Slc27a1 Cas9-CKO Strategy

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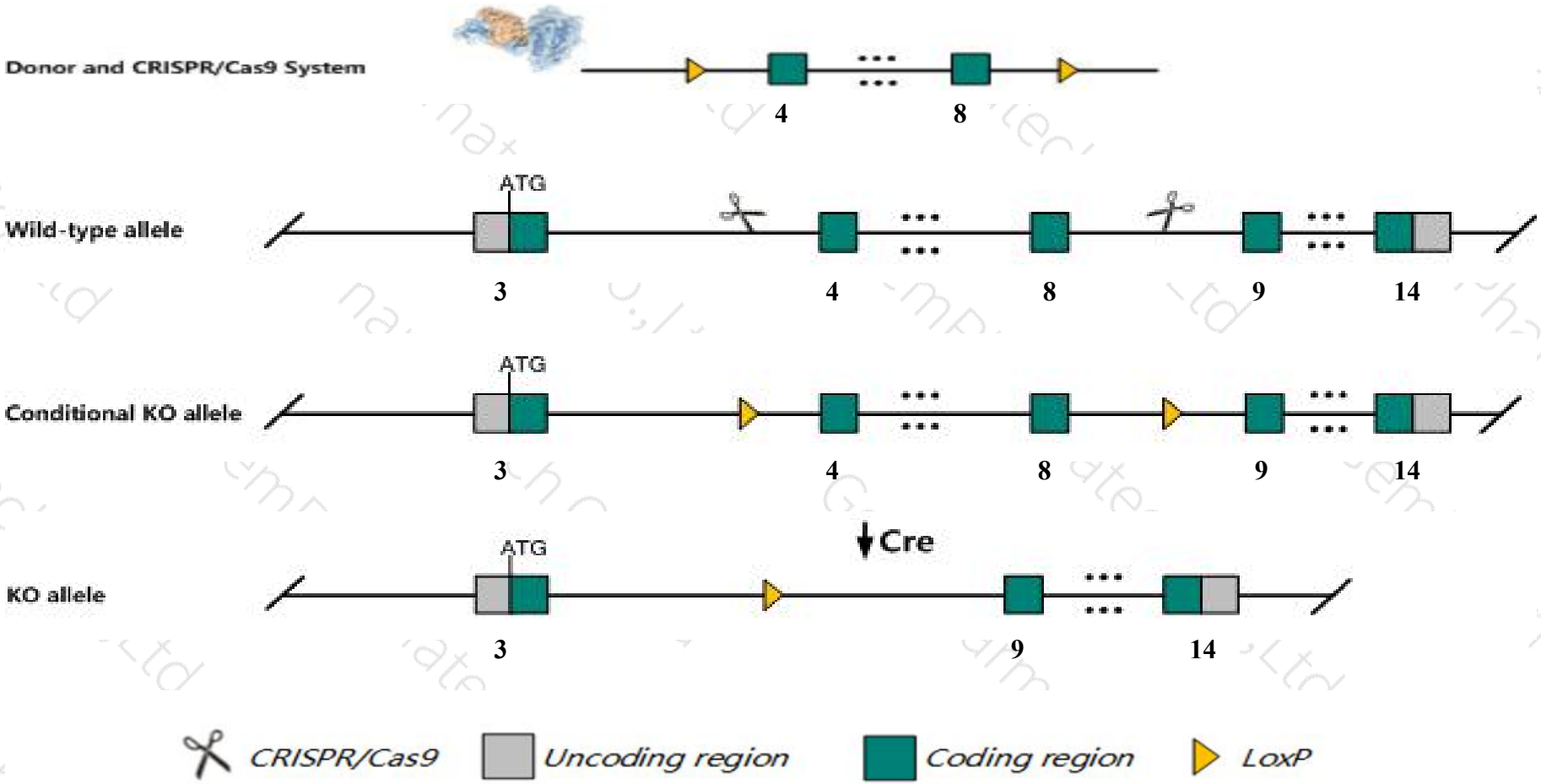
Project Overview

Project Name	***Slc27a1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc27a1* gene. The schematic diagram is as follows:



Technical routes

- The *Slc27a1* gene has 9 transcripts. According to the structure of *Slc27a1* gene, exon4-exon8 of *Slc27a1-201* (ENSMUST00000034267.4) transcript is recommended as the knockout region.The region contains 829bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc27a1* 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.

Notice

- According to the existing MGI data,Homozygous null mutants are protected from fat-induced insulin resistance and intramuscular accumulation of fatty acid metabolites without alterations in whole body adiposity.

- Transcript *Slc27a1-208* may be unaffected.

- The *Slc27a1* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information （NCBI）

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Slc27a1 solute carrier family 27 (fatty acid transporter), member 1 [Mus musculus (house mouse)]

Gene ID: 26457, updated on 31-Jan-2019

Summary

Official Symbol	Slc27a1 provided by MGI
Official Full Name	solute carrier family 27 (fatty acid transporter), member 1 provided by MGI
Primary source	MGI:MGI:1347098
See related	Ensembl:ENSMUSG00000031808
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	FATP1, Fatp
Expression	Broad expression in mammary gland adult (RPKM 230.7), adrenal adult (RPKM 183.8) and 18 other tissues See more
Orthologs	human all

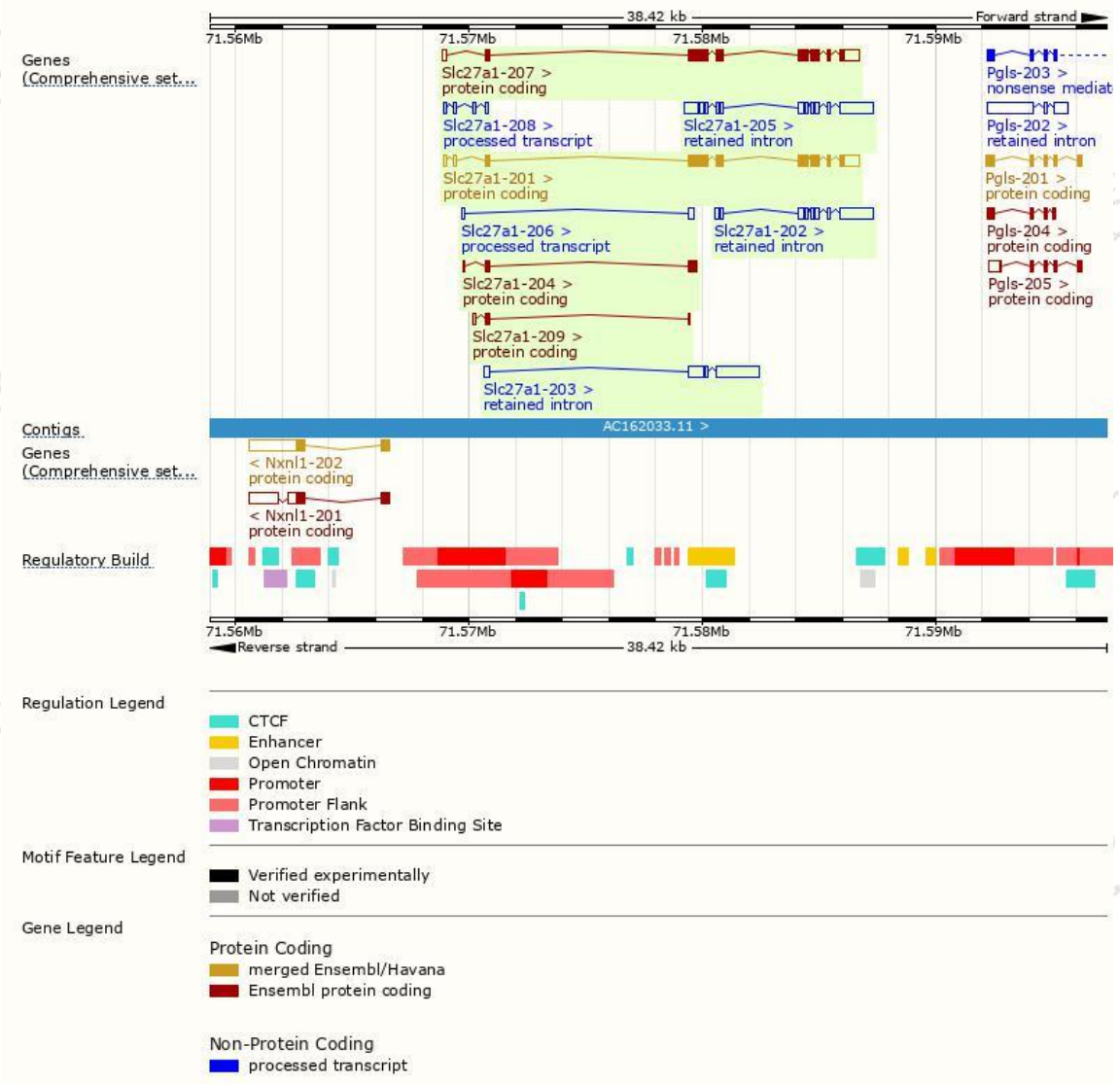
Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc27a1-201	ENSMUST00000034267.4	2795	646aa	Protein coding	CCDS40386	Q544D7 Q60714	TSL:1 GENCODE basic APPRIS P1
Slc27a1-207	ENSMUST00000212889.1	2730	646aa	Protein coding	CCDS40386	Q544D7 Q60714	TSL:1 GENCODE basic APPRIS P1
Slc27a1-204	ENSMUST00000212111.1	641	182aa	Protein coding	-	A0A1D5RLC0	CDS 3' incomplete TSL:2
Slc27a1-209	ENSMUST00000213100.1	384	80aa	Protein coding	-	A0A1D5RM39	CDS 3' incomplete TSL:3
Slc27a1-208	ENSMUST00000212989.1	432	No protein	Processed transcript	-	-	TSL:2
Slc27a1-206	ENSMUST00000212225.1	415	No protein	Processed transcript	-	-	TSL:2
Slc27a1-205	ENSMUST00000212211.1	3207	No protein	Retained intron	-	-	TSL:1
Slc27a1-203	ENSMUST00000211886.1	2809	No protein	Retained intron	-	-	TSL:1
Slc27a1-202	ENSMUST00000211811.1	2484	No protein	Retained intron	-	-	TSL:1

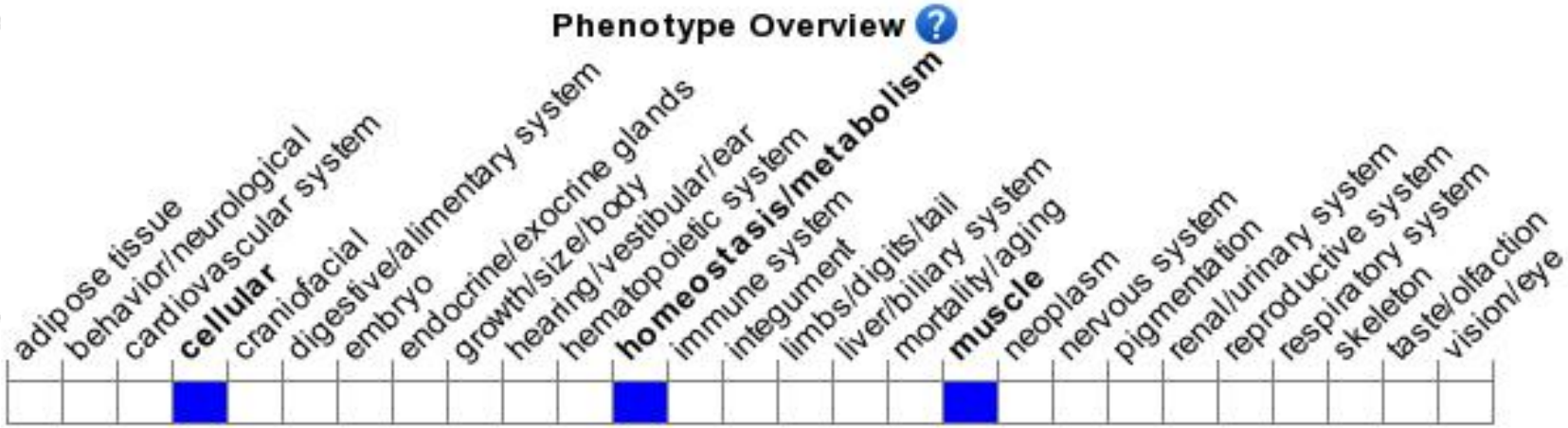
The strategy is based on the design of *Slc27a1-201* transcript,The transcription is shown below

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,Homozygous null mutants are protected from fat-induced insulin resistance and intramuscular accumulation of fatty acid metabolites without alterations in whole body adiposity.

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

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