

# *Atp2c1* Cas9-CKO Strategy

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**Reviewer:** Huimin Su

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# Project Overview

**Project Name**

*Atp2c1*

**Project type**

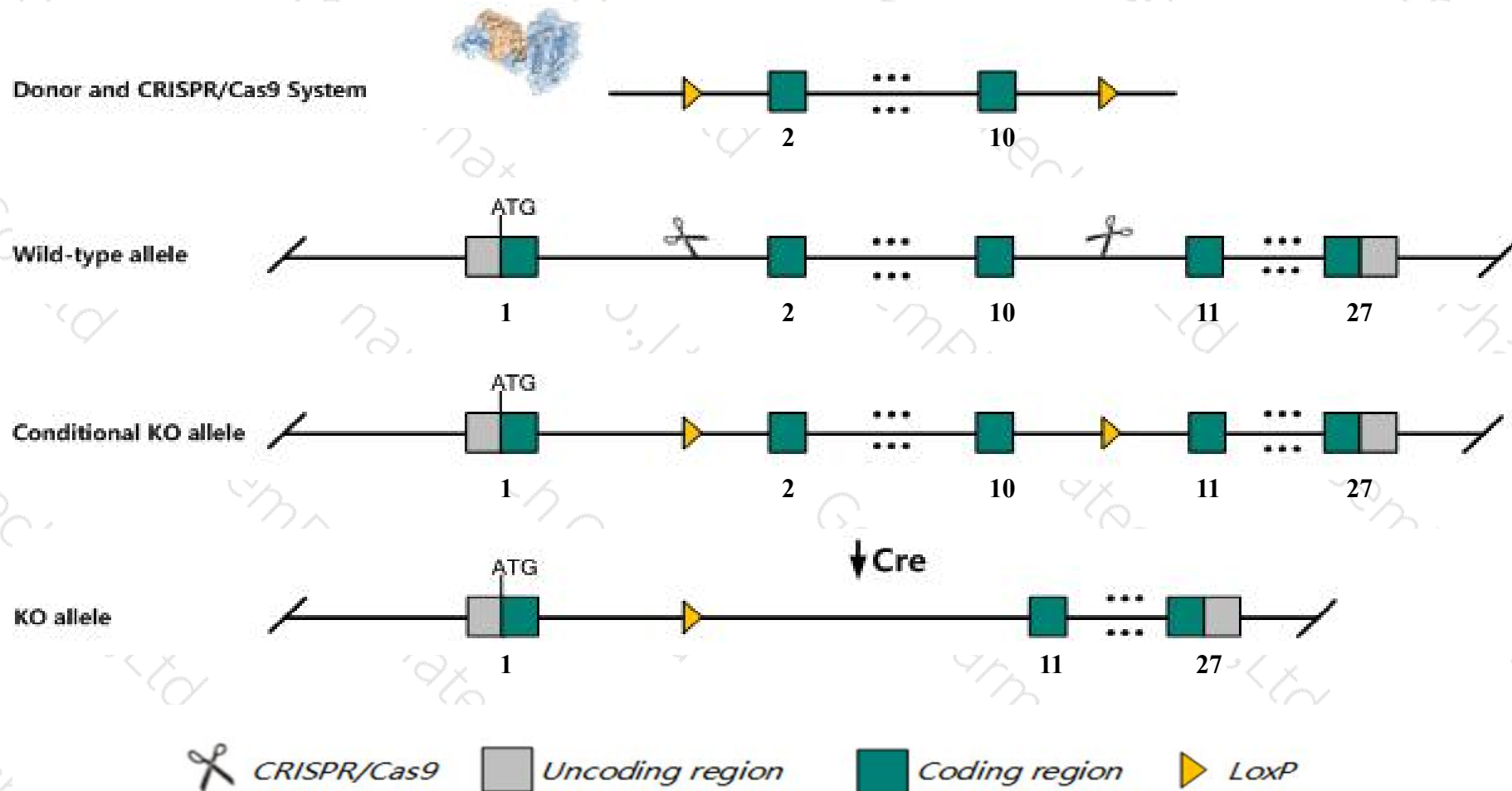
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2c1* gene. The schematic diagram is as follows:



- The *Atp2c1* gene has 21 transcripts. According to the structure of *Atp2c1* gene, exon2-exon10 of *Atp2c1*-202 (ENSMUST00000085133.12) transcript is recommended as the knockout region. The region contains 823bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2c1* 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 knock-out allele show embryonic growth retardation, failure of rostral neural tube closure, golgi and endoplasmic reticulum stress, increased apoptosis, accumulation of intracellular lipid droplets and midgestational lethality. aged heterozygotes develop squamous cell tumors.
- The *Atp2c1* gene is located on the Chr9. 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)

## Atp2c1 ATPase, Ca<sup>++</sup>-sequestering [Mus musculus (house mouse)]

Gene ID: 235574, updated on 13-Mar-2020

### Summary



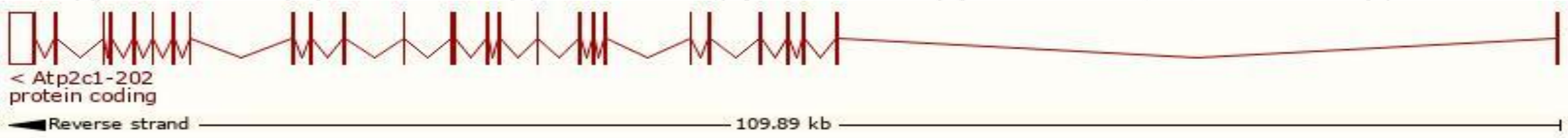
<b>Official Symbol</b>	Atp2c1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ATPase, Ca <sup>++</sup> -sequestering provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1889008</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032570</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1700121J11Rik, ATP2C1A, AW061228, BCPM, D930003G21Rik, HHD, SPCA, pmr1
<b>Expression</b>	Ubiquitous expression in CNS E18 (RPKM 19.7), frontal lobe adult (RPKM 16.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

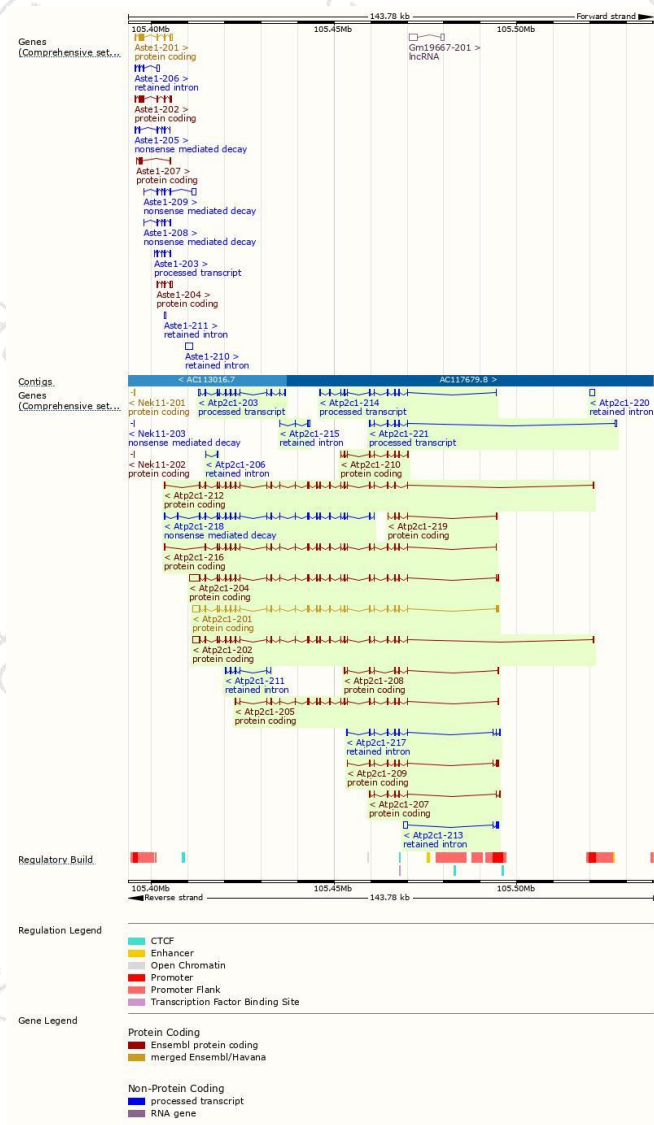
The gene has 21 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2c1-204	<a href="#">ENSMUST00000112558.9</a>	5642	<a href="#">918aa</a>	Protein coding	<a href="#">CCDS40752</a>	<a href="#">Q80XR2</a>	TSL:1 GENCODE basic APPRIS P3
Atp2c1-201	<a href="#">ENSMUST00000038118.14</a>	4876	<a href="#">918aa</a>	Protein coding	<a href="#">CCDS40752</a>	<a href="#">Q80XR2</a>	TSL:1 GENCODE basic APPRIS P3
Atp2c1-202	<a href="#">ENSMUST00000085133.12</a>	4665	<a href="#">952aa</a>	Protein coding	<a href="#">CCDS57698</a>	<a href="#">Q3UZR5</a>	TSL:1 GENCODE basic APPRIS ALT2
Atp2c1-205	<a href="#">ENSMUST00000163879.8</a>	2408	<a href="#">669aa</a>	Protein coding	<a href="#">CCDS57697</a>	<a href="#">Q8BMS7</a>	TSL:1 GENCODE basic
Atp2c1-212	<a href="#">ENSMUST00000176770.7</a>	2781	<a href="#">926aa</a>	Protein coding	-	<a href="#">H3BIX7</a>	TSL:5 GENCODE basic
Atp2c1-216	<a href="#">ENSMUST00000177074.7</a>	2664	<a href="#">887aa</a>	Protein coding	-	<a href="#">H3BL44</a>	TSL:5 GENCODE basic APPRIS ALT2
Atp2c1-209	<a href="#">ENSMUST00000176363.8</a>	1082	<a href="#">230aa</a>	Protein coding	-	<a href="#">H3BJY0</a>	CDS 3' incomplete TSL:5
Atp2c1-210	<a href="#">ENSMUST00000176651.7</a>	899	<a href="#">253aa</a>	Protein coding	-	<a href="#">H3BLC2</a>	CDS 3' incomplete TSL:5
Atp2c1-208	<a href="#">ENSMUST00000176190.7</a>	823	<a href="#">208aa</a>	Protein coding	-	<a href="#">H3BKB1</a>	CDS 3' incomplete TSL:5
Atp2c1-207	<a href="#">ENSMUST00000176036.7</a>	710	<a href="#">177aa</a>	Protein coding	-	<a href="#">H3BJJ5</a>	CDS 3' incomplete TSL:5
Atp2c1-219	<a href="#">ENSMUST00000177334.1</a>	578	<a href="#">111aa</a>	Protein coding	-	<a href="#">H3BJ99</a>	CDS 3' incomplete TSL:5
Atp2c1-218	<a href="#">ENSMUST00000177293.7</a>	2476	<a href="#">786aa</a>	Nonsense mediated decay	-	<a href="#">H3BLI6</a>	CDS 5' incomplete TSL:5
Atp2c1-203	<a href="#">ENSMUST00000112557.8</a>	1514	No protein	Processed transcript	-	-	TSL:1
Atp2c1-214	<a href="#">ENSMUST00000176960.7</a>	1072	No protein	Processed transcript	-	-	TSL:5
Atp2c1-221	<a href="#">ENSMUST00000190802.1</a>	833	No protein	Processed transcript	-	-	TSL:5
Atp2c1-213	<a href="#">ENSMUST00000176787.1</a>	1449	No protein	Retained intron	-	-	TSL:1
Atp2c1-220	<a href="#">ENSMUST00000186495.1</a>	1413	No protein	Retained intron	-	-	TSL:NA
Atp2c1-217	<a href="#">ENSMUST00000177189.7</a>	939	No protein	Retained intron	-	-	TSL:1
Atp2c1-211	<a href="#">ENSMUST00000176656.1</a>	691	No protein	Retained intron	-	-	TSL:3
Atp2c1-215	<a href="#">ENSMUST00000177000.1</a>	642	No protein	Retained intron	-	-	TSL:3
Atp2c1-206	<a href="#">ENSMUST00000175697.1</a>	255	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Atp2c1-202* transcript,the transcription is shown below:

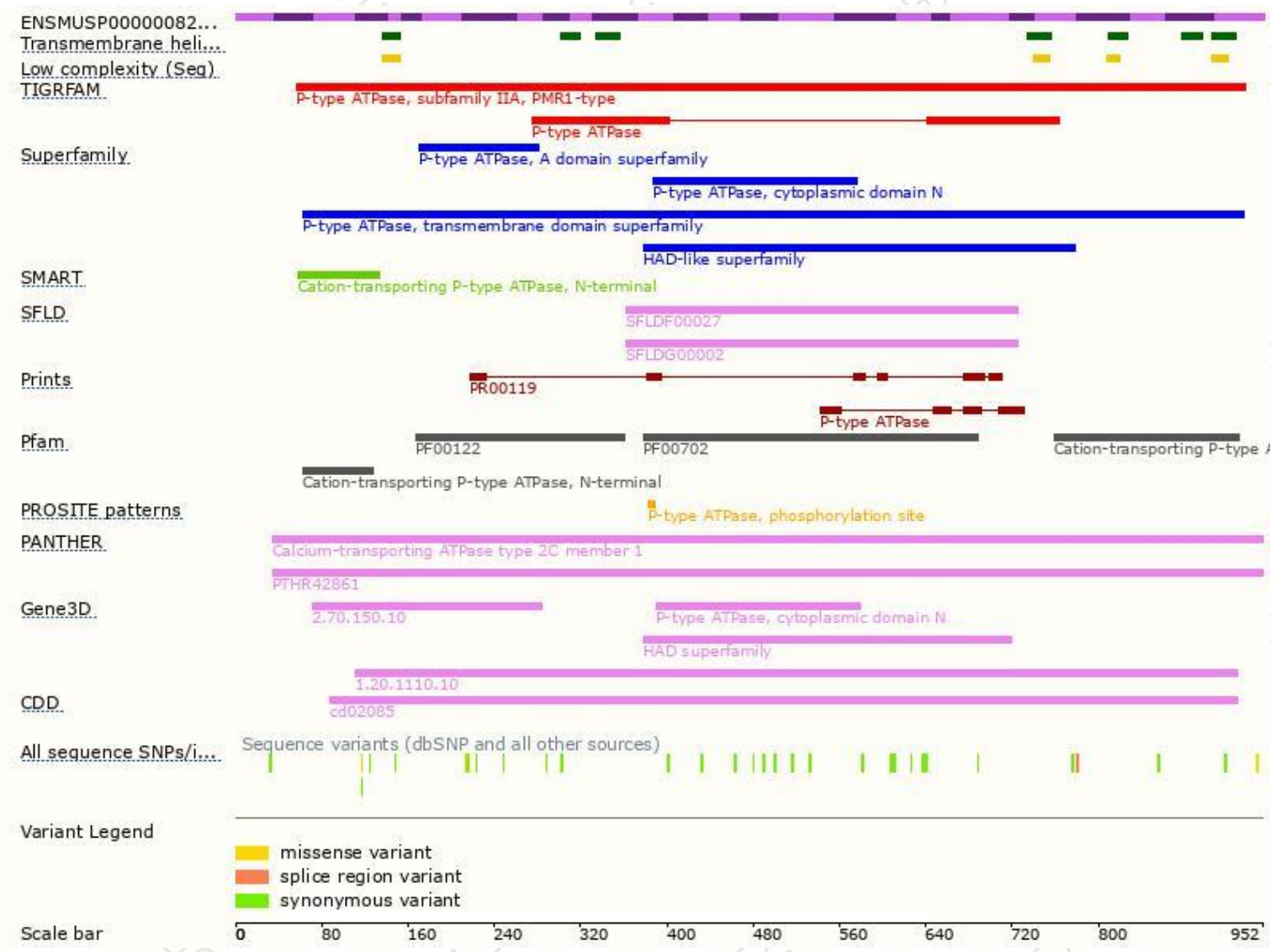


# Genomic location distribution



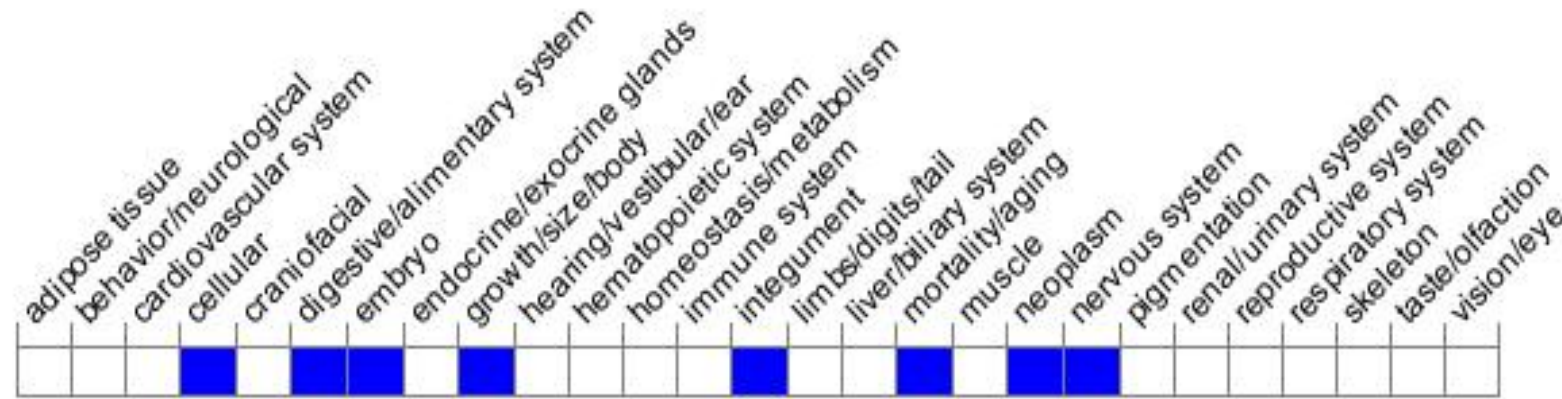


# Protein domain



# Mouse phenotype description(MGI)

Phenotype Overview



*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 knock-out allele show embryonic growth retardation, failure of rostral neural tube closure, Golgi and endoplasmic reticulum stress, increased apoptosis, accumulation of intracellular lipid droplets and midgestational lethality. Aged heterozygotes develop squamous cell tumors.

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

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