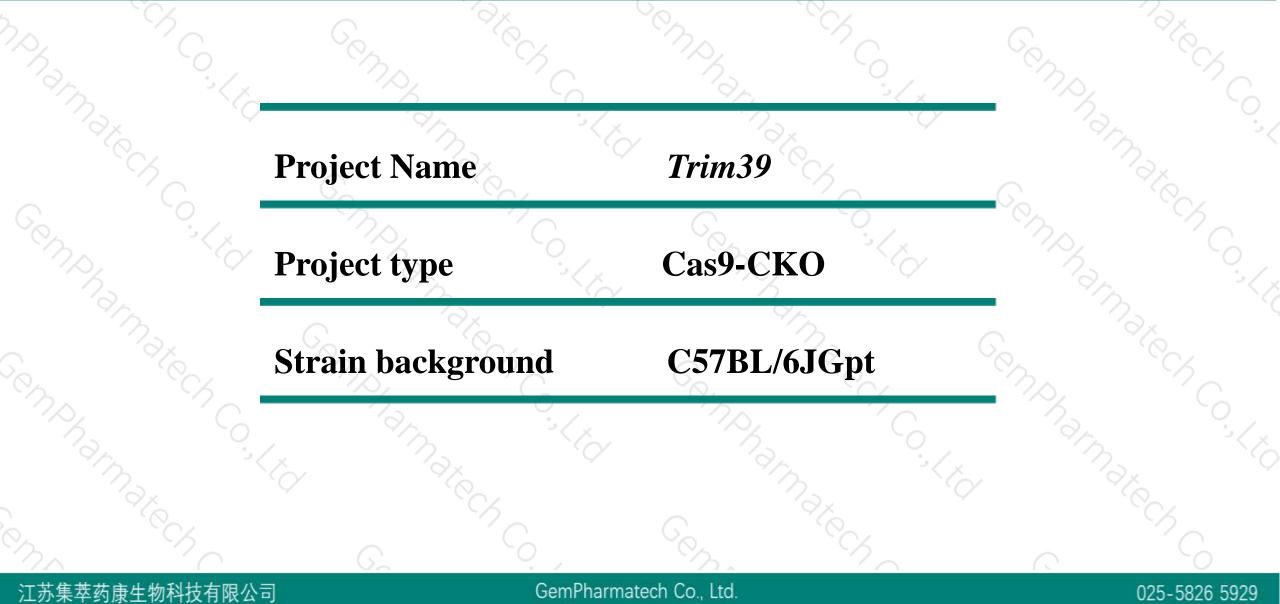


# Trim39 Cas9-CKO Strategy

Designer: Reviewer: Design Date: Baocheng Zhuang Yang Zeng 2018-6-19

### **Project Overview**

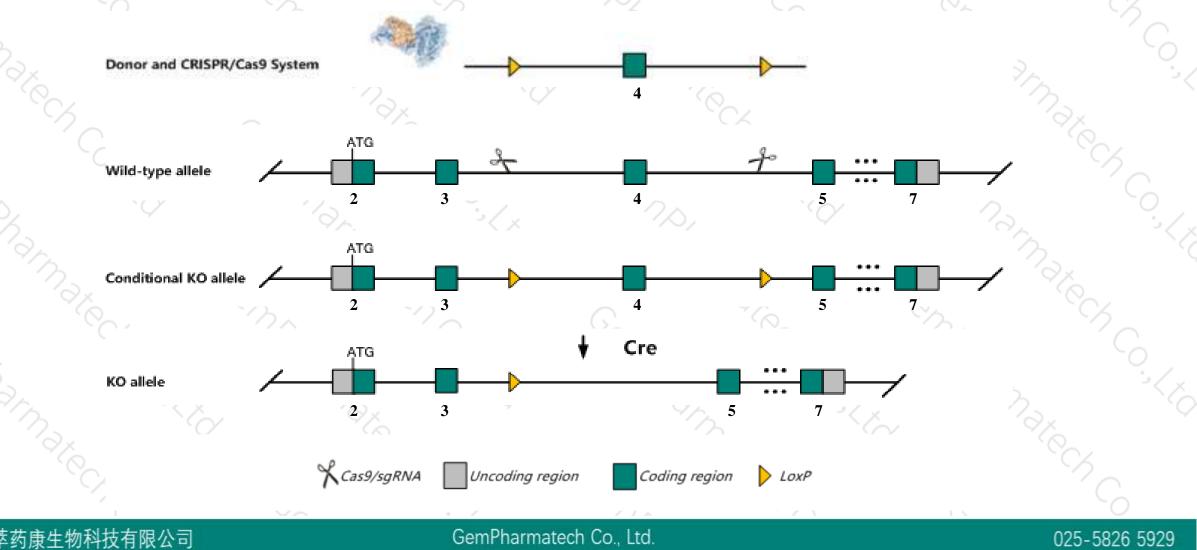




### **Conditional Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Trim39* gene. The schematic diagram is as follows:





- The *Trim39* gene has 7 transcripts. According to the structure of *Trim39* gene, exon4 of *Trim39-203* (ENSMUST00000113706.9) transcript is recommended as the knockout region. The region contains 231bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trim39* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA and Donor 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 flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

### Notice



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- > The KO region is close to 5'UTR region of the *Rpp21* gene. Knockout the region may affect the expression of *Rpp21* gene.
- The Trim39 gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

### Gene information (NCBI)



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### Trim39 tripartite motif-containing 39 [ Mus musculus (house mouse) ]

Gene ID: 79263, updated on 14-Aug-2019

#### Summary

Official Symbol Trim39 provided by MGI Official Full Name tripartite motif-containing 39 provided by MGI Primary source MGI:MGI:1890659 Ensembl:ENSMUSG0000045409 See related protein coding Gene type RefSeg status VALIDATED Organism Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Lineage Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus Also known as tfp; Rnf23; mKIAA4179; RBCC-B30.2; 1100001D15Rik; E130103K13Rik Ubiguitous expression in testis adult (RPKM 12.6), CNS E14 (RPKM 11.4) and 28 other tissues See more Expression Orthologs human all



## **Transcript information (Ensembl)**

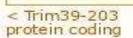


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The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trim39-203	ENSMUST00000113706.9	3204	<u>488aa</u>	Protein coding	CCDS37611	E9QLN4	TSL:1 GENCODE basic APPRIS P1
Trim39-201	ENSMUST0000042717.12	3085	<u>488aa</u>	Protein coding	CCDS37611	E9QLN4	TSL:1 GENCODE basic APPRIS P1
Trim39-205	ENSMUST00000173369.1	2914	<u>496aa</u>	Protein coding	-	G3UWI0	TSL:1 GENCODE basic
Trim39-206	ENSMUST00000173665.7	2974	<u>60aa</u>	Nonsense mediated decay	-	G3UX29	CDS 5' incomplete TSL:1
Trim39-202	ENSMUST00000113704.9	1465	No protein	Processed transcript	-	-	TSL:1
Trim39-207	ENSMUST00000174197.7	633	No protein	Processed transcript	-	-	TSL:3
Trim39-204	ENSMUST00000172832.1	4718	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of Trim39-203 transcript, The transcription is shown below

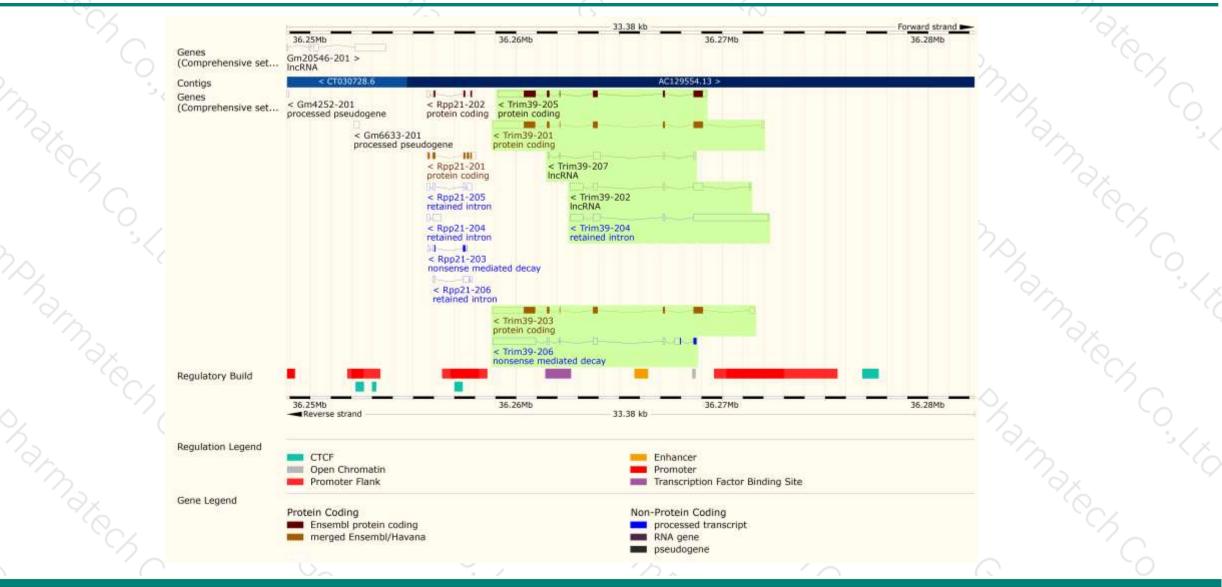


Reverse strand -

### **Genomic location distribution**



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### **Protein domain**



						12	
53	ENSMUSP00000109 Low complexity (Seg) Coiled-coils (Ncoils) Superfamily	SSF57850	SSF57845		Concanavalin A-like lectin/glucanase d	omain superfamily	
	SMART	Zinc finger, RING-type	B-box-type zinc finger		SPRY-associated SPRY domain		0.
	Prints Pfam	PF15227	B-box-type zinc finger		Butyrophylin-like, SPRY domain SPRY-associated SPRY domain		
	PROSITE profiles	Zinc finger, RING-type	B-box-type zinc finger		B30.2/SPRY domain		
`?)	PROSITE patterns PANTHER	Zinc finger, RING-ty PTHR24103:SF627	pe, conserved site				-0 -3{}
	Gene3D	PTHR24103 Zinc finger, RING/FYVE/PHD-type	3.30.40.200		2.60.120.920		
	CDD	cd16601	B-box-type zinc finger		TRIM39, PRY/SPRY domain		
	All sequence SNPs/i	Sequence variants (dbSNP and a	Il other sources)	H I I	n an ann	1	). .< <sub>Ko</sub>
Variant Legend		stop gained missense variant			hift variant mous variant		
	Scale bar	0 60	120 180	240	300 360	420 488	
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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



