

Zcchc8 Cas9-KO Strategy

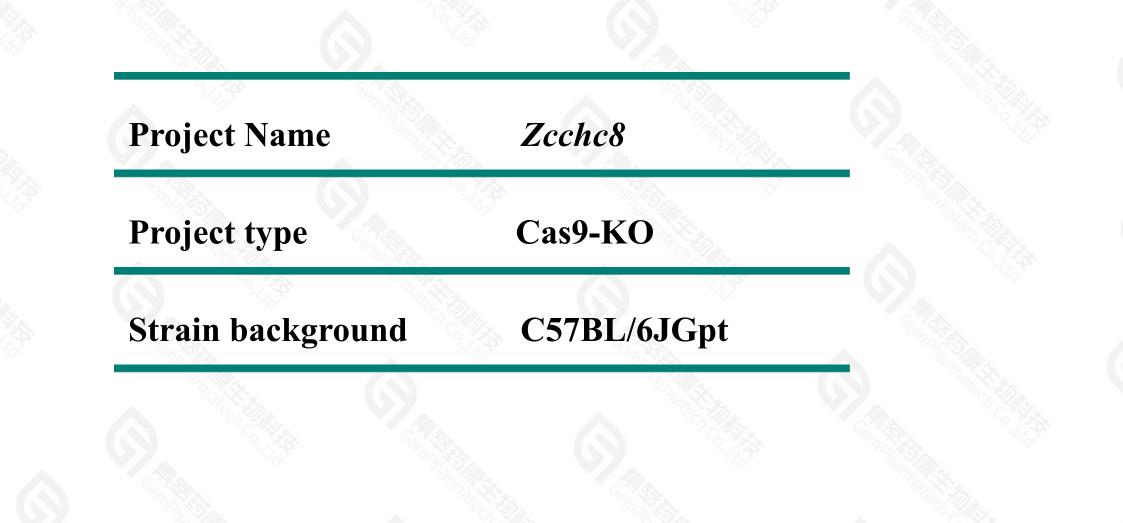
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Reviewer: Yun Li

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Project Overview





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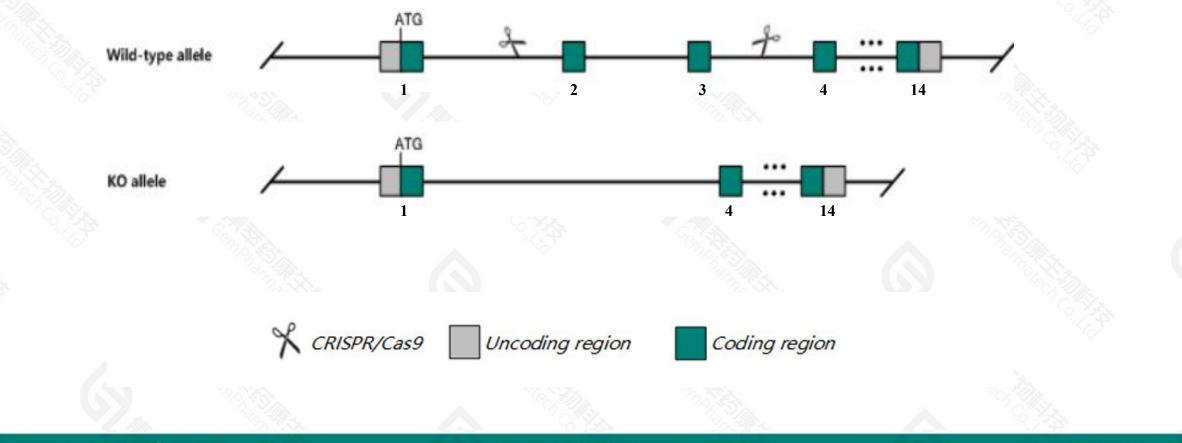
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Knockout strategy



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This model will use CRISPR/Cas9 technology to edit the Zcchc8 gene. The schematic diagram is as follows:



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➤ The Zcchc8 gene has 9 transcripts. According to the structure of Zcchc8 gene, exon2-exon3 of Zcchc8-204(ENSMUST00000196282.5) transcript is recommended as the knockout region. The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Zcchc8* 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 *Zcchc8* gene is located on the Chr5. 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.

Zcchc8 zinc finger, CCHC domain containing 8 [Mus musculus (house mouse)] Gene ID: 70650, updated on 17-Dec-2020

Summary

Official Symbol	Zcchc8 provided by MGI
Official Full Name	zinc finger, CCHC domain containing 8 provided by MGI
Primary source	MGI:MGI:1917900
See related	Ensembl:ENSMUSG0000029427
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	5730565F05Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 18.9), testis adult (RPKM 13.8) and 28 other tissues See more
Orthologs	human all

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Gene information (NCBI)



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Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zcchc8-204	ENSMUST00000196282.5	4350	<u>709aa</u>	Protein coding	CCD580406		TSL:5 , GENCODE basic , APPRIS P1
Zcchc8-201	ENSMUST0000031376.12	4286	<u>709aa</u>	Protein coding			TSL:1 , GENCODE basic , APPRIS P1
Zcchc8-208	ENSMUST00000200161.2	531	<u>103aa</u>	Protein coding	2		CDS 5' incomplete , TSL:5 ,
Zcchc8-209	ENSMUST00000200503.2	321	<u>107aa</u>	Protein coding	-		CDS 5' and 3' incomplete , TSL:3 ,
Zcchc8-206	ENSMUST00000198826.5	751	<u>105aa</u>	Nonsense mediated decay	-2		CDS 5' incomplete , TSL:5 ,
Zcchc8-205	ENSMUST00000196333.5	690	<u>173aa</u>	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Zcchc8-202	ENSMUST00000196001.2	506	<u>54aa</u>	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Zcchc8-207	ENSMUST00000199875.2	1868	No protein	Retained intron	-		TSL:1,
Zcchc8-203	ENSMUST00000196042.2	738	No protein	Retained intron	-		TSL:2,

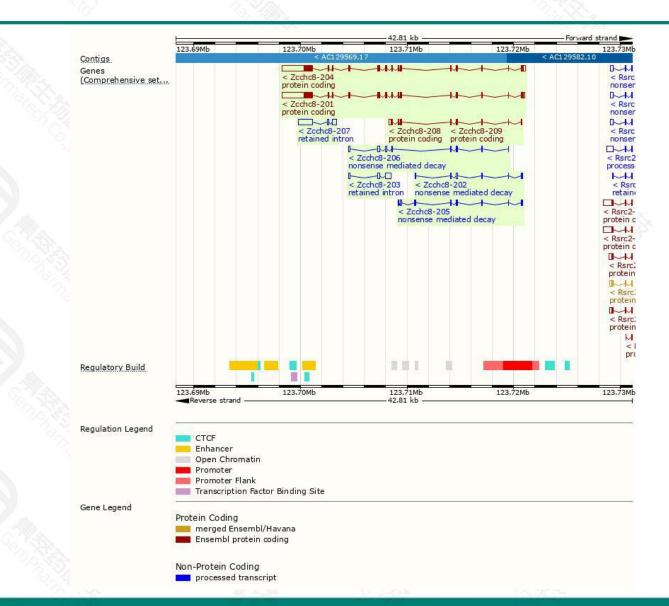
The strategy is based on the design of Zcchc8-204 transcript, the transcription is shown below:

Zcchc8-204 rotein coding	T	8			-	
Reverse strand			22.81 kb			
TD &	1 - Alle	2015.00	0 225	20.202		

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Genomic location distribution





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Protein domain



ENSMUSP00000142 MobiDB lite Low complexity (Seq) Coiled-coils (Ncoils)						-			×		
SMART			Zinc finge	PSR proline-r	ich						
<u>fam</u>			Zinc finge	PSP, proline-	rich						
ROSITE profiles			Zinc finge	ar, CCHC-type							
ANTHER	PTHR13316										
	PTHR13316:SF0										
All sequence SNPs/i	Sequence varian	s (dbSNP and a	all other sources	;)		II	n a	ili n	ener	Ŧ.	1
Variant Legend	missense va splice region synonymou:	n variant									
Scale bar	60 60	120 18	30 240	300	360	420	480	540	600		709

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



