Srf Cas9-KO Strategy

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Project Overview

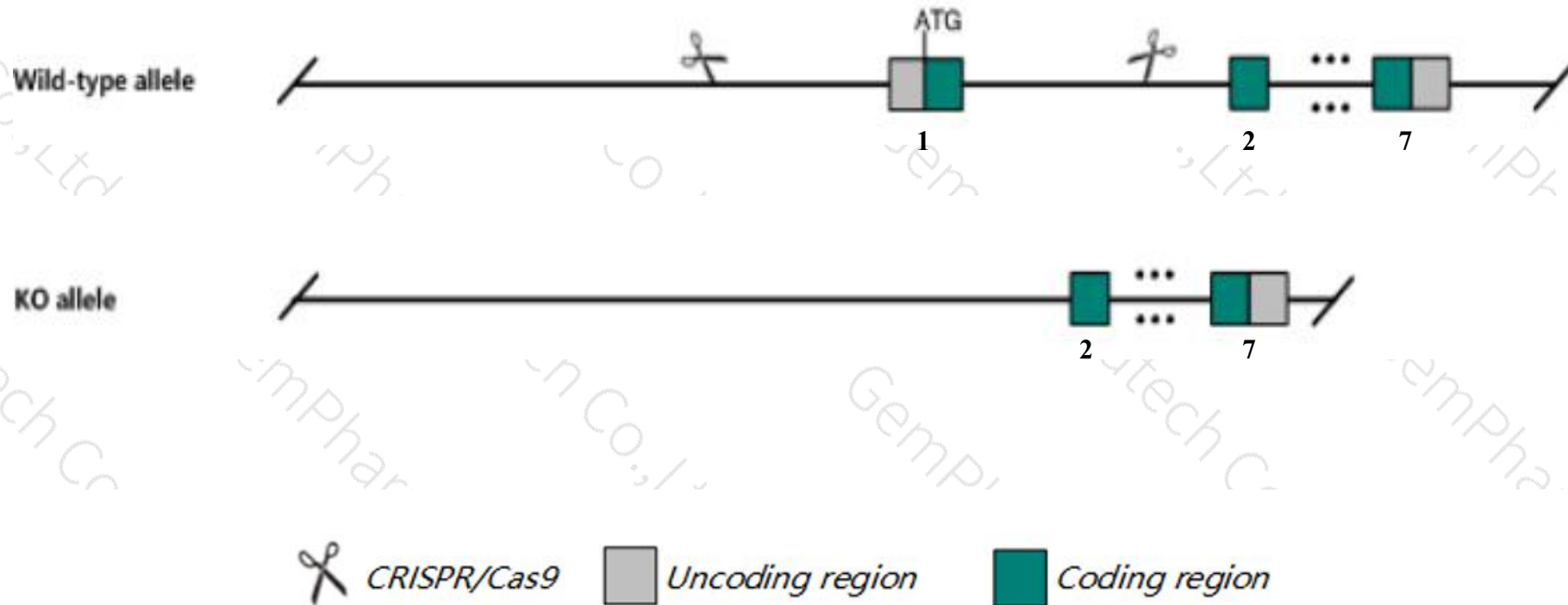|	
Project Name	*Srf*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Srf* gene has 4 transcripts. According to the structure of *Srf* gene, exon1 of *Srf-201* (ENSMUST00000015749.6) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

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

Notice

➤ According to the existing MGI data,homozygous null mice exhibit embryonic lethality, abnormal gastrulation, no mesoderm or primitive streak formation and reduced embryo size.

➤ *Srf-202* will not be affected.

➤ The *Srf* gene is located on the Chr17. 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）

Srf serum response factor [Mus musculus (house mouse)]

Gene ID: 20807, updated on 13-Mar-2020

Summary

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Official Symbol	Srf provided by MGI
Official Full Name	serum response factor provided by MGI
Primary source	MGI:MGI:106658
See related	Ensembl:ENSMUSG00000015605
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	AW049942, AW240594
Expression	Ubiquitous expression in ovary adult (RPKM 59.4), colon adult (RPKM 43.3) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srf-201	ENSMUST00000015749.6	2616	504aa	Protein coding	CCDS28831	Q9JM73	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
Srf-202	ENSMUST00000233104.1	376	97aa	Protein coding	-	A0A3B2WCW1	CDS 5' incomplete
Srf-203	ENSMUST00000233767.1	637	No protein	Retained intron	-	-	
Srf-204	ENSMUST00000233797.1	595	No protein	Retained intron	-	-	

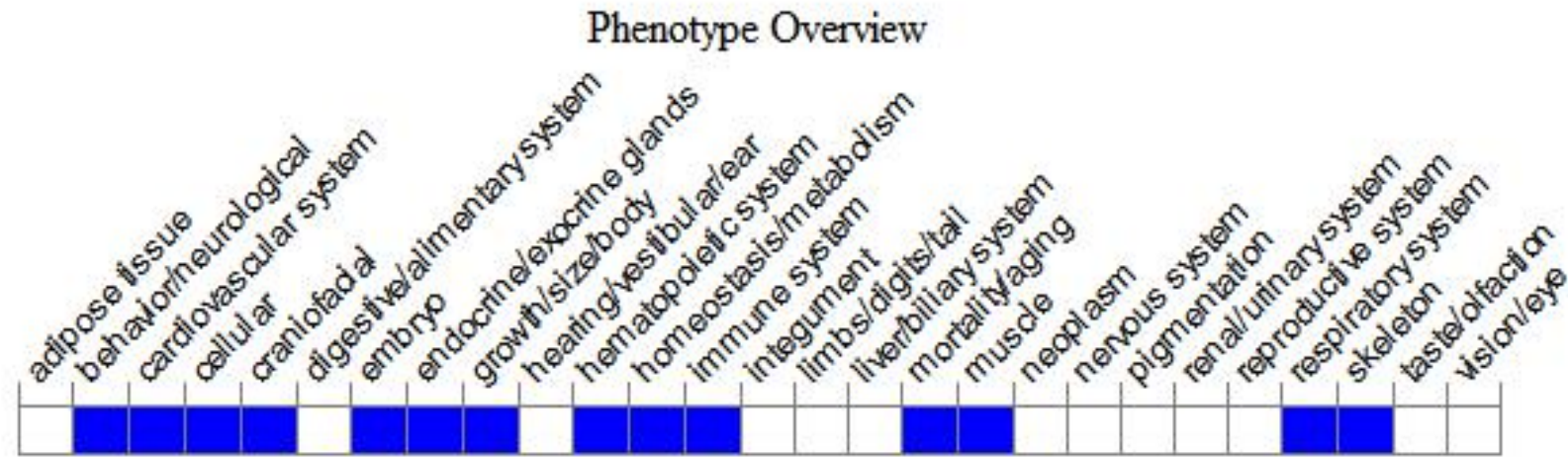The strategy is based on the design of *Srf-201* transcript,the transcription is shown below

< Srf-201
protein coding

Reverse strand

7.85 kb
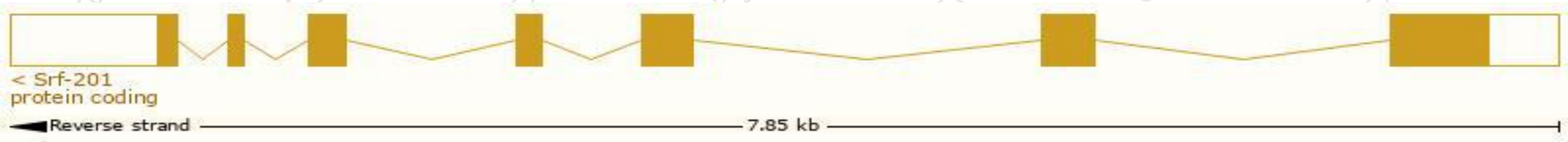
Genomic location distribution
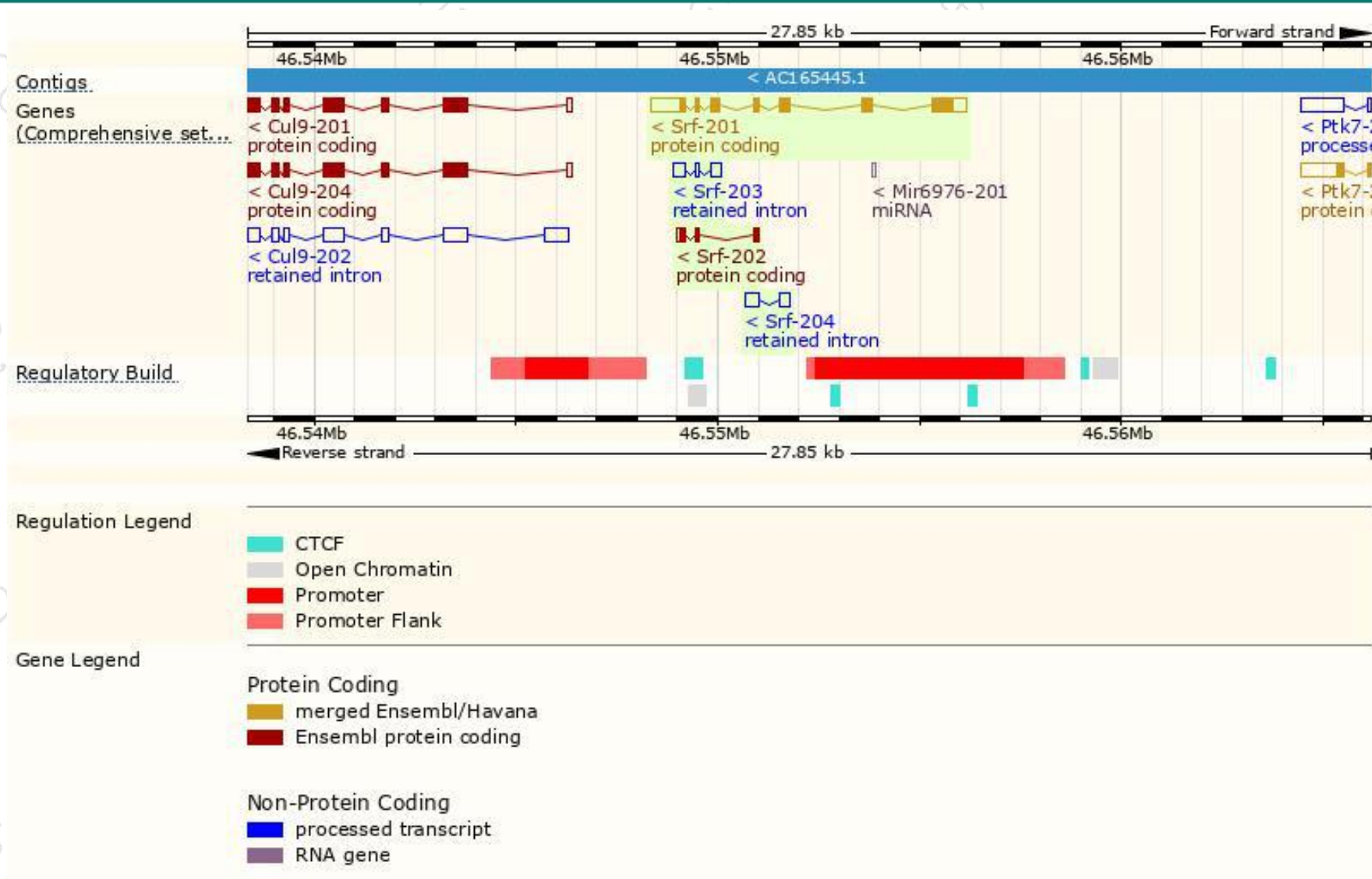
Protein domain
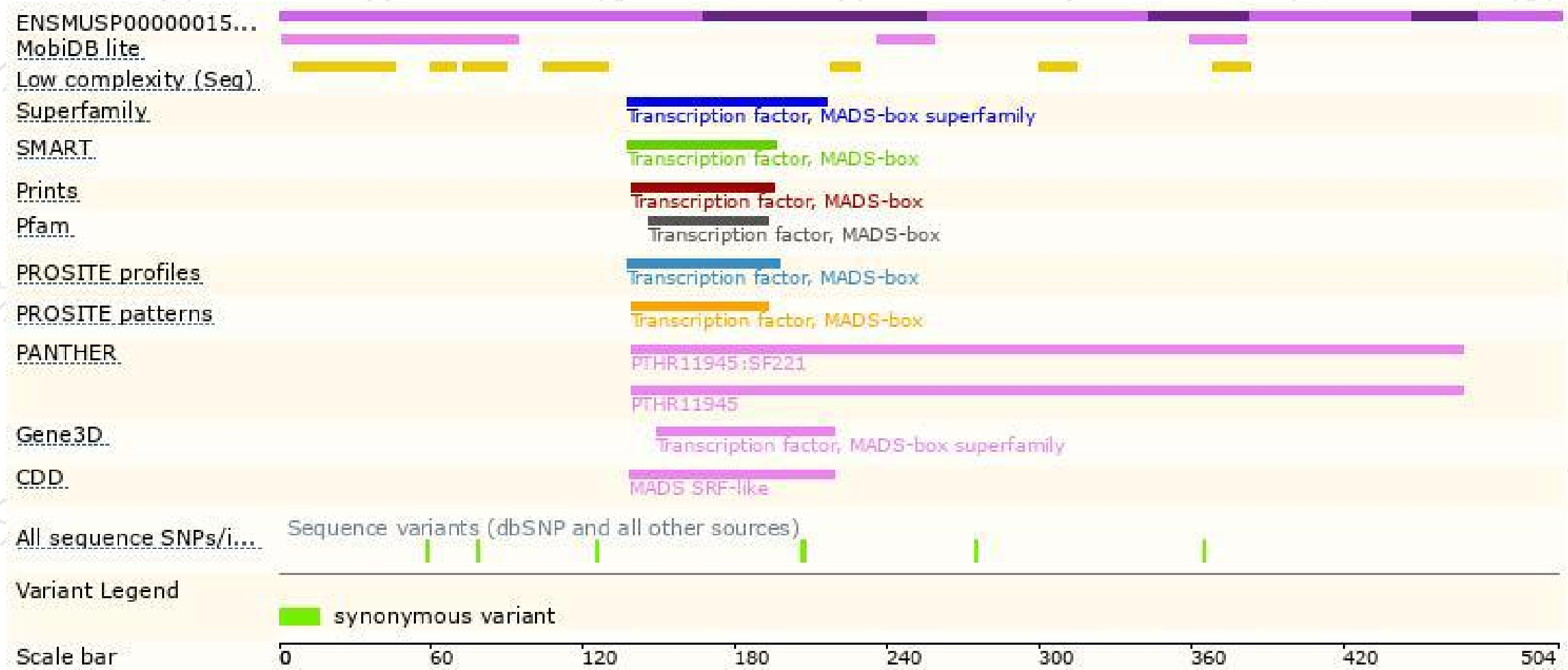
Mouse phenotype description(MGI)

Phenotype Overview

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,homozygous null mice exhibit embryonic lethality, abnormal gastrulation, no mesoderm or primitive streak formation and reduced embryo size.

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