

Derl3 Cas9-KO Strategy

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Design Date: 2020-4-26

Project Overview

Project Name

Derl3

Project type

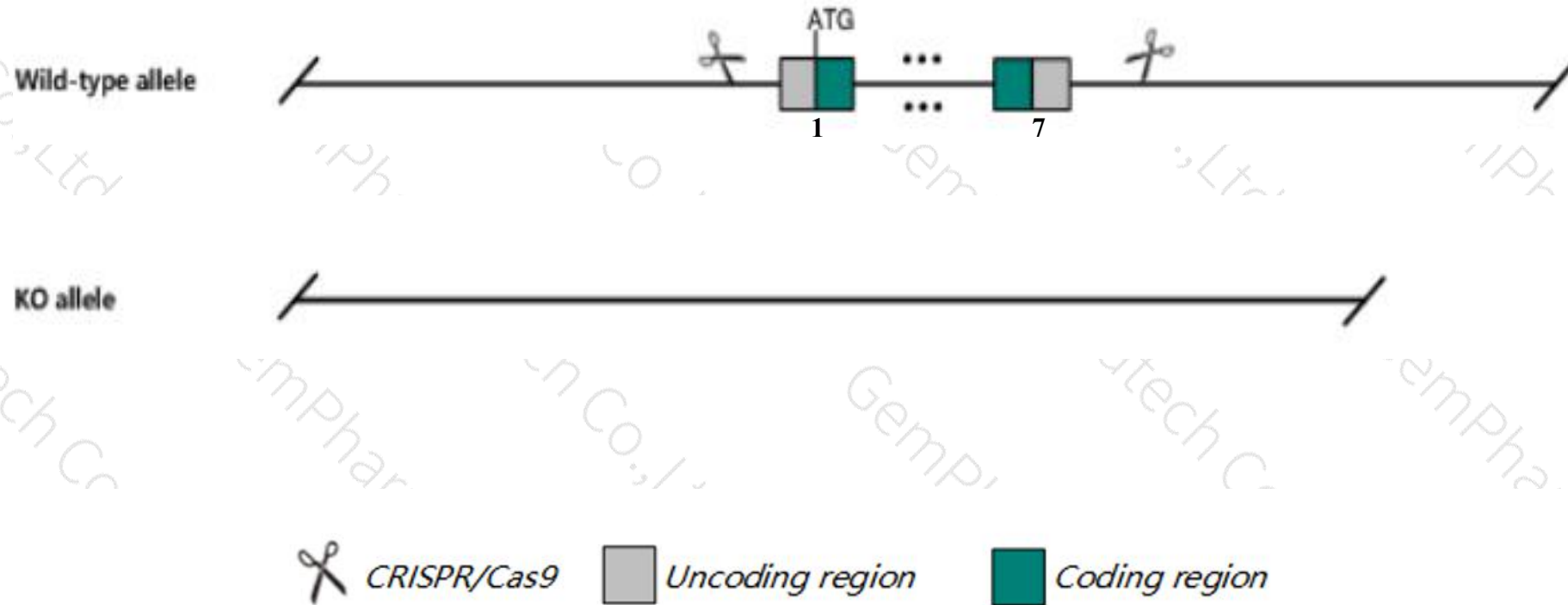
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Derl3* gene. The schematic diagram is as follows:



- The *Derl3* gene has 8 transcripts. According to the structure of *Derl3* gene, exon1-exon7 of *Derl3-201* (ENSMUST00000009236.5) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Derl3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for this gene trapped allele show no obvious phenotype alterations.
- The *Derl3* gene is located on the Chr10. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Derl3 Der1-like domain family, member 3 [Mus musculus (house mouse)]

Gene ID: 70377, updated on 13-Mar-2020

Summary



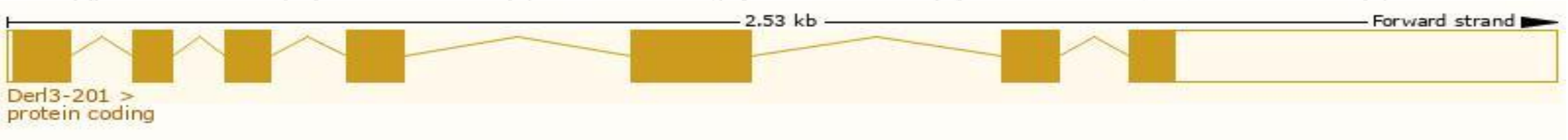
Official Symbol	Derl3 provided by MGI
Official Full Name	Der1-like domain family, member 3 provided by MGI
Primary source	MGI:MGI:1917627
See related	Ensembl:ENSMUSG000000009092
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810006I20Rik, 1810063P04Rik, IZP6, derlin-3
Expression	Biased expression in ovary adult (RPKM 82.9), genital fat pad adult (RPKM 42.8) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

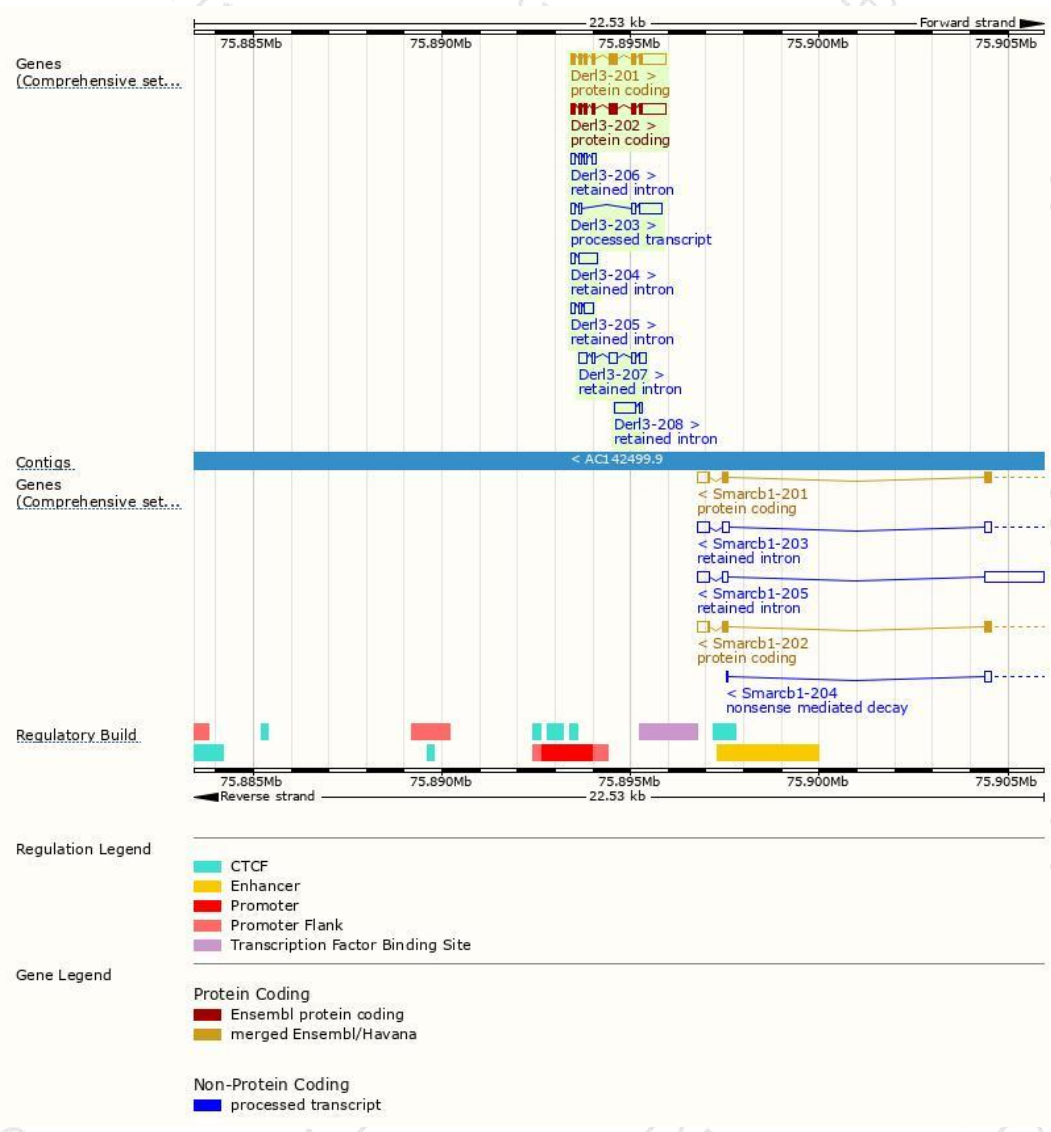
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Der13-201	ENSMUST0000009236.5	1321	228aa	Protein coding	CCDS23935	Q14C34_Q9D8K3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Der13-202	ENSMUST00000217811.1	1316	227aa	Protein coding	-	A0A1W2P7B5	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Der13-203	ENSMUST00000218506.1	815	No protein	Processed transcript	-	-	TSL:3
Der13-207	ENSMUST00000219994.1	774	No protein	Retained intron	-	-	TSL:3
Der13-208	ENSMUST00000220190.1	604	No protein	Retained intron	-	-	TSL:2
Der13-204	ENSMUST00000218718.1	579	No protein	Retained intron	-	-	TSL:3
Der13-205	ENSMUST00000218932.1	395	No protein	Retained intron	-	-	TSL:2
Der13-206	ENSMUST00000219568.1	362	No protein	Retained intron	-	-	TSL:2

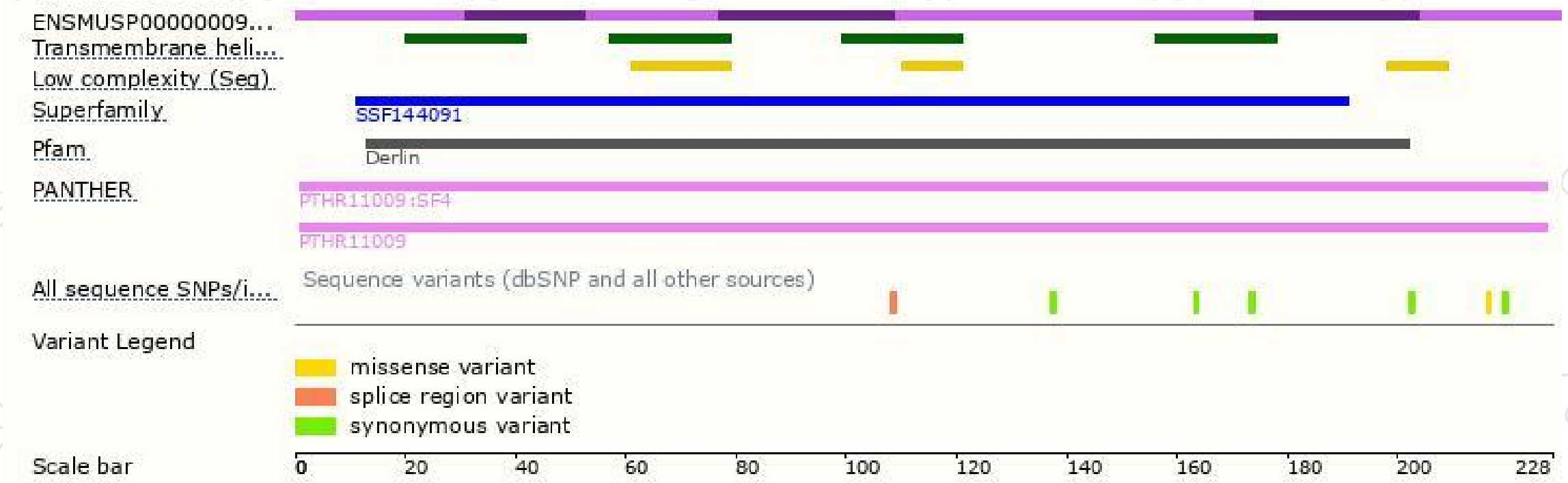
The strategy is based on the design of *Der13-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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