

Slc2a12 Cas9-KO Strategy

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Project Overview

Project Name

Slc2a12

Project type

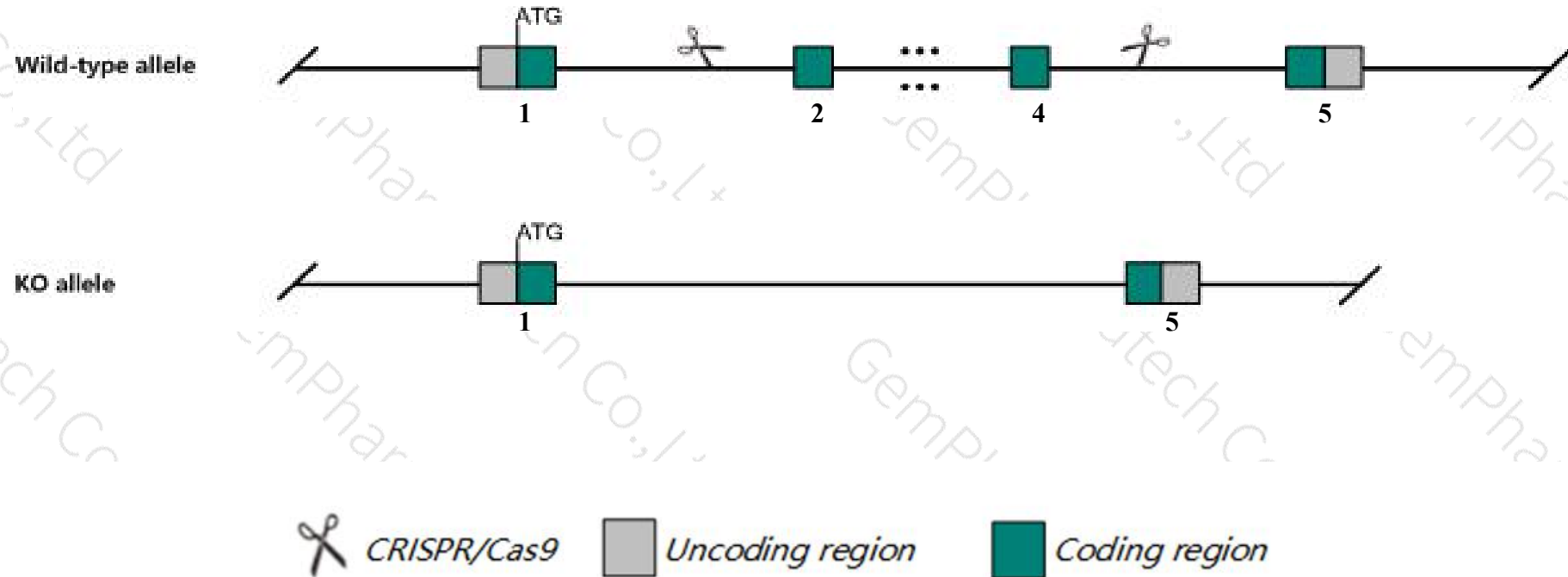
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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)

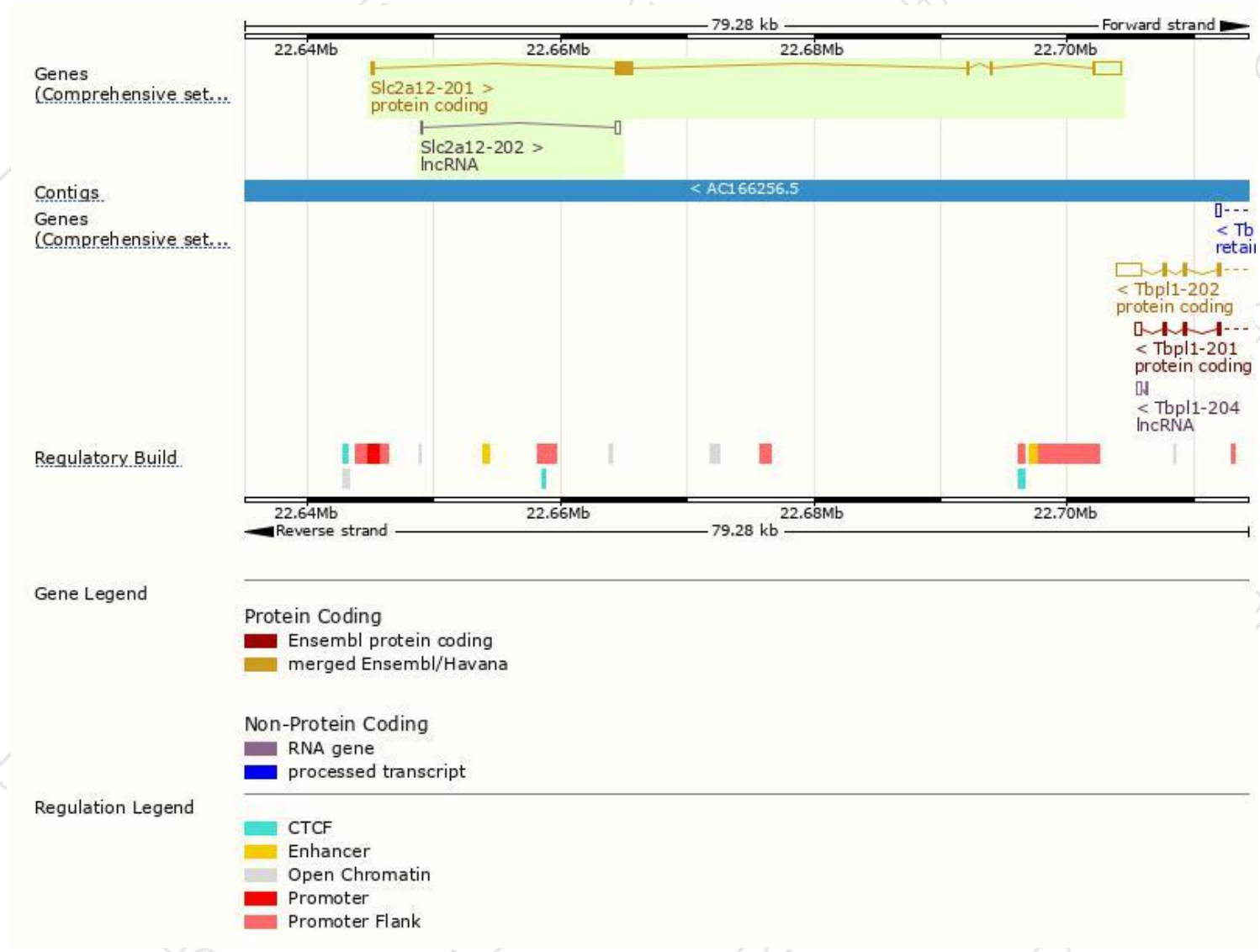
The gene has 2 transcripts,all transcripts are shown below:

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

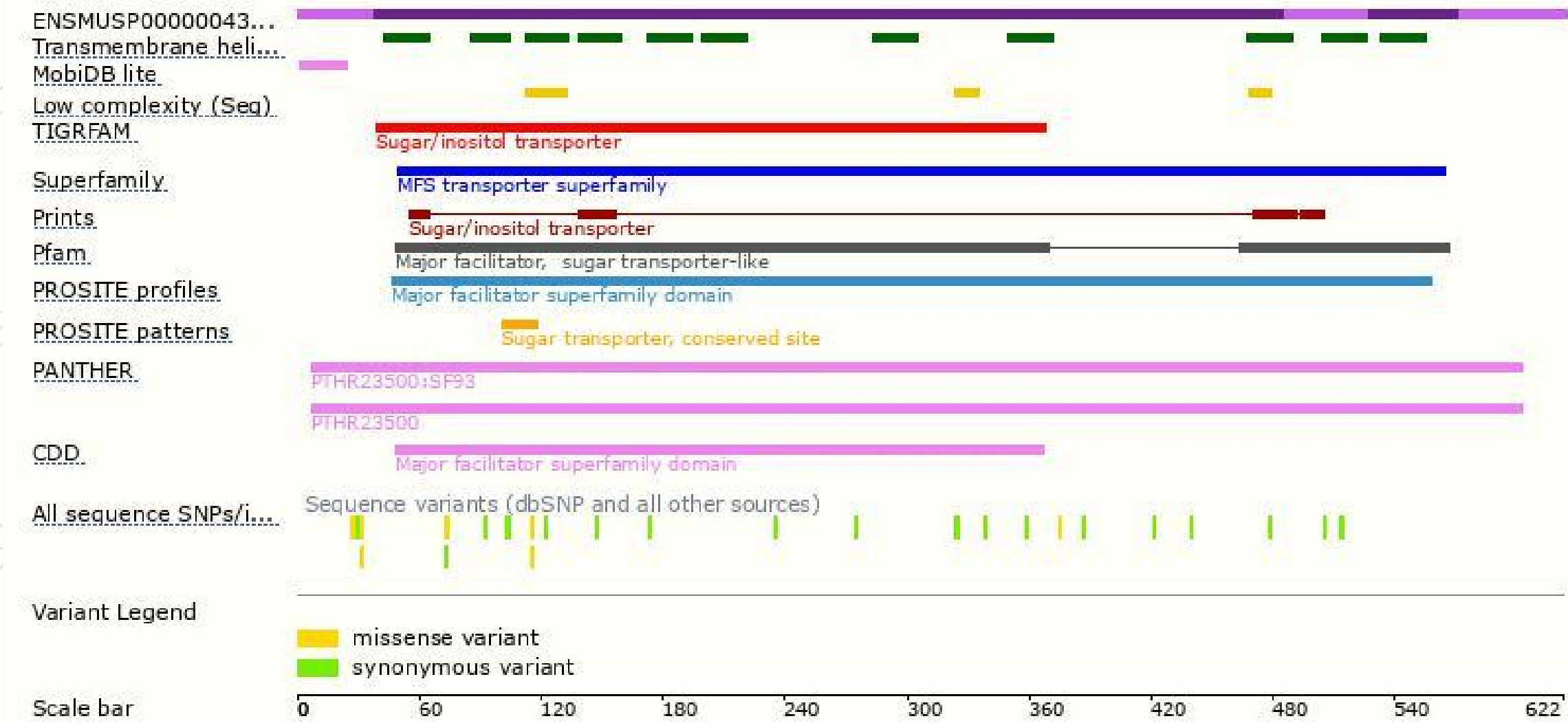
The strategy is based on the design of *Slc2a12-201* transcript,The transcription is shown below



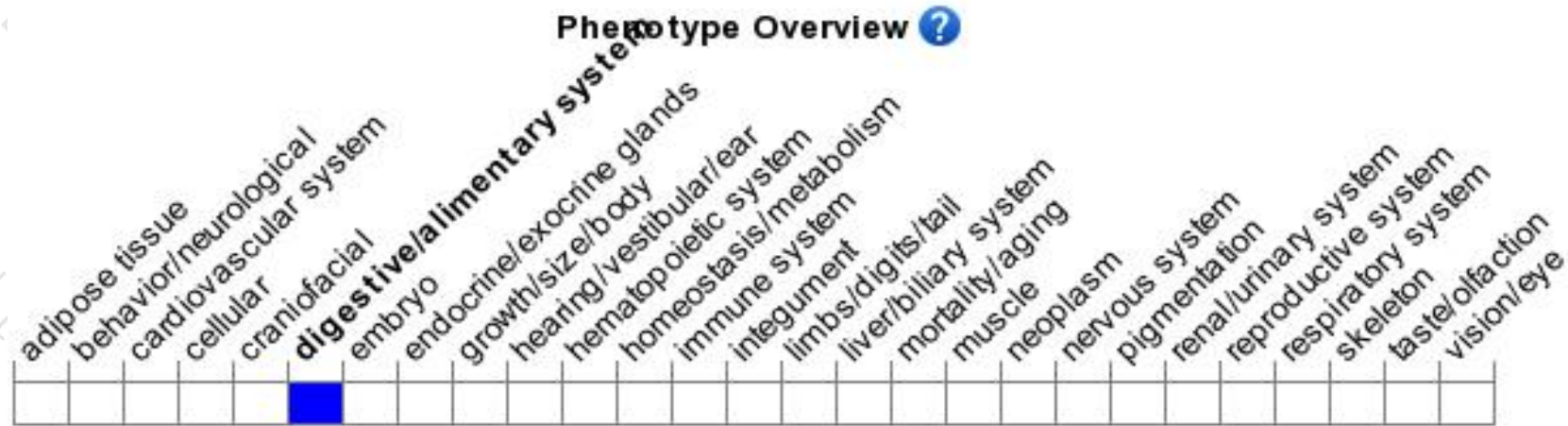
Genomic location distribution



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/>).

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

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