# *Tcf7l1* Cas9-KO Strategy


**Designer:** Yang Zeng
**Reviewer:** Ruirui Zhang


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# Project Overview

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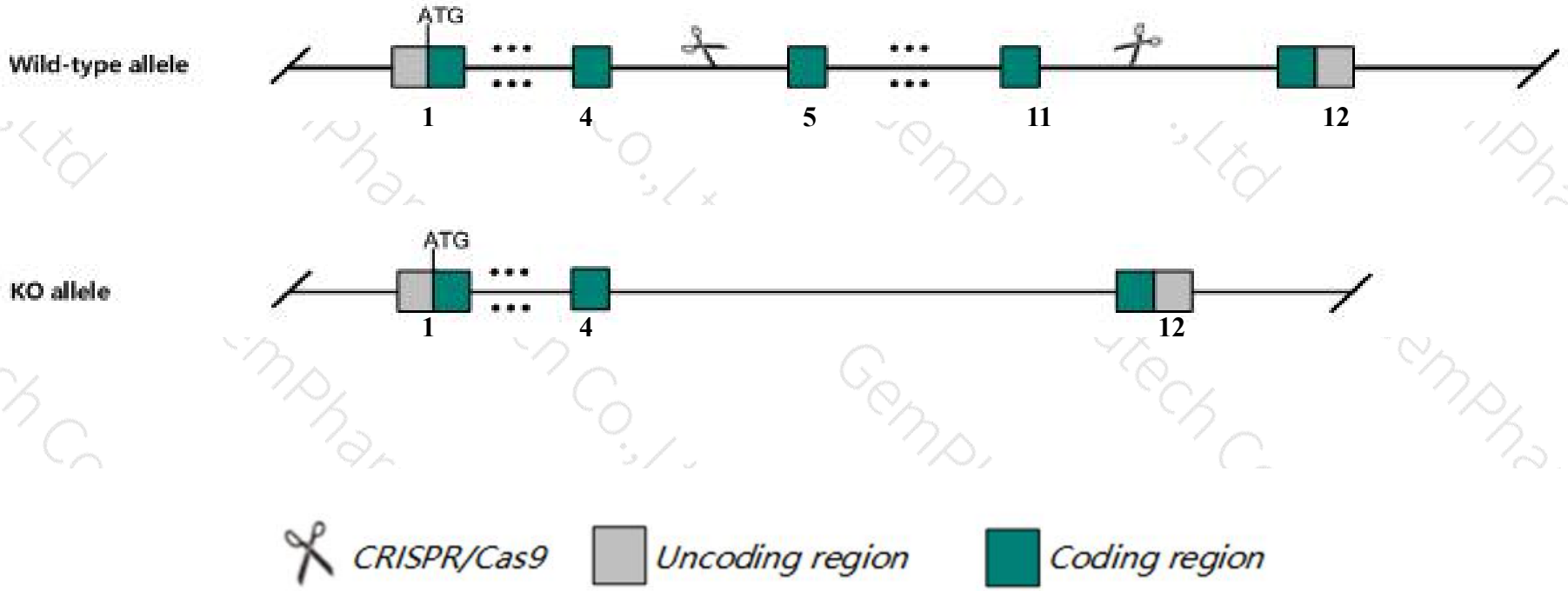
|---|---|
| **Project Name** | ***Tcf7l1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tcf7l1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Tcf7l1* gene has 5 transcripts. According to the structure of *Tcf7l1* gene, exon5-exon11 of *Tcf7l1-201* (ENSMUST00000069536.11) transcript is recommended as the knockout region.The region contains 805bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tcf7l1* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

- According to the existing MGI data,Animals homozygous for a targeted mutation exhibit severe embryological defects particularly affecting the cardiovascular system, nervous system, and digestive system. No homozygous embryos survive beyond E11.

- The KO region contains functional region of the *Gm15401* and *Gm37969* gene. Knockout the region may affect the function of Gm15401 and Gm37969 gene.

- The *Tcf7l1* gene is located on the Chr6. 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）

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## Tcf7l1 transcription factor 7 like 1 (T cell specific, HMG box) [ *Mus musculus* (house mouse) ]

Gene ID: 21415, updated on 24-Dec-2019

### Summary

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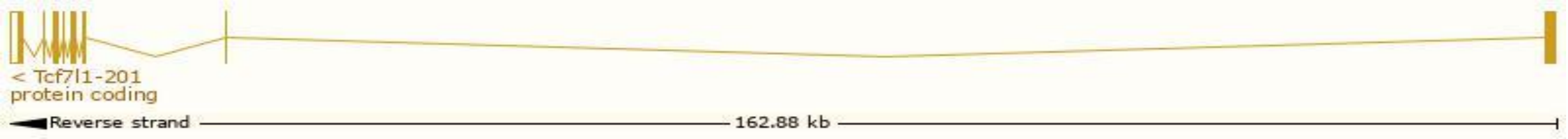
|---|---|
| **Official Symbol** | Tcf7l1 provided by MGI |
| **Official Full Name** | transcription factor 7 like 1 (T cell specific, HMG box) provided by MGI |
| **Primary source** | MGI:MGI:1202876 |
| **See related** | Ensembl:ENSMUSG00000055799 |
| **Gene type** | protein coding |
| **RefSeq status** | 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** | Tcf3; Tcf-3; bHLHb21 |
| **Expression** | Broad expression in colon adult (RPKM 24.3), limb E14.5 (RPKM 24.1) and 24 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

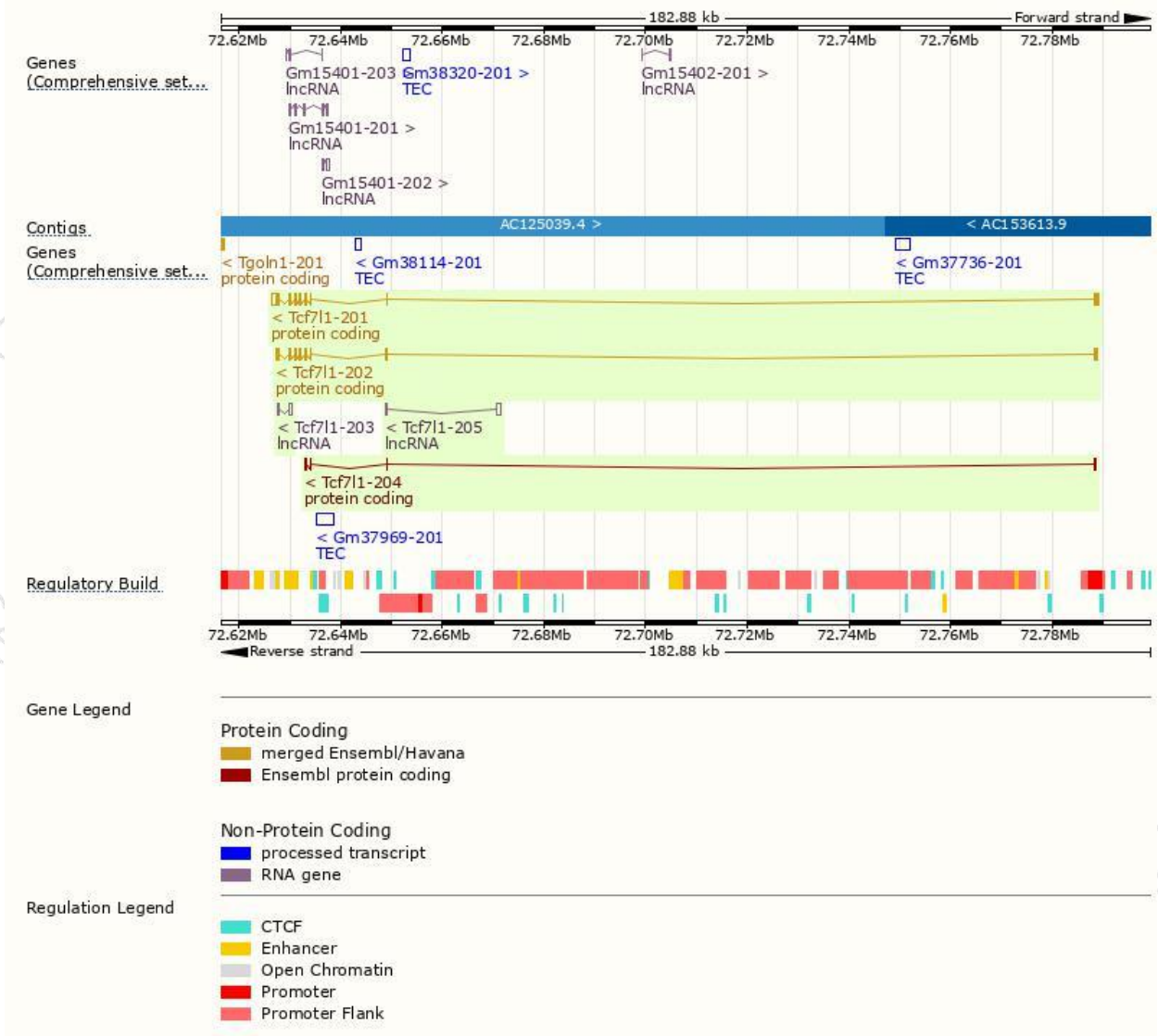
The gene has 5 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Tcf7l1-201 | ENSMUST00000069536.11 | 3042 | 585aa | Protein coding | CCDS20245 | A1A550 | TSL:1 GENCODE basic APPRIS P3 |
| Tcf7l1-202 | ENSMUST00000114053.8 | 1888 | 599aa | Protein coding | CCDS39517 | A1A549 | TSL:1 GENCODE basic APPRIS ALT2 |
| Tcf7l1-204 | ENSMUST00000149446.2 | 463 | 154aa | Protein coding | - | F6VNH1 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3 |
| Tcf7l1-205 | ENSMUST00000182651.1 | 713 | No protein | lncRNA | - | - | TSL:5 |
| Tcf7l1-203 | ENSMUST00000141743.1 | 518 | No protein | lncRNA | - | - | TSL:2 |

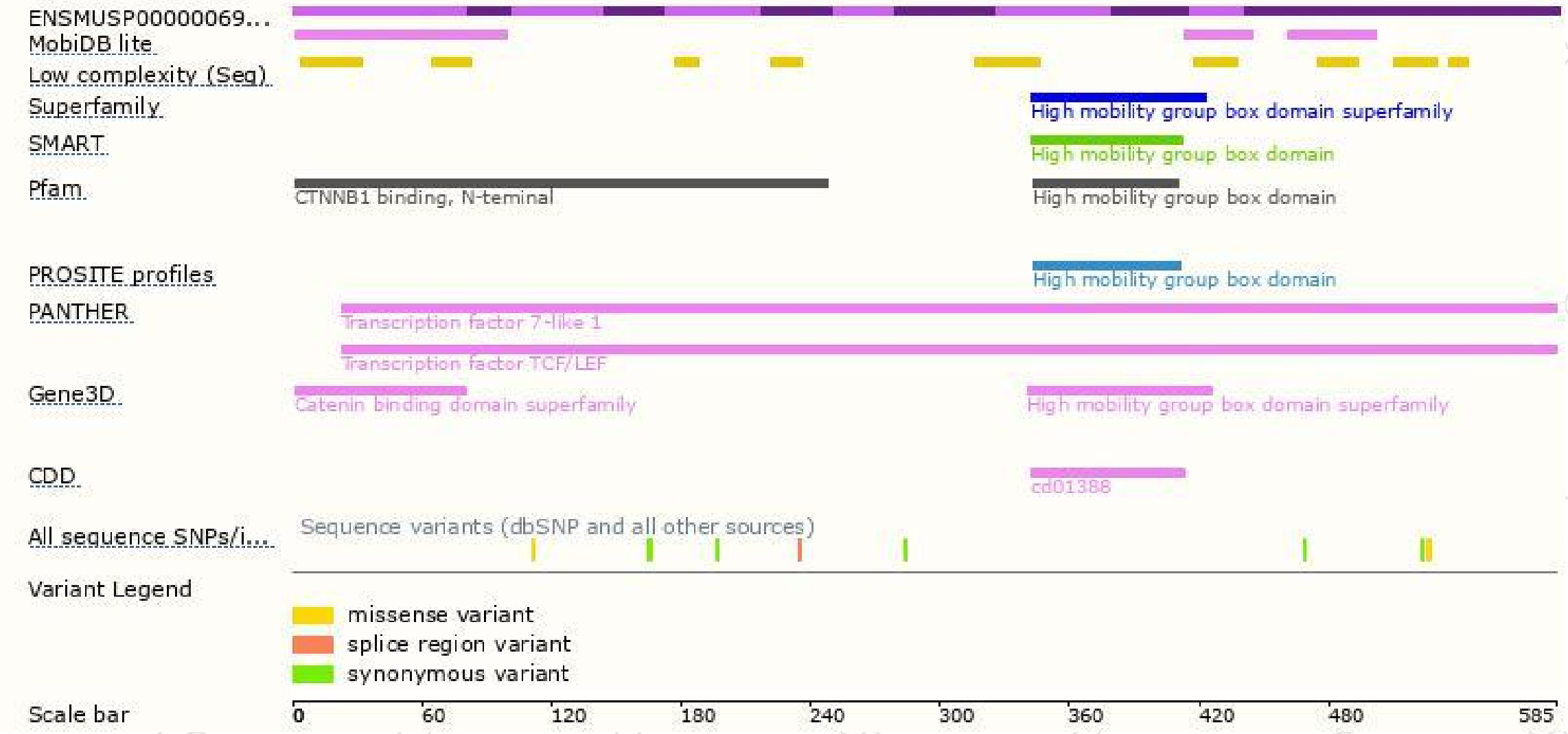
The strategy is based on the design of *Tcf7l1-201* transcript,The transcription is shown below



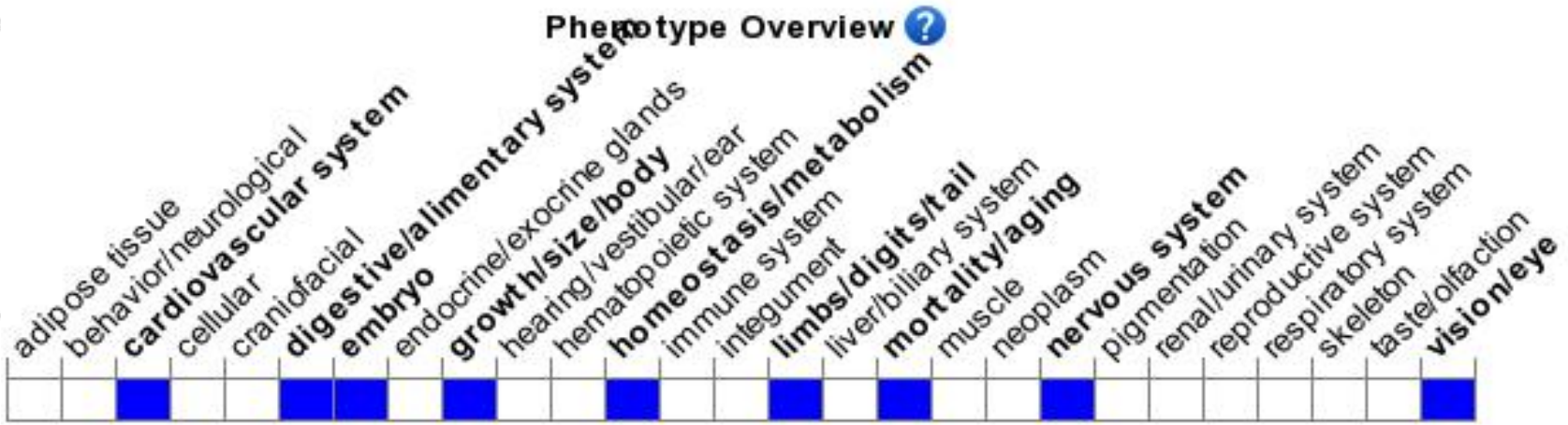
# Genomic location distribution



# 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,Animals homozygous for a targeted mutation exhibit severe embryological defects particularly affecting the cardiovascular system, nervous system, and digestive system. No homozygous embryos survive beyond E11.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd