

# *Arid3a* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

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**Project Name**

*Arid3a*

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**Project type**

**Cas9-CKO**

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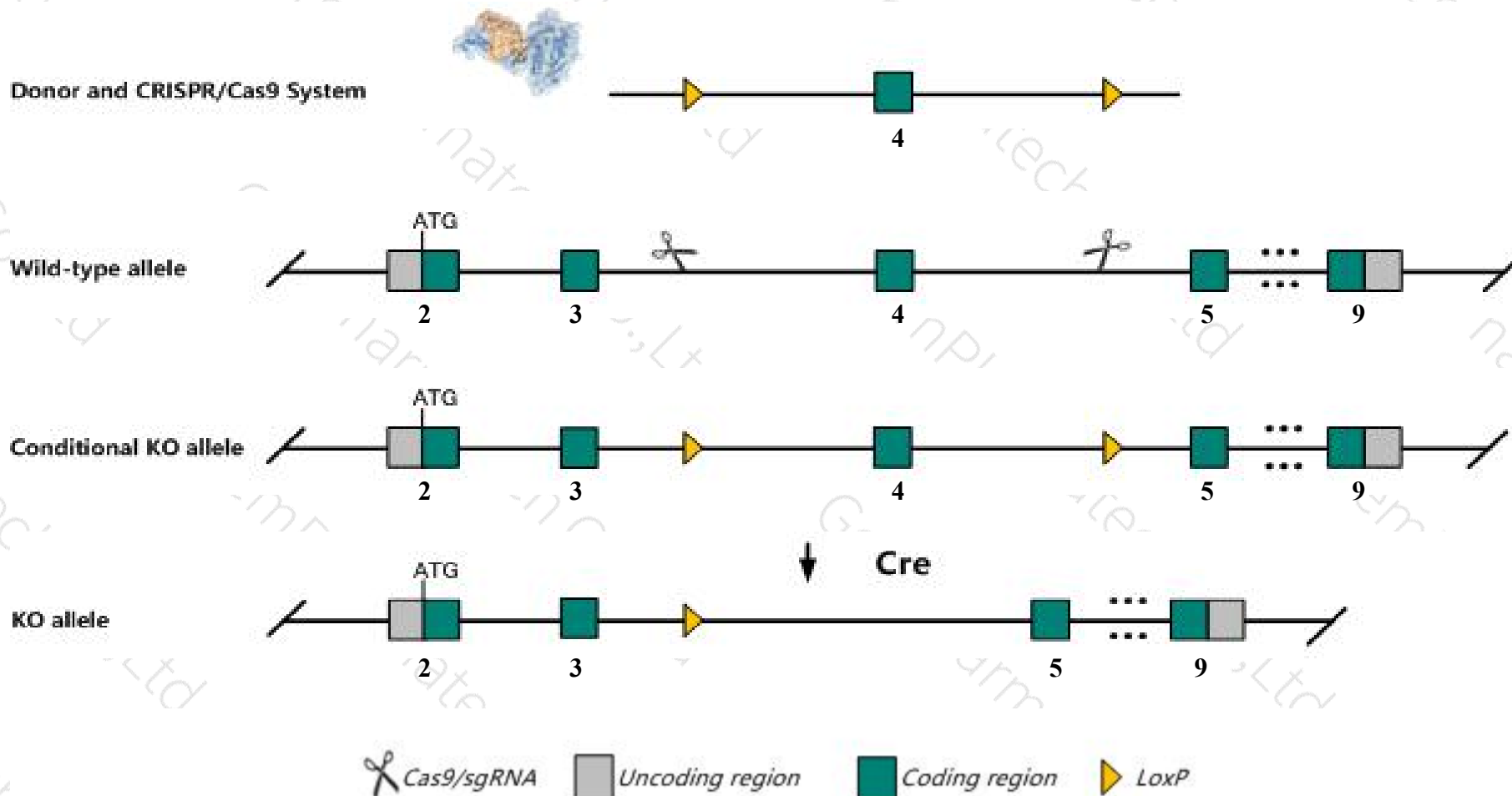
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arid3a* gene. The schematic diagram is as follows:



- The *Arid3a* gene has 5 transcripts. According to the structure of *Arid3a* gene, exon4 of *Arid3a-201* (ENSMUST00000019708.11) transcript is recommended as the knockout region. The region contains 73bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arid3a* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor 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.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit embryonic lethality between E11.5 and E13.5 due to impaired erythropoiesis.
- Transcript *Arid3a-204* may not be affected.
- The *Arid3a* gene is located on the Chr10. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



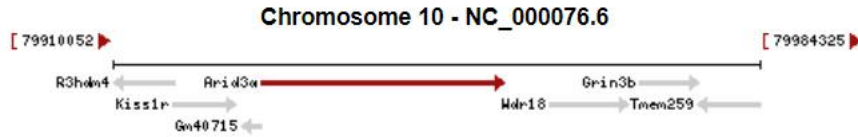
# Gene information (NCBI)

## Arid3a AT rich interactive domain 3A (BRIGHT-like) [ *Mus musculus* (house mouse) ]

Gene ID: 13496, updated on 10-Oct-2019

### Summary

Official Symbol	Arid3a provided by MGI
Official Full Name	AT rich interactive domain 3A (BRIGHT-like) provided by MGI
Primary source	MGI:MGI:1328360
See related	Ensembl:ENSMUSG00000019564
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Dri1; Dril1; Bright
Expression	Ubiquitous expression in placenta adult (RPKM 13.2), testis adult (RPKM 6.1) and 25 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>



# Transcript information (Ensembl)

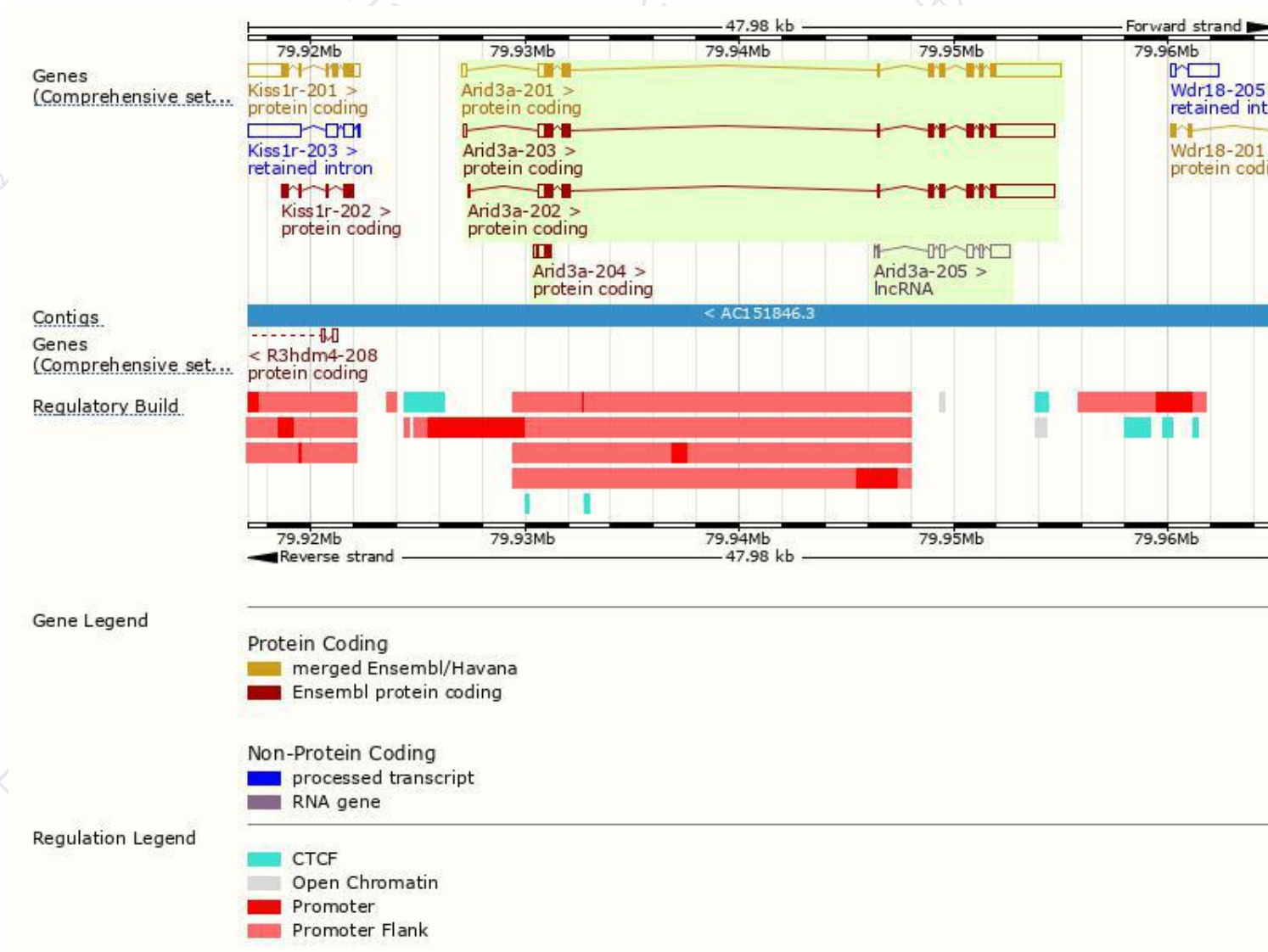
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Arid3a-201	<a href="#">ENSMUST00000019708.11</a>	5361	<a href="#">601aa</a>	<a href="#">ENSMUSP00000019708.5</a>	Protein coding	<a href="#">CCDS23999</a>	<a href="#">Q62431</a>	TSL:1 GENCODE basic APPRIS P3
Arid3a-203	<a href="#">ENSMUST00000105377.7</a>	4952	<a href="#">599aa</a>	<a href="#">ENSMUSP00000101016.1</a>	Protein coding	<a href="#">CCDS78851</a>	<a href="#">A0A0R4J1A7</a>	TSL:1 GENCODE basic APPRIS ALT2
Arid3a-202	<a href="#">ENSMUST00000105376.1</a>	4892	<a href="#">601aa</a>	<a href="#">ENSMUSP00000101015.1</a>	Protein coding	<a href="#">CCDS23999</a>	<a href="#">Q62431</a>	TSL:1 GENCODE basic APPRIS P3
Arid3a-204	<a href="#">ENSMUST00000131118.1</a>	691	<a href="#">108aa</a>	<a href="#">ENSMUSP00000114261.1</a>	Protein coding	-	<a href="#">D3YVQ2</a>	CDS 3' incomplete TSL:3
Arid3a-205	<a href="#">ENSMUST00000135005.1</a>	1839	No protein	-	lncRNA	-	-	TSL:1

The strategy is based on the design of *Arid3a-201* transcript,The transcription is shown below

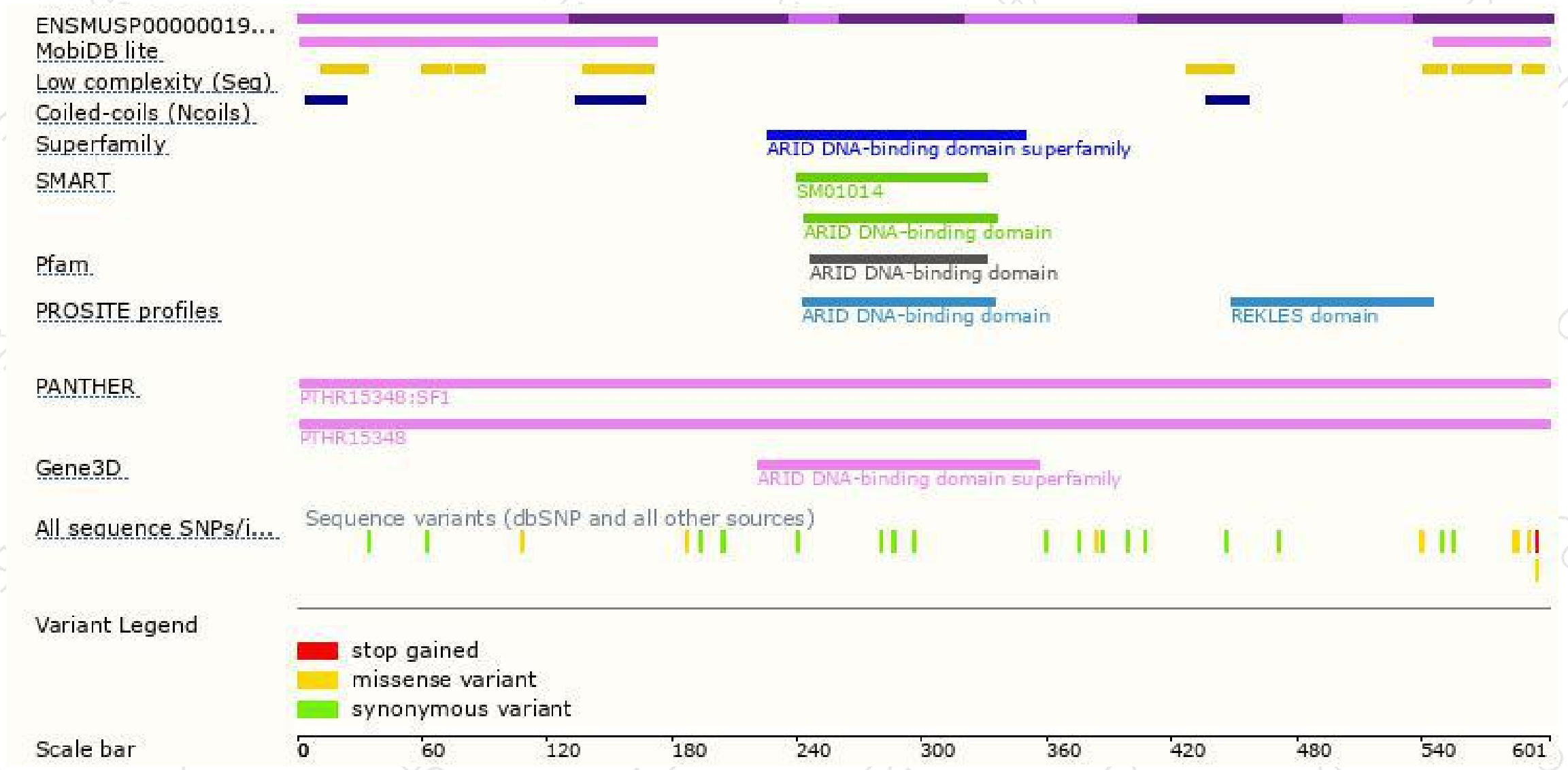


# Genomic location distribution



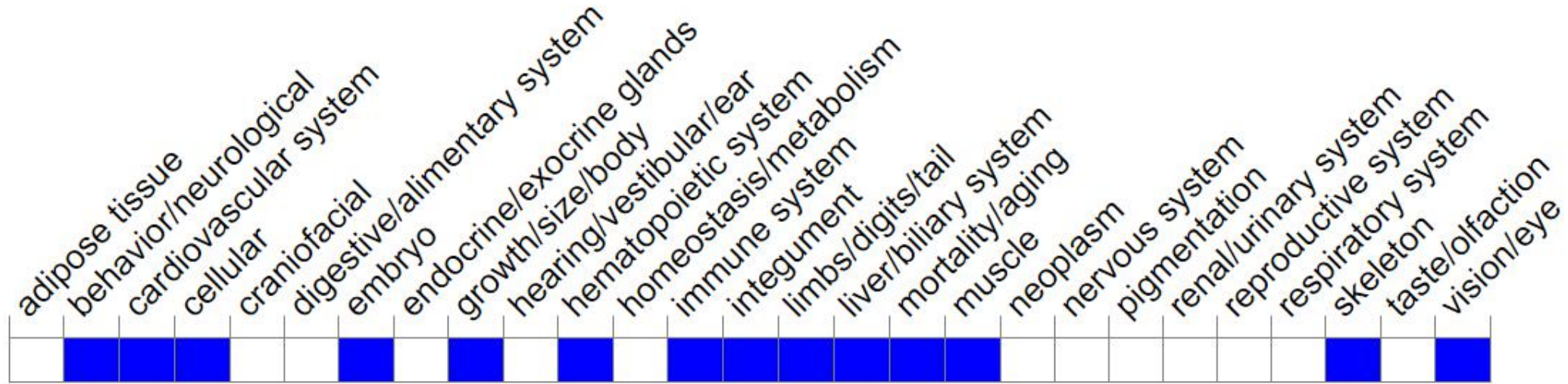


# Protein domain



# Mouse phenotype description(MGI)

## Phenotype Overview ?



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 knock-out allele exhibit embryonic lethality between E11.5 and E13.5 due to impaired erythropoiesis.

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

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