Slc26a3 Cas9-CKO Strategy

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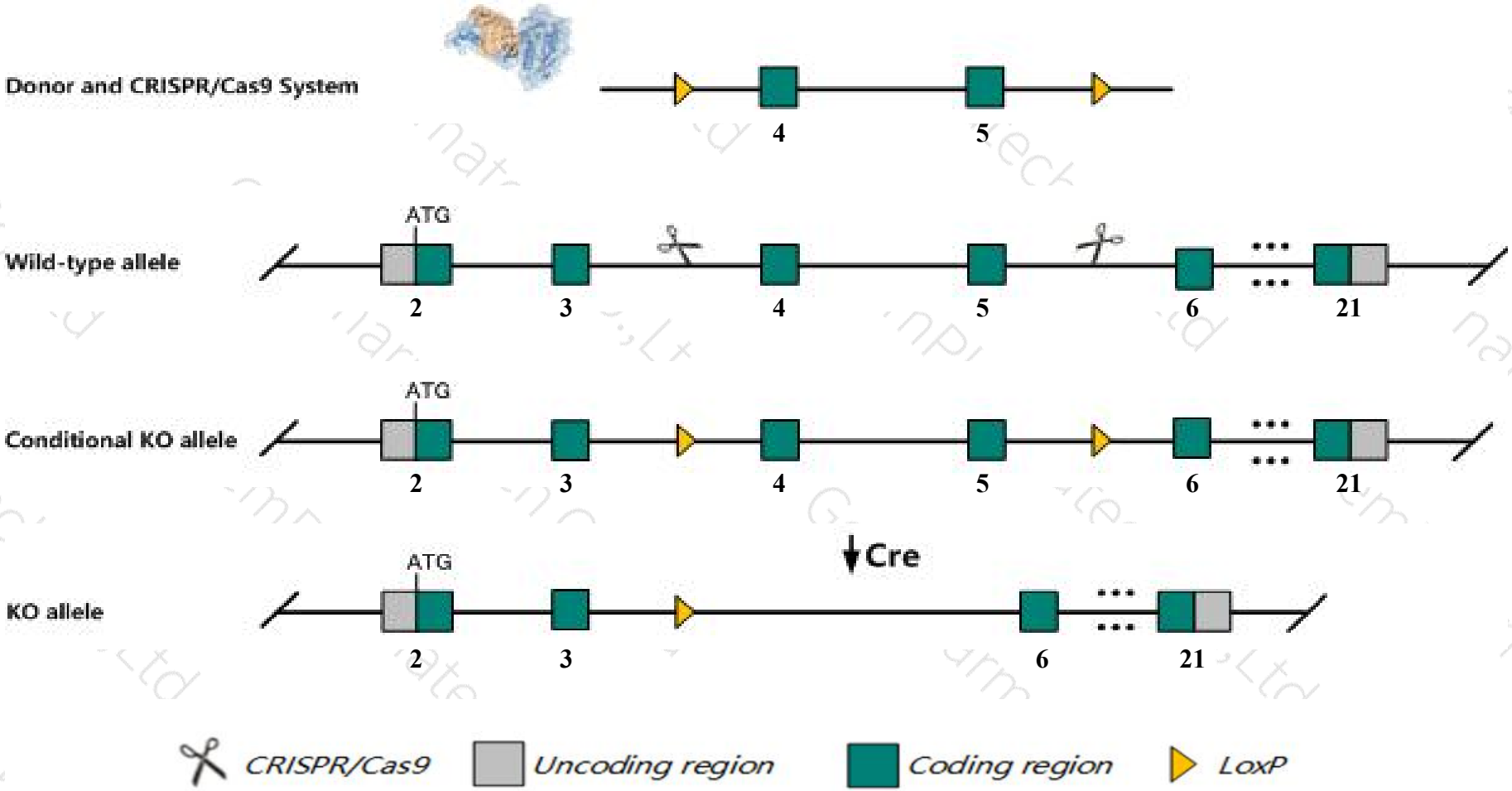
Design Date:2019-8-12

Project Overview

Project Name	***Slc26a3***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc26a3* gene. The schematic diagram is as follows:



Technical routes

- The *Slc26a3* gene has 7 transcripts. According to the structure of *Slc26a3* gene, exon4-exon5 of *Slc26a3-201* (ENSMUST00000001254.5) transcript is recommended as the knockout region.The region contains 278bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc26a3* 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,Homozygotes for a null allele display partial postnatal lethality; survivors are small and show lower luminal Cl-/HCO3- exchange activity, acidic chloridorrhea, volume depletion, upregulation of ion transporters, dilated colons, higher crypt proliferation and plasma aldosterone, and premature death.
- Transcript *Slc26a3*-202 may not be affected.
- The *Slc26a3* gene is located on the Chr12. 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）

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Slc26a3 solute carrier family 26, member 3 [Mus musculus (house mouse)]

Gene ID: 13487, updated on 12-Mar-2019

Summary

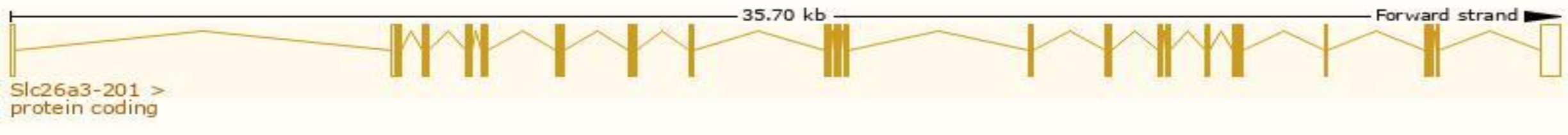
Official Symbol	Slc26a3 provided by MGI
Official Full Name	solute carrier family 26, member 3 provided byMGI
Primary source	MGI:MGI:107181
See related	Ensembl:ENSMUSG00000001225
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9030623B18Rik, 9130013M11Rik, AV376035, Dra
Summary	This gene encodes a member of the solute carrier/sulfate transporter family. The encoded protein is predominantly expressed in the intestine where it is essential for chloride absorption. Disruption of this gene results in chloride-rich diarrhea and compensatory up-regulation of ion-absorbing transporters. [provided by RefSeq, Dec 2012]
Expression	Biased expression in colon adult (RPKM 52.2), large intestine adult (RPKM 13.2) and 2 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

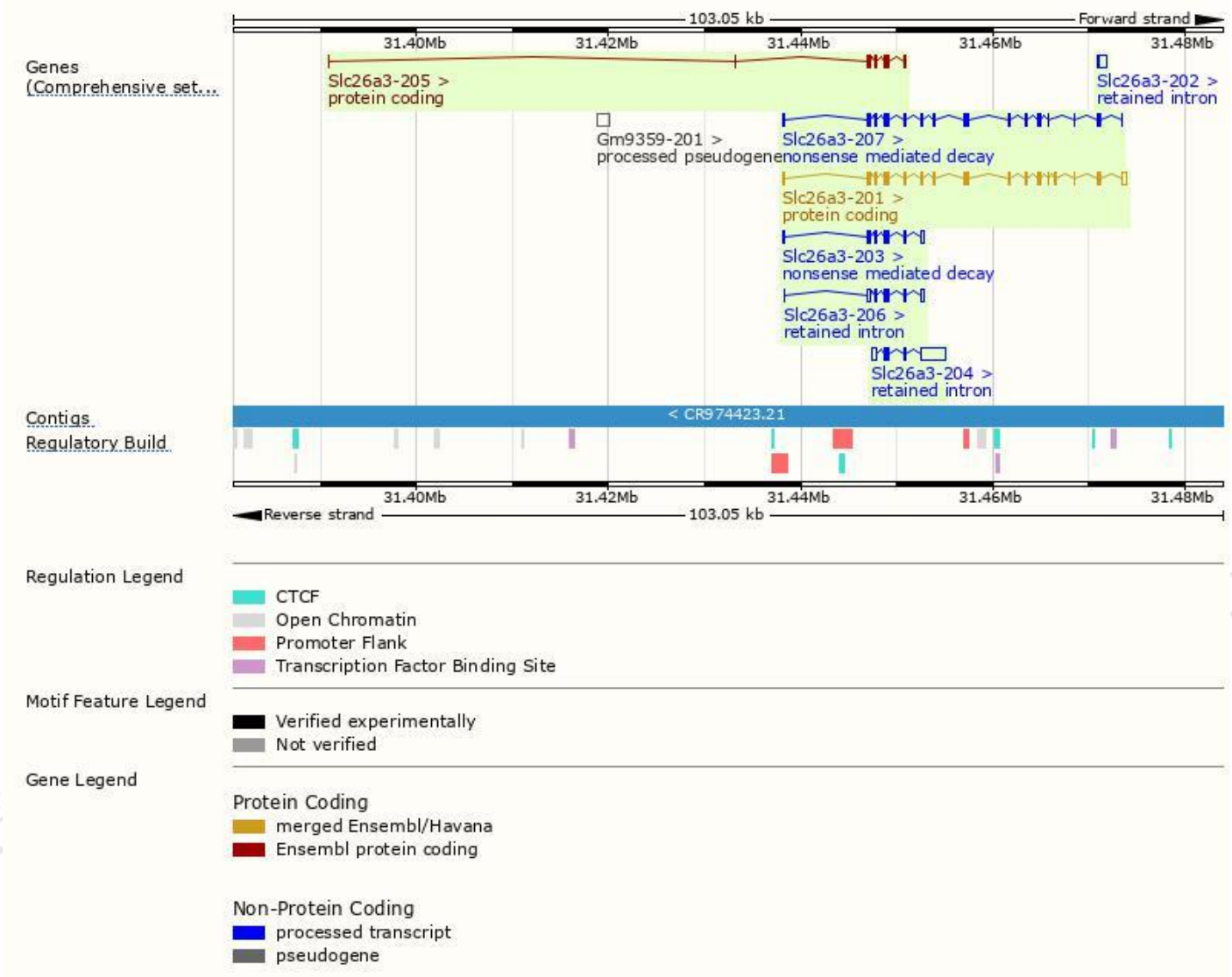
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc26a3-201	ENSMUST00000001254.5	2908	757aa	Protein coding	CCDS25863	Q9WVC8	TSL:1 GENCODE basic APPRIS P1
Slc26a3-205	ENSMUST00000167432.7	942	235aa	Protein coding	-	E9QAZ3	CDS 3' incomplete TSL:3
Slc26a3-207	ENSMUST00000171616.7	2204	58aa	Nonsense mediated decay	-	E9PY22	TSL:5
Slc26a3-203	ENSMUST00000110854.8	1245	58aa	Nonsense mediated decay	-	E9PY22	TSL:2
Slc26a3-204	ENSMUST00000165816.1	3462	No protein	Retained intron	-	-	TSL:1
Slc26a3-206	ENSMUST00000168209.7	1307	No protein	Retained intron	-	-	TSL:2
Slc26a3-202	ENSMUST00000109275.2	847	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Slc26a3-201* transcript,The transcription is shown below

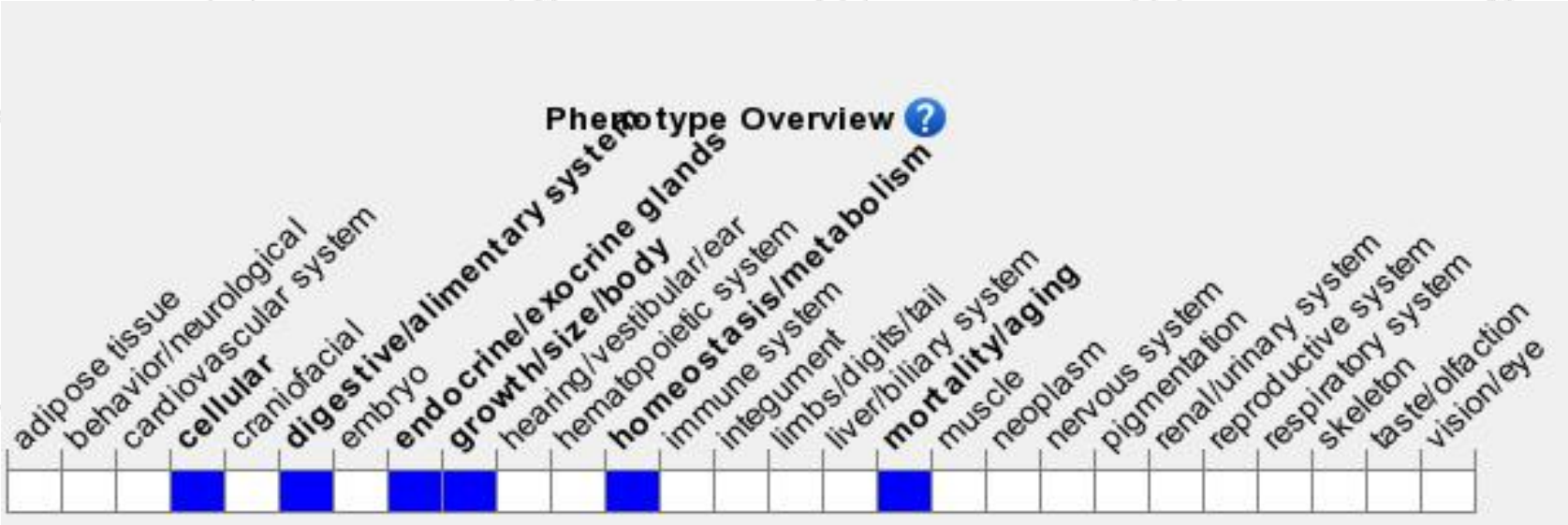


Genomic location distribution



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/).

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

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