

# ***Chd2* Cas9-CKO Strategy**

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# Project Overview

**Project Name**

*Chd2*

**Project type**

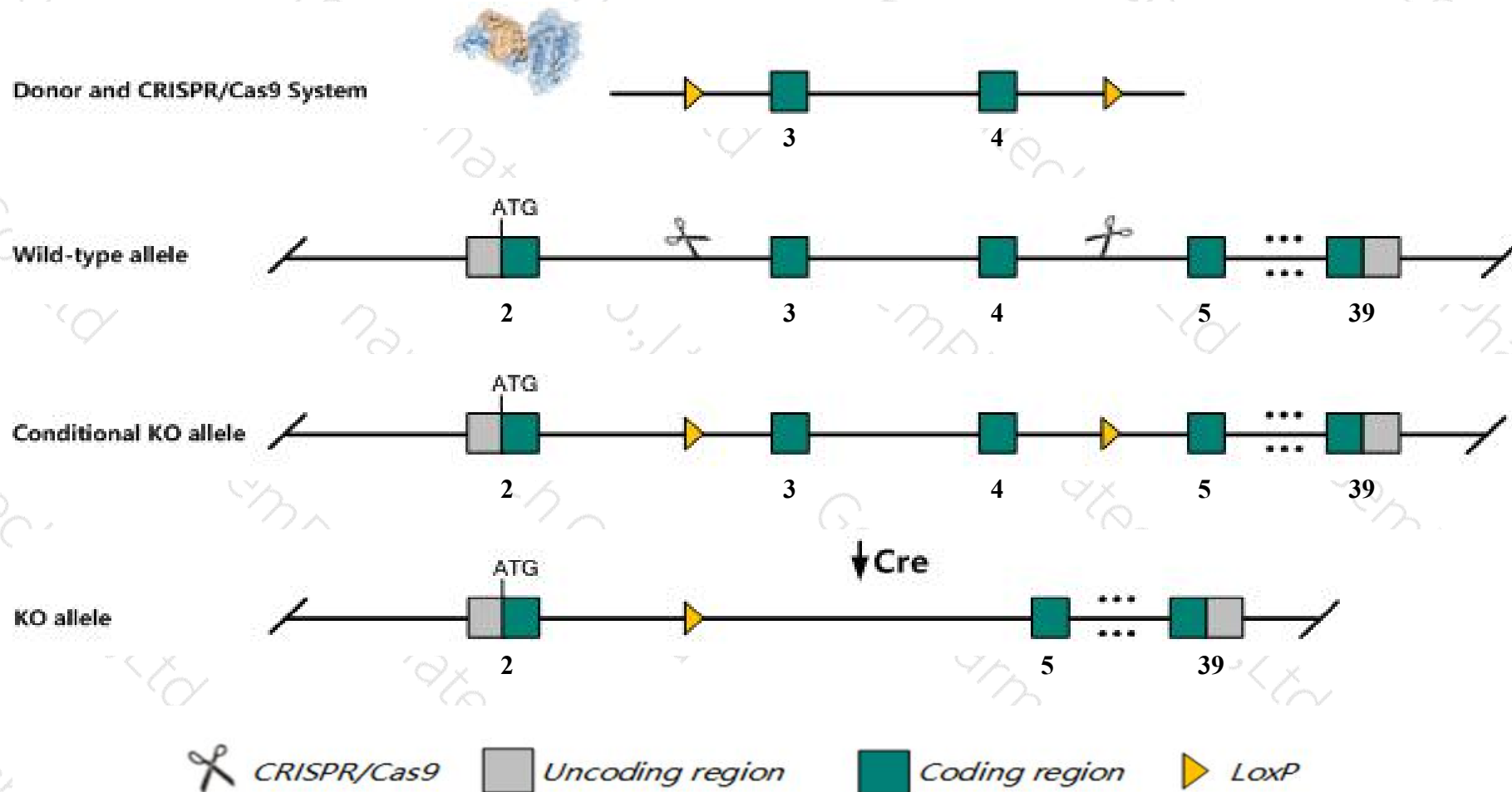
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chd2* gene. The schematic diagram is as follows:



# Technical routes

- The *Chd2* gene has 18 transcripts. According to the structure of *Chd2* gene, exon3-exon4 of *Chd2*-203(ENSMUST00000169922.8) transcript is recommended as the knockout region. The region contains 319bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Chd2* 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, mice homozygous for a gene trap allele exhibit early postnatal lethality associated with fetal growth retardation. Mice heterozygous for a gene trap allele exhibit postnatal lethality and premature death after weaning associated with growth retardation and multi-organ defects.
- The *Chd2* 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)

## Chd2 chromodomain helicase DNA binding protein 2 [ *Mus musculus* (house mouse) ]

Gene ID: 244059, updated on 26-Jun-2020

### Summary

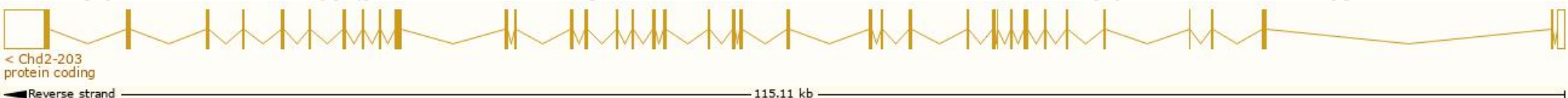
Official Symbol	Chd2 provided by <a href="#">MGI</a>
Official Full Name	chromodomain helicase DNA binding protein 2 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2448567</a>
See related	<a href="#">Ensembl:ENSMUSG00000078671</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CHD-2; AI851092; BC029703; 2810013C04Rik; 2810040A01Rik; 5630401D06Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 9.7), limb E14.5 (RPKM 9.5) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

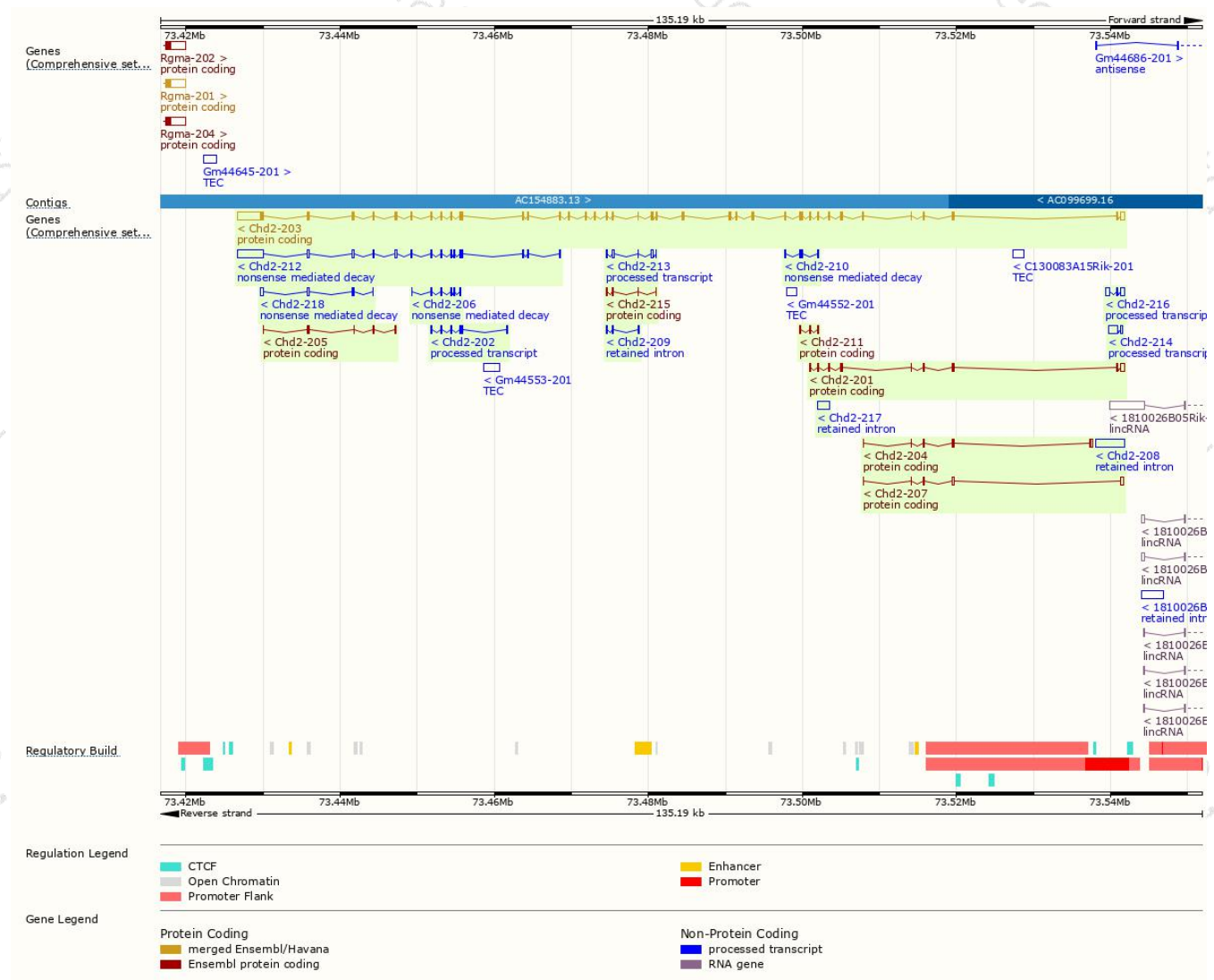
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chd2-218	<a href="#">ENSMUST00000208458.1</a>	745	<a href="#">34aa</a>	Nonsense mediated decay	-	<a href="#">A0A140LJE4</a>	CDS 5' incomplete TSL:5
Chd2-206	<a href="#">ENSMUST00000181971.5</a>	667	<a href="#">35aa</a>	Nonsense mediated decay	-	<a href="#">M0QWT0</a>	CDS 5' incomplete TSL:5
Chd2-207	<a href="#">ENSMUST00000197642.1</a>	896	<a href="#">57aa</a>	Protein coding	-	<a href="#">A0A0G2JDK8</a>	CDS 3' incomplete TSL:5
Chd2-210	<a href="#">ENSMUST00000199601.1</a>	558	<a href="#">74aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JFK1</a>	CDS 5' incomplete TSL:5
Chd2-215	<a href="#">ENSMUST00000200423.1</a>	339	<a href="#">113aa</a>	Protein coding	-	<a href="#">A0A0G2JES5</a>	CDS 5' and 3' incomplete TSL:5
Chd2-211	<a href="#">ENSMUST00000199641.1</a>	360	<a href="#">120aa</a>	Protein coding	-	<a href="#">A0A0G2JEP1</a>	CDS 5' and 3' incomplete TSL:5
Chd2-205	<a href="#">ENSMUST00000173785.1</a>	487	<a href="#">163aa</a>	Protein coding	-	<a href="#">G3UXJ4</a>	CDS 5' and 3' incomplete TSL:5
Chd2-204	<a href="#">ENSMUST00000172704.5</a>	748	<a href="#">178aa</a>	Protein coding	-	<a href="#">G3UZG2</a>	CDS 3' incomplete TSL:5
Chd2-212	<a href="#">ENSMUST00000199809.4</a>	5289	<a href="#">220aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JEZ3</a>	CDS 5' incomplete TSL:5
Chd2-201	<a href="#">ENSMUST00000026895.13</a>	1571	<a href="#">333aa</a>	Protein coding	-	<a href="#">F7CDZ7</a>	CDS 3' incomplete TSL:5
Chd2-203	<a href="#">ENSMUST00000169922.8</a>	9085	<a href="#">1827aa</a>	Protein coding	<a href="#">CCDS52274</a>	<a href="#">E9PZM4</a>	TSL:5 GENCODE basic APPRIS P1
Chd2-214	<a href="#">ENSMUST00000200218.1</a>	1387	No protein	Processed transcript	-	-	TSL:1
Chd2-216	<a href="#">ENSMUST00000200492.1</a>	1196	No protein	Processed transcript	-	-	TSL:5
Chd2-202	<a href="#">ENSMUST00000038366.8</a>	755	No protein	Processed transcript	-	-	TSL:1
Chd2-213	<a href="#">ENSMUST00000199831.1</a>	582	No protein	Processed transcript	-	-	TSL:5
Chd2-208	<a href="#">ENSMUST00000197800.1</a>	3741	No protein	Retained intron	-	-	TSL:NA
Chd2-217	<a href="#">ENSMUST00000206665.1</a>	1632	No protein	Retained intron	-	-	TSL:NA
Chd2-209	<a href="#">ENSMUST00000198225.1</a>	392	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Chd2-203* transcript,the transcription is shown below:

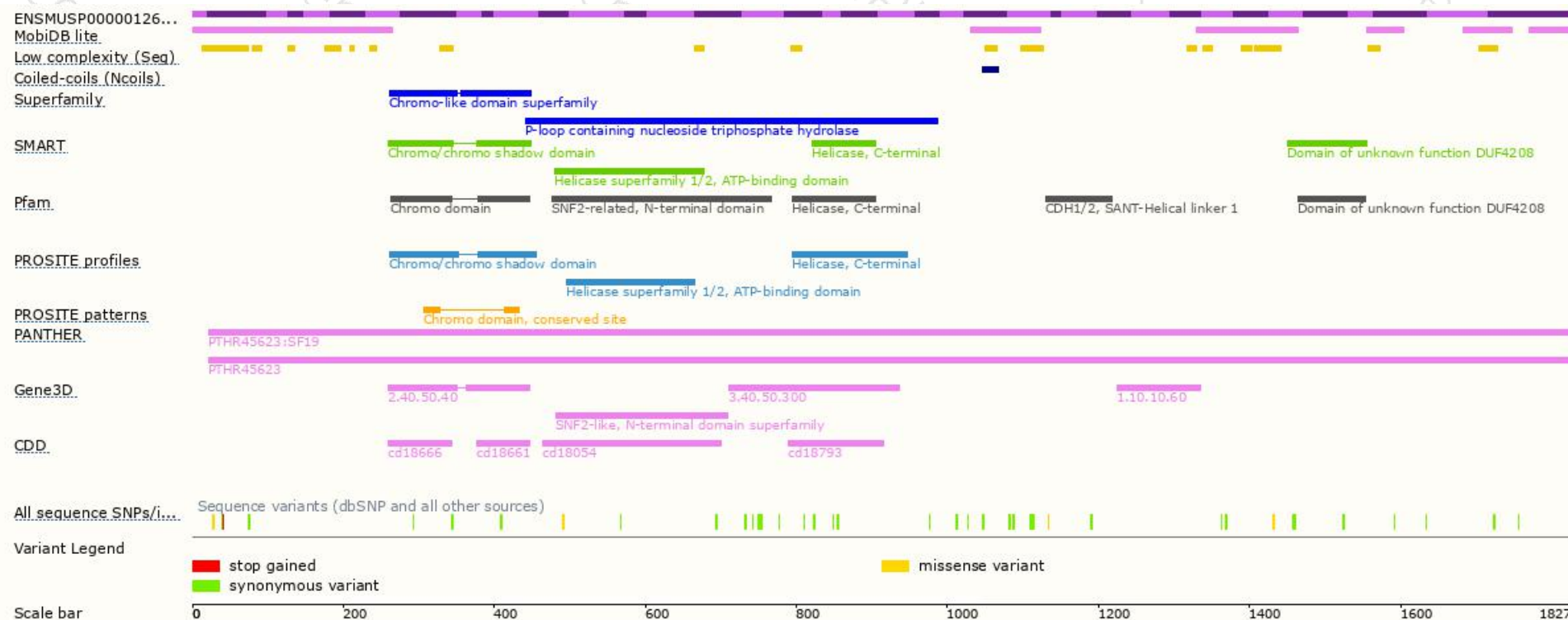


# Genomic location distribution

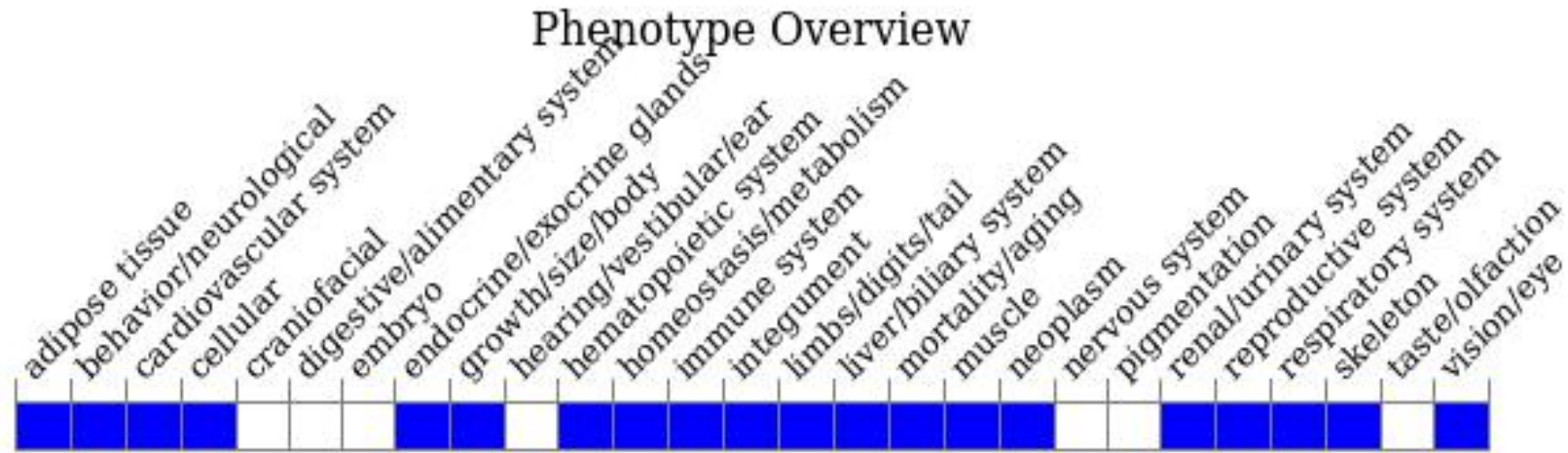




# Protein domain



# 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, mice homozygous for a gene trap allele exhibit early postnatal lethality associated with fetal growth retardation. Mice heterozygous for a gene trap allele exhibit postnatal lethality and premature death after weaning associated with growth retardation and multi-organ defects.

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

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