

***Tnk1* Cas9-CKO Strategy**

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Project Overview

Project Name

Tnk1

Project type

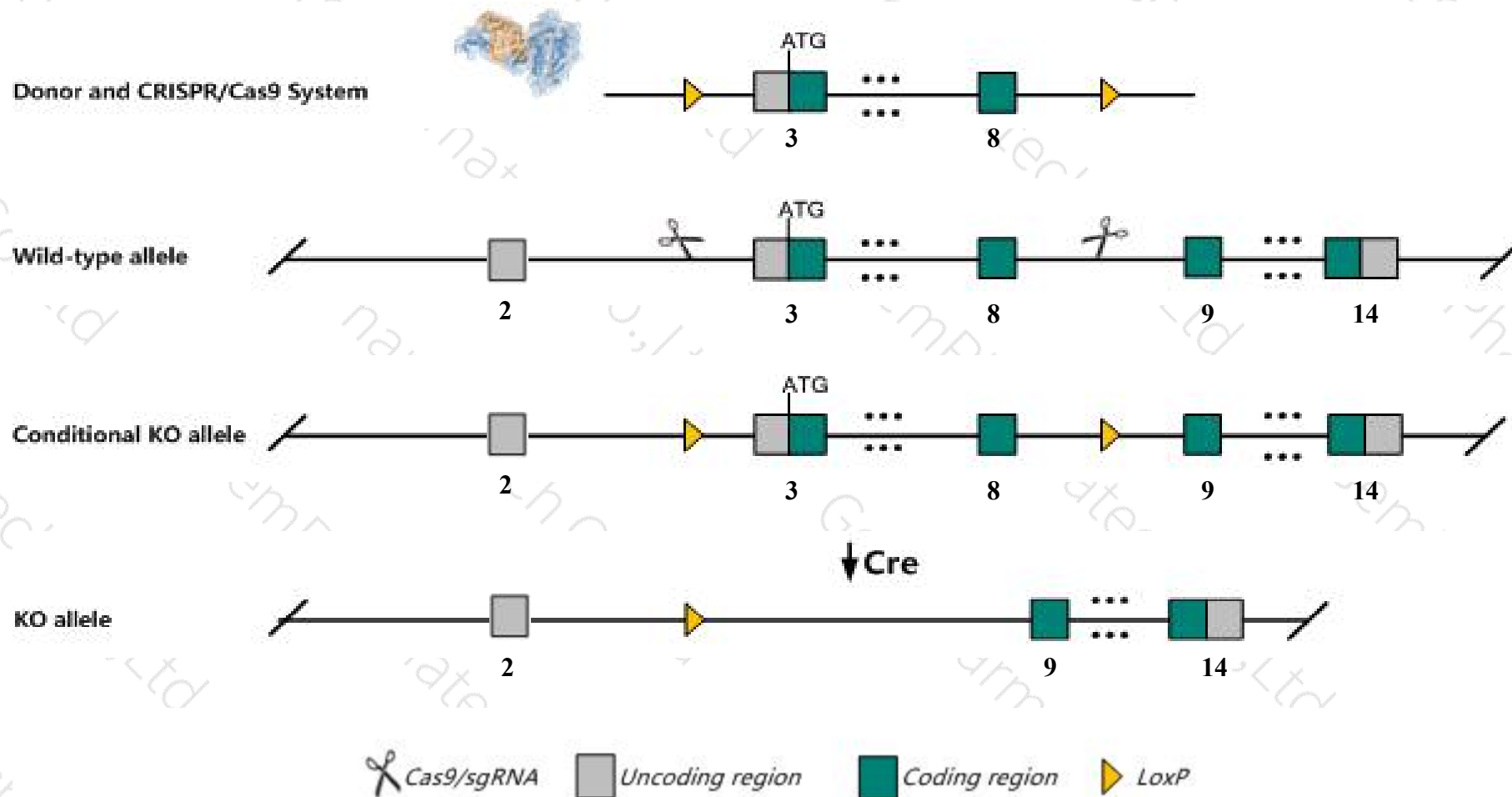
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Tnkl* gene has 5 transcripts. According to the structure of *Tnkl* gene, exon3-exon8 of *Tnkl*-201 (ENSMUST00000001626.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tnkl* 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 either heterozygous or homozygous for a knock-out allele develop spontaneous tumors, including lymphomas and carcinomas, at high rates.
- The *Tnkl* gene is located on the Chr11. 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)

Tnk1 tyrosine kinase, non-receptor, 1 [*Mus musculus* (house mouse)]

Gene ID: 83813, updated on 4-Jun-2020

Summary

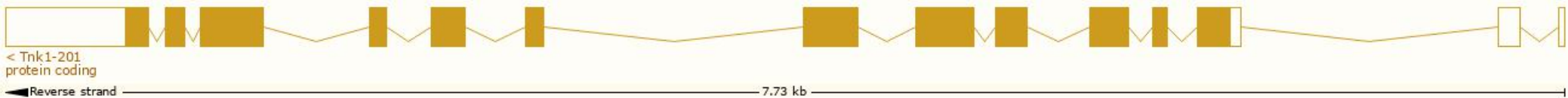
Official Symbol	Tnk1 provided by MGI
Official Full Name	tyrosine kinase, non-receptor, 1 provided by MGI
Primary source	MGI:MGI:1930958
See related	Ensembl:ENSMUSG000000001583
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Kos1; Tnk1a; Tnk1b
Expression	Ubiquitous expression in colon adult (RPKM 21.8), large intestine adult (RPKM 15.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

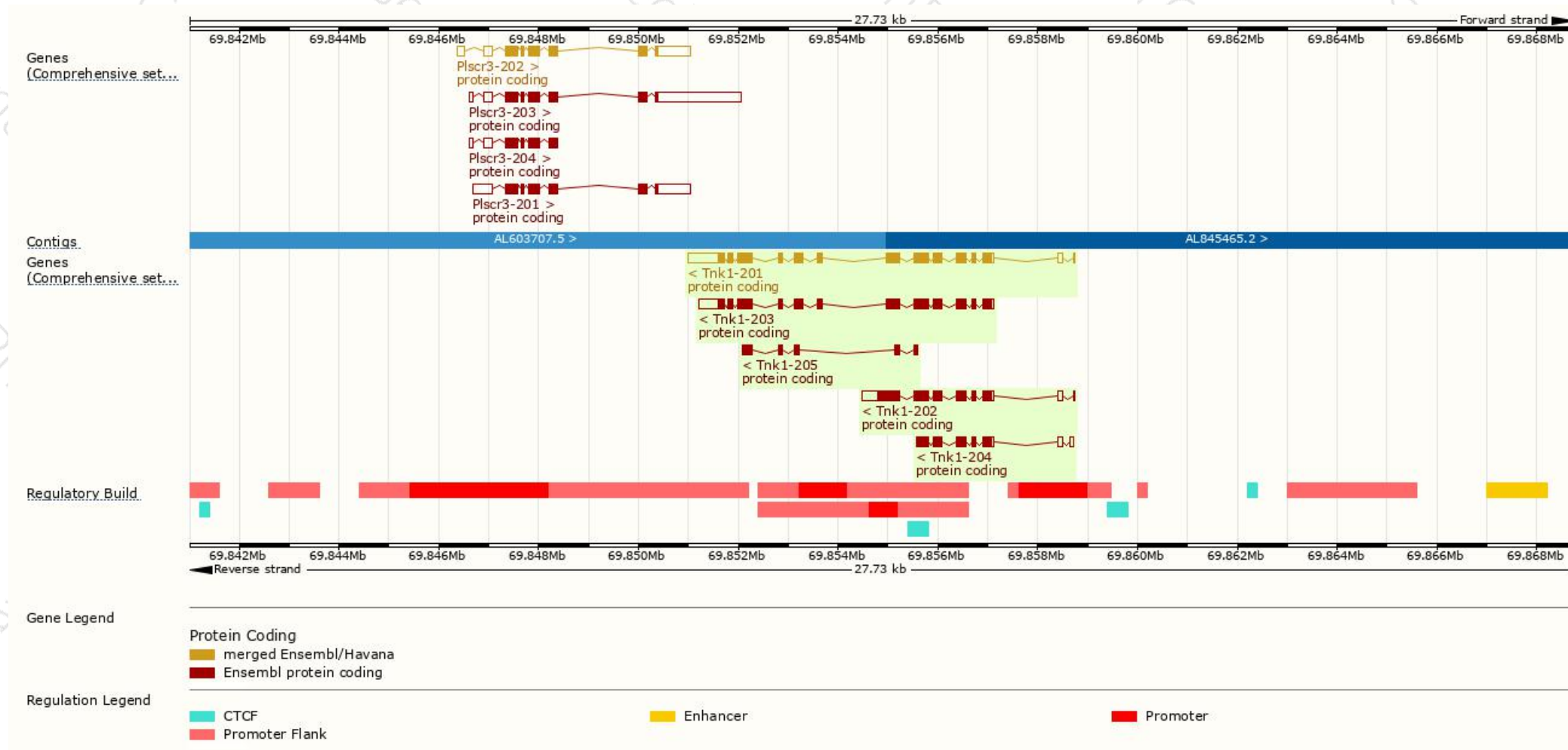
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnk1-201	ENSMUST00000001626.9	2778	666aa	Protein coding	CCDS24917	Q99ML2	TSL:1 GENCODE basic APPRIS P2
Tnk1-203	ENSMUST00000108628.7	2450	671aa	Protein coding	-	Q5F2B4	TSL:5 GENCODE basic APPRIS ALT2
Tnk1-202	ENSMUST00000108626.7	1798	434aa	Protein coding	-	Q99ML2	TSL:1 GENCODE basic
Tnk1-204	ENSMUST00000125571.1	1021	268aa	Protein coding	-	A2ARN2	CDS 3' incomplete TSL:3
Tnk1-205	ENSMUST00000156507.1	560	186aa	Protein coding	-	Q5F2B6	CDS 5' and 3' incomplete TSL:3

The strategy is based on the design of *Tnk1-201* transcript,the transcription is shown below:



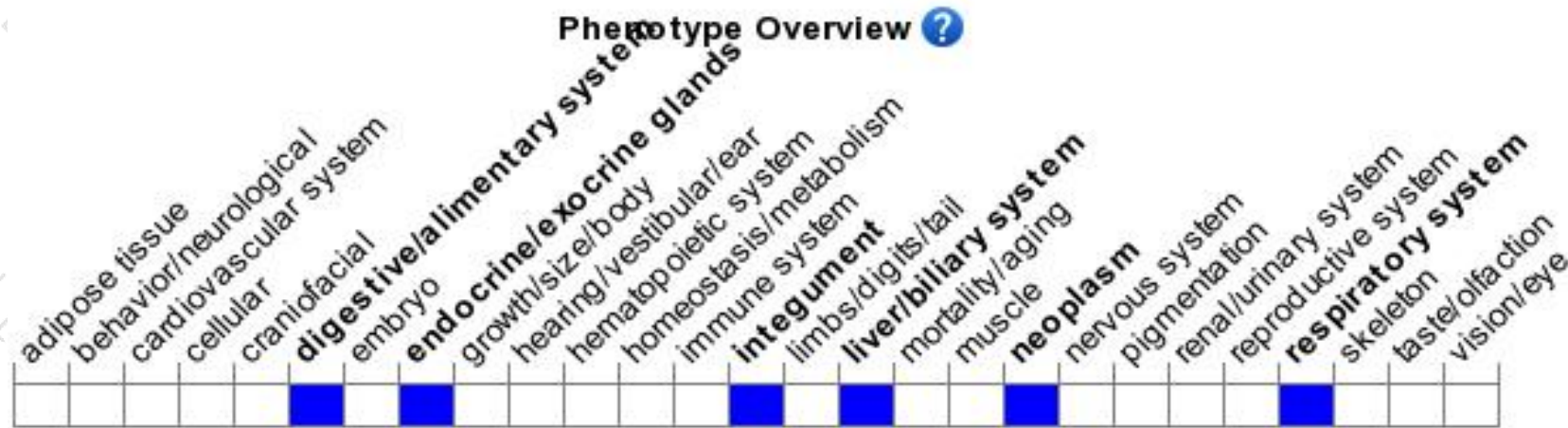
Genomic location distribution



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 either heterozygous or homozygous for a knock-out allele develop spontaneous tumors, including lymphomas and carcinomas, at high rates.

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

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