

Dhrs3 Cas9-CKO Strategy

Designer: Rui Xiong

Reviewer: Longyun Hu

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Project Overview



Project Name Dhrs3

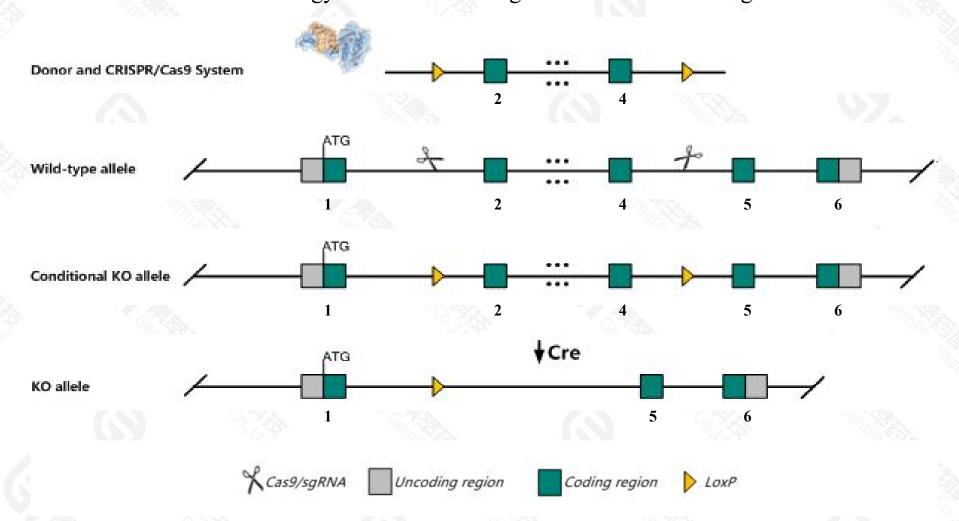
Project type Cas9-CKO

Strain background C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Dhrs3* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Dhrs3* gene has 7 transcripts. According to the structure of *Dhrs3* gene, exon2-exon4 of *Dhrs3*206(ENSMUST00000154208.8) transcript is recommended as the knockout region. The region contains 503bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Dhrs3* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor was constructed.Cas9, sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- > The flox mice was 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.

Notice



- > According to the existing MGI data, mice homozygous for a targeted mutation die before weaning age. Mice homozygous for a gene trap allele exhibit perinatal lethality, altered retinoid metabolism and heart, craniofacial and skeletal defects.
- > The *Dhrs3* gene is located on the Chr4. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes 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 existing technological level.

Gene information (NCBI)



Dhrs3 dehydrogenase/reductase (SDR family) member 3 [Mus musculus (house mouse)]

Gene ID: 20148, updated on 17-Dec-2020

Summary



Official Symbol Dhrs3 provided by MGI

Official Full Name dehydrogenase/reductase (SDR family) member 3 provided byMGI

Primary source MGI:MGI:1315215

See related Ensembl:ENSMUSG00000066026

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 Rs, Rsdr1, retS, retSDR1

Expression Broad expression in kidney adult (RPKM 53.4), bladder adult (RPKM 42.8) and 22 other tissuesSee more

Orthologs <u>human all</u>

Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

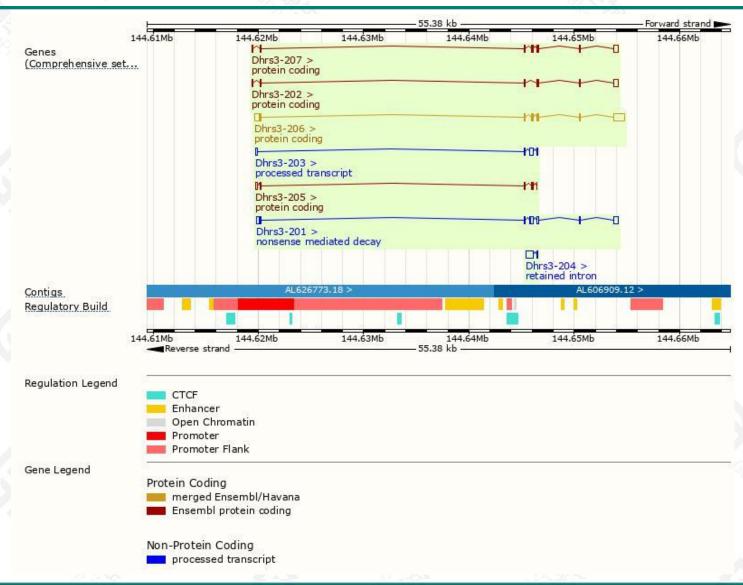
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dhrs3-206	ENSMUST00000154208.8	2337	302aa	Protein coding	CCDS18912		TSL:1 , GENCODE basic , APPRIS P1
Dhrs3-207	ENSMUST00000171001.8	1349	276aa	Protein coding	CCDS51368		TSL:5 , GENCODE basic ,
Dhrs3-202	ENSMUST00000105744.8	1226	236aa	Protein coding	29		TSL:1 , GENCODE basic ,
Dhrs3-205	ENSMUST00000142808.8	686	146aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Dhrs3-201	ENSMUST00000084184.7	1780	123aa	Nonsense mediated decay	2		TSL:1,
Dhrs3-203	ENSMUST00000128926.8	796	No protein	Processed transcript	-		TSL:3,
Dhrs3-204	ENSMUST00000133265.2	758	No protein	Retained intron			TSL:3,

The strategy is based on the design of *Dhrs3-206* transcript, the transcription is shown below:



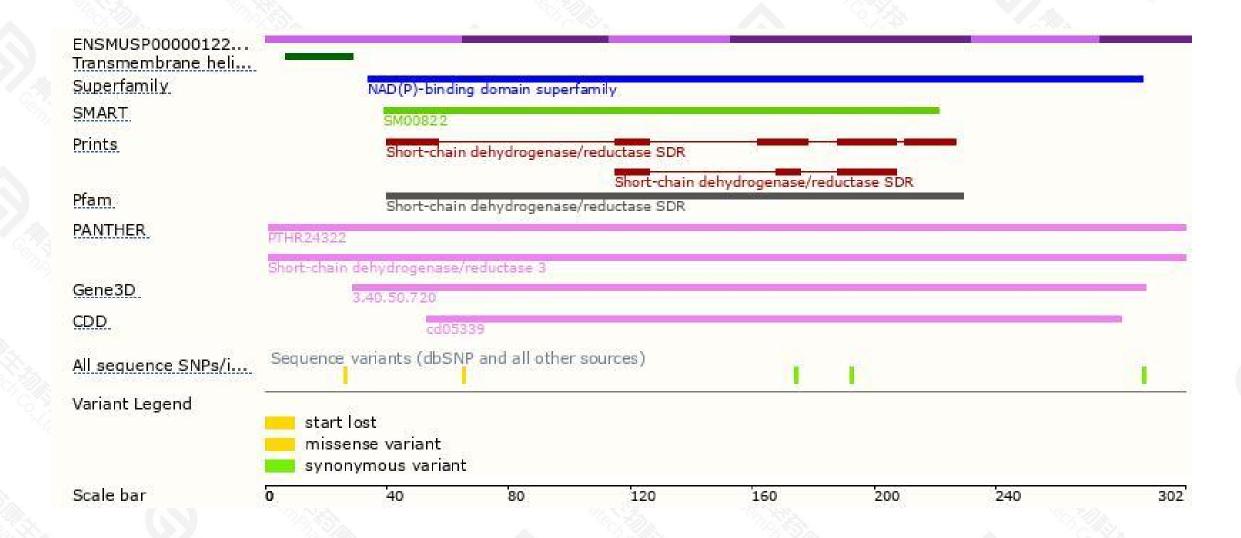
Genomic location distribution





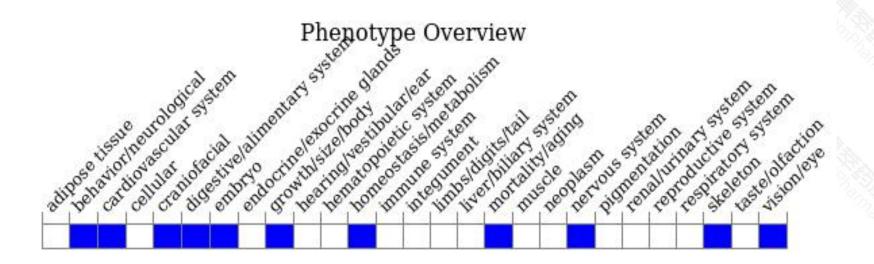
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, mice homozygous for a targeted mutation die before weaning age. Mice homozygous for a gene trap allele exhibit perinatal lethality, altered retinoid metabolism and heart, craniofacial and skeletal defects.



If you have any questions, you are welcome to inquire.

Tel: 025-5864 1534





