GemPharmatech™

Dhrs1 Cas9-CKO Strategy

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Overview

Target Gene Name

- Dhrs1

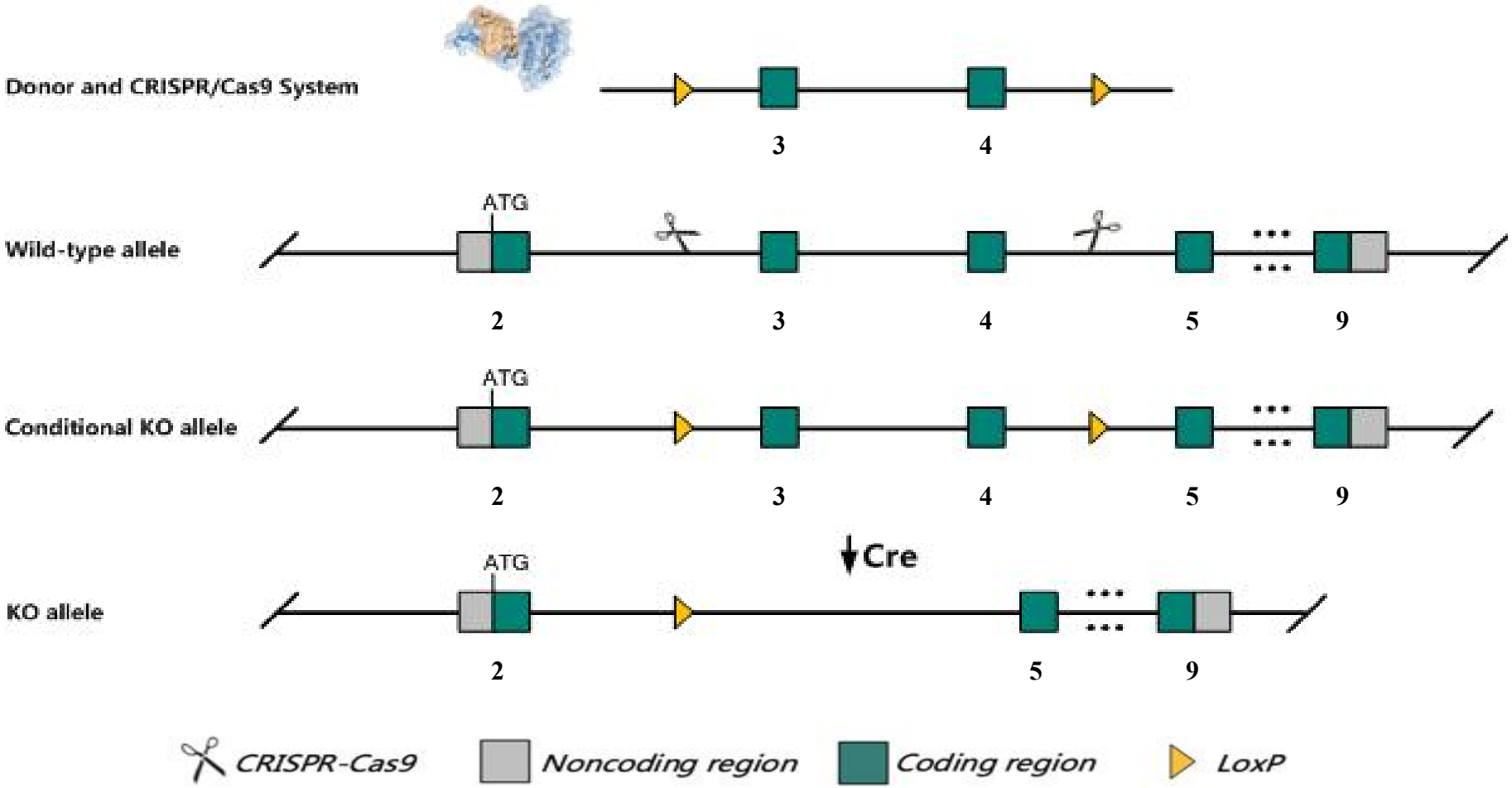
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Dhrs1* gene.

Technical Information

- The *Dhrs1* gene has 4 transcripts. According to the structure of *Dhrs1* gene, exon3-exon4 of *Dhrs1*-201 (ENSMUST00000002403.10) transcript is recommended as the knockout region. The region contains 224bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Dhrs1* 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

Dhrs1 dehydrogenase/reductase 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 52585, updated on 23-Nov-2023

Summary

Official Symbol	Dhrs1 provided by MGI
Official Full Name	dehydrogenase/reductase 1 provided by MGI
Primary source	MGI:MGI:1196314
See related	Ensembl:ENSMUSG00000002332 AllianceGenome:MGI:1196314
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	D14Ertd484e; 1110029G07Rik
Summary	Predicted to enable oxidoreductase activity. Located in mitochondrial inner membrane. Is expressed in dorsal root ganglion; glossopharyngeal ganglion; and trigeminal ganglion. Orthologous to human DHRS1 (dehydrogenase/reductase 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in duodenum adult (RPKM 54.6), testis adult (RPKM 52.1) and 28 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

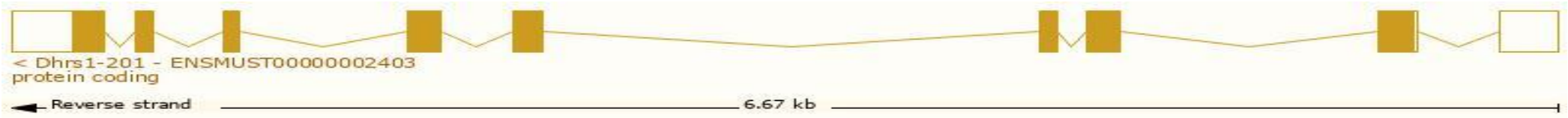
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

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

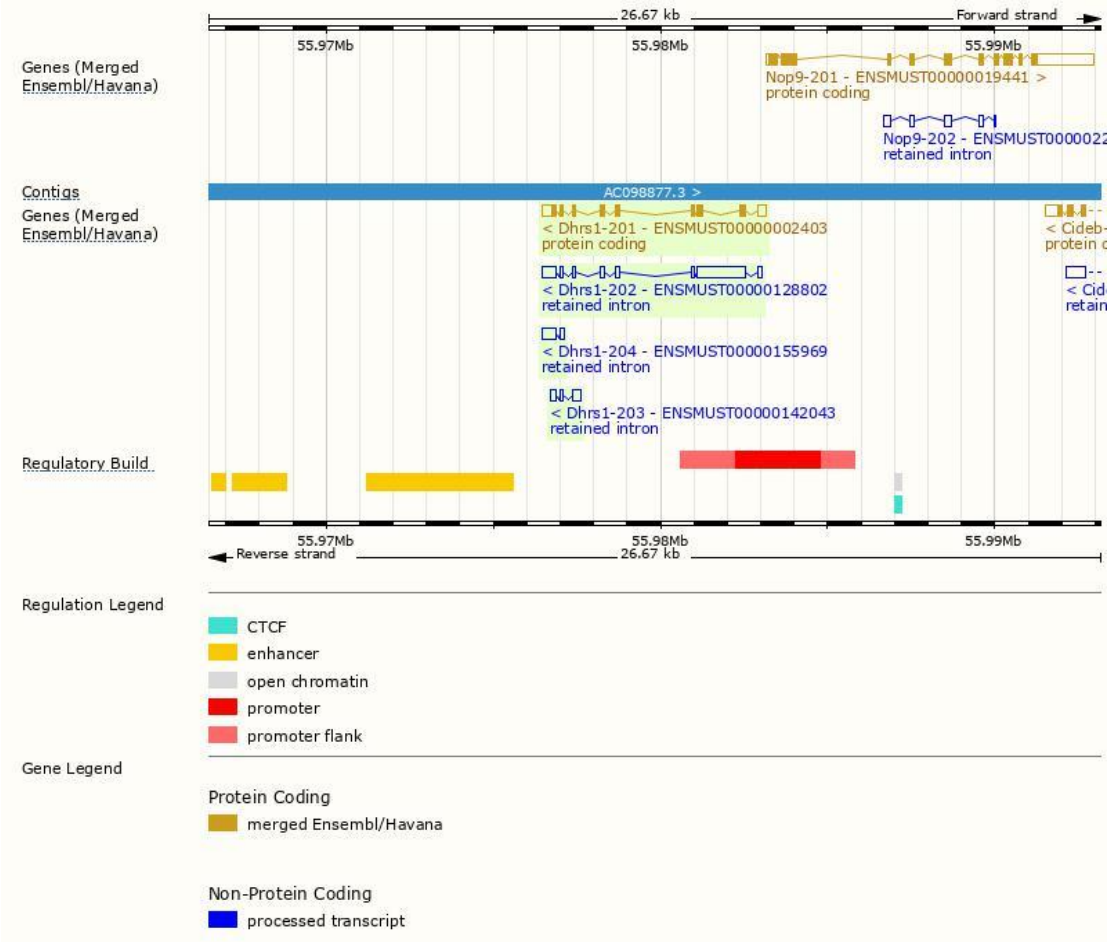
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000002403.10	Dhrs1-201	1477	313aa	Protein coding	CCDS36934	Q99L04	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000128802.8	Dhrs1-202	2502	No protein	Retained intron		-	TSL:1
ENSMUST00000155969.8	Dhrs1-204	510	No protein	Retained intron		-	TSL:2
ENSMUST00000142043.2	Dhrs1-203	477	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Dhrs1*-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

Important Information

- The floxed region is near to the N-terminal of *Nop9* gene,this strategy may influence the regulatory function of the N-terminal of *Nop9* gene.
- *Dhrs1* is located on Chr14. 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.