Rnf111 Cas9-KO Strategy

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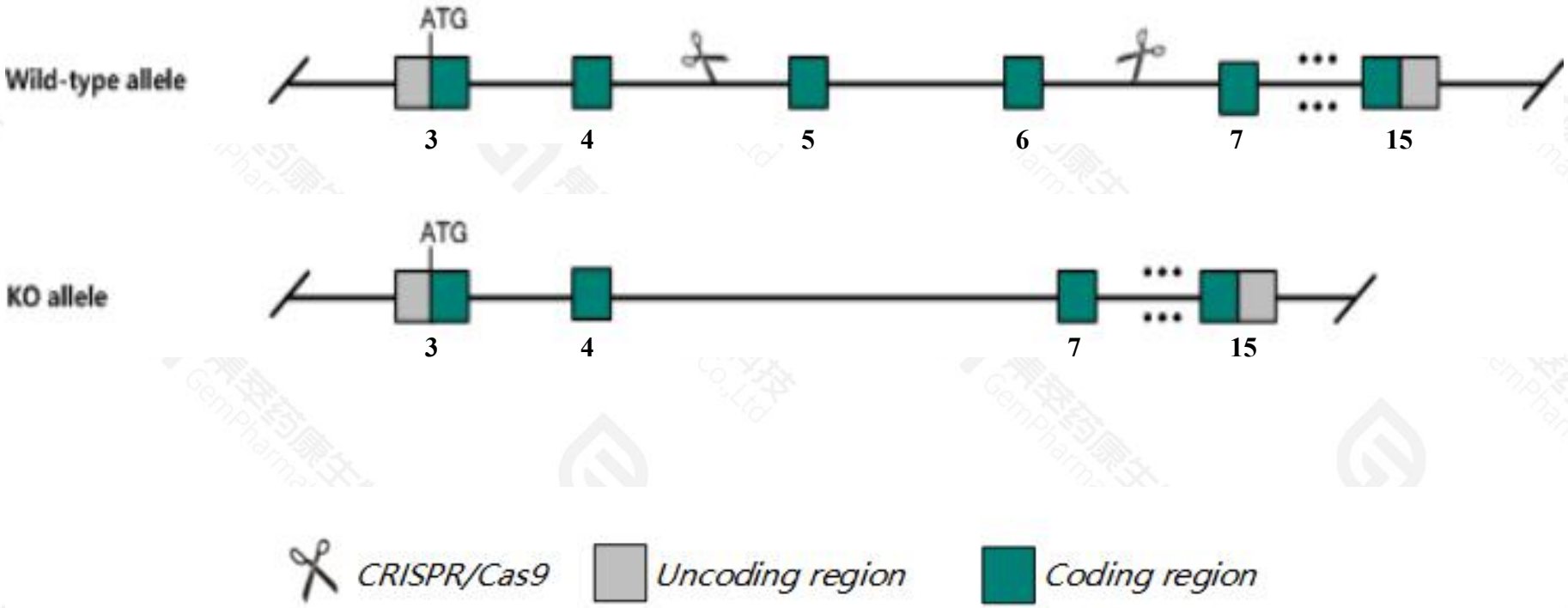
Project Overview

Project Name	***Rnf111***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf111* gene. The schematic diagram is as follows:



Technical routes

➢ The *Rnf111* gene has 8 transcripts. According to the structure of *Rnf111* gene, exon5-exon6 of *Rnf111-201*(ENSMUST00000034739.12) transcript is recommended as the knockout region.The region contains 359bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rnf111* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,mice homozygous for a gene trap allele fail to develop anterior structures and midline with failure to develop anterior endoderm, node and mesendoderm.

➢ The *Rnf111* gene is located on the Chr9. 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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Rnf111 ring finger 111 [Mus musculus (house mouse)]

Gene ID: 93836, updated on 31-Jan-2019

Summary

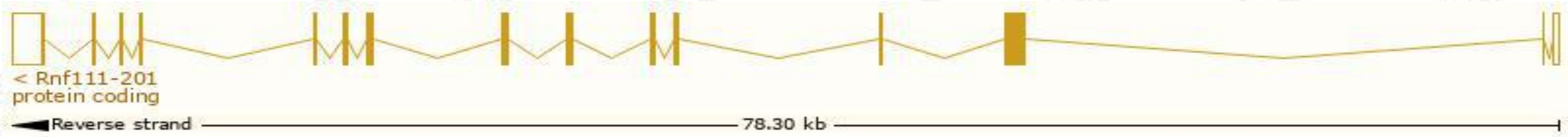
Official Symbol	Rnf111 provided by MGI
Official Full Name	ring finger 111 provided by MGI
Primary source	MGI:MGI:1934919
See related	Ensembl:ENSMUSG00000032217
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ARK, Arkadia
Expression	Ubiquitous expression in thymus adult (RPKM 22.4), spleen adult (RPKM 21.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

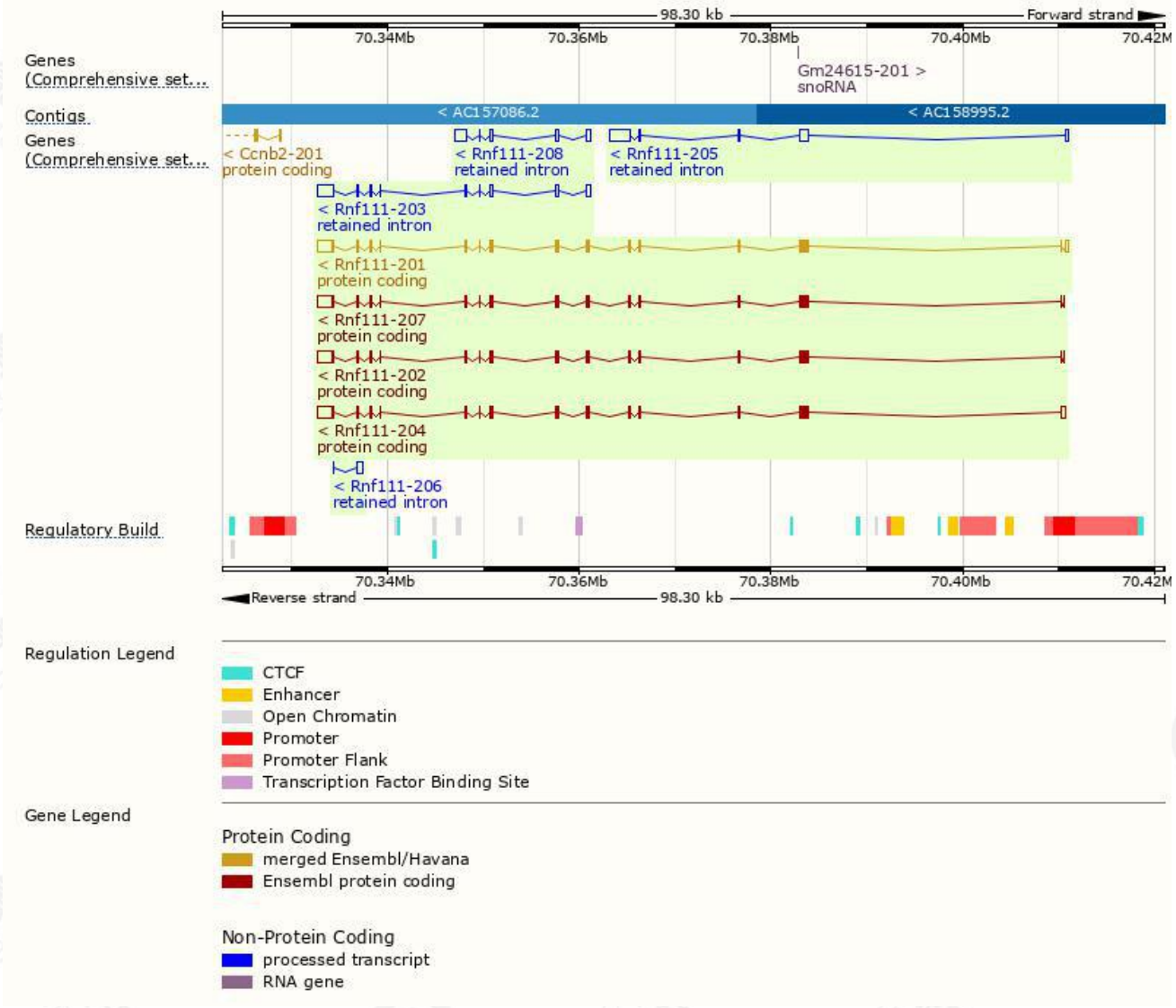
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf111-201	ENSMUST00000034739.11	4880	989aa	Protein coding	CCDS23321	Q99ML9	TSL:1 GENCODE basic APPRIS P2
Rnf111-202	ENSMUST00000113595.1	4735	989aa	Protein coding	CCDS23321	Q99ML9	TSL:5 GENCODE basic APPRIS P2
Rnf111-204	ENSMUST00000213647.1	4961	980aa	Protein coding	-	A0A1L1SRK3	TSL:1 GENCODE basic APPRIS ALT2
Rnf111-207	ENSMUST00000215848.1	4712	981aa	Protein coding	-	Q99ML9	TSL:1 GENCODE basic APPRIS ALT2
Rnf111-205	ENSMUST00000213694.1	3555	No protein	Retained intron	-	-	TSL:1
Rnf111-203	ENSMUST00000213208.1	3293	No protein	Retained intron	-	-	TSL:1
Rnf111-208	ENSMUST00000215948.1	2266	No protein	Retained intron	-	-	TSL:1
Rnf111-206	ENSMUST00000213996.1	671	No protein	Retained intron	-	-	TSL:2

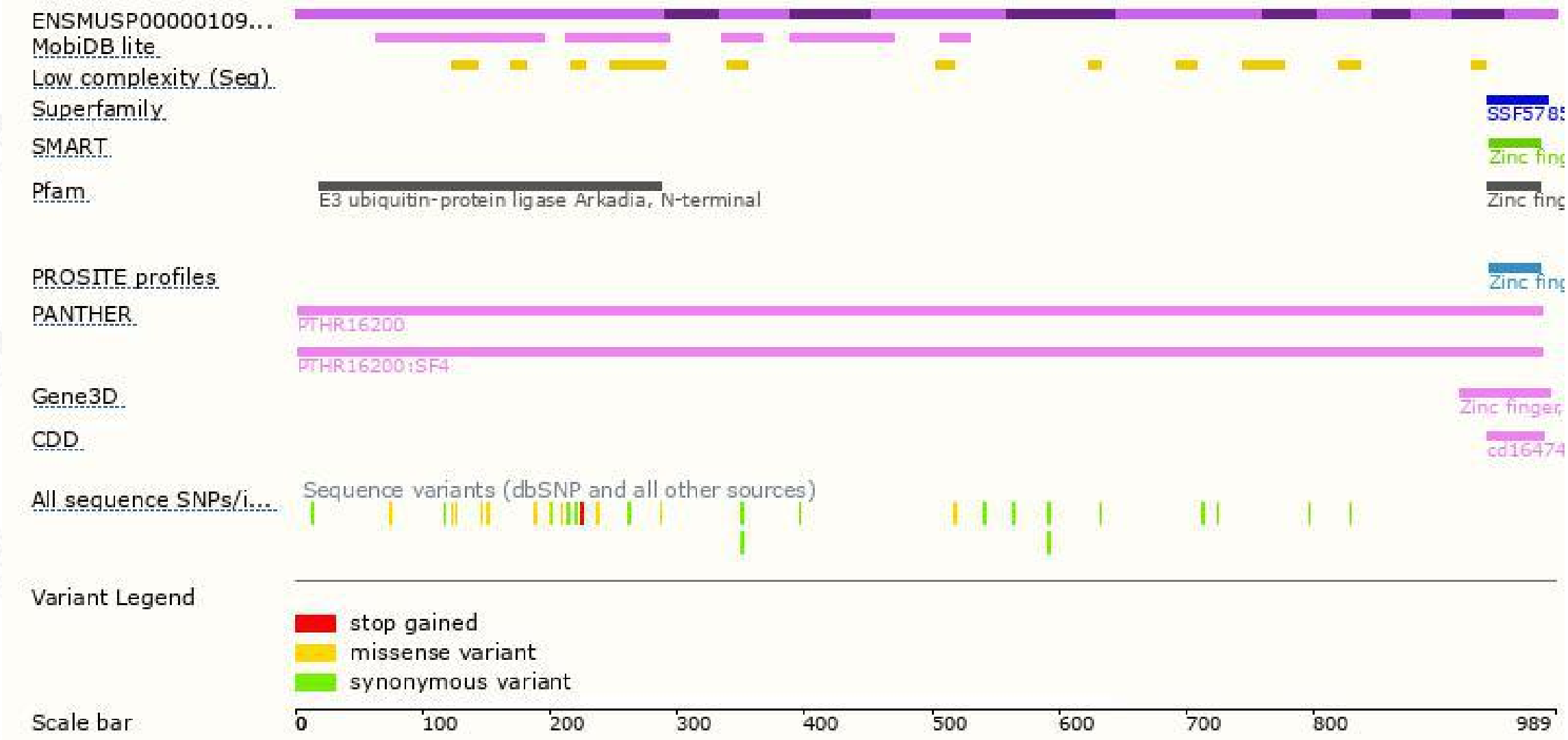
The strategy is based on the design of *Rnf111-201* transcript,the transcription is shown below:



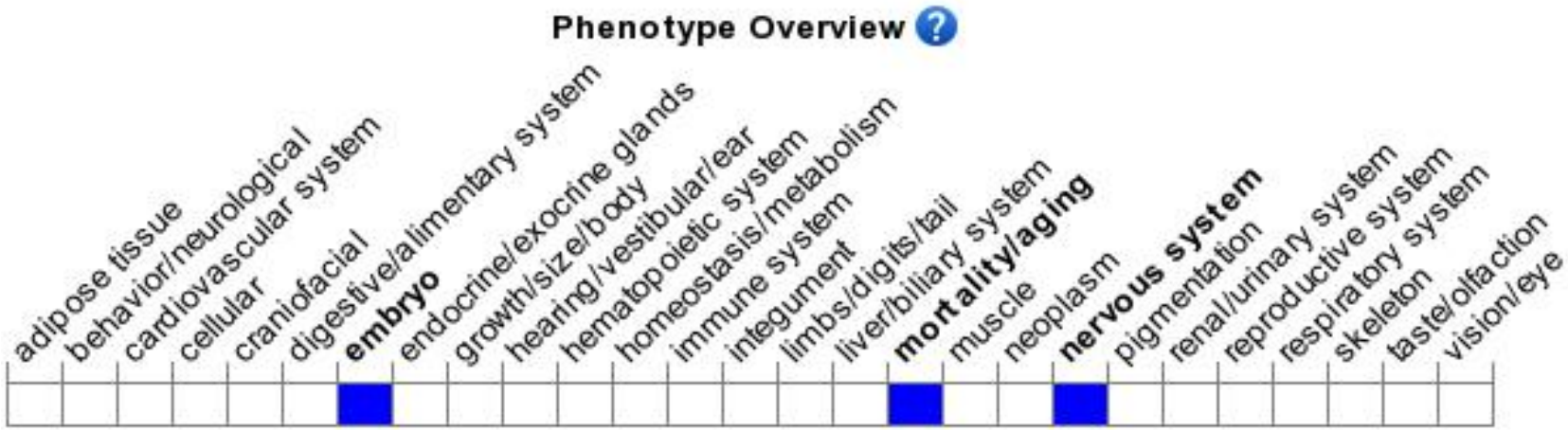
Genomic location distribution



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 a gene trap allele fail to develop anterior structures and midline with failure to develop anterior endoderm, node and mesendoderm.

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