

Dclre1a Cas9-CKO Strategy

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Project Overview

Project Name

Dclre1a

Project type

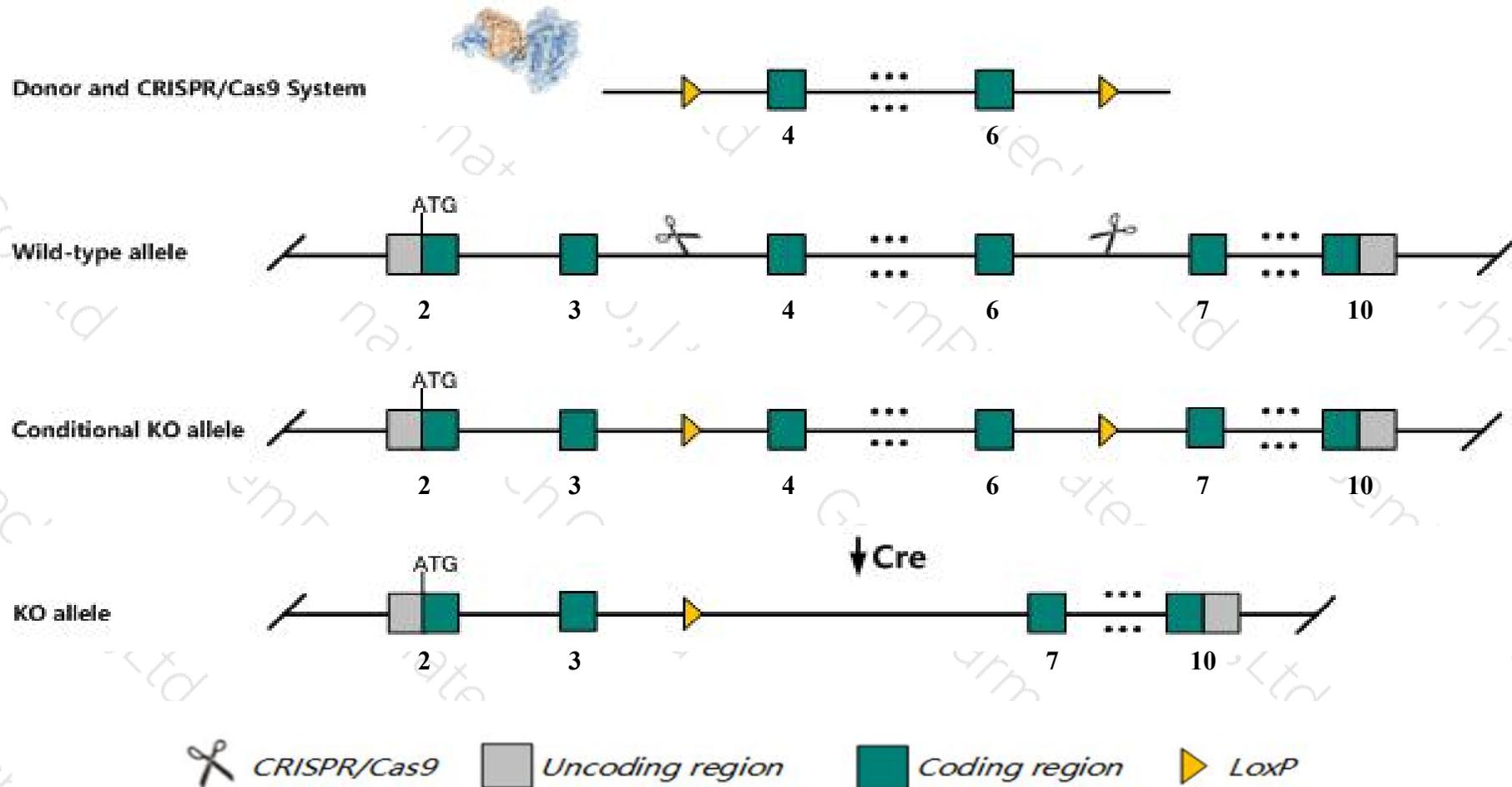
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Dclre1a* gene has 6 transcripts. According to the structure of *Dclre1a* gene, exon4-exon6 of *Dclre1a-204* (ENSMUST00000182276.1) transcript is recommended as the knockout region. The region contains 394bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dclre1a* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

- According to the existing MGI data, Mice homozygous for a targeted null mutation are viable and fertile but exhibit increased sensitivity to the DNA interstrand cross-linking agent mitomycin C.
- The *Dclrel1a* gene is located on the Chr19. 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)

Dclre1a DNA cross-link repair 1A [*Mus musculus* (house mouse)]

Gene ID: 55947, updated on 13-Mar-2020

Summary

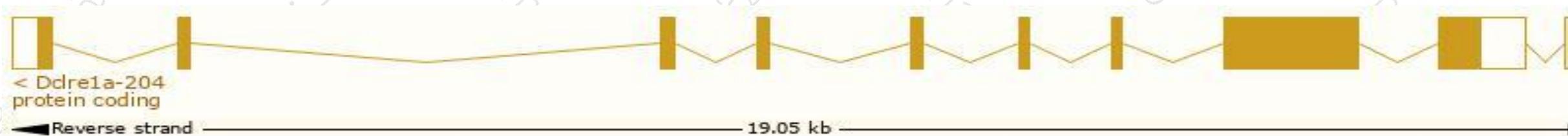
Official Symbol	Dclre1a provided by MGI
Official Full Name	DNA cross-link repair 1A provided by MGI
Primary source	MGI:MGI:1930042
See related	Ensembl:ENSMUSG00000025077
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Pso2; Snm1; Smn1a; AU022226; mKIAA0086; 2810043H12Rik
Expression	Ubiquitous expression in liver E14 (RPKM 4.9), liver E14.5 (RPKM 4.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

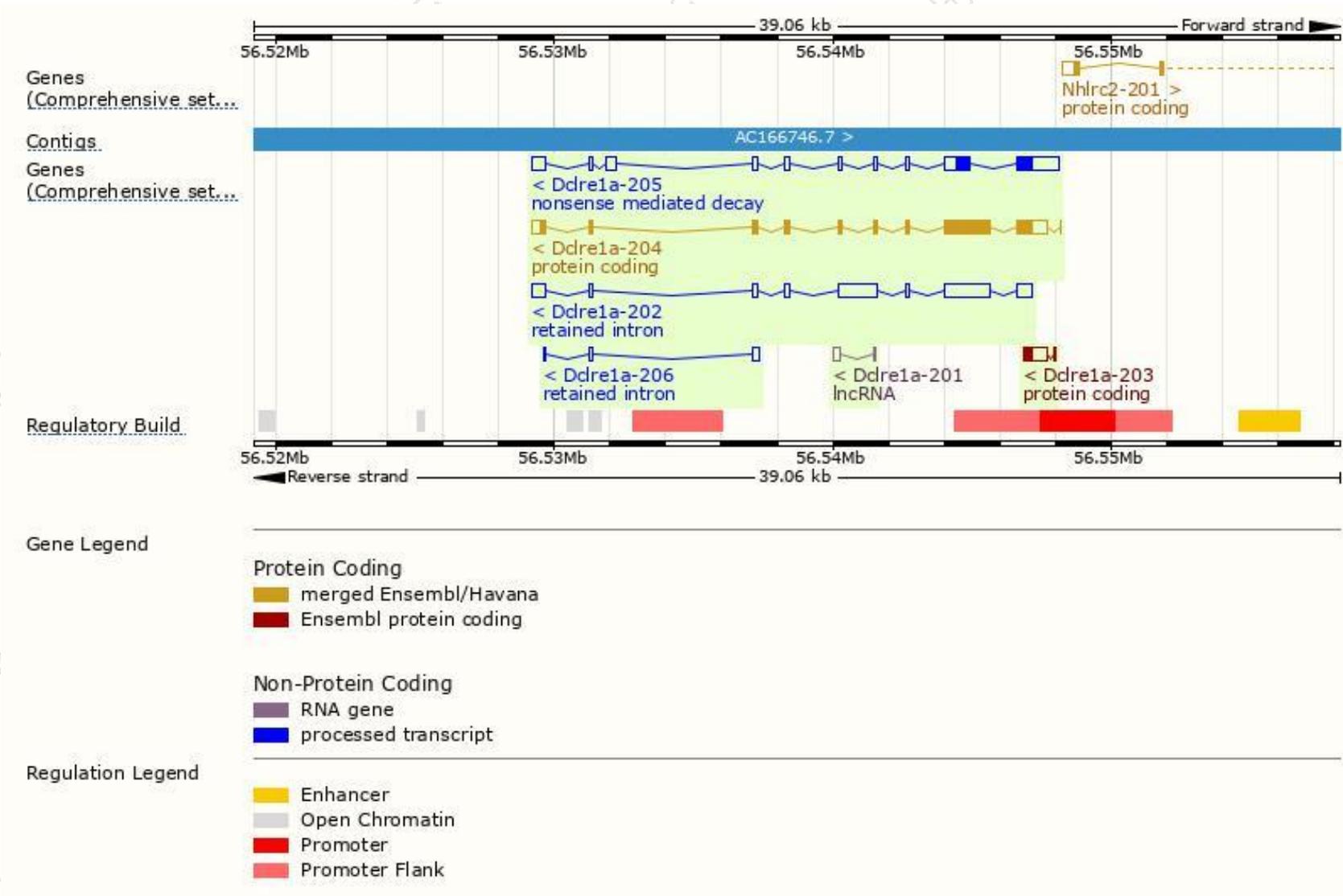
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dclre1a-204	ENSMUST00000182276.1	4066	1047aa	Protein coding	CCDS29917	S4R1N2	TSL:1 GENCODE basic APPRIS P1
Dclre1a-203	ENSMUST00000182059.1	899	97aa	Protein coding	-	S4R1T3	CDS 3' incomplete TSL:2
Dclre1a-205	ENSMUST00000183143.7	4156	314aa	Nonsense mediated decay	-	S4R284	TSL:1
Dclre1a-201	ENSMUST00000181992.1	322	No protein	Processed transcript	-	-	TSL:3
Dclre1a-202	ENSMUST00000182058.7	4664	No protein	Retained intron	-	-	TSL:2
Dclre1a-206	ENSMUST00000183216.1	478	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Dclre1a-204* transcript, The transcription is shown below



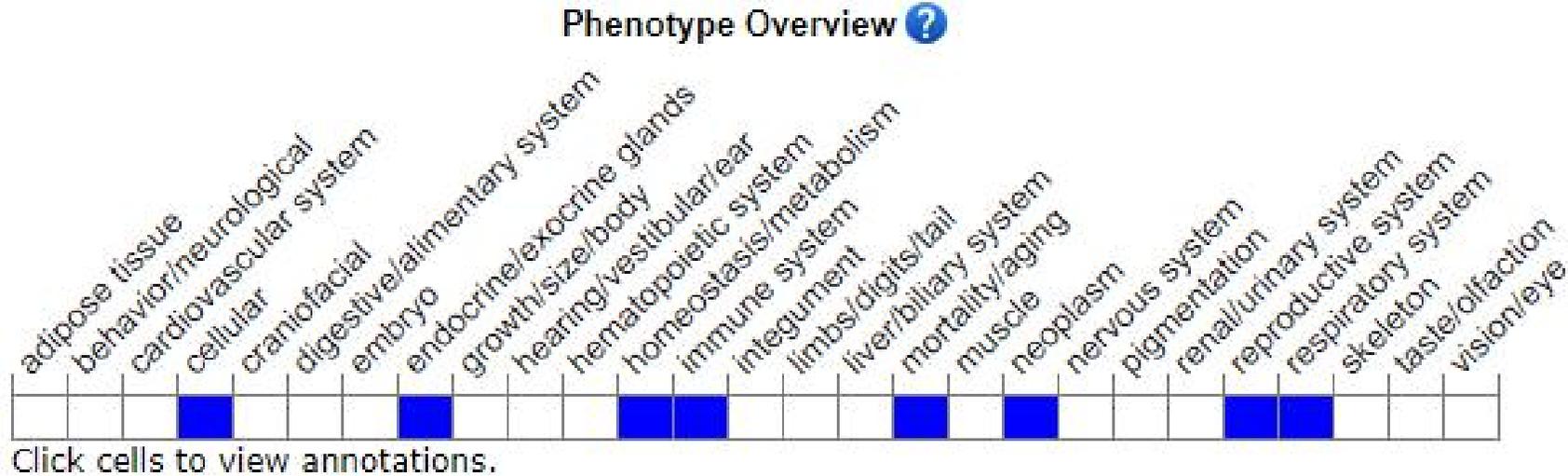
Genomic location distribution



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 null mutation are viable and fertile but exhibit increased sensitivity to the DNA interstrand cross-linking agent mitomycin C.

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

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