

Nek2 Cas9-KO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2022-8-23

Overview

Target Gene Name

• Nek2

Project Type

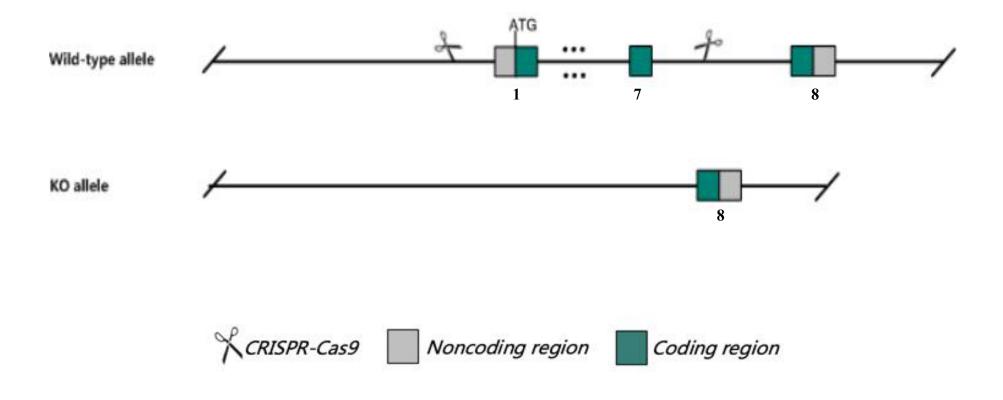
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy

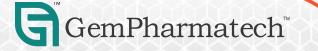


Schematic representation of CRISPR-Cas9 engineering used to edit the Nek2 gene.

GemPharmatech

Technical Information

- The *Nek2* gene has 4 transcripts. According to the structure of *Nek2* gene, exon1exon7 of *Nek2*-201 (ENSMUST0000027931.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Nek2* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



Gene Information

Nek2 NIMA (never in mitosis gene a)-related expressed kinase 2 [Mus musculus (house mouse)]

Gene ID: 18005, updated on 12-Jul-2022

 Summary 		\$
Official Symbol	Nek2 provided by MGI	
Official Full Name	NIMA (never in mitosis gene a)-related expressed kinase 2 provided byMGI	
Primary source	MGI:MGI:109359	
See related	Ensembl:ENSMUSG0000026622	
Gene type	protein coding	
RefSeq status	VALIDATED	
Organism	Mus musculus	
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia	i;
	Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus	
Also known as	AA617254, C77054	
Expression	Broad expression in testis adult (RPKM 25.4), CNS E11.5 (RPKM 10.9) and 15 other tissuesSee more	
Orthologs	human all	

Source: https://www.ncbi.nlm.nih.gov/



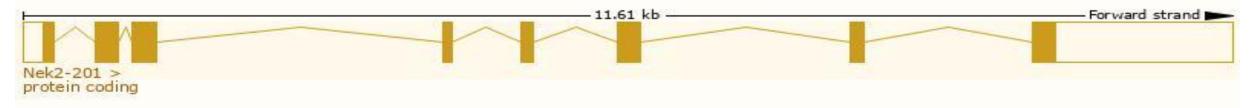
\$?

Transcript Information

The gene has 4 transcripts, all transcripts are shown below:

Transcript ID	Name 🍵	bp 👘	Protein	Biotype	CCDS	UniProt Match		Flags		\$	
ENSMUST0000027931.8	Nek2-201	3227	<u>443aa</u>	Protein coding	CCDS15623@	<u>035942</u>	Ensembl Canonical	GENCODE basic	APPRIS P1	TSL:1	
ENSMUST00000136733.2	Nek2-203	452	No protein	Processed transcript			TSL:3				
ENSMUST00000126446.8	Nek2-202	2044	No protein	Retained intron		53 <u>1</u> %		TSL:2			
ENSMUST00000150839.2	Nek2-204	767	No protein	Retained intron		1.00		TSL:3			

The strategy is based on the design of Nek2-201 transcript, the transcription is shown below:

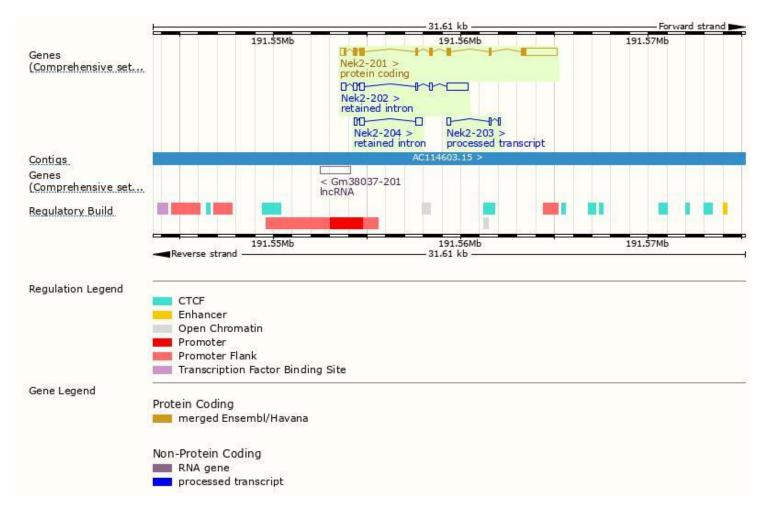


Source: https://www.ensembl.org



Genomic Information

GemPharmatech[™]



Source: : https://www.ensembl.org

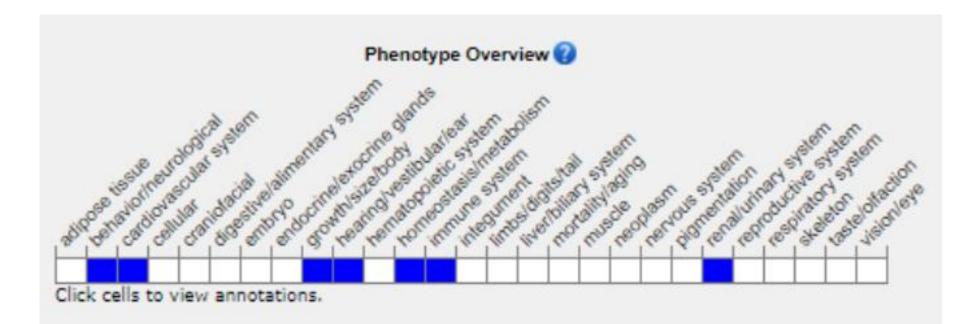
Protein Information

ENSMUSP00000027 MobiDB lite Low complexity (Seg)								-		1		
Coiled-coils (Ncoils) Superfamily SMART	Contraction of the local division of the loc	to an	domain sup	erfamily				1	* <u> </u>			
Pfam	and the second se	kinase do	107204									
PROSITE profiles		kinase do kinase do	1289-256-11									
PROSITE patterns		Serine/threonine-protein kinase, active site										
PANTHER	PTHR448	99										
Gene3D	PTHR445	0,20	10.10									
CDD.	cd08217	0.27.000044	10,10					-				
All sequence SNPs/i	Sequenc	e variant	s (dbSNP a	ind all oth	er sources)	(in		11	1.1	0.0		
Variant Legend	📕 spli		riant 1 variant 5 variant						111.			30
Scale bar	0	40	80	120	160	200	240	280	320	360	400	443

Source: : https://www.ensembl.org

GemPharmatech

Mouse Phenotype Information (MGI)



Source: https://www.informatics.jax.org

GemPharmatech

Important Information

- *Nek2* is located on Chr1. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

