

Srebf1 Cas9-KO Strategy

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Overview

Target Gene Name

• Srebf1

Project Type

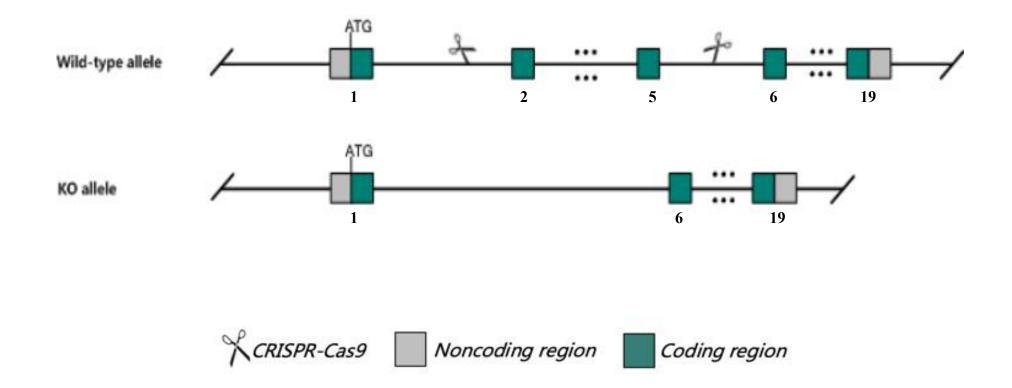
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Strn4 gene.

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Technical Information

- The *Srebf1* gene has 12 transcripts. According to the structure of Srebf1 gene, exon2-exon5 of Srebf1-201(ENSMUST0000020846.8) transcript is recommended as the knockout region. The region contains 959bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify Srebf1 gene. The brief process is as follows: CRISPR-Cas9 system 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.



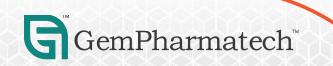
Gene Information

Srebf1 sterol regulatory element binding transcription factor 1 [Mus musculus (house mouse)]

Gene ID: 20787, updated on 12-Jul-2022

Summary	
Official Symbol	Srebf1 provided by MGI
Official Full Name	sterol regulatory element binding transcription factor 1 provided by MGI
Primary source	MGI:MGI:107606
See related	Ensembl:ENSMUSG0000020538
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	ADD1, SREBP1, bHLHd1
Summary	This gene encodes a transcription factor that binds to the sterol regulatory element-1 (SRE1), which is a decamer flanking the low density lipoprotein receptor gene and some genes involved in sterol biosynthesis. The protein is synthesized as a precursor that is attached to the nuclear membrane and endoplasmic reticulum. Following cleavage, the mature protein translocates to the nucleus and activates transcription by binding to the SRE1. Sterols inhibit the cleavage of the precursor, and the mature nuclear form is rapidly catabolized, thereby reducing transcription. The protein is a member of the basic helix-loop-helix-leucine zipper (bHLH-Zip) transcription factor family. Alternatively spliced transcript variants have been characterized for this gene. [provided by RefSeg, Nov 2017]
Expression	Broad expression in mammary gland adult (RPKM 175.8), adrenal adult (RPKM 151.4) and 25 other tissuesSee more
Orthologs	human all

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



Transcript Information

The gene has 12 transcripts, all transcripts are shown below:

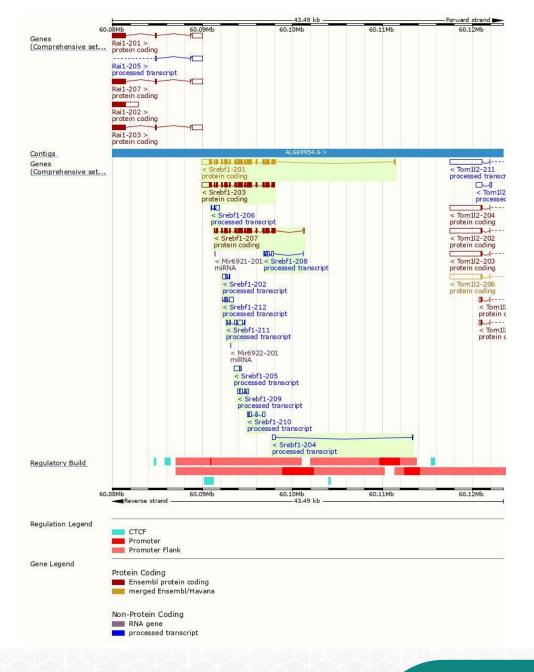
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srebf1-201	ENSMUST0000020846.8	4299	<u>1134aa</u>	Protein coding	CCD524785		TSL:1, GENCODE basic, APPRIS P1,
Srebf1-203	ENSMUST00000134660.8	4063	<u>1076aa</u>	Protein coding	-		CDS 5' incomplete , TSL:1 ,
Srebf1-207	ENSMUST00000144942.2	3177	<u>1022aa</u>	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Srebf1-211	ENSMUST00000154925.2	945	No protein	Processed transcript			TSL:5,
Srebf1-209	ENSMUST00000149238.2	826	No protein	Processed transcript	-		TSL:2 ,
Srebf1-212	ENSMUST00000156304.2	755	No protein	Processed transcript	-		TSL:3 ,
Srebf1-205	ENSMUST00000136426.2	750	No protein	Processed transcript	-		TSL:2,
Srebf1-208	ENSMUST00000147967.2	686	No protein	Processed transcript	14		TSL:3 ,
Srebf1-210	ENSMUST00000154620.2	662	No protein	Processed transcript	-		TSL:2,
Srebf1-206	ENSMUST00000141161.2	540	No protein	Processed transcript	-		TSL:2 ,
Srebf1-202	ENSMUST00000129869.8	516	No protein	Processed transcript	12		TSL:1,
Srebf1-204	ENSMUST00000136215.2	367	No protein	Processed transcript	-		TSL:3 ,

The strategy is based on the design of *Srebf1-201* transcript, the transcription is shown below:



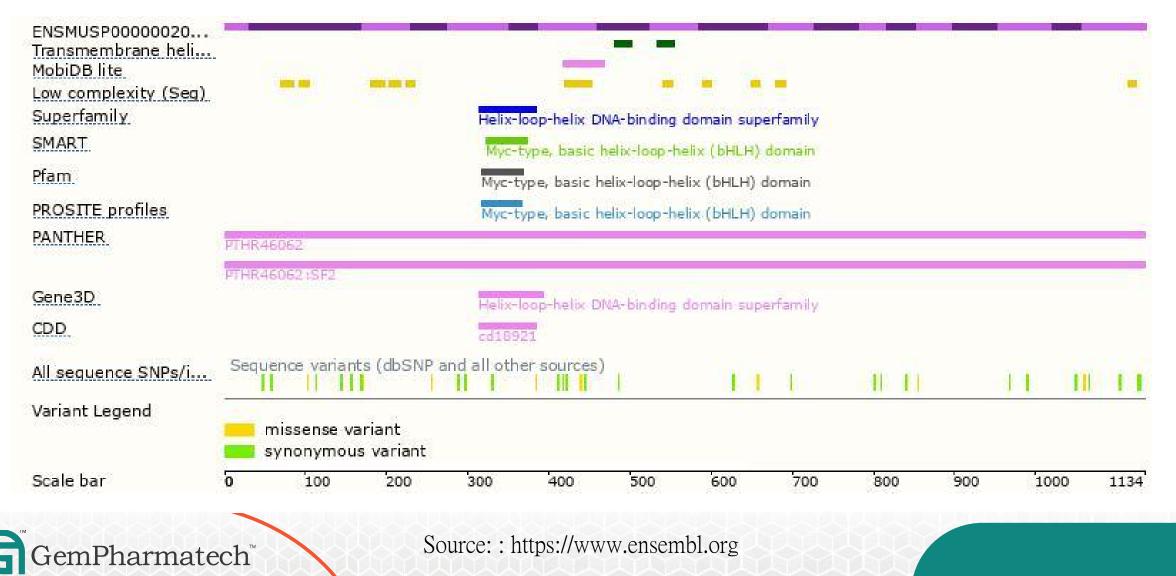
Genomic Information

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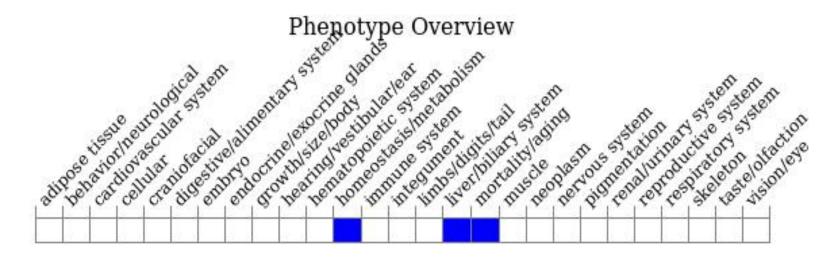


Source: : https://www.ensembl.org

Protein Information



Mouse Phenotype Information (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,mice homozygous for a knock-out allele of transcript A die between E11.5 and E14.5. Mice homozygous for a knock-out allele of transcript C exhibit decreased circulating triglyceride levels. Mice homozygous for a gene trap allele exhibit decreased hepatictriglyceride storage.

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Source: https://www.informatics.jax.org

Important Information

- The *Srebf1* gene is located on the Chr11. 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.

