

Atp2b1 Cas9-CKO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

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Project Overview

Project Name

Atp2b1

Project type

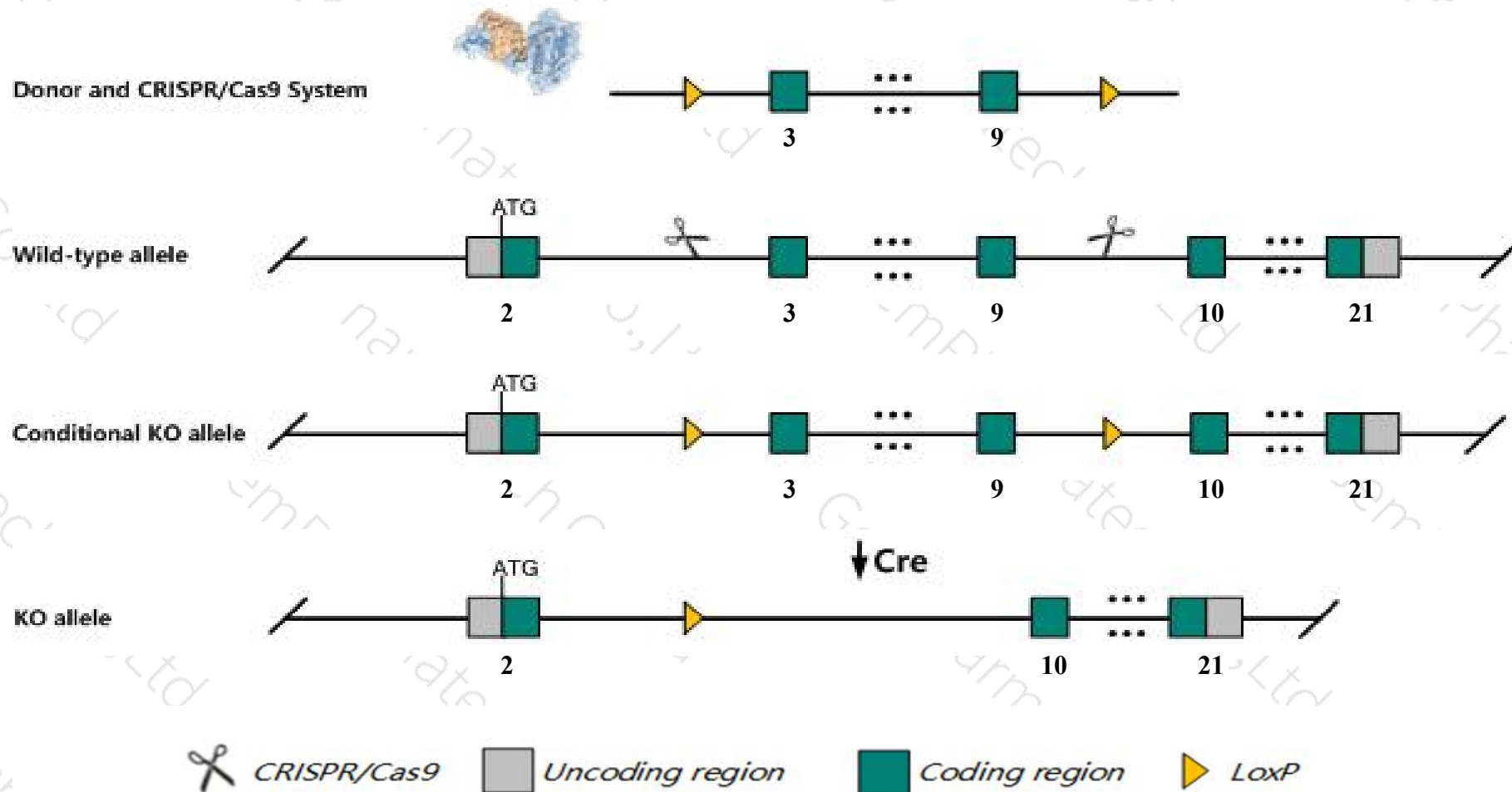
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2b1* gene. The schematic diagram is as follows:



Technical routes

- The *Atp2b1* gene has 11 transcripts. According to the structure of *Atp2b1* gene, exon3-exon9 of *Atp2b1-201* (ENSMUST00000020107.7) transcript is recommended as the knockout region. The region contains 1136bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2b1* 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 complete embryonic lethality between implantation and somite formation. cultured blastocysts form outgrowths with apparent inner cell mass but no trophectoderm or primitive endoderm cells.
- The *Atp2b1* gene is located on the Chr10. 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)

Atp2b1 ATPase, Ca⁺⁺ transporting, plasma membrane 1 [Mus musculus (house mouse)]

Gene ID: 67972, updated on 13-Mar-2020

Summary



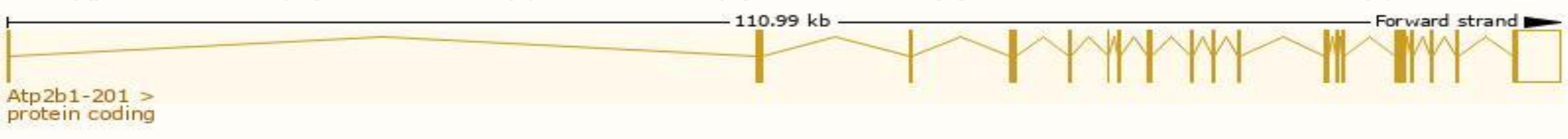
Official Symbol	Atp2b1 provided by MGI
Official Full Name	ATPase, Ca ⁺⁺ transporting, plasma membrane 1 provided by MGI
Primary source	MGI:MGI:104653
See related	Ensembl:ENSMUSG00000019943
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810442I22Rik, E130111D10Rik, Pmca1
Expression	Broad expression in frontal lobe adult (RPKM 30.2), cortex adult (RPKM 27.6) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

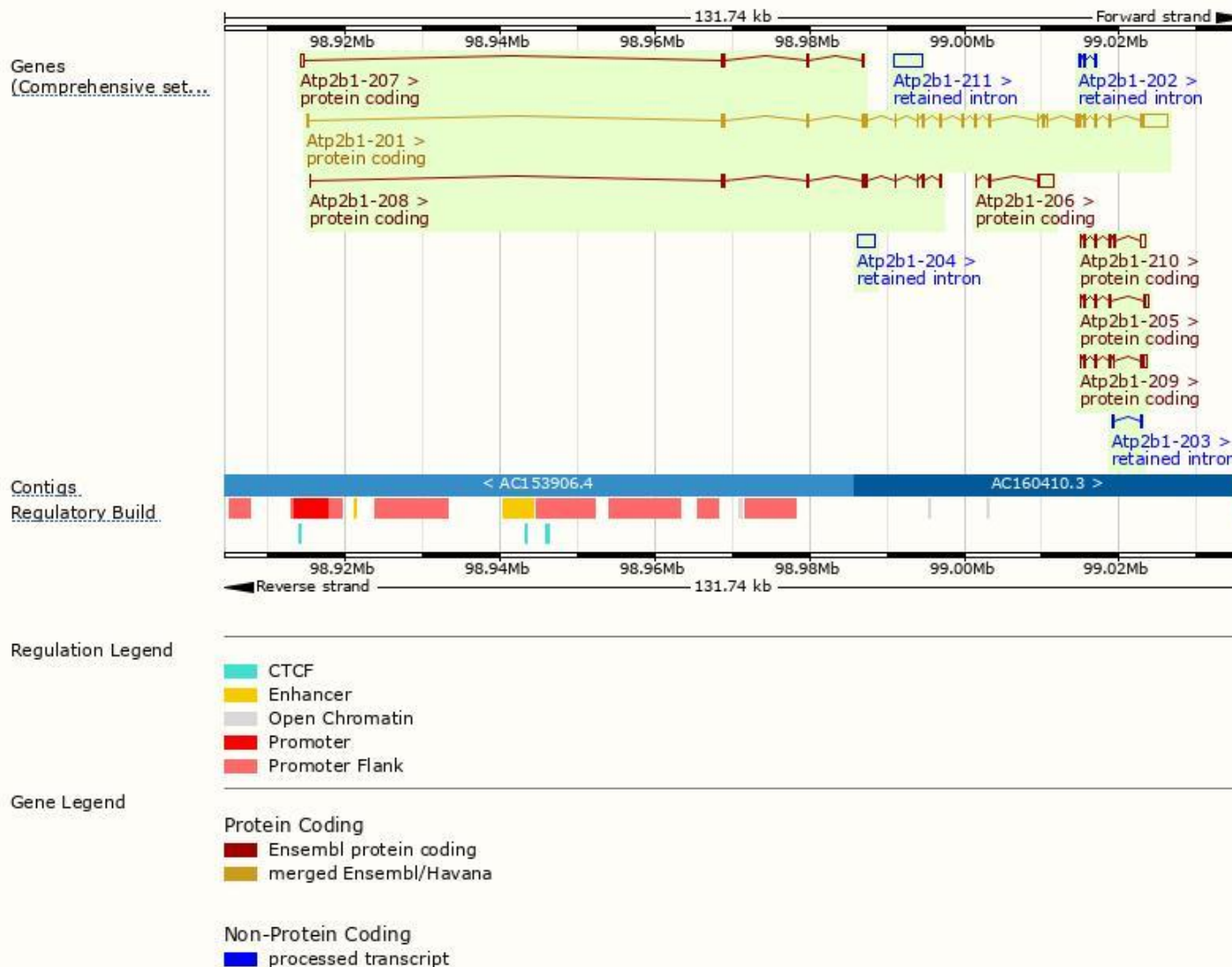
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2b1-201	ENSMUST00000020107.7	7130	1220aa	Protein coding	CCDS24145	G5E829	TSL:5 GENCODE basic APPRIS P1
Atp2b1-206	ENSMUST00000219090.1	2393	175aa	Protein coding	-	A0A1W2P867	CDS 5' incomplete TSL:2
Atp2b1-208	ENSMUST00000219624.1	1588	430aa	Protein coding	-	A0A1W2P7C7	CDS 3' incomplete TSL:5
Atp2b1-210	ENSMUST00000220124.1	1460	279aa	Protein coding	-	A0A1W2P882	CDS 5' incomplete TSL:5
Atp2b1-209	ENSMUST00000220104.1	1404	317aa	Protein coding	-	A0A1W2P772	CDS 5' incomplete TSL:5
Atp2b1-207	ENSMUST00000219557.1	1249	212aa	Protein coding	-	A0A1W2P7R3	CDS 3' incomplete TSL:2
Atp2b1-205	ENSMUST00000218948.1	1224	245aa	Protein coding	-	A0A1W2P6X7	CDS 5' incomplete TSL:5
Atp2b1-211	ENSMUST00000220358.1	3688	No protein	Retained intron	-	-	TSL:NA
Atp2b1-204	ENSMUST00000218695.1	2334	No protein	Retained intron	-	-	TSL:NA
Atp2b1-202	ENSMUST00000218312.1	604	No protein	Retained intron	-	-	TSL:3
Atp2b1-203	ENSMUST00000218419.1	454	No protein	Retained intron	-	-	TSL:3

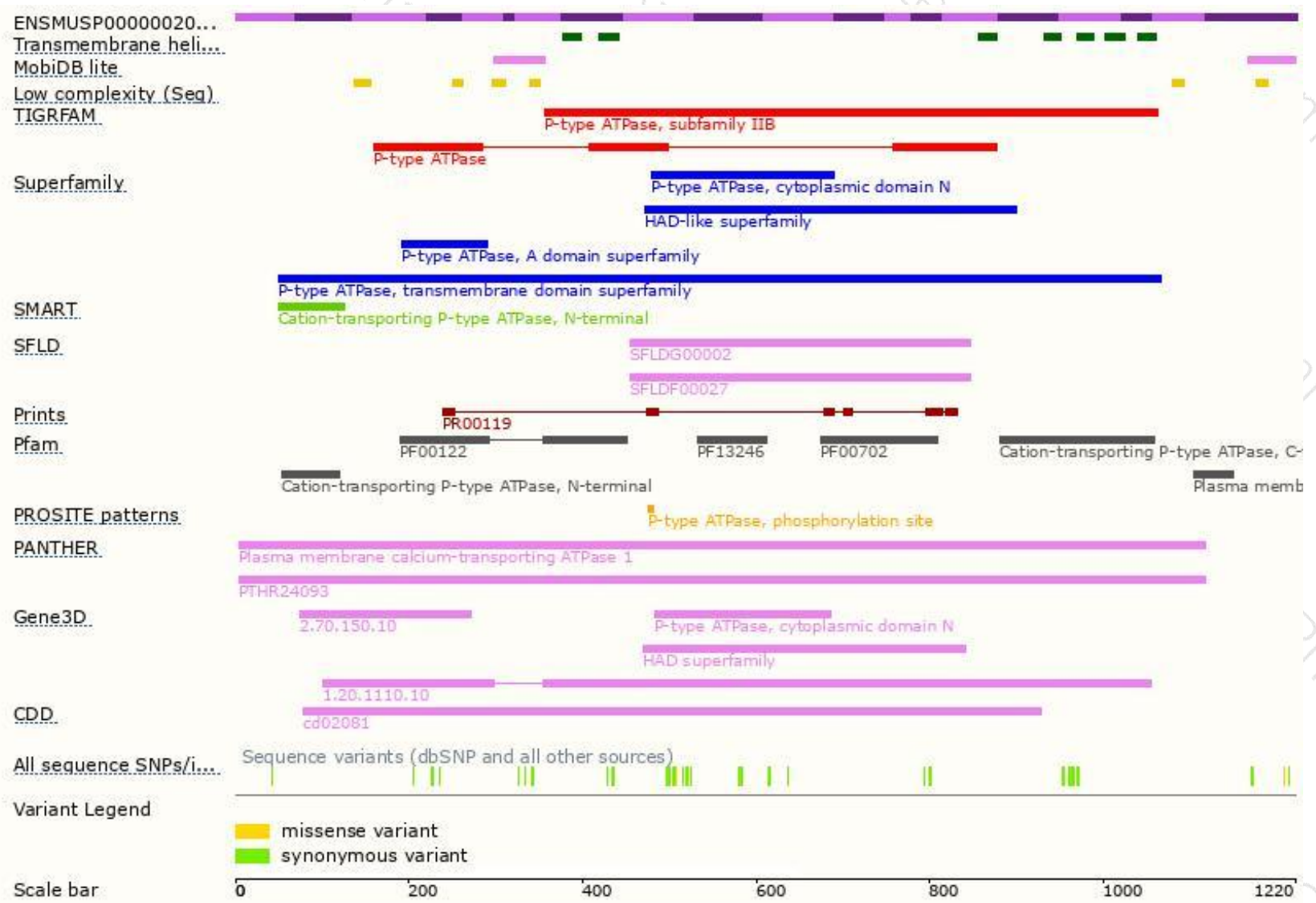
The strategy is based on the design of *Atp2b1-201* transcript,the transcription is shown below:



Genomic location distribution

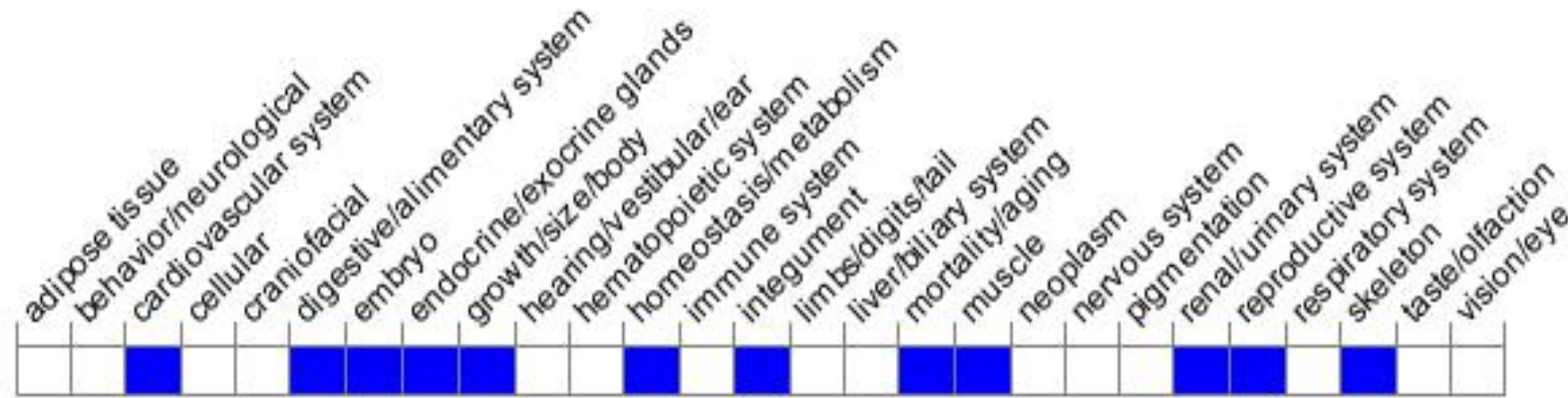


Protein domain



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 complete embryonic lethality between implantation and somite formation. Cultured blastocysts form outgrowths with apparent inner cell mass but no trophectoderm or primitive endoderm cells.

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

Tel: 400-9660890

