

# ***Bag3 Cas9-CKO Strategy***

**Designer:**

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**Design Date:**

**2019-7-26**

# Project Overview

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**Project Name**

***Bag3***

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**Project type**

**Cas9-CKO**

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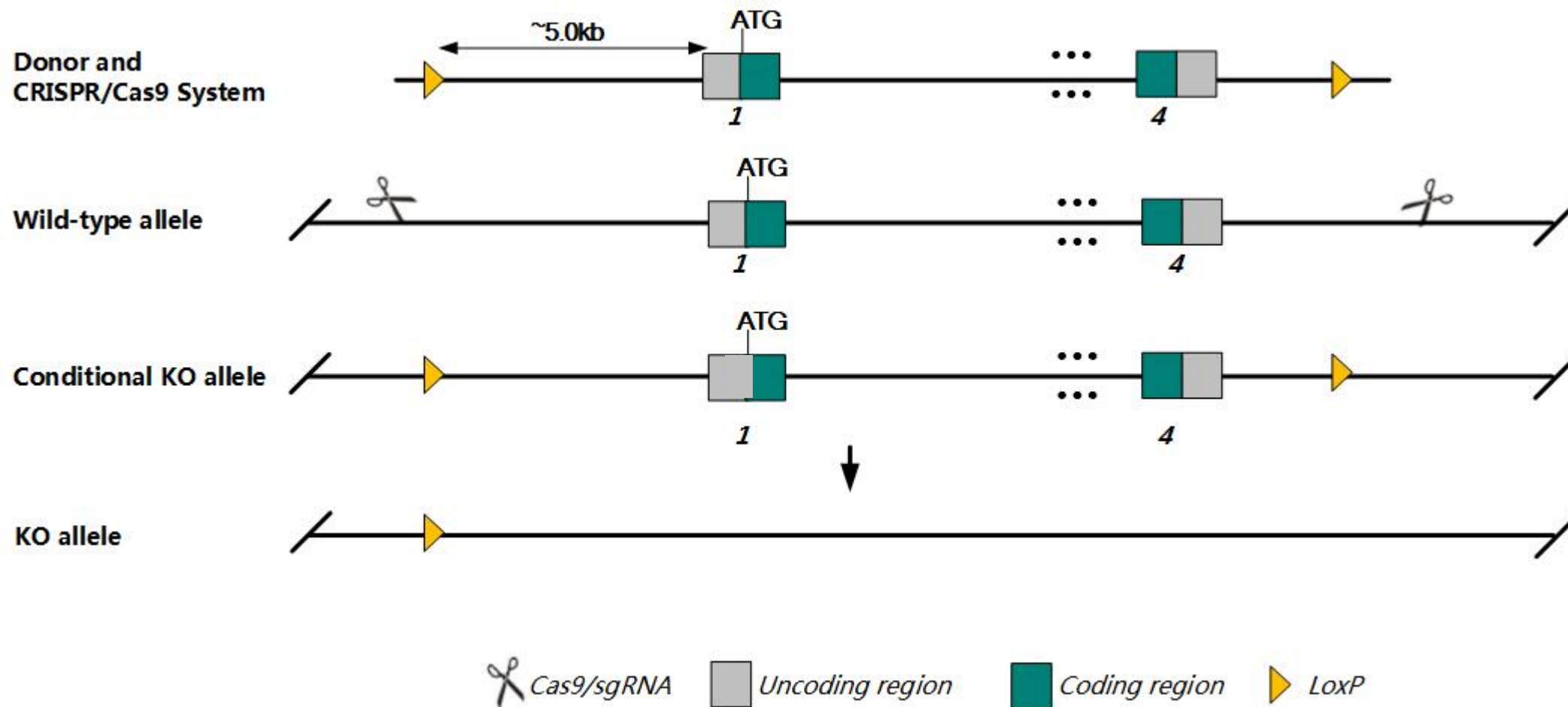
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bag3* gene. The schematic diagram is as follows:



- The *Bag3* gene has 1 transcript. According to the structure of *Bag3* gene, the predicted promoter region and exon1-4 of *Bag3*-201 (ENSMUST00000033136.8) transcript is recommended as the knockout region. The region contains the predicted promoter sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bag3* 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 or cell types.

- According to the existing MGI data: Mice homozygous for a gene trap allele exhibit postnatal lethality, growth retardation, cardiomyocyte and skeletal myocyte degeneration, and pulmonary edema. Mice homozygous for a null allele also exhibit postnatal lethality and growth retardation but lack the myocyte degeneration phenotype.
- The *Bag3* 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 the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Bag3 BCL2-associated athanogene 3 [ *Mus musculus* (house mouse) ]

Gene ID: 29810, updated on 30-Sep-2018

### Summary

**Official Symbol** Bag3 provided by [MGI](#)

**Official Full Name** BCL2-associated athanogene 3 provided by [MGI](#)

**Primary source** [MGI:MGI:1352493](#)

**See related** [Ensembl:ENSMUSG00000030847](#) [Vega:OTTMUSG00000058717](#)

**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** Bis; mg638; AA407278

**Expression** Broad expression in adrenal adult (RPKM 127.9), heart adult (RPKM 49.8) and 16 other tissues [See more](#)

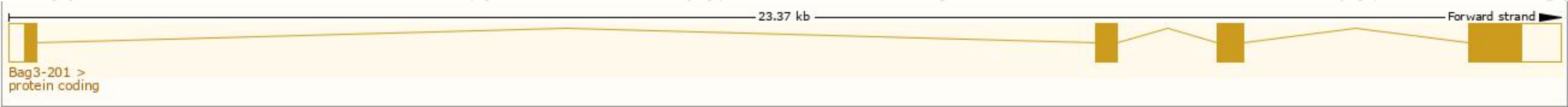
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

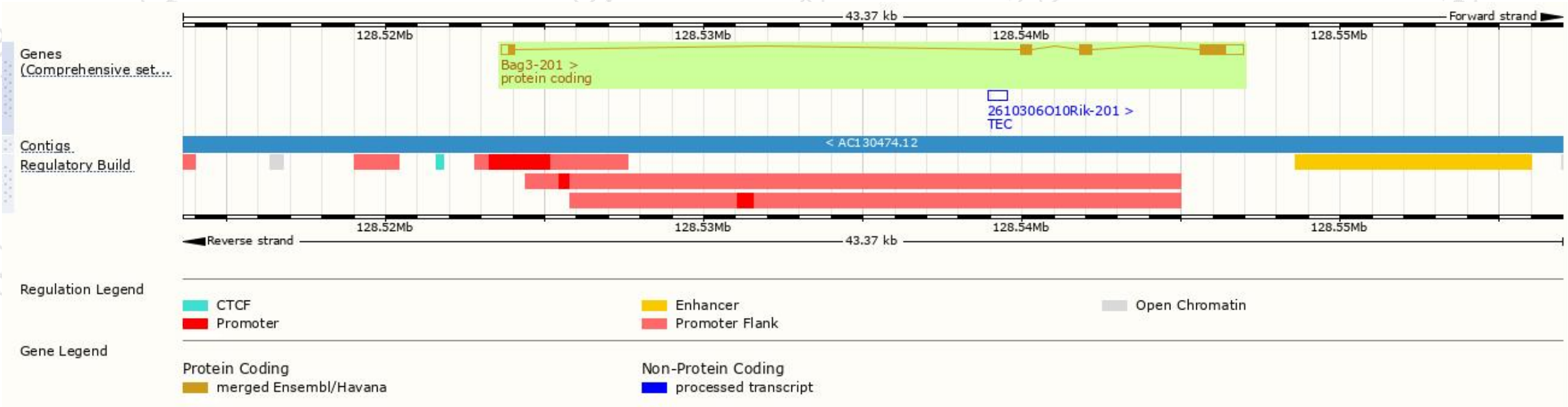
The gene has 1 transcript, and all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Bag3-201	<a href="#">ENSMUST00000033136.8</a>	2562	<a href="#">577aa</a>	Protein coding	<a href="#">CCDS21898</a>	<a href="#">Q9JLV1</a>	TSL:1 Gencode basic APPRIS P1

The strategy is based on the design of *Bag3-201* transcript, The transcription is shown below

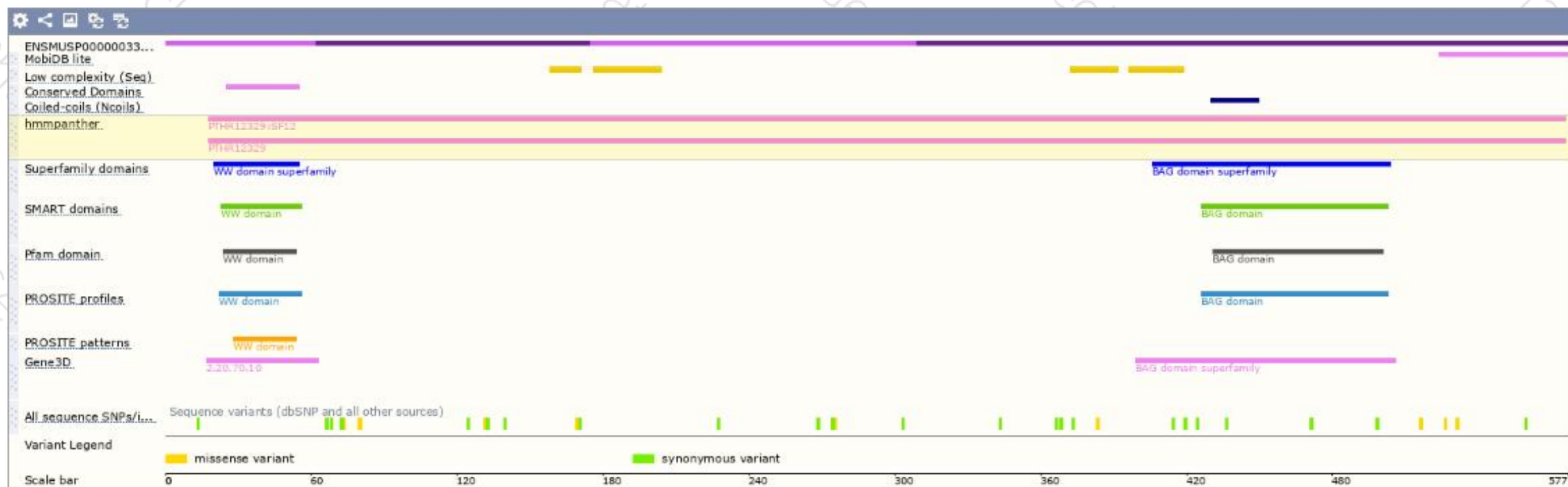


# Genomic location distribution

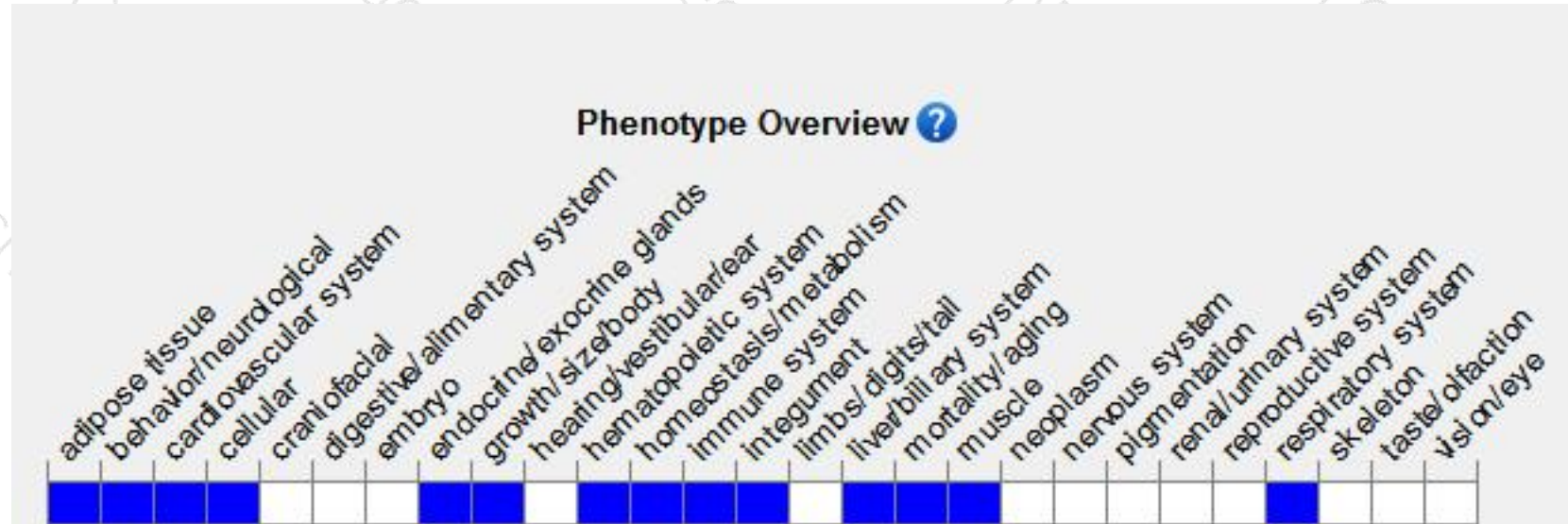




# Protein domain



# Mouse phenotype description(MGI)



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>) .*

Mice homozygous for a gene trap allele exhibit postnatal lethality, growth retardation, cardiomyocyte and skeletal myocyte degeneration, and pulmonary edema. Mice homozygous for a null allele also exhibit postnatal lethality and growth retardation but lack the myocyte degeneration phenotype.

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