

L3mbtl1 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

L3mbtl1

Project type

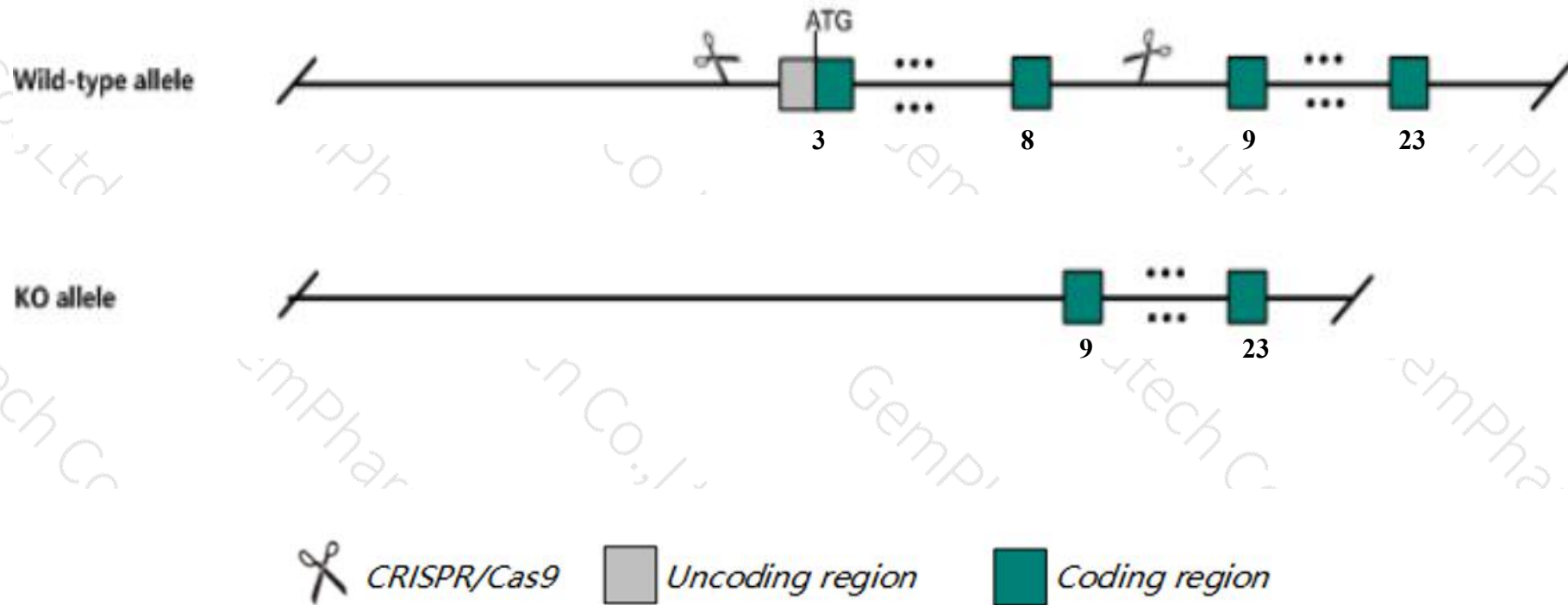
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *L3mbtl1* gene. The schematic diagram is as follows:



- The *L3mbtl1* gene has 7 transcripts. According to the structure of *L3mbtl1* gene, exon3-exon8 of *L3mbtl1-201* (ENSMUST00000035751.11) 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 *L3mbtl1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit normal nervous system phenotype, hematopoietic system phenotype, immune system phenotype, cellular phenotype, and lifespan.
- The *L3mbtl1* gene is located on the Chr2. 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)

L3mbtl1 L3MBTL1 histone methyl-lysine binding protein [*Mus musculus* (house mouse)]

Gene ID: 241764, updated on 13-Mar-2020

Summary

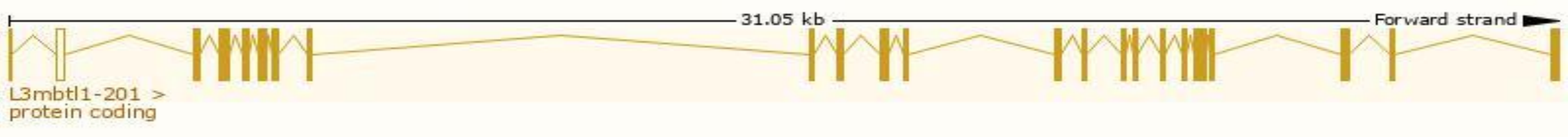
Official Symbol	L3mbtl1 provided by MGI
Official Full Name	L3MBTL1 histone methyl-lysine binding protein provided by MGI
Primary source	MGI:MGI:2676663
See related	Ensembl:ENSMUSG00000035576
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	L3mbtl; mKIAA0681; C630004G01
Expression	Biased expression in cortex adult (RPKM 2.6), CNS E18 (RPKM 2.4) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

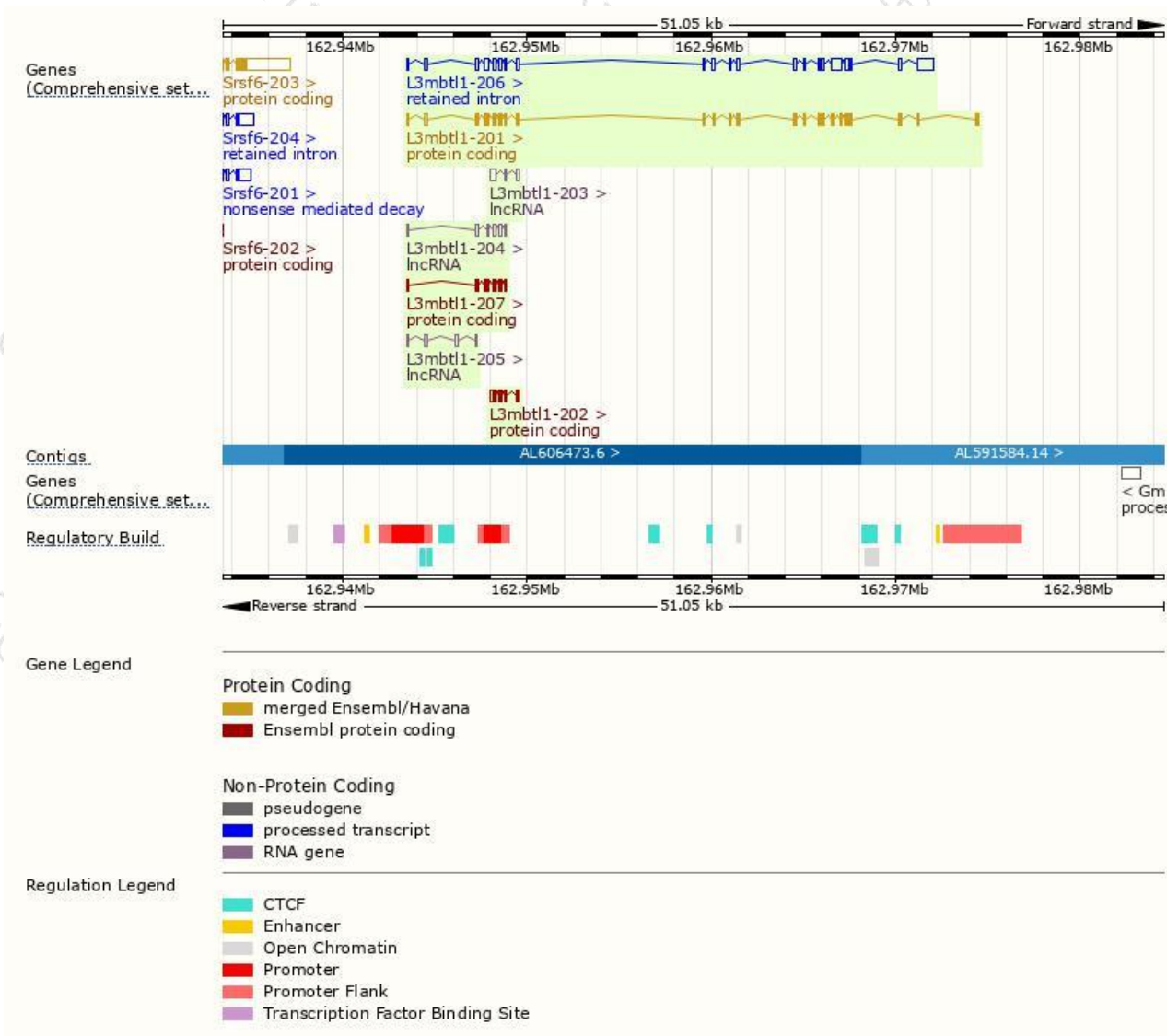
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
L3mbtl1-201	ENSMUST00000035751.11	2724	826aa	Protein coding	CCDS38314	A2A5N8	TSL:5 Gencode basic APPRIS P1
L3mbtl1-207	ENSMUST00000156954.7	803	244aa	Protein coding	-	Q3V558	CDS 3' incomplete TSL:5
L3mbtl1-202	ENSMUST00000124264.2	616	144aa	Protein coding	-	A2A6Y5	CDS 3' incomplete TSL:1
L3mbtl1-204	ENSMUST00000137108.7	675	No protein	Processed transcript	-	-	TSL:5
L3mbtl1-203	ENSMUST00000125296.1	468	No protein	Processed transcript	-	-	TSL:1
L3mbtl1-205	ENSMUST00000149447.1	409	No protein	Processed transcript	-	-	TSL:3
L3mbtl1-206	ENSMUST00000153416.7	3763	No protein	Retained intron	-	-	TSL:5

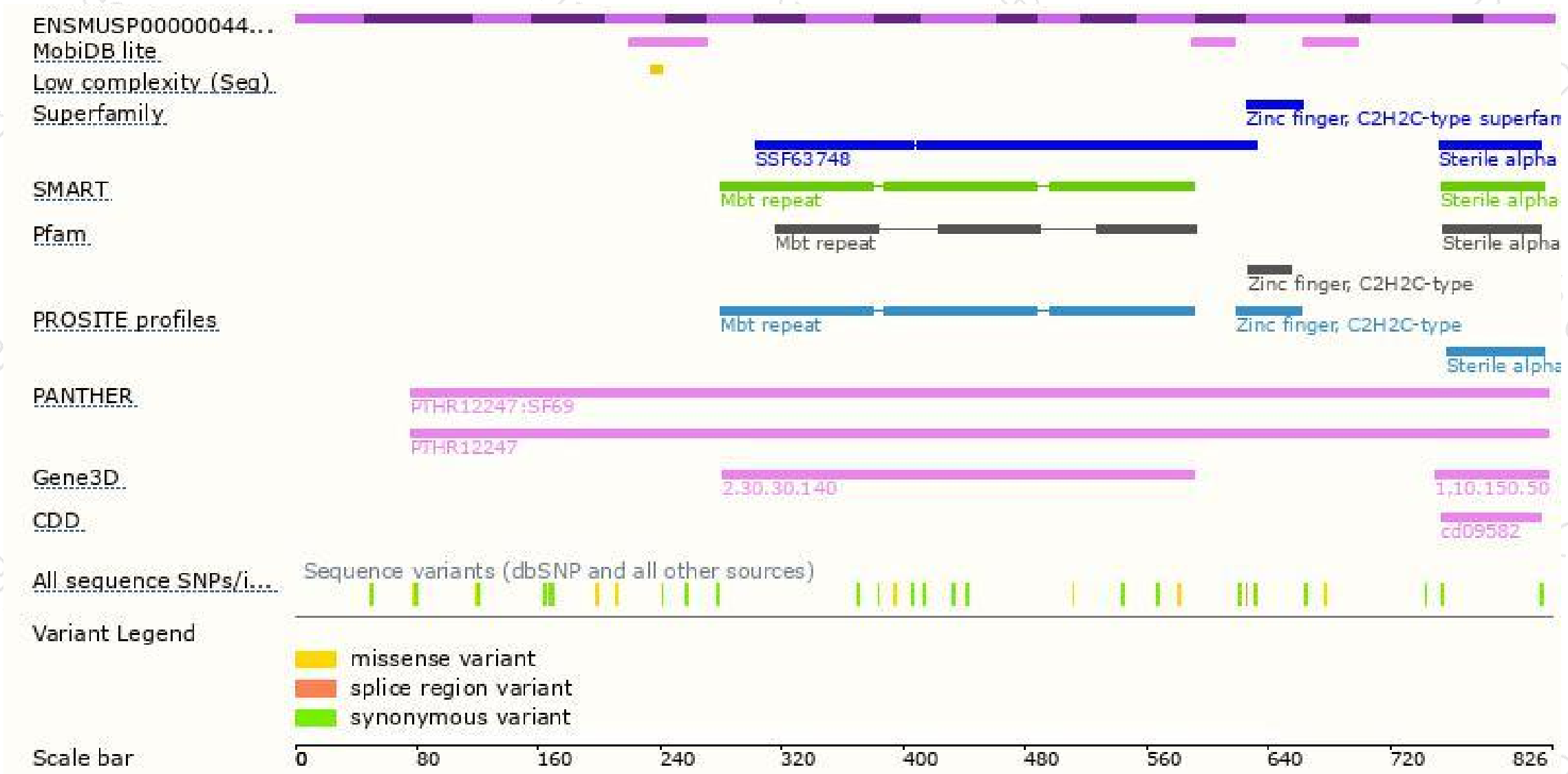
The strategy is based on the design of *L3mbtl1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

