

Neo1 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Neo1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Neo1* gene has 6 transcripts. According to the structure of *Neo1* gene, exon2-exon4 of *Neo1-201* (ENSMUST00000068664.6) transcript is recommended as the knockout region. The region contains 748bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Neo1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a gene trap allele display perinatal lethality and abnormal trigeminal nerve development.
- The *Neol* gene is located on the Chr9. 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)

Neo1 neogenin [Mus musculus (house mouse)]

Gene ID: 18007, updated on 2-Apr-2019

Summary



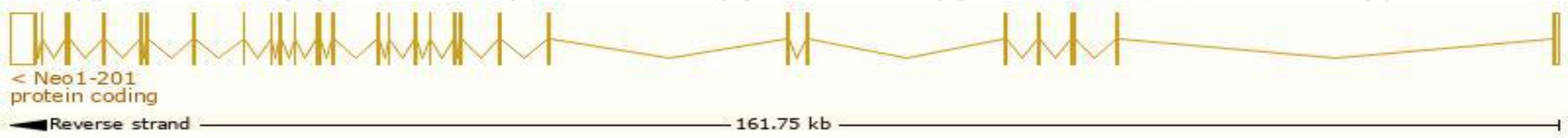
Official Symbol	Neo1 provided by MGI
Official Full Name	neogenin provided by MGI
Primary source	MGI:MGI:1097159
See related	Ensembl:ENSMUSG00000032340
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610028H22Rik, A1327052, D930014N22Rik, Igdcc2
Expression	Ubiquitous expression in CNS E18 (RPKM 24.1), limb E14.5 (RPKM 22.5) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

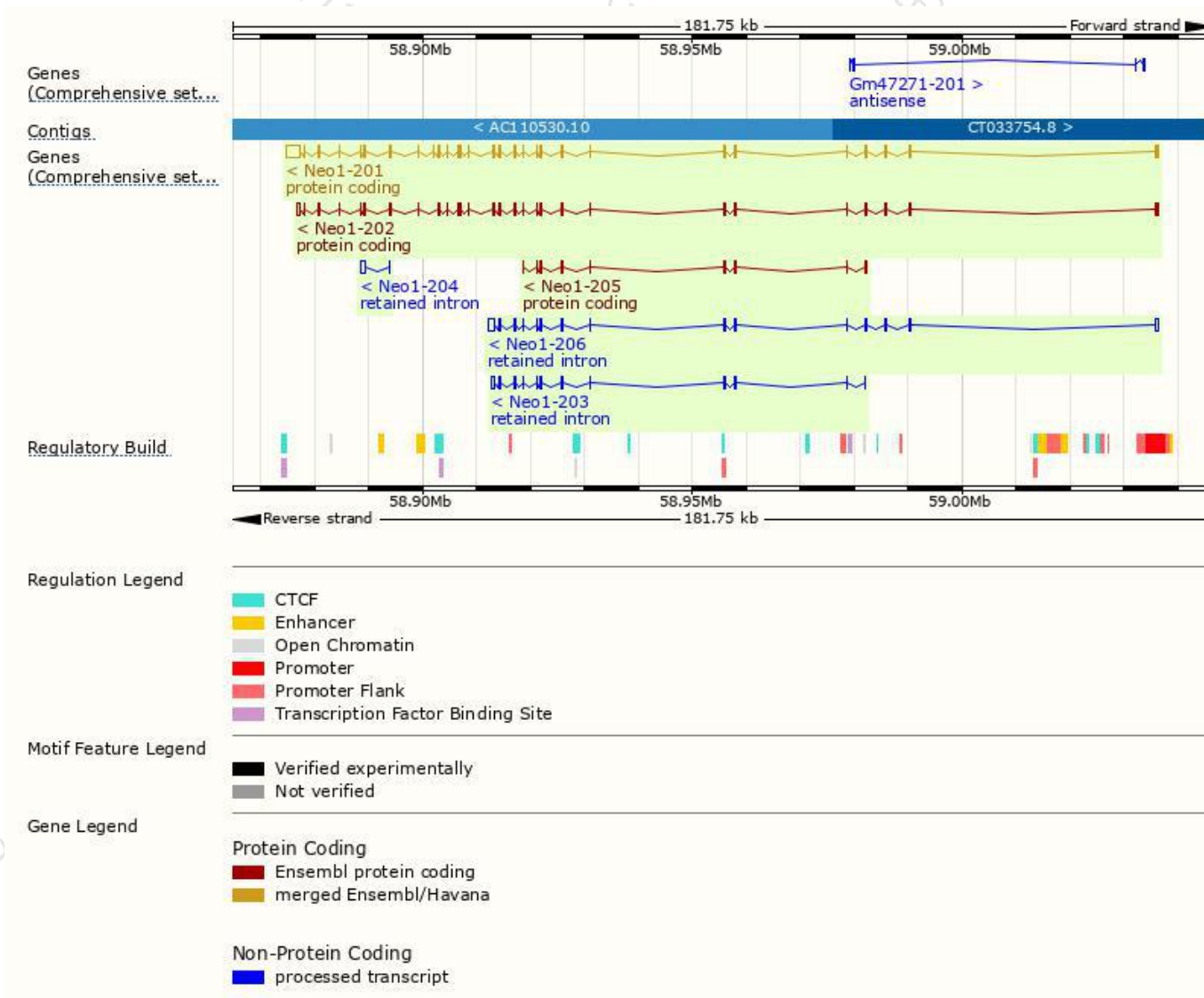
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Neo1-201	ENSMUST00000068664.6	7379	1492aa	Protein coding	CCDS23246	E9QK04	TSL:1 GENCODE basic APPRIS P2
Neo1-202	ENSMUST00000214547.1	5414	1465aa	Protein coding	-	Q7TQG5	TSL:1 GENCODE basic APPRIS ALT2
Neo1-205	ENSMUST00000216964.1	1215	405aa	Protein coding	-	A0A1L1SRD6	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
Neo1-206	ENSMUST00000217545.1	3639	No protein	Retained intron	-	-	TSL:1
Neo1-203	ENSMUST00000215026.1	1865	No protein	Retained intron	-	-	TSL:1
Neo1-204	ENSMUST00000215165.1	795	No protein	Retained intron	-	-	TSL:2

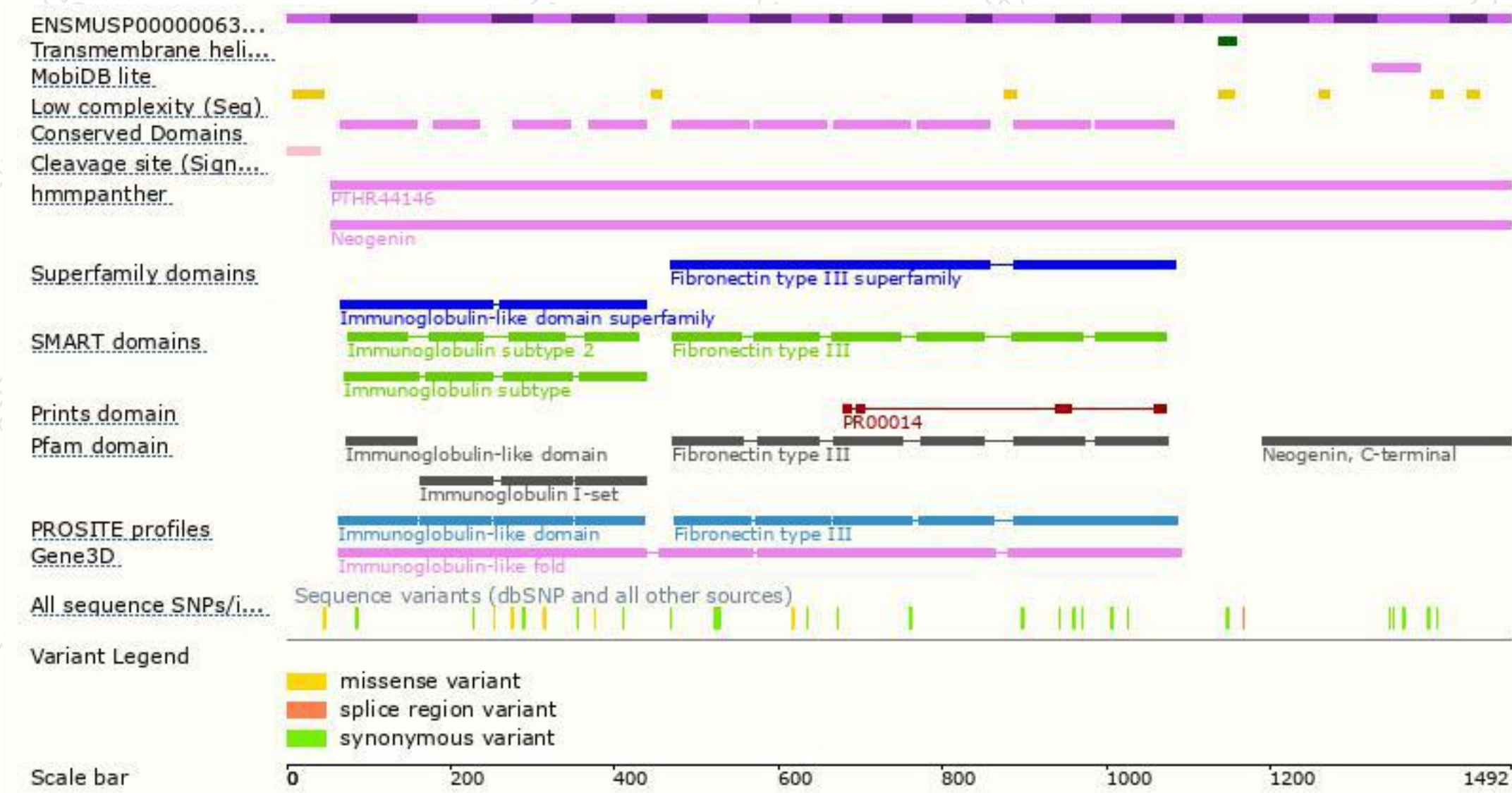
The strategy is based on the design of *Neo1-201* transcript,The transcription is shown below



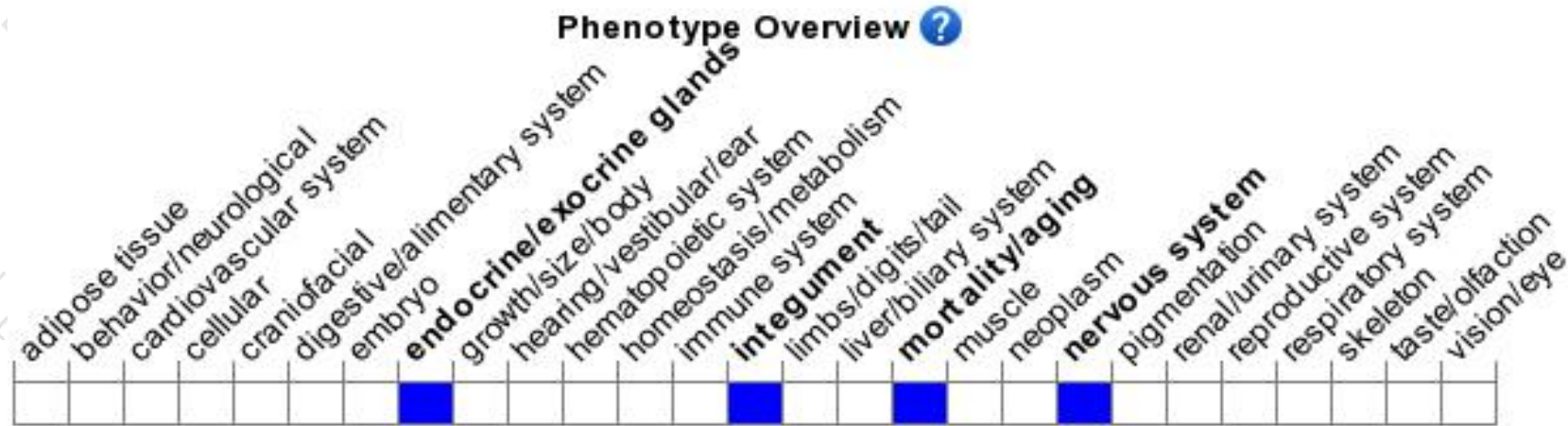
Genomic location distribution



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 gene trap allele display perinatal lethality and abnormal trigeminal nerve development.

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

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