

Scap Cas9-KO Strategy

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Project Overview

Project Name

Scap

Project type

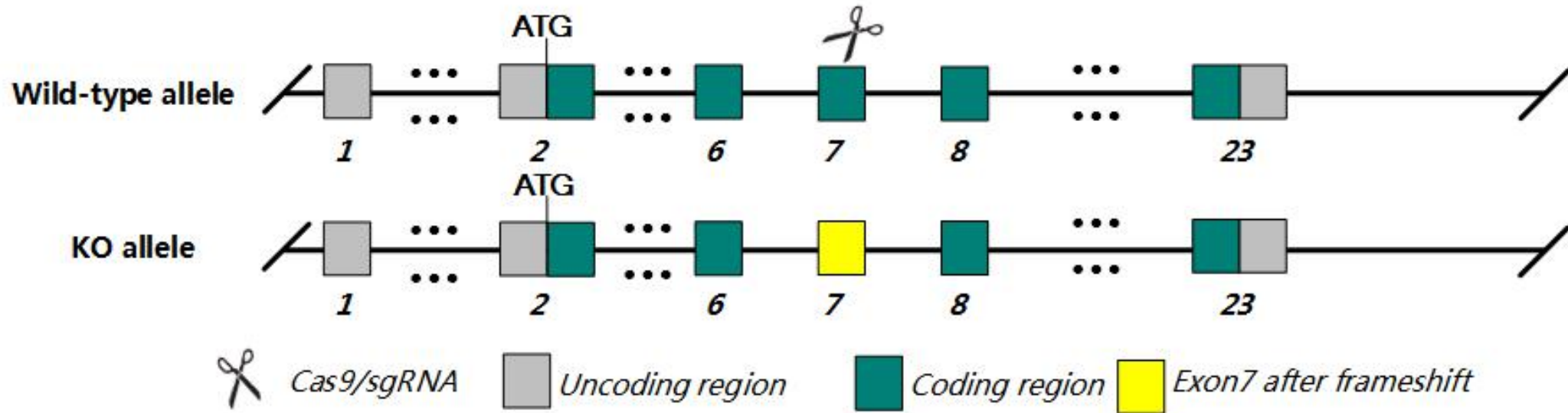
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

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



- The *Scap* gene has 10 transcripts. According to the structure of *Scap* gene, partial sequence of exon7 of *Scap-201* (ENSMUST00000098350.9) transcript is recommended as the knockout. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Scap* 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, Mice homozygous for a transgenic gene disruption exhibit decreased body size.
- The *Scap* gene is located on the Chr9. 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)

Scap SREBF chaperone [Mus musculus (house mouse)]

Gene ID: 235623, updated on 9-Apr-2019

Summary



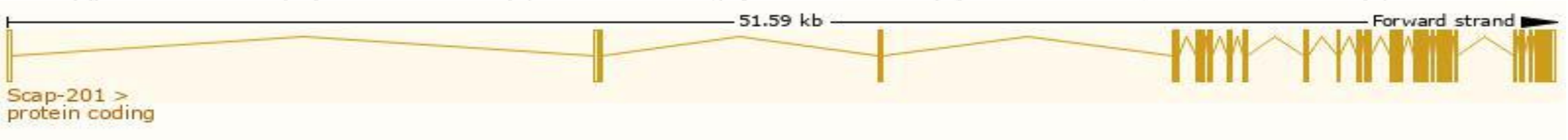
Official Symbol	Scap provided by MGI
Official Full Name	SREBF chaperone provided by MGI
Primary source	MGI:MGI:2135958
See related	Ensembl:ENSMUSG00000032485
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9530044G19, mKIAA0199
Expression	Ubiquitous expression in ovary adult (RPKM 50.5), adrenal adult (RPKM 43.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

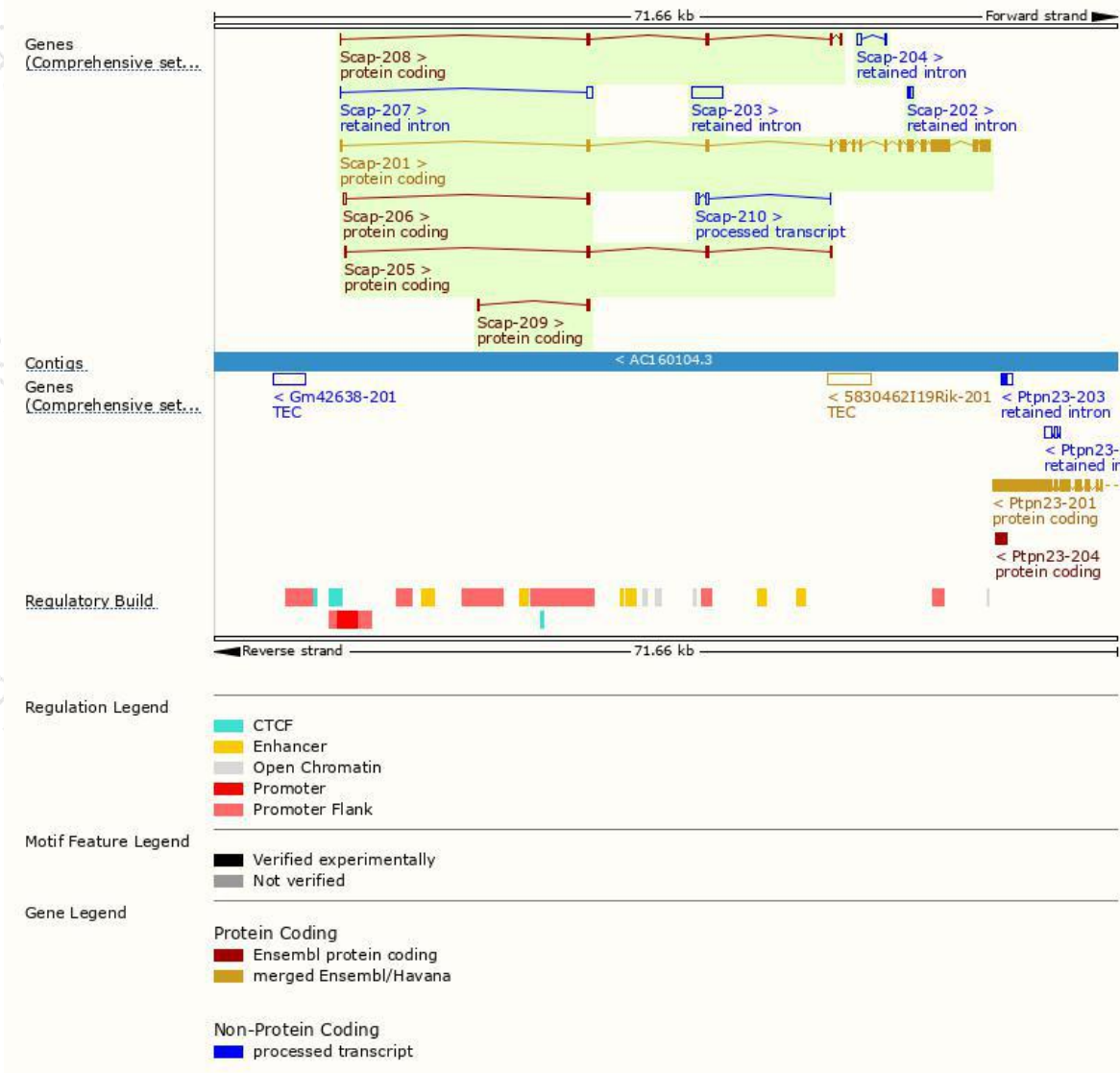
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scap-201	ENSMUST00000098350.9	4227	1276aa	Protein coding	CCDS23564	Q6GQT6	TSL:1 GENCODE basic APPRIS P1
Scap-208	ENSMUST00000198976.4	619	153aa	Protein coding	-	A0A0G2JFZ9	CDS 3' incomplete TSL:5
Scap-205	ENSMUST00000197630.2	597	123aa	Protein coding	-	A0A0G2JEV4	CDS 3' incomplete TSL:3
Scap-206	ENSMUST00000198761.4	432	40aa	Protein coding	-	A0A0G2JDQ3	CDS 3' incomplete TSL:2
Scap-209	ENSMUST00000199709.2	362	40aa	Protein coding	-	A0A0G2JDQ3	CDS 3' incomplete TSL:2
Scap-210	ENSMUST00000199886.1	353	No protein	Processed transcript	-	-	TSL:3
Scap-203	ENSMUST00000196465.1	2501	No protein	Retained intron	-	-	TSL:NA
Scap-204	ENSMUST00000196775.1	460	No protein	Retained intron	-	-	TSL:3
Scap-207	ENSMUST00000198871.1	425	No protein	Retained intron	-	-	TSL:2
Scap-202	ENSMUST00000196424.1	358	No protein	Retained intron	-	-	TSL:2

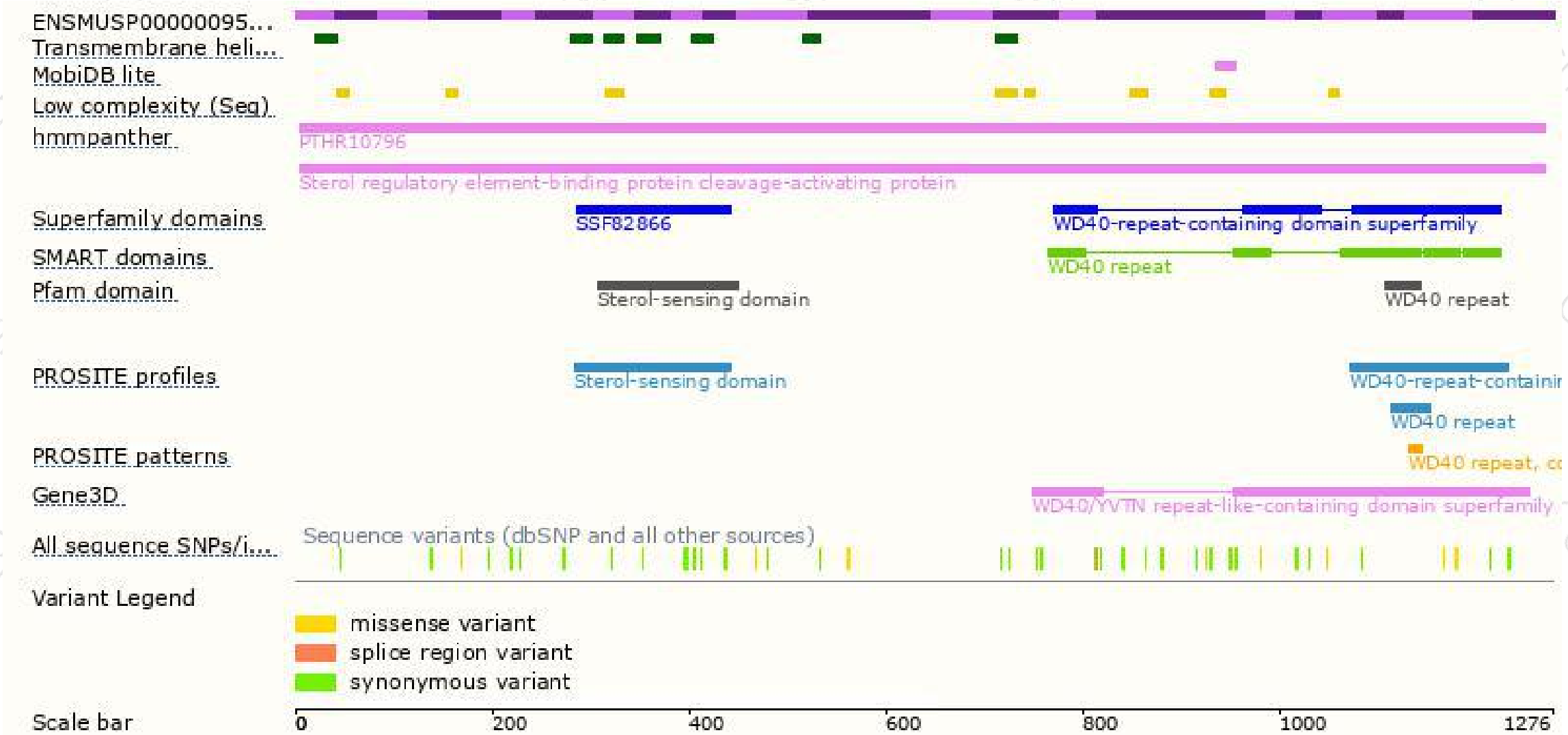
The strategy is based on the design of *Scap-201* transcript,The transcription is shown below



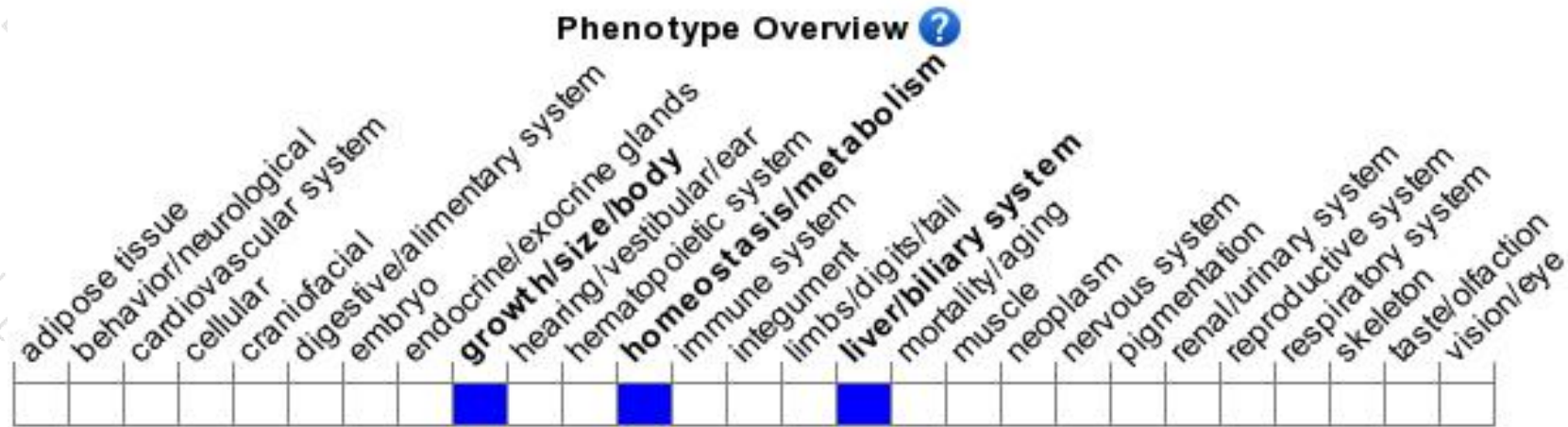
Genomic location distribution



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, Mice homozygous for a transgenic gene disruption exhibit decreased body size.

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

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