

# *Adam8* Cas9-CKO Strategy

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<b>Design Date:</b>	<b>2019-12-17</b>

# Project Overview

**Project Name**

*Adam8*

**Project type**

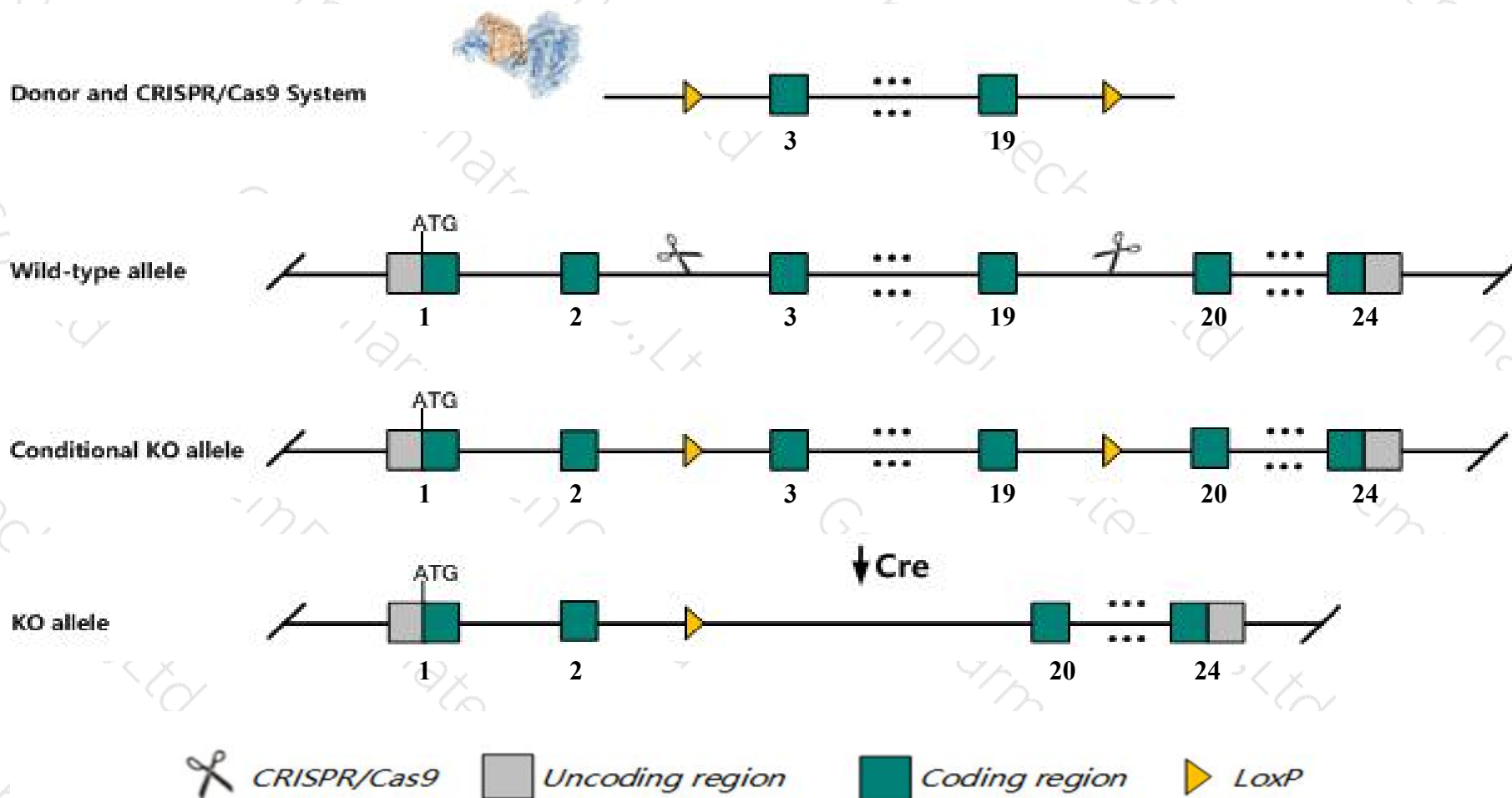
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adam8* gene. The schematic diagram is as follows:



# Technical routes

- The *Adam8* gene has 8 transcripts. According to the structure of *Adam8* gene, exon3-exon19 of *Adam8-202* (ENSMUST00000106069.8) transcript is recommended as the knockout region. The region contains 1934bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Adam8* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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 will be 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.

# Notice

- According to the existing MGI data, Homozygous mutant mice do not exhibit any morphological or pathological abnormalities. Mice homozygous for a different knock-out allele exhibit reduced osteoclast differentiation and calvarial fibrosis in response to TNF-alpha treatment.
- The KO region contains functional region of the *Mir7062* gene. Knockout the region will affect the function of *Mir7062* gene.
- The *Adam8* gene is located on the Chr7. 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)

## Adam8 a disintegrin and metallopeptidase domain 8 [Mus musculus (house mouse)]

Gene ID: 11501, updated on 17-Feb-2019

### Summary



**Official Symbol** Adam8 provided by [MGI](#)

**Official Full Name** a disintegrin and metallopeptidase domain 8 provided by [MGI](#)

**Primary source** [MGI:MGI:107825](#)

**See related** [Ensembl:ENSMUSG00000025473](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** ADAM 8, CD156, CD156a, E430039A18Rik, MS2

**Summary** This gene encodes a member of the Adam family of proteins that contain the disintegrin and metalloprotease domains. The encoded protein is localized to the cell surface, where it is involved in the remodeling of extracellular matrix and cell migration. Mice lacking the encoded protein display persistent inflammation upon treatment with allergens. Alternative splicing of this gene results in multiple variants. [provided by RefSeq, Mar 2015]

**Expression** Broad expression in ovary adult (RPKM 21.0), thymus adult (RPKM 6.6) and 19 other tissues [See more](#)

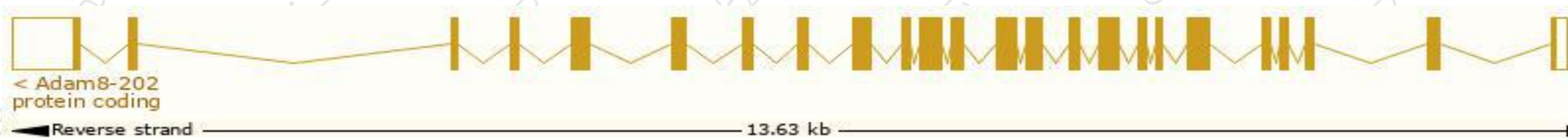
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

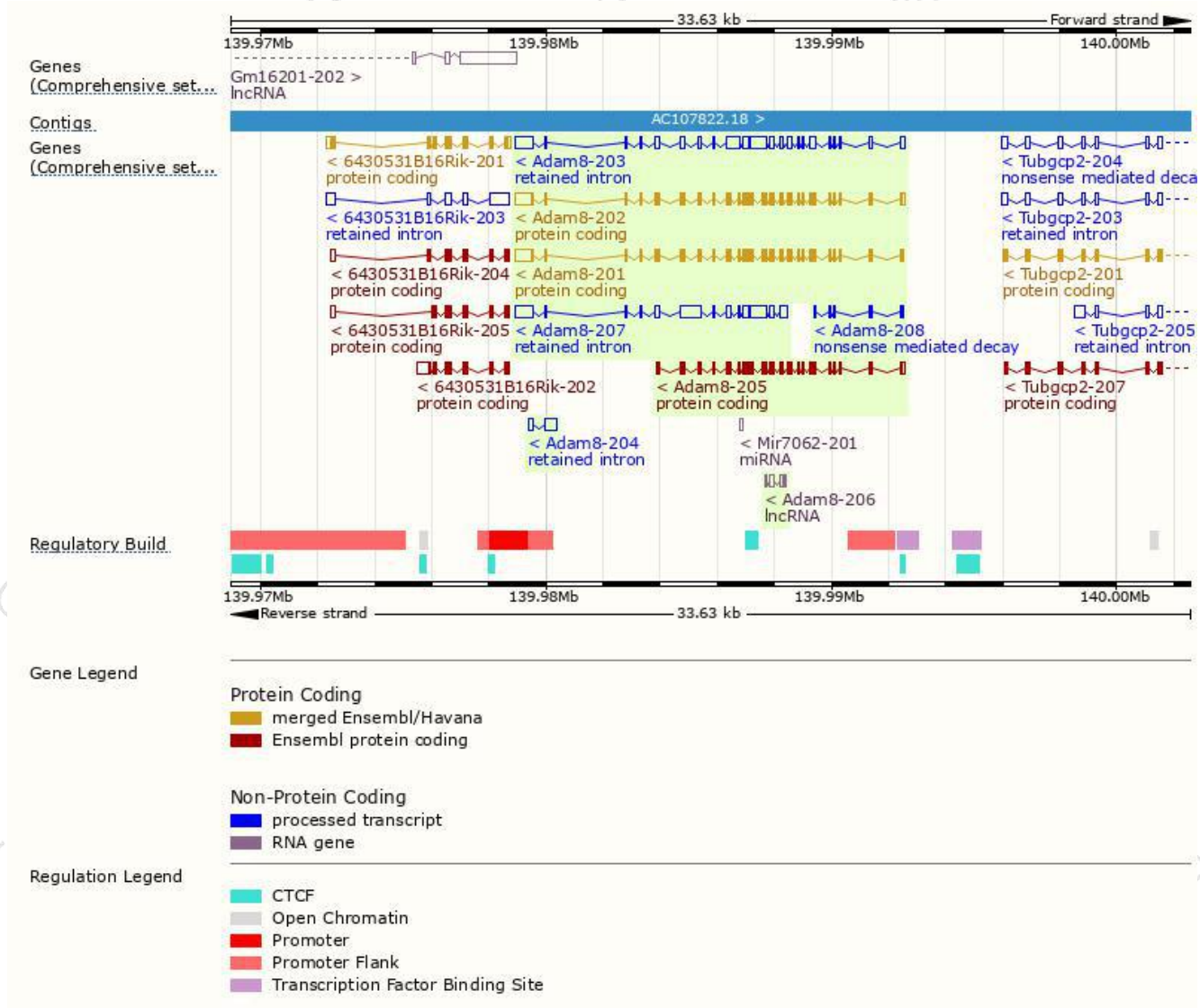
The gene has 8 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adam8-202	<a href="#">ENSMUST00000106069.8</a>	3117	<a href="#">826aa</a>	Protein coding	<a href="#">CCDS21959</a>	<a href="#">Q05910 Q3U1J7</a>	TSL:1 GENCODE basic APPRIS P3
Adam8-201	<a href="#">ENSMUST00000026546.15</a>	3100	<a href="#">825aa</a>	Protein coding	<a href="#">CCDS72064</a>	<a href="#">Q3U7G2</a>	TSL:1 GENCODE basic APPRIS ALT2
Adam8-205	<a href="#">ENSMUST00000148670.7</a>	2325	<a href="#">744aa</a>	Protein coding	-	<a href="#">E9Q359</a>	CDS 3' incomplete TSL:1
Adam8-208	<a href="#">ENSMUST00000173209.1</a>	343	<a href="#">64aa</a>	Nonsense mediated decay	-	<a href="#">G3UXF8</a>	TSL:5
Adam8-203	<a href="#">ENSMUST00000128332.7</a>	3669	No protein	Retained intron	-	-	TSL:2
Adam8-207	<a href="#">ENSMUST00000156647.7</a>	3089	No protein	Retained intron	-	-	TSL:2
Adam8-204	<a href="#">ENSMUST00000132903.1</a>	543	No protein	Retained intron	-	-	TSL:2
Adam8-206	<a href="#">ENSMUST00000149915.1</a>	367	No protein	lncRNA	-	-	TSL:2

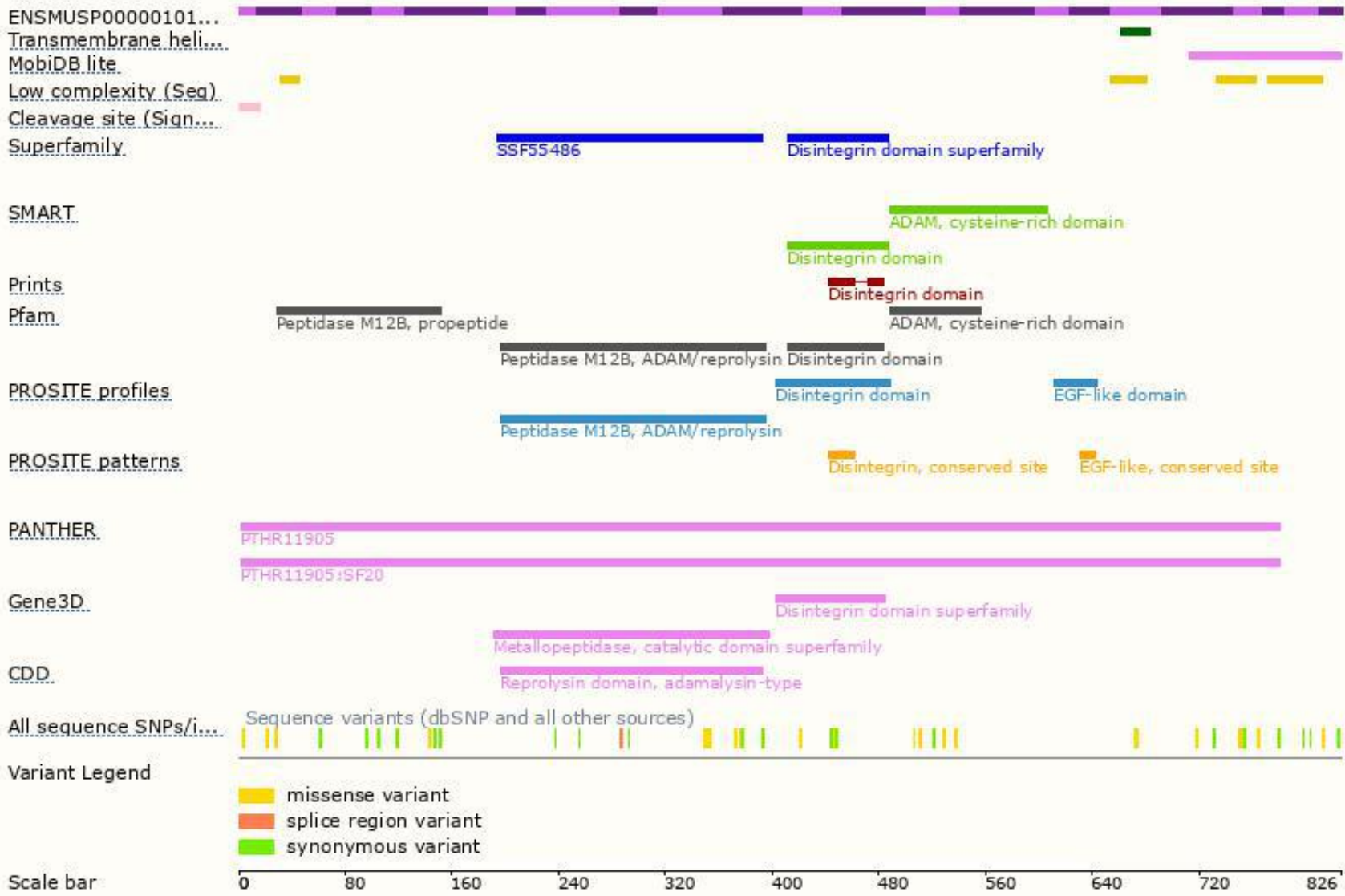
The strategy is based on the design of *Adam8-202* transcript, The transcription is shown below



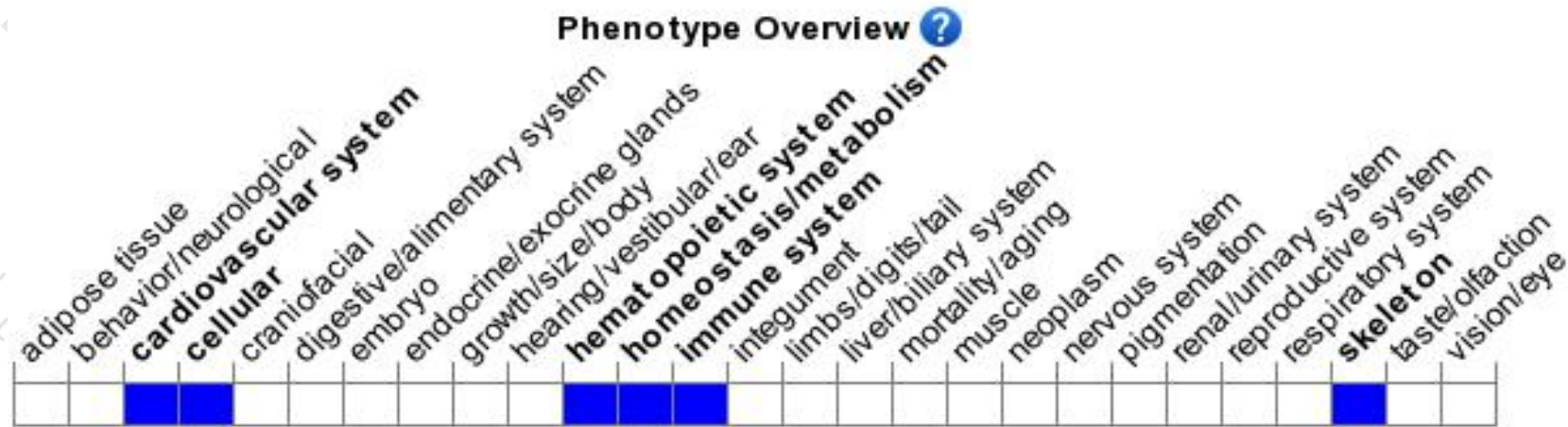
# Genomic location distribution



# 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/>).*

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