Slc17a9 Cas9-KO Strategy

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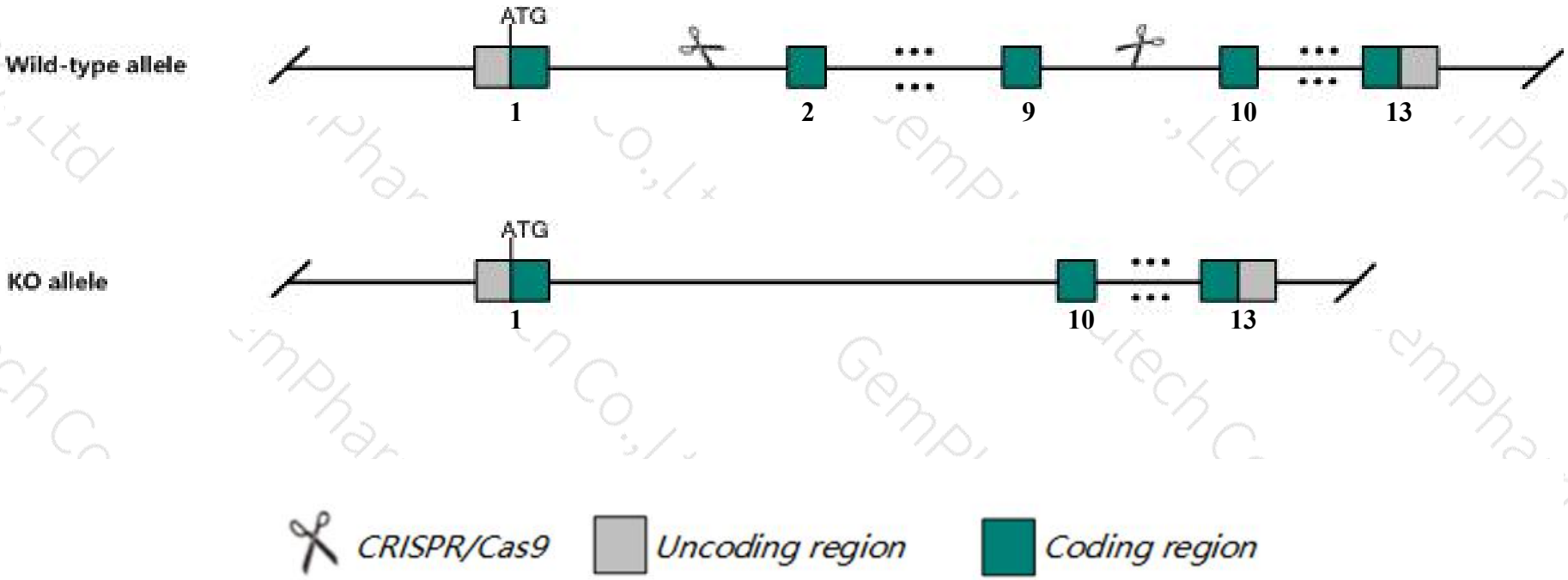
Design Date: 2020-2-14

Project Overview

Project Name	***Slc17a9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc17a9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc17a9* gene has 5 transcripts. According to the structure of *Slc17a9* gene, exon2-exon9 of *Slc17a9-201* (ENSMUST00000094218.3) transcript is recommended as the knockout region.The region contains 886bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc17a9* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Homozygous knockout affects the neuroendocrine system, resulting in hypoglycemia, increased glucose tolerance and increased insulin sensitivity.

- The *Slc17a9* gene is located on the Chr2. 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）

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Slc17a9 solute carrier family 17, member 9 [Mus musculus (house mouse)]

Gene ID: 228993, updated on 6-Apr-2019

Summary

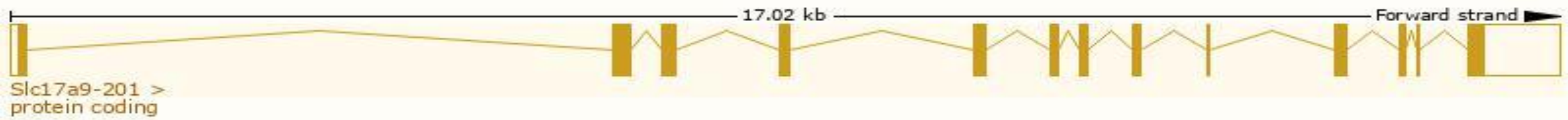
Official Symbol	Slc17a9 provided by MGI
Official Full Name	solute carrier family 17, member 9 provided by MGI
Primary source	MGI:MGI:1919107
See related	Ensembl:ENSMUSG00000023393
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700019H03Rik, BC019537, Vnut
Expression	Biased expression in colon adult (RPKM 55.9), genital fat pad adult (RPKM 48.4) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

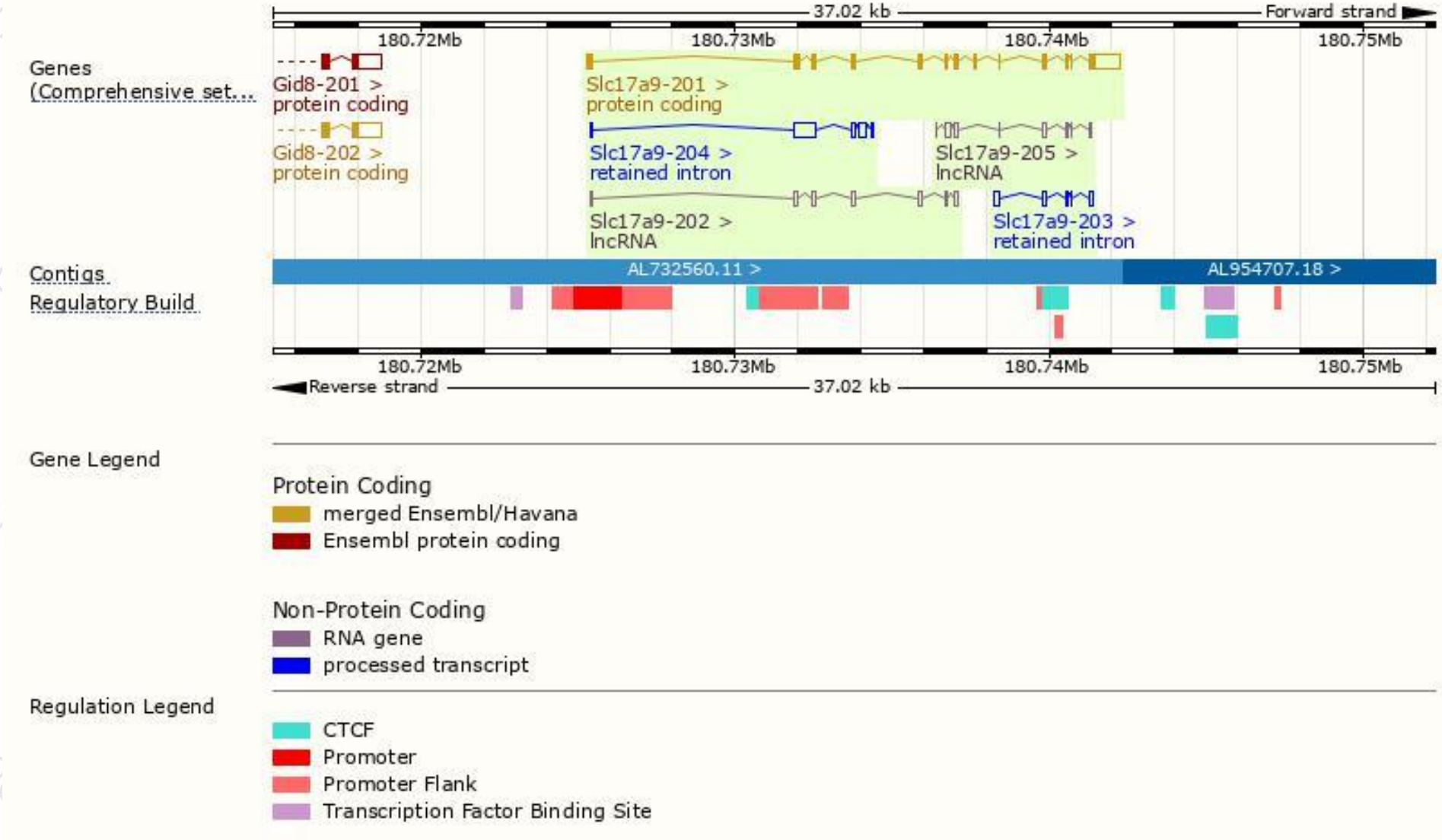
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc17a9-201	ENSMUST00000094218.3	2275	447aa	Protein coding	CCDS38378	Q8VCL5	TSL:5 GENCODE basic APPRIS P1
Slc17a9-204	ENSMUST00000151882.7	1158	No protein	Retained intron	-	-	TSL:5
Slc17a9-203	ENSMUST00000140955.1	506	No protein	Retained intron	-	-	TSL:3
Slc17a9-202	ENSMUST00000139817.1	754	No protein	lncRNA	-	-	TSL:5
Slc17a9-205	ENSMUST00000154882.7	621	No protein	lncRNA	-	-	TSL:1

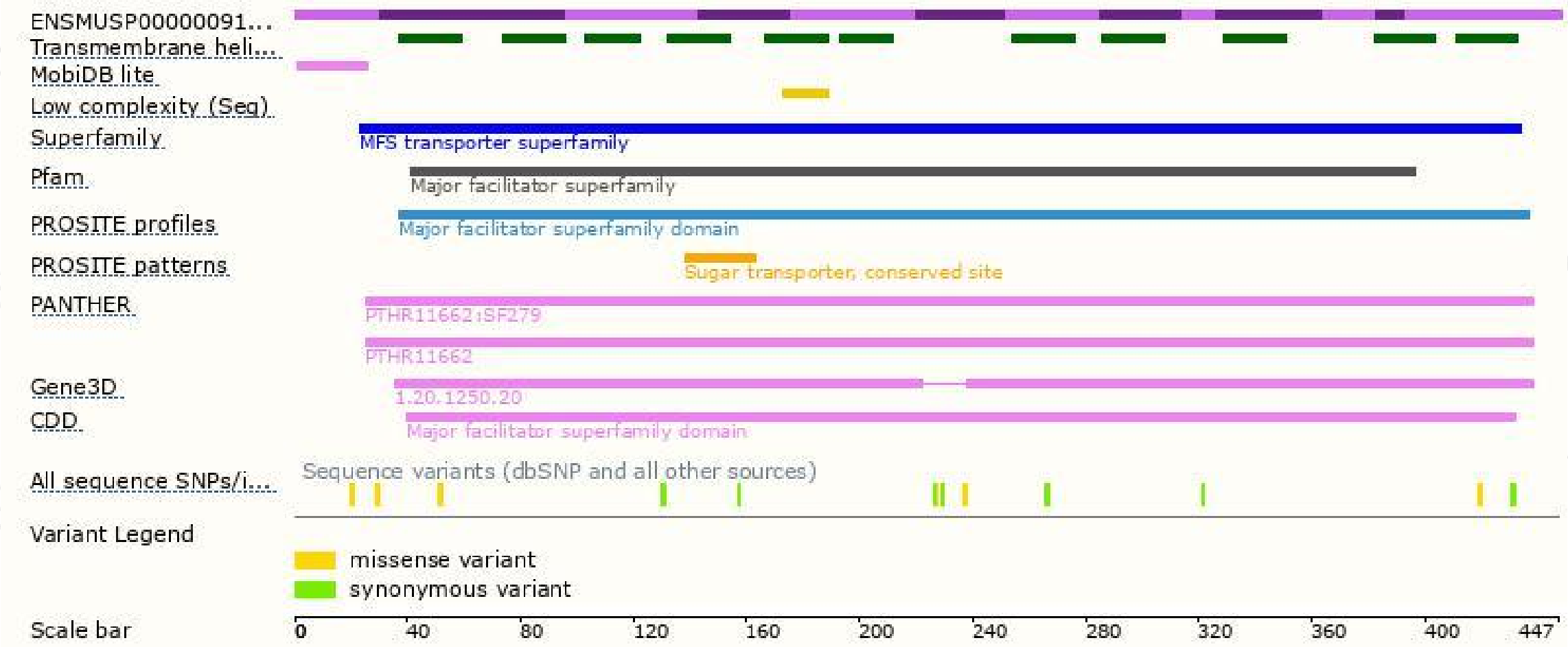
The strategy is based on the design of *Slc17a9-201* transcript,The transcription is shown below



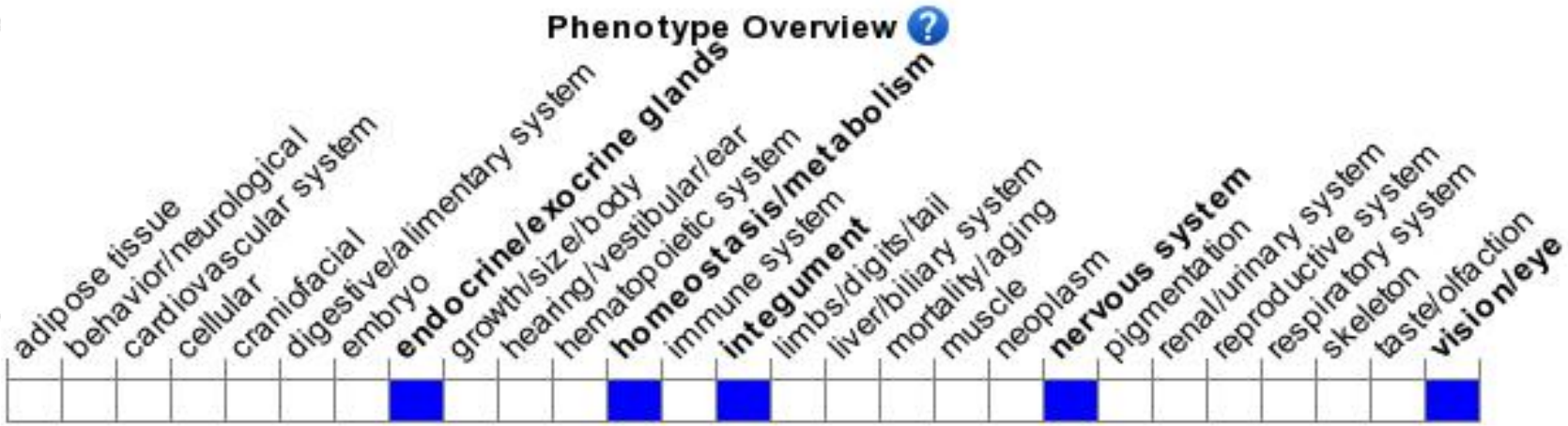
Genomic location distribution



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 knockout affects the neuroendocrine system, resulting in hypoglycemia, increased glucose tolerance and increased insulin sensitivity.

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

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