

Sdf4 Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Shen

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Project Overview

Project Name

Sdf4

Project type

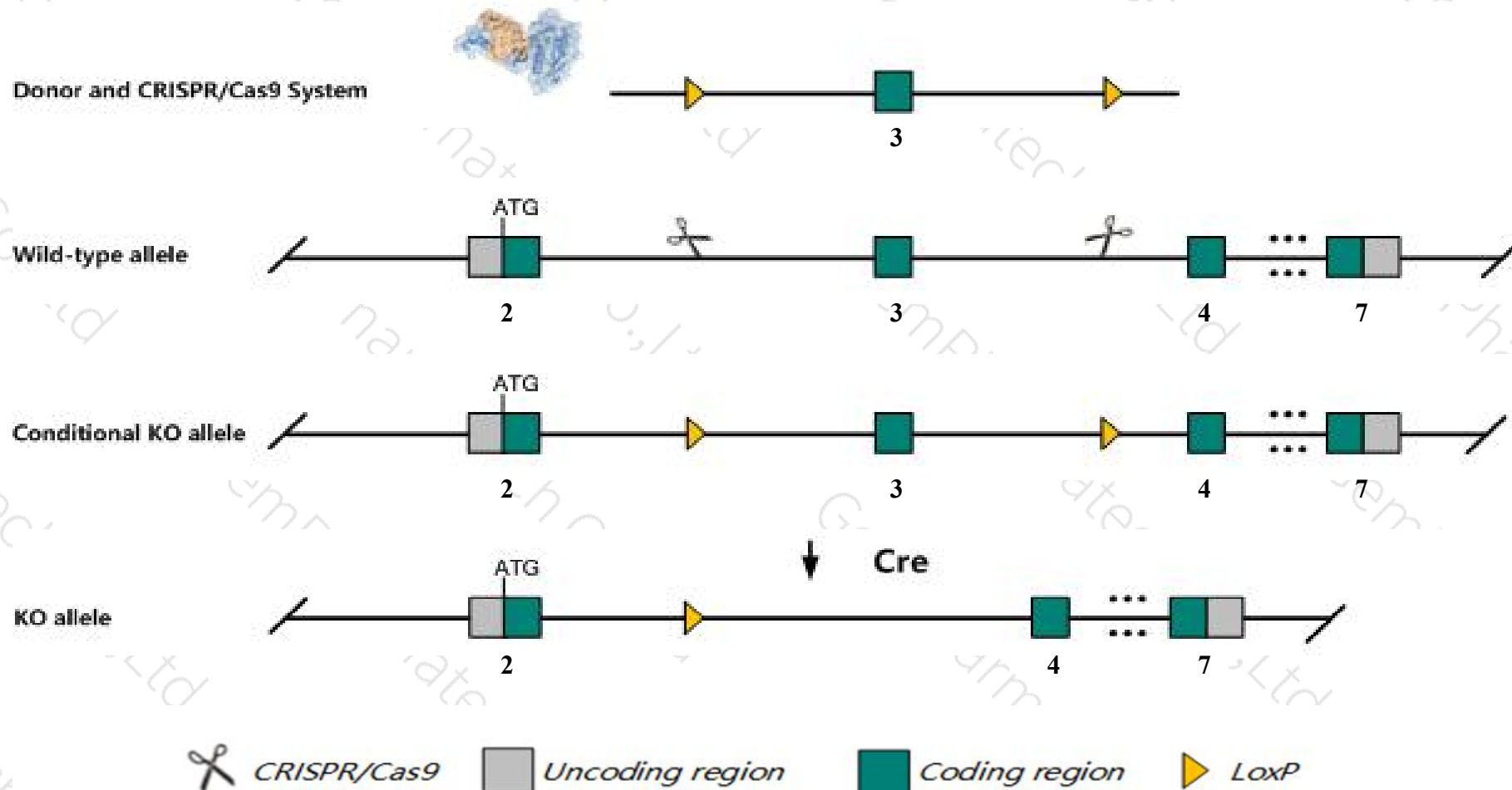
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sdf4* gene. The schematic diagram is as follows:



Technical routes

- The *Sdf4* gene has 6 transcripts. According to the structure of *Sdf4* gene, exon3 of *Sdf4-201* (ENSMUST00000050078.12) transcript is recommended as the knockout region. The region contains 137bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sdf4* 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.

Notice

- The *Sdf4* gene is located on the Chr4. 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.
- Transcript *Sdf4*-206 may not be affected.
- 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)

Sdf4 stromal cell derived factor 4 [Mus musculus (house mouse)]

Gene ID: 20318, updated on 13-Mar-2020

Summary

Official Symbol Sdf4 provided by [MGI](#)

Official Full Name stromal cell derived factor 4 provided by [MGI](#)

Primary source [MGI:MGI:108079](#)

See related [Ensembl:ENSMUSG00000029076](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Cab45

Summary This gene encodes a member of the CREC family. The encoded protein contains multiple calcium-binding EF-hand motifs. This protein localizes to the Golgi lumen and may be involved in regulating calcium dependent cellular activities. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2014]

Expression Ubiquitous expression in frontal lobe adult (RPKM 24.3), genital fat pad adult (RPKM 24.0) and 28 other tissues [See more](#)

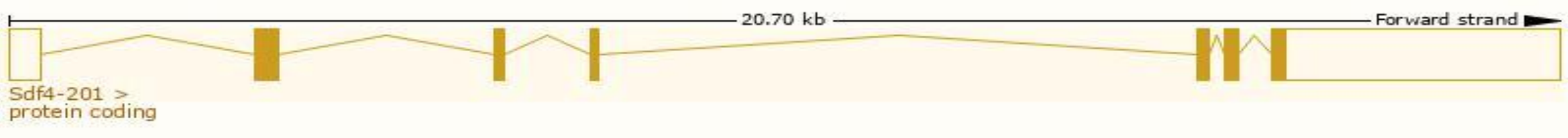
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

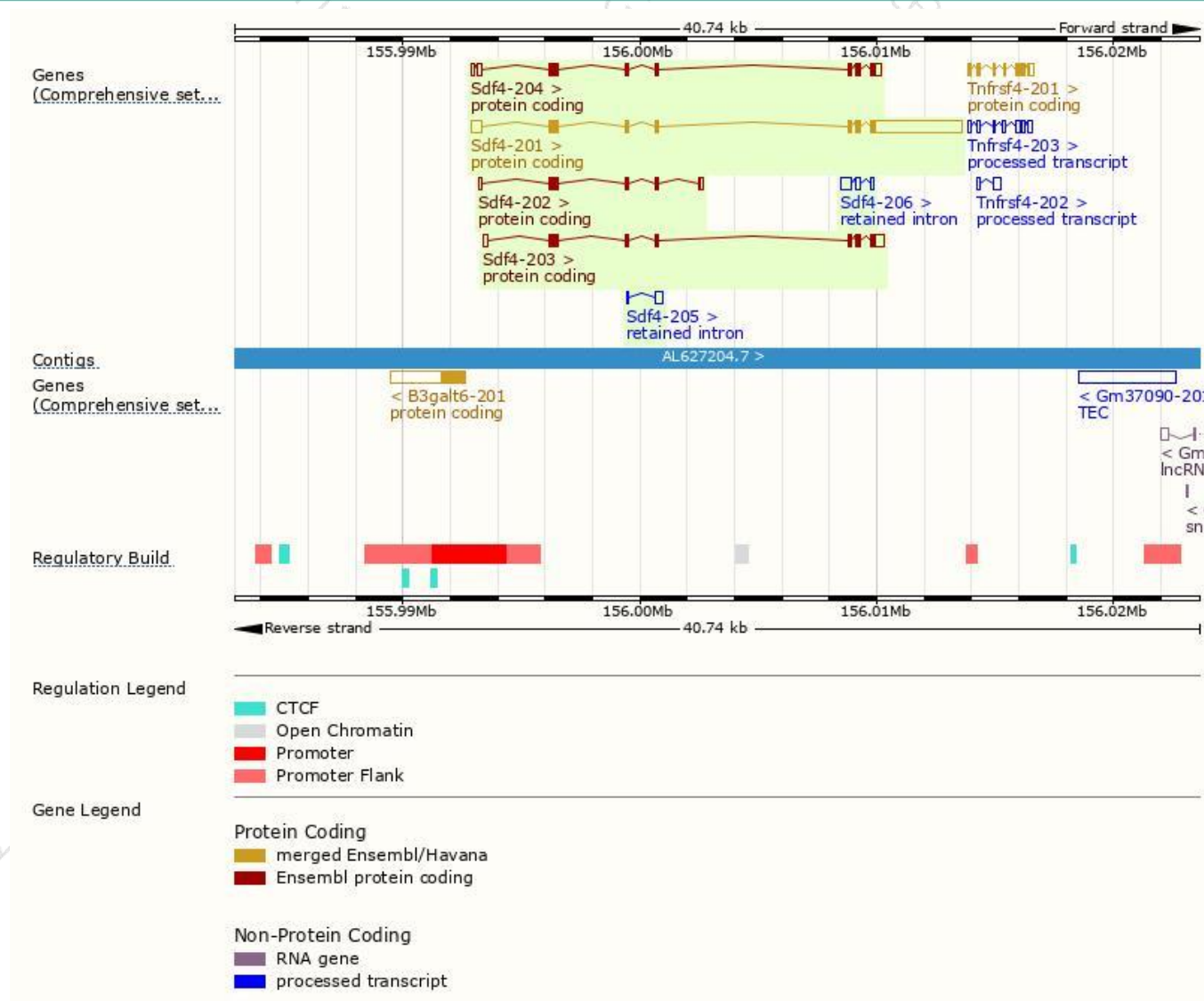
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sdf4-201	ENSMUST00000050078.12	5177	361aa	Protein coding	CCDS19054	Q61112	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Sdf4-204	ENSMUST00000105579.7	1670	361aa	Protein coding	CCDS19054	Q61112	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Sdf4-203	ENSMUST00000105578.1	1654	361aa	Protein coding	CCDS19054	Q61112	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Sdf4-202	ENSMUST00000097734.10	973	218aa	Protein coding	CCDS80198	Q61112	TSL:1 GENCODE basic
Sdf4-206	ENSMUST00000149971.1	696	No protein	Retained intron	-	-	TSL:1
Sdf4-205	ENSMUST00000124872.1	403	No protein	Retained intron	-	-	TSL:2

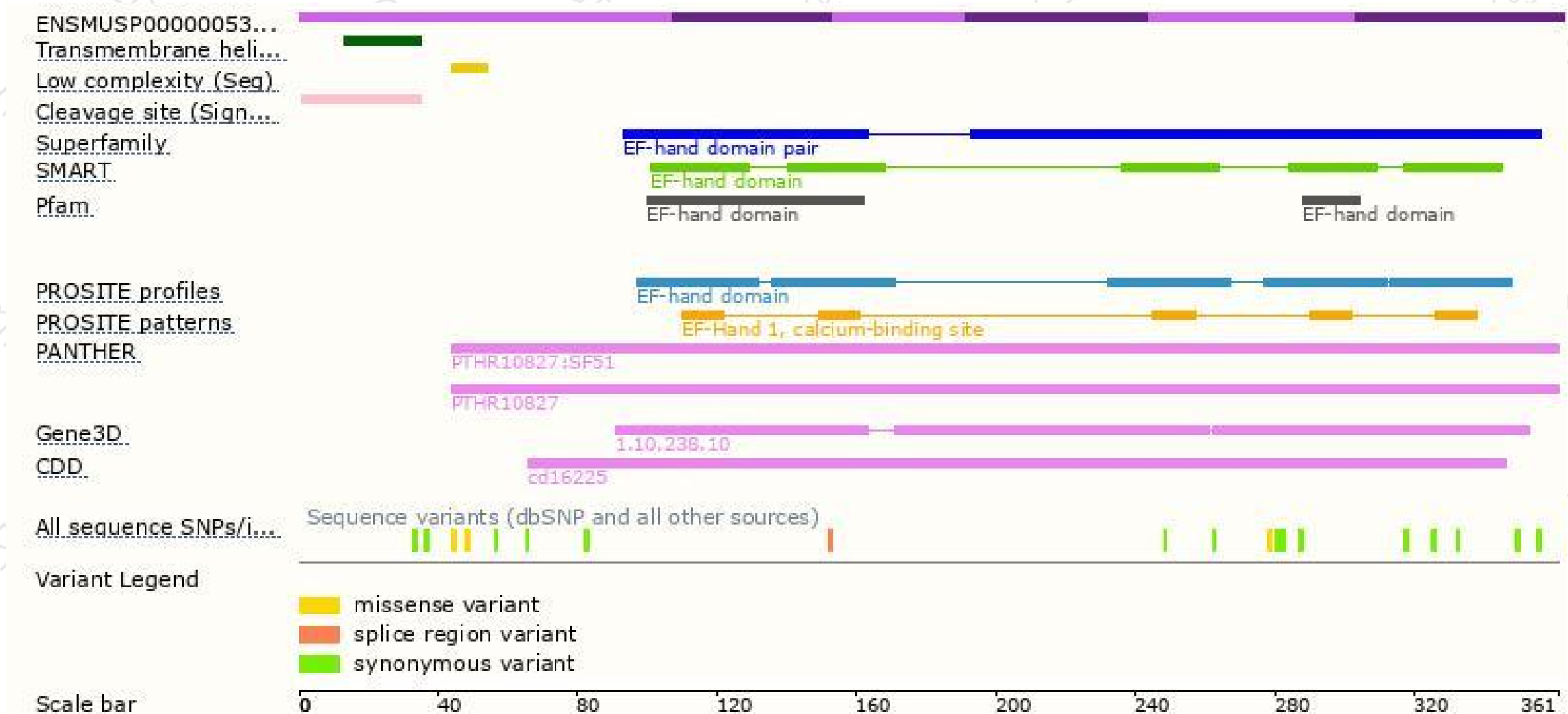
The strategy is based on the design of *Sdf4-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

