

# *Chn1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Chn1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chn1* gene. The schematic diagram is as follows:



- The *Chn1* gene has 15 transcripts. According to the structure of *Chn1* gene, exon8-exon10 of *Chn1-203* (ENSMUST00000112024.9) transcript is recommended as the knockout region. The region contains 337bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Chn1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homologous for a null allele exhibit transient postnatal size reduction, abnormal gait and abnormal innervation of the spinal cord. Part of null homozygous show preweaning lethality.
- Transcript *Chn1-205* may not be affected.
- The *Chn1* gene is located on the Chr2. 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)

## Chn1 chimerin 1 [ *Mus musculus* (house mouse) ]

Gene ID: 108699, updated on 19-Nov-2019

### Summary

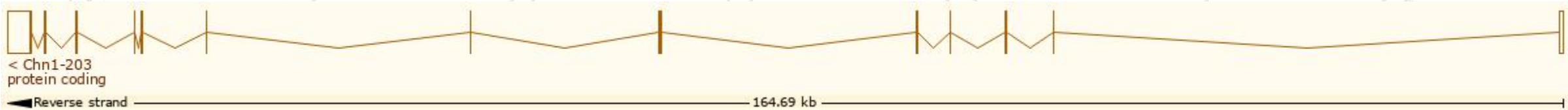
<b>Official Symbol</b>	Chn1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	chimerin 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1915674</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000056486</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	ARHGAP2; AI413815; 0610007I19Rik; 0710001E19Rik; 1700112L09Rik; 2900046J01Rik
<b>Expression</b>	Biased expression in cortex adult (RPKM 122.5), frontal lobe adult (RPKM 81.5) and 6 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:

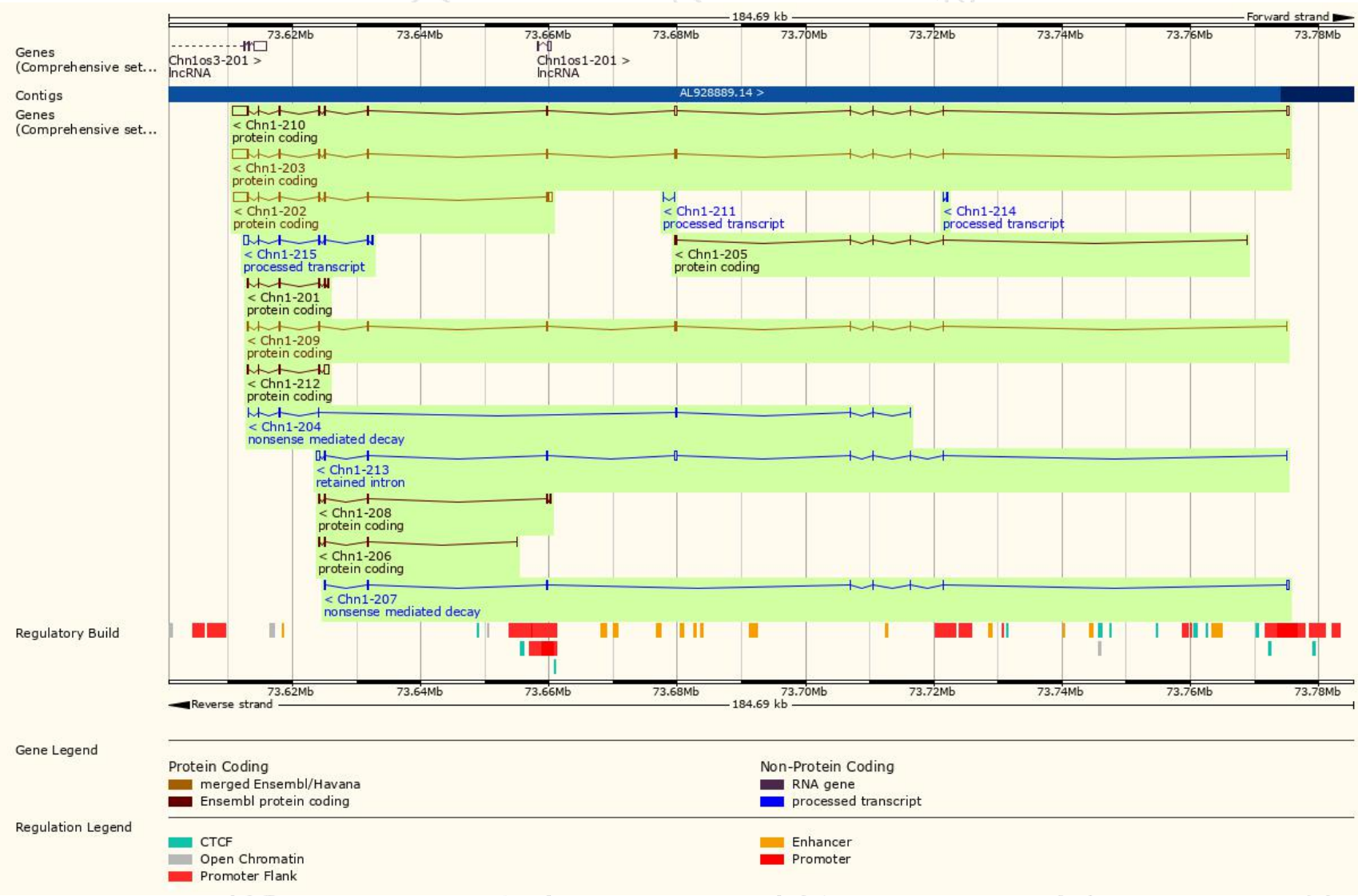
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chn1-203	<a href="#">ENSMUST00000112024.9</a>	4050	<a href="#">459aa</a>	Protein coding	<a href="#">CCDS50608</a>	<a href="#">Q91V57</a>	TSL:1 GENCODE basic APPRIS P1
Chn1-210	<a href="#">ENSMUST00000180045.7</a>	4050	<a href="#">210aa</a>	Protein coding	<a href="#">CCDS38145</a>	<a href="#">A7VK14</a> <a href="#">Q91V57</a>	TSL:1 GENCODE basic
Chn1-202	<a href="#">ENSMUST00000102677.10</a>	3760	<a href="#">334aa</a>	Protein coding	<a href="#">CCDS16133</a>	<a href="#">Q91V57</a>	TSL:1 GENCODE basic
Chn1-212	<a href="#">ENSMUST00000229731.1</a>	1403	<a href="#">210aa</a>	Protein coding	<a href="#">CCDS38145</a>	<a href="#">A7VK14</a> <a href="#">Q91V57</a>	GENCODE basic
Chn1-209	<a href="#">ENSMUST00000166199.8</a>	1324	<a href="#">401aa</a>	Protein coding	<a href="#">CCDS50607</a>	<a href="#">A7VK13</a>	TSL:1 GENCODE basic
Chn1-201	<a href="#">ENSMUST00000070579.6</a>	1023	<a href="#">210aa</a>	Protein coding	<a href="#">CCDS38145</a>	<a href="#">A7VK14</a> <a href="#">Q91V57</a>	TSL:1 GENCODE basic
Chn1-208	<a href="#">ENSMUST00000154258.7</a>	712	<a href="#">95aa</a>	Protein coding	-	<a href="#">B2FDI0</a>	CDS 3' incomplete TSL:5
Chn1-205	<a href="#">ENSMUST00000135904.1</a>	631	<a href="#">128aa</a>	Protein coding	-	<a href="#">B2FDI2</a>	CDS 3' incomplete TSL:2
Chn1-206	<a href="#">ENSMUST00000136953.1</a>	413	<a href="#">81aa</a>	Protein coding	-	<a href="#">B2FDI1</a>	CDS 3' incomplete TSL:3
Chn1-207	<a href="#">ENSMUST00000139252.1</a>	881	<a href="#">87aa</a>	Nonsense mediated decay	-	<a href="#">D6RCX8</a>	TSL:3
Chn1-204	<a href="#">ENSMUST00000124450.1</a>	643	<a href="#">29aa</a>	Nonsense mediated decay	-	<a href="#">F7C3N6</a>	CDS 5' incomplete TSL:3
Chn1-215	<a href="#">ENSMUST00000231013.1</a>	1544	No protein	Processed transcript	-	-	-
Chn1-214	<a href="#">ENSMUST00000230959.1</a>	205	No protein	Processed transcript	-	-	-
Chn1-211	<a href="#">ENSMUST00000229312.1</a>	20	No protein	Processed transcript	-	-	-
Chn1-213	<a href="#">ENSMUST00000229987.1</a>	1431	No protein	Retained intron	-	-	-

The strategy is based on the design of *Chn1-203* transcript, the transcription is shown below:



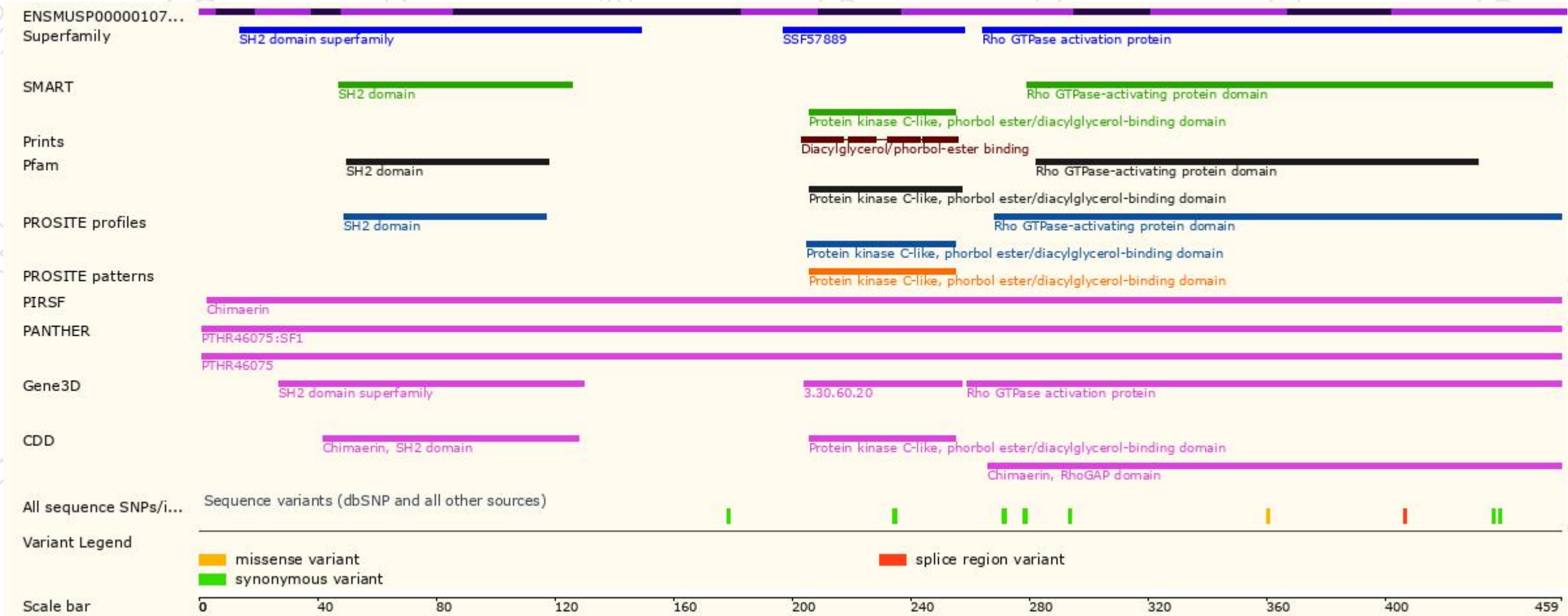


# Genomic location distribution

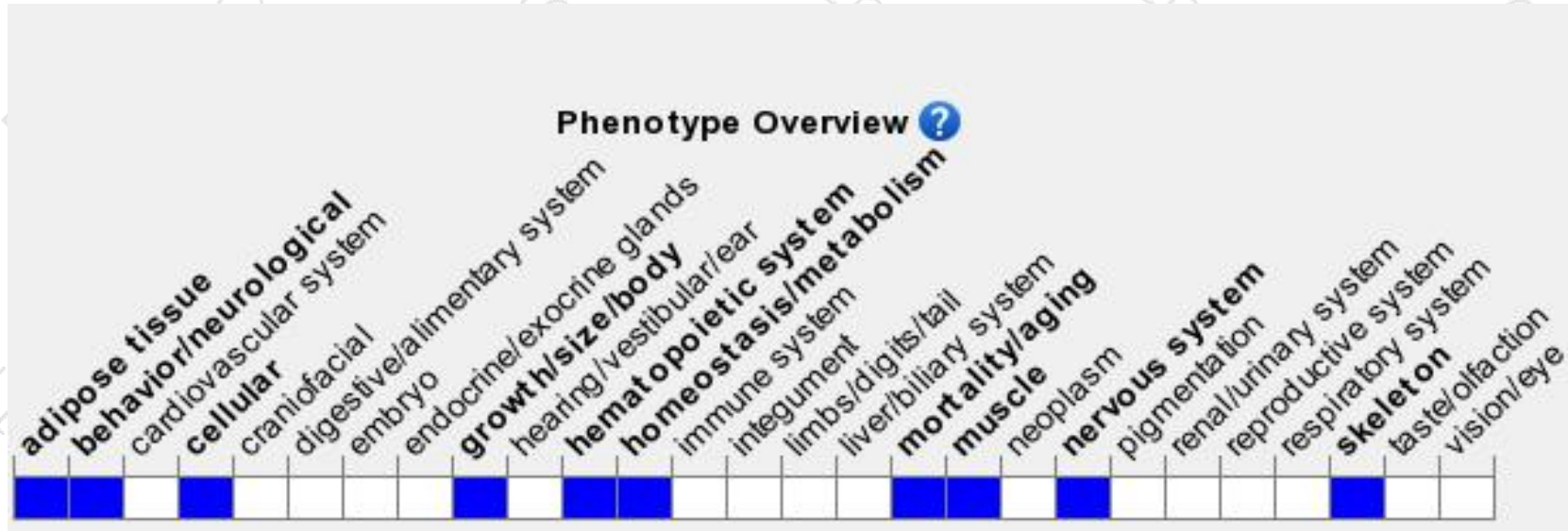




# Protein domain



# 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 homologous for a null allele exhibit transient postnatal size reduction, abnormal gait and abnormal innervation of the spinal cord. Part of null homozygous show preweaning lethality.

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

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