Decr1 Cas9-KO Strategy

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Reviewer: Shanhong Tao

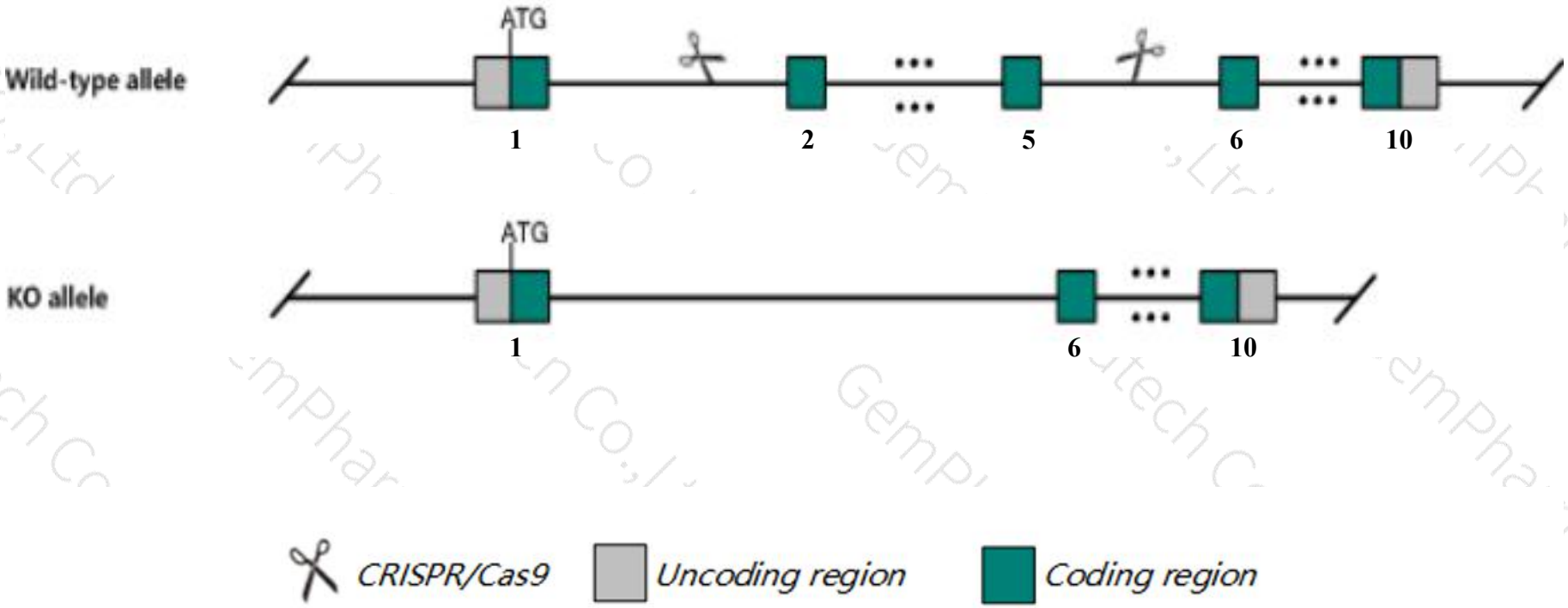
Design Date: 2020-8-4

Project Overview

Project Name	***Decr1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Decr1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Decr1* gene has 3 transcripts. According to the structure of *Decr1* gene, exon2-exon5 of *Decr1-201* (ENSMUST00000029877.8) transcript is recommended as the knockout region.The region contains 496bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Decr1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit increased sensitivity to fasting and cold stresses.
- The *Decr1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Decr1 2,4-dienoyl CoA reductase 1, mitochondrial [Mus musculus (house mouse)]

Gene ID: 67460, updated on 13-Mar-2020

Summary

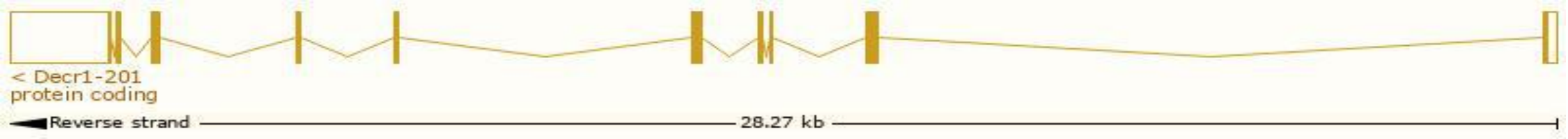
Official Symbol	Decr1 provided by MGI
Official Full Name	2,4-dienoyl CoA reductase 1, mitochondrial provided byMGI
Primary source	MGI:MGI:1914710
See related	Ensembl:ENSMUSG00000028223
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200012F07Rik, Decr, Nadph
Expression	Broad expression in heart adult (RPKM 41.1), liver E18 (RPKM 22.5) and 19 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

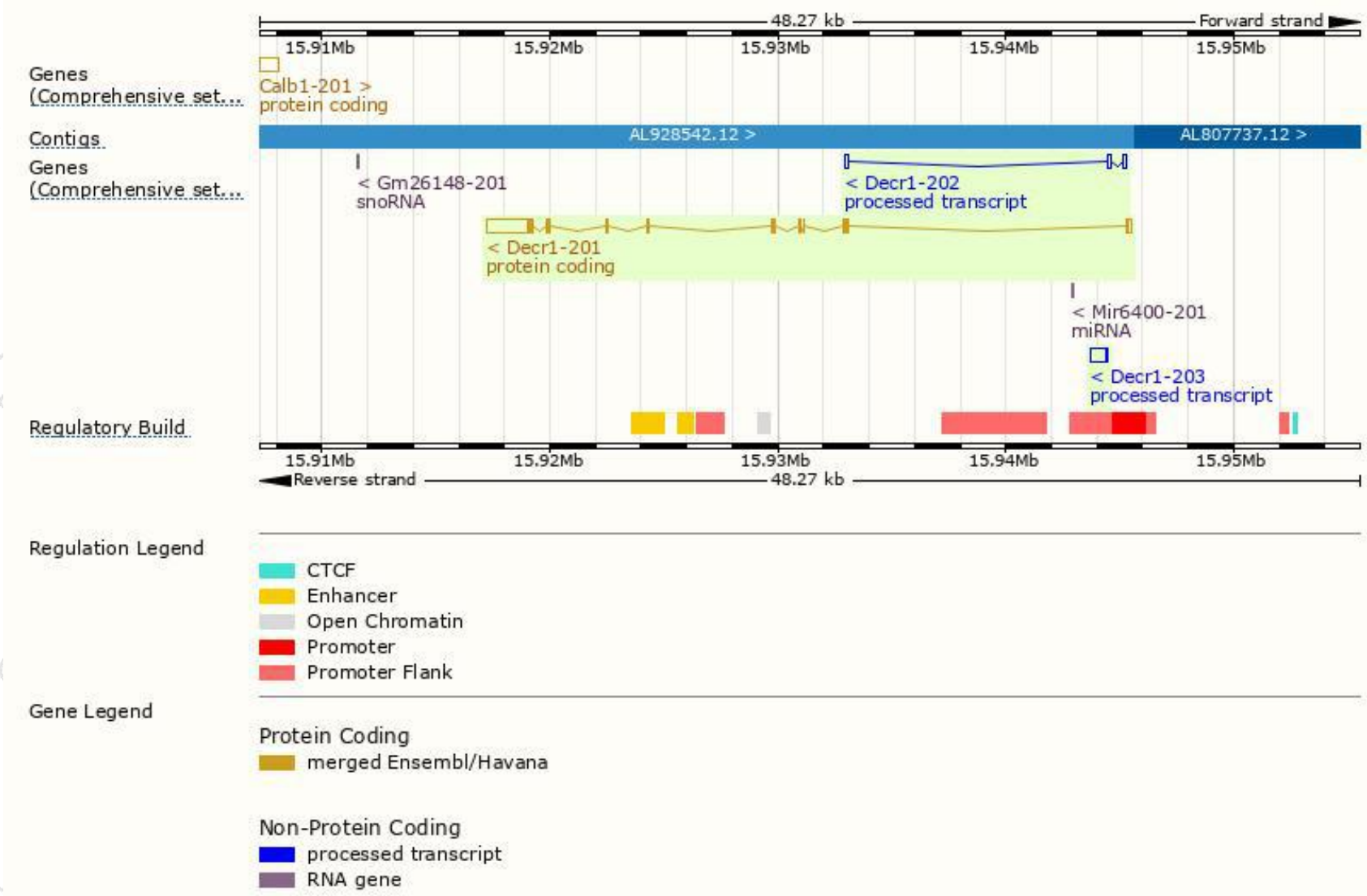
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Decr1-201	ENSMUST00000029877.8	2959	335aa	Protein coding	CCDS17985	Q4FJK0 Q9CQ62	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 P1
Decr1-203	ENSMUST00000154639.1	700	No protein	Processed transcript	-	-	TSL:3
Decr1-202	ENSMUST00000150464.1	366	No protein	Processed transcript	-	-	TSL:3

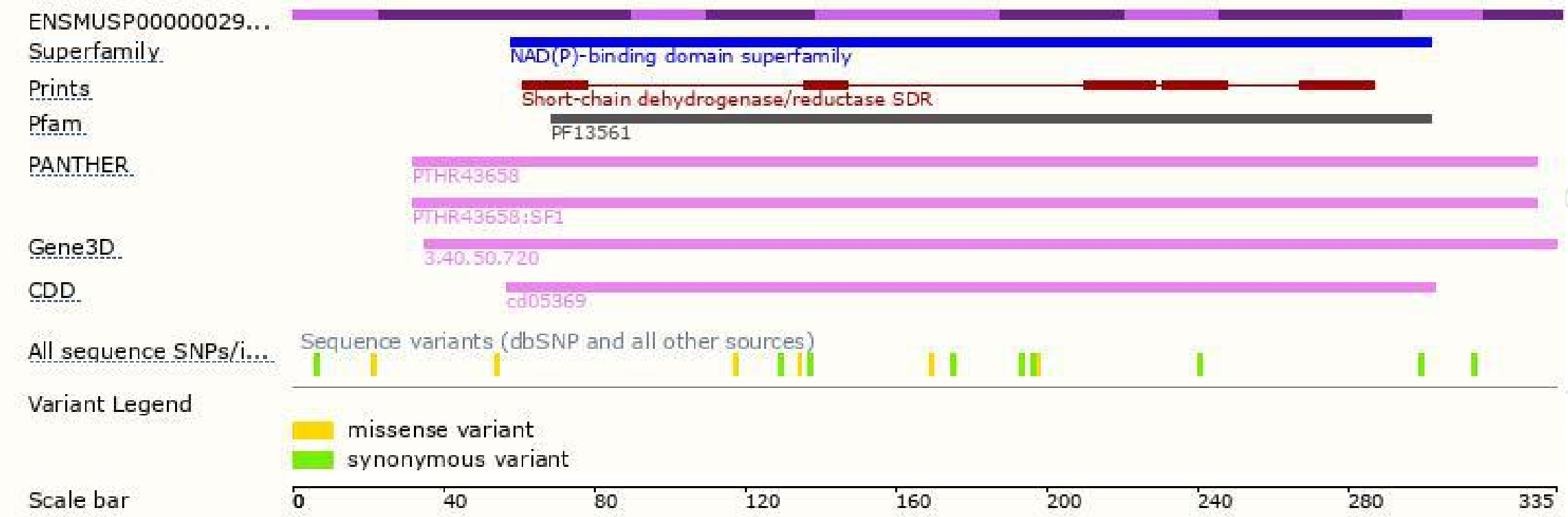
The strategy is based on the design of *Decr1-201* transcript,the transcription is shown below:



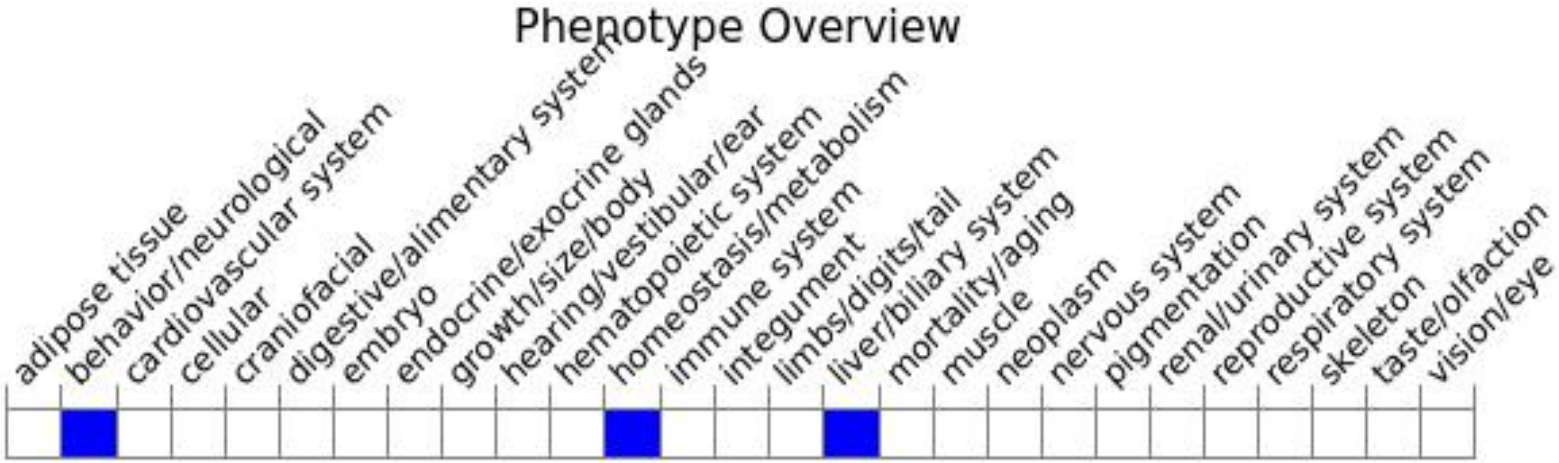
Genomic location distribution



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 null allele exhibit increased sensitivity to fasting and cold stresses.

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

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