

Tnk1 Cas9-KO Strategy

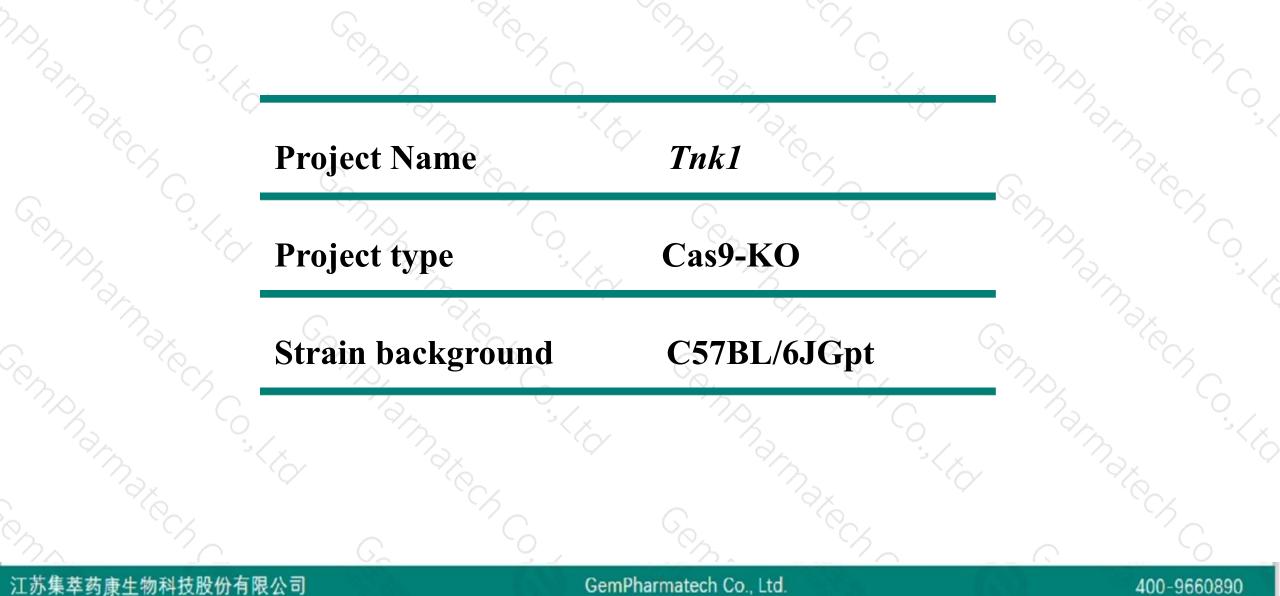
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Reviewer: Ruiuri Zhang

Design Date: 2020-6-16

Project Overview

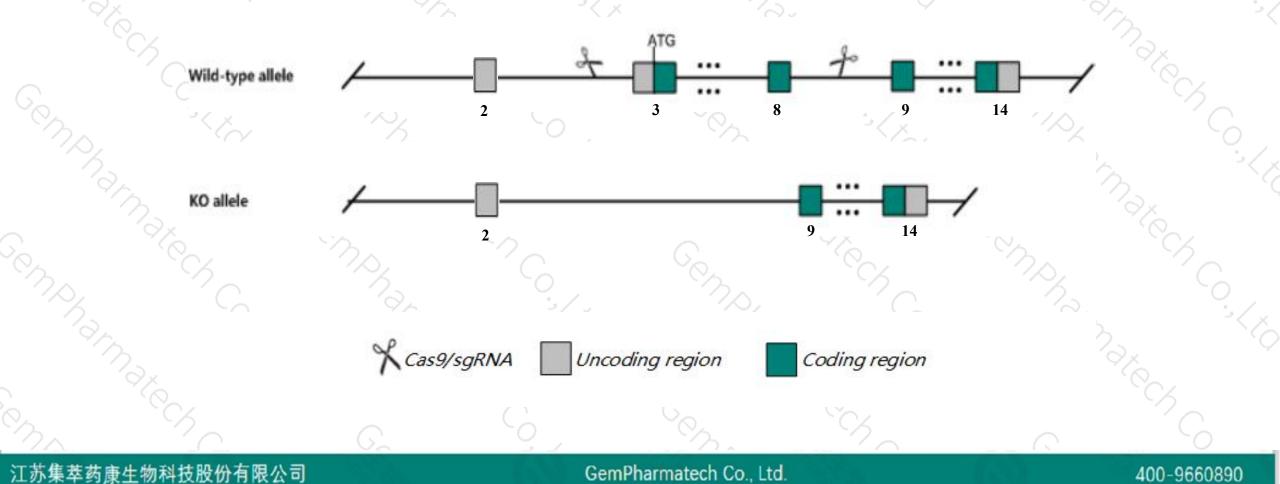




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Tnk1* gene. The schematic diagram is as follows:





- The *Tnk1* gene has 5 transcripts. According to the structure of *Tnk1* gene, exon3-exon8 of *Tnk1-201* (ENSMUST0000001626.9) 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 *Tnk1* gene. The brief process is as follows: CRISPR/Cas9 system v

- 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 *Tnk1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Notice

Gene information (NCBI)



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

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

- Summary

Of	ficial Symbol	Tnk1 provided by MGI						
Offic	ial Full Name	tyrosine kinase, non-receptor, 1 pro	wided by MGI					
Pri Pri	imary source	MGI:MGI:1930958						
~ 2	See related	Ensembl:ENSMUSG0000001583						
	Gene type	protein coding						
F	lefSeq status	VALIDATED						
	Organism	Mus musculus						
	Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea;						
0		Muridae; Murinae; Mus; Mus						
A A	lso known as	Kos1; Tnk1a; Tnk1b						
	Expression	Ubiquitous expression in colon adu	It (RPKM 21.8), large intestine ad	dult (RPKM 15.1) and 28 other tiss	ues See more			
	Orthologs	human all						
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400-9660890

Transcript information (Ensembl)



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

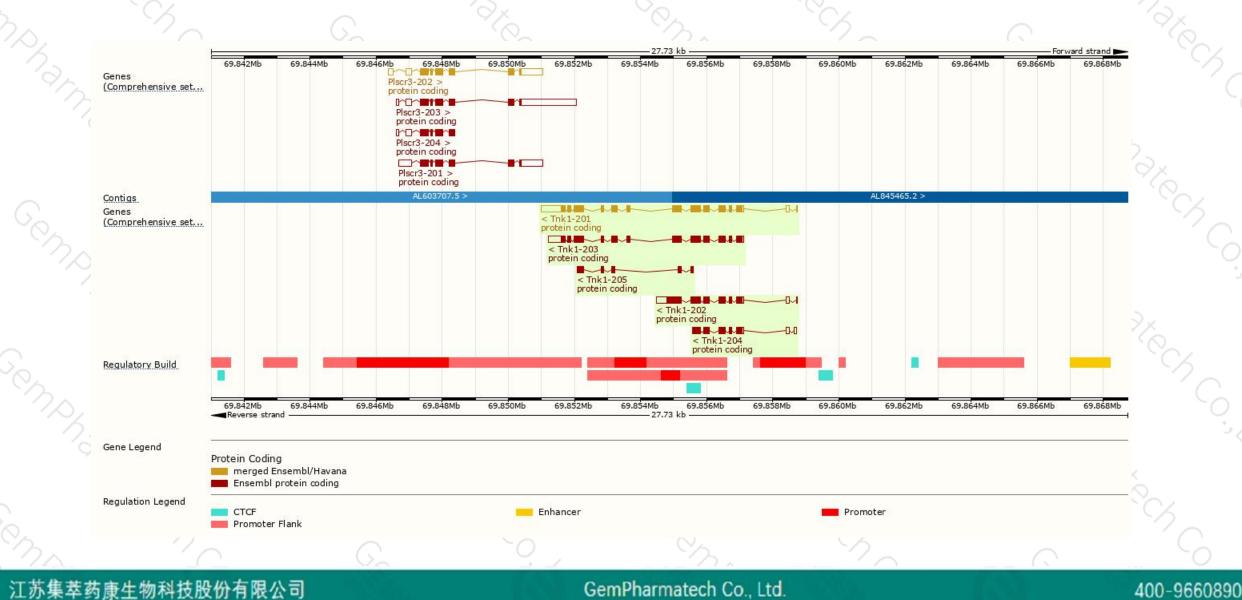
Name 🖕	Transcript ID	bp 🍦	Protein 🖕	Biotype 💧	CCDS 🖕	UniProt 🖕	Flags	
Tnk1-201	ENSMUST0000001626.9	2778	<u>666aa</u>	Protein coding	<u>CCDS24917</u> 교	<u>Q99ML2</u> 교	TSL:1 GENCODE basic APPRIS P2	
Tnk1-203	ENSMUST00000108628.7	2450	<u>671aa</u>	Protein coding		<u>Q5F2B4</u> ₽	TSL:5 GENCODE basic APPRIS ALT2	
Tnk1-202	ENSMUST00000108626.7	1798	<u>434aa</u>	Protein coding		<u>Q99ML2</u> 교	TSL:1 GENCODE basic	
Tnk1-204	ENSMUST00000125571.1	1021	<u>268aa</u>	Protein coding		A2ARN2	CDS 3' incomplete TSL:3	
Tnk1-205	ENSMUST00000156507.1	560	<u>186aa</u>	Protein coding	-	<u>Q5F2B6</u> &	CDS 5' and 3' incomplete TSL:3	

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

< Tnk1-201

Genomic location distribution





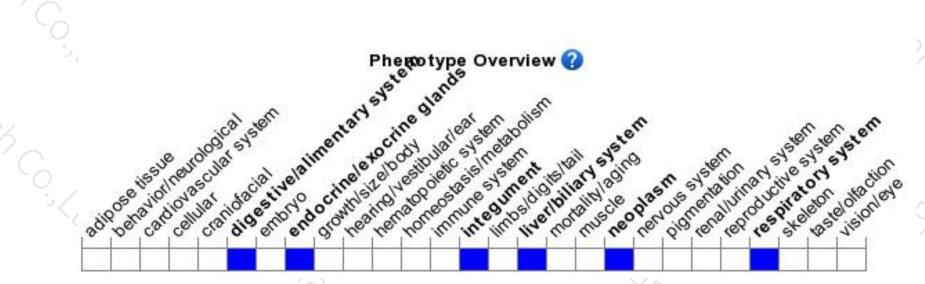
Protein domain



702	20			- Chr	$\sim \gamma_{c}$		
narm-	ENSMUSP00000001 MobiDB lite Low complexity (Seg) Superfamily	-	Protein kinase-like domain superfamily		SH3-like domain super	amily	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	SMART		Tyrosine-protein kinase, catalytic domai	in			د .
	Prints Pfam			Serine-threonine/tyrosine-protein kinase	e, catalytic domain		
	PROSITE profiles		Serine-threonine/tyrosine-protein kinas Protein kinase domain	se, catalytic domain			
G.	PROSITE patterns		Protein kinase, ATP binding site	Tyrosine-protein kinase, active site	SH3 domain		°C/S
	PANTHER	PTHR24418					
n n n n n n n n n n n n n n n n n n n	Gene3D	PTHR24418;SF263	200.20 1.10.510.	.10	2,30,30.40		
	CDD	cd09539					
	All sequence SNPs/i	Sequence variants (dbSNP and	all other sources)	CHO: 201-103	TOT T	1	
	Variant Legend	inframe deletion	-	missense variant		synonymous variant	
noparty.	Scale bar	0 iso	120 180	240 300	360 420	480 540	600 666
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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. Tel: 400-9660890



