

Tead2 Cas9-KO Strategy

Designer:

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Design Date:

2019-7-25

Project Overview

Project Name

Tead2

Project type

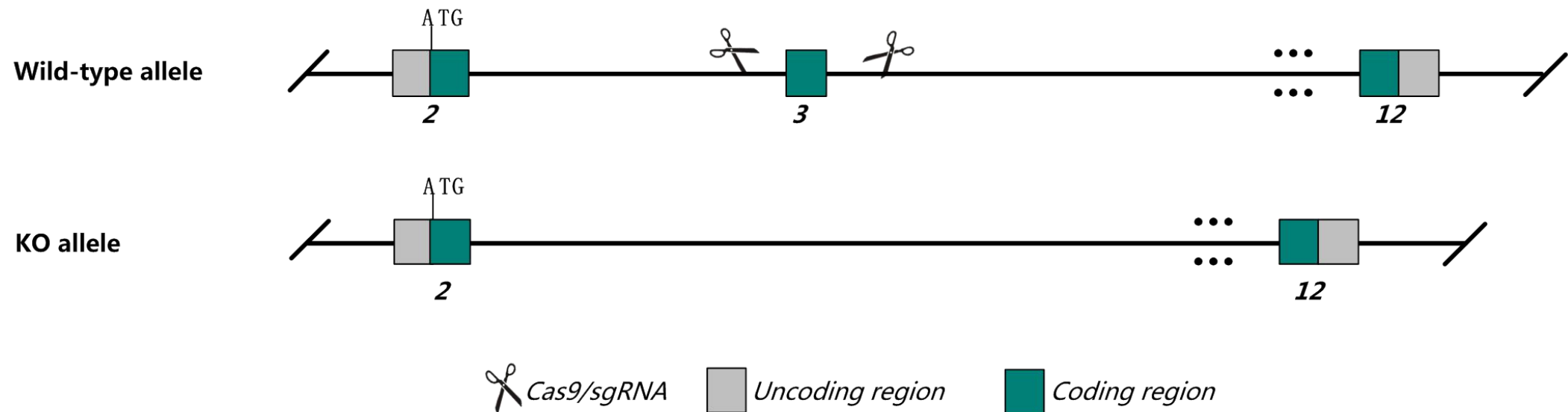
Cas9-KO

Strain background

C57BL/6JGpt

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This model will use CRISPR/Cas9 technology to edit the *Tead2* gene. The schematic diagram is as follows:



- The *Tead2* gene has 17 transcripts. According to the structure of *Tead2* gene, exon3 of *Tead2-201* (ENSMUST00000033060.13) transcript is recommended as the knockout region. The region contains 65bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tead2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a functionally null allele of this gene exhibit no gross abnormalities and are fertile.
- Transcript *Tead2-207* may not be affected.
- The *Tead2* gene is located on the Chr7. 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)

Tead2 TEA domain family member 2 [Mus musculus (house mouse)]

Gene ID: 21677, updated on 5-Feb-2019

Summary



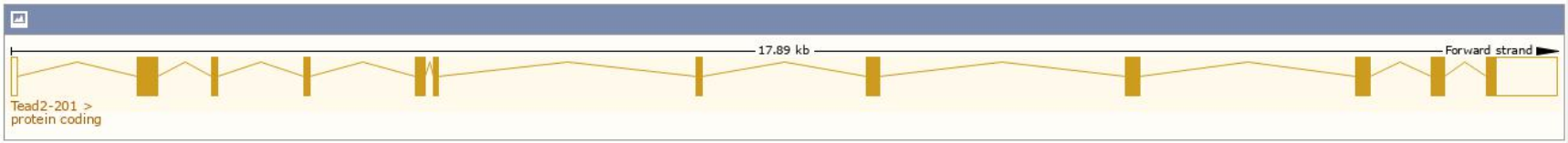
Official Symbol	Tead2 provided by MGI
Official Full Name	TEA domain family member 2 provided by MGI
Primary source	MGI:MGI:104904
See related	Ensembl:ENSMUSG00000030796
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ETEF-1, ETF, Etdf, TEAD-2, TEF-4, TEF4
Expression	Biased expression in CNS E11.5 (RPKM 109.8), limb E14.5 (RPKM 100.2) and 12 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

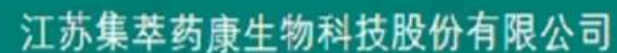
The gene has 17 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tead2-203	ENSMUST00000107801.9	3396	445aa	Protein coding	CCDS21236	P48301 Q3UPV9	TSL:1 GENCODE basic APPRIS P1
Tead2-201	ENSMUST00000033060.13	2140	445aa	Protein coding	CCDS21236	P48301 Q3UPV9	TSL:1 GENCODE basic APPRIS P1
Tead2-202	ENSMUST00000097216.4	1948	410aa	Protein coding	CCDS71957	Q80UL2	TSL:1 GENCODE basic
Tead2-211	ENSMUST00000210447.1	793	245aa	Protein coding	-	A0A1B0GT36	CDS 3' incomplete TSL:5
Tead2-216	ENSMUST00000211744.1	592	175aa	Protein coding	-	A0A1B0GRZ4	CDS 3' incomplete TSL:5
Tead2-205	ENSMUST00000209343.1	560	184aa	Protein coding	-	A0A1B0GS07	CDS 3' incomplete TSL:5
Tead2-206	ENSMUST00000209437.1	435	107aa	Protein coding	-	A0A1B0GSN2	CDS 3' incomplete TSL:3
Tead2-207	ENSMUST00000209478.1	400	129aa	Protein coding	-	A0A1B0GQX1	CDS 5' incomplete TSL:5
Tead2-208	ENSMUST00000209678.1	388	129aa	Protein coding	-	A0A1B0GR00	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Tead2-204	ENSMUST00000209222.1	460	No protein	Processed transcript	-	-	TSL:2
Tead2-210	ENSMUST00000209818.1	272	No protein	Processed transcript	-	-	TSL:5
Tead2-213	ENSMUST00000210814.1	178	No protein	Processed transcript	-	-	TSL:3
Tead2-212	ENSMUST00000210570.1	895	No protein	Retained intron	-	-	TSL:2
Tead2-209	ENSMUST00000209708.1	811	No protein	Retained intron	-	-	TSL:2
Tead2-214	ENSMUST00000211138.1	701	No protein	Retained intron	-	-	TSL:3
Tead2-217	ENSMUST00000211778.1	403	No protein	Retained intron	-	-	TSL:3
Tead2-215	ENSMUST00000211594.1	387	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Tead2-201* transcript,The transcription is shown below



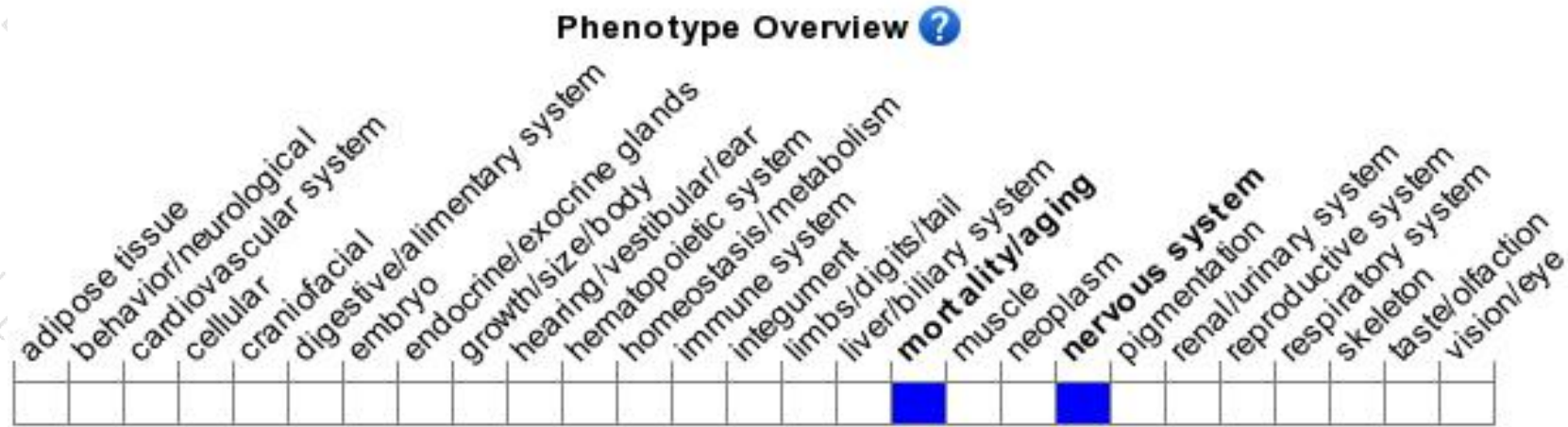
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Protein domain



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 functionally null allele of this gene exhibit no gross abnormalities and are fertile.

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

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