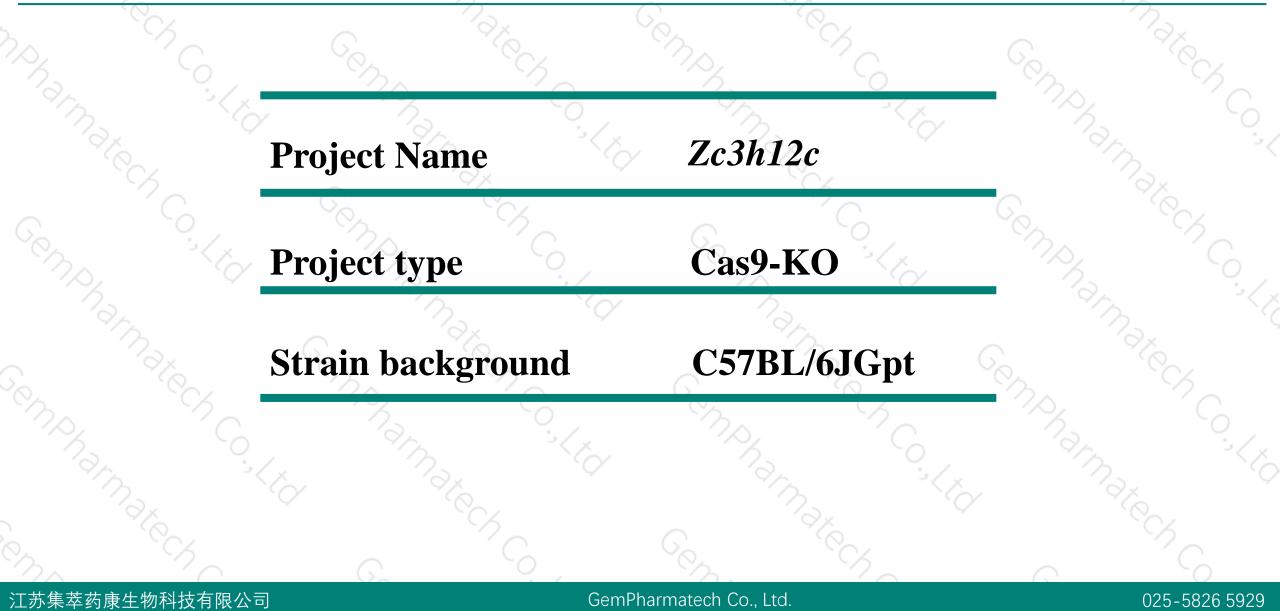
Zc3h12c Cas9-KO Strategy

Designer: Design Date: Daohua Xu 2019-7-18

Project Overview

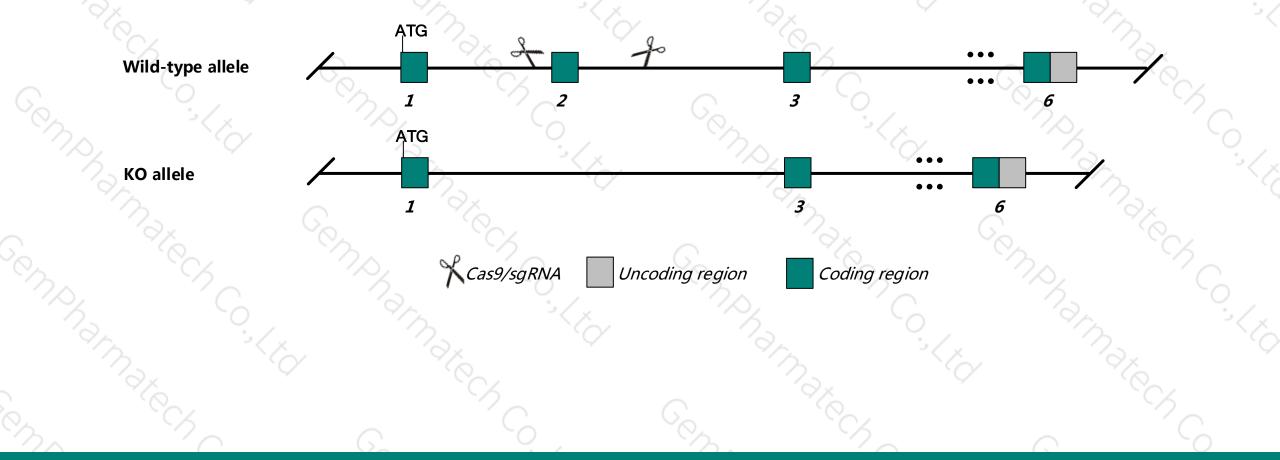




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Zc3h12c gene. The schematic diagram is as follows:



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- The Zc3h12c gene has 2 transcripts. According to the structure of Zc3h12c gene, exon2 of Zc3h12c-201 (ENSMUST00000165519.1) transcript is recommended as the knockout region. The region contains 752bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify Zc3h12c gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9, 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.

- The Zc3h12c gene is located on the Chr9. 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)



Zc3h12c zinc finger CCCH type containing 12C [Mus musculus (house mouse)]

Gene ID: 244871, updated on 8-Dec-2018

Summary

Official Symbol	Zc3h12c provided by MGI
Official Full Name	zinc finger CCCH type containing 12C provided by MGI
Primary source	<u>MGI:MGI:3026959</u>
See related	Ensembl:ENSMUSG00000035164
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; 💛
	Muroidea; Murinae; Mus; Mus
Also known as	mKIAA1726; A230108E06; C230027N18Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 3.2), whole brain E14.5 (RPKM 3.1) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)



The gene has 2 transcripts, and all transcripts are shown below:

Show/hide	columns (1 hidden)							Filter	
Name 🍦	Transcript ID 🖕	bp 🖕	Protein 🖕	Biotype 🍦	CCDS 🖕	UniProt 🖕	RefSeq 🖕	Flags	-
Zc3h12c-201	ENSMUST00000165519.1	6133	<u>903aa</u>	Protein coding	<u>CCDS52794</u> @	<u>E9Q1I3</u> &	<u>NM 001162921</u> ജ NP 001156393ജ	TSL:5 GENCODE basic	
Zc3h12c-202	ENSMUST00000213645.1	6764	<u>884aa</u>	Protein coding	-	<u>Q5DTV4</u> മ	-	TSL:5 GENCODE basic APPRIS	P1

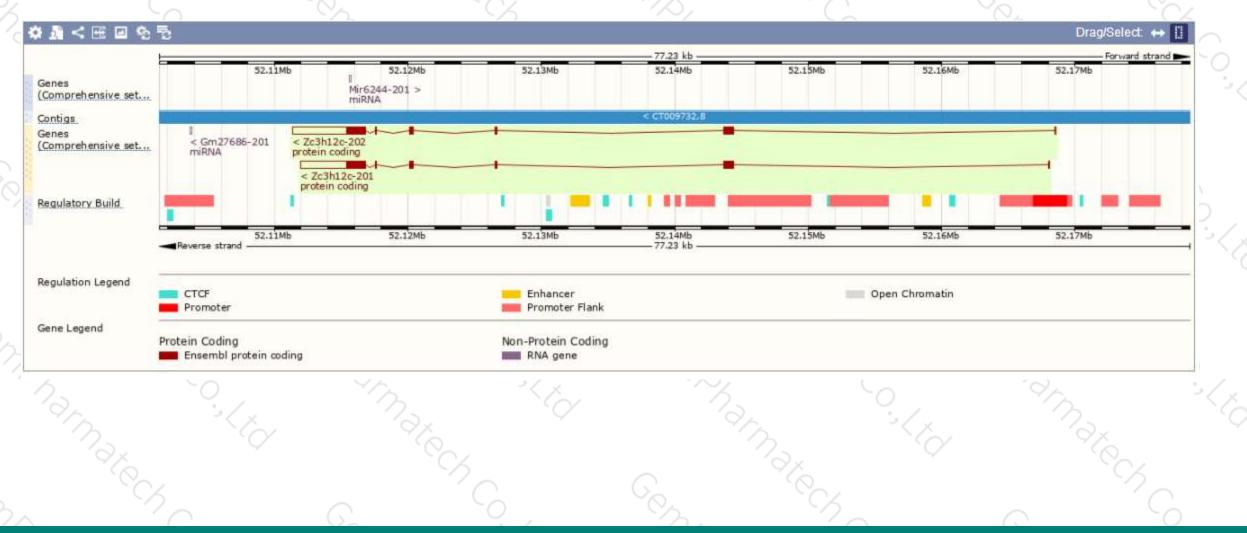
The strategy is based on the design of Zc3h12c-201 transcript, The transcription is shown below

1					_
c3h12c-201 tein coding					
Reverse strand			3 kb		
	7.1	20	N		

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Genomic location distribution





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Protein domain



 ☆ < ☑ ☆ 5 ENSMUSP00000127 MobiDB lite Low complexity (Sea) hmmpanther. 		HR1287615F36					-	
Pfam_domain PROSITE profiles Gene3D All sequence SNPs/i		HR12076 IbSNP and all other sources	Ribonuclease Zc3h12a-1 9.46.50.11980		: CCCH-type	11211		1
Maniput Language								
Variant Legend	missense variar			egion variant	480	synonymous		800 903
Variant Legend Scale bar	missense variar		240 320	egion variant 400	490	synonymous 560 640		800 903

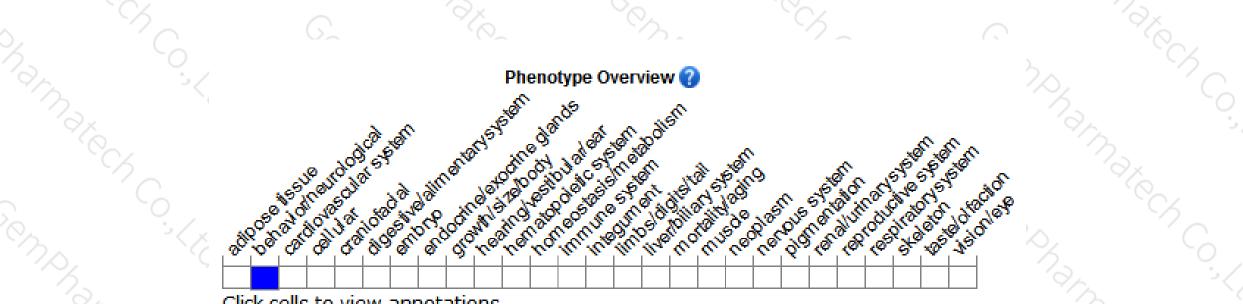
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Mouse phenotype description(MGI)





Click cells to view annotations.

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: 025-5864 1534



