

Mgl Cas9-KO Strategy

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Project Overview

Project Name

Mgll

Project type

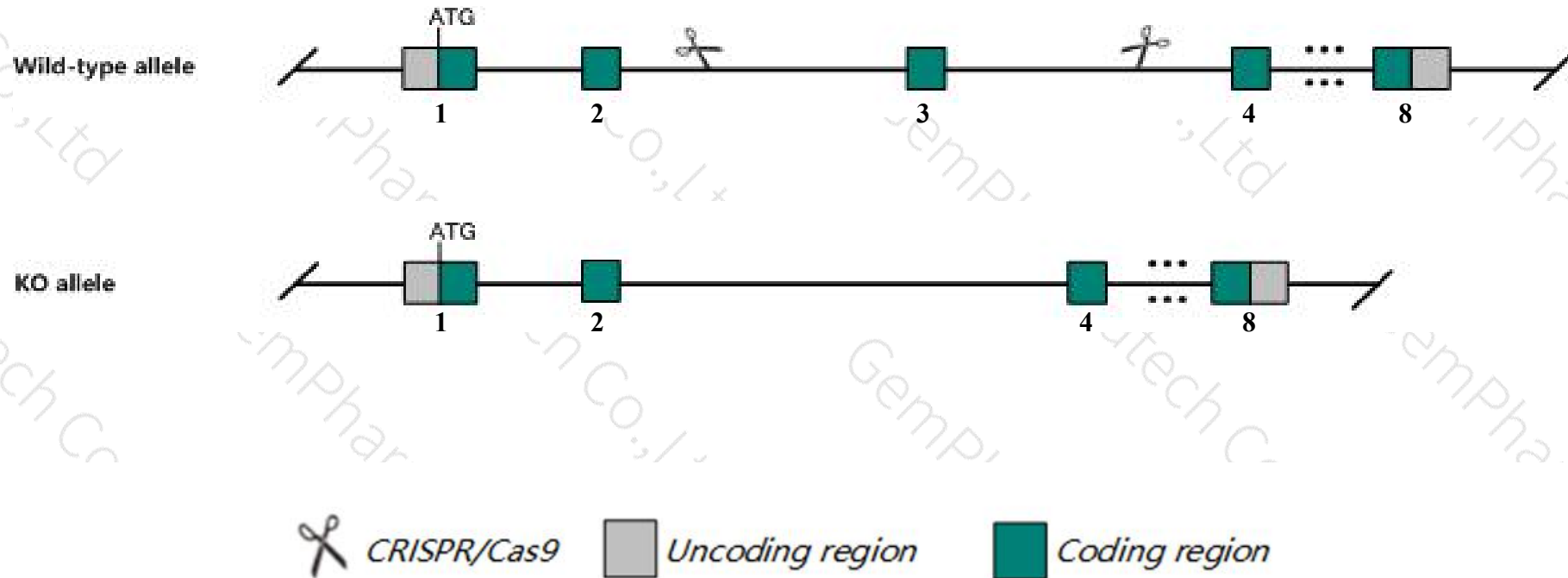
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Mgll* gene has 10 transcripts. According to the structure of *Mgll* gene, exon3 of *Mgll*-207 (ENSMUST00000163271.7) transcript is recommended as the knockout region. The region contains 107bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mgll* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a gene trapped allele exhibit hypoalgesia, increased body temperature, and decreased fatty acid levels. Mice homozygous for a targeted allele exhibit impaired lipolysis and improved glucose homeostasis on a high-fat diet.
- Transcript *Mgll*-206&210 may not be affected.
- The *Mgll* gene is located on the Chr6. 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)

Mgll monoglyceride lipase [Mus musculus (house mouse)]

Gene ID: 23945, updated on 31-Jan-2019

Summary



Official Symbol Mgll provided by [MGI](#)

Official Full Name monoglyceride lipase provided by [MGI](#)

Primary source [MGI:MGI:1346042](#)

See related [Ensembl:ENSMUSG00000033174](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AA589436, Magl, Mgl

Summary This gene encodes a monoglyceride lipase, which catalyzes the hydrolysis of monoglycerides into fatty acids and glycerol. This enzyme is also thought to hydrolyze the endocannabinoid 2-arachidonoylglycerol. Alternatively spliced transcript variants have been described. [provided by RefSeq, Oct 2009]

Expression Biased expression in subcutaneous fat pad adult (RPKM 221.3), genital fat pad adult (RPKM 144.9) and 14 other tissues [See more](#)

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

Transcript information (Ensembl)

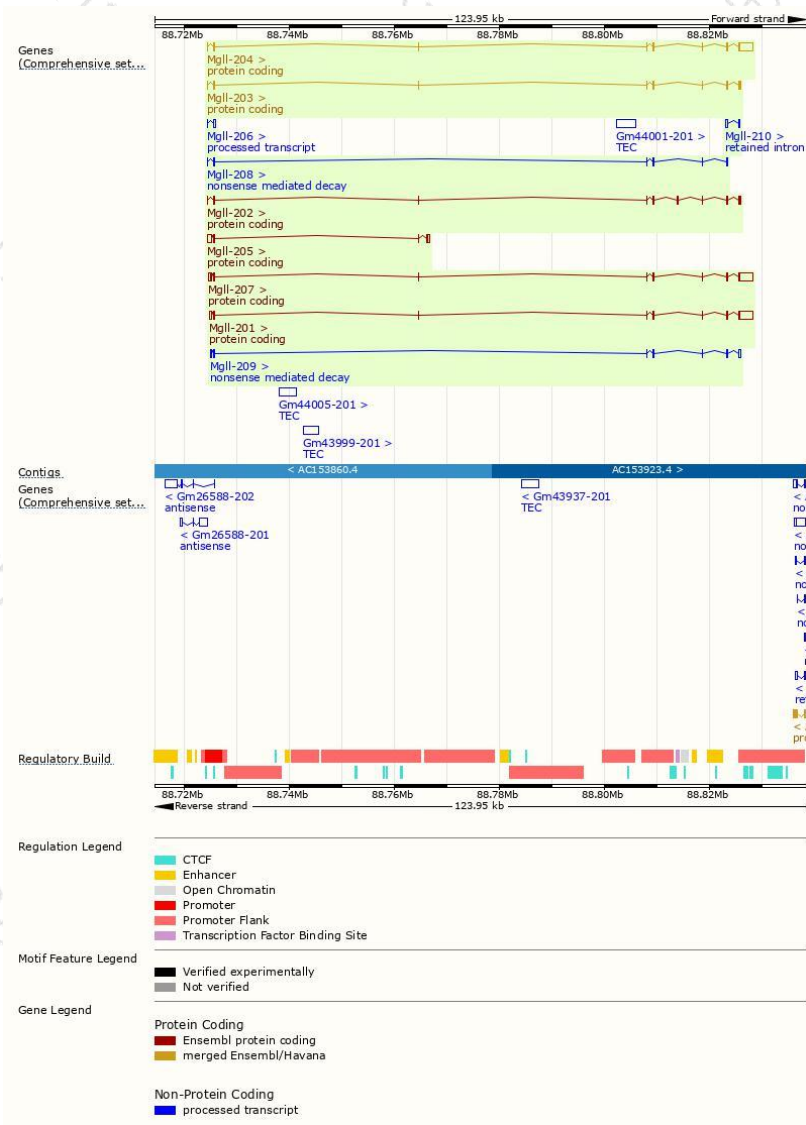
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
MgII-207	ENSMUST00000163271.7	3991	319aa	Protein coding	CCDS51843	E9Q3B9	TSL:1 GENCODE basic
MgII-201	ENSMUST00000089449.4	3867	303aa	Protein coding	CCDS20338	O35678	TSL:1 GENCODE basic APPRIS P1
MgII-204	ENSMUST00000113585.8	3676	303aa	Protein coding	CCDS20338	O35678	TSL:1 GENCODE basic APPRIS P1
MgII-203	ENSMUST00000113582.7	1034	258aa	Protein coding	CCDS51844	Q3UFN1	TSL:1 GENCODE basic
MgII-205	ENSMUST00000150180.3	1312	116aa	Protein coding	-	O35678	TSL:1 GENCODE basic
MgII-202	ENSMUST00000113581.7	1308	331aa	Protein coding	-	D3YYS6	TSL:5 GENCODE basic
MgII-209	ENSMUST00000203824.1	1025	47aa	Nonsense mediated decay	-	A0A0N4SUZ2	TSL:5
MgII-208	ENSMUST00000203608.2	767	47aa	Nonsense mediated decay	-	A0A0N4SUZ2	TSL:3
MgII-206	ENSMUST00000151699.3	443	No protein	Processed transcript	-	-	TSL:2
MgII-210	ENSMUST00000205045.1	460	No protein	Retained intron	-	-	TSL:2

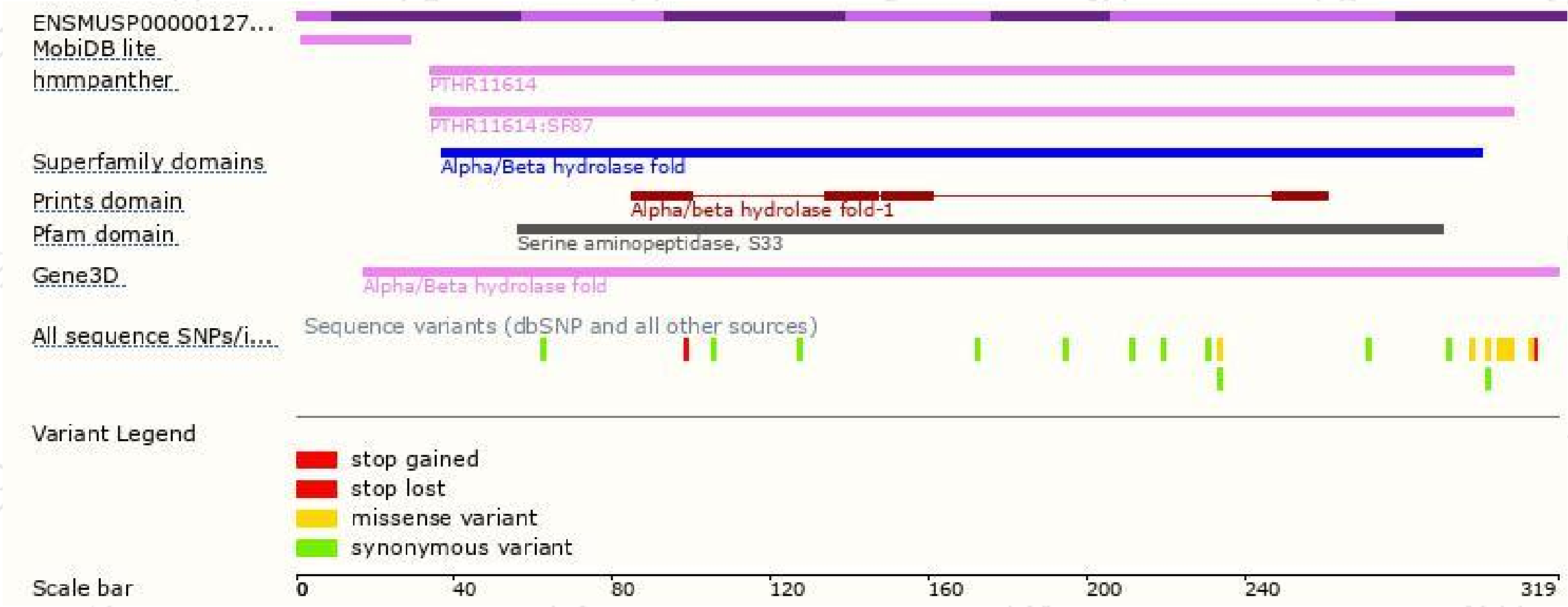
The strategy is based on the design of *MgII-207* transcript,The transcription is shown below



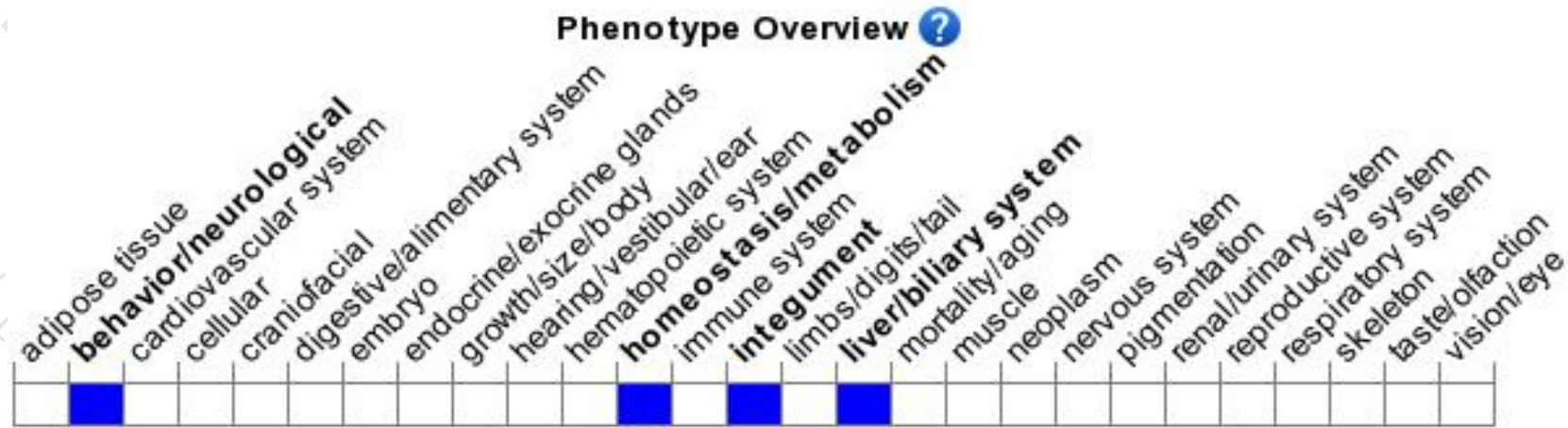
Genomic location distribution



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 trapped allele exhibit hypoalgesia, increased body temperature, and decreased fatty acid levels. Mice homozygous for a targeted allele exhibit impaired lipolysis and improved glucose homeostasis on a high-fat diet.

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

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