

Tac1 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

Design Date:

2020-3-30

Project Overview

Project Name

Tac1

Project type

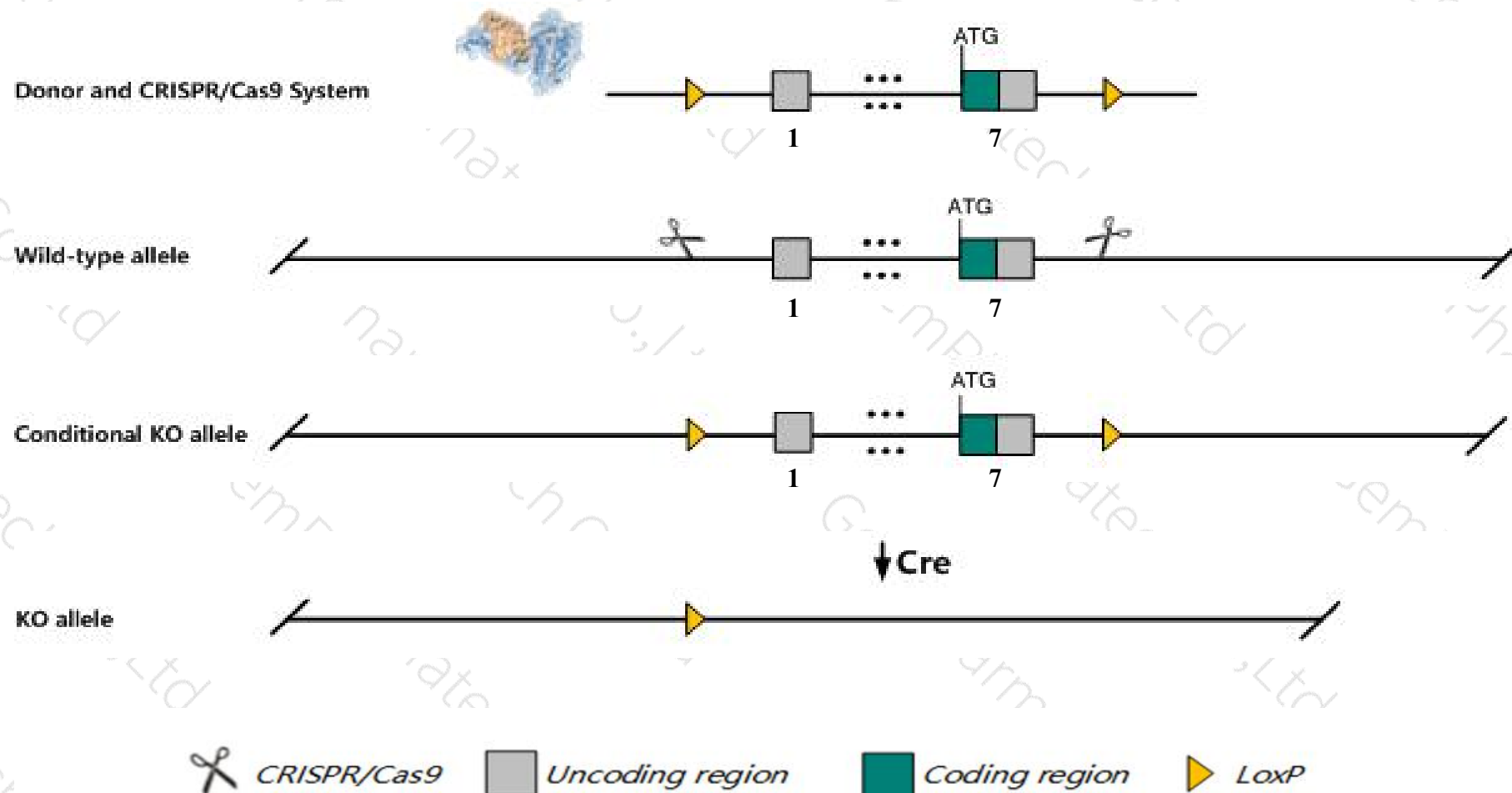
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tac1* gene. The schematic diagram is as follows:



Technical routes

- The *Tac1* gene has 5 transcripts. According to the structure of *Tac1* gene, exon1-exon7 of *Tac1*-205 (ENSMUST00000185187.7) 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 *Tac1* 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.

Notice

- The *Tac1* gene is located on the Chr6. 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)

Tac1 tachykinin 1 [Mus musculus (house mouse)]

Gene ID: 21333, updated on 19-Mar-2019

Summary



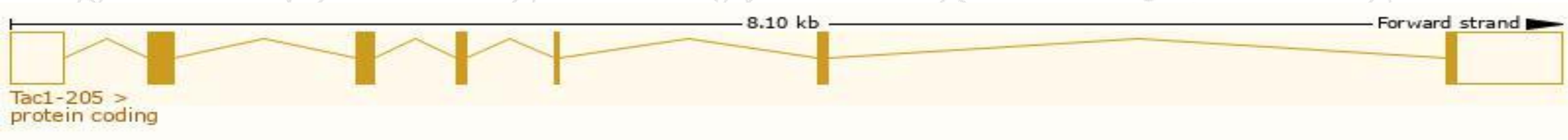
Official Symbol	Tac1 provided by MGI
Official Full Name	tachykinin 1 provided by MGI
Primary source	MGI:MGI:98474
See related	Ensembl:ENSMUSG00000061762
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930528L02Rik, NK-1, NK1, Nkna, PPT-A, PPTA, SP
Expression	Biased expression in CNS E18 (RPKM 16.9), whole brain E14.5 (RPKM 7.7) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

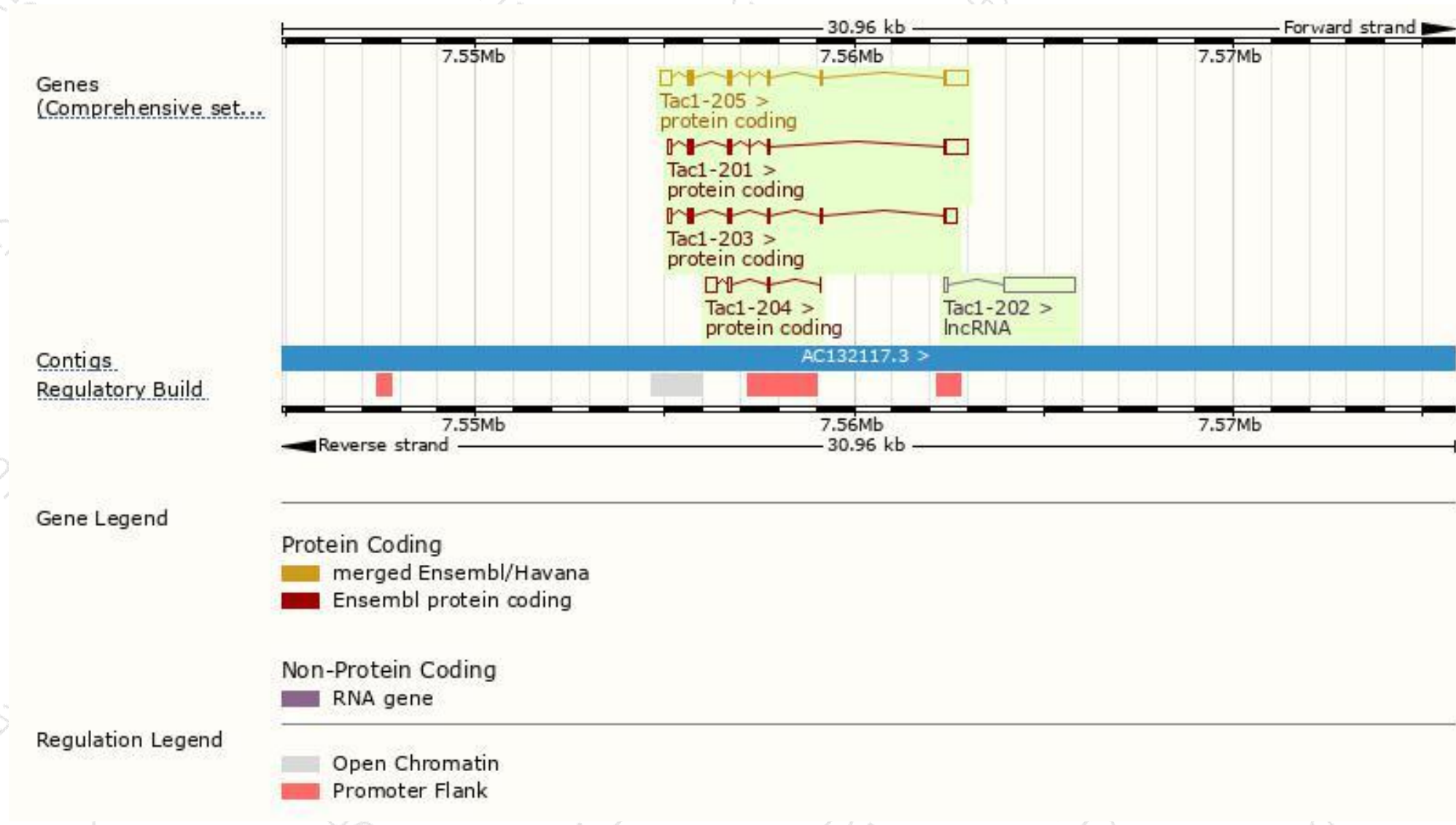
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tac1-205	ENSMUST00000185187.7	1230	130aa	Protein coding	CCDS19906	P41539 Q149W7	TSL:1 GENCODE basic APPRIS P1
Tac1-203	ENSMUST00000184986.1	691	115aa	Protein coding	CCDS80486	B7ZMQ2 P41539	TSL:1 GENCODE basic
Tac1-201	ENSMUST00000090679.8	980	112aa	Protein coding	-	A0A0A0MQA8	TSL:5 GENCODE basic
Tac1-204	ENSMUST00000185130.1	434	15aa	Protein coding	-	V9GX83	CDS 3' incomplete TSL:5
Tac1-202	ENSMUST00000184481.1	1975	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Tac1-205* transcript,The transcription is shown below



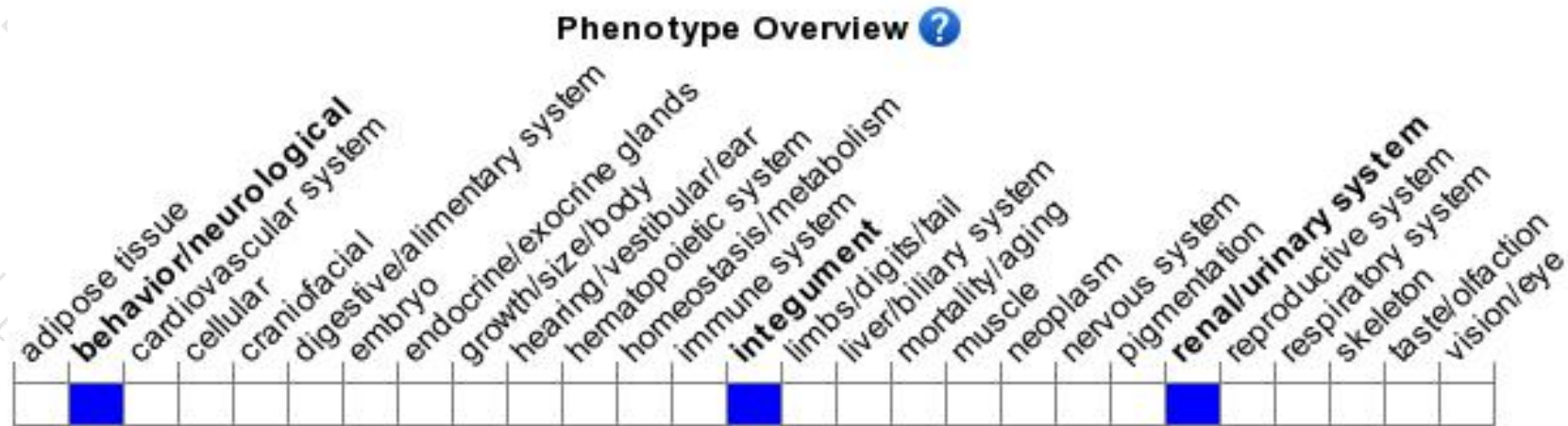
Genomic location distribution



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/>).

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

Tel: 400-9660890

