GemPharmatech™

Wdr88 Cas9-KO Strategy

Designer: Jinling Wang

Reviewer: Longyun Hu

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Overview

Target Gene Name

- Wdr88

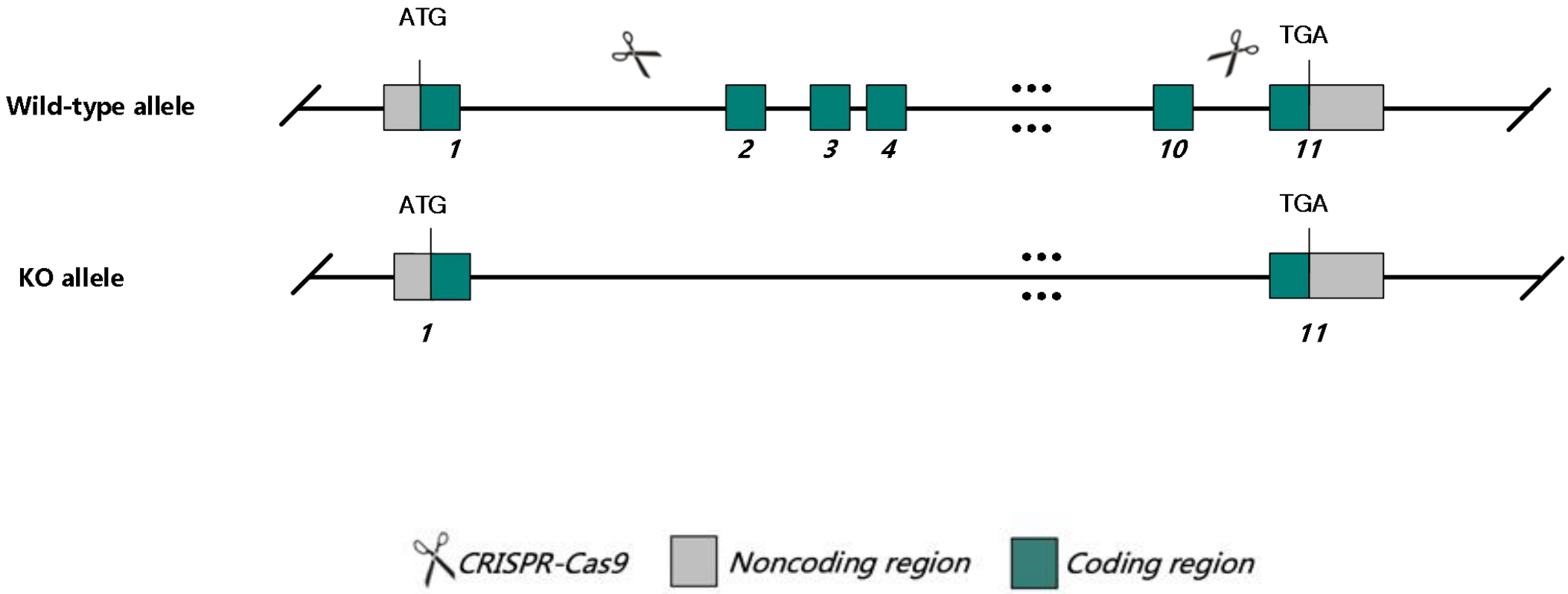
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Wdr88* gene.

Technical Information

- The *Wdr88* gene has 3 transcripts. According to the structure of *Wdr88* gene, exon2-exon10 of *Wdr88*-NP_001357815.1 transcript is recommended as the knockout region. The region contains most coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Wdr88* 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

Wdr88 WD repeat domain 88 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 384605, updated on 5-Mar-2024

Summary

Official Symbol	Wdr88 provided by MGI
Official Full Name	WD repeat domain 88 provided by MGI
Primary source	MGI:MGI:2686275
See related	Ensembl:ENSMUSG00000118454 AllianceGenome:MGI:2686275
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	Pqwd; Gm1429
Summary	Orthologous to human WDR88 (WD repeat domain 88). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Restricted expression toward testis adult (RPKM 6.8) See more
Orthologs	human all

NEW Try the new Gene table

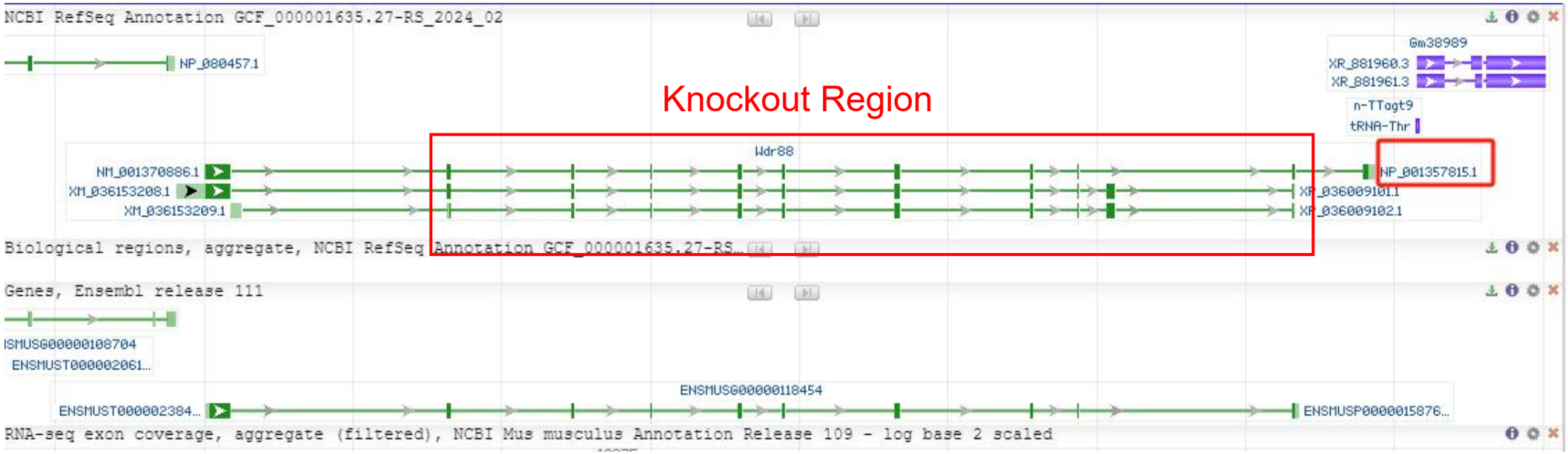
Try the new Transcript table

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

Transcript Information

The gene has 3 transcripts, and the transcripts are shown below:

Gene ID	Gene symbol	Transcript	Length (nt)	Protein	Length (aa)	Protein name	Isofo
384605	Wdr88	NM_001370886.1	2248	NP_001357815.1	654	WD repeat-containing protein 88	
384605	Wdr88	XM_036153208.1	3065	XP_036009101.1	667	WD repeat-containing protein 88	X1
384605	Wdr88	XM_036153209.1	1597	XP_036009102.1	369	WD repeat-containing protein 88	X2



Transcript Information

The strategy is based on the design of *Wdr88*-NP_001357815.1 transcript, the transcription is shown below:

1. NM_001370886.1 → NP_001357815.1 **WD repeat-containing protein 88**

Status: VALIDATED

Source sequence(s)	AC150683, AC154126
UniProtKB/TrEMBL	A0A571BF50
Related	ENSMUSP00000158765.2, ENSMUST00000238407.2

Conserved Domains (3) summary

PRK02224 Location:95 → 189	PRK02224; DNA double-strand break repair Rad50 ATPase
cd00200 Location:281 → 578	WD40; WD40 domain, found in a number of eukaryotic proteins that cover a wide variety of functions including adaptor/regulatory modules in signal transduction, pre-mRNA processing and cytoskeleton assembly; typically contains a GH dipeptide 11-24 residues from ...
sd00039 Location:292 → 330	7WD40; WD40 repeat [structural motif]

Source: https://www.ensembl.org

Important Information

- The lethality of homozygous mice after *Wdr88* gene knockout is unknown.
- This strategy is designed based on information from the NCBI website.
- The knockout region is about 3.8kb away from the 5' end of *Gm38989* and *n-TTagt9* gene, this strategy may affect the nomal function of this two genes.
- *Wdr88* 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.