

Scara5 Cas9-KO Strategy

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Project Overview

Project Name

Scara5

Project type

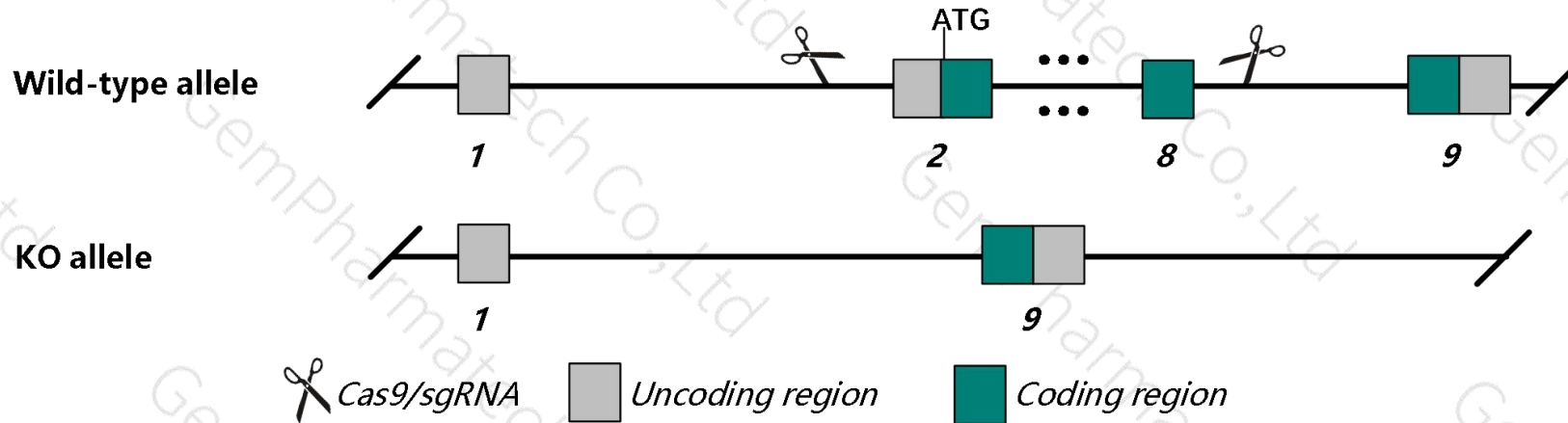
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scara5* gene. The schematic diagram is as follows:



- The *Scara5* gene has 3 transcripts. According to the structure of *Scara5* gene, exon2-exon8 of *Scara5-201* (ENSMUST00000022610.14) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Scara5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous deletion of this gene results in decreased male fertility and lymphocytic infiltration of the stroma of various tissues, particularly in the lungs.
- The *Scara5* gene is located on the Chr14. 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)

Scara5 scavenger receptor class A, member 5 [*Mus musculus* (house mouse)]

Gene ID: 71145, updated on 12-Aug-2019

Summary

- Official Symbol** Scara5 provided by MGI
- Official Full Name** scavenger receptor class A, member 5 provided by MGI
- Primary source** MGI:MGI:1918395
- See related** Ensembl:ENSMUSG00000022032
- 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** Tesr; AV278087; 4932433F15Rik; 4933425F03Rik
- Expression** Biased expression in bladder adult (RPKM 37.1), mammary gland adult (RPKM 14.4) and 10 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 14; 14 D1 See Scara5 in [Genome Data Viewer](#)

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	14	NC_000080.6 (65666403..65764826)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	14	NC_000080.5 (66285240..66383663)

Transcript information (Ensembl)

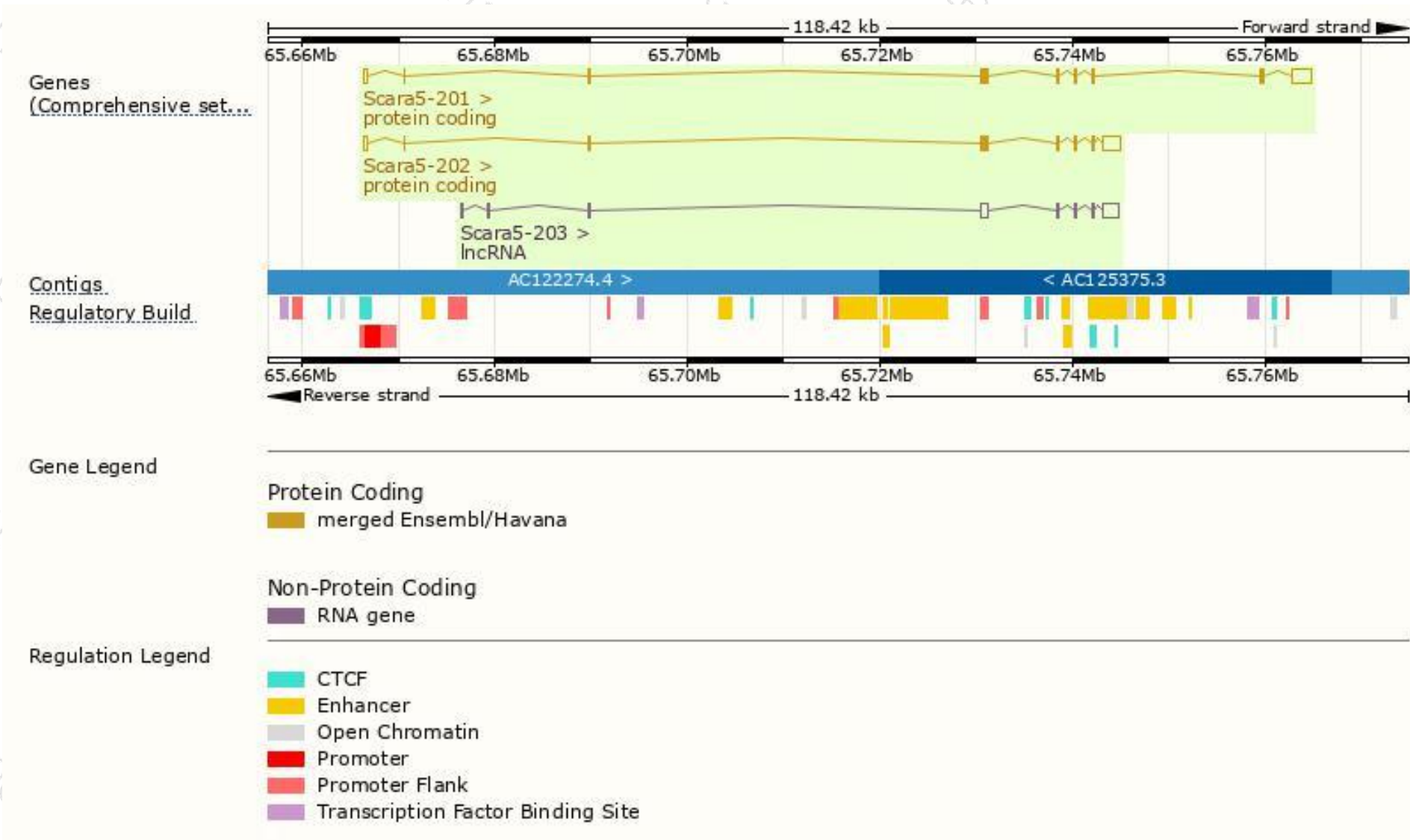
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scara5-201	ENSMUST00000022610.14	3794	491aa	Protein coding	CCDS27214	Q8K299	TSL:1 GENCODE basic APPRIS P1
Scara5-202	ENSMUST00000069226.6	3262	387aa	Protein coding	CCDS49523	Q8K299	TSL:1 GENCODE basic
Scara5-203	ENSMUST00000154373.1	3179	No protein	lncRNA	-	-	TSL:1

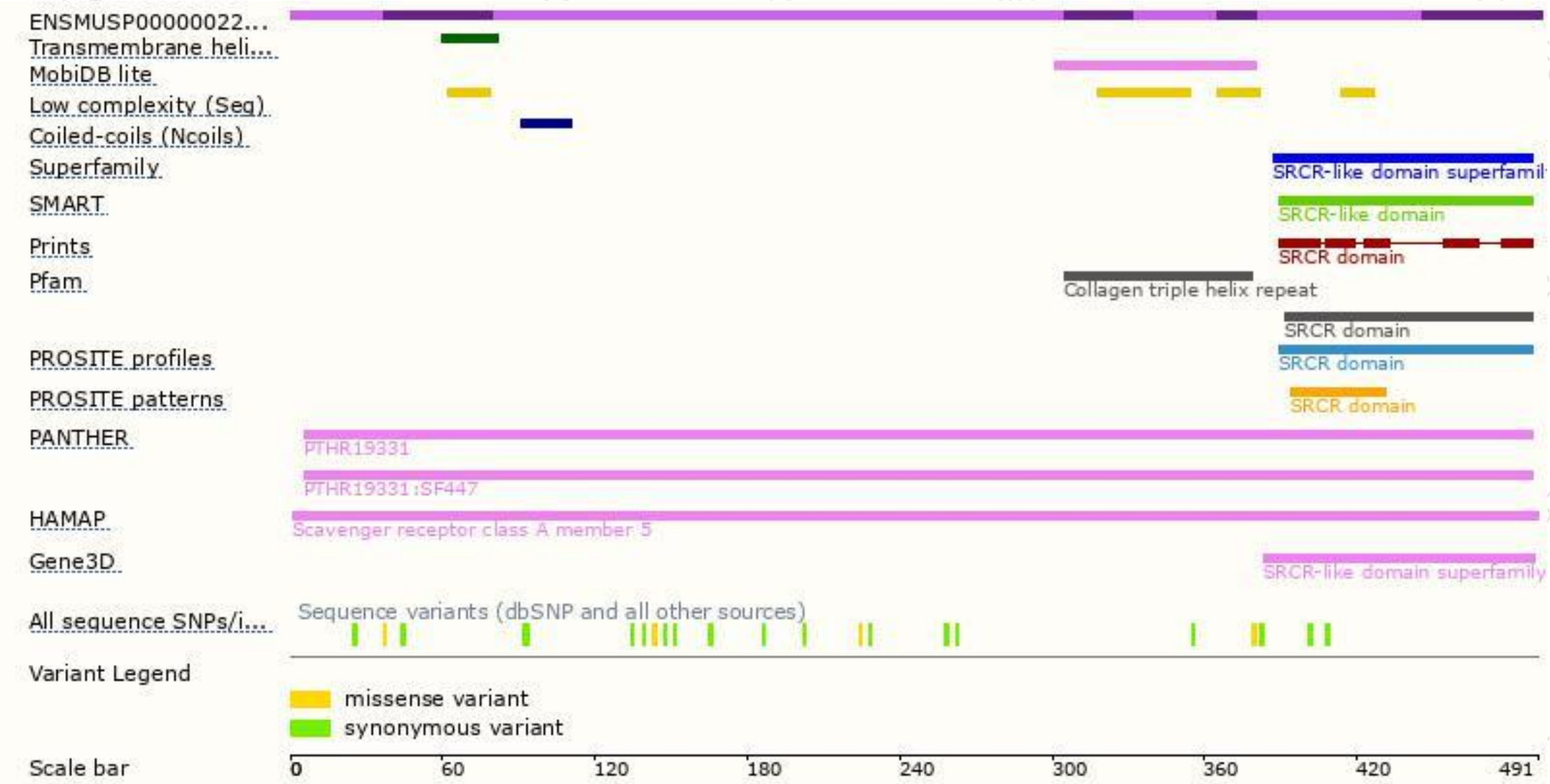
The strategy is based on the design of *Scara5-201* transcript,The transcription is shown below



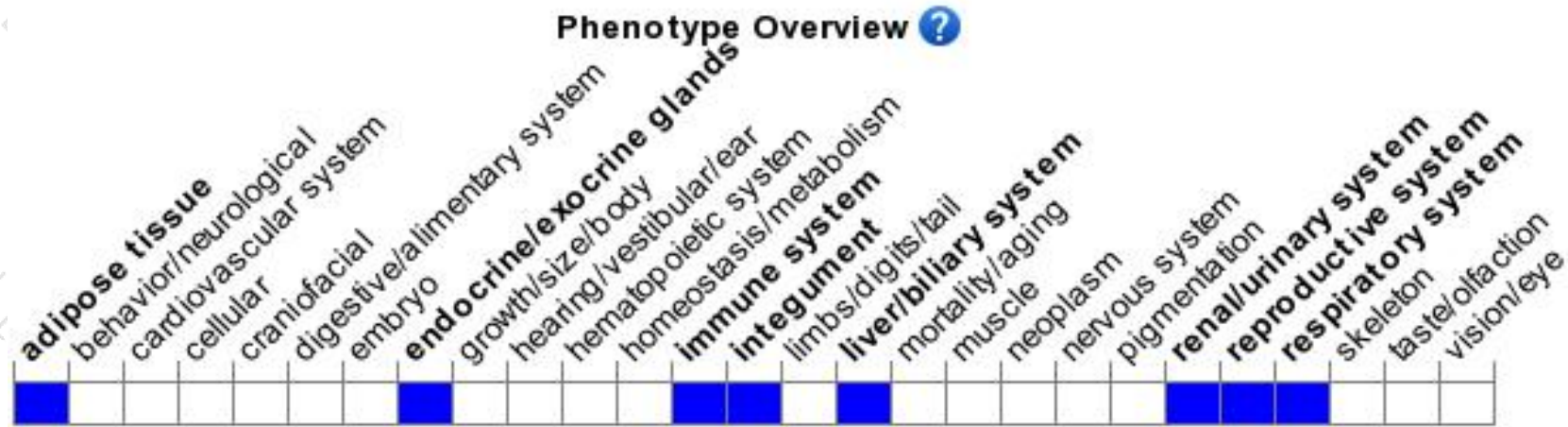
Genomic location distribution



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 deletion of this gene results in decreased male fertility and lymphocytic infiltration of the stroma of various tissues, particularly in the lungs.

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

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