GemPharmatech™

Wdr24 Cas9-KO Strategy

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Overview

Target Gene Name

- Wdr24

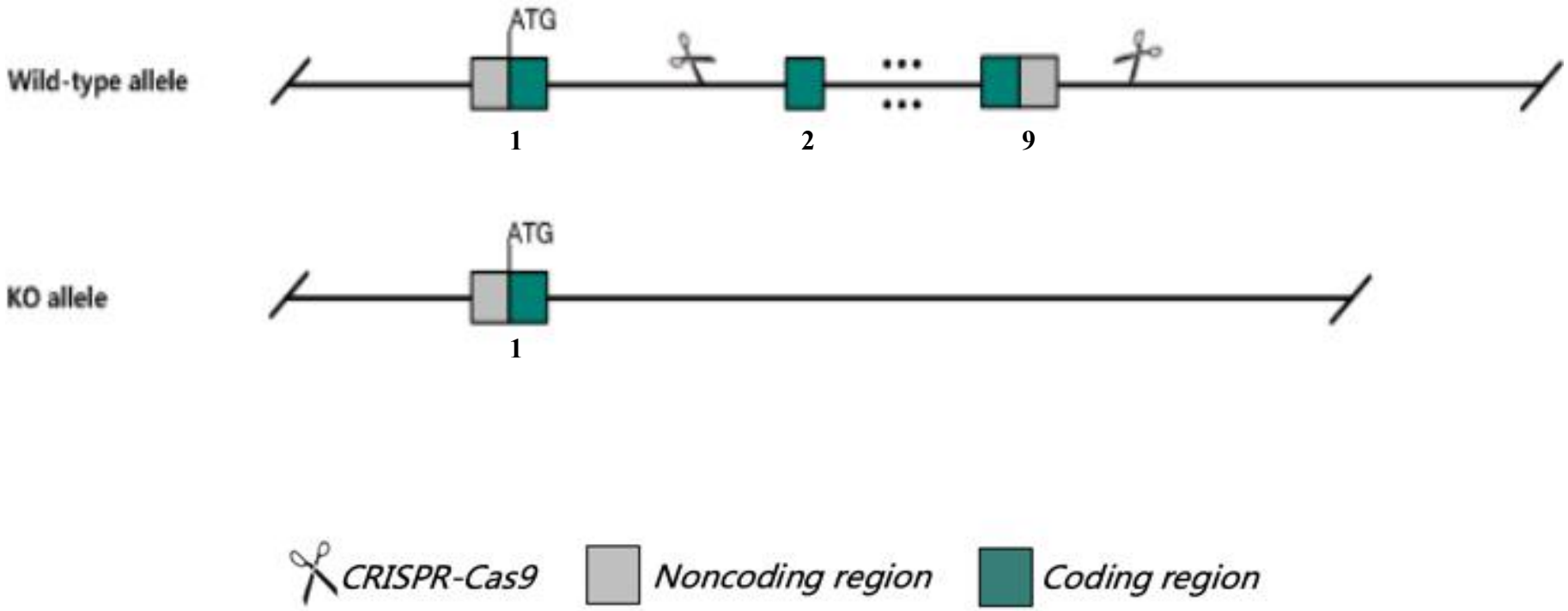
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Technical Information

- The *Wdr24* gene has 4 transcripts. According to the structure of *Wdr24* gene, exon2-exon9 of *Wdr24*-201 (ENSMUST00000026833.6) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Wdr24* 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

Wdr24 WD repeat domain 24 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 268933, updated on 23-Nov-2023

Summary

Official Symbol	Wdr24 provided by MGI
Official Full Name	WD repeat domain 24 provided by MGI
Primary source	MGI:MGI:2446285
See related	Ensembl:ENSMUSG00000025737 AllianceGenome:MGI:2446285
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	Predicted to be involved in cellular response to amino acid starvation; positive regulation of TOR signaling; and regulation of autophagy. Predicted to act upstream of or within autophagy. Predicted to be located in cytosol and lysosomal membrane. Predicted to be part of GATOR2 complex. Is expressed in several structures, including adrenal gland; genitourinary system; gut; lung; and spinal cord. Orthologous to human WDR24 (WD repeat domain 24). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in thymus adult (RPKM 26.9), ovary adult (RPKM 24.9) and 28 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

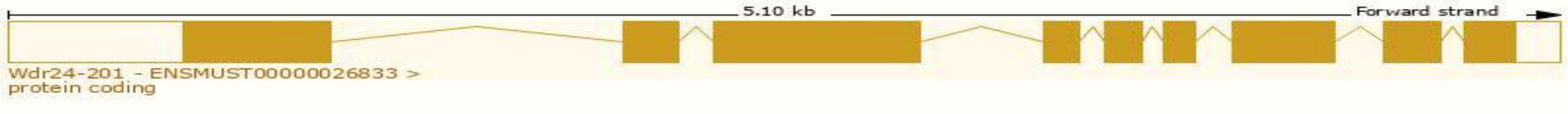
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 4 transcripts,all transcripts are shown below:

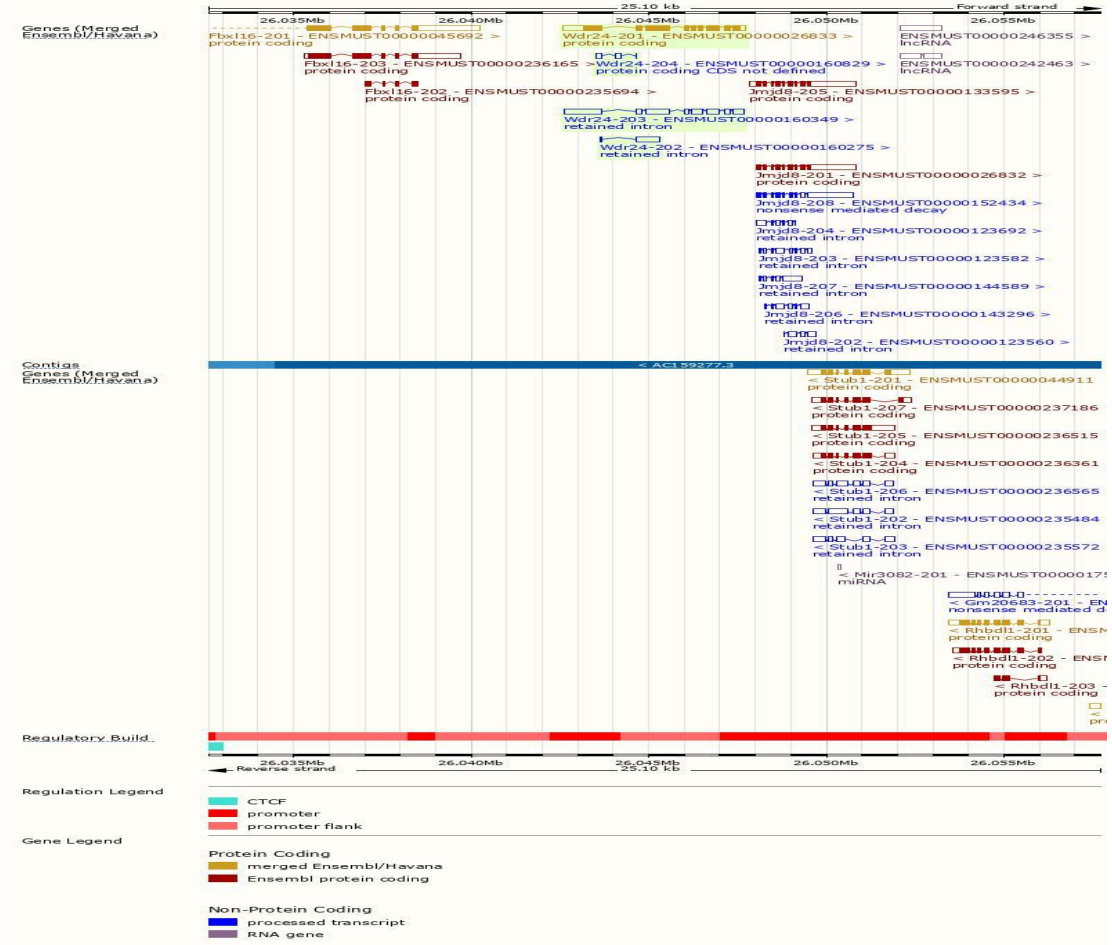
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000026833.6	Wdr24-201	3099	790aa	Protein coding	CCDS28531	Q8CFJ9	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000160829.2	Wdr24-204	317	No protein	Protein coding CDS not defined		-	TSL:5
ENSMUST00000160349.2	Wdr24-203	3139	No protein	Retained intron		-	TSL:1
ENSMUST00000160275.2	Wdr24-202	716	No protein	Retained intron		-	TSL:3

The strategy is based on the design of *Wdr24*-201 transcript, the transcription is shown below:



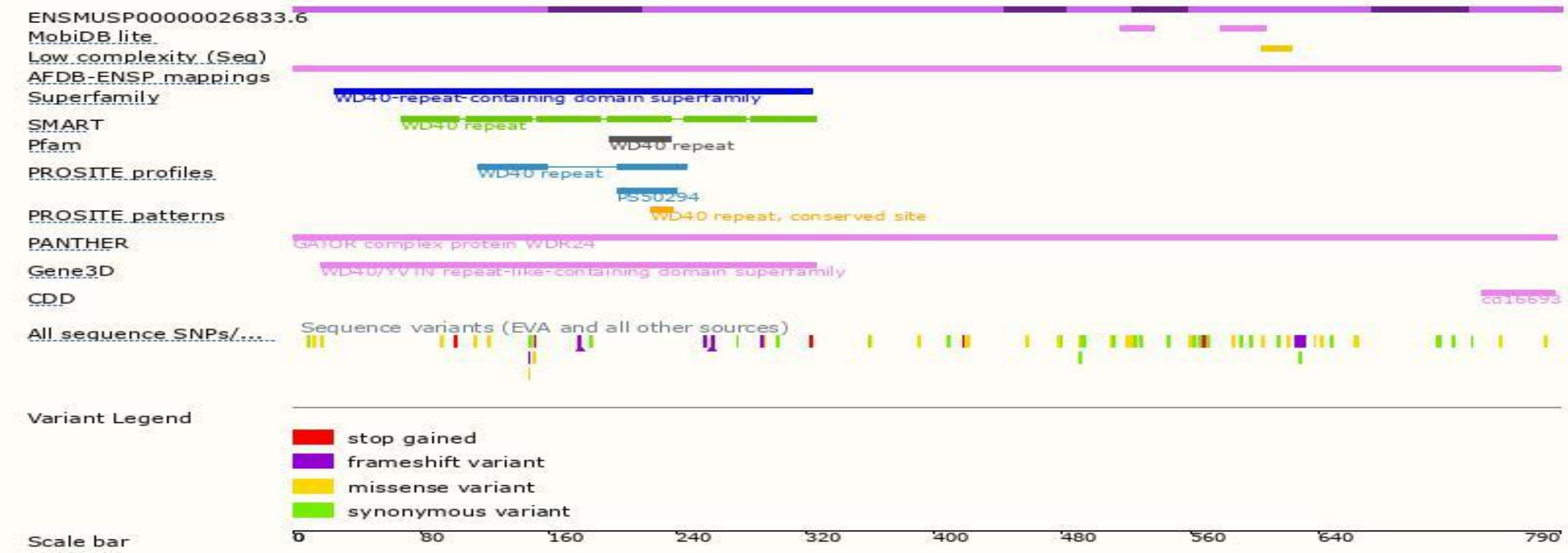
Source: https://www.ensembl.org

Genomic Information



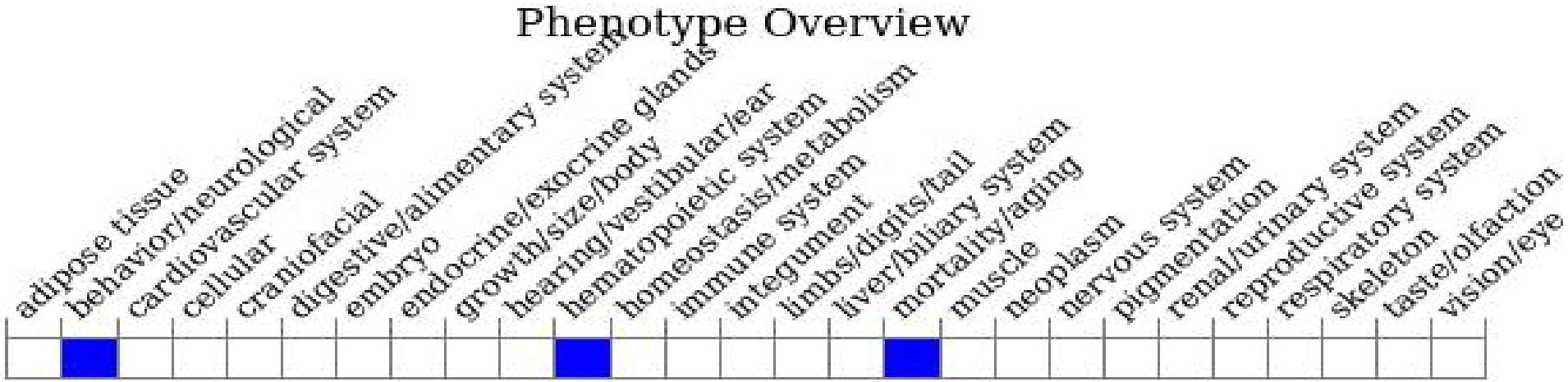
Source: : https://www.ensembl.org

Protein Information



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

Mouse Phenotype Information (MGI)



- Homozygosity for a phosphomimetic mutation at *Ser155* is early embryonic lethal. Homozygosity for a phosphoblocking mutation at *Ser155* affects glucose sensing.

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

Important Information

- According to MGI information,homozygosity for a phosphomimetic mutation at *Ser155* is early embryonic lethal. Homozygosity for a phosphoblocking mutation at *Ser155* affects glucose sensing.
- This strategy may affect the 5-terminal regulation of the *Jmjd8* gene.
- *Wdr24* is located on Chr17. 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.