

# Tpst2 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

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# **Project Overview**



**Project Name** 

Tpst2

**Project type** 

Cas9-KO

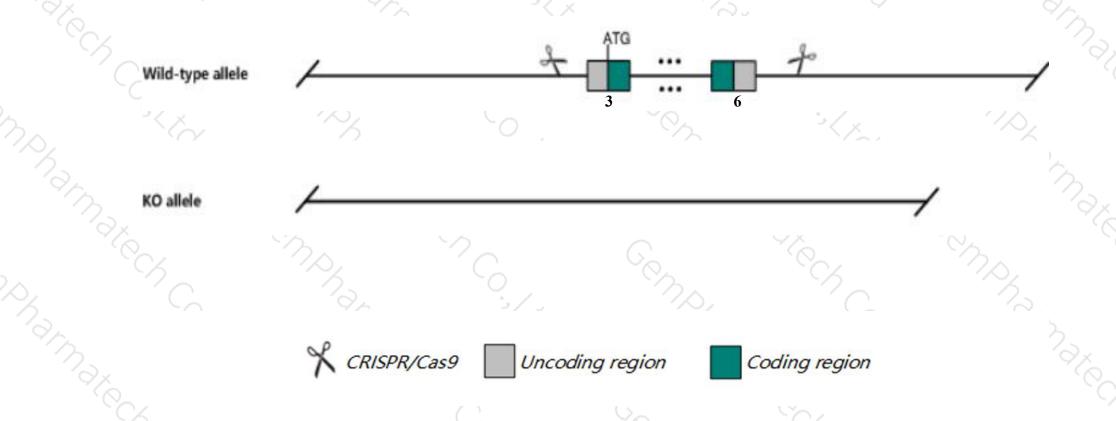
Strain background

**C57BL/6J** 

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Tpst2* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Tpst2* gene has 7 transcripts. According to the structure of *Tpst2* gene, exon3-exon6 of *Tpst2-201* (ENSMUST00000031287.10) 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 *Tpst2* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- > According to the existing MGI data, spontaneous mutants show a delayed rise and a prolonged deficit of pituitary growth hormone resulting in delayed pubertal growth, hypothyroidism, and an enlarged adenohypophysis with aberrant chromophobic cells. homozygous null mice show a modest but transient pubertal growth lag and male sterility.
- > The *Tpst2* gene is located on the Chr5. 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)



#### Tpst2 protein-tyrosine sulfotransferase 2 [Mus musculus (house mouse)]

Gene ID: 22022, updated on 13-Mar-2020

#### Summary

☆ ?

Official Symbol Tpst2 provided by MGI

Official Full Name protein-tyrosine sulfotransferase 2 provided by MGI

Primary source MGI:MGI:1309516

See related Ensembl: ENSMUSG00000029344

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 Al448750, D5Ucla3, Tango13b, grm, grt

Expression Broad expression in genital fat pad adult (RPKM 79.3), adrenal adult (RPKM 73.7) and 25 other tissuesSee more

Orthologs <u>human</u> all

# Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

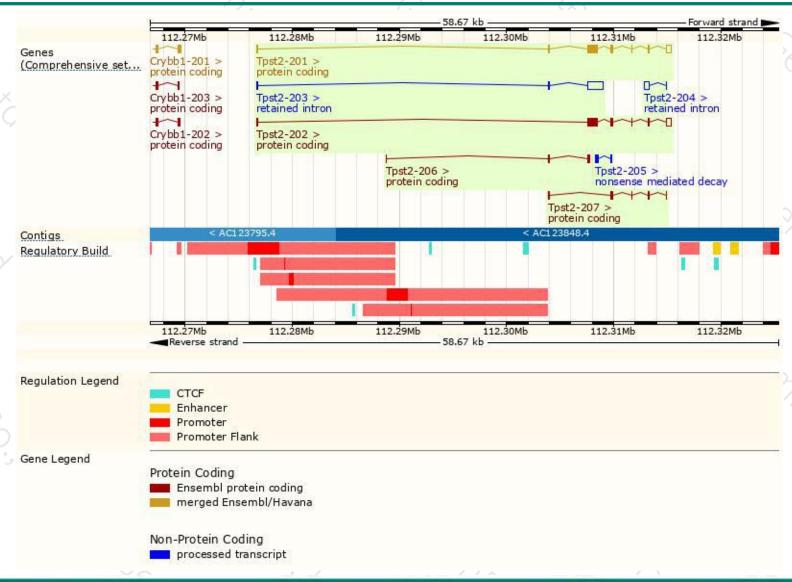
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tpst2-201	ENSMUST00000031287.10	1835	390aa	Protein coding	CCDS19538	Q3TQN1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Tpst2-202	ENSMUST00000071455.5	1741	390aa	Protein coding	CCDS19538	Q3TQN1	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
Tpst2-207	ENSMUST00000198502.1	442	<u>122aa</u>	Protein coding	(99)	A0A0G2JE92	CDS 5' incomplete TSL:5
Tpst2-206	ENSMUST00000151947.1	294	<u>46aa</u>	Protein coding	-	D3YV96	CDS 3' incomplete TSL:3
Tpst2-205	ENSMUST00000140262.1	388	<u>63aa</u>	Nonsense mediated decay	-	F7BM44	CDS 5' incomplete TSL:3
Tpst2-203	ENSMUST00000134071.7	1607	No protein	Retained intron		-8	TSL:2
Tpst2-204	ENSMUST00000139482.1	471	No protein	Retained intron	(2)	24	TSL:2

The strategy is based on the design of *Tpst2-201* transcript, the transcription is shown below:

Tpst2-201 > protein coding

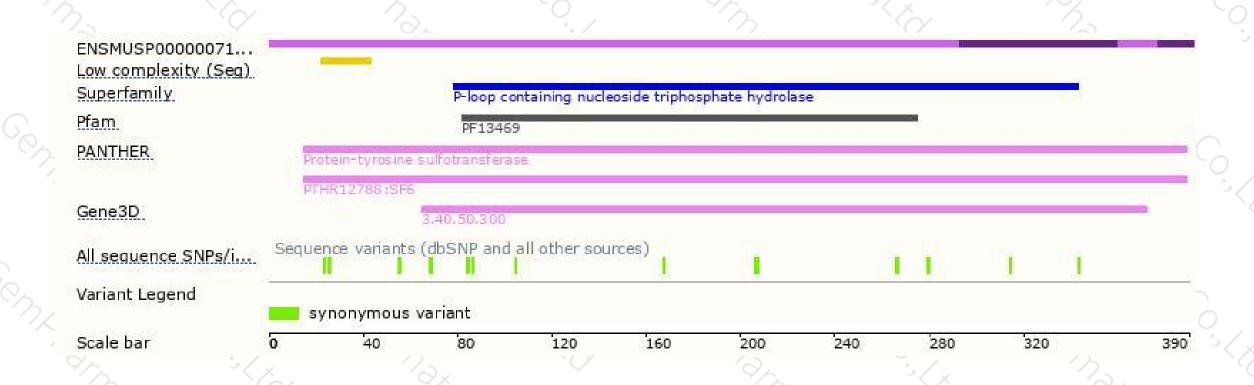
### Genomic location distribution





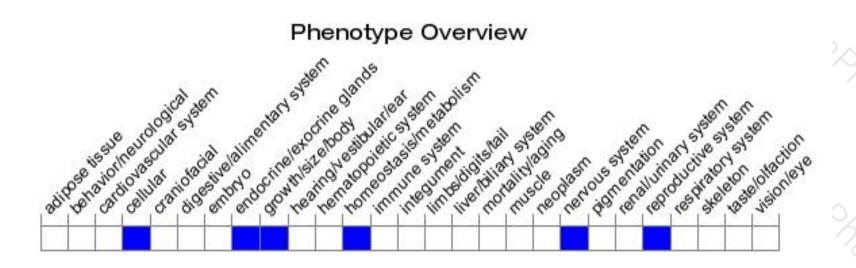
### Protein domain





## Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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If you have any questions, you are welcome to inquire. Tel: 400-9660890





