Tead3 Cas9-CKO Strategy

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Project Overview

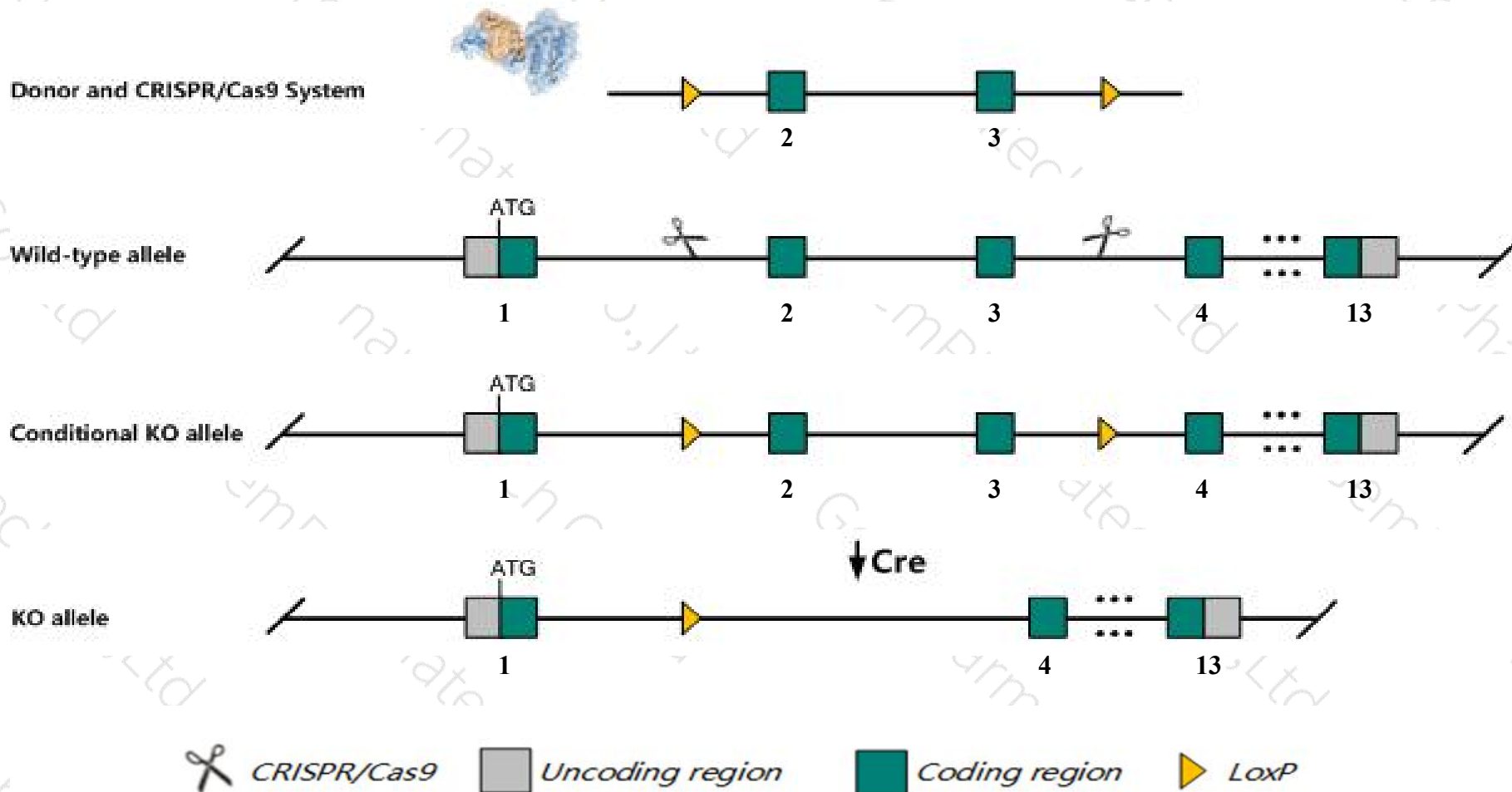|	
Project Name	*Tead3*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional 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 Ens 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 and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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

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

▲ Summary

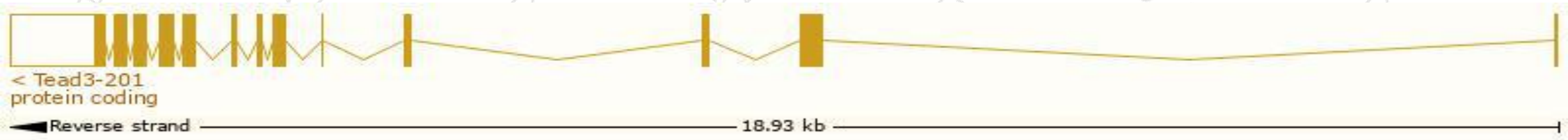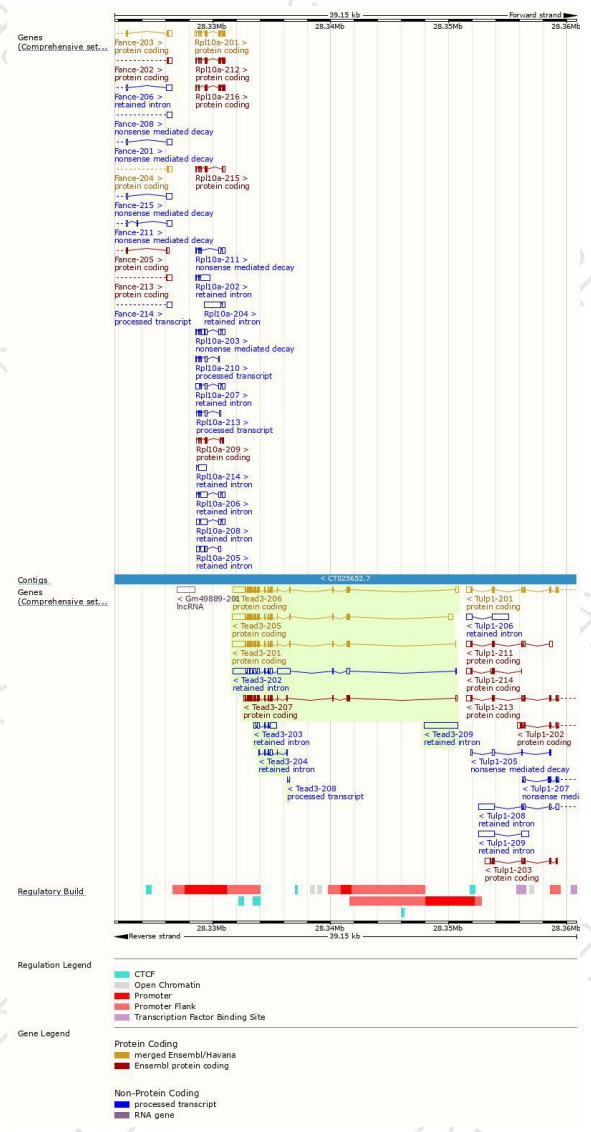|	
Official Symbol	Tead3 provided by MGI
Official Full Name	TEA domain family member 3 provided by MGI
Primary source	MGI:MGI:109241
See related	Ensembl:ENSMUSG00000002249
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 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 tissuesSee 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

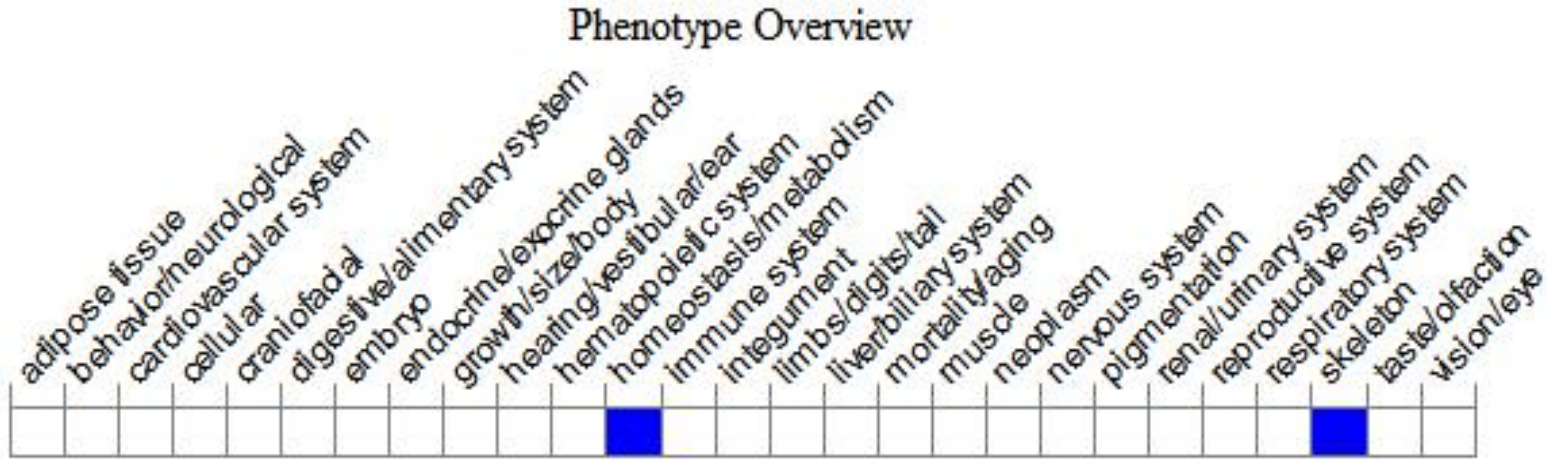The strategy is based on the design of *Tead3-201* transcript,the transcription is shown below:

< Tead3-201
protein coding

◄ Reverse strand

18.93 kb

Genomic location distribution

Protein domain

ENSMUSP00000110...	
MobiDB lite	
Low complexity (Seg)	
SMART	TEA/ATTS domain
Prints	TEA/ATTS domain
Pfam	TEA/ATTS domain YAP binding domain
PROSITE profiles	TEA/ATTS domain
PROSITE patterns	TEA/ATTS domain
PIRSF	Transcriptional enhancer factor, metazoa
	Transcriptional enhancer factor TEF-5 (TEAD3)
PANTHER	PTHR11834
	PTHR11834:SF4
Gene3D	TEA/ATTS domain superfamily 2.70.50.80
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)
Variant Legend	

Variant Legend

- 🟧 missense variant
- 🟩 synonymous variant

Scale bar

0   40   80   120   160   200   240   280   320   360   400   465

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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