

Spop Cas9-KO Strategy

Designer: Shilei Zhu



Project Overview

Project Name

Spop

Project type

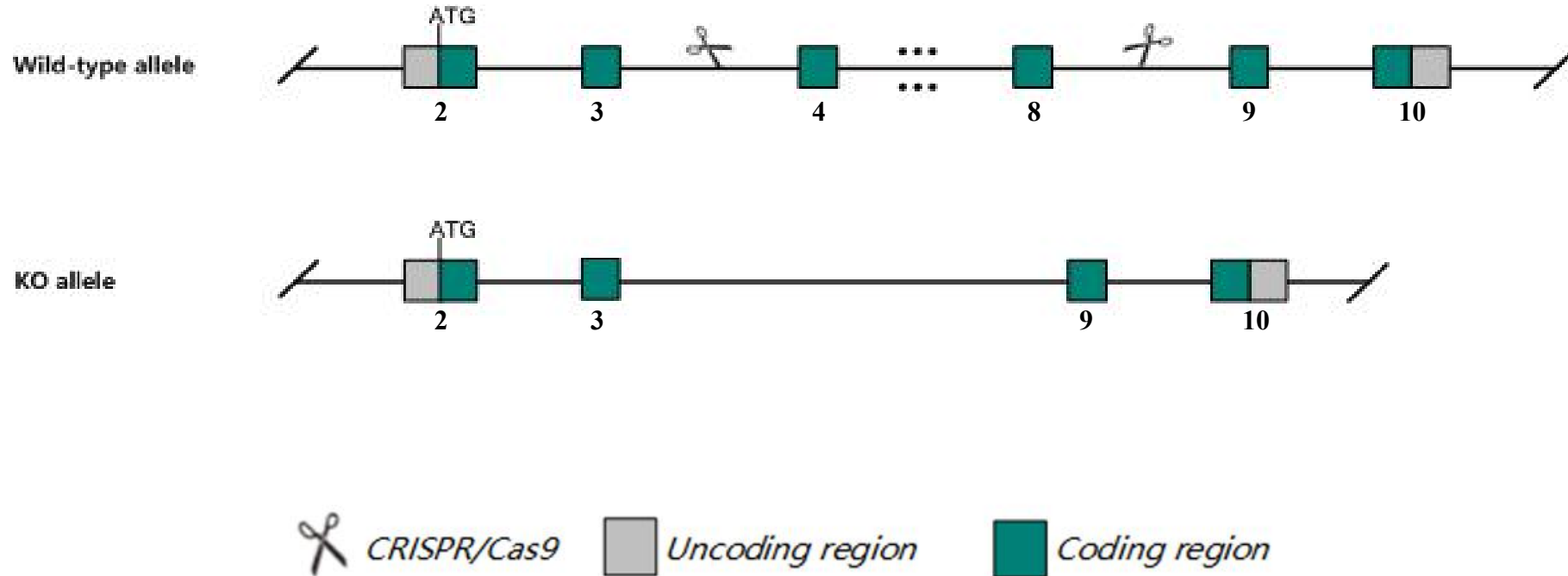
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



The *Spop* gene has 5 transcripts. According to the structure of *Spop* gene, exon4-exon8 of *Spop-201* (ENSMUST00000107722.7) transcript is recommended as the knockout region. The region contains 637bp coding sequence. Knock out the region will result in disruption of protein function.

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

According to the existing MGI data, Mice homozygous for a gene trap allele exhibit increased beta cell area and lethality between E18.5 and P1.

The *Spop* gene is located on the Chr11. 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.

Spop speckle-type POZ protein [Mus musculus (house mouse)]

Gene ID: 20747, updated on 9-Apr-2019

Summary

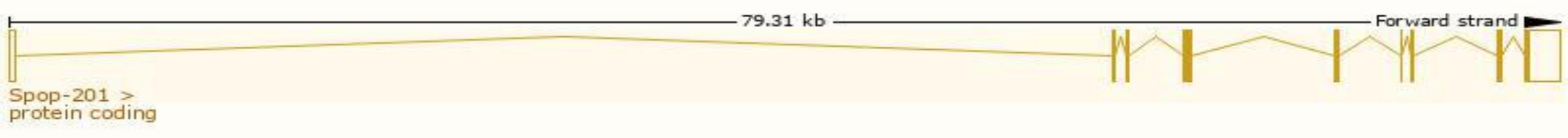
Official Symbol	Spop provided by MGI
Official Full Name	speckle-type POZ protein provided by MGI
Primary source	MGI:MGI:1343085
See related	Ensembl:ENSMUSG00000057522
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI315626, Pcif1, TEF2
Expression	Ubiquitous expression in cerebellum adult (RPKM 32.0), bladder adult (RPKM 30.6) and 28 other tissues See more
Orthologs	human all

Transcript information Ensembl

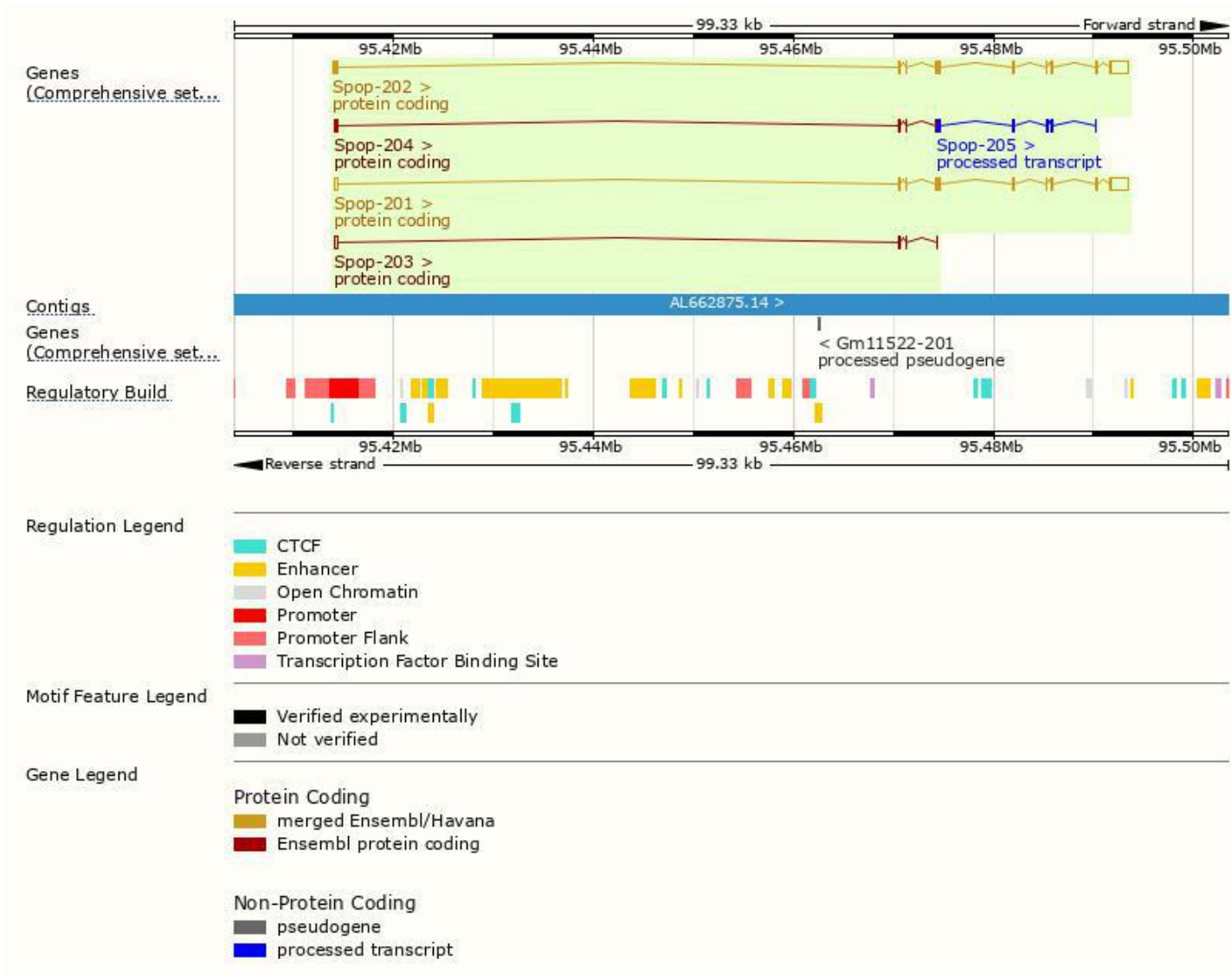
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Spop-201	ENSMUST00000107722.7	3063	374aa	Protein coding	CCDS36286	Q6ZWS8	TSL:1 GENCODE basic APPRIS P1
Spop-202	ENSMUST00000107724.8	2881	374aa	Protein coding	CCDS36286	Q6ZWS8	TSL:1 GENCODE basic APPRIS P1
Spop-204	ENSMUST00000150884.7	470	94aa	Protein coding	-	B1ATK6	CDS 3' incomplete TSL:3
Spop-203	ENSMUST00000127713.1	458	76aa	Protein coding	-	B1ATK7	CDS 3' incomplete TSL:3
Spop-205	ENSMUST00000150922.1	658	No protein	Processed transcript	-	-	TSL:3

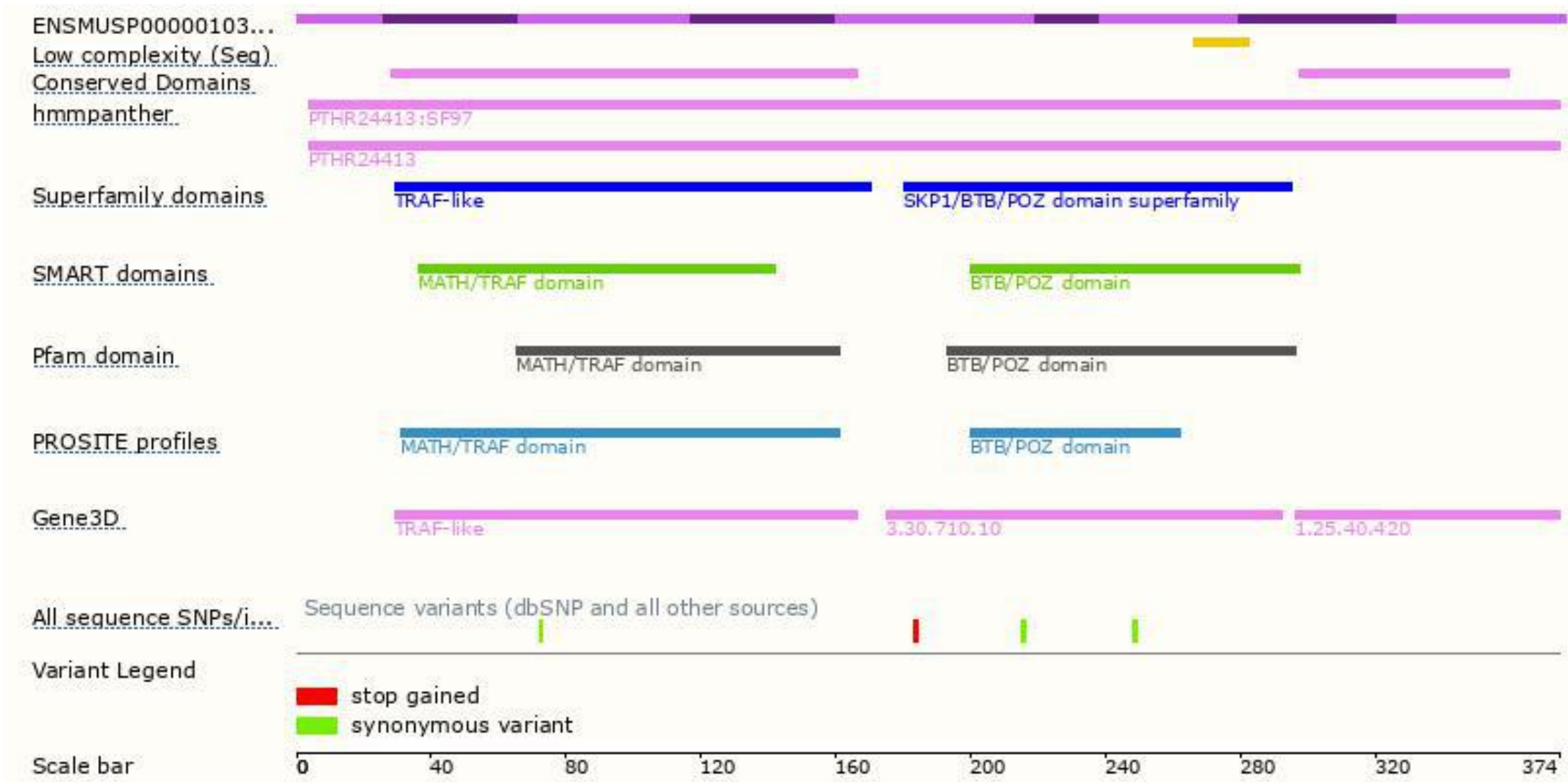
The strategy is based on the design of *Spop-201* transcript,The transcription is shown below



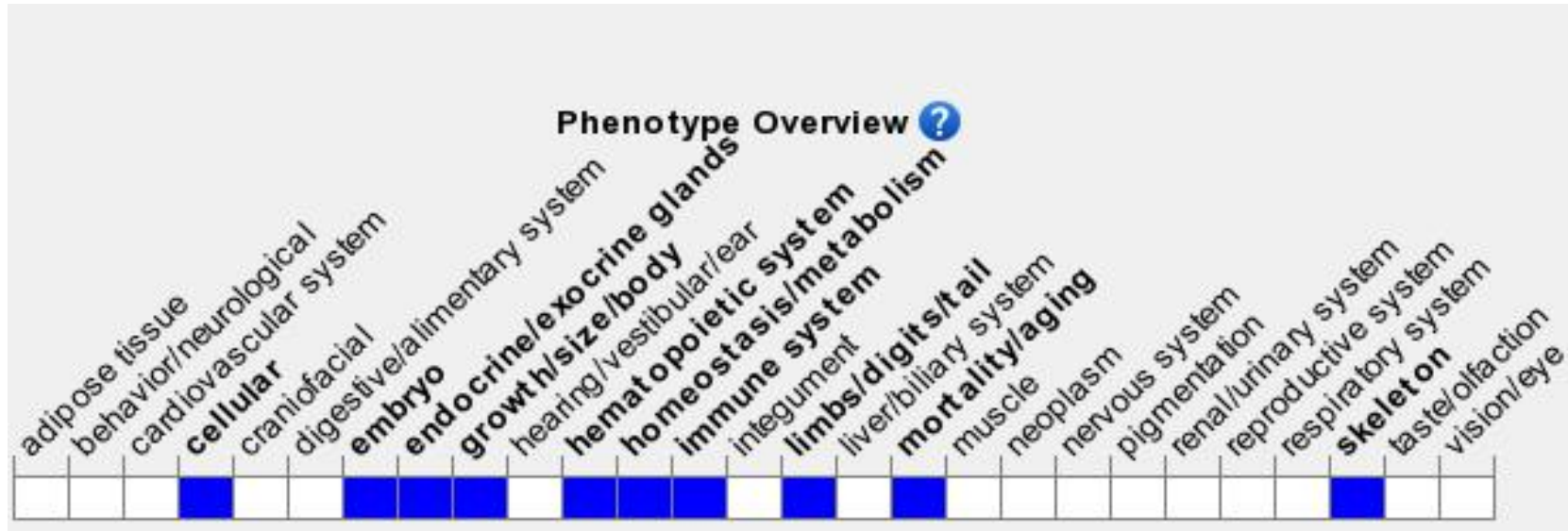
Genomic location distribution



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 exhibit increased beta cell area and lethality between E18.5 and P1.

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

