

Tep1 Cas9-KO Strategy

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Project Overview

Project Name

Tep1

Project type

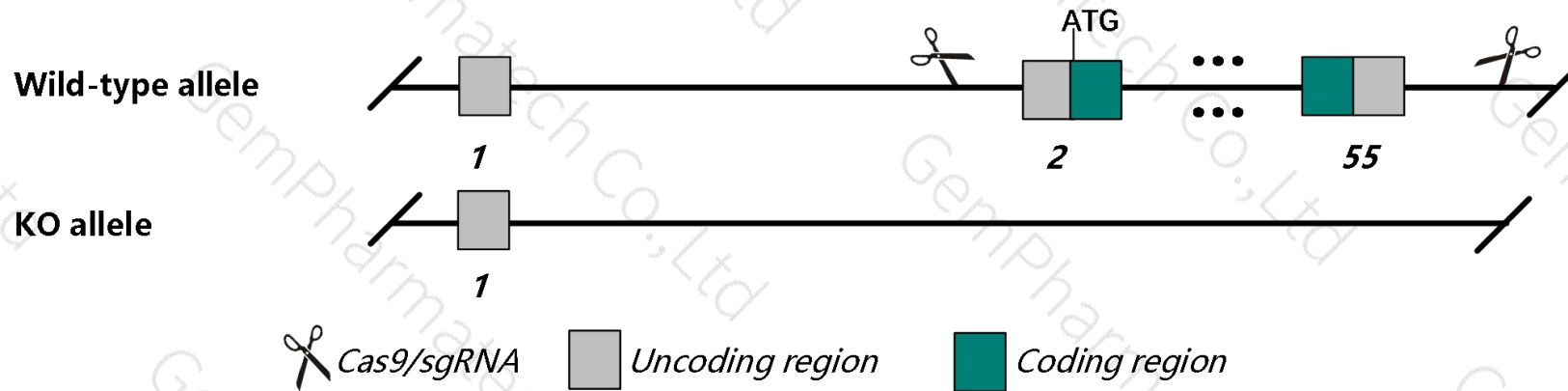
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tep1* gene. The schematic diagram is as follows:



- The *Tep1* gene has 8 transcripts. According to the structure of *Tep1* gene, exon2-exon55 of *Tep1-201* (ENSMUST00000006444.8) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tep1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a disruption in this gene show no obvious phenotype.
No changes are seen in telomerase activity or telomere length.
- The knockout region is near to the N-terminal of *Gm26782* gene, this strategy may influence the regulatory function of the N-terminal of *Gm26782* gene.
- The *Tep1* gene is located on the Chr14. 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)

Tep1 telomerase associated protein 1 [*Mus musculus* (house mouse)]

Gene ID: 21745, updated on 12-Aug-2019

Summary

Official Symbol	Tep1 provided by MGI
Official Full Name	telomerase associated protein 1 provided by MGI
Primary source	MGI:MGI:109573
See related	Ensembl:ENSMUSG00000006281
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	Tp1
Expression	Broad expression in large intestine adult (RPKM 17.7), colon adult (RPKM 17.6) and 21 other tissues See more
Orthologs	human all

Genomic context

Location: 14 C1; 14 26.26 cM

See Tep1 in [Genome Data Viewer](#)

Exon count: 56

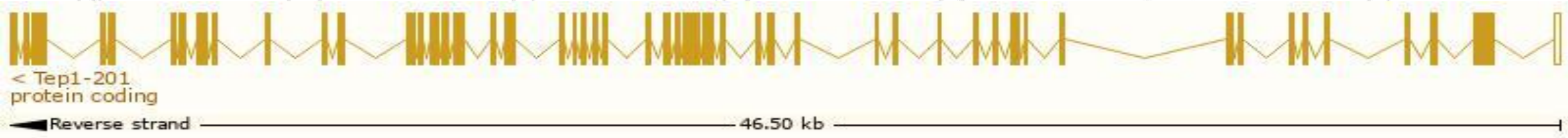
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	14	NC_000080.6 (50824059..50870579, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	14	NC_000080.5 (51443736..51490229, complement)

Transcript information (Ensembl)

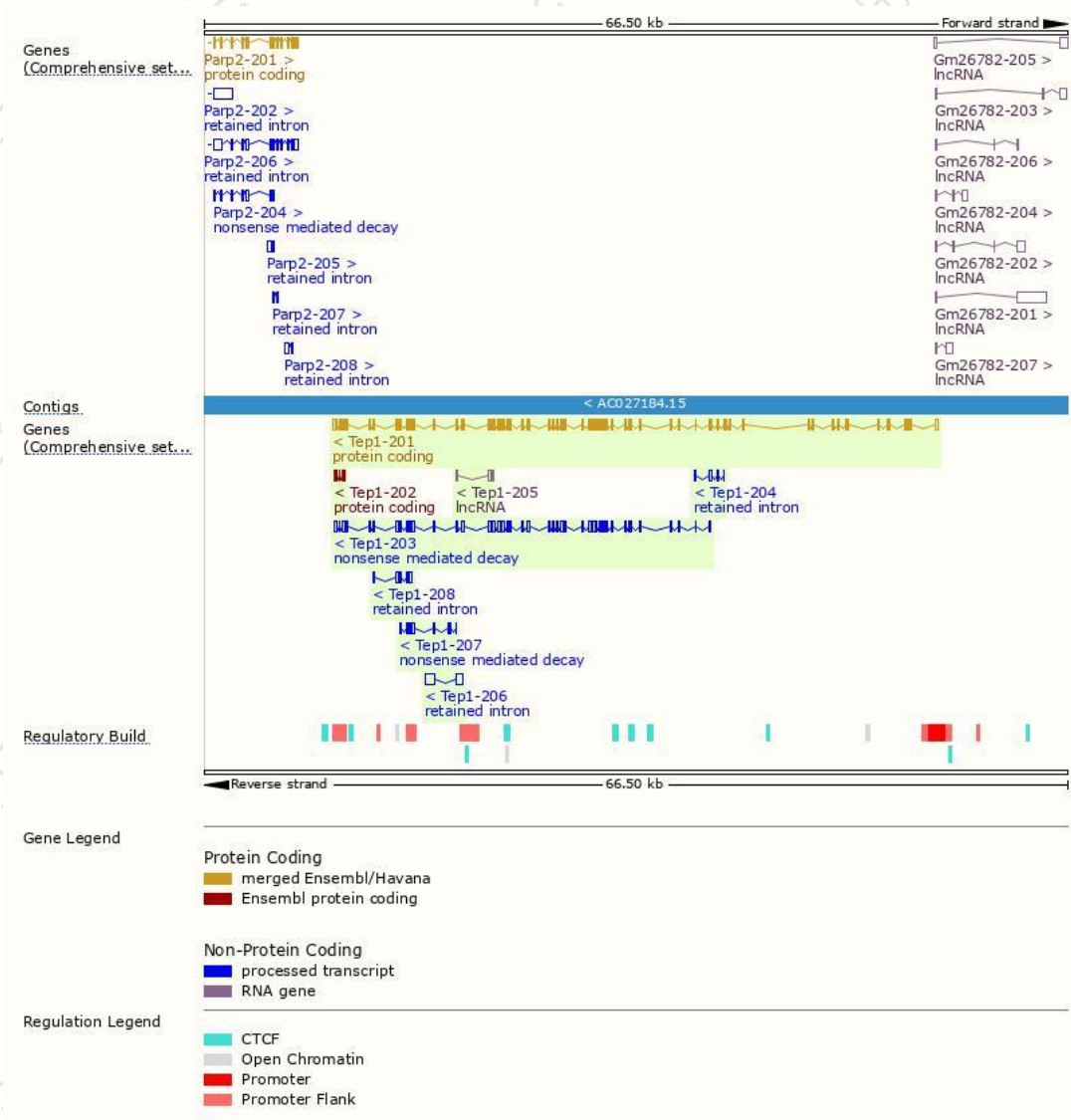
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tep1-201	ENSMUST00000006444.8	8171	2629aa	Protein coding	CCDS36907	P97499	TSL:1 GENCODE basic APPRIS P1
Tep1-202	ENSMUST00000226222.1	434	79aa	Protein coding	-	A0A2I3BRB1	CDS 5' incomplete
Tep1-203	ENSMUST00000226430.1	5690	489aa	Nonsense mediated decay	-	A0A2I3BR80	CDS 5' incomplete
Tep1-207	ENSMUST00000227526.1	737	51aa	Nonsense mediated decay	-	A0A2I3BQ06	CDS 5' incomplete
Tep1-206	ENSMUST00000227228.1	1274	No protein	Retained intron	-	-	
Tep1-208	ENSMUST00000228562.1	702	No protein	Retained intron	-	-	
Tep1-204	ENSMUST00000226789.1	551	No protein	Retained intron	-	-	
Tep1-205	ENSMUST00000227193.1	380	No protein	lncRNA	-	-	

The strategy is based on the design of *Tep1-201* transcript,The transcription is shown below



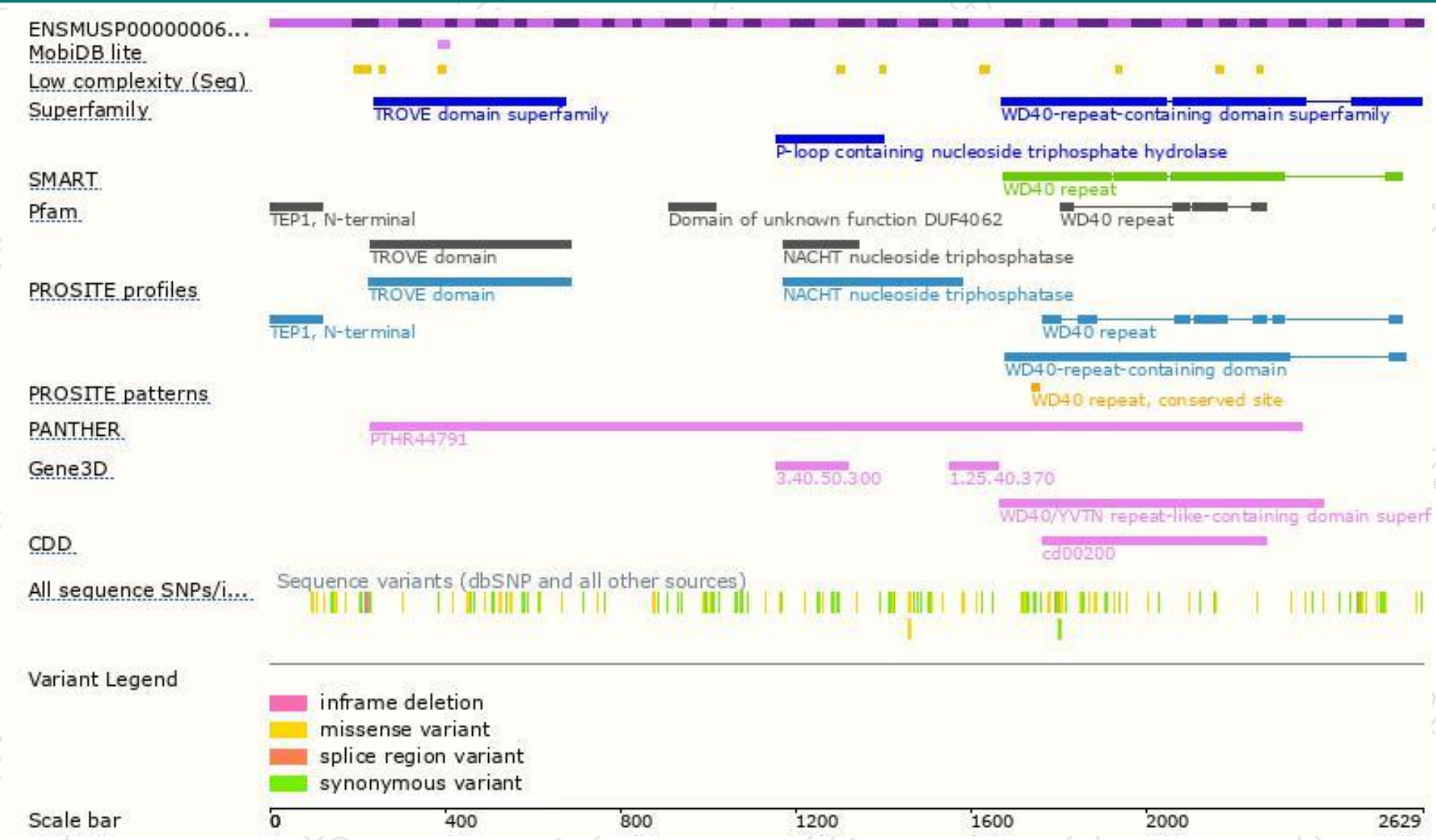
Genomic location distribution



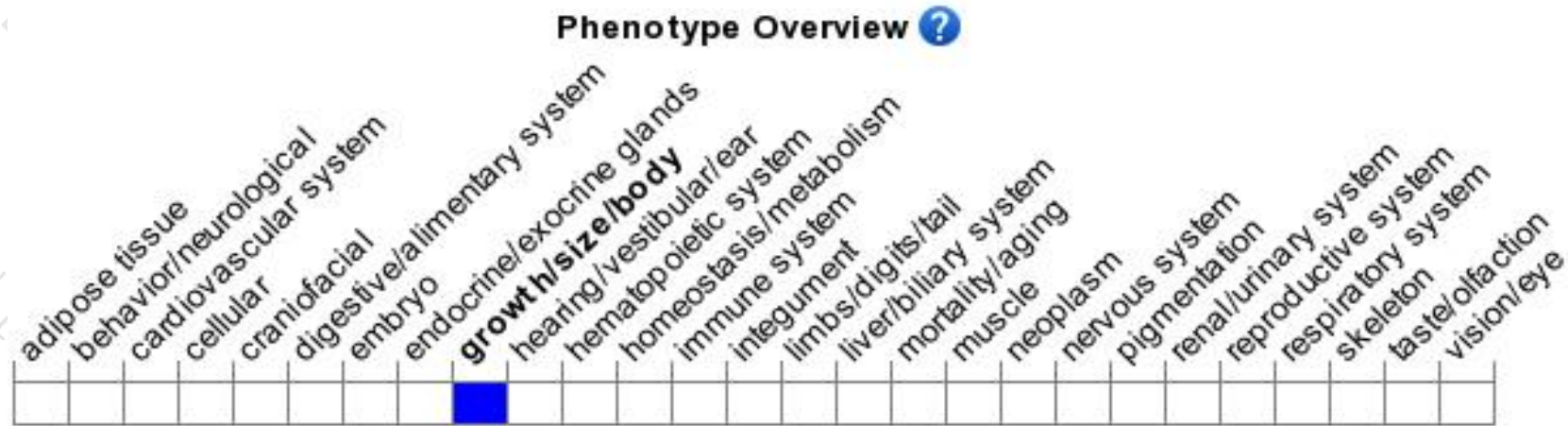
Protein domain



集萃药康
GemPharmatech



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 disruption in this gene show no obvious phenotype. No changes are seen in telomerase activity or telomere length.

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

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