

Fap Cas9-KO Strategy

Designer: Huan Wang

Reviewer: Lingyan Wu

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Project Overview

Project Name

Fap

Project type

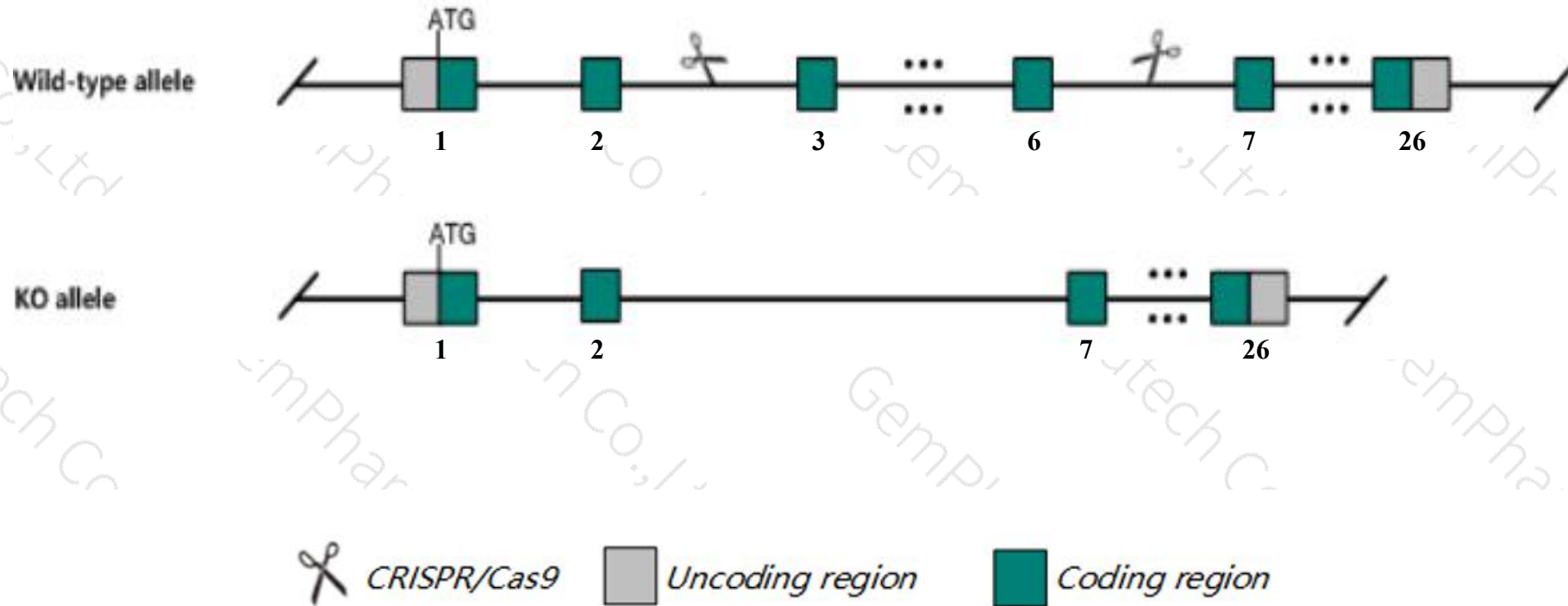
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Fap* gene has 9 transcripts. According to the structure of *Fap* gene, exon3-exon6 of *Fap*-202(ENSMUST00000102732.9) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fap* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, mice homozygous for a targeted null mutations exhibit no discernable phenotype; mice are viable and fertile with no change in cancer susceptibility.
- The *Fap* gene is located on the Chr2. 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)

Fap fibroblast activation protein [Mus musculus (house mouse)]

Gene ID: 14089, updated on 13-Mar-2020

Summary

Official Symbol Fap provided by [MGI](#)

Official Full Name fibroblast activation protein provided by [MGI](#)

Primary source [MGI:MGI:109608](#)

See related [Ensembl:ENSMUSG00000000392](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as SIMP

Summary This gene belongs to the serine protease family. The encoded protein is an inducible cell-surface bound glycoprotein specifically expressed in tumor-associated fibroblasts and pericytes of epithelial tumors and has protease and gelatinase activity. The protein plays a role in remodeling of the extracellular matrix (ECM) and may affect tumorigenesis and tissue repair. Alternately spliced transcript variants of this gene are described in the literature (PMID 9139873), but the full-length sequence of these variants is not available. [provided by RefSeq, Apr 2013]

Expression Biased expression in limb E14.5 (RPKM 7.4), mammary gland adult (RPKM 2.8) and 9 other tissues [See more](#)

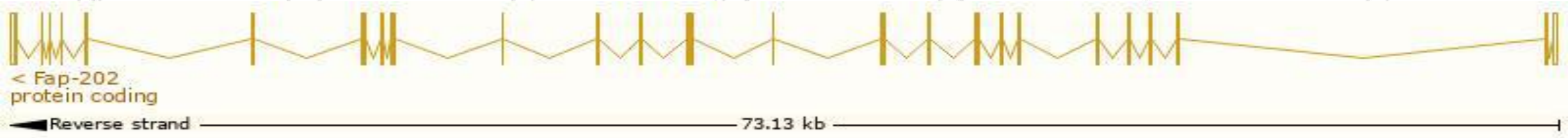
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

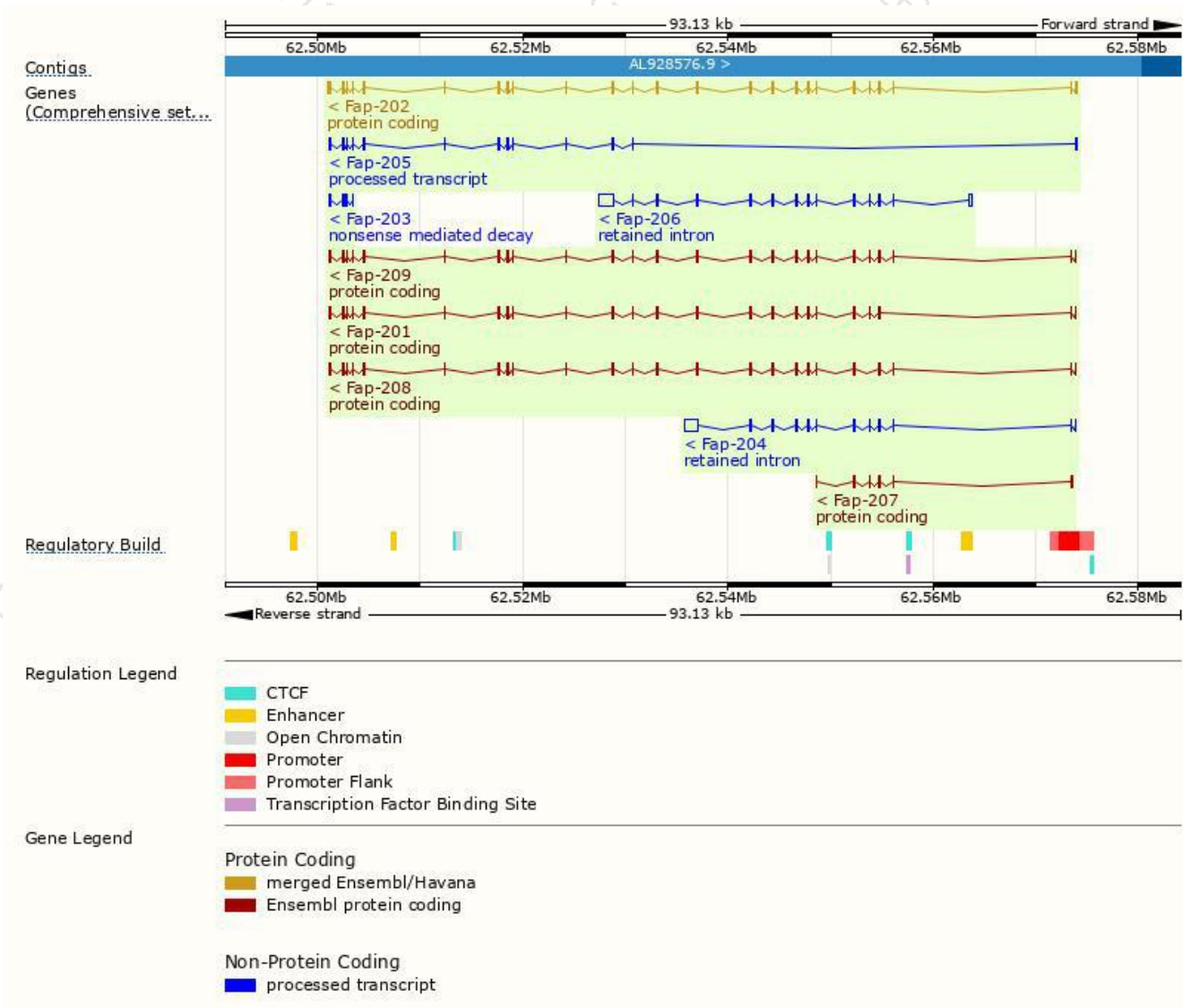
The gene has 9 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|---|
| Fap-202 | ENSMUST00000102732.9 | 2751 | 761aa | Protein coding | CCDS16067 | P97321 | 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 |
| Fap-209 | ENSMUST00000174448.7 | 2271 | 756aa | Protein coding | - | P97321 | TSL:5 GENCODE basic |
| Fap-208 | ENSMUST00000174234.7 | 2211 | 736aa | Protein coding | - | G3UXR2 | TSL:5 GENCODE basic |
| Fap-201 | ENSMUST00000000402.15 | 2187 | 728aa | Protein coding | - | P97321 | TSL:5 GENCODE basic |
| Fap-207 | ENSMUST00000173745.1 | 503 | 63aa | Protein coding | - | G3UZ14 | CDS 3' incomplete TSL:3 |
| Fap-203 | ENSMUST00000128139.2 | 467 | 47aa | Nonsense mediated decay | - | G3UYG3 | CDS 5' incomplete TSL:5 |
| Fap-205 | ENSMUST00000152085.8 | 1269 | No protein | Processed transcript | - | - | TSL:5 |
| Fap-206 | ENSMUST00000172676.7 | 2867 | No protein | Retained intron | - | - | TSL:1 |
| Fap-204 | ENSMUST00000136297.7 | 2343 | No protein | Retained intron | - | - | TSL:1 |

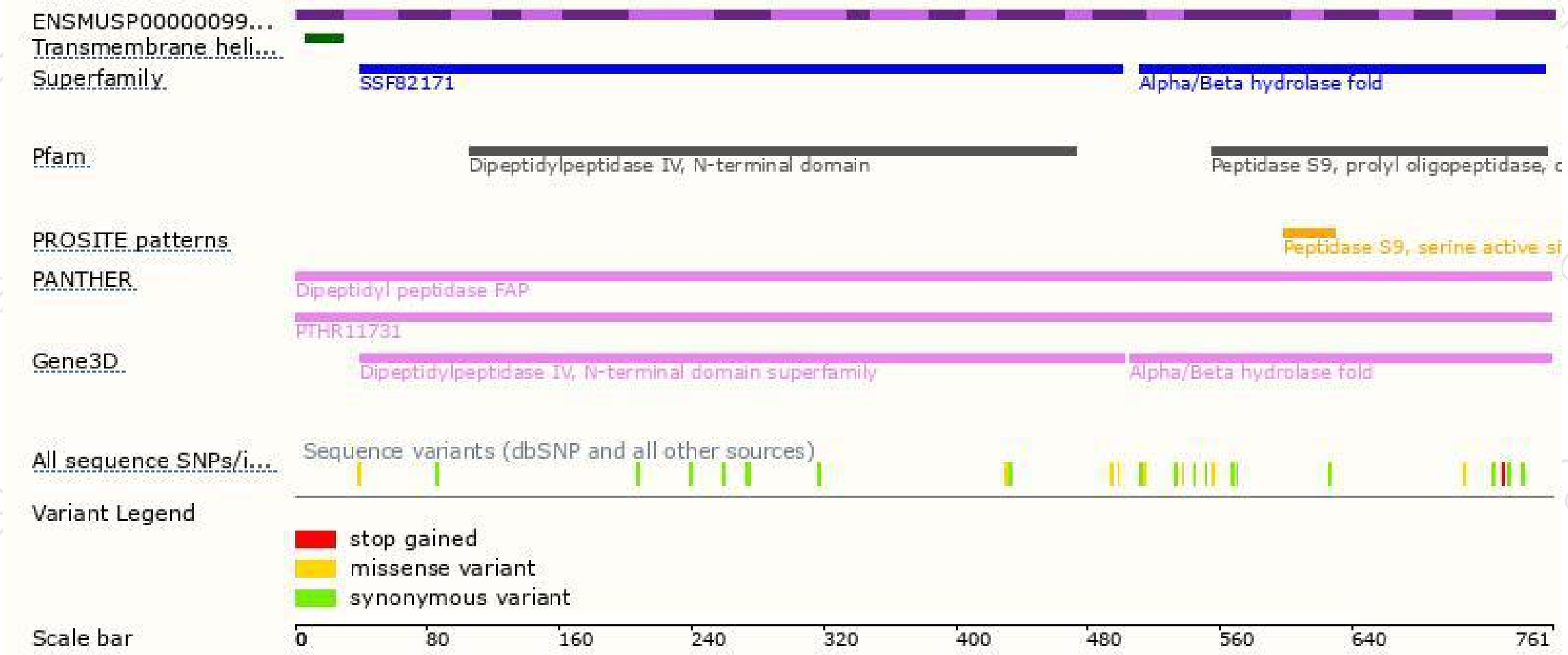
The strategy is based on the design of *Fap-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

