

Naa25 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Miaomiao Cui

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Project Overview

Project Name

Naa25

Project type

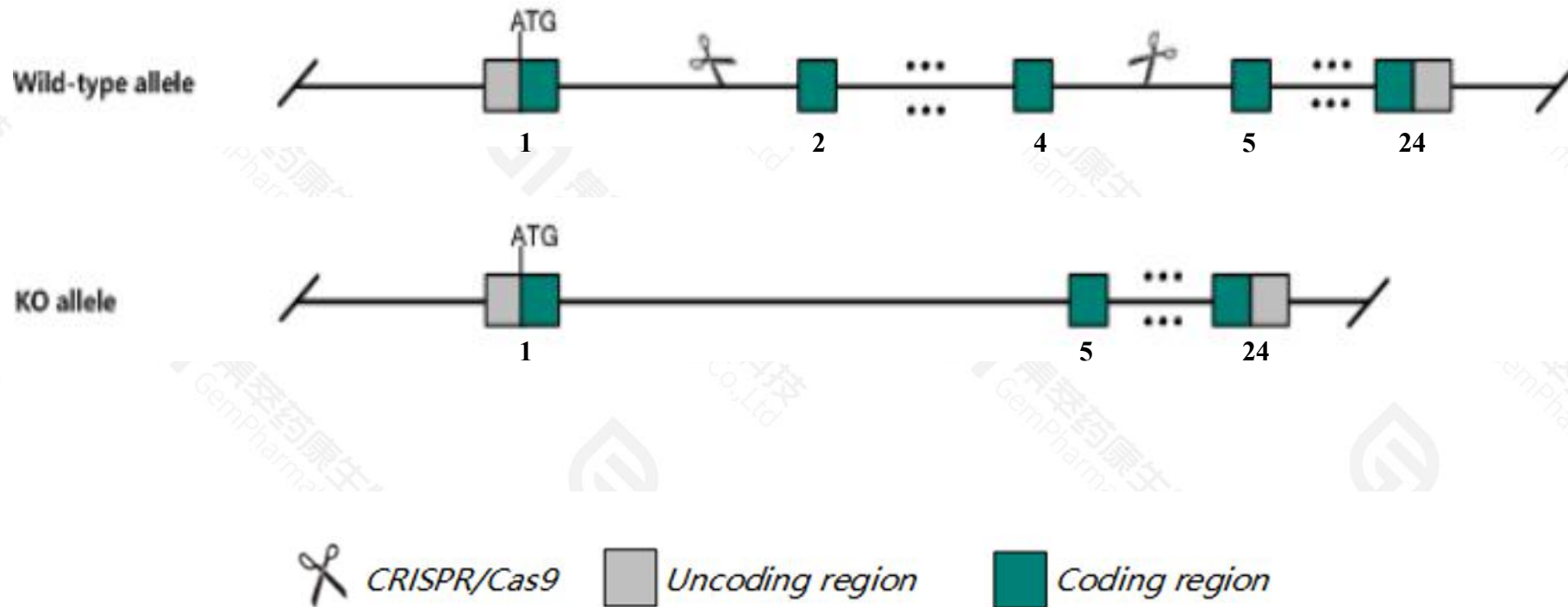
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Naa25* gene. The schematic diagram is as follows:



- The *Naa25* gene has 6 transcripts. According to the structure of *Naa25* gene, exon2-exon4 of *Naa25*-201(ENSMUST00000042163.15) transcript is recommended as the knockout region. The region contains 344bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Naa25* 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.

- Transcript *Naa25*-204 may not be affected.
- The *Naa25* gene is located on the Chr5. 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.

Naa25 N(alpha)-acetyltransferase 25, NatB auxiliary subunit [Mus musculus (house mouse)]

Gene ID: 231713, updated on 10-Oct-2020

Summary



Official Symbol Naa25 provided by [MGI](#)

Official Full Name N(alpha)-acetyltransferase 25, NatB auxiliary subunit provided by [MGI](#)

Primary source [MGI:MGI:2442563](#)

See related [Ensembl:ENSMUSG00000042719](#)

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 4833422K13Rik, A630046C11, A1450868, C330023M02Rik, Mdm20

Expression Ubiquitous expression in CNS E18 (RPKM 10.4), whole brain E14.5 (RPKM 8.5) and 28 other tissues [See more](#)

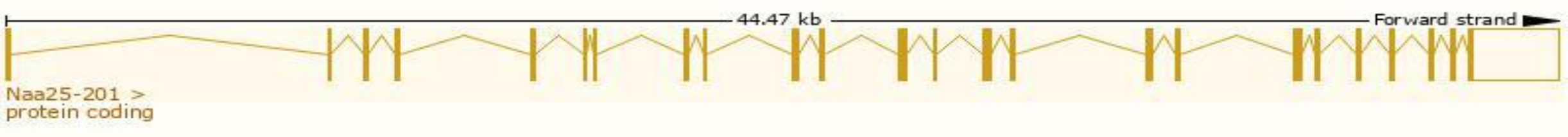
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

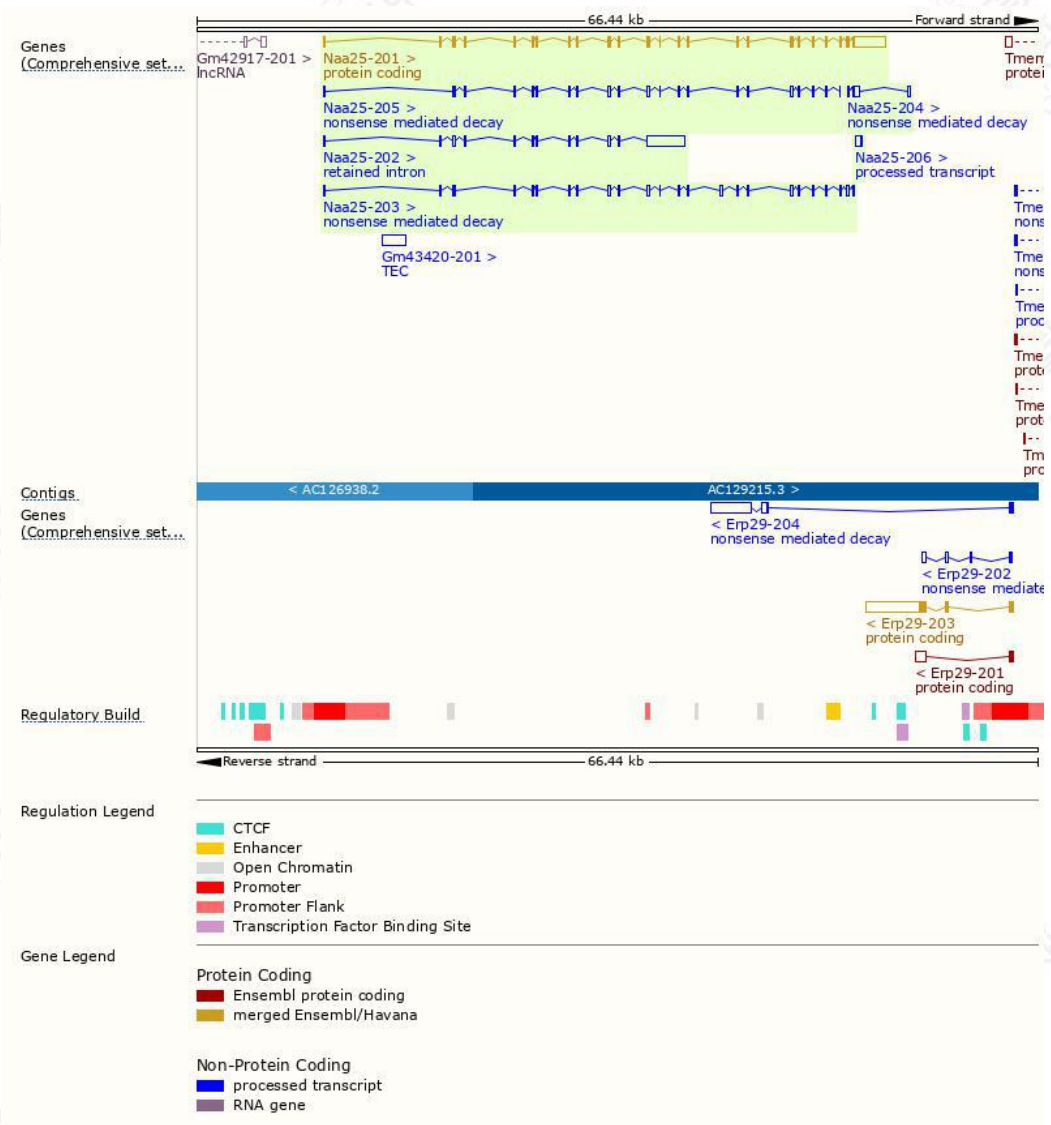
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Naa25-201	ENSMUST00000042163.15	5447	972aa	Protein coding	CCDS19633		TSL:1 , GENCODE basic , APPRIS P1 ,
Naa25-203	ENSMUST00000151458.4	2910	100aa	Nonsense mediated decay	-		TSL:5 ,
Naa25-205	ENSMUST00000173895.8	2556	45aa	Nonsense mediated decay	-		TSL:1 ,
Naa25-204	ENSMUST00000172908.2	757	62aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:2 ,
Naa25-206	ENSMUST00000174322.2	452	No protein	Processed transcript	-		TSL:3 ,
Naa25-202	ENSMUST00000131598.8	4143	No protein	Retained intron	-		TSL:1 ,

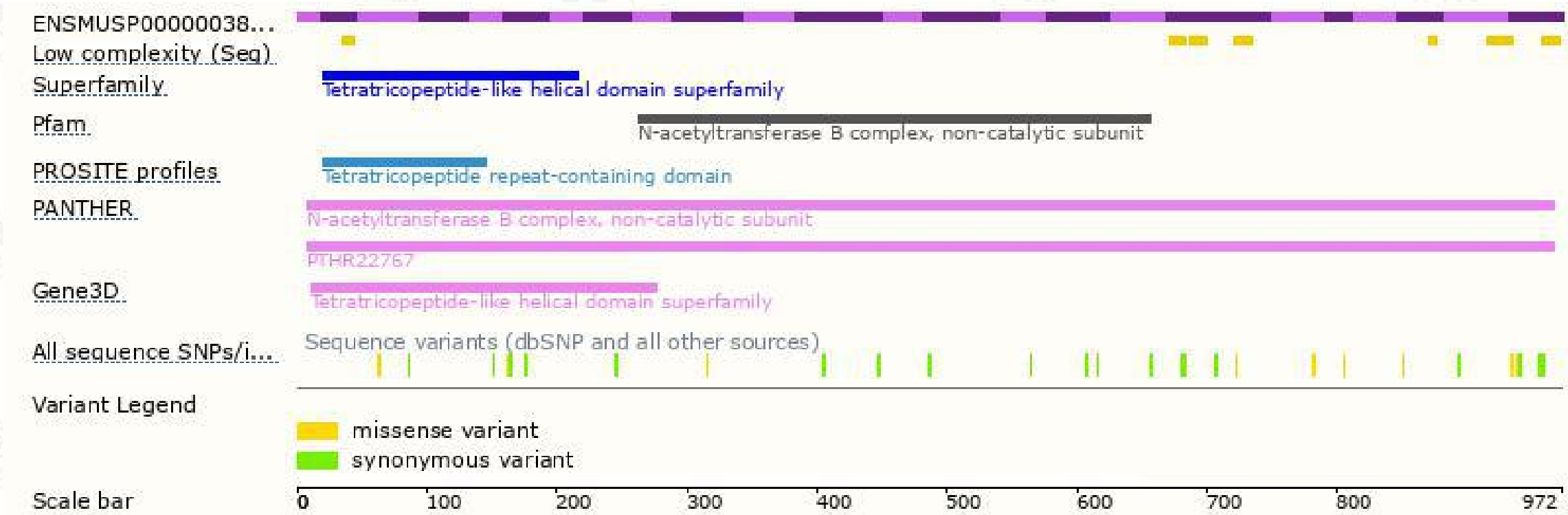
The strategy is based on the design of *Naa25-201* transcript,the transcription is shown below:



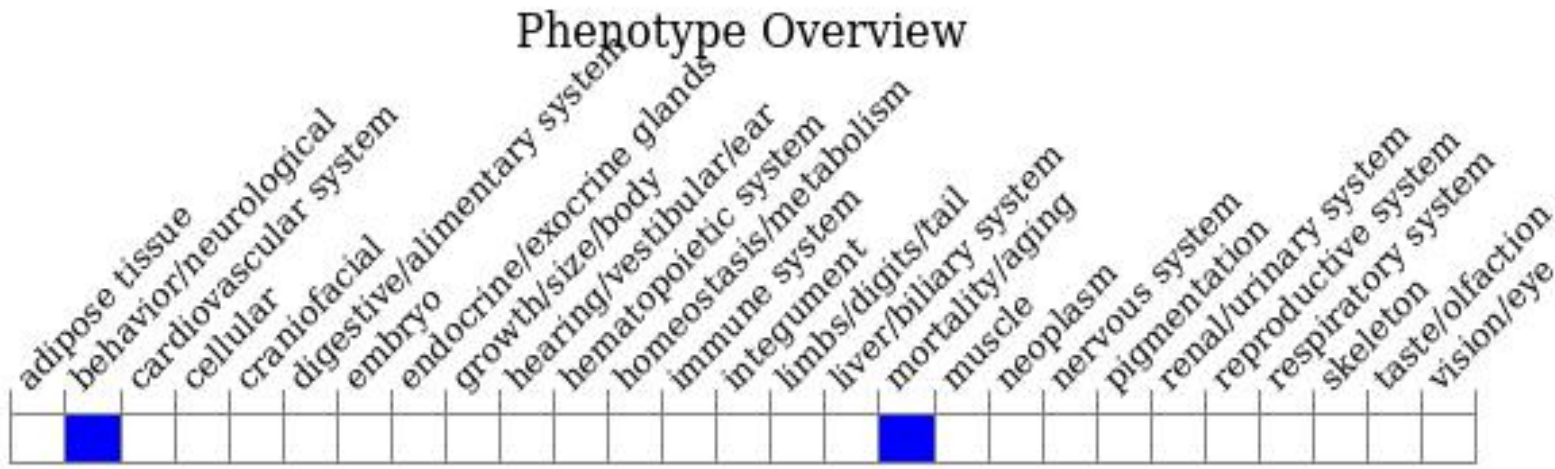
Genomic location distribution



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/>).

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

