Slc4a2 Cas9-CKO Strategy

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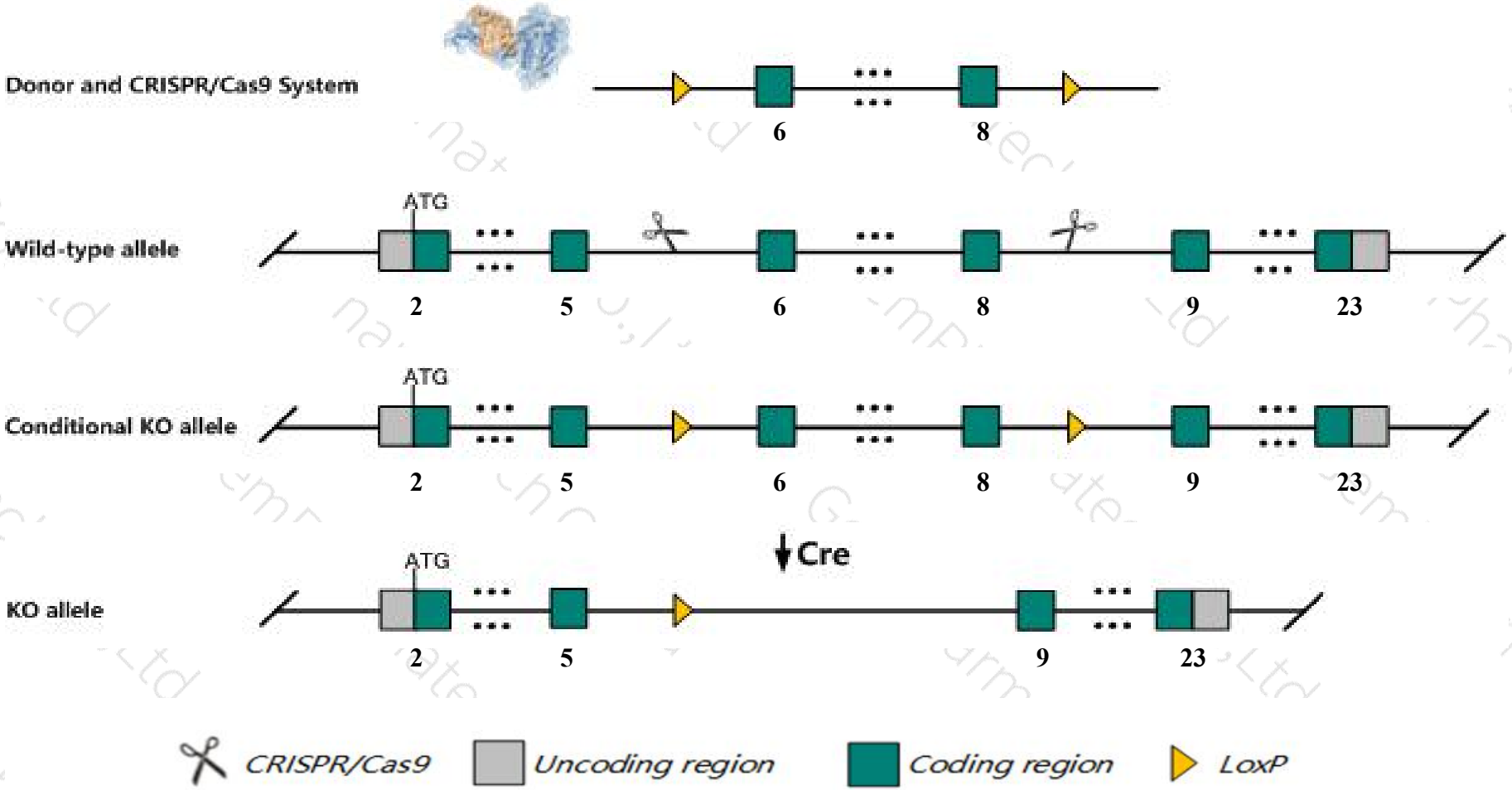
Project Overview

Project Name	***Slc4a2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc4a2* gene. The schematic diagram is as follows:



Technical routes

- The *Slc4a2* gene has 15 transcripts. According to the structure of *Slc4a2* gene, exon6-exon8 of *Slc4a2-201* (ENSMUST00000080067.12) transcript is recommended as the knockout region.The region contains 557bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc4a2* 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,mice carrying an isoform-specific allele display male infertility associated with disrupted spermiogenesis and germ cell apoptosis. mice homozygous for a null allele display perinatal and postnatal lethality, loss of gastric acid secretion, failure of tooth eruption, aphagia, and deafness.
- Transcripts *Slc4a2-209*, *Slc4a2-212* and *Slc4a2-213* are incomplete, so the effect on them are unknown.
- The *Slc4a2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Slc4a2 solute carrier family 4 (anion exchanger), member 2 [*Mus musculus* (house mouse)]

Gene ID: 20535, updated on 13-Mar-2020

Summary

Official Symbol	Slc4a2 provided by MGI
Official Full Name	solute carrier family 4 (anion exchanger), member 2 provided by MGI
Primary source	MGI:MGI:109351
See related	Ensembl:ENSMUSG00000028962
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	Ae2; B3RP
Expression	Ubiquitous expression in stomach adult (RPKM 54.7), colon adult (RPKM 48.2) and 28 other tissues See more
Orthologs	human all

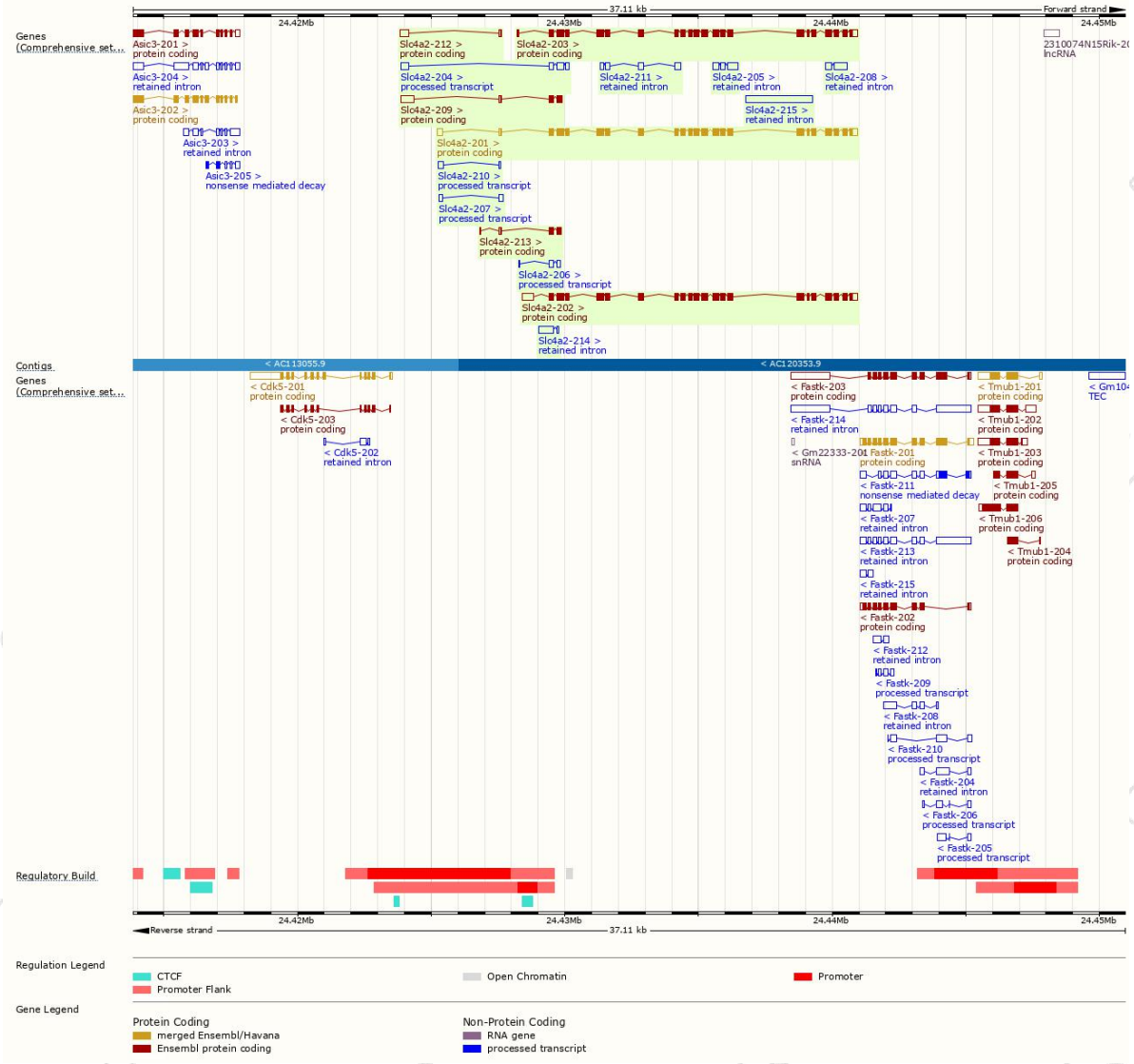
Transcript information（Ensembl）

The gene has 15 transcripts,all transcripts are shown below:

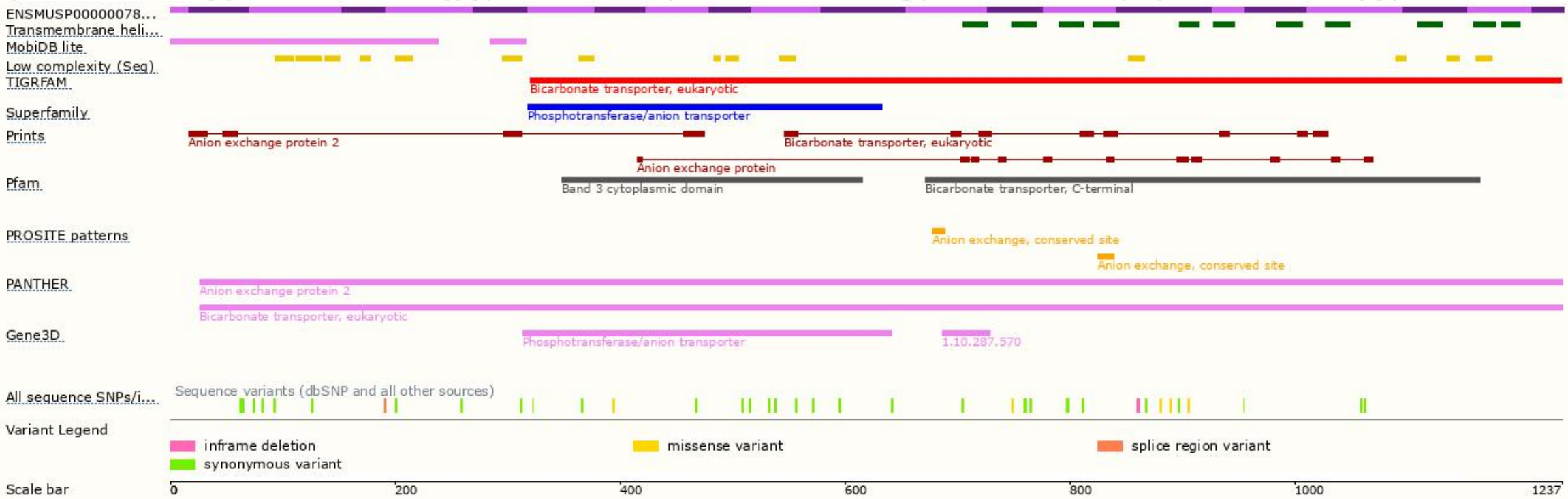
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc4a2-201	ENSMUST00000080067.12	4179	1237aa	Protein coding	CCDS19119	A0A0R4J101	TSL:1 GENCODE basic APPRIS P2
Slc4a2-202	ENSMUST00000115047.2	4264	1223aa	Protein coding	-	A0A0R4J1K4	TSL:5 GENCODE basic APPRIS ALT2
Slc4a2-203	ENSMUST00000115049.8	3924	1228aa	Protein coding	-	A0A0R4J1K9	TSL:5 GENCODE basic APPRIS ALT2
Slc4a2-209	ENSMUST00000141966.7	966	131aa	Protein coding	-	D3Z5G3	CDS 3' incomplete TSL:2
Slc4a2-213	ENSMUST00000155598.7	453	121aa	Protein coding	-	D3YUF1	CDS 3' incomplete TSL:5
Slc4a2-212	ENSMUST00000153274.1	405	9aa	Protein coding	-	A0A1C7ZN01	CDS 3' incomplete TSL:2
Slc4a2-204	ENSMUST00000127315.7	826	No protein	Processed transcript	-	-	TSL:3
Slc4a2-206	ENSMUST00000136440.1	355	No protein	Processed transcript	-	-	TSL:2
Slc4a2-207	ENSMUST00000139081.1	332	No protein	Processed transcript	-	-	TSL:2
Slc4a2-210	ENSMUST00000144305.1	234	No protein	Processed transcript	-	-	TSL:3
Slc4a2-215	ENSMUST00000198786.1	2497	No protein	Retained intron	-	-	TSL:NA
Slc4a2-205	ENSMUST00000132505.1	776	No protein	Retained intron	-	-	TSL:2
Slc4a2-208	ENSMUST00000140722.1	737	No protein	Retained intron	-	-	TSL:1
Slc4a2-211	ENSMUST00000146765.1	679	No protein	Retained intron	-	-	TSL:3
Slc4a2-214	ENSMUST00000155636.1	637	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Slc4a2-201* transcript, the transcription is shown below

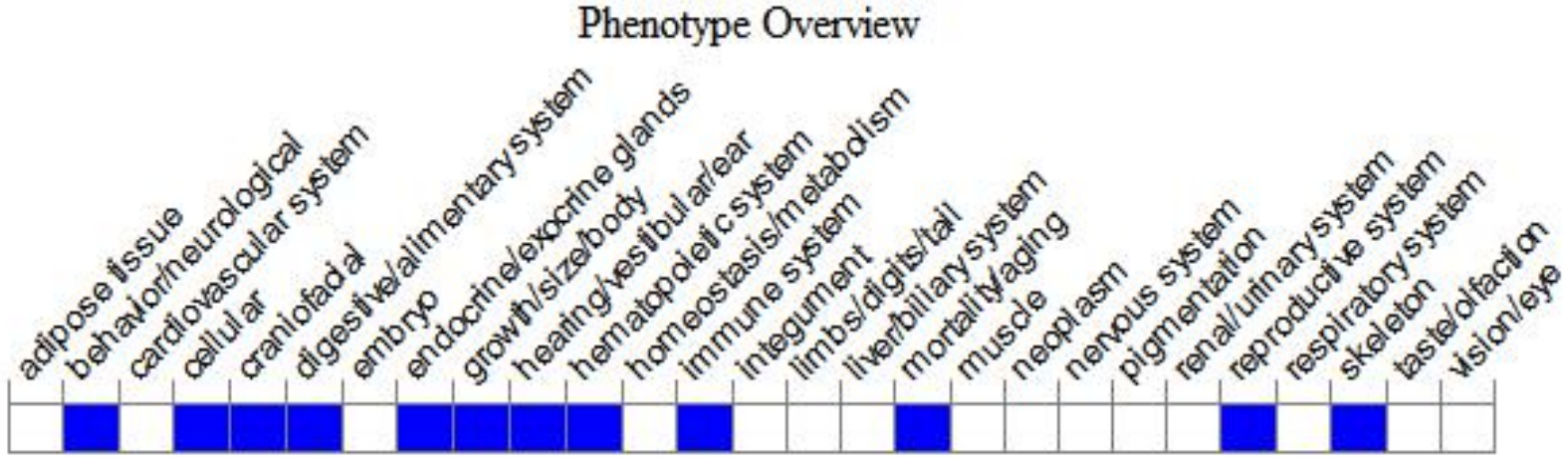
Genomic location distribution



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 carrying an isoform-specific allele display male infertility associated with disrupted spermiogenesis and germ cell apoptosis. Mice homozygous for a null allele display perinatal and postnatal lethality, loss of gastric acid secretion, failure of tooth eruption, aphagia, and deafness.

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

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