

Lzts2 Cas9-CKO Strategy

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Project Overview

Project Name

Lzts2

Project type

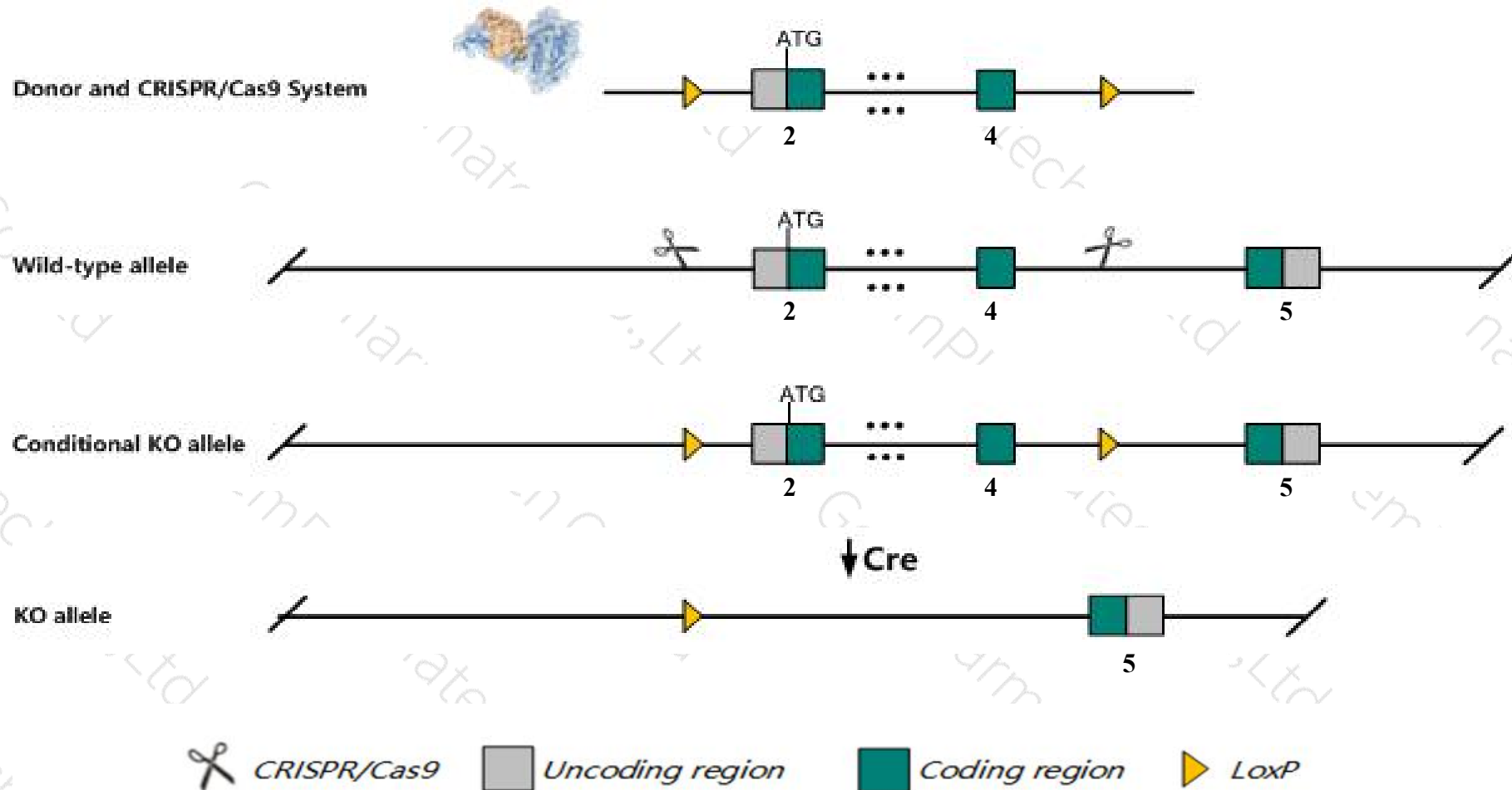
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lzts2* gene. The schematic diagram is as follows:



- The *Lzts2* gene has 8 transcripts. According to the structure of *Lzts2* gene, exon2-exon4 of *Lzts2-201* (ENSMUST00000039016.13) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lzts2* 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.

- According to the existing MGI data, Mice homozygous for a null mutation display defects in urinary tract development.
- The *Lzts2* gene is located on the Chr19. 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)

Lzts2 leucine zipper, putative tumor suppressor 2 [Mus musculus (house mouse)]

Gene ID: 226154, updated on 31-Jan-2019

Summary



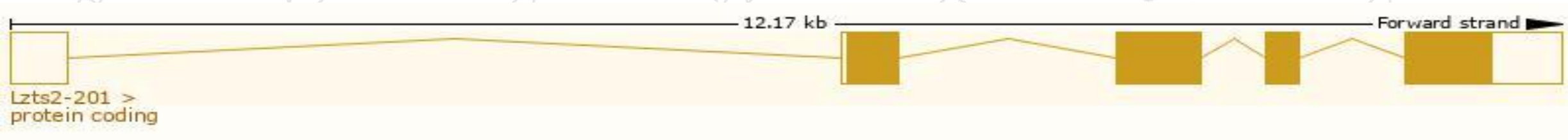
Official Symbol	Lzts2 provided by MGI
Official Full Name	leucine zipper, putative tumor suppressor 2 provided by MGI
Primary source	MGI:MGI:2385095
See related	Ensembl:ENSMUSG00000035342
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC014695, LAPSER1, mKIAA1813
Expression	Broad expression in adrenal adult (RPKM 94.4), ovary adult (RPKM 63.9) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

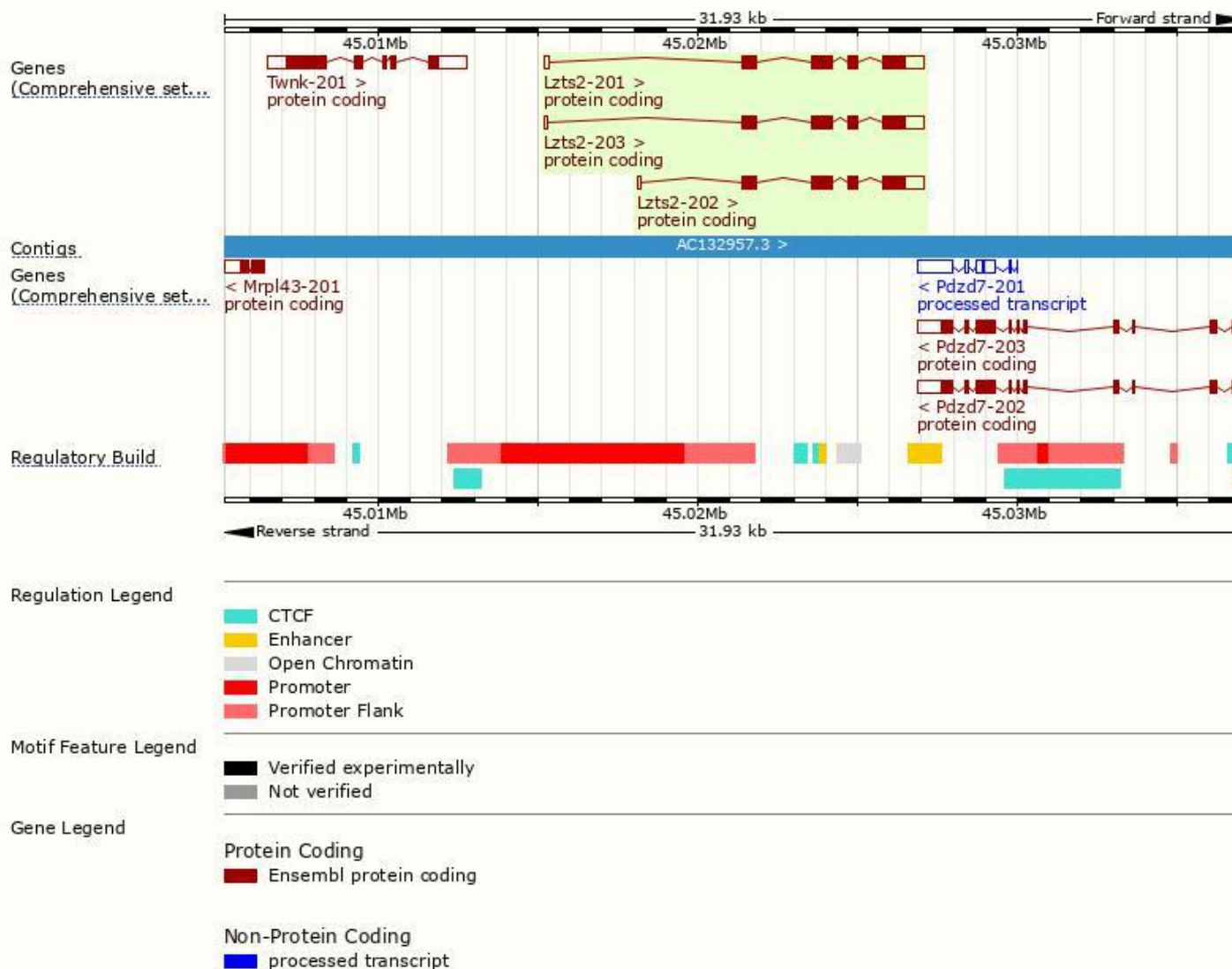
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lzts2-201	ENSMUST00000039016.13	3062	671aa	Protein coding	CCDS29855	Q91YU6	TSL:1 GENCODE basic APPRIS P1
Lzts2-203	ENSMUST00000179108.8	2798	671aa	Protein coding	CCDS29855	Q91YU6	TSL:1 GENCODE basic APPRIS P1
Lzts2-202	ENSMUST00000178087.2	2694	671aa	Protein coding	CCDS29855	Q91YU6	TSL:1 GENCODE basic APPRIS P1
Lzts2-206	ENSMUST00000237043.1	1595	283aa	Protein coding	-	-	GENCODE basic
Lzts2-204	ENSMUST00000236377.1	883	270aa	Protein coding	-	-	CDS 3' incomplete
Lzts2-207	ENSMUST00000237148.1	398	41aa	Protein coding	-	-	CDS 3' incomplete
Lzts2-208	ENSMUST00000237396.1	348	42aa	Protein coding	-	-	CDS 3' incomplete
Lzts2-205	ENSMUST00000236512.1	789	No protein	Processed transcript	-	-	

The strategy is based on the design of *Lzts2-201* transcript,The transcription is shown below



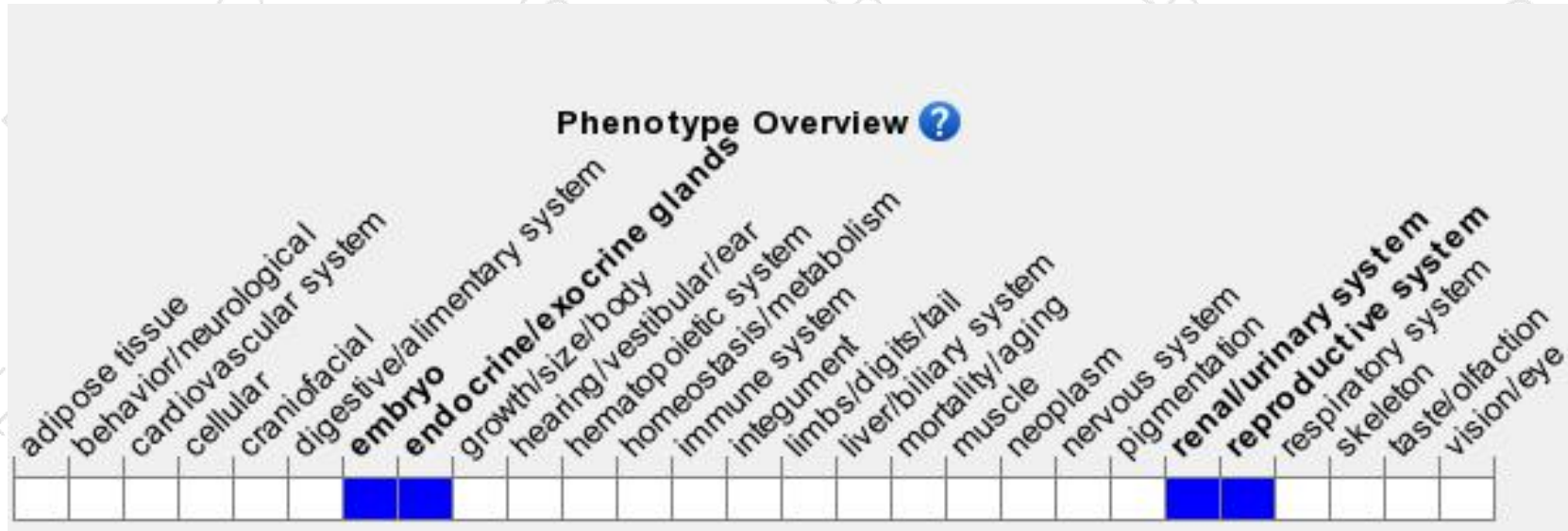
Genomic location distribution



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 null mutation display defects in urinary tract development.

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

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