

***Nup107* Cas9-KO Strategy**

Designer: Huan Wang

Reviewer: Wenjing Li

Design Date: 2020-8-1

Project Overview

Project Name

Nup107

Project type

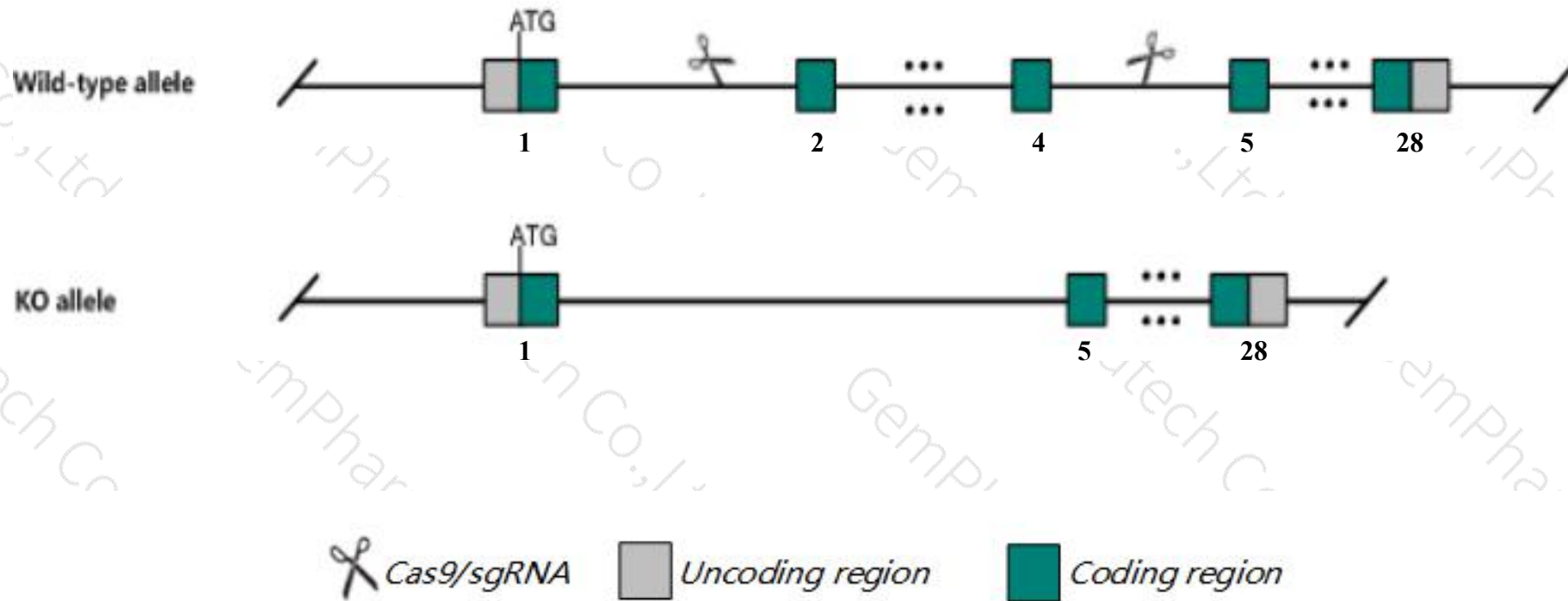
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nup107* gene. The schematic diagram is as follows:



- The *Nup107* gene has 8 transcripts. According to the structure of *Nup107* gene, exon2-exon4 of *Nup107-201*(ENSMUST00000064848.6) transcript is recommended as the knockout region. The region contains 298bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nup107* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, mice homozygous for a CRISPR-generated allele exhibit reduced female fertility.
- The *Nup107* gene is located on the Chr10. 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)

Nup107 nucleoporin 107 [Mus musculus (house mouse)]

Gene ID: 103468, updated on 13-Mar-2020

Summary



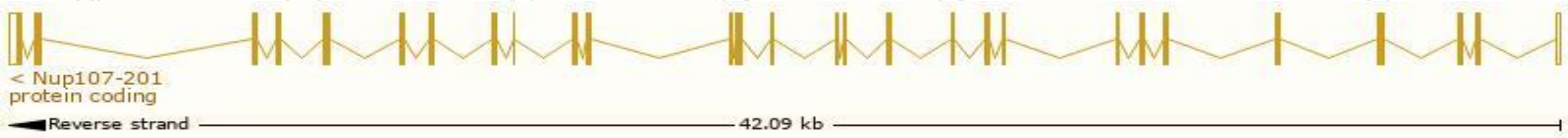
Official Symbol	Nup107 provided by MGI
Official Full Name	nucleoporin 107 provided by MGI
Primary source	MGI:MGI:2143854
See related	Ensembl:ENSMUSG00000052798
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW541137, C76801
Expression	Broad expression in CNS E11.5 (RPKM 27.0), placenta adult (RPKM 18.7) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

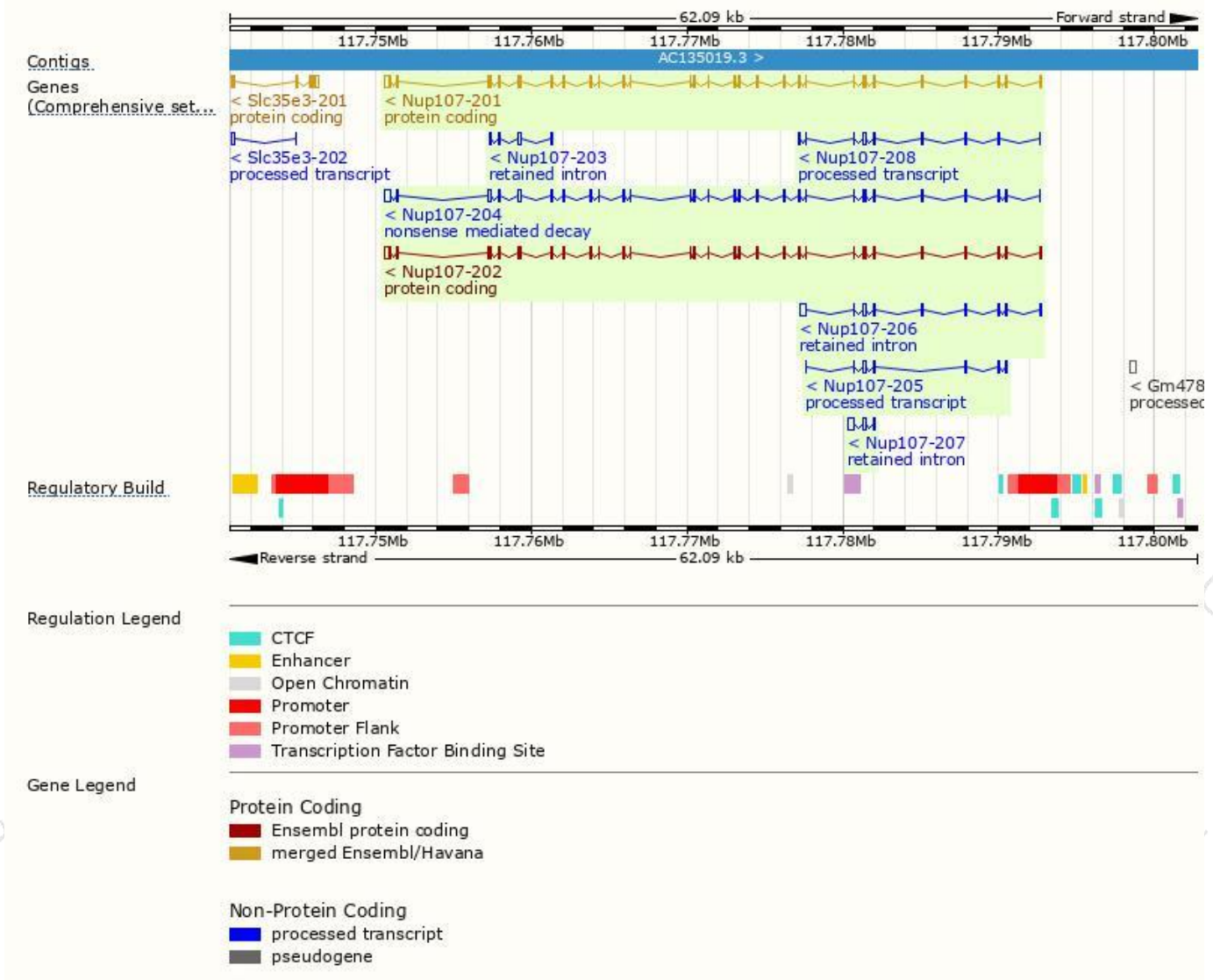
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nup107-201	ENSMUST00000064848.6	3114	926aa	Protein coding	CCDS36068	Q8BH74	TSL:1 GENCODE basic APPRIS P2
Nup107-202	ENSMUST00000167943.7	3098	924aa	Protein coding	-	E9Q4V9	TSL:1 GENCODE basic APPRIS ALT1
Nup107-204	ENSMUST00000218576.1	3092	336aa	Nonsense mediated decay	-	A0A1W2P7R1	TSL:1
Nup107-208	ENSMUST00000220323.1	837	No protein	Processed transcript	-	-	TSL:3
Nup107-205	ENSMUST00000218777.1	643	No protein	Processed transcript	-	-	TSL:3
Nup107-206	ENSMUST00000218810.1	1233	No protein	Retained intron	-	-	TSL:1
Nup107-207	ENSMUST00000220203.1	594	No protein	Retained intron	-	-	TSL:5
Nup107-203	ENSMUST00000218375.1	496	No protein	Retained intron	-	-	TSL:3

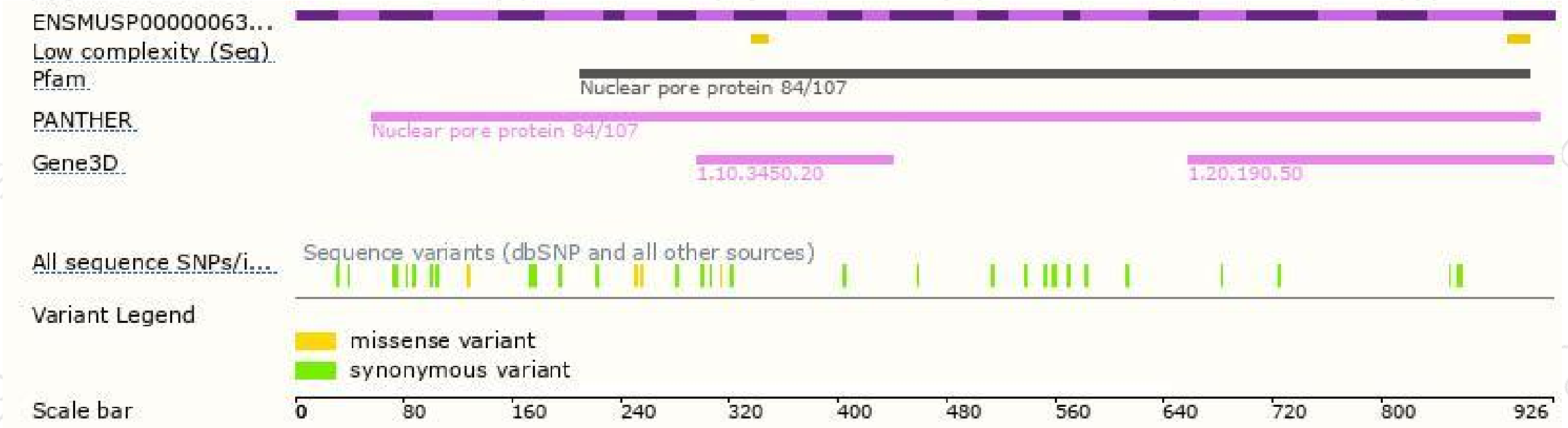
The strategy is based on the design of *Nup107-201* transcript,the transcription is shown below:



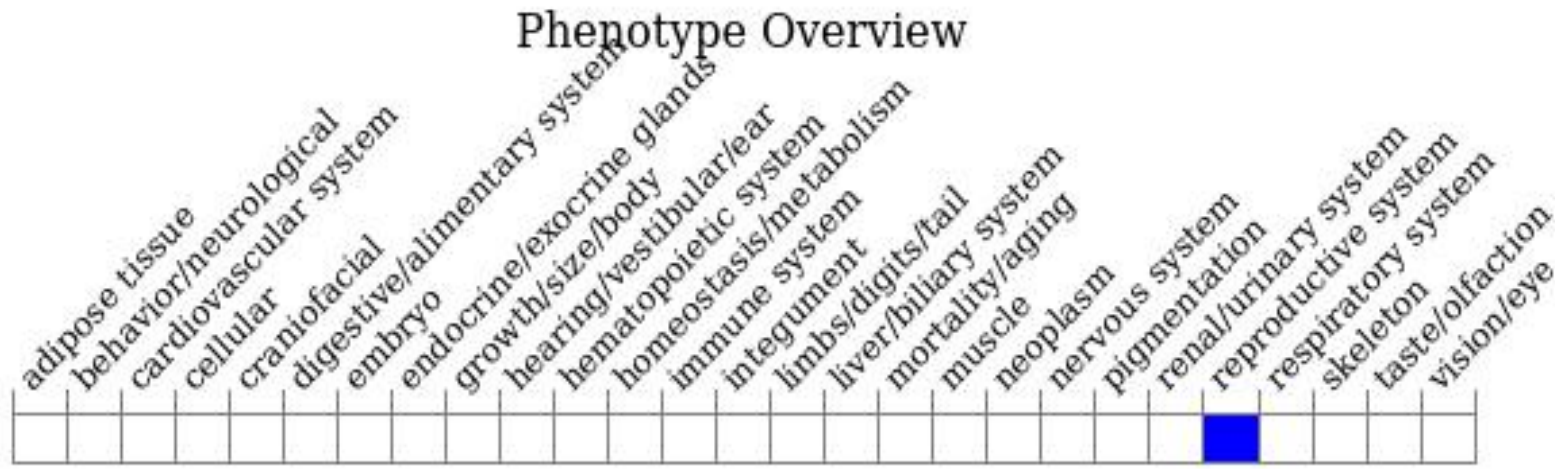
Genomic location distribution



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/>).

According to the existing MGI data,mice homozygous for a CRISPR-generated allele exhibit reduced female fertility.

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

Tel: 025-5864 1534

