L3mbtl3 Cas9-CKO Strategy

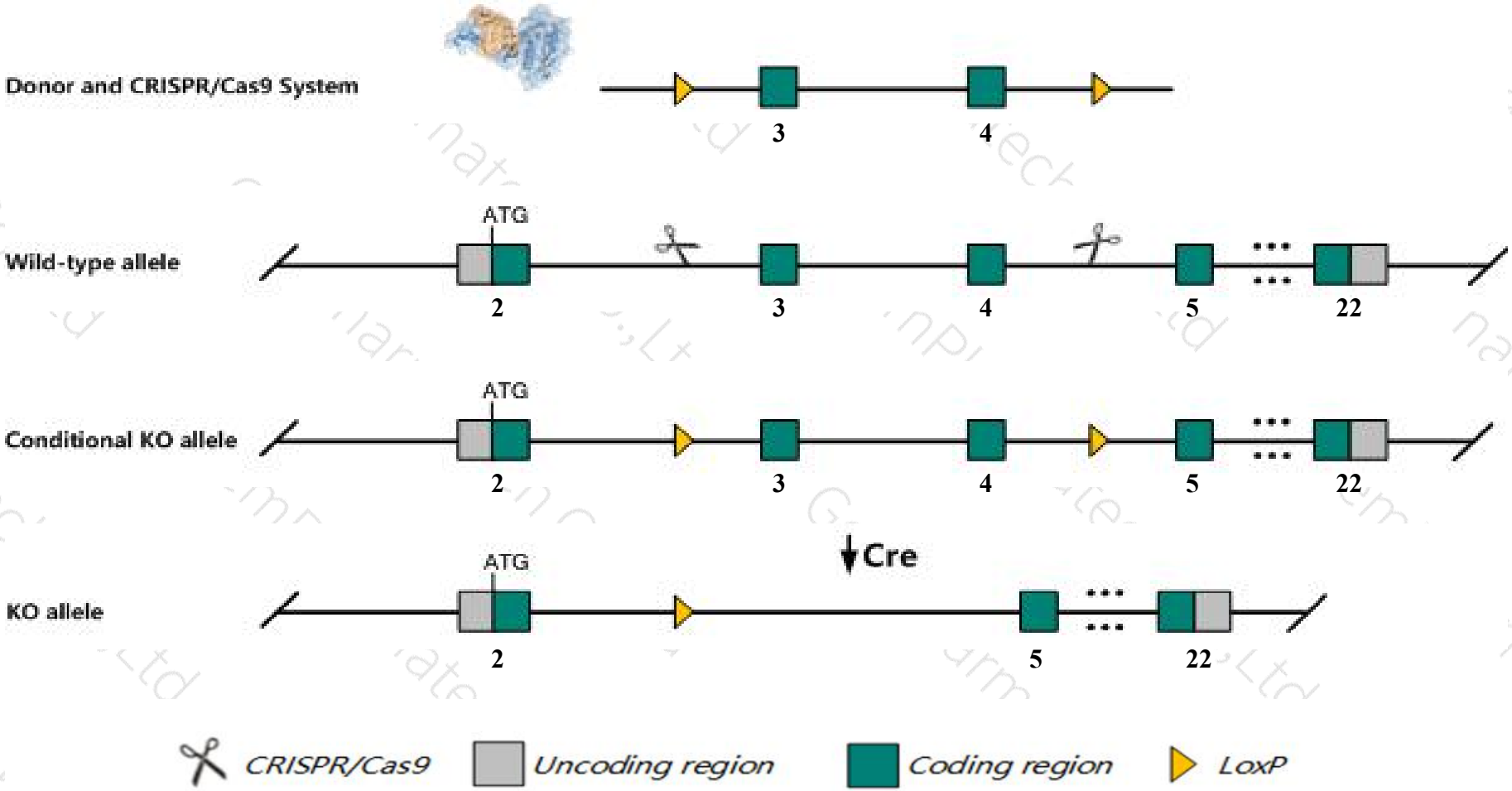
Designer: Xiaojing Li
Design Date: 2019-9-11
Reviewer: JiaYu

Project Overview

Project Name	***L3mbtl3***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *L3mbtl3* gene. The schematic diagram is as follows:



Technical routes

集萃药康 GemPharmatech

- The *L3mbtl3* gene has 7 transcripts. According to the structure of *L3mbtl3* gene, exon3-exon4 of *L3mbtl3-201* (ENSMUST00000040219.12) transcript is recommended as the knockout region.The region contains 187bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *L3mbtl3* 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 homozygous for a null mutation die between E17.5 ? 19.5 due to disturbed erythropoiesis which result in anemia.

- The *L3mbtl3* gene is located on the Chr10. 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）

集萃药康 GemPharmatech

L3mbtl3 L3MBTL3 histone methyl-lysine binding protein [Mus musculus (house mouse)]

Gene ID: 237339, updated on 9-Feb-2019

Summary

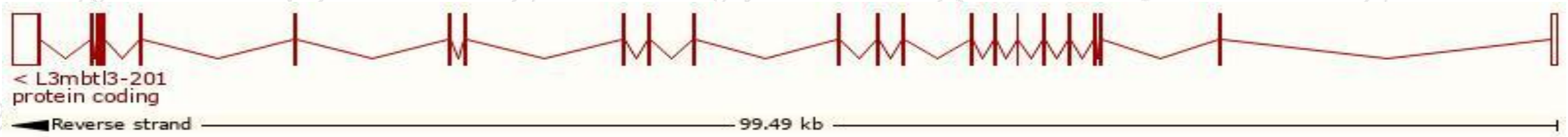
Official Symbol	L3mbtl3 provided by MGI
Official Full Name	L3MBTL3 histone methyl-lysine binding protein provided byMGI
Primary source	MGI:MGI:2143628
See related	Ensembl:ENSMUSG00000039089
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI481284, MBT-1
Expression	Broad expression in limb E14.5 (RPKM 9.7), CNS E18 (RPKM 6.9) and 25 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

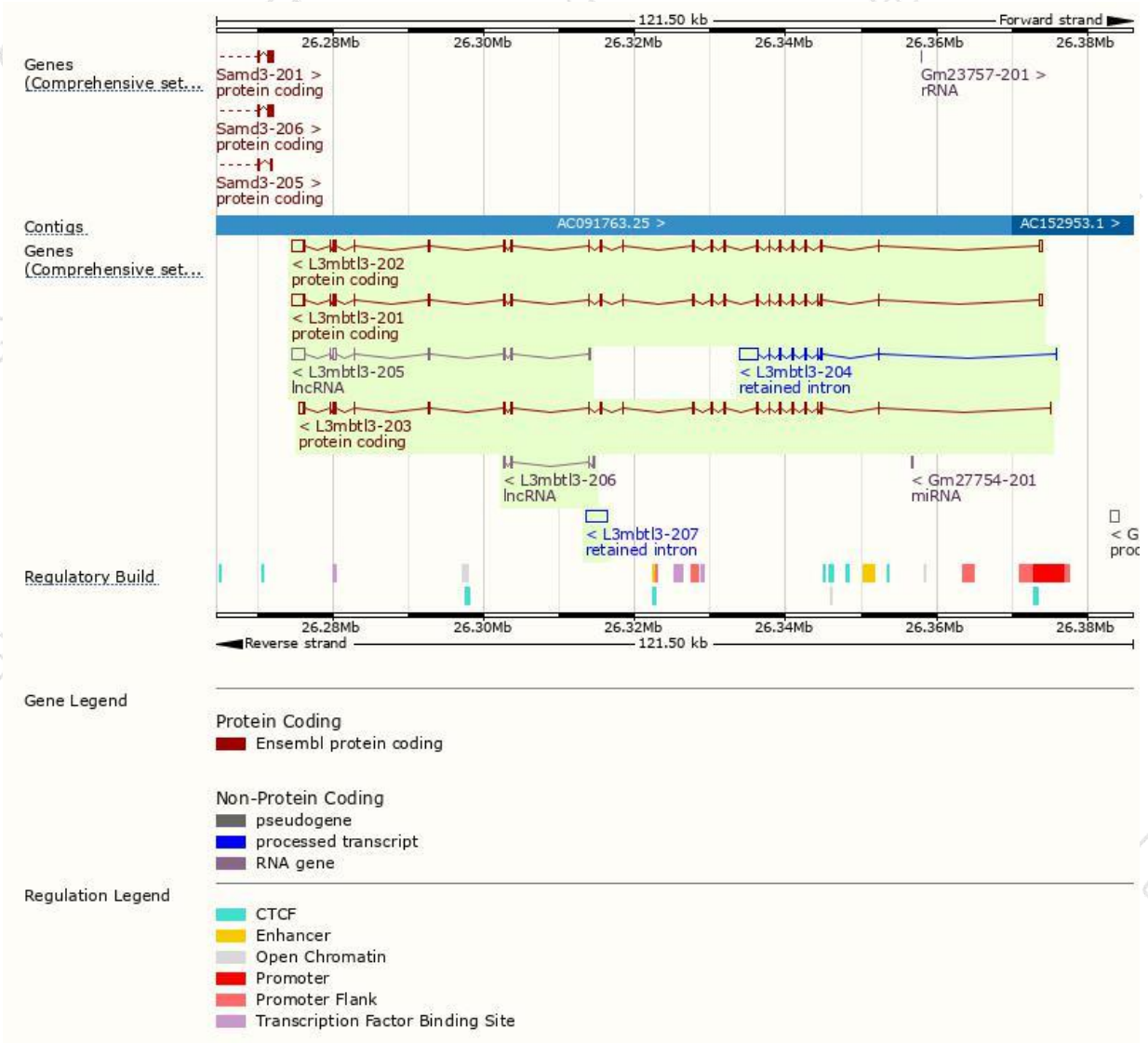
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
L3mbtl3-201	ENSMUST00000040219.12	4572	883aa	Protein coding	CCDS23756	Q8BLB7	TSL:5 GENCODE basic APPRIS P3
L3mbtl3-202	ENSMUST00000105519.9	4500	858aa	Protein coding	CCDS83689	Q8BLB7	TSL:1 GENCODE basic APPRIS ALT2
L3mbtl3-203	ENSMUST00000174766.1	3411	883aa	Protein coding	CCDS23756	Q8BLB7	TSL:1 GENCODE basic APPRIS P3
L3mbtl3-205	ENSMUST00000218585.1	2989	No protein	Processed transcript	-	-	TSL:1
L3mbtl3-206	ENSMUST00000218665.1	386	No protein	Processed transcript	-	-	TSL:3
L3mbtl3-204	ENSMUST00000217699.1	3315	No protein	Retained intron	-	-	TSL:1
L3mbtl3-207	ENSMUST00000218909.1	2823	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *L3mbtl3-201* transcript,The transcription is shown below

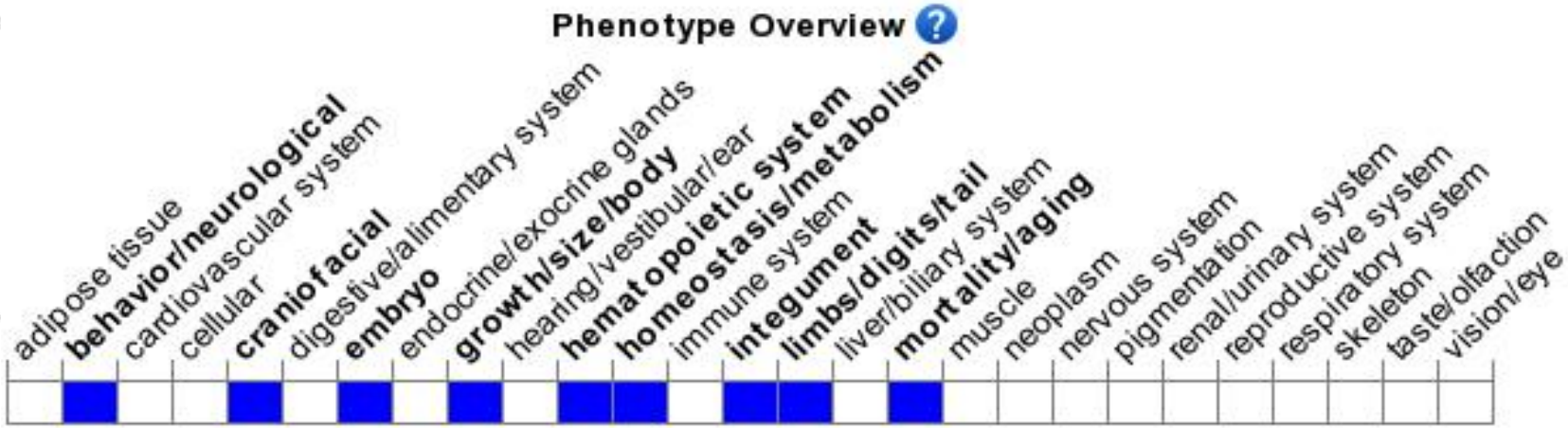


Genomic location distribution



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 die between E17.5 ? 19.5 due to disturbed erythropoiesis which result in anemia.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd