

Agpat2 Cas9-KO Strategy

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Design Date:

2019-11-5

Project Overview

Project Name

Agpat2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Agpat2* gene. The schematic diagram is as follows:



- The *Agpat2* gene has 5 transcripts. According to the structure of *Agpat2* gene, exon2-exon4 of *Agpat2-201* (ENSMUST00000028286.11) transcript is recommended as the knockout region. The region contains 406bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Agpat2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit loss of white and brown adipose tissue, insulin resistance, and hepatic steatosis.
- The KO region contains functional region of the *Gm20532* gene. Knockout the region may affect the function of *Gm20532* gene.
- The *Agpat2* 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)

Agpat2 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) [Mus musculus (house mouse)]

Gene ID: 67512, updated on 31-Jan-2019

Summary



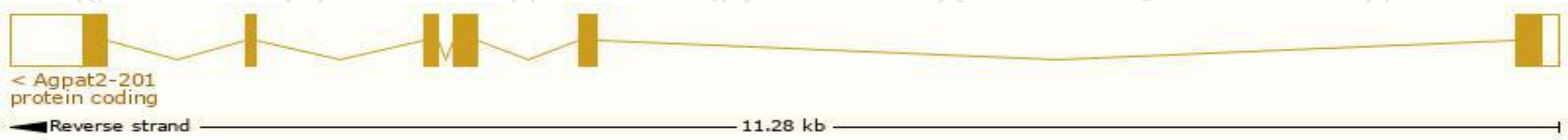
Official Symbol	Agpat2 provided by MGI
Official Full Name	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) provided by MGI
Primary source	MGI:MGI:1914762
See related	Ensembl:ENSMUSG00000026922
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2510002J07Rik, AV000834, BSCL, BSCL1, LPAAB, LPAAT-beta
Expression	Broad expression in subcutaneous fat pad adult (RPKM 450.2), mammary gland adult (RPKM 425.2) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

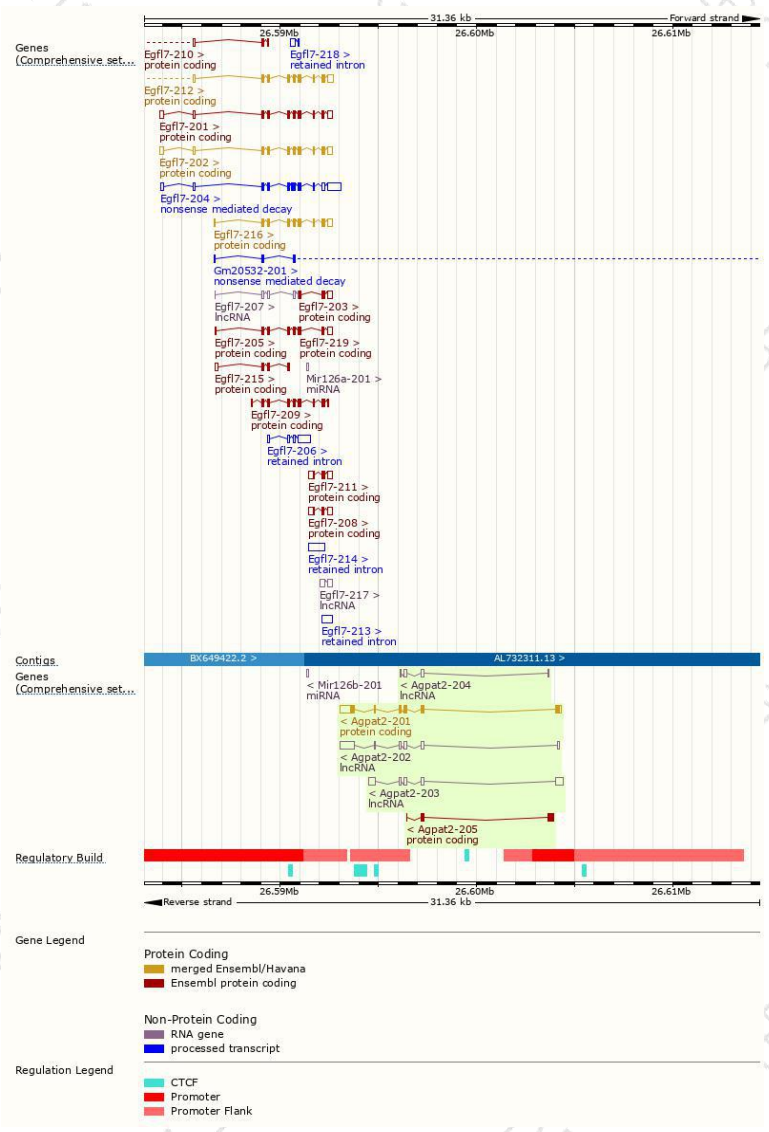
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Agpat2-201	ENSMUST00000028286.11	1489	278aa	Protein coding	CCDS15809	Q059U0 Q8K3K7	TSL:1 GENCODE basic APPRIS P1
Agpat2-205	ENSMUST00000154753.1	438	129aa	Protein coding	-	A2AI22	CDS 3' incomplete TSL:3
Agpat2-202	ENSMUST00000131940.7	1273	No protein	lncRNA	-	-	TSL:5
Agpat2-203	ENSMUST00000140386.7	1145	No protein	lncRNA	-	-	TSL:1
Agpat2-204	ENSMUST00000140508.1	424	No protein	lncRNA	-	-	TSL:5

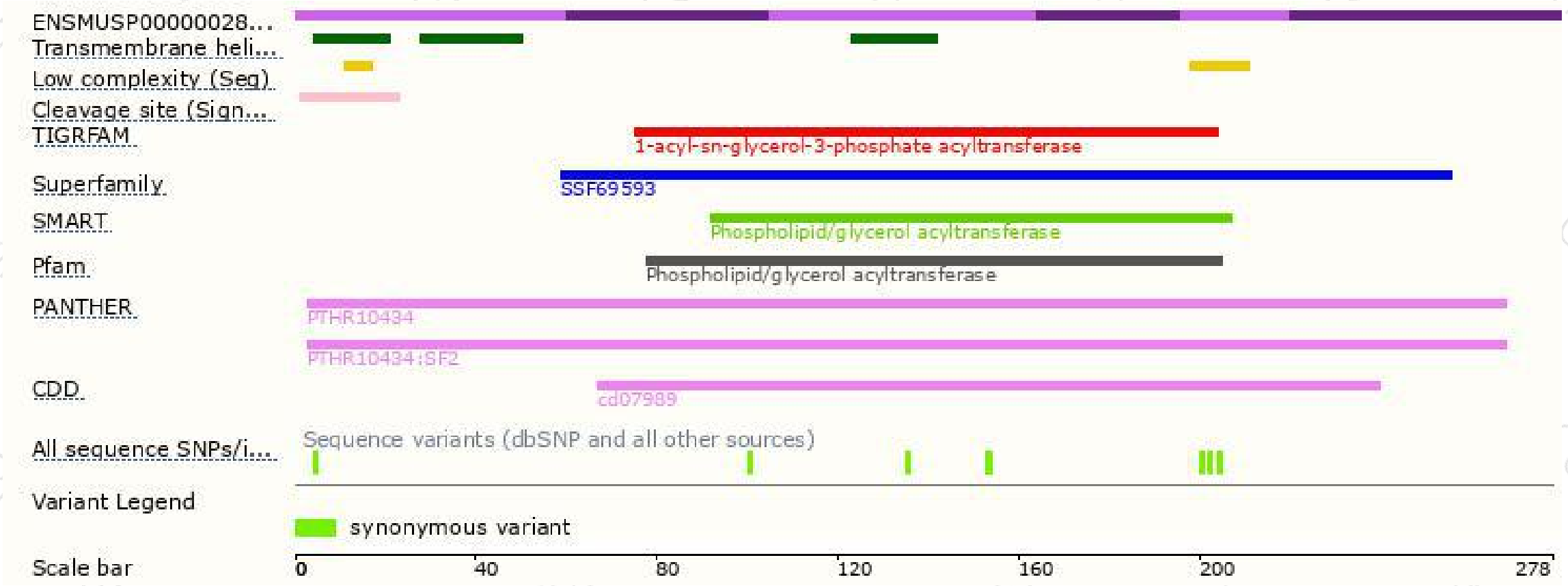
The strategy is based on the design of *Agpat2-201* transcript,The transcription is shown below



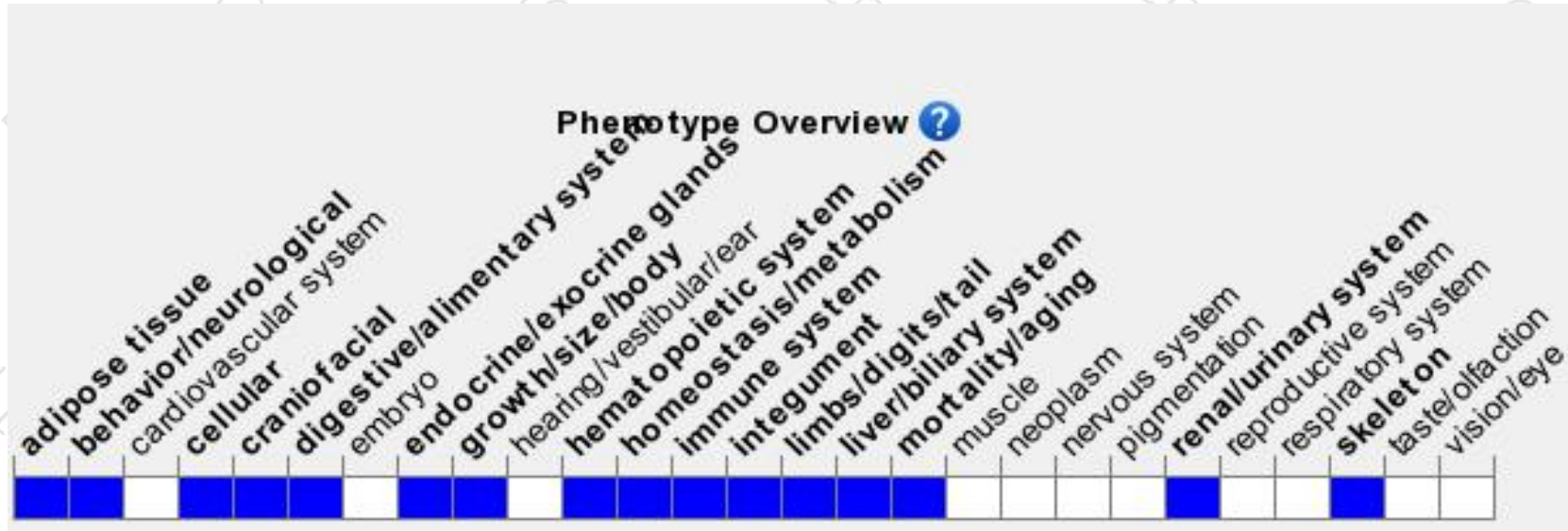
Genomic location distribution



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 loss of white and brown adipose tissue, insulin resistance, and hepatic steatosis.

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

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