

Slc15a3 Cas9-KO Strategy

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Project Overview

Project Name

Slc15a3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc15a3* gene. The schematic diagram is as follows:



- The *Slc15a3* gene has 4 transcripts. According to the structure of *Slc15a3* gene, exon2 of *Slc15a3-201* (ENSMUST00000025646.2) transcript is recommended as the knockout region. The region contains 284bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc15a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, The gene is involved in pathogen sensing by dendritic cells.
Homozygous KO results in a reduction of the number of these cells displaying tubular endo-lysosomes after LPS treatment.
- The *Slc15a3* gene is located on the Chr19. 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)

Slc15a3 solute carrier family 15, member 3 [Mus musculus (house mouse)]

Gene ID: 65221, updated on 31-Jan-2019

Summary



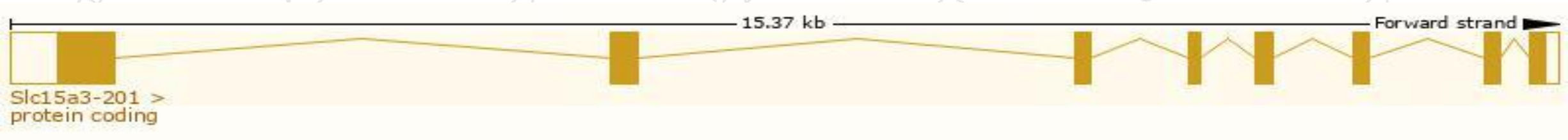
Official Symbol	Slc15a3 provided by MGI
Official Full Name	solute carrier family 15, member 3 provided by MGI
Primary source	MGI:MGI:1929691
See related	Ensembl:ENSMUSG00000024737
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ci1, cl-1
Expression	Broad expression in spleen adult (RPKM 18.7), lung adult (RPKM 15.6) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

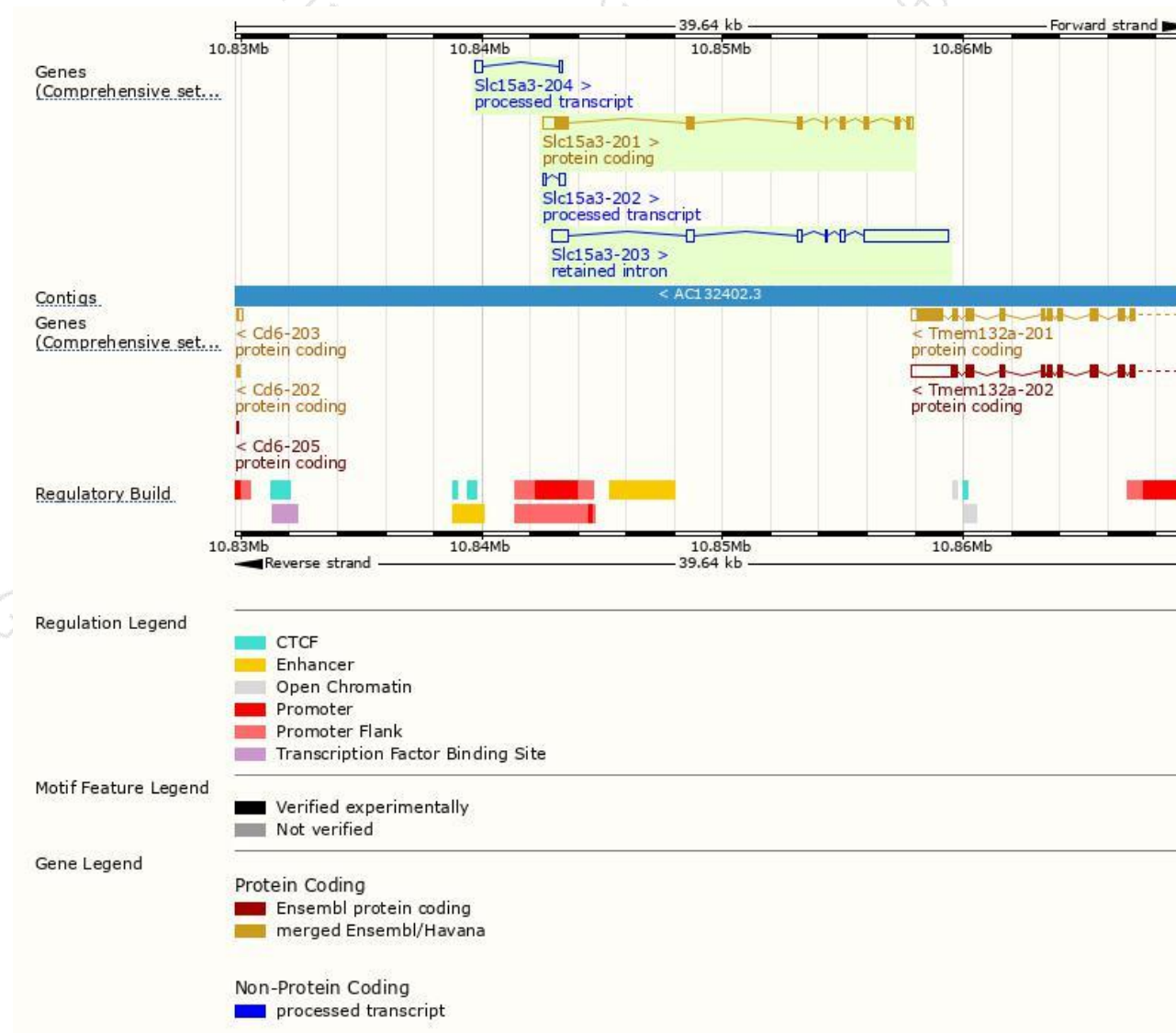
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc15a3-201	ENSMUST00000025646.2	2345	578aa	Protein coding	CCDS29588	Q8BPX9	TSL:1 GENCODE basic APPRIS P1
Slc15a3-204	ENSMUST00000138380.1	414	No protein	Processed transcript	-	-	TSL:2
Slc15a3-202	ENSMUST00000131010.1	361	No protein	Processed transcript	-	-	TSL:3
Slc15a3-203	ENSMUST00000138263.1	4868	No protein	Retained intron	-	-	TSL:1

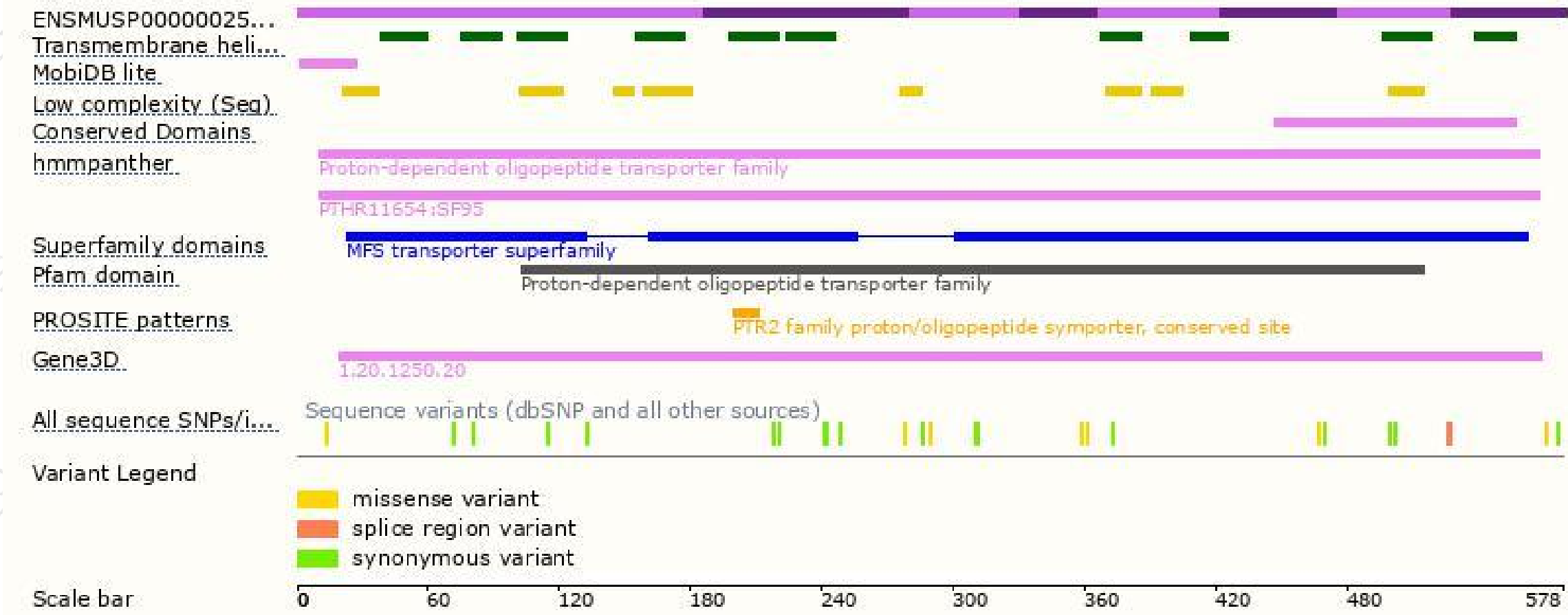
The strategy is based on the design of *Slc15a3-201* transcript,The transcription is shown below



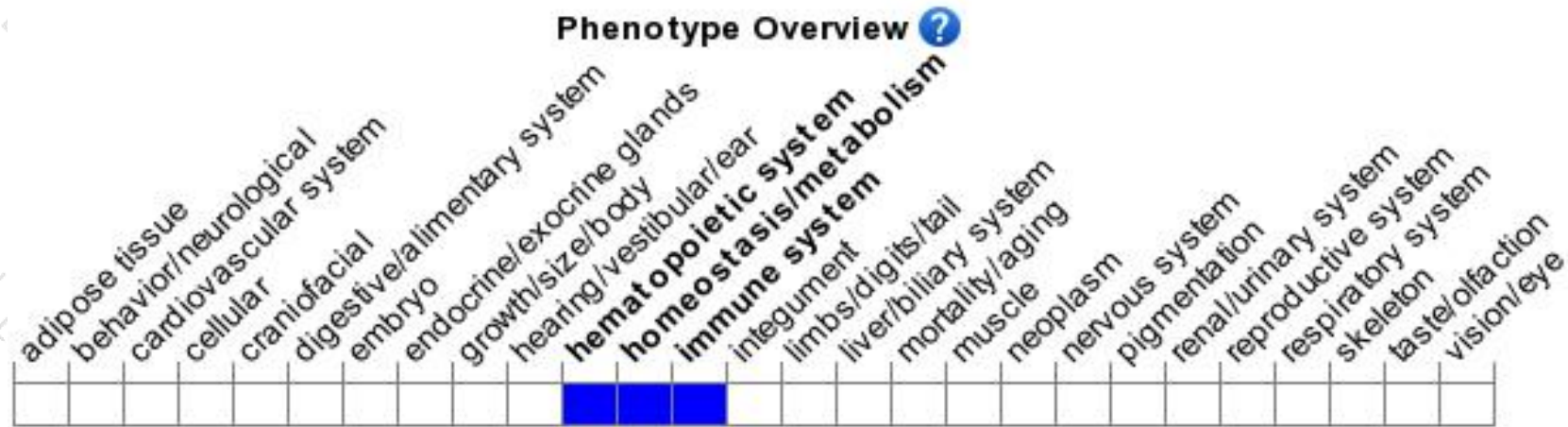
Genomic location distribution



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, The gene is involved in pathogen sensing by dendritic cells. Homozygous KO results in a reduction of the number of these cells displaying tubular endo-lysosomes after LPS treatment.

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

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