Slc2a9 Cas9-CKO Strategy

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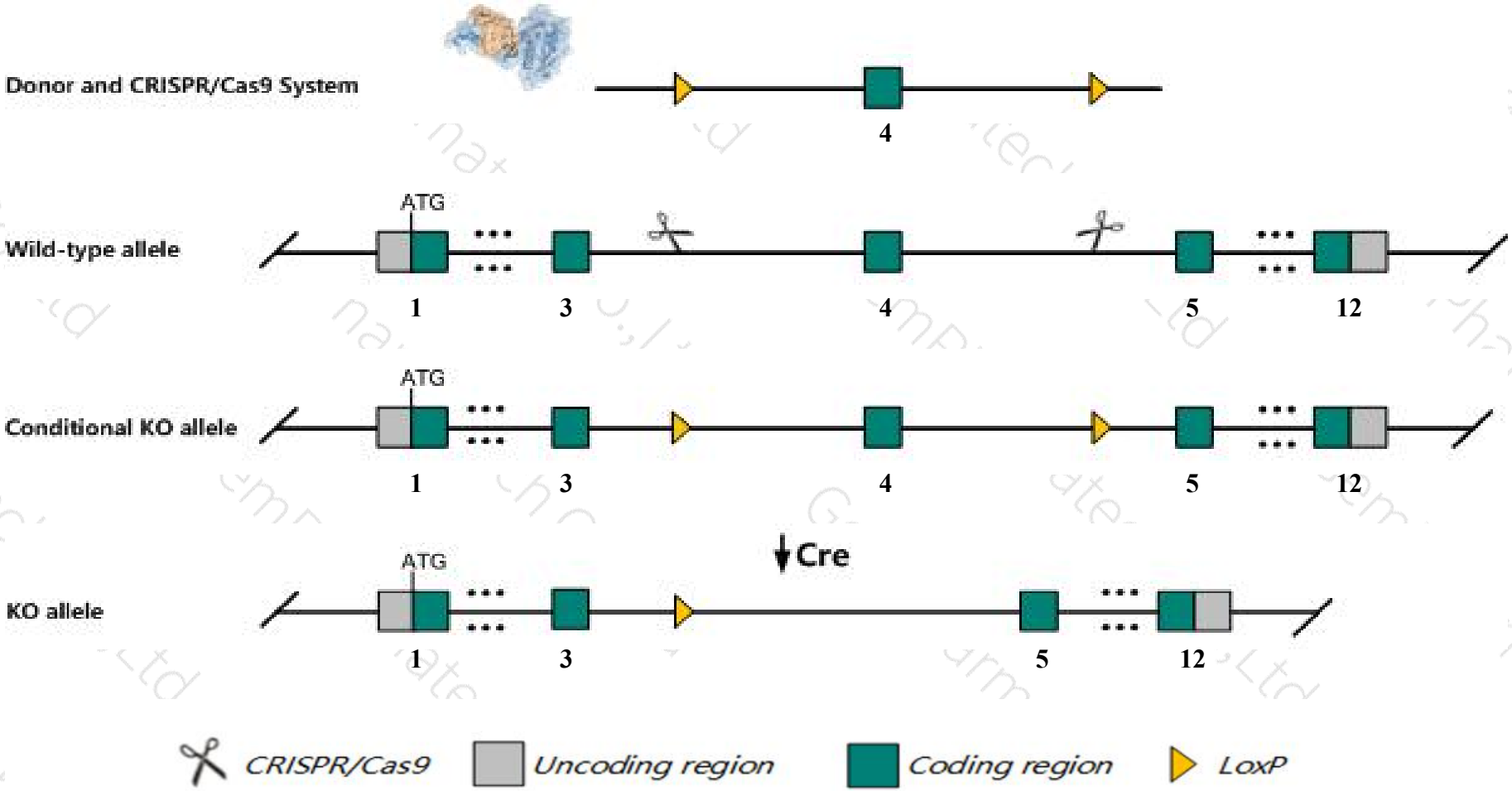
Project Overview

Project Name	***Slc2a9***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc2a9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc2a9* gene has 12 transcripts. According to the structure of *Slc2a9* gene, exon4 of *Slc2a9-203*(ENSMUST00000067886.11) transcript is recommended as the knockout region.The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc2a9* 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 knock-out allele show partial prenatal lethality, polydipsia, hyperuricemia, hyperuricosuria and polyuria, and develop urate nephropathy, characterized by obstructive lithiasis, tubulointerstitial inflammation, cortical fibrosis, renal insufficiency and reduced male weight.

➢ Transcript *Slc2a9-212* may not be affected.

➢ The *Slc2a9* gene is located on the Chr5. 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）

集萃药康 GemPharmatech

Slc2a9 solute carrier family 2 (facilitated glucose transporter), member 9 [*Mus musculus* (house mouse)]

Gene ID: 117591, updated on 26-Jun-2020

Summary

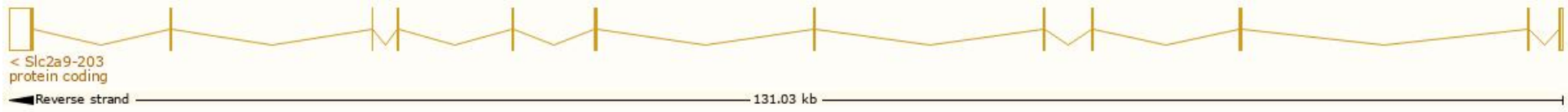
Official Symbol	Slc2a9 provided by MGI
Official Full Name	solute carrier family 2 (facilitated glucose transporter), member 9 provided by MGI
Primary source	MGI:MGI:2152844
See related	Ensembl:ENSMUSG00000005107
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Glut9; GLUT-9; SLC2A9B; SLC2a9A
Expression	Broad expression in liver adult (RPKM 6.8), large intestine adult (RPKM 5.0) and 16 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

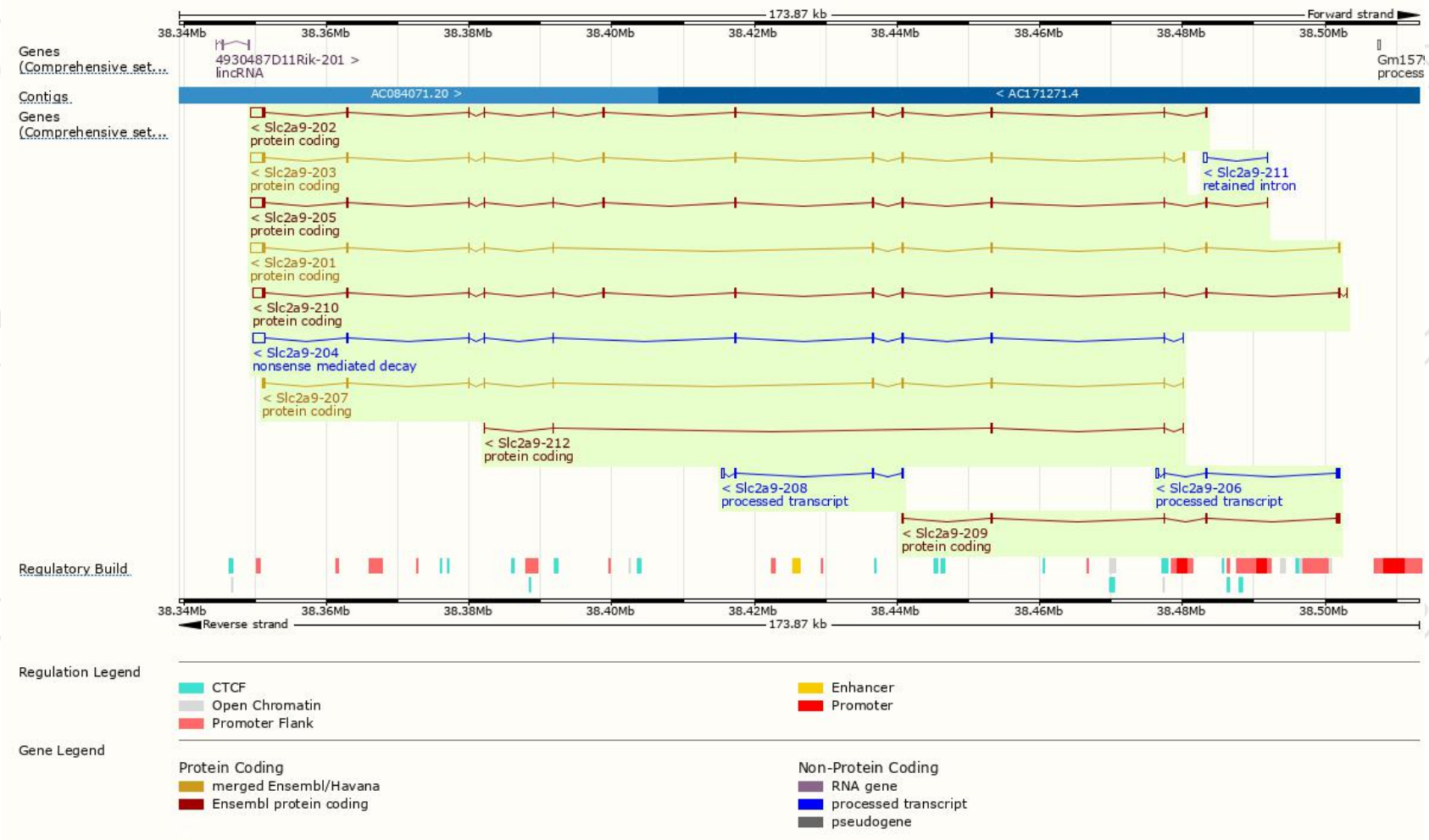
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein ▲	Biotype	CCDS	UniProt	Flags
Slc2a9-209	ENSMUST00000147664.7	652	144aa	Protein coding	-	A0A5H1ZRL9	CDS 3' incomplete TSL:2
Slc2a9-212	ENSMUST00000156272.7	526	158aa	Protein coding	-	A0A5H1ZRN5	CDS 3' incomplete TSL:5
Slc2a9-204	ENSMUST00000122970.7	2900	281aa	Nonsense mediated decay	-	A0A5H1ZRL6	TSL:1
Slc2a9-201	ENSMUST00000005238.12	3243	416aa	Protein coding	CCDS19256	Q3T9X0	TSL:1 GENCODE basic
Slc2a9-207	ENSMUST00000143758.7	1296	431aa	Protein coding	CCDS51482	Q3T9X0	TSL:1 GENCODE basic
Slc2a9-205	ENSMUST00000129099.7	3462	523aa	Protein coding	CCDS51484	Q3T9X0	TSL:5 GENCODE basic APPRIS ALT2
Slc2a9-202	ENSMUST00000067872.11	3403	523aa	Protein coding	CCDS51484	Q3T9X0	TSL:1 GENCODE basic APPRIS ALT2
Slc2a9-210	ENSMUST00000155634.7	3164	523aa	Protein coding	CCDS51484	Q3T9X0	TSL:5 GENCODE basic APPRIS ALT2
Slc2a9-203	ENSMUST00000067886.11	3602	538aa	Protein coding	CCDS51483	Q3T9X0	TSL:1 GENCODE basic APPRIS P4
Slc2a9-206	ENSMUST00000140462.1	776	No protein	Processed transcript	-	-	TSL:3
Slc2a9-208	ENSMUST00000144290.1	770	No protein	Processed transcript	-	-	TSL:3
Slc2a9-211	ENSMUST00000156076.1	427	No protein	Retained intron	-	-	TSL:3

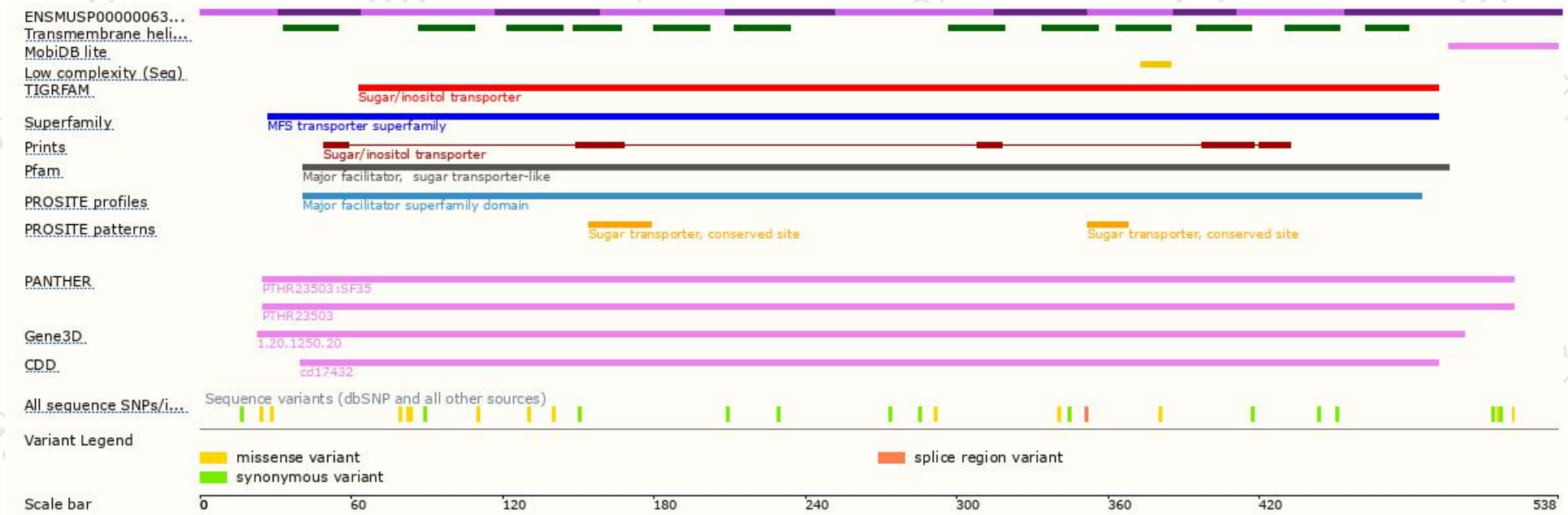
The strategy is based on the design of *Slc2a9-203* transcript,the transcription is shown below:



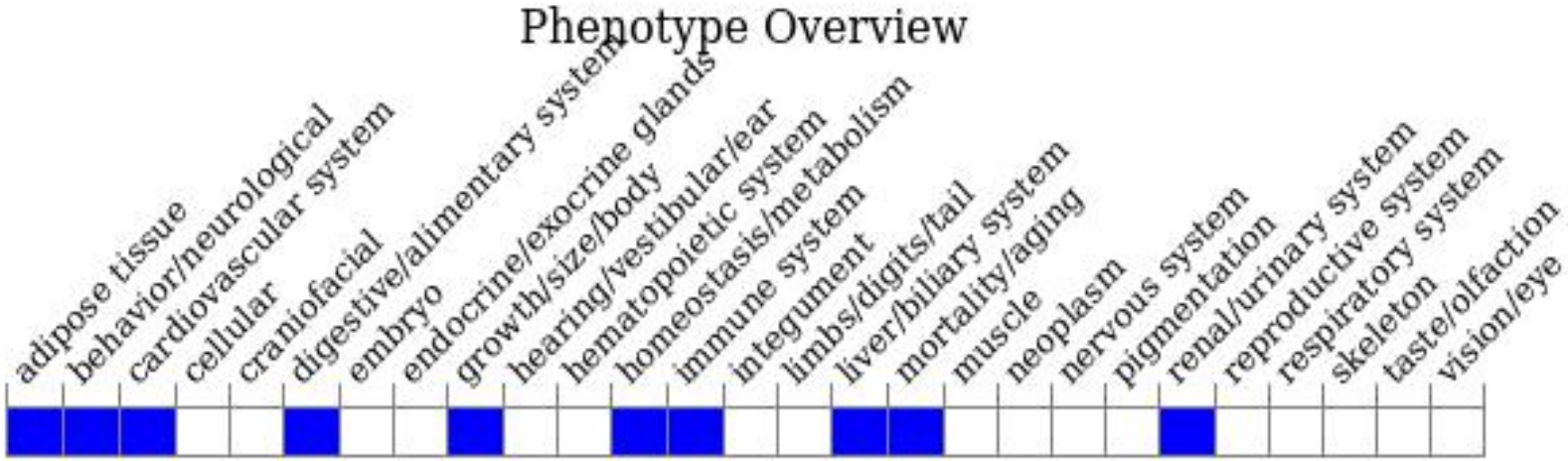
Genomic location distribution



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,mice homozygous for a knock-out allele show partial prenatal lethality, polydipsia, hyperuricemia, hyperuricosuria and polyuria, and develop urate nephropathy, characterized by obstructive lithiasis, tubulointerstitial inflammation, cortical fibrosis, renal insufficiency and reduced male weight.

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

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