

# **Dnajc19** Cas9-KO Strategy

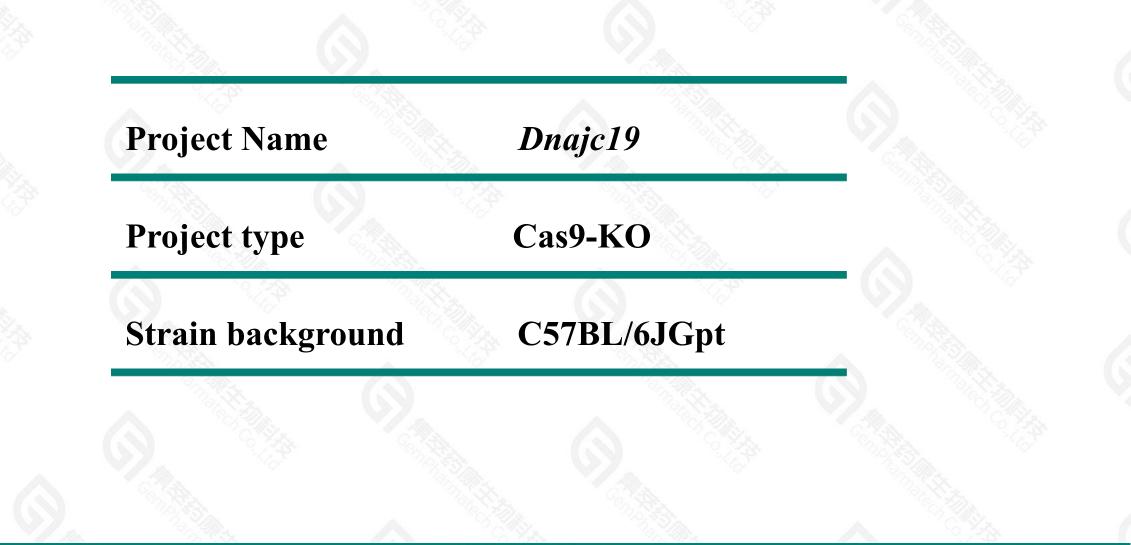
**Designer: Yumeng wang** 

**Reviewer: Huan wang** 

**Design Date: 2021-9-26** 

### **Project Overview**

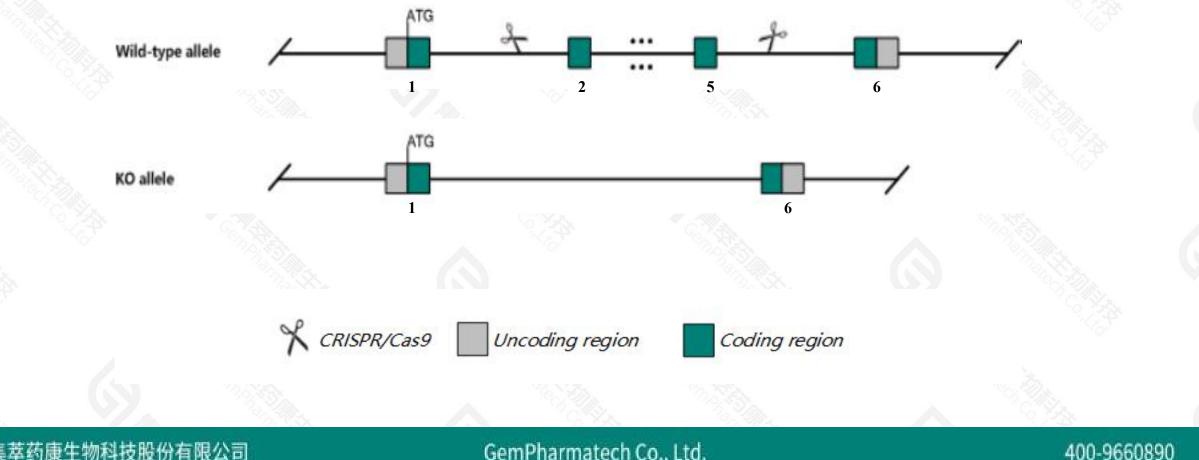




### **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Dnajc19* gene. The schematic diagram is as follows:



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> The *Dnajc19* gene has 5 transcripts. According to the structure of *Dnajc19* gene, exon2-exon5 of *Dnajc19*-201(ENSMUST00000011029.12) transcript is recommended as the knockout region. The region contains 277bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Dnajc19* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Dnajc19* gene is located on the Chr3. 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.

## **Gene information (NCBI)**



☆ ?

### Dnajc19 DnaJ heat shock protein family (Hsp40) member C19 [Mus musculus (house mouse)]

Gene ID: 67713, updated on 12-Feb-2021

#### Summary

Official Symbol	Dnajc19 provided by MGI
<b>Official Full Name</b>	DnaJ heat shock protein family (Hsp40) member C19 provided by MGI
<b>Primary source</b>	MGI:MGI:1914963
See related	Ensembl:ENSMUSG0000027679
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	1810055D05Rik, AA959924, Tim14
Expression	Ubiquitous expression in kidney adult (RPKM 15.5), duodenum adult (RPKM 11.5) and 28 other tissuesSee more
Orthologs	human all

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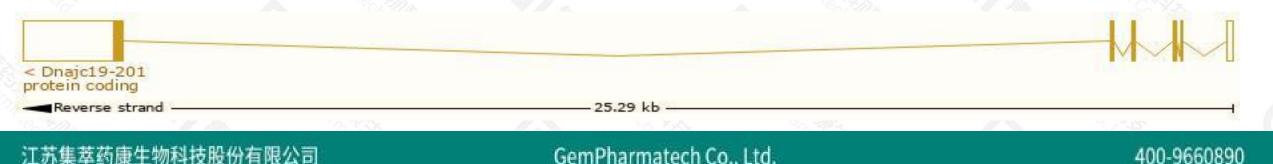
### **Transcript information (Ensembl)**



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

Name Transcript ID		bp	Protein	Biotype	CCDS	UniProt	Flags	
Dnajc19-201	ENSMUST00000011029.12	2499	<u>157aa</u>	Protein coding	CCDS38411		TSL:1 , GENCODE basic ,	
Dnajc19-203	ENSMUST00000117223.4	1695	<u>130aa</u>	Protein coding	CCDS71233		TSL:1 , GENCODE basic ,	
Dnajc19-202	ENSMUST00000108195.10	659	<u>116aa</u>	Protein coding	CCD538412		TSL:1, GENCODE basic, APPRIS P1,	
Dnajc19-204	ENSMUST00000120805.8	551	<u>110aa</u>	Protein coding	CCDS71234		TSL:2 , GENCODE basic ,	
Dnajc19-205	ENSMUST00000197111.2	419	No protein	Retained intron	-	1	TSL:2,	

The strategy is based on the design of *Dnajc19-201* transcript, the transcription is shown below:



### **Genomic location distribution**



45.30 kt Forward strand 34.11Mb 34.12Mb 34.13Mb 34.14Mb 1111 Genes Gm43668-201 > Fxr1-201 > (Comprehensive set... protein coding TEC rono 10 Fxr1-207 > nonsense mediated decar mart Fxr1-202 > protein coding man Fxr1-206 > protein coding mant Fxr1-208 > protein coding mm m 10 Fxr1-204 > protein coding Fxr1-205 > protein coding Fxr1-209 > retained intron AC068294.26 Contigs Genes < Gm43667-201 TEC < Dnajc19-202 protein coding (Comprehensive set... < Dnajc19-201 protein coding MMM < Dnajc19-204 protein coding MM < Dnajc19-205 retained intron < Dnajc19-203 protein coding Regulatory Build 34.13Mb 34.11Mb 34.12Mb 34.14Mb Reverse strand 45.30 kb **Regulation** Legend CTCF Promoter Promoter Flank Gene Legend Protein Coding merged Ensembl/Havana Ensembl protein coding Non-Protein Coding processed transcript

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### **Protein domain**



ENSMUSP00000011 Transmembrane heli Low complexity (Seg) Superfamily		2	haperone J-dom	ain superfamily				
PANTHER	PTHR12763:SF8					_		
	PTHR12763							
Gene3D		Chap	erone J-domain	superfamily				
<u>CDD</u>			DnaJ	domain	- N			
All sequence SNPs/i	Sequence variants (dbSNP	and all other	sources)	1		I	1	
Variant Legend	frameshift variant stop lost inframe deletion missense variant synonymous variant							;
Scale bar	0 20	40	60	80	100	120		157

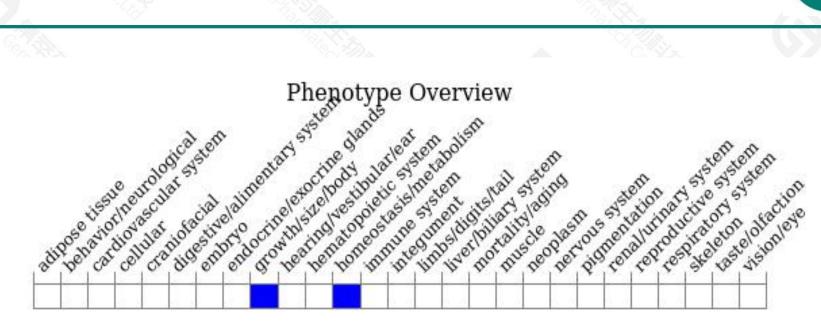
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### Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(http://www.informatics.jax.org/).



If you have any questions, you are welcome to inquire. Tel: 400-9660890



