

# *Pias1* Cas9-KO Strategy

**Designer: Longyun Hu**

**Reviewer: Rui Xiong**

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# Project Overview

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**Project Name**

*Pias1*

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**Project type**

**Cas9-KO**

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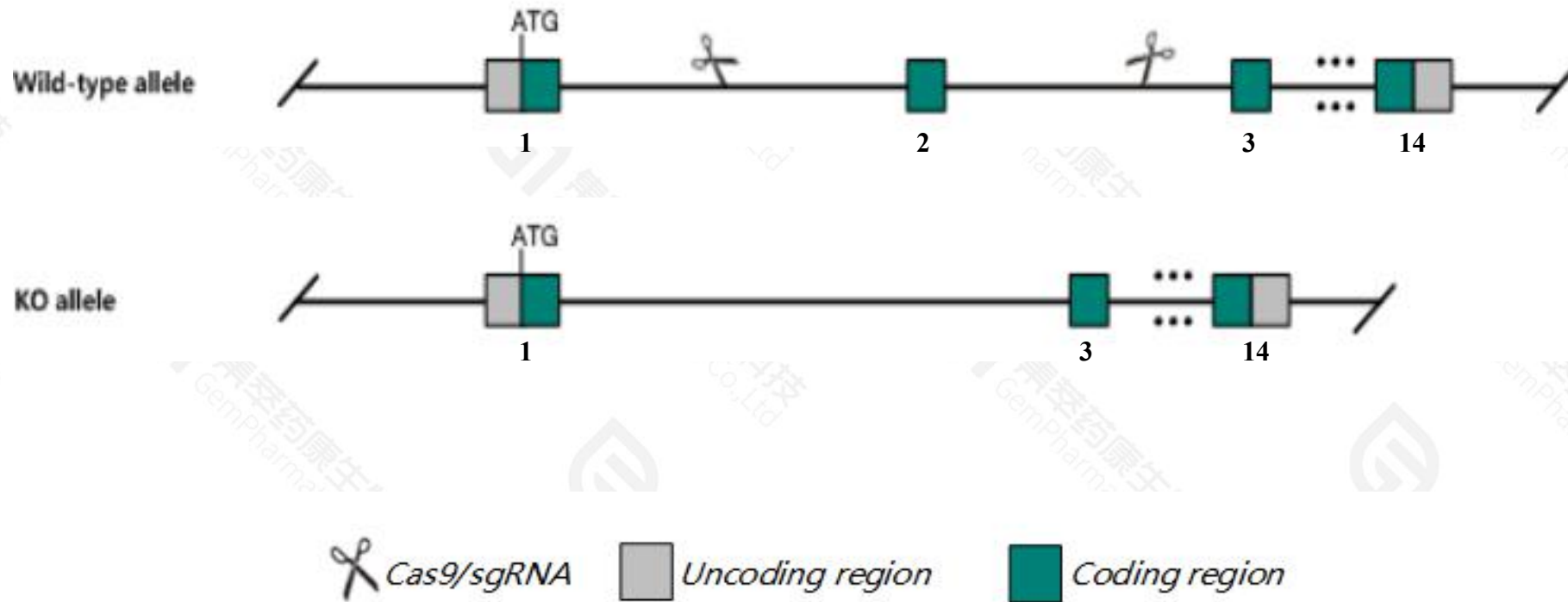
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pias1* gene. The schematic diagram is as follows:



- The *Pias1* gene has 5 transcripts. According to the structure of *Pias1* gene, exon2 of *Pias1-201*(ENSMUST00000098651.6) transcript is recommended as the knockout region. The region contains 445bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pias1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.



- According to the existing MGI data, homozygous null mice display partial perinatal lethality, reduced body size, decreased susceptibility to viral infection, and increased susceptibility to bacterial infection and LPS-induced endotoxin shock.
- The *Pias1* 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.

## Pias1 protein inhibitor of activated STAT 1 [Mus musculus (house mouse)]

Gene ID: 56469, updated on 17-Dec-2020

### Summary



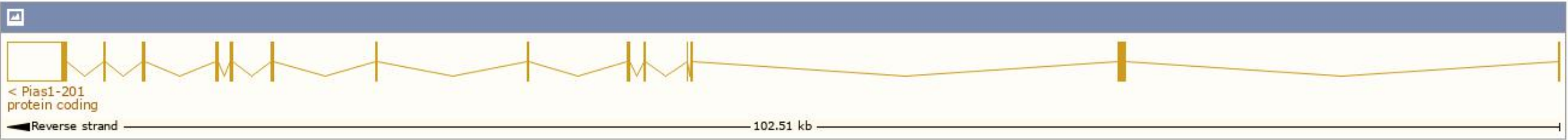
<b>Official Symbol</b>	Pias1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	protein inhibitor of activated STAT 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1913125</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032405</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	2900068C24Rik, Ddxbp, Ddxbp1, GB, GBP
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 32.8), lung adult (RPKM 10.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

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

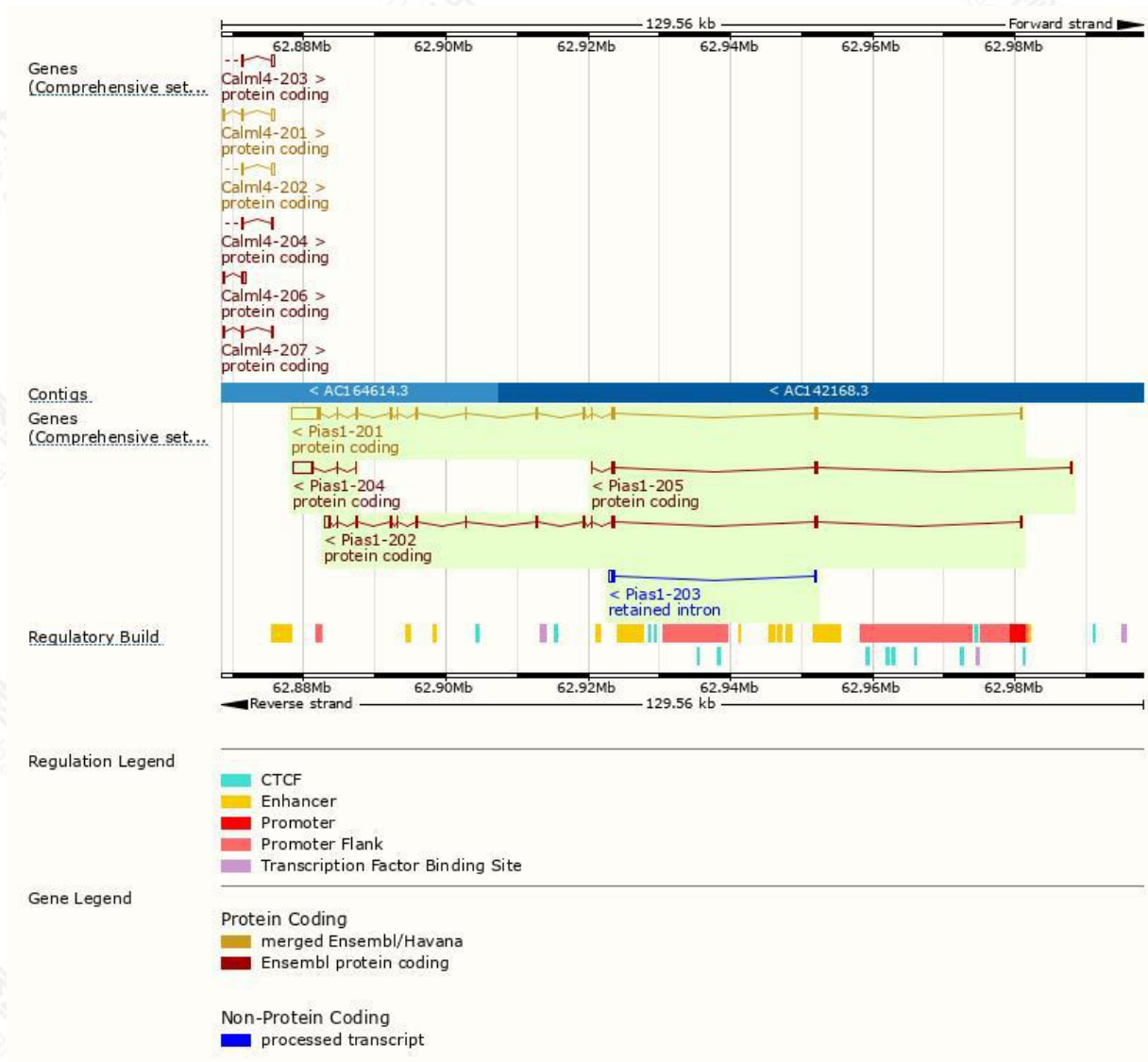
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pias1-201	<a href="#">ENSMUST00000098651.6</a>	5564	<a href="#">651aa</a>	Protein coding	<a href="#">CCDS40665</a>		TSL:1 , GENCODE basic , APPRIS P1 ,
Pias1-204	<a href="#">ENSMUST00000215501.2</a>	2895	<a href="#">85aa</a>	Protein coding	-		CDS 5' incomplete , TSL:1 ,
Pias1-202	<a href="#">ENSMUST00000214830.2</a>	2492	<a href="#">577aa</a>	Protein coding	-		TSL:1 , GENCODE basic ,
Pias1-205	<a href="#">ENSMUST00000216209.2</a>	739	<a href="#">222aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Pias1-203	<a href="#">ENSMUST00000215455.2</a>	748	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Pias1-201* transcript,the transcription is shown below:



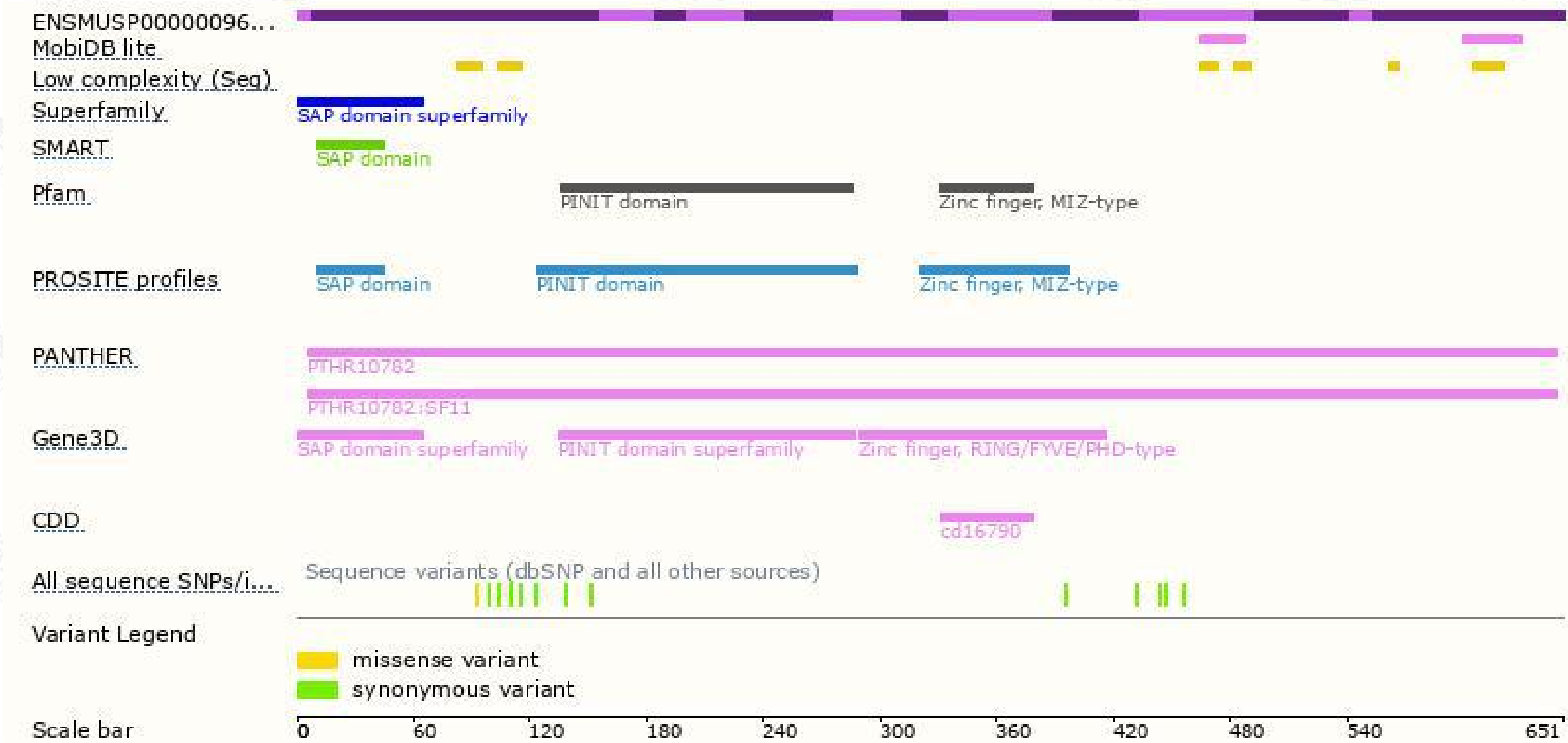


# Genomic location distribution

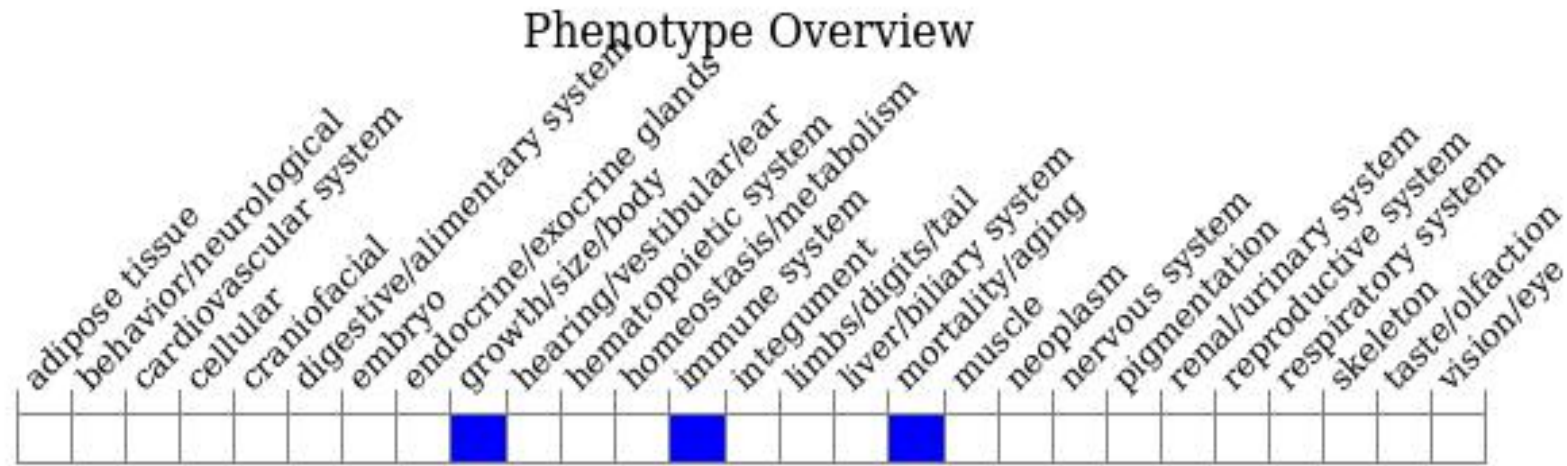




# Protein domain



# 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, homozygous null mice display partial perinatal lethality, reduced body size, decreased susceptibility to viral infection, and increased susceptibility to bacterial infection and LPS-induced endotoxin shock.

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

Tel: 025-5864 1534

