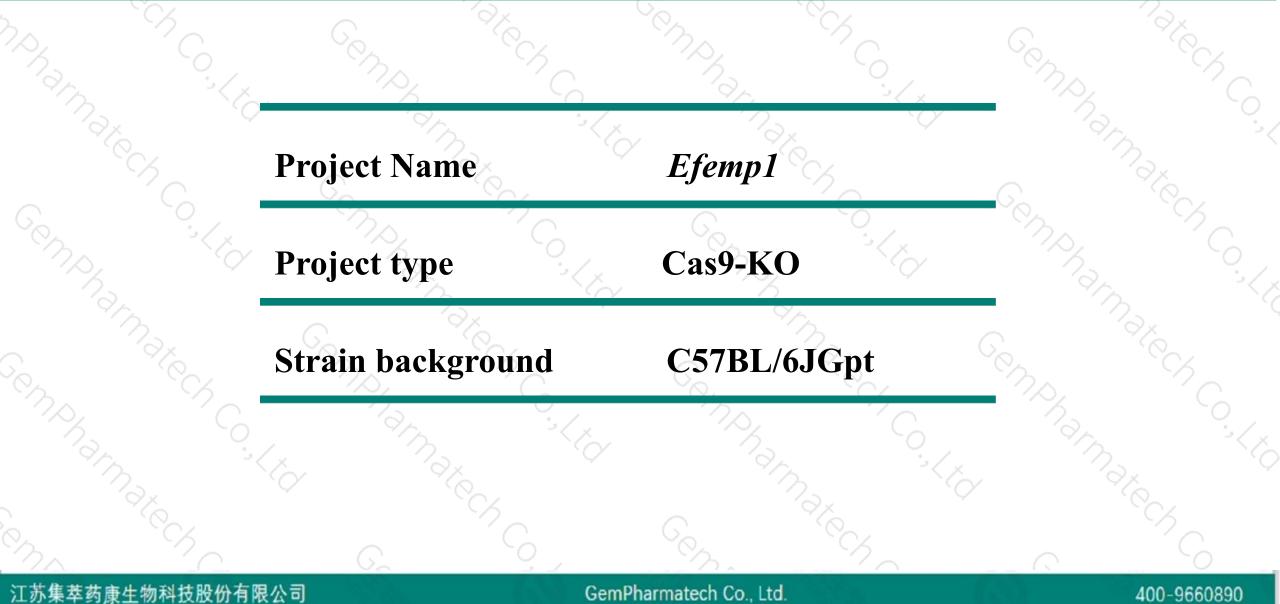


Efemp1 Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-1-17

Project Overview

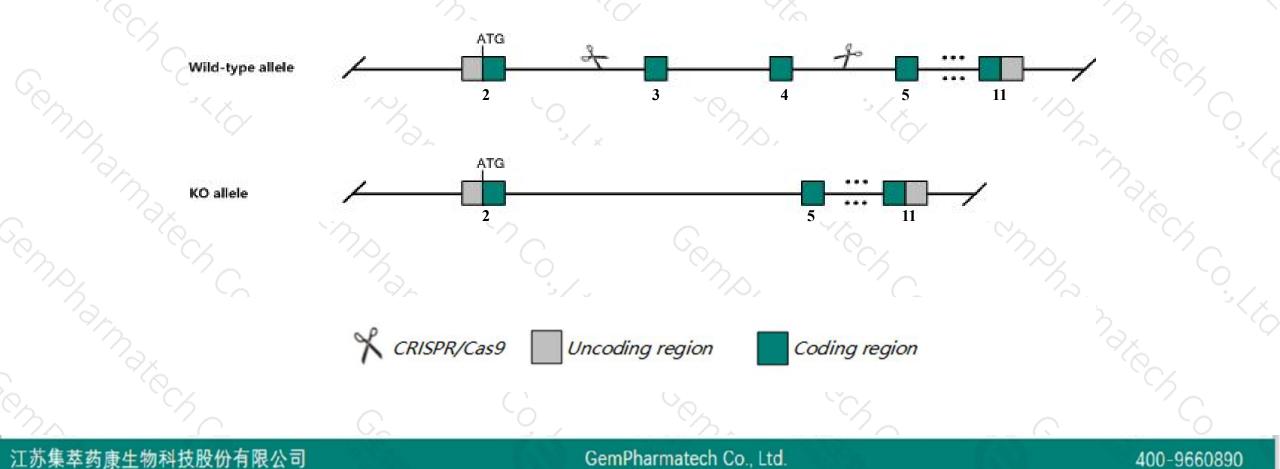




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Efemp1* gene. The schematic diagram is as follows:





- The *Efemp1* gene has 3 transcripts. According to the structure of *Efemp1* gene, exon3-exon4 of *Efemp1-201* (ENSMUST0000020759.11) transcript is recommended as the knockout region. The region contains 436bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Efemp1* gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Mice homozygous for disruptions in this gene display a normal phenotype.
 Mice homozygous for a single amino acid substitution develop deposits below the retinal pigment epithelium.
- Transcript 203 CDS 5' incomplete the influences is unknown.
- The *Efemp1* gene is located on the Chr11. 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.

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Gene information (NCBI)



Efemp1 epidermal growth factor-containing fibulin-like extracellular matrix protein 1 [Mus musculus (house mouse)]

Gene ID: 216616, updated on 3-Feb-2019

Summary

Official SymbolEfemp1 provided by MGIOfficial Full Nameepidermal growth factor-containing fibulin-like extracellular matrix protein 1 provided byMGIPrimary sourceMGI:MGI:1339998See relatedEnsembl:ENSMUSG0000020467Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusExpressionBroad expression in subcutaneous fat pad adult (RPKM 63.1), bladder adult (RPKM 60.9) and 17 other tissues
See more
human all

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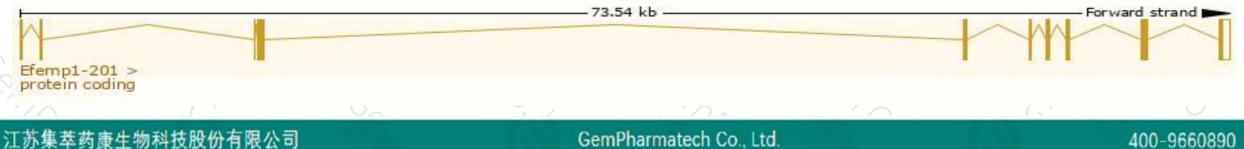
Transcript information (Ensembl)



The gene has 3 transcripts, all transcripts are shown below:

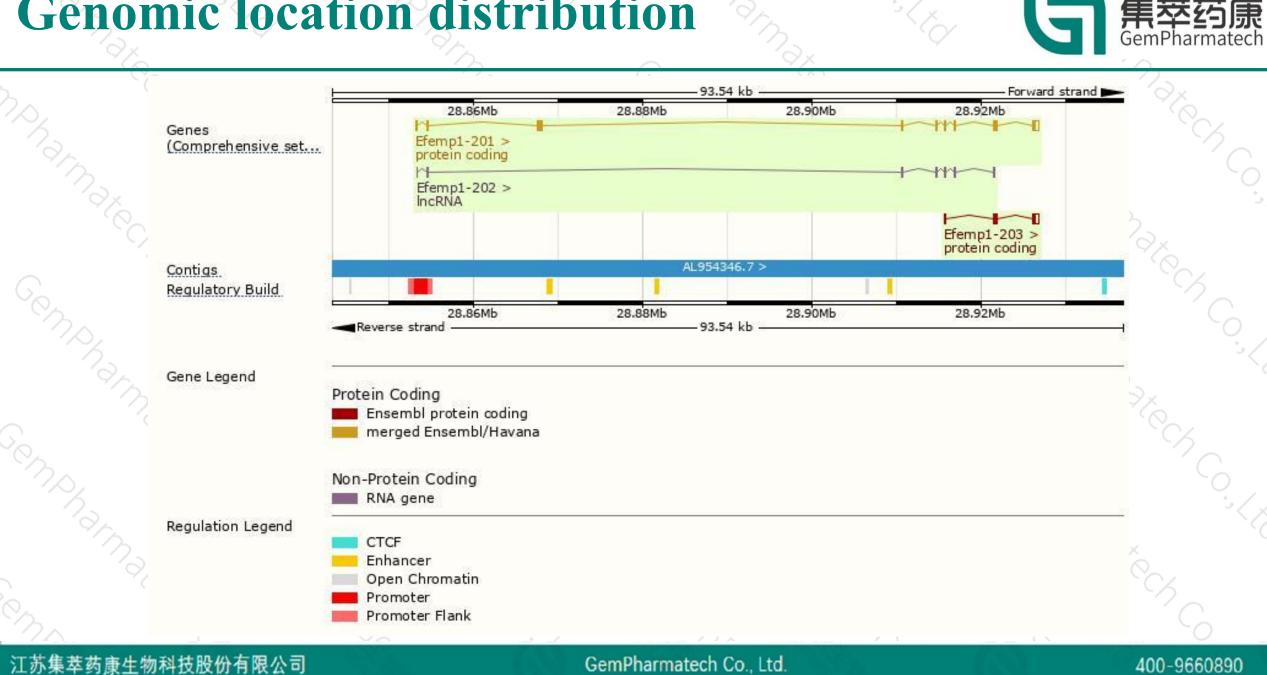
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Efemp1-201	ENSMUST00000020759.11	2037	<u>493aa</u>	Protein coding	CCDS48761	Q8BPB5	TSL:1 GENCODE basic APPRIS P1
Efemp1-203	ENSMUST00000139713.1	1021	<u>198aa</u>	Protein coding	-	F6ZFS0	CDS 5' incomplete TSL:3
Efemp1-202	ENSMUST00000124103.1	778	No protein	IncRNA	2	1040	TSL:5

The strategy is based on the design of *Efemp1-201* transcript, The transcription is shown below



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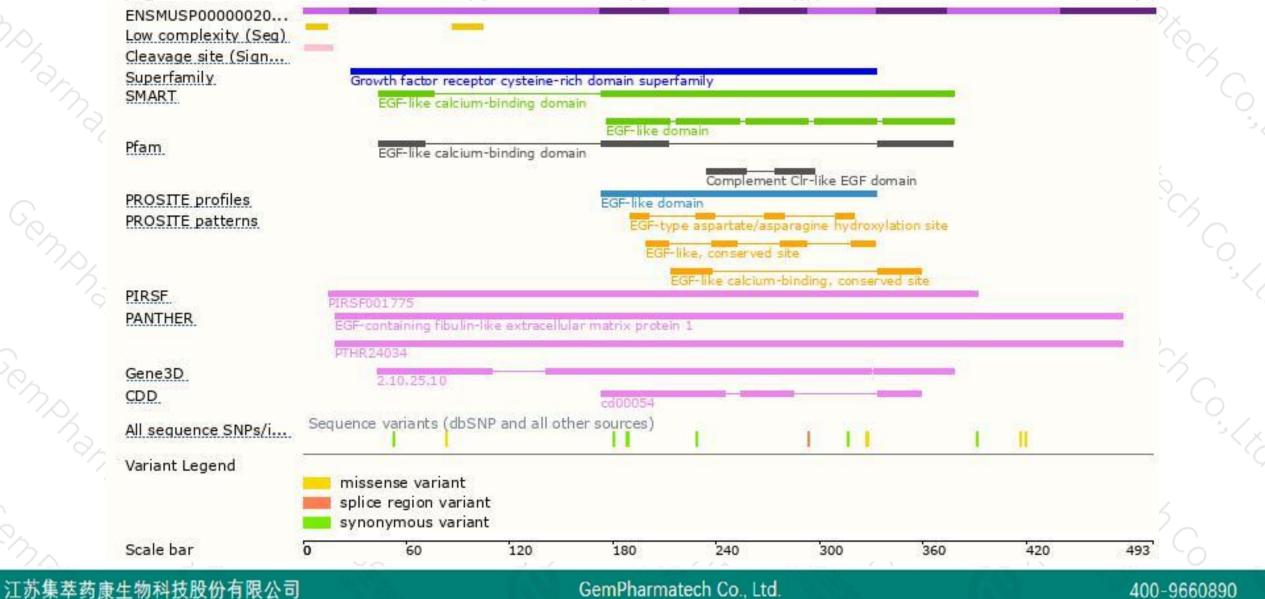
Genomic location distribution



集萃药

Protein domain

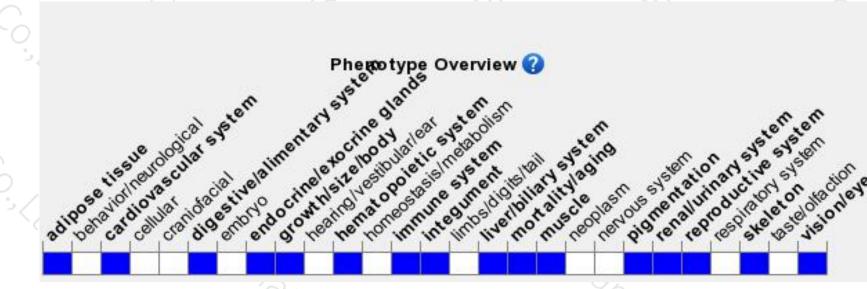




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Mouse phenotype description(MGI)





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 disruptions in this gene display a normal phenotype. Mice homozygous for a single amino acid substitution develop deposits below the retinal pigment epithelium.



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



