Slc7a2 Cas9-KO Strategy

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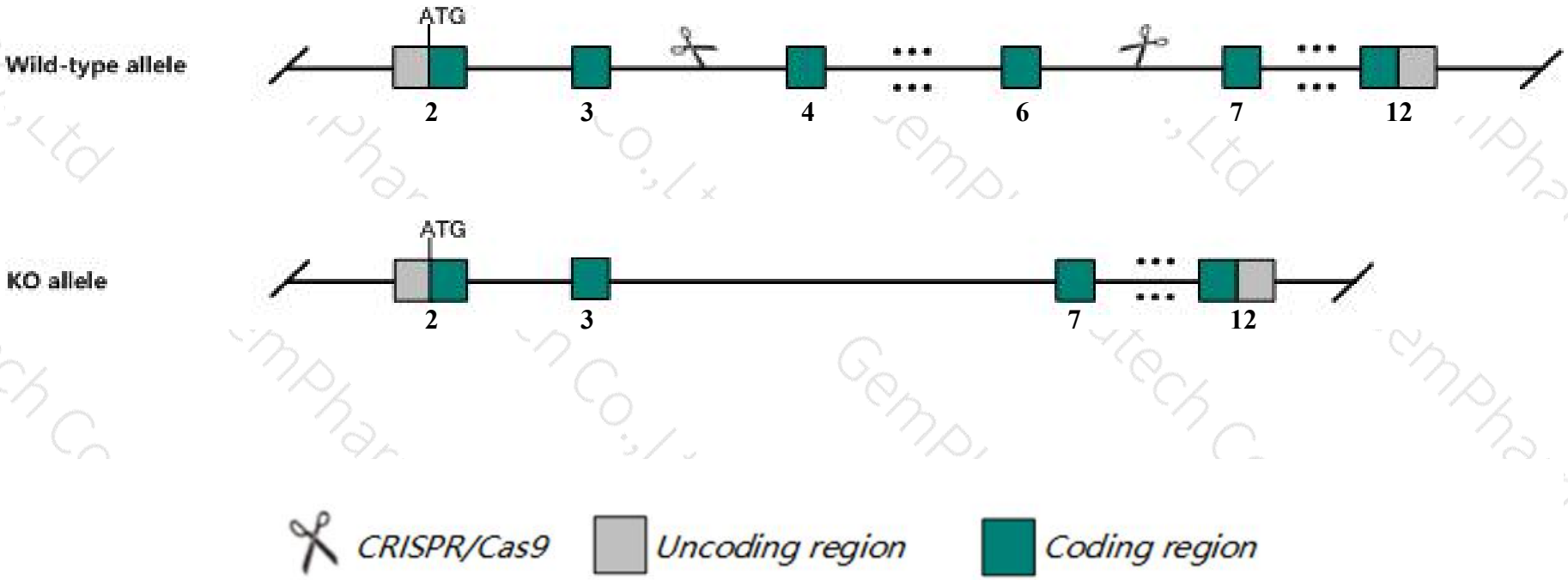
Project Overview

Project Name	***Slc7a2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc7a2* gene has 5 transcripts. According to the structure of *Slc7a2* gene, exon4-exon6 of *Slc7a2-201* (ENSMUST00000057784.14) transcript is recommended as the knockout region.The region contains 523bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc7a2* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

➢ According to the existing MGI data,Homozygotes for a targeted null allele exhibit a marked reduction of nitric oxide production by cytokine-activated macrophages.

➢The CDS of transcript *Slc7a2*-205 is incomplete ,whether it will be affected is unknown.

➢ The *Slc7a2* gene is located on the Chr8. 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）

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Slc7a2 solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 [*Mus musculus* (house mouse)]

Gene ID: 11988, updated on 12-Aug-2019

Summary

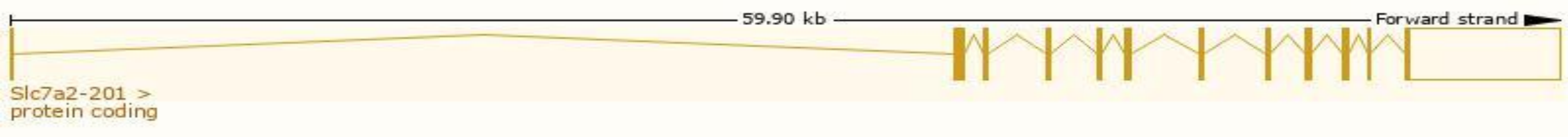
Official Symbol	Slc7a2 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 provided by MGI
Primary source	MGI:MGI:99828
See related	Ensembl:ENSMUSG00000031596
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Tea; 20.5; Cat2; Atrc2; CAT-2; AI158848
Expression	Biased expression in liver adult (RPKM 24.2), liver E18 (RPKM 9.0) and 14 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

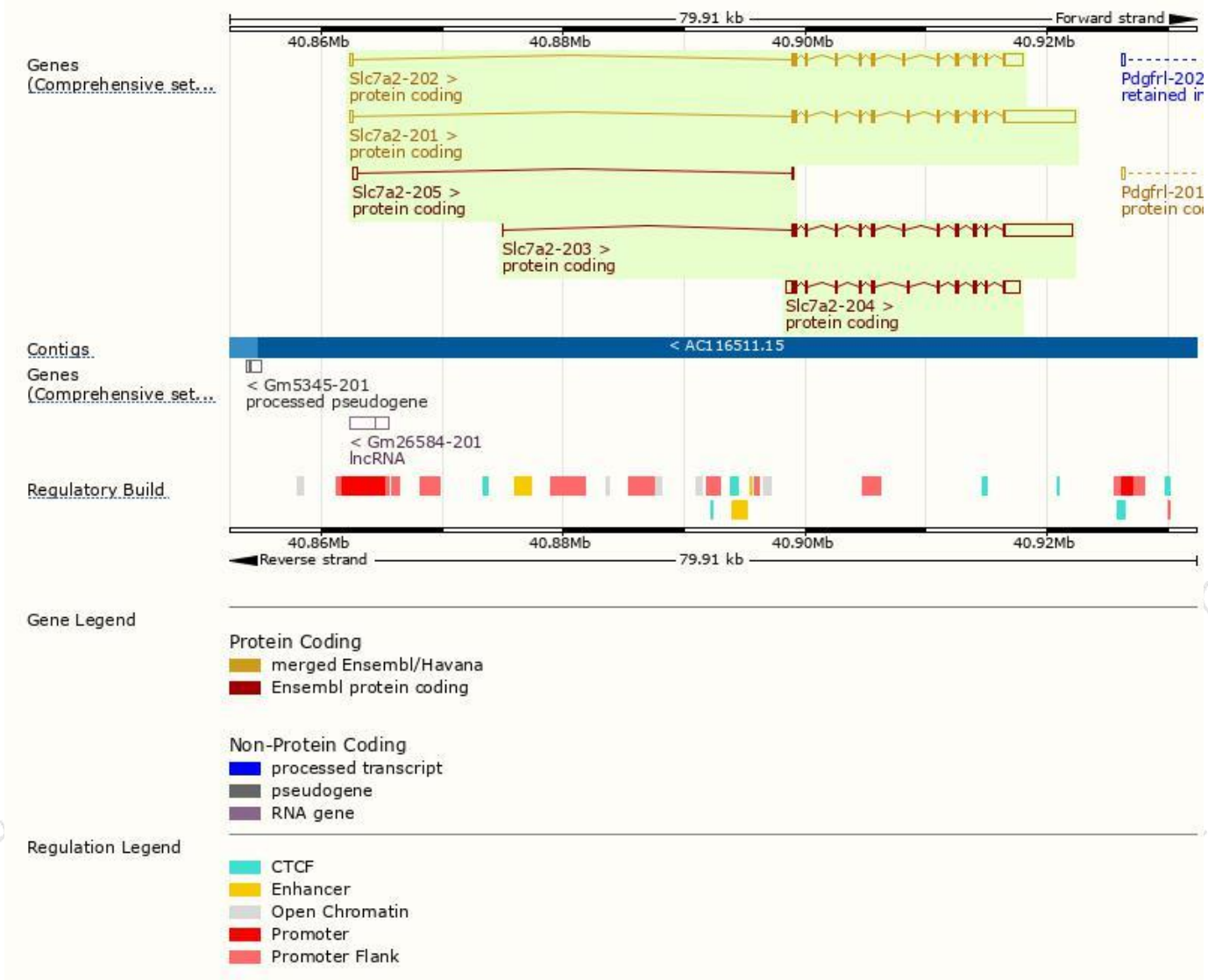
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a2-201	ENSMUST00000057784.14	7910	657aa	Protein coding	CCDS22258	P18581	TSL:1 GENCODE basic APPRIS P3
Slc7a2-203	ENSMUST00000117077.7	7626	658aa	Protein coding	CCDS40327	P18581	TSL:1 GENCODE basic APPRIS ALT1
Slc7a2-202	ENSMUST00000098816.9	3677	658aa	Protein coding	CCDS40327	P18581	TSL:1 GENCODE basic APPRIS ALT1
Slc7a2-204	ENSMUST00000118432.1	3681	674aa	Protein coding	-	E9QJY0	TSL:1 GENCODE basic
Slc7a2-205	ENSMUST00000141505.1	519	10aa	Protein coding	-	A0A1C7ZMY5	CDS 3' incomplete TSL:2

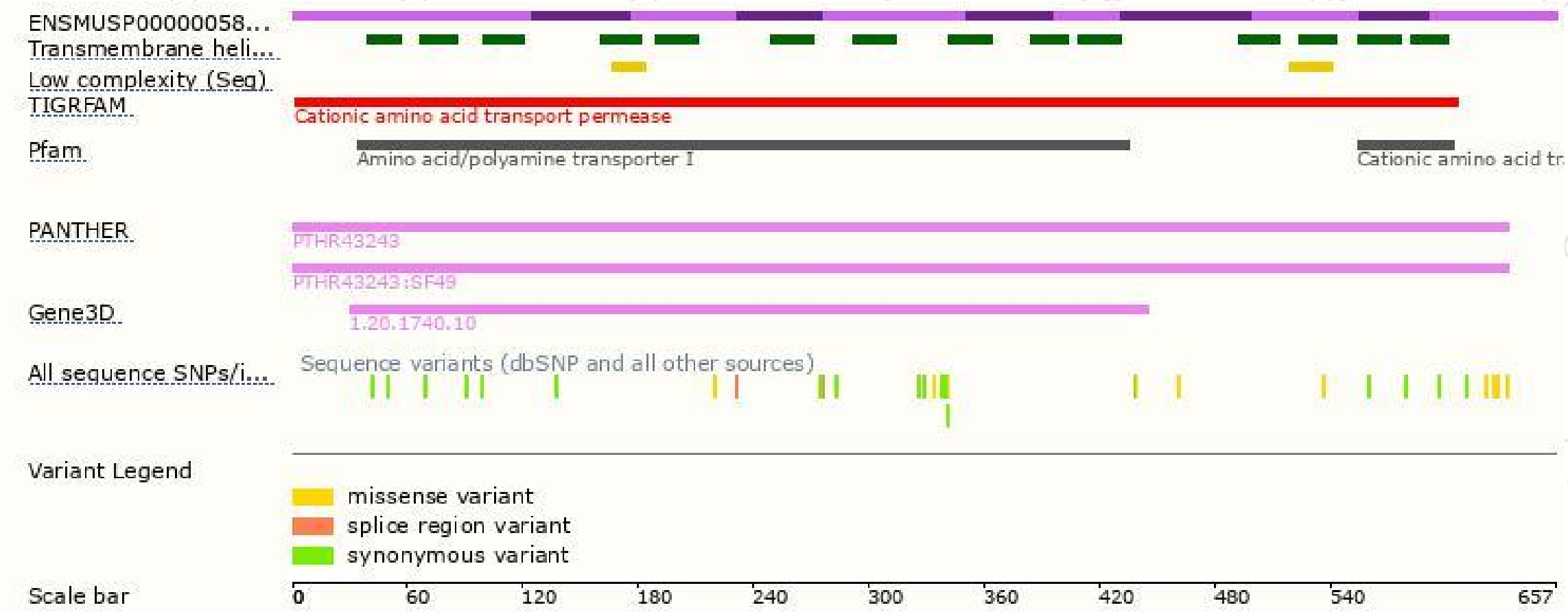
The strategy is based on the design of *Slc7a2-201* transcript,The transcription is shown below



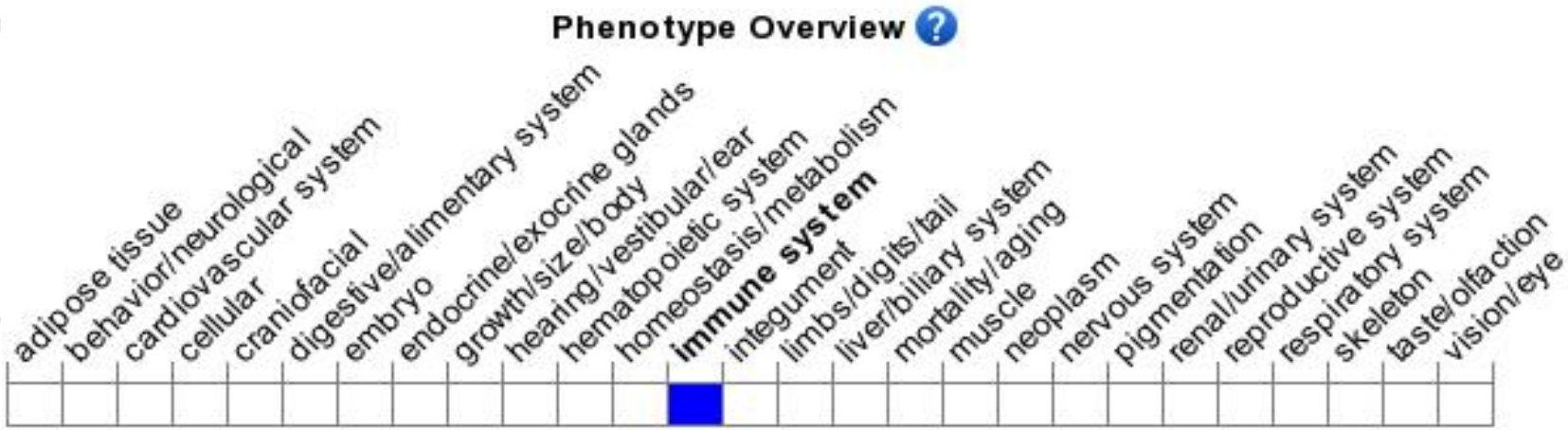
Genomic location distribution



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,Homozygotes for a targeted null allele exhibit a marked reduction of nitric oxide production by cytokine-activated macrophages.

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

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