

Sf3a2 Cas9-CKO Strategy

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Overview

Target Gene Name

- Sf3a2

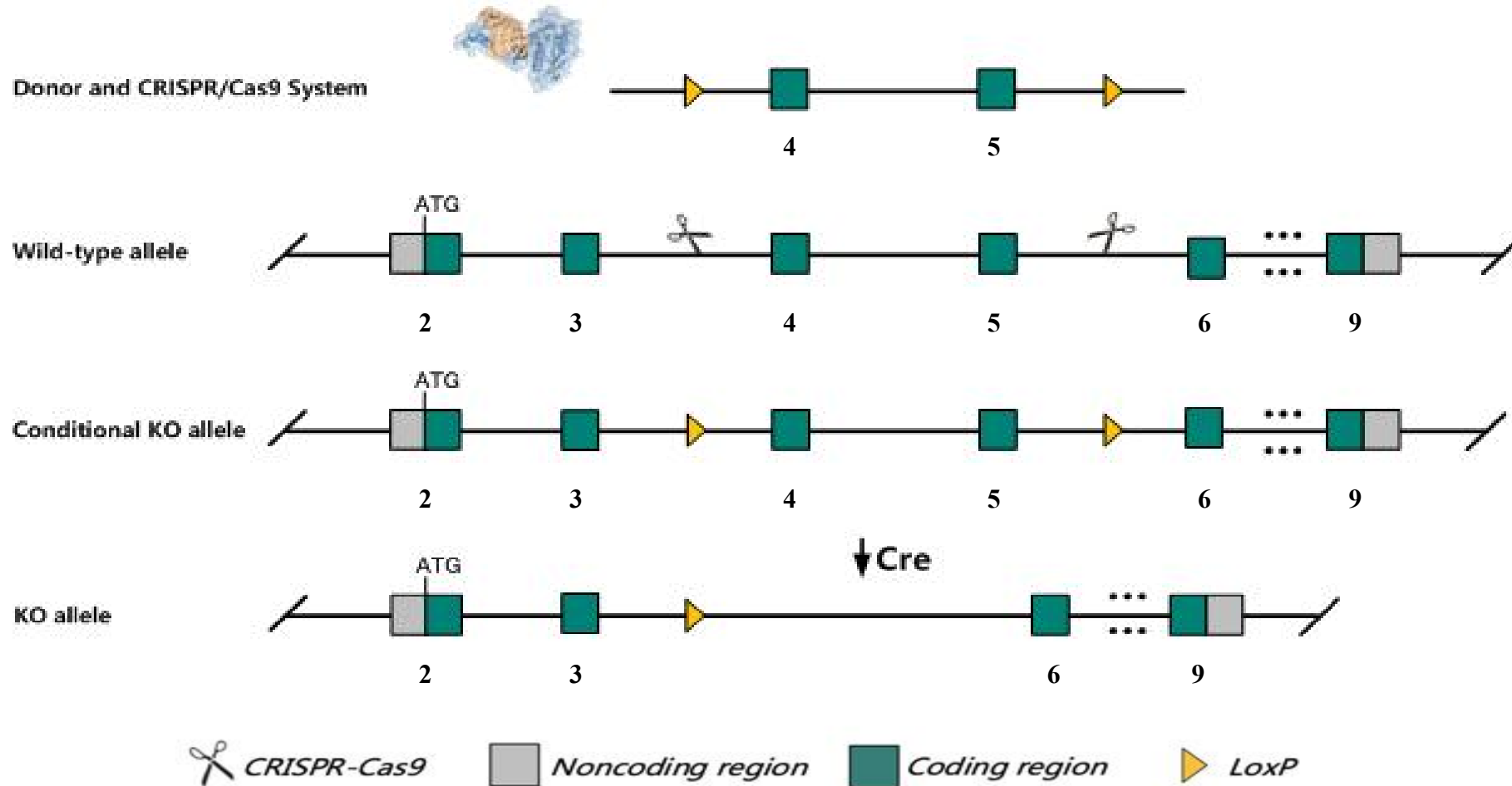
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Sf3a2* gene.

Technical Information

- The *Sf3a2* gene has 4 transcripts. According to the structure of *Sf3a2* gene, exon4-exon5 of *Sf3a2*-203 (ENSMUST00000148665.8) transcript is recommended as the knockout region. The region contains 157 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Sf3a2* 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

Sf3a2 splicing factor 3a, subunit 2 [*Mus musculus* (house mouse)]

Gene ID: 20222, updated on 23-Nov-2023

 Download Datasets

Summary

Official Symbol Sf3a2 provided by MGI
Official Full Name splicing factor 3a, subunit 2 provided by MGI
Primary source [MGI:MGI:104912](#)
See related [Ensembl:ENSMUSG00000020211](#) [AllianceGenome:MGI:104912](#)
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 66kDa; PRP11; SFA66; Sap62
Summary Predicted to be involved in U2-type prespliceosome assembly and positive regulation of neuron projection development. Predicted to act upstream of or within RNA splicing, via transesterification reactions. Part of U2 snRNP. Is expressed in several structures, including brain; genitourinary system; liver; lung; and spleen. Orthologous to human SF3A2 (splicing factor 3a subunit 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression Ubiquitous expression in adrenal adult (RPKM 42.2), ovary adult (RPKM 32.7) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)
 [Try the new Gene table](#)
[Try the new Transcript table](#)

Genomic context

Location: 10 C1; 10 39.72 cM

[See Sf3a2 in Genome Data Viewer](#)

Exon count: 9

| Annotation release | Status | Assembly | Chr | Location |
|--------------------|-------------------|--|-----|----------------------------------|
| RS_2023_04 | current | GRCm39 (GCF_000001635.27) | 10 | NC_000076.7 (80634569..80640756) |
| 108.20200622 | previous assembly | GRCm38.p6 (GCF_000001635.26) | 10 | NC_000076.6 (80798735..80804922) |

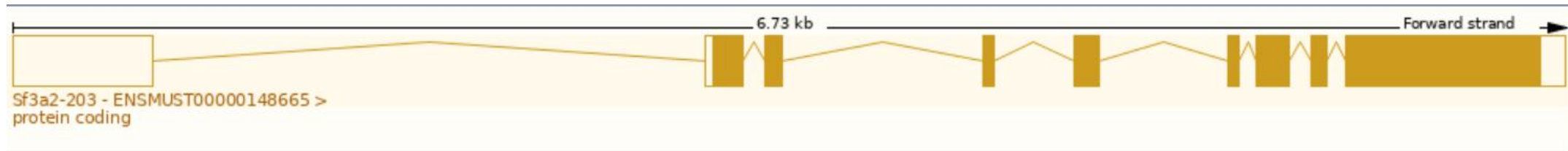
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 4 transcripts, all transcripts are shown below:

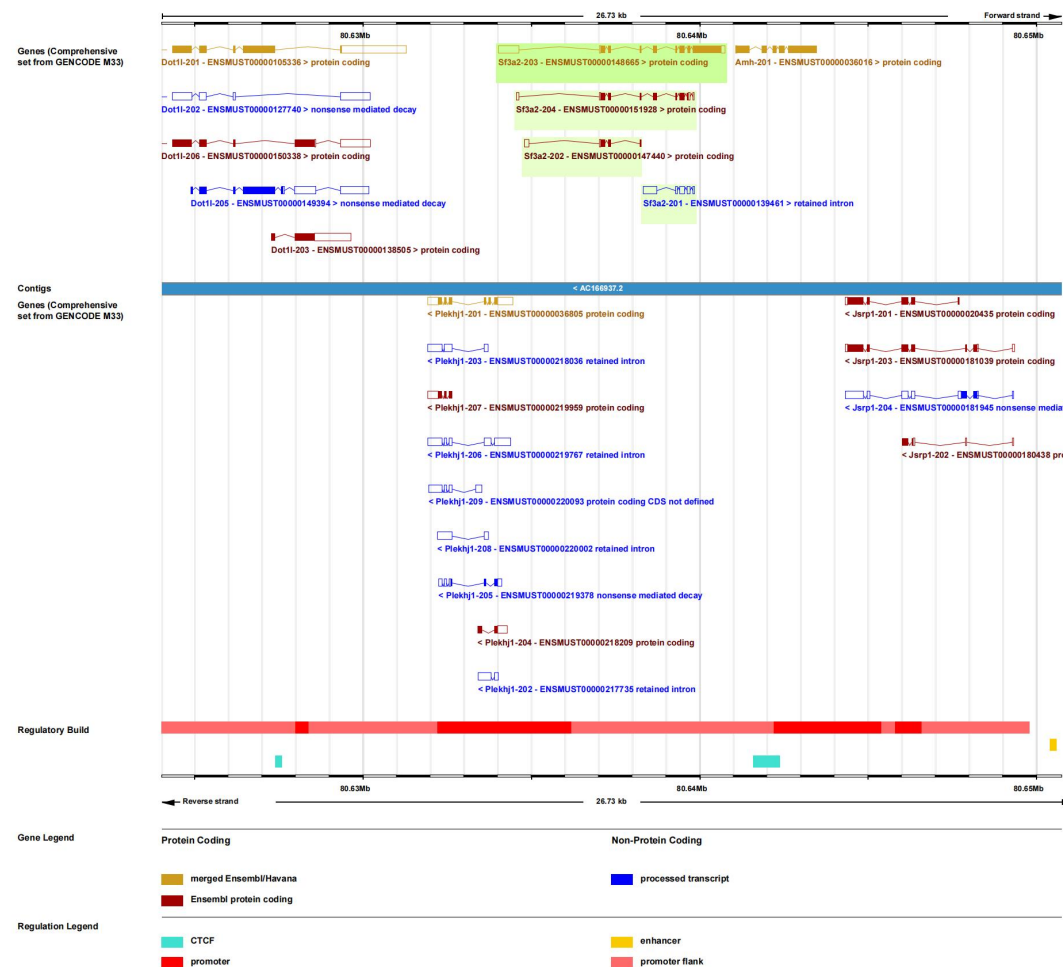
| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
|--------------------------------------|-----------|------|-----------------------|-----------------|---------------------------|------------------------|---|
| ENSMUST00000148665.8 | Sf3a2-203 | 2213 | 485aa | Protein coding | CCDS35986 | G3UVU2 | Ensembl Canonical GENCODE basic APPRIS P1 TSL:1 |
| ENSMUST00000151928.8 | Sf3a2-204 | 781 | 194aa | Protein coding | | D3YW09 | GENCODE basic TSL:5 |
| ENSMUST00000139461.2 | Sf3a2-201 | 727 | No protein | Retained intron | | - | TSL:3 |
| ENSMUST00000147440.2 | Sf3a2-202 | 373 | 67aa | Protein coding | | D3Z5A6 | TSL:5 CDS 3' incomplete |

The strategy is based on the design of *Sf3a2*-203 transcript, the transcription is shown below:

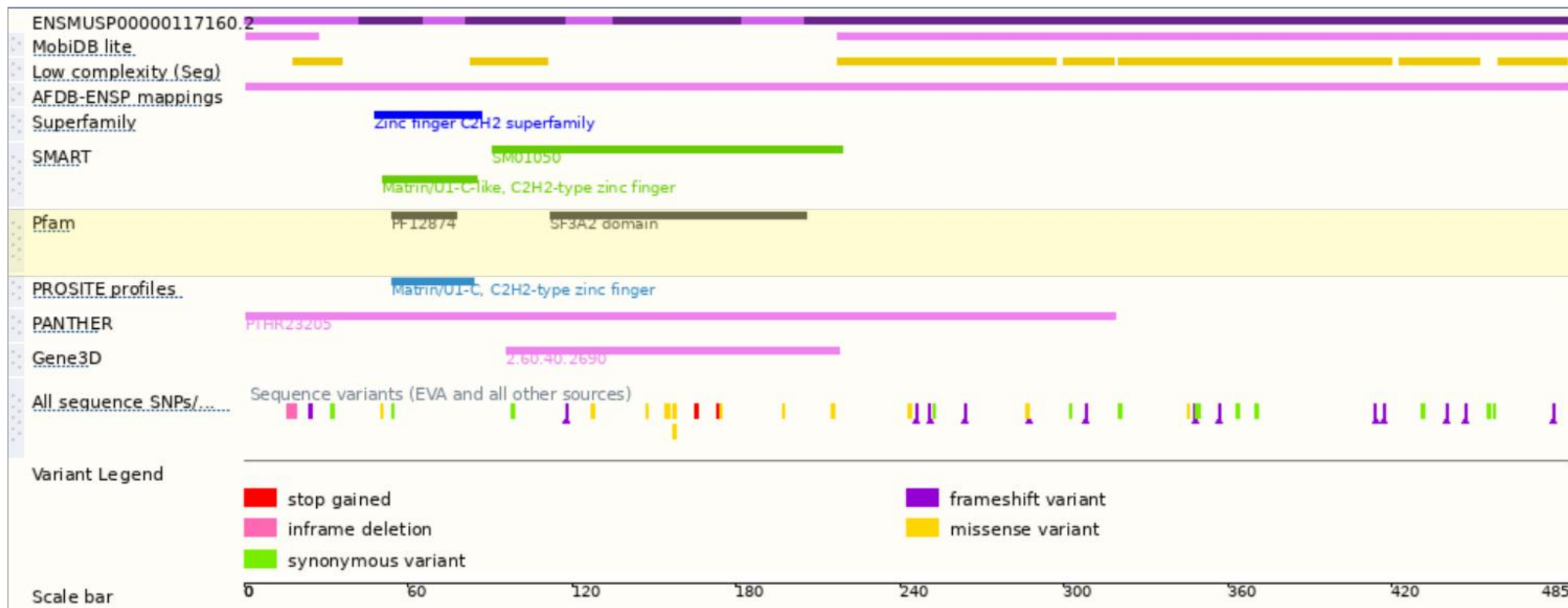


Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Important Information

- *Sf3a2* is located on Chr10. 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.
- The knockout region is located about 3 kb at the 5' end of the *Plekhj1*, 2 kb at the 5' end of the *Amh*, which may affect its transcriptional regulation.
- The intron 5-6 is 558 bp, the loxp insertion may affect the regulation of *Sf3a2* gene.
- 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.