Nln Cas9-KO Strategy

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Reviewer: Xiaojing Li

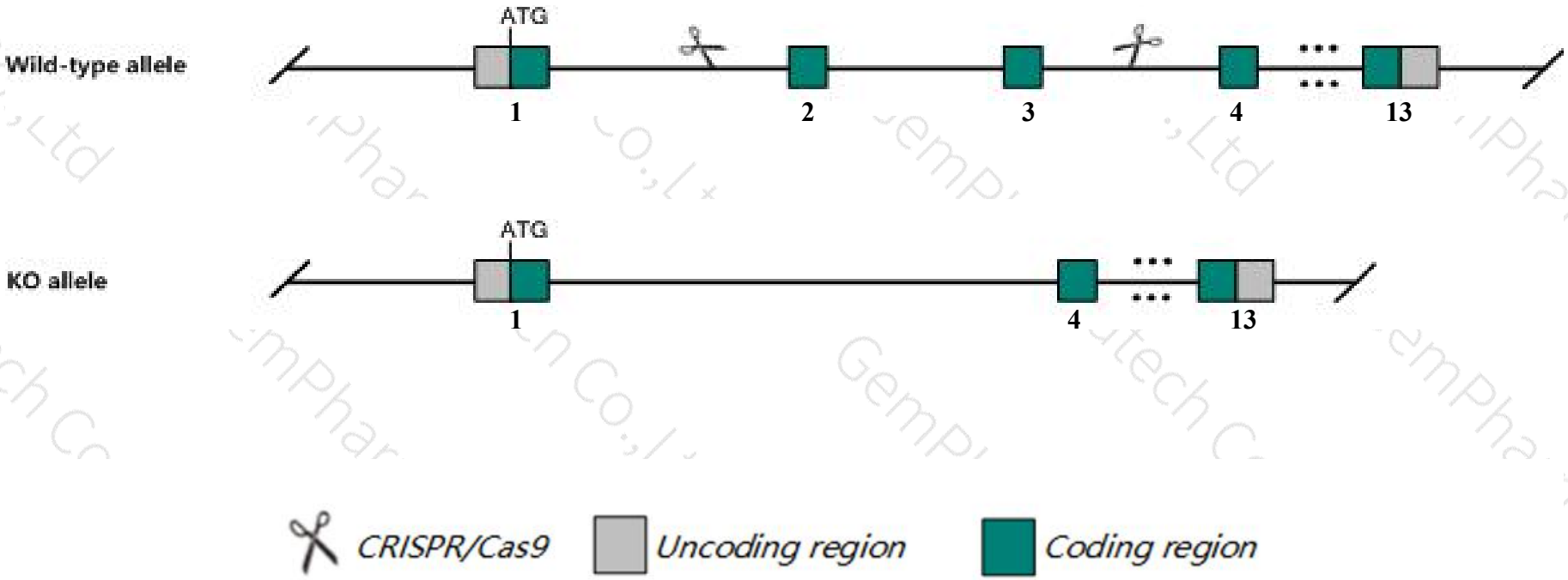
Design Date: 2020-2-19

Project Overview

Project Name	***Nln***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Nln* gene has 8 transcripts. According to the structure of *Nln* gene, exon2-exon3 of *Nln-201* (ENSMUST00000109315.4) transcript is recommended as the knockout region.The region contains 409bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nln* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Mice homozygous for a null allele exhibit increased glucose tolerance, insulin sensitivity, and gluconeogensis. Mice also show decreased body weight and run less in a low intensity regime to exhaustion.

- Transcript 206 CDS 5' and 3' incomplete the influences is unknown.

- The *Nln* gene is located on the Chr13. 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）

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Nln neurolysin (metallopeptidase M3 family) [Mus musculus (house mouse)]

Gene ID: 75805, updated on 31-Jan-2019

Summary

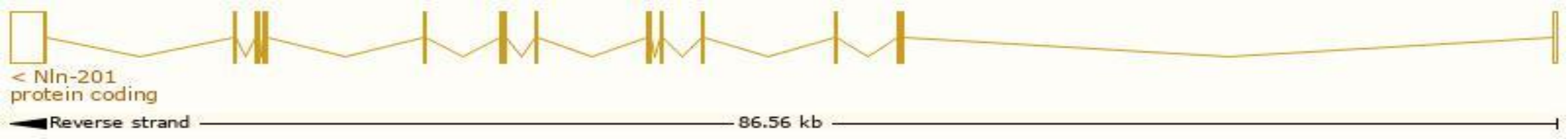
Official Symbol	Nln provided by MGI
Official Full Name	neurolysin (metallopeptidase M3 family) provided by MGI
Primary source	MGI:MGI:1923055
See related	Ensembl:ENSMUSG00000021710
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930472G13Rik, C79345
Expression	Ubiquitous expression in CNS E18 (RPKM 12.4), whole brain E14.5 (RPKM 7.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

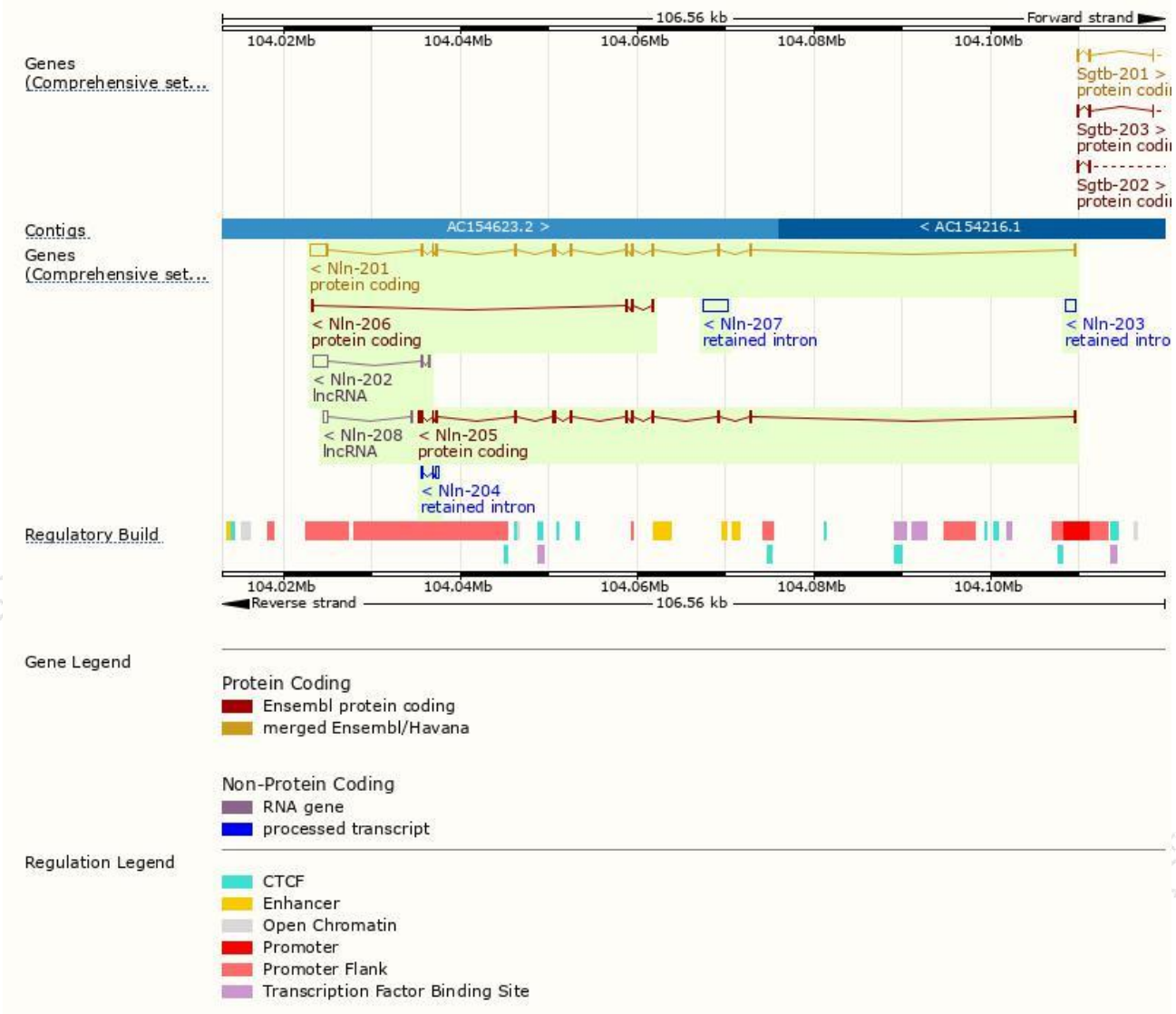
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nln-201	ENSMUST00000109315.4	4162	704aa	Protein coding	CCDS36772	Q91YP2	TSL:1 GENCODE basic APPRIS P1
Nln-205	ENSMUST00000224945.1	2486	683aa	Protein coding	-	A0A286YD12	GENCODE basic
Nln-206	ENSMUST00000225324.1	453	151aa	Protein coding	-	A0A286YD77	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Nln-207	ENSMUST00000225478.1	2720	No protein	Retained intron	-	-	
Nln-203	ENSMUST00000224086.1	1213	No protein	Retained intron	-	-	
Nln-204	ENSMUST00000224475.1	560	No protein	Retained intron	-	-	
Nln-202	ENSMUST00000224058.1	1924	No protein	lncRNA	-	-	
Nln-208	ENSMUST00000225704.1	564	No protein	lncRNA	-	-	

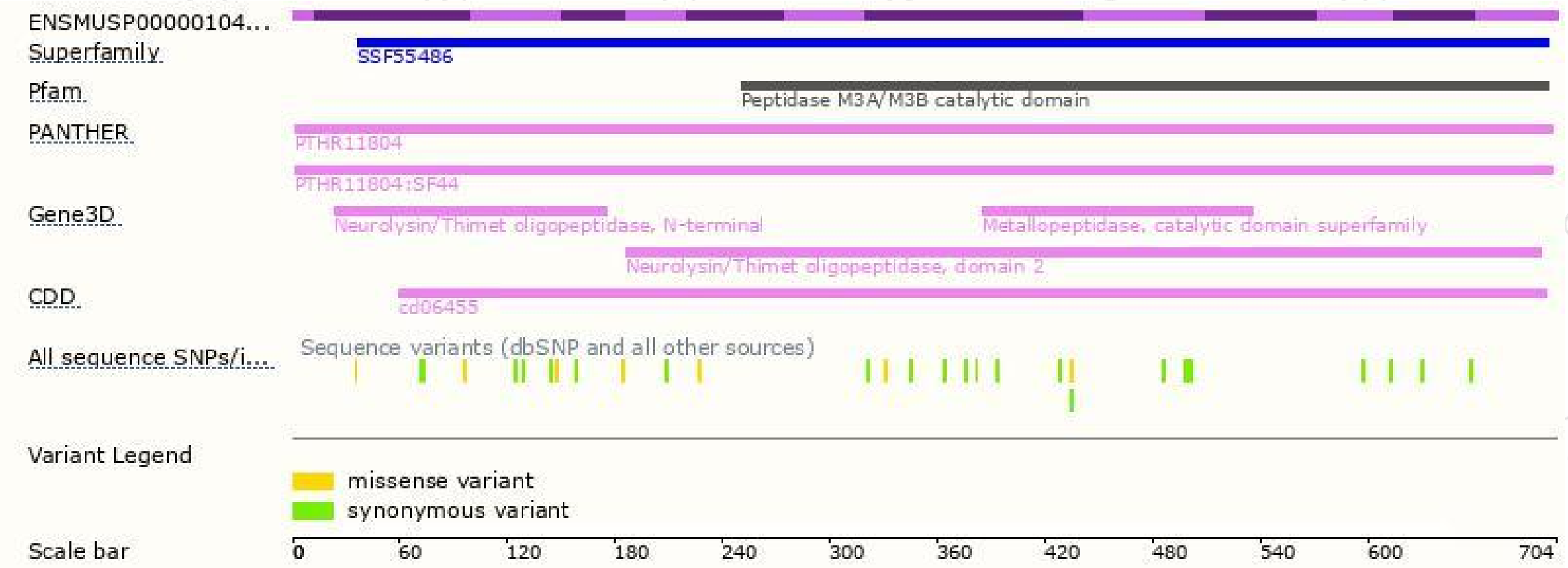
The strategy is based on the design of *Nln-201* transcript,The transcription is shown below



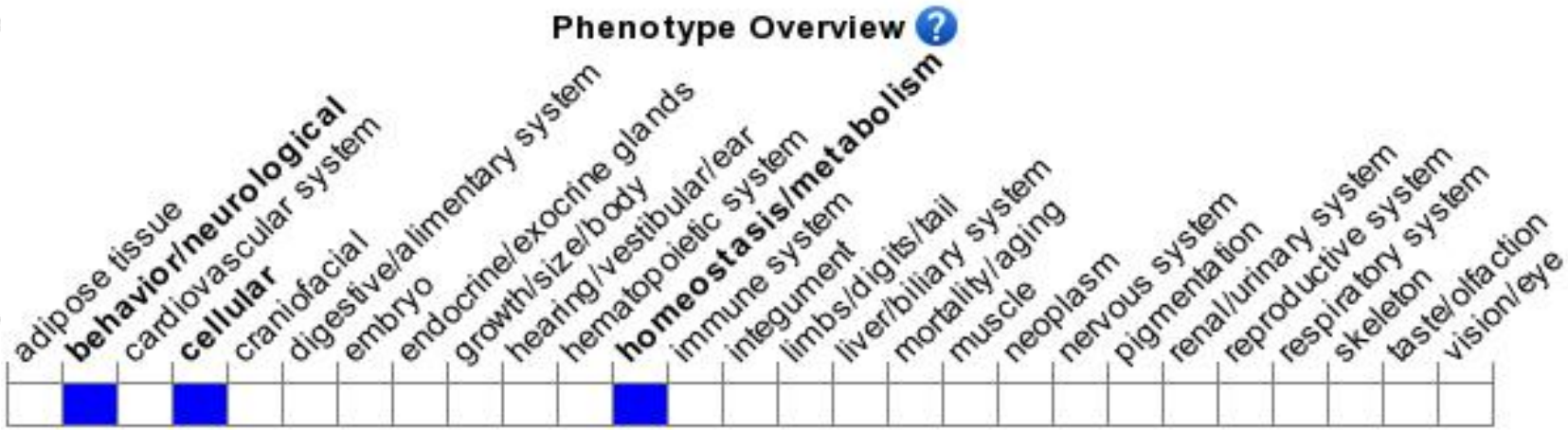
Genomic location distribution



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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