Tns2 Cas9-KO Strategy Rondhamater Co. Ltd Companyation and the second se

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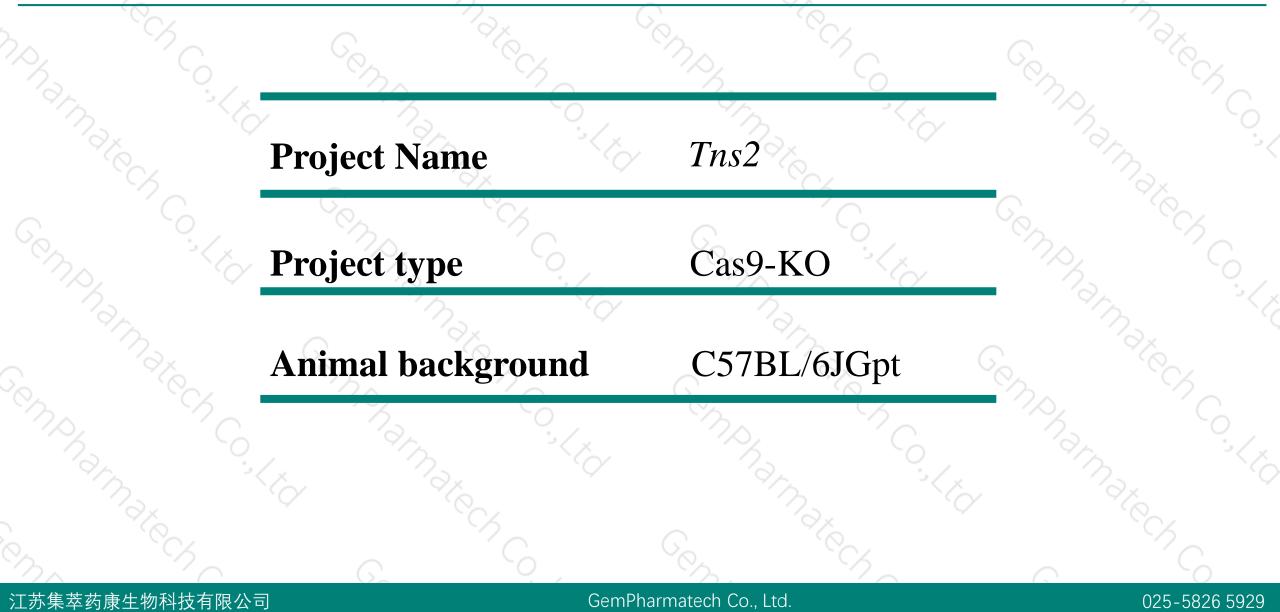
Designer:Daohua Xu Enphamaten C. It Thate Chost

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Project Overview



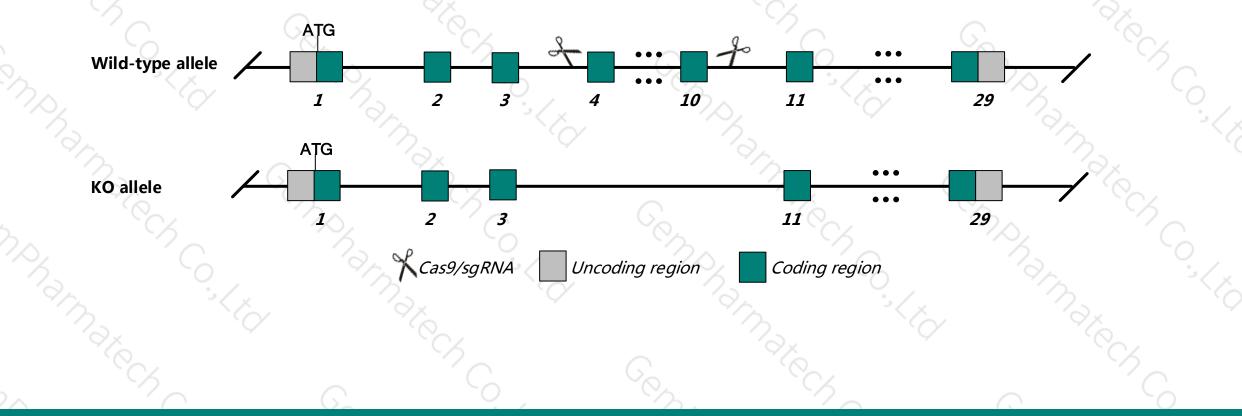


Conditional Knockout strategy



025-5826 5929

This model will use CRISPR/Cas9 technology to edit the *Tns2* gene. The schematic diagram is as follows:



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- The Tns2 gene has 9 transcripts. According to the structure of *Tns2* gene, exon4-exon10 of *Tns2*-202 transcript is recommended as the knockout region. The region contains the 539bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tns2* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice



- According to the existing MGI data, Affected mice homozygous for a spontaneous deletion show reduced female fertility, increased blood urea nitrogen, low hematocrit, proteinuria, hypoproteinemia, hypercholesterolemia, small kidneys with a yellowish granular surface, glomerular lesions and premature death; some develop systemic edema.
- The *Tns2* gene is located on the Chr15. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)



Tns2 tensin 2 [Mus musculus (house mouse)]

Gene ID: 209039, updated on 31-Jan-2019

Summary

2 ?

| ?

See Tns2 in Genome Data Viewer

Official Symbol	Tns2 provided by MGI
Official Full Name	tensin 2 provided by MGI
Primary source	MGI:MGI:2387586
See related	Ensembl:ENSMUSG0000037003
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	nep; nph; Tenc1; C1-ten
Expression	Broad expression in lung adult (RPKM 60.8), subcutaneous fat pad adult (RPKM 26.0) and 17 other tissues See more

Orthologs <u>human</u> all

Genomic context

Location: 15 F2; 15 57.29 cM

Exon count: 31

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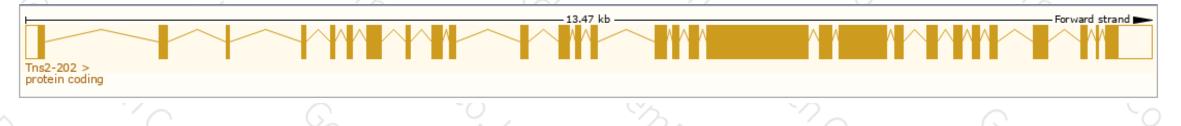
Transcript information (Ensembl)



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

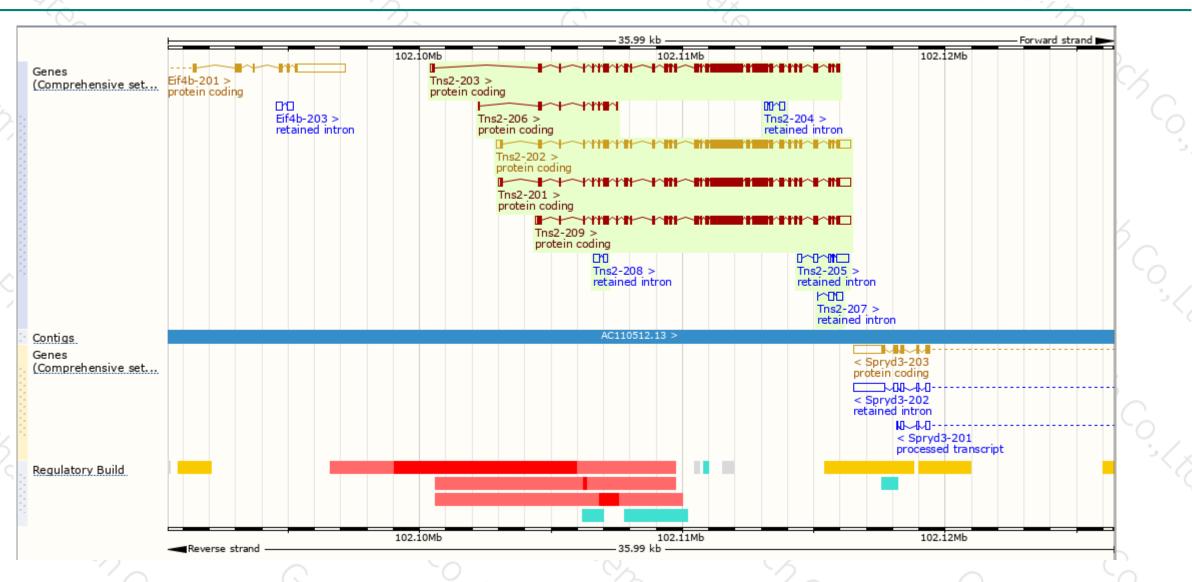
	Name 🖕	Transcript ID 💧	bp 🌲	Protein 🖕	Biotype 🍦	CCDS	UniProt 🖕	Flags 🖕	1	
-	Tns2-202	ENSMUST00000169627.8	4761	<u>1400aa</u>	Protein coding	<u>CCDS37224</u> 교	<u>Q8CGB6</u> 교	TSL:1 GENCODE basic APPRIS P2		
	Tns2-201	ENSMUST0000046144.9	4718	<u>1407aa</u>	Protein coding	-	<u>Q8CGB6</u> 교	TSL:5 GENCODE basic APPRIS ALT2		
	Tns2-209	ENSMUST0000230474.1	4637	<u>1392aa</u>	Protein coding	-	A0A2R8VHQ0	GENCODE basic APPRIS ALT2		
	Tns2-203	ENSMUST00000228958.1	4268	<u>1400aa</u>	Protein coding	-	<u>Q8CGB6</u> r	CDS 3' incomplete		
	Tns2-206	ENSMUST00000229592.1	544	<u>168aa</u>	Protein coding	-	A0A2R8W6Z5@	CDS 3' incomplete	-	
	Tns2-205	ENSMUST00000229097.1	870	No protein	Retained intron	-	-	-	-	
	Tns2-207	ENSMUST00000229800.1	468	No protein	Retained intron	-	-	-		
	Tns2-208	ENSMUST00000229908.1	365	No protein	Retained intron	-	-	-		
	Tns2-204	ENSMUST00000229035.1	359	No protein	Retained intron	-	-	-		

The strategy is based on the design of *Tns2*-202 transcript, The transcription is shown below



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Genomic location distribution



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Protein domain



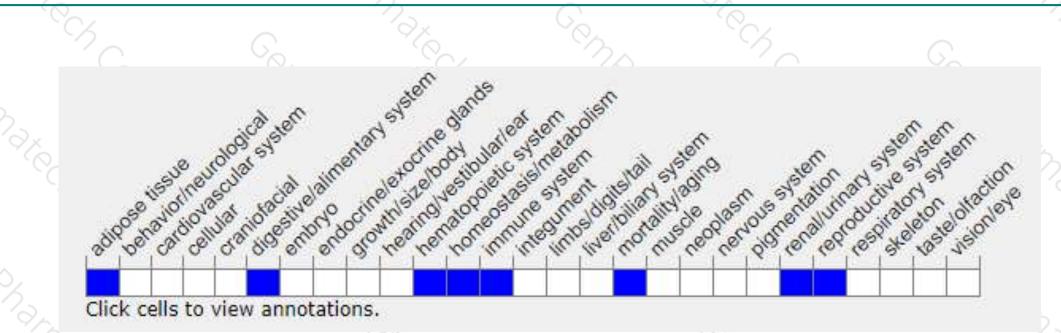
	-7_	G	~ Go	5	5		\frown	97	
	ENSMUSP00000129 MobiDB lite				_				2
	Low complexity (Seq)		-						20
	Conserved Domains								
	minipancie	PTHR12305 PTHR12305:SF58							
	. Superfamily domains	SSF57889	SSF49562				SH2 domain super	family	
		Protein-tyrosine pho	sphatase-like					SSF50729	
	SMART domains		Tensin phosphatase, C2 domain				SH2 domain	PTB/PI domain	
	24 (A)	Protein kinase C-like, phorbol est	er/diacylglycerol-binding domain						5
	Pfam domain		Tensin phosphatase, C2 domain				SH2 domain	Tensin/EPS8 phosph	0
$\sim \sim $									0
	PROSITE profiles	Tensin-type phospha					SH2 domain		31
			Tensin phosphatase, C2 domain						
	PROSITE patterns	Protein kinase C-like, phorbol est Protein kinase C-like, phorbol est							
	Gene3D	3.30.60.20 Protein-tyrosine pho						PH-like domain super	
		5.50.60.20 Protein-tyrosine pro	2.60.40.1110				SH2 domain super		
	All second collar/	Sequence variants (dbSNP and al					onz domain super	Tarriny	\bigcirc
	All sequence SNPs/i							1	0
		I				I			3/
	Variant Legend	inframe deletion		_	missense variant				
		splice region variant			synonymous variant				
	Scale bar	o 200	400	600	800	1000	1200	1400	

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Mouse phenotype description(MGI)





According to the existing MGI data, Affected mice homozygous for a spontaneous deletion show reduced female fertility, increased blood urea nitrogen, low hematocrit, proteinuria, hypoproteinemia, hypercholesterolemia, small kidneys with a yellowish granular surface, glomerular lesions and premature death; some develop systemic edema.

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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





