

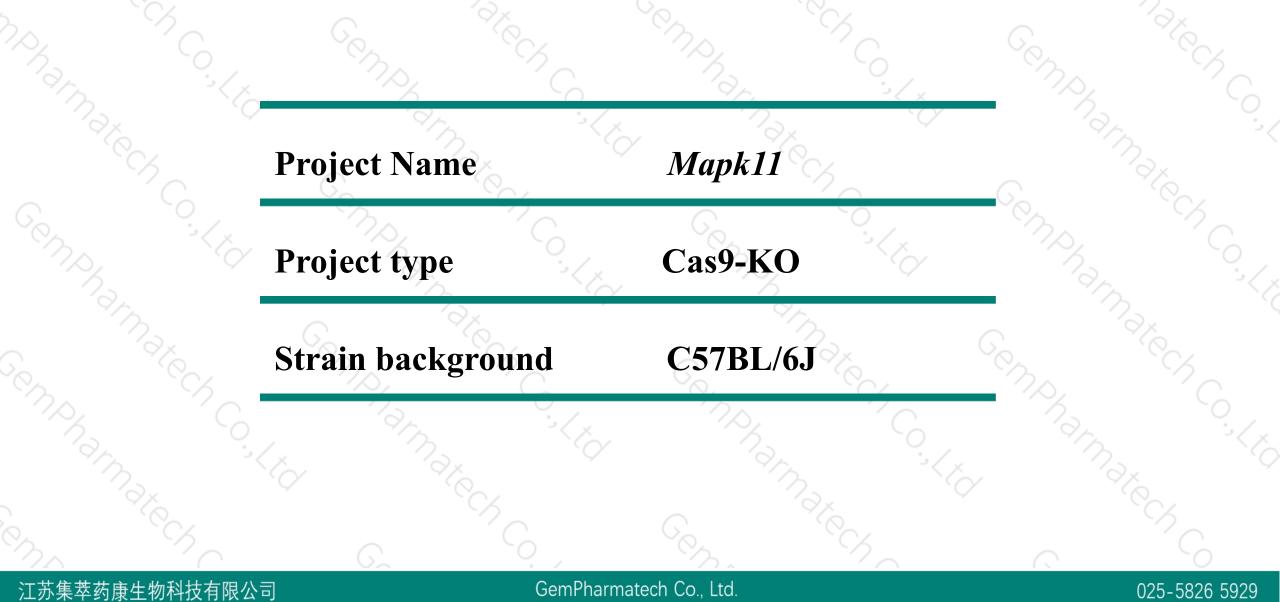
Emphamategi (Mapk11 Cas9-KO Strategy Rondhamater Co.

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Project Overview

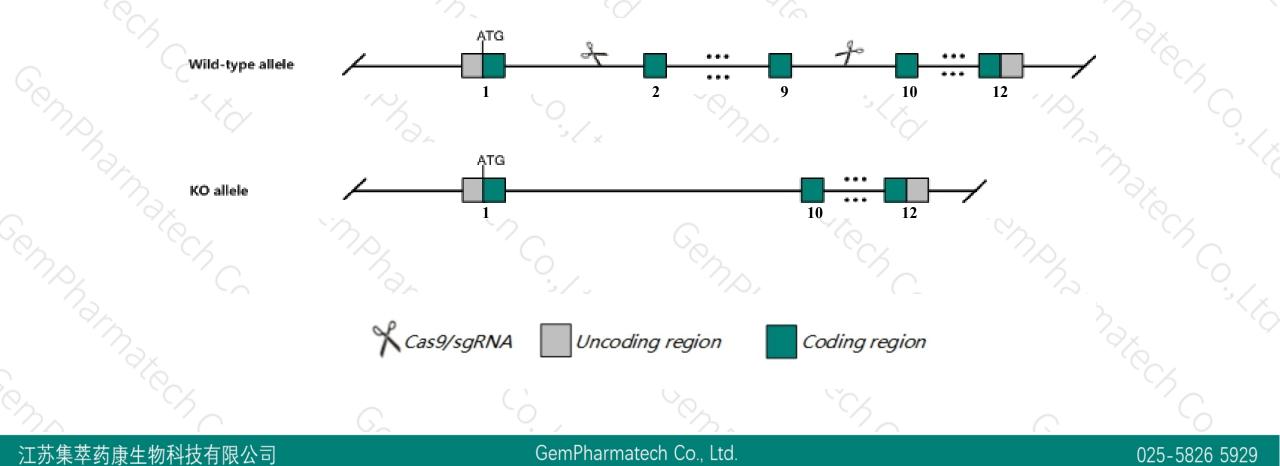




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Mapk11 gene. The schematic diagram is as follows:





- The Mapk11 gene has 4 transcripts. According to the structure of Mapk11 gene, exon2-exon9 of Mapk11-201 (ENSMUST00000088823.4) transcript is recommended as the knockout region. The region contains 646bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk11* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

025-5826 5929

- > According to the existing MGI data, Mice homozygous for a knock-out allele exhibit a normal phenotype.
- The Mapk11 gene is located on the Chr15. 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)



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Mapk11 mitogen-activated protein kinase 11 [Mus musculus (house mouse)]

Gene ID: 19094, updated on 3-Feb-2019

Summary

Official Combal	Mandada						
Official Symbol	Mapk11 provided by <u>MGI</u>						
Official Full Name	mitogen-activated protein kinase 11 provided by <u>MGI</u>						
Primary source	<u>MGI:MGI:1338024</u>						
See related	Ensembl:ENSMUSG00000053137						
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	P38b, Prkm11, Sapk2, Sapk2b, p38-2, p38beta, p38beta2						
Expression	Broad expression in cortex adult (RPKM 22.5), CNS E14 (RPKM 20.2) and 20 other tissues See more						
Orthologs	human all						

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Transcript information (Ensembl)



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The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk11-201	ENSMUST0000088823.4	2461	<u>364aa</u>	Protein coding	CCDS27741	<u>Q9WUI1</u>	TSL:1 GENCODE basic APPRIS P1
Mapk11-203	ENSMUST00000230634.1	749	No protein	Processed transcript	-	-	
Mapk11-204	ENSMUST00000230734.1	2615	No protein	Retained intron	-	-	
Mapk11-202	ENSMUST00000228967.1	534	No protein	Retained intron	_	-	

The strategy is based on the design of Mapk11-201 transcript, The transcription is shown below

< Mapk11-201 protein coding

Reverse strand

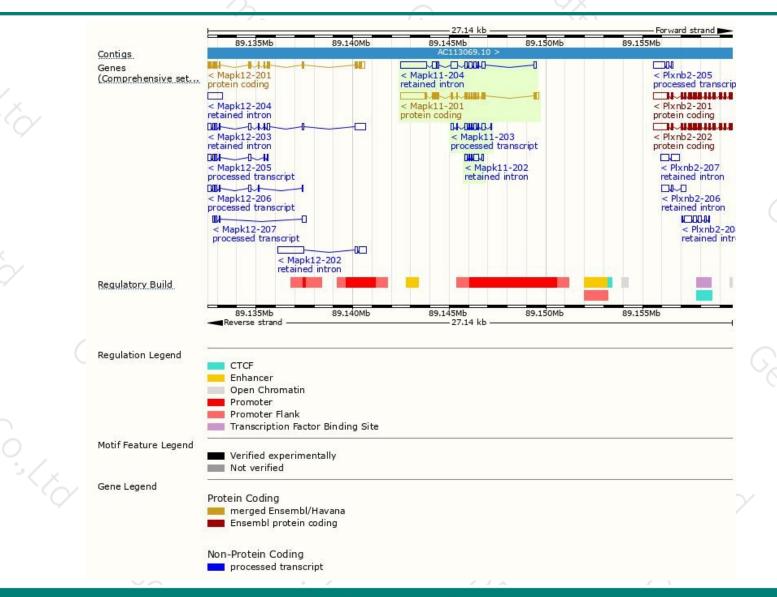
_____7.14 kb

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Genomic location distribution





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Protein domain



ENSMUSP00000086... MobiDB lite Low complexity (Seg) hmmpanther

Superfamily domains SMART domains Prints domain Pfam domain PROSITE profiles PROSITE patterns

PIRSF domain Gene3D

All sequence SNPs/i... Variant Legend

Scale bar

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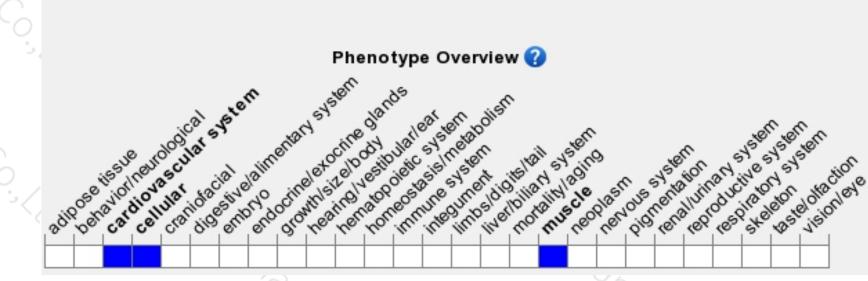
HR24055:SF1	00							
	.02							
HR.24055								
Protein kinase	-like domain superfa	mily					_	
Protein k	nase domain	``				21-0-16		
Mitogen-activ	ated protein (MAP) k	kinase p38-like						
Protein	kinase domain							
Protein k	nase domain							
Protein	kinase, ATP binding	site						
	Mitogen-activate	Contraction of the local division of the loc) kinase, cons	erved site				
PIRSEDDOG								
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		1,10,010,10						
3.30.200.20	nts (dbSNP and all	other source	0)					
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			2					
	us variant							
synonymo								
synonymo 40	80	120	160	200	240	280	320	364

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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 knock-out allele exhibit a normal phenotype.

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



