

Slc31a1 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Slc31a1

Project type

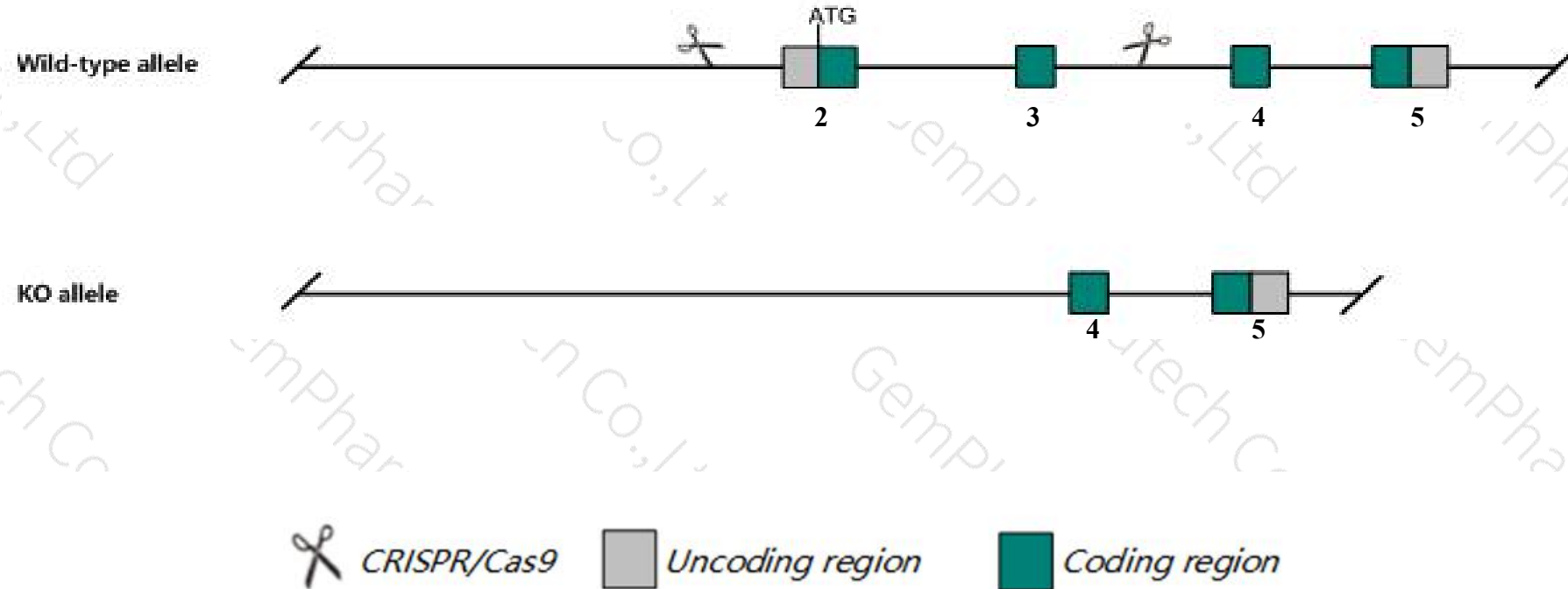
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc31a1* gene. The schematic diagram is as follows:



- The *Slc31a1* gene has 2 transcripts. According to the structure of *Slc31a1* gene, exon2-exon3 of *Slc31a1-201* (ENSMUST00000084526.11) 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 *Slc31a1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit embryonic lethality during organogenesis associated with abnormal embryogenesis. Mice heterozygous for a null allele exhibit decreased copper levels in the blood and several organs.
- The KO region contains functional region of the *Cdc26-203*. Knockout the region may affect the function of *Cdc26-203*.
- The *Slc31a1* gene is located on the Chr4. 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)

Slc31a1 solute carrier family 31, member 1 [Mus musculus (house mouse)]

Gene ID: 20529, updated on 31-Jan-2019



Summary



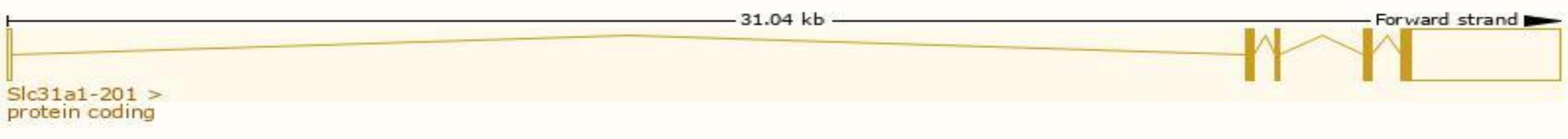
Official Symbol	Slc31a1 provided by MGI
Official Full Name	solute carrier family 31, member 1 provided by MGI
Primary source	MGI:MGI:1333843
See related	Ensembl:ENSMUSG00000066150
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930445G01Rik, AI787263, AU016967, Ctr1
Expression	Ubiquitous expression in liver adult (RPKM 31.6), large intestine adult (RPKM 31.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

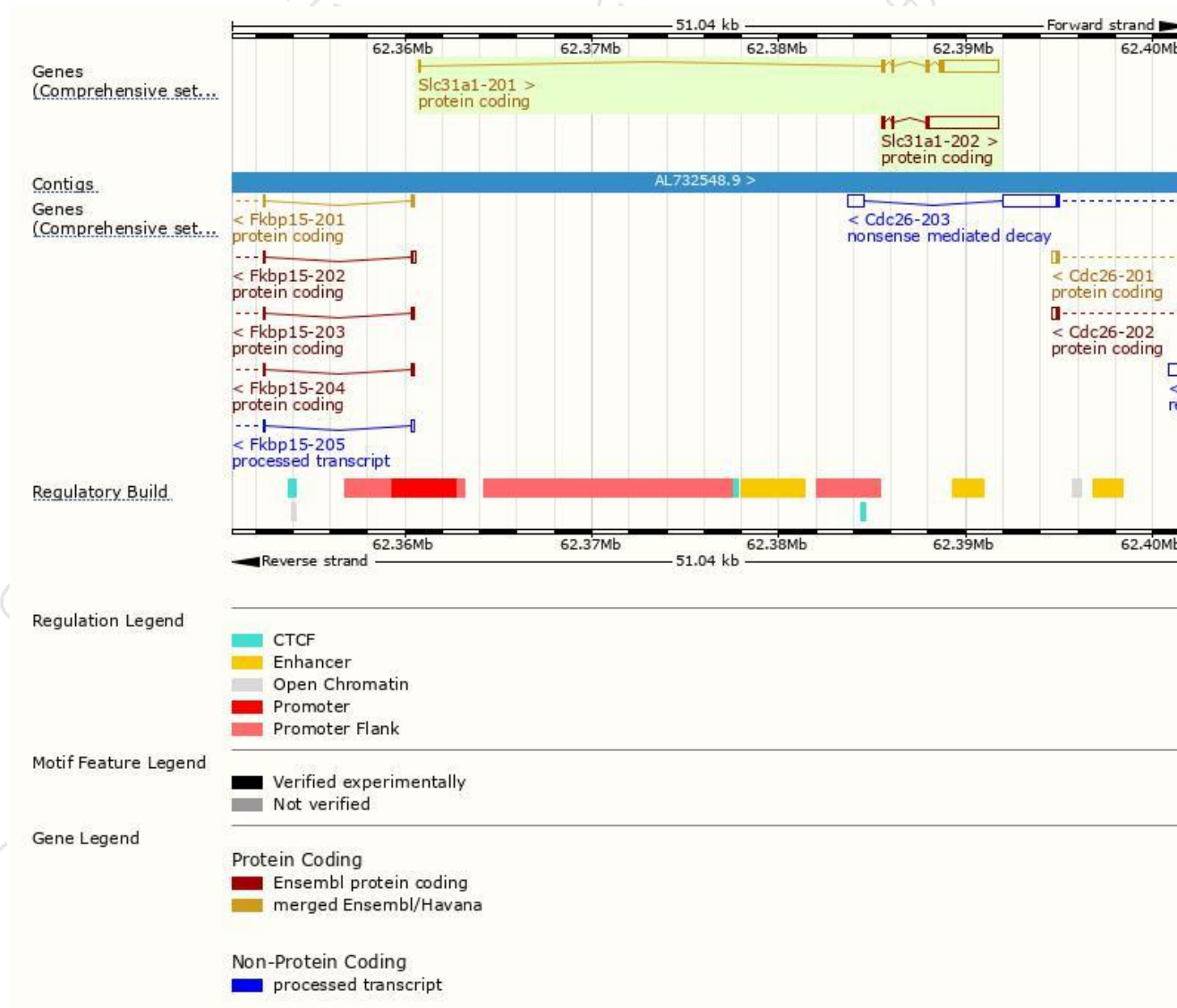
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc31a1-201	ENSMUST00000084526.11	3718	196aa	 Protein coding	CCDS18237	Q8K211	TSL:1 GENCODE basic APPRIS P1
Slc31a1-202	ENSMUST00000122092.1	4154	130aa	 Protein coding	-	A8Y5P1	TSL:1 GENCODE basic

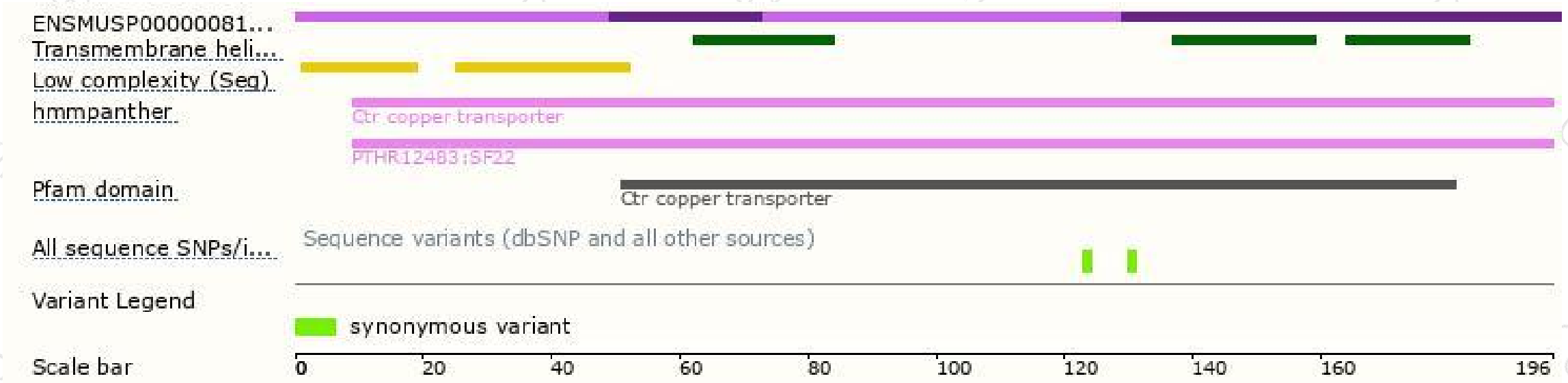
The strategy is based on the design of *Slc31a1-201* transcript,The transcription is shown below



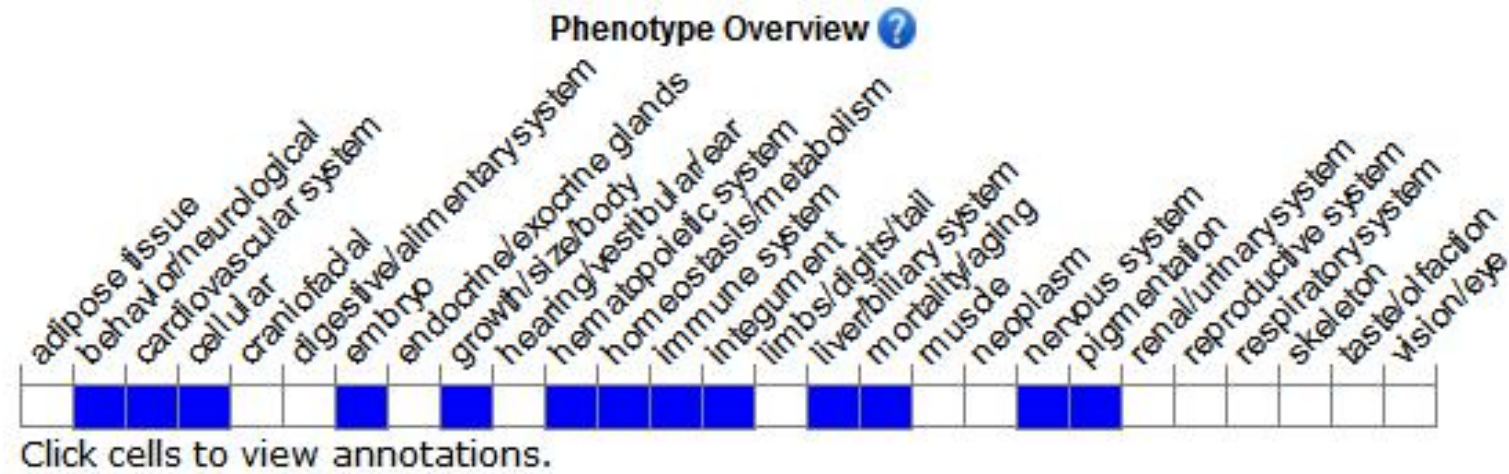
Genomic location distribution



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 embryonic lethality during organogenesis associated with abnormal embryogenesis. Mice heterozygous for a null allele exhibit decreased copper levels in the blood and several organs.

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

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