Slc7a7 Cas9-CKO Strategy

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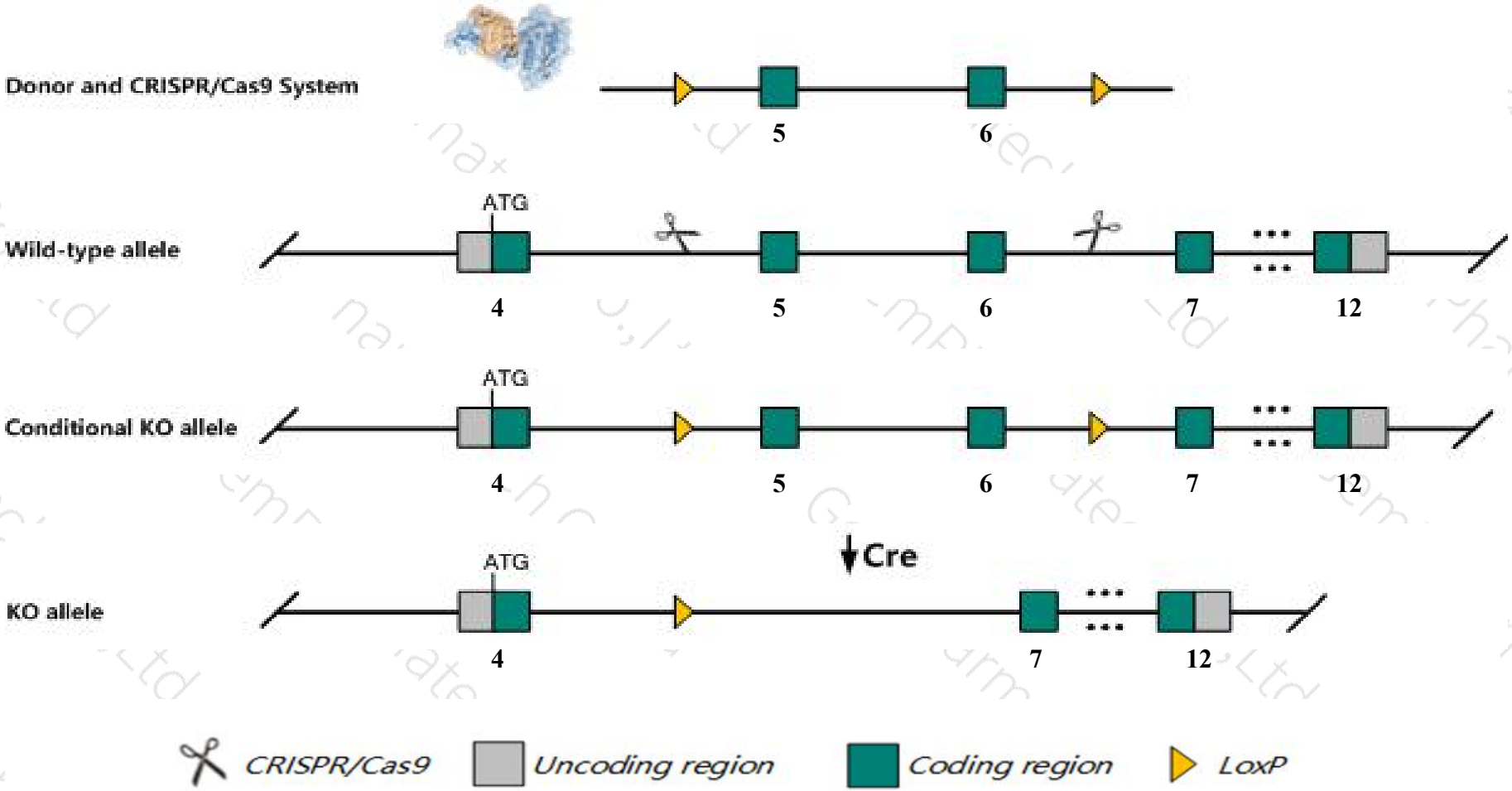
Project Overview

Project Name	***Slc7a7***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a7* gene. The schematic diagram is as follows:



Technical routes

- The *Slc7a7* gene has 12 transcripts. According to the structure of *Slc7a7* gene, exon5-exon6 of *Slc7a7-206* (ENSMUST00000197440.4) transcript is recommended as the knockout region.The region contains 271bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc7a7* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,homozygous null mice exhibit fetal growth retardation and often die neonatally. after heavy protein ingestion, surviving adults show a metabolic derangement akin to lysinuric protein intolerance and including a lasting postnatal growth retardation, splenomegaly, hyperammonemia, and aminoaciduria.
- Transcripts *Slc7a7-210,Slc7a7-203, Slc7a7-204 and Slc7a7-211* are incomplete, so the effect on them are unknown.
- The *Slc7a7* gene is located on the Chr14. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

集萃药康 GemPharmatech

Slc7a7 solute carrier family 7 (cationic amino acid transporter, y+ system), member 7 [*Mus musculus* (house mouse)]

Gene ID: 20540, updated on 7-Apr-2020

Summary

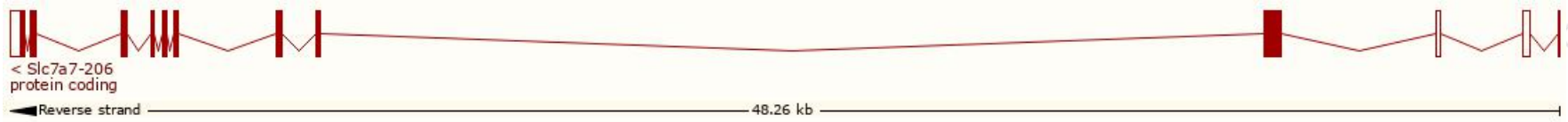
Official Symbol	Slc7a7 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7 provided by MGI
Primary source	MGI:MGI:1337120
See related	Ensembl:ENSMUSG00000000958
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	my+lat1; AI790233
Expression	Biased expression in kidney adult (RPKM 116.6), large intestine adult (RPKM 74.7) and 8 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

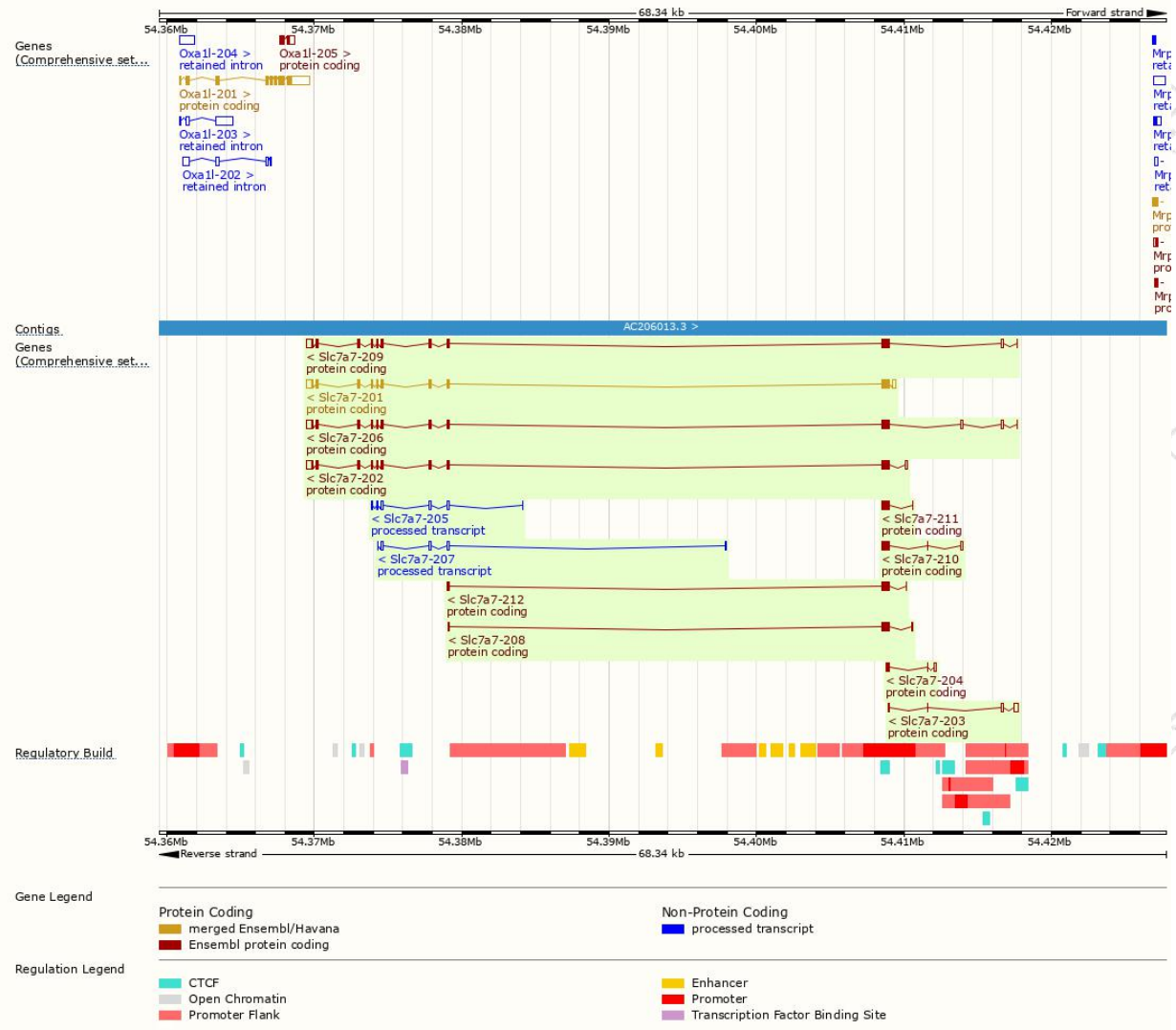
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a7-206	ENSMUST00000197440.4	2278	510aa	Protein coding	CCDS27087	Q9Z1K8	TSL:1 GENCODE basic APPRIS P1
Slc7a7-201	ENSMUST00000000984.8	2132	510aa	Protein coding	CCDS27087	Q9Z1K8	TSL:1 GENCODE basic APPRIS P1
Slc7a7-209	ENSMUST00000226753.1	2126	510aa	Protein coding	CCDS27087	Q9Z1K8	GENCODE basic APPRIS P1
Slc7a7-202	ENSMUST00000195970.4	2057	510aa	Protein coding	CCDS27087	Q9Z1K8	TSL:5 GENCODE basic APPRIS P1
Slc7a7-212	ENSMUST00000228488.1	723	209aa	Protein coding	-	A0A2I3BQX2	CDS 3' incomplete
Slc7a7-210	ENSMUST00000227334.1	711	156aa	Protein coding	-	A0A2I3BQK2	CDS 3' incomplete
Slc7a7-208	ENSMUST00000200545.1	664	186aa	Protein coding	-	A0A0G2JE10	CDS 3' incomplete TSL:3
Slc7a7-203	ENSMUST00000195999.1	622	13aa	Protein coding	-	A0A0G2JEM2	CDS 3' incomplete TSL:2
Slc7a7-211	ENSMUST00000227967.1	572	167aa	Protein coding	-	A0A2I3BPU1	CDS 3' incomplete
Slc7a7-204	ENSMUST00000196215.4	461	59aa	Protein coding	-	A0A0G2JEB8	CDS 3' incomplete TSL:3
Slc7a7-205	ENSMUST00000196966.4	638	No protein	Processed transcript	-	-	TSL:5
Slc7a7-207	ENSMUST00000197667.1	492	No protein	Processed transcript	-	-	TSL:3

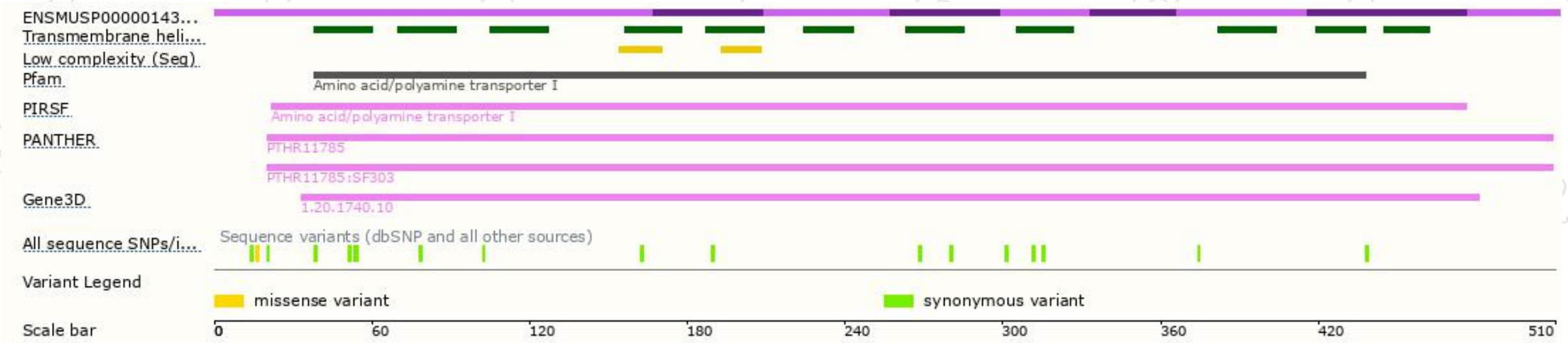
The strategy is based on the design of *Slc7a7-206* transcript, the transcription is shown below



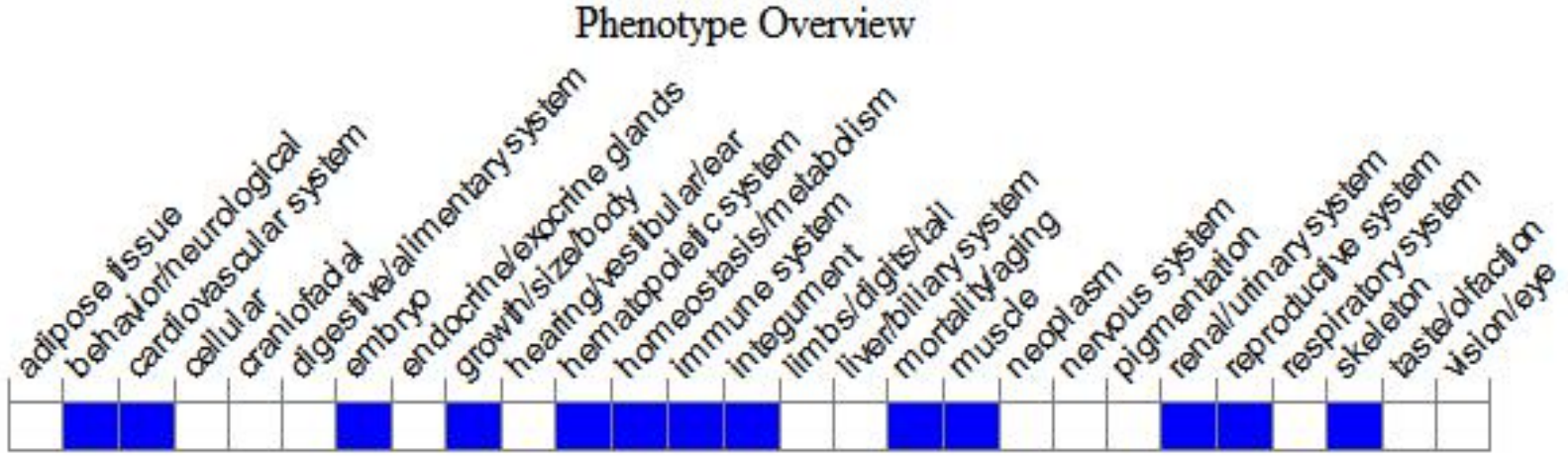
Genomic location distribution



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,Homozygous null mice exhibit fetal growth retardation and often die neonatally. After heavy protein ingestion, surviving adults show a metabolic derangement akin to lysinuric protein intolerance and including a lasting postnatal growth retardation, splenomegaly, hyperammonemia, and aminoaciduria.

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

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