

Slc35c1 Cas9-KO Strategy

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Design Date: 2021-4-19

Project Overview

Project Name

Slc35c1

Project type

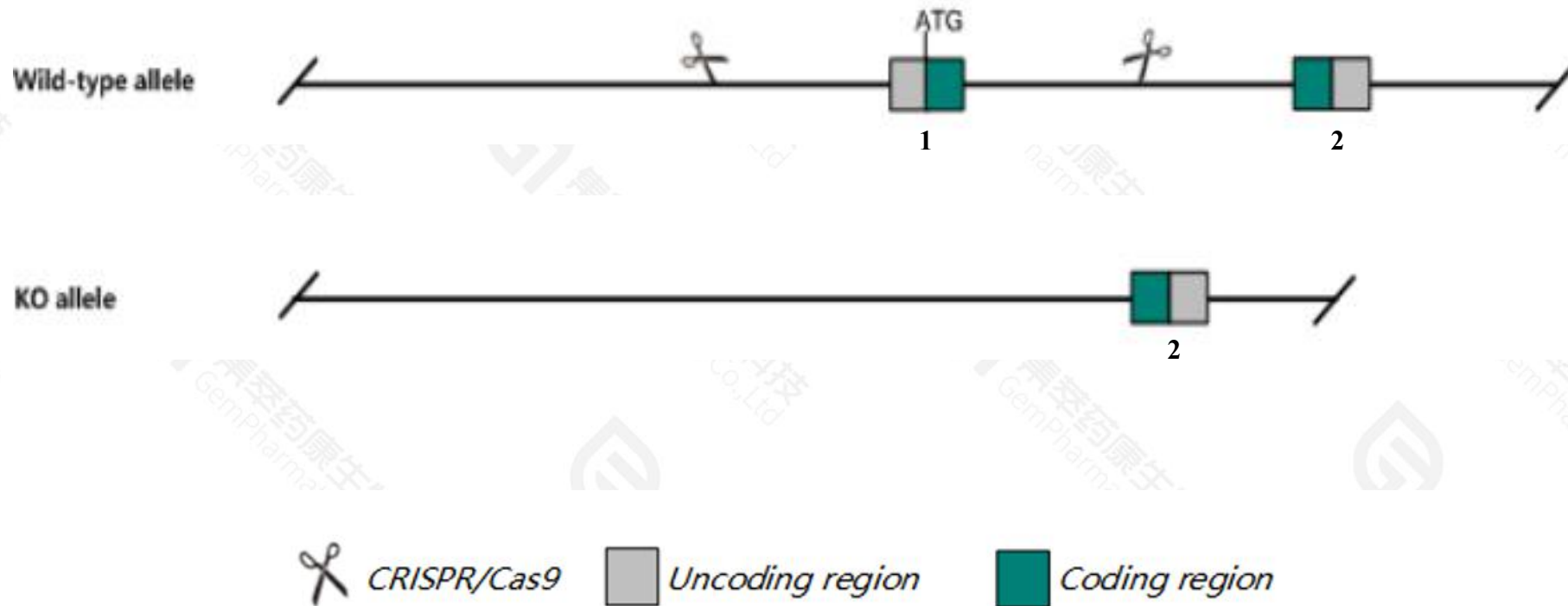
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc35c1* gene. The schematic diagram is as follows:



- The *Slc35c1* gene has 3 transcripts. According to the structure of *Slc35c1* gene, exon1 of *Slc35c1-201*(ENSMUST00000067631.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc35c1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a null allele exhibit partial perinatal and postnatal lethality, growth retardation, reduced fertility, leukocytosis, defective lung and primary lymph node development and altered lymphocyte rolling and adhesion. Mortality is increased on an inbred background.
- The *Slc35c1* gene is located on the Chr2. 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)

Slc35c1 solute carrier family 35, member C1 [Mus musculus (house mouse)]

Gene ID: 228368, updated on 17-Nov-2020

Summary



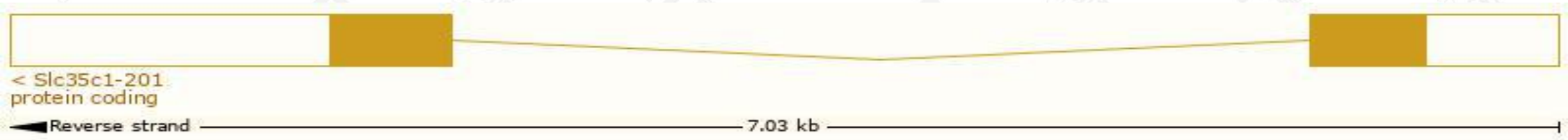
Official Symbol	Slc35c1 provided by MGI
Official Full Name	solute carrier family 35, member C1 provided by MGI
Primary source	MGI:MGI:2443301
See related	Ensembl:ENSMUSG00000049922
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E430007K15Rik, fuct1
Expression	Broad expression in colon adult (RPKM 95.4), large intestine adult (RPKM 58.1) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

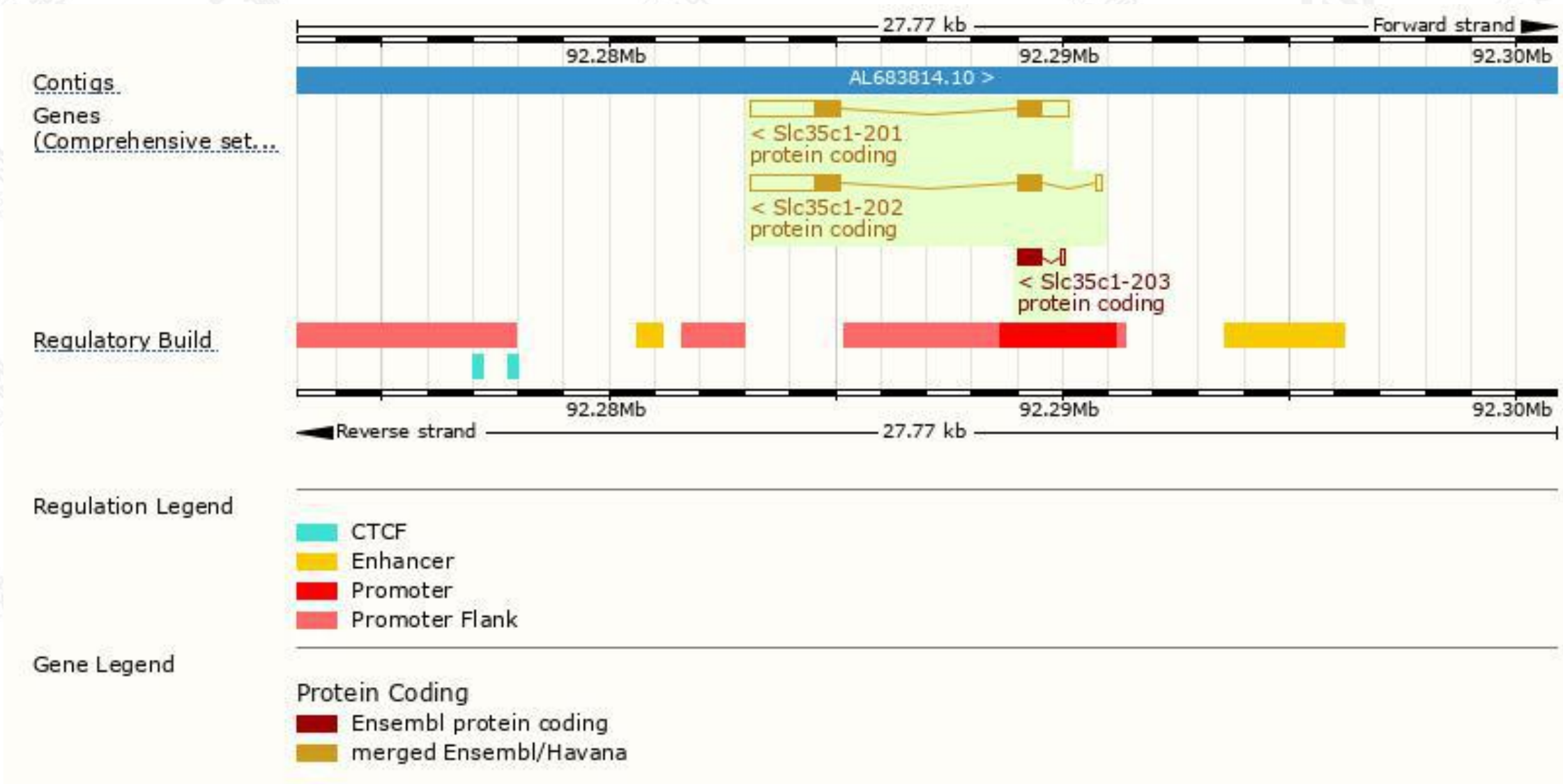
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc35c1-201	ENSMUST00000067631.7	3139	363aa	Protein coding	CCDS16448		TSL:1 , GENCODE basic , APPRIS P4 ,
Slc35c1-202	ENSMUST00000125276.2	2668	350aa	Protein coding	CCDS16449		TSL:1 , GENCODE basic , APPRIS ALT1 ,
Slc35c1-203	ENSMUST00000136718.2	606	158aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,

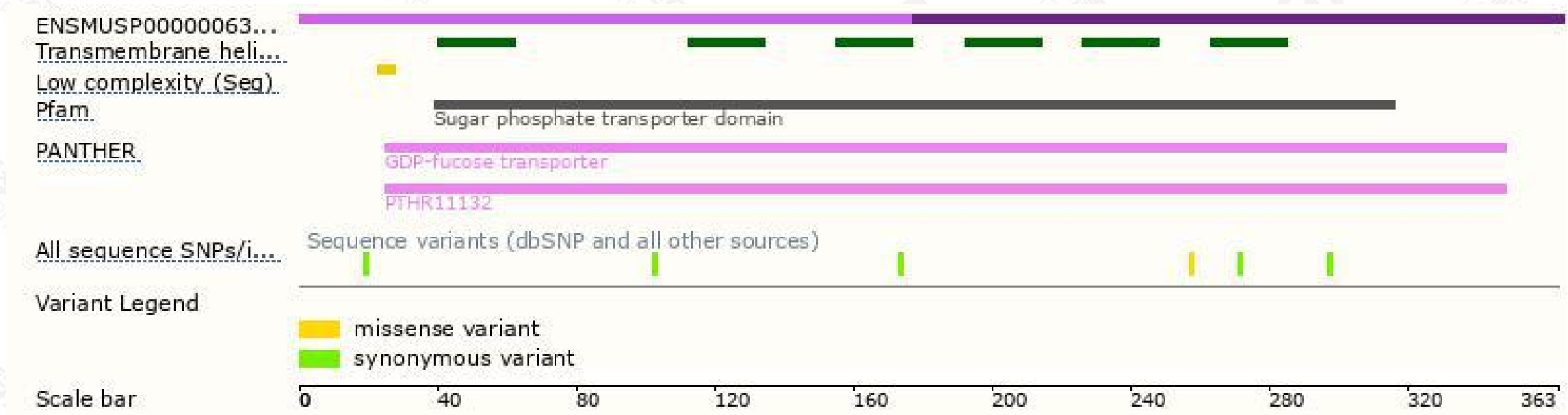
The strategy is based on the design of *Slc35c1-201* transcript,the transcription is shown below:



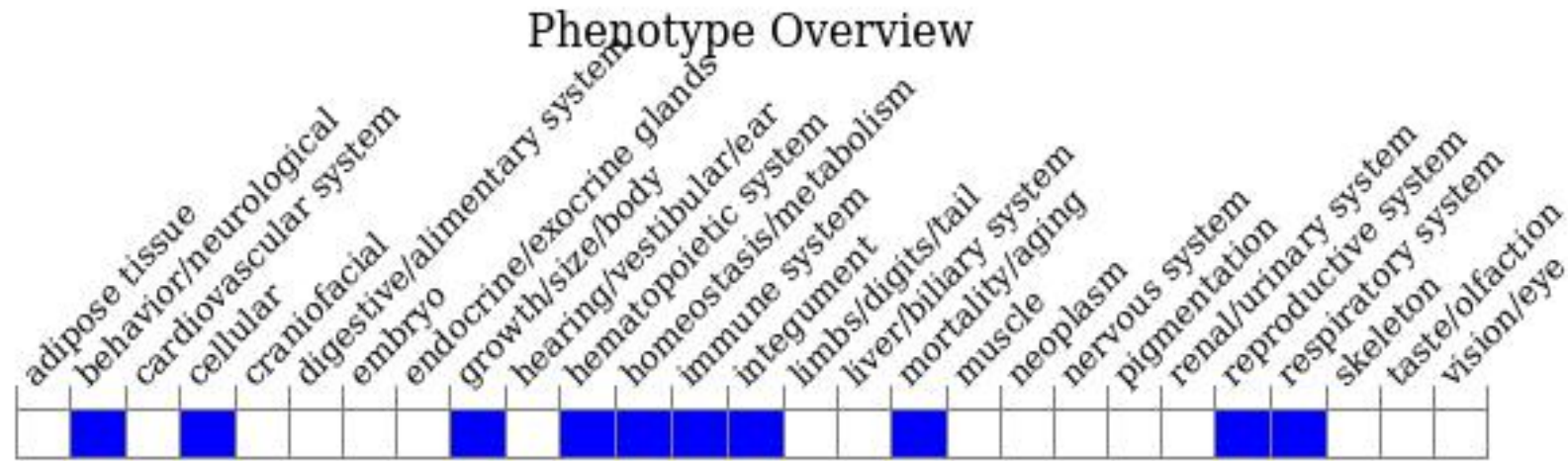
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a null allele exhibit partial perinatal and postnatal lethality, growth retardation, reduced fertility, leukocytosis, defective lung and primary lymph node development and altered lymphocyte rolling and adhesion. Mortality is increased on an inbred background.

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