

Rgs16 Cas9-CKO Strategy

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Project Overview

Project Name

Rgs16

Project type

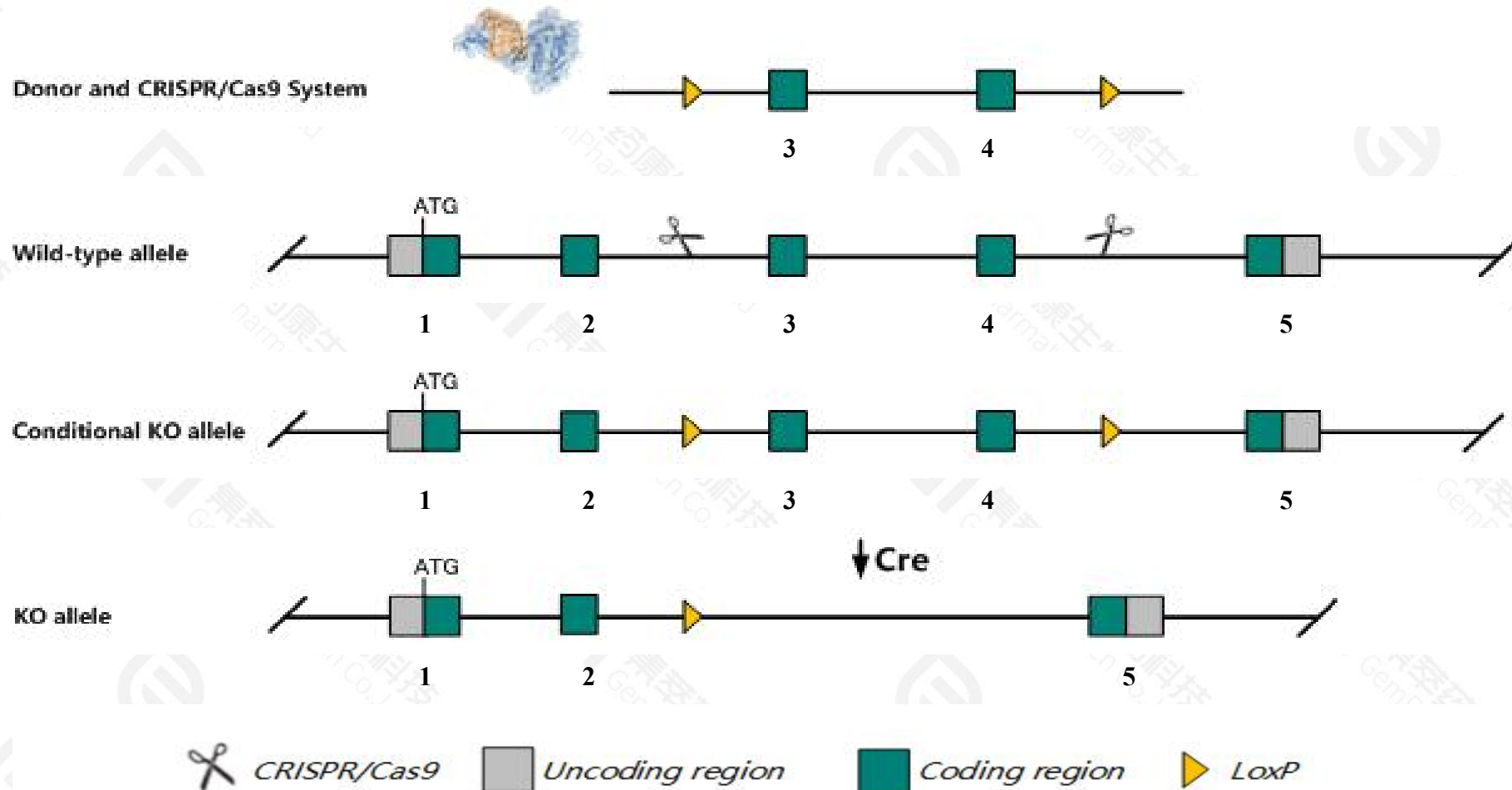
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rgs16* gene. The schematic diagram is as follows:



Technical routes

- The *Rgs16* gene has 1 transcript. According to the structure of *Rgs16* gene, exon3-exon4 of *Rgs16-201*(ENSMUST00000027748.8) transcript is recommended as the knockout region. The region contains 229bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rgs16* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased fatty acid oxidation and circulating ketone levels when fed a high-fat diet. Mice homozygous for a different knock-out allele exhibit impaired Th1 and Th2 chemotaxis and increased susceptibility to parasitic infection.
- The *Rgs16* gene is located on the Chr1. 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)

Rgs16 regulator of G-protein signaling 16 [Mus musculus (house mouse)]

Gene ID: 19734, updated on 13-Mar-2020

Summary



Official Symbol Rgs16 provided by [MGI](#)

Official Full Name regulator of G-protein signaling 16 provided by [MGI](#)

Primary source [MGI:MGI:108407](#)

See related [Ensembl:ENSMUSG00000026475](#)

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 Rgs14, Rgsr

Expression Broad expression in liver E18 (RPKM 12.8), CNS E11.5 (RPKM 10.4) and 15 other tissues [See more](#)

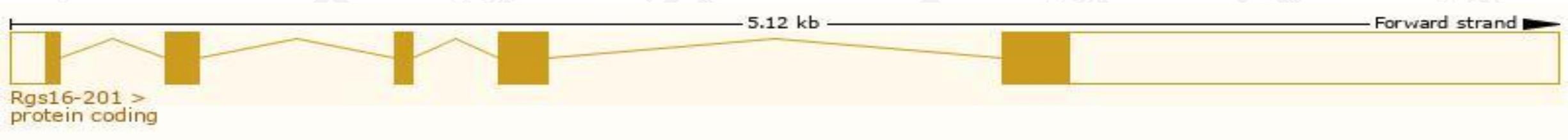
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

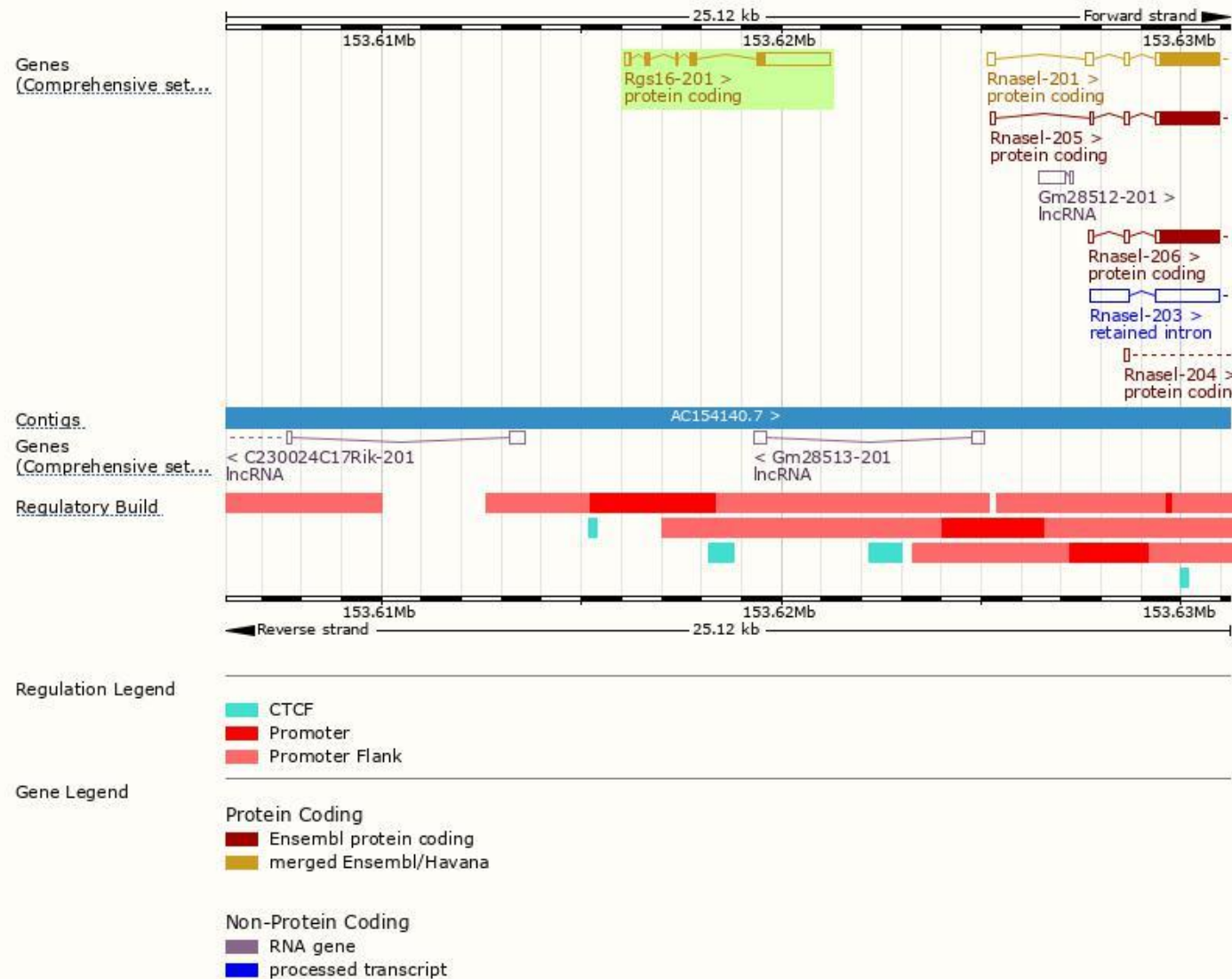
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rgs16-201	ENSMUST00000027748.7	2339	201aa	Protein coding	CCDS15376	P97428 Q542U0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

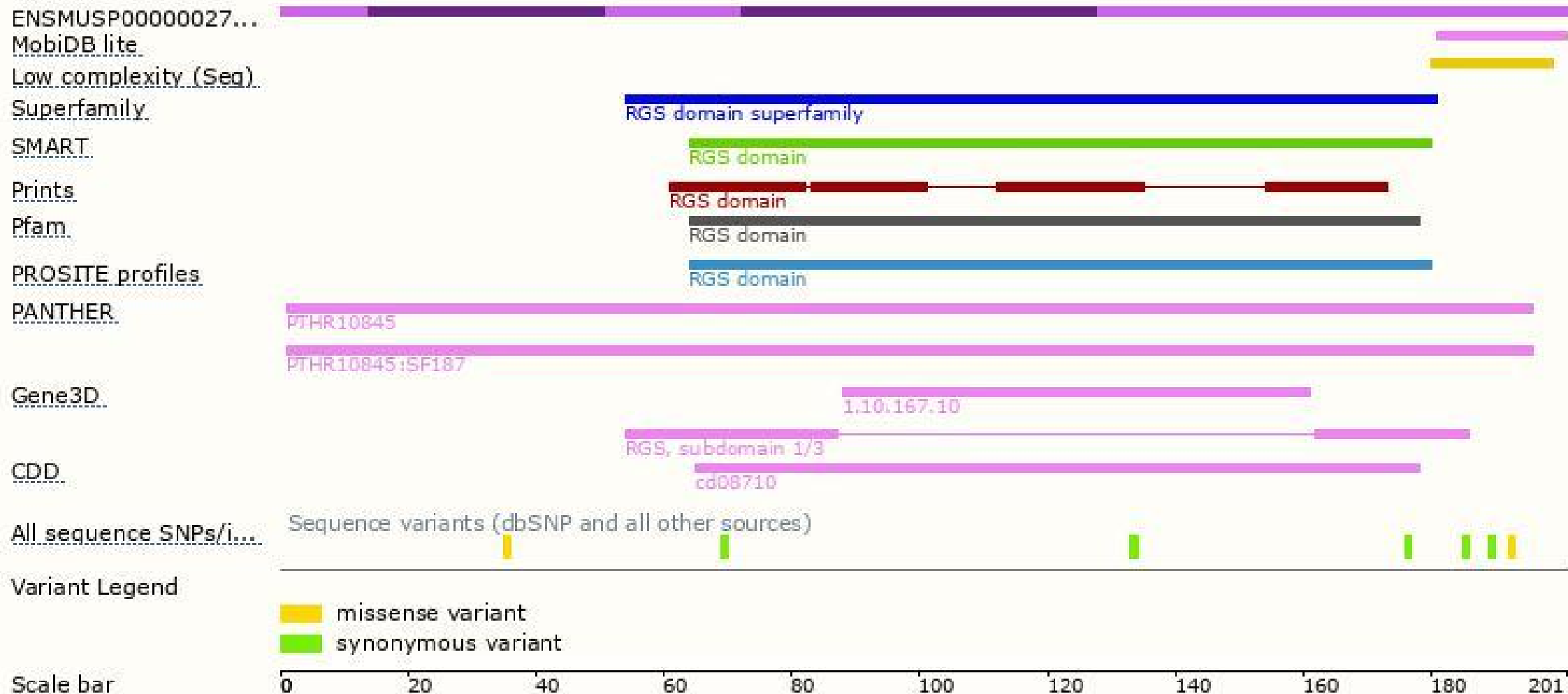
The strategy is based on the design of *Rgs16-201* transcript, the transcription is shown below:



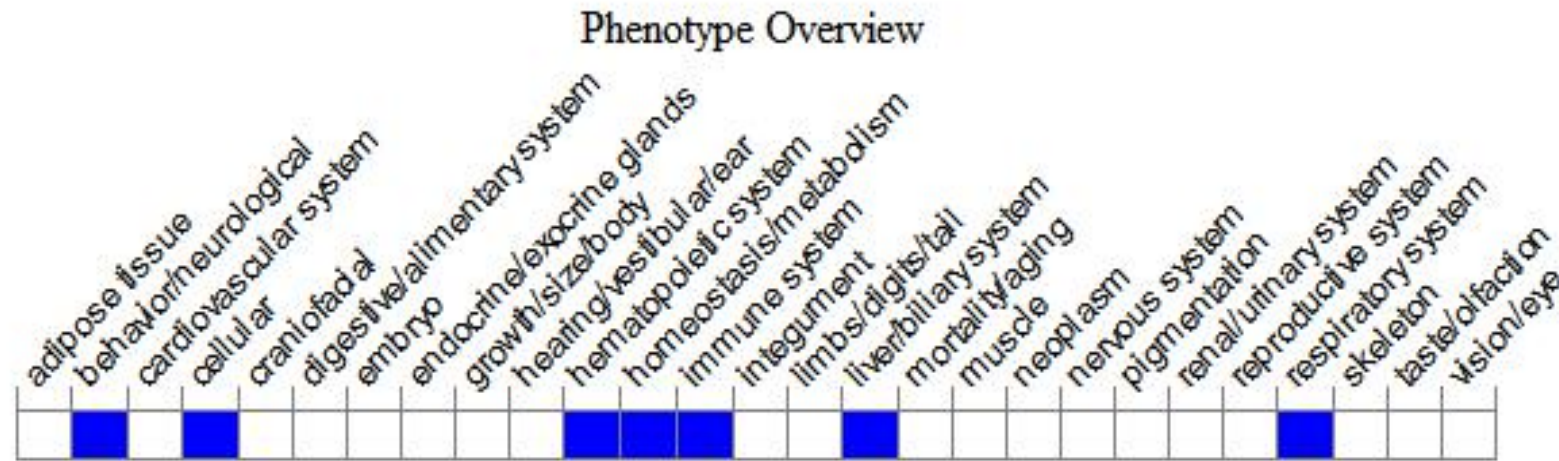
Genomic location distribution



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 knock-out allele exhibit increased fatty acid oxidation and circulating ketone levels when fed a high-fat diet. Mice homozygous for a different knock-out allele exhibit impaired Th1 and Th2 chemotaxis and increased susceptibility to parasitic infection.

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