

# *Arhgap12* Cas9-KO Strategy

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**Reviewer: Ruiuri Zhang**

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# Project Overview

**Project Name**

*Arhgap12*

**Project type**

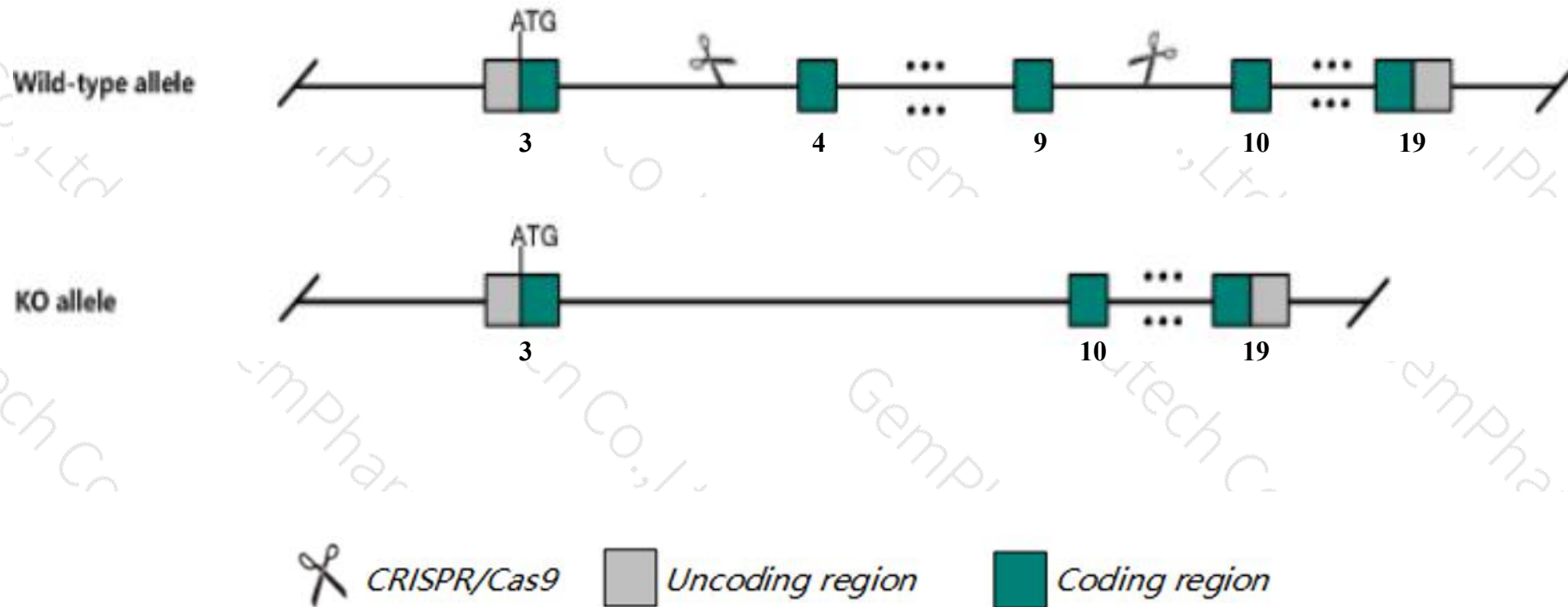
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgap12* gene. The schematic diagram is as follows:



- The *Arhgap12* gene has 15 transcripts. According to the structure of *Arhgap12* gene, exon4-exon9 of *Arhgap12*-212(ENSMUST00000182559.7) transcript is recommended as the knockout region. The region contains 746bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgap12* 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, a null gene trap mutation resulted in no notable phenotype in homozygous mutant mice.
- The *Arhgap12* gene is located on the Chr18. 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)

## Arhgap12 Rho GTPase activating protein 12 [Mus musculus (house mouse)]

Gene ID: 75415, updated on 13-Mar-2020

### Summary



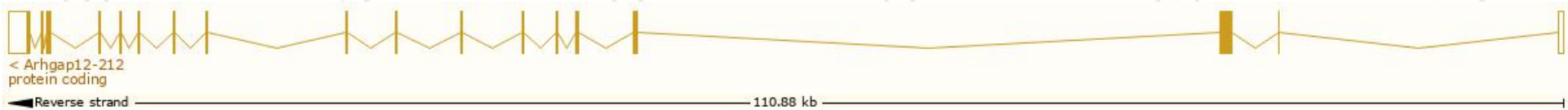
<b>Official Symbol</b>	Arhgap12 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Rho GTPase activating protein 12 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1922665</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000041225</a>
<b>Gene type</b>	protein coding
<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>	2810011M08Rik
<b>Expression</b>	Broad expression in bladder adult (RPKM 10.7), CNS E14 (RPKM 8.1) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

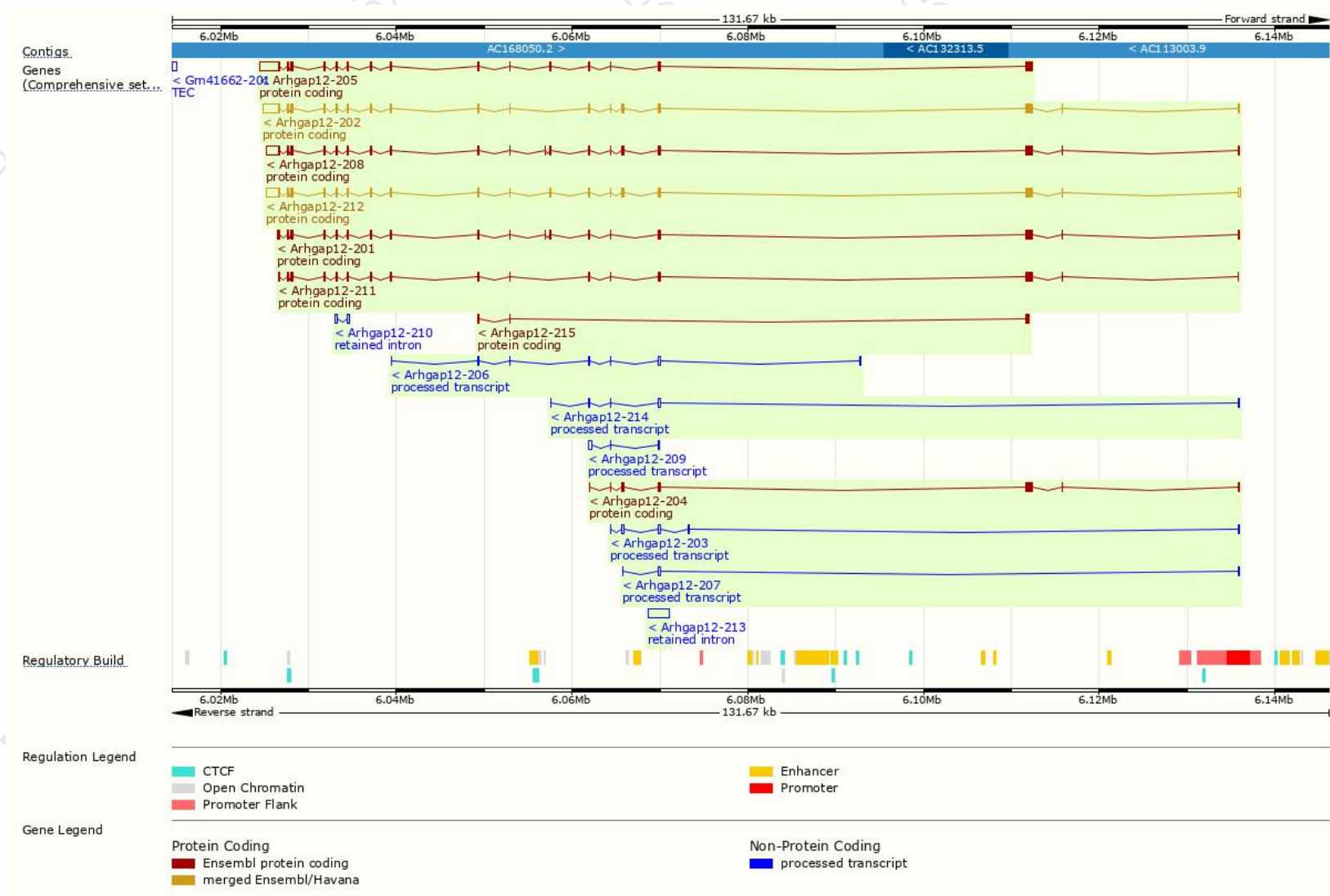
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgap12-215	<a href="#">ENSMUST00000182921.1</a>	439	<a href="#">146aa</a>	Protein coding	-	<a href="#">S4R2V0</a>	CDS 5' and 3' incomplete TSL:3
Arhgap12-204	<a href="#">ENSMUST00000182038.1</a>	1435	<a href="#">394aa</a>	Protein coding	-	<a href="#">S4R1B0</a>	CDS 3' incomplete TSL:1
Arhgap12-211	<a href="#">ENSMUST00000182383.7</a>	2500	<a href="#">766aa</a>	Protein coding	-	<a href="#">S4R203</a>	TSL:5 GENCODE basic APPRIS ALT1
Arhgap12-205	<a href="#">ENSMUST00000182066.7</a>	4506	<a href="#">791aa</a>	Protein coding	-	<a href="#">S4R248</a>	TSL:5 GENCODE basic APPRIS ALT1
Arhgap12-201	<a href="#">ENSMUST00000062584.13</a>	2718	<a href="#">796aa</a>	Protein coding	-	<a href="#">A0A0A0MQ95</a>	TSL:5 GENCODE basic
Arhgap12-202	<a href="#">ENSMUST00000077128.12</a>	4431	<a href="#">813aa</a>	Protein coding	<a href="#">CCDS37722</a>	<a href="#">B2RUJ8</a>	TSL:1 GENCODE basic APPRIS ALT1
Arhgap12-212	<a href="#">ENSMUST00000182559.7</a>	4265	<a href="#">838aa</a>	Protein coding	<a href="#">CCDS37723</a>	<a href="#">Q8C0D4</a>	TSL:1 GENCODE basic APPRIS P4
Arhgap12-208	<a href="#">ENSMUST00000182213.7</a>	4162	<a href="#">843aa</a>	Protein coding	-	<a href="#">S4R221</a>	TSL:5 GENCODE basic
Arhgap12-206	<a href="#">ENSMUST00000182101.7</a>	735	No protein	Processed transcript	-	-	TSL:3
Arhgap12-203	<a href="#">ENSMUST00000181989.7</a>	679	No protein	Processed transcript	-	-	TSL:3
Arhgap12-214	<a href="#">ENSMUST00000182614.7</a>	668	No protein	Processed transcript	-	-	TSL:3
Arhgap12-209	<a href="#">ENSMUST00000182322.1</a>	595	No protein	Processed transcript	-	-	TSL:3
Arhgap12-207	<a href="#">ENSMUST00000182178.1</a>	435	No protein	Processed transcript	-	-	TSL:3
Arhgap12-213	<a href="#">ENSMUST00000182572.1</a>	2444	No protein	Retained intron	-	-	TSL:NA
Arhgap12-210	<a href="#">ENSMUST00000182343.1</a>	556	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Arhgap12-212* transcript,the transcription is shown below:

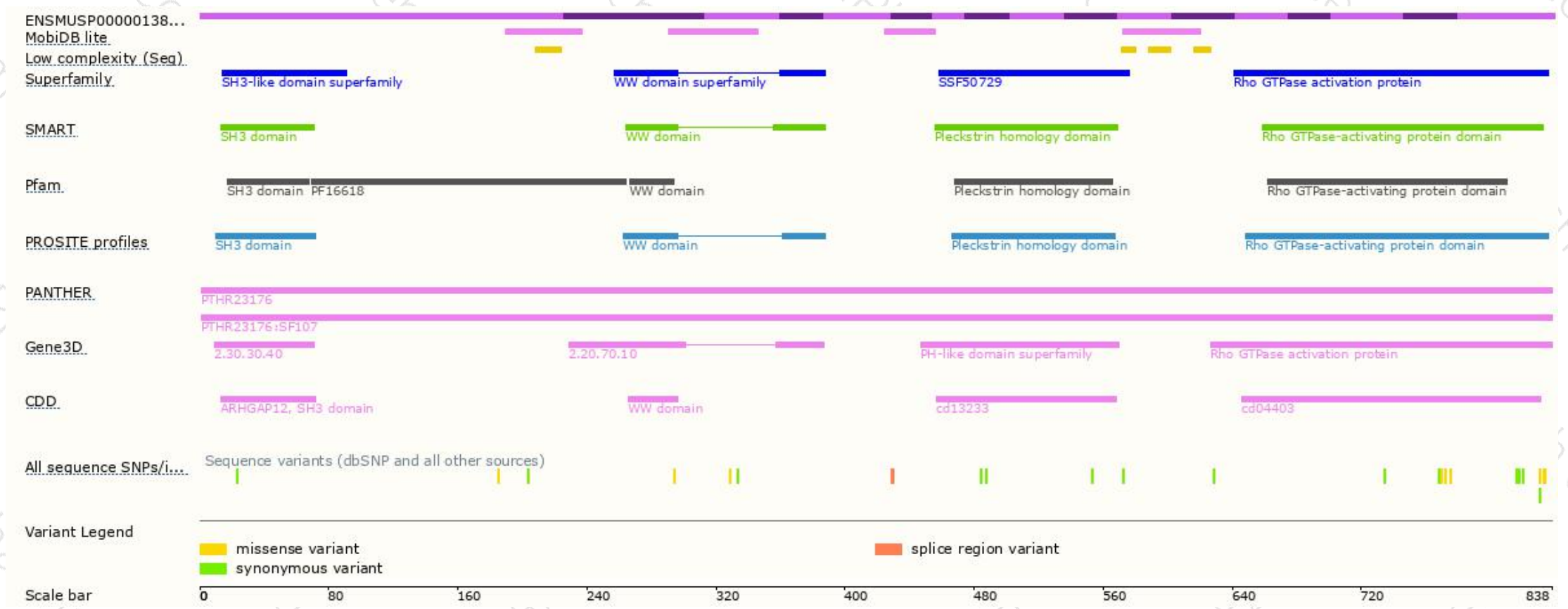


# Genomic location distribution





# Protein domain



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

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