

# ***Ankrd11* Cas9-KO Strategy**

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**Reviewer: Xueting Zhang**

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# Project Overview

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**Project Name**

*Ankrd11*

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**Project type**

**Cas9-KO**

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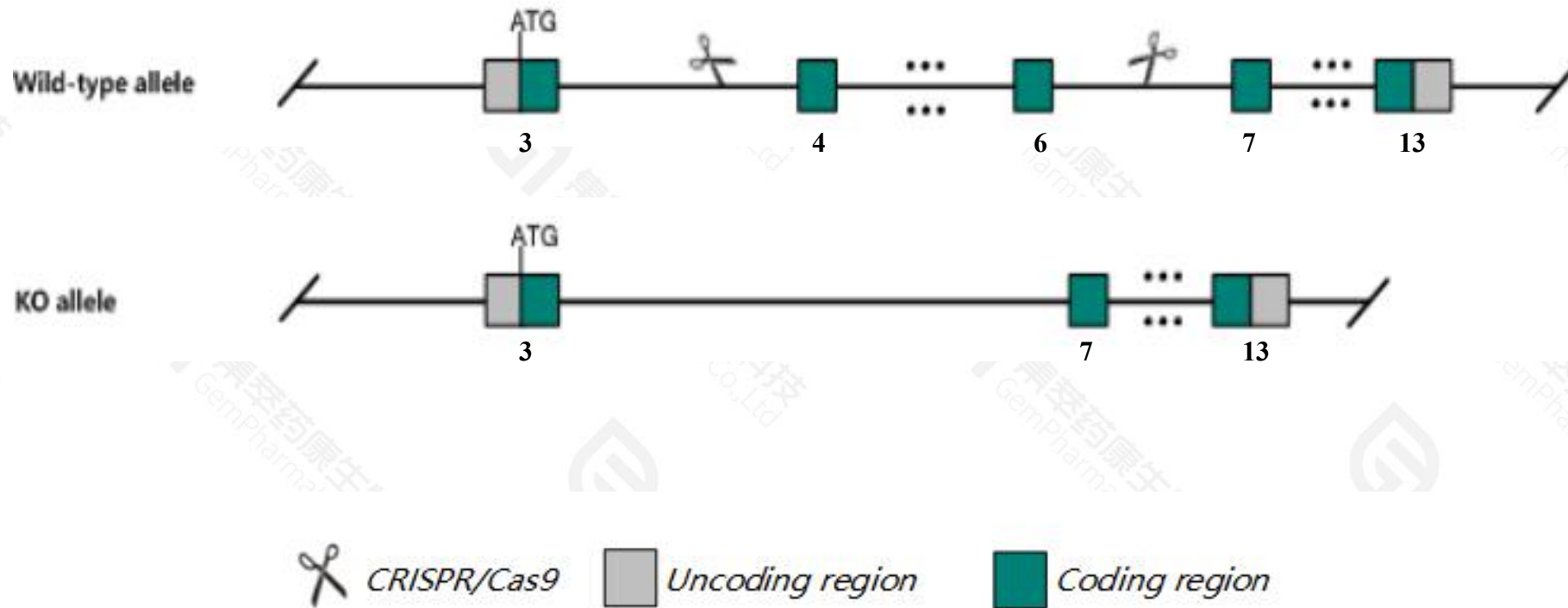
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ankrd11* gene. The schematic diagram is as follows:



- The *Ankrd11* gene has 7 transcripts. According to the structure of *Ankrd11* gene, exon4-exon6 of *Ankrd11*-202(ENSMUST00000098334.13) transcript is recommended as the knockout region. The region contains 514bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ankrd11* 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, mice homozygous for a spontaneous allele die by E9.5, are small and fail to turn. Mice heterozygous for a spontaneous allele exhibit craniofacial abnormalities, decreased weight, osteoporosis and osteopenia.
- The *Ankrd11*-207 transcript was not affected and the effect is unknown.
- This strategy can destroy *Gm45894* gene while knocking out the target gene.
- The *Ankrd11* gene is located on the Chr8. 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.

## Ankrd11 ankyrin repeat domain 11 [Mus musculus (house mouse)]

Gene ID: 77087, updated on 17-Dec-2020

### Summary



**Official Symbol** Ankrd11 provided by [MGI](#)

**Official Full Name** ankyrin repeat domain 11 provided by [MGI](#)

**Primary source** [MGI:MGI:1924337](#)

**See related** [Ensembl:ENSMUSG00000035569](#)

**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** 2410104C19Rik, 3010027A04Rik, 6330578C09Rik, 9530048I21Rik, AA930108, Gm176, Yo, Yod

**Expression** Ubiquitous expression in thymus adult (RPKM 25.9), ovary adult (RPKM 21.9) and 28 other tissues [See more](#)

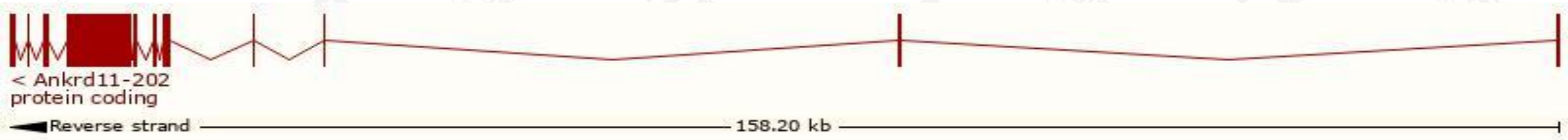
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

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

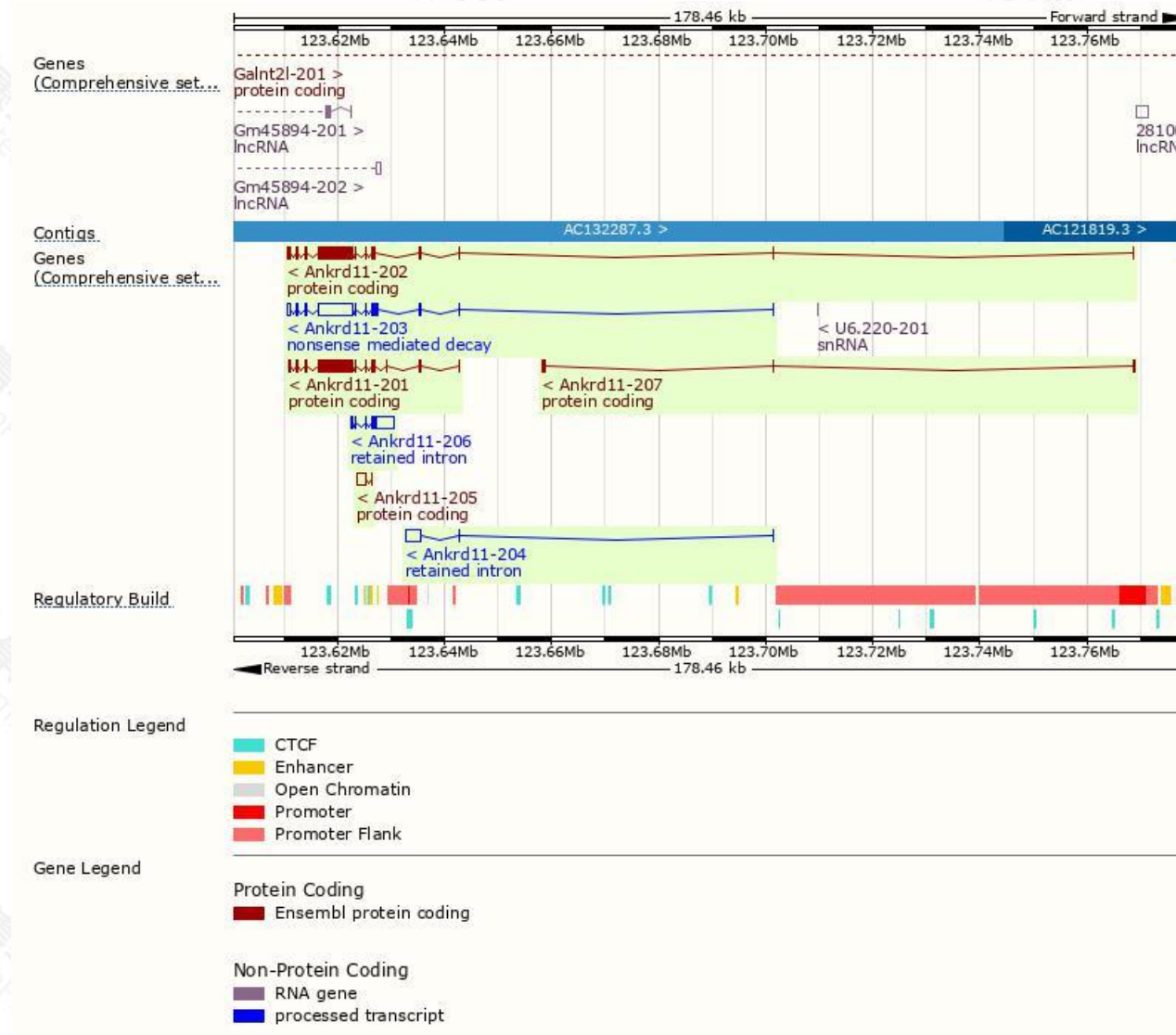
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ankrd11-202	<a href="#">ENSMUST00000098334.13</a>	8455	<a href="#">2643aa</a>	Protein coding	<a href="#">CCDS40507</a>		TSL:5 , GENCODE basic , APPRIS P2 ,
Ankrd11-201	<a href="#">ENSMUST00000098333.5</a>	7995	<a href="#">2664aa</a>	Protein coding	-		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Ankrd11-205	<a href="#">ENSMUST00000212050.2</a>	1874	<a href="#">134aa</a>	Protein coding	-		CDS 5' incomplete , TSL:1 ,
Ankrd11-207	<a href="#">ENSMUST00000212937.2</a>	943	<a href="#">121aa</a>	Protein coding	-		TSL:1 , GENCODE basic ,
Ankrd11-203	<a href="#">ENSMUST00000172906.8</a>	8481	<a href="#">97aa</a>	Nonsense mediated decay	-		TSL:1 ,
Ankrd11-206	<a href="#">ENSMUST00000212337.2</a>	4257	No protein	Retained intron	-		TSL:1 ,
Ankrd11-204	<a href="#">ENSMUST00000174833.2</a>	2934	No protein	Retained intron	-		TSL:1 ,

The strategy is based on the design of *Ankrd11-202* transcript,the transcription is shown below:



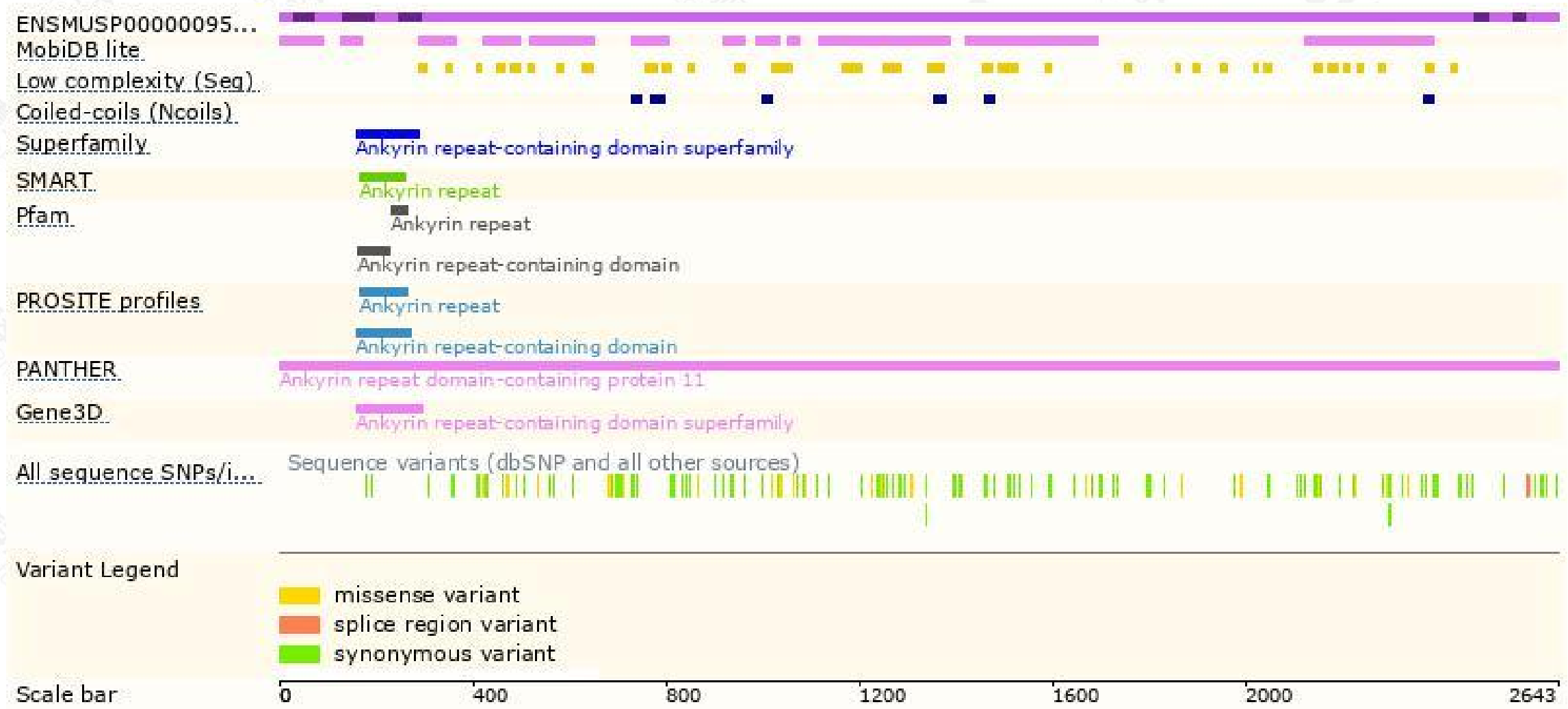


# Genomic location distribution

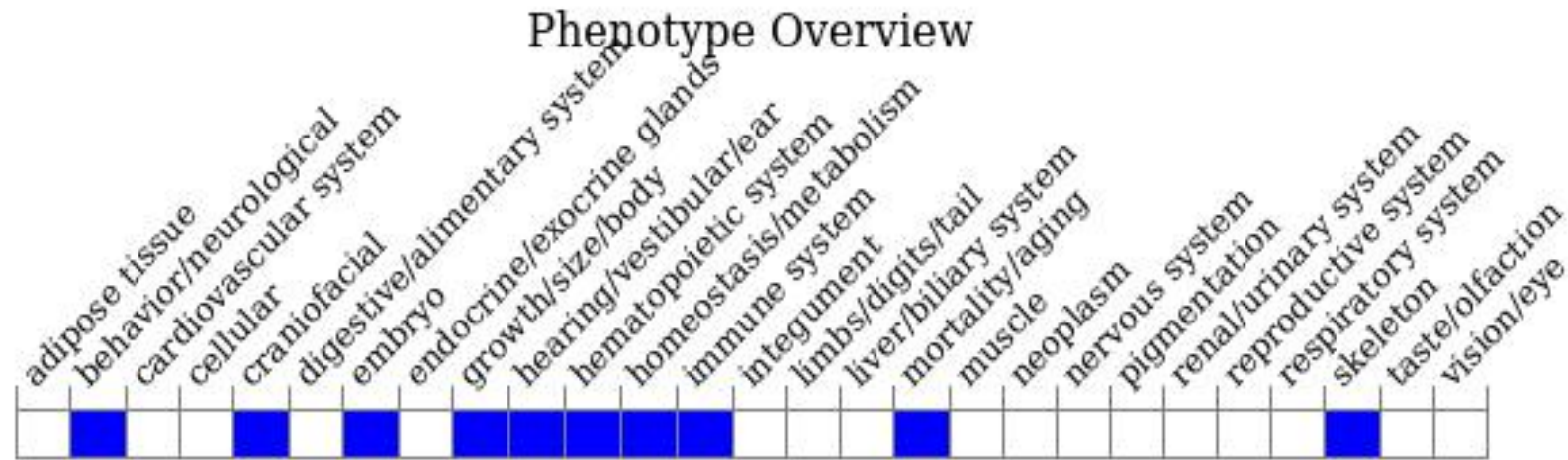




# Protein domain



# 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 homozygous for a spontaneous allele die by E9.5, are small and fail to turn.

Mice heterozygous for a spontaneous allele exhibit craniofacial abnormalities, decreased weight, osteoporosis and osteopenia.

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