



Arhgap32 Cas9-CKO Strategy

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Design Date: 2020-1-22
Reviewer: JiaYu

Project Overview

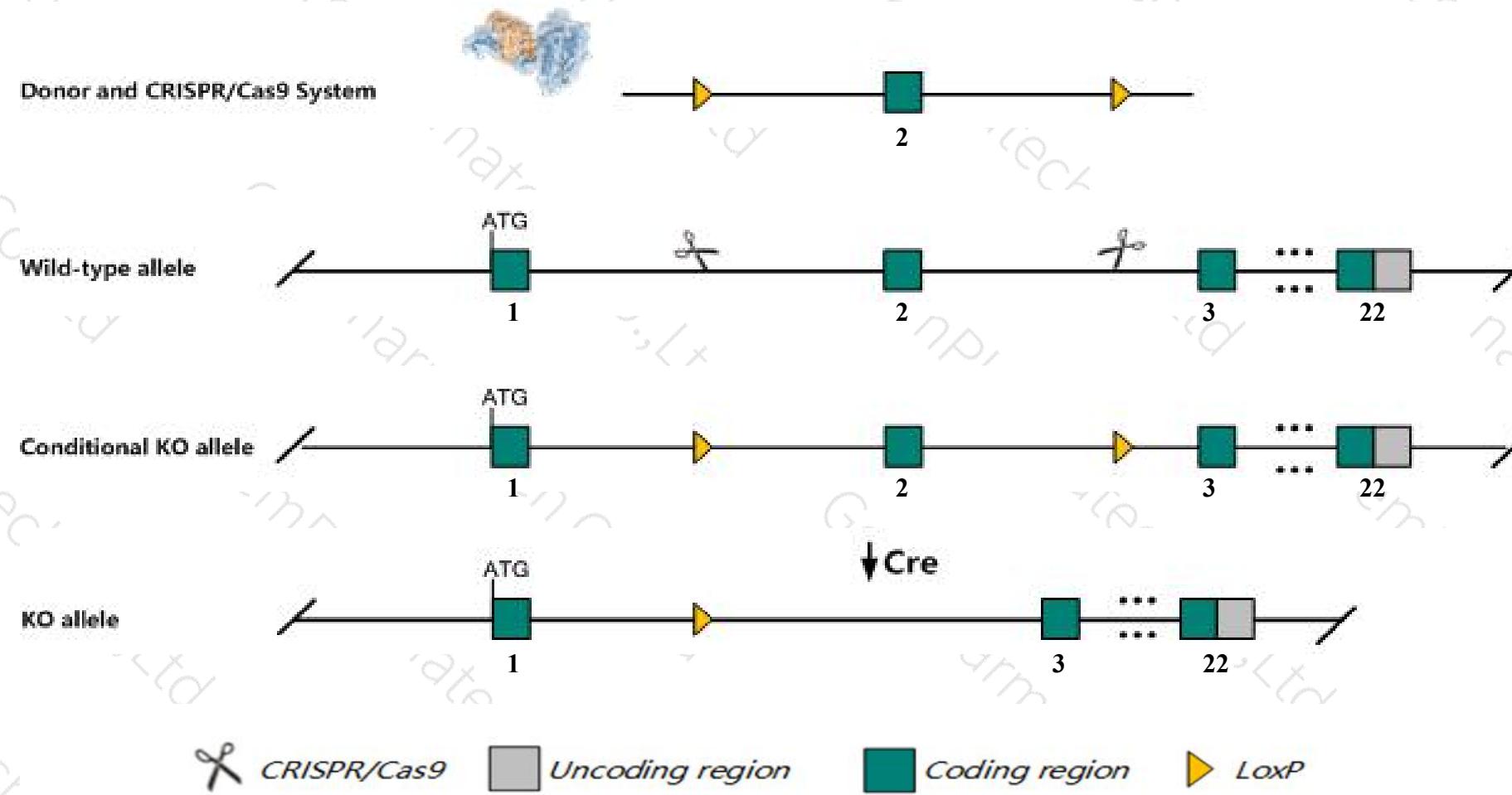
Project Name*Arhgap32*

Project type**Cas9-CKO**

Strain background**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgap32* gene. The schematic diagram is as follows:



Technical routes

- The *Arhgap32* gene has 7 transcripts. According to the structure of *Arhgap32* gene, exon2 of *Arhgap32-203* (ENSMUST00000174641.7) transcript is recommended as the knockout region. The region contains 109bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgap32* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



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Notice

- According to the existing MGI data, Mice homozygous for a null mutation are fertile but display abnormal neurite growth.
- This strategy has no effect on *Arhgap32-201*, *Arhgap32-206*, *Arhgap32-207*.
- The *Arhgap32* gene is located on the Chr9. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



Gene information (NCBI)

Arhgap32 Rho GTPase activating protein 32 [*Mus musculus* (house mouse)]

Gene ID: 330914, updated on 12-Aug-2019

Summary

Official Symbol Arhgap32 provided by [MGI](#)

Official Full Name Rho GTPase activating protein 32 provided by [MGI](#)

Primary source [MGI](#):[MGI:2450166](#)

See related [Ensembl:ENSMUSG00000041444](#)

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 Grit; Rics; Gc-gap; Px-rics; p250Gap; mKIAA0712; p200Rhogap; 3426406O18Rik

Annotation information Note: There are conflicting opinions about the protein-coding potential of this locus. [17 Jun 2011]

Expression Broad expression in cortex adult (RPKM 9.5), frontal lobe adult (RPKM 9.3) and 22 other tissues [See more](#)

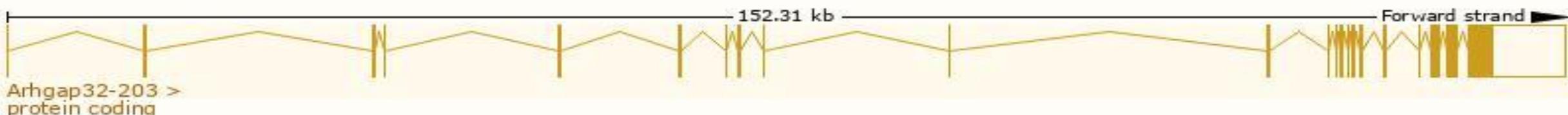
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

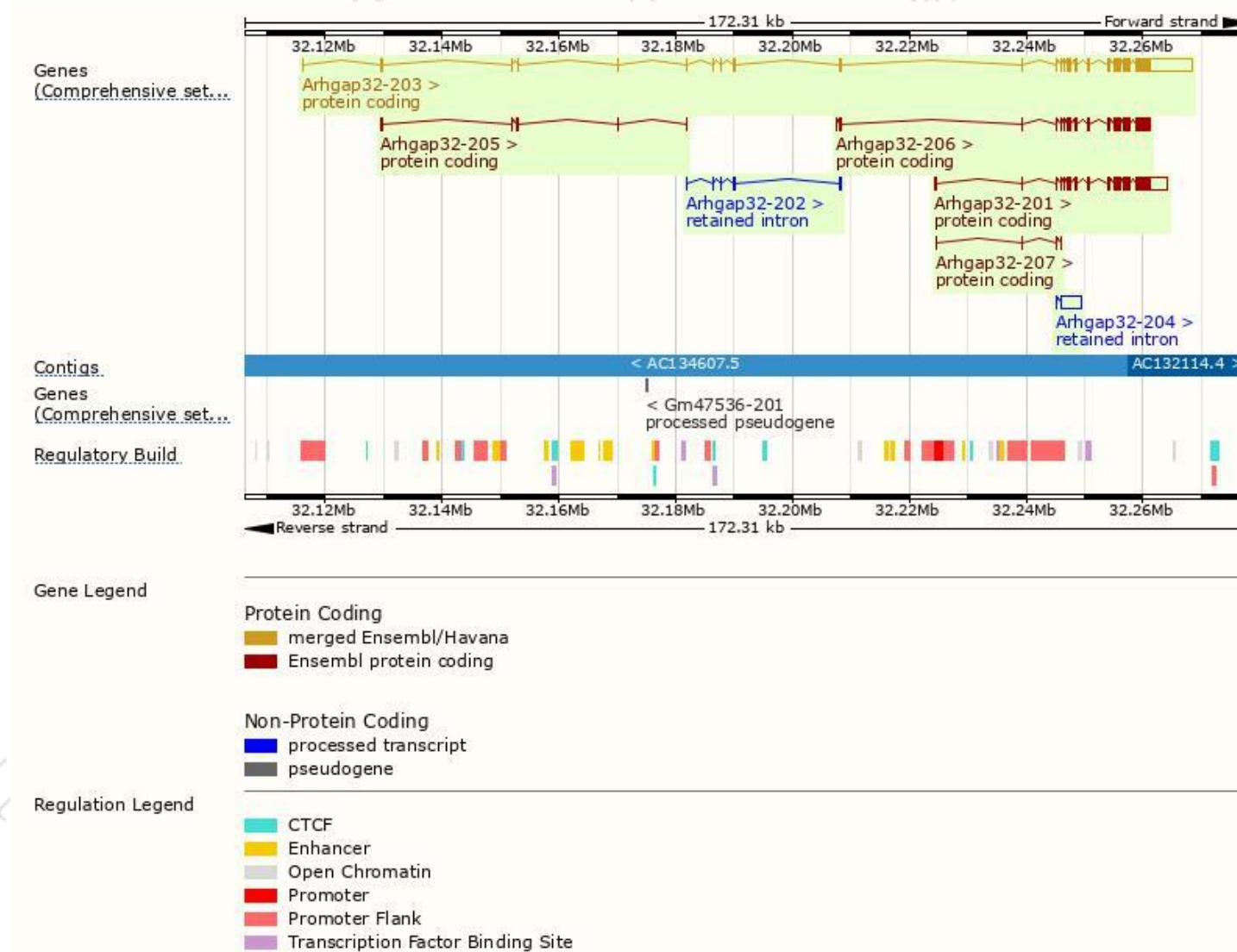
The gene has 7 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|--------------|--------------------------------------|-------|------------------------|-----------------|---------------------------|------------------------|---|
| Arhgap32-203 | ENSMUST00000174641.7 | 13568 | 2089aa | Protein coding | CCDS57666 | Q811P8 | TSL:5 GENCODE basic APPRIS P1 |
| Arhgap32-201 | ENSMUST00000168954.8 | 8703 | 1740aa | Protein coding | CCDS22951 | Q811P8 | TSL:5 GENCODE basic |
| Arhgap32-206 | ENSMUST00000182802.7 | 5621 | 1740aa | Protein coding | CCDS22951 | Q811P8 | TSL:1 GENCODE basic |
| Arhgap32-205 | ENSMUST00000182310.1 | 540 | 180aa | Protein coding | - | S4R2G6 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| Arhgap32-207 | ENSMUST00000183121.1 | 380 | 91aa | Protein coding | - | S4R2C0 | CDS 3' incomplete TSL:5 |
| Arhgap32-204 | ENSMUST00000174730.1 | 3638 | No protein | Retained intron | - | - | TSL:2 |
| Arhgap32-202 | ENSMUST00000174314.1 | 543 | No protein | Retained intron | - | - | TSL:3 |

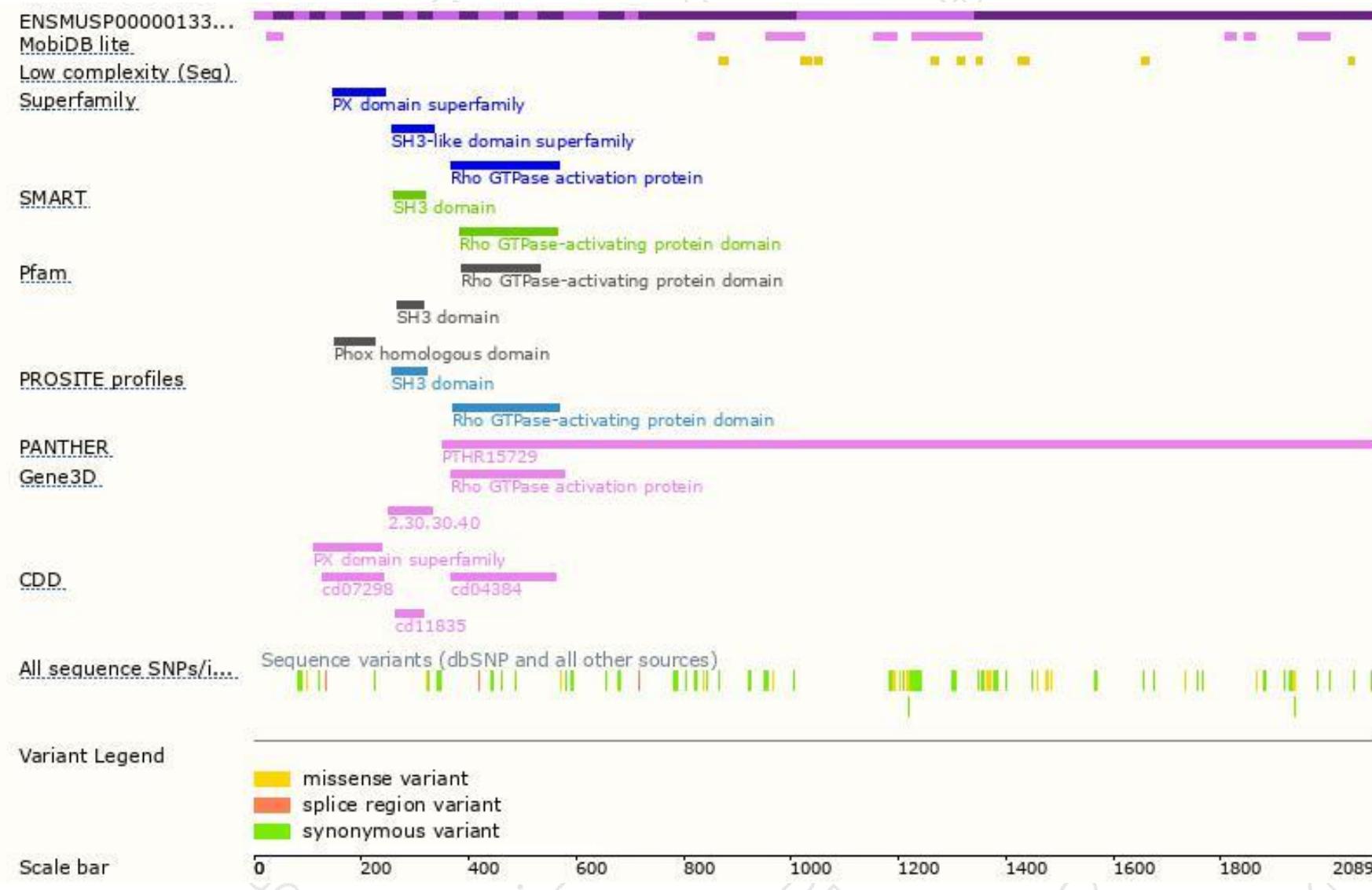
The strategy is based on the design of *Arhgap32-203* transcript, The transcription is shown below



Genomic location distribution



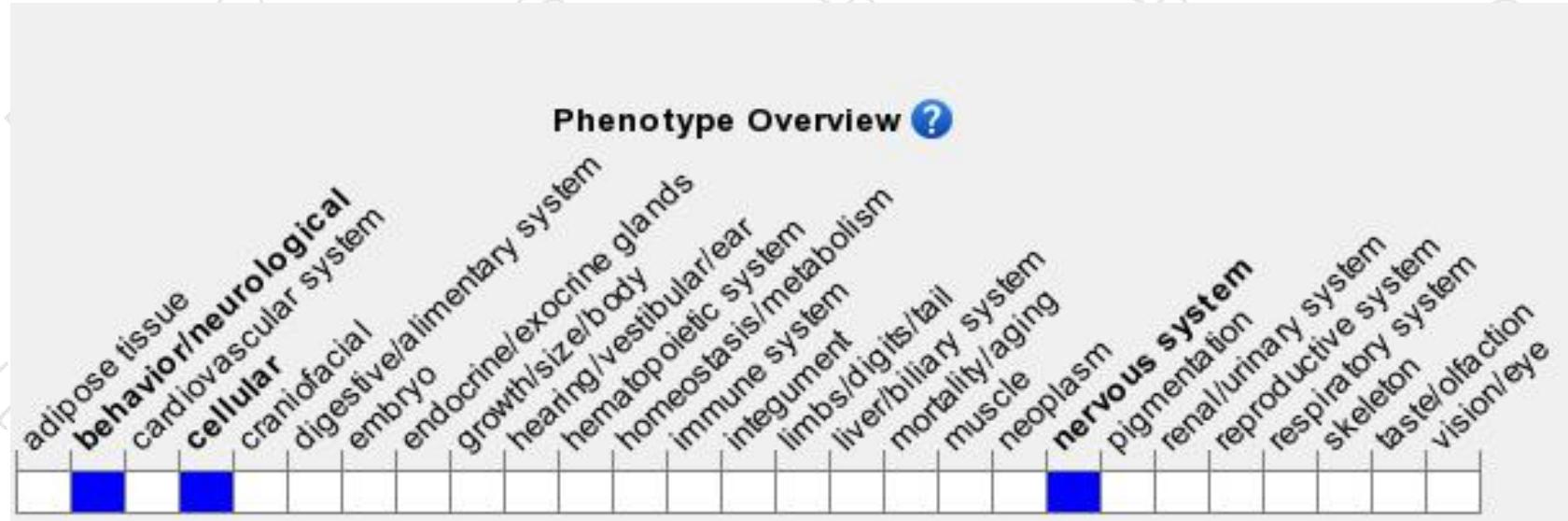
Protein domain





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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, Mice homozygous for a null mutation are fertile but display abnormal neurite growth.



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

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