

# *Axin1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Axin1*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Axin1* gene. The schematic diagram is as follows:



- The *Axin1* gene has 5 transcripts. According to the structure of *Axin1* gene, exon2-exon9 of *Axin1-201* (ENSMUST00000074370.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Axin1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mutant homozygotes die at embryonic day 8-10, exhibiting neuroectodermal defects and axial duplications. Heterozygotes exhibit skeletal, cardiac, and neurological defects including short, bent tails, and deafness with circling behavior.
- The *Axin1* 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)

## Axin1 axin 1 [Mus musculus (house mouse)]

Gene ID: 12005, updated on 19-Mar-2019

### Summary



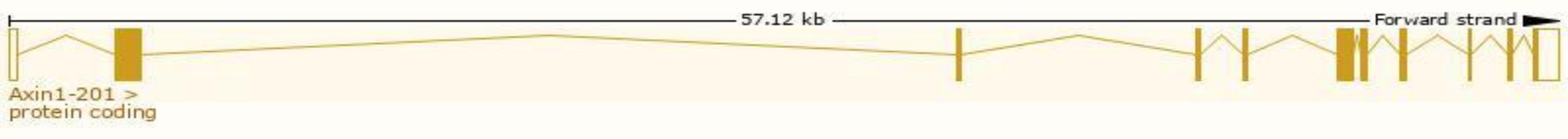
<b>Official Symbol</b>	Axin1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	axin 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1096327</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000024182</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	AI316800, Axin, Fu, Kb, Ki, fused, kinky, knobbly
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 11.6), CNS E11.5 (RPKM 10.8) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

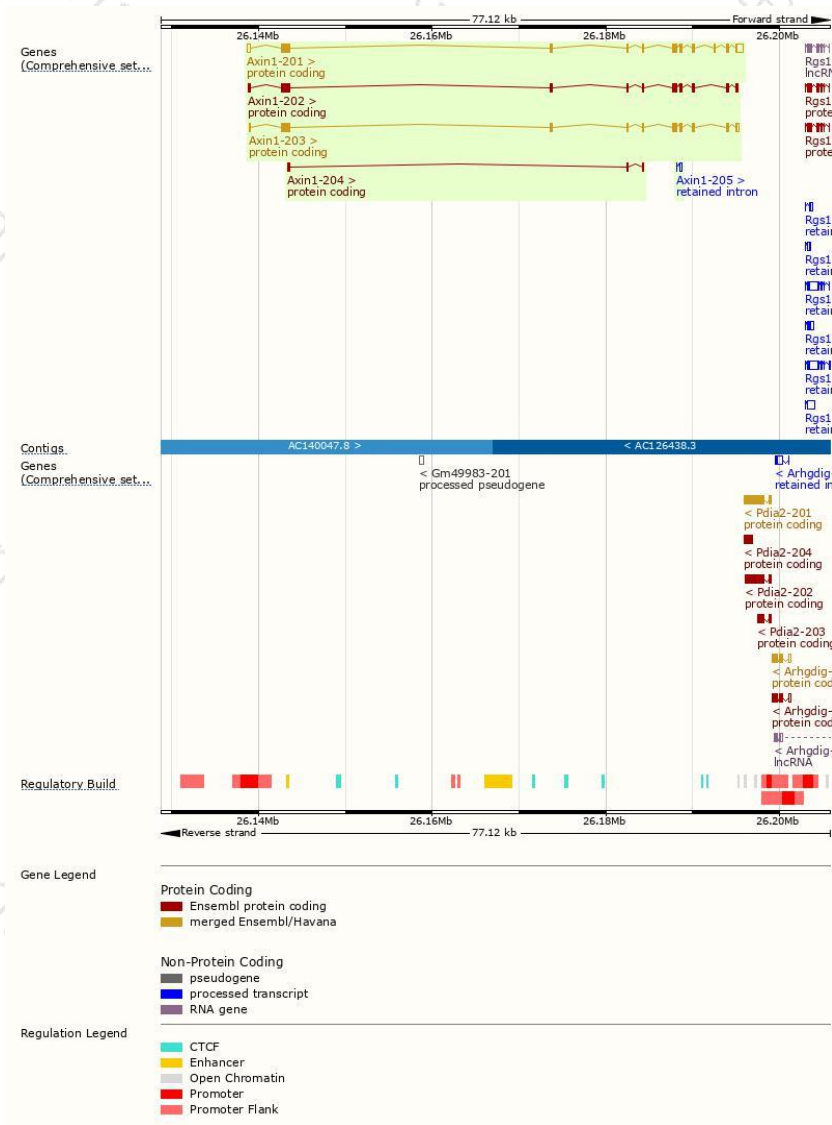
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Axin1-201	<a href="#">ENSMUST00000074370.9</a>	3777	<a href="#">868aa</a>	Protein coding	<a href="#">CCDS28547</a>	<a href="#">E9QMJ8</a>	TSL:1 GENCODE basic APPRIS P3
Axin1-203	<a href="#">ENSMUST00000163421.7</a>	2890	<a href="#">832aa</a>	Protein coding	<a href="#">CCDS50042</a>	<a href="#">Q14DJ8</a>	TSL:5 GENCODE basic APPRIS ALT2
Axin1-202	<a href="#">ENSMUST00000118904.8</a>	2833	<a href="#">832aa</a>	Protein coding	<a href="#">CCDS50042</a>	<a href="#">Q14DJ8</a>	TSL:1 GENCODE basic APPRIS ALT2
Axin1-204	<a href="#">ENSMUST00000168282.2</a>	465	<a href="#">155aa</a>	Protein coding	-	<a href="#">F6SKQ8</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Axin1-205	<a href="#">ENSMUST00000169268.1</a>	291	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Axin1-201* transcript,The transcription is shown below

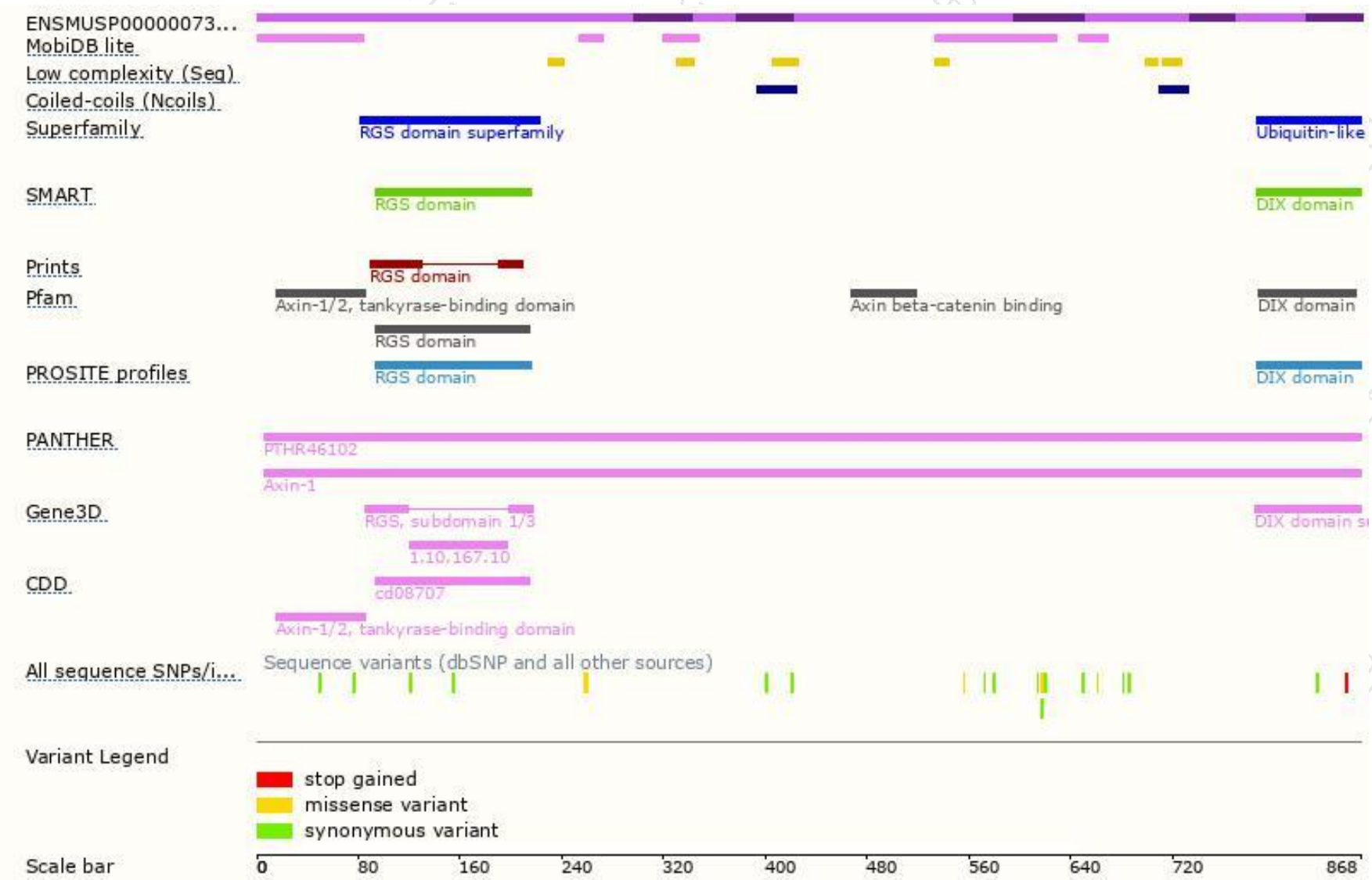


# Genomic location distribution

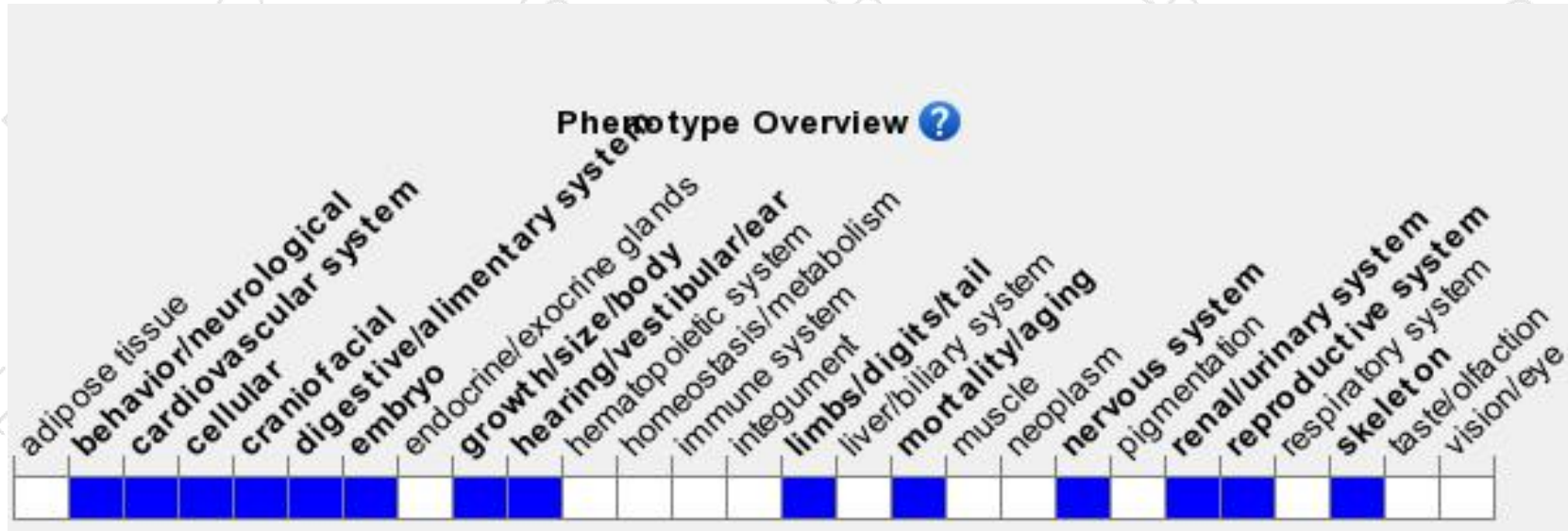




# Protein domain



# 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, Mutant homozygotes die at embryonic day 8-10, exhibiting neuroectodermal defects and axial duplications. Heterozygotes exhibit skeletal, cardiac, and neurological defects including short, bent tails, and deafness with circling behavior.

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

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