

Pabpc4 Cas9-KO Strategy

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Overview

Target Gene Name

- Pabpc4

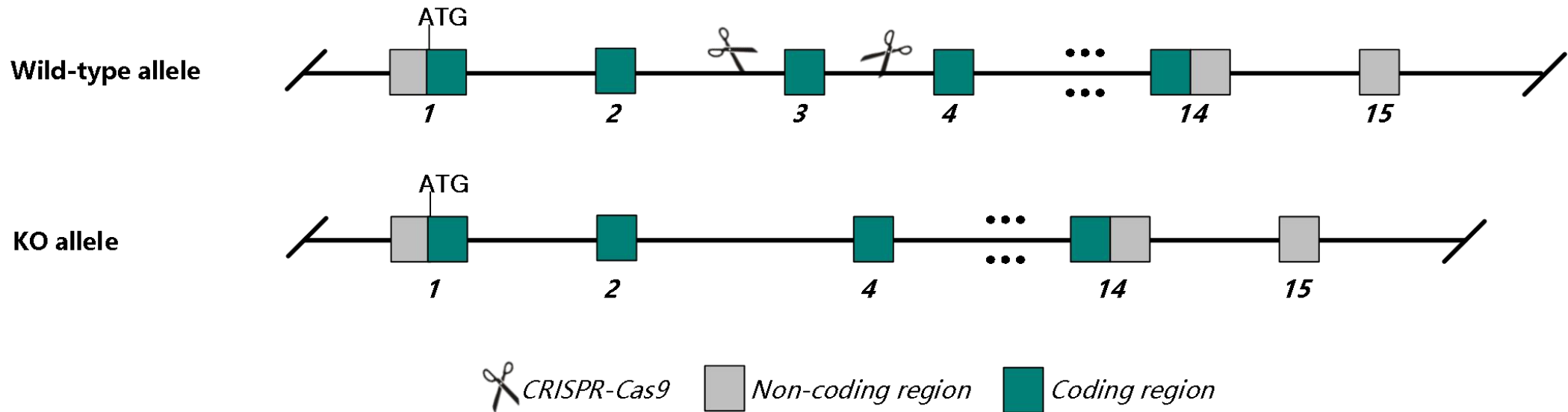
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Pabpc4* gene.

Technical Information

- The *Pabpc4* gene has 8 transcripts. According to the structure of *Pabpc4* gene, exon3 of *Pabpc4-202* (ENSMUST00000080178.13) transcript is recommended as the knockout region. The region contains 116bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Pabpc4* 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

Pabpc4 poly(A) binding protein, cytoplasmic 4 [*Mus musculus* (house mouse)]

Gene ID: 230721, updated on 24-Apr-2022

[Download Datasets](#)

Summary

Official Symbol Pabpc4 provided by MGI
Official Full Name poly(A) binding protein, cytoplasmic 4 provided by MGI
Primary source [MGI:MGI:2385206](#)
See related [Ensembl:ENSMUSG00000011257](#) [AllianceGenome:MGI:2385206](#)
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
Summary Enables mRNA binding activity. Acts upstream of or within myeloid cell development and regulation of mRNA stability. Predicted to be located in cytoplasm. Predicted to be part of ribonucleoprotein complex. Predicted to be active in cytoplasmic stress granule; cytosol; and nucleus. Is expressed in central nervous system; sensory organ; and tooth. Orthologous to human PABPC4 (poly(A) binding protein cytoplasmic 4). [provided by Alliance of Genome Resources, Apr 2022]
Expression Ubiquitous expression in liver E14 (RPKM 71.8), liver E14.5 (RPKM 71.3) and 27 other tissues [See more](#)
Orthologs [human](#) [all](#)
NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

Genomic context

Location: 4; 4 D2.2

Exon count: 15

See Pabpc4 in [Genome Data Viewer](#)

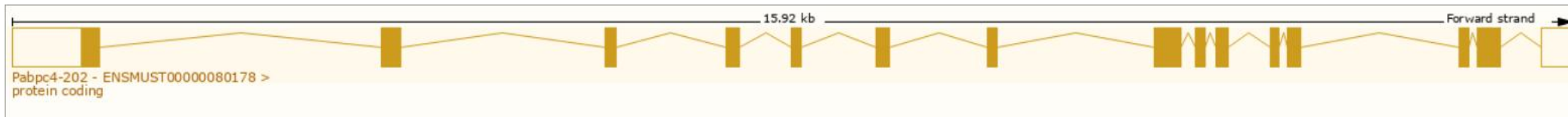
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 8 transcripts, all transcripts are shown below:

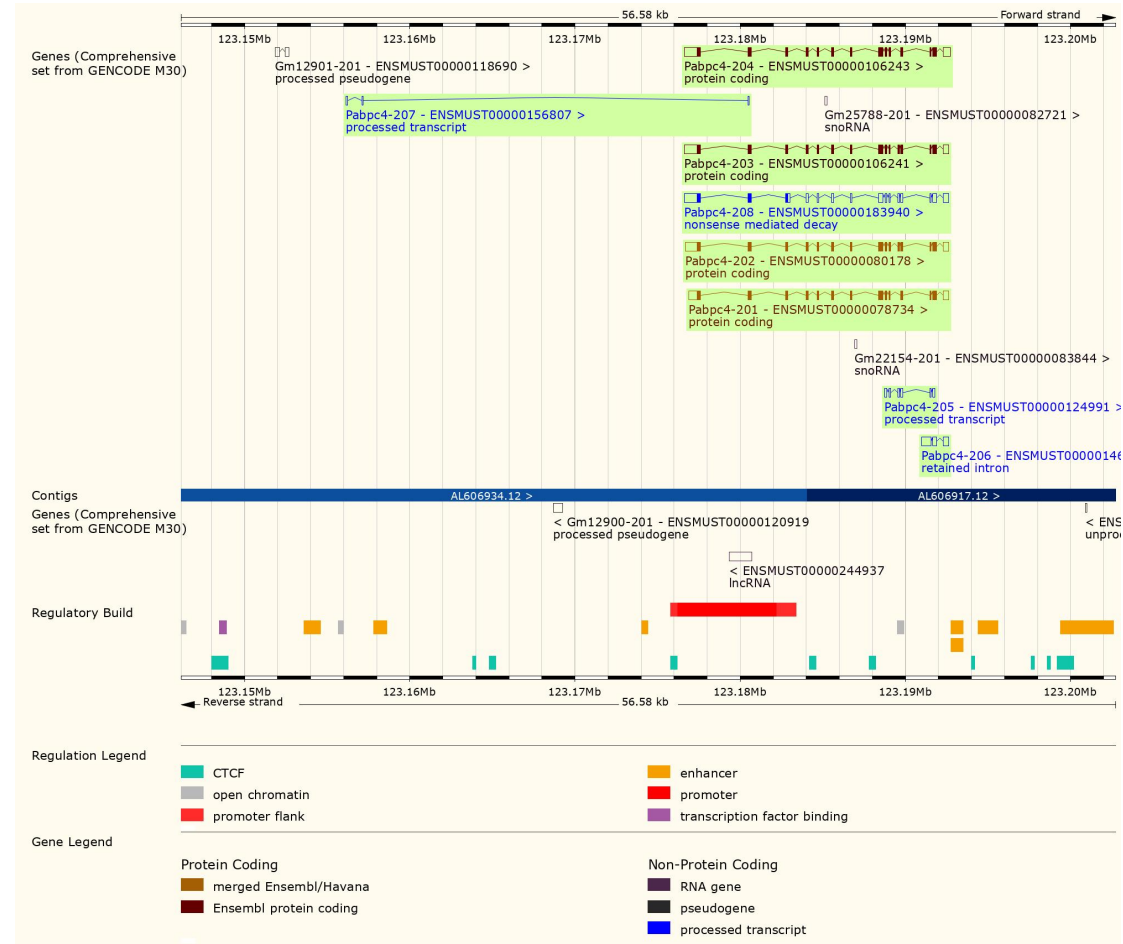
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000080178.13	Pabpc4-202	3019	660aa	Protein coding	CCDS18614	Q6PHQ9	Ensembl Canonical Gencode basic TSL:1
ENSMUST00000106243.8	Pabpc4-204	3111	631aa	Protein coding		A3KFU5	Gencode basic APPRIS P1 TSL:5
ENSMUST00000106241.8	Pabpc4-203	3050	644aa	Protein coding		A3KFU8	Gencode basic TSL:5
ENSMUST00000078734.12	Pabpc4-201	2700	615aa	Protein coding	CCDS18615	Q91YZ8	Gencode basic TSL:1
ENSMUST00000183940.8	Pabpc4-208	3166	168aa	Nonsense mediated decay		V9GXG3	TSL:1
ENSMUST00000124991.2	Pabpc4-205	692	No protein	Processed transcript		-	TSL:2
ENSMUST00000156807.2	Pabpc4-207	245	No protein	Processed transcript		-	TSL:5
ENSMUST00000146156.2	Pabpc4-206	1146	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Pabpc4-202* transcript, the transcription is shown below:

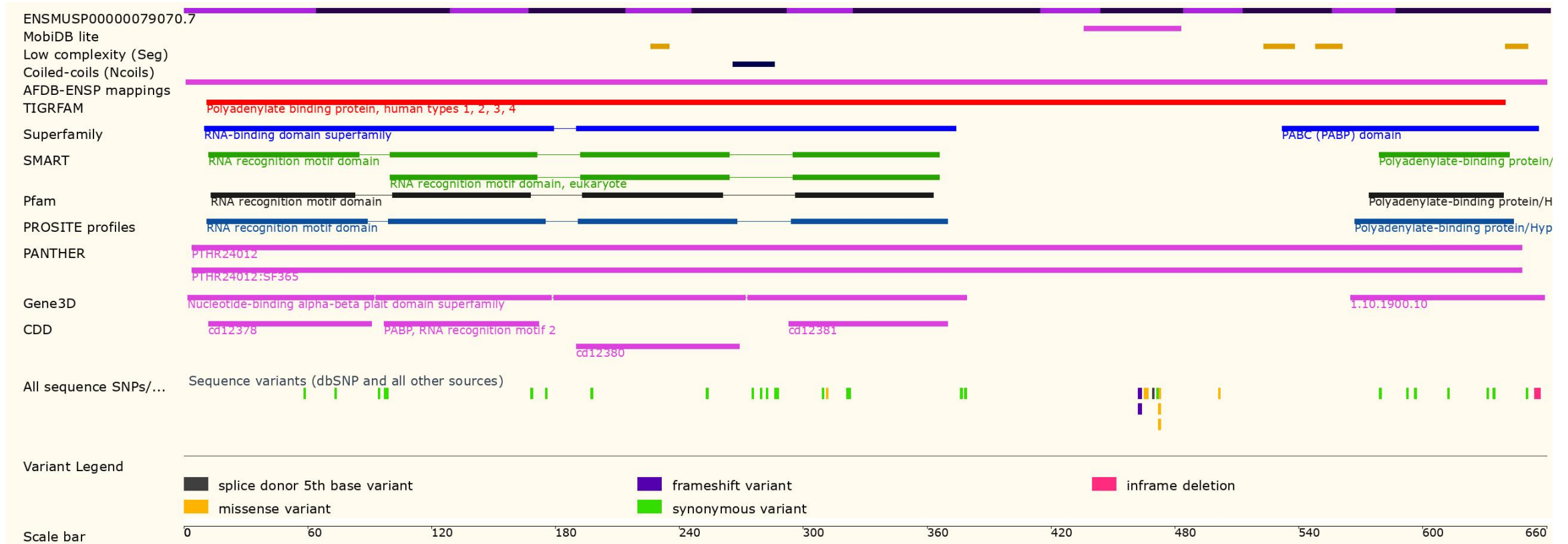


Source: <https://www.ensembl.org>

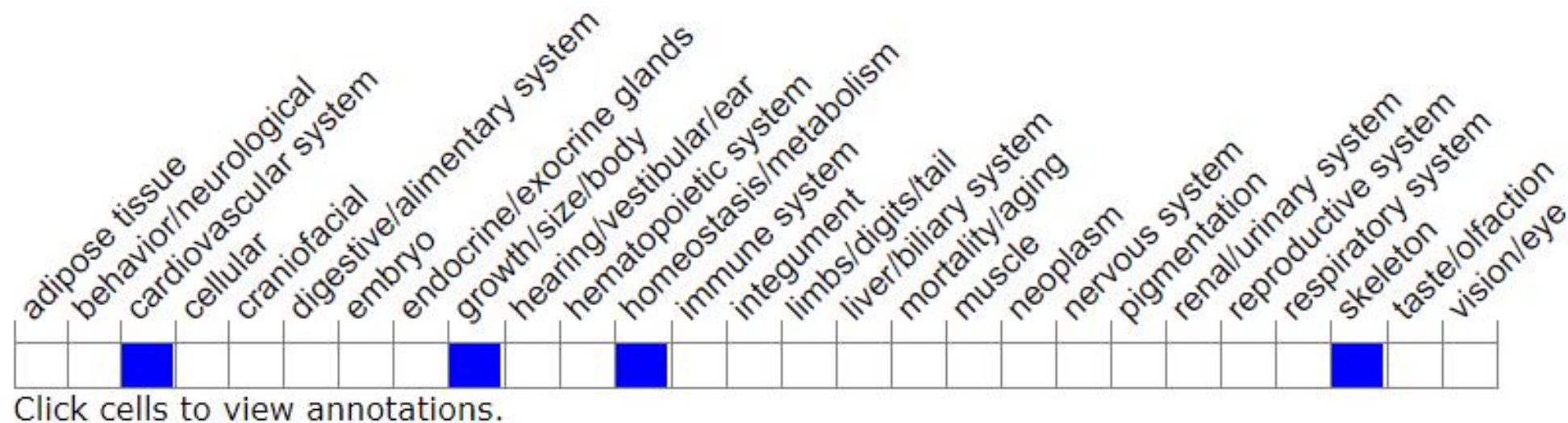
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



Important Information

- The effect of *Gm25788-201*, *Gm22154* and ENSMUST00000244937.1 gene is unknown.
- *Pabpc4* is located on Chr4. 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.