

Tcea1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Tcea1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Tcea1* gene has 2 transcripts. According to the structure of *Tcea1* gene, exon2-exon6 of *Tcea1-202* (ENSMUST00000165720.2) transcript is recommended as the knockout region. The region contains 460bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tcea1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display impaired definitive erythropoiesis with loss of late stage erythroblasts, fetal liver hypoplasia, and embryonic lethality.
- The KO region contains functional region of the *Gm37988* gene. Knockout the region may affect the function of *Gm37988* gene.
- The *Tceal* gene is located on the Chr1. 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)

Tcea1 transcription elongation factor A (SII) 1 [Mus musculus (house mouse)]

Gene ID: 21399, updated on 31-Jan-2019

Summary



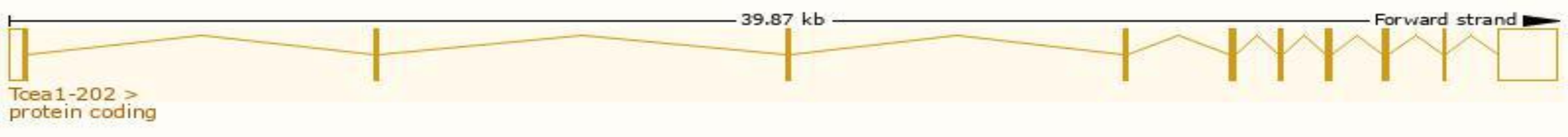
Official Symbol	Tcea1 provided by MGI
Official Full Name	transcription elongation factor A (SII) 1 provided by MGI
Primary source	MGI:MGI:1196624
See related	Ensembl:ENSMUSG00000033813
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	S-II
Expression	Broad expression in CNS E11.5 (RPKM 29.3), liver E14 (RPKM 24.7) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

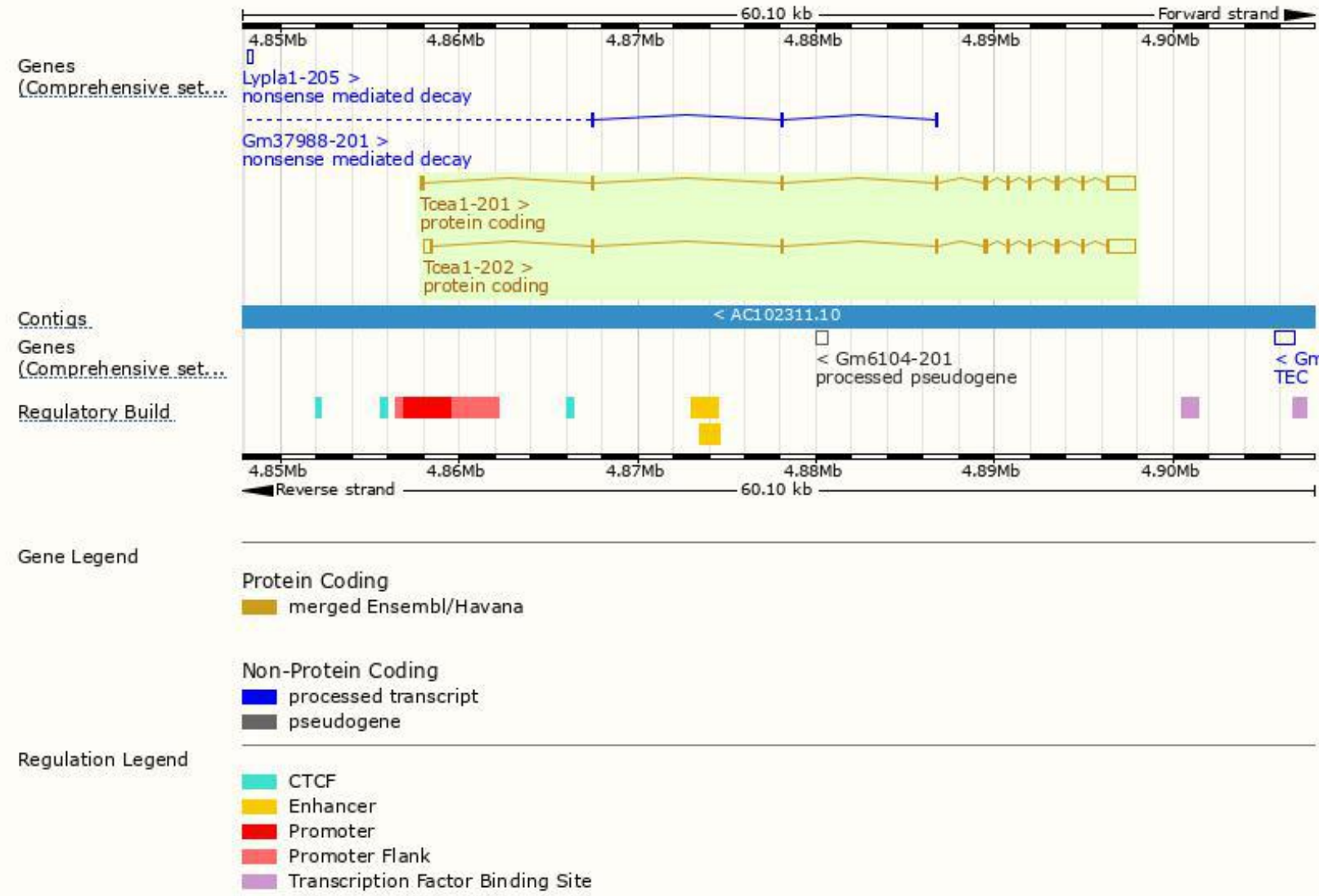
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tcea1-202	ENSMUST00000165720.2	2854	312aa	Protein coding	CCDS48212	E9PYD5	TSL:5 GENCODE basic
Tcea1-201	ENSMUST00000081551.13	2547	301aa	Protein coding	CCDS35505	P10711 Q3UWX7	TSL:1 GENCODE basic APPRIS P1

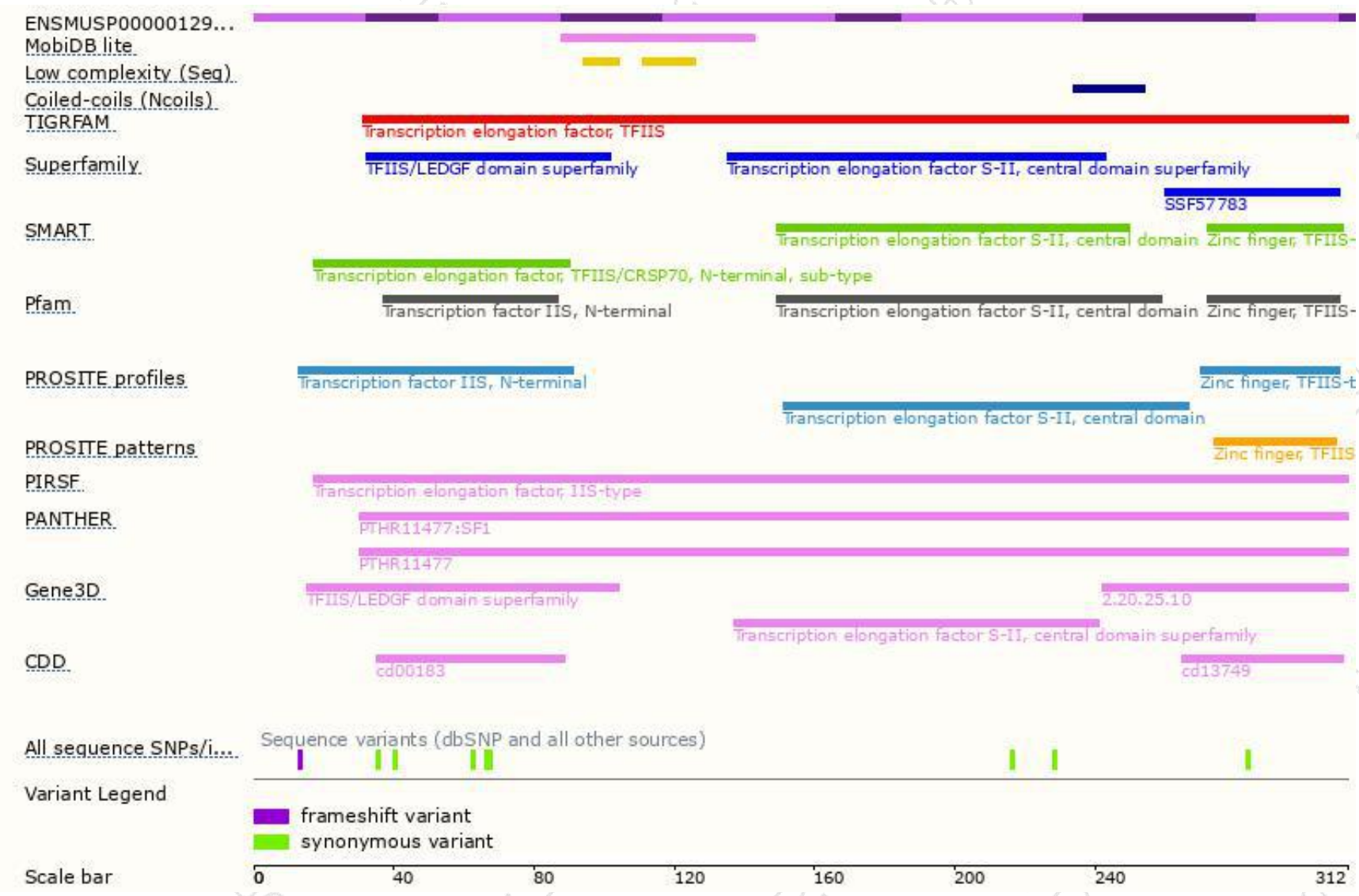
The strategy is based on the design of *Tcea1-202* transcript,The transcription is shown below



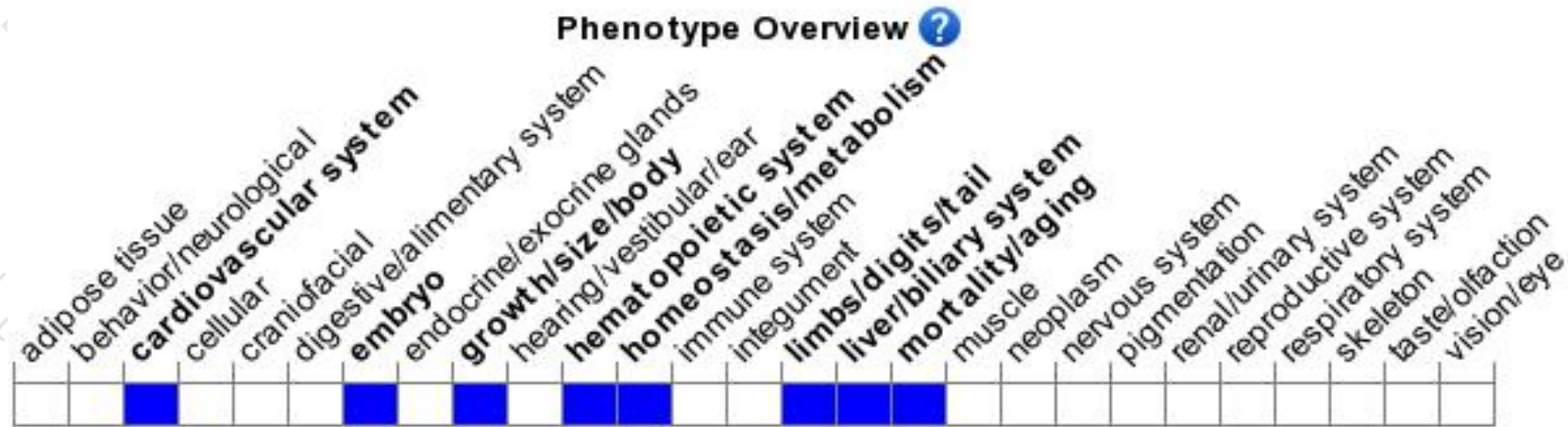
Genomic location distribution



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 null mice display impaired definitive erythropoiesis with loss of late stage erythroblasts, fetal liver hypoplasia, and embryonic lethality.

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

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