

# *Pomgnt1* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Pomgnt1*

**Project type**

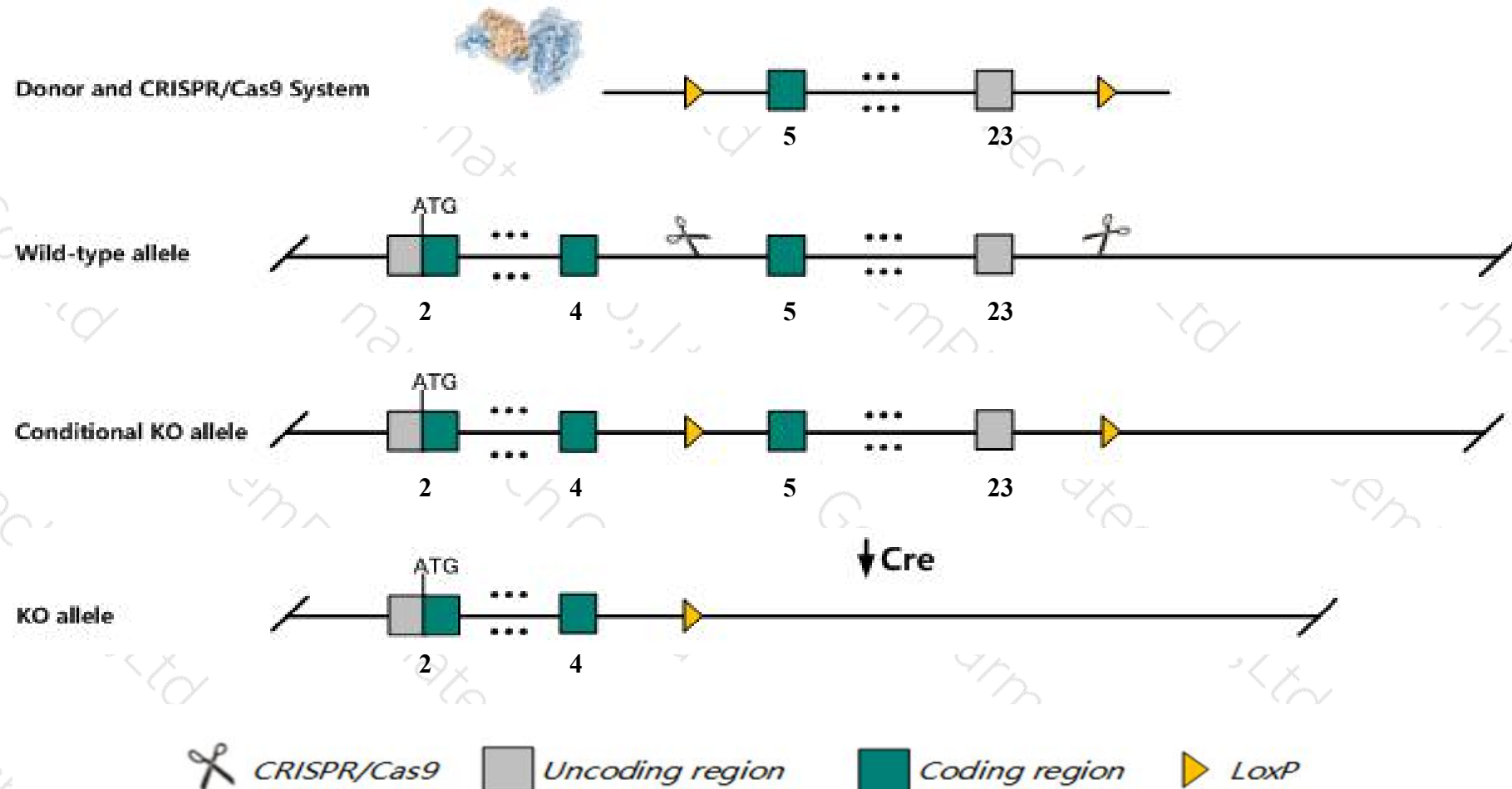
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pomgnt1* gene. The schematic diagram is as follows:



# Technical routes

- The *Pomgnt1* gene has 12 transcripts. According to the structure of *Pomgnt1* gene, exon5-exon23 of *Pomgnt1*-204(ENSMUST00000120083.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pomgnt1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, surviving homozygous null mice display a mild dystrophy despite a reduced muscle mass and myofiber number, impaired muscle regeneration and low proliferative activity of satellite cells. Mice homozygous for a gene trap allele show reduced fertility and multiple defects in muscle, eye and brain.
- The Intron4 is only 513bp, loxp insertion may affect mRNA splicing.
- The *Pomgnt1* gene is located on the Chr4. 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)

Pomgnt1 protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase [Mus musculus (house mouse)]

Gene ID: 68273, updated on 13-Mar-2020

## Summary



Official Symbol Pomgnt1 provided by [MGI](#)

Official Full Name protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase provided by [MGI](#)

Primary source [MGI:MGI:1915523](#)

See related [Ensembl:ENSMUSG00000028700](#)

Gene type protein coding

RefSeq status VALIDATED

Organism [Mus musculus](#)

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

Also known as 0610016I07Rik, 4930467B06Rik

Expression Ubiquitous expression in testis adult (RPKM 35.5), ovary adult (RPKM 18.0) and 28 other tissues [See more](#)

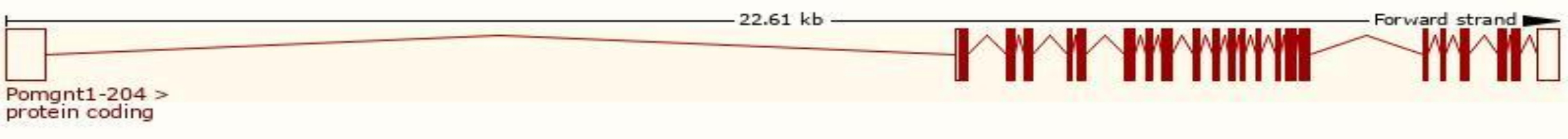
Orthologs [human all](#)

# Transcript information (Ensembl)

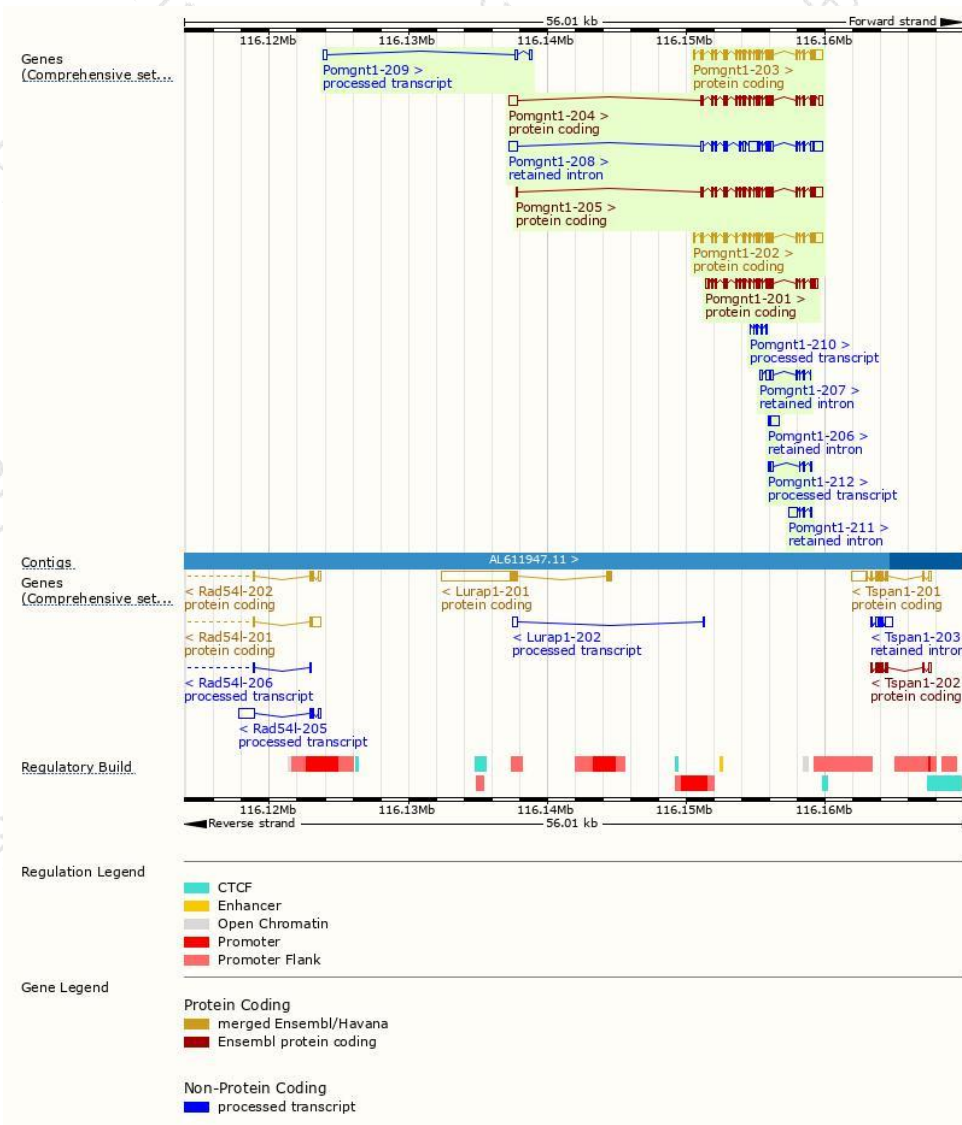
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pomgnt1-204	<a href="#">ENSMUST00000120083.7</a>	2953	<a href="#">660aa</a>	Protein coding	<a href="#">CCDS18506</a>	<a href="#">Q91X88</a>	TSL:5 GENCODE basic APPRIS P1
Pomgnt1-203	<a href="#">ENSMUST00000106498.7</a>	2719	<a href="#">660aa</a>	Protein coding	<a href="#">CCDS18506</a>	<a href="#">Q91X88</a>	TSL:1 GENCODE basic APPRIS P1
Pomgnt1-205	<a href="#">ENSMUST00000121052.7</a>	2693	<a href="#">660aa</a>	Protein coding	<a href="#">CCDS18506</a>	<a href="#">Q91X88</a>	TSL:5 GENCODE basic APPRIS P1
Pomgnt1-202	<a href="#">ENSMUST00000106496.7</a>	2613	<a href="#">627aa</a>	Protein coding	<a href="#">CCDS18507</a>	<a href="#">Q91X88</a>	TSL:1 GENCODE basic
Pomgnt1-201	<a href="#">ENSMUST00000106494.2</a>	2226	<a href="#">638aa</a>	Protein coding	<a href="#">CCDS71450</a>	<a href="#">Q91X88</a>	TSL:1 GENCODE basic
Pomgnt1-209	<a href="#">ENSMUST00000144311.1</a>	557	No protein	Processed transcript	-	-	TSL:1
Pomgnt1-212	<a href="#">ENSMUST00000155718.7</a>	449	No protein	Processed transcript	-	-	TSL:2
Pomgnt1-210	<a href="#">ENSMUST00000147612.1</a>	393	No protein	Processed transcript	-	-	TSL:3
Pomgnt1-208	<a href="#">ENSMUST00000136855.7</a>	3448	No protein	Retained intron	-	-	TSL:5
Pomgnt1-207	<a href="#">ENSMUST00000133838.7</a>	870	No protein	Retained intron	-	-	TSL:5
Pomgnt1-211	<a href="#">ENSMUST00000151325.1</a>	790	No protein	Retained intron	-	-	TSL:3
Pomgnt1-206	<a href="#">ENSMUST00000127426.1</a>	636	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Pomgnt1-204* transcript,the transcription is shown below:

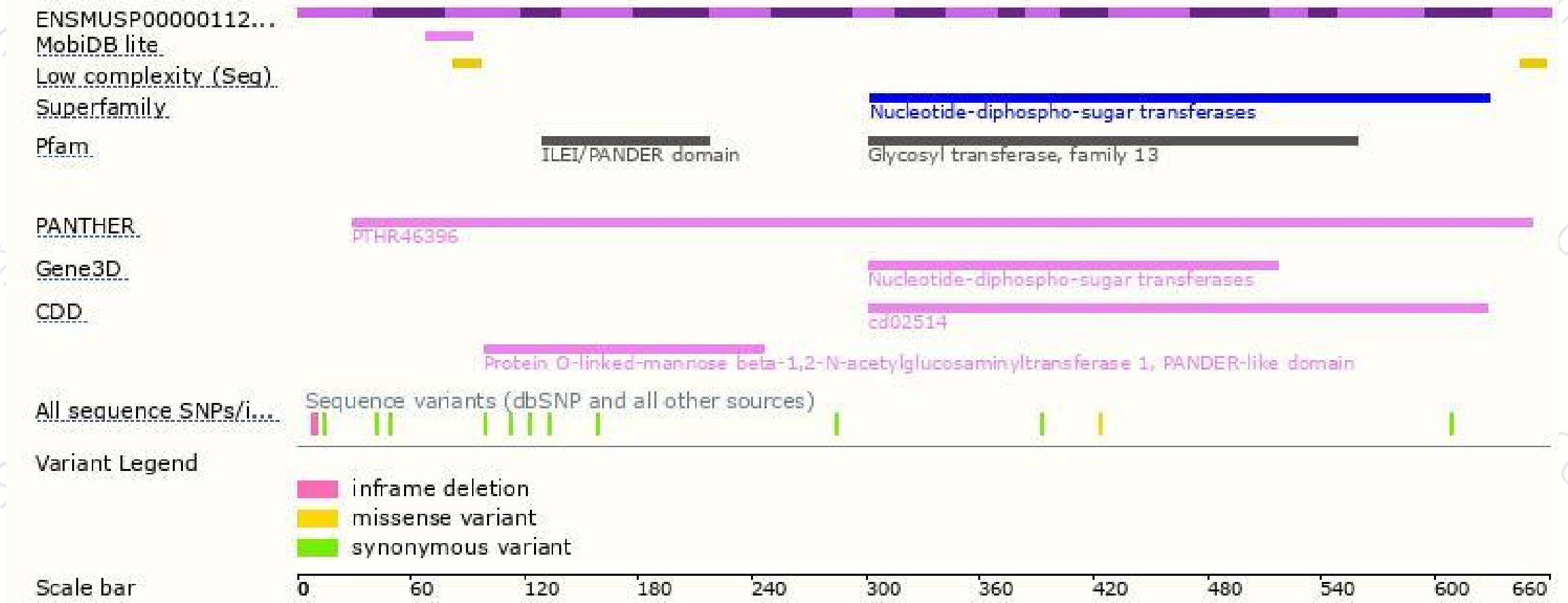


# Genomic location distribution

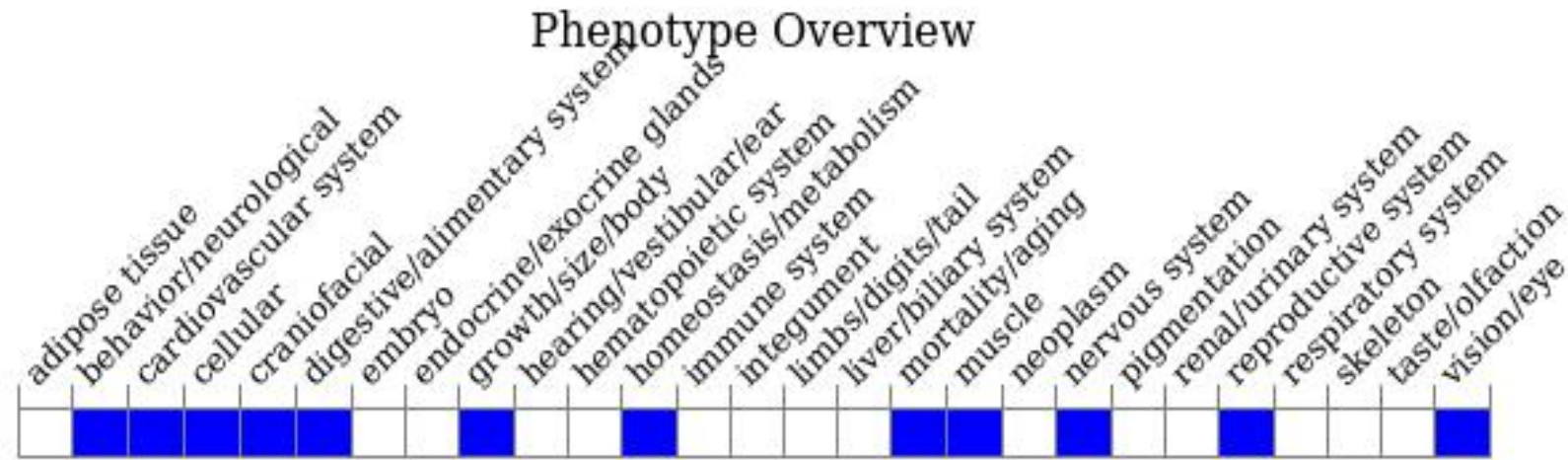




# Protein domain



# 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, surviving homozygous null mice display a mild dystrophy despite a reduced muscle mass and myofiber number, impaired muscle regeneration and low proliferative activity of satellite cells. Mice homozygous for a gene trap allele show reduced fertility and multiple defects in muscle, eye and brain.

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

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