

***Fut10* Cas9-CKO Strategy**

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Project Overview

Project Name

Fut10

Project type

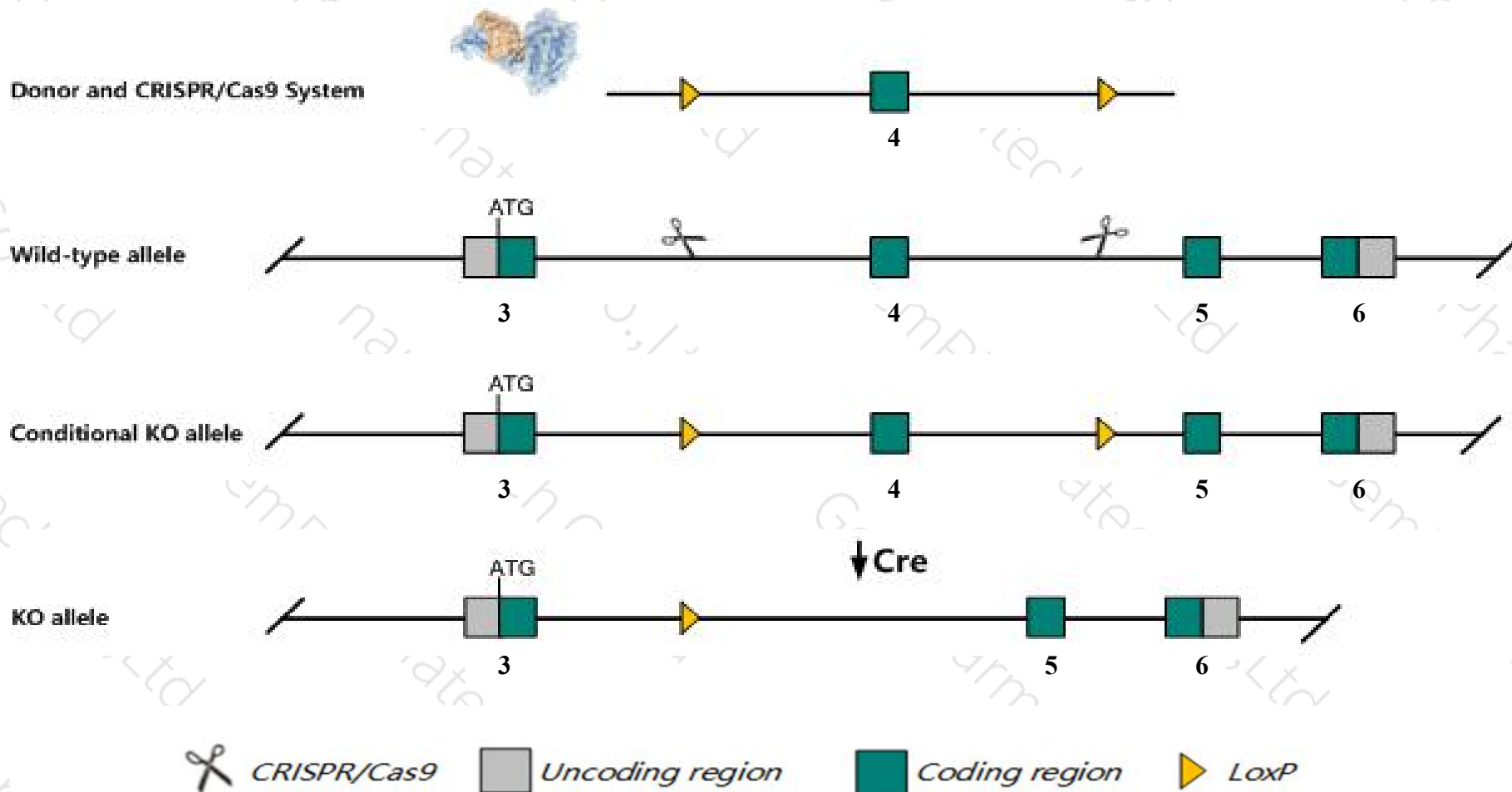
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fut10* gene. The schematic diagram is as follows:



Technical routes

- The *Fut10* gene has 5 transcripts. According to the structure of *Fut10* gene, exon4 of *Fut10*-203(ENSMUST00000161502.1) transcript is recommended as the knockout region. The region contains 295bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fut10* 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.

- The *Fut10* gene is located on the Chr8. 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)

Fut10 fucosyltransferase 10 [Mus musculus (house mouse)]

Gene ID: 171167, updated on 13-Mar-2020

Summary



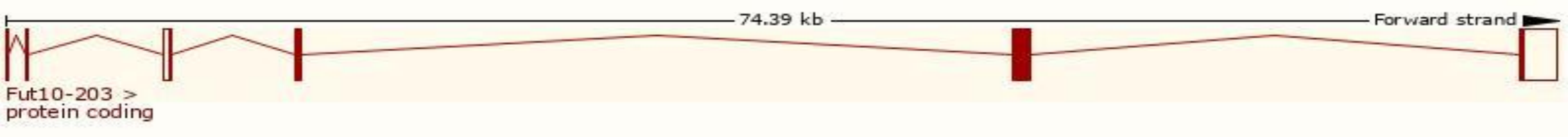
Official Symbol	Fut10 provided by MGI
Official Full Name	fucosyltransferase 10 provided by MGI
Primary source	MGI:MGI:2384748
See related	Ensembl:ENSMUSG00000046152
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	fuc-TX, fut10A
Expression	Broad expression in CNS E11.5 (RPKM 2.1), limb E14.5 (RPKM 2.1) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

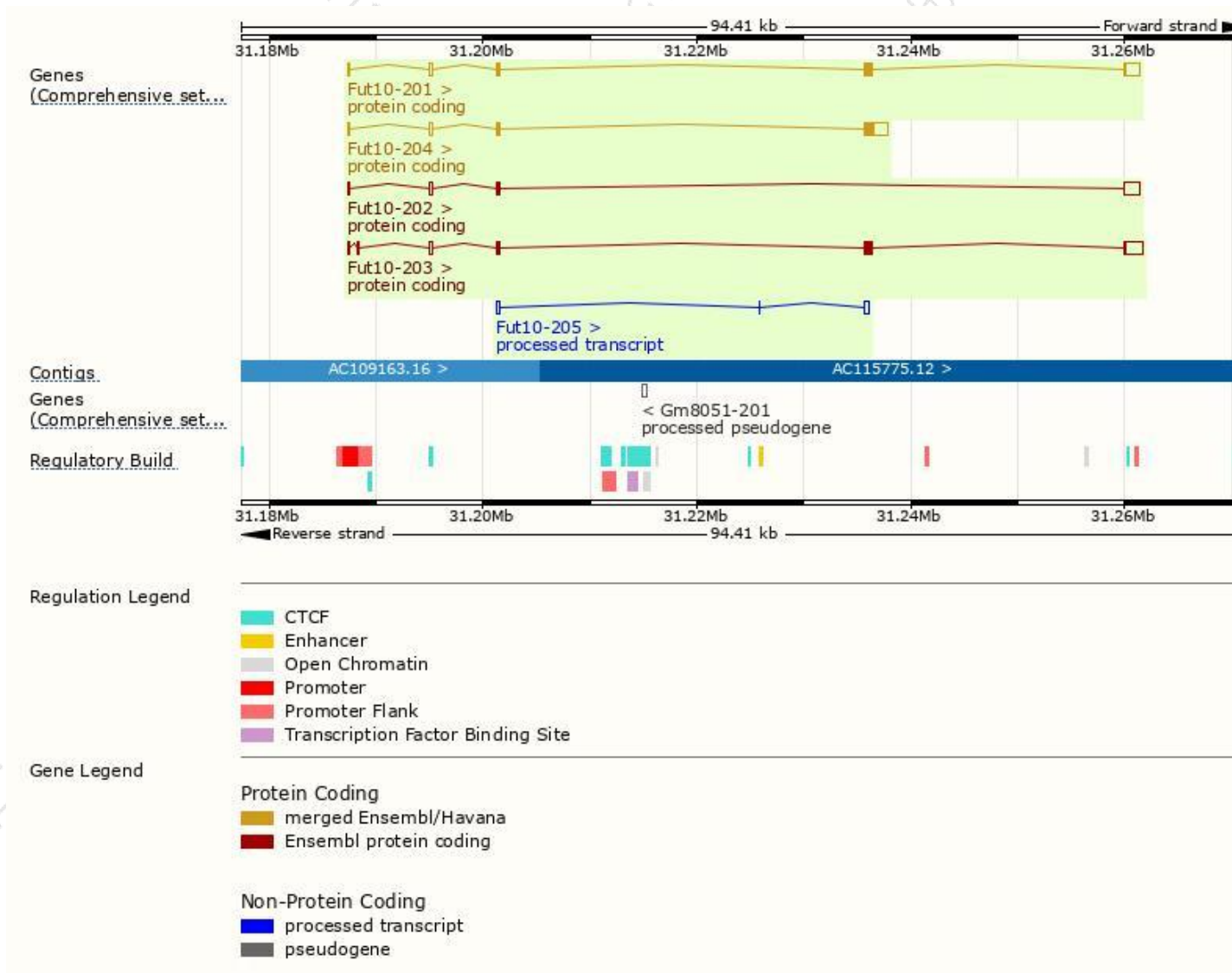
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fut10-203	ENSMUST00000161502.1	3527	481aa	Protein coding	CCDS22223	Q5F2L2	TSL:1 GENCODE basic APPRIS P3
Fut10-201	ENSMUST00000066173.11	3183	481aa	Protein coding	CCDS22223	Q5F2L2	TSL:1 GENCODE basic APPRIS P3
Fut10-204	ENSMUST00000161788.7	2962	436aa	Protein coding	CCDS52536	Q5F2L2	TSL:1 GENCODE basic APPRIS ALT2
Fut10-202	ENSMUST00000110527.8	2327	136aa	Protein coding	CCDS72111	Q5F2L2	TSL:1 GENCODE basic
Fut10-205	ENSMUST00000162162.1	771	No protein	Processed transcript	-	-	TSL:3

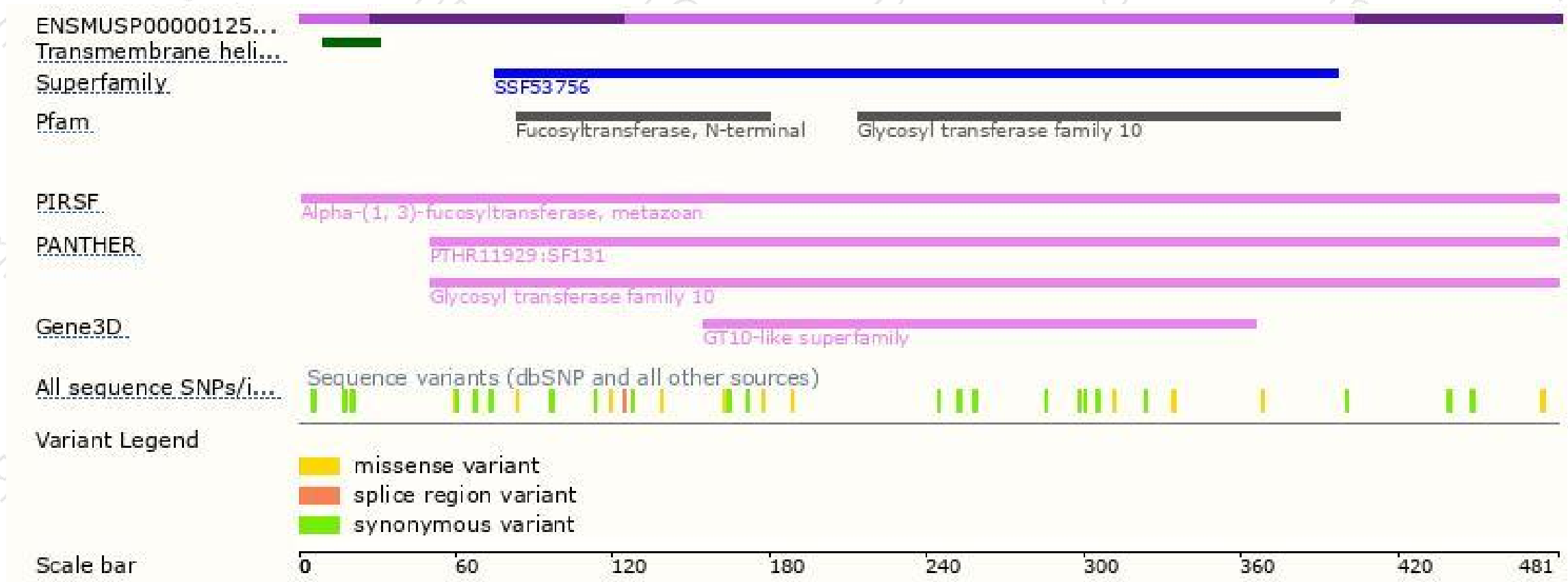
The strategy is based on the design of *Fut10-203* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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