Slc7a9 Cas9-KO Strategy

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Reviewer: Xiaojing Li

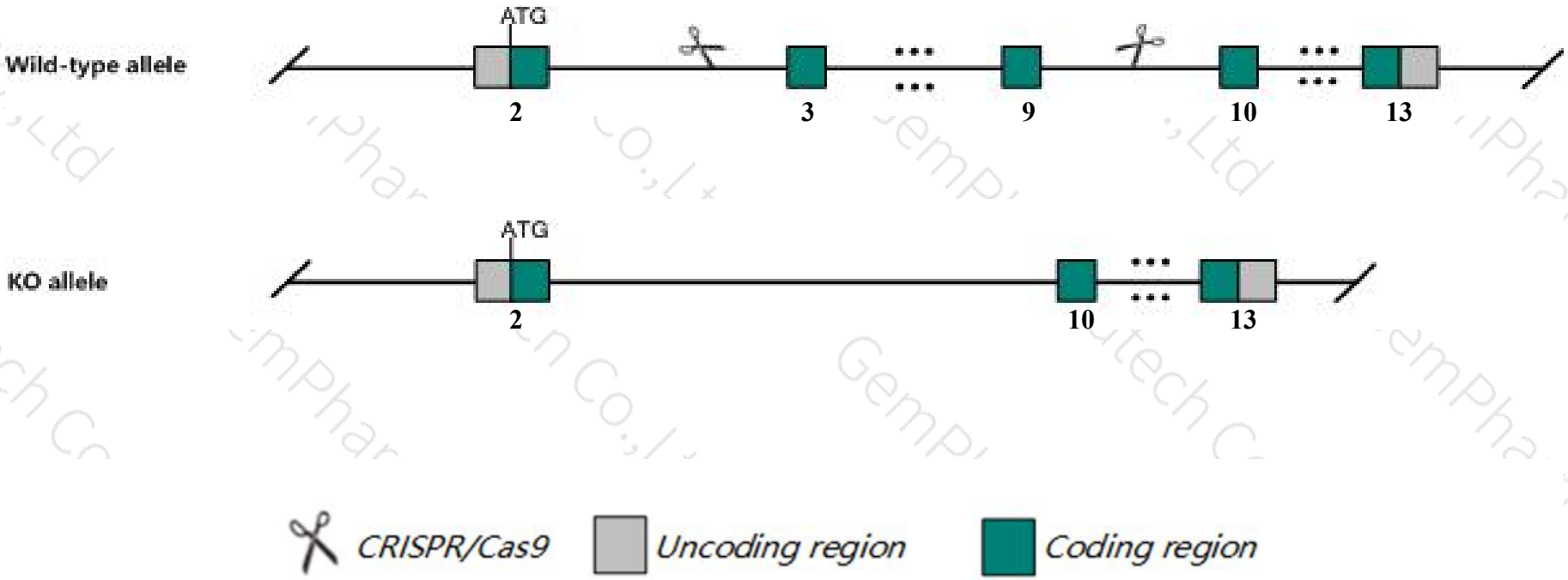
Design Date: 2020-2-18

Project Overview

Project Name	***Slc7a9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc7a9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc7a9* gene has 6 transcripts. According to the structure of *Slc7a9* gene, exon3-exon9 of *Slc7a9-201* (ENSMUST00000032703.9) transcript is recommended as the knockout region.The region contains 890bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc7a9* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Inactivation of this locus leads to renal absorption defects and cystine urolithiasis, similar to the symptoms observed in patients with cystinuria.

➢ The *Slc7a9* gene is located on the Chr7. 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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Slc7a9 solute carrier family 7 (cationic amino acid transporter, y+ system), member 9 [Mus musculus (house mouse)]

Gene ID: 30962, updated on 31-Jan-2019

Summary

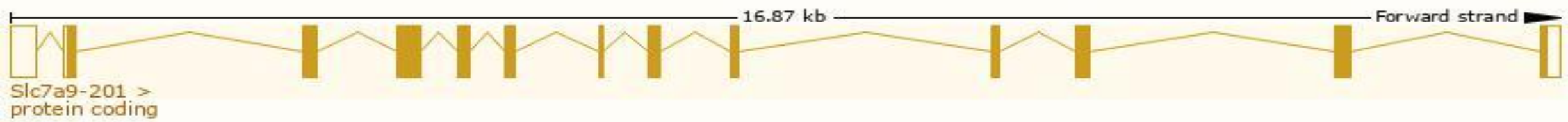
Official Symbol	Slc7a9 provided by MGI
Official Full Name	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9 provided by MGI
Primary source	MGI:MGI:1353656
See related	Ensembl:ENSMUSG00000030492
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CSNU3
Expression	Biased expression in large intestine adult (RPKM 139.5), kidney adult (RPKM 97.6) and 3 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

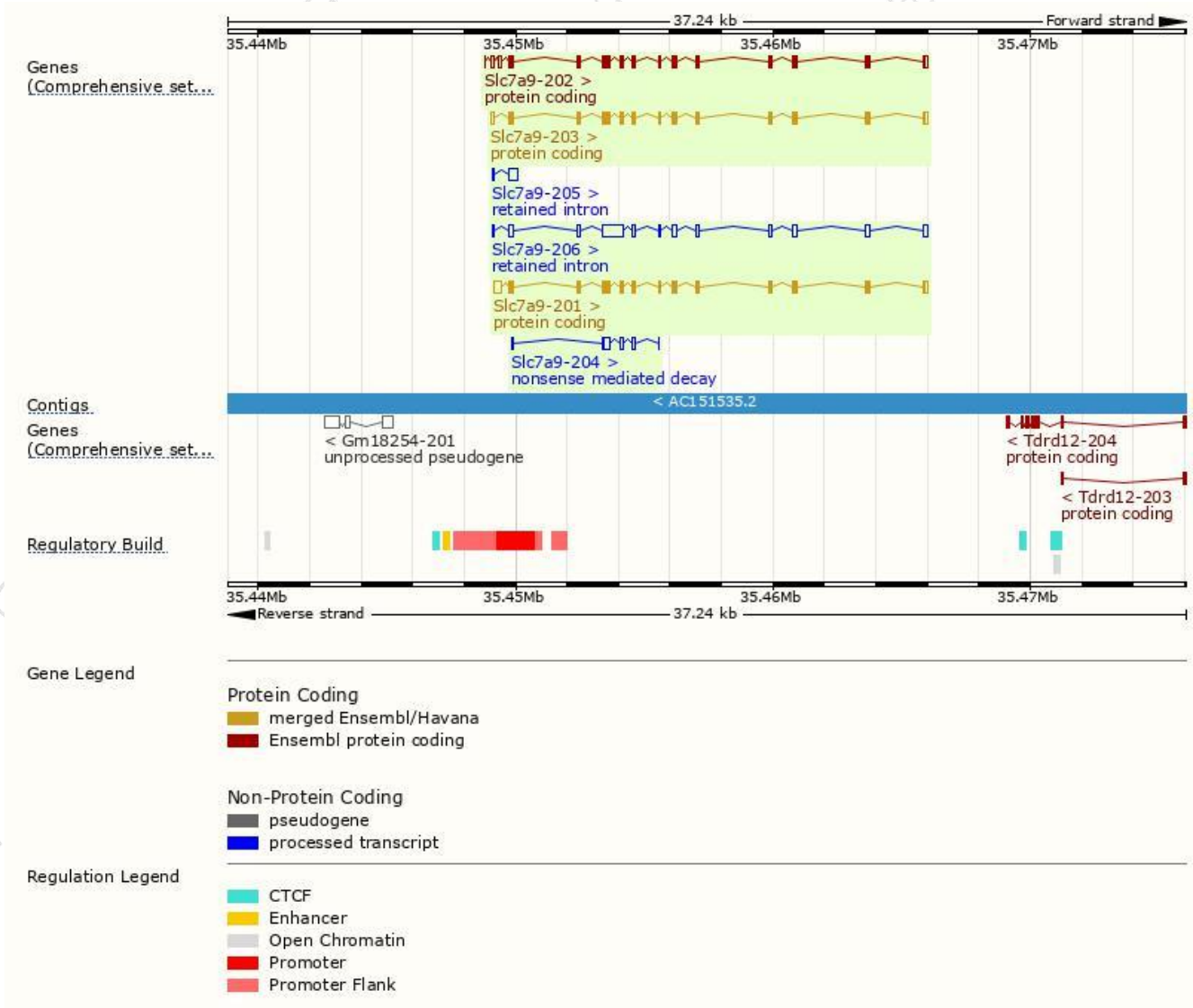
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc7a9-201	ENSMUST00000032703.9	1940	487aa	Protein coding	CCDS21150	Q3UQE3 Q9QXA6	TSL:1 GENCODE basic APPRIS P1
Slc7a9-202	ENSMUST00000118383.7	1869	487aa	Protein coding	CCDS21150	Q3UQE3 Q9QXA6	TSL:5 GENCODE basic APPRIS P1
Slc7a9-203	ENSMUST00000118969.7	1765	487aa	Protein coding	CCDS21150	Q3UQE3 Q9QXA6	TSL:1 GENCODE basic APPRIS P1
Slc7a9-204	ENSMUST00000141245.1	536	27aa	Nonsense mediated decay	-	F7AUJ6	CDS 5' incomplete TSL:5
Slc7a9-206	ENSMUST00000147026.7	2086	No protein	Retained intron	-	-	TSL:2
Slc7a9-205	ENSMUST00000141905.1	370	No protein	Retained intron	-	-	TSL:2

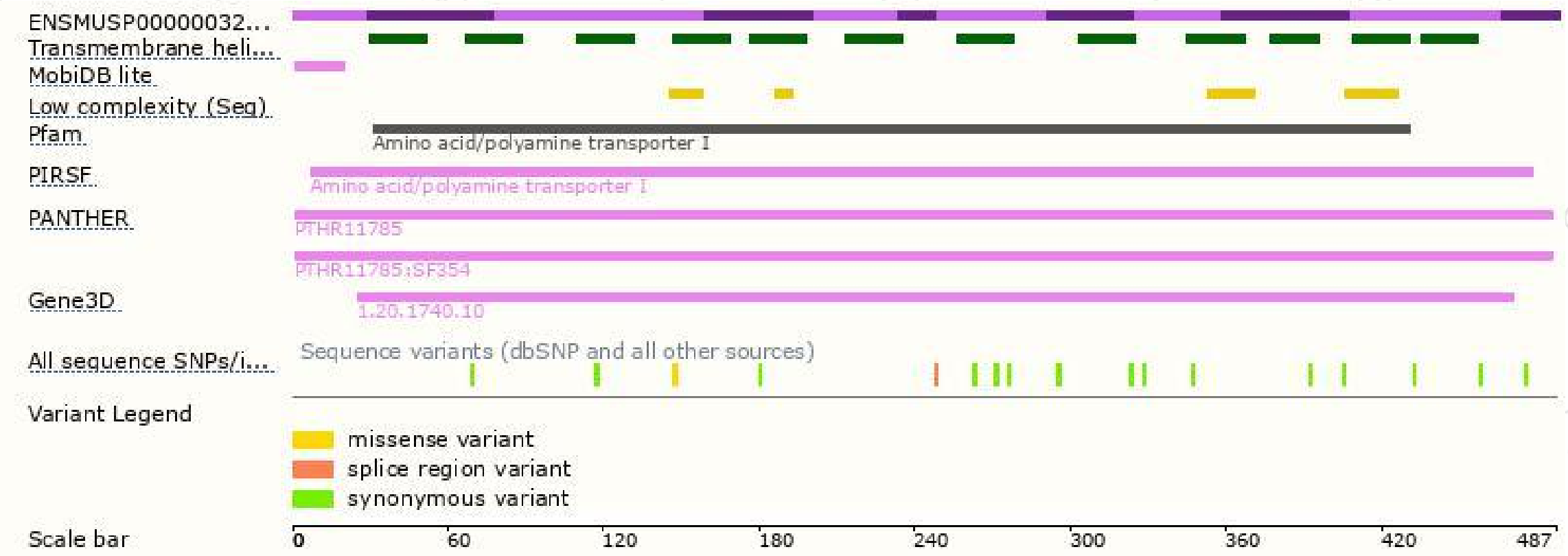
The strategy is based on the design of *Slc7a9-201* transcript,The transcription is shown below



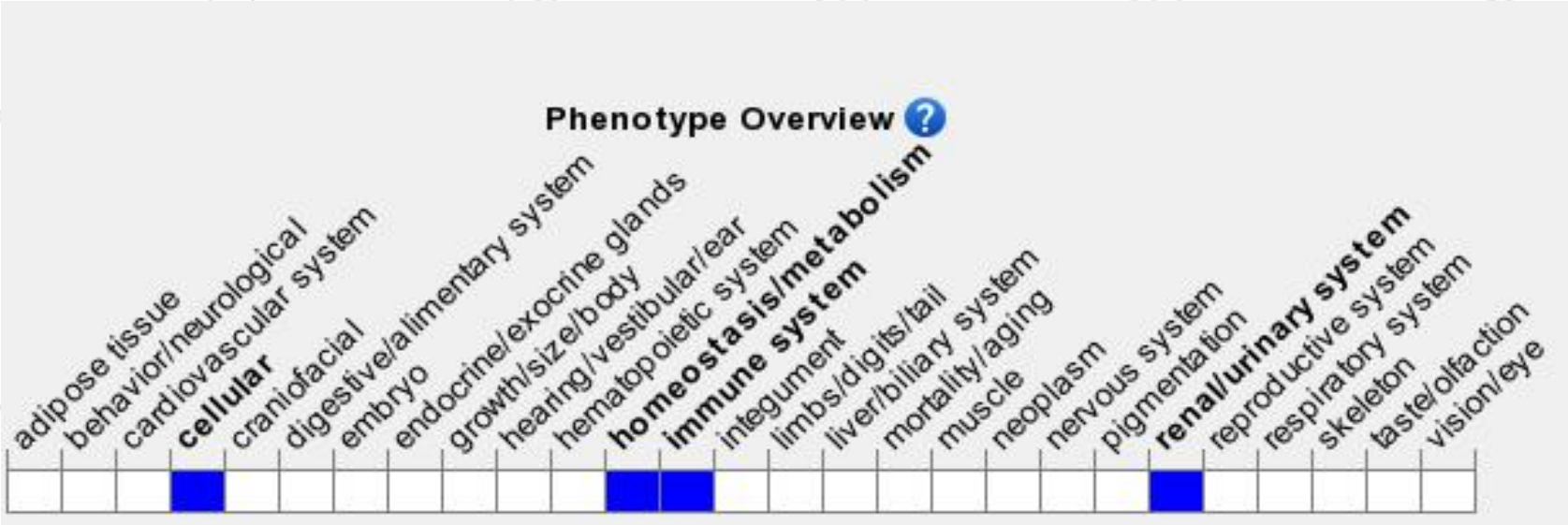
Genomic location distribution



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,Inactivation of this locus leads to renal absorption defects and cystine urolithiasis, similar to the symptoms observed in patients with cystinuria.

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

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