Nop58 Cas9-KO Strategy

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Date: 2020/1/19

Project Overview

Project Name	*Nop58*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nop58* gene. The schematic diagram is as follows:

Technical routes

➢ The *Nop58* gene has 15 transcripts. According to the structure of *Nop58* gene, exon2-exon12 of *Nop58-215* (ENSMUST00000191142.6) transcript is recommended as the knockout region.The region contains 1223bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nop58* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Nop58* gene is located on the Chr1. 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）

Nop58 NOP58 ribonucleoprotein [Mus musculus (house mouse)]

Gene ID: 55989, updated on 31-Jan-2019

▲ Summary

|	
Official Symbol	Nop58 provided by MGI
Official Full Name	NOP58 ribonucleoprotein provided by MGI
Primary source	MGI:MGI:1933184
See related	Ensembl:ENSMUSG00000026020
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	MSSP, Nol5, SIK, nop5
Expression	Broad expression in CNS E11.5 (RPKM 41.5), liver E14 (RPKM 35.5) and 20 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 15 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nop58-215	ENSMUST00000191142.6	9507	536aa	Protein coding	CCDS35587	Q6DFW4	TSL:1 GENCODE basic
Nop58-201	ENSMUST00000027174.9	1713	444aa	Protein coding	-	A0A0A0MQ76	TSL:5 GENCODE basic APPRIS P1
Nop58-211	ENSMUST00000190231.6	639	28aa	Protein coding	-	A0A087WRD9	CDS 3' incomplete TSL:2
Nop58-206	ENSMUST00000187837.6	638	213aa	Protein coding	-	A0A087WQ46	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
Nop58-207	ENSMUST00000188390.1	585	195aa	Protein coding	-	A0A087WP00	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
Nop58-203	ENSMUST00000185772.6	461	20aa	Protein coding	-	A0A087WNS6	CDS 3' incomplete TSL:3
Nop58-212	ENSMUST00000190265.6	714	191aa	Nonsense mediated decay	-	A0A087WSL8	CDS 5' incomplete TSL:5
Nop58-209	ENSMUST00000189327.6	702	60aa	Nonsense mediated decay	-	A0A087WNW0	TSL:5
Nop58-210	ENSMUST00000189919.6	598	146aa	Nonsense mediated decay	-	A0A087WSU5	CDS 5' incomplete TSL:3
Nop58-205	ENSMUST00000187491.1	373	60aa	Nonsense mediated decay	-	A0A087WQ59	CDS 5' incomplete TSL:5
Nop58-202	ENSMUST00000185368.1	891	No protein	Retained intron	-	-	TSL:3
Nop58-204	ENSMUST00000186044.1	725	No protein	Retained intron	-	-	TSL:2
Nop58-208	ENSMUST00000189289.6	653	No protein	Retained intron	-	-	TSL:2
Nop58-213	ENSMUST00000190759.6	623	No protein	Retained intron	-	-	TSL:3
Nop58-214	ENSMUST00000191088.6	576	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Nop58-215* transcript,The transcription is shown below
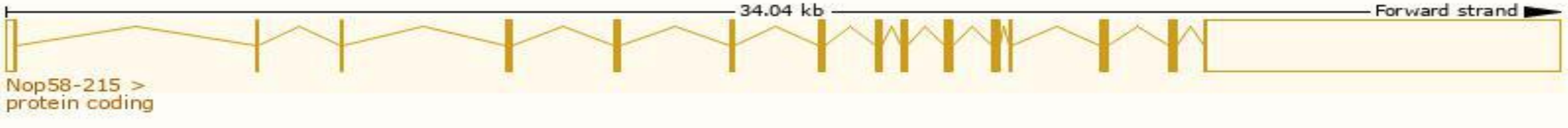
Genomic location distribution

Protein domain

| | Scale bar | 0 | 60 | 120 | 180 | 240 | 300 | 360 | 420 | 536 |
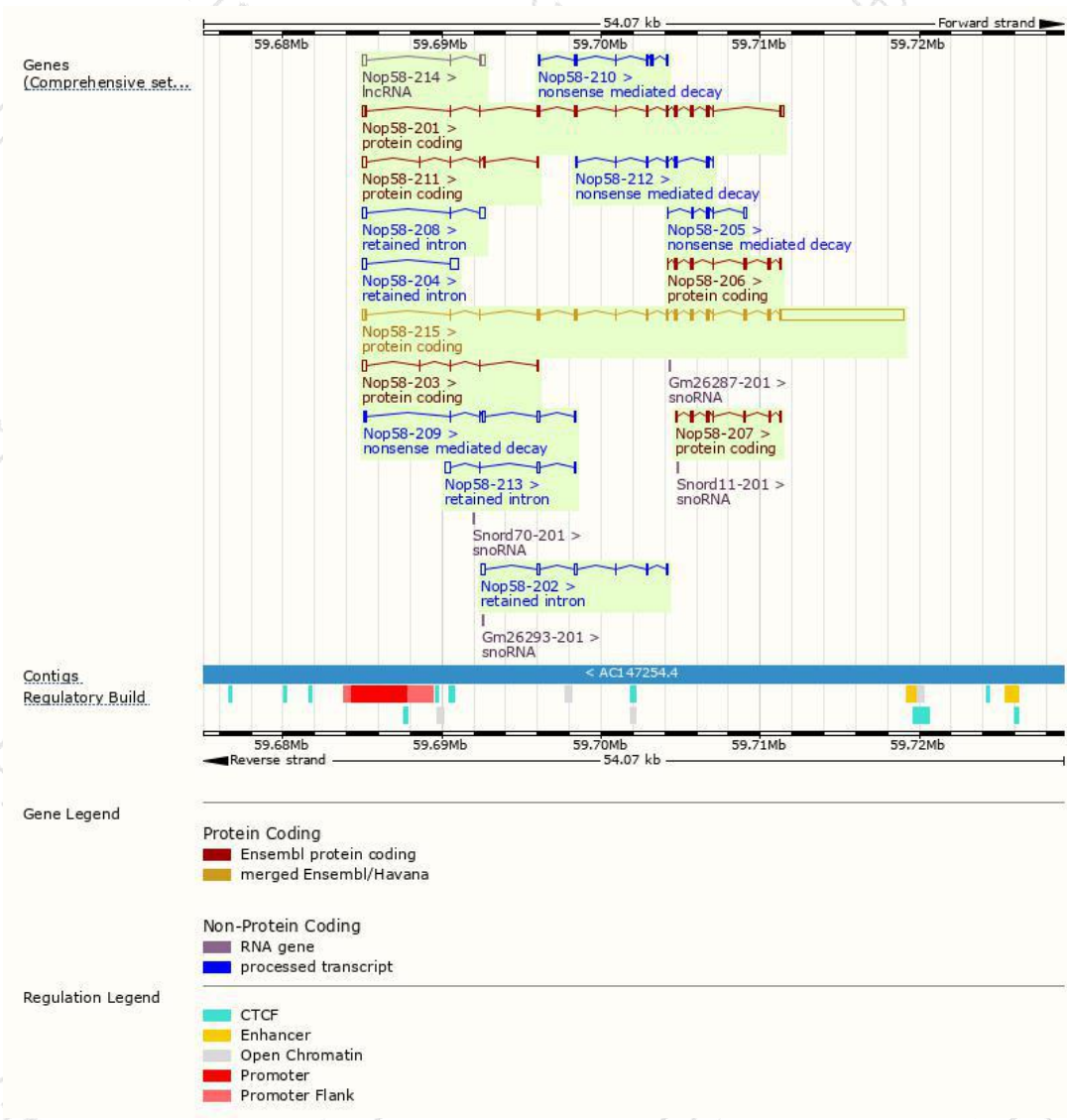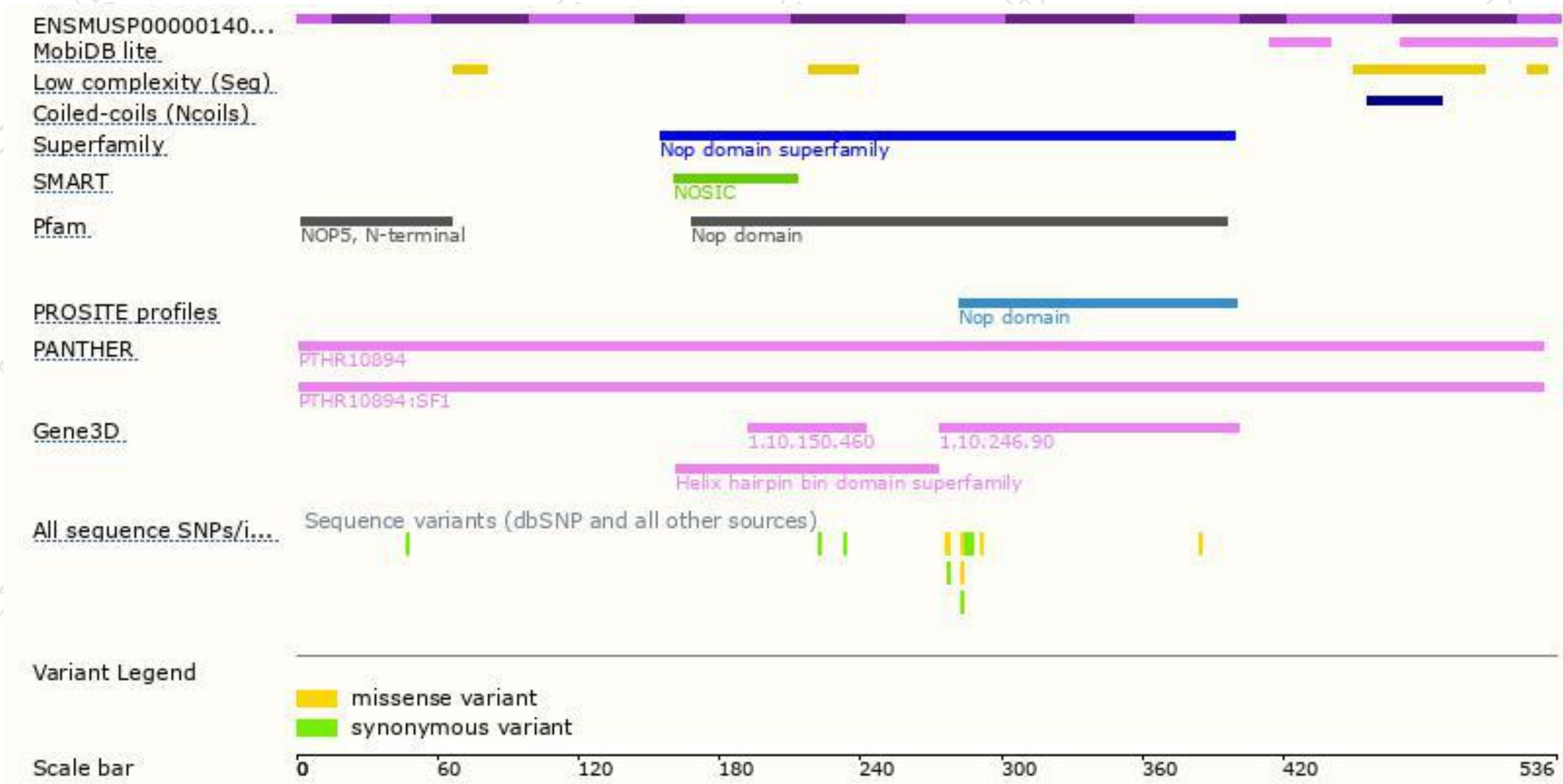
If you have any questions, you are welcome to inquire.
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