

# *Rps6ka6* Cas9-KO Strategy

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**Reviewer:** Huimin Su

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# Project Overview

**Project Name**

***Rps6ka6***

**Project type**

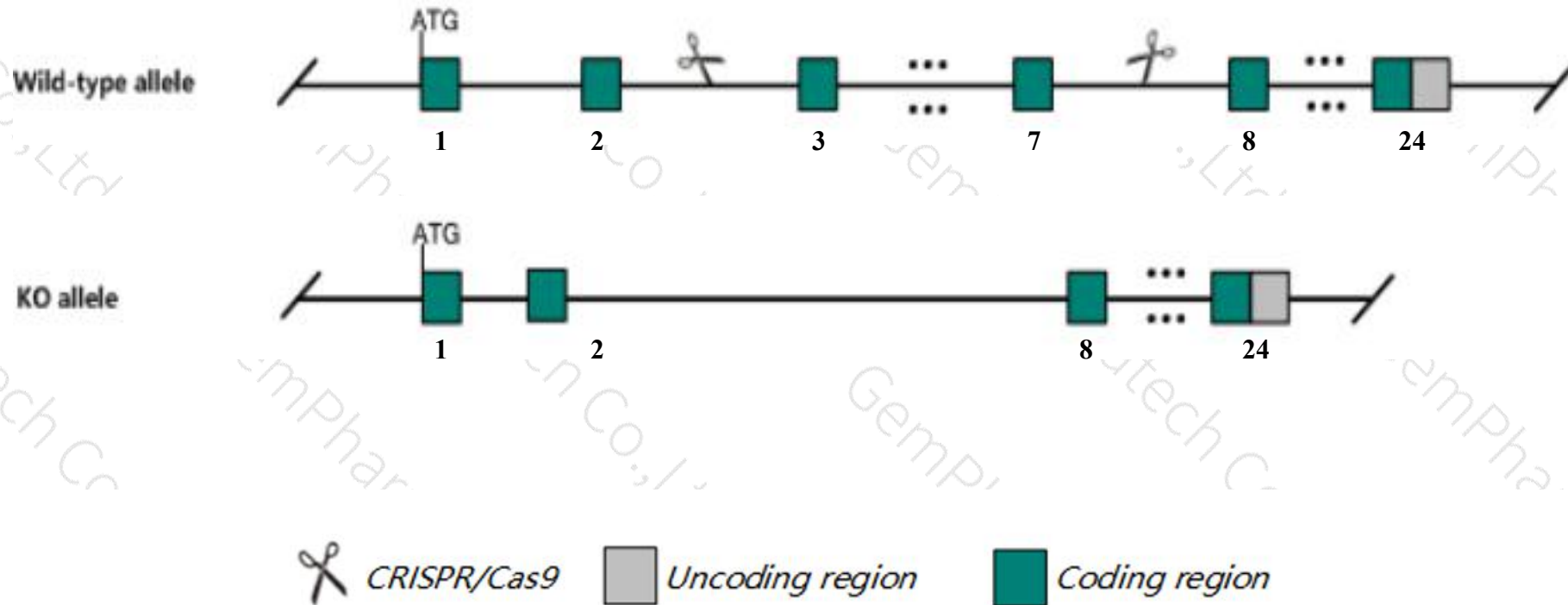
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rps6ka6* gene. The schematic diagram is as follows:



- The *Rps6ka6* gene has 12 transcripts. According to the structure of *Rps6ka6* gene, exon3-exon7 of *Rps6ka6-202* (ENSMUST00000082034.12) transcript is recommended as the knockout region. The region contains 403bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rps6ka6* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, male chimeras hemizygous for a gene trapped allele exhibit a possible gastrulation defect, primitive streak and node defects, failure of chorioallantoic fusion, impaired embryo turning, posterior truncation, abnormal heart development, and microcephaly.
- The *Rps6ka6* gene is located on the ChrX. 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)

## Rps6ka6 ribosomal protein S6 kinase polypeptide 6 [Mus musculus (house mouse)]

Gene ID: 67071, updated on 13-Mar-2020

### Summary



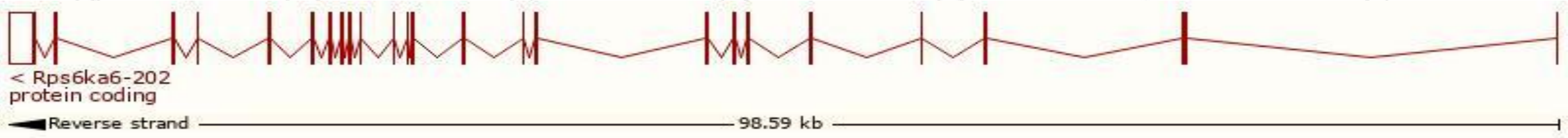
<b>Official Symbol</b>	Rps6ka6 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ribosomal protein S6 kinase polypeptide 6 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1914321</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000025665</a>
<b>Gene type</b>	protein 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>	2610524K04Rik, RSK4, S6K-alpha-6
<b>Expression</b>	Biased expression in placenta adult (RPKM 15.3), CNS E11.5 (RPKM 4.6) and 7 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

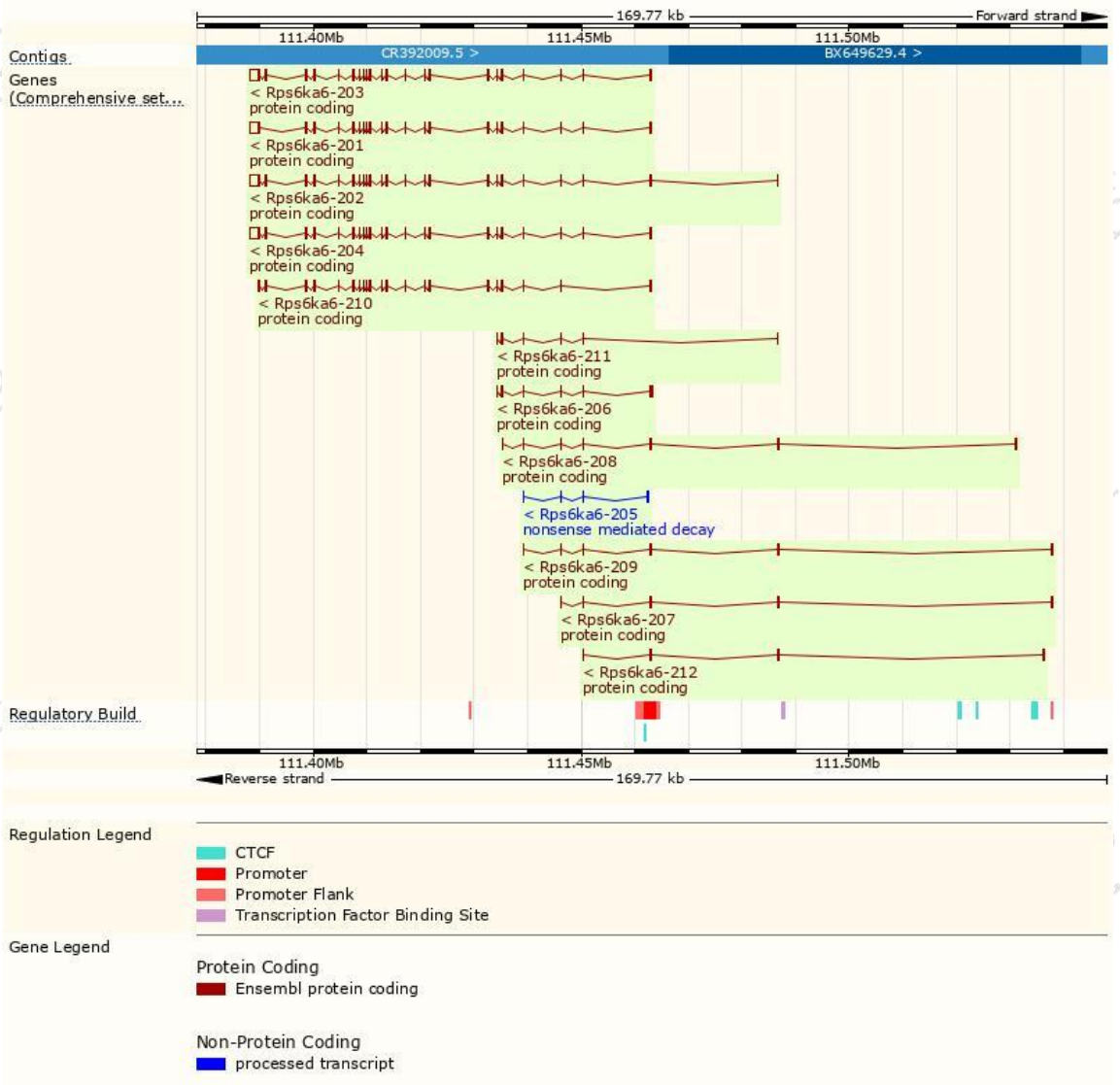
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rps6ka6-202	<a href="#">ENSMUST00000082034.12</a>	4170	<a href="#">860aa</a>	Protein coding	<a href="#">CCDS30356</a>	<a href="#">E9QK39</a>	TSL:5 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 P2
Rps6ka6-203	<a href="#">ENSMUST00000096348.9</a>	4151	<a href="#">781aa</a>	Protein coding	-	<a href="#">A2CEE7</a>	TSL:2 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 ALT2
Rps6ka6-204	<a href="#">ENSMUST00000113428.8</a>	4135	<a href="#">776aa</a>	Protein coding	-	<a href="#">E9PUP0</a>	TSL:5 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 ALT2
Rps6ka6-201	<a href="#">ENSMUST00000065976.11</a>	3867	<a href="#">737aa</a>	Protein coding	-	<a href="#">A2CEE6</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 ALT2
Rps6ka6-210	<a href="#">ENSMUST00000137712.8</a>	2410	<a href="#">760aa</a>	Protein coding	-	<a href="#">A2CEE5</a>	TSL:5 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 ALT2
Rps6ka6-206	<a href="#">ENSMUST00000123213.7</a>	798	<a href="#">163aa</a>	Protein coding	-	<a href="#">A2CEE8</a>	CDS 3' incomplete TSL:3
Rps6ka6-208	<a href="#">ENSMUST00000128819.7</a>	701	<a href="#">203aa</a>	Protein coding	-	<a href="#">B1B0X1</a>	CDS 3' incomplete TSL:5
Rps6ka6-209	<a href="#">ENSMUST00000132319.7</a>	644	<a href="#">166aa</a>	Protein coding	-	<a href="#">B1B0X2</a>	CDS 3' incomplete TSL:5
Rps6ka6-207	<a href="#">ENSMUST00000123951.7</a>	639	<a href="#">160aa</a>	Protein coding	-	<a href="#">B1B0X3</a>	CDS 3' incomplete TSL:2
Rps6ka6-212	<a href="#">ENSMUST00000156639.1</a>	507	<a href="#">130aa</a>	Protein coding	-	<a href="#">B1B0X4</a>	CDS 3' incomplete TSL:5
Rps6ka6-211	<a href="#">ENSMUST00000138645.7</a>	486	<a href="#">162aa</a>	Protein coding	-	<a href="#">B2GVN8</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
Rps6ka6-205	<a href="#">ENSMUST00000123102.1</a>	447	<a href="#">42aa</a>	Nonsense mediated decay	-	<a href="#">E9Q3H1</a>	TSL:3

The strategy is based on the design of *Rps6ka6-202* transcript,the transcription is shown below:



# Genomic location distribution

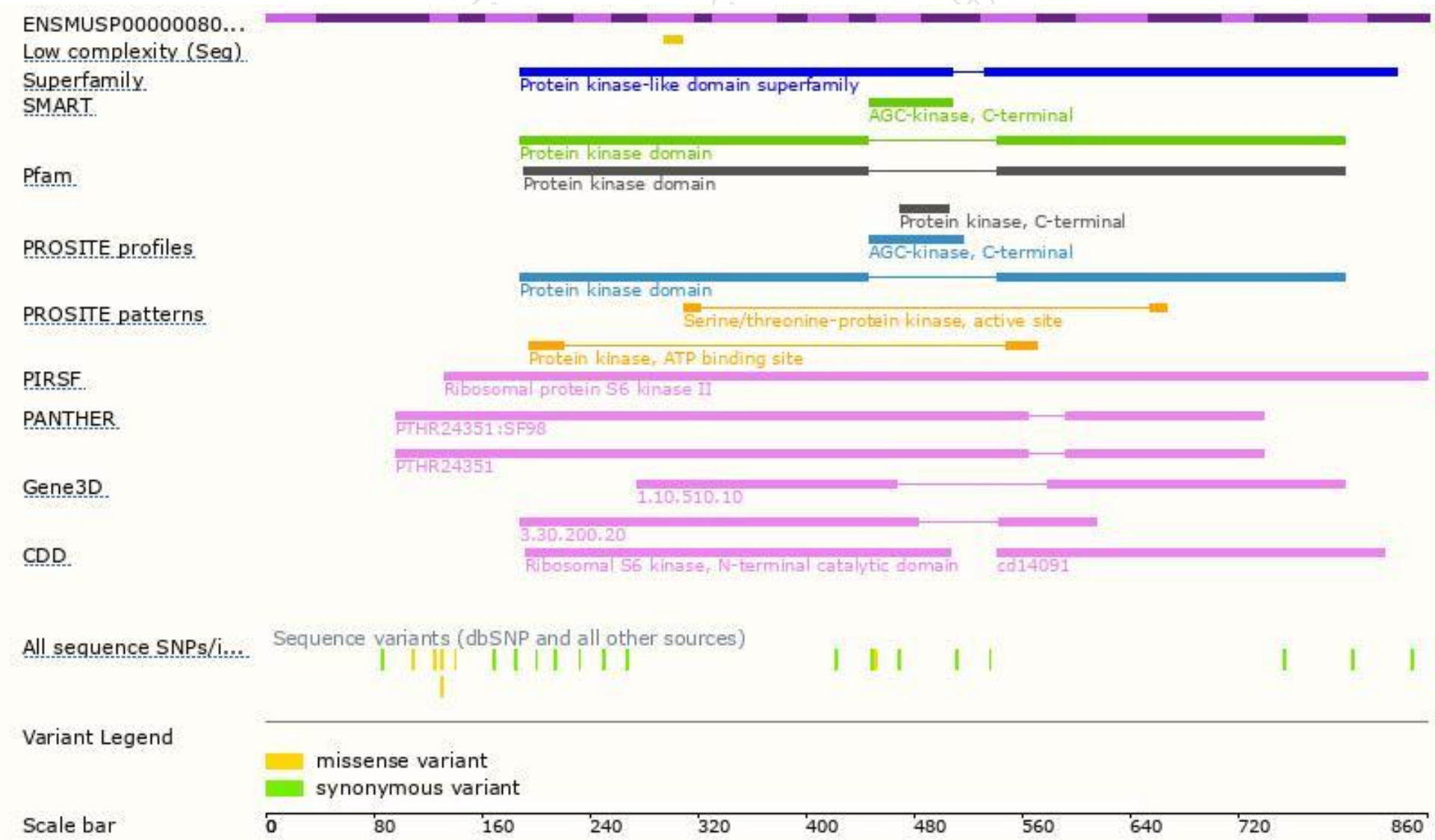




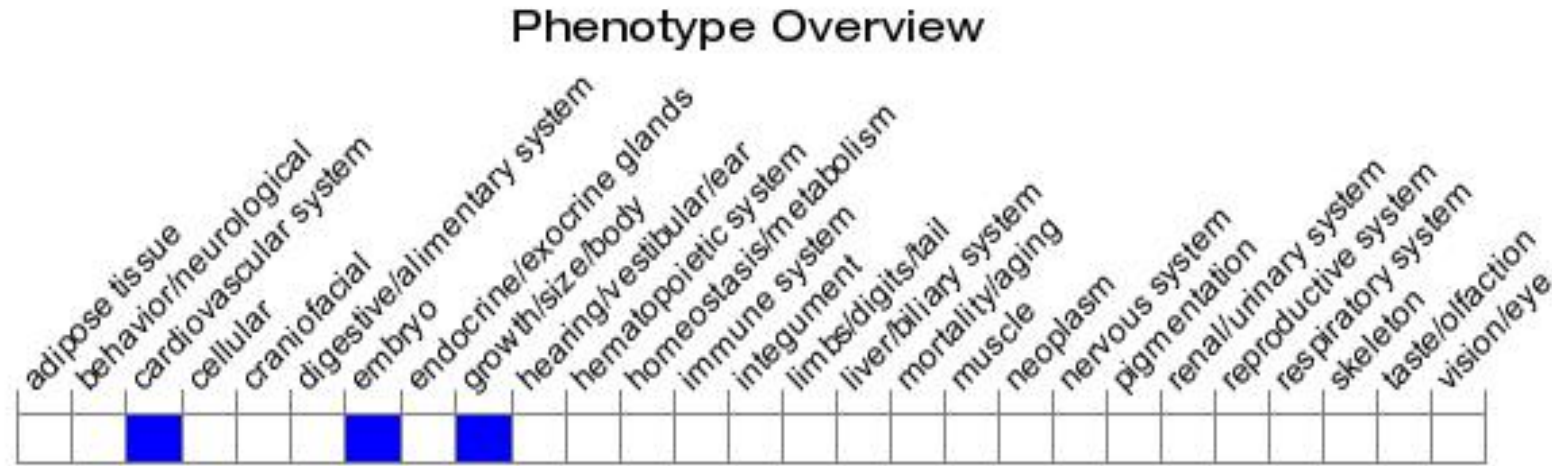
# Protein domain



集萃药康  
GemPharmatech



# 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, male chimeras hemizygous for a gene trapped allele exhibit a possible gastrulation defect, primitive streak and node defects, failure of chorioallantoic fusion, impaired embryo turning, posterior truncation, abnormal heart development, and microcephaly.

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

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