

# *Sfn* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Sfn*

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**Project type**

**Cas9-KO**

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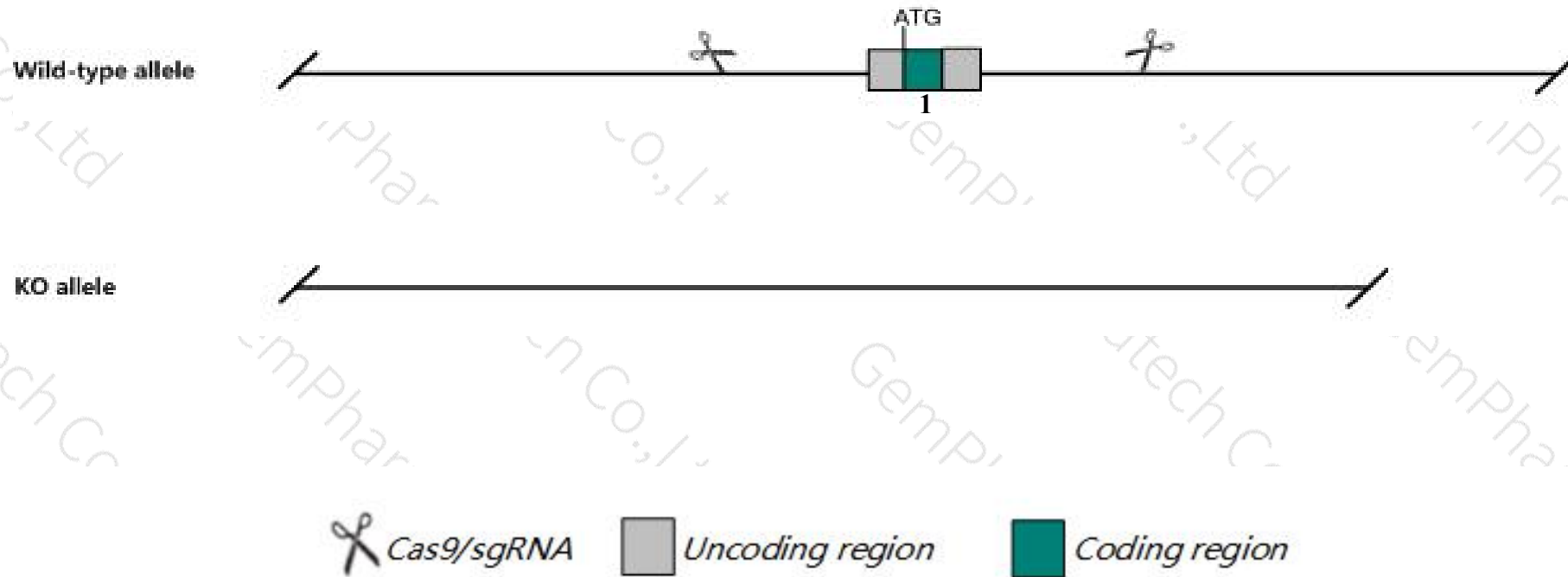
**Strain background**

**C57BL/6J**

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# Knockout strategy

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



- The *Sfn* gene has 1 transcript. According to the structure of *Sfn* gene, exon1 of *Sfn-201* (ENSMUST00000057311.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sfn* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Nullizygous mice show impaired B-cell homeostasis, BCR signaling, and T cell-independent B-cell responses. Homozygous hypomorphs show altered mammary epithelial morphology. Spontaneous mutants die at birth from respiratory stress with severe anomalies in skin, limbs, tails, face and oral cavity.
- The *Sfn* 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.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Sfn stratifin [Mus musculus (house mouse)]

Gene ID: 55948, updated on 7-Apr-2019

### Summary

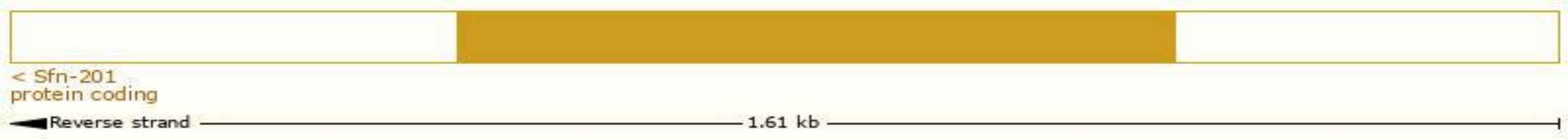
Official Symbol	Sfn provided by <a href="#">MGI</a>
Official Full Name	stratifin provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1891831</a>
See related	<a href="#">Ensembl:ENSMUSG000000047281</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Er, Mme1, Ywhas
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

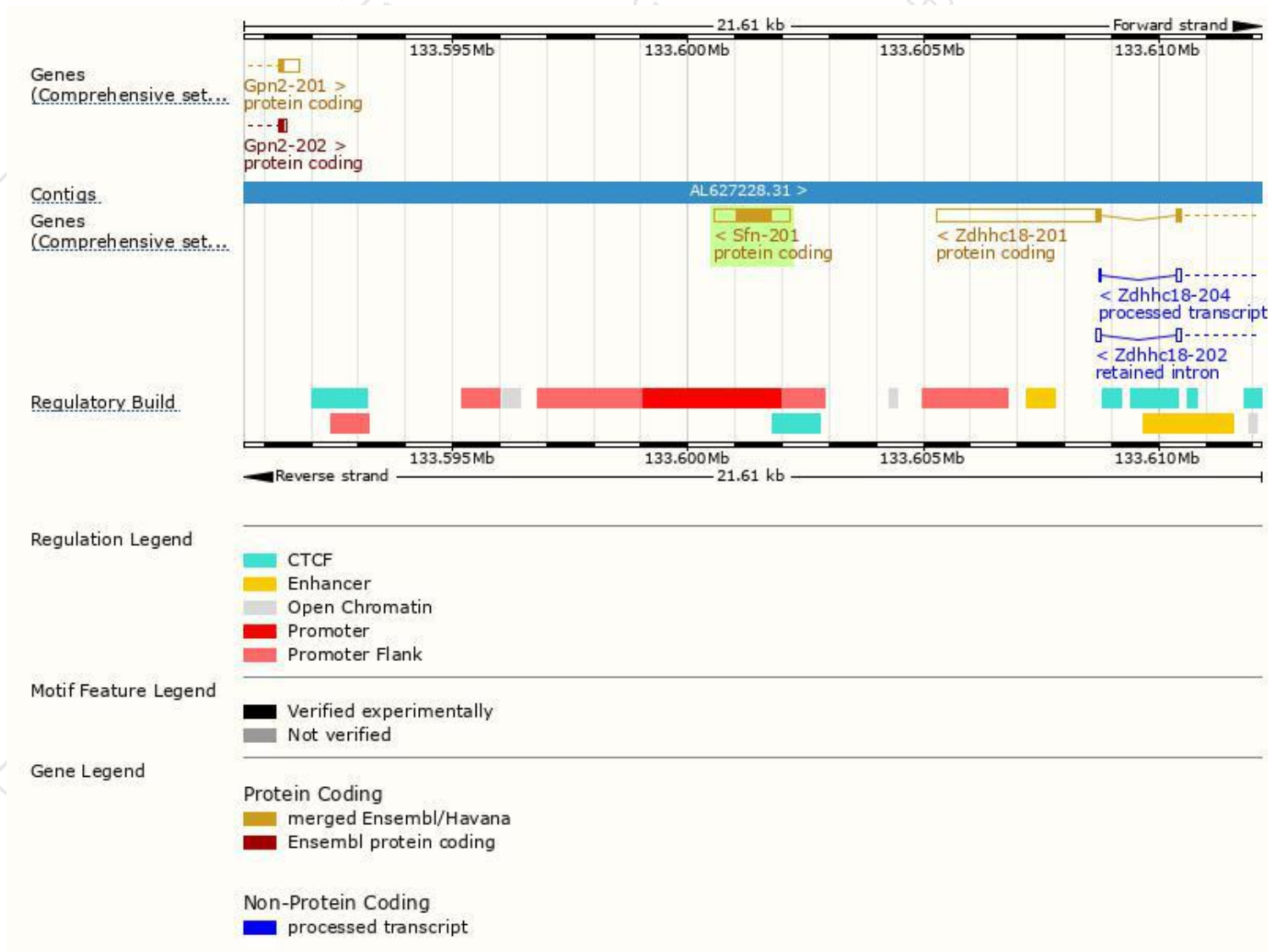
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sfn-201	<a href="#">ENSMUST00000057311.3</a>	1613	<a href="#">248aa</a>	Protein coding	<a href="#">CCDS18754</a>	<a href="#">O70456</a>	TSL:NA GENCODE basic APPRIS P1

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

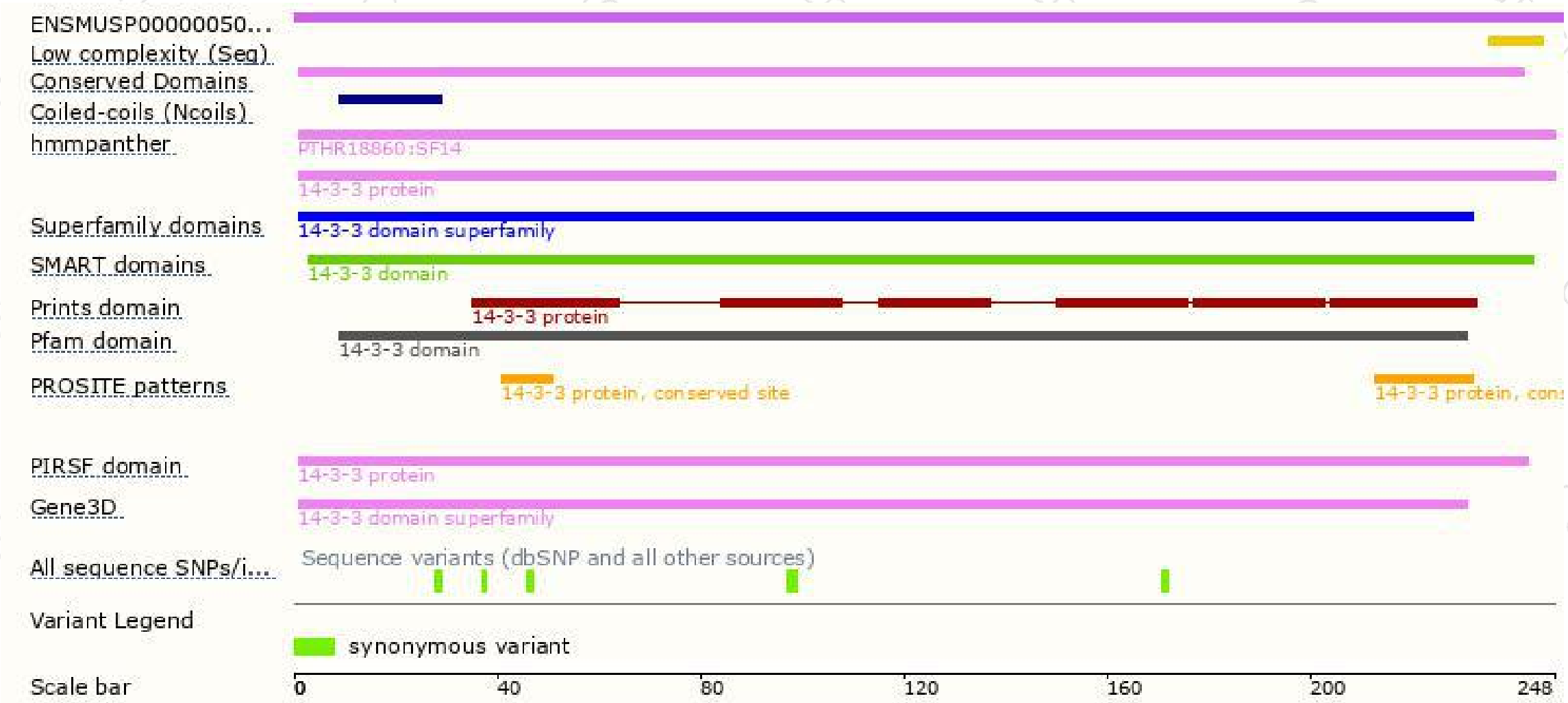


# Genomic location distribution





# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Nullizygous mice show impaired B-cell homeostasis, BCR signaling, and T cell-independent B-cell responses. Homozygous hypomorphs show altered mammary epithelial morphology. Spontaneous mu birth from respiratory stress with severe anomalies in skin, limbs, tails, face and oral cavity.

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

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