

# Fra10ac1 Cas9-CKO Strategy

Designer: Jing Chen

Reviewer: Xiangli Bian

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# Overview

## Target Gene Name

- Fra10ac1

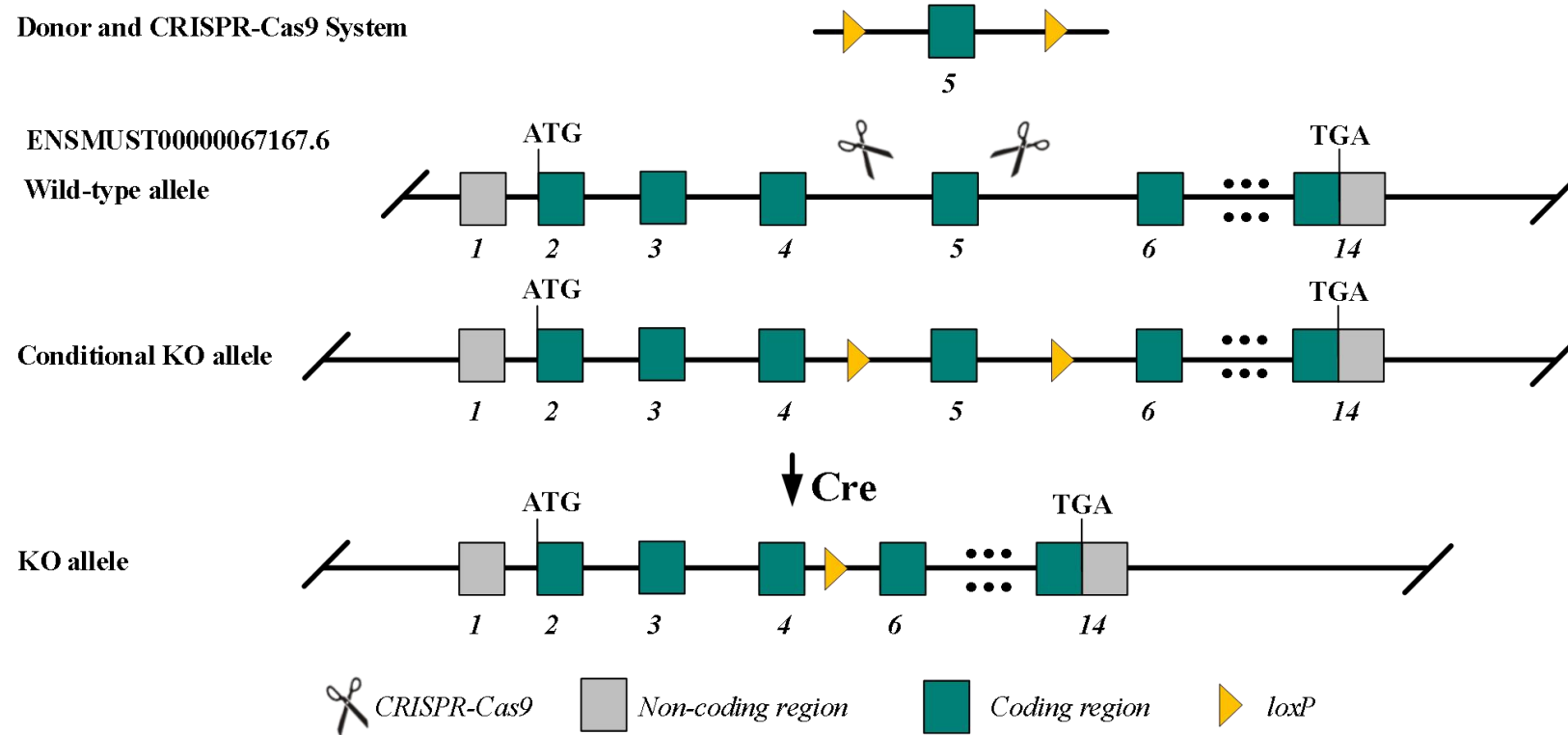
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Fra10ac1* gene.

# Technical Information

- The *Fra10ac1* gene has 3 transcripts. According to the structure of *Fra10ac1* gene, exon5 of *Fra10ac1*-201 (ENSMUST00000067167.6) transcript is recommended as the knockout region. The region contains 77 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Fra10ac1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.


# Gene Information

## Fra10ac1 FRA10A associated CGG repeat 1 [ *Mus musculus* (house mouse) ]

Gene ID: 70567, updated on 23-Nov-2023

 Download Datasets

### Summary

**Official Symbol** Fra10ac1 provided by MGI  
**Official Full Name** FRA10A associated CGG repeat 1 provided by MGI  
**Primary source** [MGI:MGI:1917817](#)  
**See related** [Ensembl:ENSMUSG00000054237](#) [AllianceGenome:MGI:1917817](#)  
**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** 5730455O13Rik  
**Summary** Predicted to enable phosphatase activity. Predicted to be involved in dephosphorylation. Predicted to be located in nucleus. Orthologous to human FRA10AC1 (FRA10A associated CGG repeat 1). [provided by Alliance of Genome Resources, Apr 2022]  
**Expression** Ubiquitous expression in CNS E11.5 (RPKM 10.1), CNS E14 (RPKM 7.3) and 27 other tissues [See more](#)  
**Orthologs** [human](#) [all](#)  
 [Try the new Gene table](#)  
[Try the new Transcript table](#)

### Genomic context

**Location:** 19 C2; 19 32.82 cM

[See Fra10ac1 in Genome Data Viewer](#)

**Exon count:** 15

Annotation release	Status	Assembly	Chr	Location
RS_2023_04	current	GRCm39 ( <a href="#">GCF_000001635.27</a> )	19	NC_000085.7 (38176925..38213078, complement)
108.20200622	previous assembly	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	19	NC_000085.6 (38188477..38224630, complement)

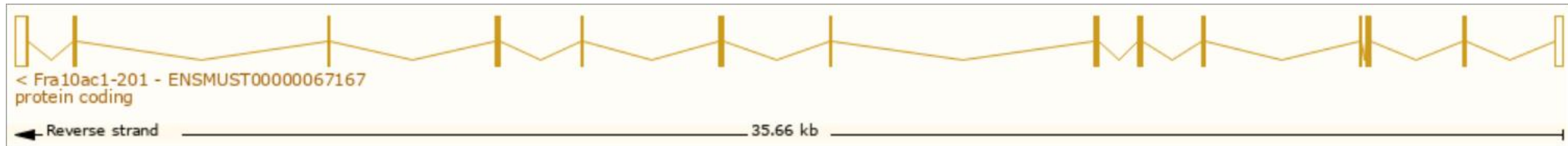
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

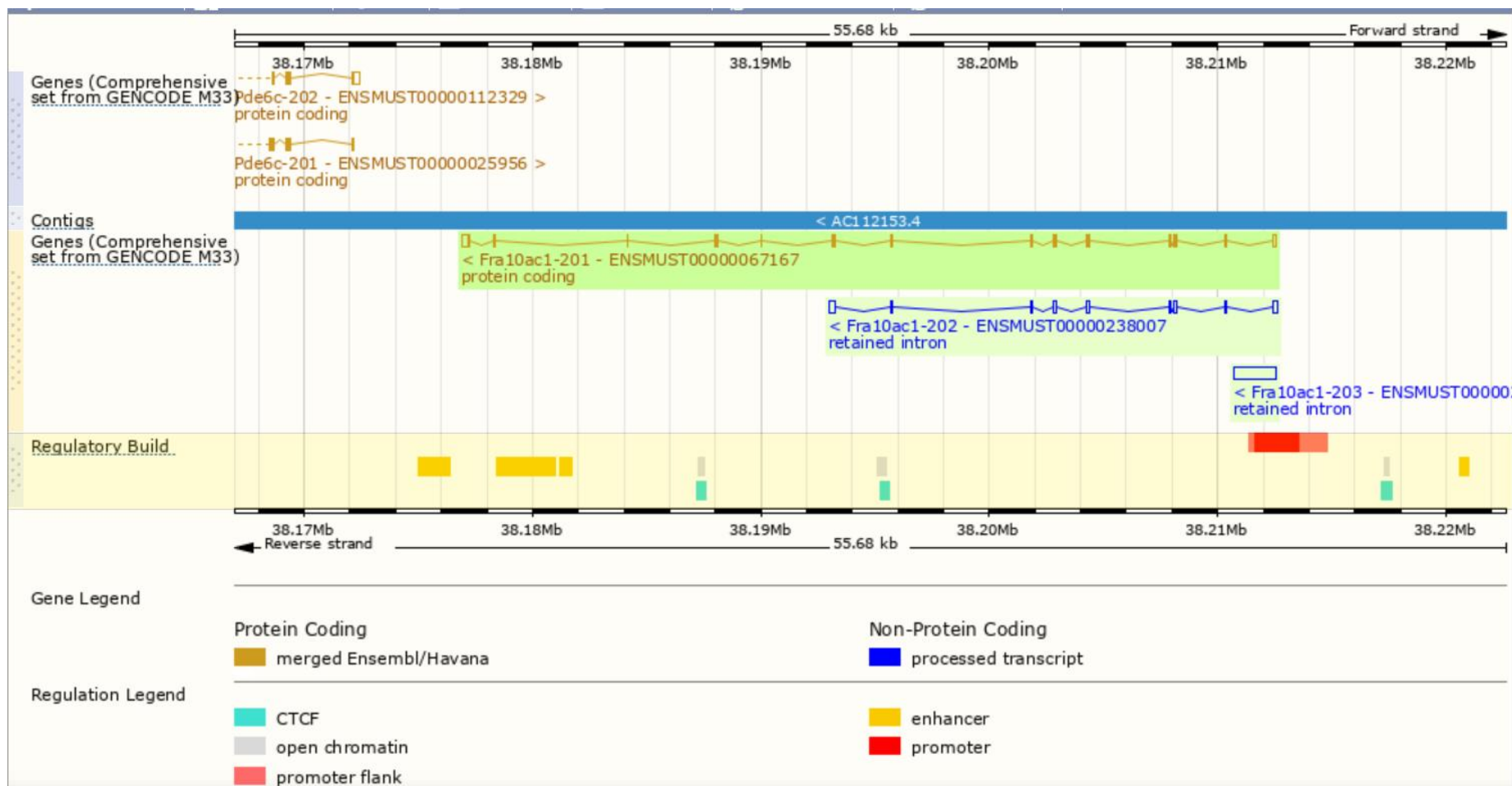
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000238154.2</a>	Fra10ac1-203	1884	No protein	Retained intron		-	-
<a href="#">ENSMUST00000238007.2</a>	Fra10ac1-202	1010	No protein	Retained intron		-	-
<a href="#">ENSMUST00000067167.6</a>	Fra10ac1-201	1402	<a href="#">315aa</a>	Protein coding	<a href="#">CCDS37972</a>	<a href="#">Q8BP78</a>	Ensembl Canonical Gencode basic APPRIS P1 TSL:1

The strategy is based on the design of *Fra10ac1*-201 transcript, the transcription is shown below:

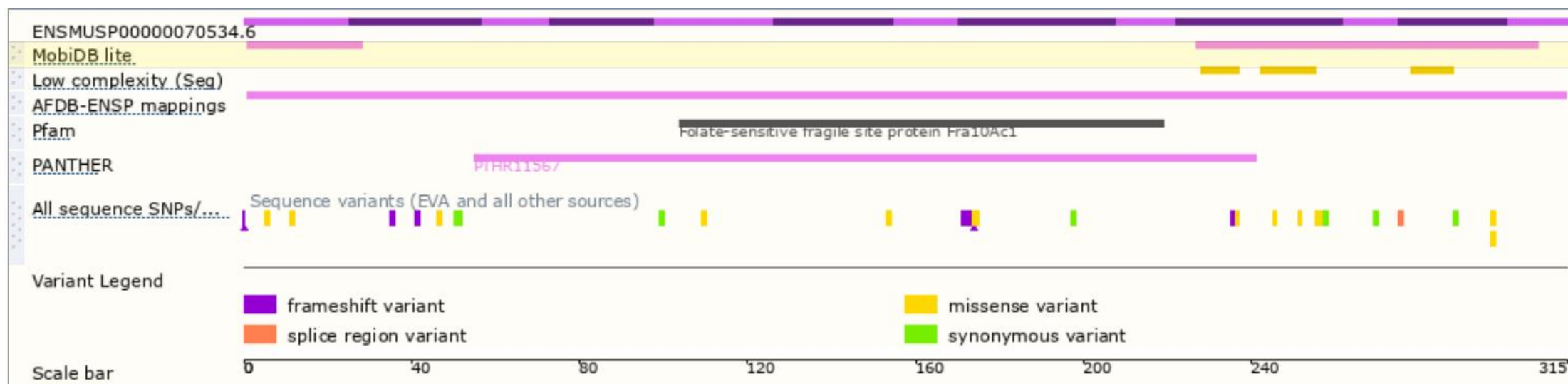


Source: <https://www.ensembl.org>

# Genomic Information



# Protein Information



# Important Information

- *Fra10ac1* is located on Chr19. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.