

Ppie Cas9-KO Strategy

Designer:

Reviewer:

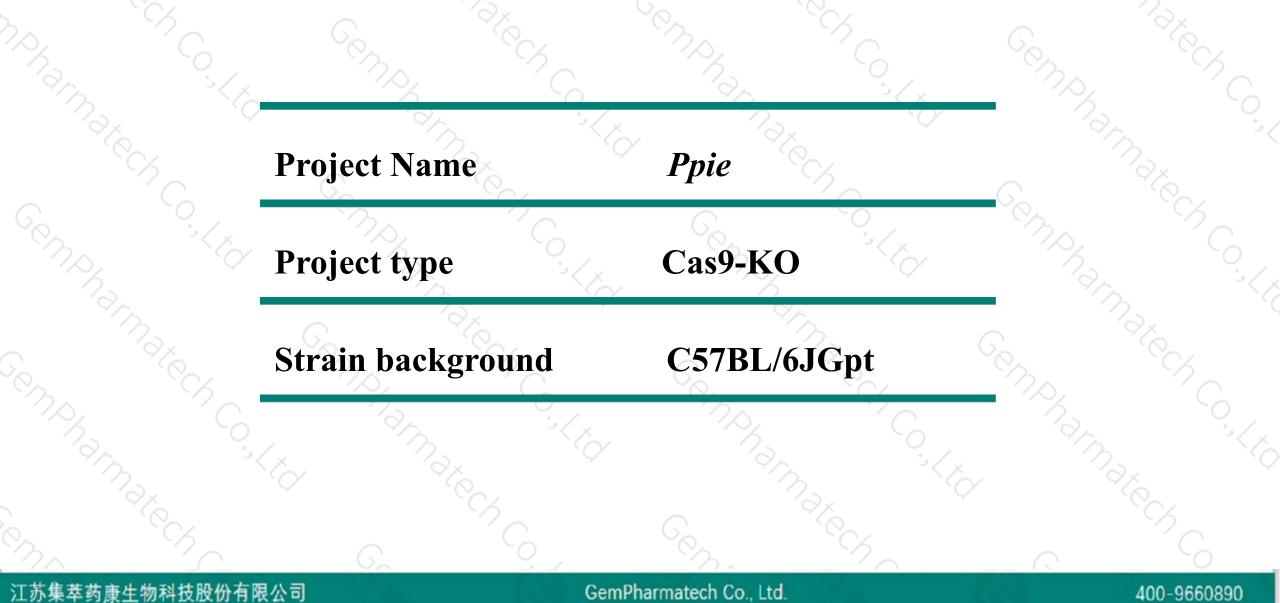
Design Date:

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2020-4-15

Project Overview

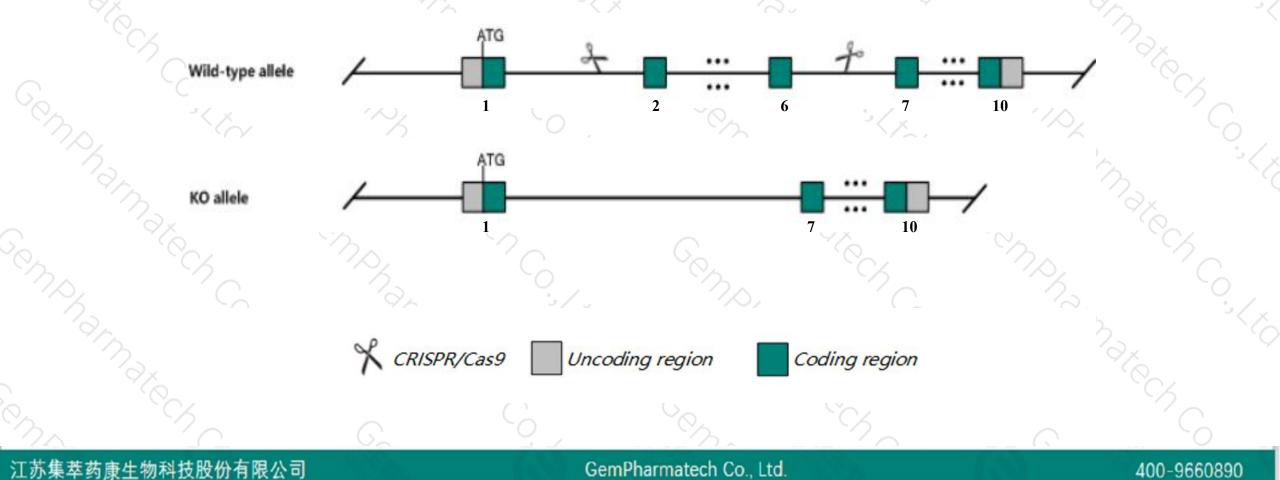




Knockout strategy



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





- The Ppie gene has 4 transcripts. According to the structure of Ppie gene, exon2-exon6 of Ppie-201 (ENSMUST00000030404.4) transcript is recommended as the knockout region. The region contains 353bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Ppie* gene. The brief process is as follows: CRISPR/Cas9 system v

- The Ppie gene is located on the Chr4. 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)



\$?

Ppie peptidylprolyl isomerase E (cyclophilin E) [Mus musculus (house mouse)]

Gene ID: 56031, updated on 13-Mar-2020

Summary

Official Symbol	Ppie provided by MGI
Official Full Name	peptidylprolyl isomerase E (cyclophilin E) provided by <u>MGI</u>
Primary source	MGI:MGI:1917118
See related	Ensembl:ENSMUSG0000028651
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	2010010D16Rik, Cyp33
Expression	Ubiquitous expression in CNS E11.5 (RPKM 21.0), limb E14.5 (RPKM 14.1) and 28 other tissues See more
Orthologs	human all

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Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppie-201	ENSMUST0000030404.4	1188	<u>301aa</u>	Protein coding	CCDS18610	<u>Q9QZH3</u>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Ppie-203	ENSMUST00000136466.7	861	No protein	Processed transcript	-8	8.	TSL:5
Ppie-202	ENSMUST00000126558.7	804	No protein	Processed transcript		84	TSL:2
Ppie-204	ENSMUST00000137778.1	669	No protein	Processed transcript	2	1	TSL:5

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

< Ppie-201 protein coding

Reverse strand

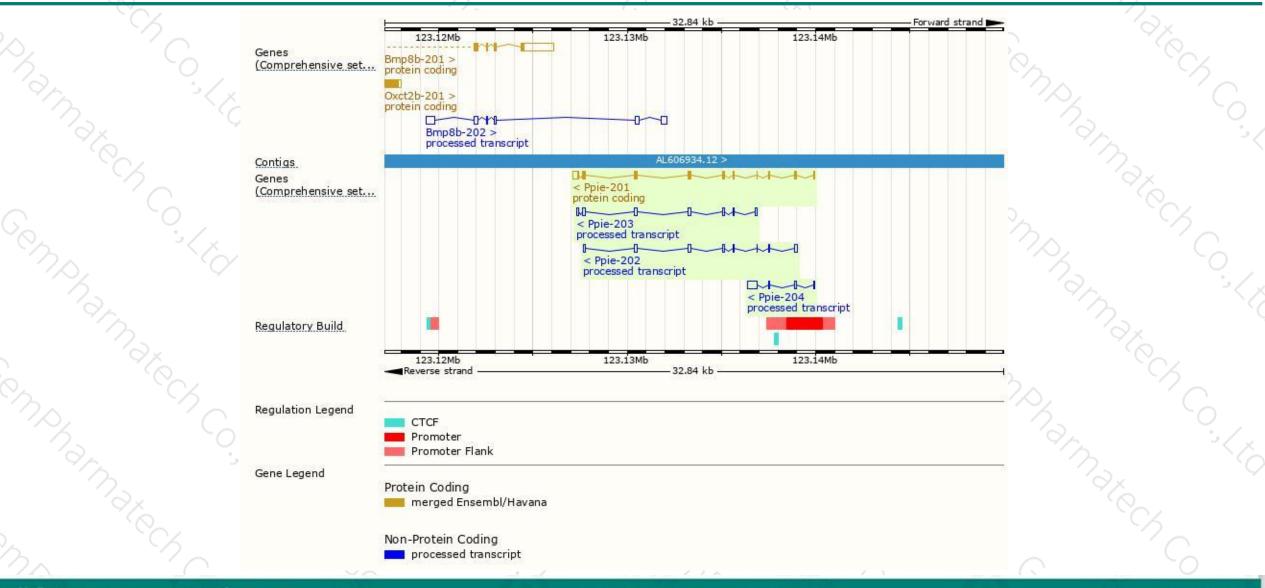
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Genomic location distribution



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Protein domain



valiant Legenu	missense variant							
Variant Legend								
All sequence SNPs/i	Sequence variants (db	SNP and all other s	sources)		1.11	1	1	
	Peptidyl-prolyl cis-trar							
CDD			cdi	01926				
Gene3D	Nucleotide-binding alpha	a-beta plait domain si	uperfamily Cycloph	ilin-like domain s	uperfamily			~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
		PTHR11071	5					
PANTHER	Peptidyl-prolyl cis-trans i	PTHR11071						
PIRSF					Cyclophilin-type	peptioyi-pro	iyi cis-trans iso	merase,
PROSITE patterns								
PROSITE profiles	RNA recognition motif (domain	o	yclophilin-type p	eptidyl-prolyl cis	-trans isome	rase domain	
Pfam.	RNA recognition motif	fdomain	0	yclophilin-type p	eptidyl-prolyl cis	-trans isome	rase domain	
Prints			_	Cyclophilin	-type peptidyl-p	rolyl cis-trans	s isomerase doi	main 5
SMART	RNA recognition motif	domain						
Superfamily	RNA-binding domain su	perfamily	Cycle	ophilin-like doma	in superfamily			
Low complexity (Seg)								
MobiDB lite			Common Statements					

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



