Slc7a1 Cas9-KO *Strategy*

Designer: **Huan Fan**

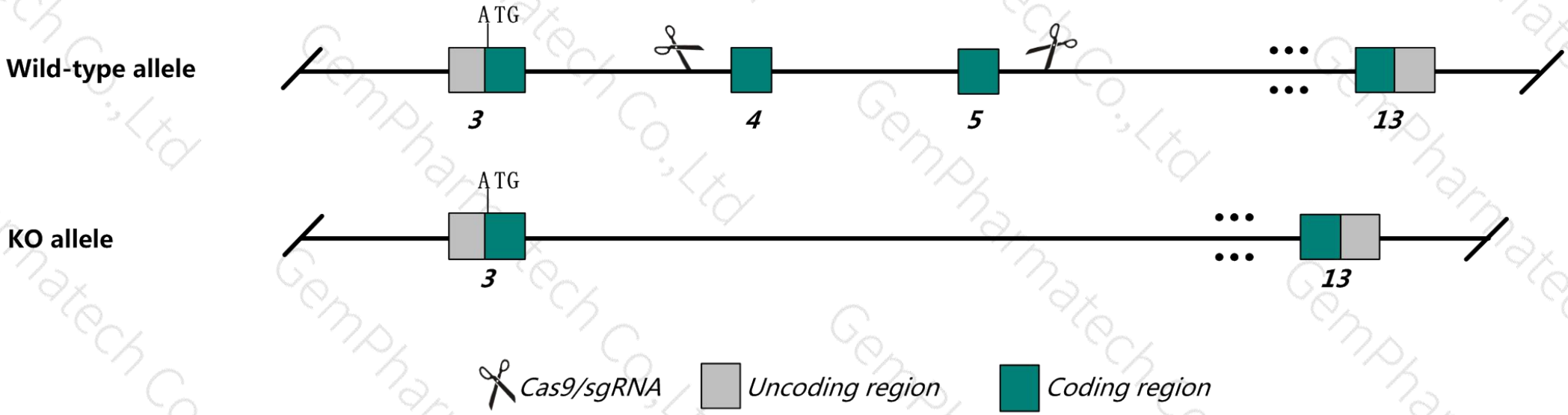
Design Date: **2019-7-25**

Project Overview

Project Name	***Slc7a1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a1* gene. The schematic diagram is as follows:



Technical routes

- The *Slc7a1* gene has 6 transcripts.According to the structure of *Slc7a1* gene, exon4-5 of *Slc7a1*-201 transcript is recommended as the knockout region.The region contains 316bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc7a1* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

- According to the existing MGI data，Homozygous mutants die on the first day of birth and are very anemic. Peripheral blood contains 50% fewer red blood cells, reduced hemoglobin levels, and a defect in erythroid maturation.
- Transcript *Slc7a1-203* may not be affected.
- The *Slc7a1* gene is located on the Chr5. 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）

集萃药康 GemPharmatech

Slc7a1 solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 [*Mus musculus* (house mouse)]

Gene ID: 11987, updated on 31-Jan-2019

Summary

Official Symbol	Slc7a1 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 provided by MGI
Primary source	MGI:MGI:88117
See related	Ensembl:ENSMUSG00000041313
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	Cat1; Atrc1; Rec-1; Rev-1; Atrc-1; mCAT-1; AI447493; 4831426K01Rik
Expression	Ubiquitous expression in adrenal adult (RPKM 11.4), genital fat pad adult (RPKM 10.4) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts, and all transcripts are shown below:

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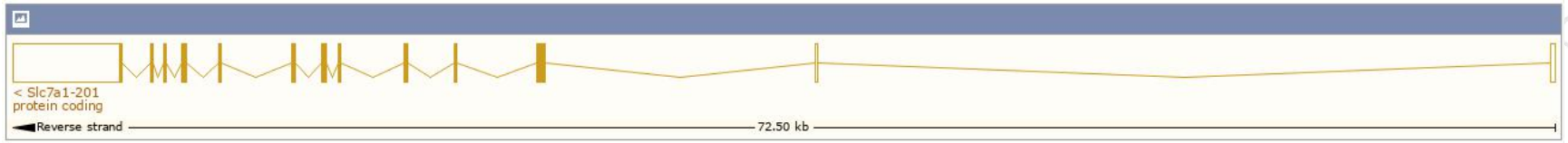
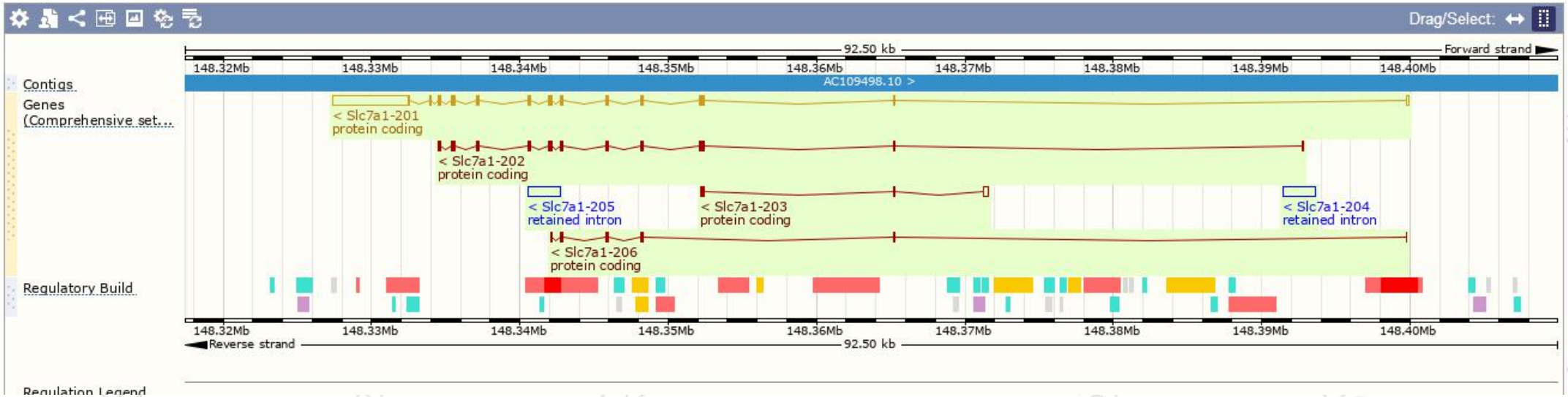
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a1-201	ENSMUST00000048116.14	7179	622aa	Protein coding	CCDS19882	Q09143 Q3UGD6	TSL:1 GENCODE basic APPRIS P1
Slc7a1-202	ENSMUST00000138257.7	1792	542aa	Protein coding	-	E9Q3N1	CDS 3' incomplete TSL:5
Slc7a1-203	ENSMUST00000138596.1	675	94aa	Protein coding	-	D3Z161	CDS 3' incomplete TSL:3
Slc7a1-206	ENSMUST00000202457.3	663	142aa	Protein coding	-	A0A0J9YU45	CDS 3' incomplete TSL:5
Slc7a1-204	ENSMUST00000201348.1	2232	No protein	Retained intron	-	-	TSL:NA
Slc7a1-205	ENSMUST00000201860.1	2151	No protein	Retained intron	-	-	TSL:NA

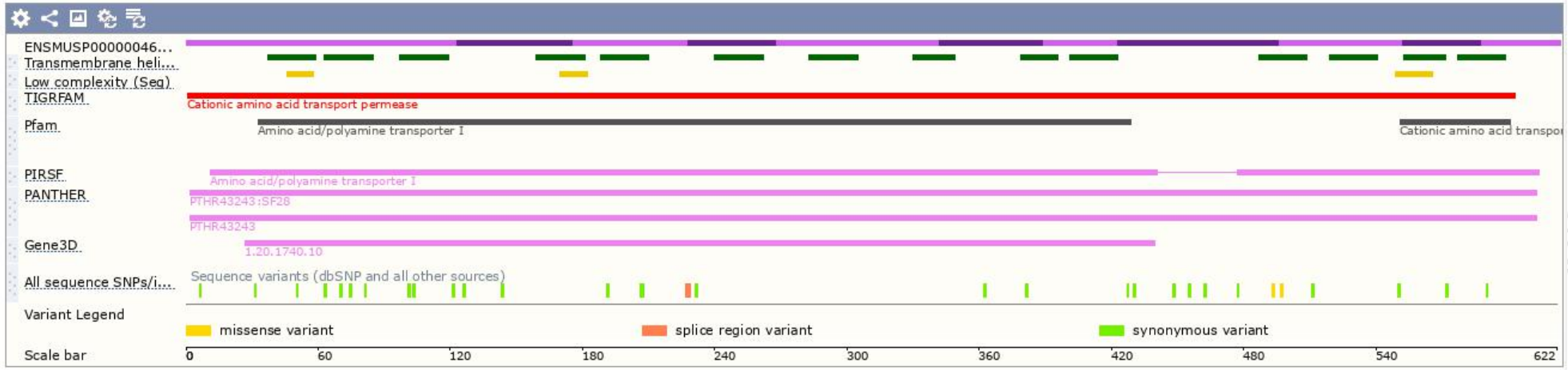
The strategy is based on the design of *Slc7a1*-201 transcript,The transcription is shown below



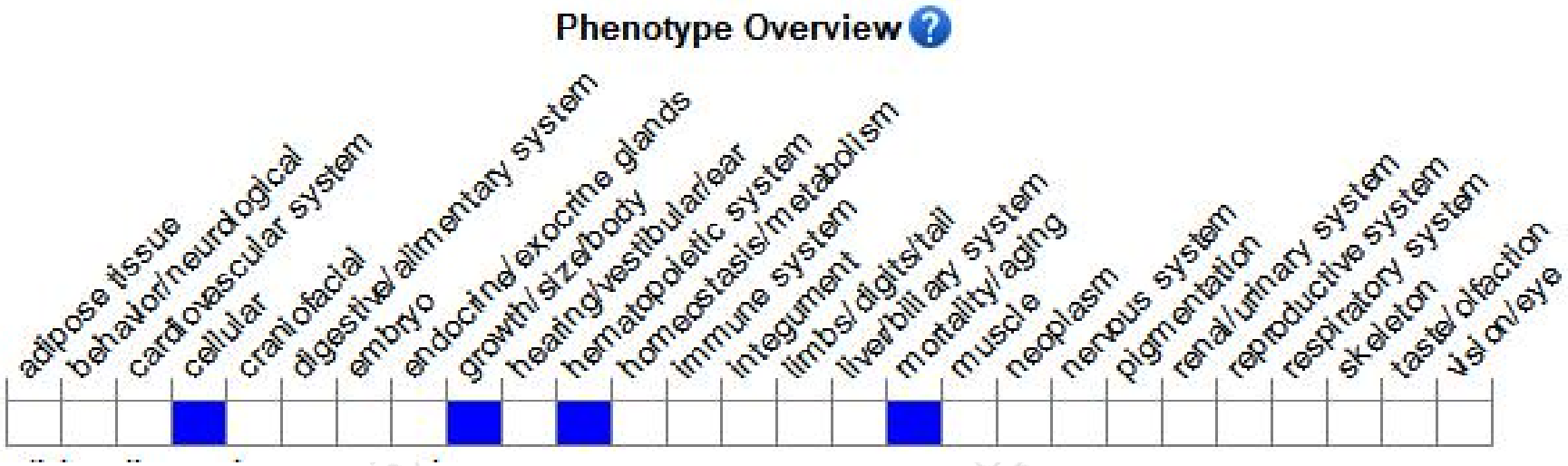
Genomic location distribution



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,Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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