

# *Sh2d1a* Cas9-KO Strategy

|                     |                  |
|---------------------|------------------|
| <b>Designer:</b>    | <b>Huan Wang</b> |
| <b>Reviewer:</b>    | <b>Huan Fan</b>  |
| <b>Design Date:</b> | <b>2020-4-22</b> |

# Project Overview

**Project Name**

*Sh2d1a*

**Project type**

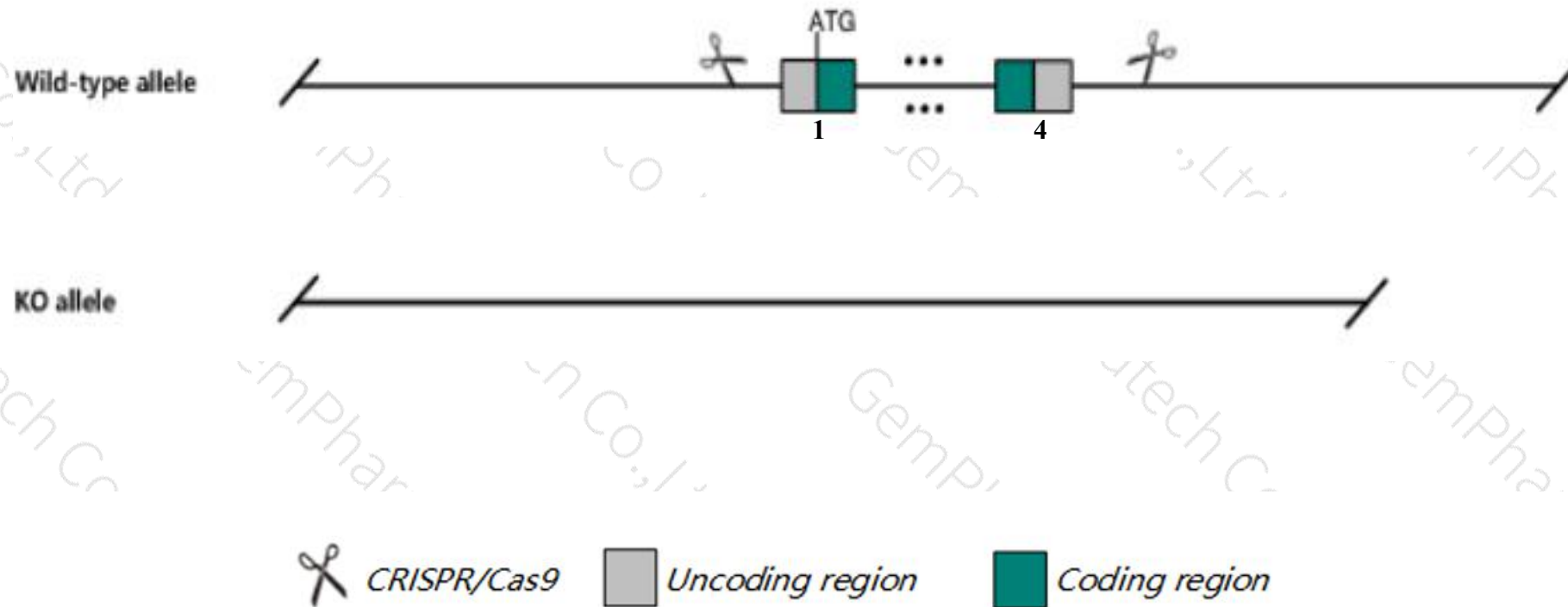
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sh2d1a* gene. The schematic diagram is as follows:



- The *Sh2d1a* gene has 7 transcripts. According to the structure of *Sh2d1a* gene, exon1-exon4 of *Sh2d1a-201* (ENSMUST00000005839.10) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sh2d1a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for disruptions in this gene display various immune system abnormalities.
- The *Sh2d1a* gene is located on the ChrX. 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)

## Sh2d1a SH2 domain containing 1A [Mus musculus (house mouse)]

Gene ID: 20400, updated on 13-Mar-2020

### Summary



**Official Symbol** Sh2d1a provided by [MGI](#)

**Official Full Name** SH2 domain containing 1A provided by [MGI](#)

**Primary source** [MGI:MGI:1328352](#)

**See related** [Ensembl:ENSMUSG000000005696](#)

**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** Gm686, SAP

**Expression** Restricted expression toward thymus adult (RPKM 26.6)[See more](#)

**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

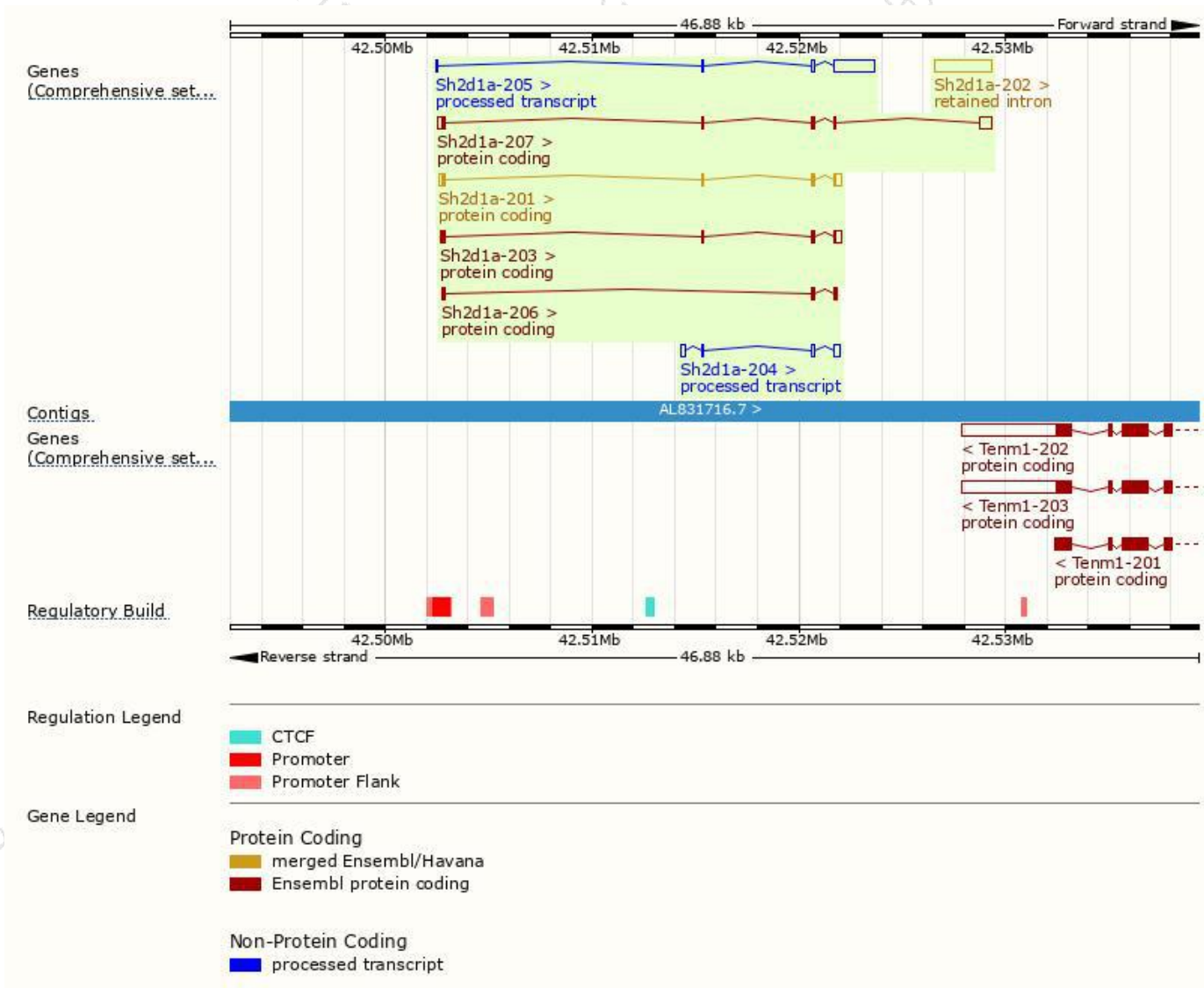
The gene has 7 transcripts,all transcripts are shown below:

| Name       | Transcript ID                        | bp   | Protein               | Biotype              | CCDS                      | UniProt                       | Flags   |
|------------|--------------------------------------|------|-----------------------|----------------------|---------------------------|-------------------------------|---|
| Sh2d1a-207 | <a href="#">ENSMUST00000189753.6</a> | 1223 | <a href="#">126aa</a> | Protein coding       | <a href="#">CCDS30099</a> | <a href="#">O88890_Q544F1</a> | TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Sh2d1a-201 | <a href="#">ENSMUST0000005839.10</a> | 883  | <a href="#">126aa</a> | Protein coding       | <a href="#">CCDS30099</a> | <a href="#">O88890_Q544F1</a> | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Sh2d1a-203 | <a href="#">ENSMUST00000115070.7</a> | 782  | <a href="#">123aa</a> | Protein coding       | <a href="#">CCDS85770</a> | <a href="#">O88890</a>        | TSL:1 GENCODE basic   |
| Sh2d1a-206 | <a href="#">ENSMUST00000153948.1</a> | 400  | <a href="#">93aa</a>  | Protein coding       | -                         | <a href="#">S4R2F6</a>        | CDS 5' incomplete TSL:3   |
| Sh2d1a-205 | <a href="#">ENSMUST00000129855.7</a> | 2269 | No protein            | Processed transcript | -                         | -                             | TSL:1   |
| Sh2d1a-204 | <a href="#">ENSMUST00000128393.1</a> | 625  | No protein            | Processed transcript | -                         | -                             | TSL:3   |
| Sh2d1a-202 | <a href="#">ENSMUST00000101619.3</a> | 2746 | No protein            | Retained intron      | -                         | -                             | TSL:NA  |

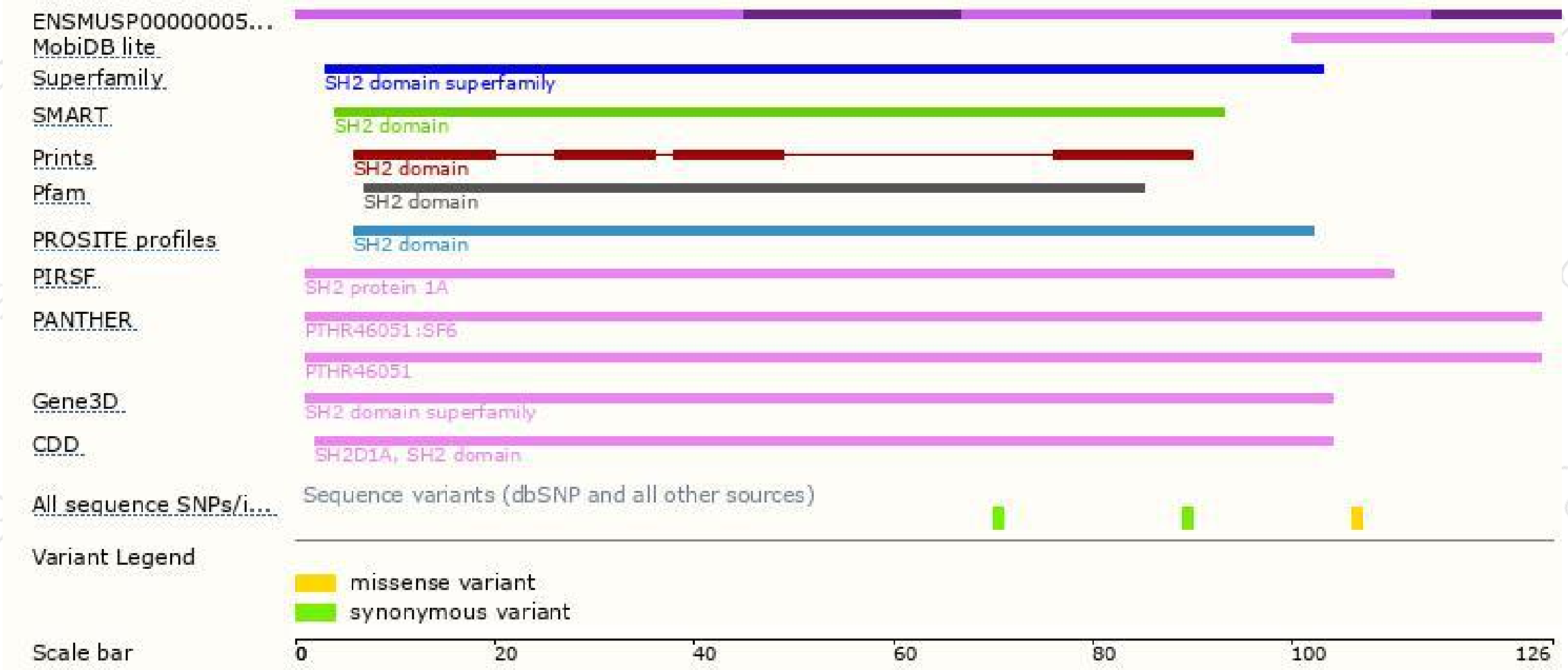
The strategy is based on the design of *Sh2d1a-201* transcript, the transcription is shown below:



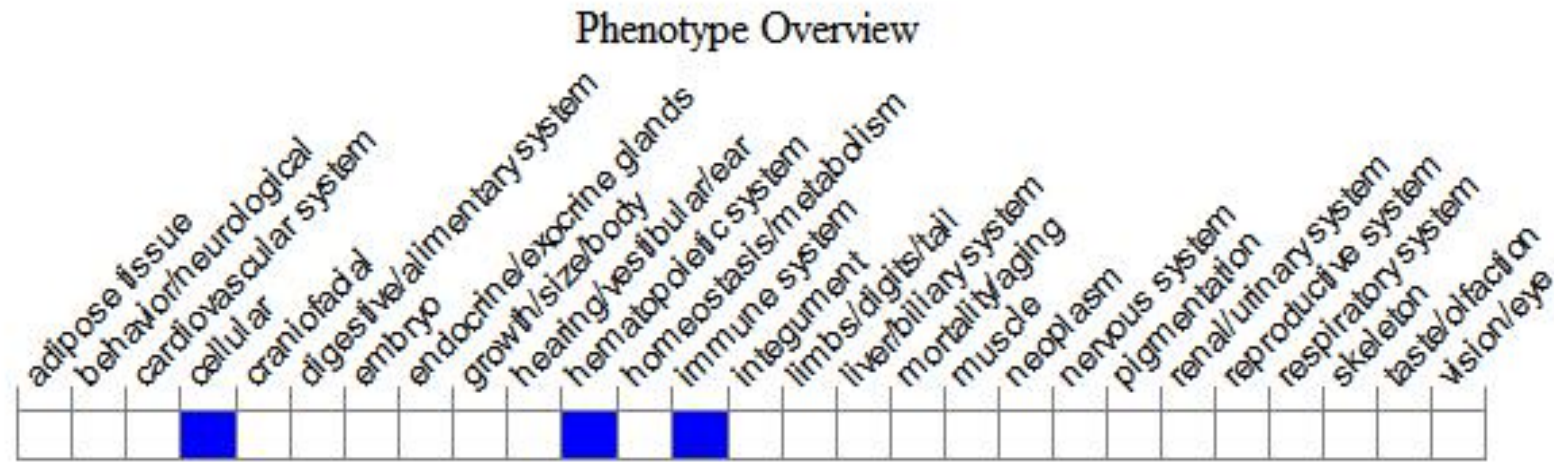
# Genomic location distribution



# 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 disruptions in this gene display various immune system abnormalities.

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

Tel: 400-9660890

