

Naa50 Cas9-KO Strategy

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Project Overview



Project Name

Naa50

Project type

Cas9-KO

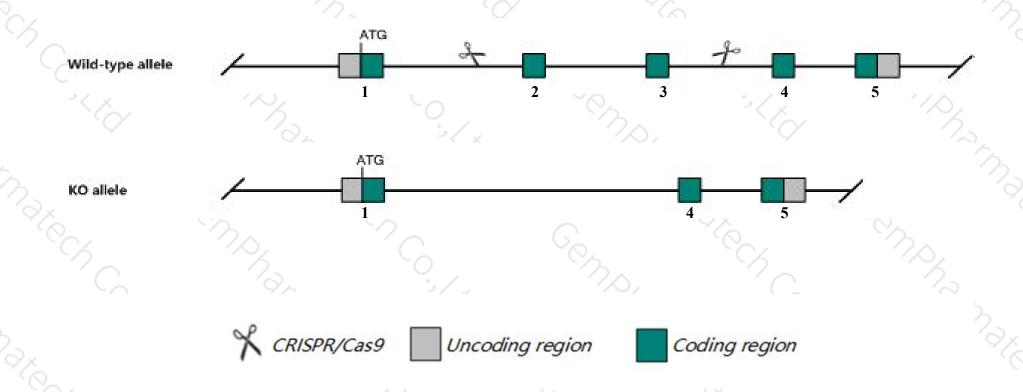
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Naa50* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Naa50* gene has 4 transcripts. According to the structure of *Naa50* gene, exon2-exon3 of *Naa50-204*(ENSMUST00000161326.7) transcript is recommended as the knockout region. The region contains 257bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Naa50* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > The *Naa50* gene is located on the Chr16. 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)



Naa50 N(alpha)-acetyltransferase 50, NatE catalytic subunit [Mus musculus (house mouse)]

Gene ID: 72117, updated on 15-Aug-2019

Summary

☆ ?

Official Symbol Naa50 provided by MGI

Official Full Name N(alpha)-acetyltransferase 50, NatE catalytic subunit provided by MGI

Primary source MGI:MGI:1919367

See related Ensembl: ENSMUSG00000022698

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 San; Mak3; Nat5; Mak3p; Nat13; AW112078; 2600005K24Rik; 2810441M03Rik

Expression Ubiquitous expression in CNS E11.5 (RPKM 17.1), liver E14 (RPKM 15.4) and 28 other tissues See more

Orthologs human all

Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

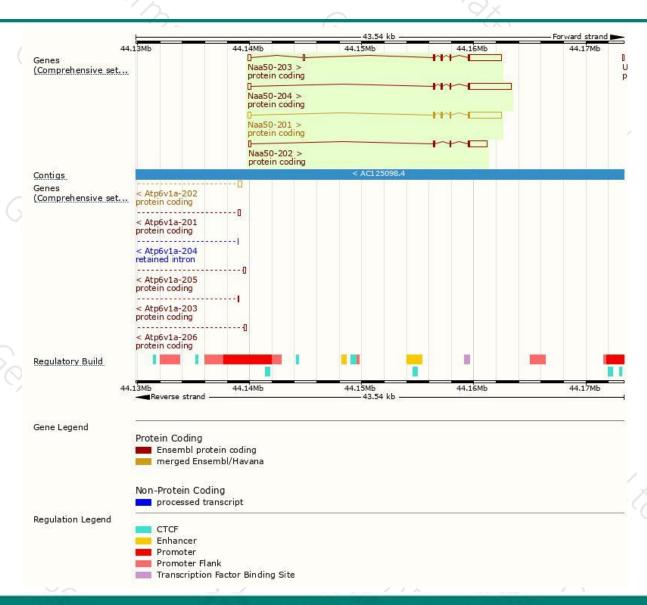
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Naa50-204	ENSMUST00000161326.7	4487	<u>169aa</u>	Protein coding	CCDS84236	Q6PGB6	TSL:1 GENCODE basic APPRIS ALT1
Naa50-201	ENSMUST00000063520.14	3557	<u>168aa</u>	Protein coding	CCDS28183	Q6PGB6	TSL:1 GENCODE basic APPRIS P3
Naa50-203	ENSMUST00000159514.7	3756	<u>175aa</u>	Protein coding	-	Q6PGB6	TSL:1 GENCODE basic
Naa50-202	ENSMUST00000063542.7	2136	129aa	Protein coding	2	Q6PGB6	TSL:1 GENCODE basic

The strategy is based on the design of Naa50-204 transcript, The transcription is shown below

Naa50-204 > protein coding

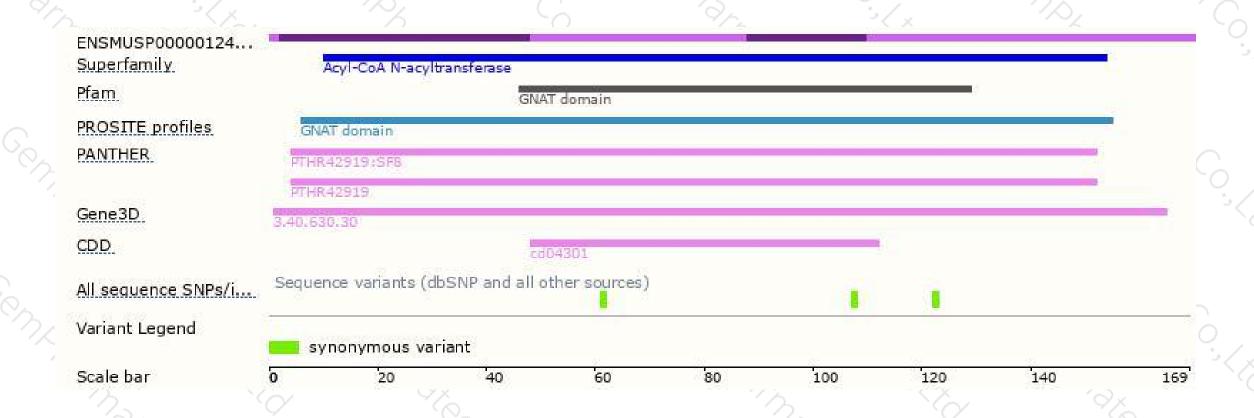
Genomic location distribution





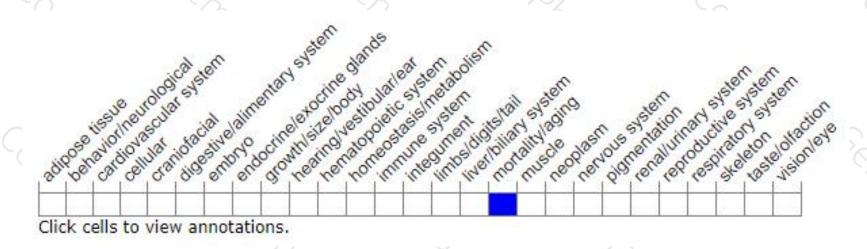
Protein domain





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





