

Fat3 Cas9-KO Strategy

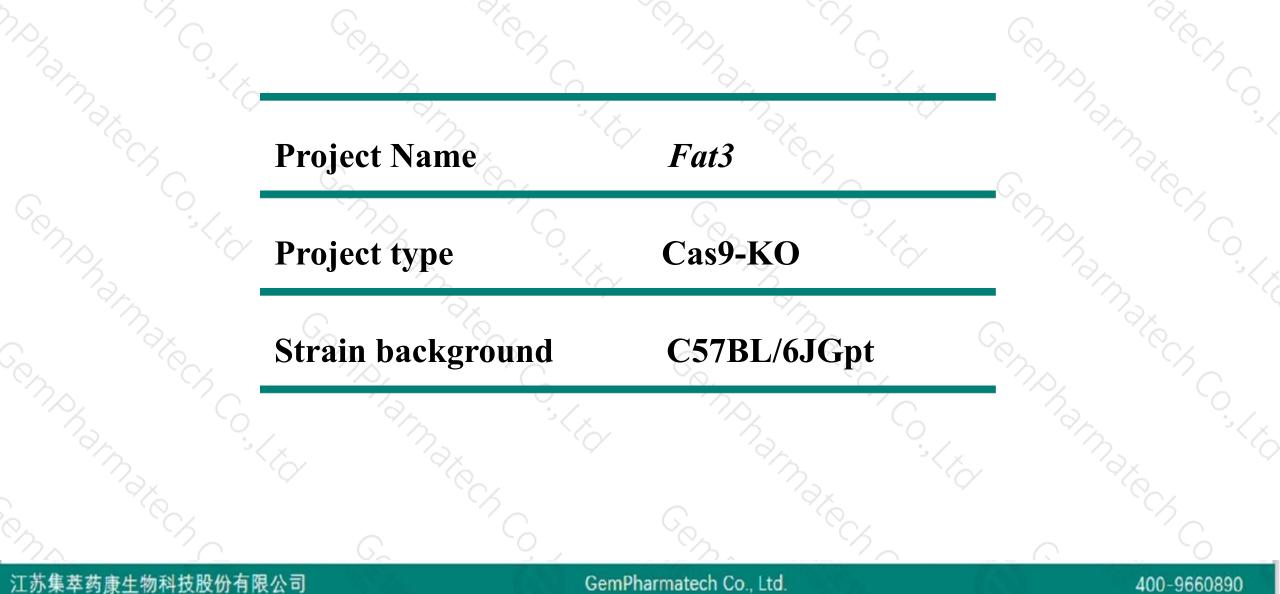
Designer: Design Date:

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Jinling Wang 2019-9-30

Project Overview

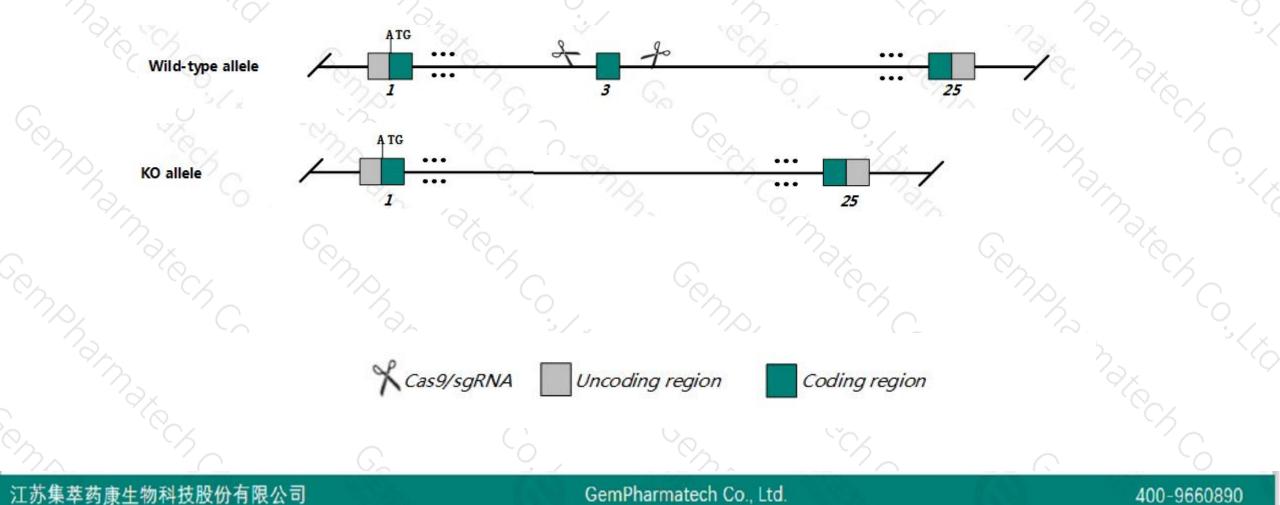




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Fat3 gene. The schematic diagram is as follows:





- The *Fat3* gene has 5 transcripts. According to the structure of *Fat3* gene, exon4 of *Fat3-201* (ENSMUST0000082170.5) transcript is recommended as the knockout region. The region contains 62bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Fat3 gene. The brief process is as follows: CRISPR/Cas9 system v

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- According to the existing MGI data, Mice homozgyous for a knock-out allele exhibit abnormal amacrine cell differentiation and migration that result in the formation of two additional plexiform layers and thickened retinal ganglion layer.
- The Fat3 gene is located on the Chr9. 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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Fat3 FAT atypical cadherin 3 [Mus musculus (house mouse)]

Gene ID: 270120, updated on 12-Mar-2019

Summary

Official SymbolFat3 provided by MGIOfficial Full NameFAT atypical cadherin 3 provided byMGIPrimary soureMGI:MGI:2444314See relateEnsembl:ENSMUSG0000074505Gene typeprotein codingprotein codingVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusAlso knownas9430076A06Rik, D430038H04Rik, Gm1132, Gm510, MFAT3FExpressionBiased expression in whole brain E14.5 (RPKM 3.7), frontal lobe adult (RPKM 3.2) and 12 other tissuesSee more
human all

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Transcript information (Ensembl)



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The gene has 5 transcripts, all transcripts are shown below:

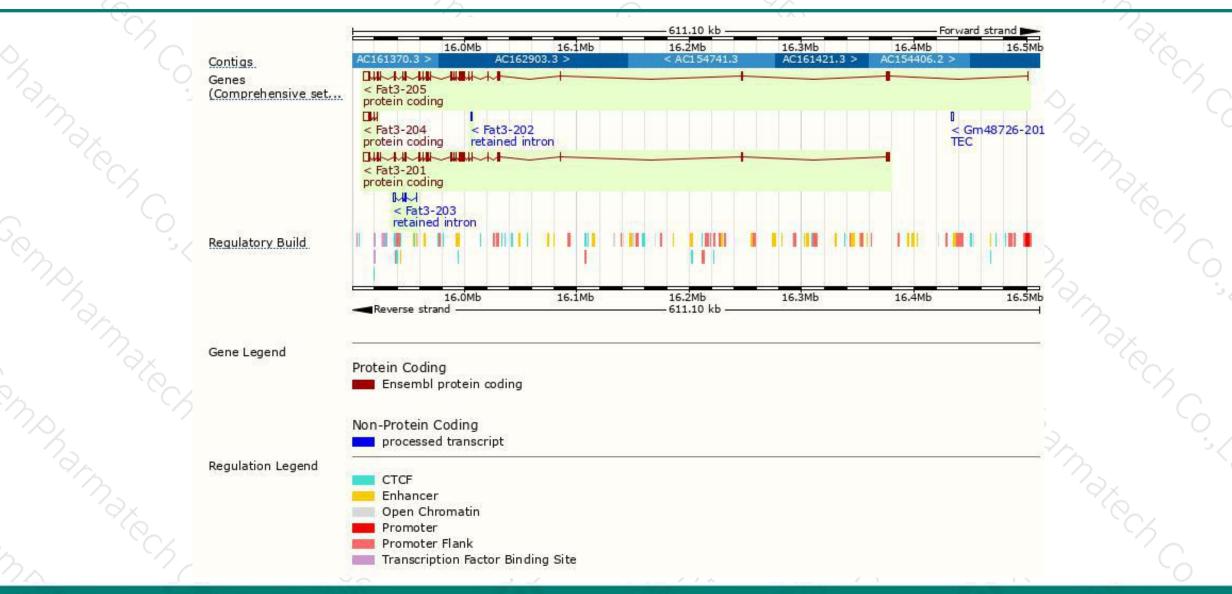
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1 March 1990							
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fat3-205	ENSMUST00000217308.1	18760	<u>4551aa</u>	Protein coding	CCDS40539	E9QK16	TSL:5 GENCODE basic APPRIS P1
Fat3-201	ENSMUST0000082170.5	18456	<u>4551aa</u>	Protein coding	CCDS40539	E9QK16	TSL:5 GENCODE basic APPRIS P1
Fat3-204	ENSMUST00000217187.1	6024	<u>404aa</u>	Protein coding	8 4	A0A1L1SU86	CDS 5' incomplete TSL:3
Fat3-203	ENSMUST00000215388.1	2214	No protein	Retained intron	62	20	TSL:1
Fat3-202	ENSMUST00000213517.1	SMUST00000213517.1 1391 No prote		Retained intron	15	T.(TSL:NA

The strategy is based on the design of *Fat3-201* transcript, The transcription is shown below



Genomic location distribution



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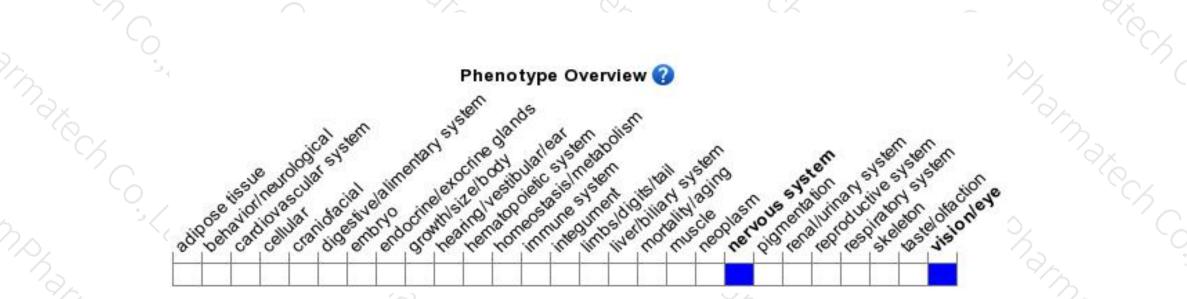
Protein domain



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	SMART domains	Cadherin										EGF-like domain Laminin G 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 homozgyous for a knock-out allele exhibit abnormal amacrine cell differentiation and migration that result in the formation of two additional plexiform layers and thickened retinal ganglion lay



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



