

Cdc42ep1 Cas9-KO Strategy

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Project Overview

Project Name

Cdc42ep1

Project type

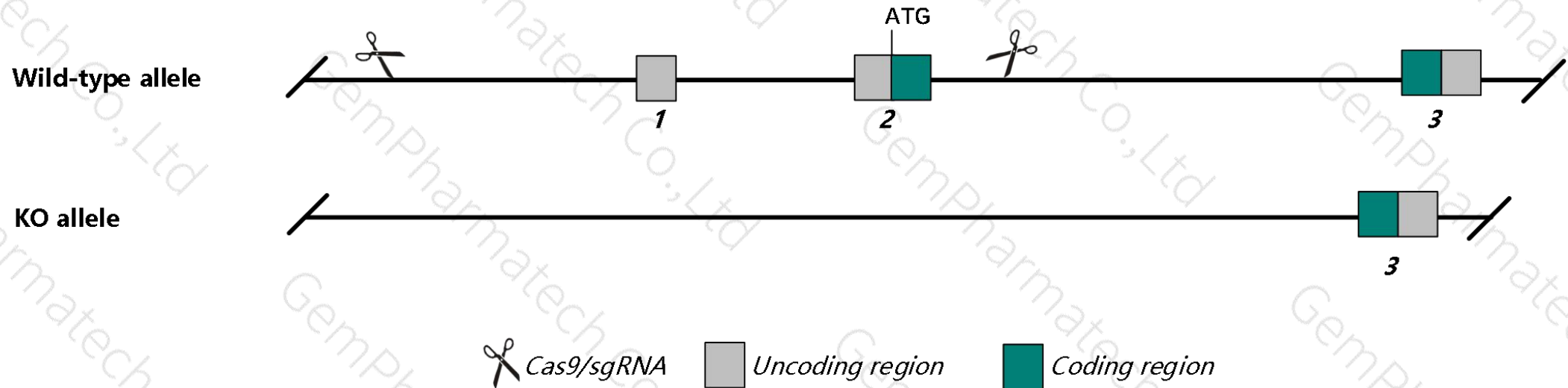
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cdc42ep1* gene. The schematic diagram is as follows:



- The *Cdc42ep1* gene has 1 transcript. According to the structure of *Cdc42ep1* gene, exon1-exon2 of *Cdc42ep1-201* (ENSMUST00000059619.2) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cdc42ep1* gene. The brief process is as follows: CRISPR/Cas9 sys

- The *Cdc42ep1* gene is located on the Chr15. 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)

Cdc42ep1 CDC42 effector protein (Rho GTPase binding) 1 [Mus musculus (house mouse)]

Gene ID: 104445, updated on 13-Mar-2020

Summary



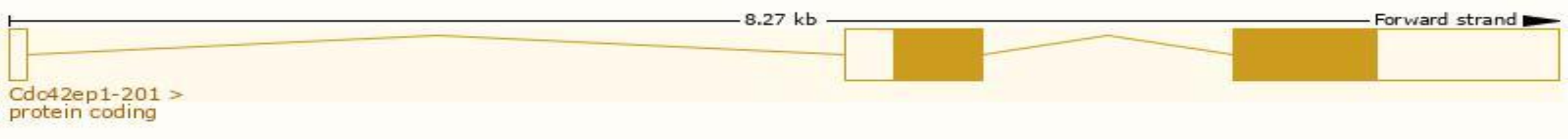
Official Symbol	Cdc42ep1 provided by MGI
Official Full Name	CDC42 effector protein (Rho GTPase binding) 1 provided by MGI
Primary source	MGI:MGI:1929763
See related	Ensembl:ENSMUSG00000049521
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810058K22Rik, AA980734, Borg5, CEP1, MSE55
Expression	Broad expression in lung adult (RPKM 172.0), subcutaneous fat pad adult (RPKM 83.5) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

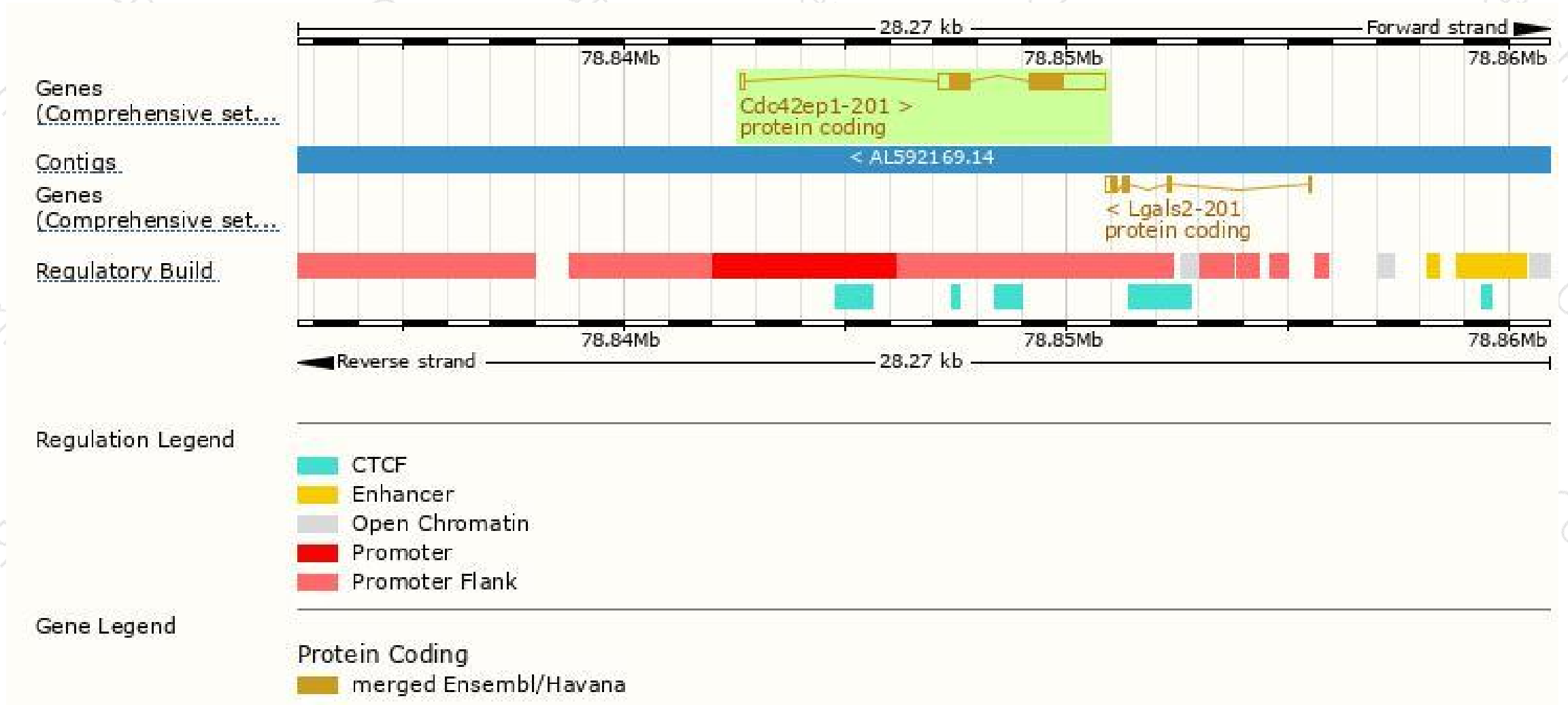
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cdc42ep1-201	ENSMUST00000059619.2	2560	409aa	Protein coding	CCDS27624	A0A0R4J0S1	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

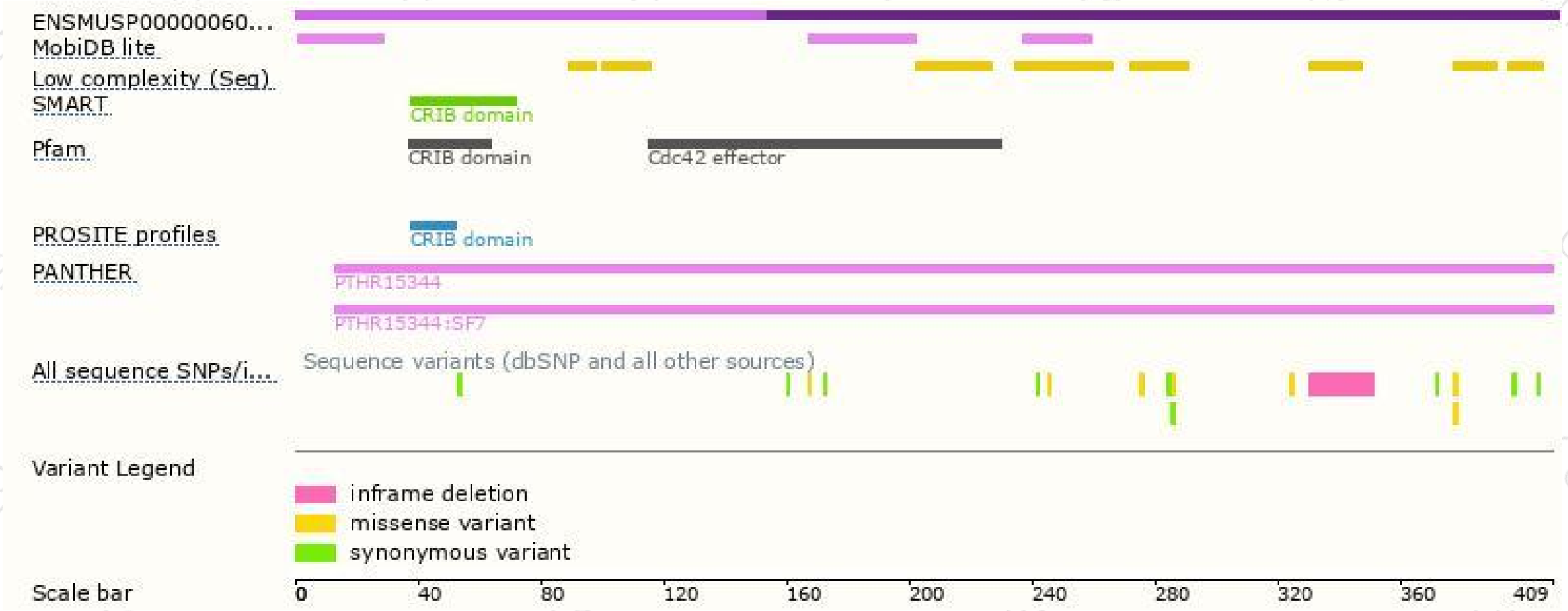
The strategy is based on the design of *Cdc42ep1-201* transcript, The transcription is shown below



Genomic location distribution



Protein domain



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

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