

# ***Zbtb16* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Zbtb16***

**Project type**

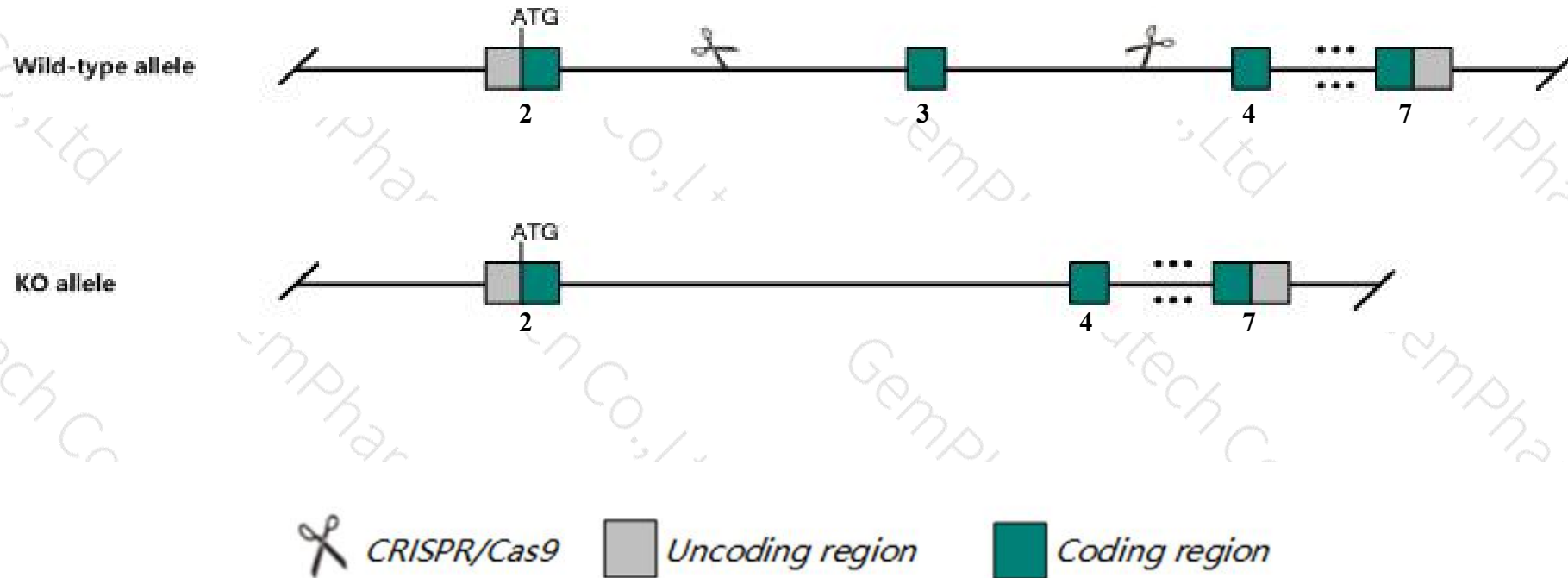
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb16* gene. The schematic diagram is as follows:



- The *Zbtb16* gene has 2 transcripts. According to the structure of *Zbtb16* gene, exon3 of *Zbtb16-201* (ENSMUST00000093852.4) transcript is recommended as the knockout region. The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zbtb16* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutants exhibit abnormal anterior-posterior patterning, with skeletal abnormalities of the limb, especially the hindlimb, and homeotic transformations of anterior skeletal elements into posterior structures. Males develop infertility due to loss of germline cells with age.
- The *Zbtb16* gene is located on the Chr9. 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)

## Zbtb16 zinc finger and BTB domain containing 16 [Mus musculus (house mouse)]

Gene ID: 235320, updated on 19-Mar-2019

### Summary



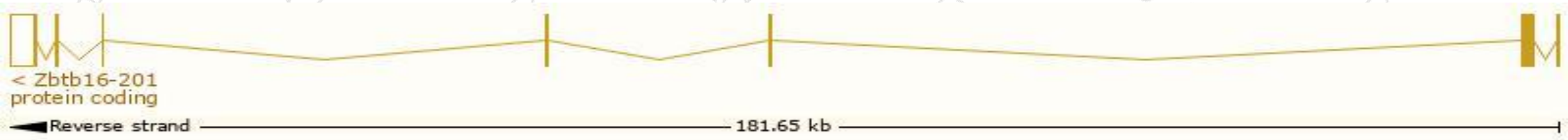
<b>Official Symbol</b>	Zbtb16 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	zinc finger and BTB domain containing 16 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:103222</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000066687</a>
<b>Gene type</b>	protein 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>	AI467657, PLZF, Zfp145, lu
<b>Expression</b>	Broad expression in lung adult (RPKM 8.1), subcutaneous fat pad adult (RPKM 7.3) and 24 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

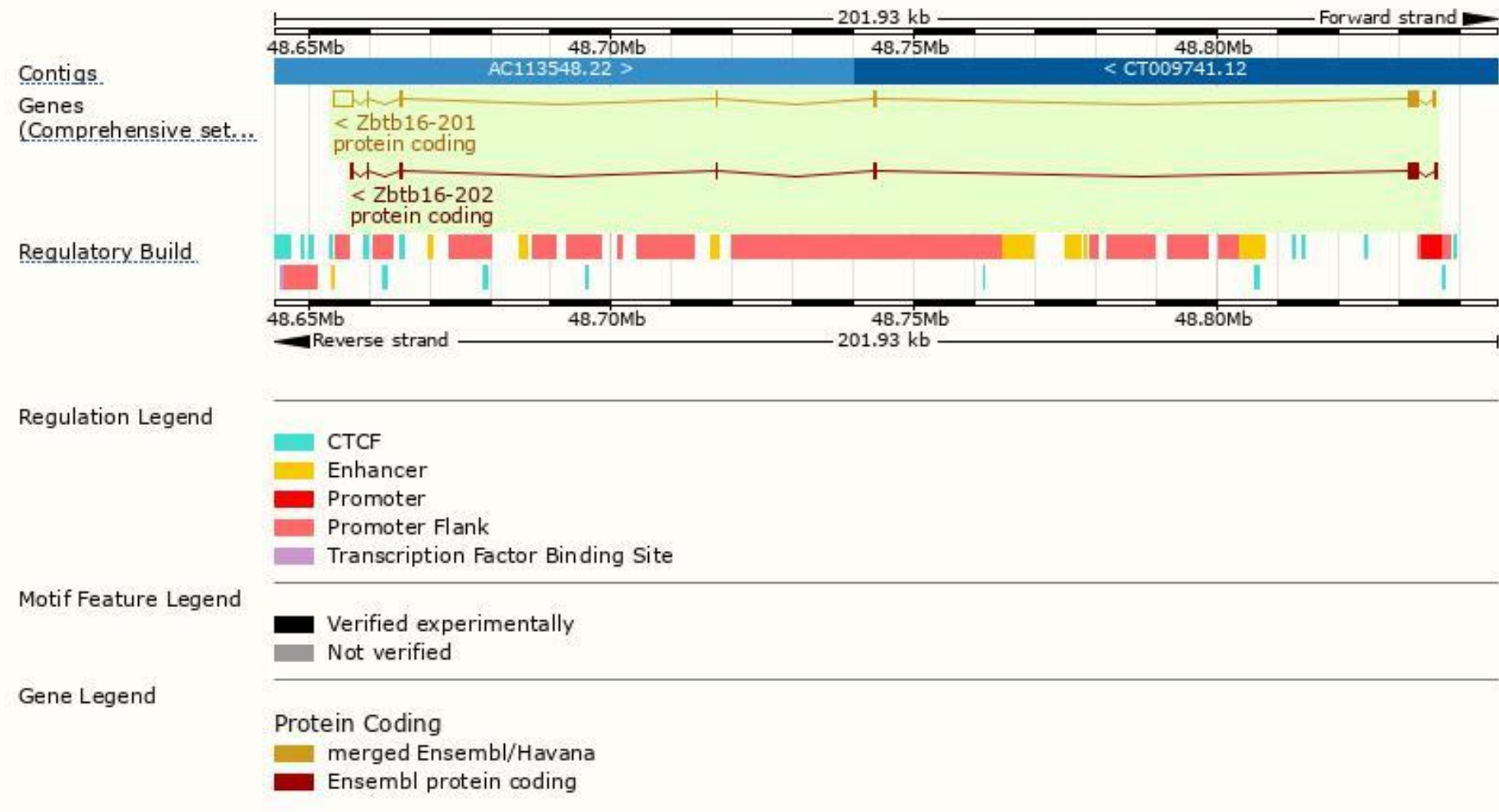
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb16-201	<a href="#">ENSMUST00000093852.4</a>	5114	<a href="#">673aa</a>	Protein coding	<a href="#">CCDS23158</a>	<a href="#">Q3UQ17</a>	TSL:1 GENCODE basic APPRIS P1
Zbtb16-202	<a href="#">ENSMUST00000216150.1</a>	2505	<a href="#">673aa</a>	Protein coding	<a href="#">CCDS23158</a>	<a href="#">Q3UQ17</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Zbtb16-201* transcript,The transcription is shown below

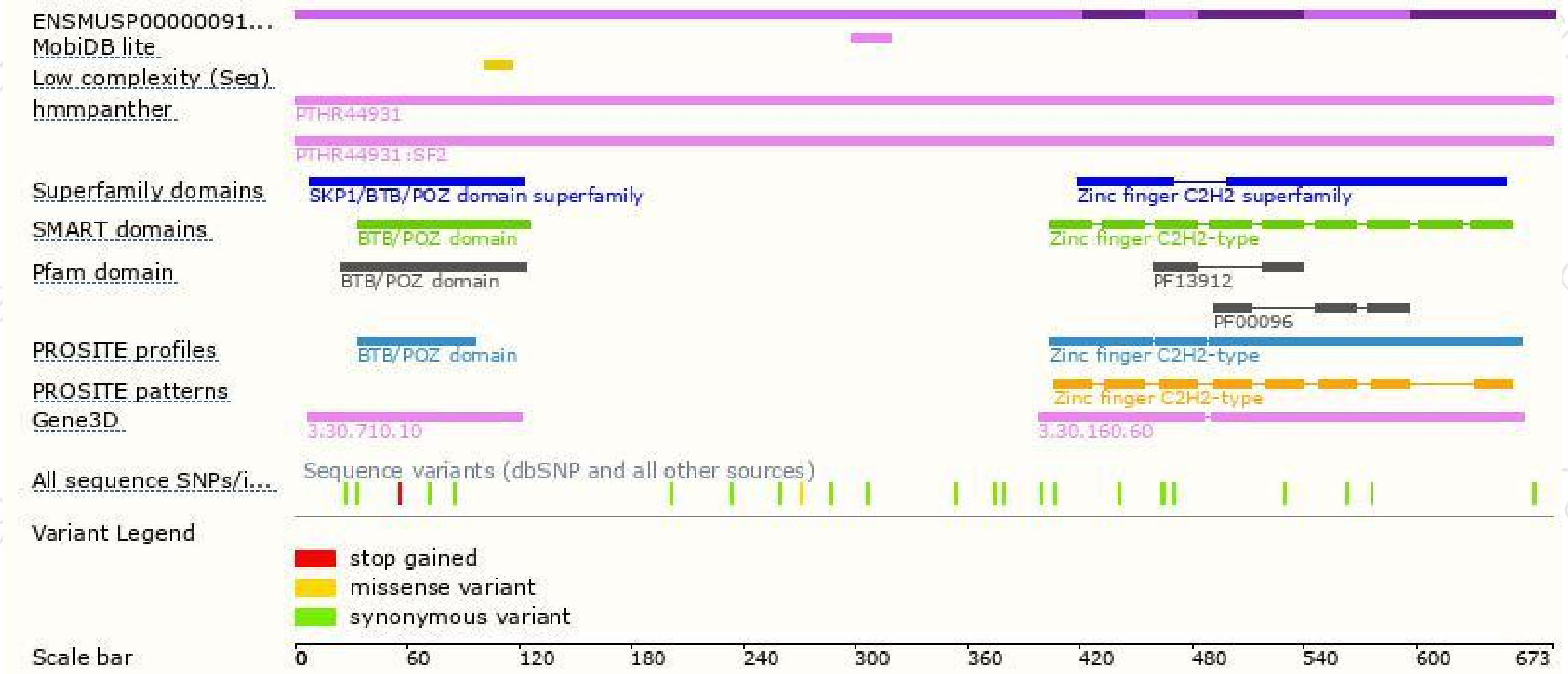


# Genomic location distribution

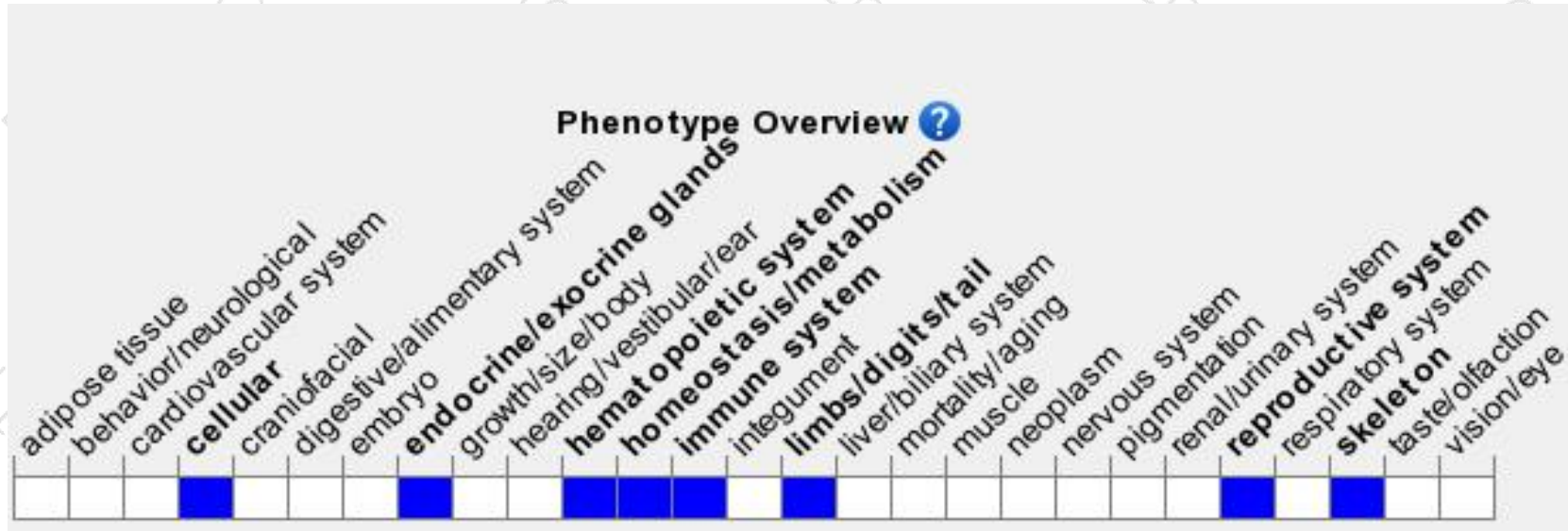




# Protein domain



# 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, Homozygous mutants exhibit abnormal anterior-posterior patterning, with skeletal abnormalities of the limb, especially the hindlimb, and homeotic transformations of anterior skeletal elements into posterior structures. Males develop infertility due to loss of germline cells with age.

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

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