

Nin Cas9-KO Strategy

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Design Date: 2020-2-14

Project Overview

Project Name

Nin

Project type

Cas9-KO

Strain background

C57BL/6J

Knockout strategy

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



- The *Nin* gene has 17 transcripts. According to the structure of *Nin* gene, exon3 of *Nin-211* (ENSMUST00000222237.1) transcript is recommended as the knockout region. The region contains 82bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nin* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit partial pre- and postnatal lethality, thinner skin, delayed skin barrier formation, impaired skin barrier function, impaired differentiation of suprabasal cells, and defects in mitotic spindle orientation, desmosome assembly and lamellar body secretion.
- The *Nin* gene is located on the Chr12. 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)

Nin ninein [*Mus musculus* (house mouse)]

Gene ID: 18080, updated on 10-Oct-2019

Summary

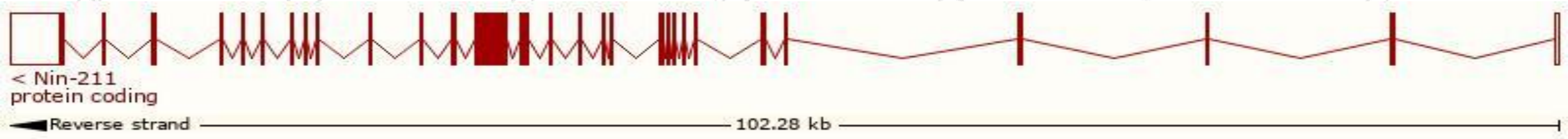
| | |
|--------------------|---|
| Official Symbol | Nin provided by MGI |
| Official Full Name | ninein provided by MGI |
| Primary source | MGI:MGI:105108 |
| See related | Ensembl:ENSMUSG000000021068 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | AI385615; AU024711; mKIAA1565; 3110068G20Rik |
| Expression | Ubiquitous expression in CNS E18 (RPKM 5.4), CNS E14 (RPKM 4.0) and 23 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

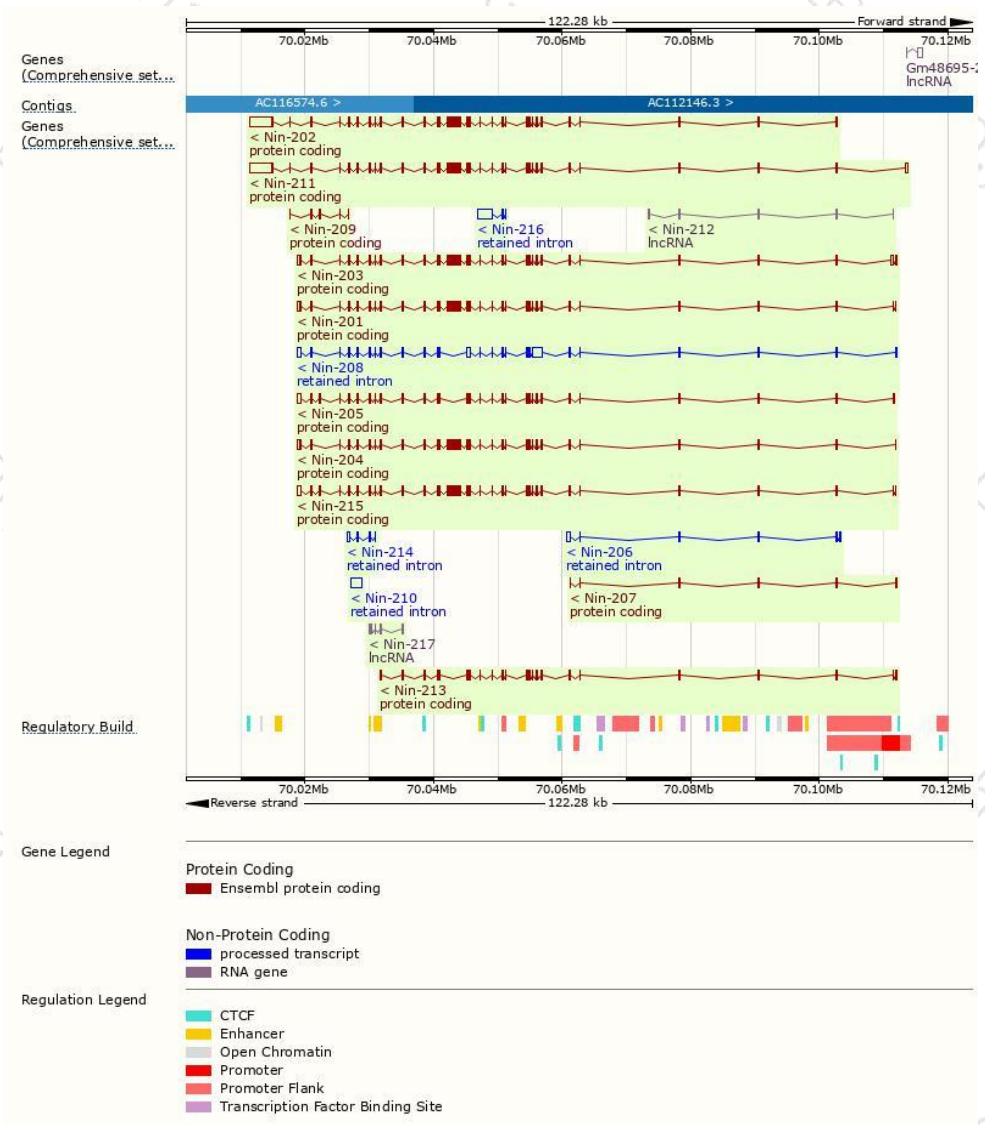
The gene has 17 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---------|---------------------------------------|------|------------------------|-----------------|---------------------------|----------------------------|---------------------------------|
| Nin-211 | ENSMUST00000222237.1 | 9919 | 2113aa | Protein coding | CCDS36468 | Q61043 | TSL:5 GENCODE basic APPRIS P4 |
| Nin-202 | ENSMUST00000085314.10 | 9675 | 2113aa | Protein coding | CCDS36468 | Q61043 | TSL:1 GENCODE basic APPRIS P4 |
| Nin-203 | ENSMUST00000095666.12 | 7183 | 2035aa | Protein coding | CCDS36469 | Q61043 | TSL:5 GENCODE basic APPRIS ALT2 |
| Nin-201 | ENSMUST00000021468.13 | 6708 | 2035aa | Protein coding | CCDS36469 | Q61043 | TSL:1 GENCODE basic APPRIS ALT2 |
| Nin-204 | ENSMUST00000169074.1 | 6636 | 2035aa | Protein coding | CCDS36469 | Q61043 | TSL:1 GENCODE basic APPRIS ALT2 |
| Nin-215 | ENSMUST00000223257.1 | 6744 | 1979aa | Protein coding | - | A0A1Y7VNC5 | TSL:1 GENCODE basic APPRIS ALT2 |
| Nin-205 | ENSMUST00000220689.1 | 4723 | 1272aa | Protein coding | - | Q61043 | TSL:1 GENCODE basic APPRIS ALT2 |
| Nin-213 | ENSMUST00000222835.1 | 3181 | 996aa | Protein coding | - | A0A1Y7VJC3 | CDS 3' incomplete TSL:1 |
| Nin-207 | ENSMUST00000221275.1 | 729 | 178aa | Protein coding | - | A0A1Y7VIQ3 | CDS 3' incomplete TSL:3 |
| Nin-209 | ENSMUST00000221579.1 | 521 | 80aa | Protein coding | - | A0A1Y7VJS5 | CDS 5' incomplete TSL:3 |
| Nin-208 | ENSMUST00000221486.1 | 5655 | No protein | Retained intron | - | - | TSL:2 |
| Nin-216 | ENSMUST00000223316.1 | 2490 | No protein | Retained intron | - | - | TSL:1 |
| Nin-210 | ENSMUST00000222137.1 | 1650 | No protein | Retained intron | - | - | TSL:NA |
| Nin-206 | ENSMUST00000221141.1 | 1397 | No protein | Retained intron | - | - | TSL:1 |
| Nin-214 | ENSMUST00000223048.1 | 656 | No protein | Retained intron | - | - | TSL:2 |
| Nin-212 | ENSMUST00000222466.1 | 846 | No protein | lncRNA | - | - | TSL:3 |
| Nin-217 | ENSMUST00000223469.1 | 488 | No protein | lncRNA | - | - | TSL:3 |

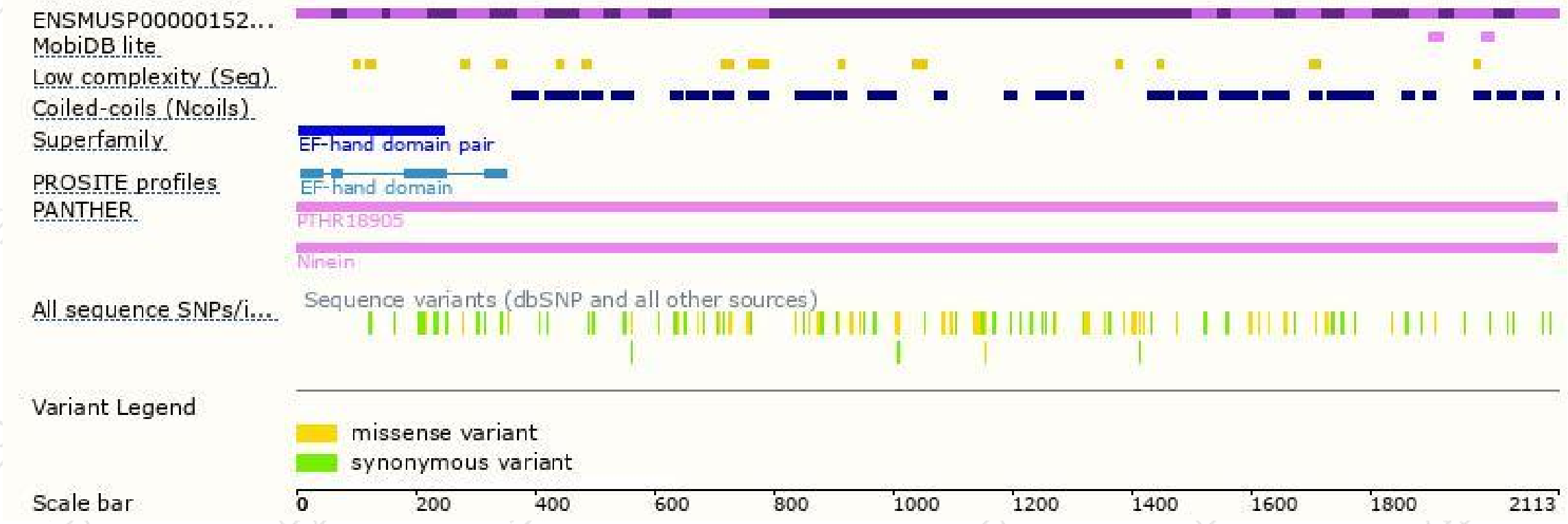
The strategy is based on the design of *Nin-211* transcript,The transcription is shown below



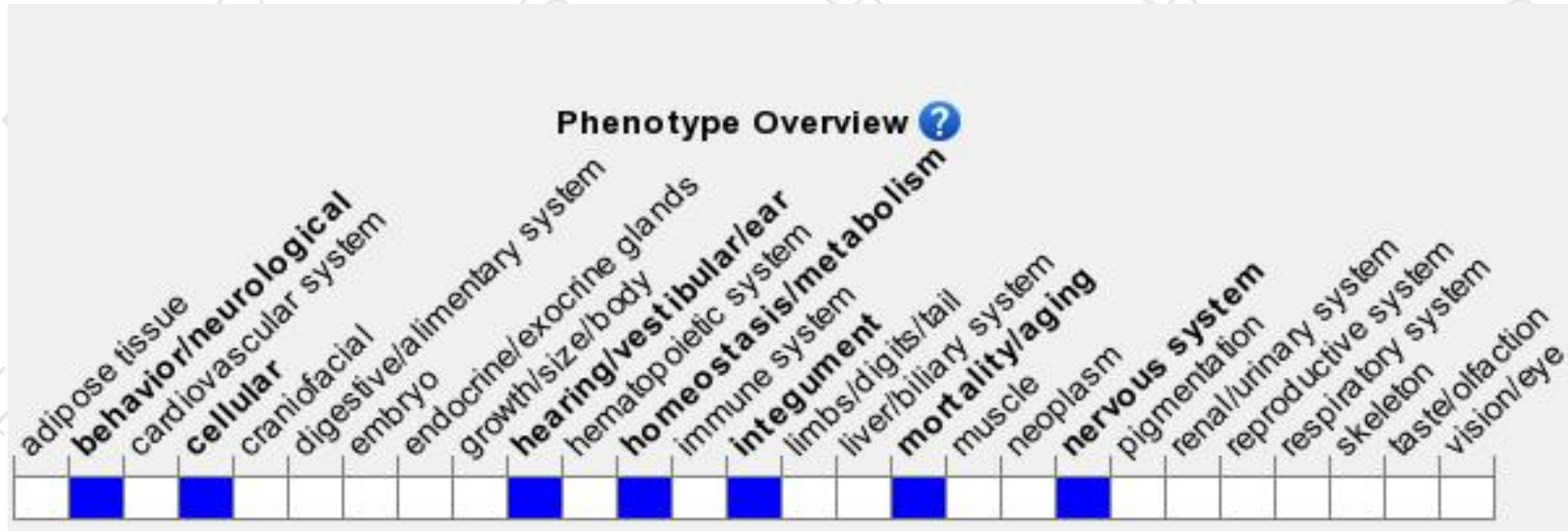
Genomic location distribution



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/>).

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

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