

# ***Bmp4* Cas9-KO Strategy**

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# Project Overview

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**Project Name**

***Bmp4***

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**Project type**

**Cas9-KO**

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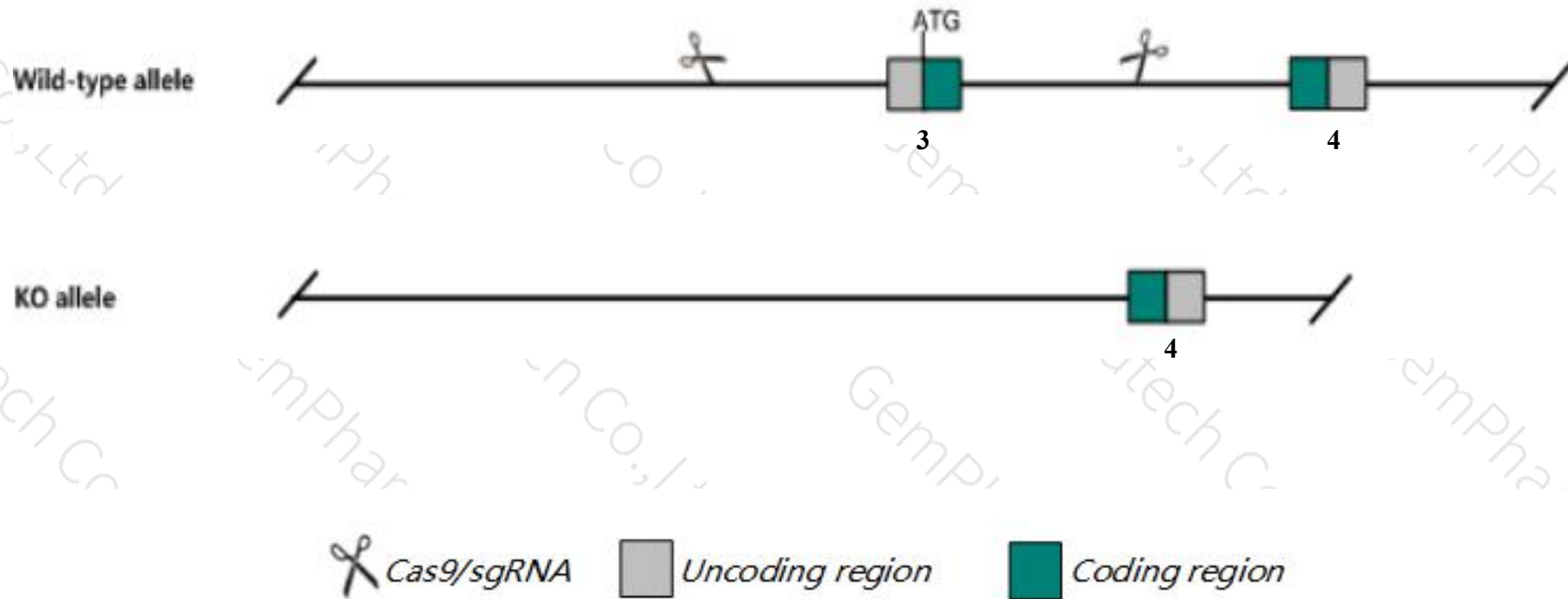
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bmp4* gene. The schematic diagram is as follows:



- The *Bmp4* gene has 4 transcripts. According to the structure of *Bmp4* gene, exon3 of *Bmp4*-201(ENSMUST00000074077.11) 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 *Bmp4* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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, targeted mutants have wide ranging effects, including embryonic lethality, aberrant mesoderm differentiation, developmental retardation and disorganized posterior structures; heterozygous null mutants display anomalies of the kidney and urinary tract; other targeted mutants display failure of lens induction and lack primordial germ cells.
- The floxed region is near to the N-terminal of *Gm15222* gene, this strategy may influence the regulatory function of the N-terminal of *Gm15222* gene.
- The *Bmp4* gene is located on the Chr14. 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)

## Bmp4 bone morphogenetic protein 4 [Mus musculus (house mouse)]

Gene ID: 12159, updated on 22-Mar-2020

### Summary

**Official Symbol** Bmp4 provided by [MGI](#)

**Official Full Name** bone morphogenetic protein 4 provided by [MGI](#)

**Primary source** [MGI:MGI:88180](#)

**See related** [Ensembl:ENSMUSG00000021835](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** Bmp-4, Bmp2b, Bmp2b-1, Bmp2b1

**Summary** This gene encodes a secreted ligand of the TGF-beta (transforming growth factor-beta) superfamily of proteins. Ligands of this family bind various TGF-beta receptors leading to recruitment and activation of SMAD family transcription factors that regulate gene expression. The encoded preproprotein is proteolytically processed to generate each subunit of the disulfide-linked homodimer. This protein regulates heart development and adipogenesis. Homozygous knockout mice die in utero, while a conditional knockout mouse exhibits defects in heart development. Transgenic mice overexpressing this gene in a neuron-specific manner exhibit a phenotype resembling the rare hereditary connective tissue disease, fibrodysplasia ossificans progressiva. [provided by RefSeq, Jul 2016]

**Expression** Broad expression in bladder adult (RPKM 26.3), lung adult (RPKM 20.8) and 18 other tissues [See more](#)

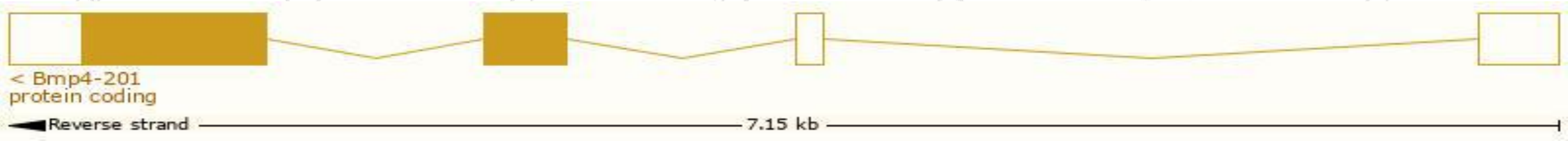
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

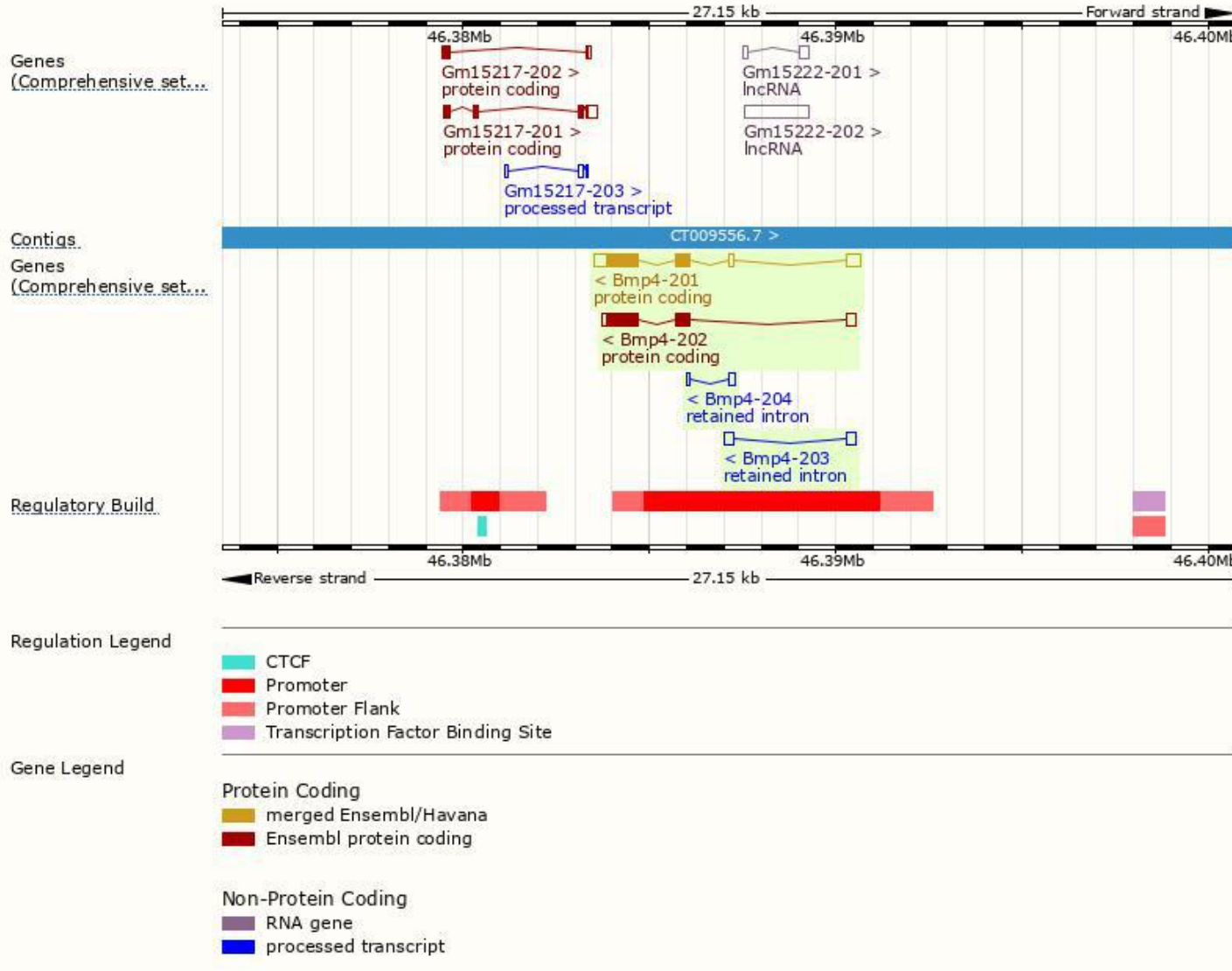
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bmp4-201	<a href="#">ENSMUST0000074077.11</a>	2064	<a href="#">408aa</a>	Protein coding	<a href="#">CCDS36897</a>	<a href="#">P21275 Q3ULR1</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Bmp4-202	<a href="#">ENSMUST00000100676.2</a>	1633	<a href="#">408aa</a>	Protein coding	<a href="#">CCDS36897</a>	<a href="#">P21275 Q3ULR1</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Bmp4-203	<a href="#">ENSMUST00000135408.1</a>	517	No protein	Retained intron	-	-	TSL:2
Bmp4-204	<a href="#">ENSMUST00000226759.1</a>	258	No protein	Retained intron	-	-	

The strategy is based on the design of *Bmp4-201* transcript,the transcription is shown below:

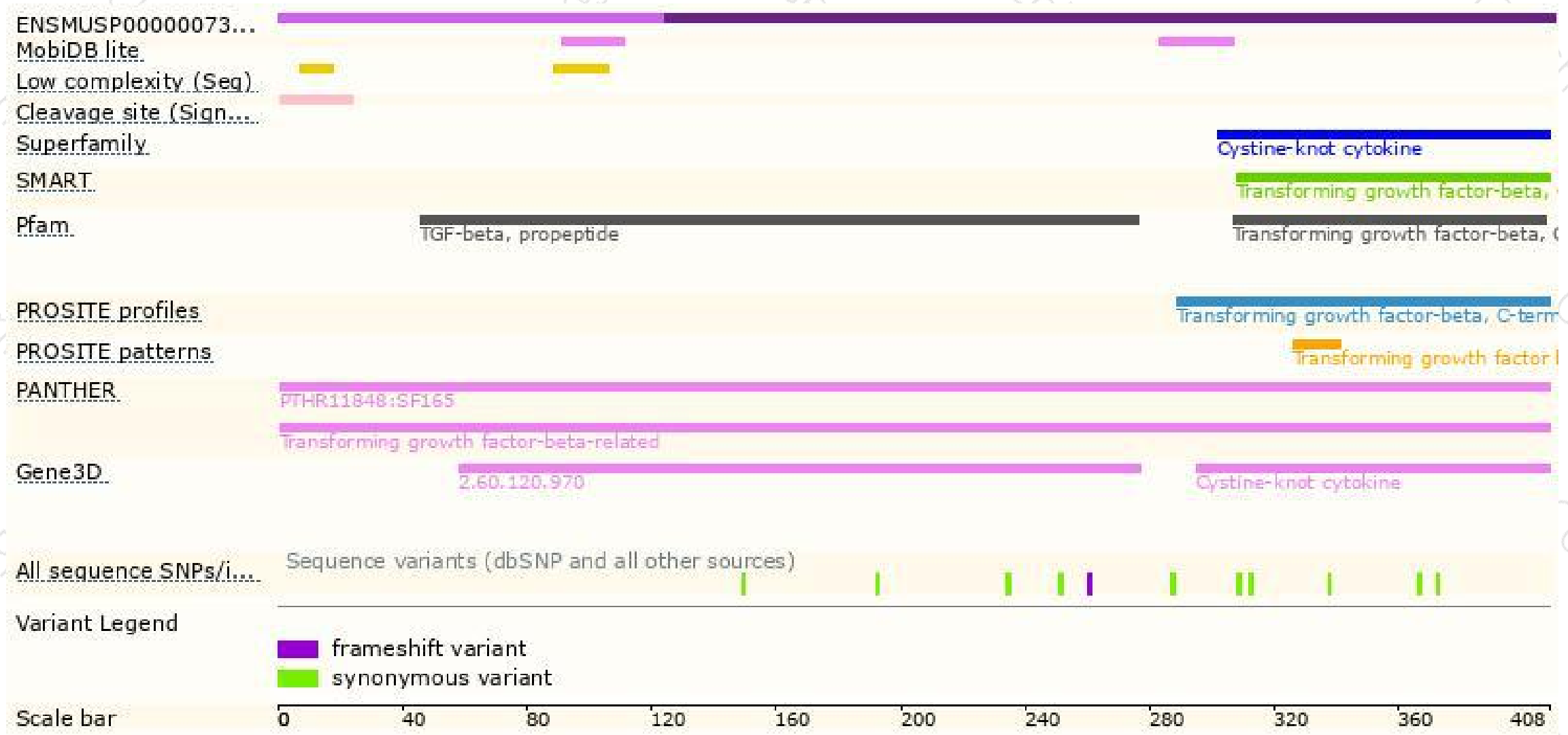


# Genomic location distribution

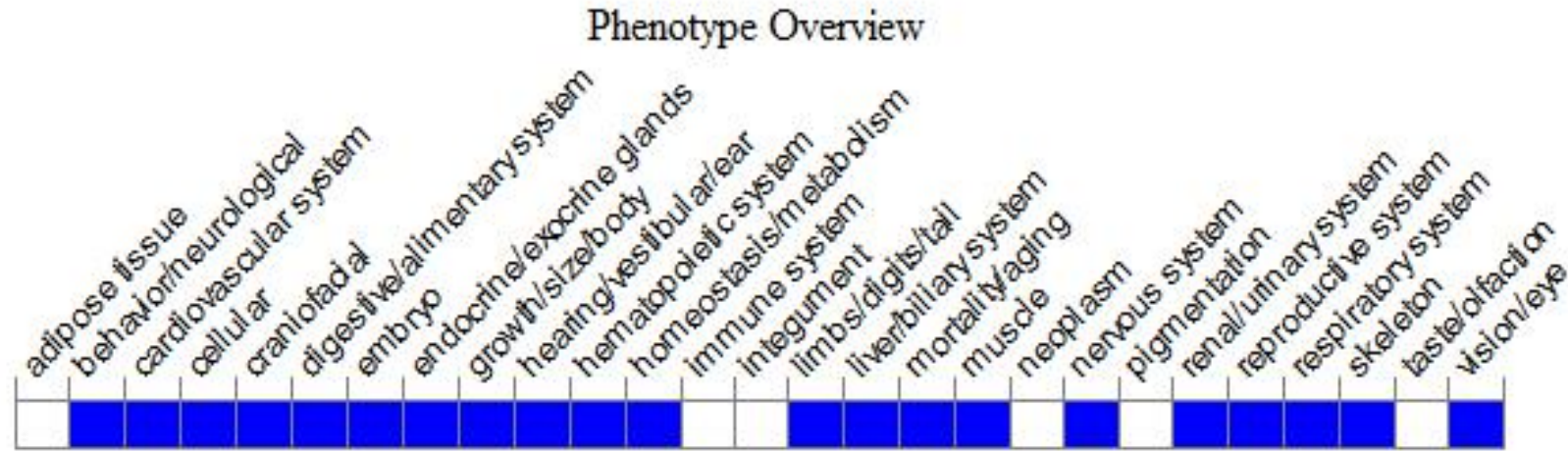




# Protein domain



# 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, targeted mutants have wide ranging effects, including embryonic lethality, aberrant mesoderm differentiation, developmental retardation and disorganized posterior structures; heterozygous null mutants display anomalies of the kidney and urinary tract; other targeted mutants display failure of lens induction and lack primordial germ cells.

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

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