

Agpat5 Cas9-CKO Strategy

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Project Overview

Project Name

Agpat5

Project type

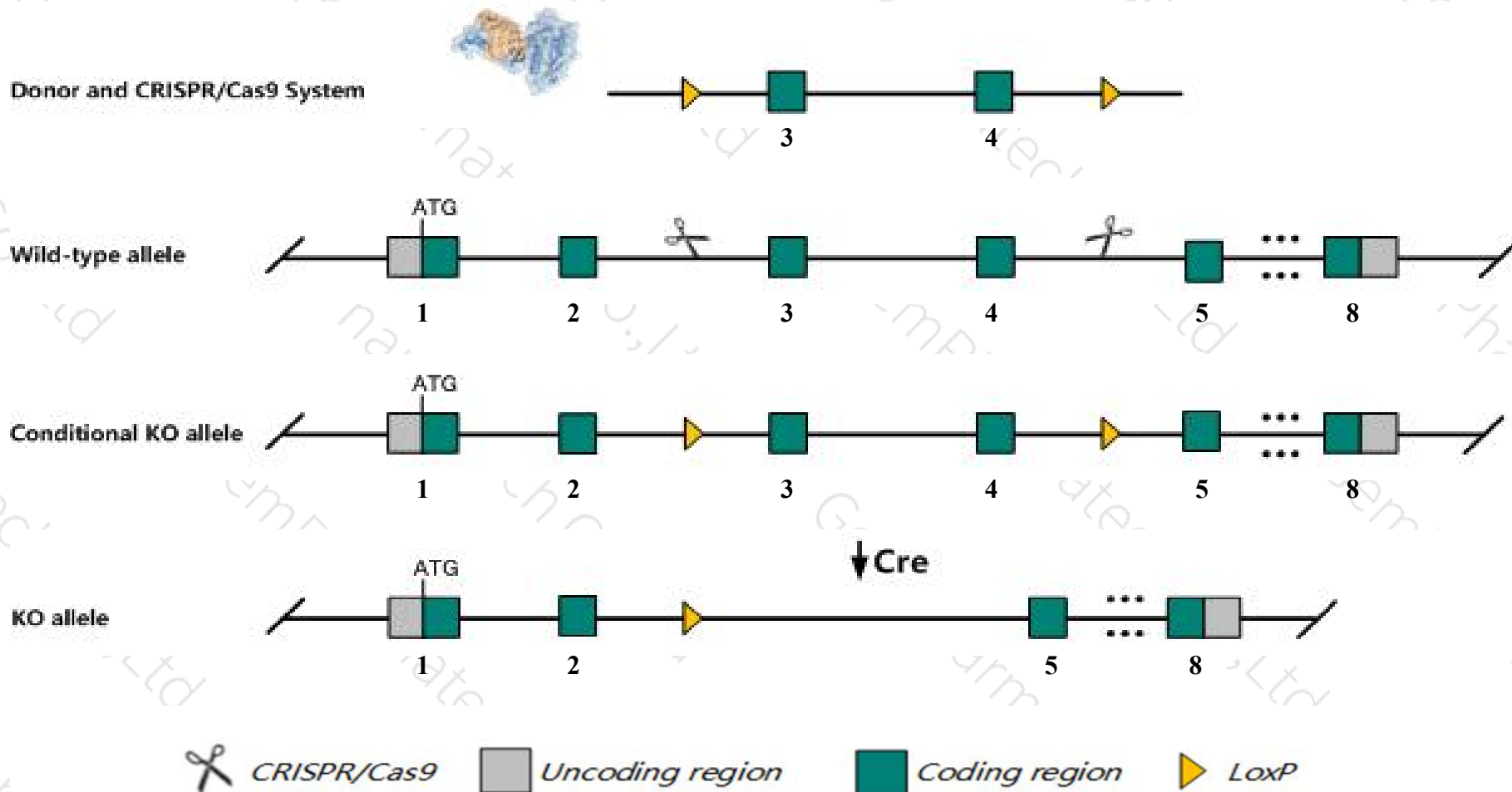
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Agpat5* gene. The schematic diagram is as follows:



- The *Agpat5* gene has 2 transcripts. According to the structure of *Agpat5* gene, exon3-exon4 of *Agpat5*-202 (ENSMUST00000149565.7) transcript is recommended as the knockout region. The region contains 206bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Agpat5* 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 disruptions in this gene display moderate fatty changes in the liver.
- The *Agpat5* gene is located on the Chr8. 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)

Agpat5 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) [Mus musculus (house mouse)]

Gene ID: 52123, updated on 13-Mar-2020

Summary



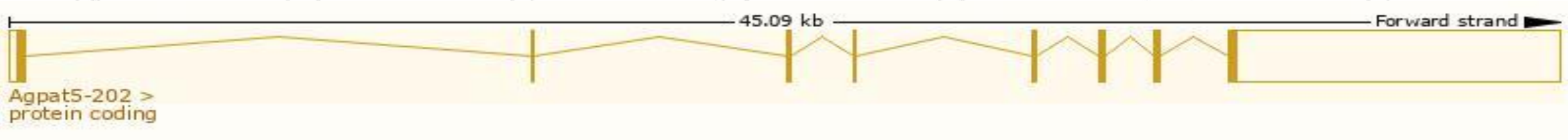
Official Symbol	Agpat5 provided by MGI
Official Full Name	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) provided by MGI
Primary source	MGI:MGI:1196345
See related	Ensembl:ENSMUSG00000031467
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110013A05Rik, D8Ertd319e
Expression	Ubiquitous expression in ovary adult (RPKM 12.3), placenta adult (RPKM 11.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Agpat5-202	ENSMUST00000149565.7	10779	365aa	Protein coding	CCDS22126	Q9D1E8	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 P2
Agpat5-201	ENSMUST00000033847.4	2841	291aa	Protein coding	-	F8WGD9	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 ALT2

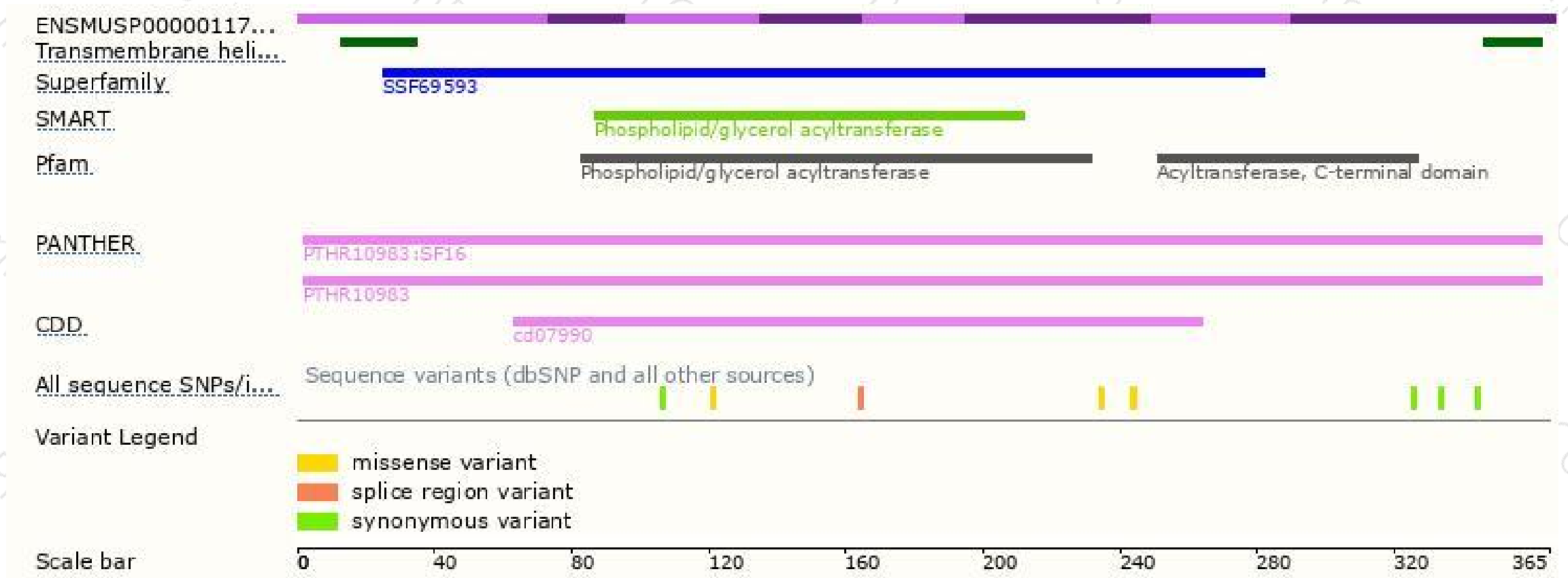
The strategy is based on the design of *Agpat5-202* transcript,The transcription is shown below



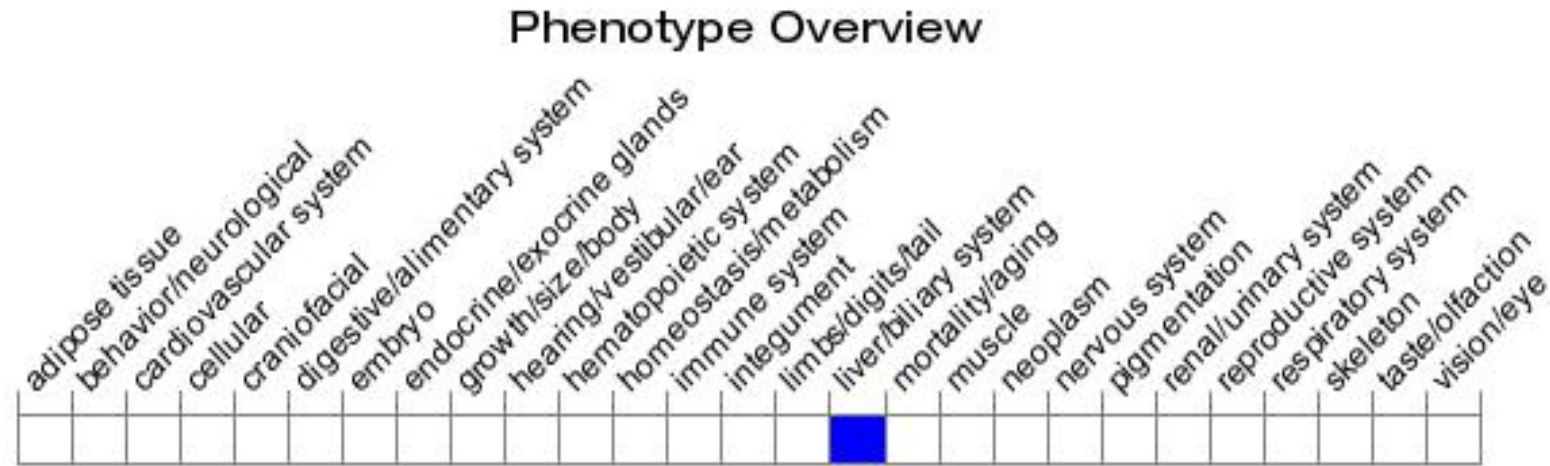
Genomic location distribution



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 disruptions in this gene display moderate fatty changes in the liver.

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

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