

Naa10 Cas9-CKO Strategy

Designer: Ruirui Zhang

Reviewer: Daohua Xu

Design Date: 2021-5-8

Project Overview

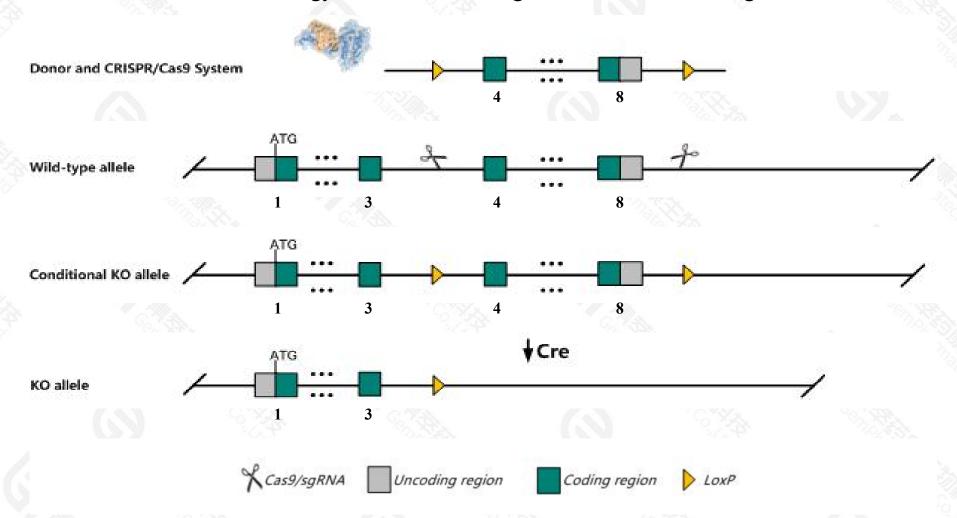


Project Name	Naa10			
Project type	Cas9-CKO			
Strain background	C57BL/6JGpt			

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Naa10* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Naa10* gene has 12 transcripts. According to the structure of *Naa10* gene, exon4-exon8 of *Naa10*-201(ENSMUST00000033763.15) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Naa10* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor was constructed.Cas9, sgRNA and Donor 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.
- > The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice



- According to the existing MGI data, male homozygous mice with Naa10 gene knocked out showed abnormal seminal vesicle morphology, enlarged seminal vesicle, small seminal vesicle, abnormal testis morphology.
- The KO region contains functional region of the *Arhgap4-209* gene. Knockout the region may affect the function of *Arhgap4* gene.
- ➤ The *Naa10* gene is located on the ChrX. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Naa10 N(alpha)-acetyltransferase 10, NatA catalytic subunit [Mus musculus (house mouse)]

♣ Download Datasets

Gene ID: 56292, updated on 6-May-2021



☆ ?

Official Symbol Naa10 provided by MGI

Official Full Name N(alpha)-acetyltransferase 10, NatA catalytic subunit provided by MGI

Primary source MGI:MGI:1915255

See related Ensembl: ENSMUSG00000031388

Gene type protein coding
RefSeq status VALIDATED
Organism Mus musculus

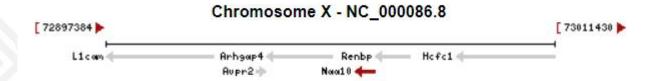
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;

Murinae; Mus; Mus

Also known as Ar; Te2; Ard1; Ard1a; 2310039H09Rik

Expression Ubiquitous expression in liver E14.5 (RPKM 30.5), large intestine adult (RPKM 29.1) and 27 other tissues See more

Orthologs human all



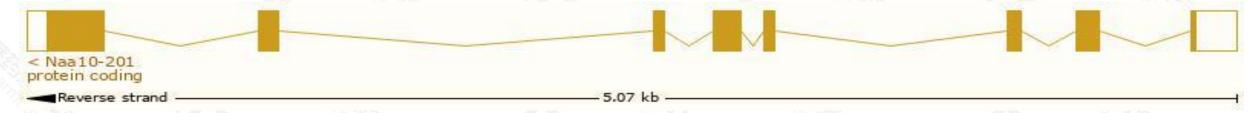
Transcript information (Ensembl)



The gene has 12 transcripts, all transcripts are shown below:

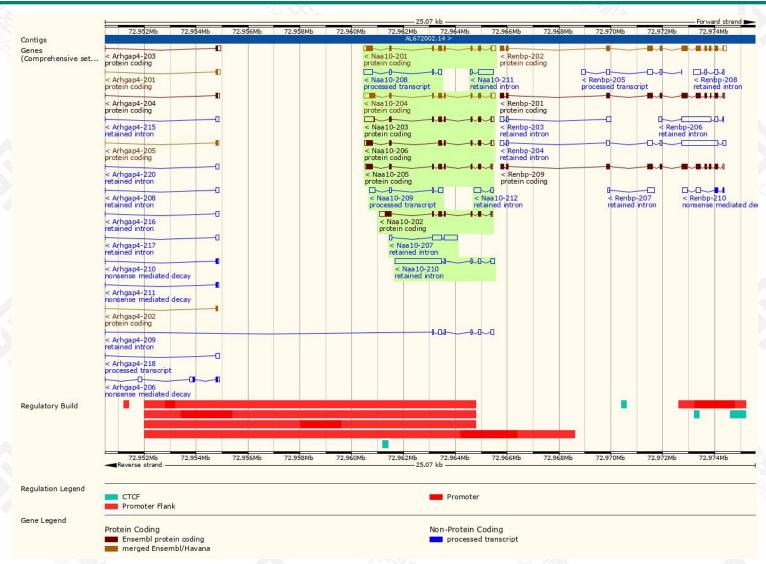
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Naa10-204	ENSMUST00000114389.10	1031	225aa	Protein coding	CCDS53102		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Naa10-203	ENSMUST00000114387.8	979	<u>170aa</u>	Protein coding	CCDS81139		TSL:2 , GENCODE basic , APPRIS ALT2
Naa10-201	ENSMUST00000033763.15	962	235aa	Protein coding	CCDS30217		TSL:1 , GENCODE basic , APPRIS P3 ,
Naa10-202	ENSMUST00000096316.4	892	206aa	Protein coding	650		TSL:2 , GENCODE basic , APPRIS ALT2
Naa10-206	ENSMUST00000114391.10	834	220aa	Protein coding	(54)		TSL:5 , GENCODE basic ,
Naa10-205	ENSMUST00000114390.8	797	233aa	Protein coding	450		TSL:5 , GENCODE basic ,
Naa10-208	ENSMUST00000139105.8	551	No protein	Processed transcript	1.0		TSL:5 ,
Naa10-209	ENSMUST00000141211.2	479	No protein	Processed transcript	-		TSL:2,
Naa10-210	ENSMUST00000143076.2	2156	No protein	Retained intron	575		TSL:1,
Naa10-207	ENSMUST00000124446.2	963	No protein	Retained intron	-		TSL:5 ,
Naa10-211	ENSMUST00000149591.2	649	No protein	Retained intron	121		TSL:2,
Naa10-212	ENSMUST00000153929.2	355	No protein	Retained intron			TSL:2,

The strategy is based on the design of *Naa10-201* transcript, the transcription is shown below:



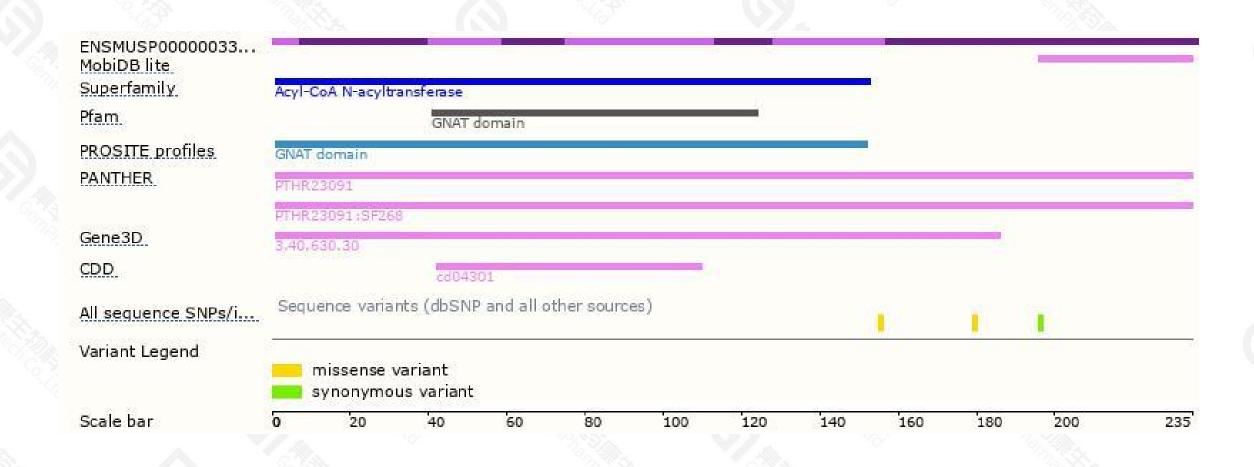
Genomic location distribution





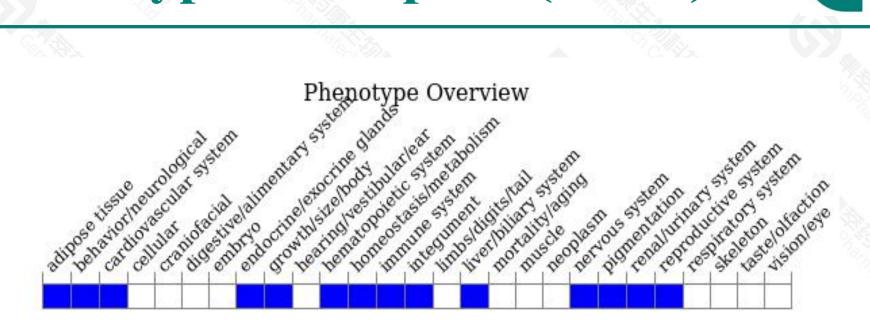
Protein domain



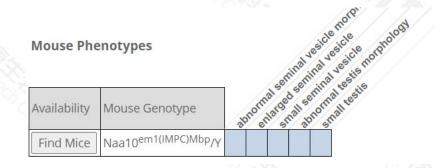


Mouse phenotype description(MGI)





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: 025-5864 1534





