

Slc27a5 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Slc27a5

Project type

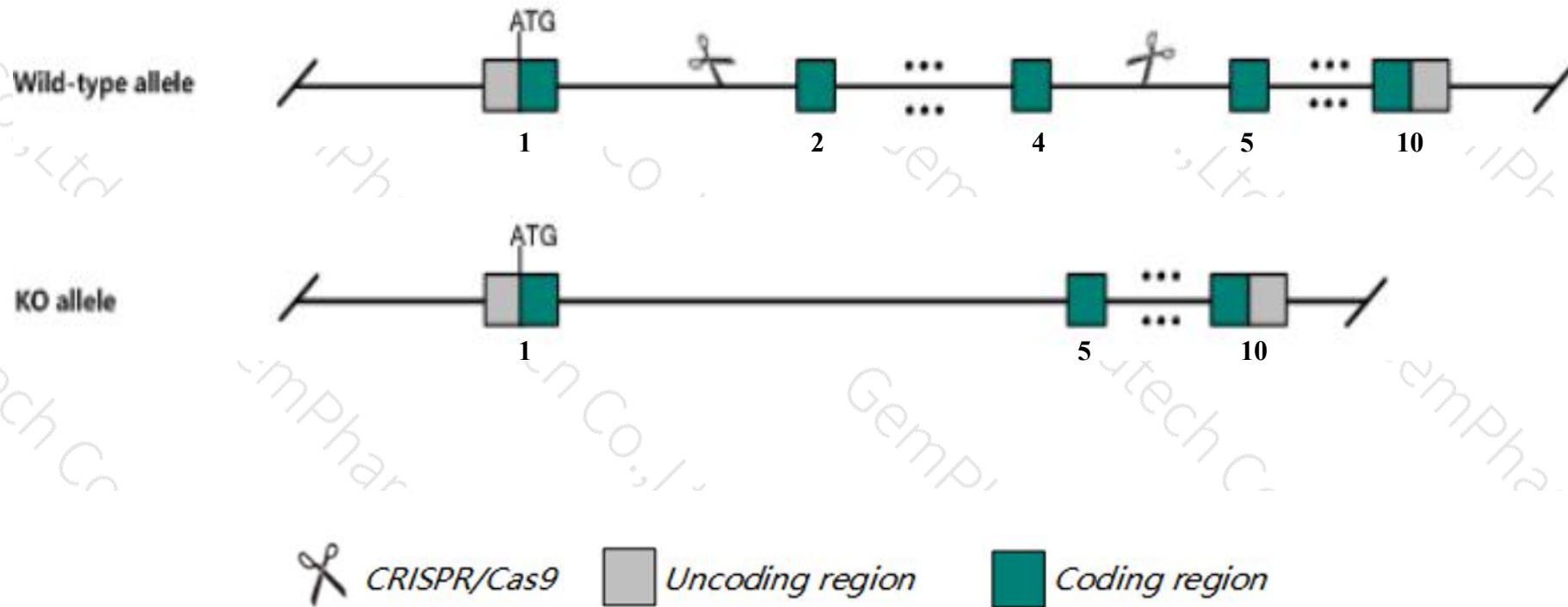
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc27a5* gene. The schematic diagram is as follows:



- The *Slc27a5* gene has 4 transcripts. According to the structure of *Slc27a5* gene, exon2-exon4 of *Slc27a5-201* (ENSMUST00000032539.13) transcript is recommended as the knockout region. The region contains 494bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc27a5* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a null allele exhibit altered lipid homeostasis.
- The *Slc27a5* gene is located on the Chr7. 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)

Slc27a5 solute carrier family 27 (fatty acid transporter), member 5 [*Mus musculus* (house mouse)]

Gene ID: 26459, updated on 27-Feb-2020

Summary

- Official Symbol** Slc27a5 provided by [MGI](#)
- Official Full Name** solute carrier family 27 (fatty acid transporter), member 5 provided by [MGI](#)
- Primary source** [MGI:MGI:1347100](#)
- See related** [Ensembl:ENSMUSG00000030382](#)
- 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** FATP5; FACVL3; VLCSH2; Vlacr; VLCS-H2
- Expression** Restricted expression toward liver adult (RPKM 472.5) [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 7; 7 A1 [See Slc27a5 in Genome Data Viewer](#)

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (12988346..12998192, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (13573695..13583541, complement)

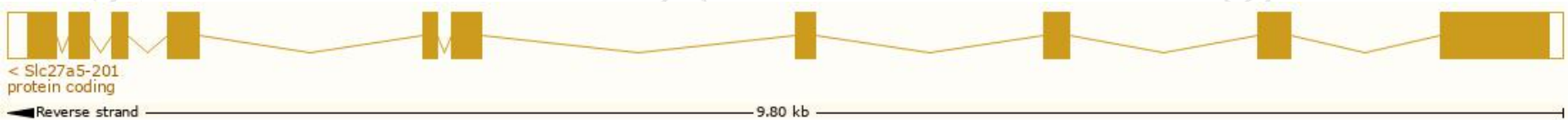


Transcript information (Ensembl)

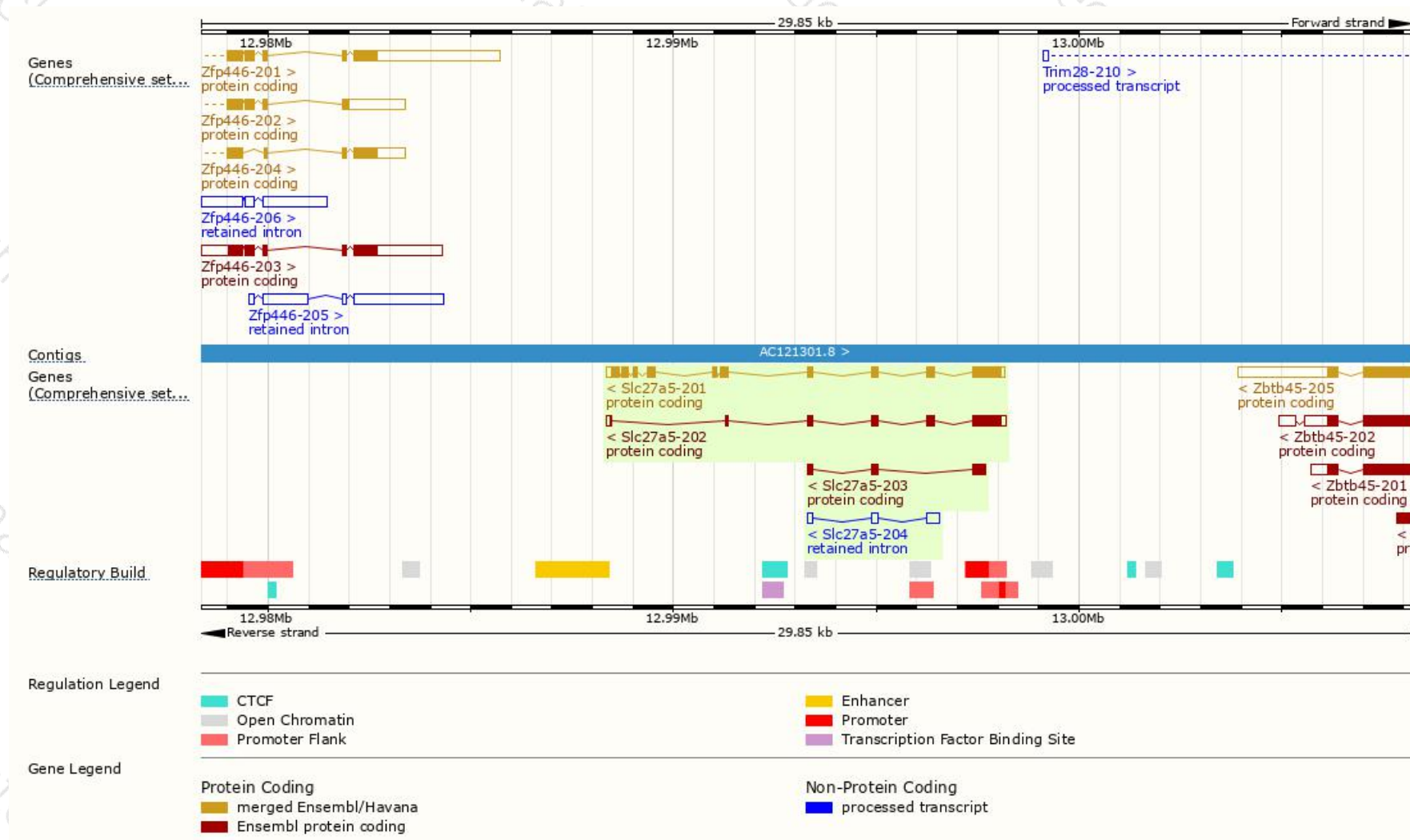
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc27a5-201	ENSMUST00000032539.13	2288	689aa	Protein coding	CCDS20821	Q4LDG0	TSL:1 GENCODE basic APPRIS P1
Slc27a5-202	ENSMUST00000120903.7	1468	418aa	Protein coding	-	E9PXV4	TSL:1 GENCODE basic
Slc27a5-203	ENSMUST00000133977.2	584	195aa	Protein coding	-	F6YDR6	CDS 5' and 3' incomplete TSL:3
Slc27a5-204	ENSMUST00000155192.1	602	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Slc27a5-201* transcript, the transcription is shown below



Genomic location distribution

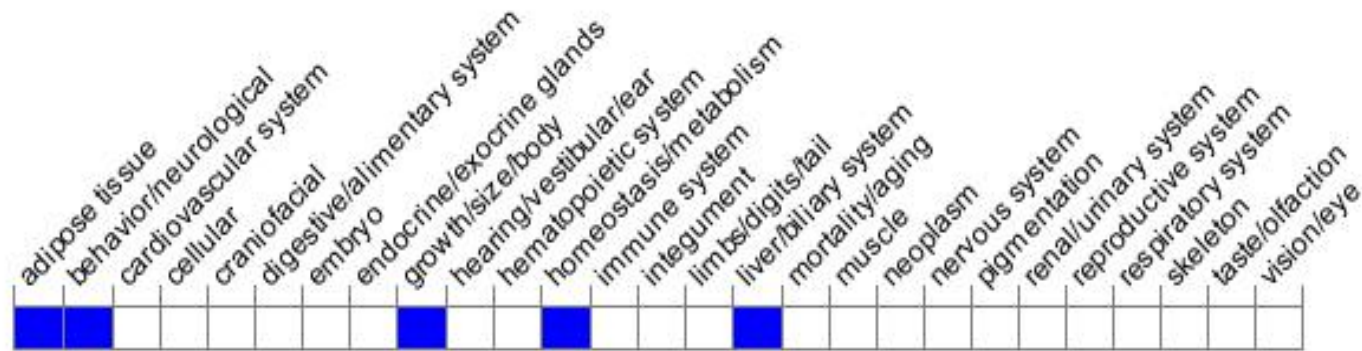


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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 null allele exhibit altered lipid homeostasis.

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

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