

Tal1 Cas9-KO Strategy

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Project Overview

Project Name

Tal1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Tall* gene has 4 transcripts. According to the structure of *Tall* gene, exon3-exon5 of *Tall*-201 (ENSMUST00000030489.8) 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 *Tall* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous targeted null mutants show retarded growth, edema, lack yolk sac hematopoiesis and die at embryonic day 9.5-10.5. Conditional mutants show loss of megakaryocyte and erythrocyte progenitors resulting in low hematocrit and platelet count.
- The *Tall* gene is located on the Chr4. 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)

Tal1 T cell acute lymphocytic leukemia 1 [Mus musculus (house mouse)]

Gene ID: 21349, updated on 24-Feb-2019

Summary



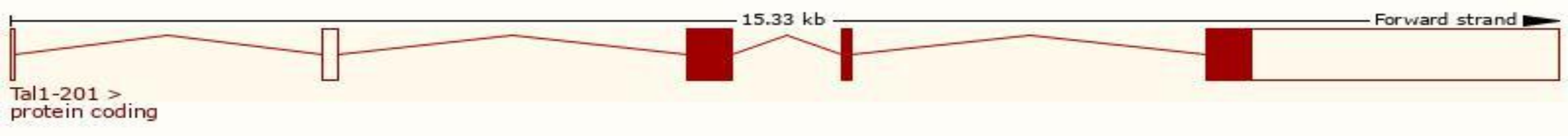
Official Symbol	Tal1 provided by MGI
Official Full Name	T cell acute lymphocytic leukemia 1 provided by MGI
Primary source	MGI:MGI:98480
See related	Ensembl:ENSMUSG00000028717
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Hpt, SCL/tal-1, Scl, bHLHa17, tal-1
Expression	Biased expression in liver E14.5 (RPKM 43.3), liver E14 (RPKM 39.2) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

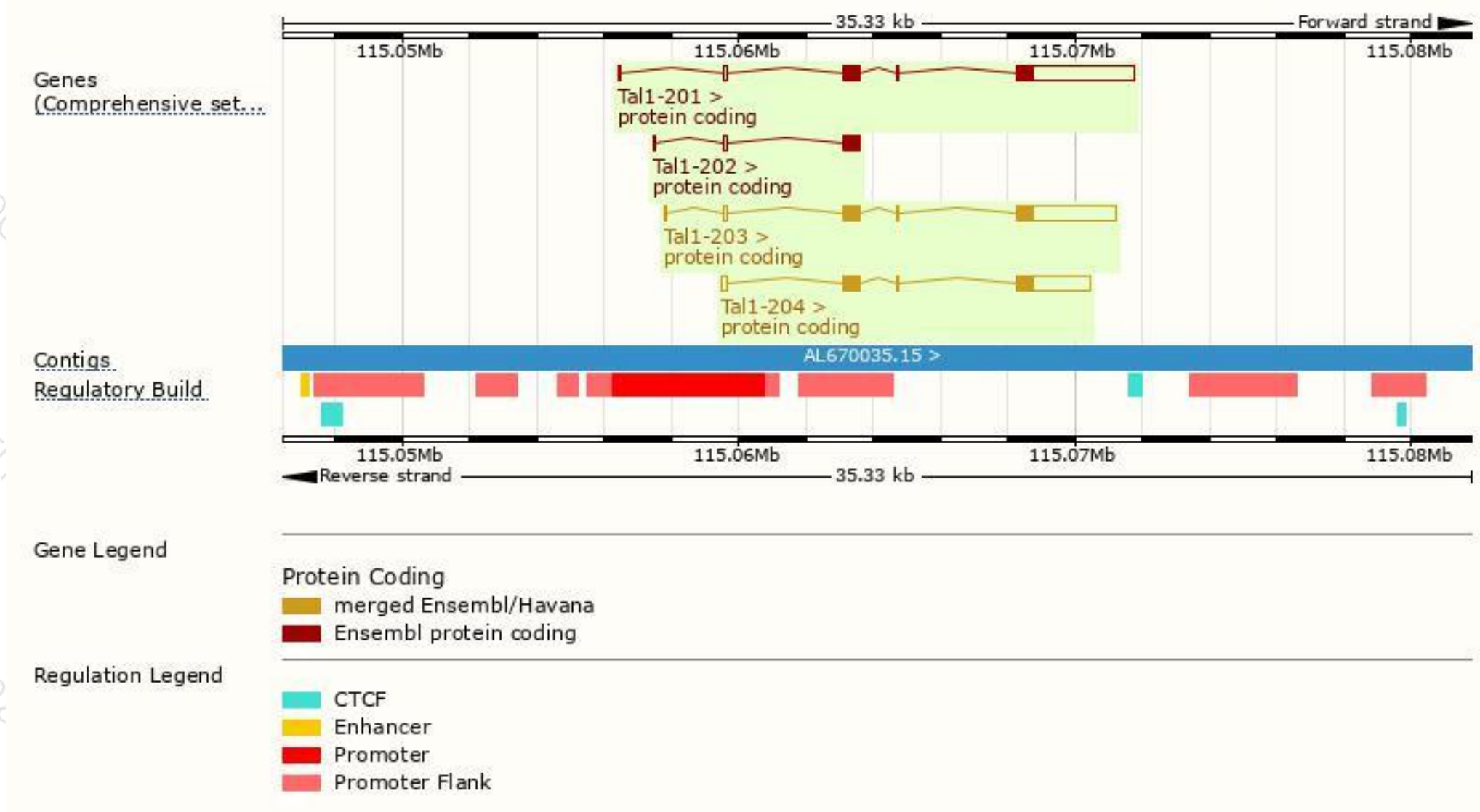
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tal1-201	ENSMUST00000030489.8	4213	329aa	Protein coding	CCDS18486	P22091 Q3TZH7	TSL:1 GENCODE basic APPRIS P1
Tal1-203	ENSMUST00000161601.7	3703	329aa	Protein coding	CCDS18486	P22091 Q3TZH7	TSL:1 GENCODE basic APPRIS P1
Tal1-204	ENSMUST00000162489.1	2894	329aa	Protein coding	CCDS18486	P22091 Q3TZH7	TSL:1 GENCODE basic APPRIS P1
Tal1-202	ENSMUST00000136946.7	683	146aa	Protein coding	-	A2AD40	CDS 3' incomplete TSL:3

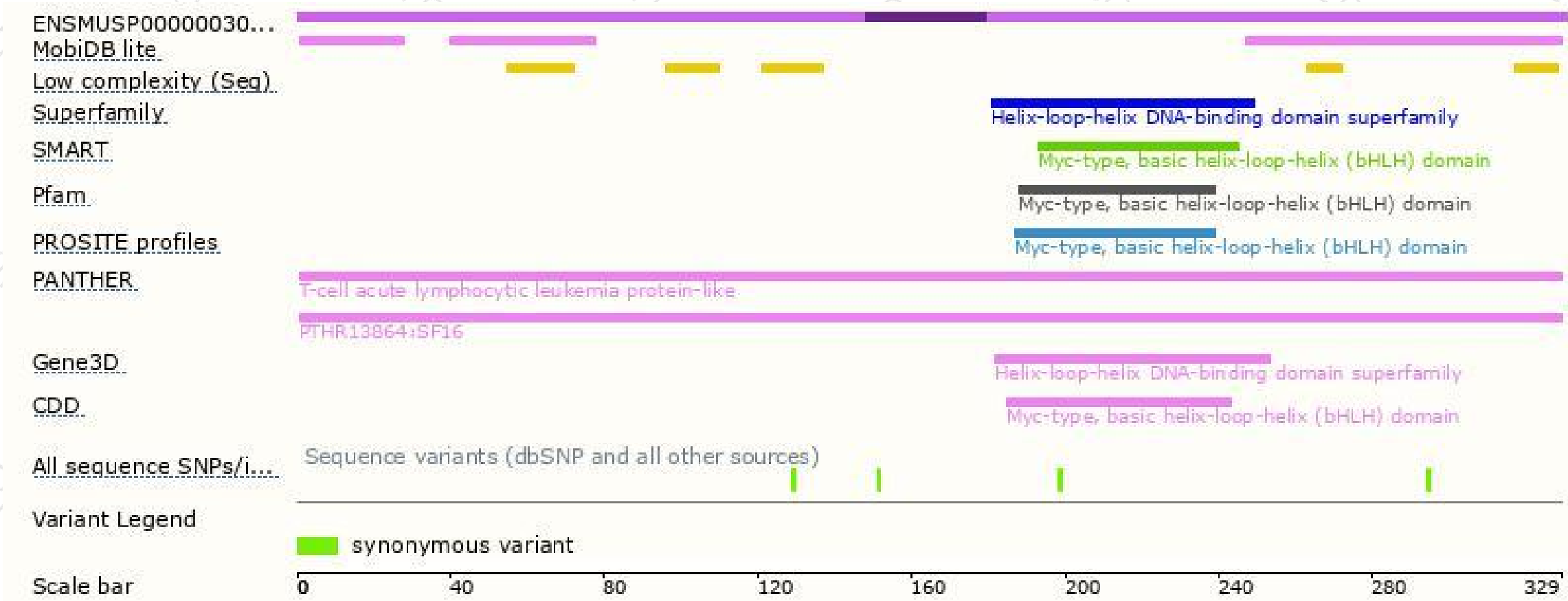
The strategy is based on the design of *Tal1-201* transcript,The transcription is shown below



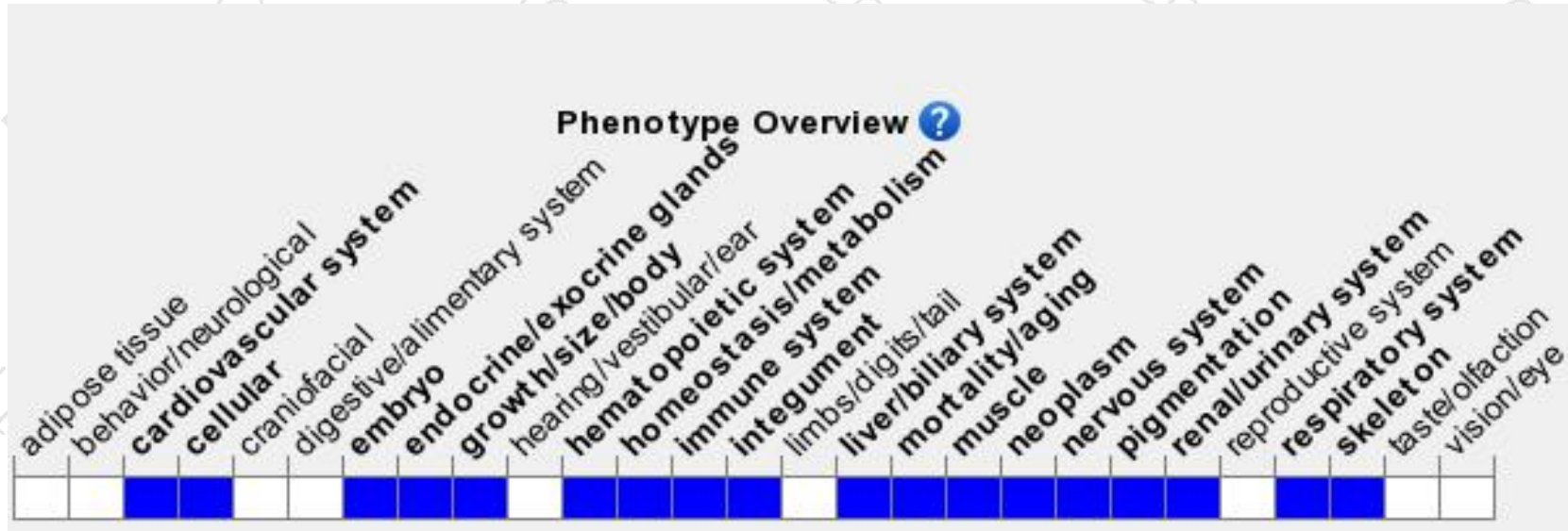
Genomic location distribution



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, Homozygous targeted null mutants show retarded growth, edema, lack yolk sac hematopoiesis and die at embryonic day 9.5-10.5. Conditional mutants show loss of megakaryocyte and erythrocyte progeni resulting in low hematocrit and platelet count.

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

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