

Tead3 Cas9-KO Strategy

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Project Overview

Project Name

Tead3

Project type

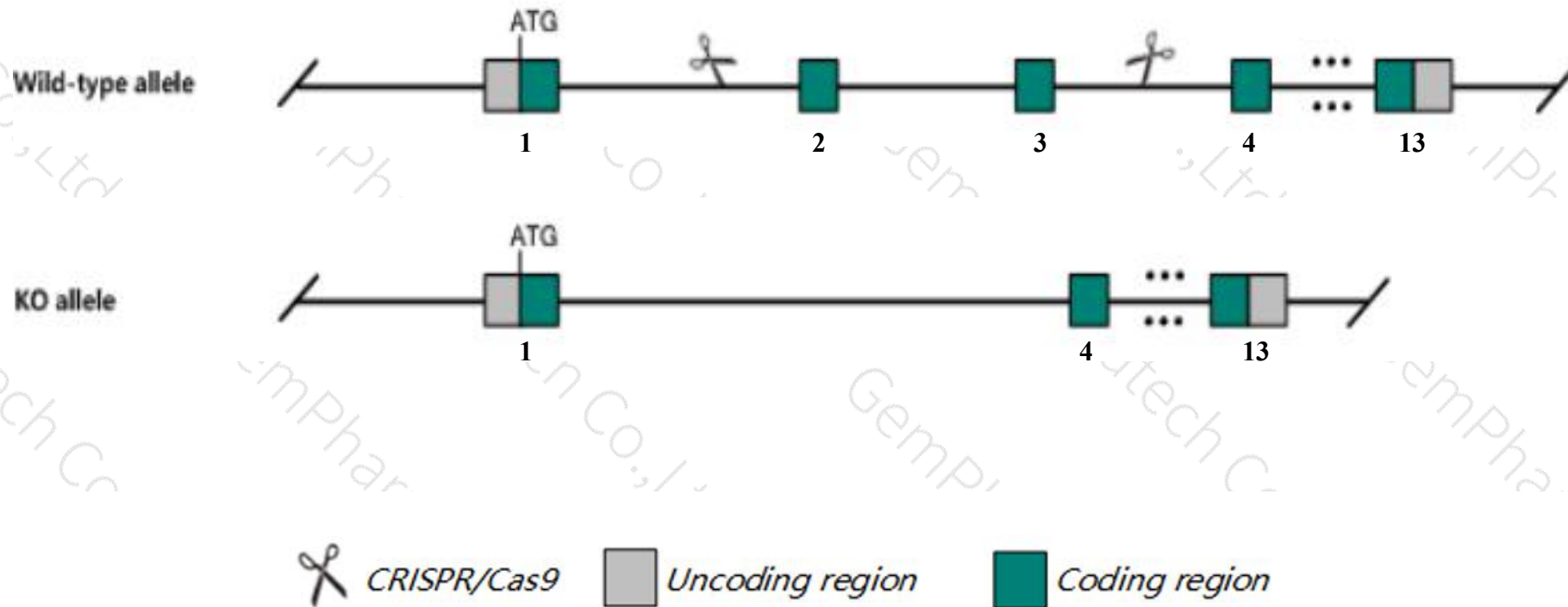
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tead3* gene. The schematic diagram is as follows:



Technical routes

- The *Tead3* gene has 9 transcripts. According to the structure of *Tead3* gene, exon2-exon3 of *Tead3*-201(ENSMUST00000114799.7) transcript is recommended as the knockout region. The region contains 317bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tead3* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Tead3* gene is located on the Chr17. 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.
- Transcript *Tead3-203, 204, 208* may not be affected.
- 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)

Tead3 TEA domain family member 3 [Mus musculus (house mouse)]

Gene ID: 21678, updated on 13-Mar-2020

Summary

Official Symbol Tead3 provided by [MGI](#)

Official Full Name TEA domain family member 3 provided by [MGI](#)

Primary source [MGI:MGI:109241](#)

See related [Ensembl:ENSMUSG00000002249](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as DTEF-1, ETFR-1, TEAD-3, TEF-5, Tcf13r2

Summary This gene product is a member of the transcriptional enhancer factor (TEF) family of transcription factors, which contain the TEA/ATTS DNA-binding domain. It is predominantly expressed in the placenta and thought to play a role in placental gene regulation and development. Alternative splicing, and alternate use of an upstream AUG translation initiation codon, and an in-frame downstream non-AUG (AUA) codon, results in 2 isoforms. [provided by RefSeq, Jul 2008]

Expression Broad expression in limb E14.5 (RPKM 22.9), bladder adult (RPKM 15.0) and 22 other tissues [See more](#)

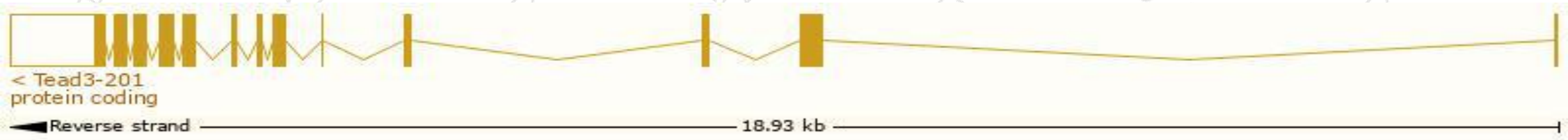
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

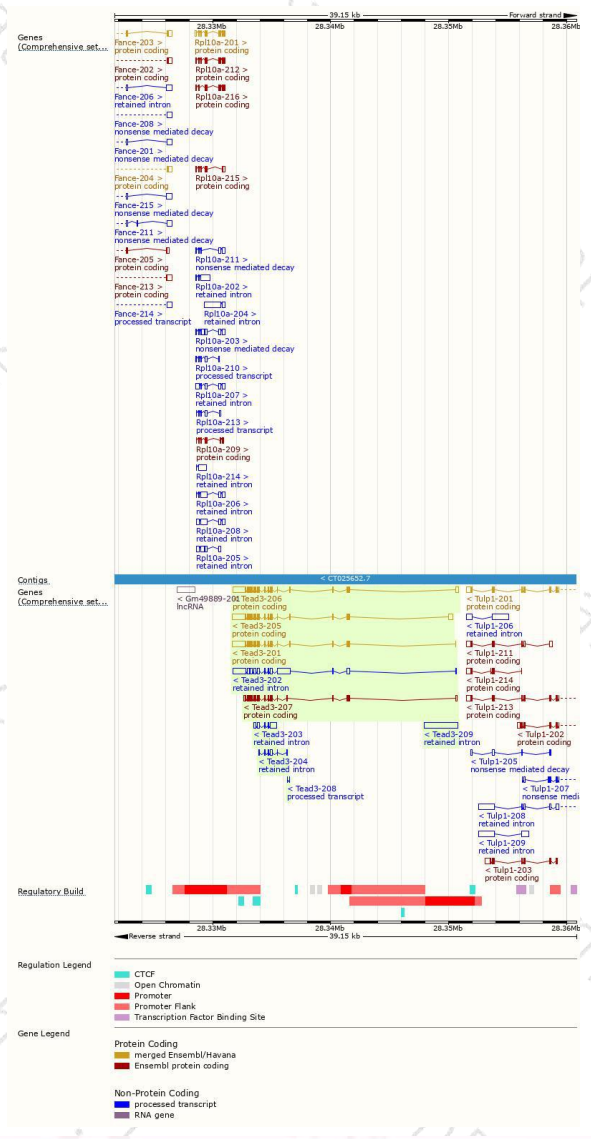
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tead3-201	ENSMUST00000114799.7	2448	465aa	Protein coding	CCDS50046	F8VPU0	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
Tead3-205	ENSMUST00000154873.8	2775	439aa	Protein coding	-	F6TTJ9	TSL:1 GENCODE basic
Tead3-206	ENSMUST00000156862.2	2585	439aa	Protein coding	-	F6TTJ9	TSL:1 GENCODE basic
Tead3-207	ENSMUST00000219703.2	1579	439aa	Protein coding	-	A0A3F2YNR7	TSL:1 GENCODE basic
Tead3-208	ENSMUST00000226172.1	11	No protein	Processed transcript	-	-	
Tead3-202	ENSMUST00000127212.8	3443	No protein	Retained intron	-	-	TSL:2
Tead3-209	ENSMUST00000233330.1	2870	No protein	Retained intron	-	-	
Tead3-203	ENSMUST00000146668.8	944	No protein	Retained intron	-	-	TSL:3
Tead3-204	ENSMUST00000151557.1	347	No protein	Retained intron	-	-	TSL:5

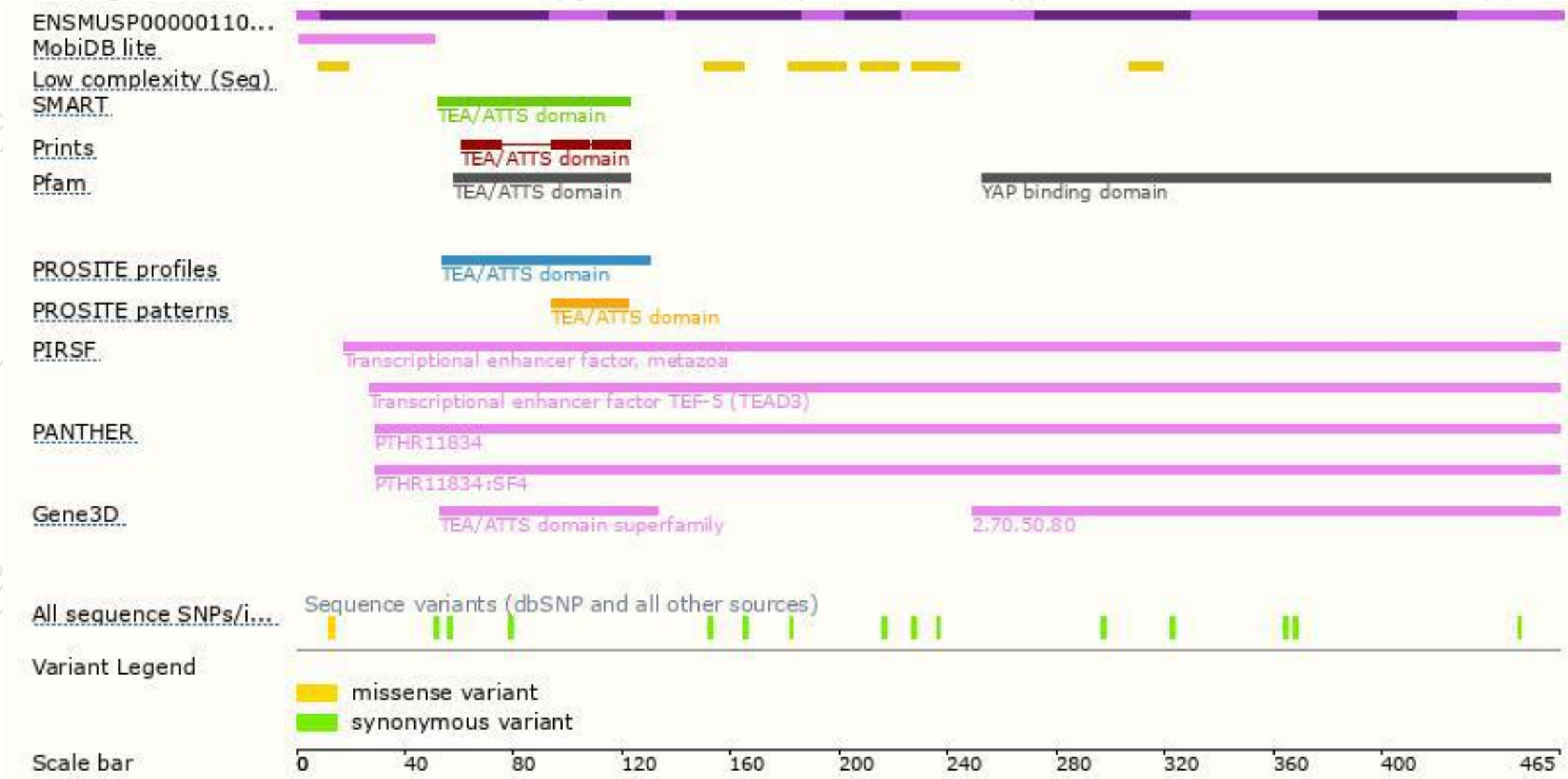
The strategy is based on the design of *Tead3-201* transcript,the transcription is shown below:



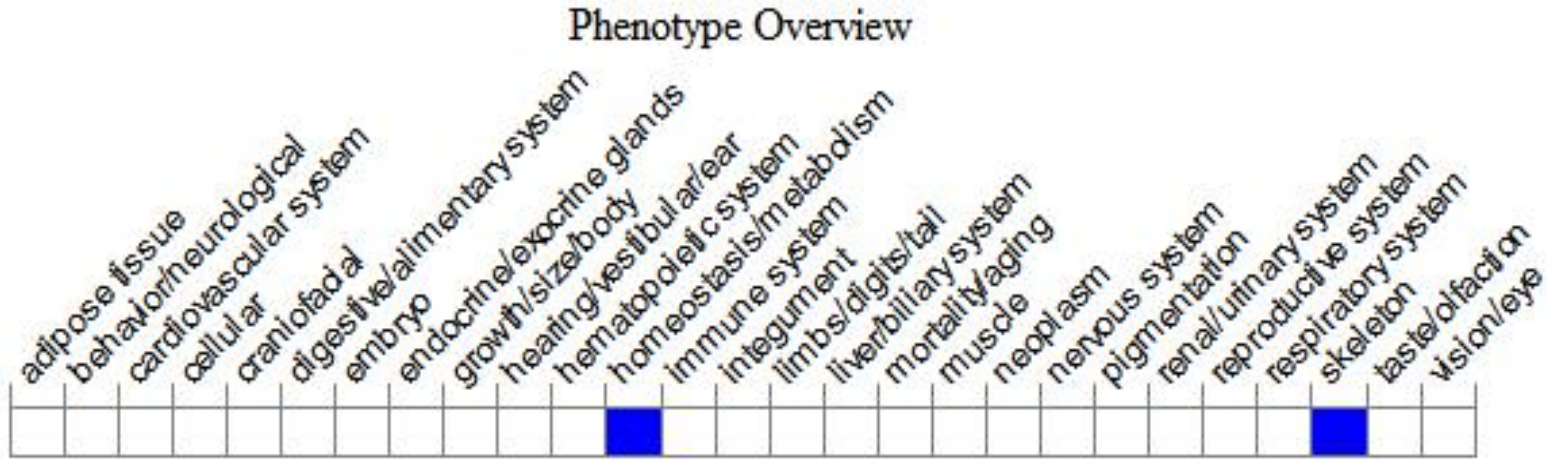
Genomic location distribution



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/>).

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

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