

# *Ctsk* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Ctsk*

**Project type**

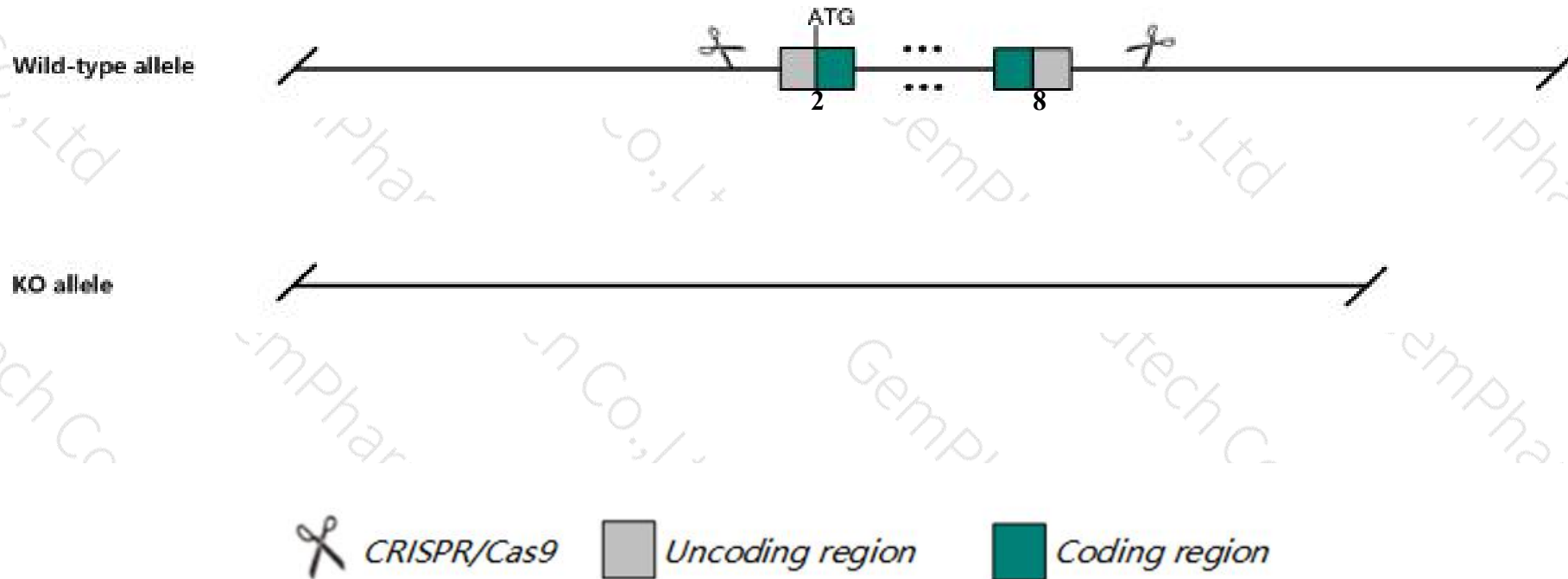
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Ctsk* gene has 1 transcript. According to the structure of *Ctsk* gene, exon2-exon8 of *Ctsk-201* (ENSMUST00000015664.4) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ctsk* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for disruptions in this gene survive well and are fertile. They have osteopetrosis, reduced levels of thyroxine and increased pulmonary fibrosis.
- The *Ctsk* gene is located on the Chr3. 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)

## Ctsk cathepsin K [Mus musculus (house mouse)]

Gene ID: 13038, updated on 23-Mar-2019

### Summary



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

**Official Full Name** cathepsin K provided by [MGI](#)

**Primary source** [MGI:MGI:107823](#)

**See related** [Ensembl:ENSMUSG00000028111](#)

**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** AI323530, MMS10-Q, Ms10q, catK

**Summary** This gene encodes a member of the cathepsin family of cysteine proteases that is highly expressed in osteoclasts and is involved in the degradation of collagen and other matrix proteins in bone. The encoded preproprotein undergoes proteolytic processing to generate a mature, functional enzyme. Mice lacking the encoded protein exhibit phenotypic features of pycnodysostosis such as increased bone density and bone deformity, which become progressively more pronounced with age. [provided by RefSeq, Jan 2016]

**Expression** Biased expression in bladder adult (RPKM 27.4), limb E14.5 (RPKM 13.7) and 12 other tissues [See more](#)

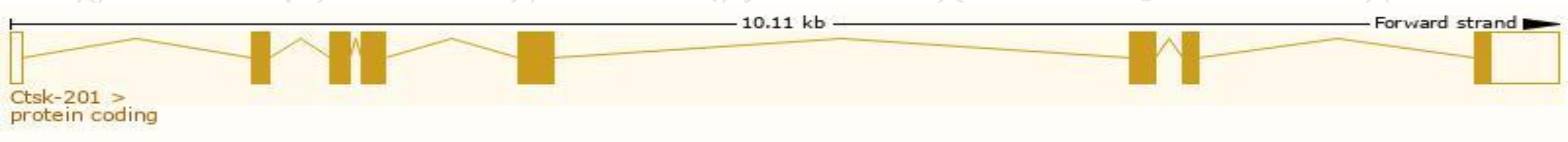
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

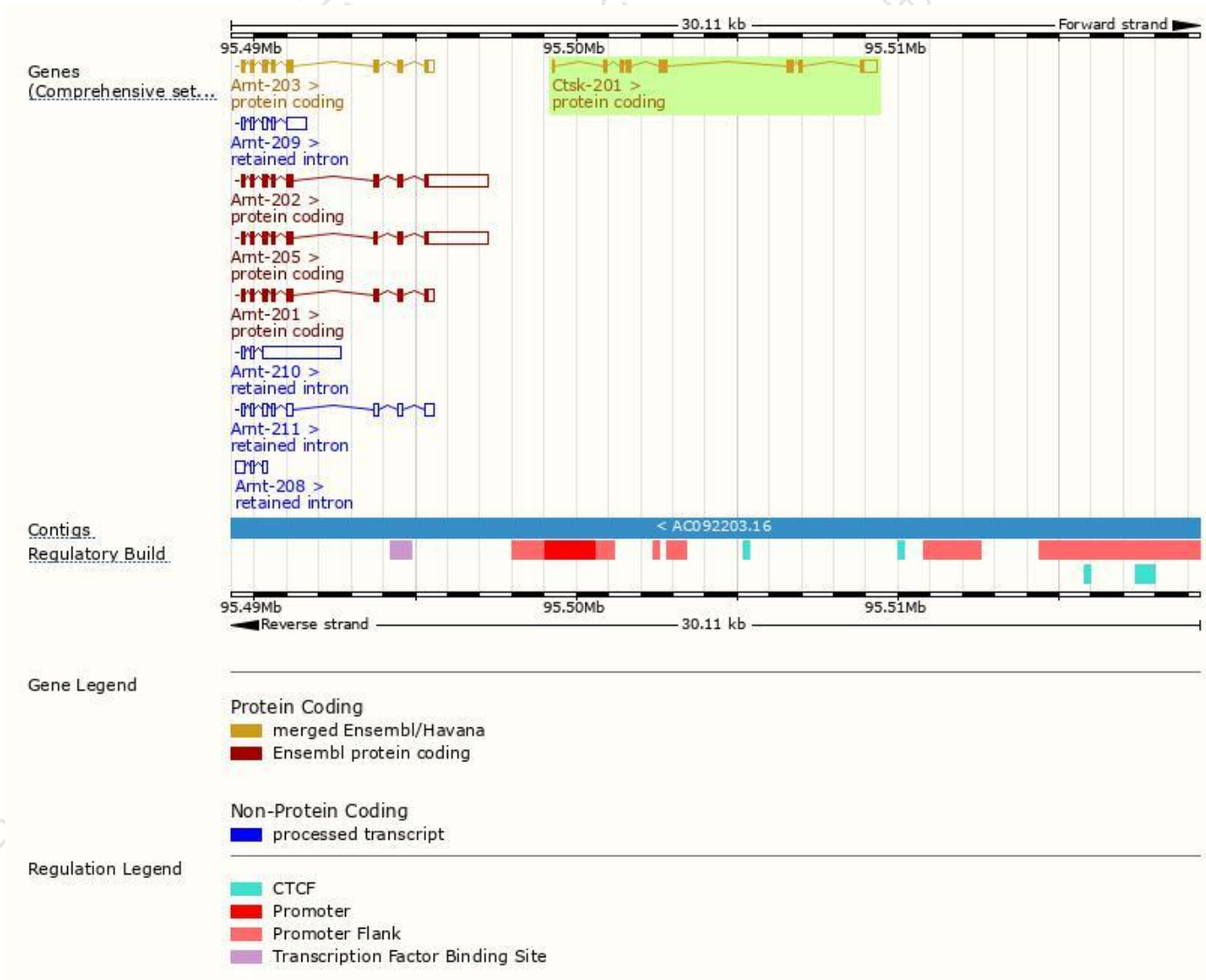
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ctsk-201	<a href="#">ENSMUST00000015664.4</a>	1512	<a href="#">329aa</a>	Protein coding	<a href="#">CCDS17615</a>	<a href="#">P55097 Q545T0</a>	TSL:1 GENCODE basic APPRIS P1

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

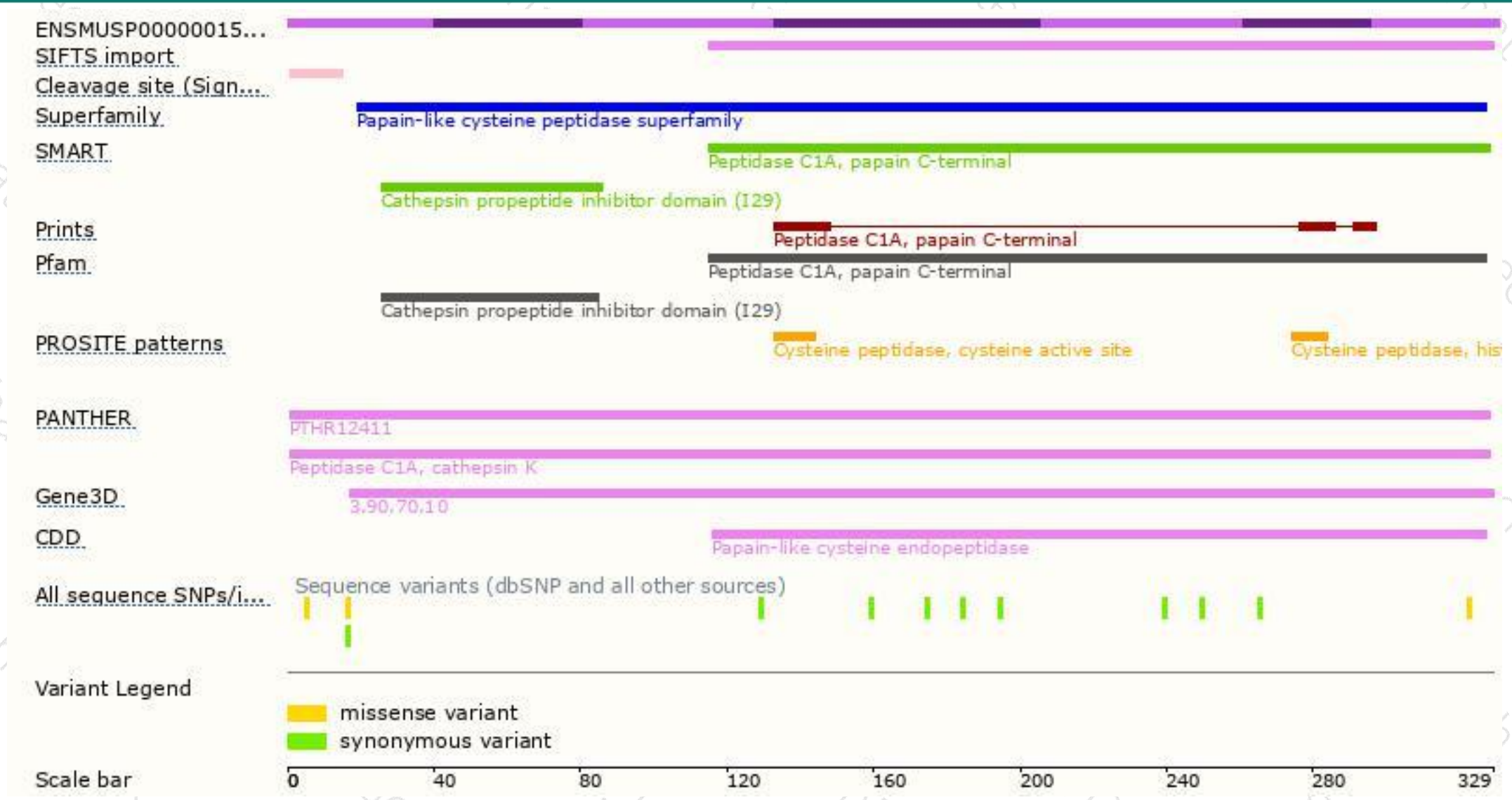


# Genomic location distribution

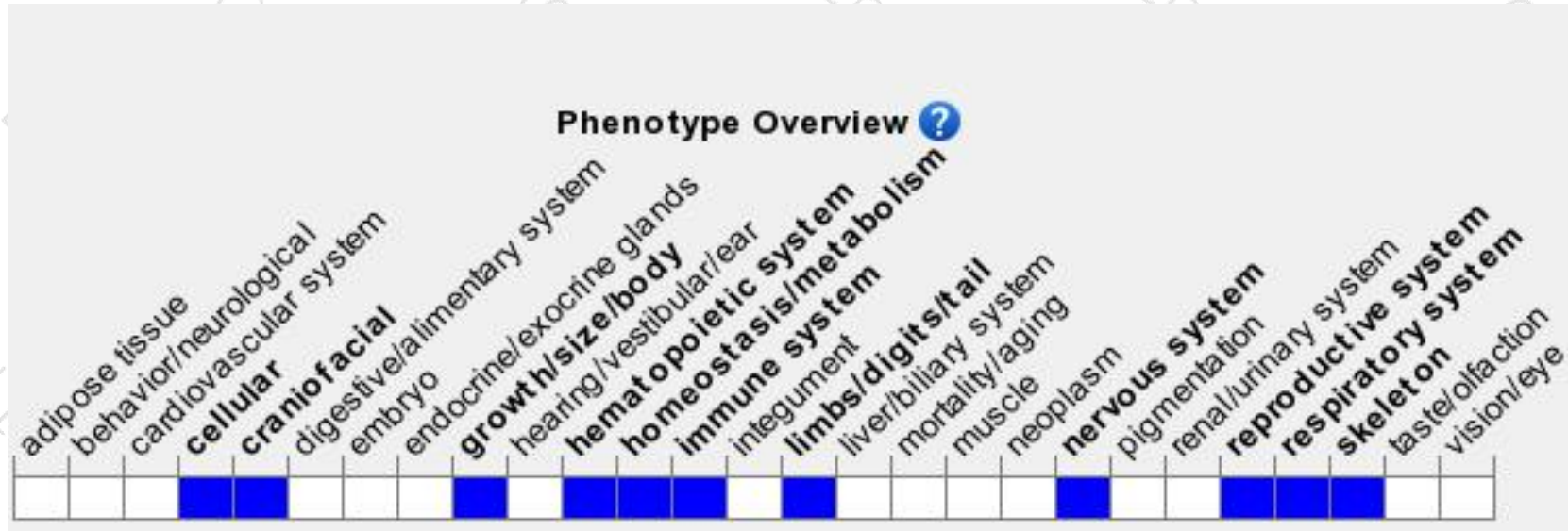




# Protein domain



# 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, Mice homozygous for disruptions in this gene survive well and are fertile. They have osteopetrosis, reduced levels of thyroxine and increased pulmonary fibrosis.

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

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