

Trim9 Cas9-KO Strategy Enphamaten C.- Lt

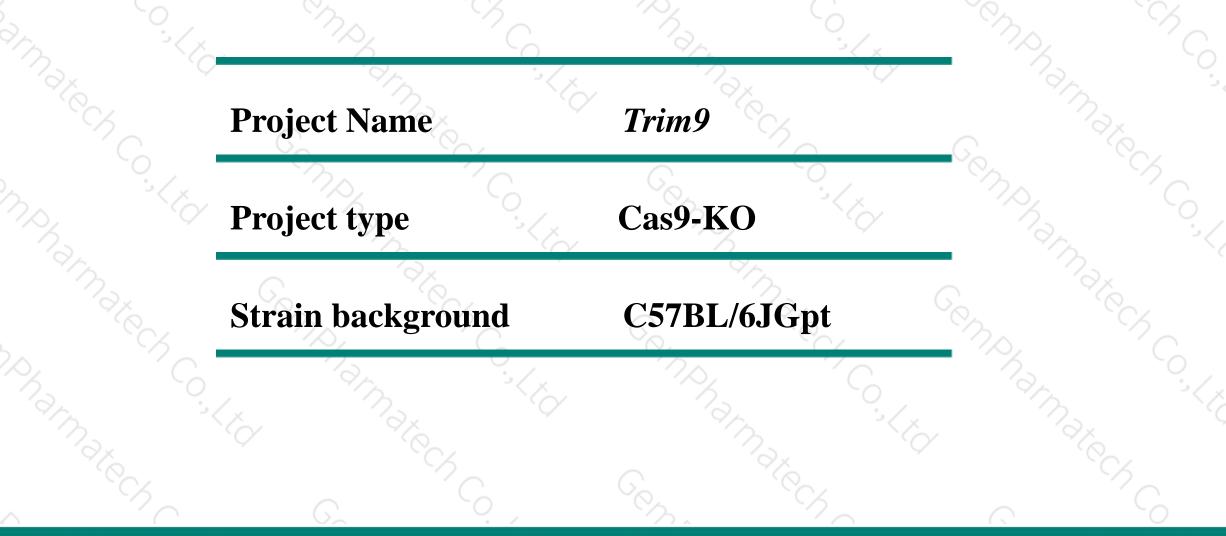
Cemphamatech, Cemphamaten Co. Designer: Qiong Zhou

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Project Overview

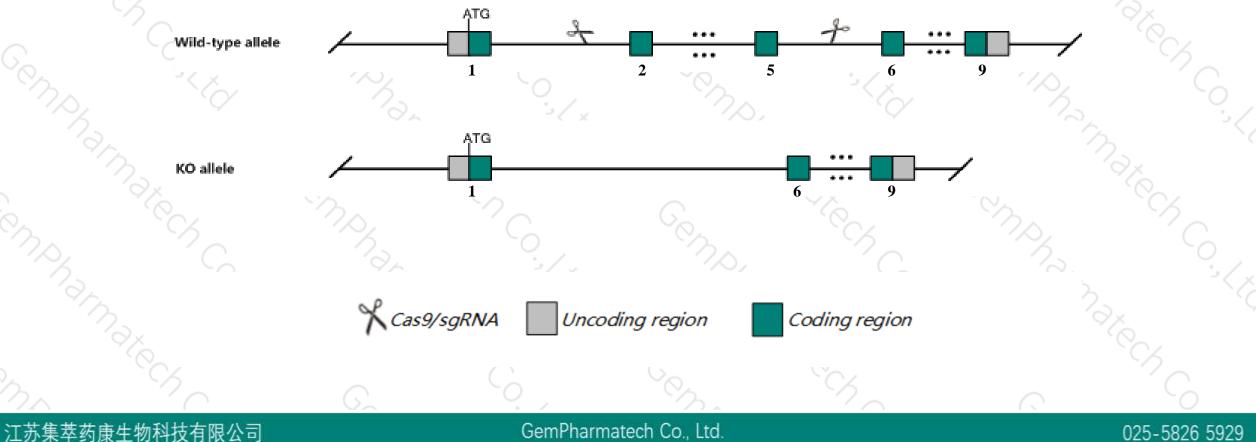


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This model will use CRISPR/Cas9 technology to edit the Trim9 gene. The schematic diagram is as follows:





- The *Trim9* gene has 12 transcripts. According to the structure of *Trim9* gene, exon2-exon5 of *Trim9-202* (ENSMUST00000110522.9) transcript is recommended as the knockout region. The region contains 484bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trim9* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and 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.





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- According to the existing MGI data, Mice homozygous for a null mutation display increased axonal branching and increased corpus callosum thickness.
- The Trim9 gene is located on the Chr12. 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)



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Trim9 tripartite motif-containing 9 [Mus musculus (house mouse)]

Gene ID: 94090, updated on 3-Mar-2019

Summary

Official Symbol	Trim9 provided by MGI
Official Full Name	tripartite motif-containing 9 provided by <u>MGI</u>
Primary source	<u>MGI:MGI:2137354</u>
See related	Ensembl:ENSMUSG00000021071
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
Expression	Biased expression in frontal lobe adult (RPKM 15.7), cortex adult (RPKM 12.9) and 5 other tissuesSee more
Orthologs	human all

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Transcript information (Ensembl)



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The gene has 12 transcripts, all transcripts are shown below:

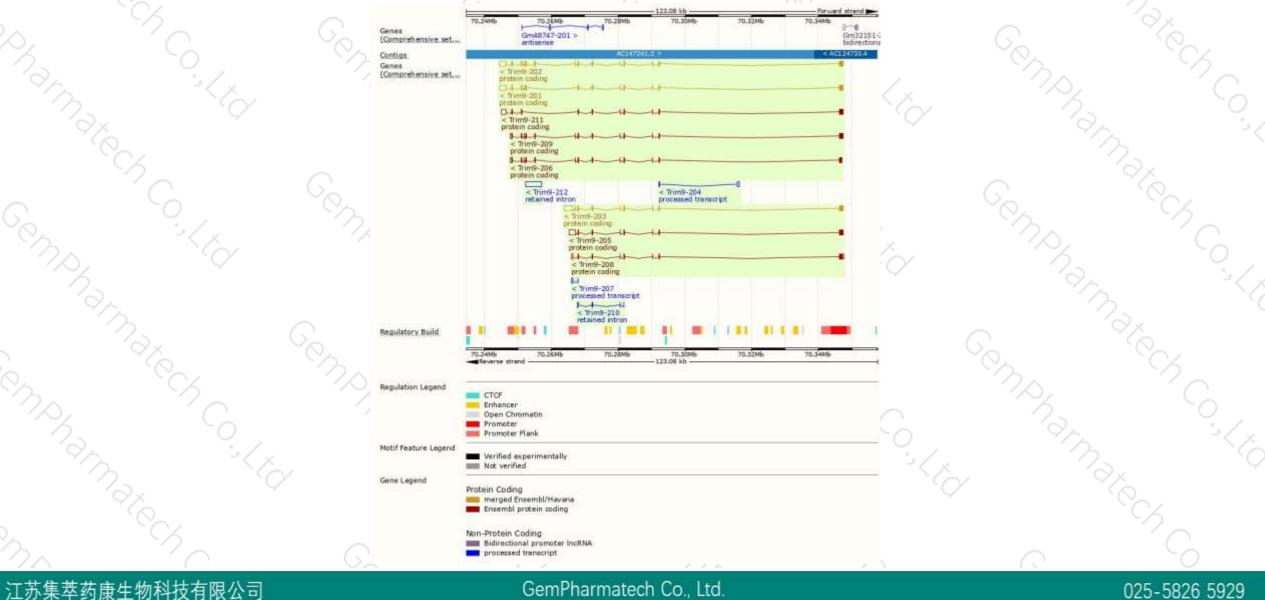
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trim9-203	ENSMUST00000167755.2	4559	<u>547aa</u>	Protein coding	CCDS49079	<u>E9Q524</u>	TSL:1 GENCODE basic
Trim9-202	ENSMUST00000110522.9	4405	<u>788aa</u>	Protein coding	CCDS49078	E9QLH4	TSL:1 GENCODE basic
Trim9-201	ENSMUST00000110520.9	4156	<u>714aa</u>	Protein coding	CCDS49077	<u>Q8C7M3</u>	TSL:1 GENCODE basic
Trim9-205	ENSMUST00000221041.1	3767	<u>565aa</u>	Protein coding	-	<u>Q8C7M3</u>	TSL:1 GENCODE basic
Trim9-211	ENSMUST00000223160.1	3574	<u>710aa</u>	Protein coding	-	A0A1Y7VP88	TSL:5 GENCODE basic APPRIS P1
Trim9-209	ENSMUST00000222316.1	3049	<u>817aa</u>	Protein coding	-	<u>Q8C7M3</u>	TSL:2 GENCODE basic
Trim9-206	ENSMUST00000221294.1	2752	<u>772aa</u>	Protein coding	-	A0A1Y7VJX8	CDS 5' incomplete TSL:1
Trim9-208	ENSMUST00000221370.1	2393	<u>536aa</u>	Protein coding	-	<u>Q8C7M3</u>	TSL:1 GENCODE basic
Trim9-204	ENSMUST00000220557.1	642	No protein	Processed transcript	-	-	TSL:2
Trim9-207	ENSMUST00000221306.1	399	No protein	Processed transcript	-	-	TSL:3
Trim9-212	ENSMUST00000223518.1	4807	No protein	Retained intron	-	-	TSL:NA
Trim9-210	ENSMUST00000222603.1	719	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of Trim9-202 transcript, The transcription is shown below

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Genomic location distribution





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Protein domain

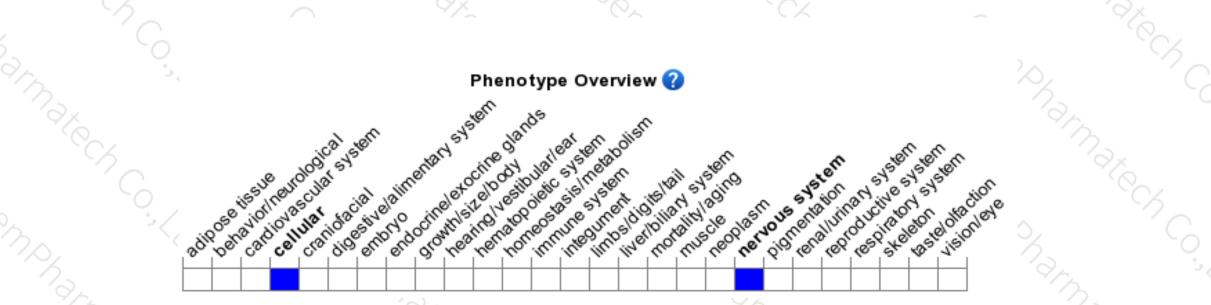


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		Y X	$\sim N_{\perp}$ $\sim CZ$		
ENSMUSP00000106 Low complexity (Seg) Coiled-coils (Ncoils) Superfamily	SSF57850	SSF57845	Fibronectin type III superfamily	Concanavalin A-like le	tin/glucanase domain superfar
SMART	Zinc finger: RING type	B-box-type zinc finger B-box, Otterminal	Fibronectin type III	SPRY do	main
Pfam.	RING-type zinc-finger, UsH dimensation motif	B-box-type zinc finger	Fibronectin type III		SPRY domain
PROSITE profiles	Zinc finger, RING-type	B-box-type zinc finger	COS domain Pibronectin type III	B30.2/SPRV domain	
PROSITE patterns PANTHER	Zinc finger, RINO-type, conserved site MHR20095				5
Gene3D	PTHE2409915F13 Zinc Tinger, TUPK/PTVE/PtrD-type 3.3	9,40.90 3.30.40,200	Immunogtabulin-file fold	2.60.120.920	
CDD.	cd16755		Fibronectin type [1]	cd12689	<u> </u>
All sequence SNPs/i Variant Legend	Sequence variants (dbSNP and all other sour	tes)	1.1. 1. 1. 1.		<u> </u>
Scale bar	o iso	160 240 320	400 460	560 640	788
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		C.	Con Ch		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

Mouse phenotype description(MGI)





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

According to the existing MGI data, Mice homozygous for a null mutation display increased axonal branching and increased corpus callosum thickness.





If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



