

Naa40 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Naa40

Project type

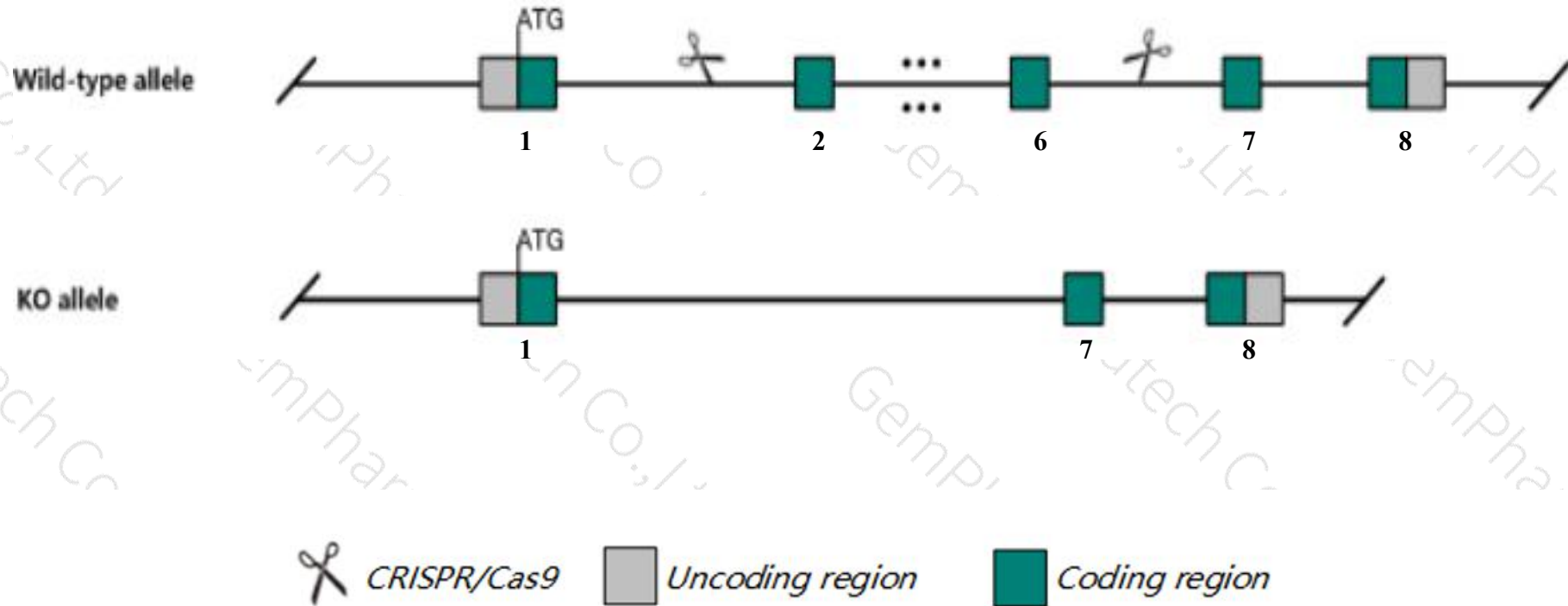
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Naa40* gene. The schematic diagram is as follows:



- The *Naa40* gene has 5 transcripts. According to the structure of *Naa40* gene, exon2-exon6 of *Naa40-201* (ENSMUST00000025675.10) transcript is recommended as the knockout region. The region contains 488bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Naa40* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a conditional allele activated in hepatocytes exhibit protection from age-induced but not high fat diet-induced steatosis with altered lipid homeostasis.
- Transcript *Naa40-202* may not be affected.
- The *Naa40* gene is located on the Chr19. 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)

Naa40 N(alpha)-acetyltransferase 40, NatD catalytic subunit [*Mus musculus* (house mouse)]

Gene ID: 70999, updated on 12-Aug-2019

Summary

- Official Symbol** Naa40 provided by [MGI](#)
- Official Full Name** N(alpha)-acetyltransferase 40, NatD catalytic subunit provided by [MGI](#)
- Primary source** [MGI:MGI:1918249](#)
- See related** [Ensembl:ENSMUSG00000024764](#)
- 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** NatD; Nat11; AU023197; 4931433E08Rik
- Expression** Ubiquitous expression in testis adult (RPKM 26.2), whole brain E14.5 (RPKM 19.6) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 19; 19 A See Naa40 in [Genome Data Viewer](#)

Exon count: 8

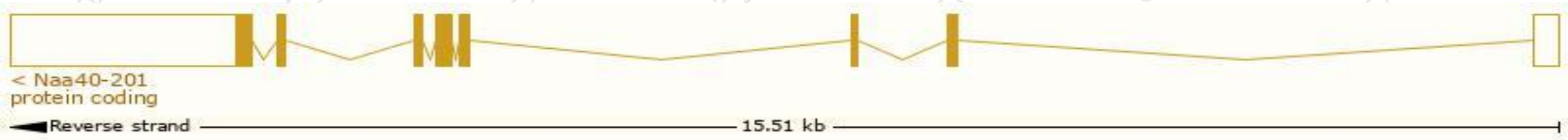
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (7225668..7241222, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (7300158..7315712, complement)

Transcript information (Ensembl)

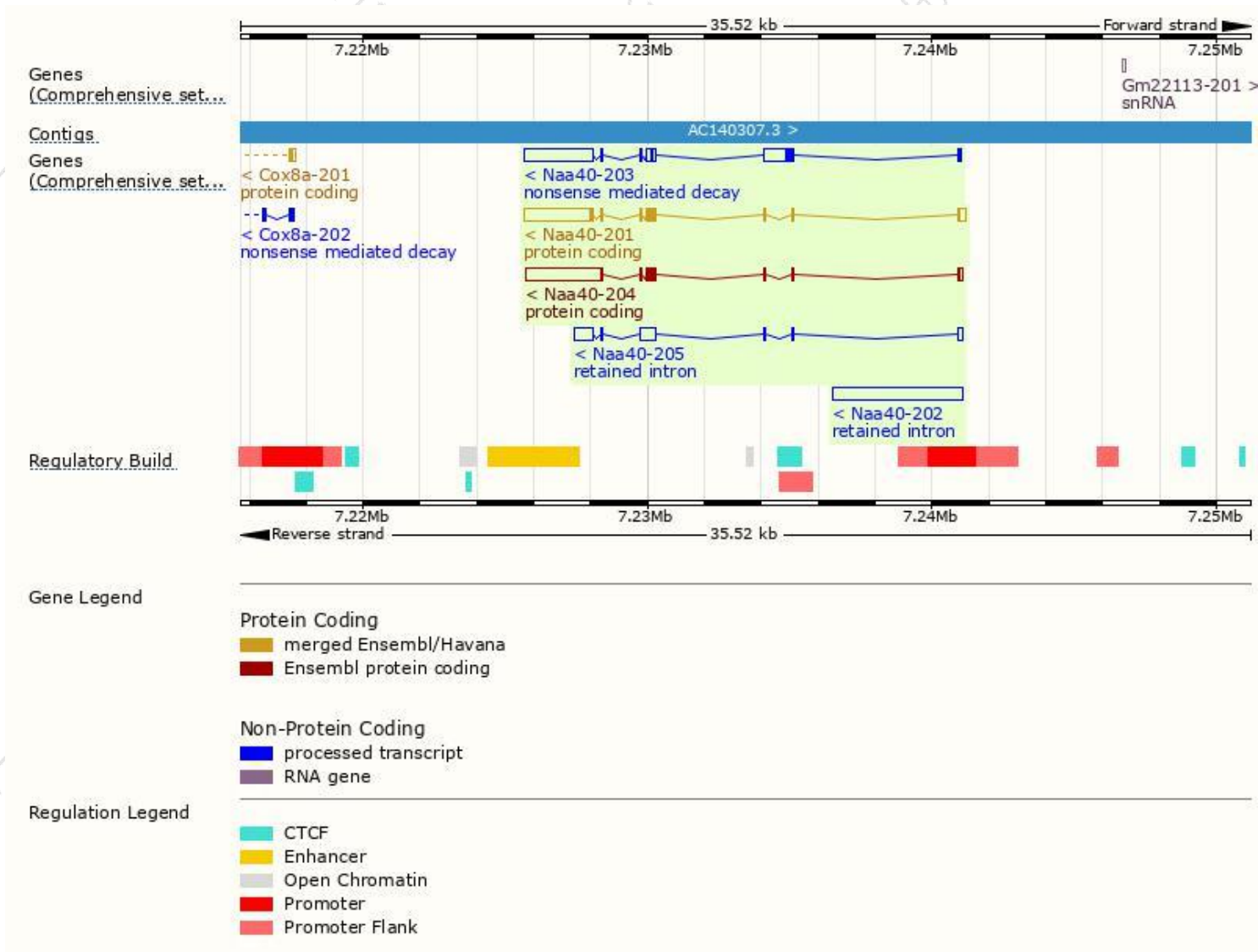
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Naa40-201	ENSMUST00000025675.10	3231	237aa	Protein coding	CCDS50377	Q8VE10	TSL:1 GENCODE basic APPRIS P1
Naa40-204	ENSMUST000000236769.1	3324	191aa	Protein coding	-	-	GENCODE basic
Naa40-203	ENSMUST000000236628.1	3993	102aa	Nonsense mediated decay	-	-	
Naa40-202	ENSMUST000000235323.1	4520	No protein	Retained intron	-	-	
Naa40-205	ENSMUST000000237834.1	1569	No protein	Retained intron	-	-	

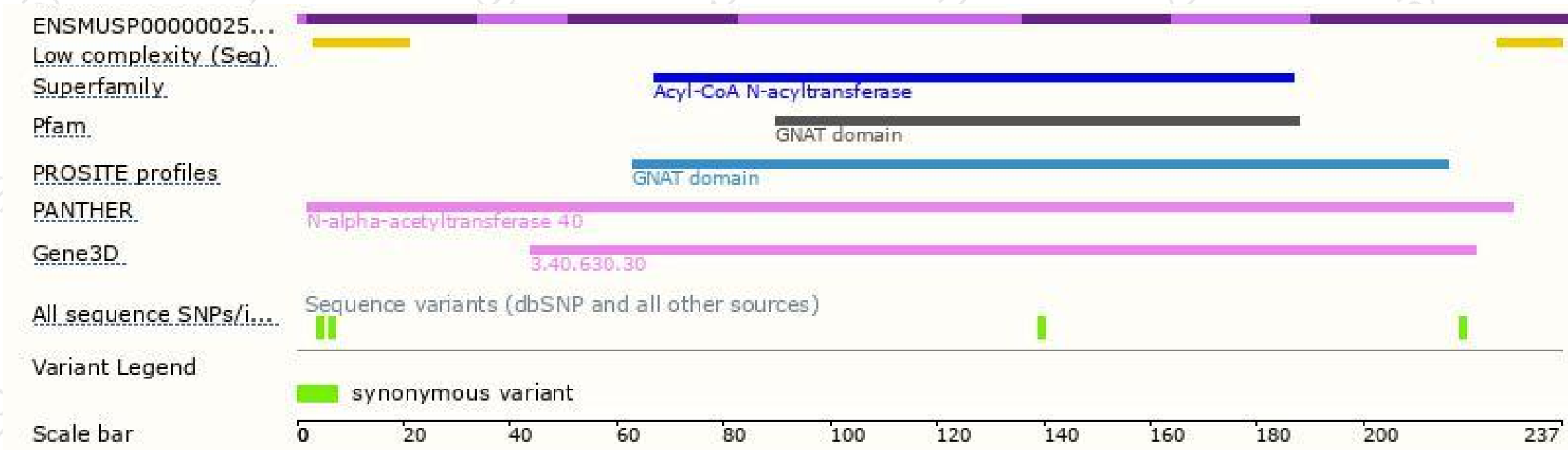
The strategy is based on the design of *Naa40-201* transcript,The transcription is shown below



Genomic location distribution

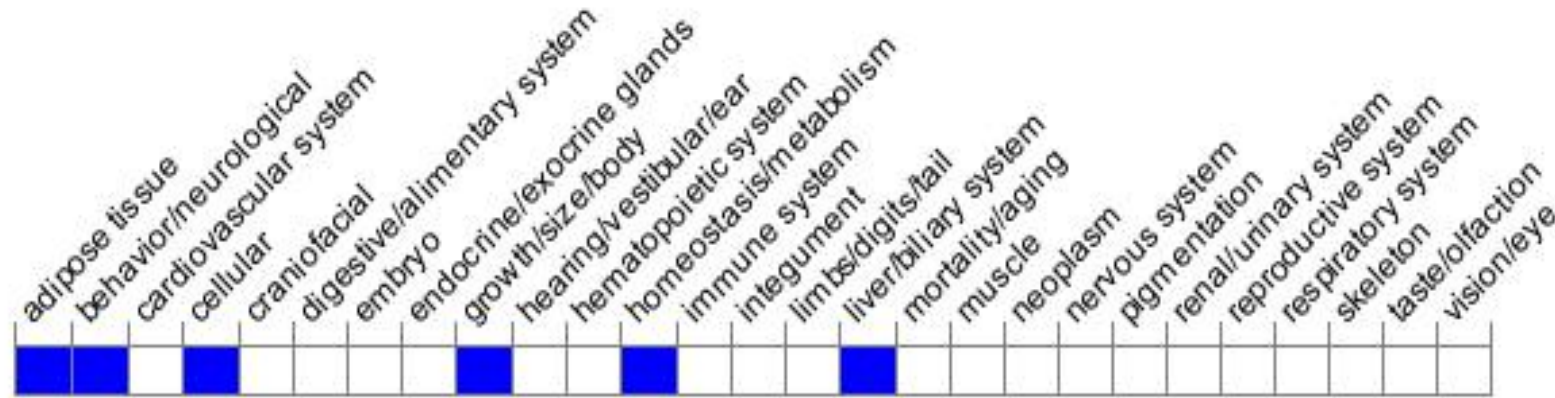


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice homozygous for a conditional allele activated in hepatocytes exhibit protection from age-induced but not high fat diet-induced steatosis with altered lipid homeostasis.

If you have any questions, you are welcome to inquire.

Tel: 400-9660890

