

Fbxw10 Cas9-CKO Strategy

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Reviewer: Yao Yu

Design Date: 2023-12-25

Overview

Target Gene Name

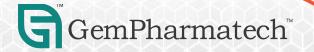
• Fbxw10

Project Type

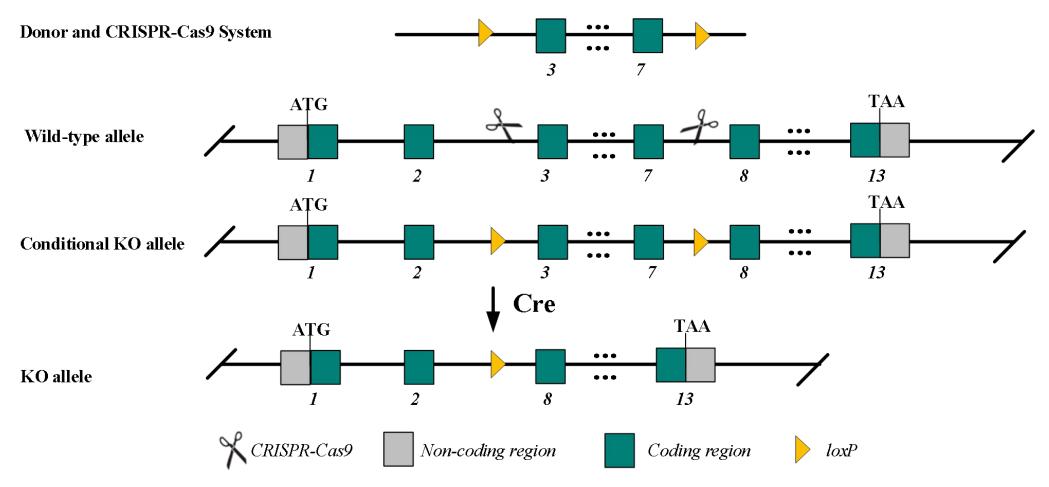
• Cas9-CKO

Genetic Background

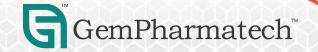
• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Fbxw10 gene.



Technical Information

- The *Fbxw10* gene has 6 transcripts. According to the structure of *Fbxw10* gene, exon 3-exon 7 of *Fbxw10*-205 (ENSMUST00000176577.2) transcript is recommended as the knockout region. The region contains 763bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Fbxw10* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



Gene Information

Fbxw10 F-box and WD-40 domain protein 10 [Mus musculus (house mouse)]

Toxin to 1 box and the 40 domain protein to [mas massaras (nodes modes)

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☆ ?



Official Symbol Fbxw10 provided by MGI

Official Full Name F-box and WD-40 domain protein 10 provided by MGI

Primary source MGI:MGI:3052463

Gene ID: 213980, updated on 7-Sep-2023

See related Ensembl:ENSMUSG00000090173 AllianceGenome:MGI:3052463

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; Muridae; Mus; Mus

Also known as HREP; Fbw10; SM25H2; SM2SH2

Summary Orthologous to several human genes including FBXW10 (F-box and WD repeat domain containing 10). [provided by Alliance of Genome Resources, Apr 2022]

Expression Biased expression in testis adult (RPKM 31.0) and thymus adult (RPKM 1.3) See more

Orthologs human all

NEW

Try the new Gene table

Try the new <u>Transcript table</u>

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

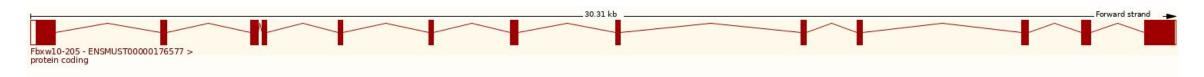


Transcript Information

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

Transcript ID	Name	bp 🌲	Protein ▼	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000036085.11	Fbxw10-201	3354	<u>1030aa</u>	Protein coding		Q5SUS0-1@	Ensembl Canonical GENCODE basic APPRIS ALT2 TSL:5
ENSMUST00000176577.2	Fbxw10-205	3254	<u>1025aa</u>	Protein coding	CCDS78968 ₪	H3BLP9₽	GENCODE basic APPRIS P2 TSL:1
ENSMUST00000150989.8	Fbxw10-203	3267	1020aa	Protein coding	CCDS24833 ₽	B7ZC91@	GENCODE basic APPRIS ALT2 TSL:5
ENSMUST00000177336.8	Fbxw10-206	3230	689aa	Nonsense mediated decay		H3BK87₽	TSL:1
ENSMUST00000127646.2	Fbxw10-202	461	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000175804.2	Fbxw10-204	1412	No protein	Retained intron		=	TSL:1

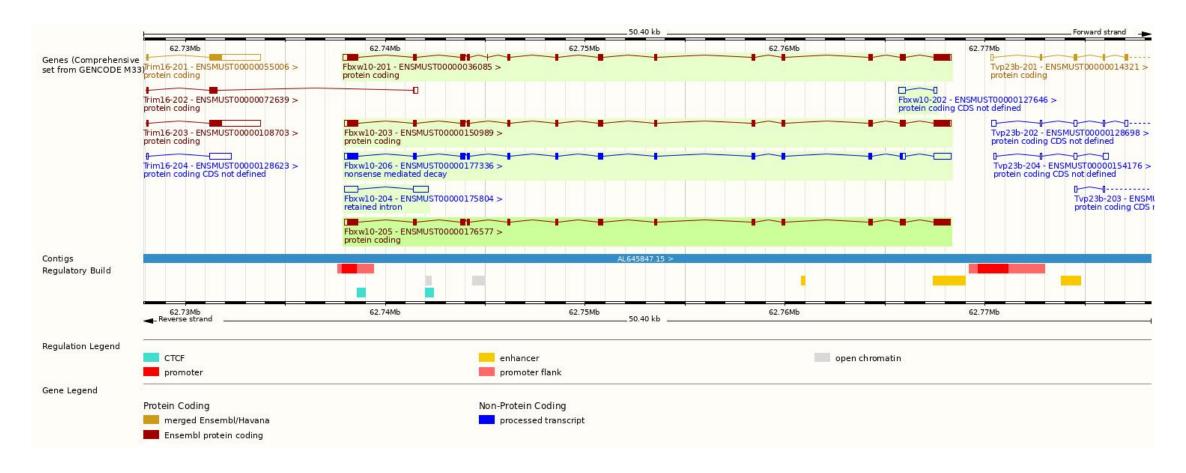
The strategy is based on the design of Fbxw10-205 transcript, the transcription is shown below:



Source: https://www.ensembl.org



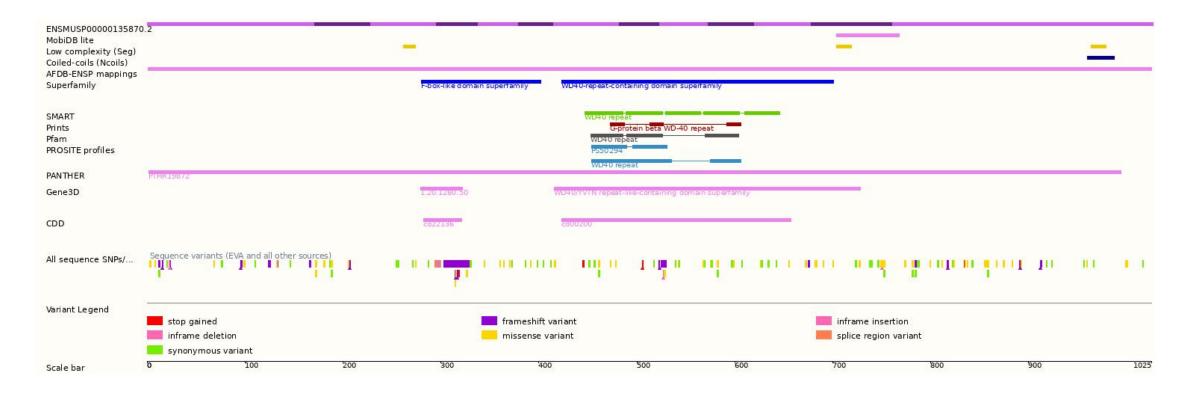
Genomic Information





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

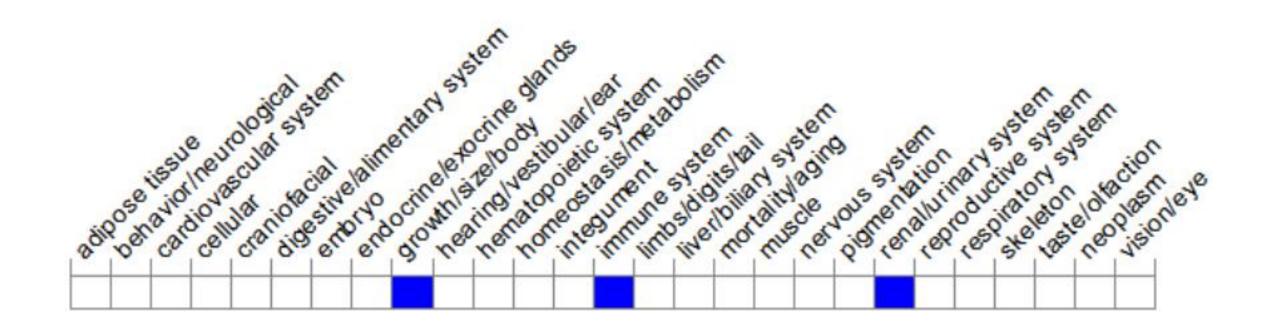
Protein Information





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

Mouse Phenotype Information (MGI)





Important Information

- After cross cre, 228 amino acids remained at the N-terminus of this strategy, with unknown effects.
- This strategy may affect the 3-terminal regulatory function of *Trim16*.
- *Fbxw10* is located on Chr11. 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

