Dad1 Cas9-KO Strategy

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Reviewer: Yanhua Shen

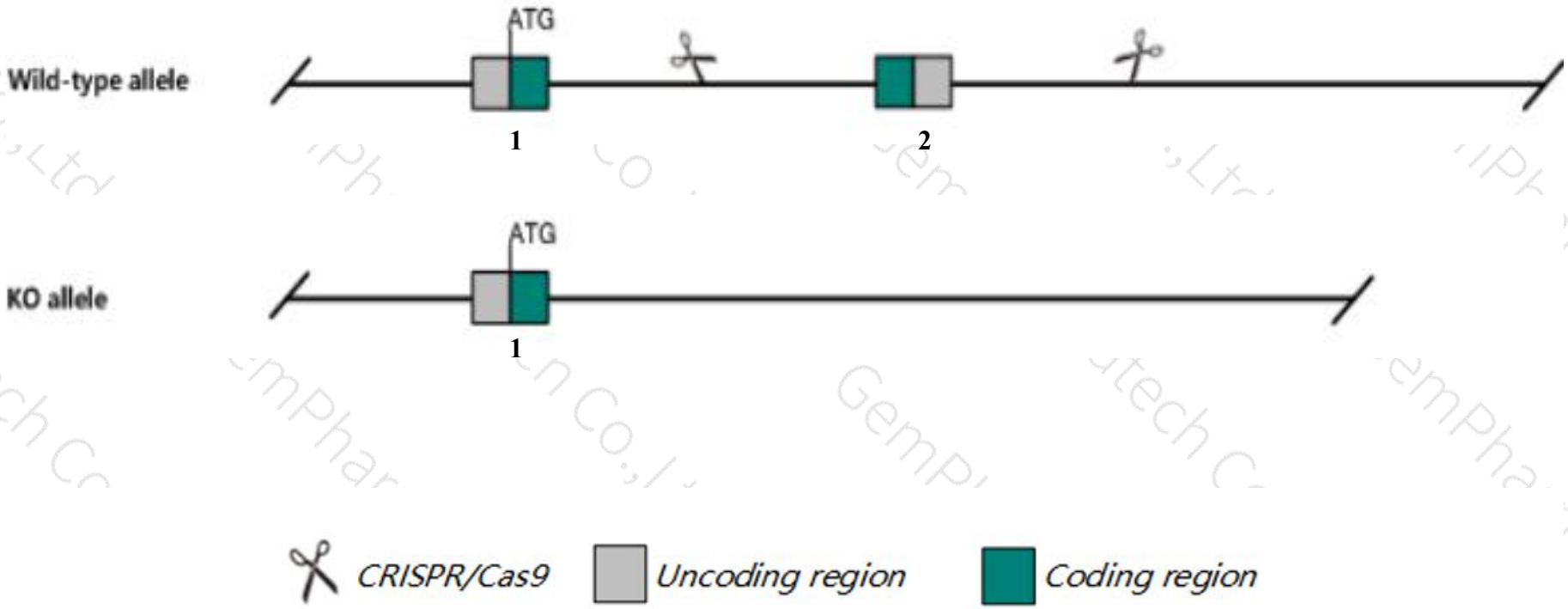
Design Date: 2020-4-14

Project Overview

Project Name	***Dad1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dad1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Dad1* gene has 2 transcripts. According to the structure of *Dad1* gene, exon2 of *Dad1-201* (ENSMUST00000022781.7) transcript is recommended as the knockout region.The region contains most 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 *Dad1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,homozygous null mice display fully penetrant embryonic lethality before somite formation and impaired growth. Heterozygous null mice display incompletely penetrant embryonic lethality, impaired embryonic growth, syndactyly, and mild thymic hypoplasia.
- ➢ The N-terminal of *Dad1* gene will remain several amino acids ,it may remain the partial function of *Dad1* gene.
- The *Dad1* gene is located on the Chr14. 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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Dad1 defender against cell death 1 [Mus musculus (house mouse)]

Gene ID: 13135, updated on 13-Mar-2020

Summary

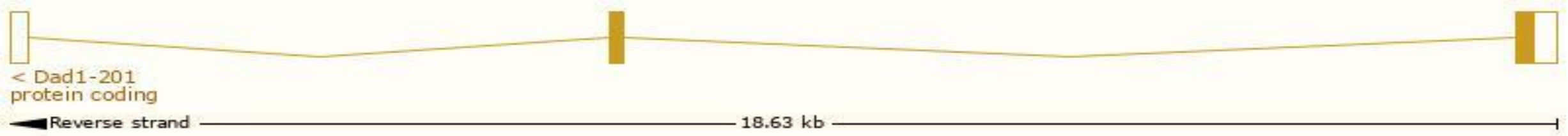
Official Symbol	Dad1 provided by MGI
Official Full Name	defender against cell death 1 provided by MGI
Primary source	MGI:MGI:101912
See related	Ensembl:ENSMUSG00000022174
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323713
Expression	Ubiquitous expression in adrenal adult (RPKM 143.6), duodenum adult (RPKM 96.9) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

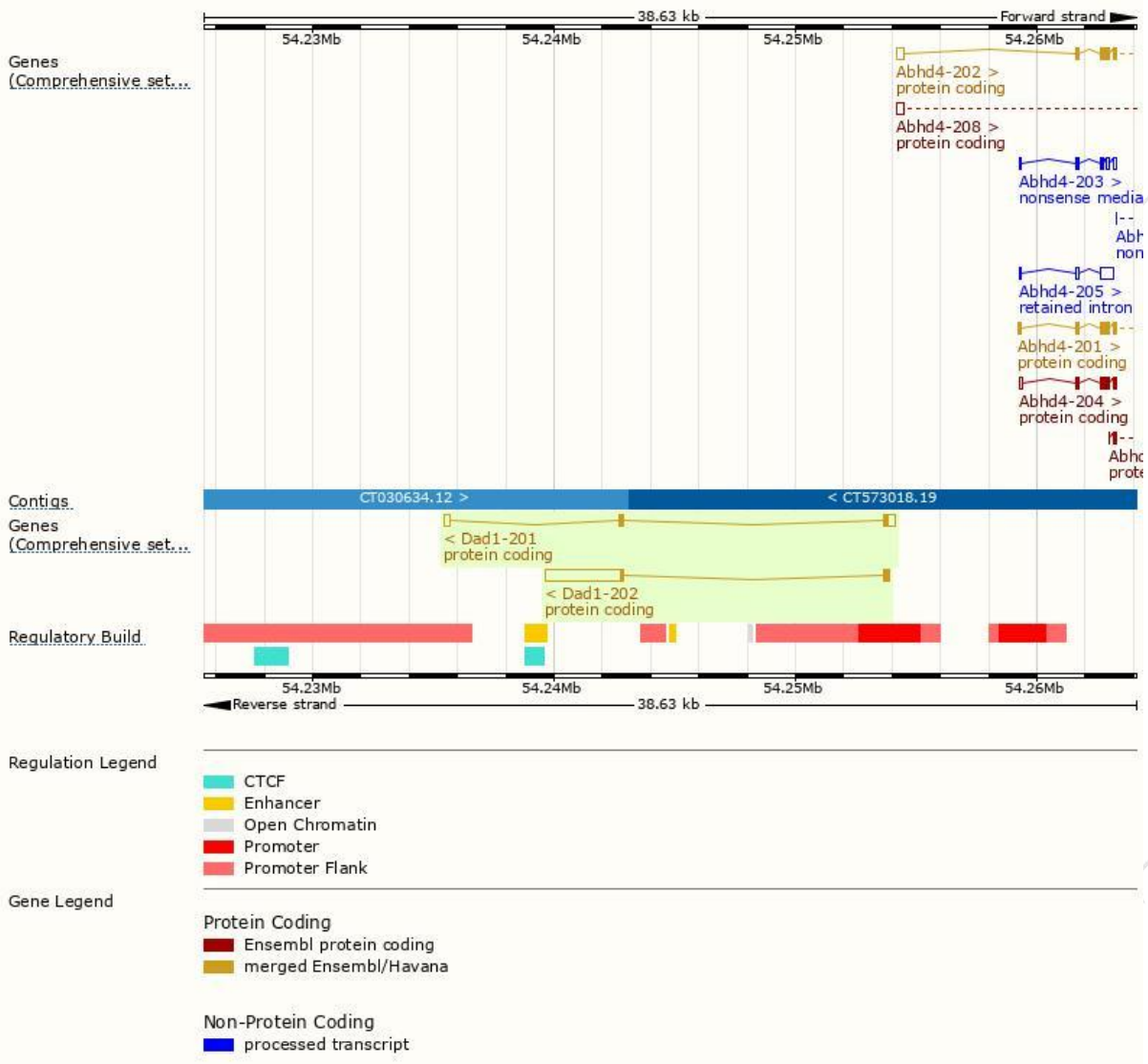
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dad1-202	ENSMUST00000128231.1	3491	113aa	Protein coding	CCDS27084	P61804	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
Dad1-201	ENSMUST00000022781.7	878	113aa	Protein coding	CCDS27084	P61804	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

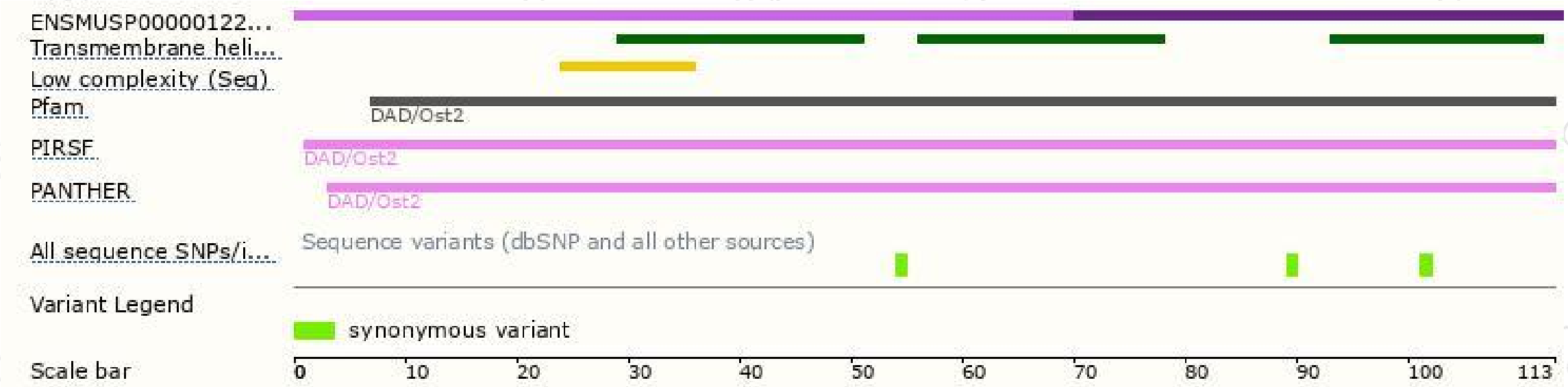
The strategy is based on the design of *Dad1-201* transcript,the transcription is shown below



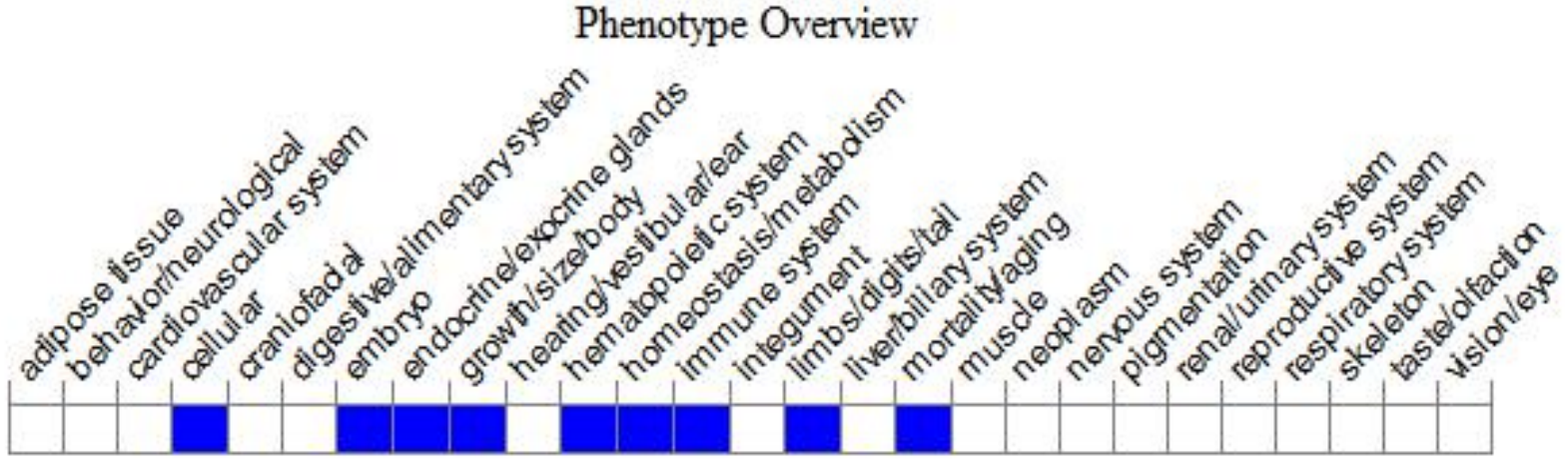
Genomic location distribution



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/).

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

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