Tjp1 Cas9-CKO Strategy

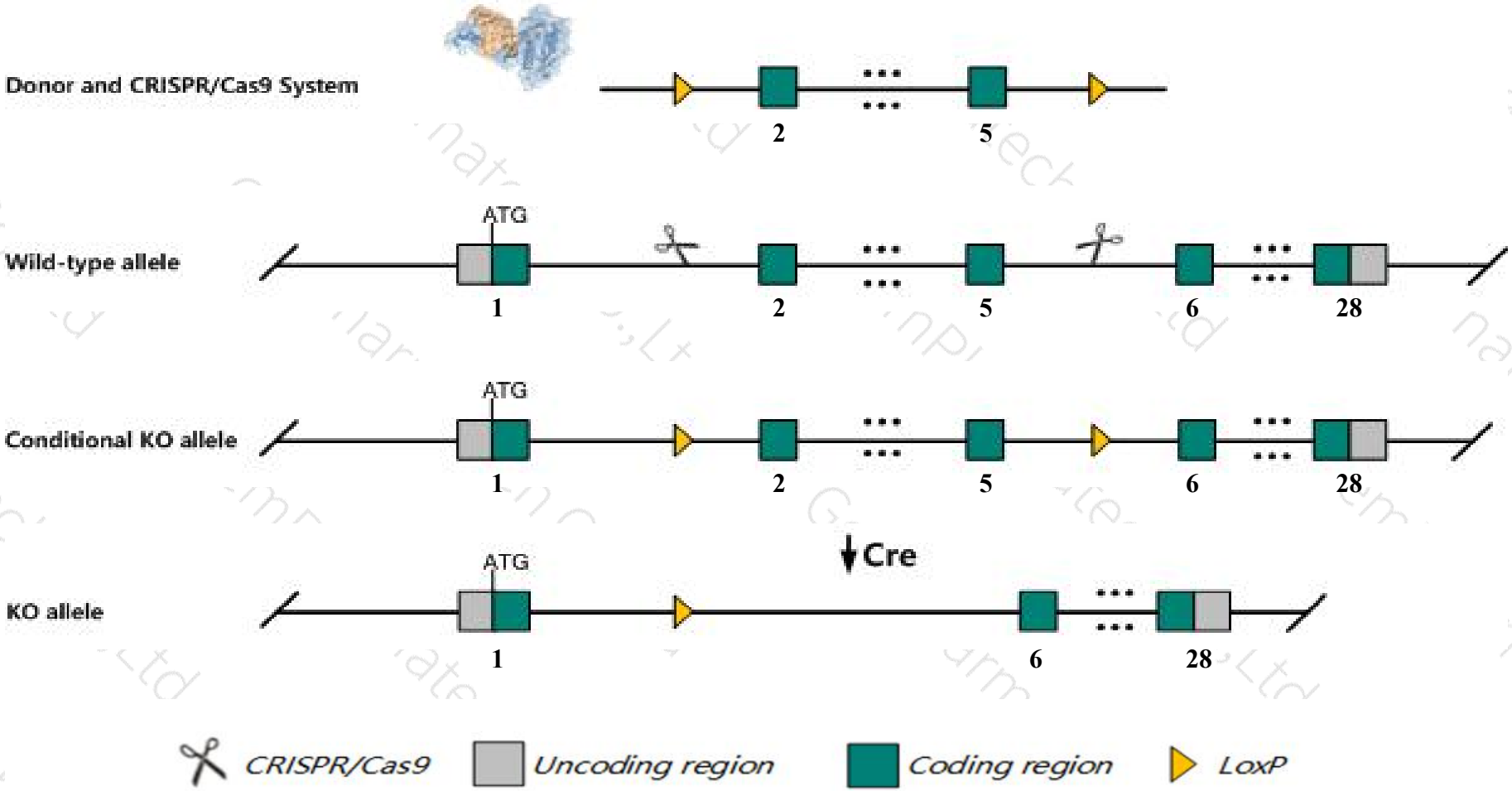
Designer: Daohua Xu
Reviewer: Huimin Su
Design Date: 2019-11-14

Project Overview

Project Name	***Tjp1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tjp1* gene. The schematic diagram is as follows:



Technical routes

- The *Tjp1* gene has 7 transcripts. According to the structure of *Tjp1* gene, exon2-exon5 of *Tjp1-202* (ENSMUST00000102592.9) transcript is recommended as the knockout region.The region contains 562bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Tjp1* 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 null allele show embryonic lethality and growth retardation, failure of embryo turning and chorioallantoic fusion, defective yolk sac angiogenesis, and increased apoptosis in the notochord, neural tube, somite and allantois. Homozygotes for a reporter allele are overtly normal.

- The *Tjp1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

集萃药康 GemPharmatech

Tjp1 tight junction protein 1 [Mus musculus (house mouse)]

Gene ID: 21872, updated on 23-Mar-2019

Summary

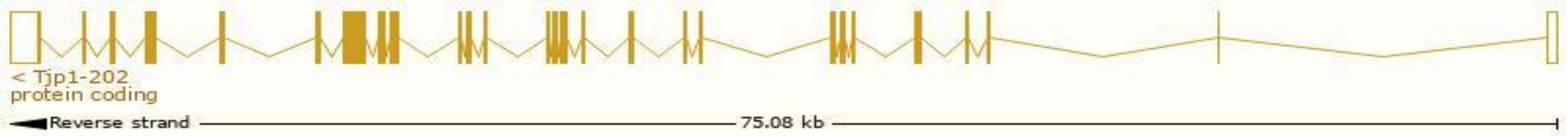
Official Symbol	Tjp1 provided by MGI
Official Full Name	tight junction protein 1 provided byMGI
Primary source	MGI:MGI:98759
See related	Ensembl:ENSMUSG00000030516
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ZO1
Expression	Ubiquitous expression in lung adult (RPKM 23.6), bladder adult (RPKM 20.6) and 26 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

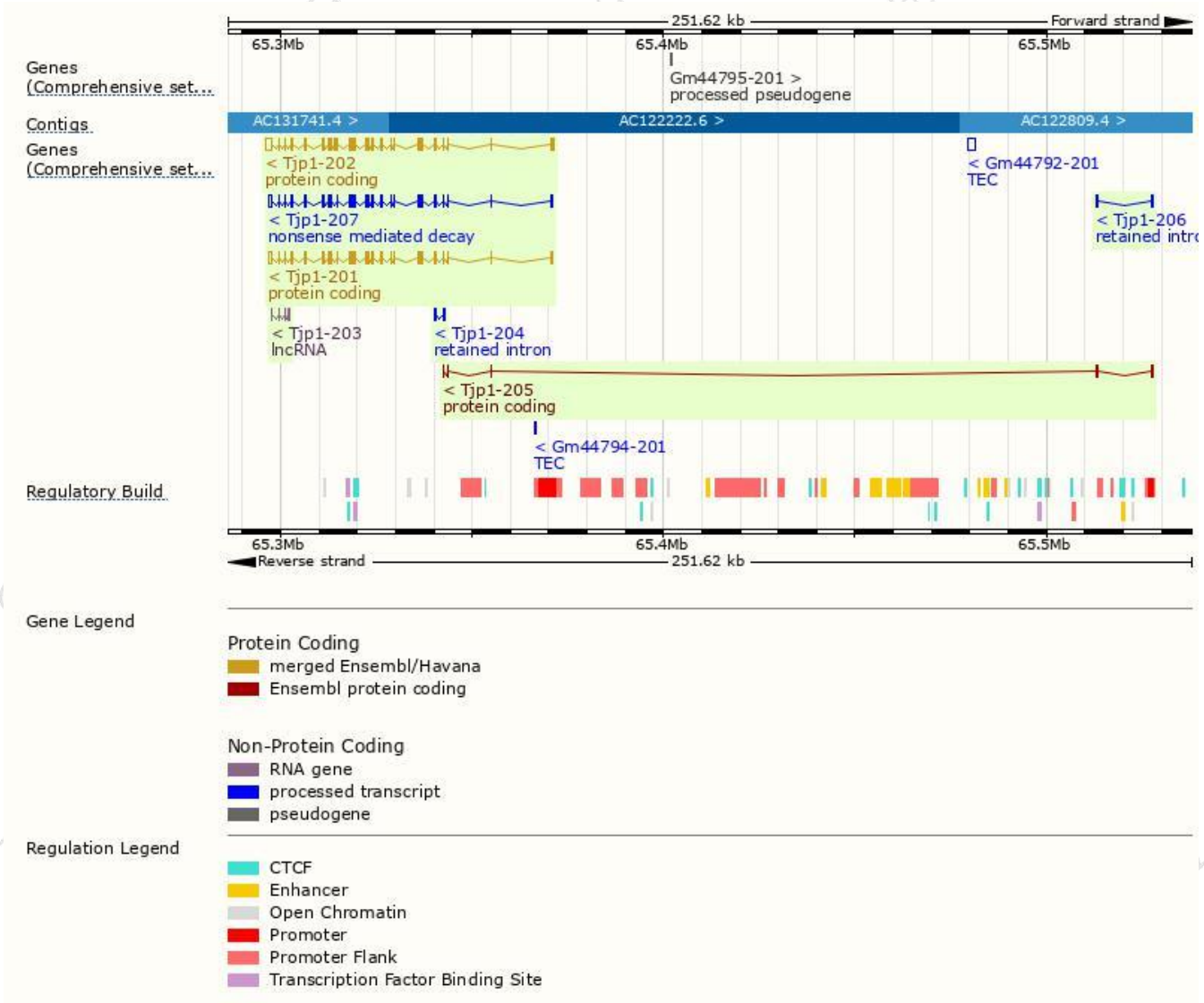
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tjp1-202	ENSMUST00000102592.9	7049	1745aa	Protein coding	CCDS21338	P39447	TSL:1 GENCODE basic APPRIS P3
Tjp1-201	ENSMUST00000032729.7	6102	1685aa	Protein coding	CCDS52266	B9EHJ3	TSL:1 GENCODE basic APPRIS ALT2
Tjp1-205	ENSMUST00000206228.1	551	171aa	Protein coding	-	A0A0U1RPB2	CDS 3' incomplete TSL:5
Tjp1-207	ENSMUST00000206612.1	5938	1128aa	Nonsense mediated decay	-	A0A0U1RPW2	TSL:1
Tjp1-206	ENSMUST00000206438.1	451	No protein	Retained intron	-	-	TSL:3
Tjp1-204	ENSMUST00000144961.1	385	No protein	Retained intron	-	-	TSL:3
Tjp1-203	ENSMUST00000132036.1	699	No protein	lncRNA	-	-	TSL:1

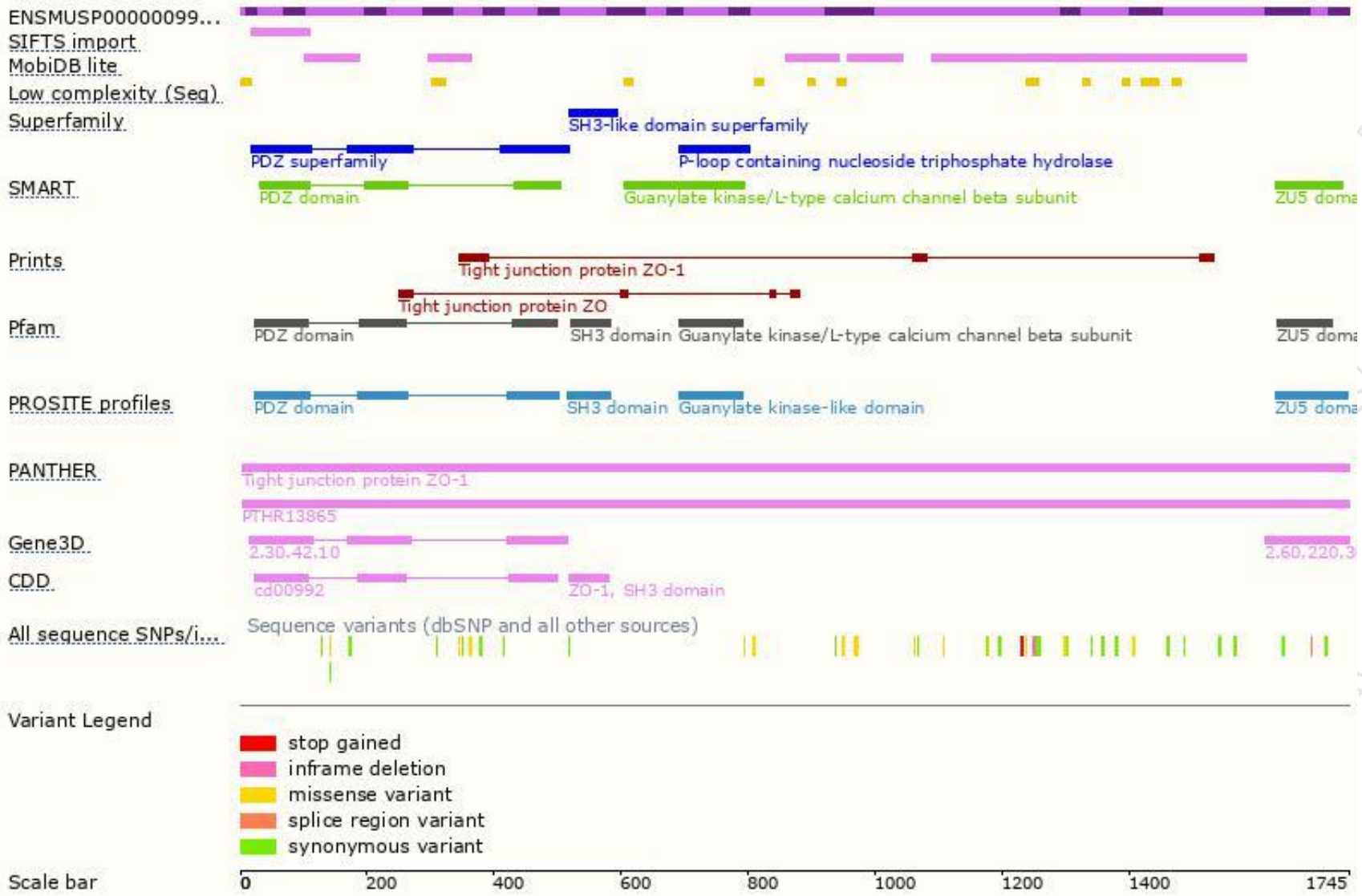
The strategy is based on the design of *Tjp1-202* transcript,The transcription is shown below



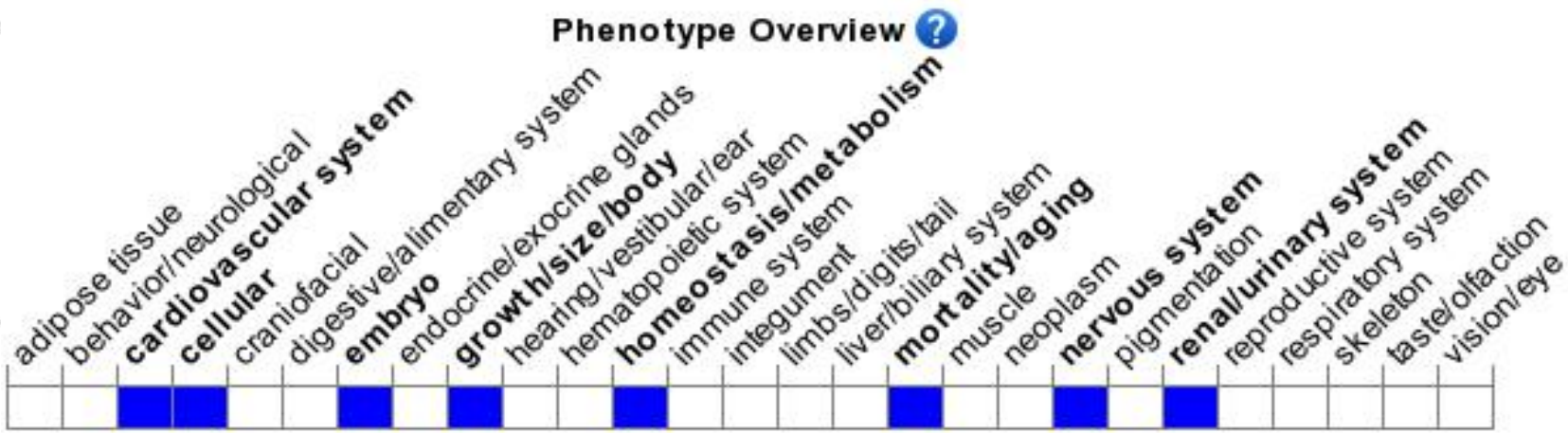
Genomic location distribution



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 null allele show embryonic lethality and growth retardation, failure of embryo turning and chorioallantoic fusion, defective yolk sac angiogenesis, and increased apoptosis in the notochord, neural tube, somite and allantois. Homozygotes for a reporter allele are overtly normal.

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