

Nbeal1 Cas9-KO Strategy

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Overview

Target Gene Name

- Nbeal1

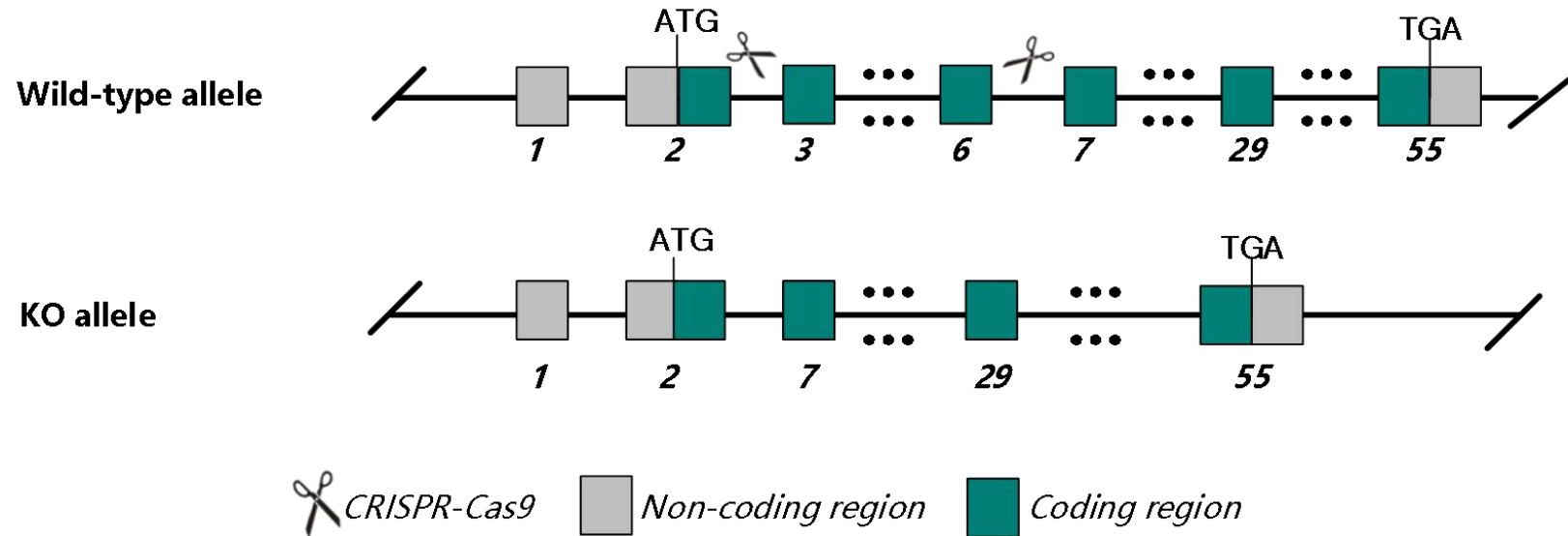
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Nbeal1* gene.

Technical Information

- The *Nbeal1* gene has 10 transcripts. According to the structure of *Nbeal1* gene, exon 3-exon 6 of *Nbeal1*-203 (ENSMUST00000160834.8) transcript is recommended as the knockout region. The region contains 464 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Nbeal1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Nbeal1 neurobeachin like 1 [*Mus musculus* (house mouse)]

Gene ID: 269198, updated on 5-Aug-2023

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Summary

Official Symbol	Nbeal1 provided by MGI
Official Full Name	neurobeachin like 1 provided by MGI
Primary source	MGI:MGI:2444343
See related	Ensembl:ENSMUSG00000073664 AllianceGenome:MGI:2444343
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	ALS2CR17; 2310076G13Rik; A530050O19Rik; A530083I02Rik
Summary	Predicted to enable protein kinase binding activity. Predicted to be involved in protein localization. Predicted to be active in cytosol and membrane. Orthologous to human NBEAL1 (neurobeachin like 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in bladder adult (RPKM 3.9), CNS E18 (RPKM 1.7) and 25 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

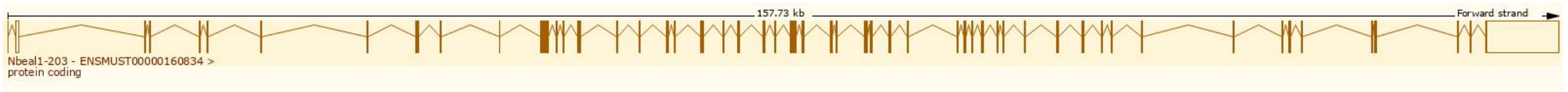
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 10 transcripts, and the transcripts are shown below:

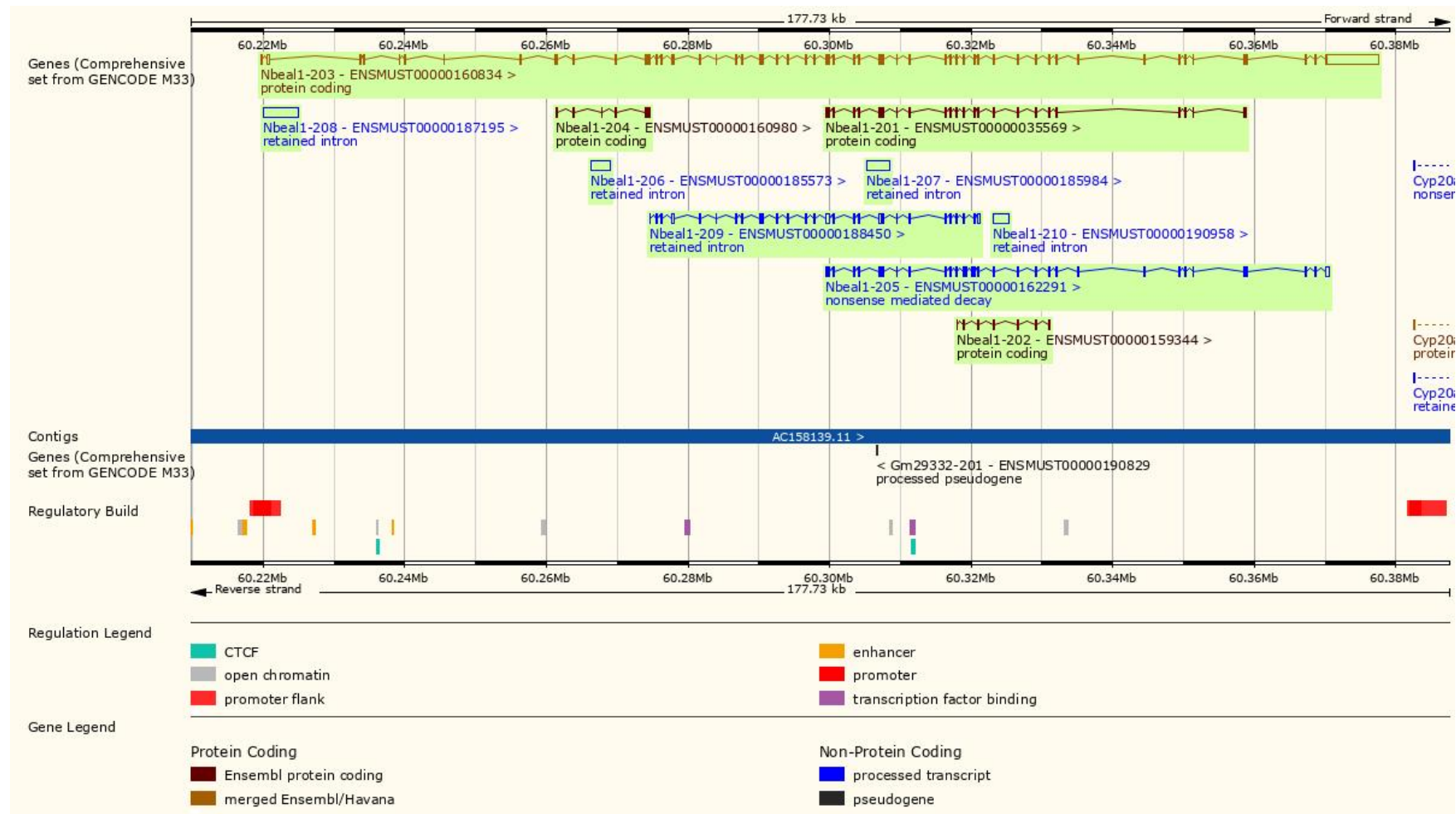
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST0000035569.12	Nbeal1-201	3536	1179aa	Protein coding		E9PV03	TSL:5	CDS 5' and 3' incomplete
ENSMUST00000159344.2	Nbeal1-202	736	246aa	Protein coding		F6U6E8	TSL:5	CDS 5' and 3' incomplete
ENSMUST00000160834.8	Nbeal1-203	15731	2688aa	Protein coding	CCDS48274	E9PYP2	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:5
ENSMUST00000160980.3	Nbeal1-204	1130	376aa	Protein coding		F7D418	TSL:3	CDS 5' and 3' incomplete
ENSMUST00000162291.8	Nbeal1-205	5000	734aa	Nonsense mediated decay		F7BJ98	TSL:1	CDS 5' incomplete
ENSMUST00000185573.2	Nbeal1-206	2677	No protein	Retained intron		-	TSL:NA	
ENSMUST00000185984.2	Nbeal1-207	3218	No protein	Retained intron		-	TSL:NA	
ENSMUST00000187195.2	Nbeal1-208	5087	No protein	Retained intron		-	TSL:NA	
ENSMUST00000188450.7	Nbeal1-209	4543	No protein	Retained intron		-	TSL:1	
ENSMUST00000190958.2	Nbeal1-210	2262	No protein	Retained intron		-	TSL:NA	

The strategy is based on the design of *Nbeal1*-203 transcript, the transcription is shown below:

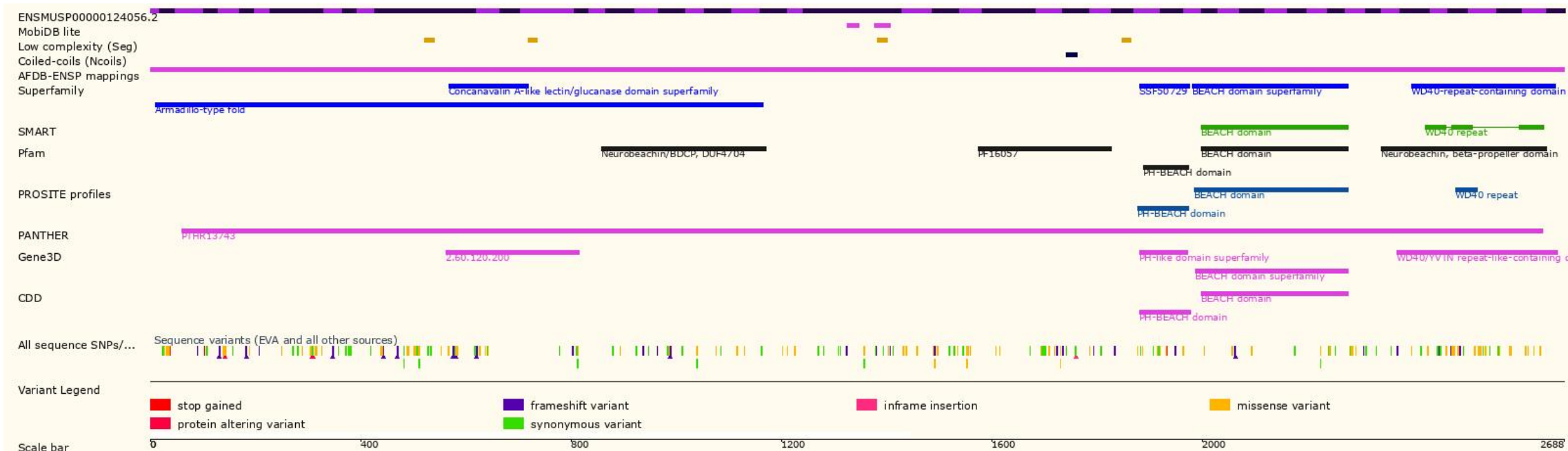


Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Important Information

- The effect of this strategy on *Nbeal1-201* transcript, *Nbeal1-202* transcript, *Nbeal1-204* transcript, *Nbeal1-205* transcript is unknown.
- The *Nbeal1* gene is located on Chr1. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.