI
Official Full Name	nucleolar protein 9 provided by MGI
Primary source	MGI:MGI:1921285
See related	Ensembl:ENSMUSG00000028948
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4632412I24Rik, 6030462G04Rik, AI449622, AW490720
Expression	Ubiquitous expression in ovary adult (RPKM 14.1), thymus adult (RPKM 12.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

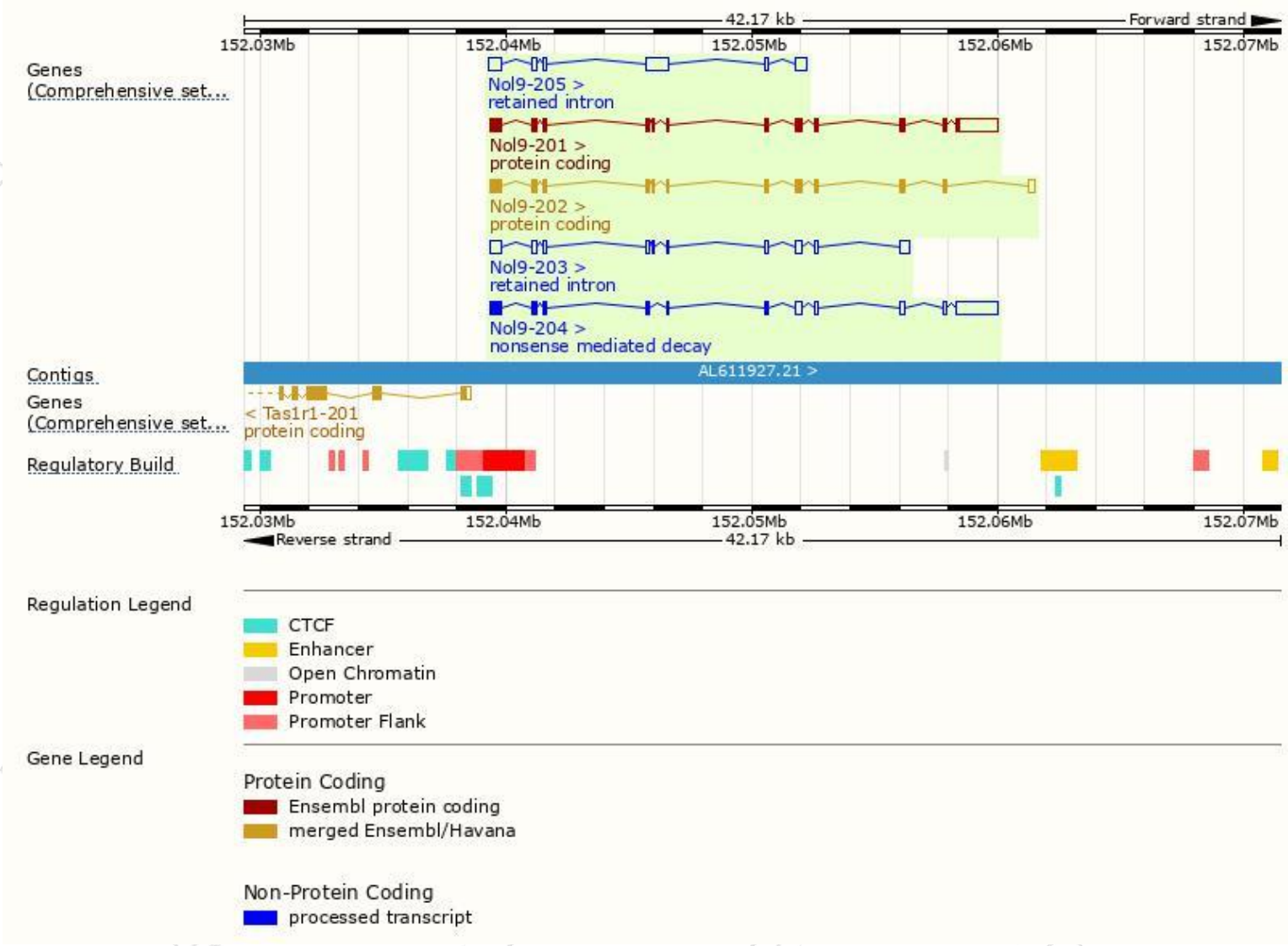
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nol9-201	ENSMUST00000084116.12	3722	714aa	Protein coding	CCDS51389	Q3TZX8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Nol9-202	ENSMUST00000103197.4	2271	671aa	Protein coding	CCDS18986	Q3TZX8	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Nol9-204	ENSMUST00000131696.2	3616	361aa	Nonsense mediated decay	-	A0A0U1RPV7	CDS 5' incomplete TSL:1
Nol9-205	ENSMUST00000147797.7	2419	No protein	Retained intron	-	-	TSL:2
Nol9-203	ENSMUST00000105663.7	2064	No protein	Retained intron	-	-	TSL:1

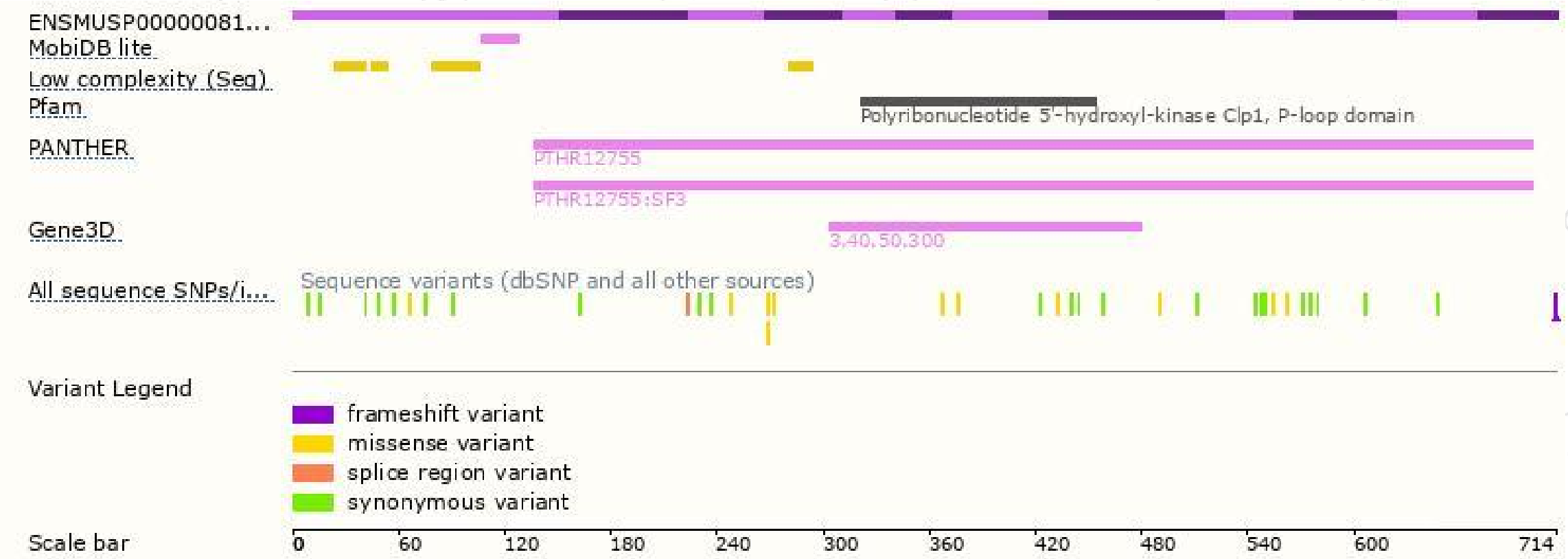
The strategy is based on the design of *Nol9-201* transcript,the transcription is shown below:



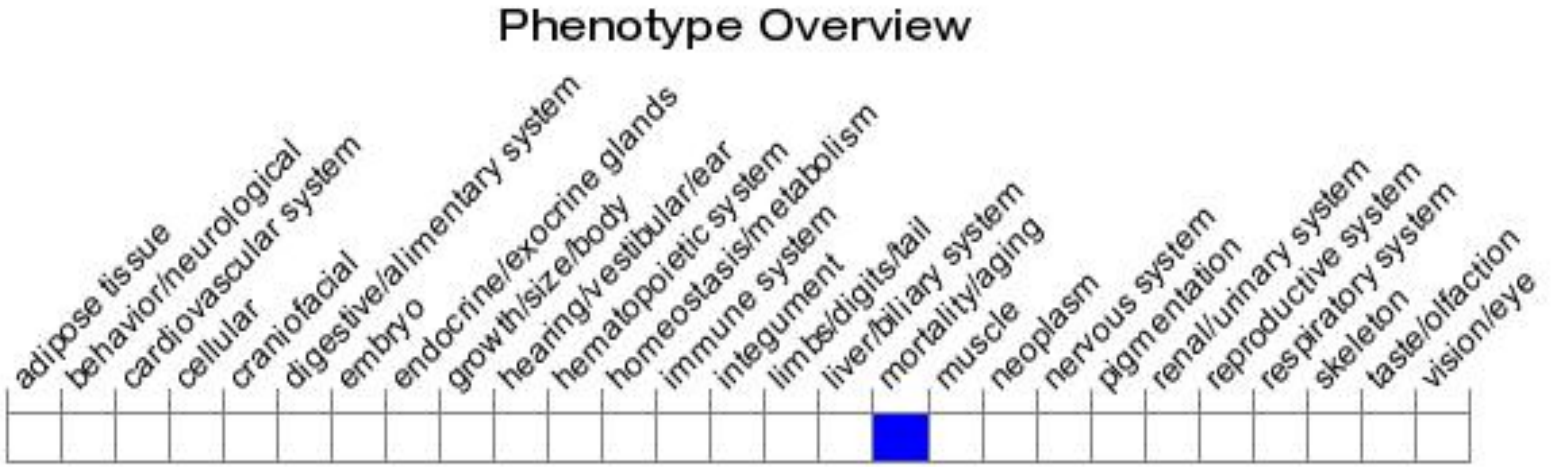
Genomic location distribution



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/).

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

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