

Slc27a6 Cas9-KO Strategy

Designer:

Reviewer:

Design Date:

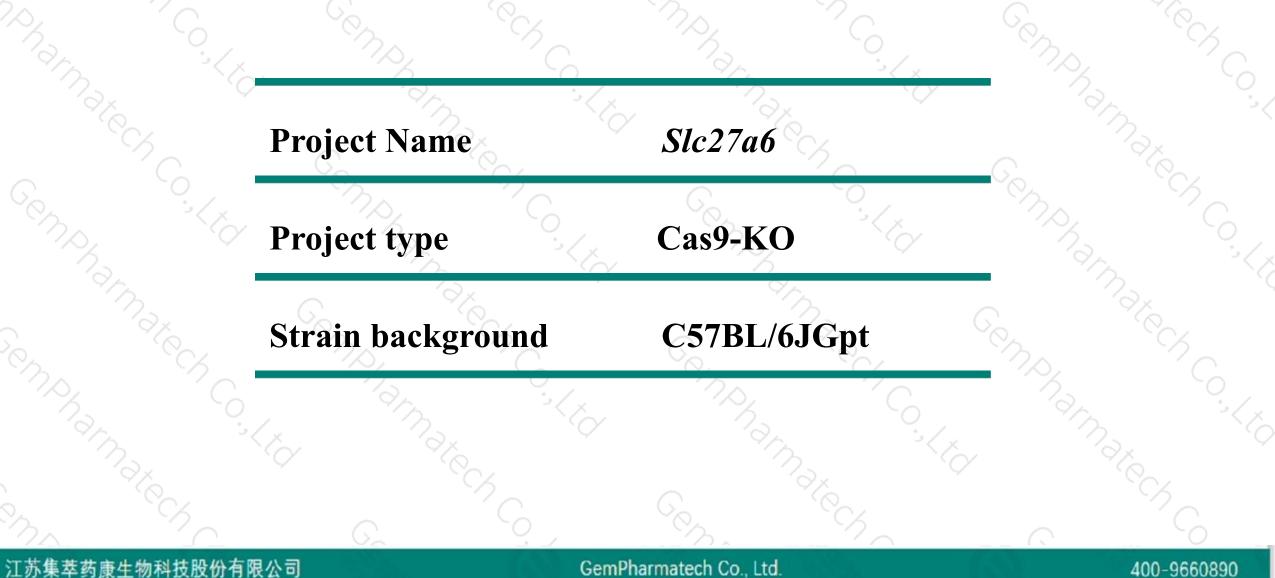
Daohua Xu

Huimin Su

2020-4-15

Project Overview





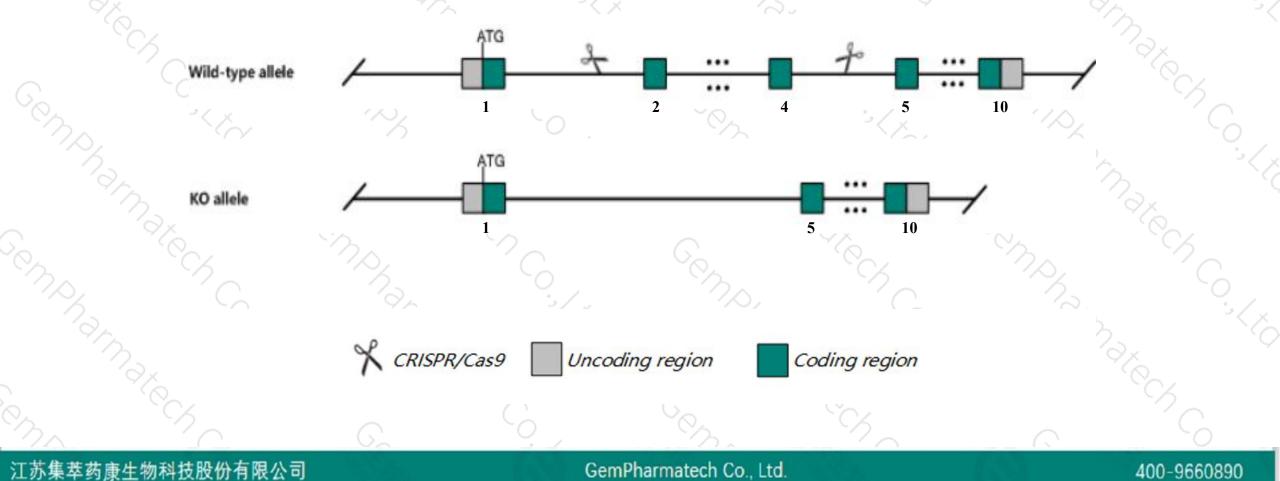
江苏集萃药康生物科技股份有限公司

GemPharmatech Co., Ltd.

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Slc27a6* gene. The schematic diagram is as follows:





- The Slc27a6 gene has 1 transcript. According to the structure of Slc27a6 gene, exon2-exon4 of Slc27a6-201 (ENSMUST00000025500.6) transcript is recommended as the knockout region. The region contains 488bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Slc27a6 gene. The brief process is as follows: CRISPR/Cas9 syste

- > The *Slc27a6* gene is located on the Chr18. 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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SIc27a6 solute carrier family 27 (fatty acid transporter), member 6 [Mus musculus (house mouse)]

Gene ID: 225579, updated on 13-Mar-2020

Summary

Official Symbol	SIc27a6 provided by MGI
Official Full Name	solute carrier family 27 (fatty acid transporter), member 6 provided by MGI
Primary source	MGI:MGI:3036230
See related	Ensembl:ENSMUSG00000024600
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
	Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4732438L20Rik, FACVL2, FATP6, VLCS-H1
Expression	Biased expression in placenta adult (RPKM 5.5), testis adult (RPKM 2.2) and 6 other tissues See more
Orthologs	human all

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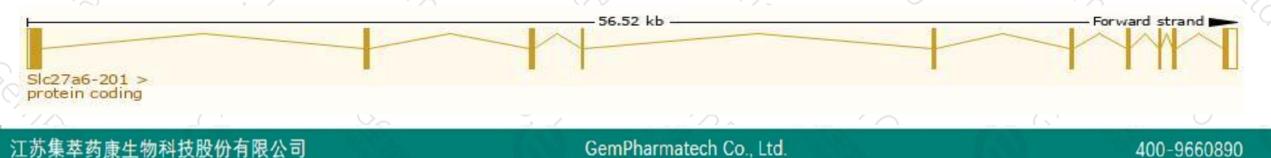
Transcript information (Ensembl)



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

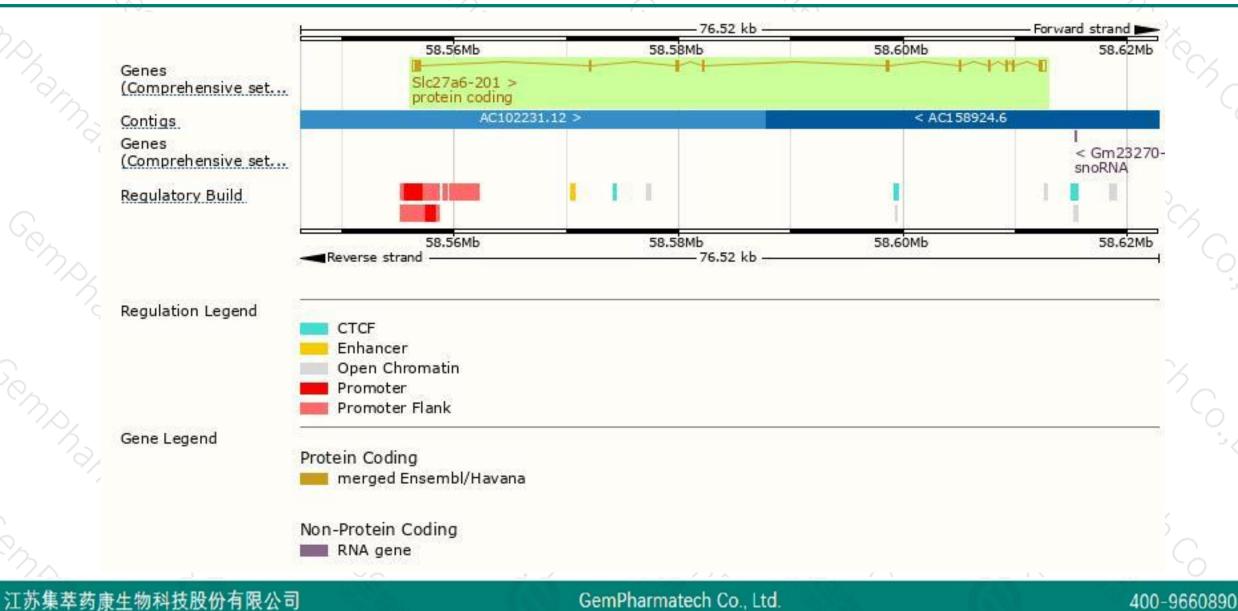
Name	Transcript ID		Protein	otein Biotype	CCDS	UniProt	Flags						
SIc27a6-201	ENSMUST00000025500.6	2485	<u>619aa</u>	Protein coding	CCDS37828	E9Q9W4	TSL:1 GENCODE basic APPRIS is a system to annotate alt	ernatively spliced transcripts based on a rang	ge of computational methods to id	dentify the most functionally import	ant transcript(s) of a gene. APPRIS P1		
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The strategy is based on the design of *Slc27a6-201* transcript, the transcription is shown below:



Genomic location distribution





Protein domain



ENSMUSP00000025 Low complexity (Seq) Superfamily. Pfam. AMP-dependent synthetase/ligase AMP-binding enzyme, C-ten PROSITE patterns. AMP-binding, conserved site PANTHER. Patty add transport protein 5 PTHR43107 Gene3D. AMP-dependent synthetase-like superfamily 3.30.300.30 CDD. cd05938 All sequence SNPs/L Sequence variant (dbSNP and all other sources) II IIII IIIIIIIIIIIIIIIIIIIIIIIIIIII					<	- 00 ×		`°~z				70×	
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Gene3D. AMP-dependent synthetase-like superfamily 3.30,300.30 CDD. cd05938 All sequence SNPs/i Sequence variants (dbSNP and all other sources) Variant Legend missense variant splice region variants Scale bar 0 6 120 180 240 300 360 420 480		PROSITE patterns				AMP-binding,	conserved :	site					
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



