

***Tut7* Cas9-CKO Strategy**

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Project Overview

Project Name

Tut7

Project type

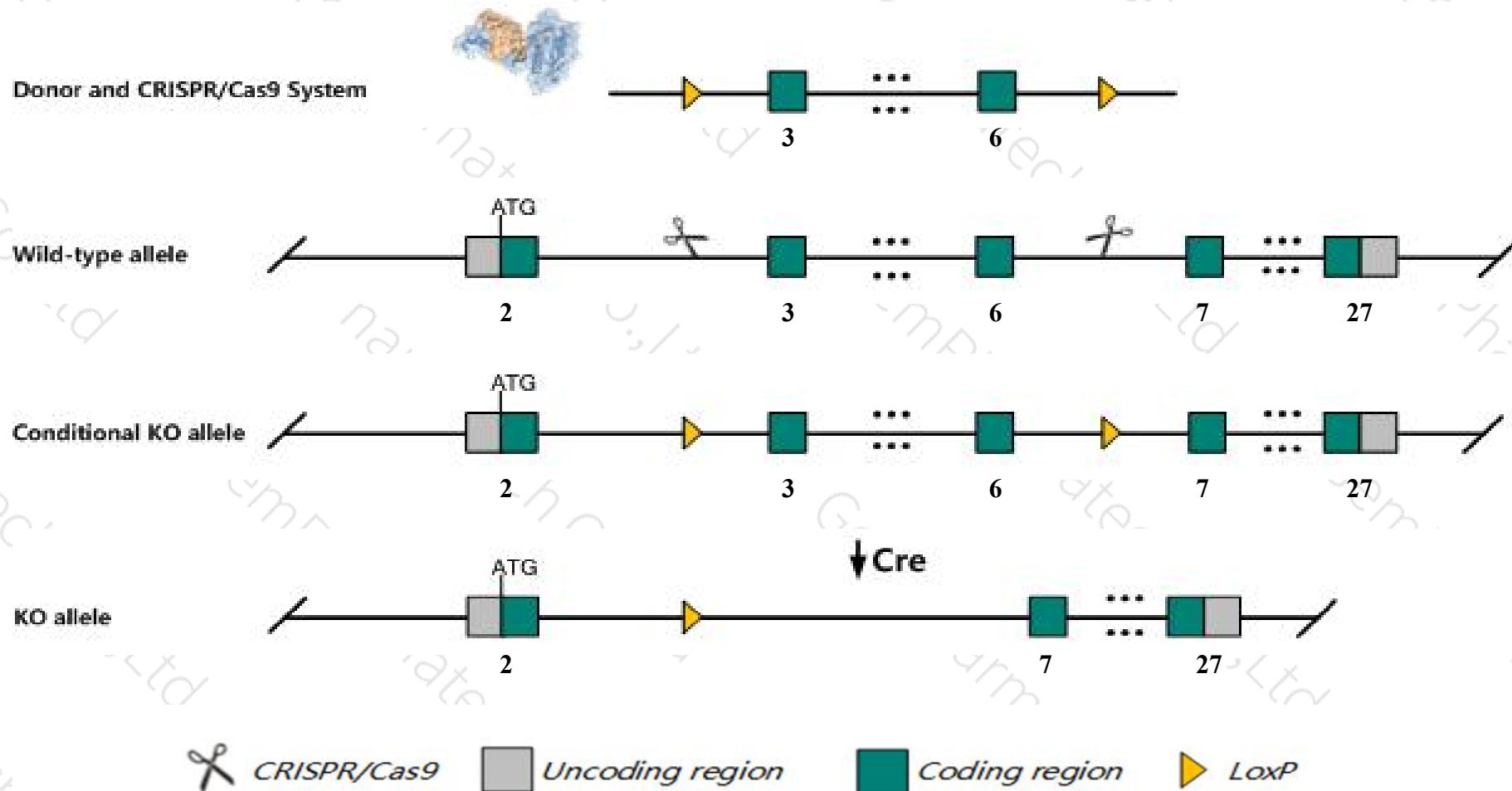
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tut7* gene. The schematic diagram is as follows:



Technical routes

- The *Tut7* gene has 10 transcripts. According to the structure of *Tut7* gene, exon3-exon6 of *Tut7-201* (ENSMUST00000071703.5) transcript is recommended as the knockout region. The region contains 566bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tut7* 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.

- According to the existing MGI data, mice homozygous for conditional alleles of *tut4* and *tut7* activated in oocytes exhibit female infertility due to abnormal female meiosis i.
- The *Tut7* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Tut7 terminal uridylyl transferase 7 [Mus musculus (house mouse)]

Gene ID: 214290, updated on 13-Mar-2020

Summary



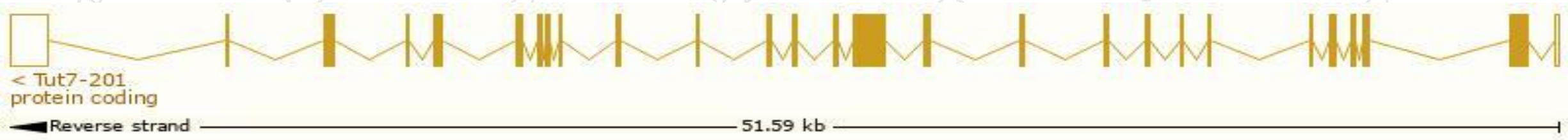
| | |
|---------------------------|---|
| Official Symbol | Tut7 provided by MGI |
| Official Full Name | terminal uridylyl transferase 7 provided by MGI |
| Primary source | MGI:MGI:2387179 |
| See related | Ensembl:ENSMUSG00000035248 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 6030448M23Rik, AA420405, Tent3b, Zcchc6 |
| Expression | Ubiquitous expression in liver E14 (RPKM 11.4), liver E14.5 (RPKM 9.7) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

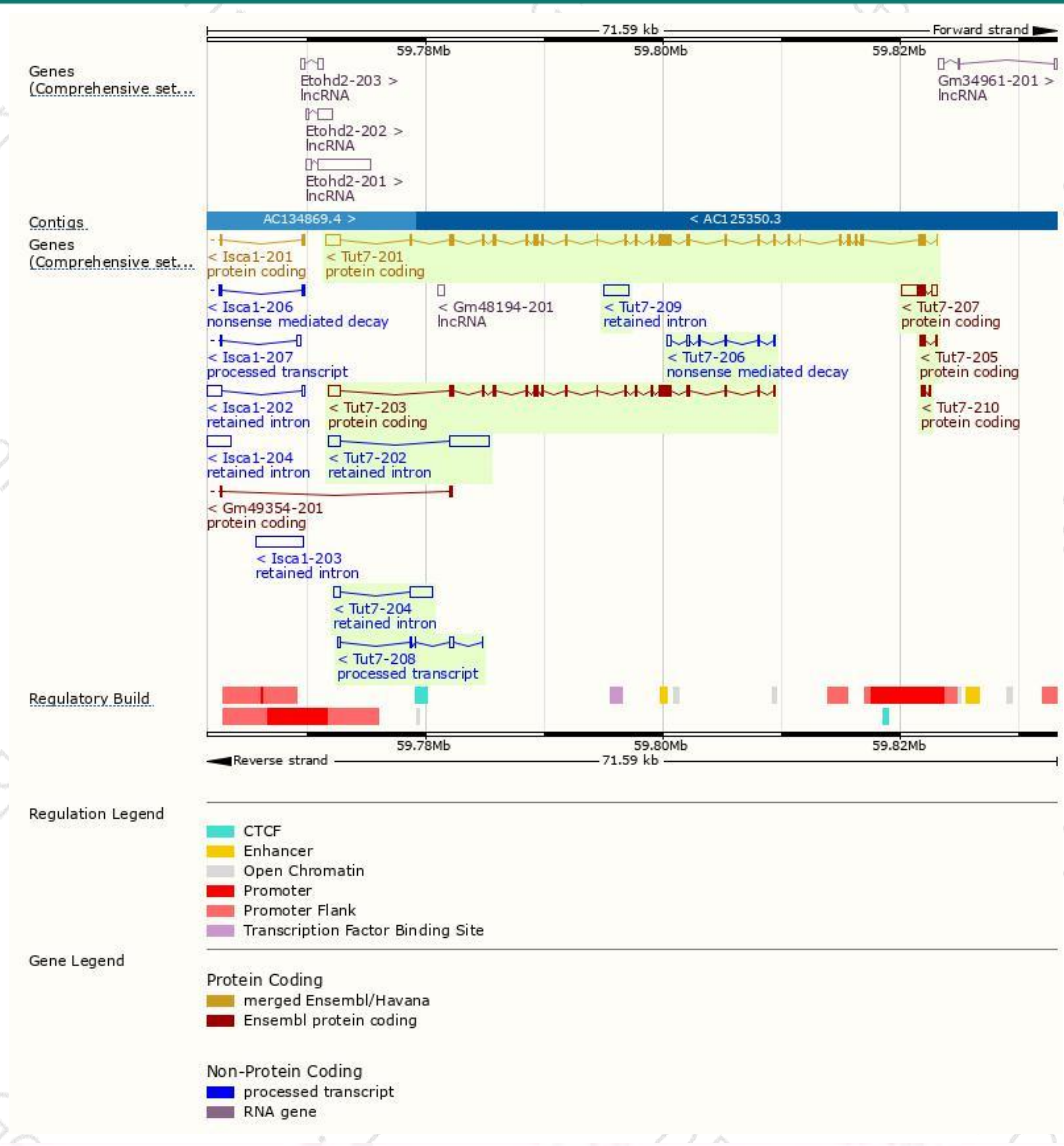
The gene has 10 transcripts,all transcripts are shown below:

| Name ▲ | Transcript ID ▲ | bp ▲ | Protein ▲ | Biotype ▲ | CCDS ▲ | UniProt ▲ | Flags ▲ |
|----------|--------------------------------------|------|------------------------|-------------------------|---------------------------|----------------------------|-------------------------------|
| Tut7-201 | ENSMUST00000071703.5 | 5869 | 1474aa | Protein coding | CCDS36689 | E9PUA2 | TSL:1 Gencode basic APPRIS P1 |
| Tut7-202 | ENSMUST00000224320.1 | 4337 | No protein | Retained intron | - | - | - |
| Tut7-203 | ENSMUST00000224480.1 | 4186 | 1089aa | Protein coding | - | A0A286YDD7 | CDS 5' incomplete |
| Tut7-204 | ENSMUST00000224845.1 | 2452 | No protein | Retained intron | - | - | - |
| Tut7-205 | ENSMUST00000225179.1 | 619 | 149aa | Protein coding | - | A0A286YDR9 | CDS 3' incomplete |
| Tut7-206 | ENSMUST00000225241.1 | 1056 | 148aa | Nonsense mediated decay | - | A0A286YDH2 | CDS 5' incomplete |
| Tut7-207 | ENSMUST00000225576.1 | 2499 | 210aa | Protein coding | - | A0A286YD79 | Gencode basic |
| Tut7-208 | ENSMUST00000225607.1 | 757 | No protein | Processed transcript | - | - | - |
| Tut7-209 | ENSMUST00000225944.1 | 2095 | No protein | Retained intron | - | - | - |
| Tut7-210 | ENSMUST00000225987.1 | 435 | 90aa | Protein coding | - | A0A286YCY9 | CDS 3' incomplete |

The strategy is based on the design of *Tut7-201* transcript,The transcription is shown below



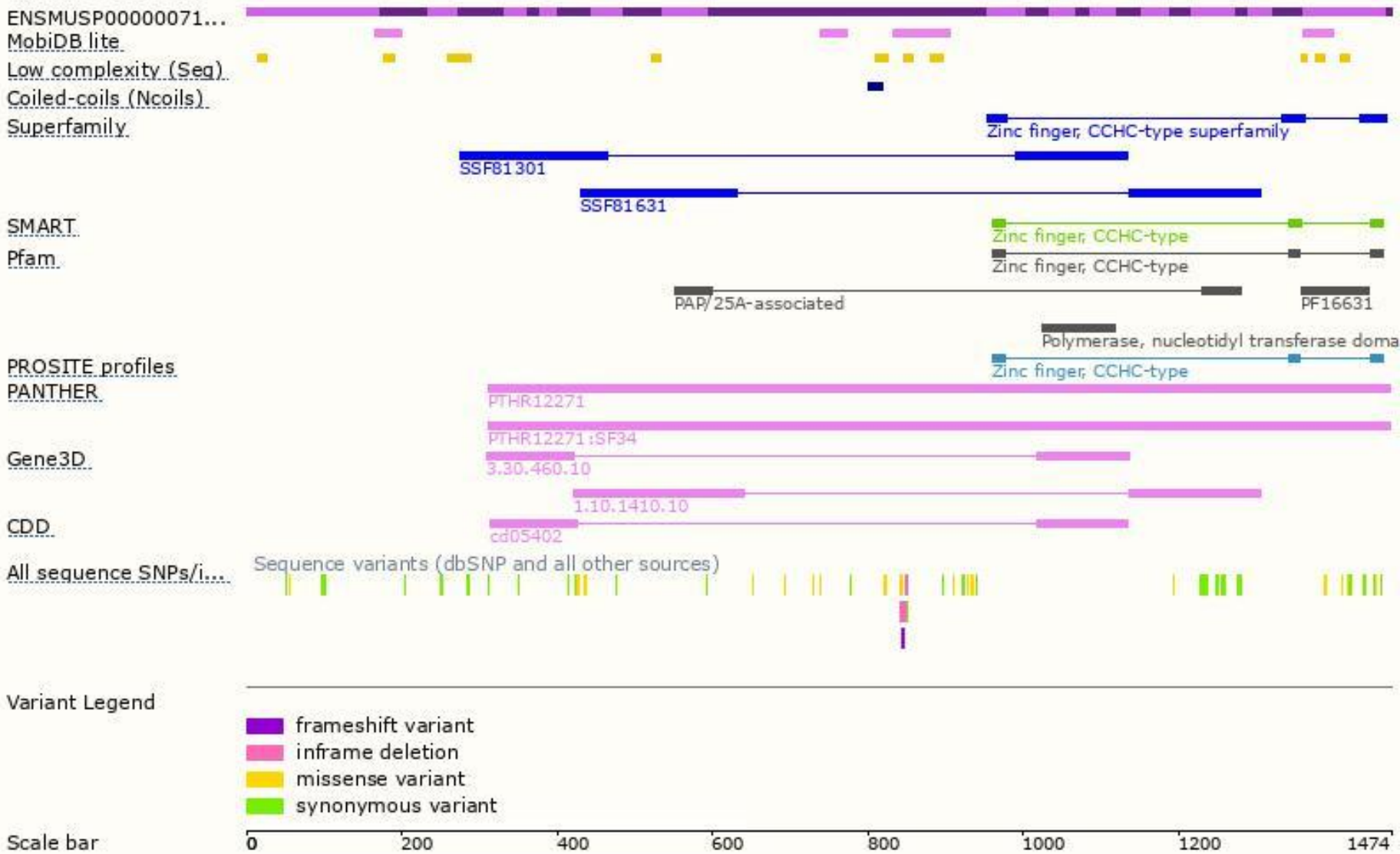
Genomic location distribution



Protein domain



集萃药康
GemPharmatech



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

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