

Fap Cas9-CKO Strategy

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Design Date: 2020-7-2

Project Overview

Project Name

Fap

Project type

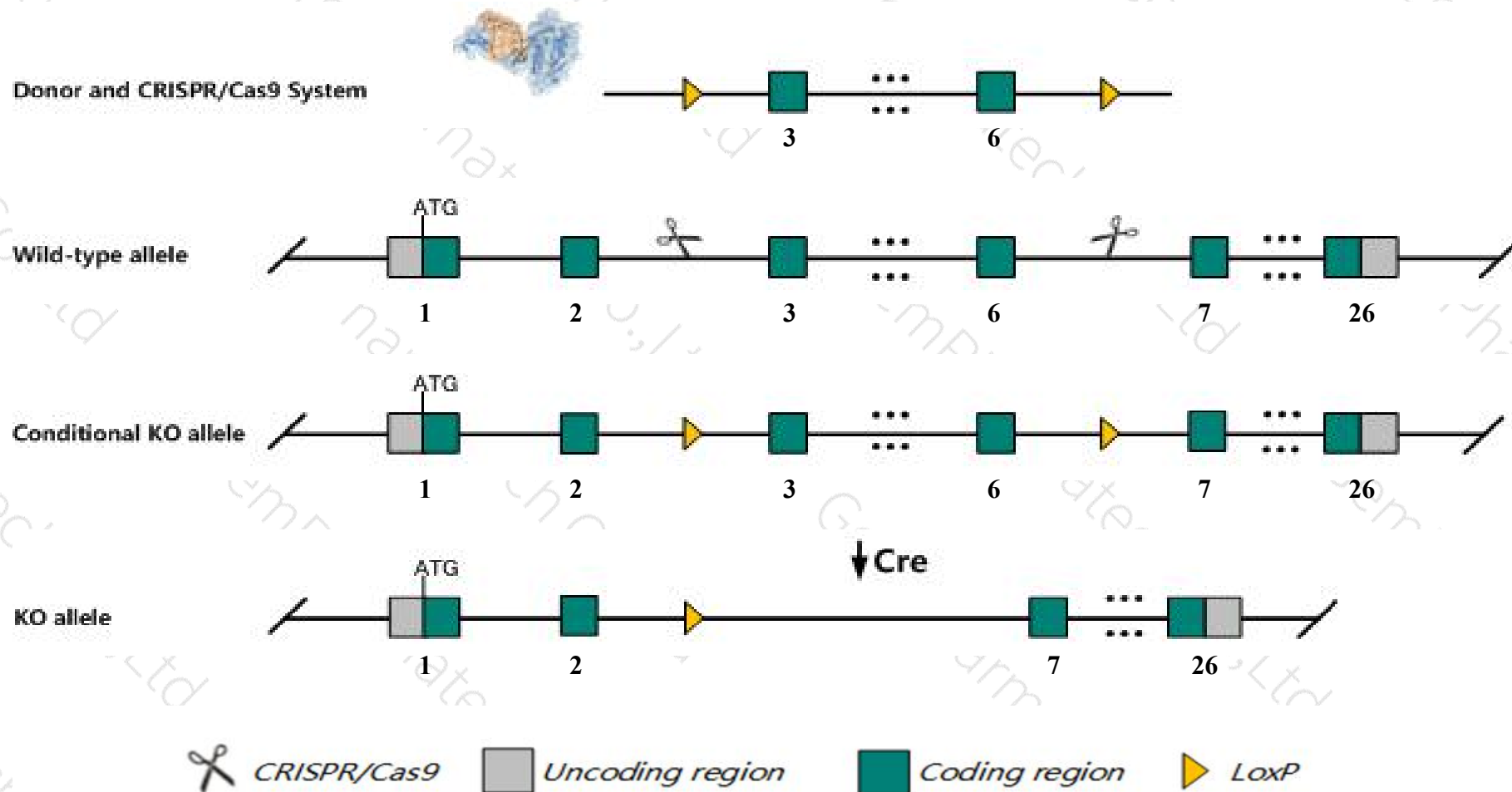
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- 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: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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](#)

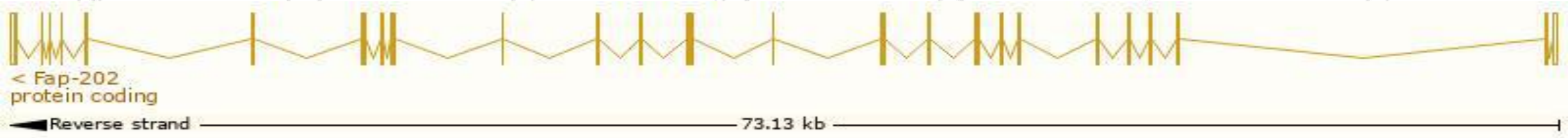
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

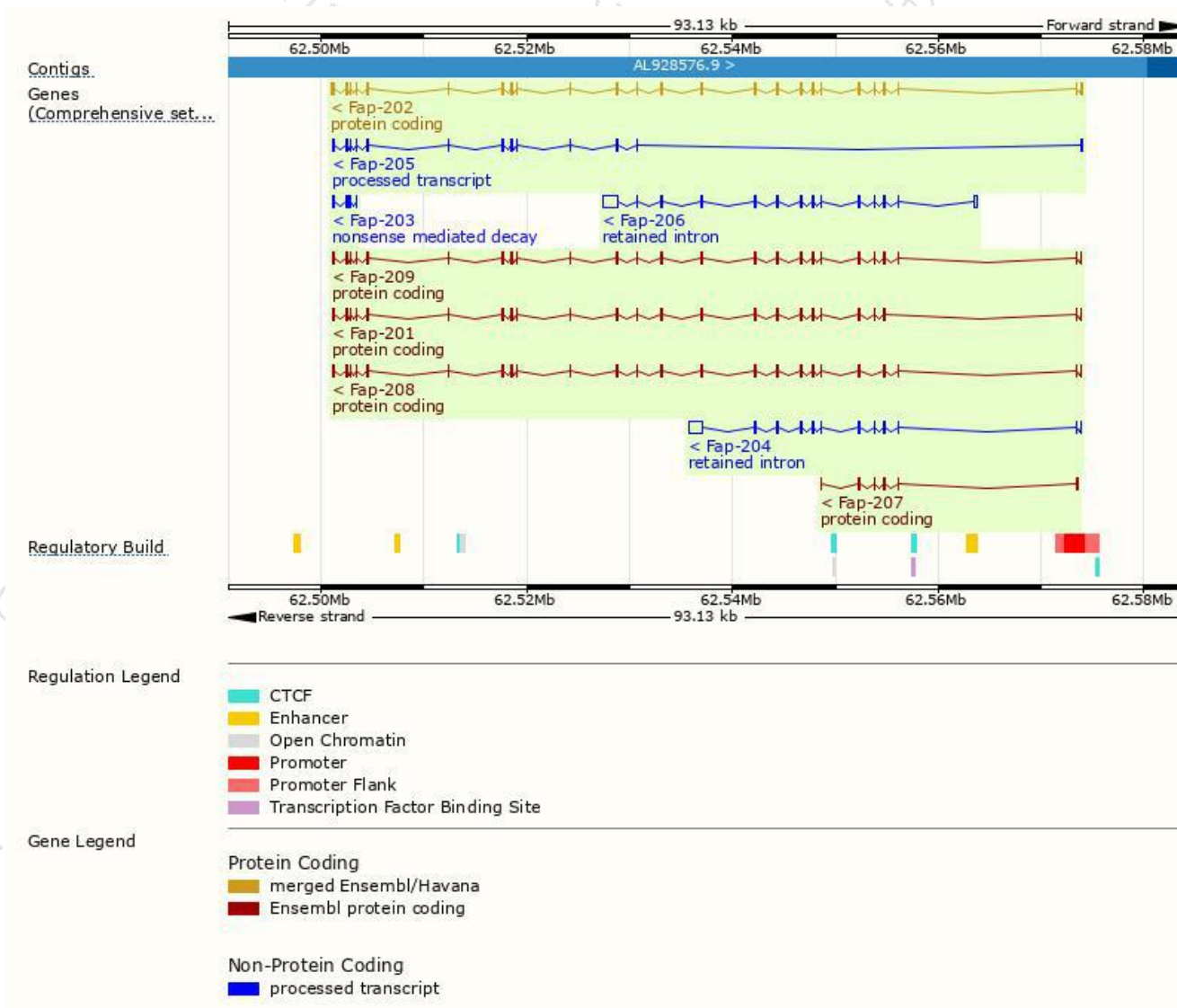
The gene has 9 transcripts,all transcripts are shown below:

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

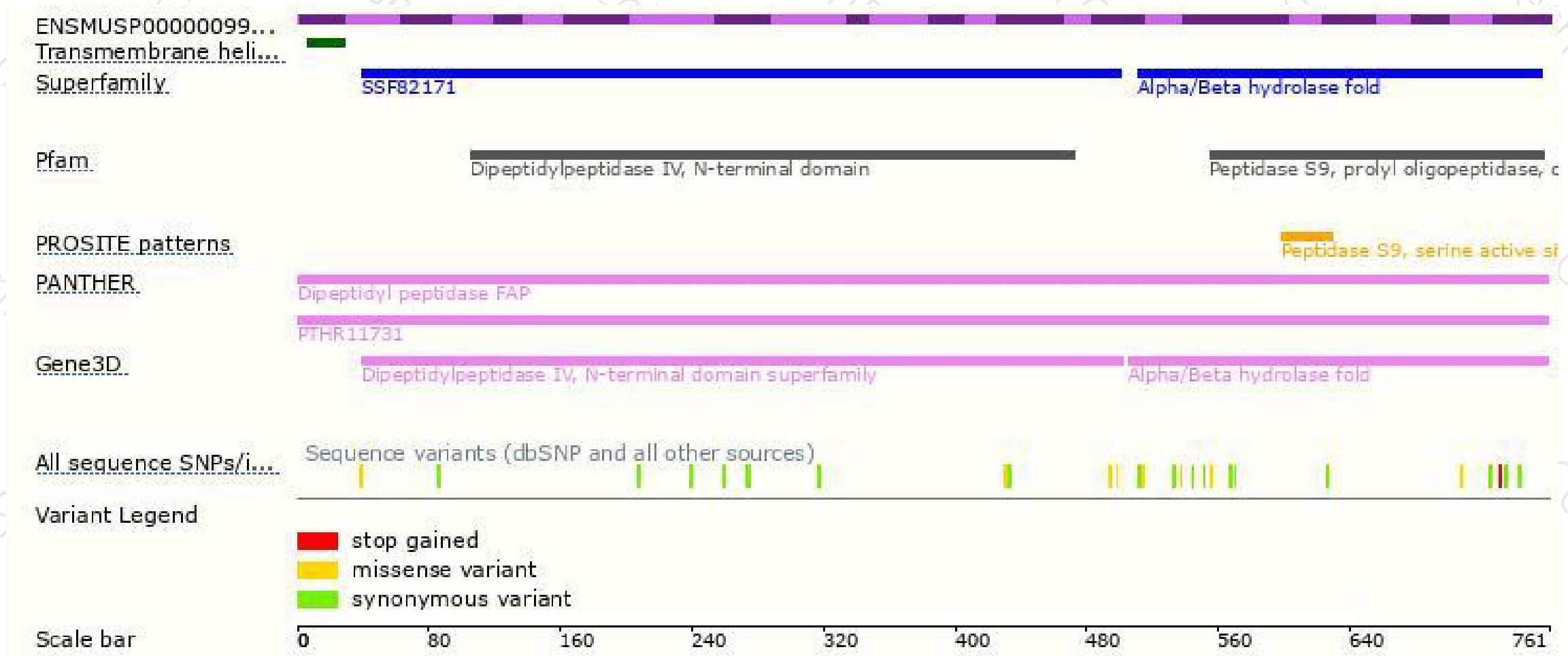
The strategy is based on the design of *Fap-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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