

Tnrc18 Cas9-KO Strategy

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Overview

Target Gene Name

- *Tnrc18*

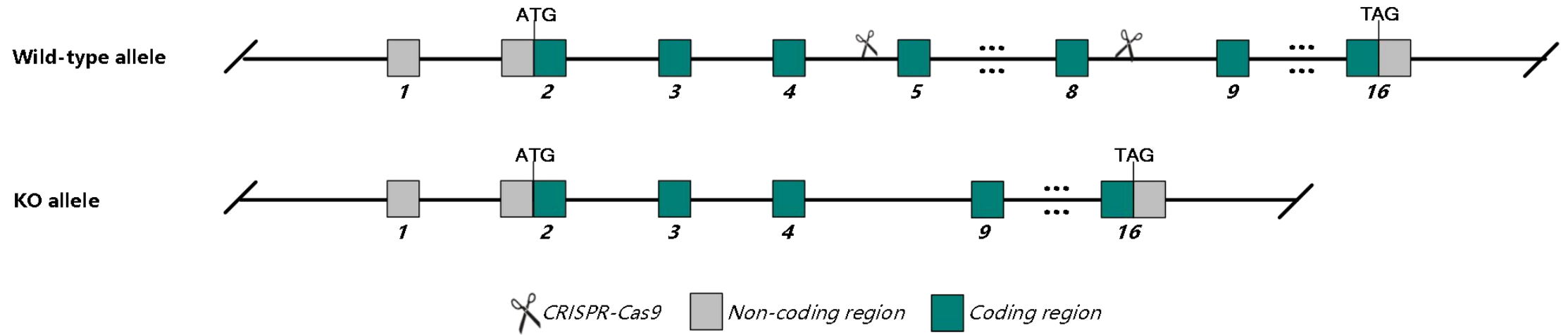
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Tnrc18* gene.

Technical Information

- The *Tnrc18* gene has 7 transcripts. According to the structure of *Tnrc18* gene, exon 5-8 of *Tnrc18*-201 (ENSMUST00000151477.8) is recommended as the knockout region. The region contains 641 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Tnrc18* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Tnrc18 trinucleotide repeat containing 18 [*Mus musculus* (house mouse)]

Gene ID: 231861, updated on 6-Oct-2023

[Download Datasets](#)

Summary

Official Symbol	Tnrc18 provided by MGI
Official Full Name	trinucleotide repeat containing 18 provided by MGI
Primary source	MGI:MGI:3648294
See related	Ensembl:ENSMUSG00000039477 AllianceGenome:MGI:3648294
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	Zfp469; EG381742
Summary	Predicted to enable chromatin binding activity. Predicted to be located in cytosol; mitochondrion; and nucleus. Orthologous to human TNRC18 (trinucleotide repeat containing 18). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in ovary adult (RPKM 24.2), colon adult (RPKM 14.8) and 25 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

Location: 5 G2; 5 81.73 cM

Exon count: 34

See Tnrc18 in [Genome Data Viewer](#)

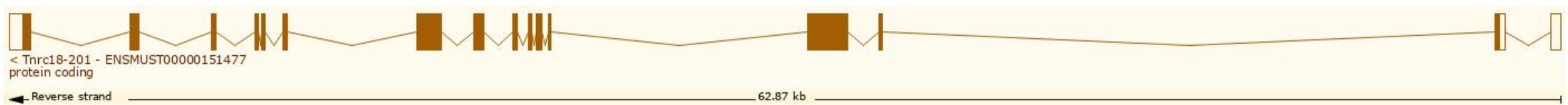
<https://www.ncbi.nlm.nih.gov/gene/231861>

Transcript Information

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

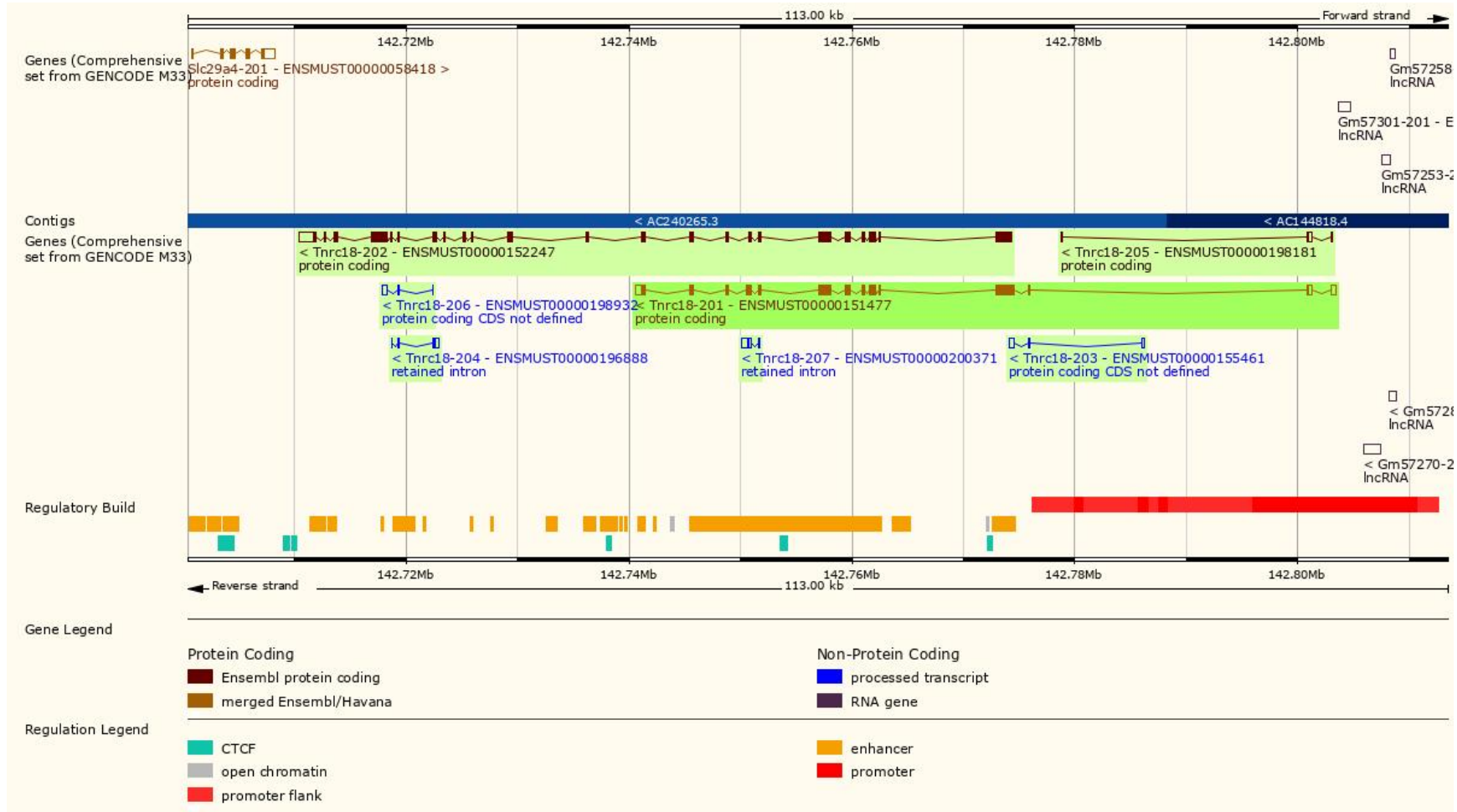
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000152247.8	Tnrc18-202	9342	2673aa	Protein coding		F6Z7L1	Ensembl Canonical TSL:5 CDS 5' incomplete
ENSMUST00000151477.8	Tnrc18-201	6487	1755aa	Protein coding	CCDS19830	D3YV17	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000198181.2	Tnrc18-205	696	114aa	Protein coding		A0A0G2JFH8	TSL:5 CDS 3' incomplete
ENSMUST00000155461.2	Tnrc18-203	712	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000198932.5	Tnrc18-206	600	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000200371.2	Tnrc18-207	830	No protein	Retained intron		-	TSL:3
ENSMUST00000196888.2	Tnrc18-204	647	No protein	Retained intron		-	TSL:3

The strategy is based on the design of *Tnrc18-201* transcript, the transcription is shown below:

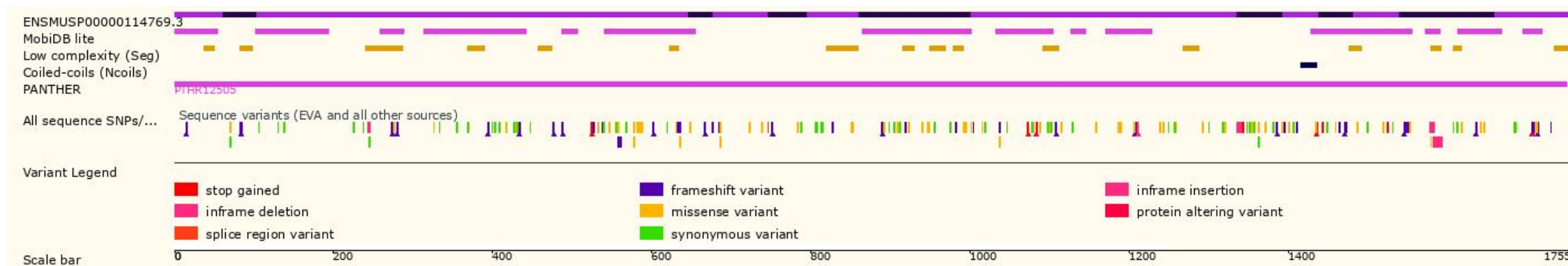


Source: <http://asia.ensembl.org/>

Genomic Information



Protein Information



Important Information

- Since the *Tnrc18*-202 transcript 5' is incomplete, the effect of this strategy on *Tnrc18*-202 transcript is unknown.
- Since the *Tnrc18*-205 transcript 3' is incomplete, the effect of this strategy on *Tnrc18*-205 transcript is unknown.
- This strategy may not affect *Tnrc18*-203, *Tnrc18*-204, *Tnrc18*-206, and *Tnrc18*-207 transcript.
- A part of amino acid sequence (646 aa) will still remain at the N-terminal of *Tnrc18* gene.
- *Tnrc18* is located on Chr 5. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.