

# *Sh2d3c* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Sh2d3c*

**Project type**

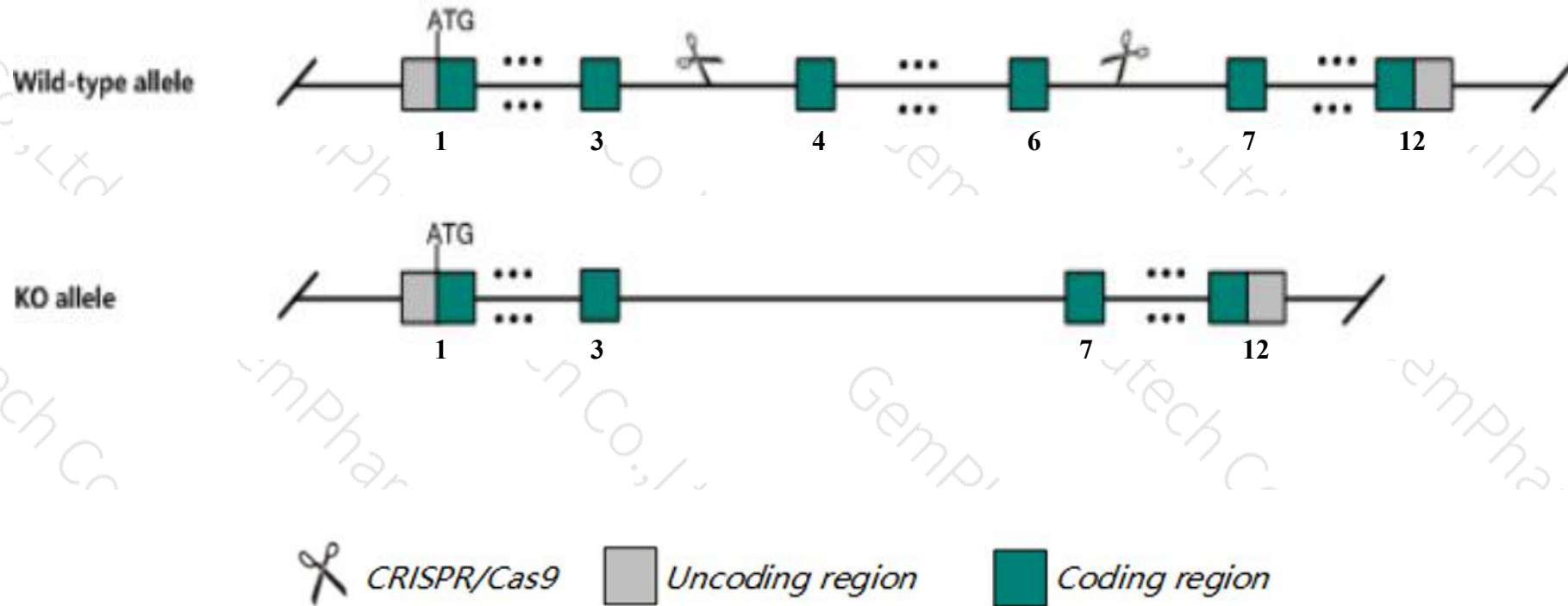
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sh2d3c* gene. The schematic diagram is as follows:



- The *Sh2d3c* gene has 6 transcripts. According to the structure of *Sh2d3c* gene, exon4-exon6 of *Sh2d3c*-201(ENSMUST00000074248.10) transcript is recommended as the knockout region. The region contains 709bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sh2d3c* 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 neonatal lethality with absence of gastric milk. Surviving mice exhibit abnormal olfactory bulb innervation, fewer gonadotrophin positive cells in the hypothalamus, and decreased testes size.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The flox region is about 3 kb away from the 5th end of the 6330409D20Rik gene, which may affect the regulation of this gene.
- The *Sh2d3c* gene is located on the Chr2. 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)

## Sh2d3c SH2 domain containing 3C [Mus musculus (house mouse)]

Gene ID: 27387, updated on 13-Mar-2020

### Summary



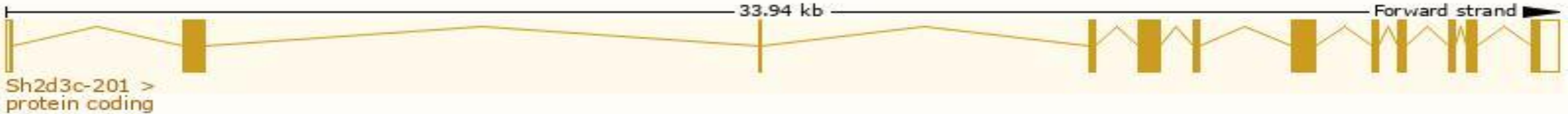
<b>Official Symbol</b>	Sh2d3c provided by <a href="#">MGI</a>
<b>Official Full Name</b>	SH2 domain containing 3C provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1351631</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000059013</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Chat, Nsp3, Shep1
<b>Expression</b>	Broad expression in lung adult (RPKM 40.4), spleen adult (RPKM 34.7) and 24 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

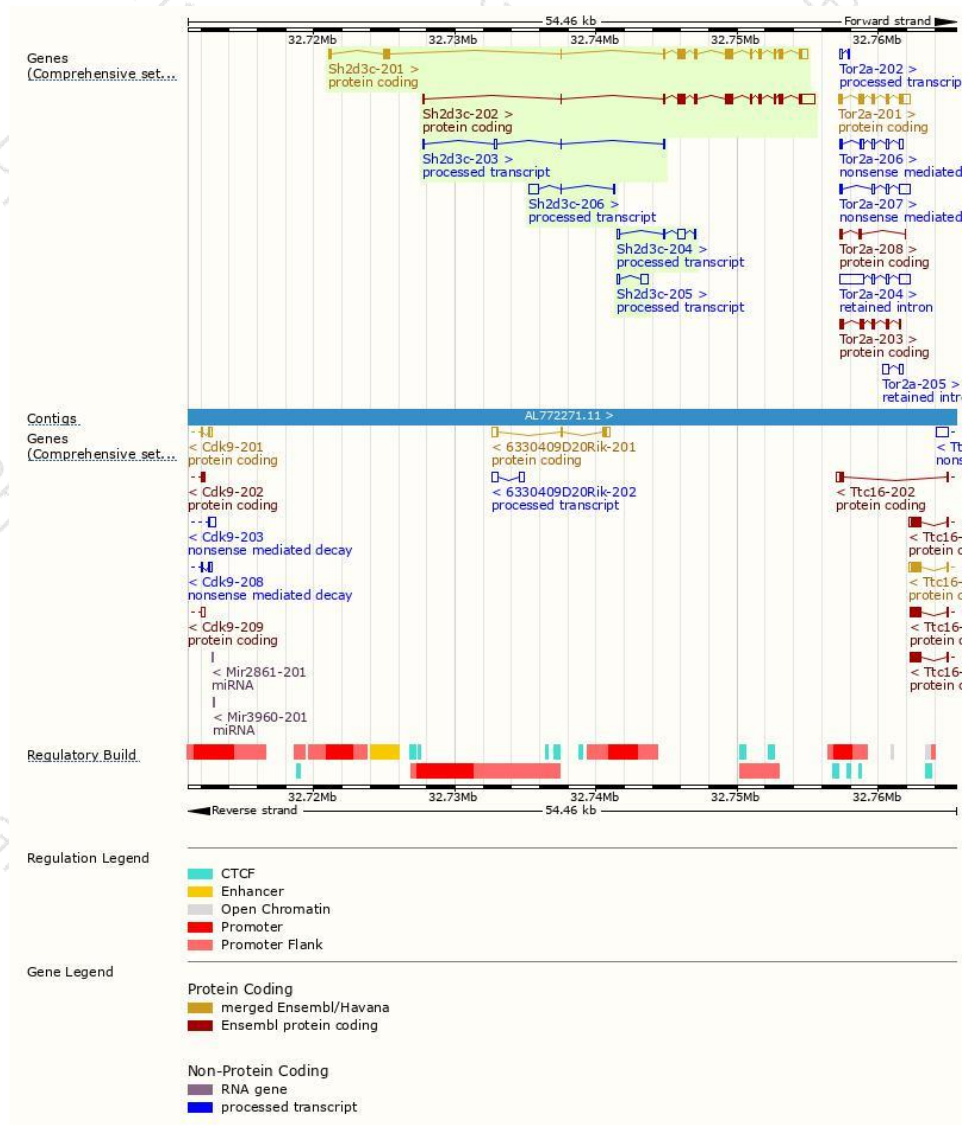
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sh2d3c-202	<a href="#">ENSMUST00000113242.4</a>	3107	<a href="#">702aa</a>	Protein coding	<a href="#">CCDS57168</a>	<a href="#">Q9QZS8</a>	TSL:1 GENCODE basic APPRIS P1
Sh2d3c-201	<a href="#">ENSMUST00000074248.10</a>	3092	<a href="#">854aa</a>	Protein coding	<a href="#">CCDS15928</a>	<a href="#">Q9QZS8</a>	TSL:1 GENCODE basic
Sh2d3c-204	<a href="#">ENSMUST00000131101.2</a>	805	No protein	Processed transcript	-	-	TSL:5
Sh2d3c-206	<a href="#">ENSMUST00000141670.1</a>	794	No protein	Processed transcript	-	-	TSL:3
Sh2d3c-205	<a href="#">ENSMUST00000139563.1</a>	632	No protein	Processed transcript	-	-	TSL:3
Sh2d3c-203	<a href="#">ENSMUST00000124133.7</a>	369	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Sh2d3c-201* transcript,the transcription is shown below:

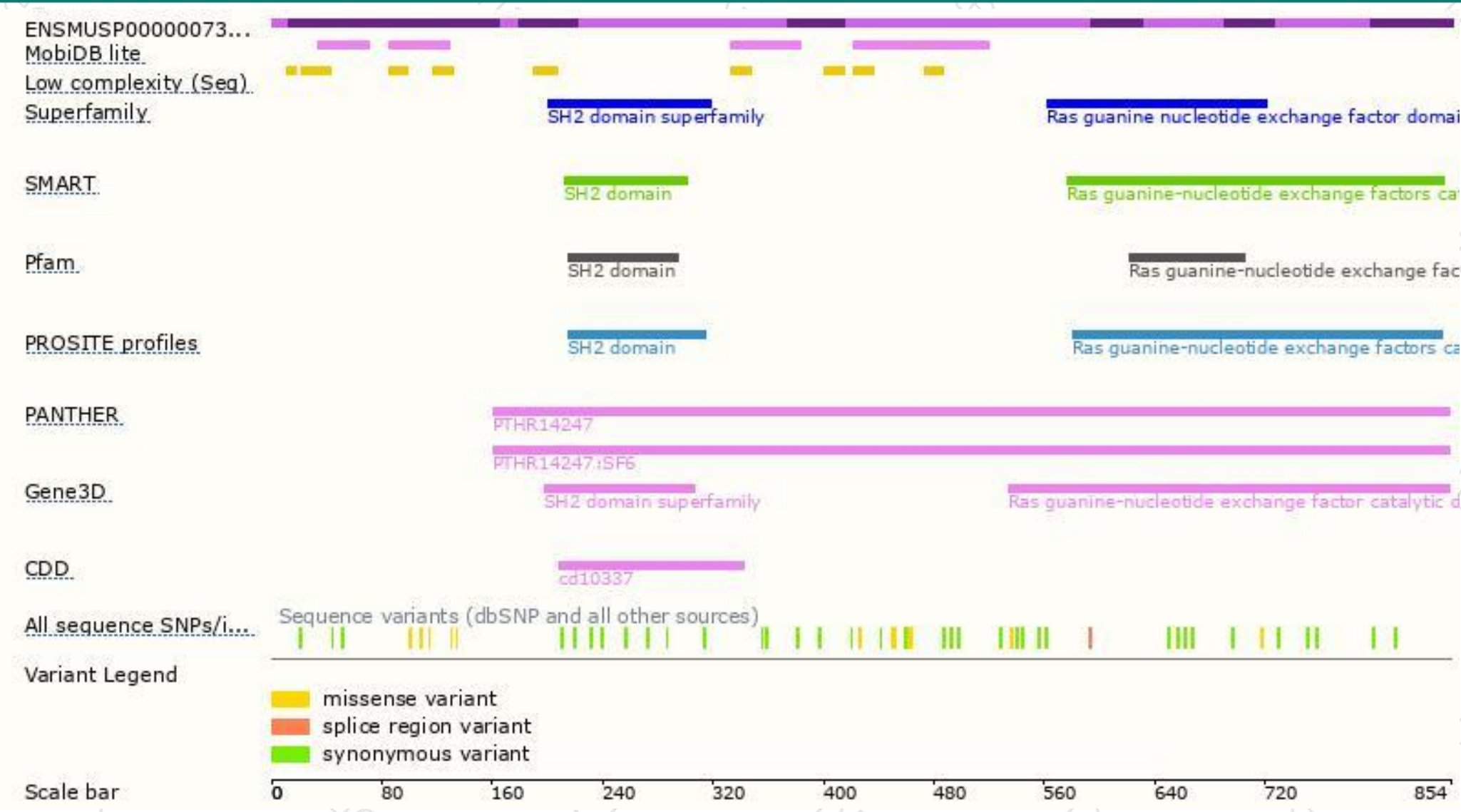


# Genomic location distribution

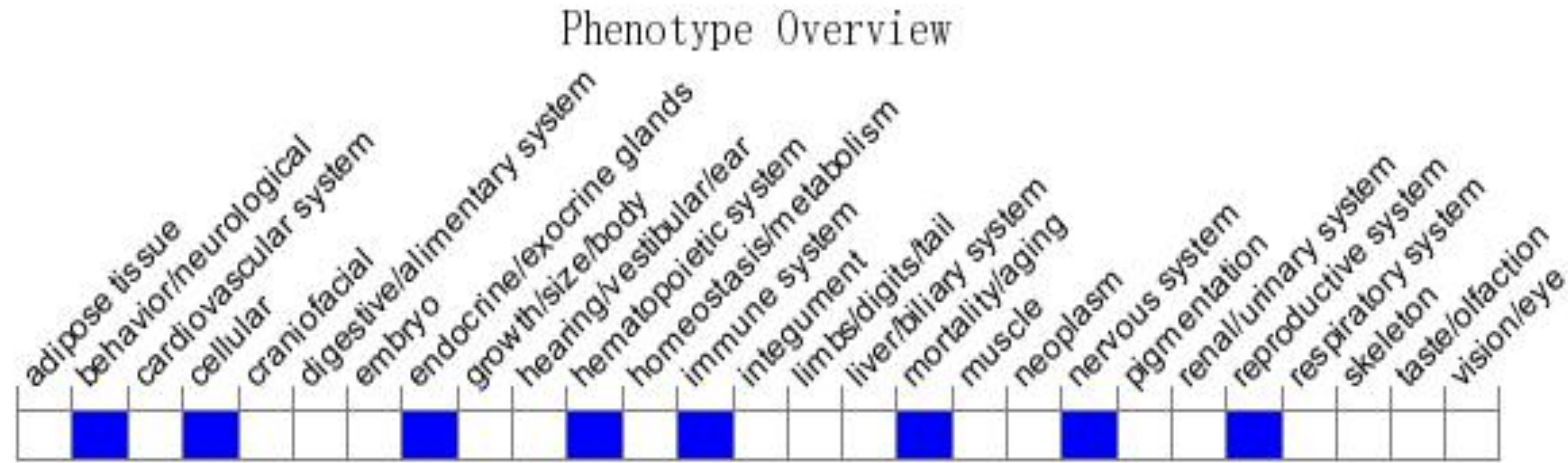




# Protein domain



# 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 neonatal lethality with absence of gastric milk. Surviving mice exhibit abnormal olfactory bulb innervation, fewer gonadotrophin positive cells in the hypothalamus, and decreased testes size.

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

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