# *Camsap3* Cas9-CKO Strategy

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| **Reviewer:** | **Huimin Su** |
| **Design Date:** | **2019-9-17** |

# Project Overview

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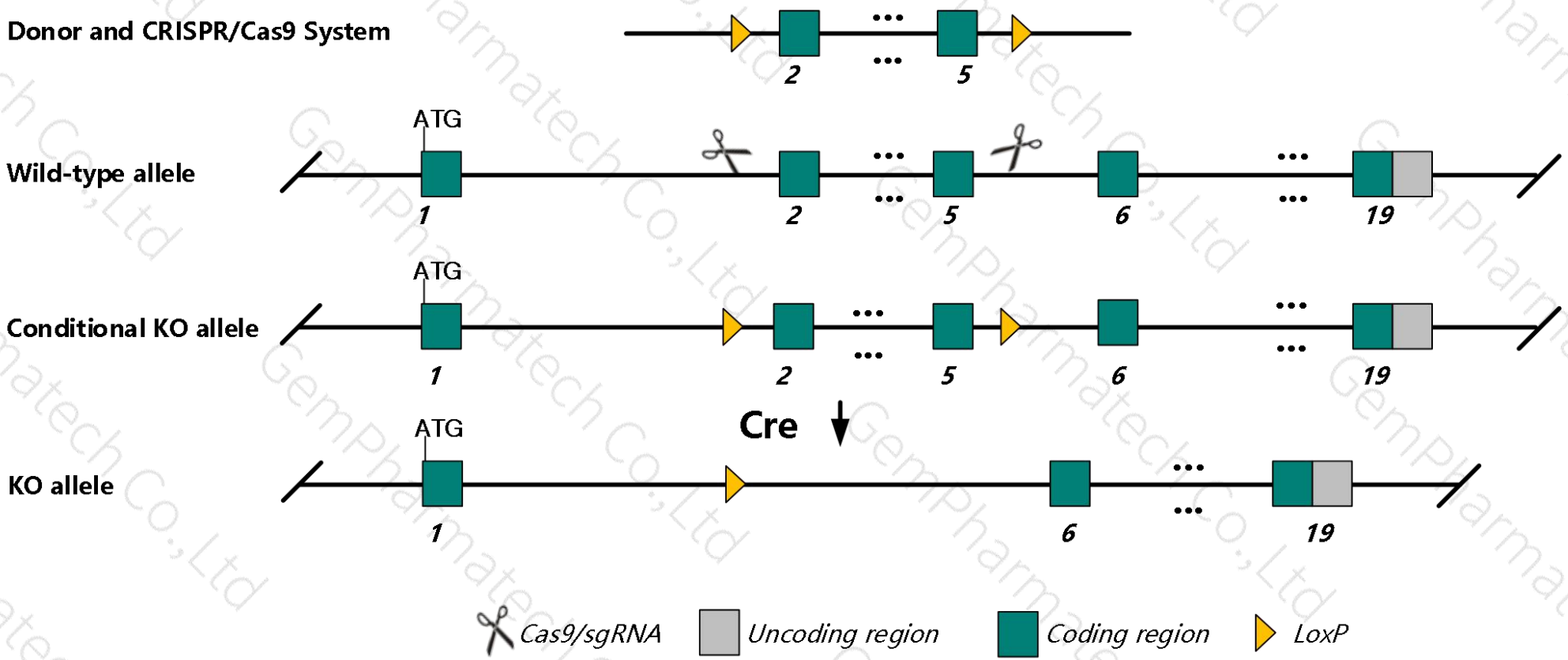
| **Project Name** | ***Camsap3*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Camsap3* gene. The schematic diagram is as follows:



# Technical routes

- The *Camsap3* gene has 12 transcripts. According to the structure of *Camsap3* gene, exon2-exon5 of *Camsap3-205* (ENSMUST00000207432.1) transcript is recommended as the knockout region.The region contains 506 bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Camsap3* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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.

# Notice

- According to the existing MGI data,Mice homozygous for a null allele display variable penetrance of vascular, liver, nervous system, rib and eye abnormalities. Mice homozygous for an allele with loss of microtubule binding show partial lethality, decreased body size and abnormal alignment of microtubles in polarized epithelial cells.

- The *Camsap3* gene is located on the Chr8. 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）

集萃药康 GemPharmatech

**Camsap3 calmodulin regulated spectrin-associated protein family, member 3 [ *Mus musculus* (house mouse) ]**

Gene ID: 69697, updated on 14-Aug-2019

**Summary**

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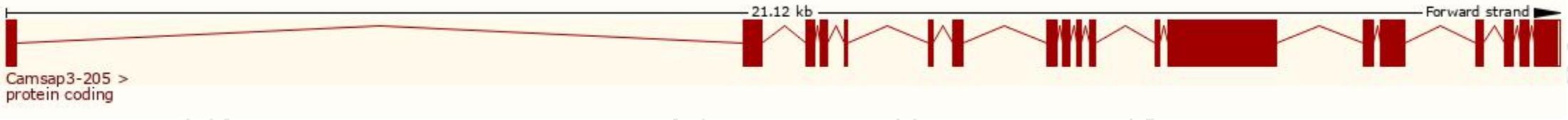
| **Official Symbol** | Camsap3 provided by MGI |
| **Official Full Name** | calmodulin regulated spectrin-associated protein family, member 3 provided by MGI |
| **Primary source** | MGI:MGI:1916947 |
| **See related** | Ensembl:ENSMUSG00000044433 |
| **Gene type** | protein coding |
| **RefSeq status** | 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** | Nezha; Kiaa1543; 2310057J16Rik |
| **Expression** | Broad expression in colon adult (RPKM 25.0), small intestine adult (RPKM 23.5) and 23 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

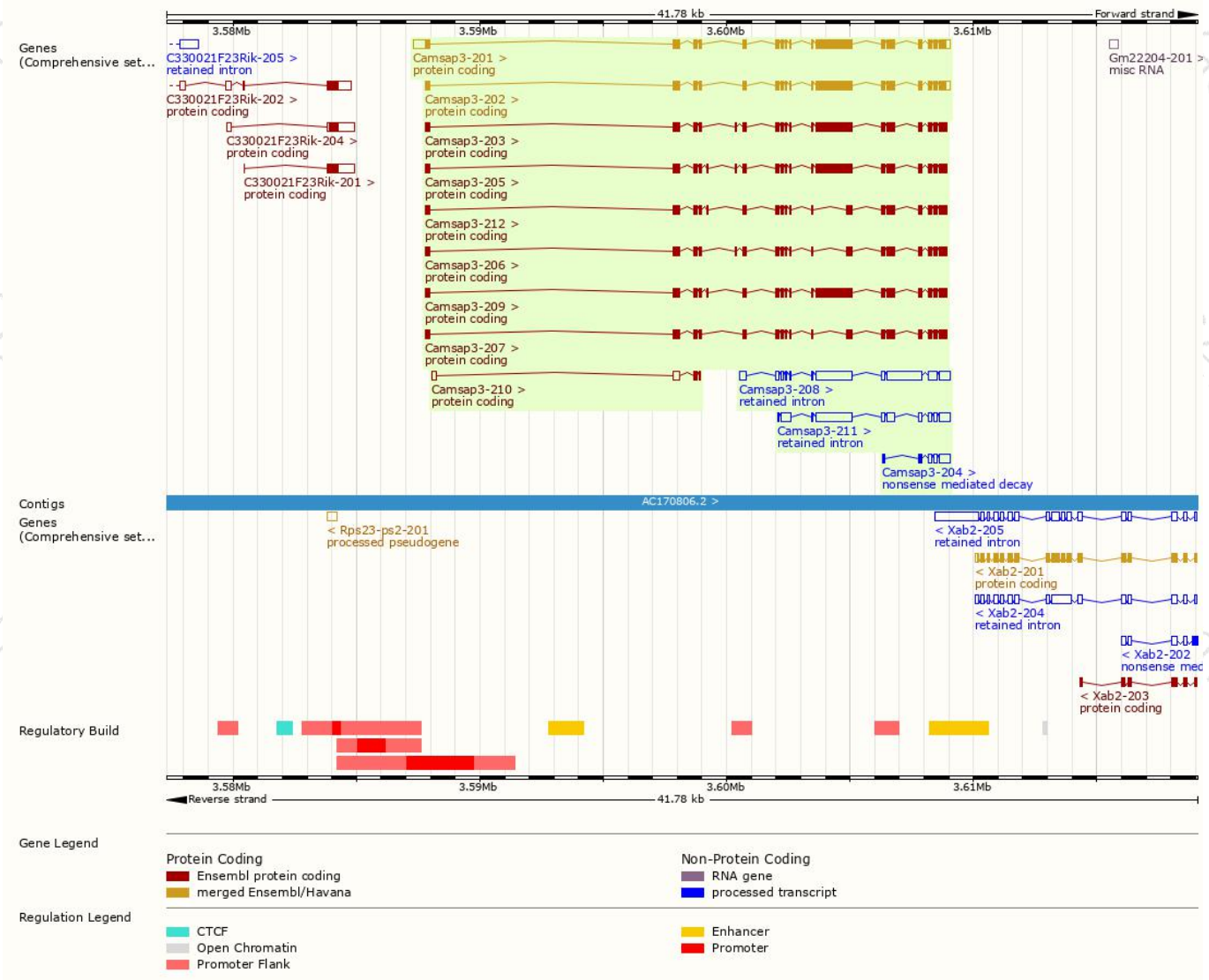
The gene has 12 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Camsap3-201 | ENSMUST00000057028.14 | 4450 | 1252aa | Protein coding | CCDS22064 | Q80VC9 | TSL:1 GENCODE basic APPRIS P3 |
| Camsap3-202 | ENSMUST00000171962.2 | 3925 | 1253aa | Protein coding | CCDS52469 | Q80VC9 | TSL:1 GENCODE basic APPRIS ALT2 |
| Camsap3-205 | ENSMUST00000207432.1 | 3865 | 1279aa | Protein coding | CCDS85488 | Q80VC9 | TSL:1 GENCODE basic APPRIS ALT2 |
| Camsap3-203 | ENSMUST00000207077.1 | 3832 | 1268aa | Protein coding | CCDS85490 | Q80VC9 | TSL:1 GENCODE basic APPRIS ALT2 |
| Camsap3-209 | ENSMUST00000207970.1 | 3817 | 1263aa | Protein coding | CCDS85489 | Q80VC9 | TSL:1 GENCODE basic APPRIS ALT2 |
| Camsap3-206 | ENSMUST00000207533.1 | 2584 | 852aa | Protein coding | - | Q80VC9 | TSL:1 GENCODE basic |
| Camsap3-212 | ENSMUST00000208240.1 | 2572 | 848aa | Protein coding | - | Q80VC9 | TSL:1 GENCODE basic |
| Camsap3-207 | ENSMUST00000207712.1 | 2539 | 837aa | Protein coding | - | Q80VC9 | TSL:1 GENCODE basic |
| Camsap3-210 | ENSMUST00000208036.1 | 591 | 53aa | Protein coding | - | A0A140LJI9 | CDS 3' incomplete TSL:3 |
| Camsap3-204 | ENSMUST00000207152.1 | 846 | 47aa | Nonsense mediated decay | - | A0A140LJ93 | CDS 5' incomplete TSL:1 |
| Camsap3-208 | ENSMUST00000207930.1 | 4466 | No protein | Retained intron | - | - | TSL:1 |
| Camsap3-211 | ENSMUST00000208064.1 | 3241 | No protein | Retained intron | - | - | TSL:5 |

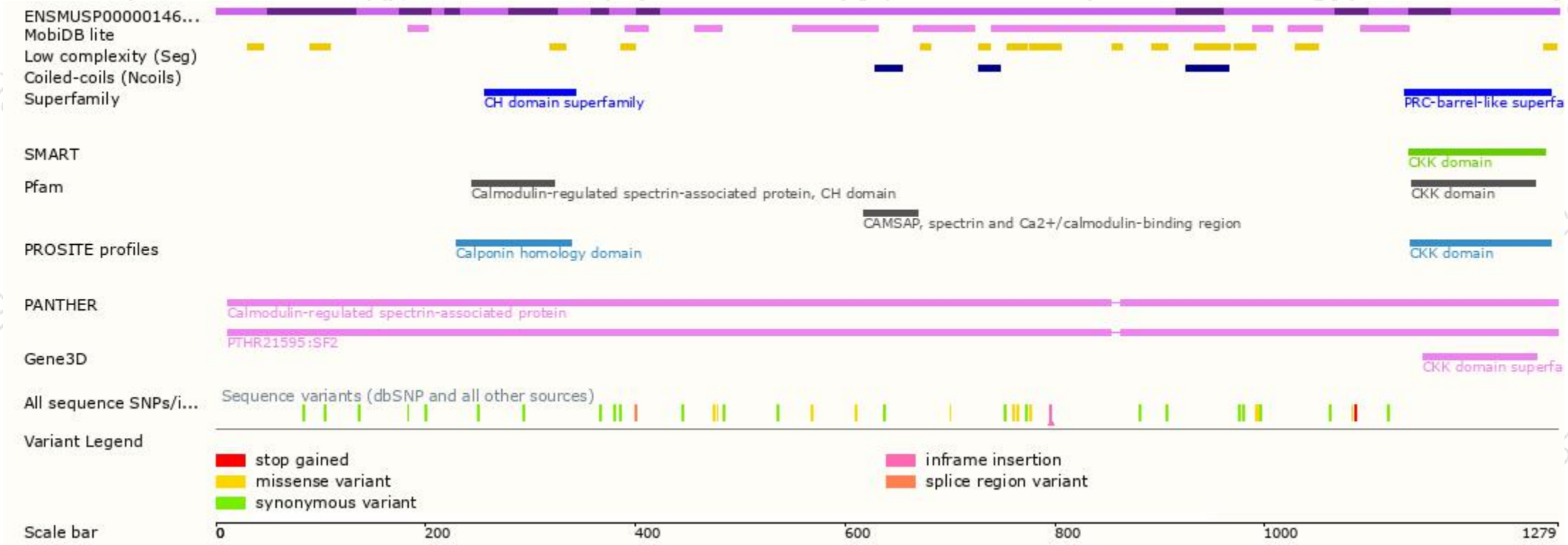
The strategy is based on the design of *Camsap3-205* transcript,The transcription is shown below



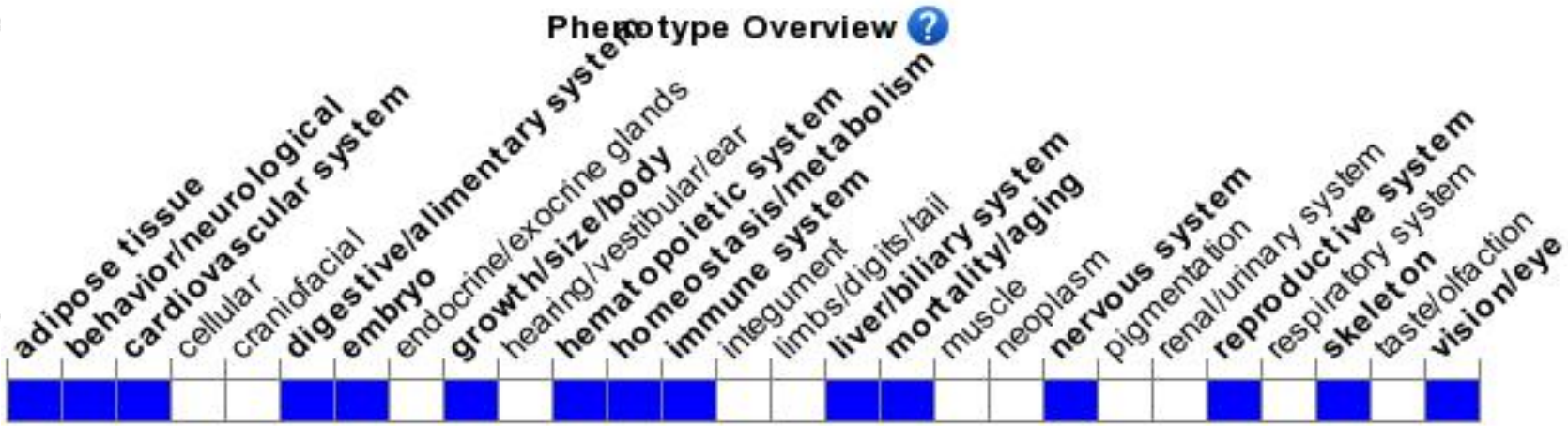
# Genomic location distribution



# 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 a null allele display variable penetrance of vascular, liver, nervous system, rib and eye abnormalities. Mice homozygous for an allele with loss of microtubule binding show partial lethality, decreased body size and abnormal alignment of microtubles in polarized epithelial cells.

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

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