Slc2a12 Cas9-CKO Strategy

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Project Overview

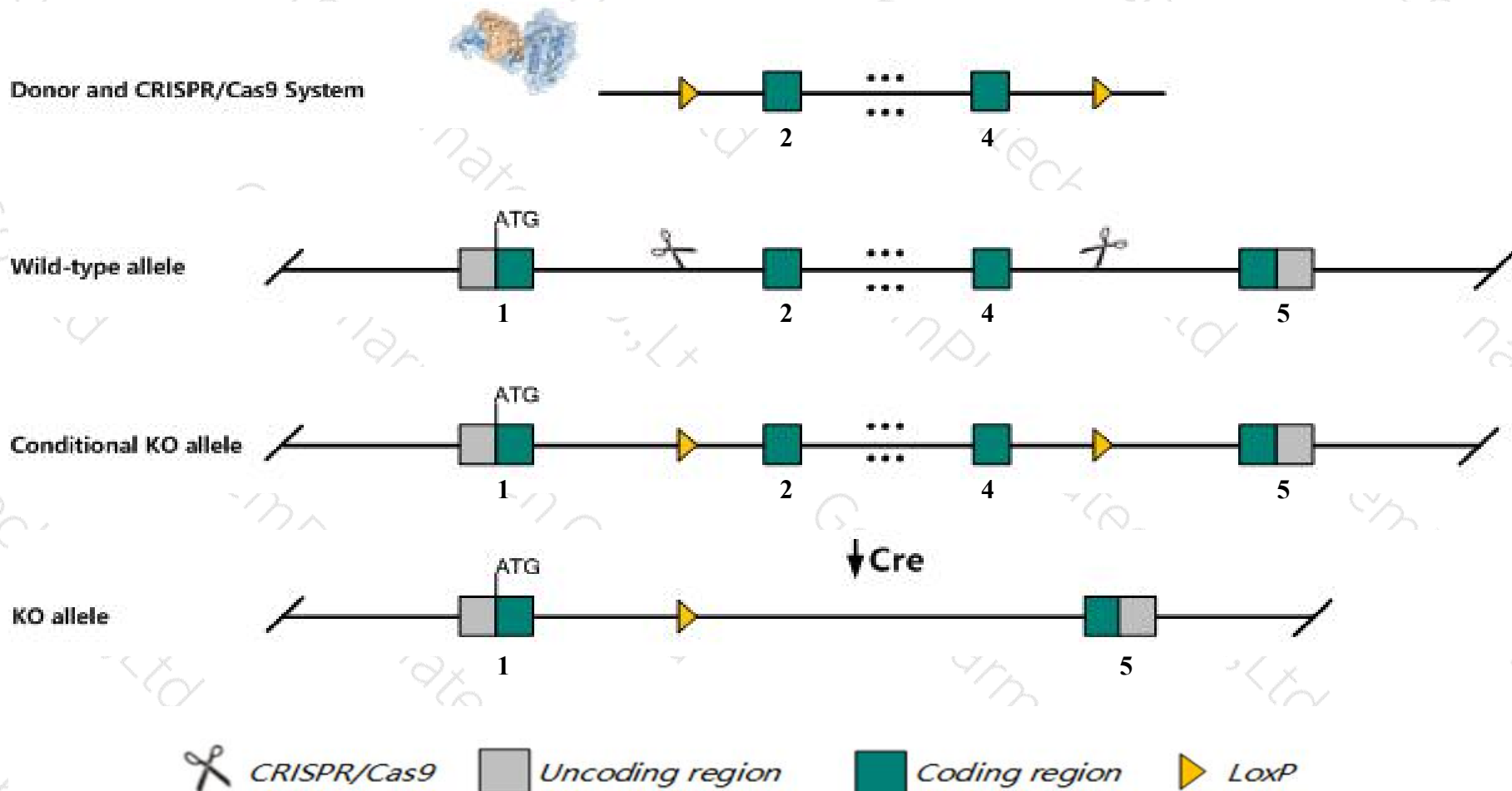|	
Project Name	*Slc2a12*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc2a12* gene. The schematic diagram is as follows:

Technical routes

➤ The *Slc2a12* gene has 2 transcripts. According to the structure of *Slc2a12* gene, exon2-exon4 of *Slc2a12-201* (ENSMUST00000042261.4) transcript is recommended as the knockout region. The region contains Ens 1600bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Slc2a12* 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 *Slc2a12* gene is located on the Chr10. 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）

Slc2a12 solute carrier family 2 (facilitated glucose transporter), member 12 [*Mus musculus* (house mouse)]

Gene ID: 353169, updated on 10-Oct-2019

Summary

Official Symbol	Slc2a12 provided by MGI
Official Full Name	solute carrier family 2 (facilitated glucose transporter), member 12 provided by MGI
Primary source	MGI:MGI:3052471
See related	Ensembl:ENSMUSG00000037490
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	Glut12; GLUT-12
Expression	Broad expression in bladder adult (RPKM 3.5), kidney adult (RPKM 1.9) and 20 other tissues See more
Orthologs	human all

Genomic context

Location: 10; 10 A3

See Slc2a12 in Genome Data Viewer

Exon count: 7

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (22644990..22703880)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (22364817..22423686)

Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

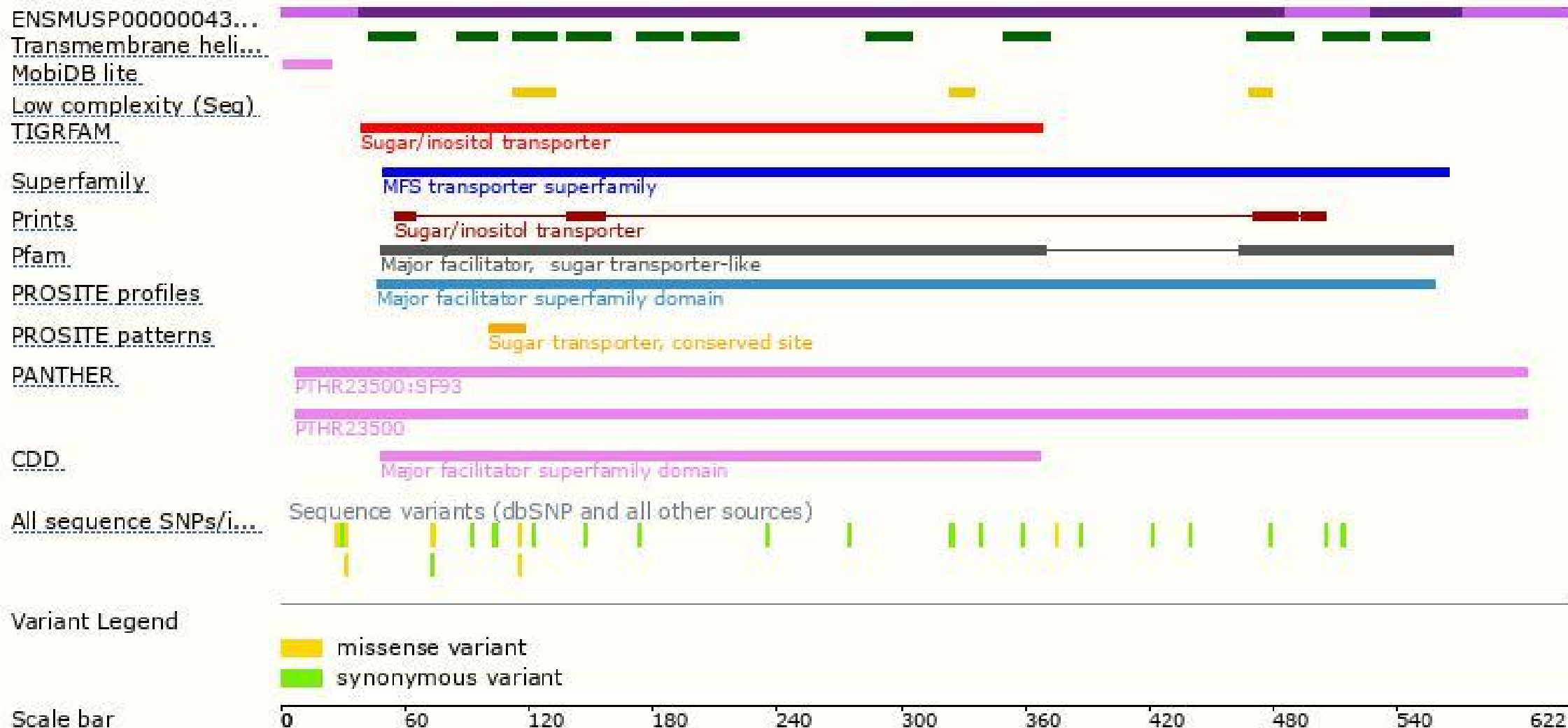| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc2a12-201	ENSMUST00000042261.4	4167	622aa	Protein coding	CCDS23729	B2RRB2 Q8BFW9	TSL:1 GENCODE basic APPRIS P1
Slc2a12-202	ENSMUST00000159174.1	398	No protein	lncRNA	-	-	TSL:2

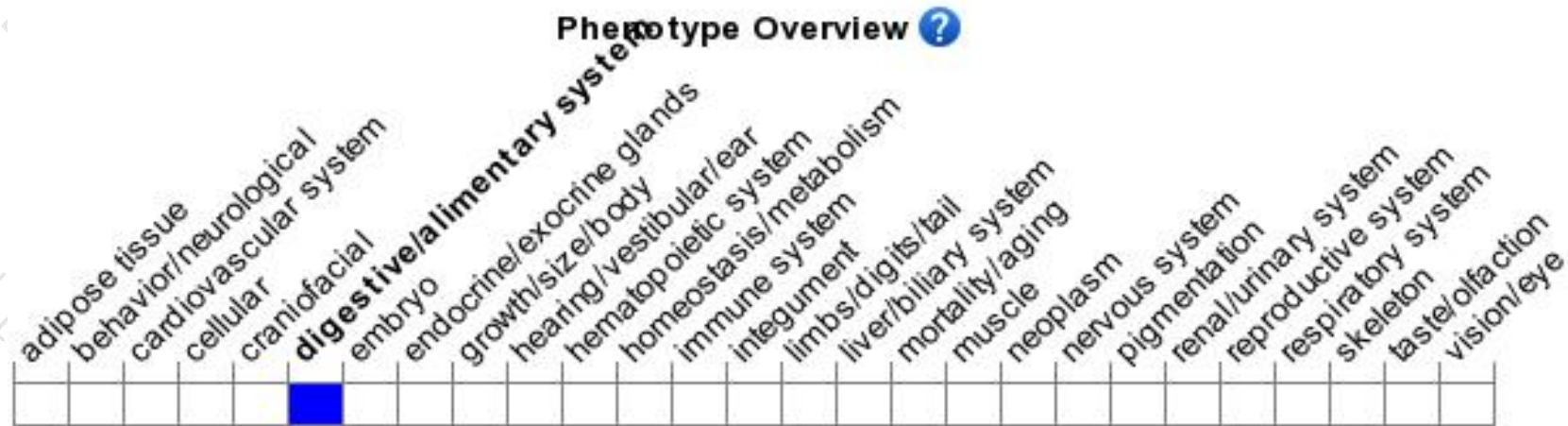The strategy is based on the design of *Slc2a12-201* transcript,The transcription is shown below

Slc2a12-201 >
protein coding

Genomic location distribution

Protein domain

ENSMUSP00000043...	
Transmembrane heli...	
MobiDB lite	
Low complexity (Seg)	
TIGRFAM	Sugar/inositol transporter
Superfamily	MFS transporter superfamily
Prints	Sugar/inositol transporter
Pfam	Major facilitator, sugar transporter-like
PROSITE profiles	Major facilitator superfamily domain
PROSITE patterns	Sugar transporter, conserved site
PANTHER	PTHR23500:SF93
	PTHR23500
CDD	Major facilitator superfamily domain
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

■ missense variant
■ synonymous variant

Scale bar

0   60   120   180   240   300   360   420   480   540   622

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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