

Sipa1l3 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

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Project Overview

Project Name

Sipa1l3

Project type

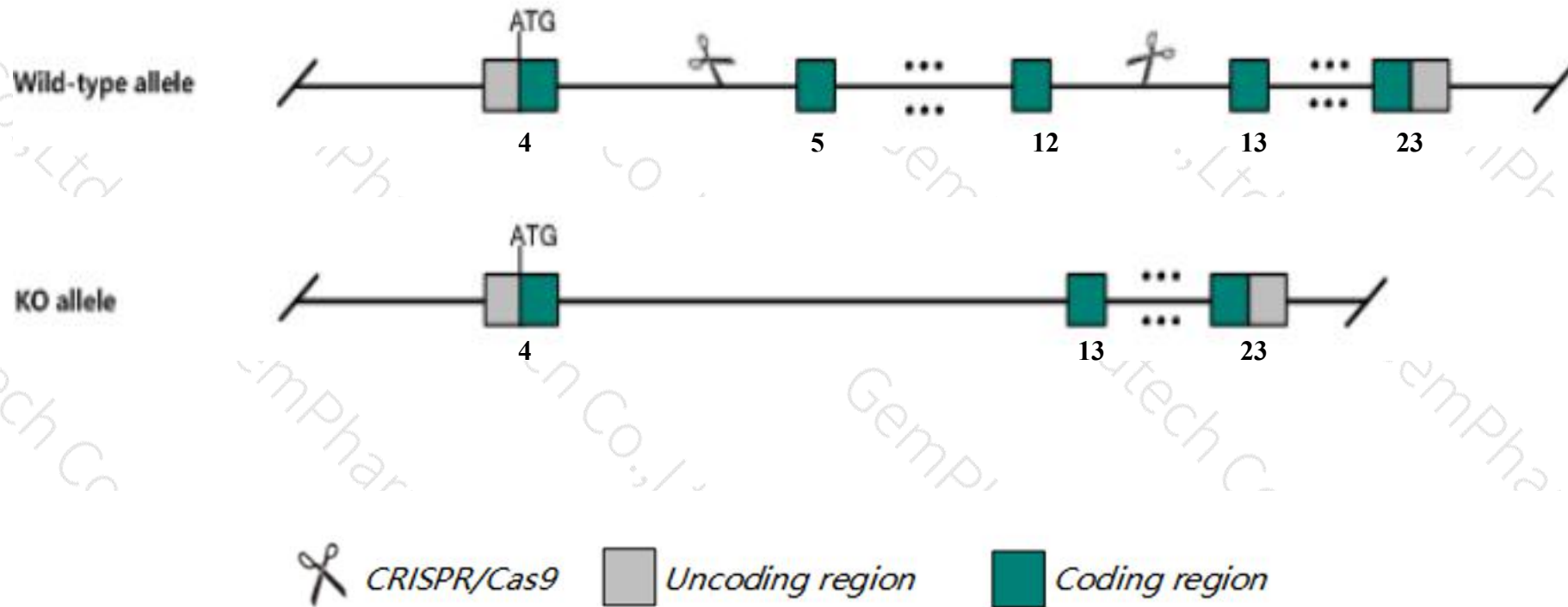
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 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.

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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)

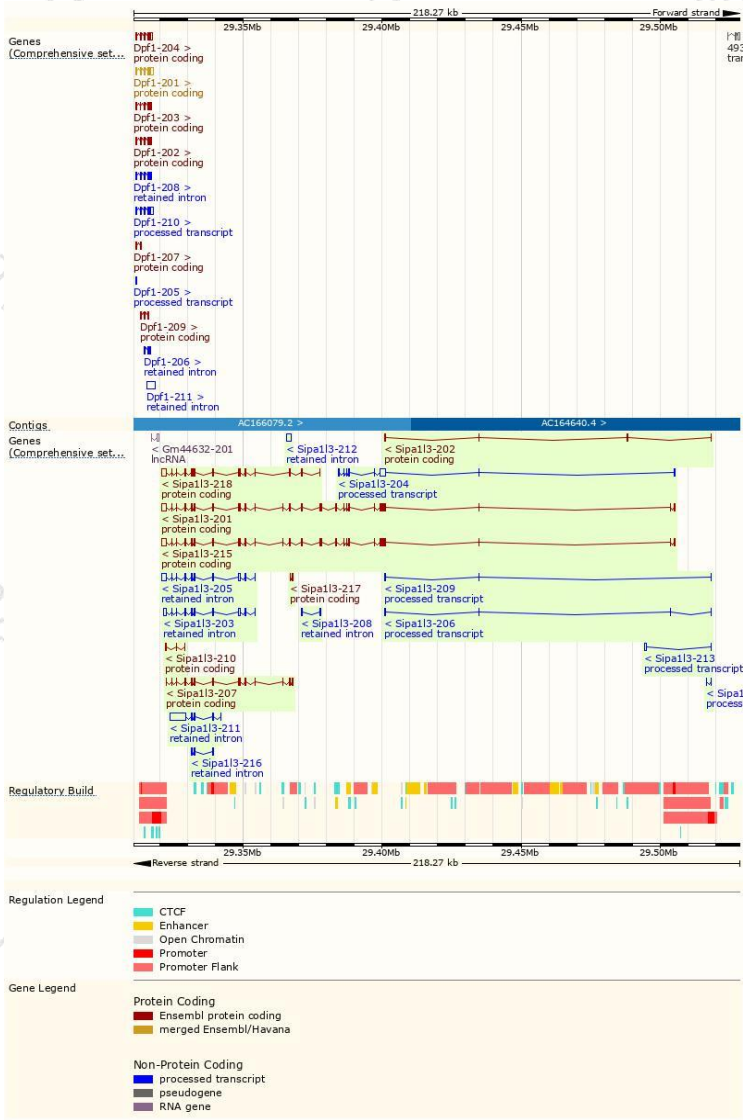
The gene has 18 transcripts,all transcripts are shown below:

| 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:



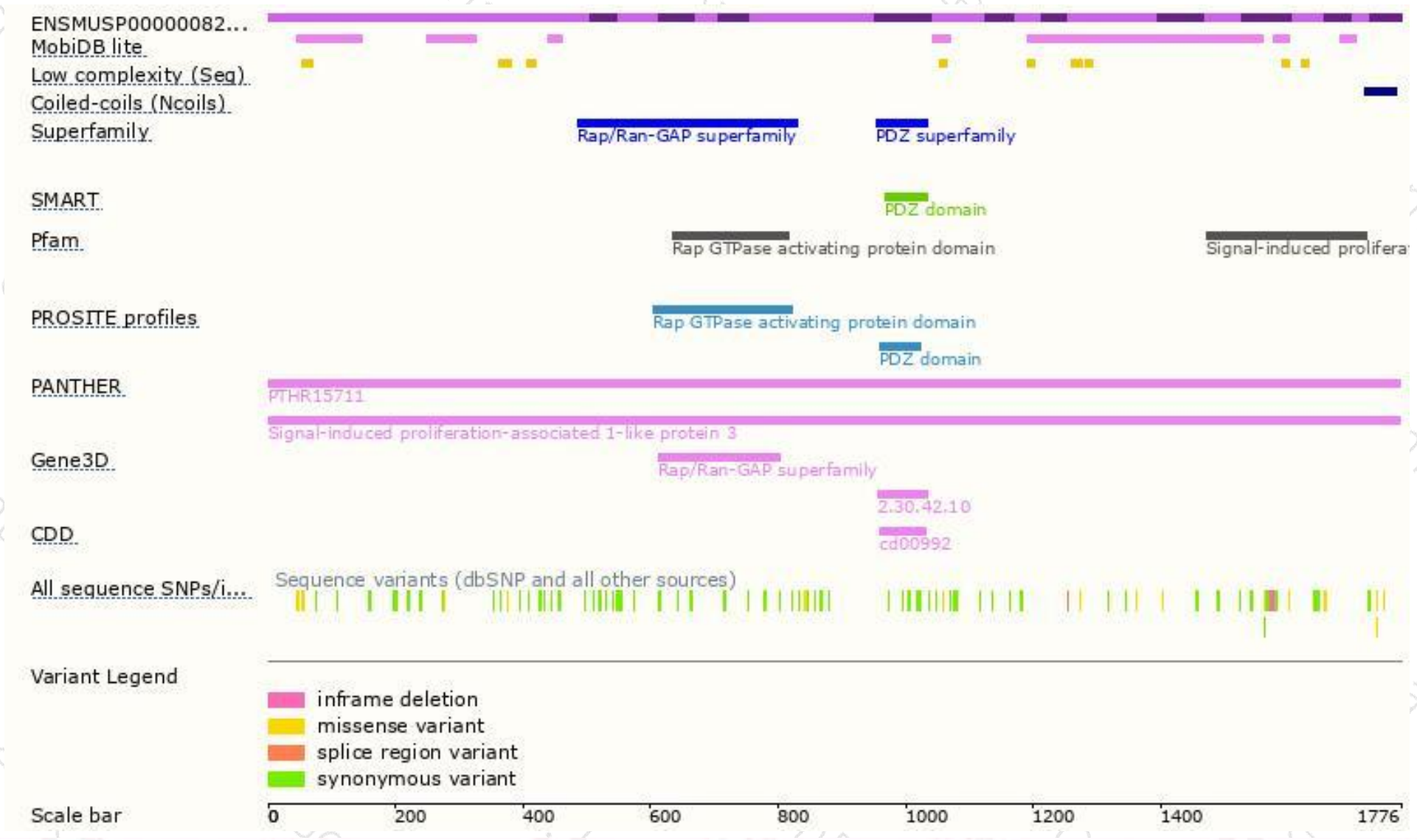
Genomic location distribution



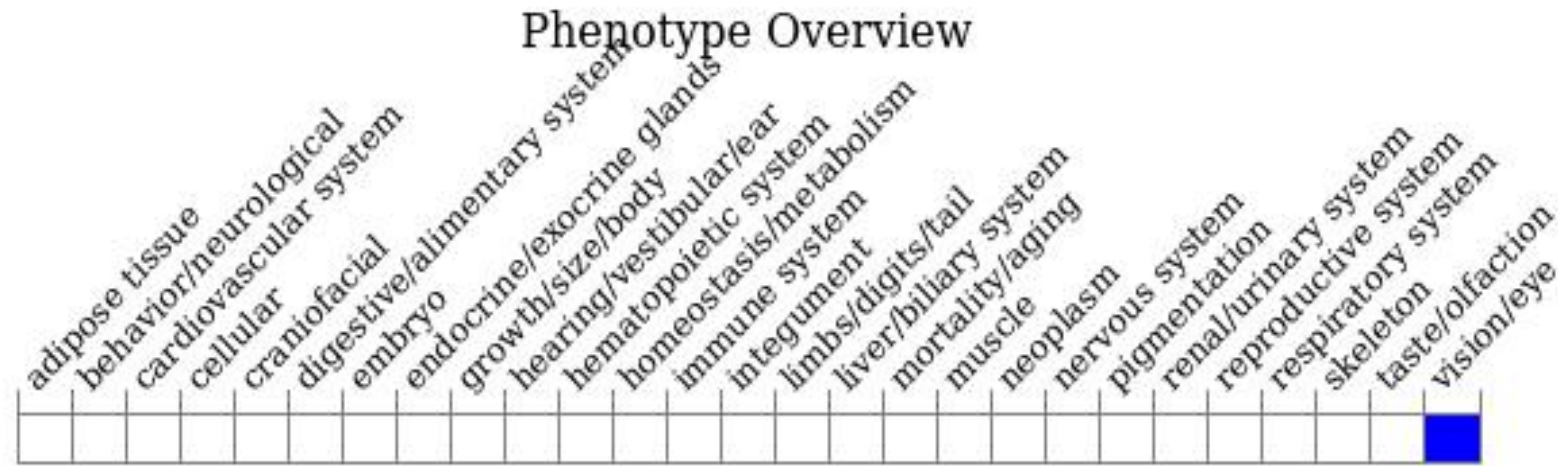
Protein domain



集萃药康
GemPharmatech



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.

Tel: 400-9660890

