

# *Chaf1b* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Chaf1b***

**Project type**

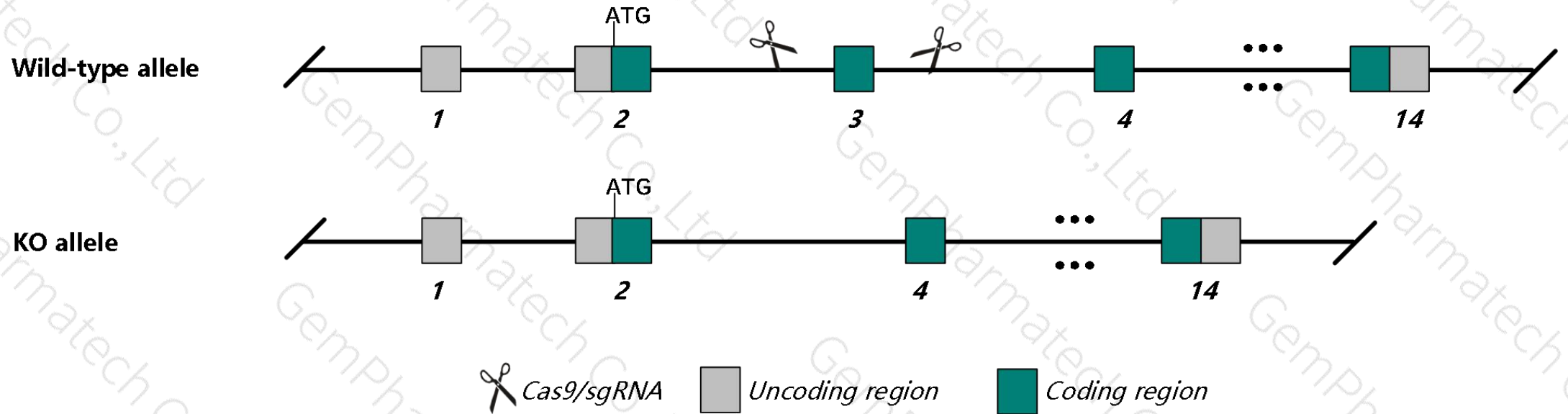
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chaf1b* gene. The schematic diagram is as follows:



- The *Chaf1b* gene has 7 transcripts. According to the structure of *Chaf1b* gene, exon3 of *Chaf1b-201* (ENSMUST00000023666.10) transcript is recommended as the knockout region. The region contains 133bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Chaf1b* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mice homozygous for a conditional allele activated in hematopoietic cells exhibit premature death, pancytopenia, reduced bone marrow and hematopoietic stem cells, and reduced hematopoietic reconstitution.
- The *Chaf1b* gene is located on the Chr16. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.



# Gene information (NCBI)

## Chaf1b chromatin assembly factor 1, subunit B (p60) [Mus musculus (house mouse)]

Gene ID: 110749, updated on 5-Mar-2019

### Summary



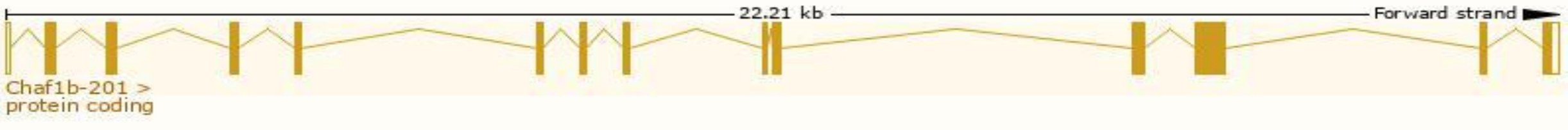
<b>Official Symbol</b>	Chaf1b provided by <a href="#">MGI</a>
<b>Official Full Name</b>	chromatin assembly factor 1, subunit B (p60) provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1314881</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022945</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<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>	2600017H24Rik, C76145, CAF-I p60, CAF-Ip60, CAF1, CAF1A, CAF1P60, MPHOSPH7
<b>Expression</b>	Broad expression in CNS E11.5 (RPKM 15.1), liver E14 (RPKM 14.2) and 20 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

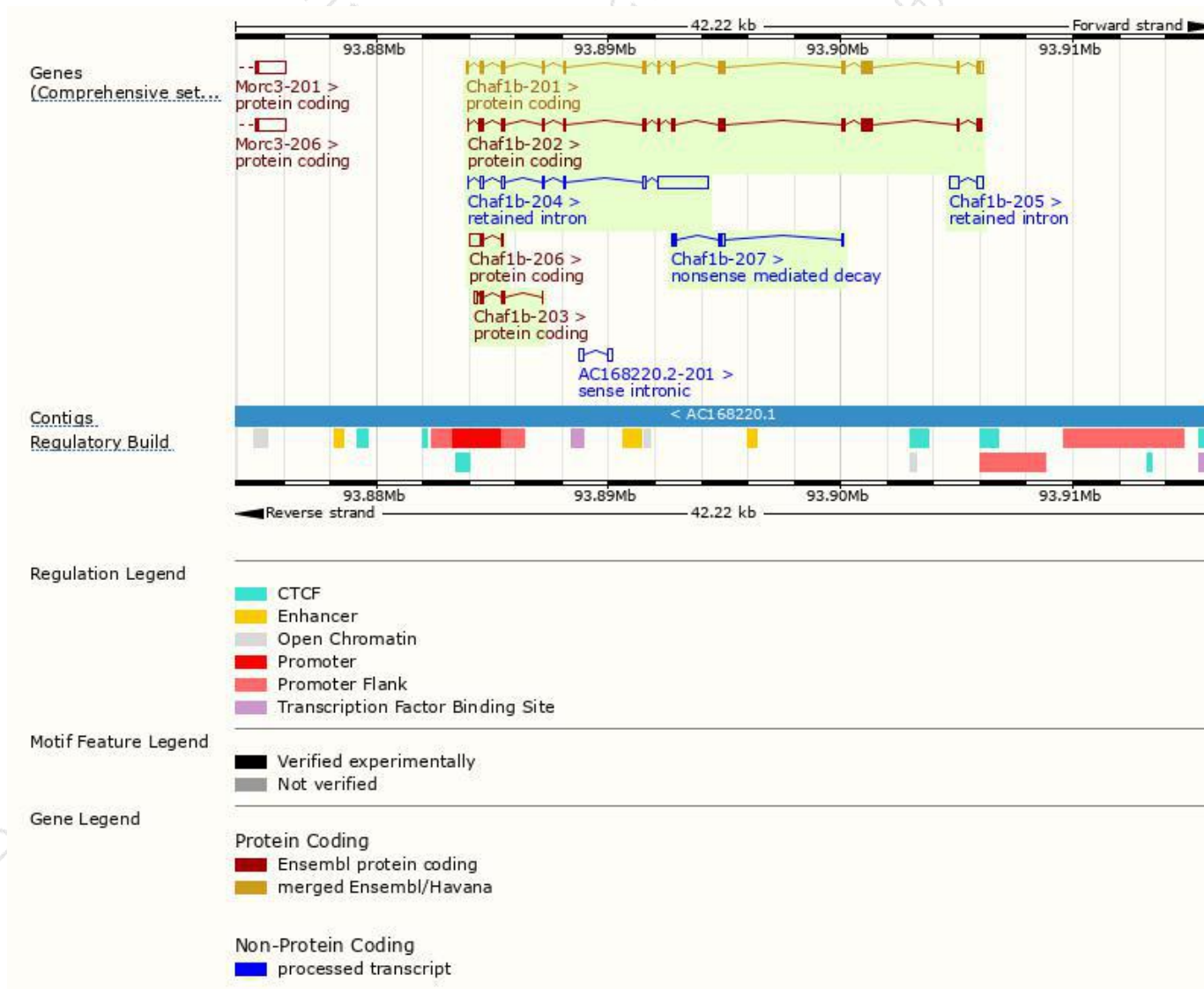
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chaf1b-201	<a href="#">ENSMUST00000023666.10</a>	1922	<a href="#">572aa</a>	Protein coding	<a href="#">CCDS28344</a>	<a href="#">Q9D0N7</a>	TSL:1 GENCODE basic APPRIS P1
Chaf1b-202	<a href="#">ENSMUST00000117099.7</a>	1894	<a href="#">572aa</a>	Protein coding	<a href="#">CCDS28344</a>	<a href="#">Q9D0N7</a>	TSL:5 GENCODE basic APPRIS P1
Chaf1b-206	<a href="#">ENSMUST00000142316.1</a>	719	<a href="#">79aa</a>	Protein coding	-	<a href="#">D3YTP6</a>	CDS 3' incomplete TSL:2
Chaf1b-203	<a href="#">ENSMUST00000120586.1</a>	484	<a href="#">96aa</a>	Protein coding	-	<a href="#">D3Z616</a>	CDS 3' incomplete TSL:5
Chaf1b-207	<a href="#">ENSMUST00000143006.1</a>	428	<a href="#">34aa</a>	Nonsense mediated decay	-	<a href="#">A0A338P679</a>	CDS 5' incomplete TSL:3
Chaf1b-204	<a href="#">ENSMUST00000124313.7</a>	2828	No protein	Retained intron	-	-	TSL:1
Chaf1b-205	<a href="#">ENSMUST00000128316.1</a>	611	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Chaf1b-201* transcript,The transcription is shown below

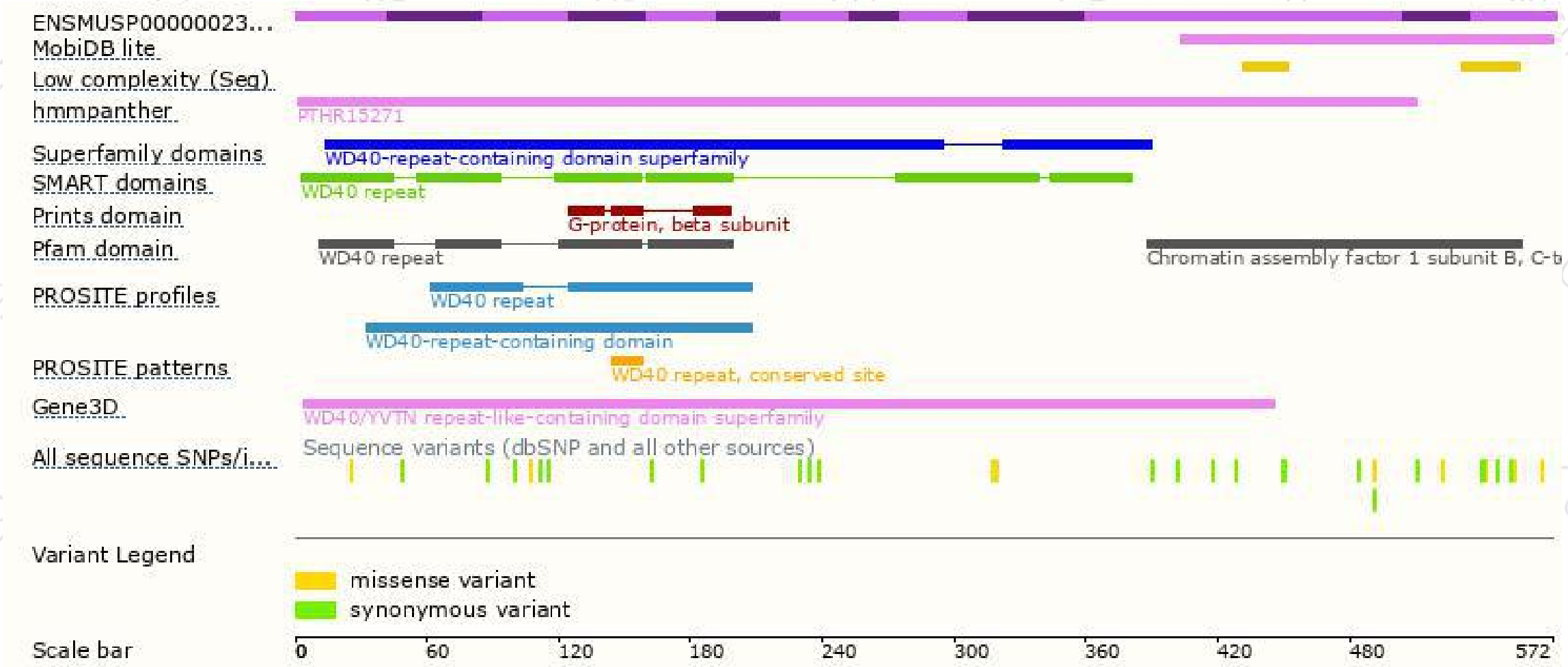


# Genomic location distribution

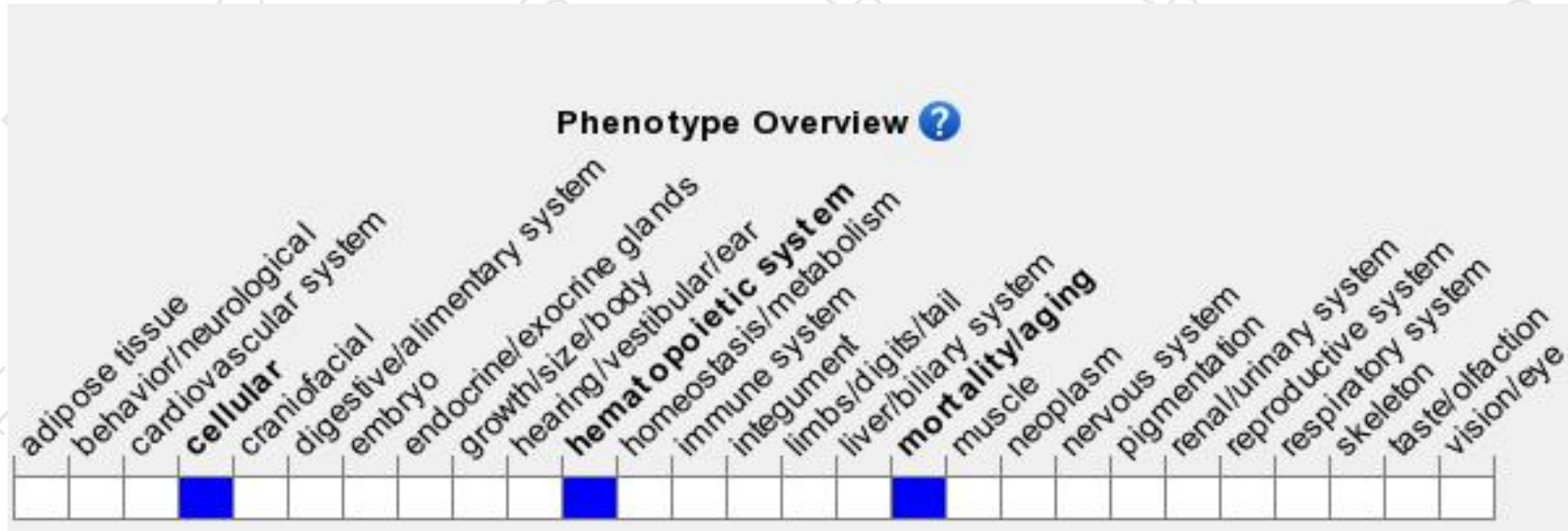




# Protein domain



# 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, Mice homozygous for a conditional allele activated in hematopoietic cells exhibit premature death, pancytopenia, reduced bone marrow and hematopoietic stem cells, and reduced hematopoietic reconstitution.

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

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