

Tent2 Cas9-KO Strategy

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Project Overview

Project Name

Tent2

Project type

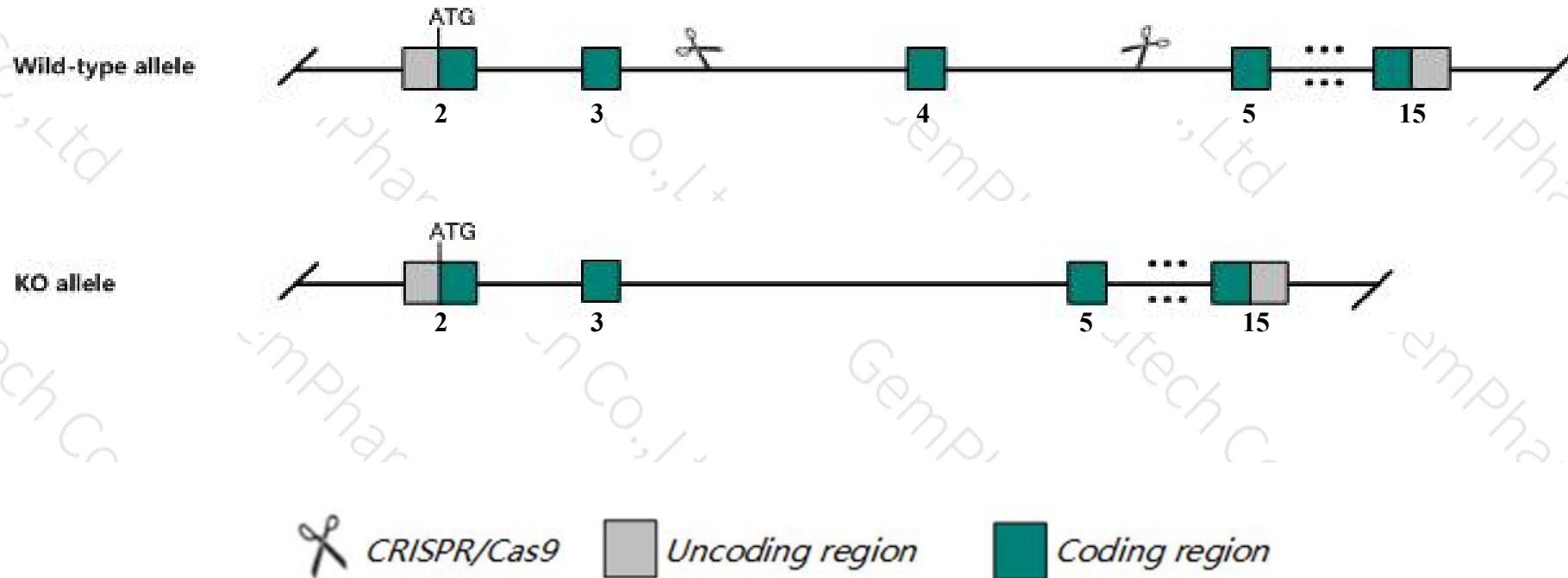
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tent2* gene. The schematic diagram is as follows:



- The *Tent2* gene has 6 transcripts. According to the structure of *Tent2* gene, exon4 of *Tent2-201* (ENSMUST00000048702.6) transcript is recommended as the knockout region. The region contains 238bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tent2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele results in disruption in polyadenylation in oocytes and somatic cells.
- Transcript 206 CDS 5' incomplete the influences is unknown.
- The *Tent2* gene is located on the Chr13. 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)

Tent2 terminal nucleotidyltransferase 2 [Mus musculus (house mouse)]

Gene ID: 100715, updated on 31-Jan-2019

Summary



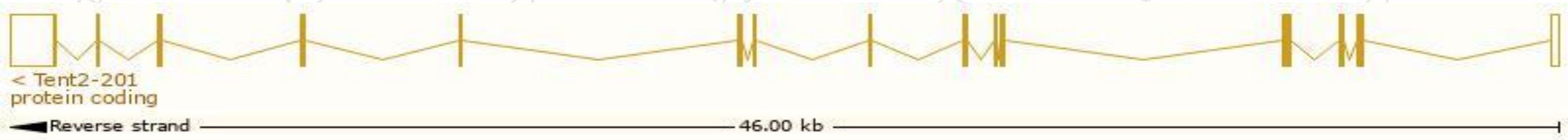
Official Symbol	Tent2 provided by MGI
Official Full Name	terminal nucleotidyltransferase 2 provided by MGI
Primary source	MGI:MGI:2140950
See related	Ensembl:ENSMUSG00000042167
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	8030446C20Rik, Al649009, GLD-2, Gld2, Papd4
Expression	Ubiquitous expression in limb E14.5 (RPKM 18.2), placenta adult (RPKM 16.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

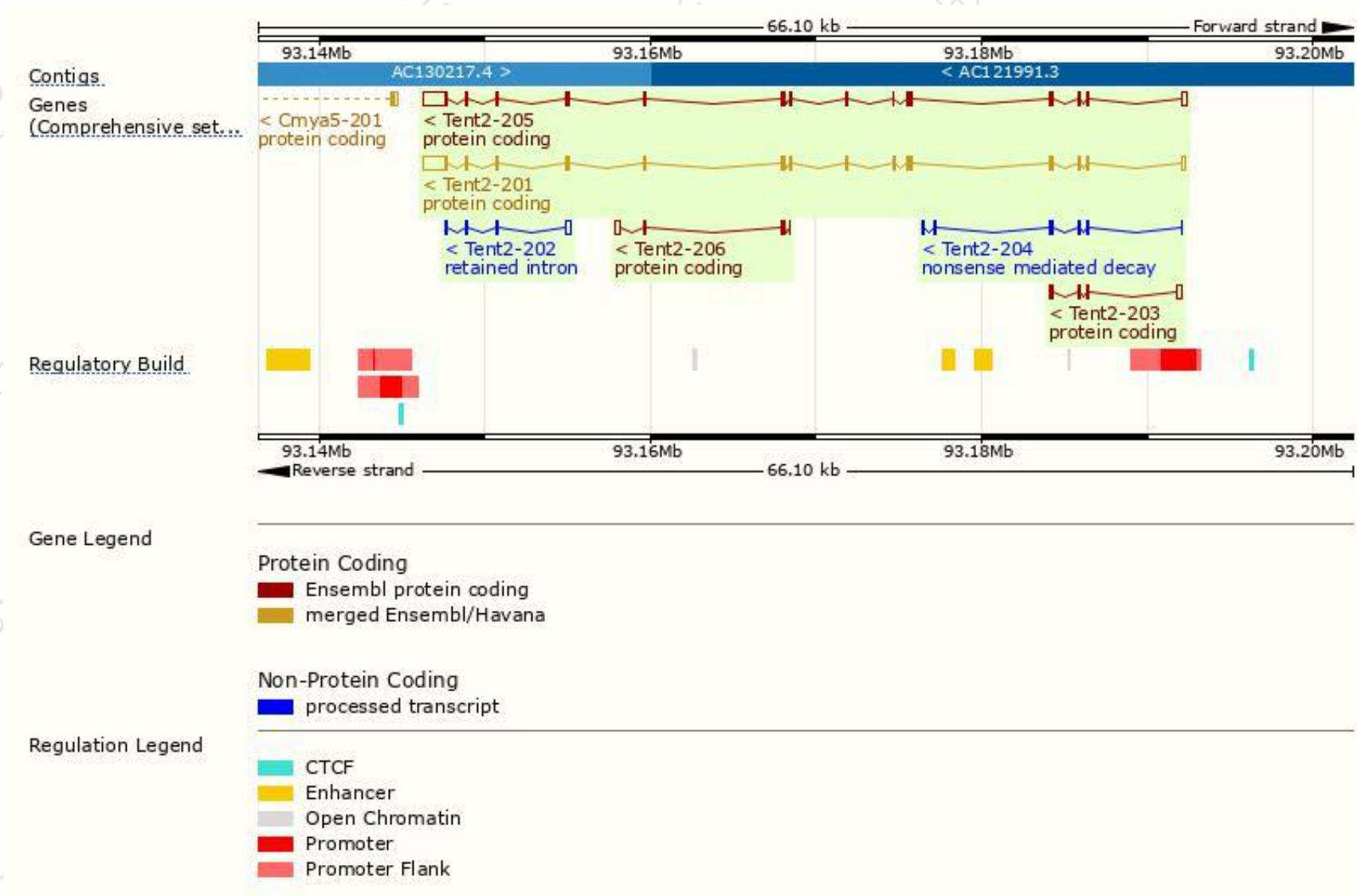
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tent2-201	ENSMUST00000048702.6	2990	484aa	Protein coding	CCDS26686	Q91YI6	TSL:1 GENCODE basic APPRIS P2
Tent2-205	ENSMUST00000225868.1	3081	480aa	Protein coding	-	Q91YI6	GENCODE basic APPRIS ALT 1
Tent2-203	ENSMUST00000224464.1	821	155aa	Protein coding	-	A0A286YCM6	CDS 3' incomplete
Tent2-206	ENSMUST00000226081.1	602	99aa	Protein coding	-	A0A286YED5	CDS 5' incomplete
Tent2-204	ENSMUST00000224545.1	788	158aa	Nonsense mediated decay	-	A0A286YDA7	
Tent2-202	ENSMUST00000223975.1	502	No protein	Retained intron	-	-	

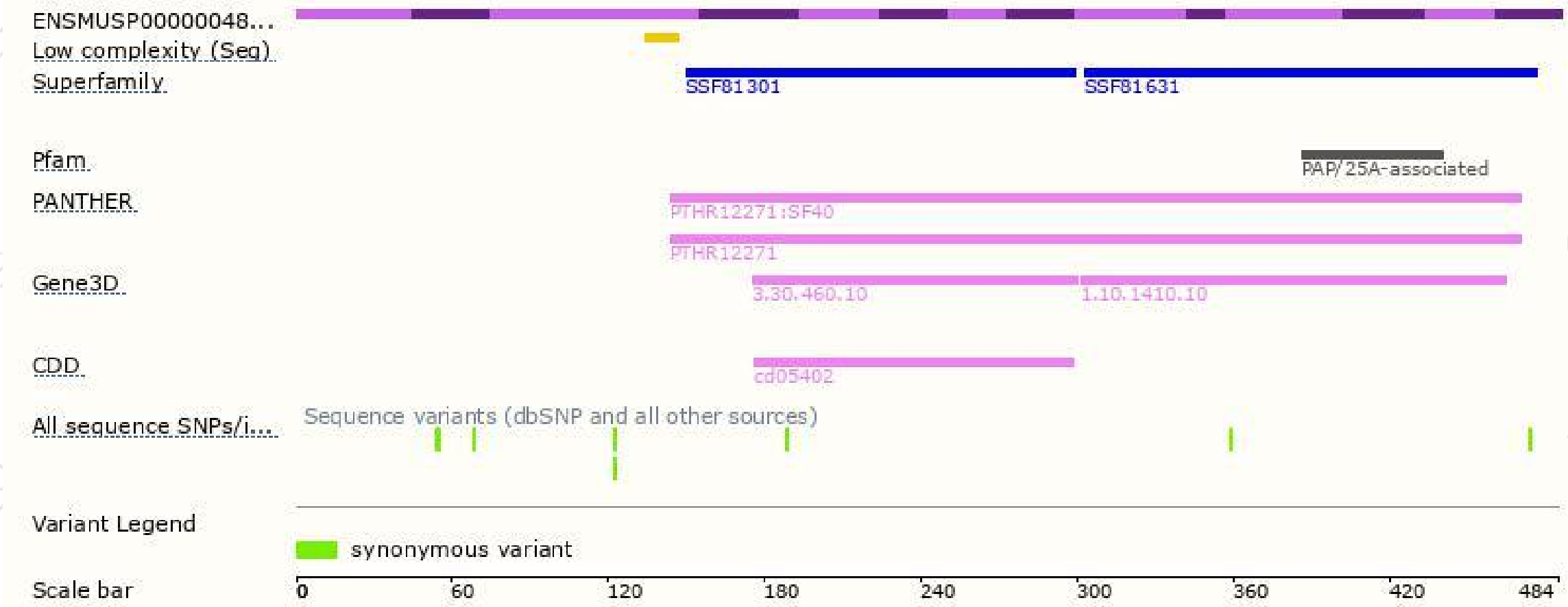
The strategy is based on the design of *Tent2-201* transcript,The transcription is shown below



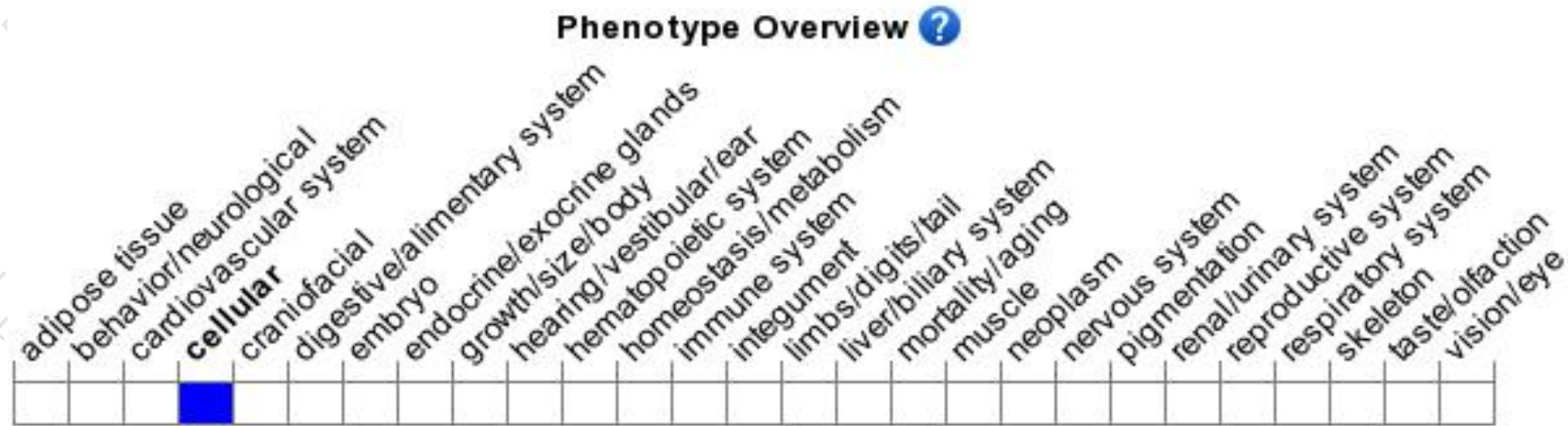
Genomic location distribution



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 a null allele results in disruption in polyadenylation in oocytes and somatic cells.

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

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