

Pacsin1 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Pacsin1

Project type

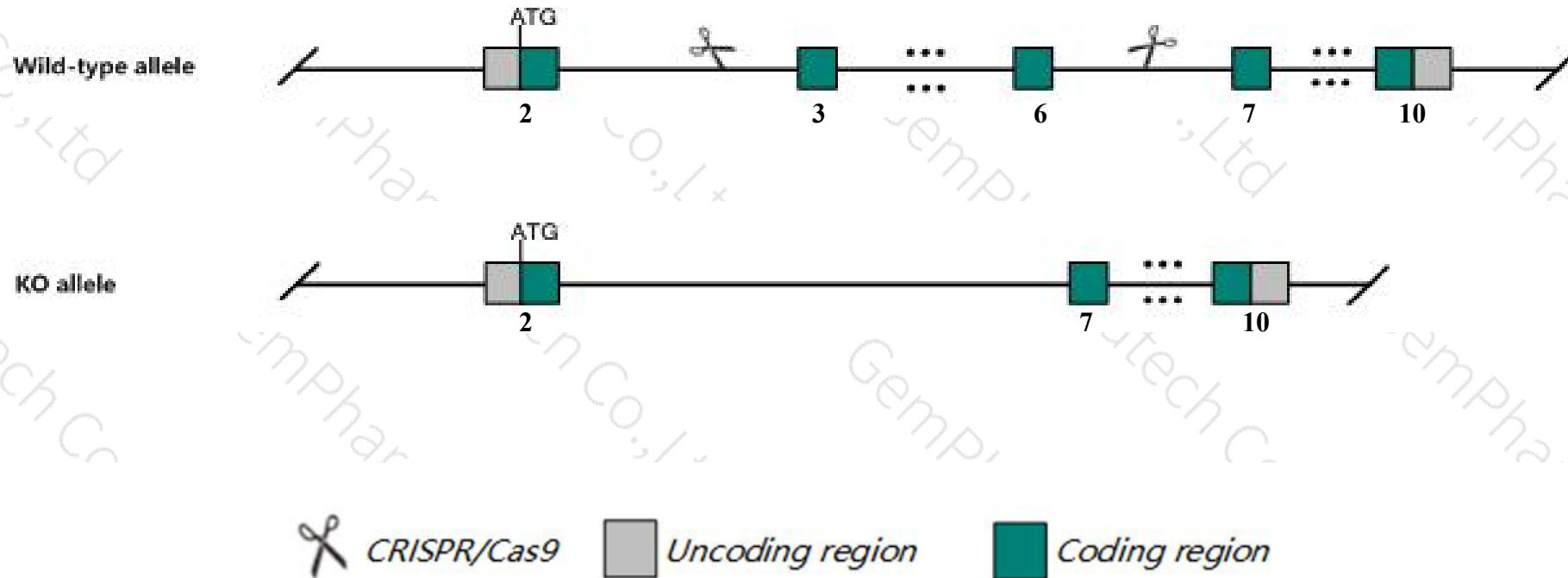
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pacsin1* gene. The schematic diagram is as follows:



- The *Pacsin1* gene has 11 transcripts. According to the structure of *Pacsin1* gene, exon3-exon6 of *Pacsin1-211* (ENSMUST00000232437.1) transcript is recommended as the knockout region. The region contains 725bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pacsin1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a gene trapped allele show altered type I interferon responses in plasmacytoid dendritic cells. Homozygotes for a null allele show impaired synaptic vesicle formation, synaptic transmission and neuronal network activity, and develop generalized seizures with tonic-clonic convulsions.
- The *Pacsin1* gene is located on the Chr17. 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)

Pacsin1 protein kinase C and casein kinase substrate in neurons 1 [Mus musculus (house mouse)]

Gene ID: 23969, updated on 7-Apr-2019

Summary



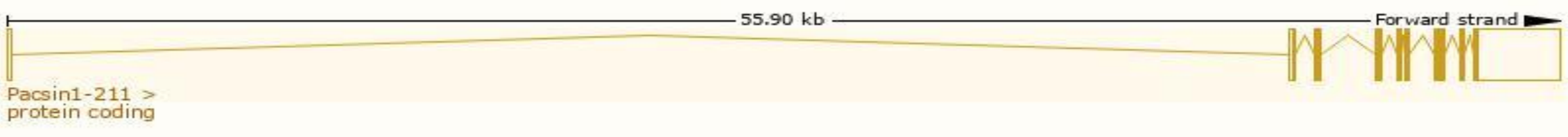
| | |
|---------------------------|---|
| Official Symbol | Pacsin1 provided by MGI |
| Official Full Name | protein kinase C and casein kinase substrate in neurons 1 provided by MGI |
| Primary source | MGI:MGI:1345181 |
| See related | Ensembl:ENSMUSG00000040276 |
| Gene type | protein coding |
| RefSeq 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 | A830061D09Rik, H74, mKIAA1379, syndapin |
| Expression | Biased expression in frontal lobe adult (RPKM 48.4), cerebellum adult (RPKM 46.5) and 8 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

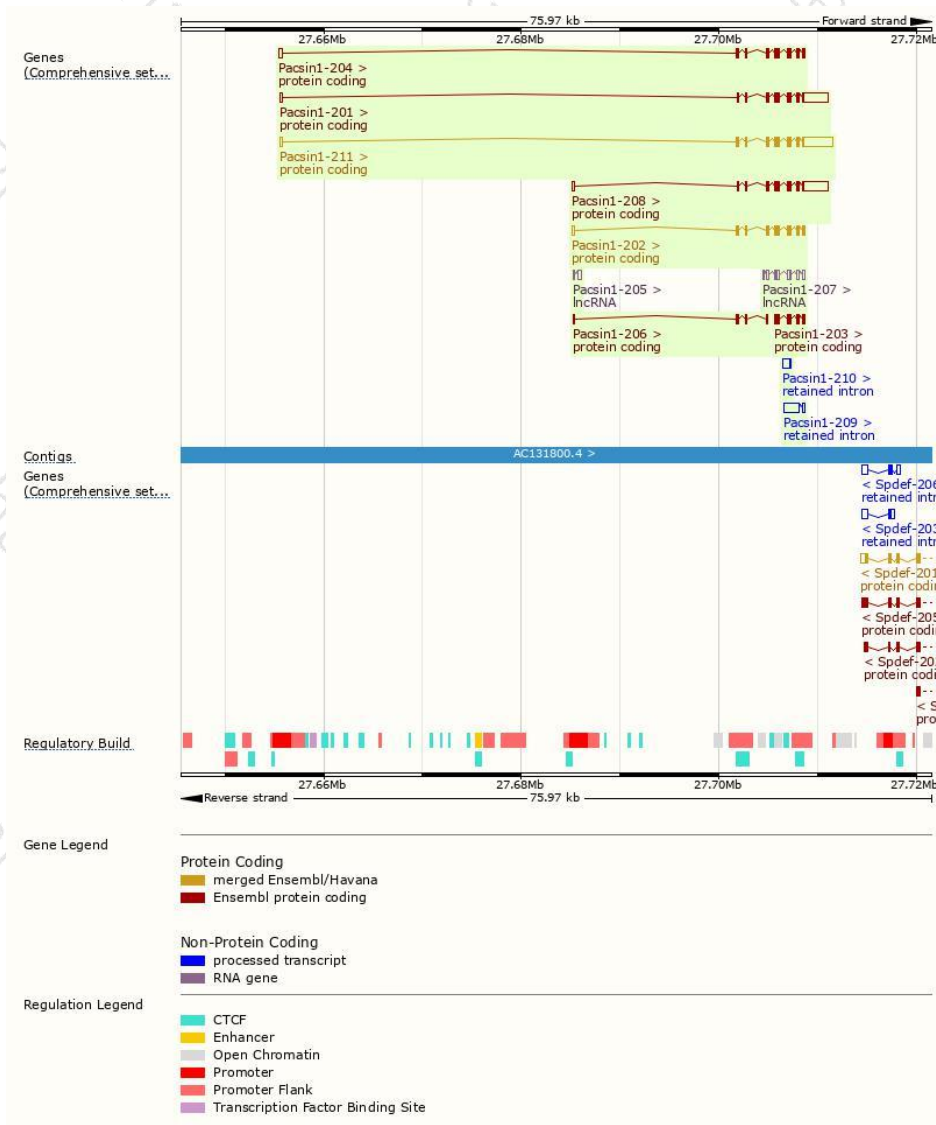
The gene has 11 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-------------|---------------------------------------|------|-----------------------|-----------------|---------------------------|---|-------------------------------|
| Pacsin1-211 | ENSMUST00000232437.1 | 4566 | 441aa | Protein coding | CCDS28567 | Q543Y7 Q61644 | GENCODE basic APPRIS P1 |
| Pacsin1-208 | ENSMUST00000231669.1 | 4209 | 441aa | Protein coding | CCDS28567 | Q543Y7 Q61644 | GENCODE basic APPRIS P1 |
| Pacsin1-201 | ENSMUST00000045896.10 | 4176 | 441aa | Protein coding | CCDS28567 | Q543Y7 Q61644 | TSL:1 GENCODE basic APPRIS P1 |
| Pacsin1-204 | ENSMUST00000114873.7 | 1857 | 441aa | Protein coding | CCDS28567 | Q543Y7 Q61644 | TSL:1 GENCODE basic APPRIS P1 |
| Pacsin1-202 | ENSMUST00000097360.2 | 1800 | 441aa | Protein coding | CCDS28567 | Q543Y7 Q61644 | TSL:1 GENCODE basic APPRIS P1 |
| Pacsin1-203 | ENSMUST00000114872.8 | 972 | 320aa | Protein coding | - | A0A384DVB1 | CDS 5' incomplete TSL:1 |
| Pacsin1-206 | ENSMUST00000231236.1 | 672 | 109aa | Protein coding | - | A0A338P6K4 | CDS 3' incomplete |
| Pacsin1-209 | ENSMUST00000231854.1 | 1786 | No protein | Retained intron | - | - | |
| Pacsin1-210 | ENSMUST00000232225.1 | 697 | No protein | Retained intron | - | - | |
| Pacsin1-207 | ENSMUST00000231350.1 | 1368 | No protein | lncRNA | - | - | |
| Pacsin1-205 | ENSMUST00000155259.1 | 552 | No protein | lncRNA | - | - | TSL:2 |

The strategy is based on the design of *Pacsin1-211* transcript,The transcription is shown below

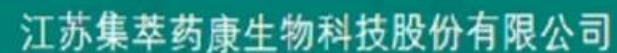


Genomic location distribution

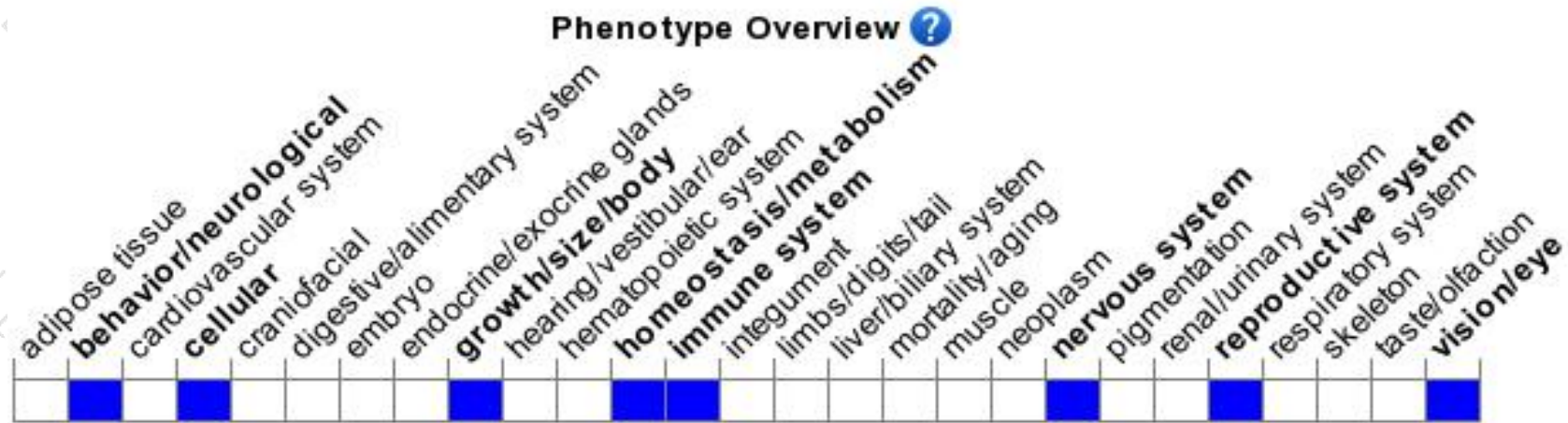




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Mouse phenotype description(MGI)



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, Homozygotes for a gene trapped allele show altered type I interferon responses in plasmacytoid dendritic cells. Homozygotes for a null allele show impaired synaptic vesicle formation, synaptic transmission and neuronal network activity, and develop generalized seizures with tonic-clonic convulsions.

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

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