Slc13a5 Cas9-CKO Strategy

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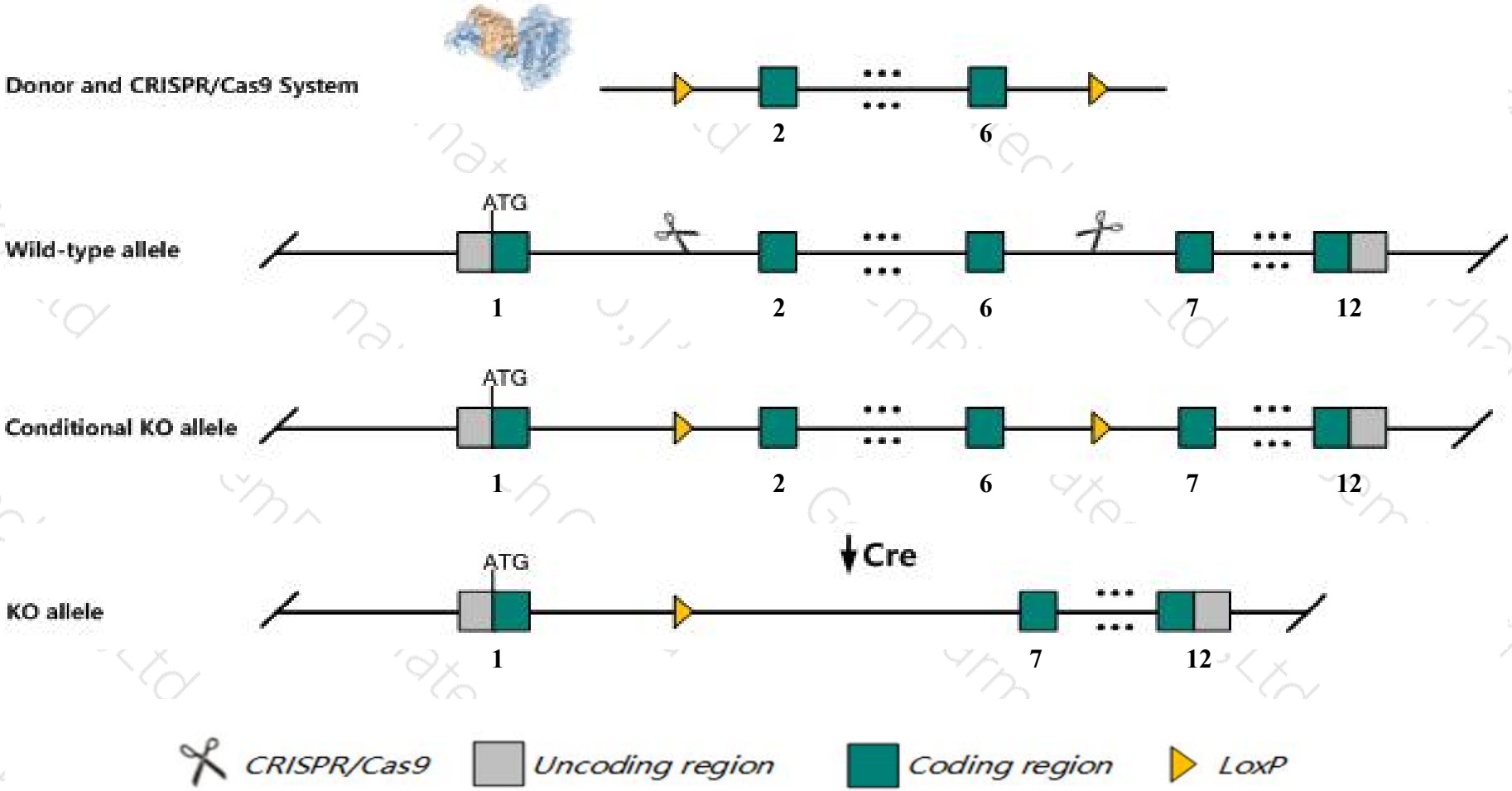
Project Overview

Project Name	***Slc13a5***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc13a5* gene. The schematic diagram is as follows:



Technical routes

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- The *Slc13a5* gene has 6 transcripts. According to the structure of *Slc13a5* gene, exon2-exon6 of *Slc13a5-201* (ENSMUST00000021161.13) transcript is recommended as the knockout region.The region contains 746bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc13a5* 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,Mice homozygous for a null allele display resistance to diet and age induced obesity, increased energy expenditure, improved glucose tolerance, and increased hepatic lipid oxidation. Mice homozygous for an ENU-induced allele exhibit reduced body weight.

➢ The *Slc13a5* gene is located on the Chr11. 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）

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Slc13a5 solute carrier family 13 (sodium-dependent citrate transporter), member 5 [Mus musculus (house mouse)]

Gene ID: 237831, updated on 13-Mar-2020

Summary

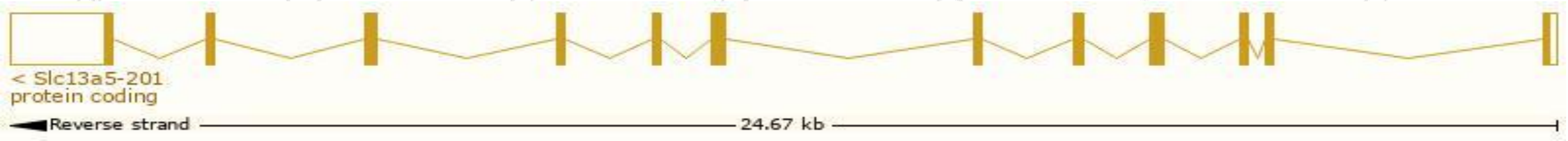
Official Symbol	Slc13a5 provided by MGI
Official Full Name	solute carrier family 13 (sodium-dependent citrate transporter), member 5 provided byMGI
Primary source	MGI:MGI:3037150
See related	Ensembl:ENSMUSG00000020805
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Indy, NaC2/NaCT, Nact, mINDY
Expression	Biased expression in testis adult (RPKM 17.5), cortex adult (RPKM 3.2) and 4 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

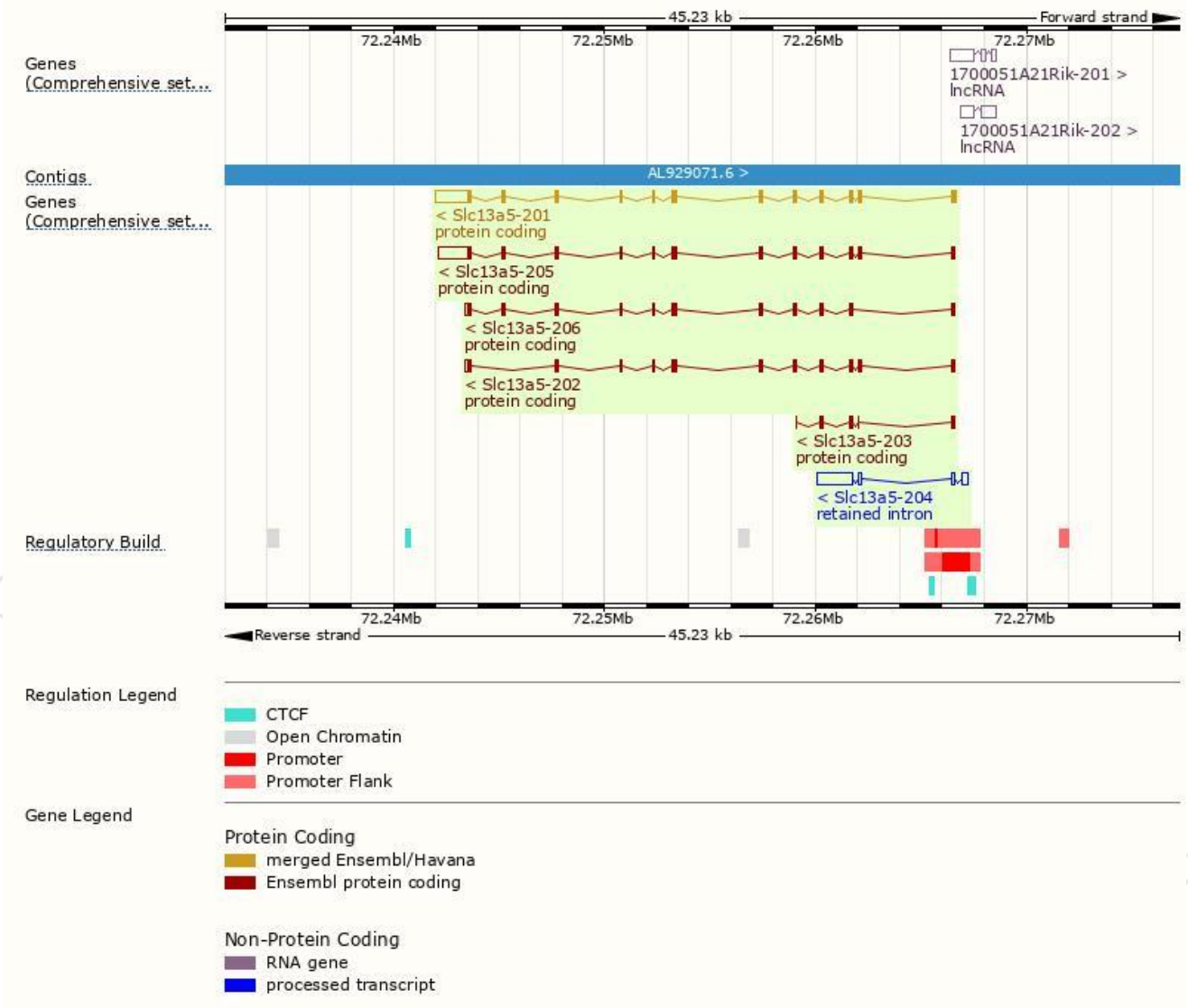
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc13a5-201	ENSMUST00000021161.13	3329	572aa	Protein coding	CCDS24983	Q67BT3	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
Slc13a5-205	ENSMUST00000208056.1	3111	555aa	Protein coding	-	A0A140LIR1	TSL:5 GENCODE basic
Slc13a5-206	ENSMUST00000208912.1	1751	529aa	Protein coding	-	A0A140LIC4	TSL:5 GENCODE basic
Slc13a5-202	ENSMUST00000137701.2	1746	526aa	Protein coding	-	Q5NBV0	TSL:5 GENCODE basic
Slc13a5-203	ENSMUST00000140167.2	542	168aa	Protein coding	-	Q5NBV1	CDS 3' incomplete TSL:5
Slc13a5-204	ENSMUST00000207990.1	2186	No protein	Retained intron	-	-	TSL:2

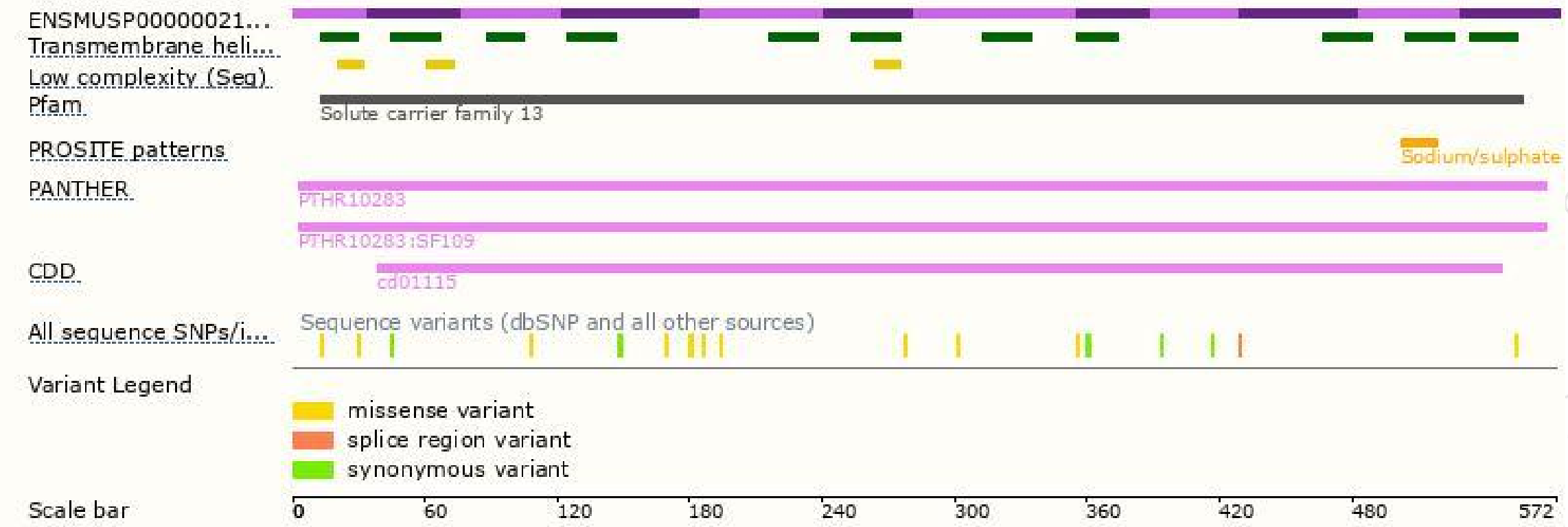
The strategy is based on the design of *Slc13a5-201* transcript,The transcription is shown below



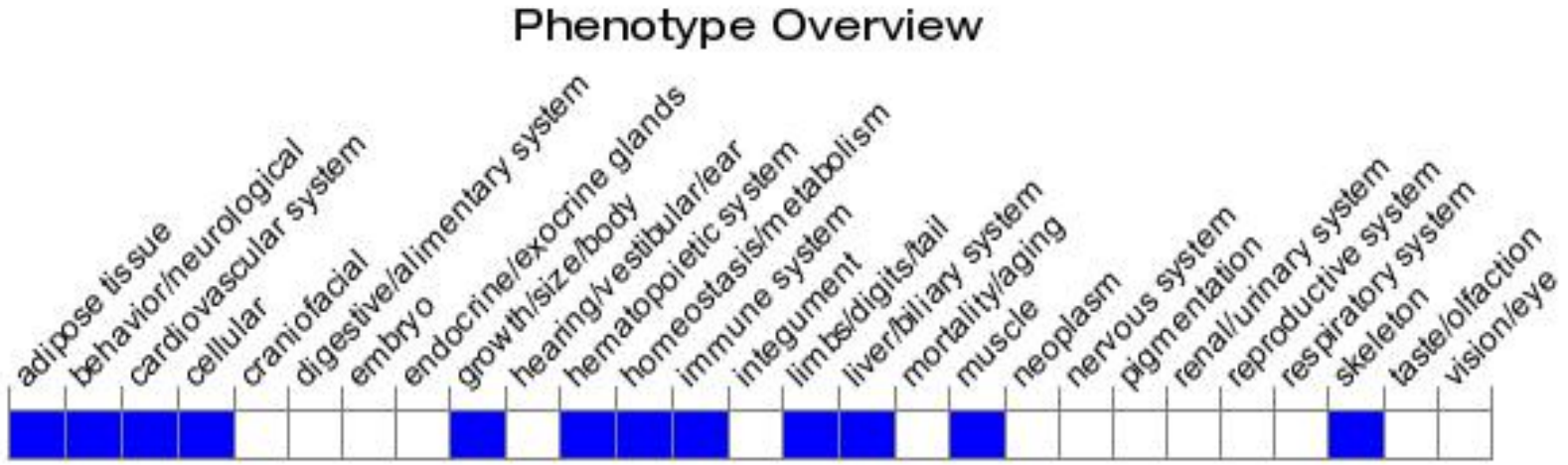
Genomic location distribution



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/).

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

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