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Ankzf1 Cas9-KO Strategy

Designer: Mingzhu Xu
Reviewer: Qian Chen
Design Date: 2024-1-19

Overview

Target Gene Name

- *Ankzf1*

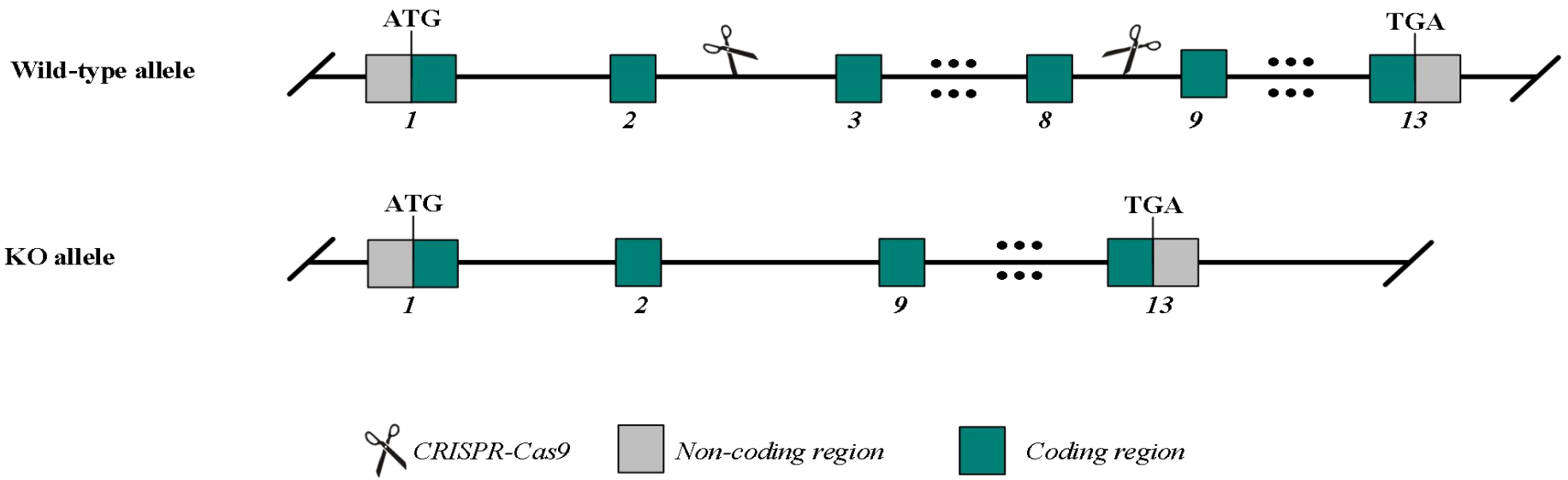
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

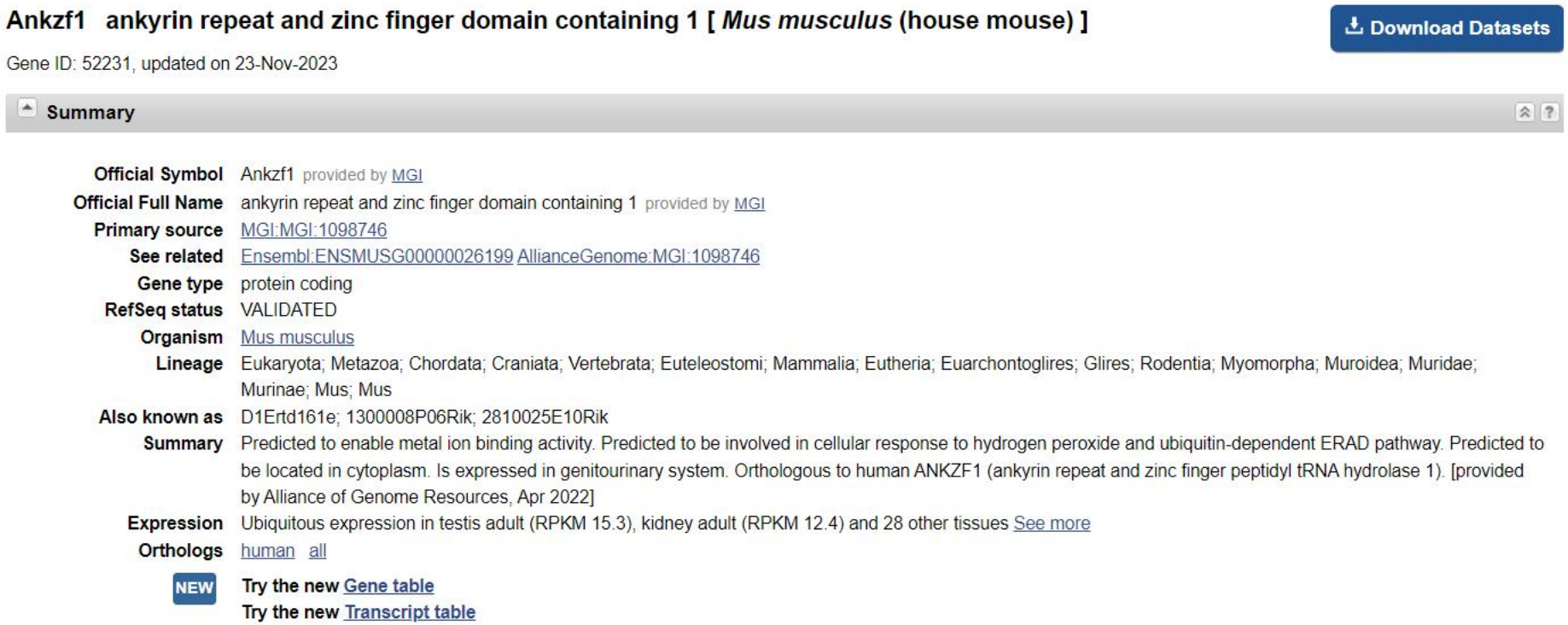


Schematic representation of CRISPR-Cas9 engineering used to edit the *Ankzf1* gene.

Technical Information

- The *Ankzf1* gene has 7 transcripts. According to the structure of *Ankzf1* gene, exon 3-8 of *Ankzf1*-207 (ENSMUST00000152233.9) transcript is recommended as the knockout region. The region contains 943 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ankzf1* 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.

Gene Information



Ankzf1 ankyrin repeat and zinc finger domain containing 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 52231, updated on 23-Nov-2023

Summary

Official Symbol	Ankzf1 provided by MGI
Official Full Name	ankyrin repeat and zinc finger domain containing 1 provided by MGI
Primary source	MGI:MGI:1098746
See related	Ensembl:ENSMUSG00000026199 AllianceGenome:MGI:1098746
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	D1Ertd161e; 1300008P06Rik; 2810025E10Rik
Summary	Predicted to enable metal ion binding activity. Predicted to be involved in cellular response to hydrogen peroxide and ubiquitin-dependent ERAD pathway. Predicted to be located in cytoplasm. Is expressed in genitourinary system. Orthologous to human ANKZF1 (ankyrin repeat and zinc finger peptidyl tRNA hydrolase 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in testis adult (RPKM 15.3), kidney adult (RPKM 12.4) 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/

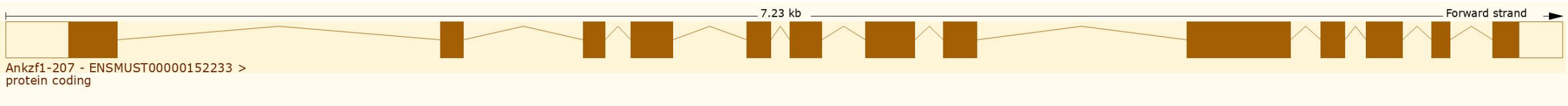
Transcript Information

The gene has 7 transcripts, and the transcript is shown below:

Show/hide columns (1 hidden) Filter

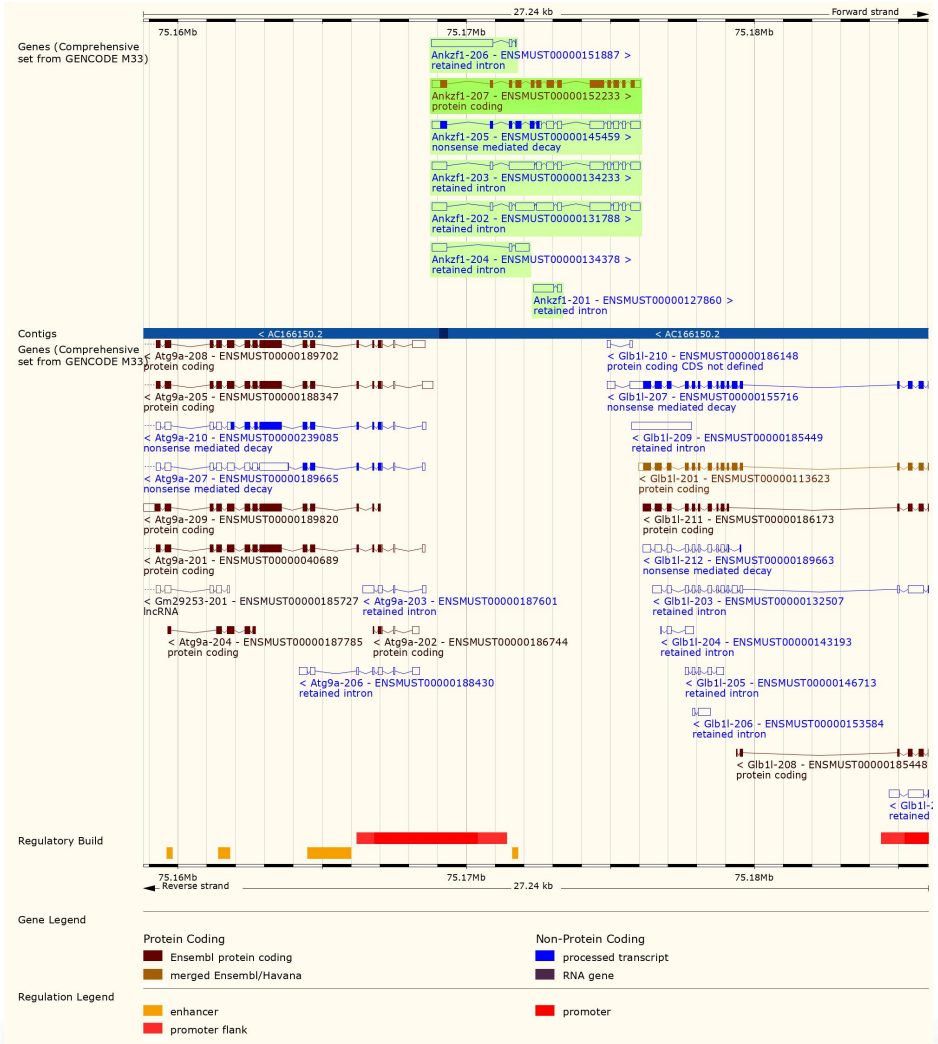
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000152233.9	Ankzf1-207	2739	748aa	Protein coding	CCDS56632	J3QM81	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000145459.9	Ankzf1-205	2770	287aa	Nonsense mediated decay		J3KMQ5	TSL:1
ENSMUST00000131788.9	Ankzf1-202	3426	No protein	Retained intron		-	TSL:2
ENSMUST00000134233.9	Ankzf1-203	3201	No protein	Retained intron		-	TSL:2
ENSMUST00000151887.9	Ankzf1-206	2259	No protein	Retained intron		-	TSL:2
ENSMUST00000134378.9	Ankzf1-204	1093	No protein	Retained intron		-	TSL:1
ENSMUST00000127860.2	Ankzf1-201	832	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Ankzf1*-207 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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

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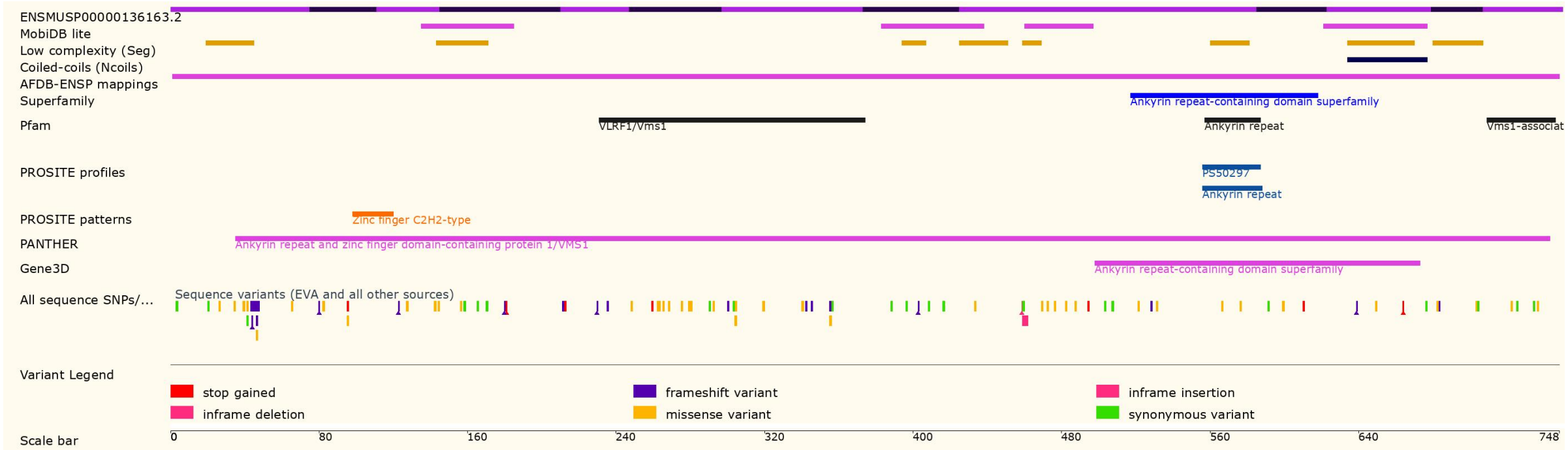
Protein Information



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

Important Information

- The knocking out region may contains the functional region of the *Atg9a* and *Glb1l* gene.Knockout the region may affect its function of *Atg9a* and *Glb1l* gene.
- *Ankzf1* is located on Chr1. 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.