GemPharmatech™

Ifitm10 Cas9-KO Strategy

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Design Date: 2023-10-27

Overview

Target Gene Name

- Ifitm10

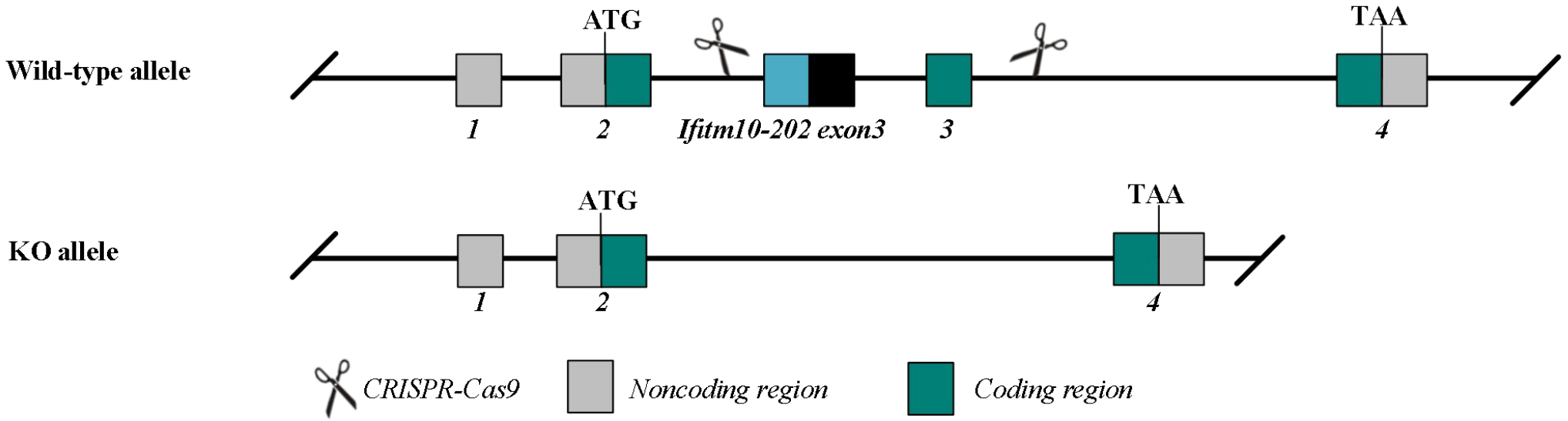
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ifitm10* gene.

Technical Information

- The *Ifitm10* gene has 6 transcripts. According to the structure of *Ifitm10* gene, exon3 of *Ifitm10*-201 (ENSMUST00000059223.15) transcript is recommended as the knockout region. The region contains 97bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ifitm10* 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

Ifitm10 interferon induced transmembrane protein 10 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 320802, updated on 7-Sep-2023

Summary

Official Symbol	Ifitm10 provided by MGI
Official Full Name	interferon induced transmembrane protein 10 provided by MGI
Primary source	MGI:MGI:2444776
See related	Ensembl:ENSMUSG00000045777 AllianceGenome:MGI:2444776
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	DSPA3; 6330512M04Rik
Summary	Predicted to be located in membrane. Predicted to be integral component of membrane. Predicted to be active in plasma membrane. Orthologous to human IFITM10 (interferon induced transmembrane protein 10). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in cerebellum adult (RPKM 9.8), lung adult (RPKM 4.5) and 8 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

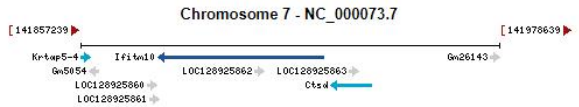
Genomic context

Location: 7 F5; 7 87.9 cM

See Ifitm10 in Genome Data Viewer

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
RS_2023_04	current	GRCm39 (GCF_000001635.27)	7	NC_000073.7 (141879572..141927526, complement)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (142325835..142373779, complement)



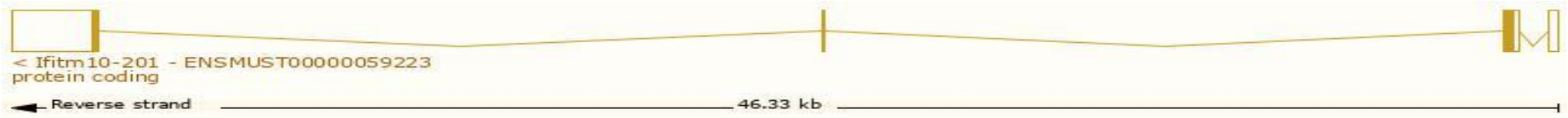
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 6 transcripts,all transcripts are shown below:

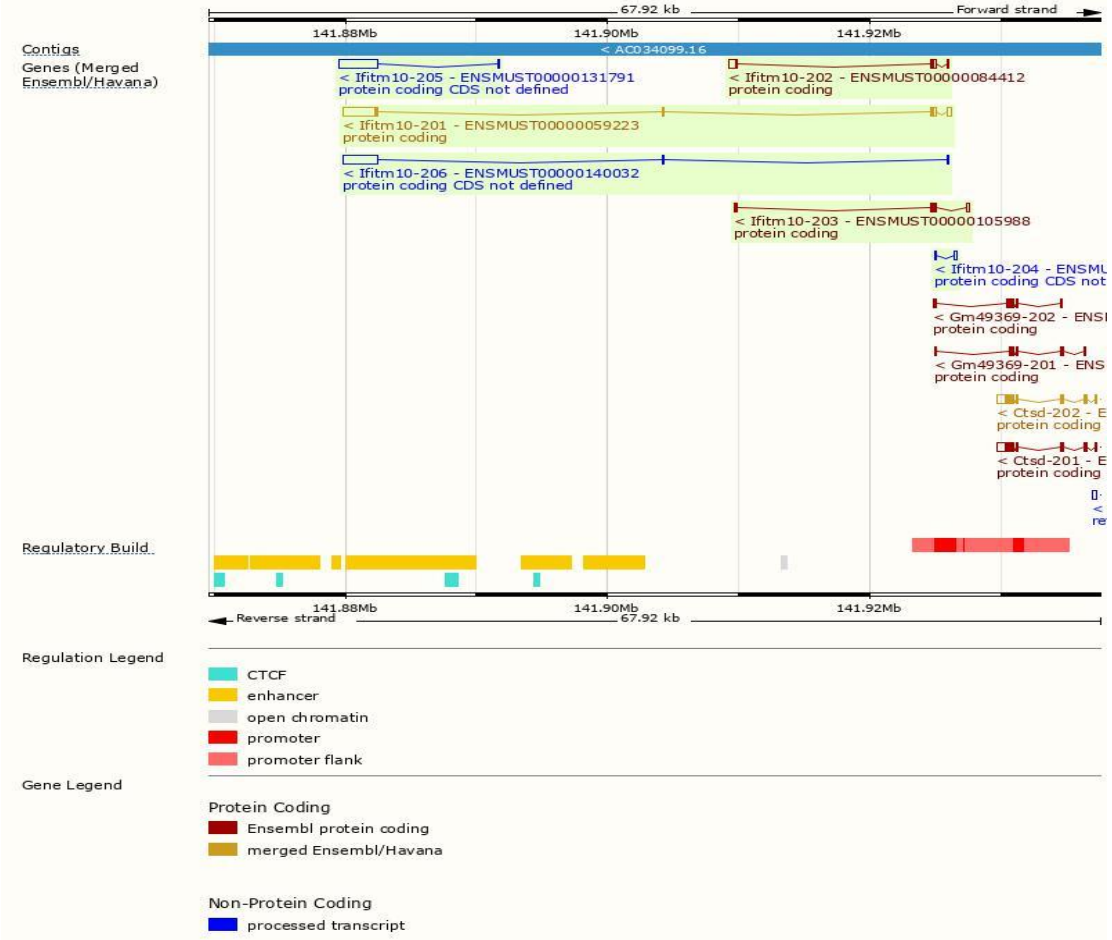
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000105988.2	Ifitm10-203	824	201aa	Protein coding	CCDS85468	Q8BR26-1	Ensembl Canonical GENCODE basic APPRIS ALT2 TSL:2
ENSMUST00000059223.15	Ifitm10-201	3412	162aa	Protein coding	CCDS40191	Q8BR26-3	GENCODE basic TSL:1
ENSMUST00000084412.6	Ifitm10-202	1158	130aa	Protein coding	CCDS85467	Q8BR26-2	GENCODE basic APPRIS P2 TSL:1
ENSMUST00000131791.2	Ifitm10-205	2973	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000140032.2	Ifitm10-206	2767	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000123543.2	Ifitm10-204	369	No protein	Protein coding CDS not defined		-	TSL:3

The strategy is based on the design of *Ifitm10*-201 transcript, the transcription is shown below:



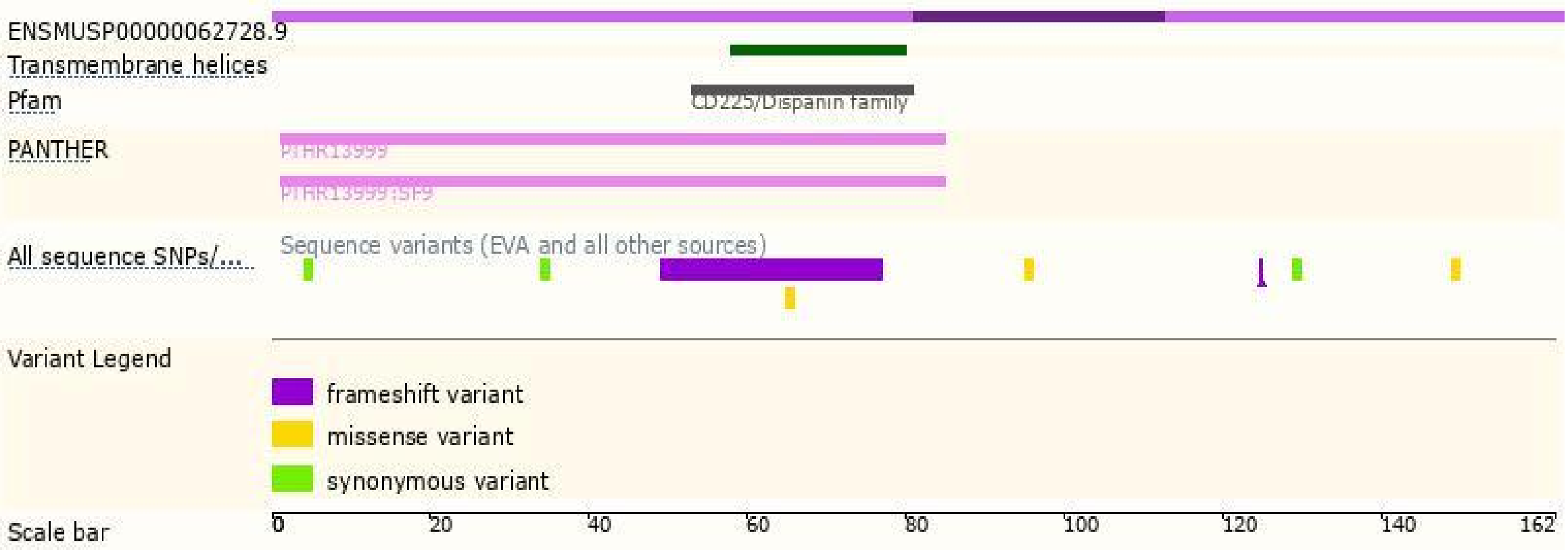
Source: https://www.ensembl.org

Genomic Information



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

Protein Information



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

Important Information

- *Ifitm10* is located on Chr7. 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.