

Nup35 Cas9-CKO Strategy

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Project Overview

Project Name

Nup35

Project type

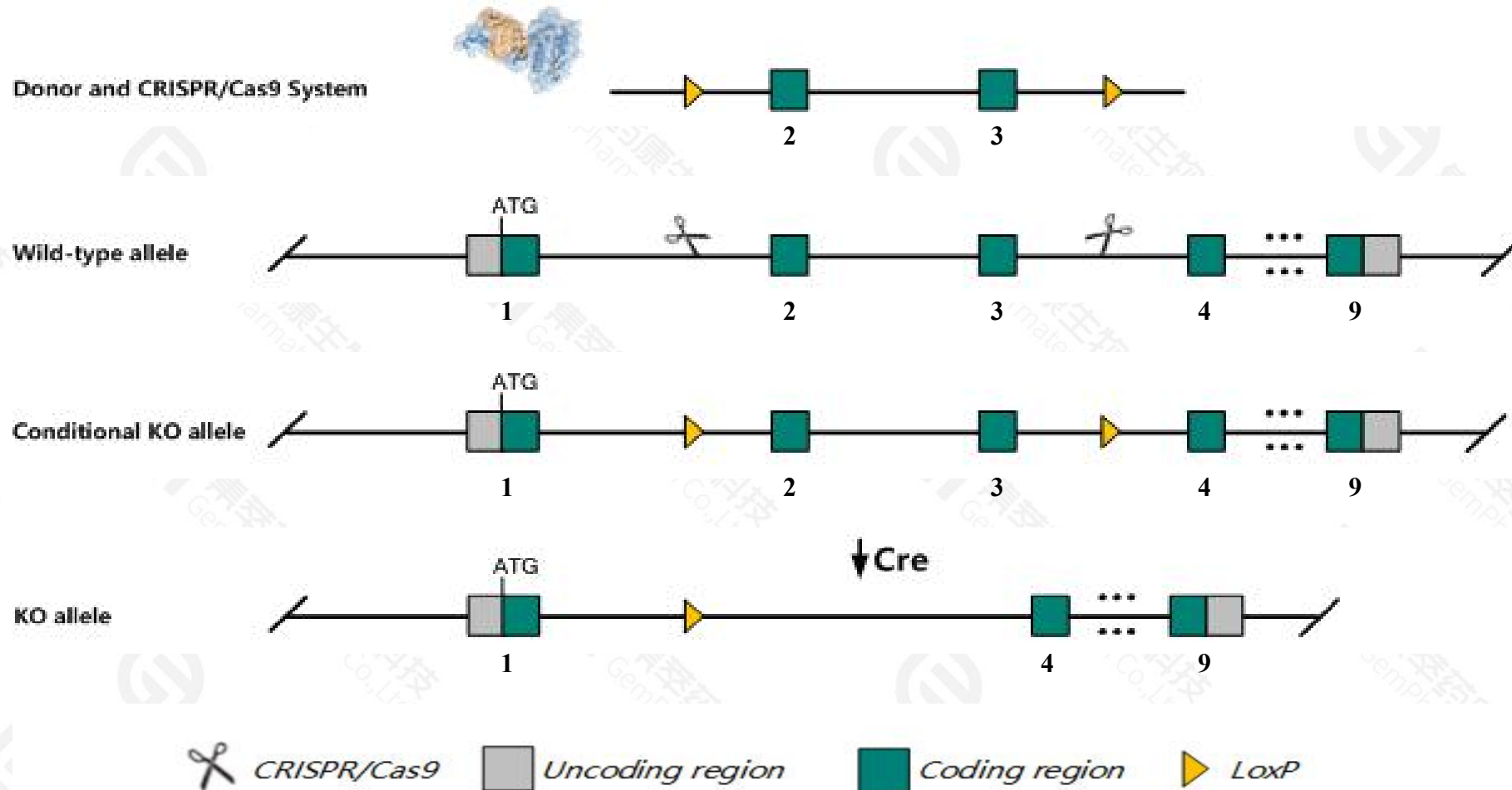
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nup35* gene. The schematic diagram is as follows:



Technical routes

- The *Nup35* gene has 5 transcripts. According to the structure of *Nup35* gene, exon2-exon3 of *Nup35-201*(ENSMUST00000028382.13) transcript is recommended as the knockout region. The region contains 299bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nup35* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, homozygous knockout through a point mutation in a critical functional domain leads to early death as a result of megacolon caused by colon myopathy.
- The *Nup35* gene is located on the Chr2. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Nup35 nucleoporin 35 [Mus musculus (house mouse)]

Gene ID: 69482, updated on 25-Sep-2020

Summary



Official Symbol	Nup35 provided by MGI
Official Full Name	nucleoporin 35 provided by MGI
Primary source	MGI:MGI:1916732
See related	Ensembl:ENSMUSG00000026999
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	2310006I24Rik, 35kDa, 5330402E05Rik, MP44, NO44
Expression	Ubiquitous expression in testis adult (RPKM 15.4), whole brain E14.5 (RPKM 7.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

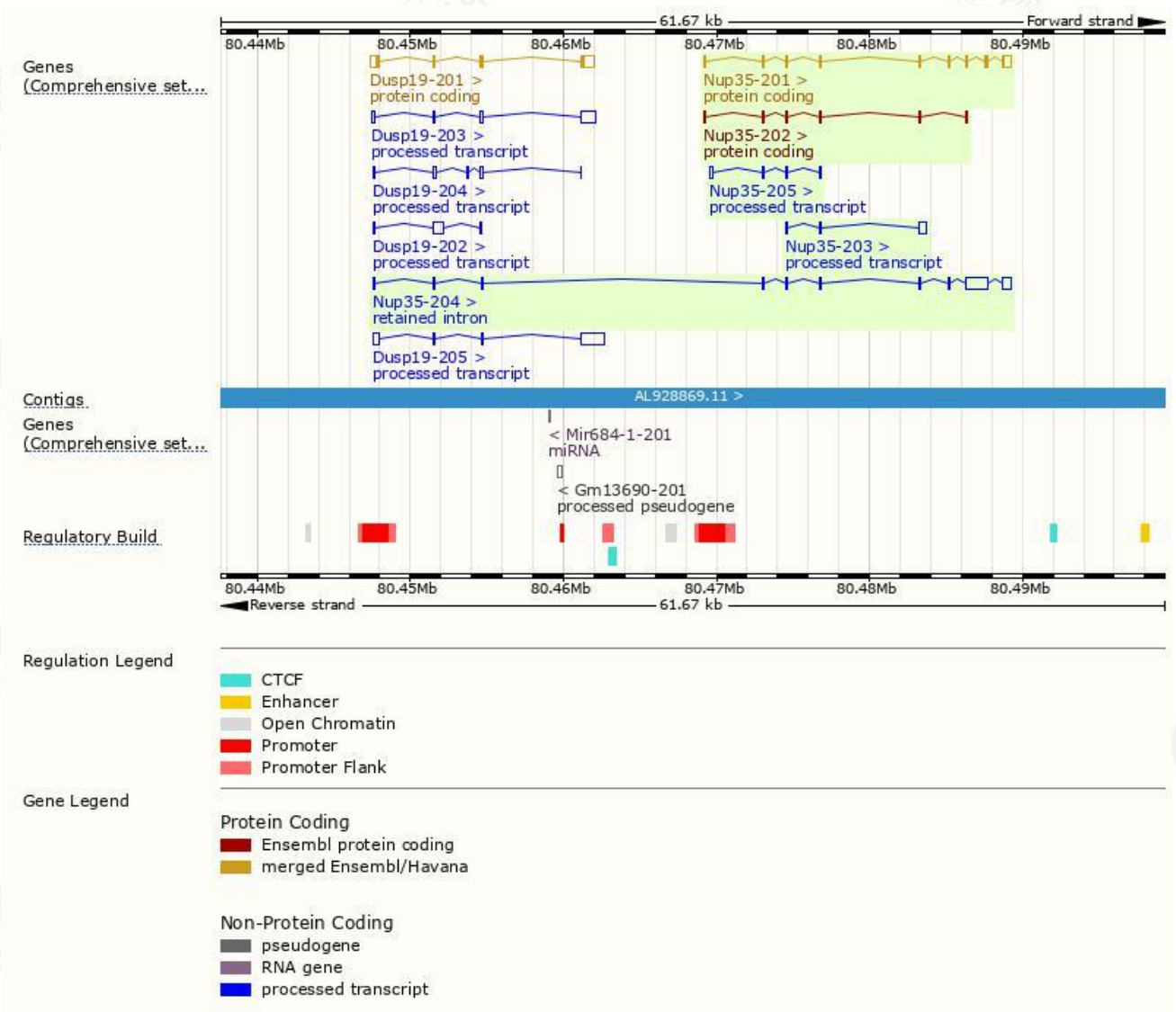
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nup35-201	ENSMUST00000028382.13	1559	325aa	Protein coding	CCDS16179		TSL:1 , GENCODE basic , APPRIS P1 ,
Nup35-202	ENSMUST00000124377.2	653	197aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Nup35-203	ENSMUST00000127926.2	692	No protein	Processed transcript	-		TSL:3 ,
Nup35-205	ENSMUST00000144697.2	496	No protein	Processed transcript	-		TSL:3 ,
Nup35-204	ENSMUST00000135305.8	2688	No protein	Retained intron	-		TSL:2 ,

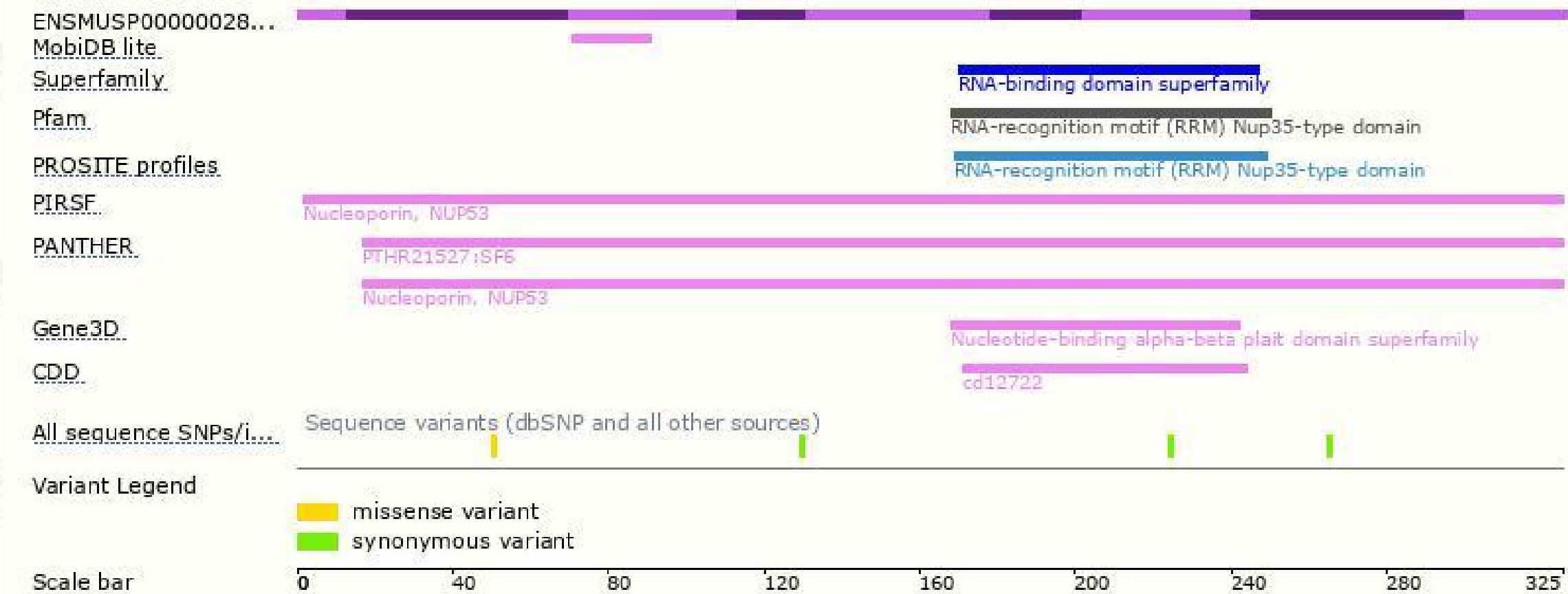
The strategy is based on the design of *Nup35-201* transcript,the transcription is shown below:



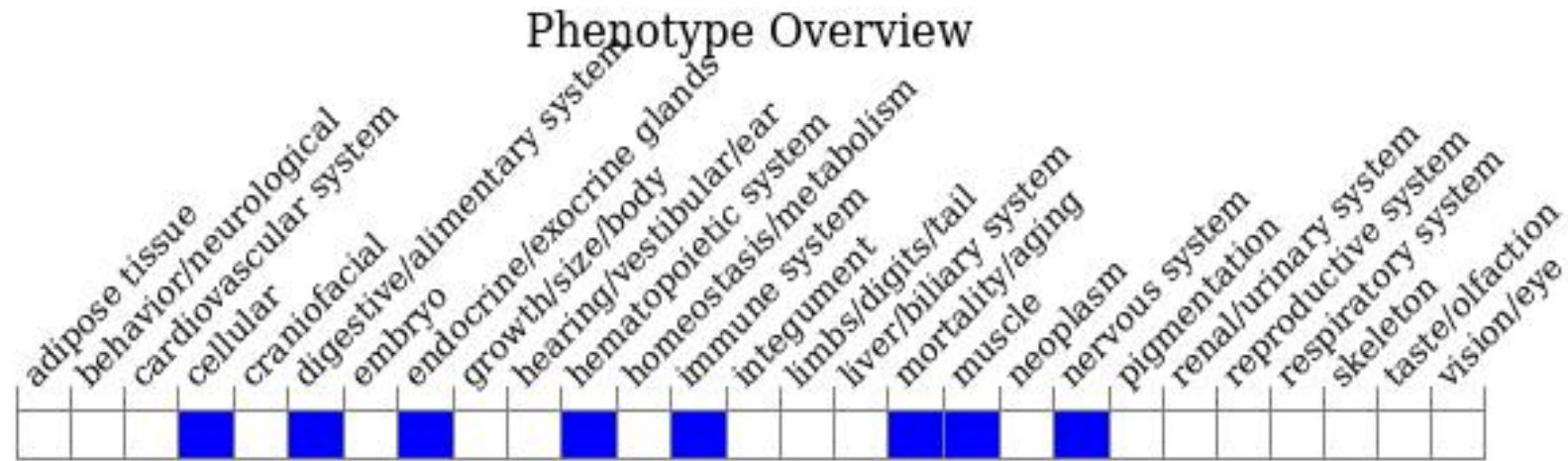
Genomic location distribution



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, homozygous knockout through a point mutation in a critical functional domain leads to early death as a result of megacolon caused by colon myopathy.

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