Slc27a6 Cas9-CKO Strategy

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Project Overview

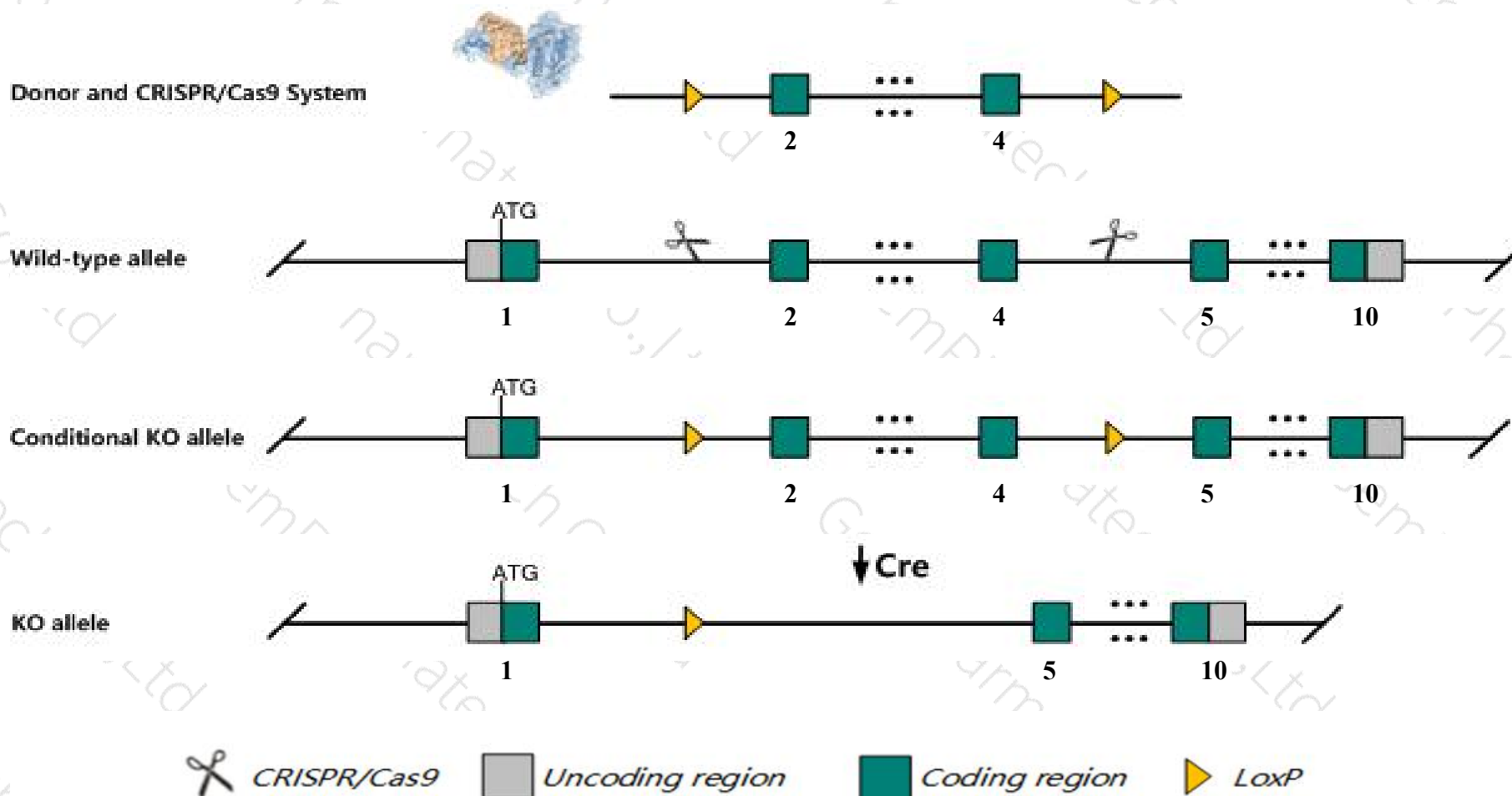|	
Project Name	*Slc27a6*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc27a6* gene. The schematic diagram is as follows:

Technical routes

➤ The *Slc27a6* gene has 1 transcript. According to the structure of *Slc27a6* gene, exon2-exon4 of *Slc27a6-201* (ENSMUST00000025500.6) transcript is recommended as the knockout region.The region contains Ens 488bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Slc27a6* 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

➢ The *Slc27a6* gene is located on the Chr18. 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）

Slc27a6 solute carrier family 27 (fatty acid transporter), member 6 [Mus musculus (house mouse)]

Gene ID: 225579, updated on 13-Mar-2020

Summary

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Official Symbol	Slc27a6 provided by MGI
Official Full Name	solute carrier family 27 (fatty acid transporter), member 6 provided by MGI
Primary source	MGI:MGI:3036230
See related	Ensembl:ENSMUSG00000024600
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4732438L20Rik, FACVL2, FATP6, VLCS-H1
Expression	Biased expression in placenta adult (RPKM 5.5), testis adult (RPKM 2.2) and 6 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc27a6-201	ENSMUST00000025500.6	2485	619aa	Protein coding	CCDS37828	E9Q9W4	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 P1

The strategy is based on the design of *Slc27a6-201* transcript,the transcription is shown below:
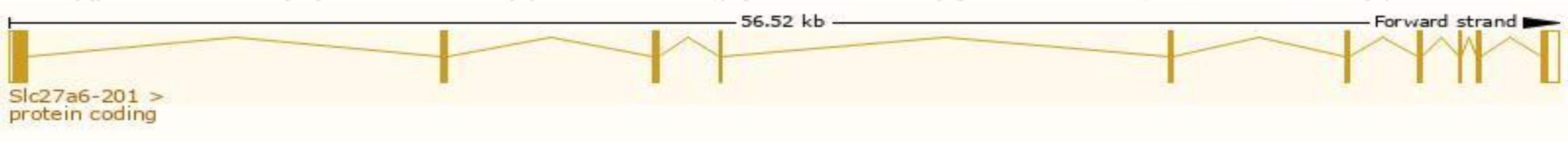
Genomic location distribution
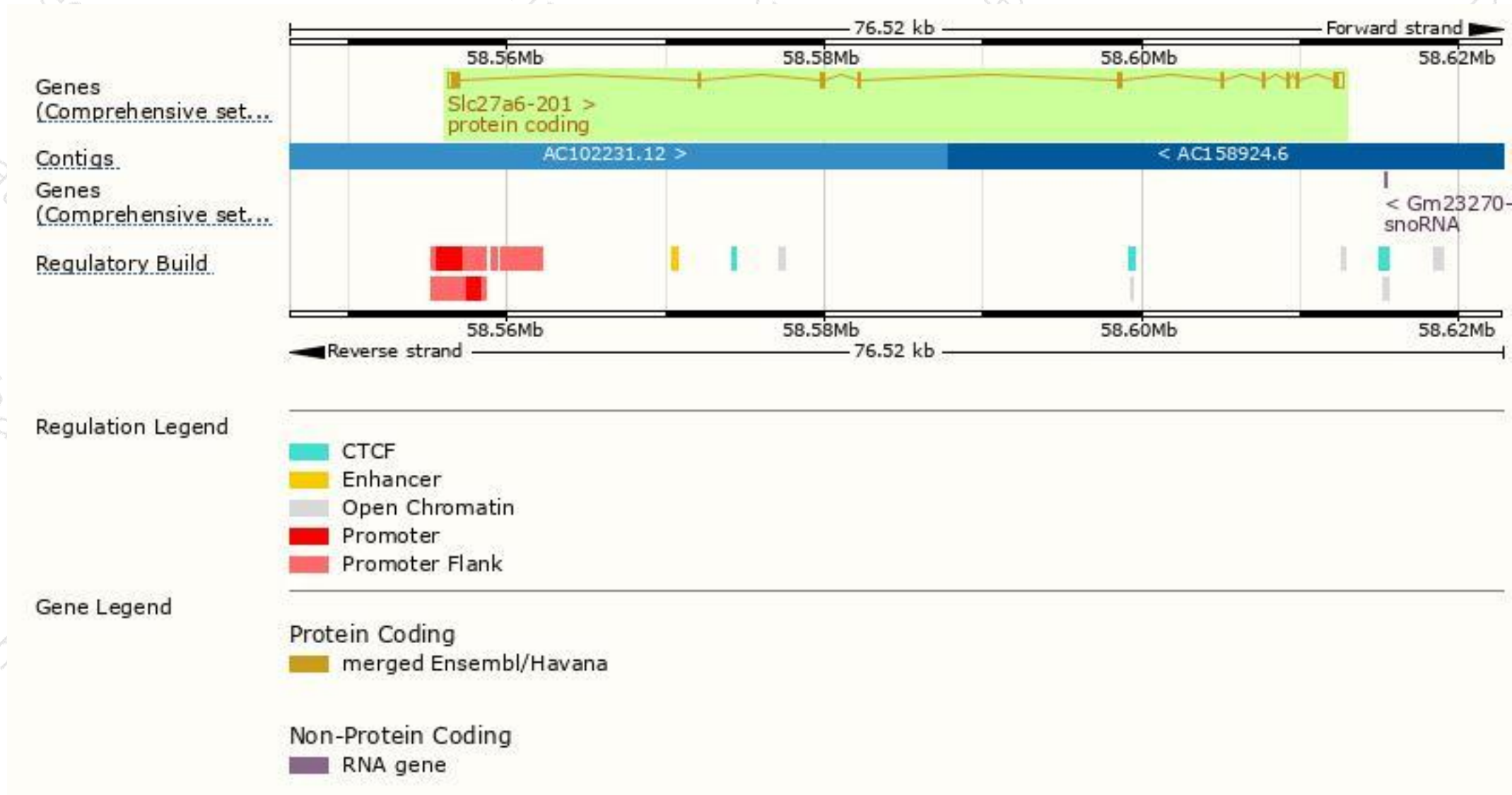
Protein domain

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