

Tm9sf4 Cas9-KO Strategy

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Project Overview

Project Name

Tm9sf4

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tm9sf4* gene. The schematic diagram is as follows:



- The *Tm9sf4* gene has 10 transcripts. According to the structure of *Tm9sf4* gene, exon2-exon17 of *Tm9sf4-201* (ENSMUST00000089027.2) transcript is recommended as the knockout region. The region contains most 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 *Tm9sf4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutants exhibit abnormal hair follicles and sebaceous glands, vertebrae and rib abnormalities, and increased circulating cholesterol, calcium, albumin, and total protein levels.
- The *Tm9sf4* gene is located on the Chr2. 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)

Tm9sf4 transmembrane 9 superfamily protein member 4 [Mus musculus (house mouse)]

Gene ID: 99237, updated on 31-Jan-2019

Summary



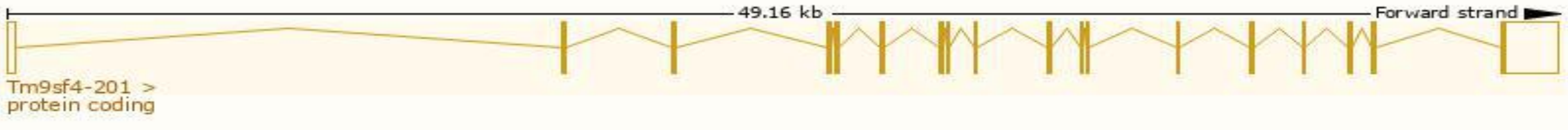
Official Symbol	Tm9sf4 provided by MGI
Official Full Name	transmembrane 9 superfamily protein member 4 provided by MGI
Primary source	MGI:MGI:2139220
See related	Ensembl:ENSMUSG00000068040
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA986553, AU045326, B930079E06, mKIAA0255
Expression	Ubiquitous expression in colon adult (RPKM 30.8), limb E14.5 (RPKM 21.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

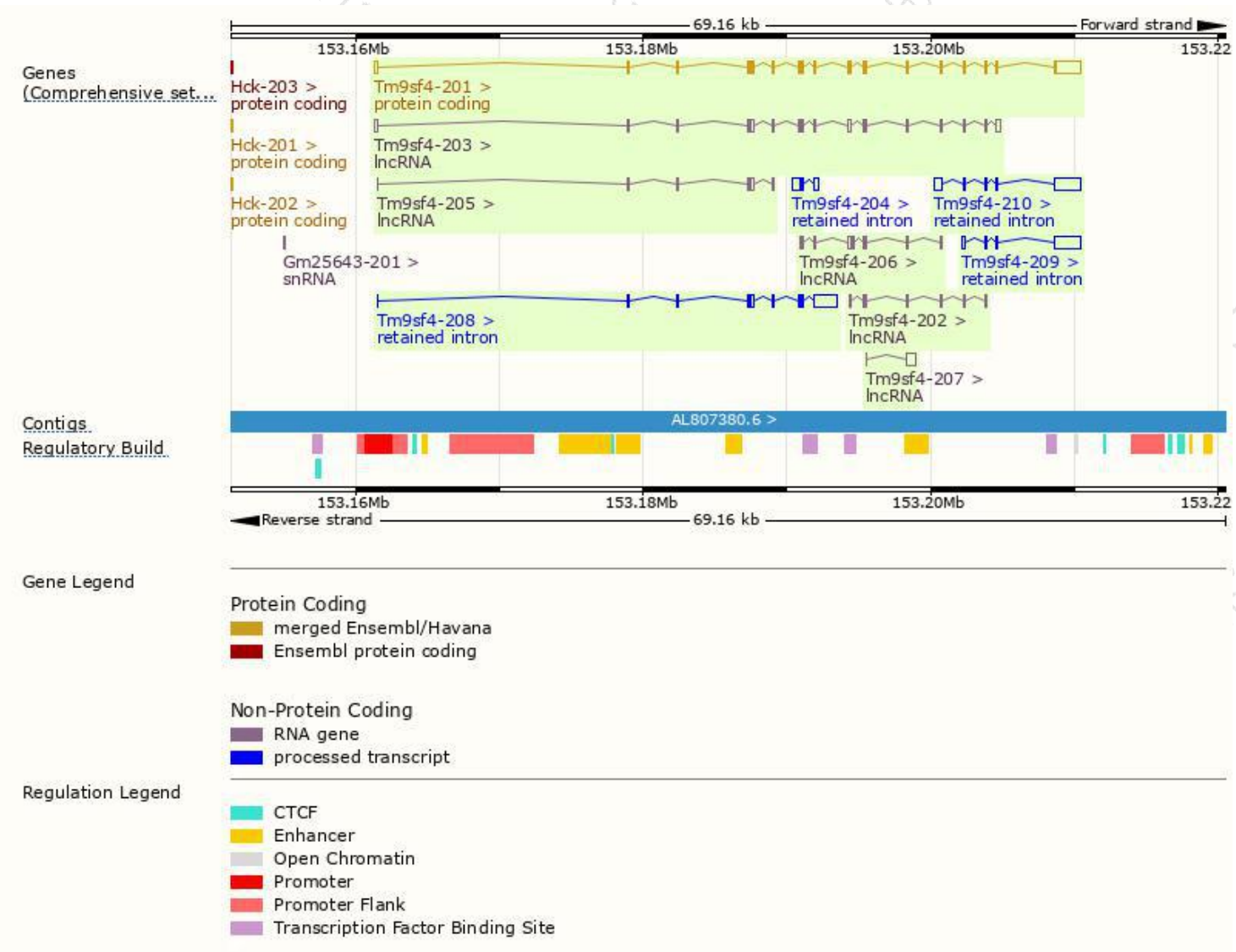
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tm9sf4-201	ENSMUST00000089027.2	3896	643aa	Protein coding	CCDS16906	Q8BH24	TSL:1 GENCODE basic APPRIS P1
Tm9sf4-210	ENSMUST00000152807.7	2705	No protein	Retained intron	-	-	TSL:1
Tm9sf4-208	ENSMUST00000147978.7	2473	No protein	Retained intron	-	-	TSL:1
Tm9sf4-209	ENSMUST00000149390.1	2338	No protein	Retained intron	-	-	TSL:1
Tm9sf4-204	ENSMUST00000140988.7	921	No protein	Retained intron	-	-	TSL:3
Tm9sf4-203	ENSMUST00000137446.7	2274	No protein	lncRNA	-	-	TSL:1
Tm9sf4-206	ENSMUST00000145010.7	794	No protein	lncRNA	-	-	TSL:5
Tm9sf4-202	ENSMUST00000134922.7	668	No protein	lncRNA	-	-	TSL:3
Tm9sf4-205	ENSMUST00000141220.7	657	No protein	lncRNA	-	-	TSL:5
Tm9sf4-207	ENSMUST00000146477.1	604	No protein	lncRNA	-	-	TSL:5

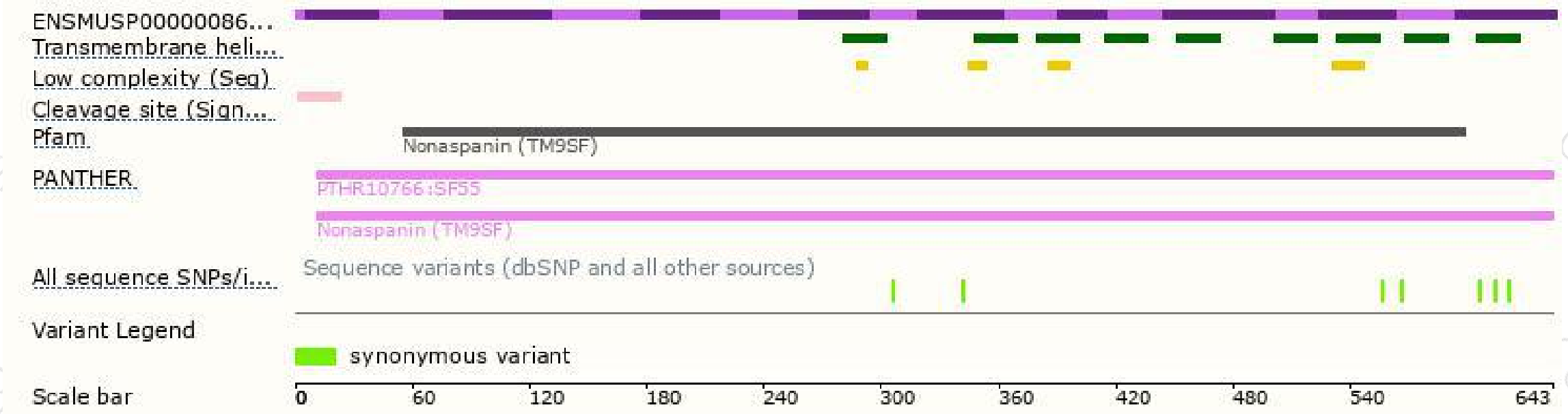
The strategy is based on the design of *Tm9sf4-201* transcript,The transcription is shown below



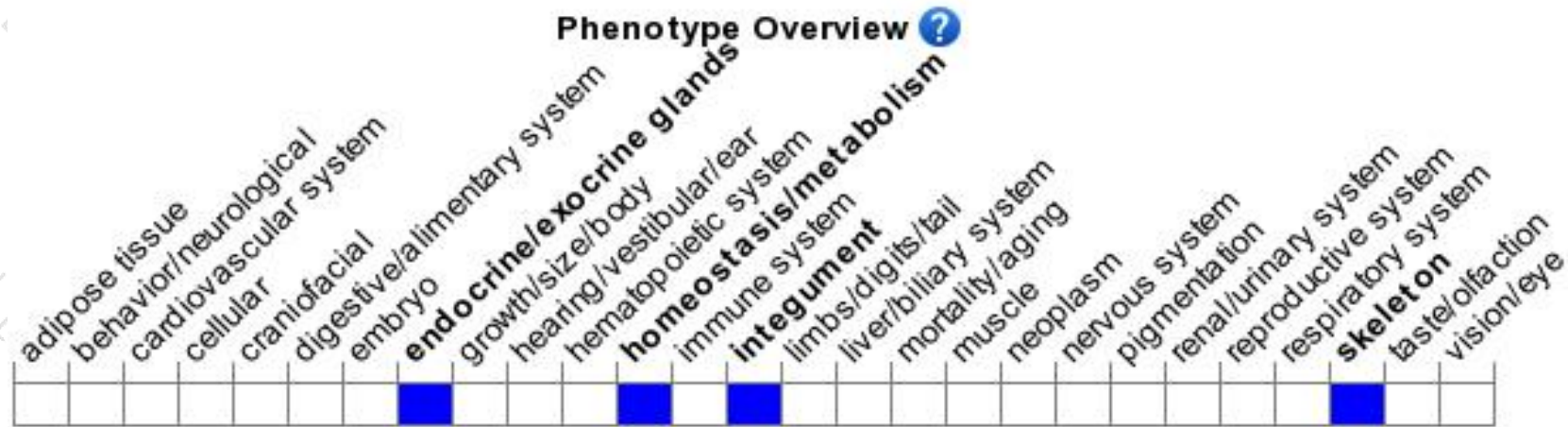
Genomic location distribution



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, Homozygous mutants exhibit abnormal hair follicles and sebaceous glands, vertebrae and rib abnormalities, and increased circulating cholesterol, calcium, albumin, and total protein levels.

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

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