Hnrnpc Cas9-CKO Strategy

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Project Overview

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

Conditional Knockout strategy

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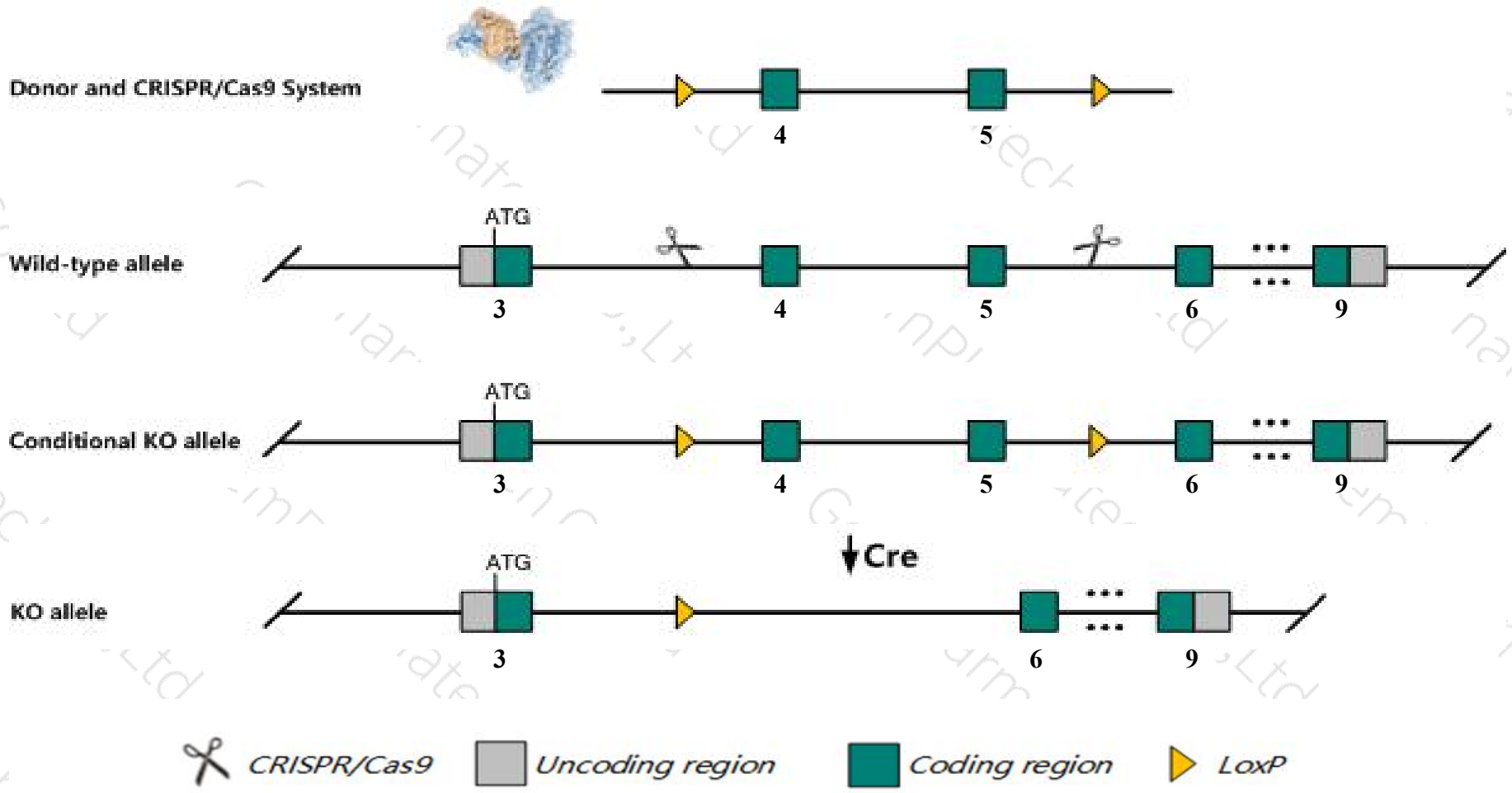
This model will use CRISPR/Cas9 technology to edit the *Hnrnpc* gene. The schematic diagram is as follows:



Technical routes

- The *Hnrnpc* gene has 13 transcripts. According to the structure of *Hnrnpc* gene, exon4-exon5 of *Hnrnpc-201* (ENSMUST00000111610.11) transcript is recommended as the knockout region.The region contains 163bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hnrnpc* gene. The brief process is as follows:CRISPR/Cas9 system 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 gene trapped allele fail to undergo gastrulation, appear to arrest at the egg cylinder stage, and are resorbed at various times thereafter.

- Transcript *Hnrnpc-203/208/212/213* may not be affected.

- The *Hnrnpc* gene is located on the Chr14. 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）

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Hnrnpc heterogeneous nuclear ribonucleoprotein C [Mus musculus (house mouse)]

Gene ID: 15381, updated on 31-Jan-2019

Summary

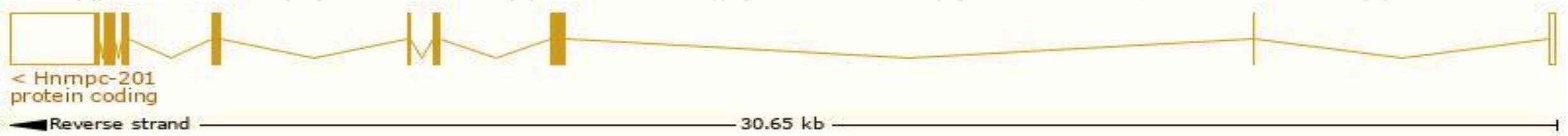
Official Symbol	Hnrnpc provided by MGI
Official Full Name	heterogeneous nuclear ribonucleoprotein C provided byMGI
Primary source	MGI:MGI:107795
See related	Ensembl:ENSMUSG00000060373
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AL022939, D14Wsu171e, Hnrpc, Hnrpc1, Hnrpc2, hnRNPC1, hnRNPC2, hnrnp-C
Expression	Broad expression in CNS E11.5 (RPKM 123.0), CNS E14 (RPKM 61.1) and 23 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

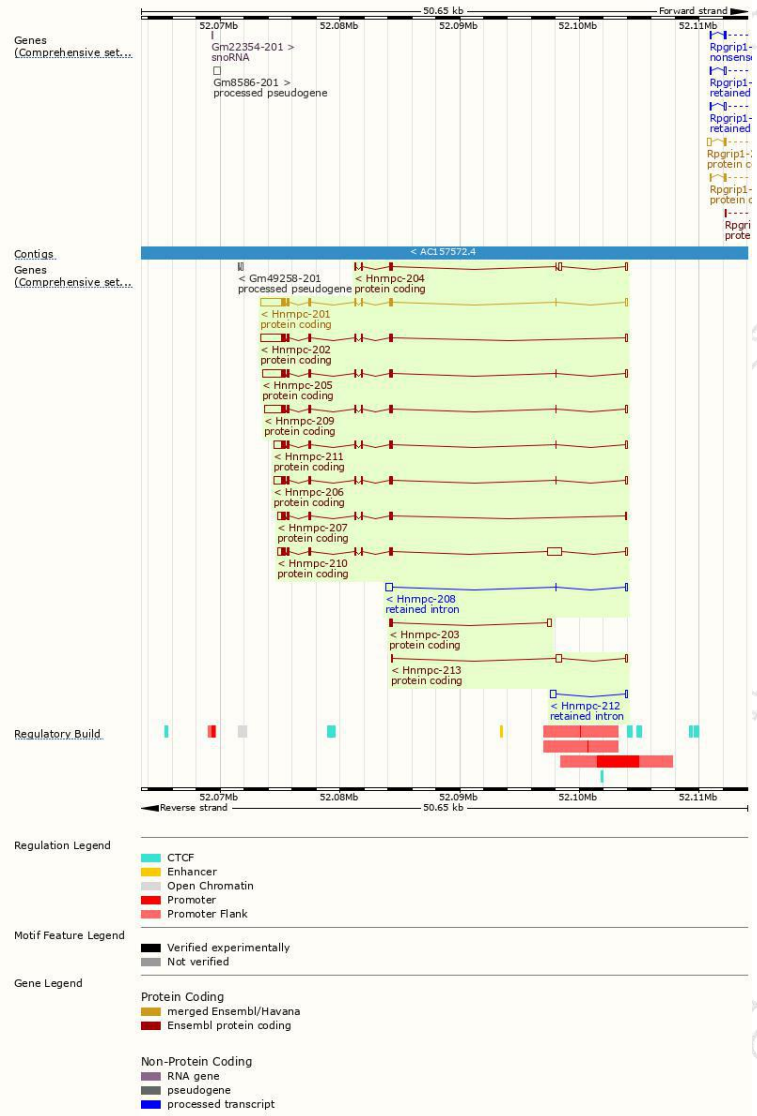
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpc-201	ENSMUST00000111610.11	2847	313aa	Protein coding	CCDS36917	Q9Z204	TSL:1 GENCODE basic
Hnrnpc-202	ENSMUST00000164655.1	2843	313aa	Protein coding	CCDS36917	Q9Z204	TSL:5 GENCODE basic
Hnrnpc-205	ENSMUST00000227242.1	2617	300aa	Protein coding	-	Q9Z204	GENCODE basic
Hnrnpc-210	ENSMUST00000228232.1	2535	293aa	Protein coding	-	Q9Z204	GENCODE basic APPRIS ALT2
Hnrnpc-209	ENSMUST00000228198.1	2498	306aa	Protein coding	-	Q9Z204	GENCODE basic APPRIS P5
Hnrnpc-211	ENSMUST00000228748.1	1691	293aa	Protein coding	-	Q9Z204	GENCODE basic APPRIS ALT2
Hnrnpc-206	ENSMUST00000227458.1	1683	292aa	Protein coding	-	Q9Z204	GENCODE basic APPRIS ALT1
Hnrnpc-207	ENSMUST00000227536.1	1301	300aa	Protein coding	-	Q9Z204	GENCODE basic
Hnrnpc-213	ENSMUST00000228815.1	755	28aa	Protein coding	-	A0A2I3BQW7	CDS 3' incomplete
Hnrnpc-204	ENSMUST00000227195.1	745	117aa	Protein coding	-	A0A2I3BRM6	CDS 3' incomplete
Hnrnpc-203	ENSMUST00000226993.1	582	80aa	Protein coding	-	A0A2I3BQH3	CDS 3' incomplete
Hnrnpc-208	ENSMUST00000228045.1	660	No protein	Retained intron	-	-	
Hnrnpc-212	ENSMUST00000228786.1	611	No protein	Retained intron	-	-	

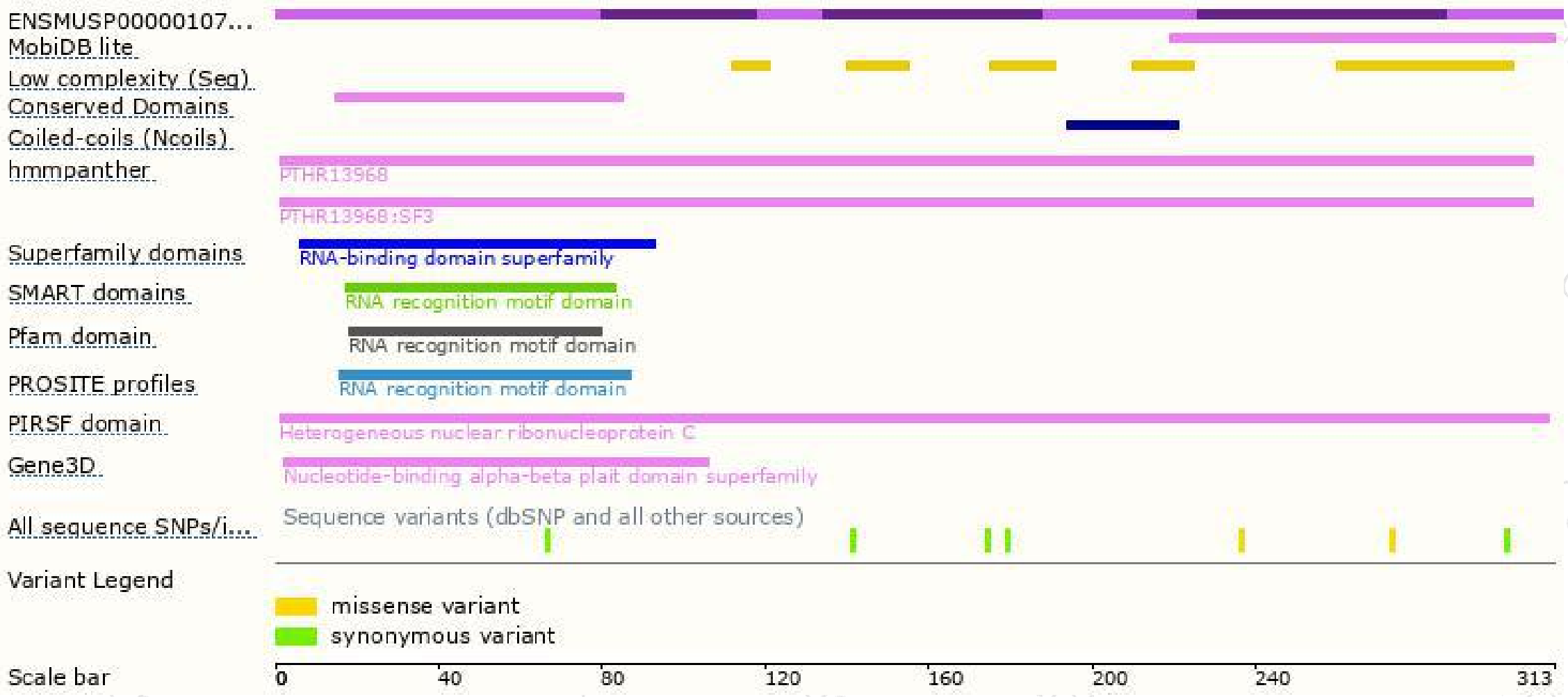
The strategy is based on the design of *Hnrnpc-201* transcript,The transcription is shown below



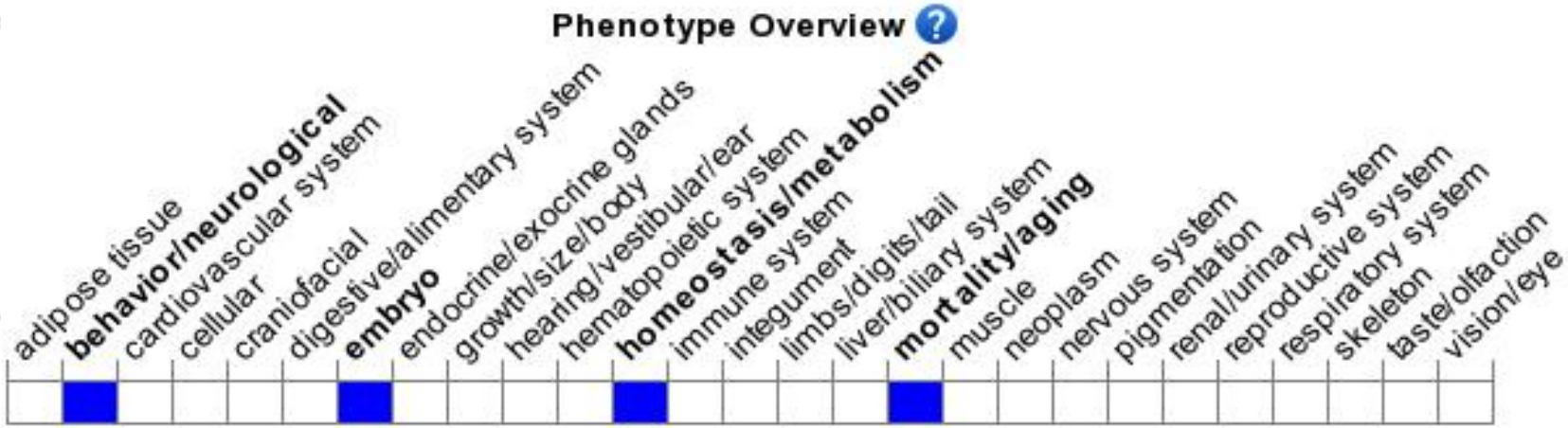
Genomic location distribution



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 trapped allele fail to undergo gastrulation, appear to arrest at the egg cylinder stage, and are resorbed at various times thereafter.

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

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