

Slc7a5 Cas9-KO Strategy

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Project Overview



Project Name

Slc7a5

Project type

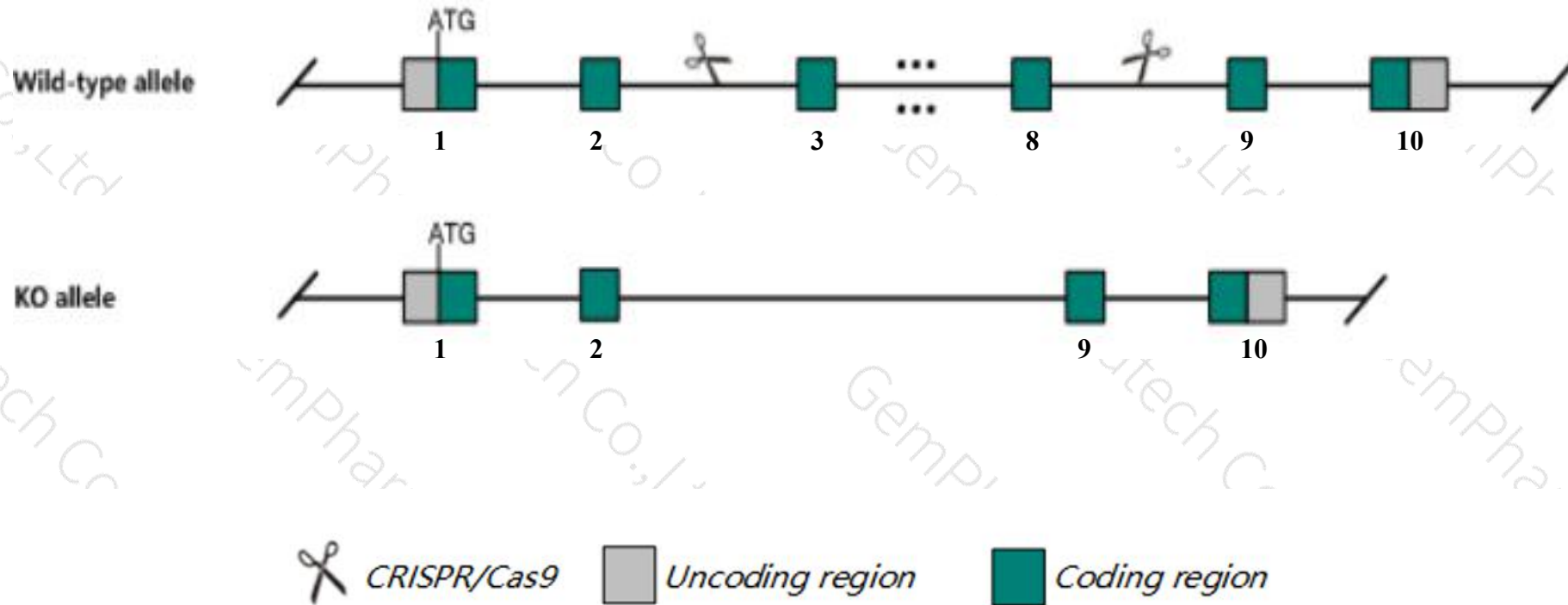
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a5* gene. The schematic diagram is as follows:



- The *Slc7a5* gene has 3 transcripts. According to the structure of *Slc7a5* gene, exon3-exon8 of *Slc7a5-201* (ENSMUST00000045557.9) transcript is recommended as the knockout region. The region contains 626bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc7a5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a targeted mutation die prenatally.
- Part of *Gm20388* will be knocked out.
- The *Slc7a5* gene is located on 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)

Slc7a5 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 [*Mus musculus* (house mouse)]

Gene ID: 20539, updated on 6-Apr-2020

Summary

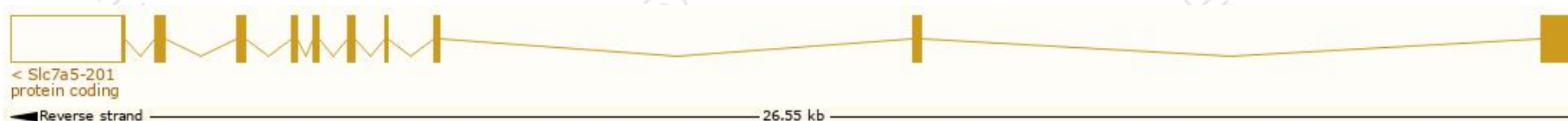
Official Symbol	Slc7a5 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 provided by MGI
Primary source	MGI:MGI:1298205
See related	Ensembl:ENSMUSG00000040010
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	TA1; LAT1; 4F2LC; D0H16S474E
Expression	Broad expression in genital fat pad adult (RPKM 202.2), ovary adult (RPKM 100.8) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

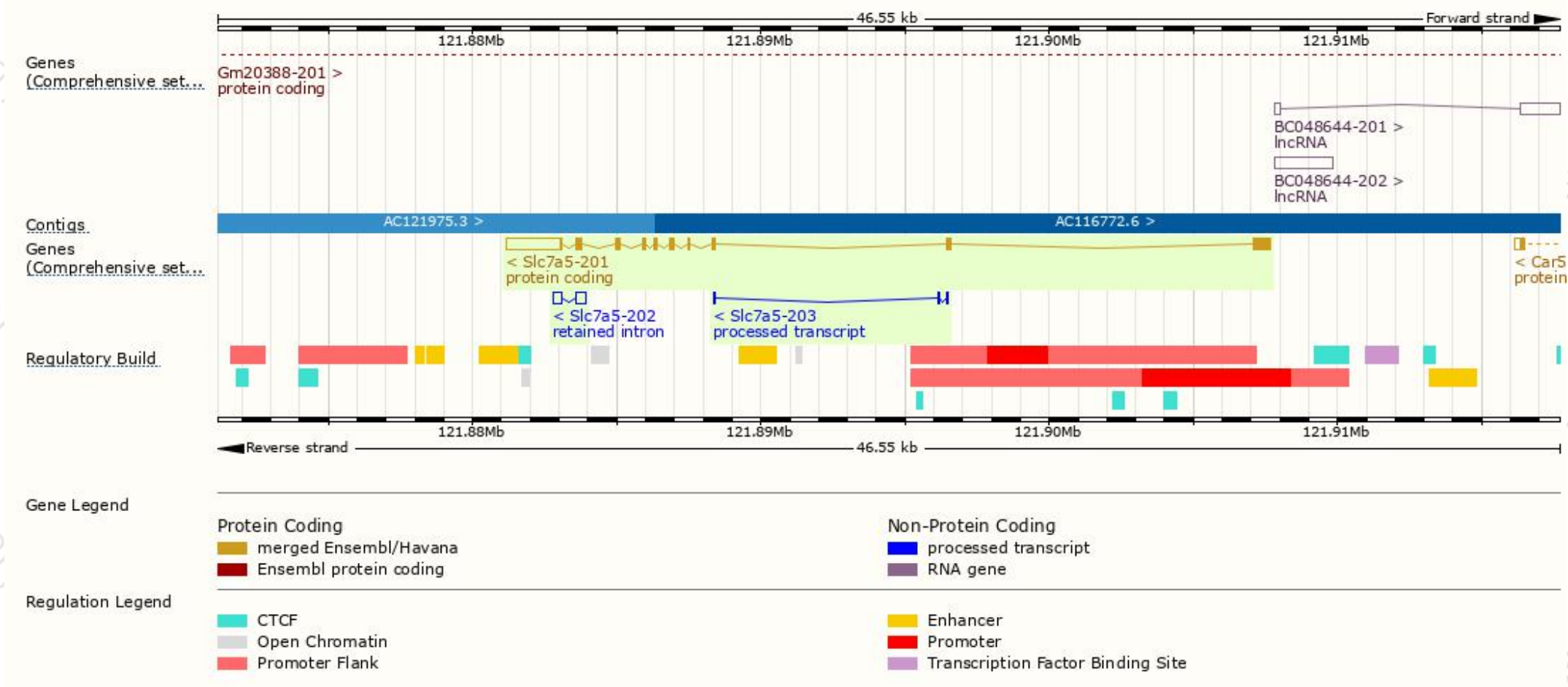
The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a5-201	ENSMUST00000045557.9	3517	512aa	Protein coding	CCDS22730	Q9Z127	TSL:1 Gencode basic APPRIS P1
Slc7a5-203	ENSMUST00000183015.1	174	No protein	Processed transcript	-	-	TSL:1
Slc7a5-202	ENSMUST00000182165.1	618	No protein	Retained intron	-	-	TSL:1

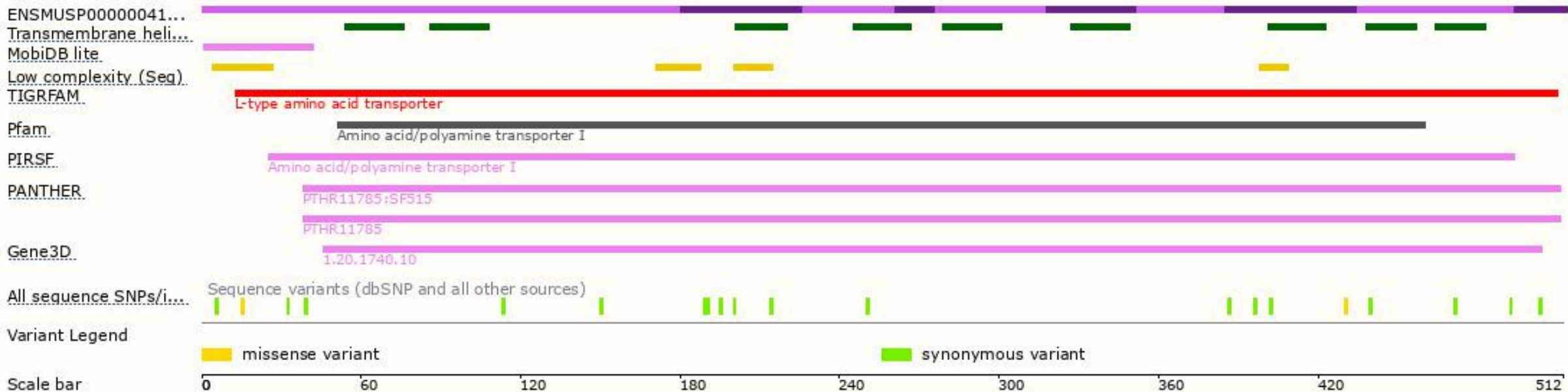
The strategy is based on the design of *Slc7a5-201* transcript, the transcription is shown below



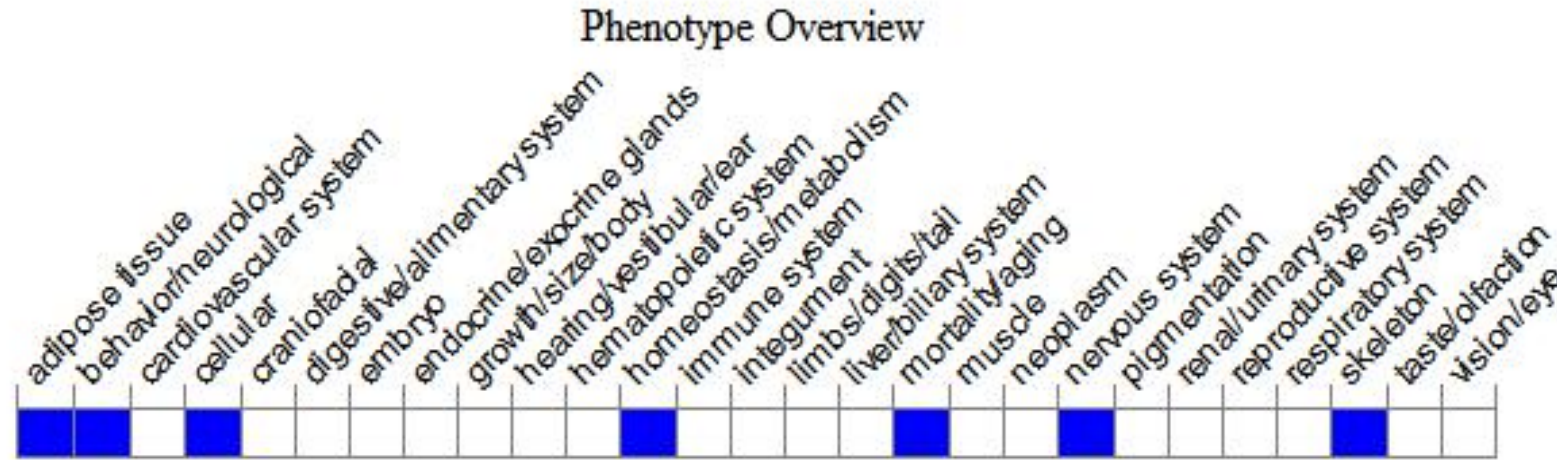
Genomic location distribution



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 targeted mutation die prenatally.

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

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