# *Hras* Cas9-KO Strategy

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# Project Overview

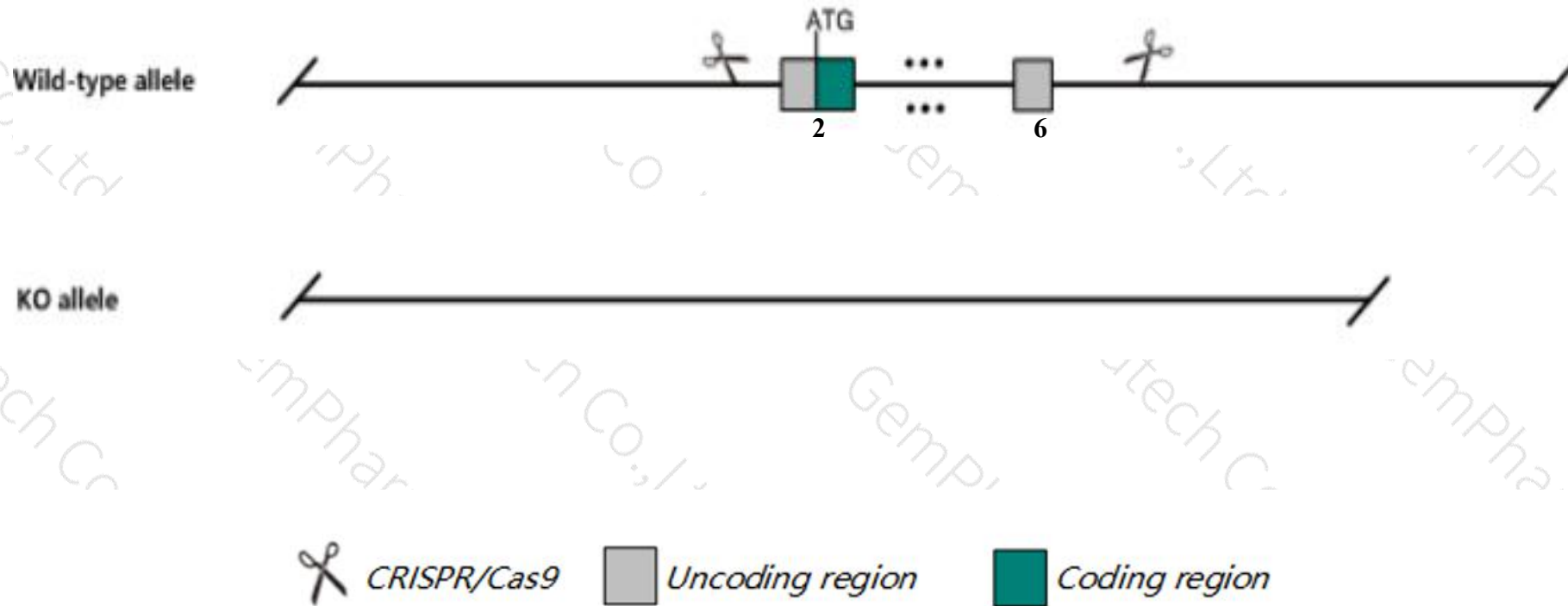| | |
|---|---|
| **Project Name** | *Hras* |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

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

# Technical routes

➢ The *Hras* gene has 7 transcripts. According to the structure of *Hras* gene, exon2-exon6 of *Hras-201*
(ENSMUST00000026572.10) transcript is recommended as the knockout region.The region contains all coding sequence.
Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hras* gene. The brief process is as follows: CRISPR/Cas9 system v

➢ According to the existing MGI data,mice homozygous for targeted null mutations are viable and fertile with no gross morphological or histological abnormalities, defects in neuronal development or defects in lymphocyte cell populations. a decreased susceptibility to dmba induced skin papillomas was also demonstrated.

➢ Knockout the region may affect the function of Lrrc56 gene.

➢ The *Hras* gene is located on the Chr7. 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）

## Hras Harvey rat sarcoma virus oncogene [Mus musculus (house mouse)]

Gene ID: 15461, updated on 13-Mar-2020

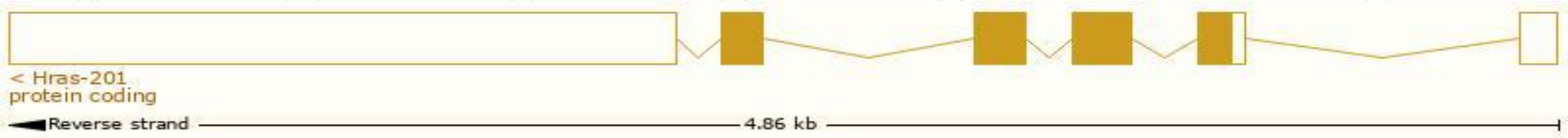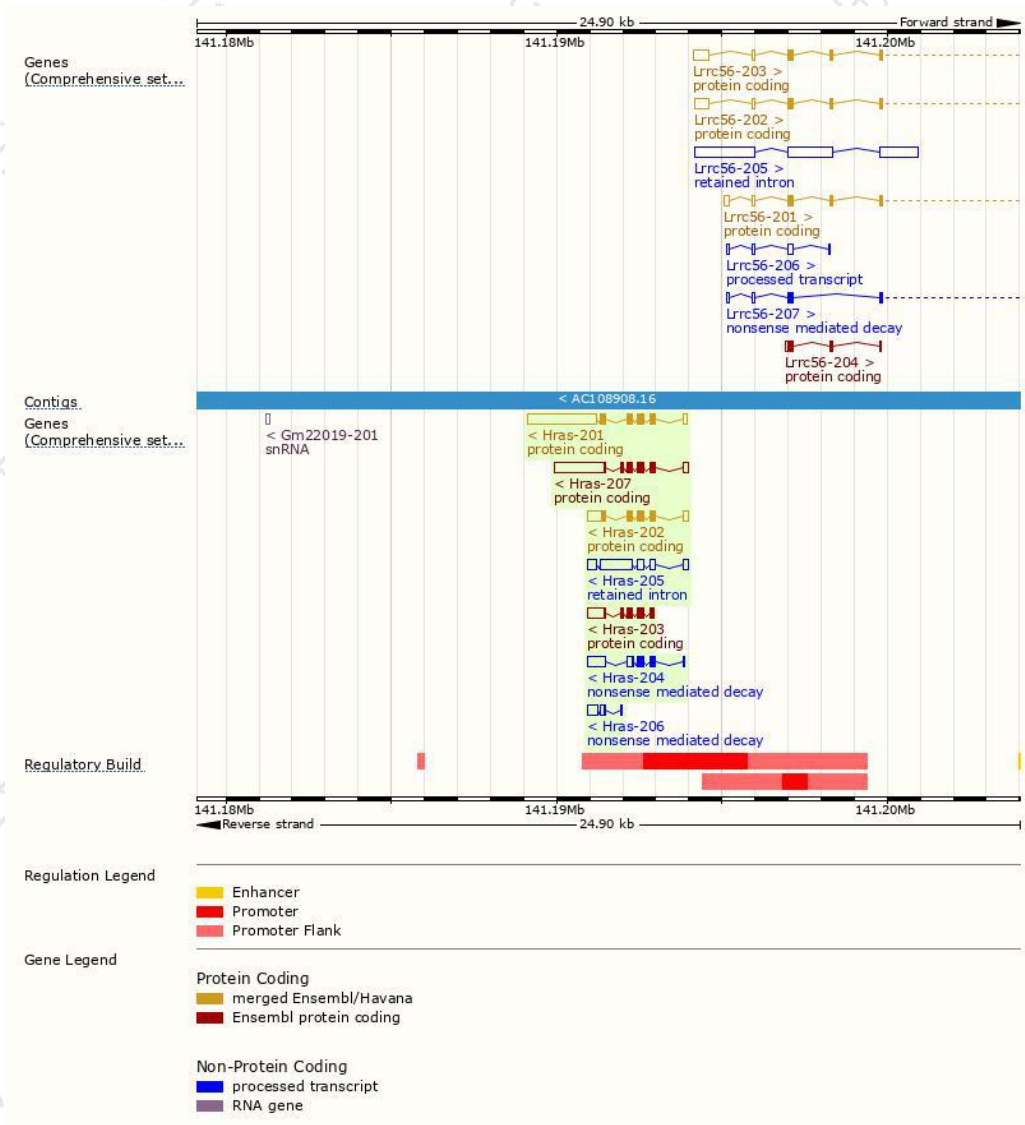| | |
|---|---|
| **Official Symbol** | Hras provided by MGI |
| **Official Full Name** | Harvey rat sarcoma virus oncogene provided by MGI |
| **Primary source** | MGI:MGI:96224 |
| **See related** | Ensembl:ENSMUSG00000025499 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | H-ras, Ha-ras, Harvey-ras, Hras-1, Hras1, Kras2, c-H-ras, c-Ha-ras, c-rasHa, ras |
| **Expression** | Ubiquitous expression in CNS E18 (RPKM 31.5), cortex adult (RPKM 31.3) and 28 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

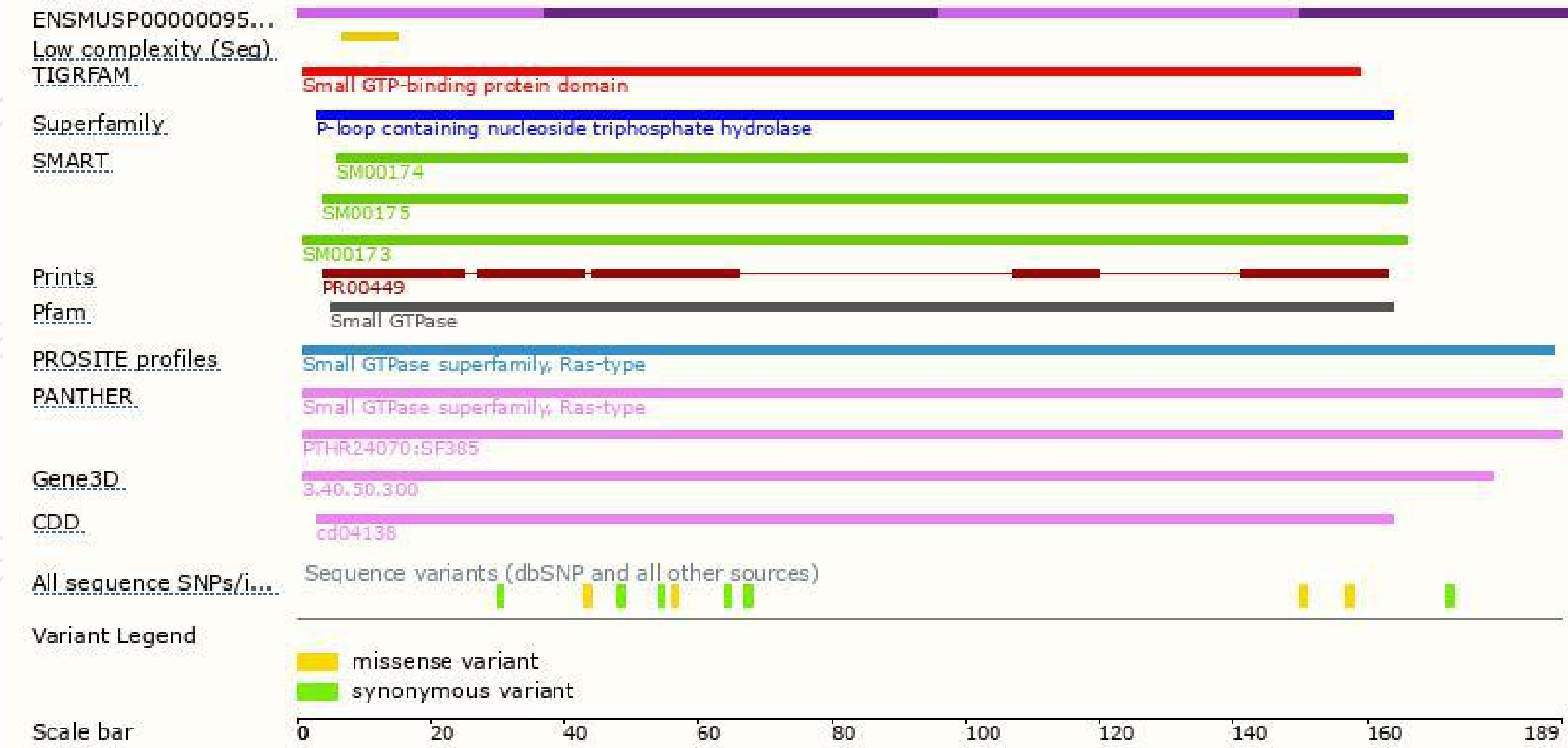| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------|---------------|-----|---------|---------|------|---------|-------|
| Hras-201 | ENSMUST00000026572.10 | 2828 | 189aa | Protein coding | CCDS22003 | Q61411 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Hras-207 | ENSMUST00000168550.7 | 2272 | 188aa | Protein coding | CCDS52439 | Q61411 | TSL:5 GENCODE basic |
| Hras-202 | ENSMUST00000097957.10 | 1199 | 189aa | Protein coding | CCDS22003 | Q61411 | TSL:2 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Hras-203 | ENSMUST00000124314.2 | 1073 | 188aa | Protein coding | CCDS52439 | Q61411 | TSL:5 GENCODE basic |
| Hras-204 | ENSMUST00000124971.1 | 1122 | 119aa | Nonsense mediated decay | - | C0H5X4 | TSL:2 |
| Hras-206 | ENSMUST00000134008.1 | 447 | 19aa | Nonsense mediated decay | - | A0A1B0GRN0 | CDS 5' incomplete TSL:5 |
| Hras-205 | ENSMUST00000128993.1 | 1704 | No protein | Retained intron | - | - | TSL:2 |

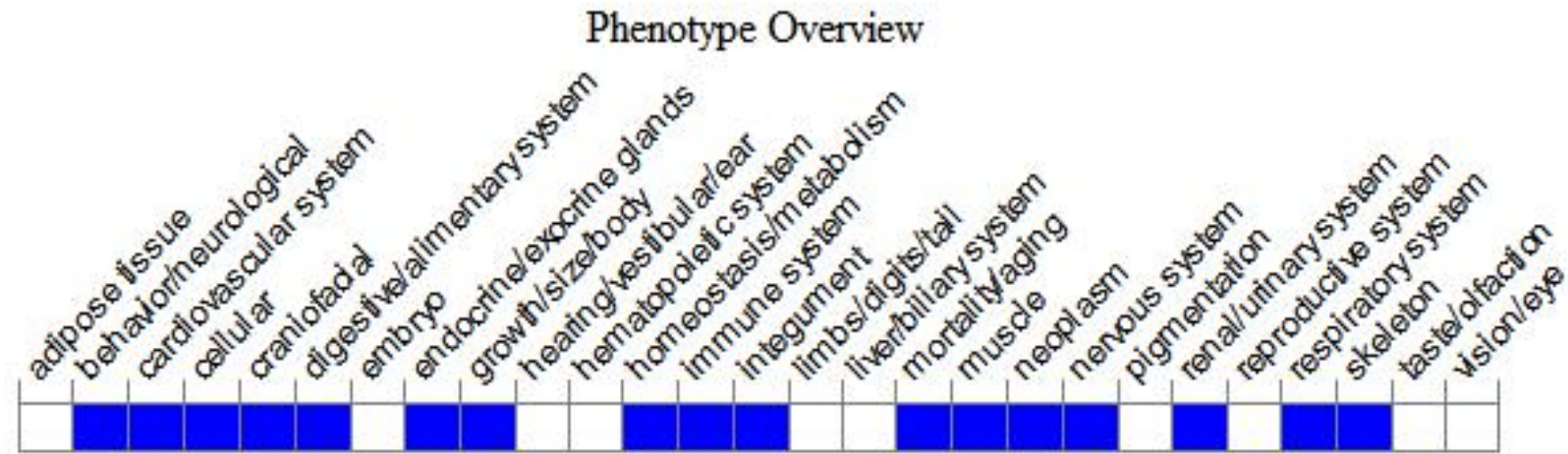The strategy is based on the design of *Hras-201* transcript,the transcription is shown below：



&lt; Hras-201
protein coding

◄ Reverse strand

4.86 kb

# Genomic location distribution

# Protein domain



| | |
|---|---|
| ENSMUSP00000095... | |
| Low complexity (Seg) | |
| TIGRFAM | Small GTP-binding protein domain |
| Superfamily | P-loop containing nucleoside triphosphate hydrolase |
| SMART | SM00174 |
| | SM00175 |
| | SM00173 |
| Prints | PR00449 |
| Pfam | Small GTPase |
| PROSITE profiles | Small GTPase superfamily, Ras-type |
| PANTHER | Small GTPase superfamily, Ras-type |
| | PTHR24070:SF385 |
| Gene3D | 3.40.50.300 |
| CDD | cd04138 |
| All sequence SNPs/i... | Sequence variants (dbSNP and all other sources) |
| Variant Legend | |

missense variant
synonymous variant

Scale bar    0    20    40    60    80    100    120    140    160    189

# 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 targeted null mutations are viable and fertile with no gross morphological or histological abnormalities, defects in neuronal development or defects in lymphocyte cell populations. A decreased susceptibility to DMBA induced skin papillomas was also demonstrated.

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