

Sipa1l3 Cas9-CKO Strategy

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Project Overview

Project Name

Sipa1l3

Project type

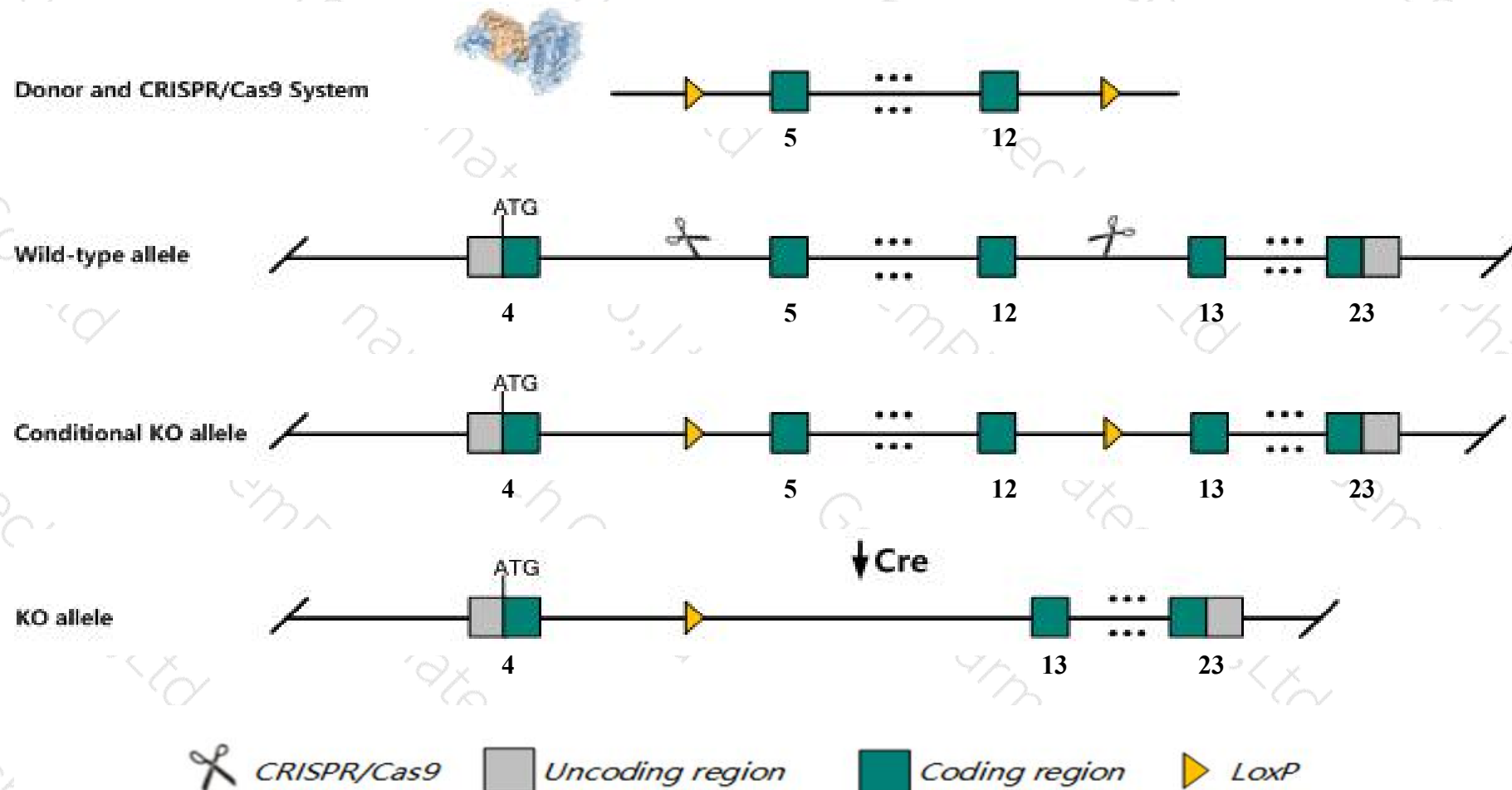
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sipa1l3* gene. The schematic diagram is as follows:



Technical routes

- The *Sipa1l3* gene has 18 transcripts. According to the structure of *Sipa1l3* gene, exon5-exon12 of *Sipa1l3*-201(ENSMUST00000085809.10) transcript is recommended as the knockout region. The region contains 1861bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sipa1l3* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit small lenses, microphthalmia, cataracts, posterior iris synechia, and abnormal lens fiber morphology.
- Transcript 210,218 CDS 5' incomplete the influences is unknown.
- Transcript 202,217 CDS 3' incomplete the influences is unknown.
- The *Sipa1l3* gene is located on the Chr7. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Sipa1l3 signal-induced proliferation-associated 1 like 3 [Mus musculus (house mouse)]

Gene ID: 74206, updated on 13-Mar-2020

Summary



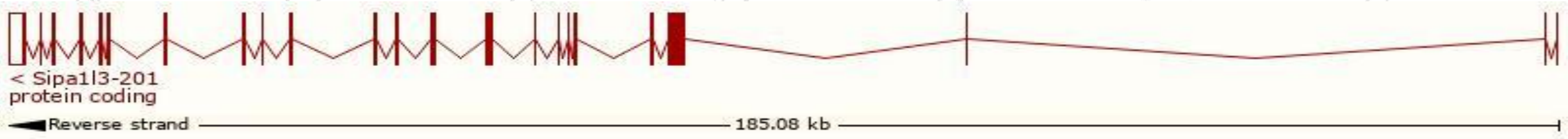
Official Symbol	Sipa1l3 provided by MGI
Official Full Name	signal-induced proliferation-associated 1 like 3 provided by MGI
Primary source	MGI:MGI:1921456
See related	Ensembl:ENSMUSG00000030583
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610511M17Rik
Expression	Ubiquitous expression in colon adult (RPKM 17.0), small intestine adult (RPKM 16.1) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

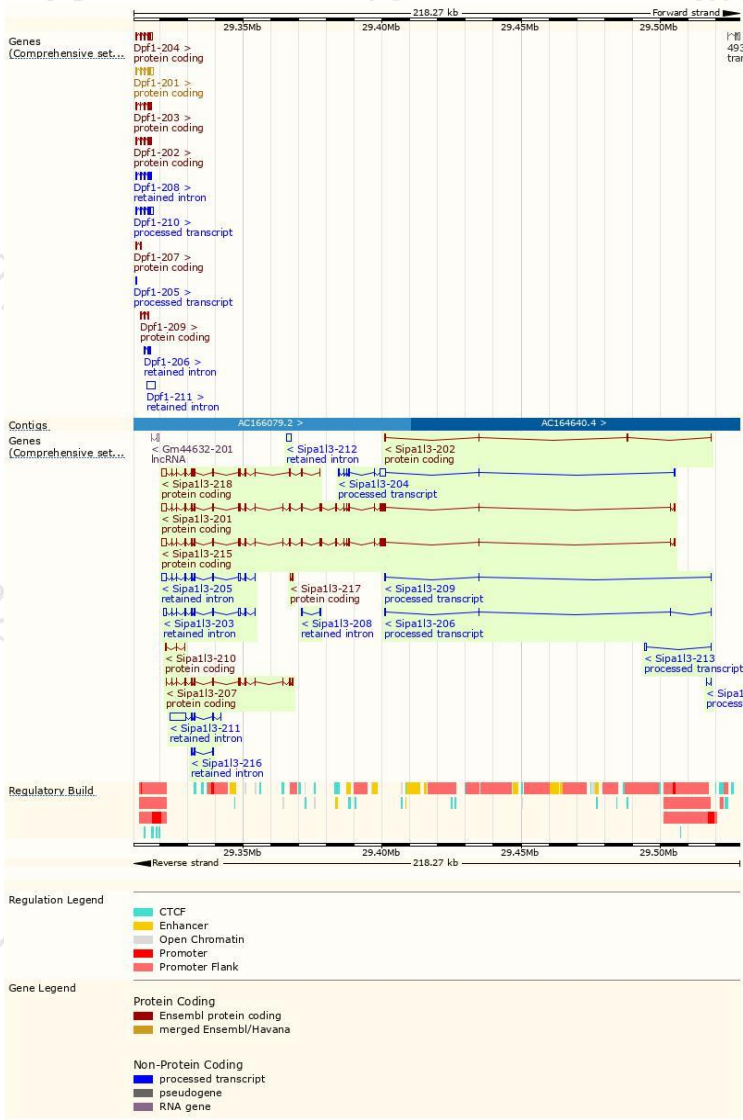
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sipa1l3-201	ENSMUST00000085809.10	7713	1776aa	Protein coding	CCDS39871	G3X9J0	TSL:5 GENCODE basic APPRIS P1
Sipa1l3-215	ENSMUST00000183096.7	7713	1776aa	Protein coding	CCDS39871	G3X9J0	TSL:5 GENCODE basic APPRIS P1
Sipa1l3-218	ENSMUST00000183330.7	4321	849aa	Protein coding	-	S4R1S0	CDS 5' incomplete TSL:5
Sipa1l3-207	ENSMUST00000182484.1	2420	726aa	Protein coding	-	S4R2N4	TSL:5 GENCODE basic
Sipa1l3-202	ENSMUST00000181975.7	678	27aa	Protein coding	-	S4R2C7	CDS 3' incomplete TSL:3
Sipa1l3-210	ENSMUST00000182780.7	601	115aa	Protein coding	-	S4R1P8	CDS 5' incomplete TSL:5
Sipa1l3-217	ENSMUST00000183275.1	452	25aa	Protein coding	-	S4R1U8	CDS 3' incomplete TSL:5
Sipa1l3-204	ENSMUST00000182011.7	2774	No protein	Processed transcript	-	-	TSL:1
Sipa1l3-213	ENSMUST00000183081.1	625	No protein	Processed transcript	-	-	TSL:1
Sipa1l3-209	ENSMUST00000182702.7	537	No protein	Processed transcript	-	-	TSL:2
Sipa1l3-206	ENSMUST00000182236.1	503	No protein	Processed transcript	-	-	TSL:3
Sipa1l3-214	ENSMUST00000183085.1	254	No protein	Processed transcript	-	-	TSL:5
Sipa1l3-211	ENSMUST00000182829.7	6385	No protein	Retained intron	-	-	TSL:1
Sipa1l3-205	ENSMUST00000182223.7	3697	No protein	Retained intron	-	-	TSL:1
Sipa1l3-203	ENSMUST00000182009.7	2660	No protein	Retained intron	-	-	TSL:1
Sipa1l3-212	ENSMUST00000182911.1	1708	No protein	Retained intron	-	-	TSL:NA
Sipa1l3-216	ENSMUST00000183164.1	712	No protein	Retained intron	-	-	TSL:3
Sipa1l3-208	ENSMUST00000182529.1	702	No protein	Retained intron	-	-	TSL:2

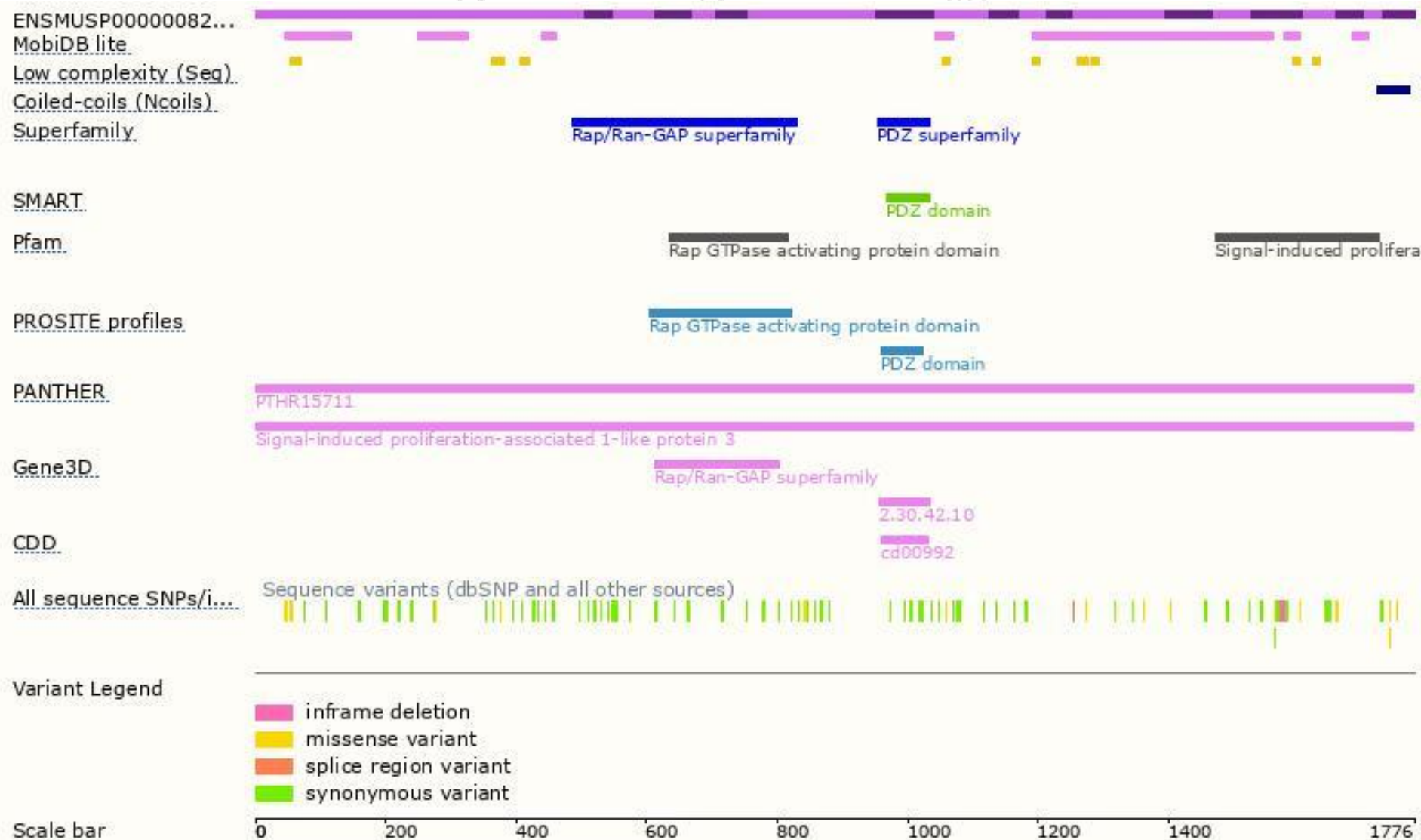
The strategy is based on the design of *Sipa1l3-201* transcript,the transcription is shown below:



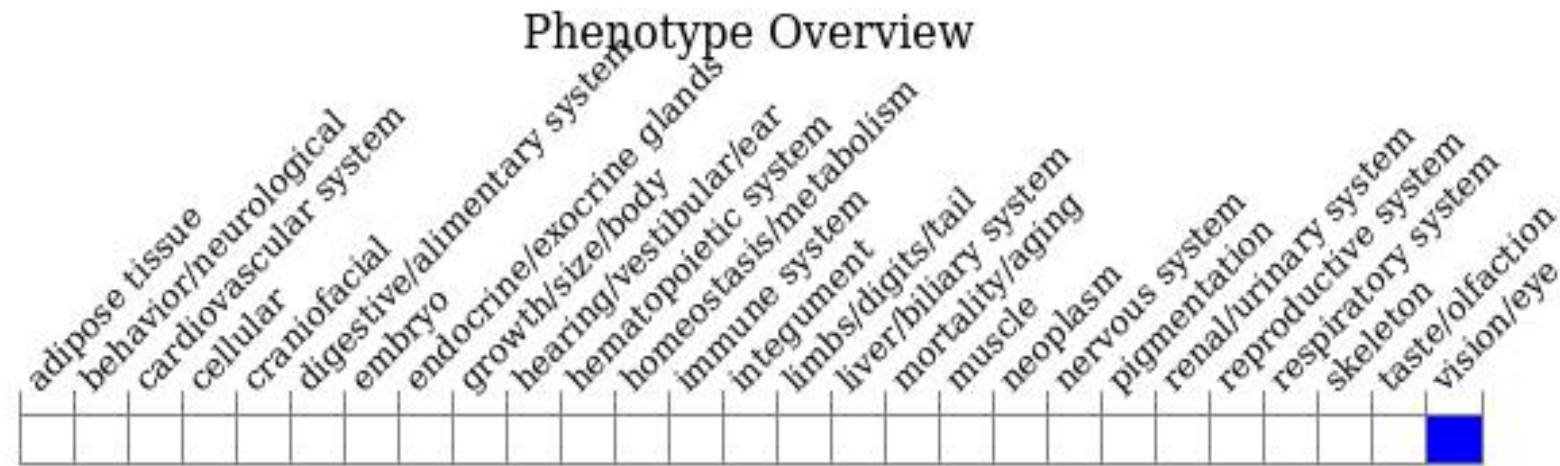
Genomic location distribution



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 knock-out allele exhibit small lenses, microphthalmia, cataracts, posterior iris synechia, and abnormal lens fiber morphology.

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

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