

Plek2 Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-3-4

Project Overview

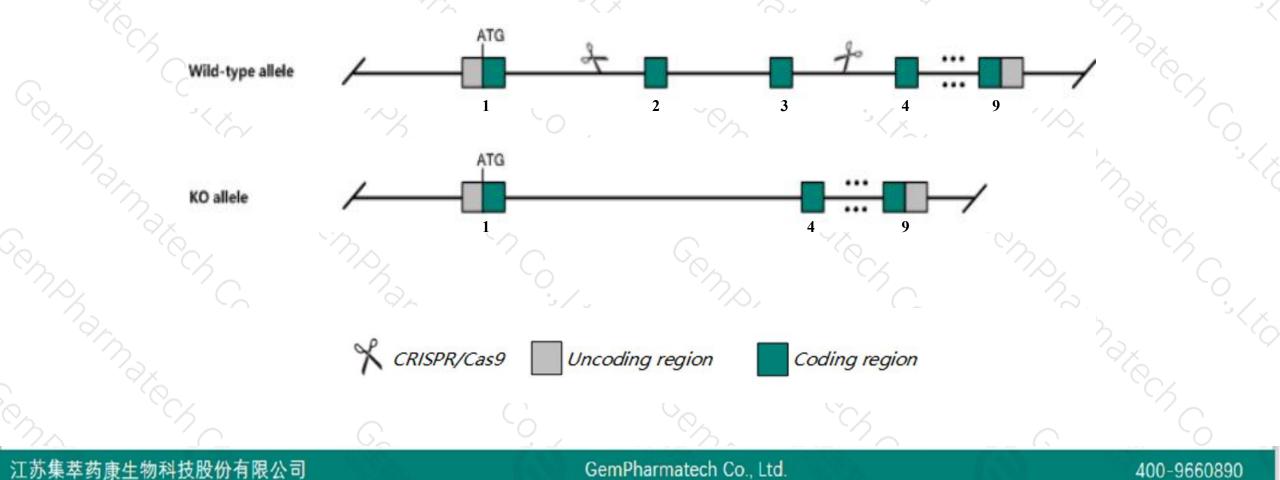




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Plek2* gene. The schematic diagram is as follows:





- The Plek2 gene has 1 transcript. According to the structure of Plek2 gene, exon2-exon3 of Plek2-201 (ENSMUST0000021544.7) transcript is recommended as the knockout region. The region contains 347bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Plek2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Plek2* 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.

Notice

Gene information (NCBI)



Plek2 pleckstrin 2 [Mus musculus (house mouse)]

Gene ID: 27260, updated on 5-Feb-2019

Summary

 Official Symbol
 Plek2 provided by MGI

 Official Full Name
 pleckstrin 2 provided byMGI

 Primary source
 MGI:MGI:1351466

 See related
 Ensembl:ENSMUSG0000021118

 Gene type
 protein coding

 RefSeq status
 PROVISIONAL

 Organism
 Mus musculus

 Lineage
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muriae; Mus; Mus

 Expression
 Biased expression in liver E14.5 (RPKM 12.3), liver E14 (RPKM 12.0) and 11 other tissuesSee more

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Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below:

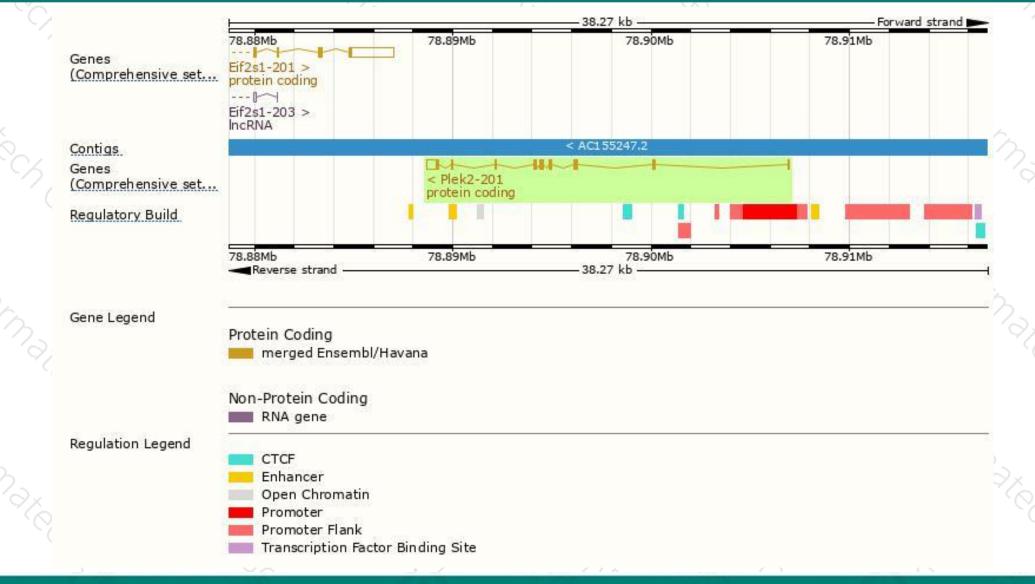
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plek2-201	ENSMUST00000021544.7	1583	<u>353aa</u>	Protein coding	CCDS26004	<u>Q9WV52</u>	TSL:1 GENCODE basic APPRIS P1
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### **Genomic location distribution**





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## **Protein domain**



Scale bar	missense variant synonymous variant 0 40 80 120 160 200 240	280 353
Variant Legend		
All sequence SNPs/i	Sequence variants (dbSNP and all other sources)	
CDD	cd13301 Winged helix-like DNA-binding domain superfamily Pleckstrin-2, DEP domain cd13302	
Gene3D	PH-like domain superfamily	
	Pleckstrin	
PANTHER	DEP domain PTHR12092:SF2	
PROSITE profiles	Pleckstrin homology domain	
	Pleckstrin homology domain DEP domain	
Pfam	DEP domain	
SMART	Winged helix DNA-binding domain superfamily Pleckstrin homology domain	
Superfamily	SSF50729	
SIFTS import Low complexity (Seg)		(



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



