

# ***Fads1* Cas9-KO Strategy**

Designer: Xiaojing Li

Reviewer: Jia Yu

Design Date: 2020-2-26

# Project Overview

**Project Name**

*Fads1*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fads1* gene. The schematic diagram is as follows:



- The *Fads1* gene has 8 transcripts. According to the structure of *Fads1* gene, exon1-exon5 of *Fads1-201* (ENSMUST00000010807.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fads1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit arachidonic acid deficiency with premature lethality and altered prostaglandin levels. Heterozygous mice exhibit an intermediate phenotype.
- The *Fads1* gene is located on the Chr19. 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)

## Fads1 fatty acid desaturase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 76267, updated on 12-Aug-2019

### Summary

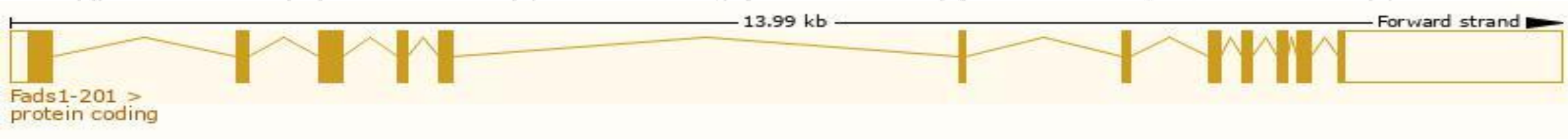
Official Symbol	Fads1 provided by <a href="#">MGI</a>
Official Full Name	fatty acid desaturase 1 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1923517</a>
See related	<a href="#">Ensembl:ENSMUSG00000010663</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	DSD; AI317215; 0710001O03Rik; A930006B21Rik
Expression	Ubiquitous expression in adrenal adult (RPKM 116.7), liver adult (RPKM 83.2) and 23 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

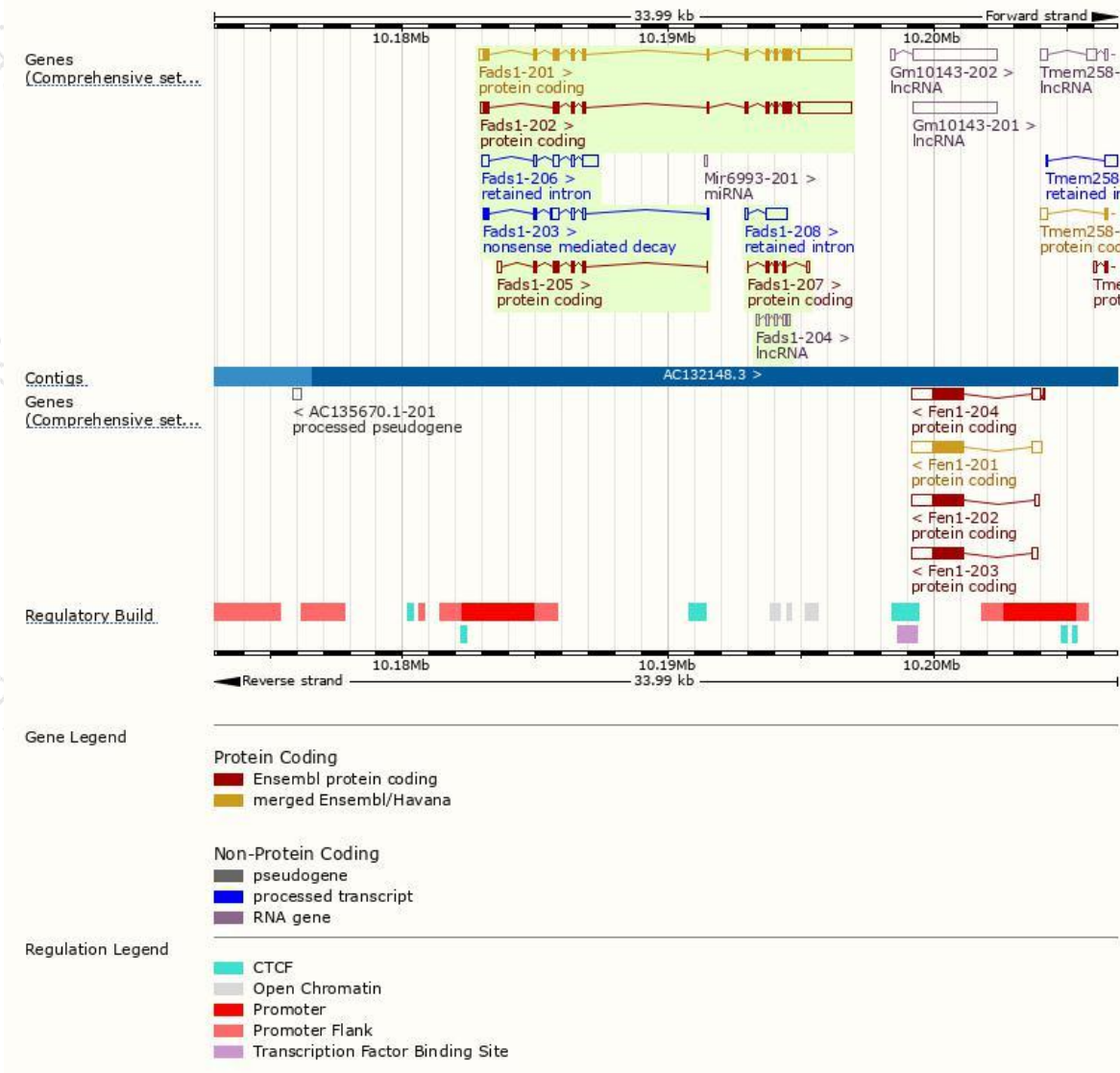
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fads1-201	<a href="#">ENSMUST00000010807.5</a>	3460	<a href="#">447aa</a>	Protein coding	<a href="#">CCDS29572</a>	<a href="#">Q920L1</a>	TSL:1 GENCODE basic APPRIS P1
Fads1-202	<a href="#">ENSMUST00000235160.1</a>	3301	<a href="#">410aa</a>	Protein coding	-	-	GENCODE basic
Fads1-205	<a href="#">ENSMUST00000236594.1</a>	742	<a href="#">179aa</a>	Protein coding	-	-	CDS 3' incomplete
Fads1-207	<a href="#">ENSMUST00000237861.1</a>	422	<a href="#">110aa</a>	Protein coding	-	-	CDS 5' incomplete
Fads1-203	<a href="#">ENSMUST00000235515.1</a>	934	<a href="#">112aa</a>	Nonsense mediated decay	-	-	
Fads1-206	<a href="#">ENSMUST00000237221.1</a>	1310	No protein	Retained intron	-	-	
Fads1-208	<a href="#">ENSMUST00000238115.1</a>	837	No protein	Retained intron	-	-	
Fads1-204	<a href="#">ENSMUST00000236385.1</a>	472	No protein	lncRNA	-	-	

The strategy is based on the design of *Fads1-201* transcript,The transcription is shown below

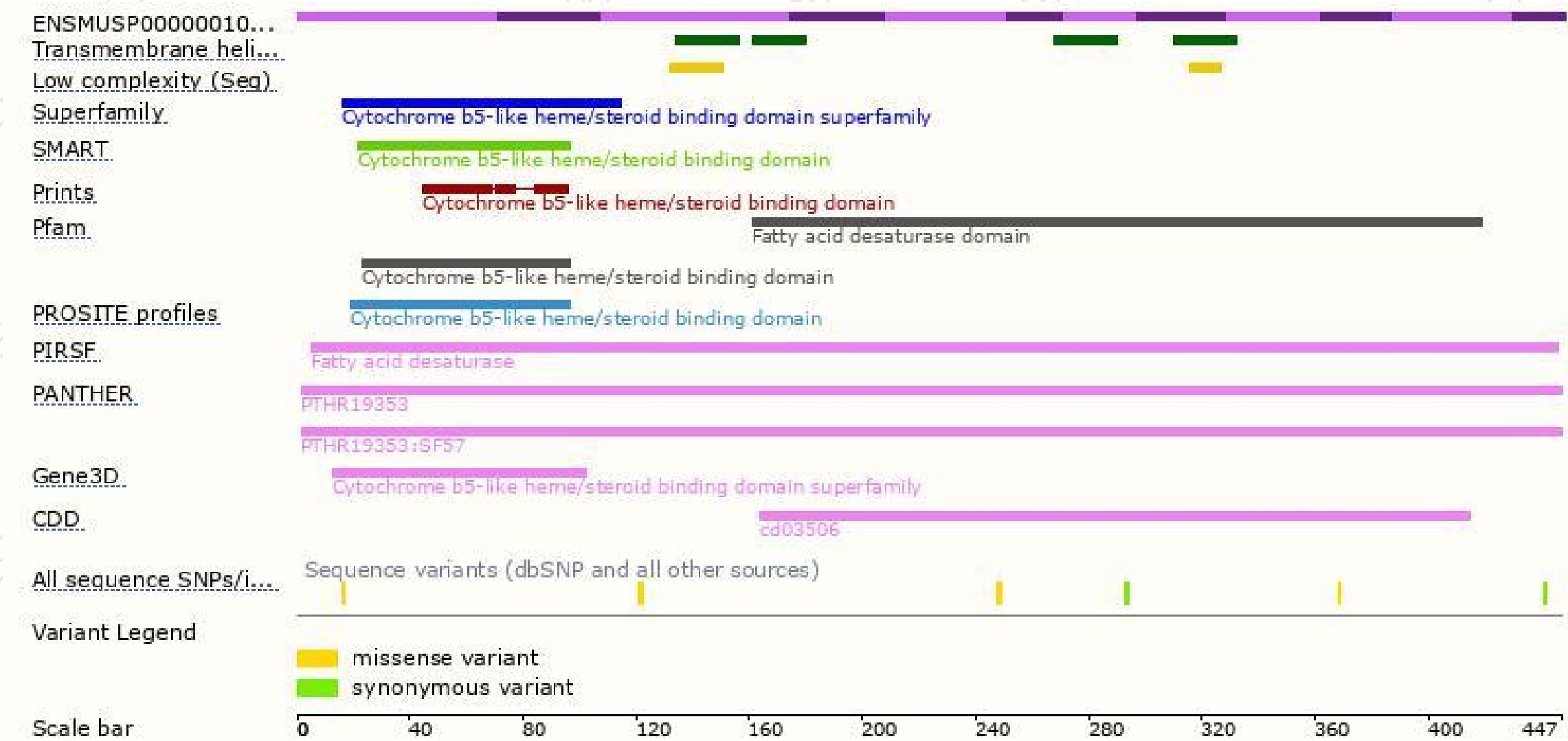


# Genomic location distribution

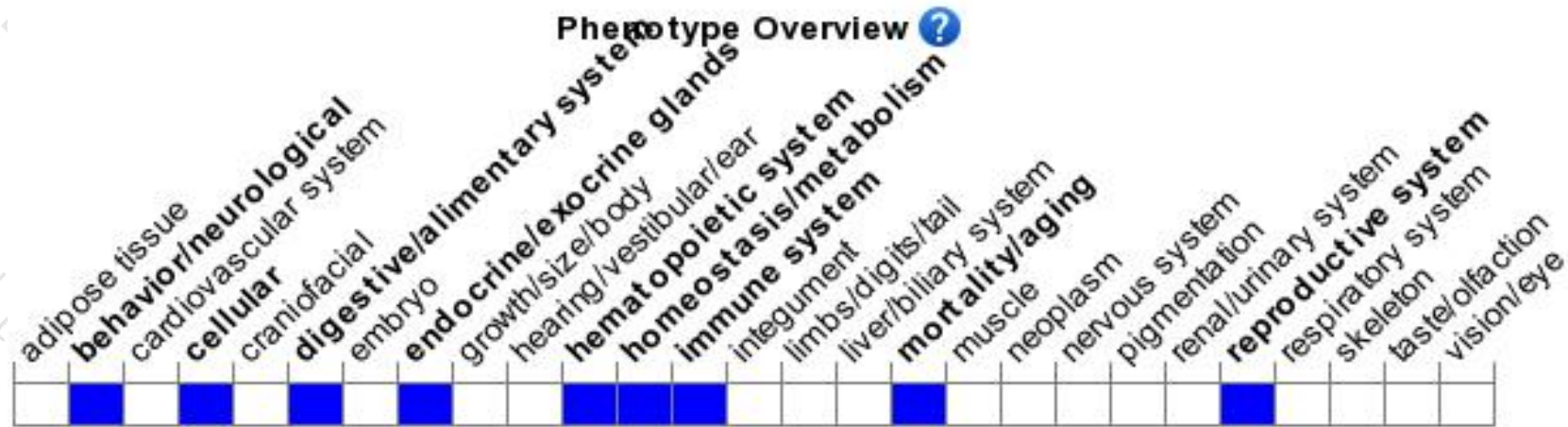




# Protein domain



# 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 arachidonic acid deficiency with premature lethality and altered prostaglandin levels. Heterozygous mice exhibit an intermediate phenotype.

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

Tel: 400-9660890

