

Naa35 Cas9-CKO Strategy

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Project Overview

Project Name

Naa35

Project type

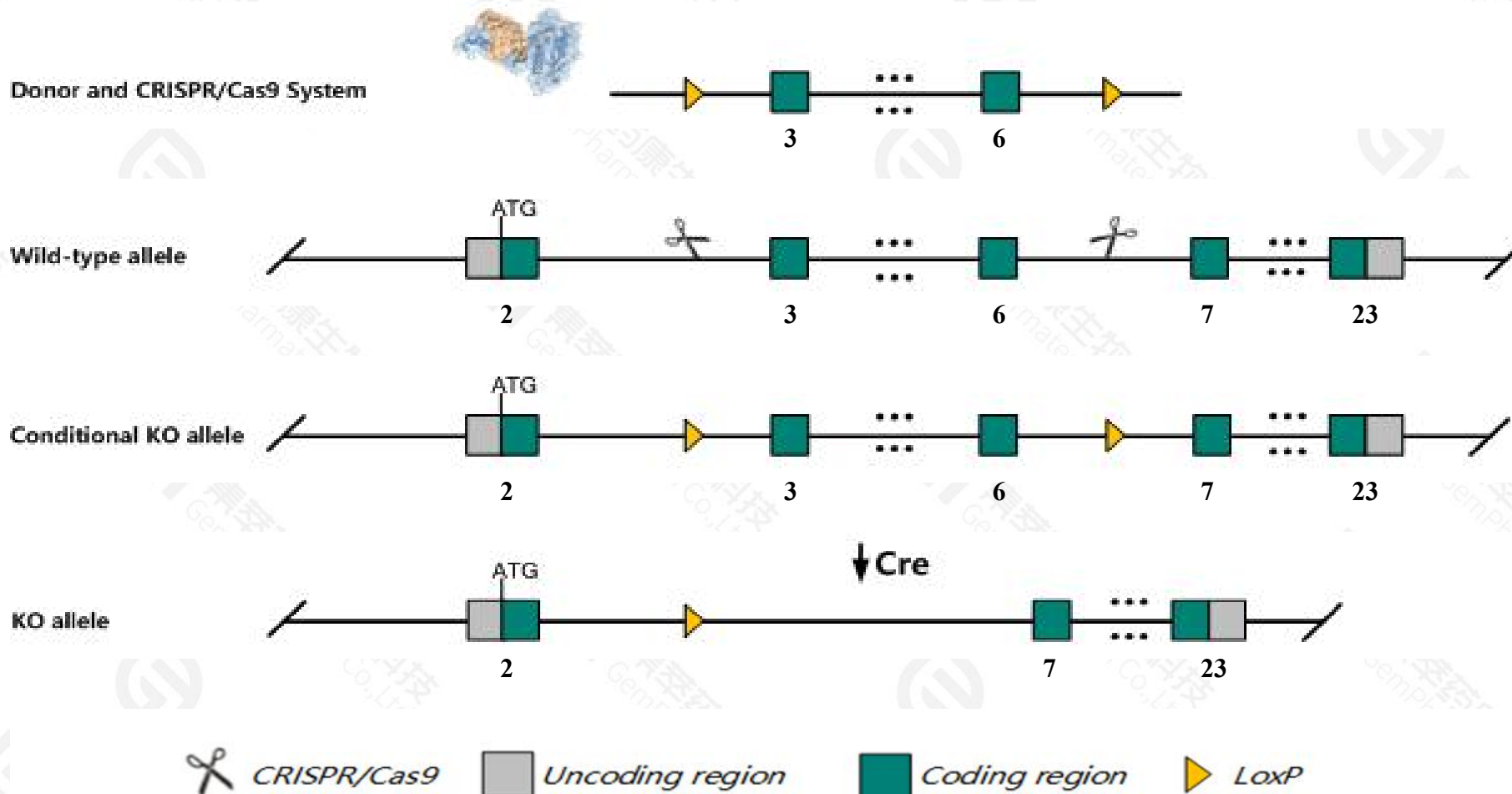
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Naa35* gene. The schematic diagram is as follows:



- The *Naa35* gene has 17 transcripts. According to the structure of *Naa35* gene, exon3-exon6 of *Naa35-201*(ENSMUST00000022038.15) transcript is recommended as the knockout region. The region contains 392bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Naa35* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be 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.

- Transcript *Naa35*-206&214 may not be affected.
- The *Naa35* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Naa35 N(alpha)-acetyltransferase 35, NatC auxiliary subunit [Mus musculus (house mouse)]

Gene ID: 78689, updated on 3-Jan-2021

Summary



Official Symbol Naa35 provided by [MGI](#)

Official Full Name N(alpha)-acetyltransferase 35, NatC auxiliary subunit provided by [MGI](#)

Primary source [MGI:MGI:1925939](#)

See related [Ensembl:ENSMUSG00000021555](#)

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 A330021G12Rik, A330027C19Rik, AI158944, C030004C14Rik, Mak1, Mak10

Expression Ubiquitous expression in CNS E14 (RPKM 22.3), CNS E11.5 (RPKM 21.9) and 28 other tissues [See more](#)

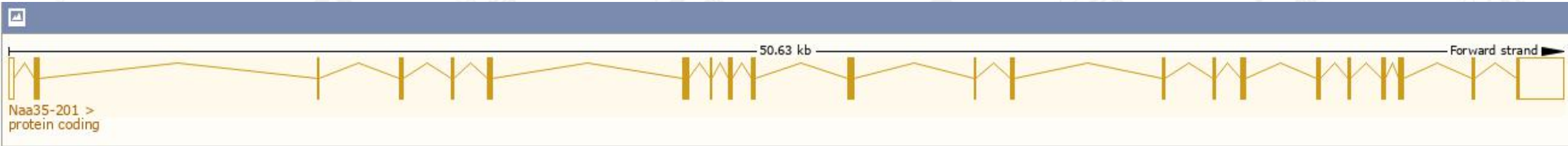
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

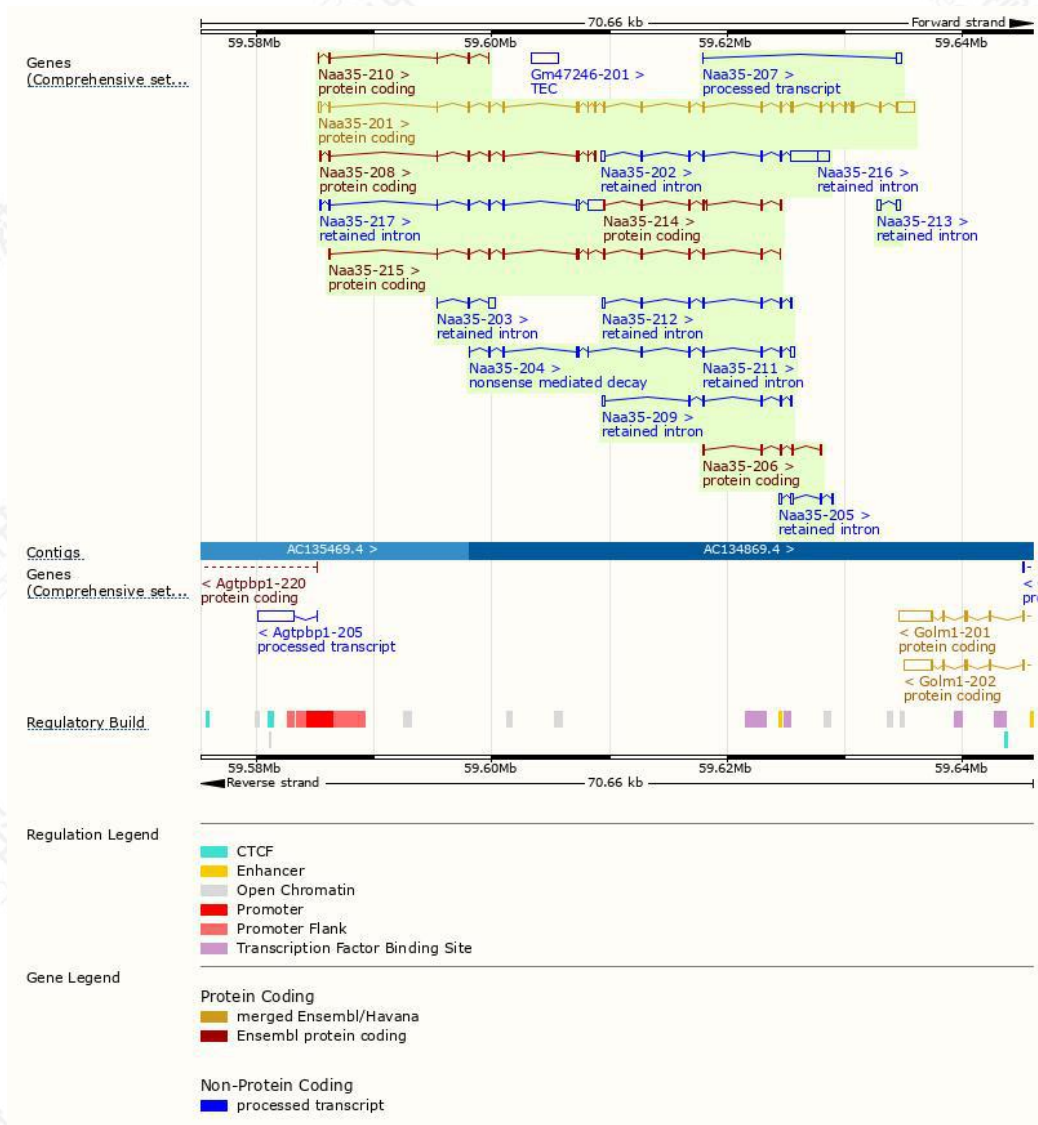
The gene has 17 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Naa35-201	ENSMUST00000022038.15	3793	725aa	Protein coding	CCDS26575		TSL:1 , GENCODE basic , APPRIS P1 ,
Naa35-215	ENSMUST00000172419.8	1207	402aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:5 ,
Naa35-208	ENSMUST00000166923.9	779	236aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Naa35-214	ENSMUST00000172166.8	638	213aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:3 ,
Naa35-206	ENSMUST00000165253.2	443	147aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:3 ,
Naa35-210	ENSMUST00000168367.8	374	111aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Naa35-204	ENSMUST00000164011.8	708	152aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Naa35-207	ENSMUST00000165841.2	371	No protein	Processed transcript	-		TSL:3 ,
Naa35-202	ENSMUST00000163395.8	3082	No protein	Retained intron	-		TSL:1 ,
Naa35-217	ENSMUST00000225670.2	2051	No protein	Retained intron	-		
Naa35-216	ENSMUST00000224194.2	1042	No protein	Retained intron	-		
Naa35-212	ENSMUST00000171391.8	754	No protein	Retained intron	-		TSL:3 ,
Naa35-203	ENSMUST00000163521.2	674	No protein	Retained intron	-		TSL:5 ,
Naa35-209	ENSMUST00000168242.8	566	No protein	Retained intron	-		TSL:3 ,
Naa35-213	ENSMUST00000172118.2	526	No protein	Retained intron	-		TSL:2 ,
Naa35-205	ENSMUST00000165129.2	506	No protein	Retained intron	-		TSL:3 ,
Naa35-211	ENSMUST00000168633.2	478	No protein	Retained intron	-		TSL:2 ,

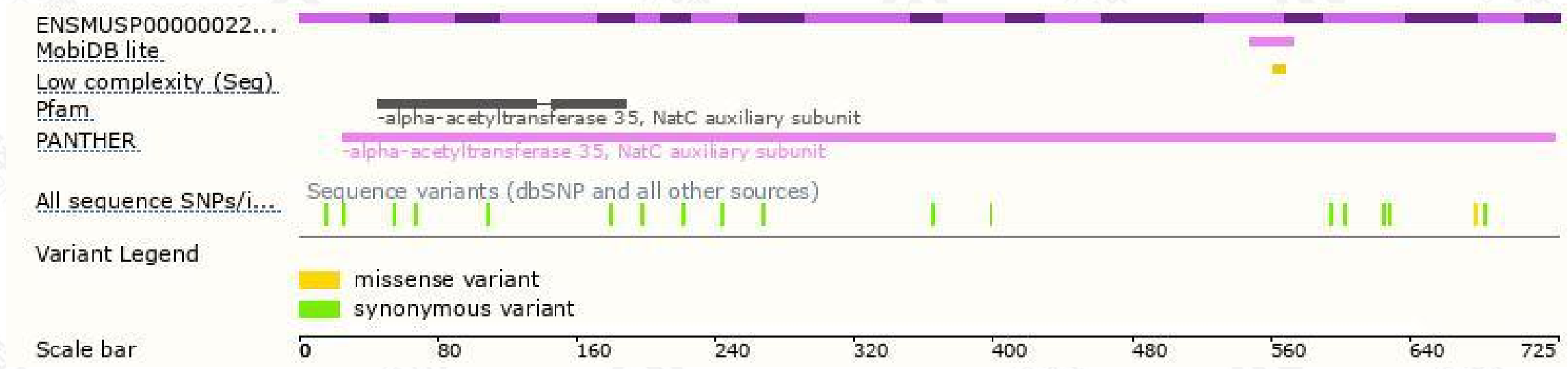
The strategy is based on the design of *Naa35-201* transcript,the transcription is shown below:



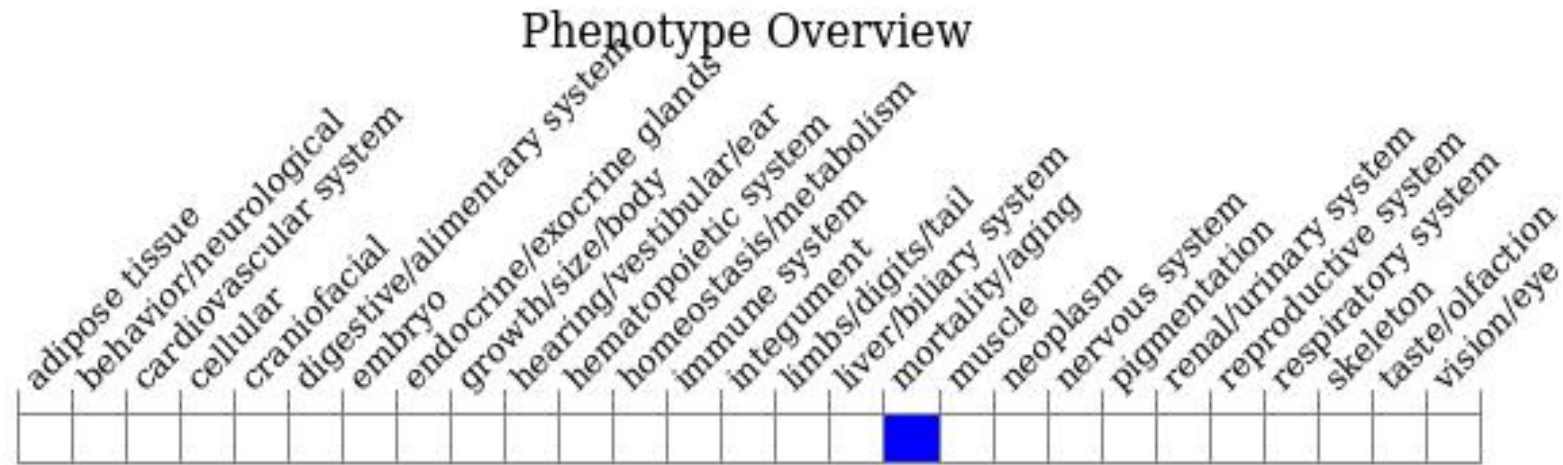
Genomic location distribution



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.
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