

***Fli1* Cas9-KO Strategy**

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Project Overview

Project Name

Fli1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Fli1* gene has 2 transcripts. According to the structure of *Fli1* gene, exon3 of *Fli1-201* (ENSMUST00000016231.13) transcript is recommended as the knockout region. The region contains 155bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fli1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, mice homozygous for most knock-out allele exhibit abnormal hematopoietic and immune systems.
- The *Flil* gene is located on the Chr9. 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)

Fli1 Friend leukemia integration 1 [Mus musculus (house mouse)]

Gene ID: 14247, updated on 13-Mar-2020

Summary

Official Symbol Fli1 provided by [MGI](#)

Official Full Name Friend leukemia integration 1 provided by [MGI](#)

Primary source [MGI:MGI:95554](#)

See related [Ensembl:ENSMUSG00000016087](#)

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 EWSR2, Fli-1, SIC-1, Sic1

Expression Broad expression in spleen adult (RPKM 10.2), thymus adult (RPKM 7.9) and 23 other tissues [See more](#)

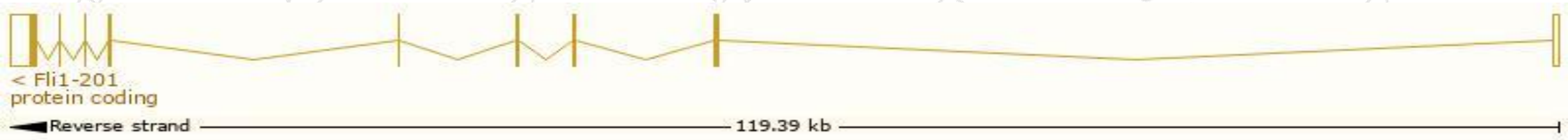
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

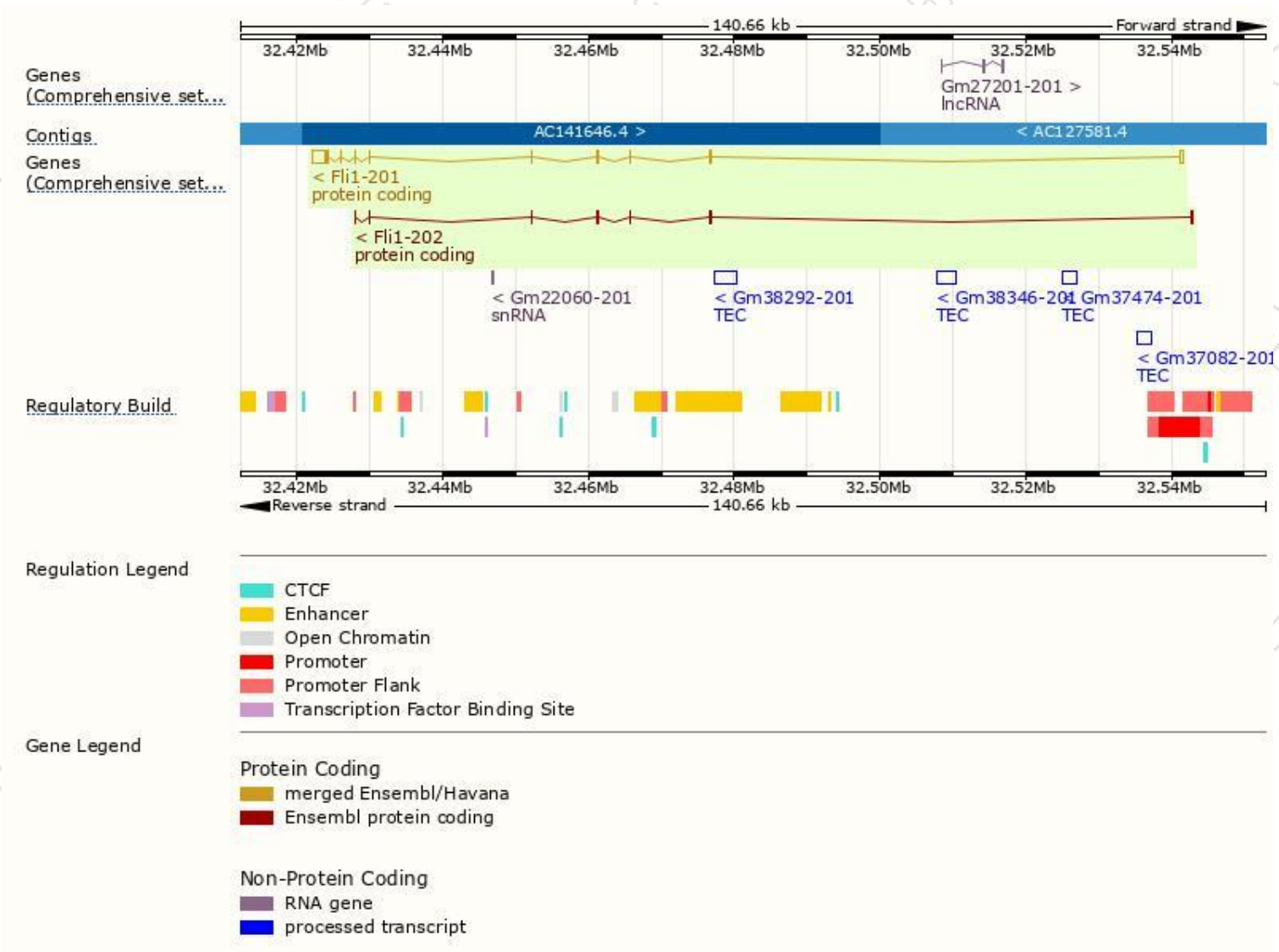
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fli1-201	ENSMUST00000016231.13	3318	452aa	Protein coding	CCDS40571	P26323 Q544B3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Fli1-202	ENSMUST000000183767.1	878	209aa	Protein coding	-	V9GX50	CDS 3' incomplete TSL:5

The strategy is based on the design of *Fli1-201* transcript,the transcription is shown below:



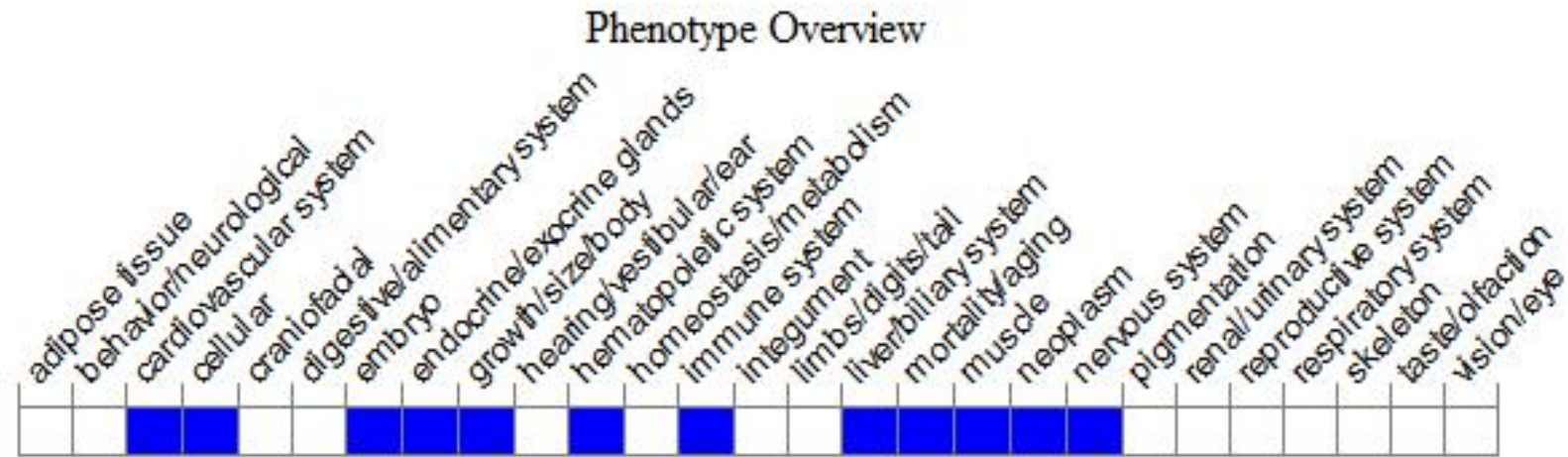
Genomic location distribution



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 most knock-out allele exhibit abnormal hematopoietic and immune systems.

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

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