

# ***Mcm4*** Cas9-KO Strategy

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# Project Overview

**Project Name**

***Mcm4***

**Project type**

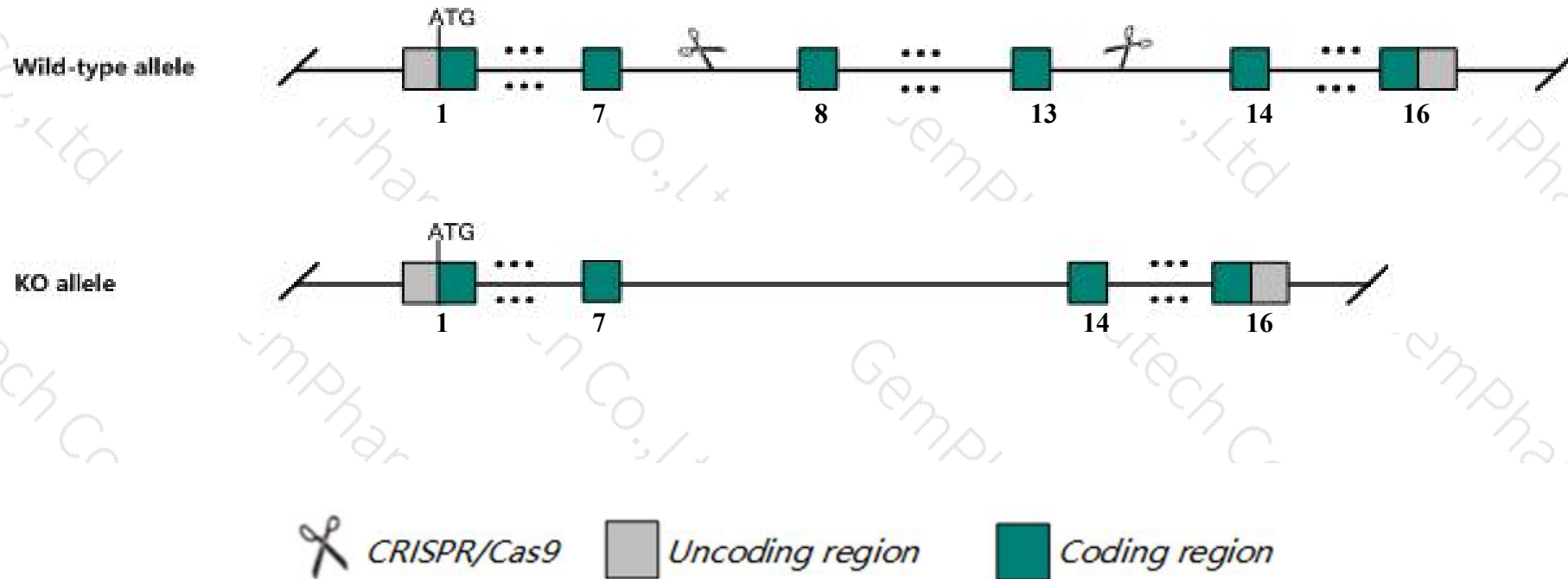
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcm4* gene. The schematic diagram is as follows:



- The *Mcm4* gene has 3 transcripts. According to the structure of *Mcm4* gene, exon8-exon13 of *Mcm4-201* (ENSMUST00000023353.3) transcript is recommended as the knockout region. The region contains 1304bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mcm4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Disruption of this allele cause chromosomal instability as assessed by micronucleus levels in erythrocytes. Mice homozygous for a spontaneous allele exhibit early onset T cell acute lymphoblastic leukemia.
- The N-terminal of *Mcm4* gene will remain 276aa, it may remain the partial function of *Mcm4* gene.
- The *Mcm4* 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 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)

## Mcm4 minichromosome maintenance complex component 4 [Mus musculus (house mouse)]

Gene ID: 17217, updated on 31-Jan-2019

### Summary



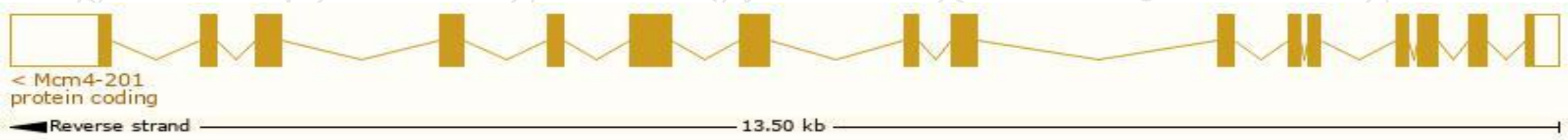
<b>Official Symbol</b>	Mcm4 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	minichromosome maintenance complex component 4 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:103199</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022673</a>
<b>Gene type</b>	protein 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>	19G, AI325074, AU045576, Cdc21, Mcmd4, mKIAA4003, mcdc21
<b>Expression</b>	Broad expression in liver E14 (RPKM 36.5), liver E14.5 (RPKM 34.4) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

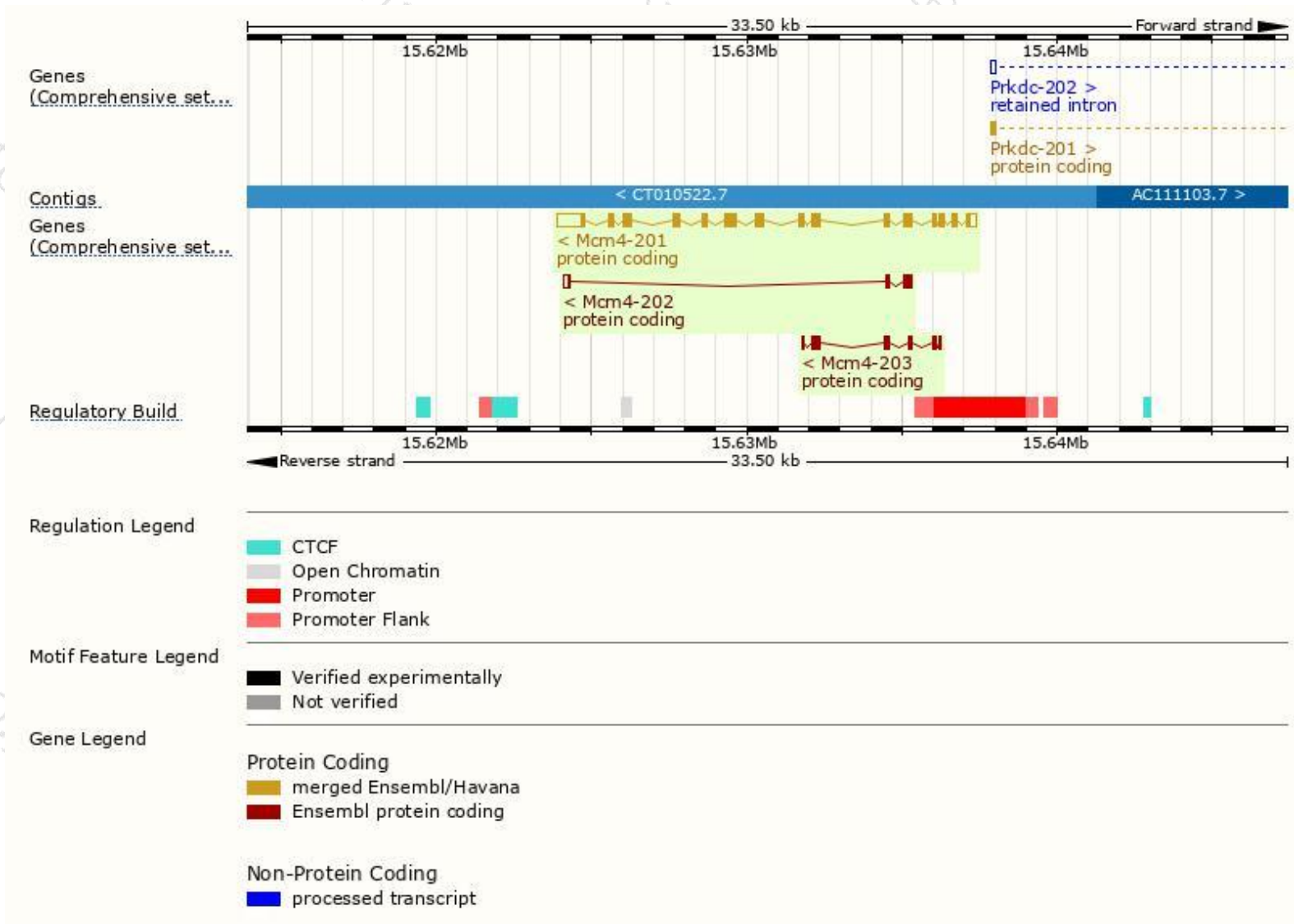
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mcm4-201	<a href="#">ENSMUST00000023353.3</a>	3589	<a href="#">862aa</a>	Protein coding	<a href="#">CCDS27977</a>	<a href="#">P49717 Q542F4</a>	TSL:1 GENCODE basic APPRIS P1
Mcm4-203	<a href="#">ENSMUST00000230437.1</a>	658	<a href="#">220aa</a>	Protein coding	-	<a href="#">A0A2R8VHP7</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Mcm4-202	<a href="#">ENSMUST00000229606.1</a>	423	<a href="#">86aa</a>	Protein coding	-	<a href="#">A0A2R8VKJ4</a>	CDS 5' incomplete

The strategy is based on the design of *Mcm4-201* transcript,The transcription is shown below

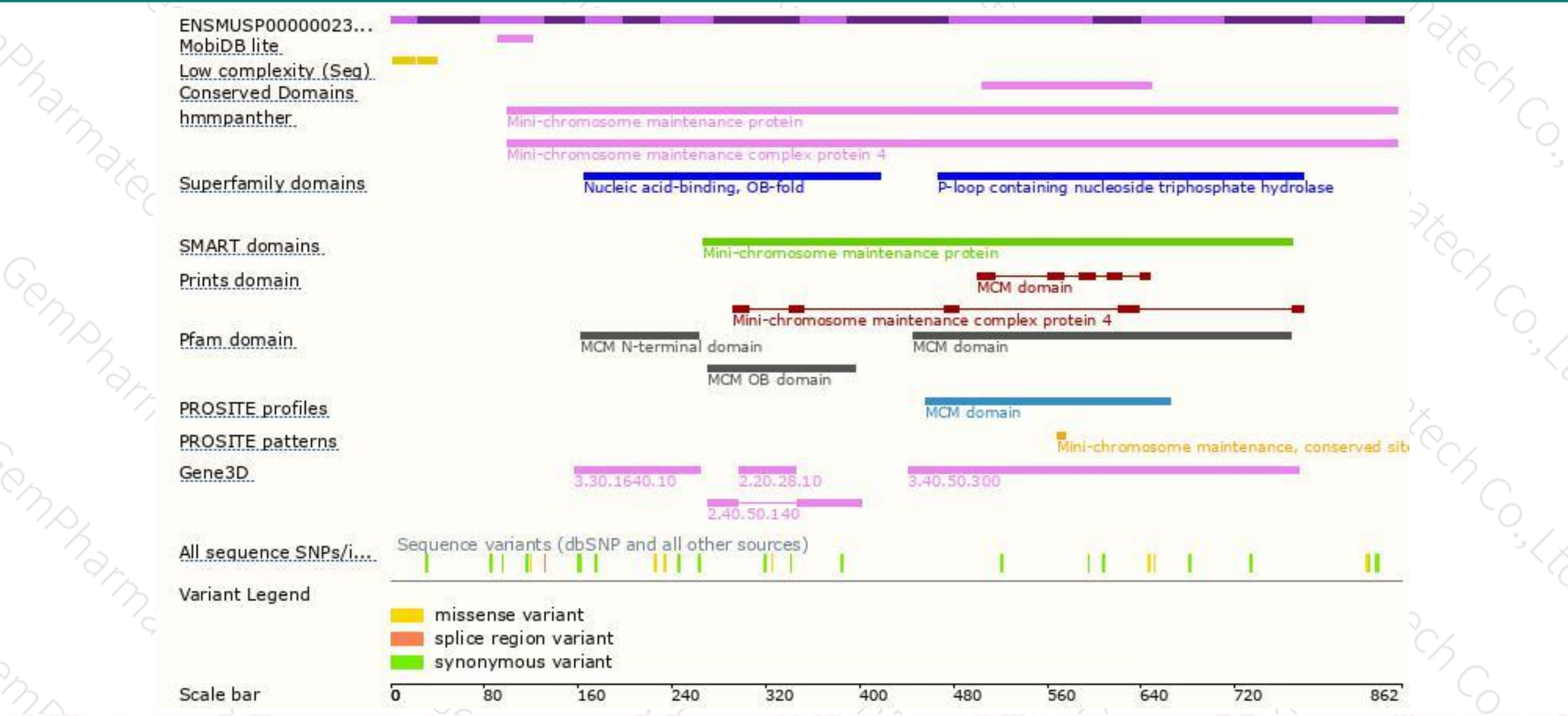


# Genomic location distribution

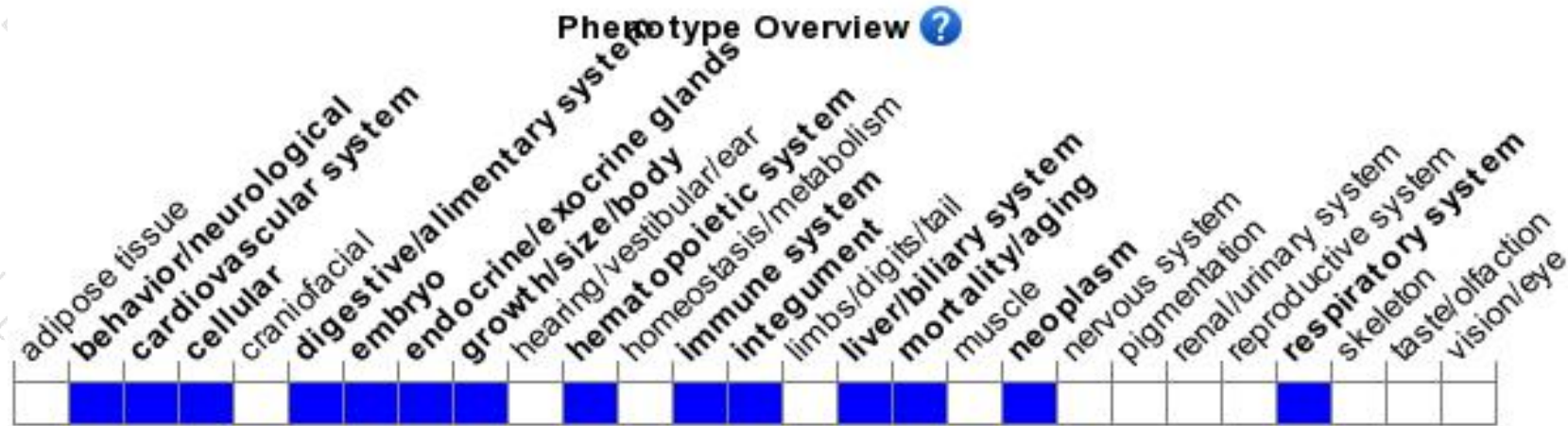




# Protein domain



# 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, Disruption of this allele cause chromosomal instability as assessed by micronucleus levels in erythrocytes. Mice homozygous for a spontaneous allele exhibit early onset T cell acute lymphoblastic leukemia.

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

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