

Neurod2 Cas9-KO Strategy

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Project Overview

Project Name

Neurod2

Project type

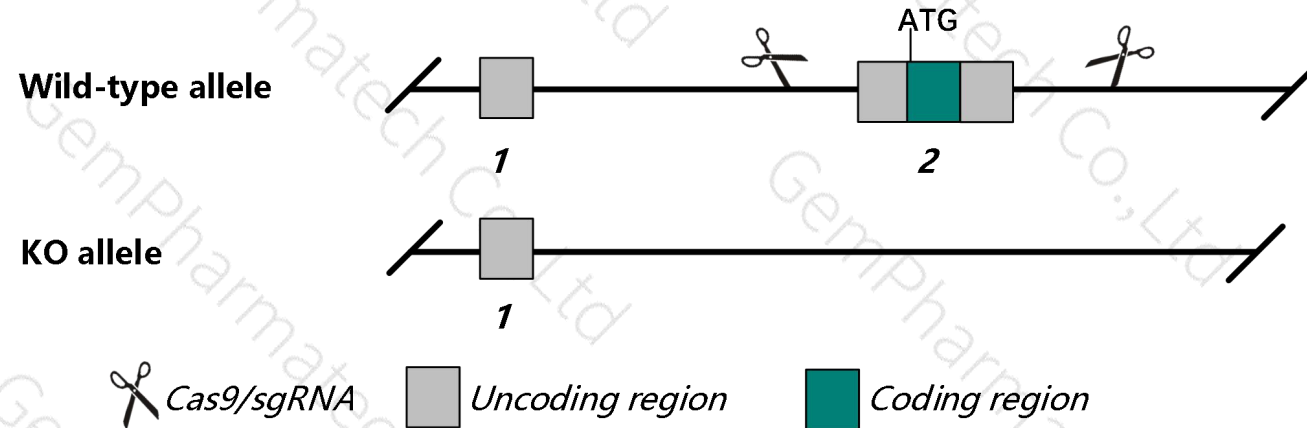
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Neurod2* gene. The schematic diagram is as follows:



- The *Neurod2* gene has 1 transcript. According to the structure of *Neurod2* gene, exon2 of *Neurod2*-201(ENSMUST00000041685.6) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Neurod2* 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.

- According to the existing MGI data, homozygotes for a targeted null mutation show elevated neuronal apoptosis resulting in ataxia, incoordination, elevated seizure susceptibility, and death by 35 days. Heterozygotes are moderately affected, and adults are subject to unexplained death.
- The *Neurod2* gene is located on the Chr11. 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)

Neurod2 neurogenic differentiation 2 [Mus musculus (house mouse)]

Gene ID: 18013, updated on 13-Mar-2020

Summary

Official Symbol Neurod2 provided by [MGI](#)

Official Full Name neurogenic differentiation 2 provided by [MGI](#)

Primary source [MGI:MGI:107755](#)

See related [Ensembl:ENSMUSG00000038255](#)

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 Ndrf, bHLHa1

Expression Biased expression in CNS E14 (RPKM 26.6), whole brain E14.5 (RPKM 24.4) and 4 other tissues [See more](#)

Orthologs [human](#) [all](#)

Transcript information (Ensembl)

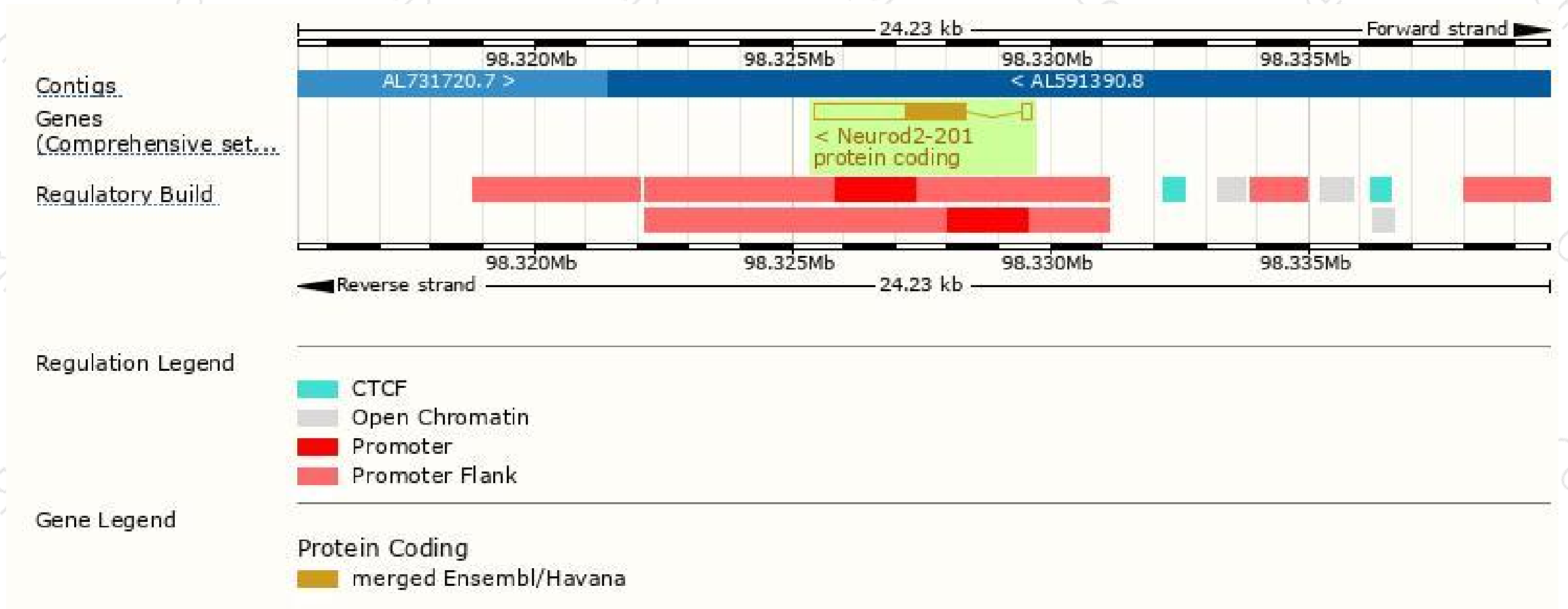
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Neurod2-201	ENSMUST00000041685.6	3142	383aa	Protein coding	CCDS25343	Q3TYB2 Q62414	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 P1

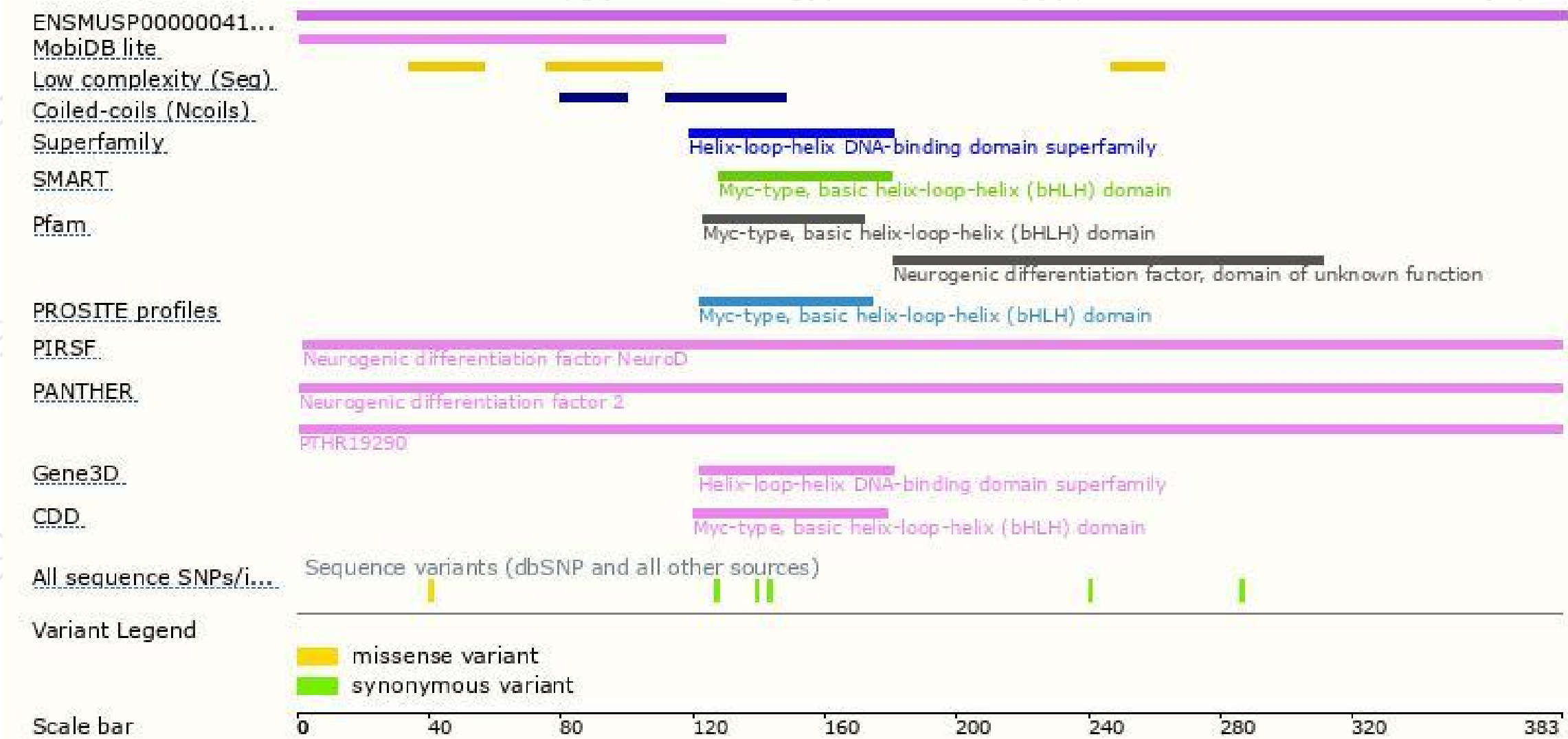
The strategy is based on the design of *Neurod2-201* transcript, the transcription is shown below:



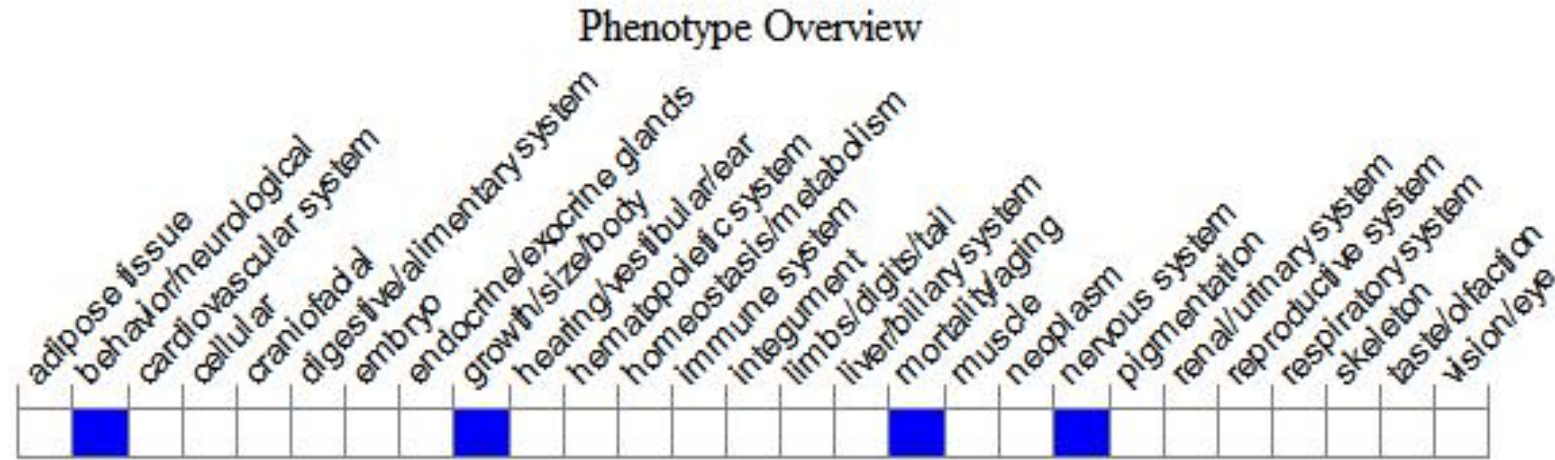
Genomic location distribution



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/>).

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

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