

Lzts1 Cas9-KO Strategy

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Project Overview

Project Name

Lzts1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lzts1* gene. The schematic diagram is as follows:



- The *Lzts1* gene has 5 transcripts. According to the structure of *Lzts1* gene, exon1-exon3 of *Lzts1-201* (ENSMUST00000037049.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lzts1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Heterozygous or homozygous inactivation of this gene leads to increased incidence of spontaneous and carcinogen-induced tumors. Homozygotes for a null allele show working memory and cognitive deficits, enhanced anxiety, defects in glutamatergic synaptic transmission, and impaired spine maturation.
- Transcript *Lzts1*-203&203&205 may not be affected.
- The *Lzts1* gene is located on the 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)

Lzts1 leucine zipper, putative tumor suppressor 1 [Mus musculus (house mouse)]

Gene ID: 211134, updated on 31-Jan-2019

Summary



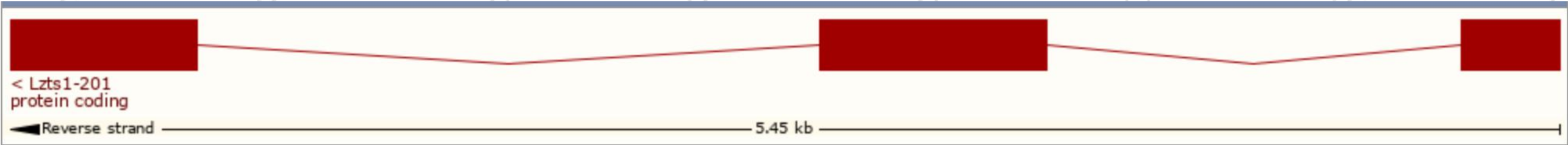
Official Symbol	Lzts1 provided by MGI
Official Full Name	leucine zipper, putative tumor suppressor 1 provided by MGI
Primary source	MGI:MGI:2684762
See related	Ensembl:ENSMUSG00000036306
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	F37, FEZ1, PSD-Zip70
Expression	Biased expression in frontal lobe adult (RPKM 14.3), cortex adult (RPKM 13.3) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

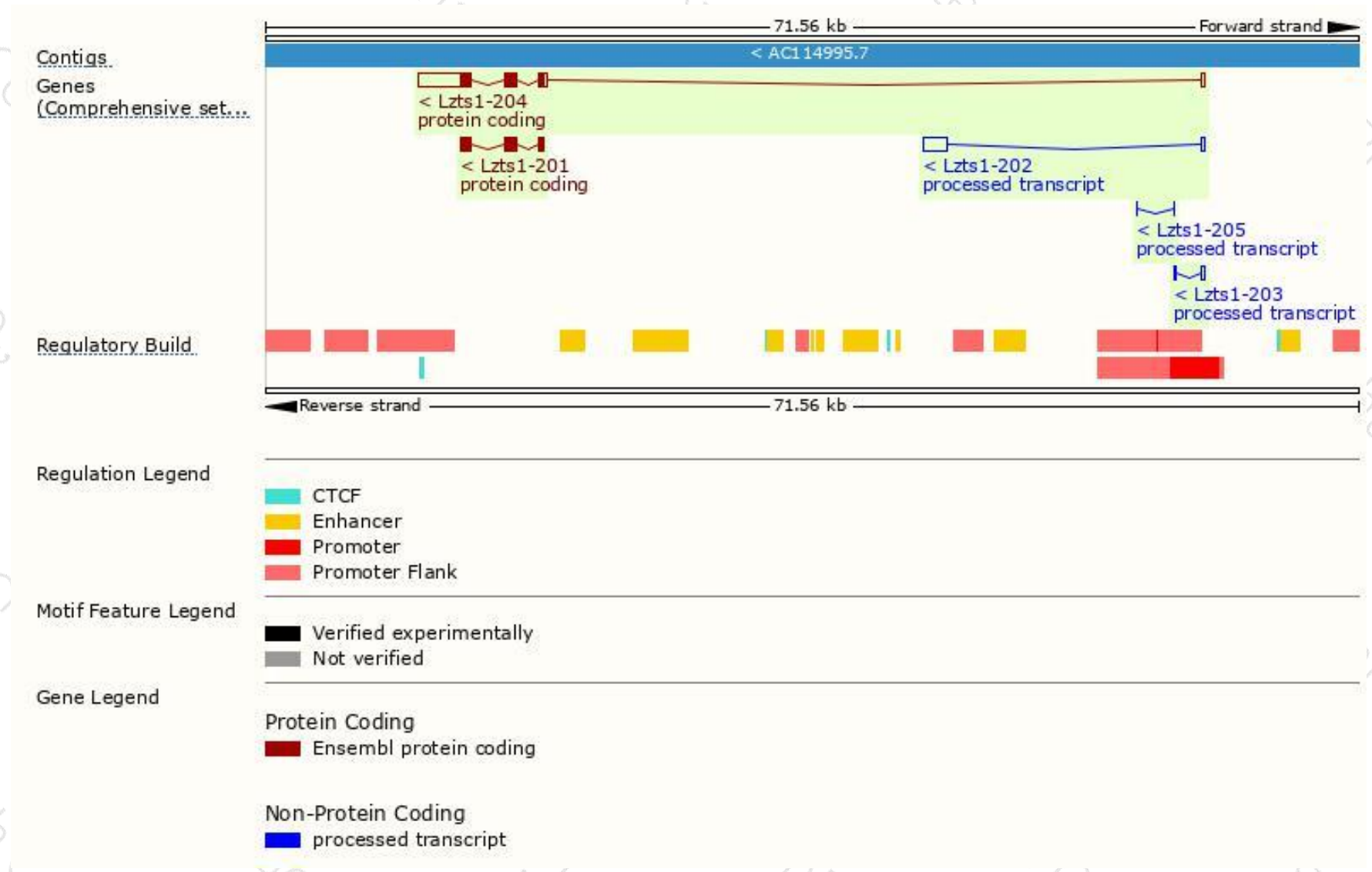
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lzts1-204	ENSMUST00000185176.7	5019	599aa	Protein coding	CCDS22345	P60853	TSL:5 GENCODE basic APPRIS P1
Lzts1-201	ENSMUST00000037049.3	1800	599aa	Protein coding	CCDS22345	P60853	TSL:1 GENCODE basic APPRIS P1
Lzts1-202	ENSMUST00000181890.1	1784	No protein	Processed transcript	-	-	TSL:1
Lzts1-203	ENSMUST00000184961.1	404	No protein	Processed transcript	-	-	TSL:2
Lzts1-205	ENSMUST00000209353.1	87	No protein	Processed transcript	-	-	TSL:5

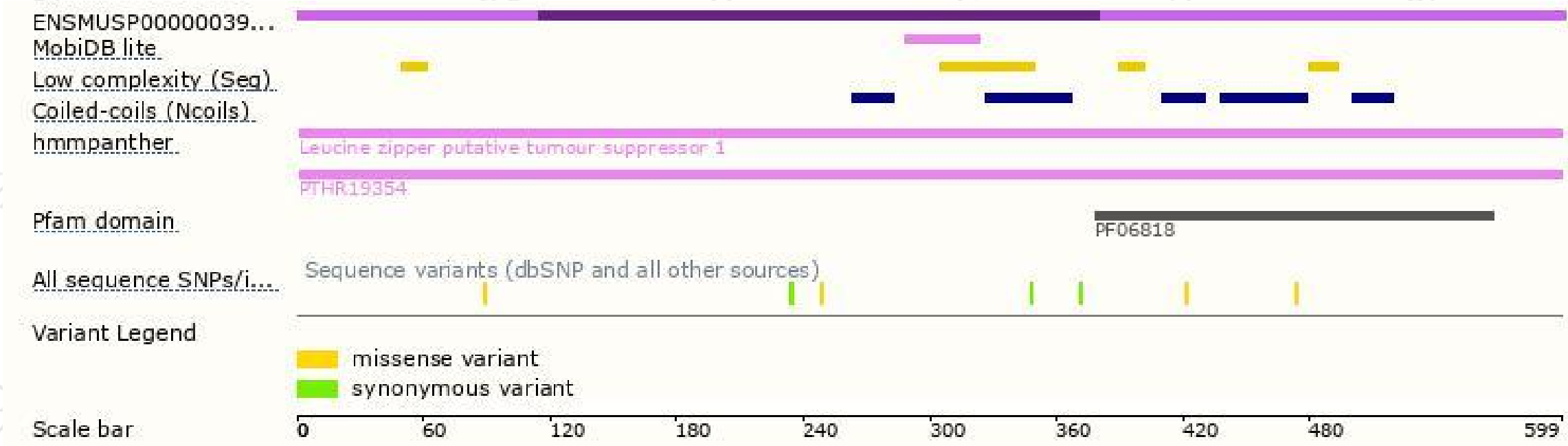
The strategy is based on the design of *Lzts1-201* transcript,The transcription is shown below



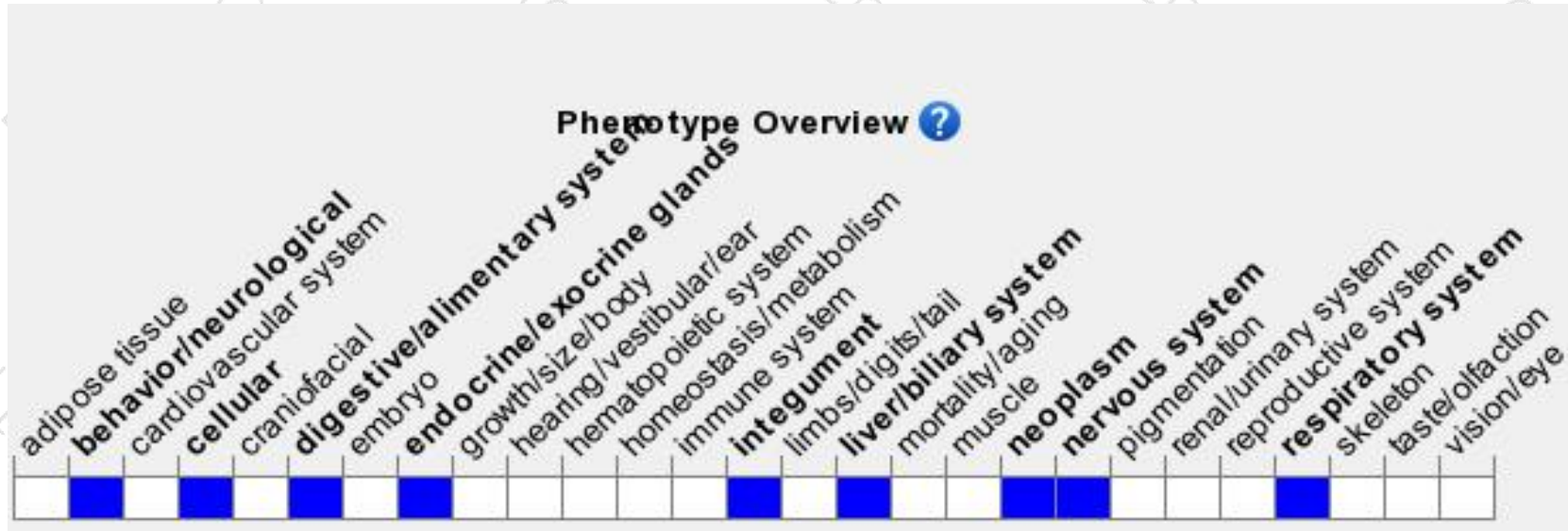
Genomic location distribution



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, Heterozygous or homozygous inactivation of this gene leads to increased incidence of spontaneous and carcinogen-induced tumors. Homozygotes for a null allele show working memory and cognitive deficits, enhanced anxiety, defects in glutamatergic synaptic transmission, and impaired spine maturation.

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

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