

# Sf3b2 Cas9-KO Strategy

Designer: Yang Yang

Reviewer: Yanhua Shen

Design Date: 2022/11/7

# Overview

## Target Gene Name

- Sf3b2

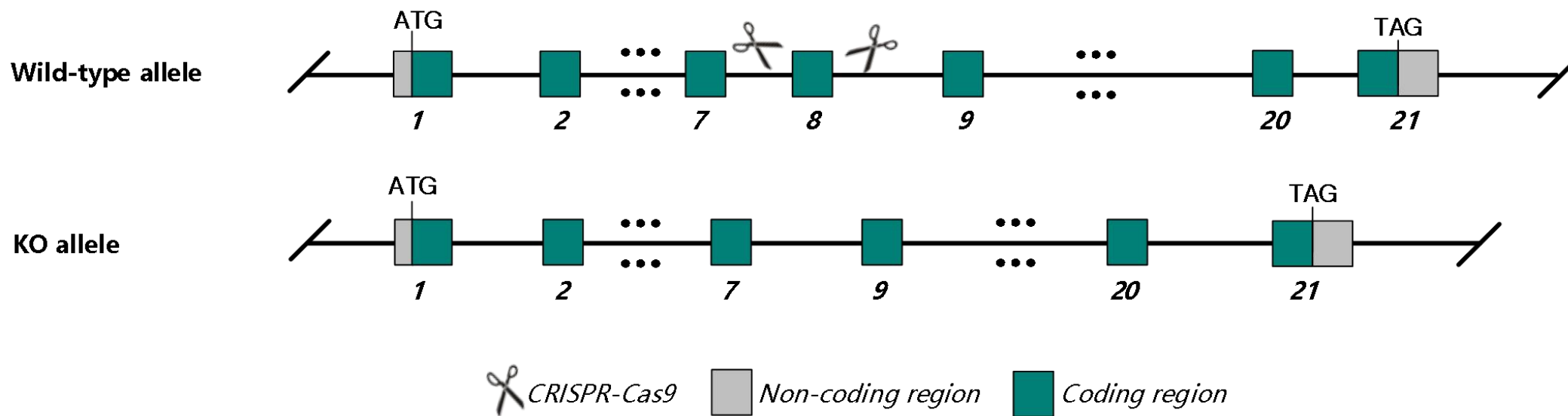
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Sf3b2* gene.

# Technical Information

- The *Sf3b2* gene has 8 transcripts. According to the structure of *Sf3b2* gene, exon 8 of *Sf3b2*-201 (ENSMUST00000025774.11) transcript is recommended as the knockout region. The region contains 92 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Sf3b2* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

# Gene Information

**Sf3b2** splicing factor 3b, subunit 2 [ *Mus musculus* (house mouse) ]

Gene ID: 319322, updated on 26-Sep-2022

[Download Datasets](#)

## Summary

Official Symbol	Sf3b2 provided by <a href="#">MGI</a>
Official Full Name	splicing factor 3b, subunit 2 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2441856</a>
See related	<a href="#">Ensembl:ENSMUSG00000024853</a> <a href="#">AllianceGenome:MGI:2441856</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SF3b1; 145kDa; SAP145; SF3b145; SF3b150; 2610311M13Rik; 2810441F20Rik; B230398H18Rik
Summary	Predicted to be involved in mRNA splicing, via spliceosome. Predicted to be located in nuclear speck. Predicted to be part of U2 snRNP and spliceosomal complex. Is expressed in early conceptus; inner cell mass; and oocyte. Orthologous to human SF3B2 (splicing factor 3b subunit 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in CNS E11.5 (RPKM 77.1), CNS E14 (RPKM 51.7) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

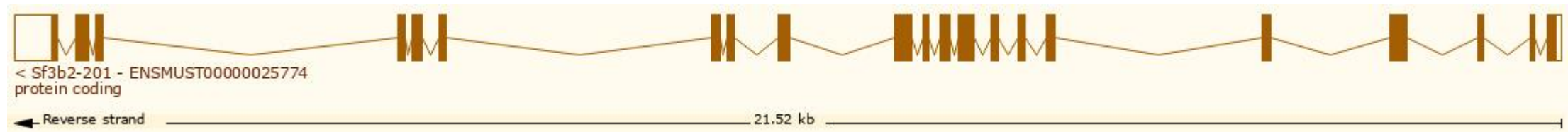
Source: [https://https://www.ncbi.nlm.nih.gov/gene/319322](https://www.ncbi.nlm.nih.gov/gene/319322)

# Transcript Information

The gene has 8 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
<a href="#">ENSMUST0000025774.11</a>	Sf3b2-201	3222	<a href="#">878aa</a>	Protein coding	<a href="#">CCDS29454</a>	<a href="#">Q3UJB0</a>	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000235182.2</a>	Sf3b2-202	933	<a href="#">308aa</a>	Protein coding		<a href="#">A0A494B9S9</a>	CDS 3' incomplete	
<a href="#">ENSMUST00000235772.2</a>	Sf3b2-204	2950	No protein	Retained intron		-	-	
<a href="#">ENSMUST00000237781.2</a>	Sf3b2-208	1894	No protein	Retained intron		-	-	
<a href="#">ENSMUST00000235368.2</a>	Sf3b2-203	963	No protein	Retained intron		-	-	
<a href="#">ENSMUST00000236695.2</a>	Sf3b2-206	673	No protein	Retained intron		-	-	
<a href="#">ENSMUST00000236014.2</a>	Sf3b2-205	539	No protein	Retained intron		-	-	
<a href="#">ENSMUST00000237512.2</a>	Sf3b2-207	455	No protein	Retained intron		-	-	

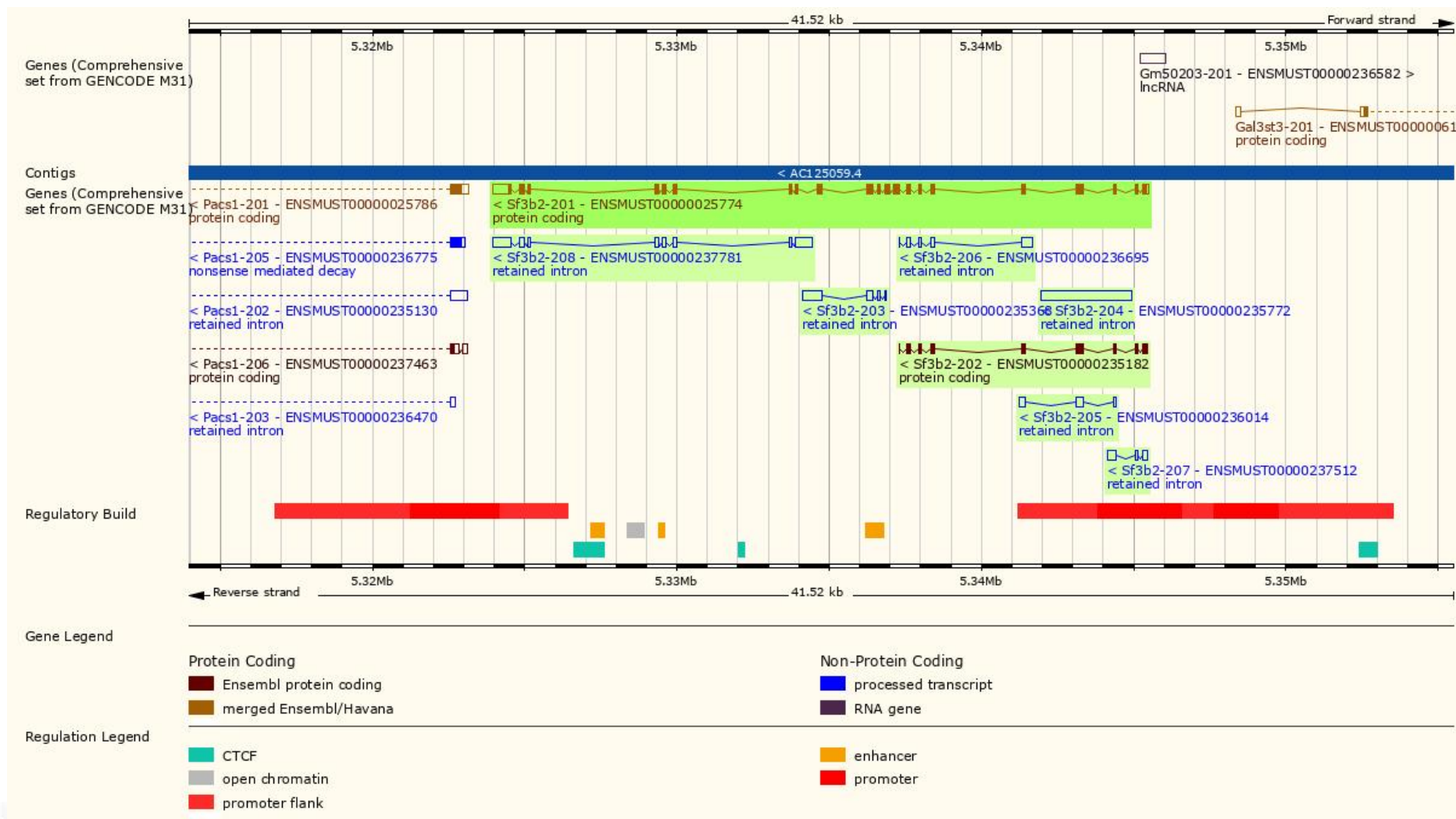
The strategy is based on the design of *Sf3b2*-201 transcript, the transcription is shown below:



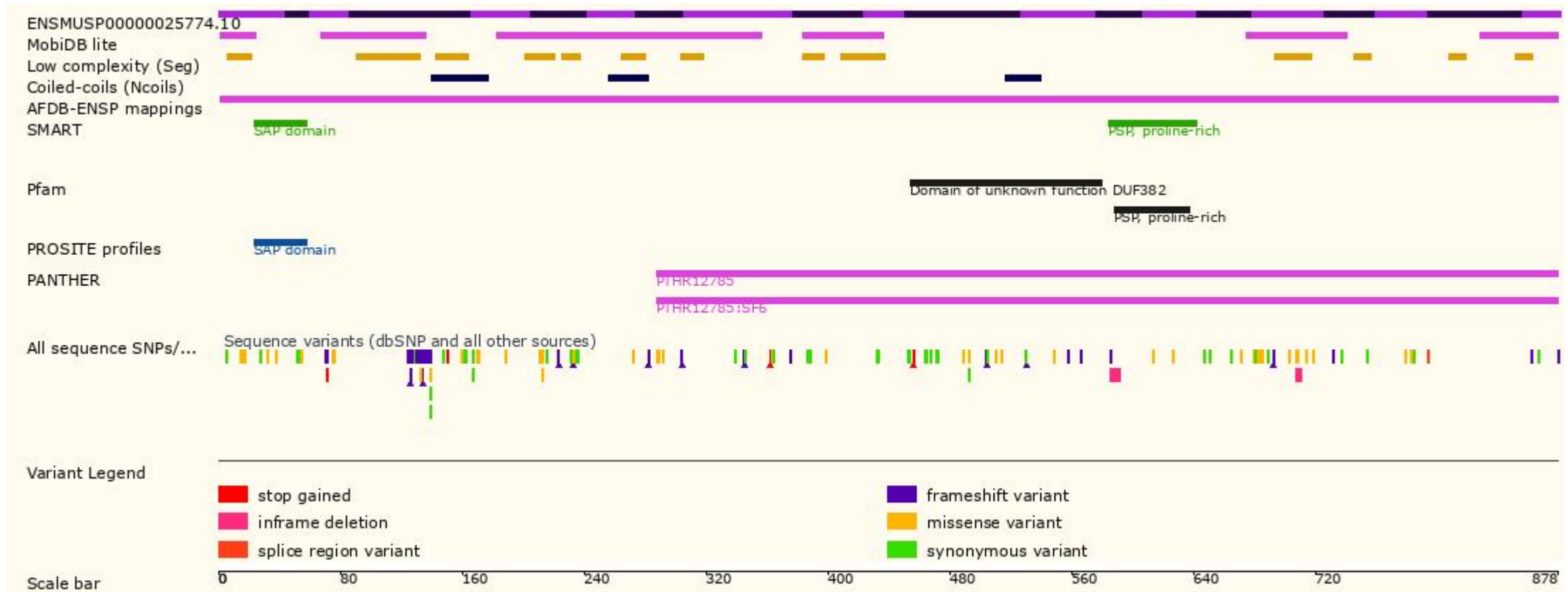
Source: <https://www.ensembl.org>



# Genomic Information



# Protein Information





# Important Information

- *Sf3b2* 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.