

Arhgap33 Cas9-KO Strategy

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Project Overview

Project Name

Arhgap33

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgap33* gene. The schematic diagram is as follows:



- The *Arhgap33* gene has 8 transcripts. According to the structure of *Arhgap33* gene, exon3-exon20 of *Arhgap33-204* (ENSMUST00000207860.1) transcript is recommended as the knockout region. The region contains 1936bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgap33* gene. The brief process is as follows: CRISPR/Cas9 sys

- According to the existing MGI data, Mice homozygous for a null mutation display region specific thinning of the cerebral cortex with reduced dendritic complexity.
- The *Arhgap33* gene is located on the Chr7. 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)

Arhgap33 Rho GTPase activating protein 33 [*Mus musculus* (house mouse)]

Gene ID: 233071, updated on 12-Aug-2019

Summary

Official Symbol Arhgap33 provided by [MGI](#)
Official Full Name Rho GTPase activating protein 33 provided by [MGI](#)
Primary source [MGI:MGI:2673998](#)
See related [Ensembl:ENSMUSG00000036882](#)
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 Snx26; TCGAP; AW324378; NOMA-GAP
Expression Broad expression in whole brain E14.5 (RPKM 45.7), CNS E14 (RPKM 41.4) and 16 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 7; 7 B1

See Arhgap33 in [Genome Data Viewer](#)

Exon count: 23

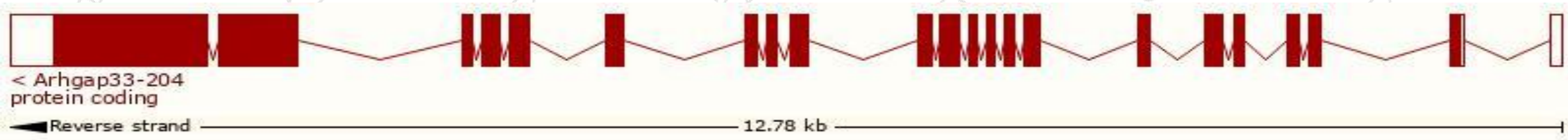
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (30522225..30535171, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (31307245..31320028, complement)

Transcript information (Ensembl)

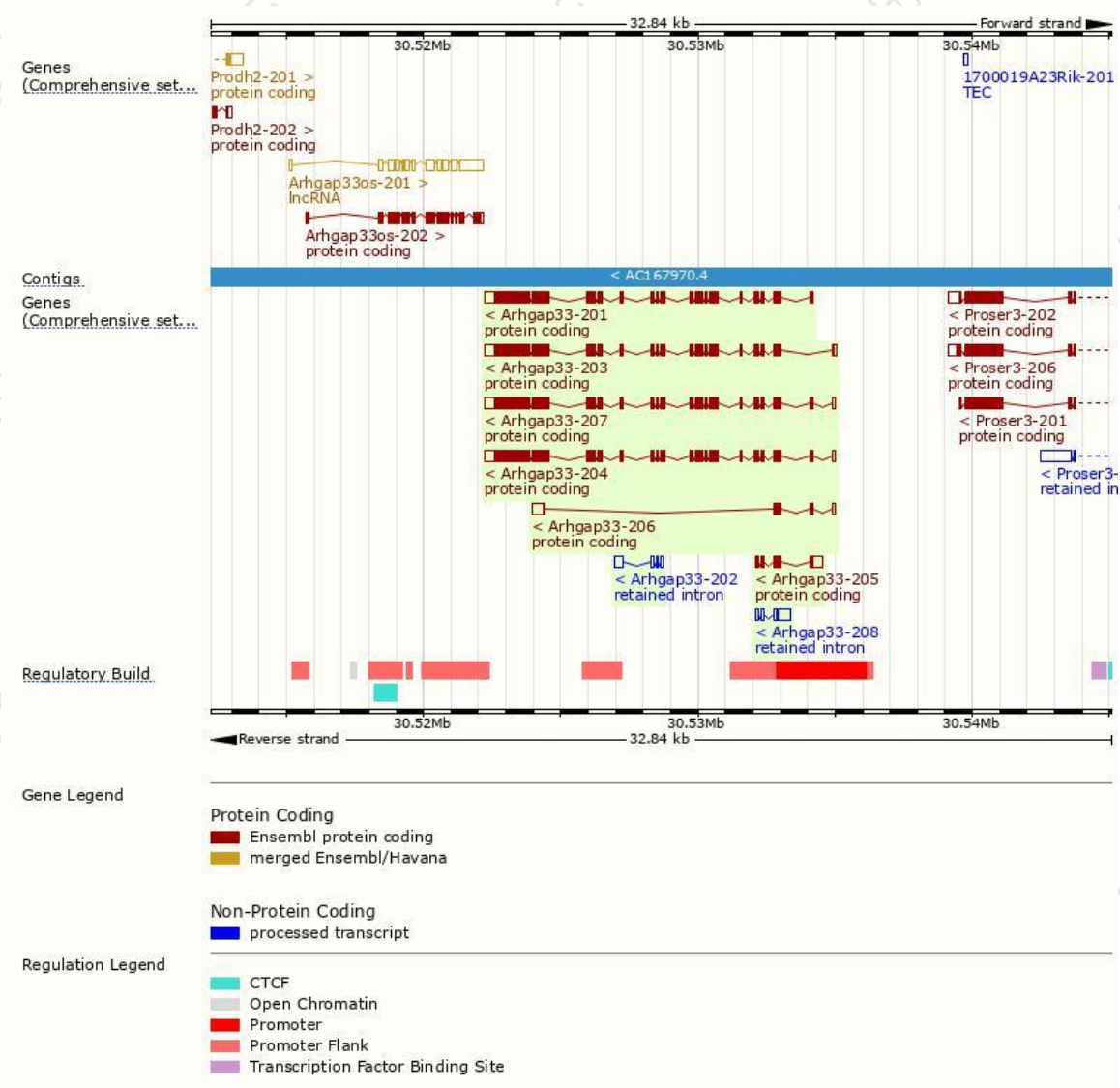
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgap33-204	ENSMUST00000207860.1	4396	1305aa	Protein coding	CCDS21095	Q80YF9	TSL:1 GENCODE basic APPRIS P3
Arhgap33-207	ENSMUST00000208538.1	4372	1305aa	Protein coding	CCDS21095	Q80YF9	TSL:1 GENCODE basic APPRIS P3
Arhgap33-203	ENSMUST00000207858.1	4337	1281aa	Protein coding	CCDS85264	A0A140LHW2	TSL:1 GENCODE basic APPRIS ALT2
Arhgap33-201	ENSMUST00000044338.4	4280	1305aa	Protein coding	CCDS21095	Q80YF9	TSL:1 GENCODE basic APPRIS P3
Arhgap33-205	ENSMUST00000208491.1	822	145aa	Protein coding	-	A0A140LIY1	CDS 3' incomplete TSL:3
Arhgap33-206	ENSMUST00000208522.1	781	97aa	Protein coding	-	A0A140LIC8	TSL:3 GENCODE basic
Arhgap33-208	ENSMUST00000208723.1	726	No protein	Retained intron	-	-	TSL:3
Arhgap33-202	ENSMUST00000207637.1	596	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Arhgap33-204* transcript,The transcription is shown below



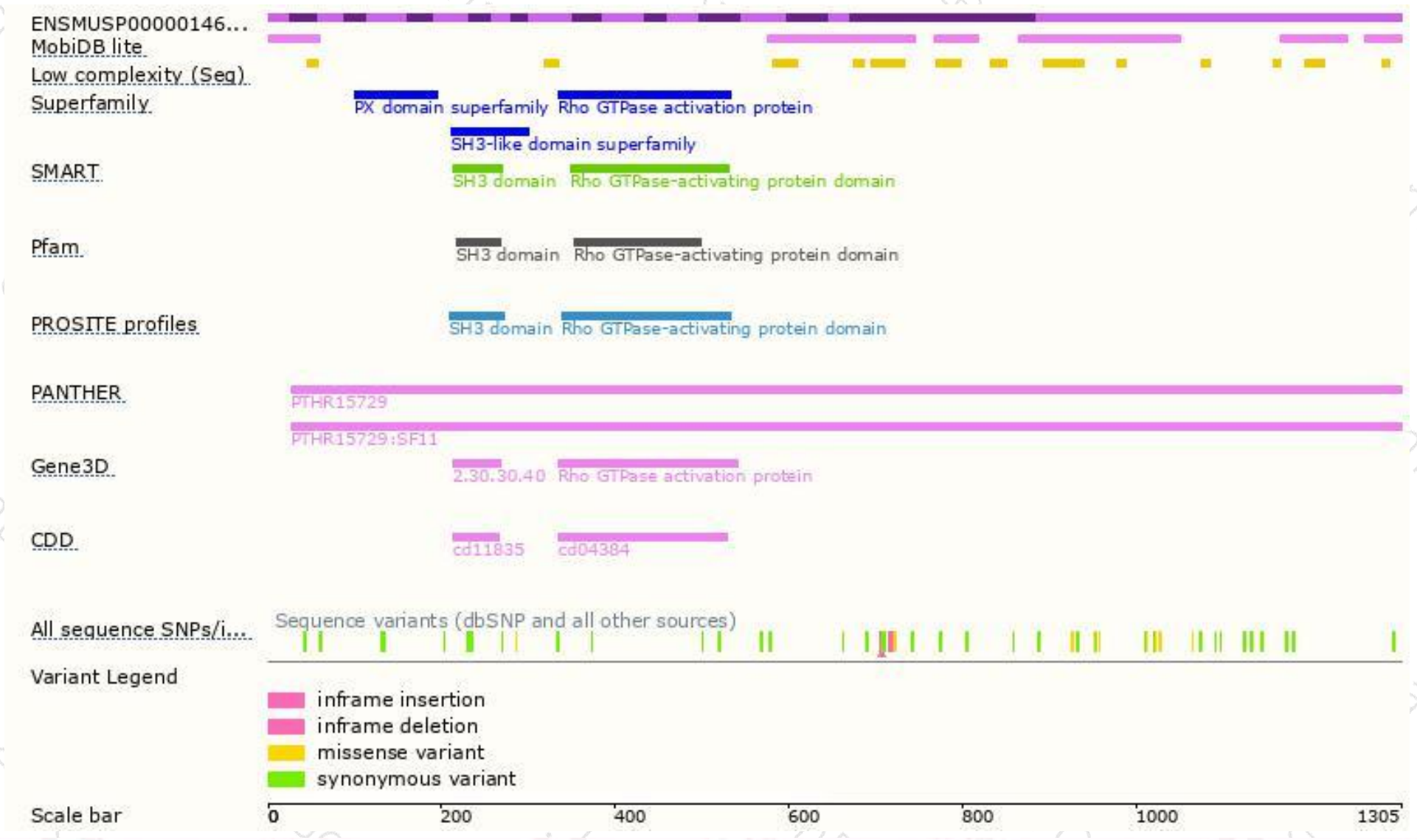
Genomic location distribution



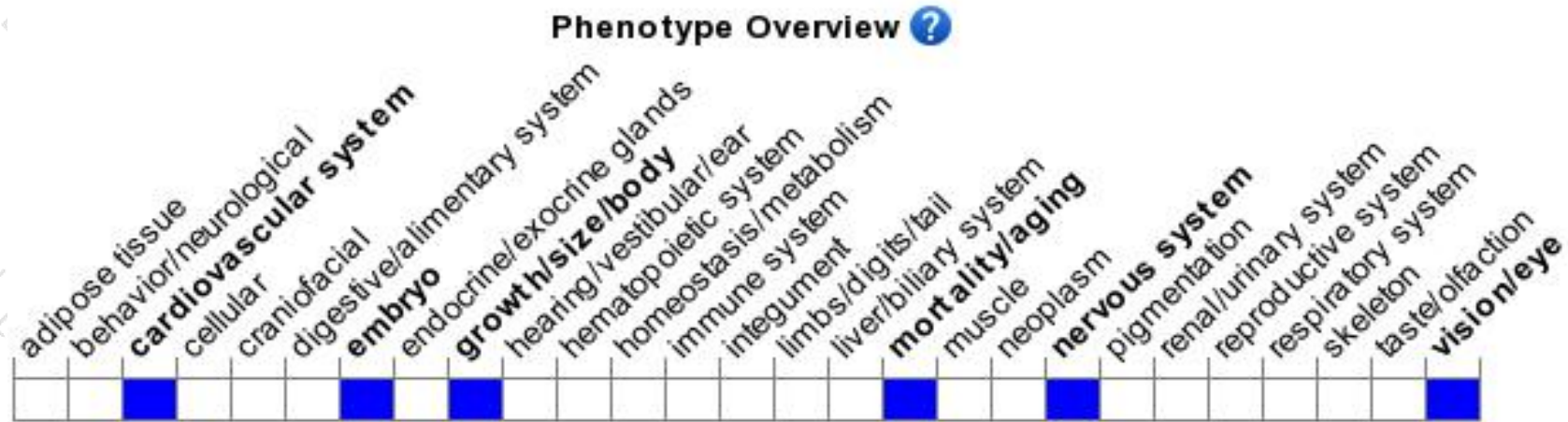
Protein domain



集萃药康
GemPharmatech



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 display region specific thinning of the cerebral cortex with reduced dendritic complexity.

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

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