

Cfap52 Cas9-KO Strategy

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Project Overview

Project Name

Cfap52

Project type

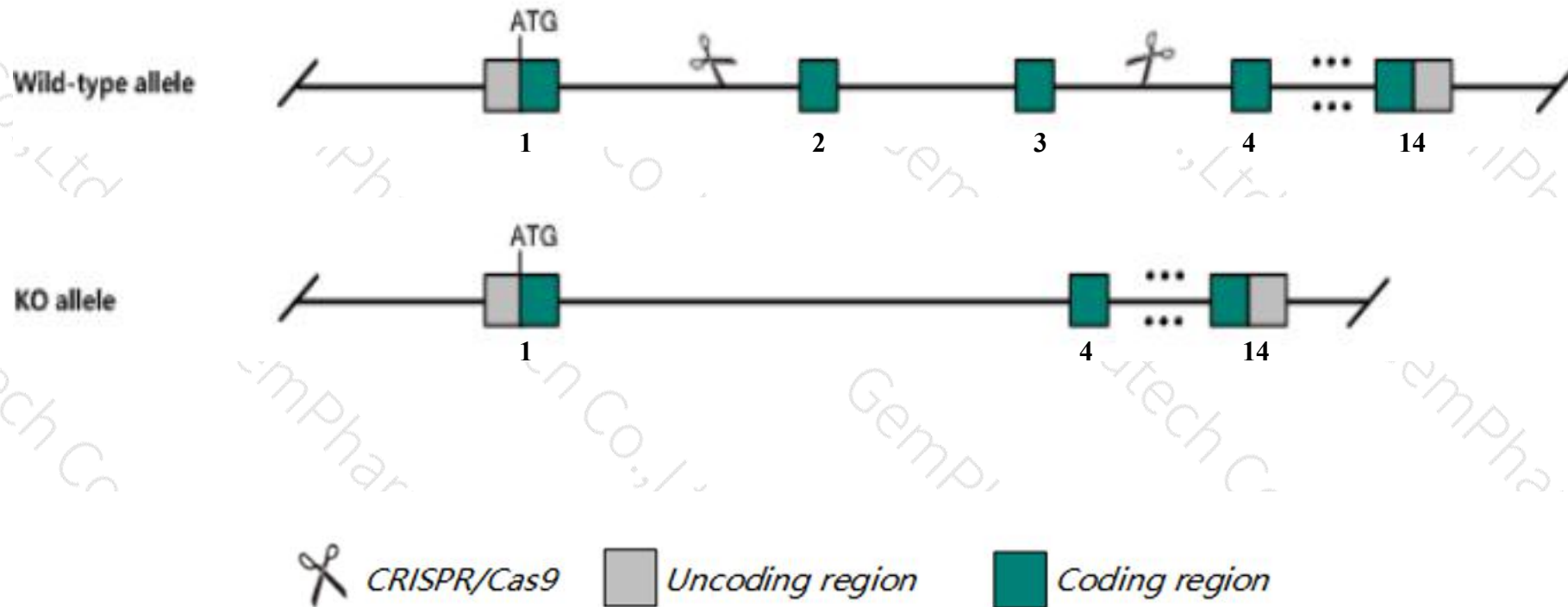
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cfap52* gene. The schematic diagram is as follows:



- The *Cfap52* gene has 4 transcripts. According to the structure of *Cfap52* gene, exon2-exon3 of *Cfap52-201* (ENSMUST00000021287.11) transcript is recommended as the knockout region. The region contains 337bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cfap52* gene. The brief process is as follows: CRISPR/Cas9 system w

- Transcripts 202,204 may not be affected.
- The *Cfap52* gene is located on the Chr11. 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)

Cfap52 cilia and flagella associated protein 52 [Mus musculus (house mouse)]

Gene ID: 71860, updated on 13-Mar-2020

Summary



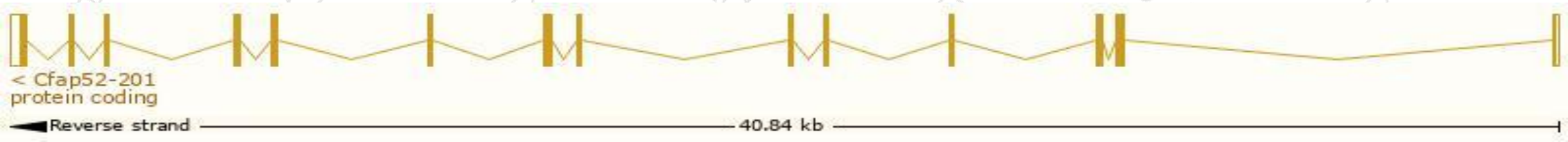
Official Symbol	Cfap52 provided by MGI
Official Full Name	cilia and flagella associated protein 52 provided by MGI
Primary source	MGI:MGI:1919110
See related	Ensembl:ENSMUSG00000020904
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700019F09Rik, 4933417B11Rik, WDRPUH, Wdr16
Expression	Biased expression in testis adult (RPKM 26.6), lung adult (RPKM 1.9) and 2 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

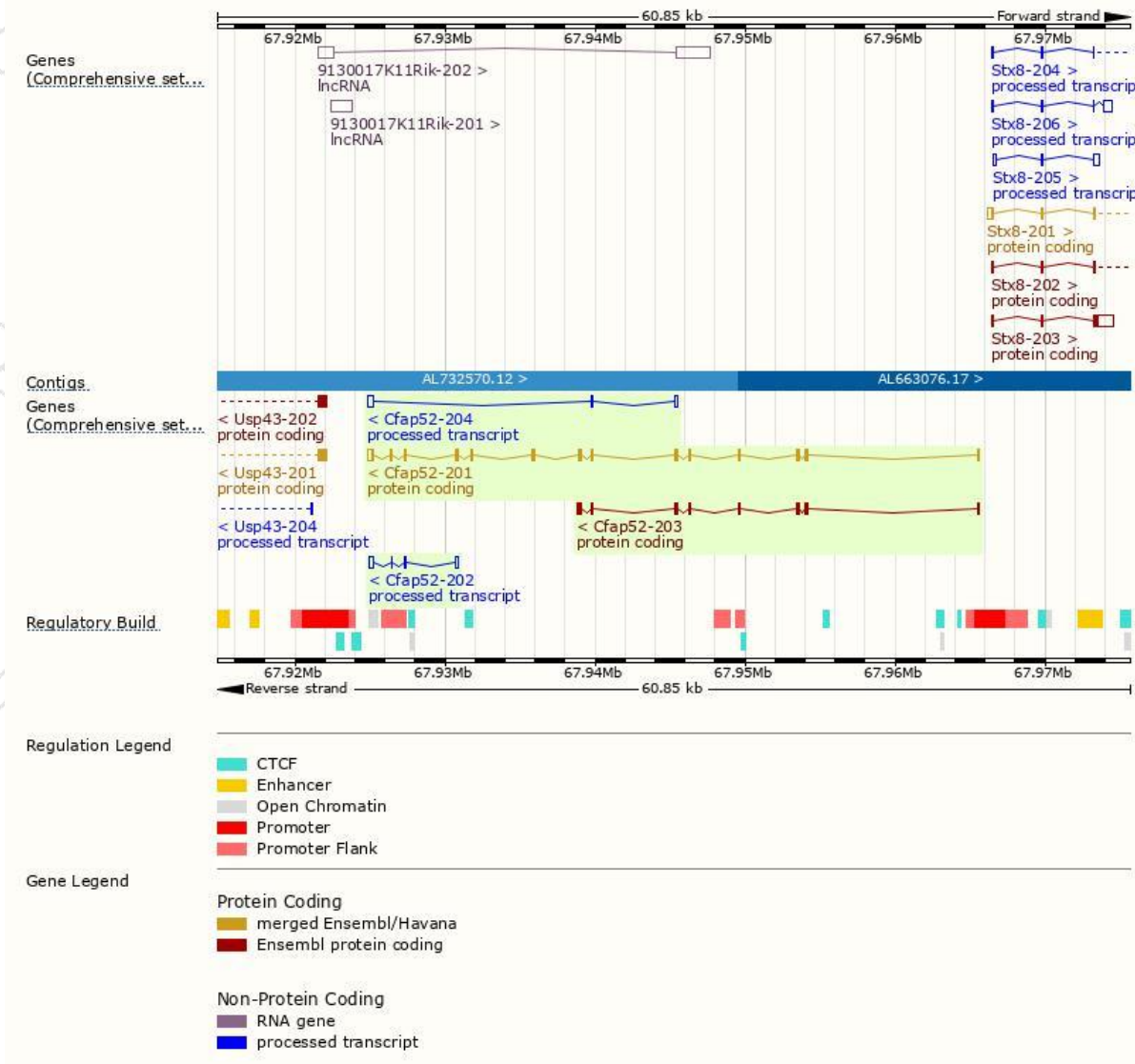
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cfap52-201	ENSMUST00000021287.1	2199	620aa	Protein coding	CCDS24862	Q147Z1 Q5F201	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
Cfap52-203	ENSMUST00000126766.1	1195	342aa	Protein coding	-	Q5F201	TSL:1
Cfap52-204	ENSMUST00000142929.1	637	No protein	Processed transcript	-	-	TSL:5
Cfap52-202	ENSMUST00000123900.1	629	No protein	Processed transcript	-	-	TSL:3

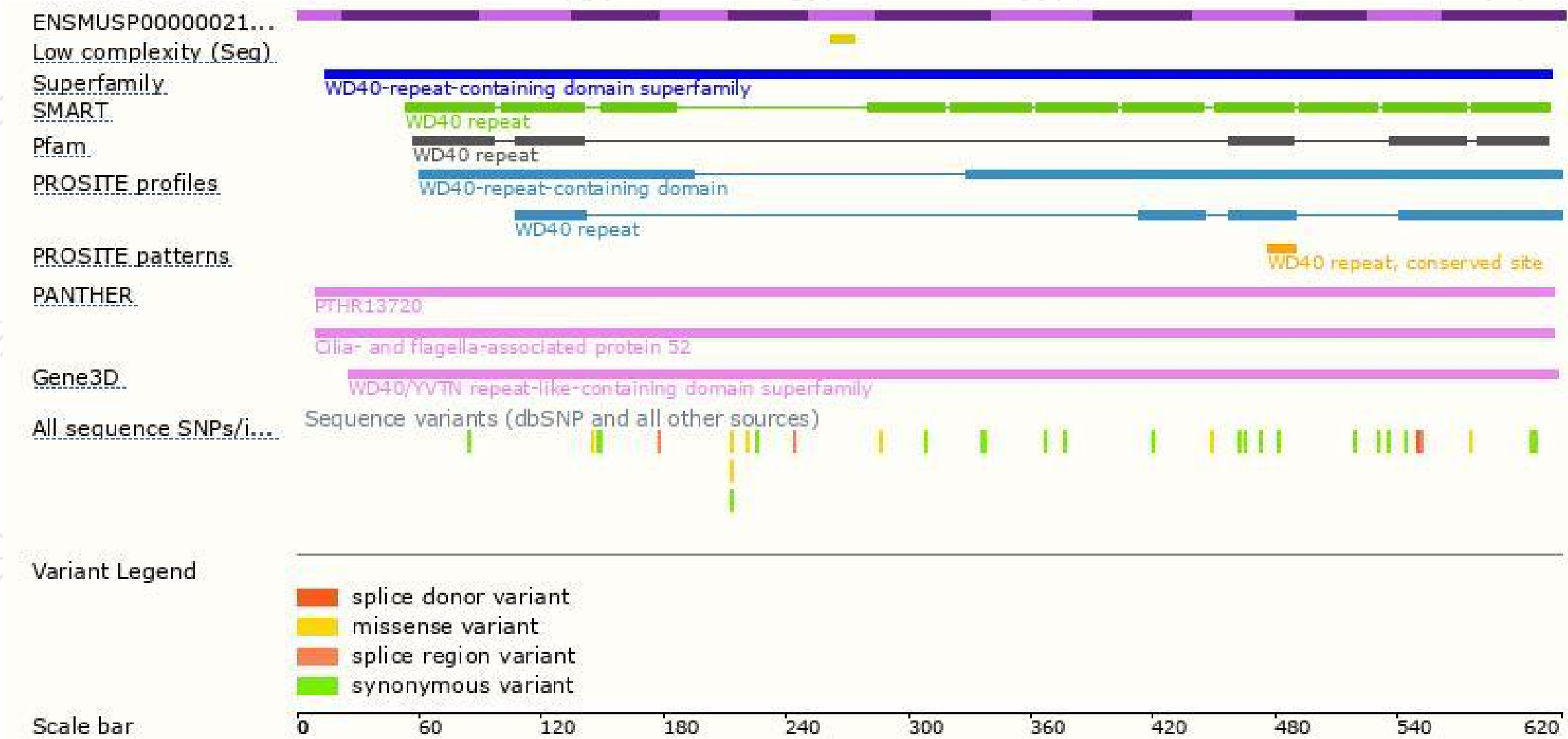
The strategy is based on the design of *Cfap52-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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