

***Smoc2* Cas9-KO Strategy**

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Project Overview

Project Name

Smoc2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smoc2* gene. The schematic diagram is as follows:



- The *Smoc2* gene has 7 transcripts. According to the structure of *Smoc2* gene, exon2 of *Smoc2-201* (ENSMUST00000024660.8) transcript is recommended as the knockout region. The region contains 172bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Smoc2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for one KO allele exhibit protection from induced kidney fibrosis and reduced interstitial myofibroblast accumulation. Another KO allele leads to shortening and widening of the skull.
- The *Smoc2* gene is located on the Chr17. 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)

Smoc2 SPARC related modular calcium binding 2 [*Mus musculus* (house mouse)]

Gene ID: 64074, updated on 14-Oct-2019

Summary

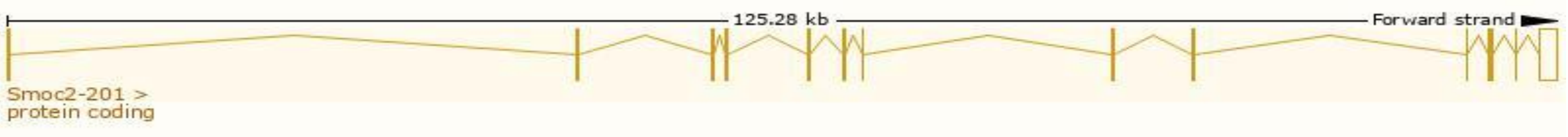
Official Symbol	Smoc2 provided by MGI
Official Full Name	SPARC related modular calcium binding 2 provided by MGI
Primary source	MGI:MGI:1929881
See related	Ensembl:ENSMUSG00000023886
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Smoc2l; 1700056C05Rik; 5430426J21Rik
Expression	Broad expression in ovary adult (RPKM 125.2), subcutaneous fat pad adult (RPKM 55.4) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

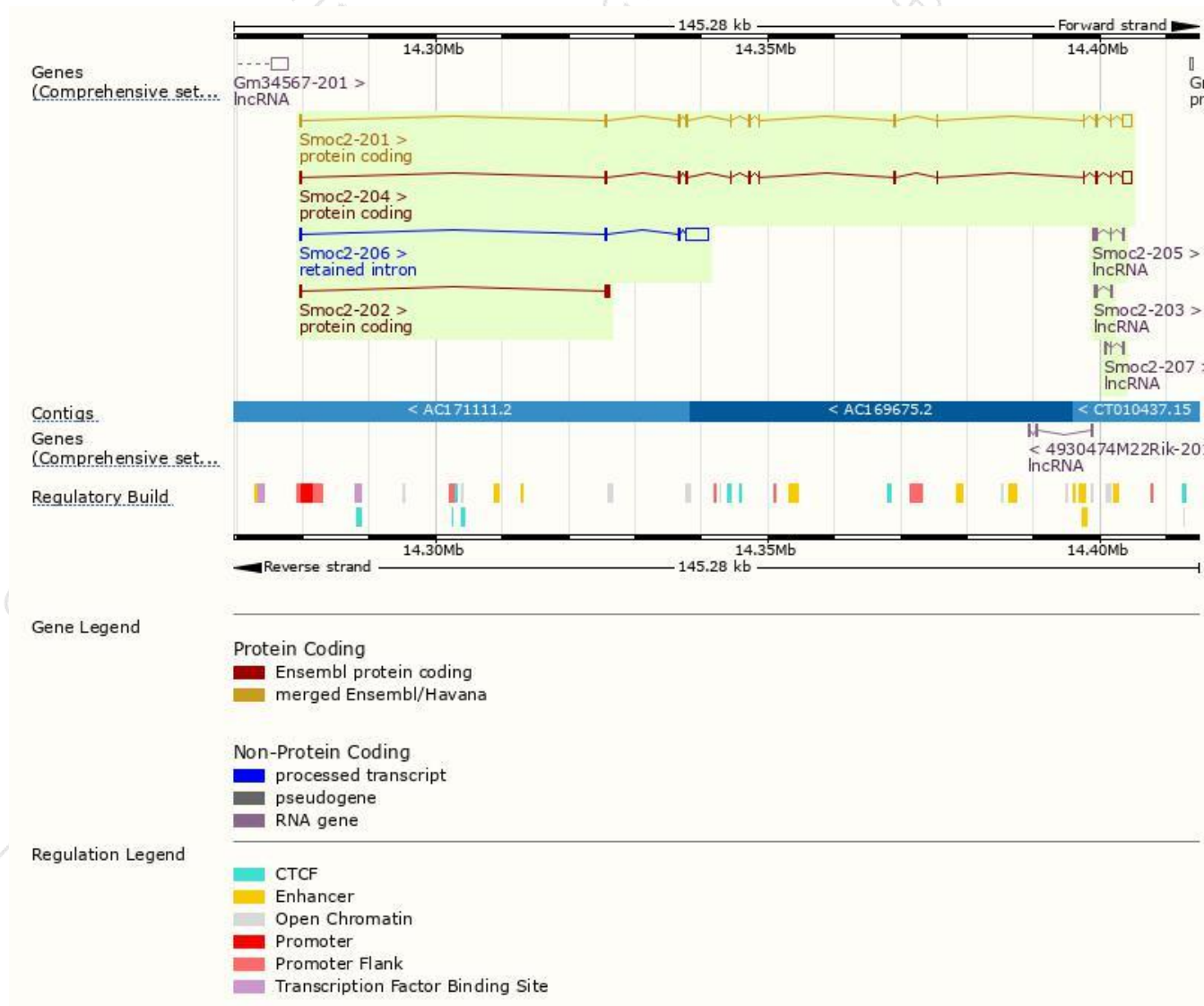
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smoc2-201	ENSMUST00000024660.8	2832	447aa	Protein coding	CCDS37442	Q8CD91	TSL:1 GENCODE basic APPRIS P1
Smoc2-204	ENSMUST00000233344.1	2817	458aa	Protein coding	-	A0A3B2WCK7	GENCODE basic
Smoc2-202	ENSMUST00000232923.1	588	89aa	Protein coding	-	A0A3B2WCQ8	GENCODE basic
Smoc2-206	ENSMUST00000233540.1	3972	No protein	Retained intron	-	-	
Smoc2-205	ENSMUST00000233526.1	572	No protein	lncRNA	-	-	
Smoc2-203	ENSMUST00000232936.1	521	No protein	lncRNA	-	-	
Smoc2-207	ENSMUST00000233686.1	337	No protein	lncRNA	-	-	

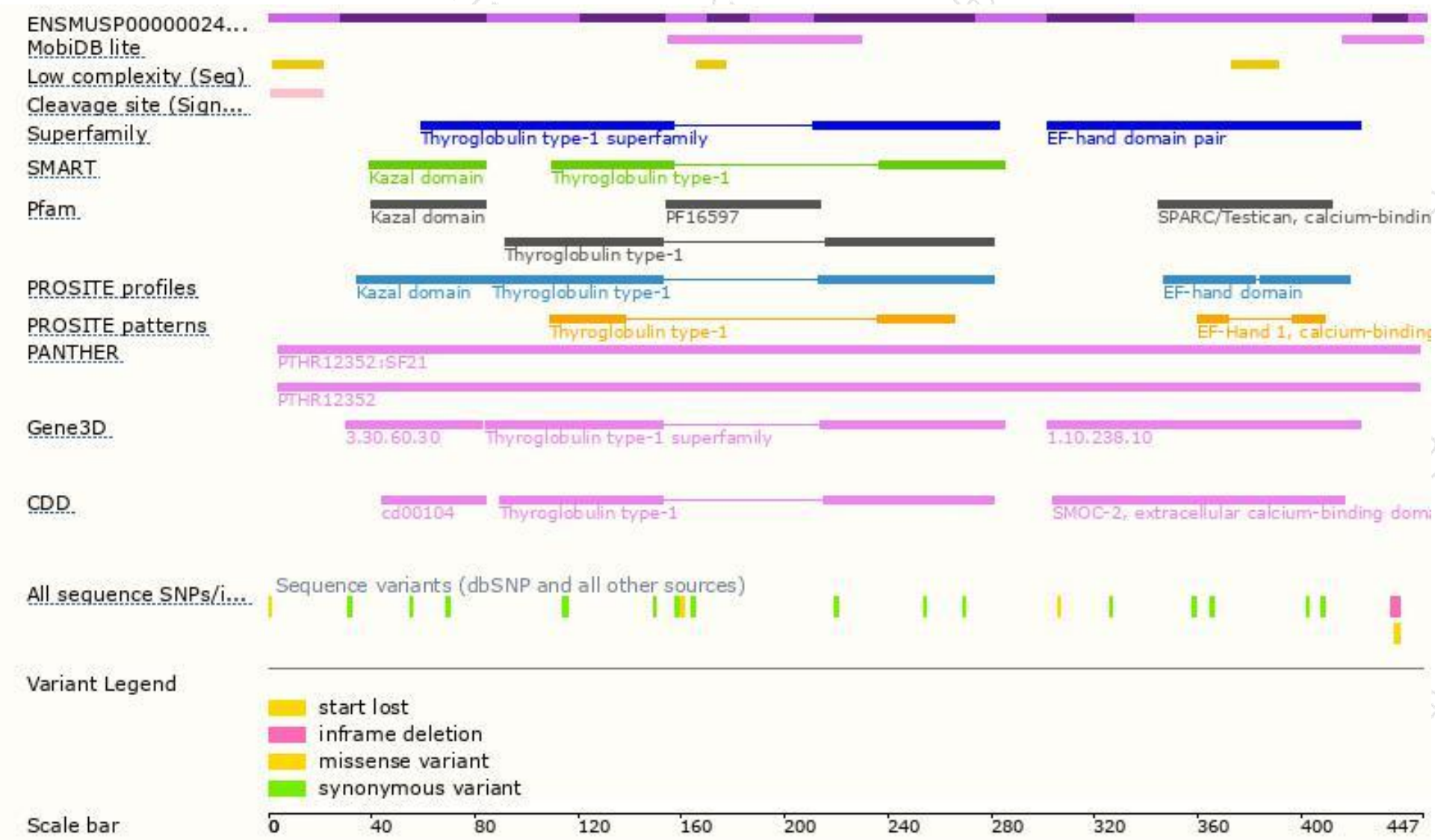
The strategy is based on the design of *Smoc2-201* transcript,The transcription is shown below



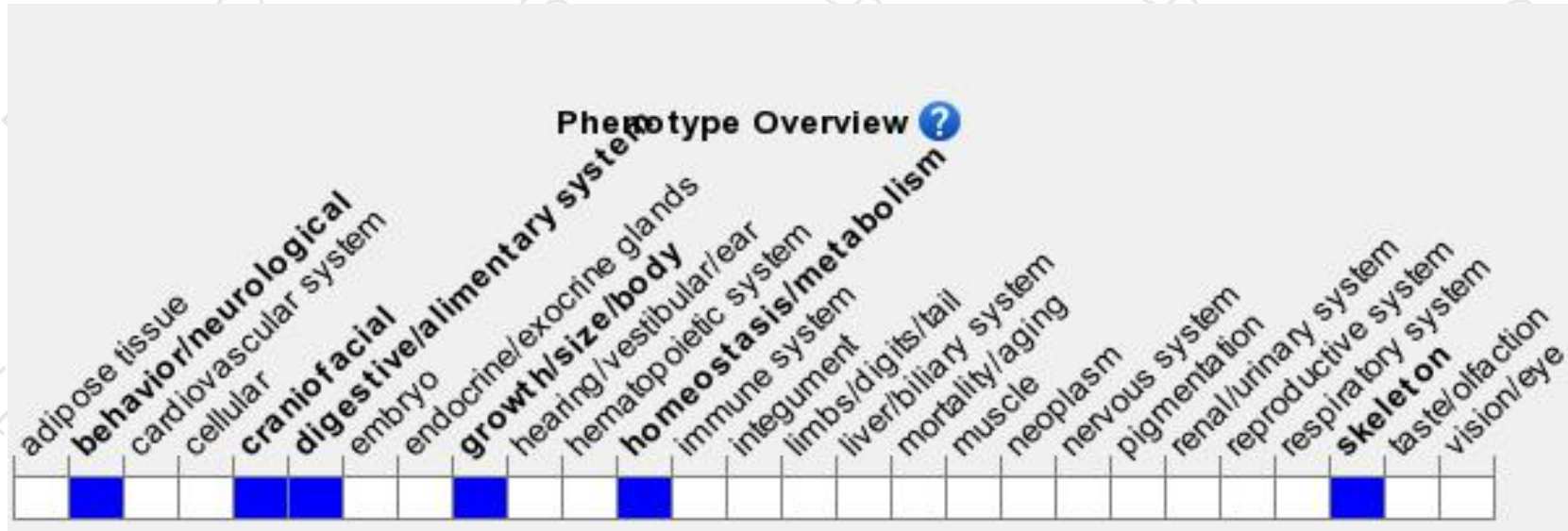
Genomic location distribution



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 one KO allele exhibit protection from induced kidney fibrosis and reduced interstitial myofibroblast accumulation. Another KO allele leads to shortening and widening of the skull.

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

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