

Scml4 Cas9-KO Strategy

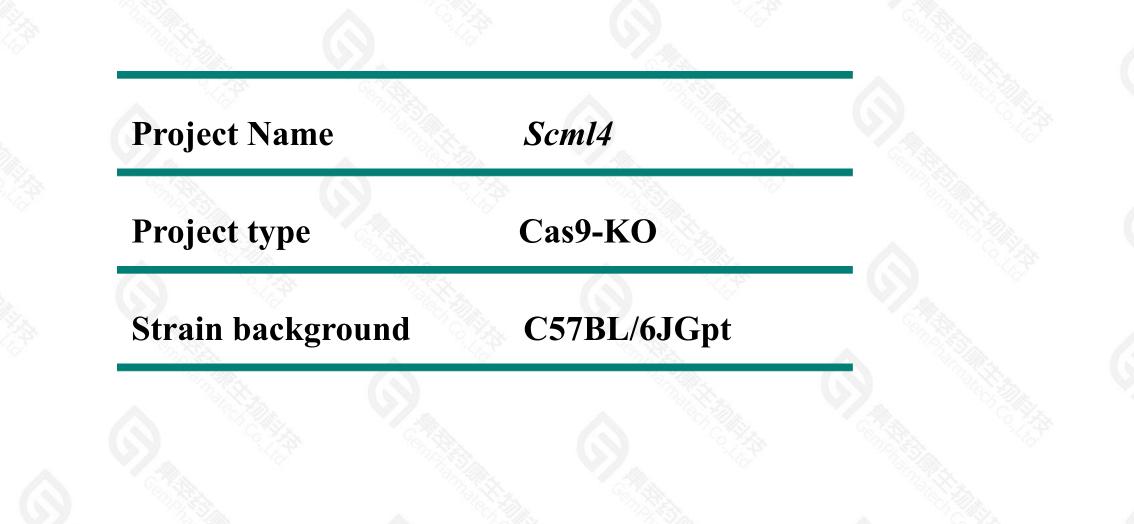
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Reviewer: Rui Xiong

Design Date: 2021-7-6

Project Overview





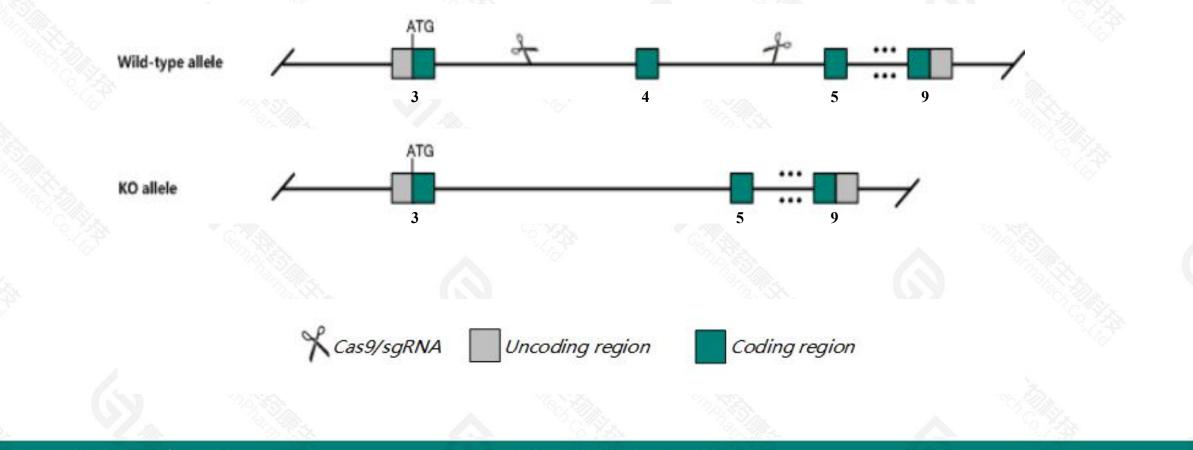
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Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Scml4* gene. The schematic diagram is as follows:



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> The *Scml4* gene has 9 transcripts. According to the structure of *Scml4* gene, exon4 of *Scml4*-201(ENSMUST00000063063.14) transcript is recommended as the knockout region. The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Scml4* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.



- > The *Scml4* gene is located on the Chr10. 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.

Scml4 Scm polycomb group protein like 4 [Mus musculus (house mouse)]

Gene ID: 268297, updated on 17-Dec-2020

Summary

Official Symbol	Scml4 provided by MGI
Official Full Name	Scm polycomb group protein like 4 provided by MGI
Primary source	MGI:MGI:2446140
See related	Ensembl:ENSMUSG00000044770
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	9330161D17, mFLJ00197
Expression	Broad expression in spleen adult (RPKM 3.2), thymus adult (RPKM 2.9) and 22 other tissuesSee more
Orthologs	human all

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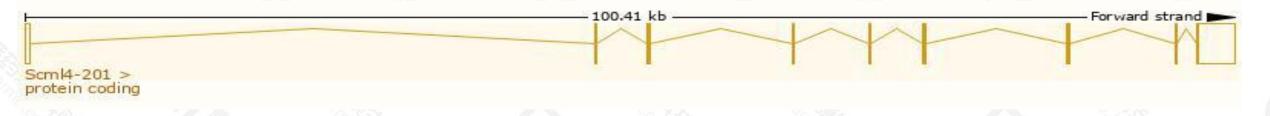
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scml4-201	ENSMUST0000063063.14	4885	<u>408aa</u>	Protein coding	CCDS23816		TSL:1 , GENCODE basic , APPRIS P1
Scml4-202	ENSMUST00000105494.8	4166	<u>350aa</u>	Protein coding	-		TSL:1 , GENCODE basic ,
Scml4-203	ENSMUST00000105495.8	1033	<u>177aa</u>	Protein coding	828		TSL:1 , GENCODE basic ,
Scml4-204	ENSMUST00000125576.2	887	<u>224aa</u>	Protein coding			CDS 3' incomplete , TSL:3 ,
Scml4-209	ENSMUST00000157071.8	365	<u>94aa</u>	Protein coding	5 2 5		CDS 3' incomplete , TSL:3 ,
Scml4-205	ENSMUST00000127675.2	2214	No protein	Processed transcript	578		TSL:1,
Scml4-207	ENSMUST00000136841.2	349	No protein	Processed transcript	-		TSL:5 ,
Scml4-206	ENSMUST00000130511.8	2381	No protein	Retained intron	020		TSL:1,
Scml4-208	ENSMUST00000153091.2	1563	No protein	Retained intron			TSL:1,

The strategy is based on the design of Scml4-201 transcript, the transcription is shown below:

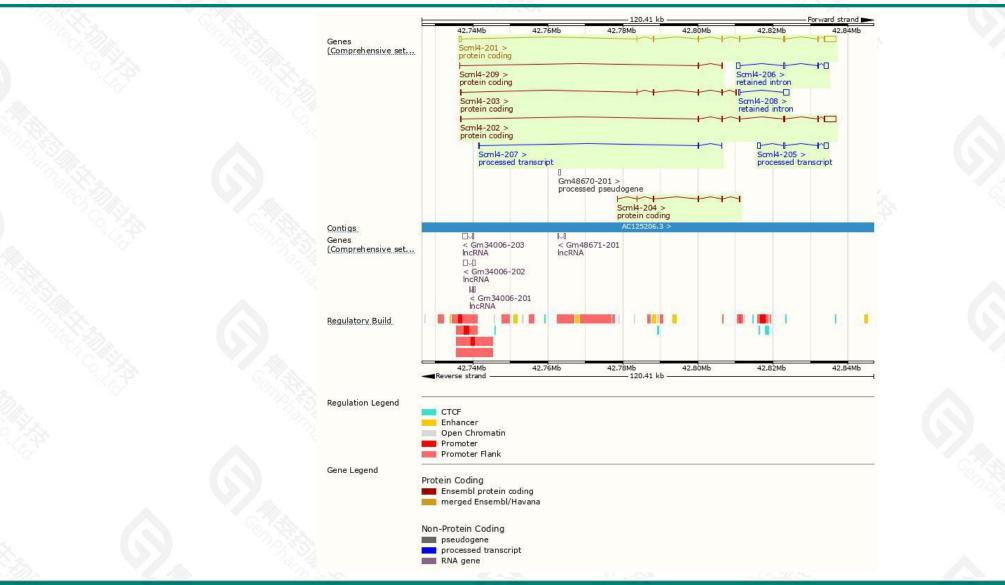


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Genomic location distribution





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Protein domain

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fam		SL	ED domain		-					motif dom:
	Polycomb group p	rotein, RNA bin	ding region							
ANTHER	PTHR12247:SF85									_
ene3D	PTHR12247	SLE	D domain sup	erfamily	-			St	erile alpha r	notif/pointe
DD								c	309578	
ll sequence SNPs/i	Sequence variar	nts (dbSNP an	d all other s			(1)	.000 1	R.	I).I	U.
ariant Legend	missense v splice regio incomplete synonymou	on variant terminal cod	lon variant							29



If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



