

***Fuca2* Cas9-CKO Strategy**

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Reviewer: JiaYu

Design Date: 2020-7-21

Project Overview

Project Name

Fuca2

Project type

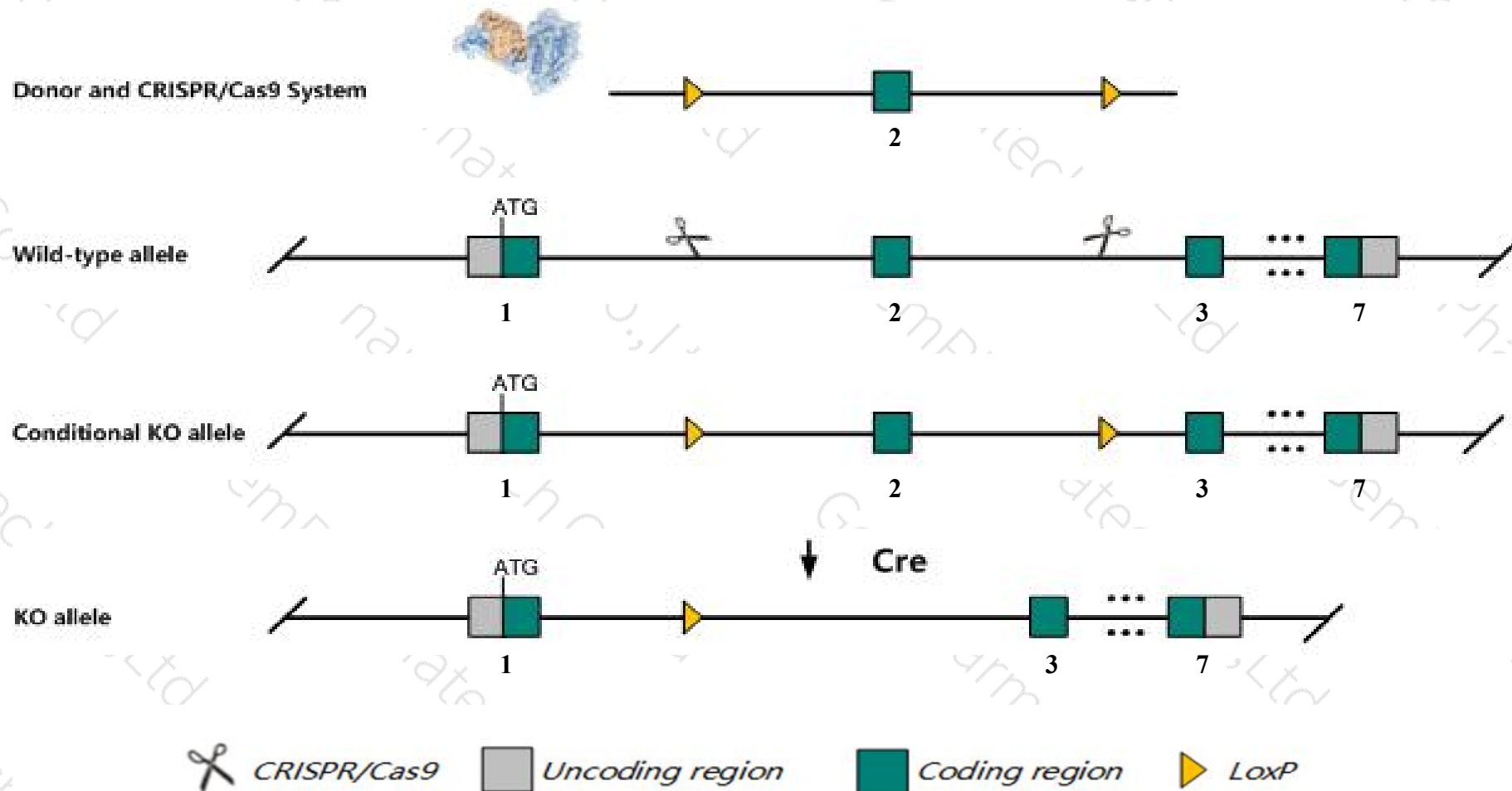
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fuca2* gene. The schematic diagram is as follows:



- The *Fuca2* gene has 6 transcripts. According to the structure of *Fuca2* gene, exon2 of *Fuca2*-203(ENSMUST00000121465.2) transcript is recommended as the knockout region. The region contains 188bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fuca2* gene. The brief process is as follows: CRISPR/Cas9 system 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, no notable phenotype was detected in a high-throughput screen of homozygous mutant mice.
- The *Fuca2* gene is located on the Chr10. 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)

Fuca2 fucosidase, alpha-L- 2, plasma [Mus musculus (house mouse)]

Gene ID: 66848, updated on 13-Mar-2020

Summary



Official Symbol [Fuca2](#) provided by [MGI](#)

Official Full Name [fucosidase, alpha-L- 2, plasma](#) provided by [MGI](#)

Primary source [MGI:MGI:1914098](#)

See related [Ensembl:ENSMUSG00000019810](#)

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 [0610025011Rik](#), [5530401P20Rik](#)

Expression Ubiquitous expression in kidney adult (RPKM 23.4), heart adult (RPKM 17.8) and 27 other tissues [See more](#)

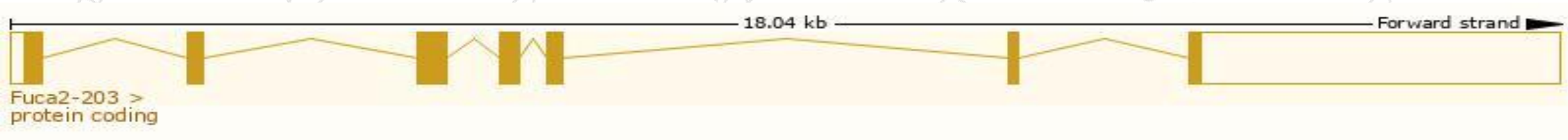
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

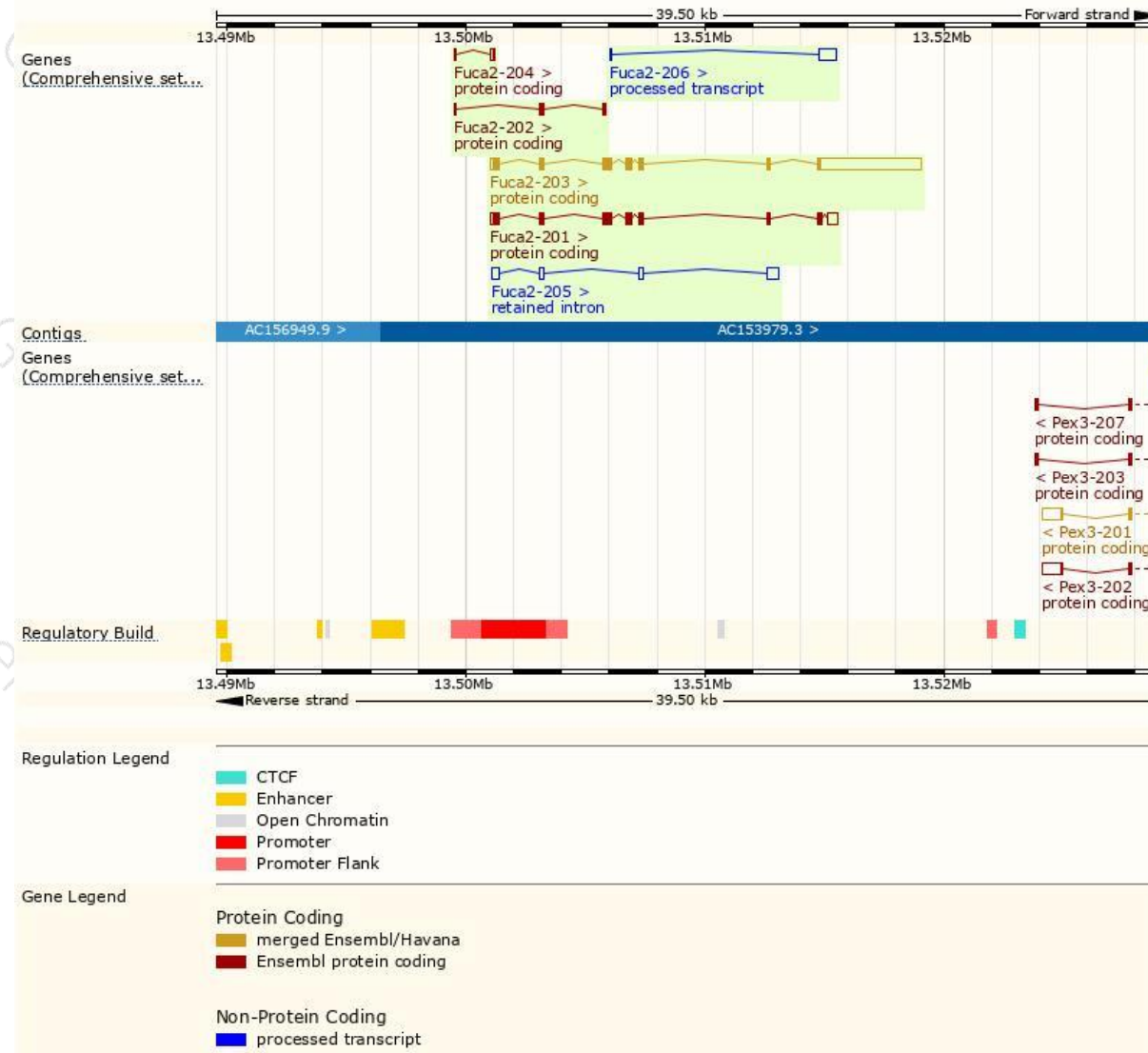
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fuca2-203	ENSMUST00000121465.2	5741	461aa	Protein coding	CCDS23701	Q505Q3 Q99KR8	TSL:1 GENCODE basic APPRIS P1
Fuca2-201	ENSMUST00000060212.12	2007	461aa	Protein coding	CCDS23701	Q505Q3 Q99KR8	TSL:1 GENCODE basic APPRIS P1
Fuca2-202	ENSMUST00000120549.1	374	95aa	Protein coding	-	D3YVV4	CDS 3' incomplete TSL:3
Fuca2-204	ENSMUST00000130865.1	223	3aa	Protein coding	-	-	CDS 3' incomplete TSL:5
Fuca2-206	ENSMUST00000166466.1	786	No protein	Processed transcript	-	-	TSL:3
Fuca2-205	ENSMUST00000150048.1	1150	No protein	Retained intron	-	-	TSL:2

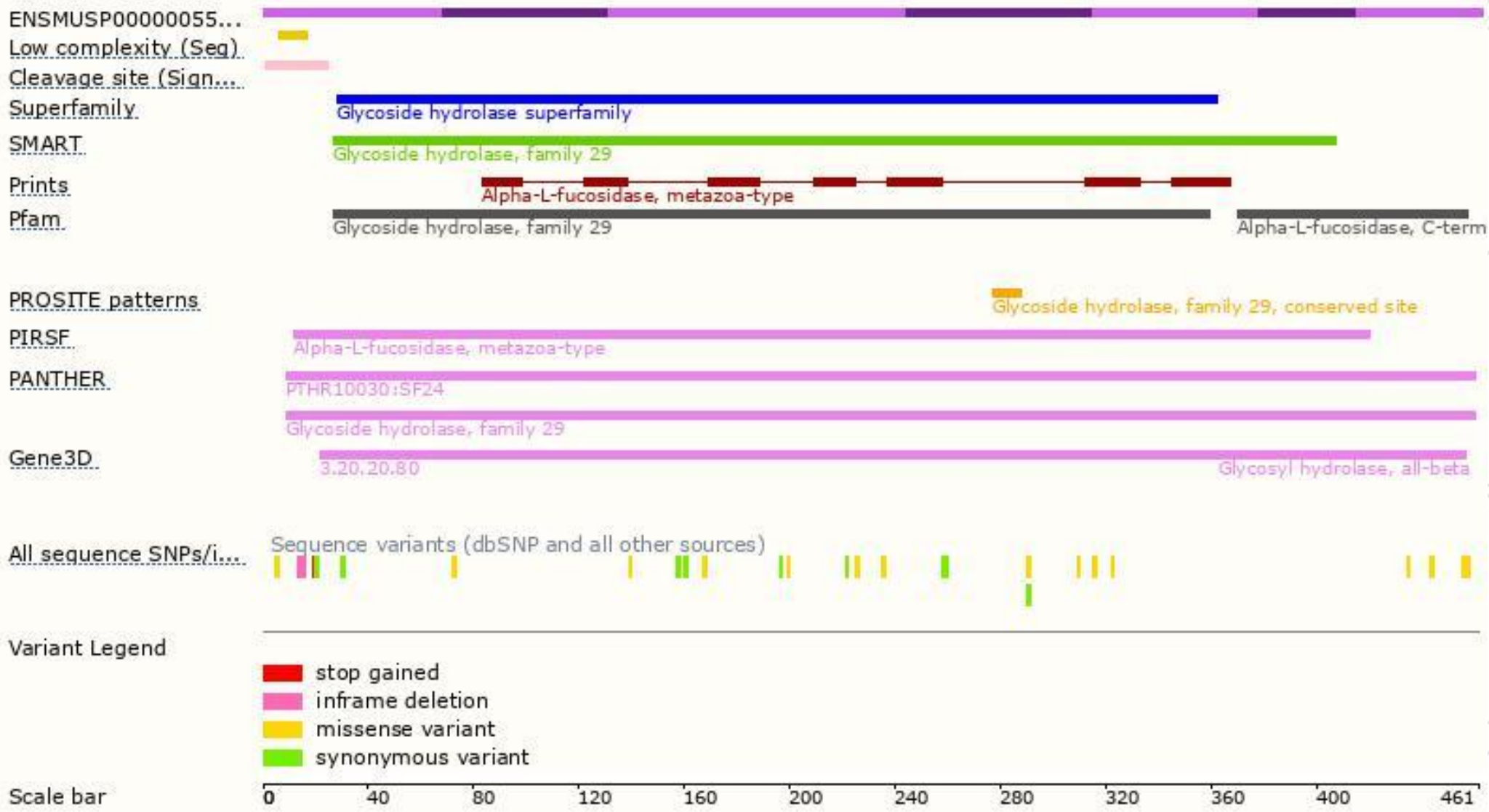
The strategy is based on the design of *Fuca2-203* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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