

Tec Cas9-KO Strategy

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Project Overview



Project Name

Tec

Project type

Cas9-KO

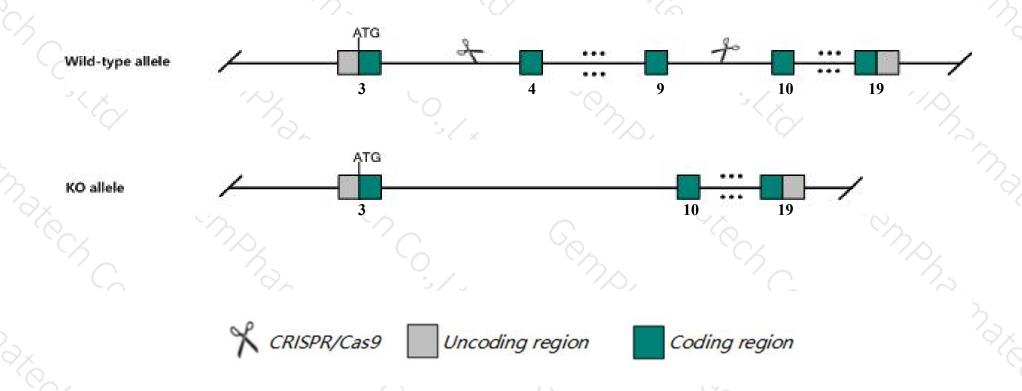
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Tec* gene has 9 transcripts. According to the structure of *Tec* gene, exon4-exon9 of *Tec-201*(ENSMUST00000071944.12) transcript is recommended as the knockout region. The region contains 596bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Tec* gene. The brief process is as follows: CRISPR/Cas9 system were

Notice



- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit a minor reduction in platetet aggregation in response to threshold concentrations of collagen-related peptide or collagen.
- > Transcript Tec-209 CDS 3' is incomplete affected, whether it will be affected is unknown.
- The *Tec* 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)



Tec tec protein tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 21682, updated on 12-Aug-2019

Summary

☆ ?

Official Symbol Tec provided by MGI

Official Full Name tec protein tyrosine kinase provided by MGI

Primary source MGI:MGI:98662

See related Ensembl: ENSMUSG00000029217

Gene type protein coding
RefSeq status VALIDATED

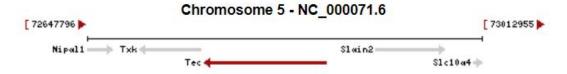
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Expression Ubiquitous expression in placenta adult (RPKM 4.6), spleen adult (RPKM 4.0) and 27 other tissues See more

Orthologs human all



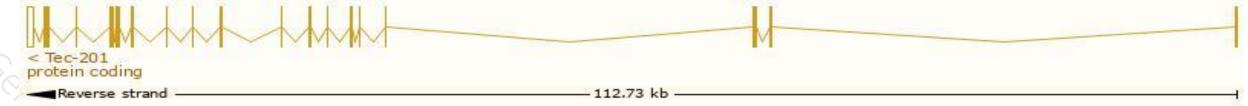
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

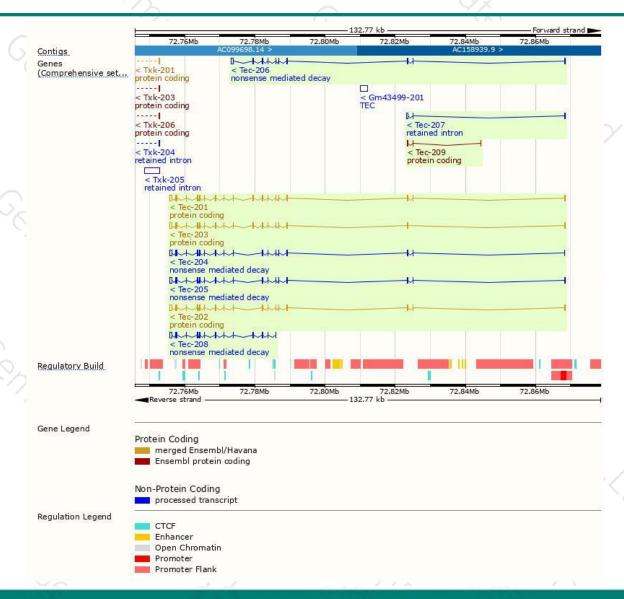
						_1
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000071944.12	2659	630aa	Protein coding	CCDS51516	Q3U436	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000113594.7	2580	630aa	Protein coding	CCDS51516	Q3U436	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000073843.12	2573	608aa	Protein coding	CCDS51515	Q8CFK4	TSL:1 GENCODE basic
ENSMUST00000202547.1	377	<u>44aa</u>	Protein coding	42	A0A0J9YV29	CDS 3' incomplete TSL:3
ENSMUST00000138842.7	2569	<u>100aa</u>	Nonsense mediated decay		A0A0R4J1V5	TSL:1
ENSMUST00000126481.7	2543	<u>184aa</u>	Nonsense mediated decay		D6RJM5	TSL:5
ENSMUST00000155342.7	2117	<u>68aa</u>	Nonsense mediated decay	ŞE.	F6W1T9	CDS 5' incomplete TSL:2
ENSMUST00000149533.7	1561	<u>100aa</u>	Nonsense mediated decay	i i	A0A0R4J1V5	TSL:1
ENSMUST00000150193.1	621	No protein	Retained intron	15	₹á	TSL:2
	ENSMUST00000113594.7 ENSMUST00000073843.12 ENSMUST000000202547.1 ENSMUST00000138842.7 ENSMUST00000126481.7 ENSMUST00000155342.7 ENSMUST00000149533.7	ENSMUST00000113594.7 2580 ENSMUST00000073843.12 2573 ENSMUST000000202547.1 377 ENSMUST00000138842.7 2569 ENSMUST00000126481.7 2543 ENSMUST00000155342.7 2117 ENSMUST00000149533.7 1561	ENSMUST00000113594.7 2580 630aa ENSMUST00000073843.12 2573 608aa ENSMUST000000202547.1 377 44aa ENSMUST00000138842.7 2569 100aa ENSMUST00000126481.7 2543 184aa ENSMUST00000155342.7 2117 68aa ENSMUST00000149533.7 1561 100aa	ENSMUST00000071944.12 2659 630aa Protein coding ENSMUST00000113594.7 2580 630aa Protein coding ENSMUST00000073843.12 2573 608aa Protein coding ENSMUST00000202547.1 377 44aa Protein coding ENSMUST00000138842.7 2569 100aa Nonsense mediated decay ENSMUST00000126481.7 2543 184aa Nonsense mediated decay ENSMUST00000155342.7 2117 68aa Nonsense mediated decay ENSMUST00000149533.7 1561 100aa Nonsense mediated decay	ENSMUST00000071944.12 2659 630aa Protein coding CCDS51516 ENSMUST00000113594.7 2580 630aa Protein coding CCDS51516 ENSMUST00000073843.12 2573 608aa Protein coding CCDS51515 ENSMUST00000202547.1 377 44aa Protein coding - ENSMUST00000138842.7 2569 100aa Nonsense mediated decay - ENSMUST00000126481.7 2543 184aa Nonsense mediated decay - ENSMUST00000155342.7 2117 68aa Nonsense mediated decay - ENSMUST00000149533.7 1561 100aa Nonsense mediated decay -	ENSMUST00000071944.12 2659 630aa Protein coding CCDS51516 Q3U436 ENSMUST00000113594.7 2580 630aa Protein coding CCDS51516 Q3U436 ENSMUST00000073843.12 2573 608aa Protein coding CCDS51515 Q8CFK4 ENSMUST00000202547.1 377 44aa Protein coding - A0A0J9YV29 ENSMUST00000138842.7 2569 100aa Nonsense mediated decay - A0A0R4J1V5 ENSMUST00000126481.7 2543 184aa Nonsense mediated decay - D6RJM5 ENSMUST00000155342.7 2117 68aa Nonsense mediated decay - A0A0R4J1V5 ENSMUST00000149533.7 1561 100aa Nonsense mediated decay - A0A0R4J1V5

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



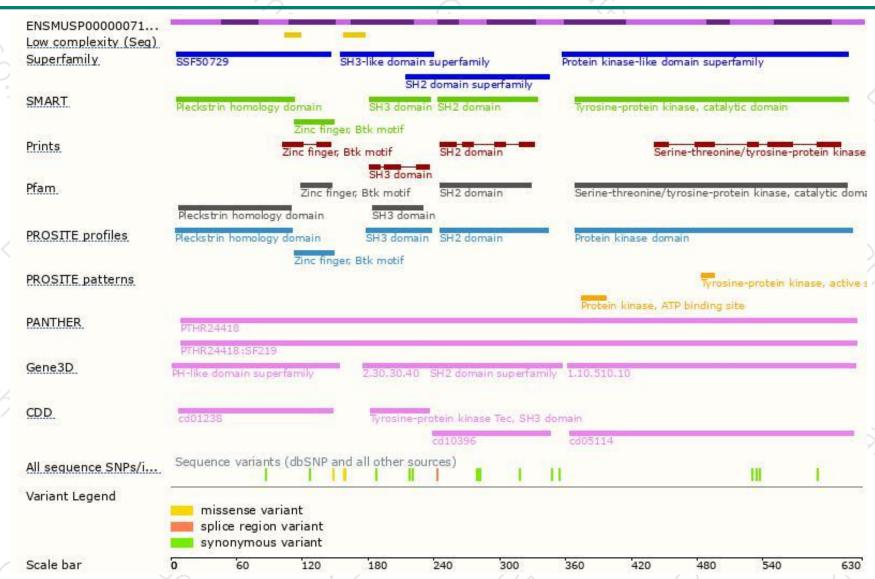
Genomic location distribution





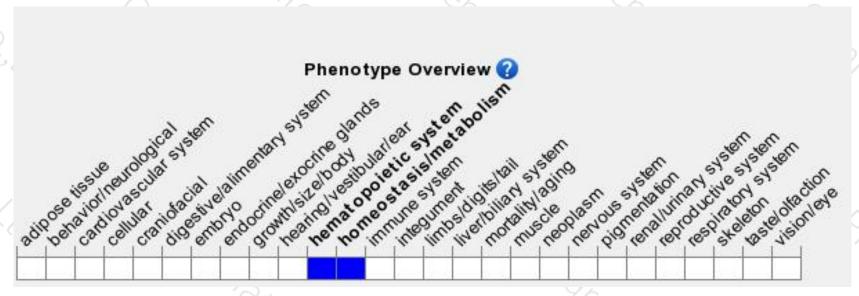
Protein domain





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 knock-out allele exhibit a minor reduction in platetet aggregation in response to threshold concentrations of collagen-related peptide or collagen.



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





