Nucb1 Cas9-KO Strategy

Designer: Huan Wang

Reviewer: Yumeng Wang

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Project Overview

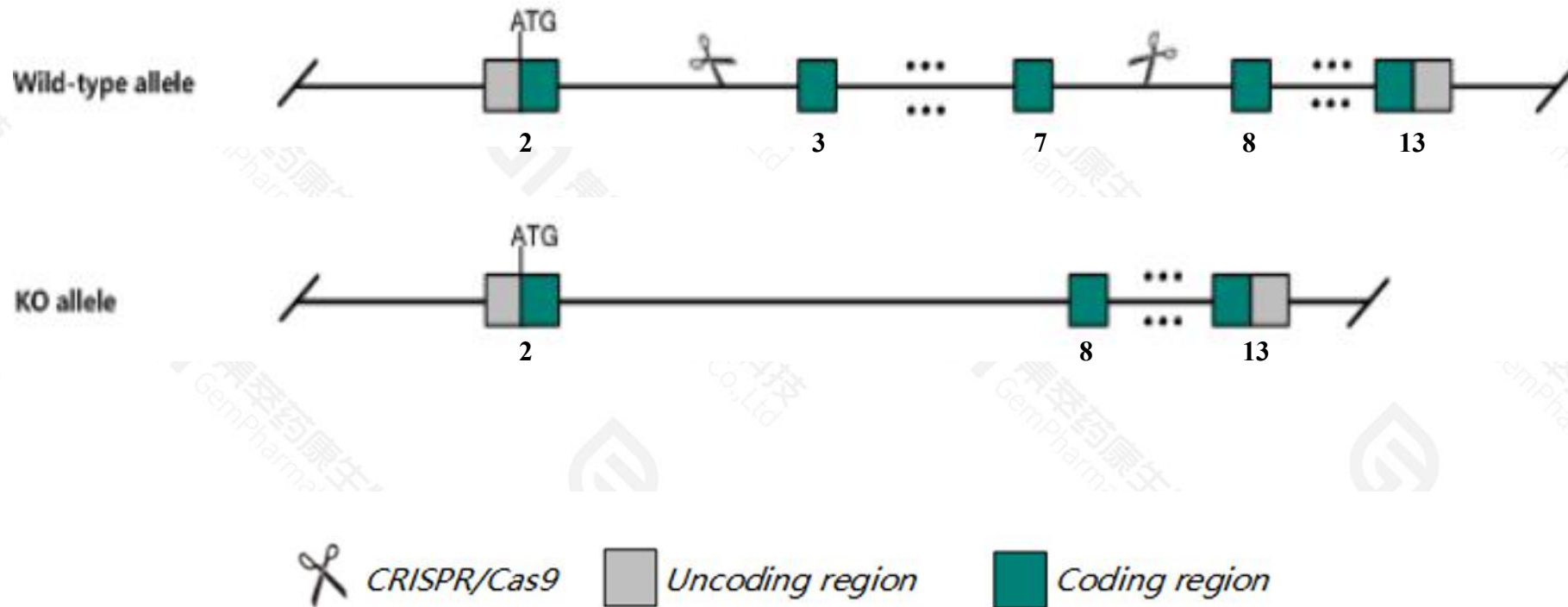|	
Project Name	*Nucb1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nucb1* gene. The schematic diagram is as follows:

Technical routes

➤ The *Nucb1* gene has 10 transcripts. According to the structure of *Nucb1* gene, exon3-exon7 of *Nucb1-210*(ENSMUST00000211765.2) transcript is recommended as the knockout region.The region contains 622bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Nucb1* gene. The brief process is as follows: CRISPR/Cas9 system 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➤ The *Nucb1* gene is located on the Chr7. 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.

➤ The KO region contains the intron of *Tulp2* gene. Knockout the region may affect the function of *Tulp2* gene.

➤ 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）

Nucb1 nucleobindin 1 [Mus musculus (house mouse)]

Gene ID: 18220, updated on 13-Mar-2020

▲ Summary

|	
Official Symbol	Nucb1 provided by MGI
Official Full Name	nucleobindin 1 provided by MGI
Primary source	MGI:MGI:97388
See related	Ensembl:ENSMUSG00000030824
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	B230337F23Rik, C77483, Calnuc, MTEST82, Nucb
Expression	Ubiquitous expression in colon adult (RPKM 160.1), genital fat pad adult (RPKM 128.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 10 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nucb1-210	ENSMUST00000211765.1	4853	459aa	Protein coding	CCDS52247	Q02819	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
Nucb1-201	ENSMUST00000033096.15	2111	455aa	Protein coding	CCDS85300	A0A1C7CYU3	TSL:5 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
Nucb1-206	ENSMUST00000210449.1	811	271aa	Protein coding	-	A0A1B0GR41	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 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
Nucb1-209	ENSMUST00000211682.1	755	220aa	Protein coding	-	A0A1B0GR92	CDS 3' incomplete TSL:2
Nucb1-202	ENSMUST00000209436.1	615	121aa	Protein coding	-	A0A1B0GT83	CDS 3' incomplete TSL:2
Nucb1-208	ENSMUST00000211343.1	559	170aa	Protein coding	-	A0A1B0GS16	CDS 3' incomplete TSL:5
Nucb1-204	ENSMUST00000210208.1	2742	No protein	Retained intron	-	-	TSL:1
Nucb1-205	ENSMUST00000210394.1	1069	No protein	Retained intron	-	-	TSL:5
Nucb1-207	ENSMUST00000210675.1	438	No protein	Retained intron	-	-	TSL:3
Nucb1-203	ENSMUST00000209509.1	433	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Nucb1-210* transcript,the transcription is shown below:
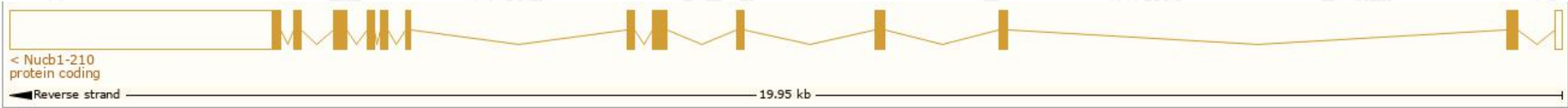
Genomic location distribution

Protein domain

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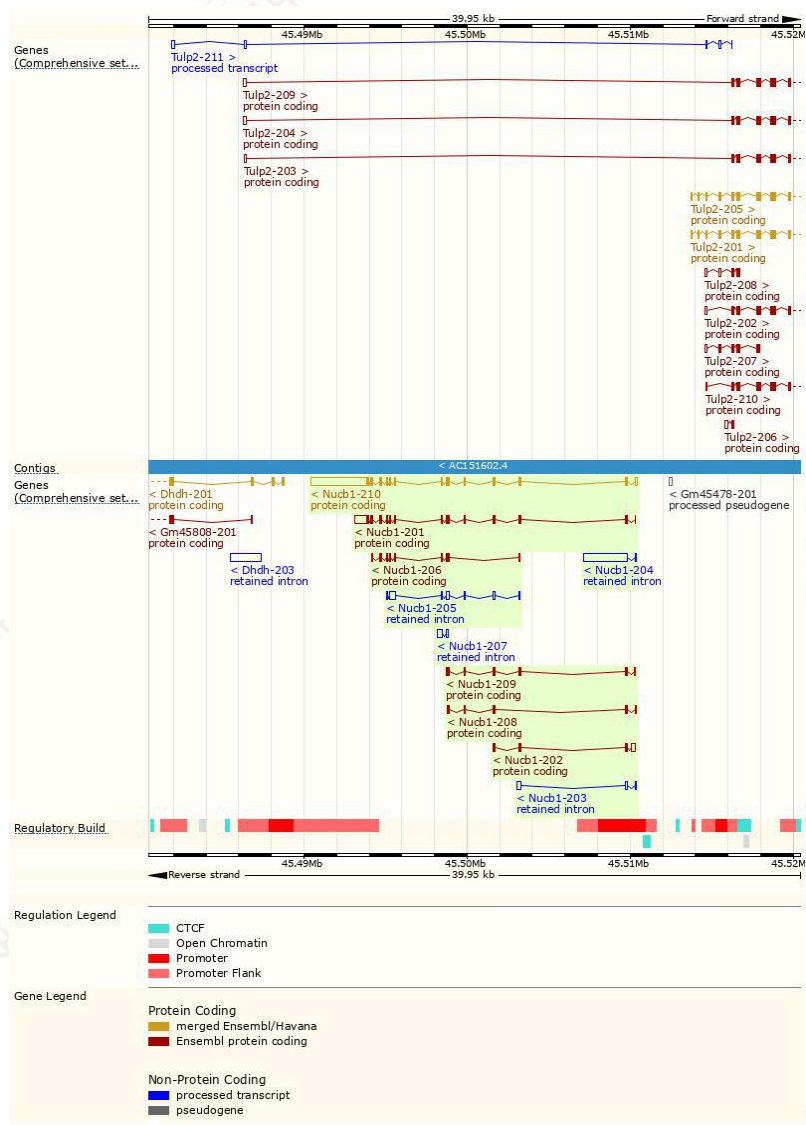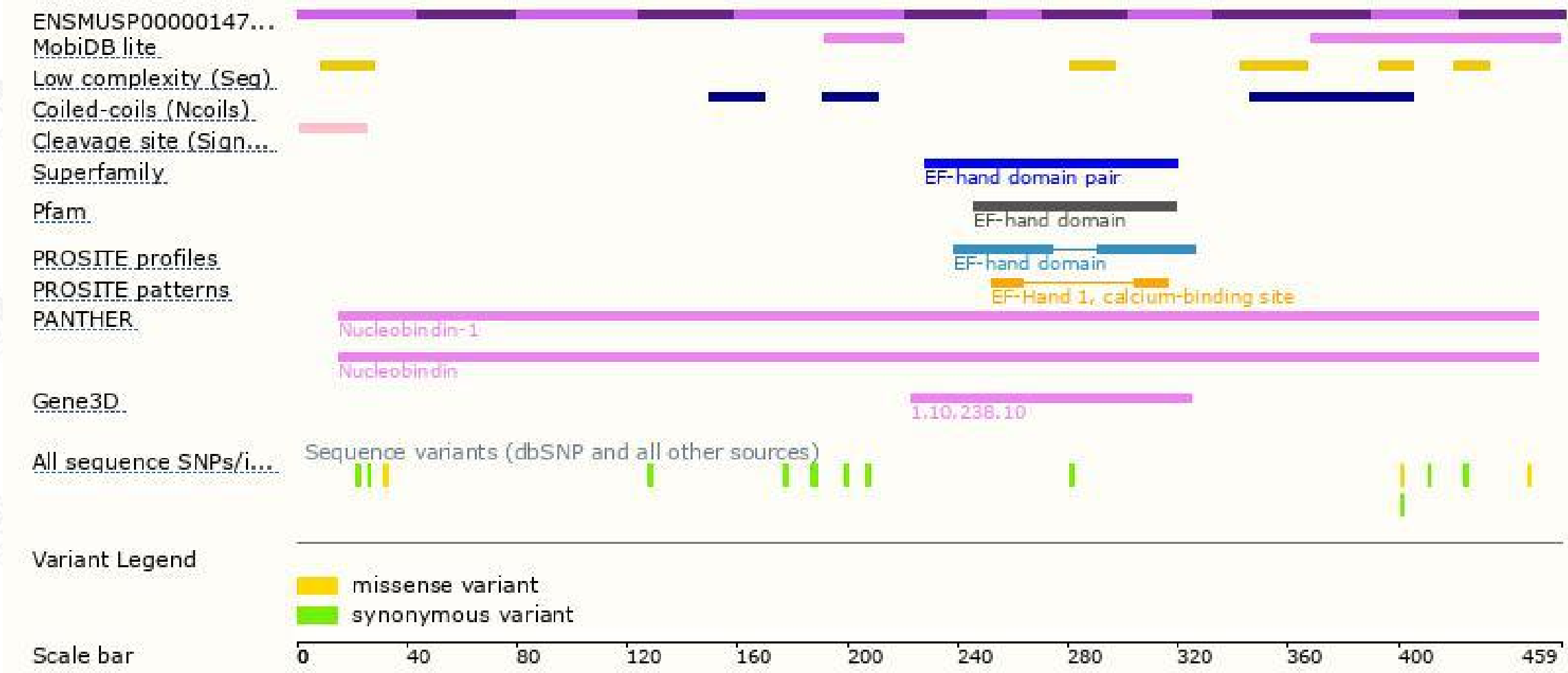
If you have any questions, you are welcome to inquire.
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