

# ***Hmgb1* Cas9-KO Strategy**

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**Reviewer: Ruirui Zhang**

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# Project Overview

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**Project Name**

*Hmgb1*

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**Project type**

**Cas9-KO**

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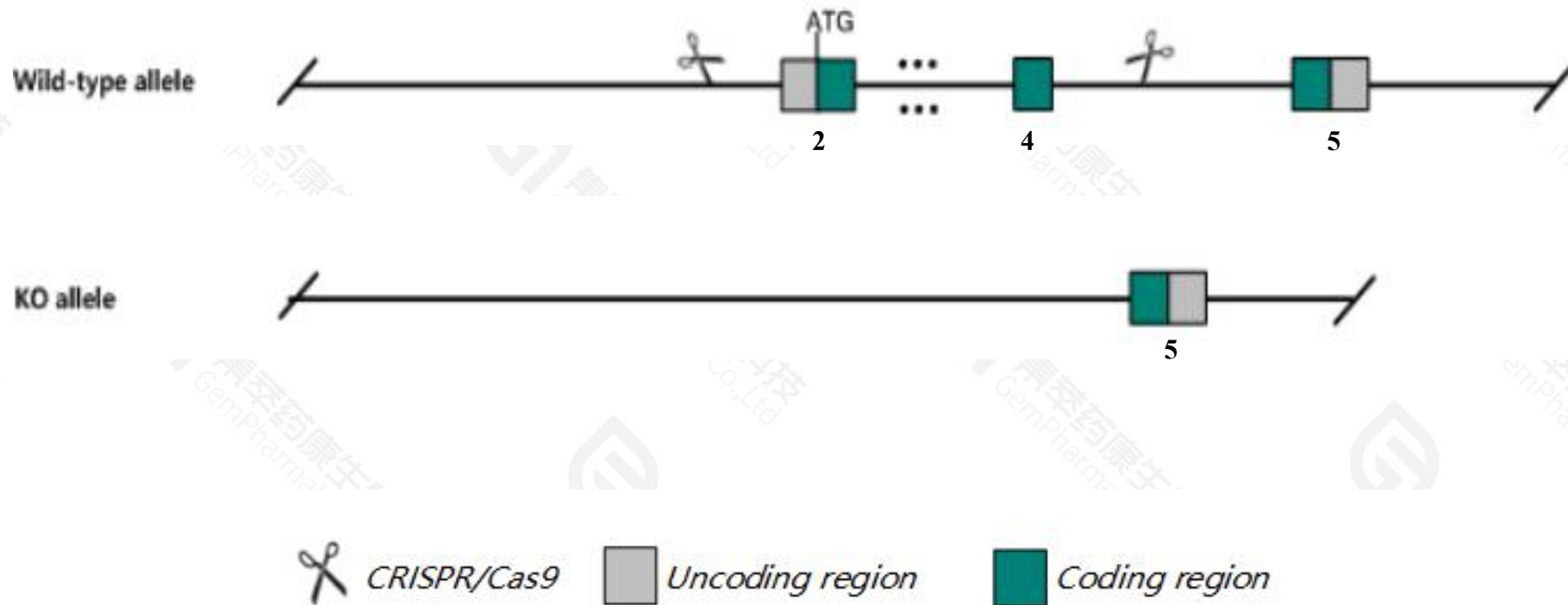
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmgb1* gene. The schematic diagram is as follows:



- The *Hmgb1* gene has 10 transcripts. According to the structure of *Hmgb1* gene, exon2-exon4 of *Hmgb1*-201(ENSMUST00000085546.13) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hmgb1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous null mice display partial or complete neonatal lethality due to hypoglycemia depending on the strain background, with open eyelids at birth, atelectasis, and lethargy.
- The *Hmgb1* gene is located on the Chr5. 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

## Hmgb1 high mobility group box 1 [Mus musculus (house mouse)]

Gene ID: 15289, updated on 13-Mar-2020

### Summary

**Official Symbol** Hmgb1 provided by [MGI](#)

**Official Full Name** high mobility group box 1 provided by [MGI](#)

**Primary source** [MGI:MGI:96113](#)

**See related** [Ensembl:ENSMUSG00000066551](#)

**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** HMG-1, Hmg1, SBP-1, p30

**Summary** This gene encodes a protein that belongs to the High Mobility Group-box superfamily. The encoded non-histone, nuclear DNA-binding protein regulates transcription, and is involved in organization of DNA. This protein plays a role in several cellular processes, including inflammation, cell differentiation and tumor cell migration. Multiple pseudogenes of this gene have been identified. Alternative splicing results in multiple transcript variants that encode the same protein. [provided by RefSeq, Sep 2015]

**Expression** Broad expression in CNS E11.5 (RPKM 22.0), liver E14 (RPKM 17.0) and 24 other tissues [See more](#)

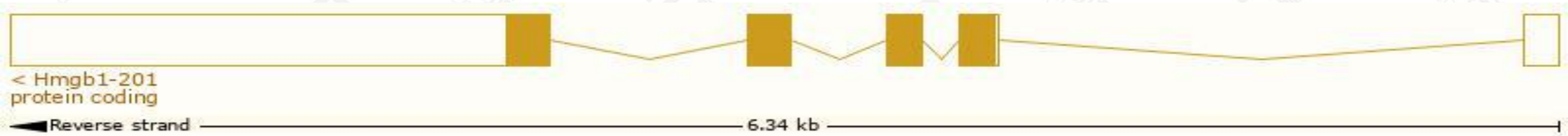
**Orthologs** [human](#) [all](#)

# Transcript information（Ensembl）

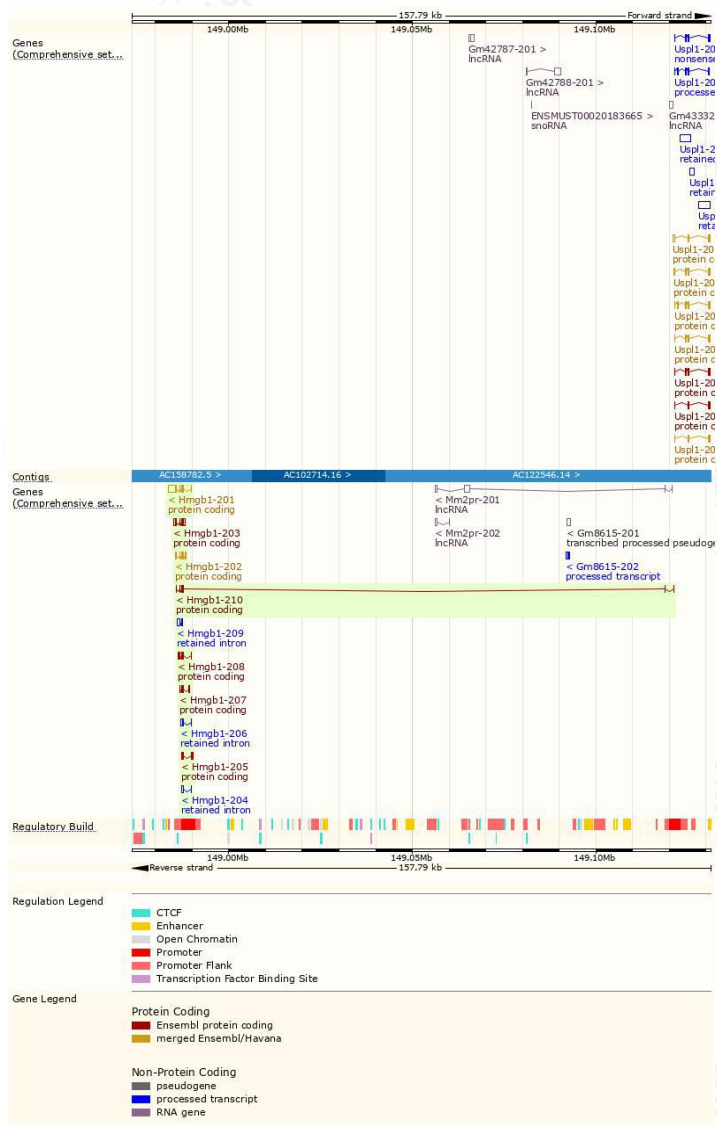
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmgb1-201	<a href="#">ENSMUST00000085546.12</a>	2838	<a href="#">215aa</a>	Protein coding	<a href="#">CCDS19883</a>	<a href="#">P63158 Q58EV5</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Hmgb1-203	<a href="#">ENSMUST00000110505.7</a>	1720	<a href="#">215aa</a>	Protein coding	<a href="#">CCDS19883</a>	<a href="#">P63158 Q58EV5</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Hmgb1-202	<a href="#">ENSMUST00000093196.10</a>	1092	<a href="#">215aa</a>	Protein coding	<a href="#">CCDS19883</a>	<a href="#">P63158 Q58EV5</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Hmgb1-208	<a href="#">ENSMUST00000139443.7</a>	923	<a href="#">171aa</a>	Protein coding	-	<a href="#">A0A0J9YUD8</a>	TSL:2 GENCODE basic
Hmgb1-210	<a href="#">ENSMUST00000202133.3</a>	685	<a href="#">211aa</a>	Protein coding	-	<a href="#">A0A0J9YUZ4</a>	CDS 3' incomplete TSL:3
Hmgb1-205	<a href="#">ENSMUST00000125605.1</a>	604	<a href="#">92aa</a>	Protein coding	-	<a href="#">D3YVC6</a>	CDS 3' incomplete TSL:5
Hmgb1-207	<a href="#">ENSMUST00000138553.7</a>	428	<a href="#">124aa</a>	Protein coding	-	<a href="#">D3YZ18</a>	CDS 3' incomplete TSL:2
Hmgb1-209	<a href="#">ENSMUST00000155086.1</a>	902	No protein	Retained intron	-	-	TSL:2
Hmgb1-206	<a href="#">ENSMUST00000133667.1</a>	654	No protein	Retained intron	-	-	TSL:2
Hmgb1-204	<a href="#">ENSMUST00000123645.1</a>	461	No protein	Retained intron	-	-	TSL:2

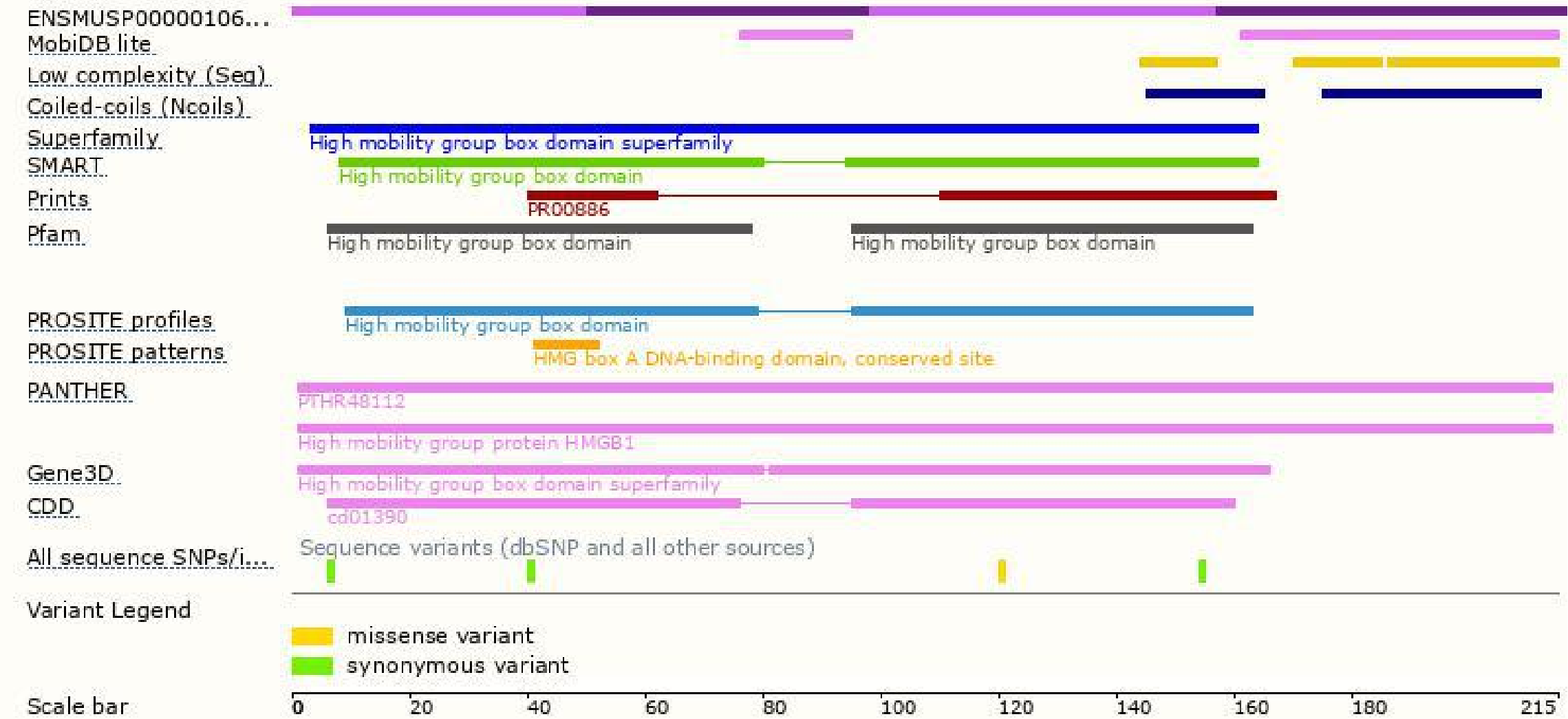
The strategy is based on the design of *Hmgb1-201* transcript,the transcription is shown below:



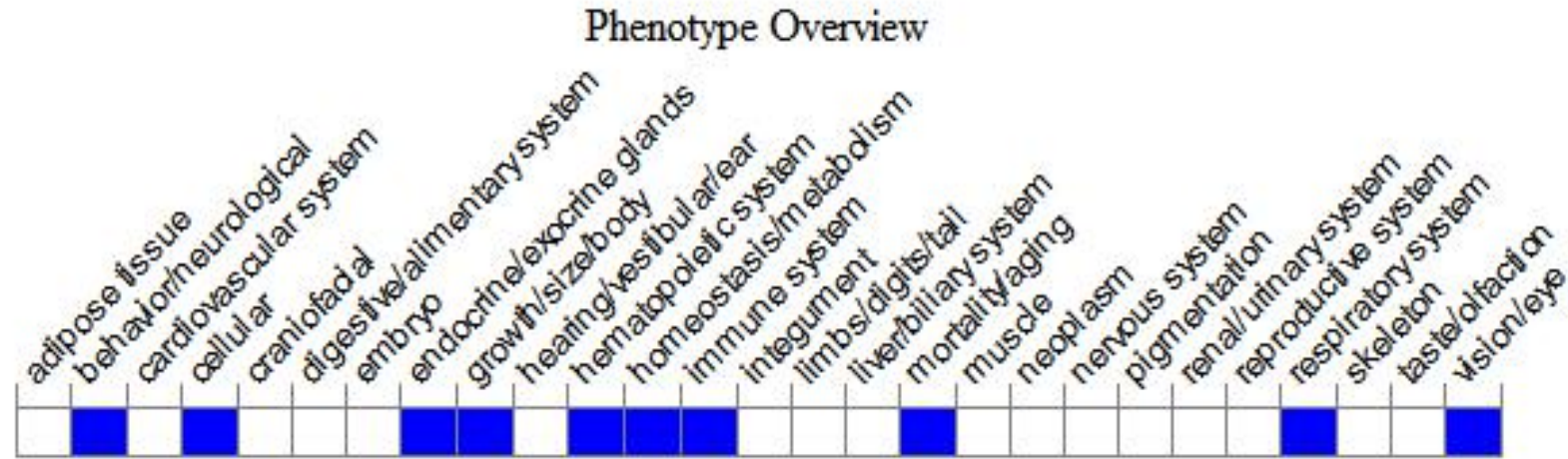
# Genomic location distribution



# 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/>).*

According to the existing MGI data, homozygous null mice display partial or complete neonatal lethality due to hypoglycemia depending on the strain background, with open eyelids at birth, atelectasis, and lethargy.

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

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