

Arhgef6 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Arhgef6

Project type

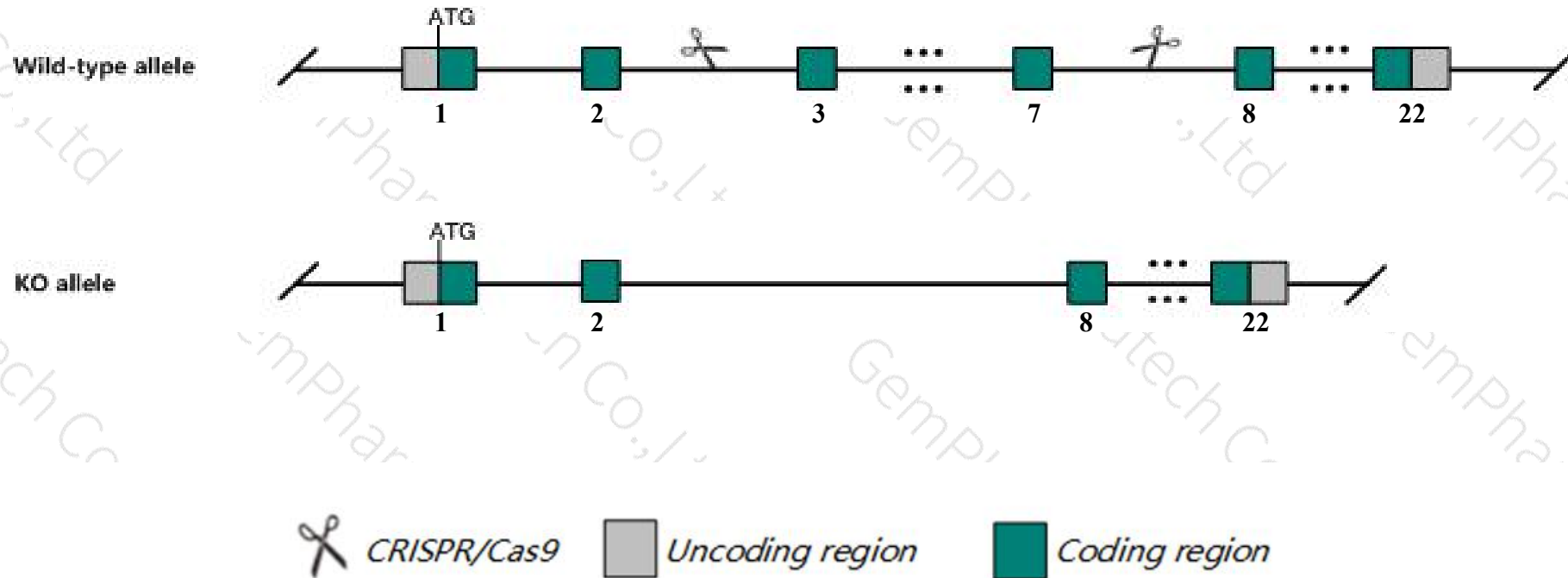
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgef6* gene. The schematic diagram is as follows:



- The *Arhgef6* gene has 8 transcripts. According to the structure of *Arhgef6* gene, exon3-exon7 of *Arhgef6-201* (ENSMUST00000033468.10) transcript is recommended as the knockout region. The region contains 575bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgef6* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a truncated allele exhibit decreased mature lymphocyte cell numbers, decreased B and T cell proliferation, and defective humeral response. Mice homozygous for a reporter allele exhibit abnormal dendrite morphology and synaptic plasticity and cognitive defects.
- The transcript *Arhgef6-207* is incomplete, so the effect on it is unknown.
- The *Arhgef6* 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)

Arhgef6 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [*Mus musculus* (house mouse)]

Gene ID: 73341, updated on 12-Aug-2019

Summary

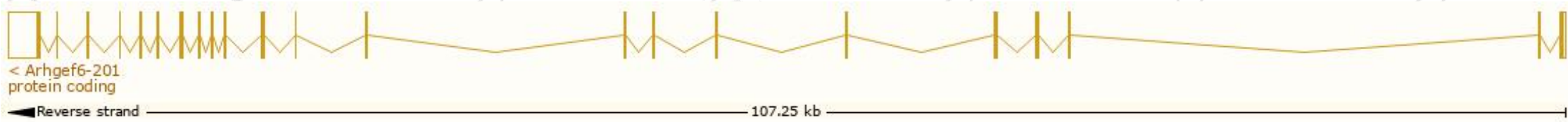
| | |
|---------------------------|---|
| Official Symbol | Arhgef6 provided by MGI |
| Official Full Name | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 provided by MGI |
| Primary source | MGI:MGI:1920591 |
| See related | Ensembl:ENSMUSG000000031133 |
| Gene type | protein coding |
| RefSeq 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 | alpha-PIX; 1600028C08Rik; 1700038J06Rik; 4930592P22Rik |
| Expression | Biased expression in placenta adult (RPKM 38.2), thymus adult (RPKM 12.8) and 12 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

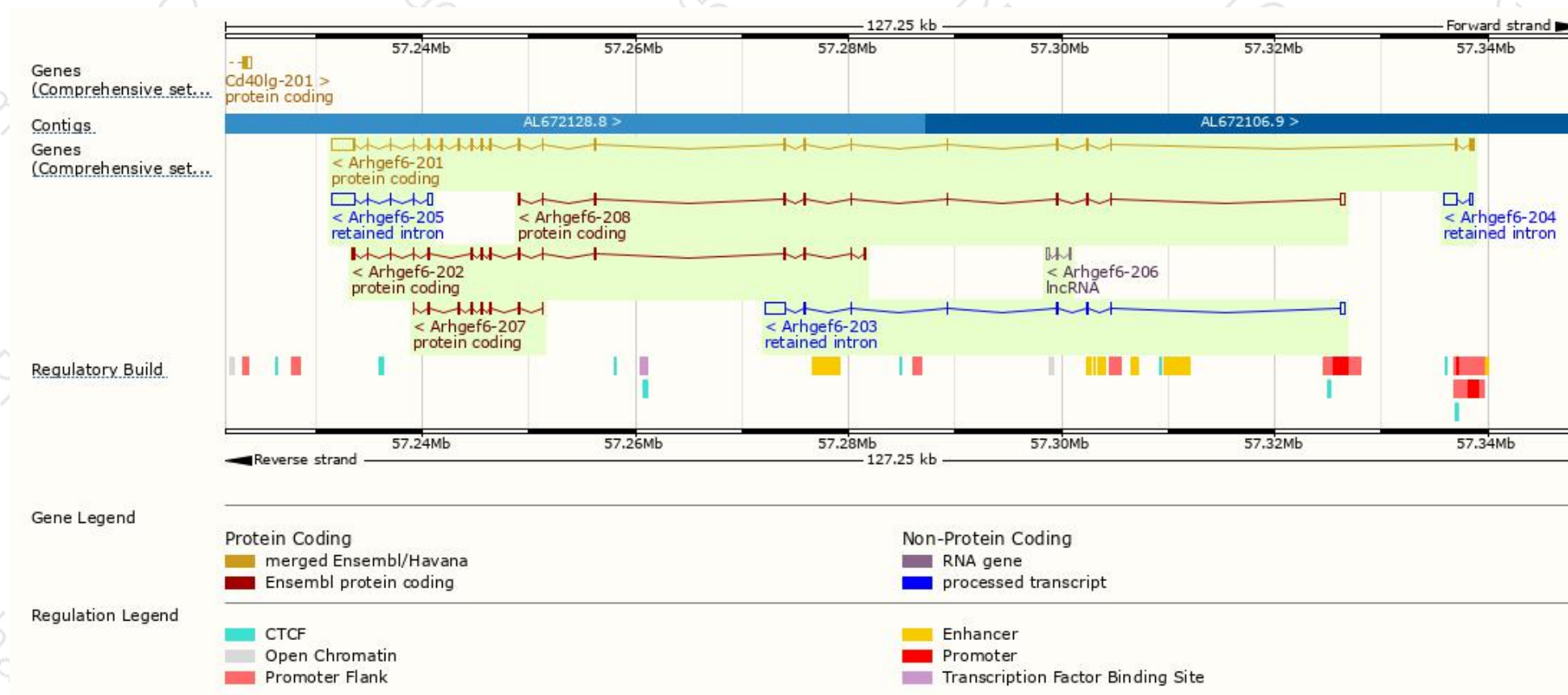
The gene has 8 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-------------|---------------------------------------|------|-----------------------|-----------------|---------------------------|------------------------|--------------------------------|
| Arhgef6-201 | ENSMUST00000033468.10 | 4569 | 795aa | Protein coding | CCDS40984 | F6WMJ3 | TSL:1 GENCODE basic APPRIS P1 |
| Arhgef6-202 | ENSMUST00000114735.8 | 1614 | 483aa | Protein coding | - | A2AFJ8 | TSL:1 GENCODE basic |
| Arhgef6-208 | ENSMUST00000176986.7 | 1604 | 302aa | Protein coding | - | H3BJ53 | CDS 3' incomplete TSL:5 |
| Arhgef6-207 | ENSMUST00000175900.1 | 748 | 250aa | Protein coding | - | H3BKQ0 | CDS 5' and 3' incomplete TSL:5 |
| Arhgef6-203 | ENSMUST00000134028.8 | 2951 | No protein | Retained intron | - | - | TSL:1 |
| Arhgef6-205 | ENSMUST00000151768.1 | 2696 | No protein | Retained intron | - | - | TSL:1 |
| Arhgef6-204 | ENSMUST00000135098.1 | 1301 | No protein | Retained intron | - | - | TSL:1 |
| Arhgef6-206 | ENSMUST00000175636.1 | 675 | No protein | lncRNA | - | - | TSL:1 |

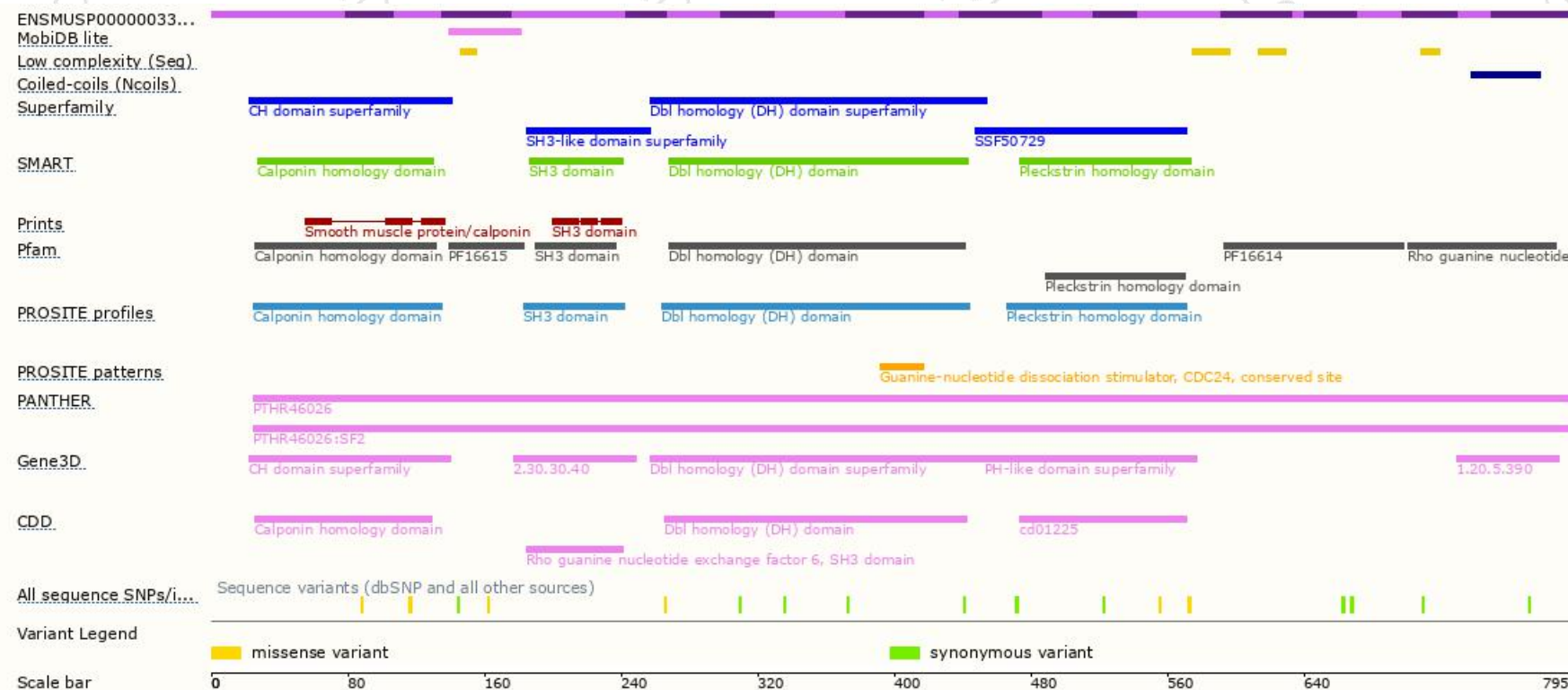
The strategy is based on the design of *Arhgef6-201* transcript,The transcription is shown below



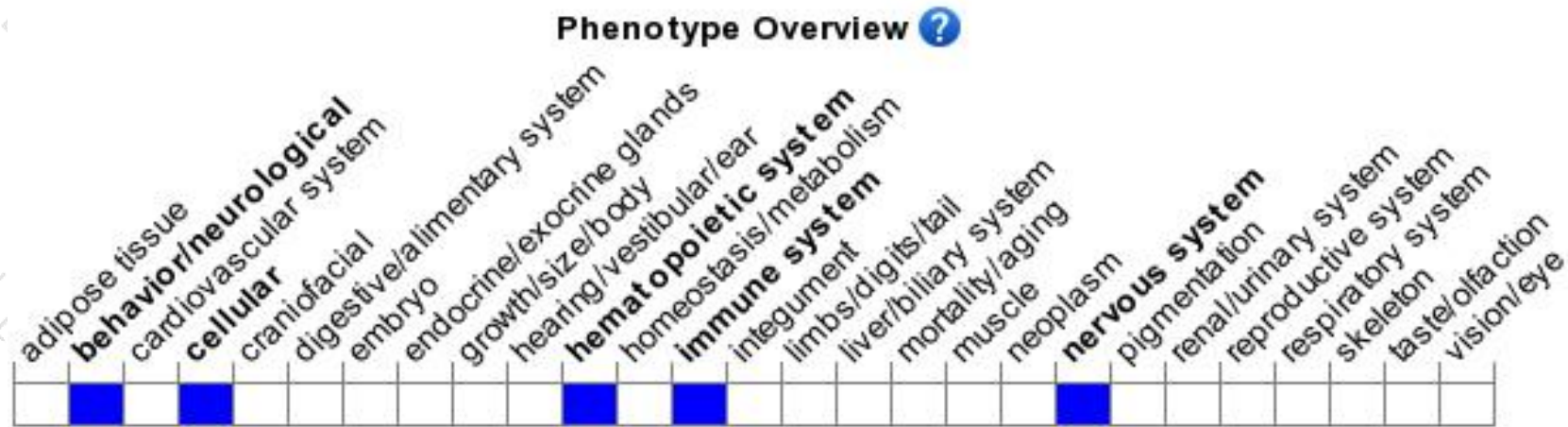
Genomic location distribution



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 truncated allele exhibit decreased mature lymphocyte cell numbers, decreased B and T cell proliferation, and defective humeral response. Mice homozygous for a reporter allele exhibit abnormal dendrite morphology and synaptic plasticity and cognitive defects.

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

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