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Fbxo7 Cas9-KO Strategy

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Reviewer: Yanhua Shen

Design Date: 2022-12-6

Overview

Target Gene Name

- Fbxo7

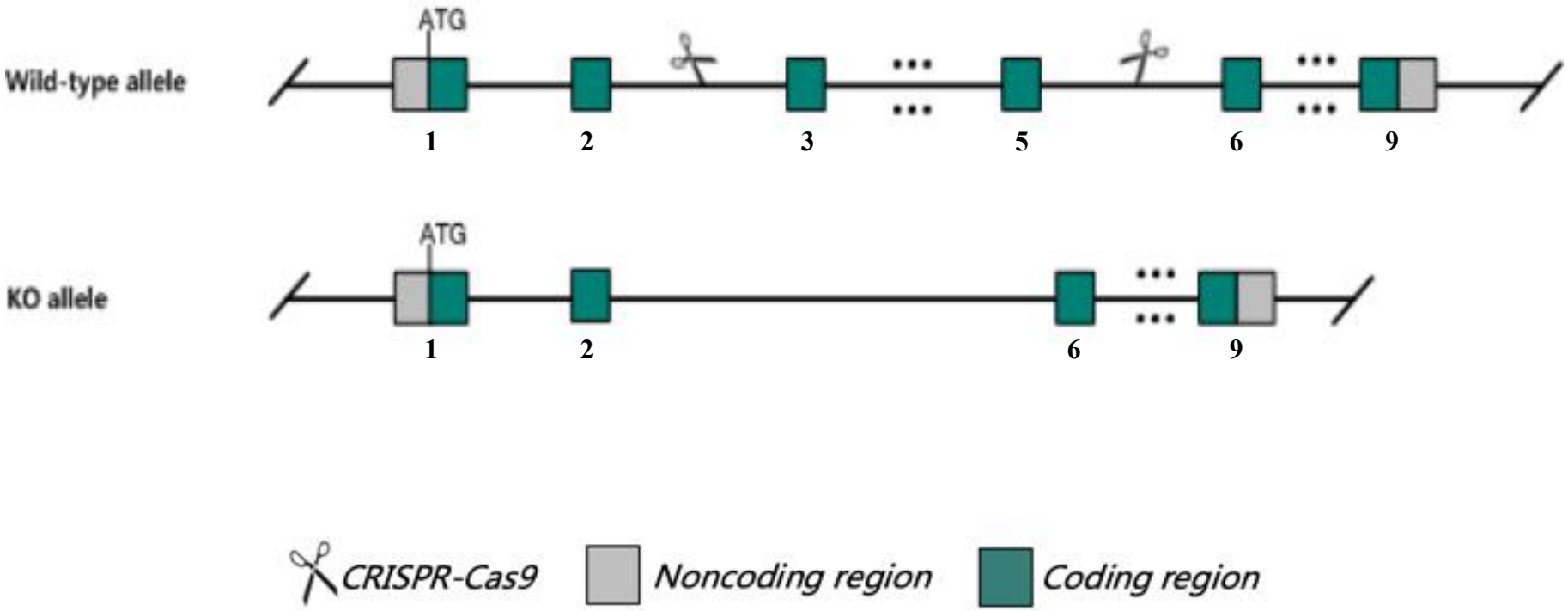
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Fbxo7* gene.

Technical Information

- The *Fbxo7* gene has 7 transcripts. According to the structure of *Fbxo7* gene, exon3-5 of *Fbxo7-204* (ENSMUST00000130320.8) transcript is recommended as the knockout region. The region contains 457bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Fbxo7* 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

Fbxo7 F-box protein 7 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 69754, updated on 4-Oct-2022

Summary

Official Symbol	Fbxo7 provided by MGI
Official Full Name	F-box protein 7 provided by MGI
Primary source	MGI:MGI:1917004
See related	Ensembl:ENSMUSG00000001786 AllianceGenome:MGI:1917004
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	2410015K21Rik; A230052G17Rik
Summary	Enables protein kinase binding activity. Acts upstream of or within negative regulation of G1/S transition of mitotic cell cycle; negative regulation of cyclin-dependent protein serine/threonine kinase activity; and negative regulation of lymphocyte differentiation. Located in mitochondrion and nucleus. Is expressed in dorsal root ganglion; gallbladder; liver; trigeminal ganglion; and vagus ganglion. Human ortholog(s) of this gene implicated in Parkinson's disease and Parkinson's disease 15. Orthologous to human FBXO7 (F-box protein 7). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in kidney adult (RPKM 26.7), liver E14.5 (RPKM 23.1) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

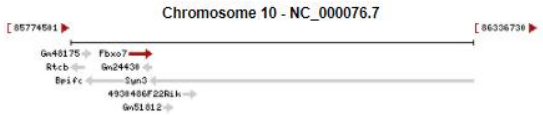
Genomic context

Location: 10; 10 C1

See Fbxo7 in Genome Data Viewer

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
109	current	GRCm39 (GCF_000001635.27)	10	NC_000076.7 (85856313..85887737)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (86020449..86051873)



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

Transcript Information

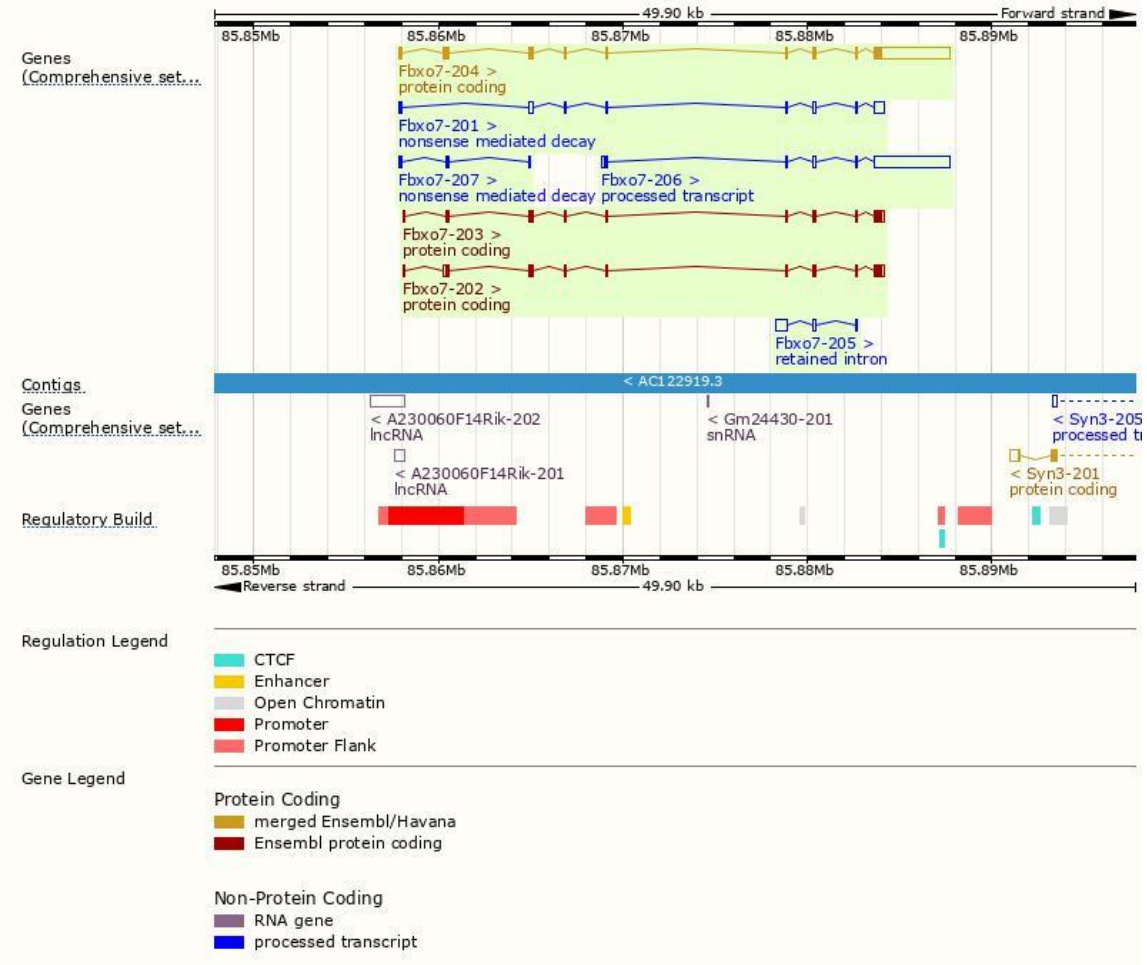
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fbxo7-204	ENSMUST00000130320.8	5388	523aa	Protein coding	CCDS24095		TSL:1 , GENCODE basic , APPRIS P3 ,
Fbxo7-202	ENSMUST00000117597.2	1799	442aa	Protein coding	CCDS83740		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Fbxo7-203	ENSMUST00000120344.8	1655	444aa	Protein coding	CCDS78875		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Fbxo7-201	ENSMUST00000001837.14	1498	56aa	Nonsense mediated decay	-		TSL:5 ,
Fbxo7-207	ENSMUST00000147168.2	385	49aa	Nonsense mediated decay	-		TSL:5 ,
Fbxo7-206	ENSMUST00000134490.8	4728	No protein	Processed transcript	-		TSL:1 ,
Fbxo7-205	ENSMUST00000130383.2	780	No protein	Retained intron	-		TSL:5 ,

The strategy is based on the design of *Fbxo7-204* transcript, the transcription is shown below:

Source: https://www.ensembl.org

Genomic Information



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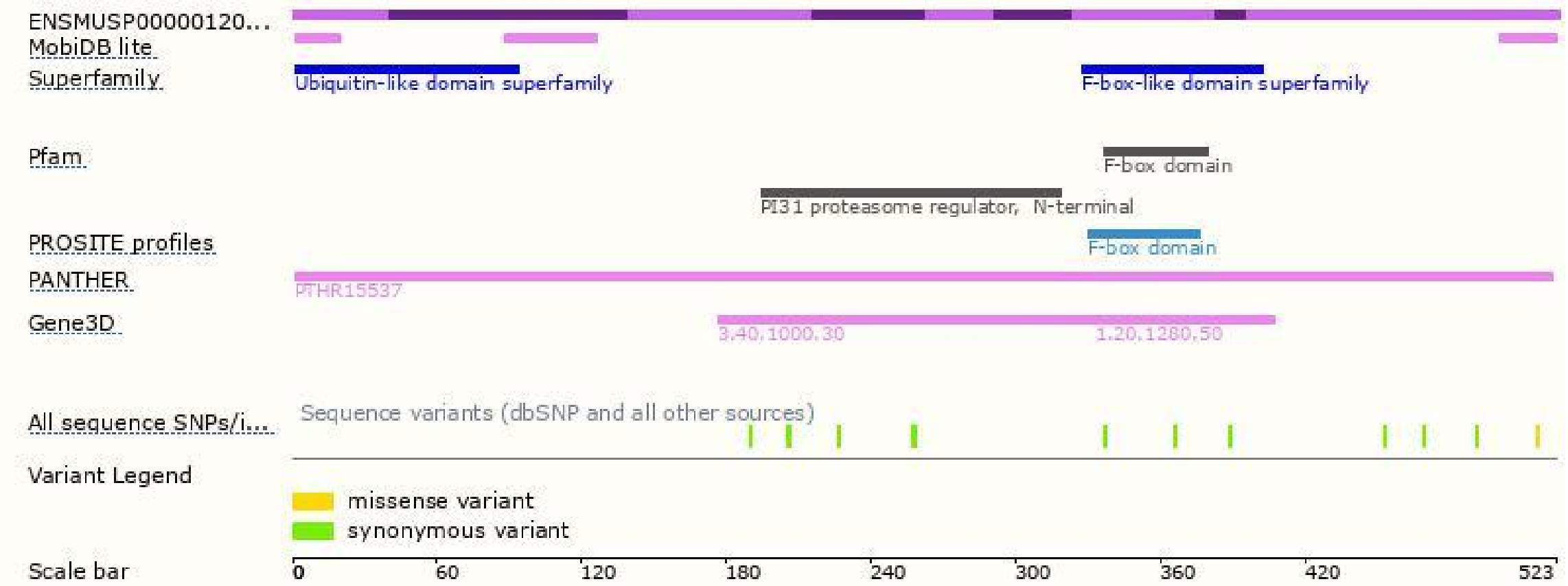
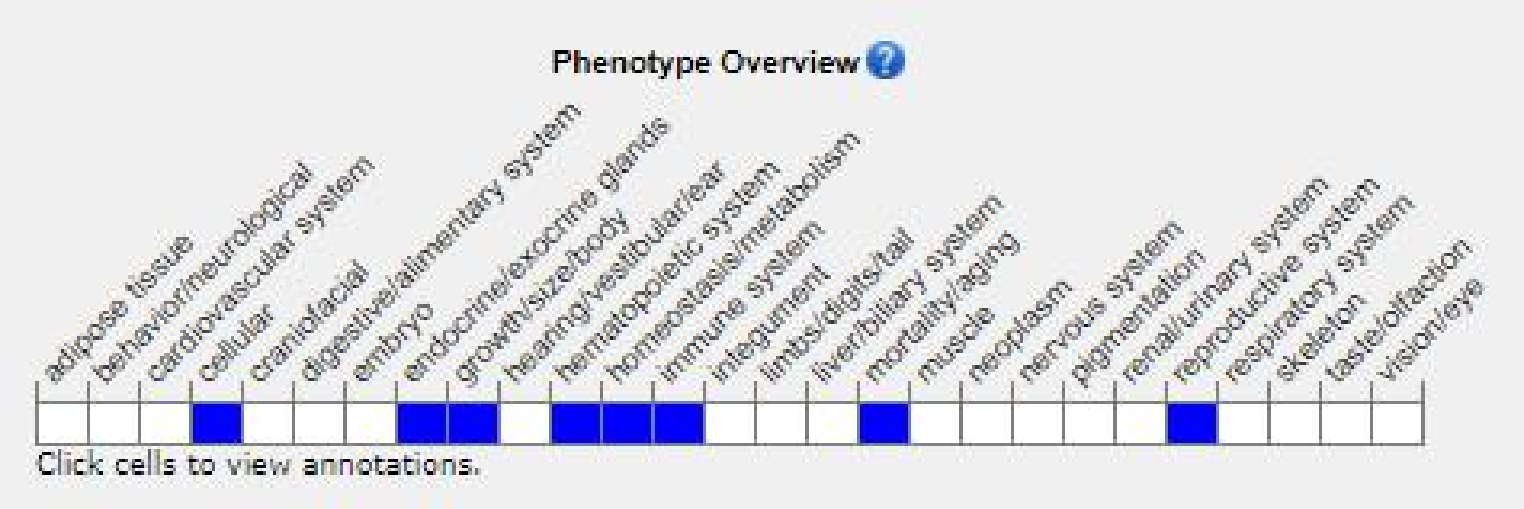
Source: : https://www.ensembl.org

Protein Information



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

Mouse Phenotype Information (MGI)



- Homozygotes for a null allele show increased pro-B cell and pro-erythroblast numbers. Homozygotes for a hypomorphic allele show anemia due to a shortened erythrocyte half-life, impaired spermatogenesis, male infertility, altered T cell phenotypes, and increased susceptibility to bacterial infection.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data,the gene knockout homozygous mice had a pre weaning death phenotype.
- The KO region is close to 5'UTR region of the *A230060F14Rik* gene. Knockout the region may affect the expression of *A230060F14Rik* gene.
- *Fbxo7* is located on Chr10. 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.