

Sipa1l1 Cas9-KO Strategy

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Project Overview

Project Name

Sipa1l1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sipa1l1* gene. The schematic diagram is as follows:



- The *Sipa111* gene has 11 transcripts. According to the structure of *Sipa111* gene, exon5-exon6 of *Sipa111*-202 (ENSMUST00000166429.8) transcript is recommended as the knockout region. The region contains 320bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sipa111* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Sipa111* gene is located on the Chr12. 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)

Sipa1l1 signal-induced proliferation-associated 1 like 1 [Mus musculus (house mouse)]

Gene ID: 217692, updated on 31-Jan-2019

Summary



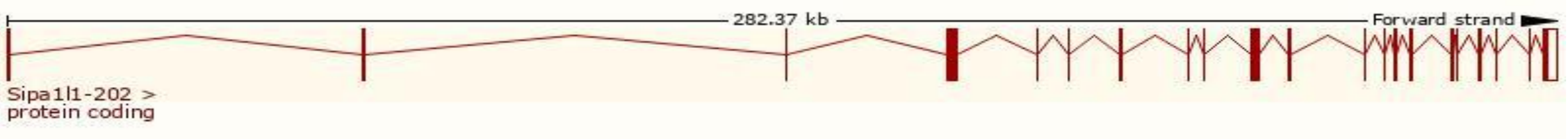
Official Symbol	Sipa1l1 provided by MGI
Official Full Name	signal-induced proliferation-associated 1 like 1 provided by MGI
Primary source	MGI:MGI:2443679
See related	Ensembl:ENSMUSG00000042700
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4931426N11Rik, AW213287, Spar, mKIAA0440
Expression	Ubiquitous expression in frontal lobe adult (RPKM 37.5), cortex adult (RPKM 30.3) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

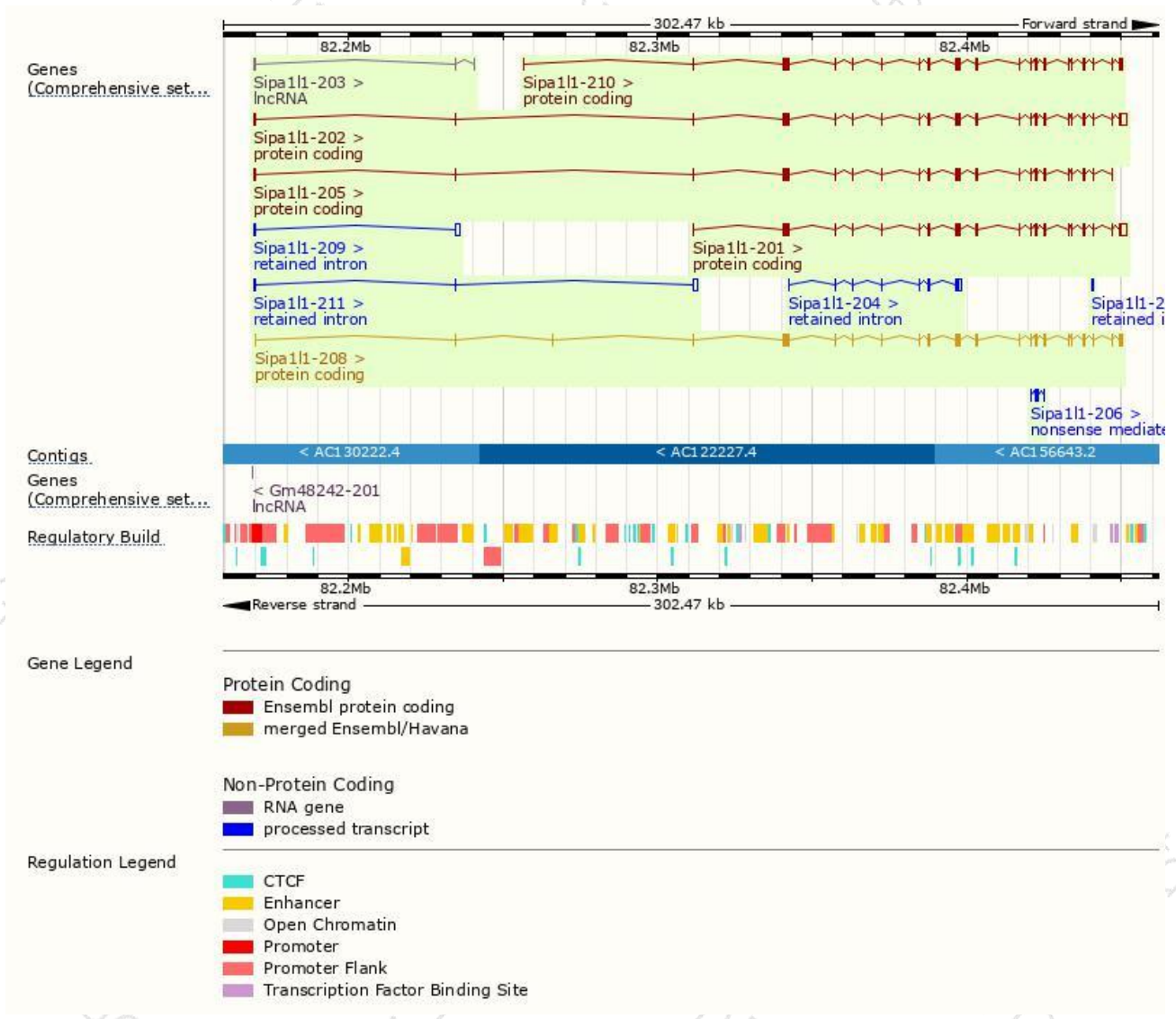
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sipa1l1-202	ENSMUST00000166429.8	8215	1782aa	Protein coding	CCDS26026	Q8C0T5	TSL:1 GENCODE basic APPRIS P3
Sipa1l1-201	ENSMUST00000053969.6	7488	1782aa	Protein coding	CCDS26026	Q8C0T5	TSL:5 GENCODE basic APPRIS P3
Sipa1l1-208	ENSMUST00000222298.1	6179	1751aa	Protein coding	CCDS49105	Q8C0T5	TSL:1 GENCODE basic APPRIS ALT2
Sipa1l1-210	ENSMUST00000222714.1	6002	1782aa	Protein coding	CCDS26026	Q8C0T5	TSL:1 GENCODE basic APPRIS P3
Sipa1l1-205	ENSMUST00000220963.1	5907	1713aa	Protein coding	-	Q4VBF8	TSL:1 GENCODE basic APPRIS ALT2
Sipa1l1-206	ENSMUST00000221169.1	728	76aa	Nonsense mediated decay	-	A0A1Y7VJM1	CDS 5' incomplete TSL:3
Sipa1l1-204	ENSMUST00000220766.1	2395	No protein	Retained intron	-	-	TSL:1
Sipa1l1-211	ENSMUST00000222849.1	1831	No protein	Retained intron	-	-	TSL:1
Sipa1l1-209	ENSMUST00000222312.1	1416	No protein	Retained intron	-	-	TSL:1
Sipa1l1-207	ENSMUST00000221327.1	414	No protein	Retained intron	-	-	TSL:NA
Sipa1l1-203	ENSMUST00000220550.1	363	No protein	lncRNA	-	-	TSL:3

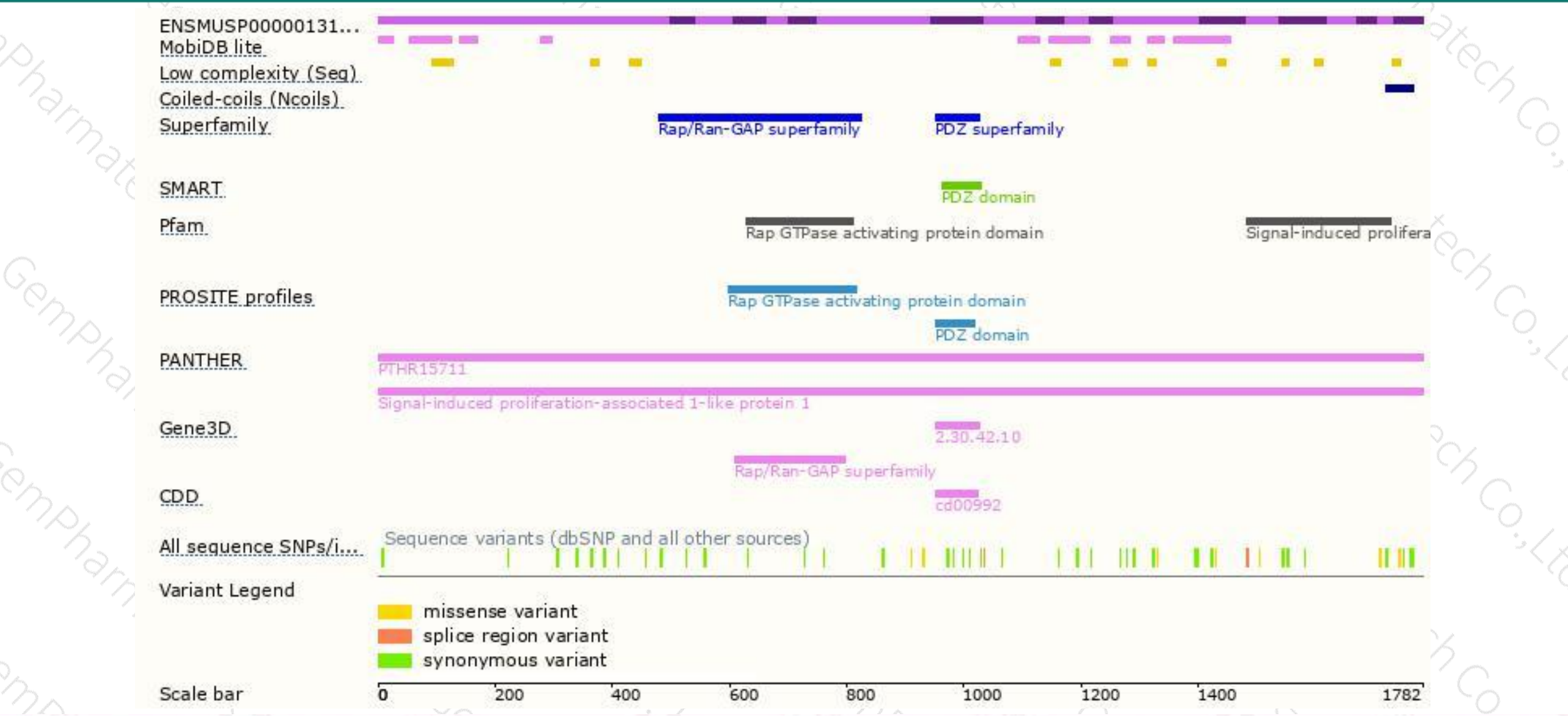
The strategy is based on the design of *Sipa1l1-202* transcript,The transcription is shown below



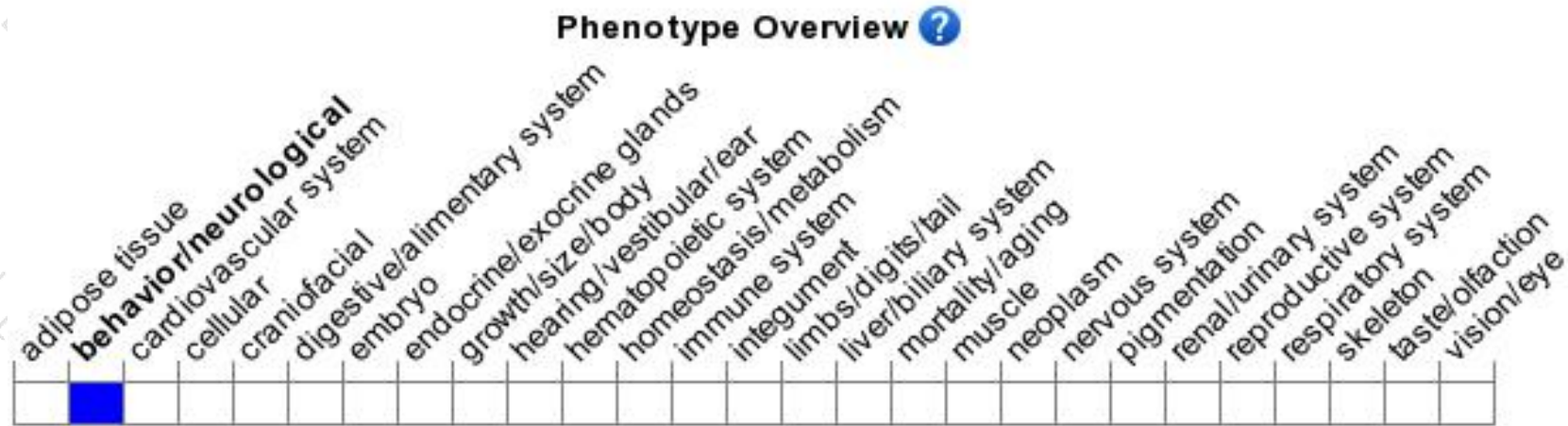
Genomic location distribution



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/>).

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

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