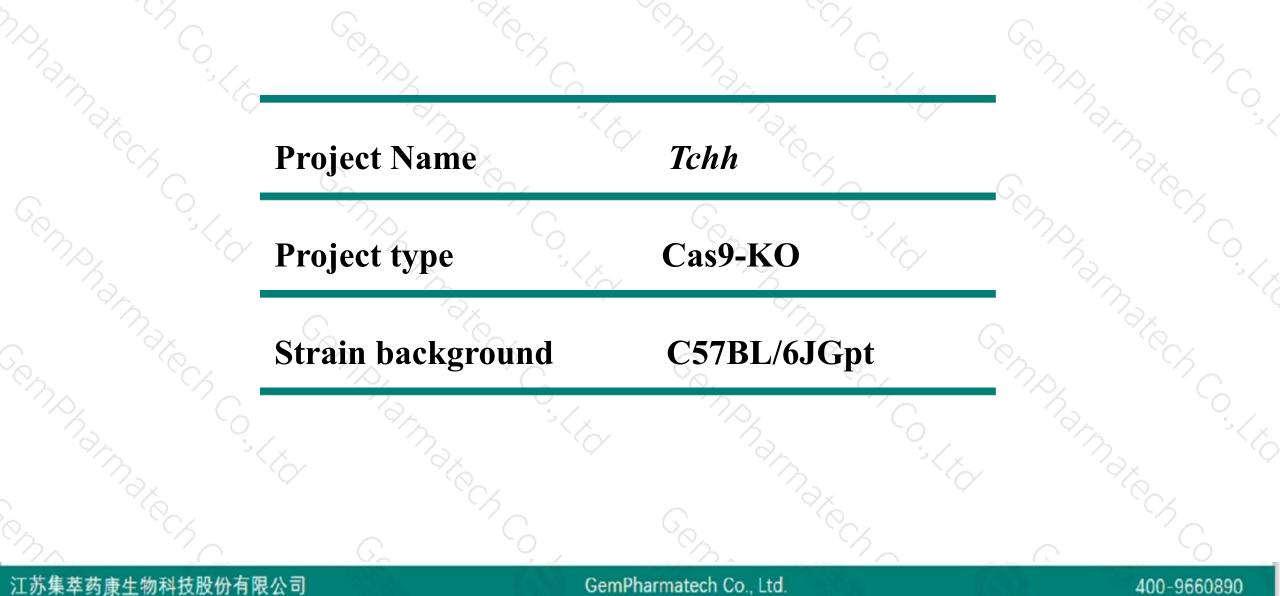


# Tchh Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-1-17

## **Project Overview**

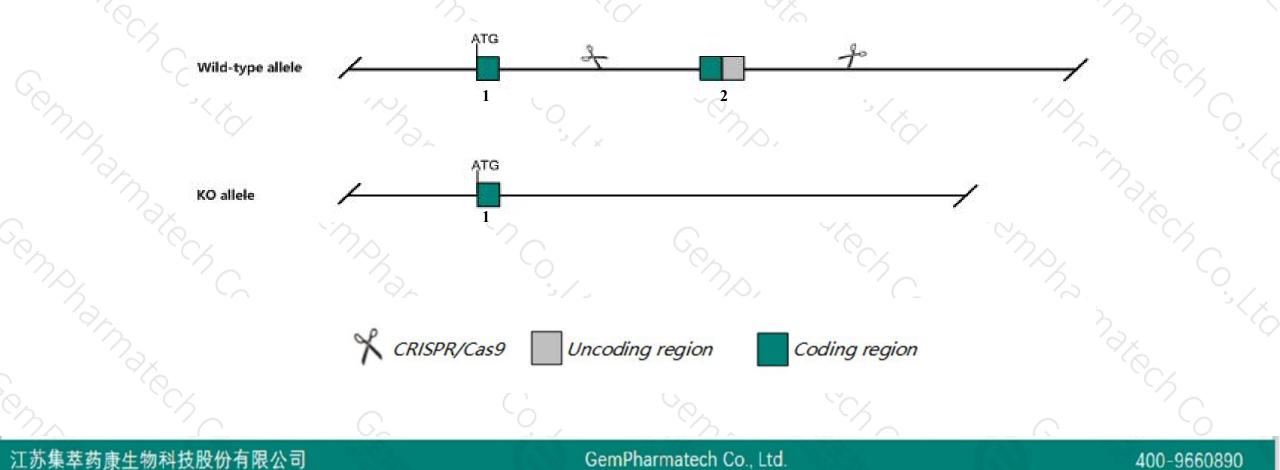




# **Knockout strategy**



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





- The *Tchh* gene has 1 transcript. According to the structure of *Tchh* gene, exon2 of *Tchh-201* (ENSMUST00000064257.5) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Tchh* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Tchh* 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.
- The targeted region is in the intron of the Gm37245 gene, which may affect the regulation of this gene.
- 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)**



☆ ?

### Tchh trichohyalin [Mus musculus (house mouse)]

Gene ID: 99681, updated on 31-Jan-2019

#### Summary

Official SymbolTchh provided by MGIOfficial Full Nametichohyalin provided byMGIPrimary sourceMGI:MGI:2177944See relatedEnsembl:ENSMUSG0000052415Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;<br/>Muroidea; Murinae; Mus; MusAlso knownasAHF, AI597080, ThhExpressionBroad expression in testis adult (RPKM 1.5), genital fat pad adult (RPKM 1.1) and 16 other tissues<br/>See moreOrthologshuman all

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# **Transcript information (Ensembl)**



The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cchh-201	ENSMUST0000064257.5	5823 <u>1599aa</u>		Protein coding	CCDS50980	A0A0B4J1F9	TSL:5 GENCODE basic APPRIS P1
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		2				NO <sup>2</sup>	12A 10
atrotoo	y is based on the design of	of Tabl	201 tran	Corint The tran	soriation is a	hown holow	5.0
- sualeg	y is based on the design (	JI ICHN	<i>i-201</i> ffall	iscript, The trai	iscription is s	nown below	
	9 <i>X</i>			6.75 kb			Forward strand

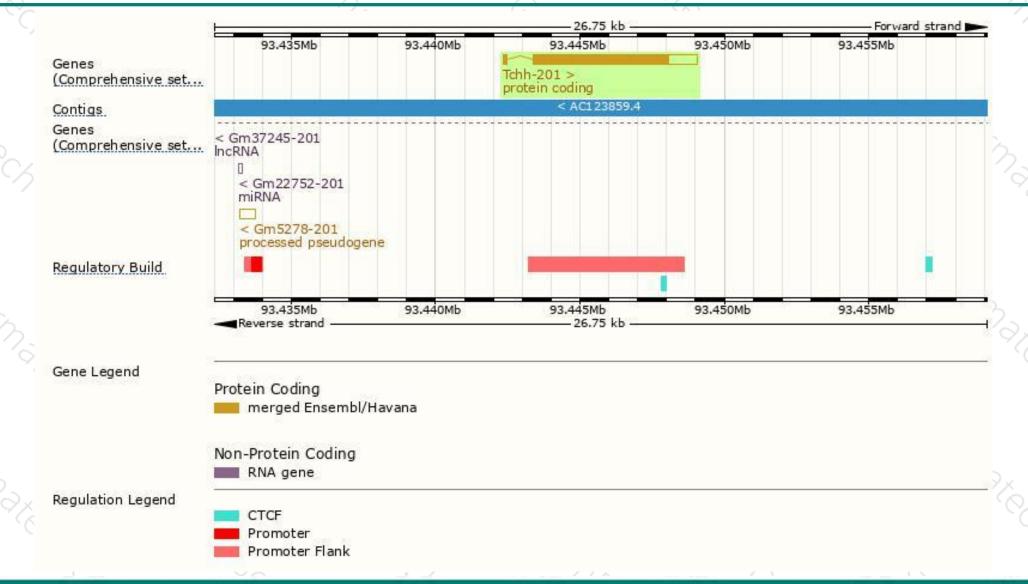
#### Tchh-201 > protein coding

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### **Genomic location distribution**





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# **Protein domain**



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2	All sequence SNPs/i	Sequence variants (	dbSNP and all other	sources)	01 01 1 1 1						
	CDD	S-100									
	PANTHER Gene3D	PTHR 34855									
	PROSITE patterns	EF-Hand 1, calcium-binding site									
	PROSITE profiles	EF-hand domain					C				
	<u>Pfam</u>	S100/CaBP-9k-type, calcium binding, subdomain									
	SMART	S100/CaBP-9k-type, c	alcium binding, subdo	main							
	Coiled-coils (Ncoils) Superfamily	EF-hand domain pair									
2	ENSMUSP00000069 MobiDB lite Low complexity (Seg)						× × × × × ×				

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



