

Kpna6 Cas9-KO Strategy

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Project Overview

Project Name

Kpna6

Project type

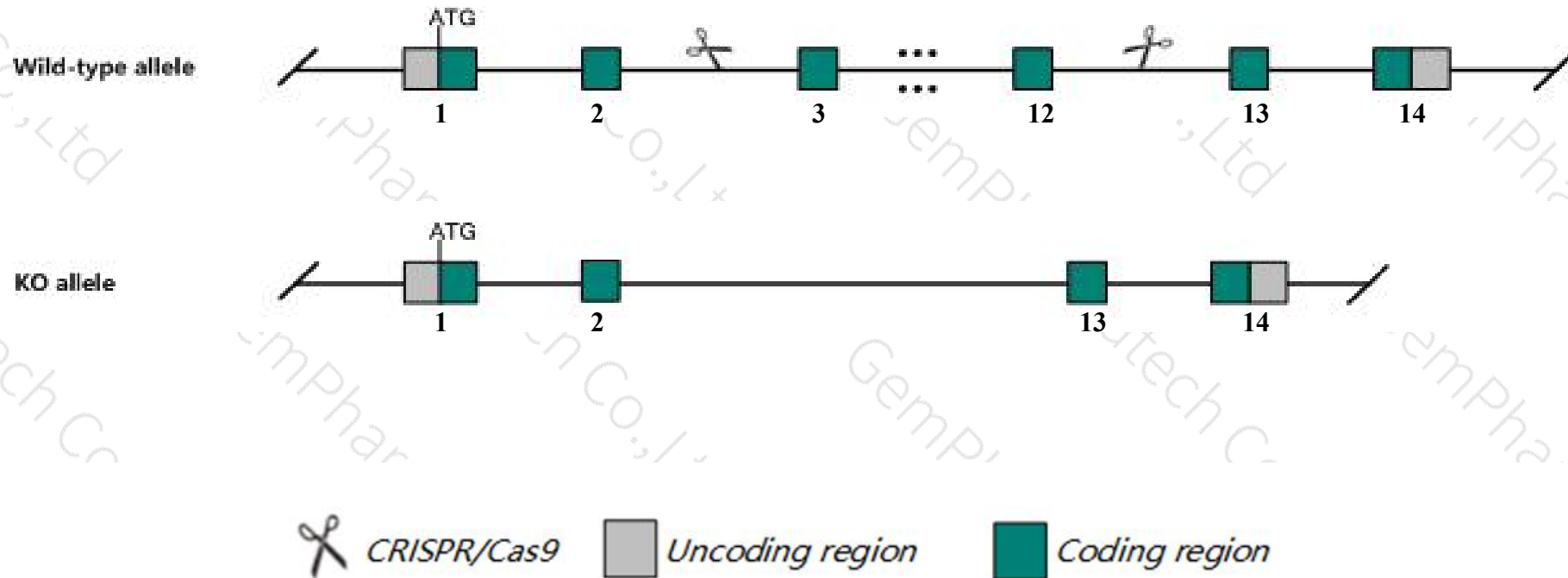
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kpna6* gene. The schematic diagram is as follows:



- The *Kpna6* gene has 6 transcripts. According to the structure of *Kpna6* gene, exon3-exon12 of *Kpna6-202* (ENSMUST00000102590.10) transcript is recommended as the knockout region. The region contains 1106bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kpna6* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Female mice homozygous for a null mutation are infertile and show a block in zygotic genome activation.
- Transcript 206 may not be affected. The effect of transcript 203 is unknown.
- The *Kpna6* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Kpna6 karyopherin (importin) alpha 6 [*Mus musculus* (house mouse)]

Gene ID: 16650, updated on 7-Jan-2020

Summary



Official Symbol	Kpna6 provided by MGI
Official Full Name	karyopherin (importin) alpha 6 provided by MGI
Primary source	MGI:MGI:1100836
See related	Ensembl:ENSMUSG00000003731
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	IPOA7; Kpna5; NPI-2
Expression	Ubiquitous expression in testis adult (RPKM 30.4), subcutaneous fat pad adult (RPKM 16.8) and 28 other tissues See more
Orthologs	human all

Genomic context



Location: 4; 4 D2.2

Exon count: 15

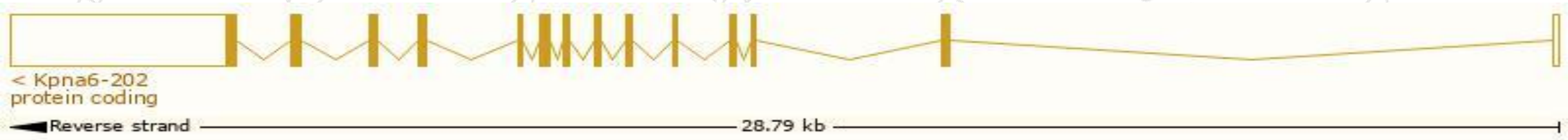
See Kpna6 in [Genome Data Viewer](#)

Transcript information (Ensembl)

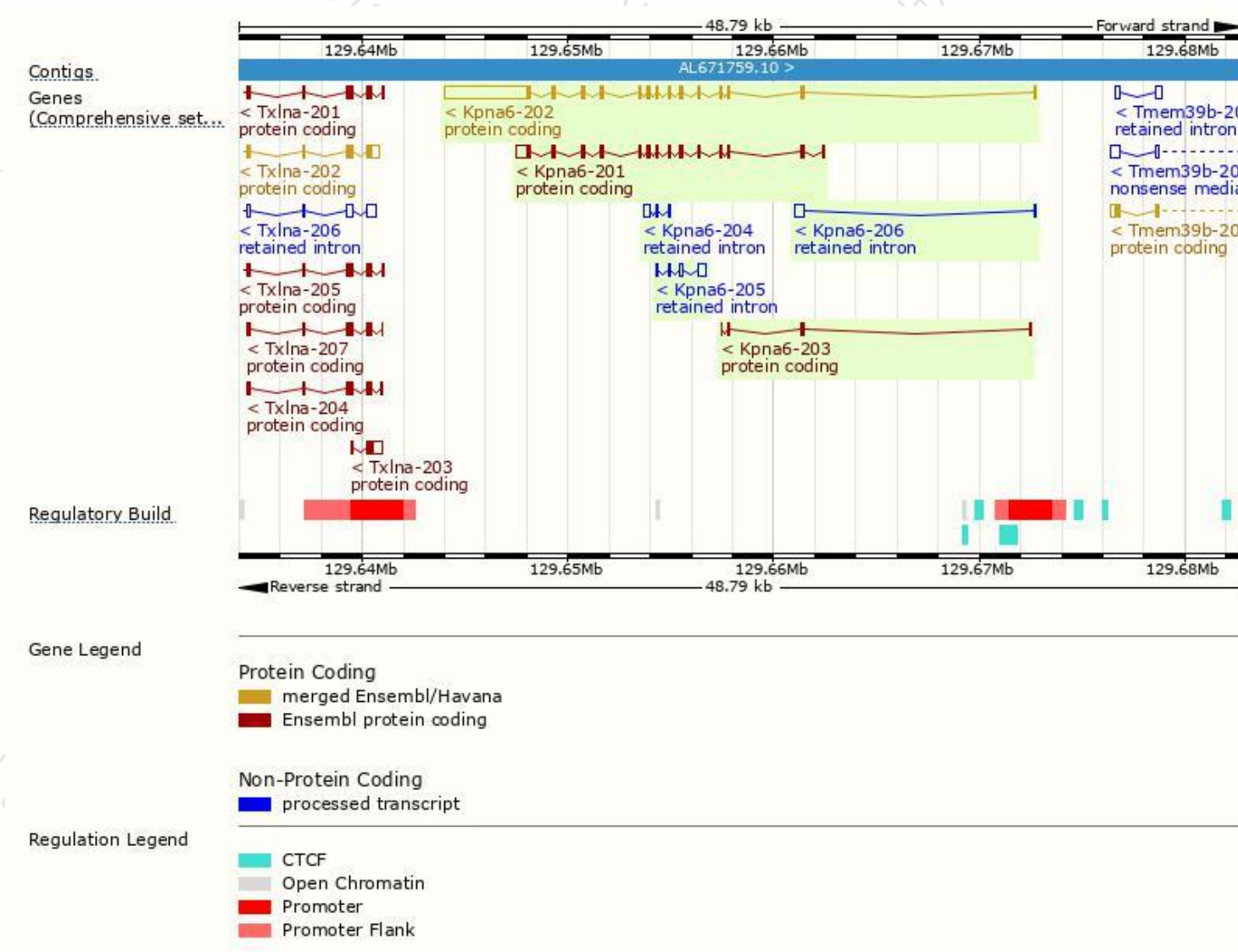
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kpna6-202	ENSMUST00000102590.10	5710	536aa	Protein coding	CCDS18701	Q35345 Q8BH30	TSL:1 GENCODE basic APPRIS P2
Kpna6-201	ENSMUST00000003828.10	2195	533aa	Protein coding	-	Q4FJZ2	TSL:5 GENCODE basic APPRIS ALT 1
Kpna6-203	ENSMUST00000126010.1	389	88aa	Protein coding	-	A2ADZ6	CDS 3' incomplete TSL:3
Kpna6-205	ENSMUST00000146215.1	724	No protein	Retained intron	-	-	TSL:3
Kpna6-206	ENSMUST00000146361.1	534	No protein	Retained intron	-	-	TSL:2
Kpna6-204	ENSMUST00000138916.1	521	No protein	Retained intron	-	-	TSL:3

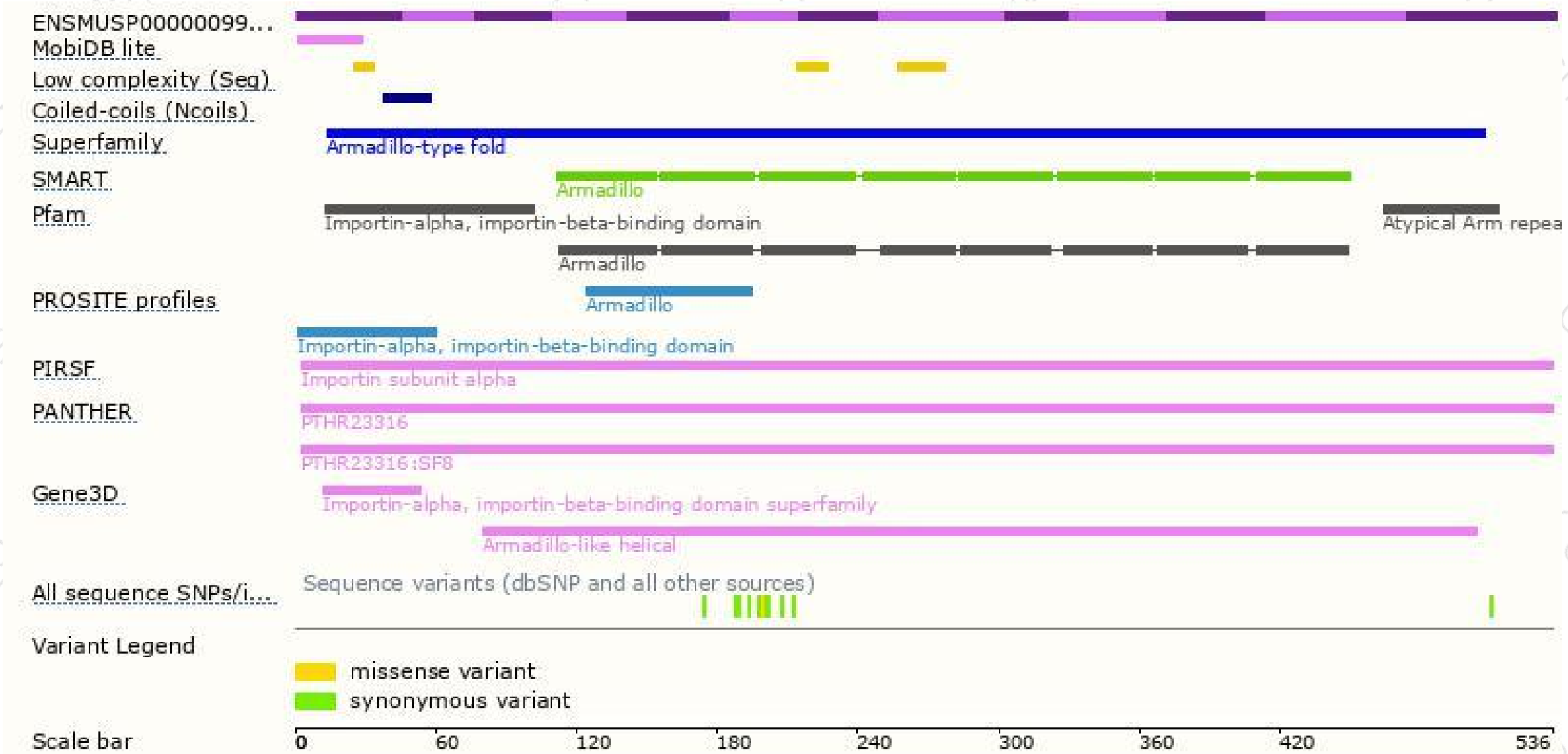
The strategy is based on the design of *Kpna6-202* transcript,The transcription is shown below



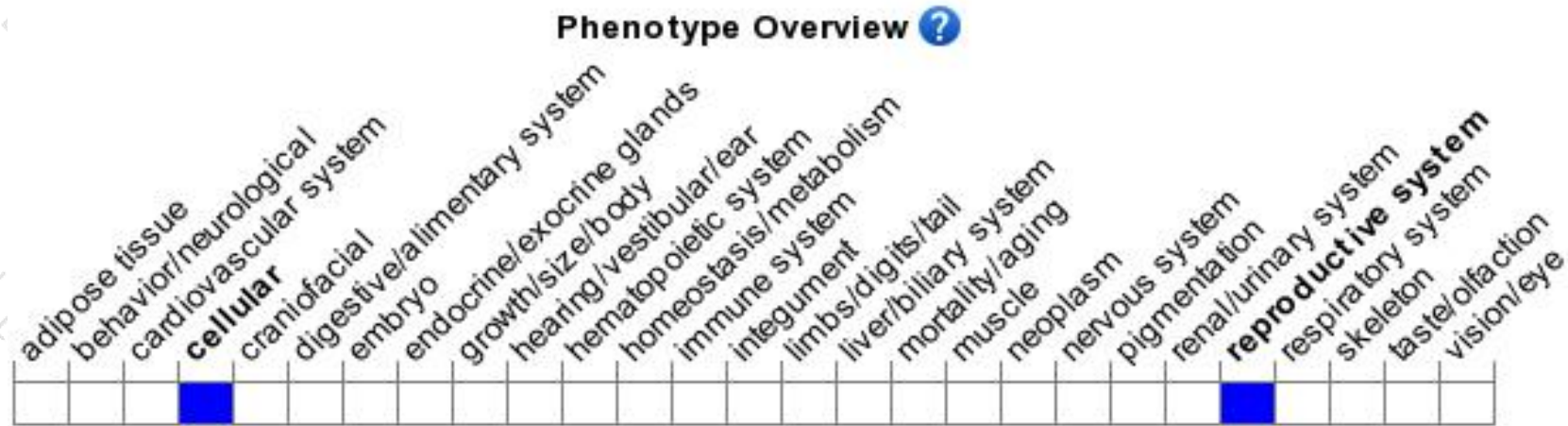
Genomic location distribution



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/>).

According to the existing MGI data, Female mice homozygous for a null mutation are infertile and show a block in zygotic genome activation.

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

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