

Slc27a4 Cas9-KO Strategy

Designer: Reviewer:

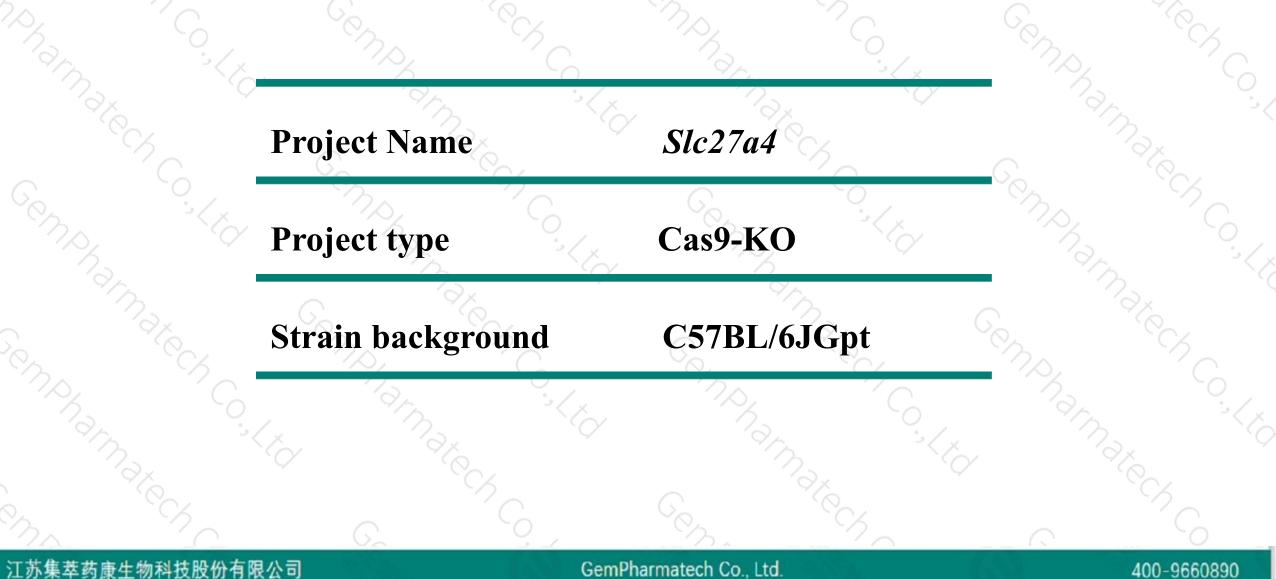
Design Date:

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2020-4-7

Project Overview



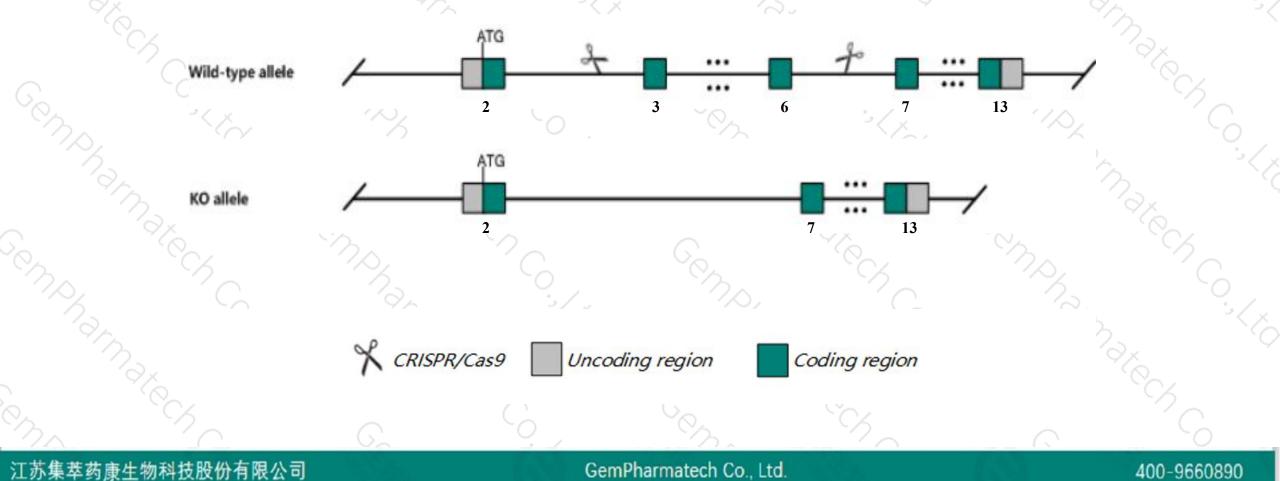


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Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Slc27a4* gene. The schematic diagram is as follows:





- The Slc27a4 gene has 2 transcripts. According to the structure of Slc27a4 gene, exon3-exon6 of Slc27a4-201 (ENSMUST0000080065.2) transcript is recommended as the knockout region. The region contains 716bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Slc27a4 gene. The brief process is as follows: CRISPR/Cas9 syste

- According to the existing MGI data, Homozygous mutant mice are not viable. While mice of one mutant line die during early development, mice of other mutant lines die at birth exhibiting abnormal skin.
- The *Slc27a4* gene is located on the Chr2. 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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SIc27a4 solute carrier family 27 (fatty acid transporter), member 4 [Mus musculus (house mouse)]

Gene ID: 26569, updated on 13-Mar-2020

Summary

Official Symbol	SIc27a4 provided by MGI
Official Full Name	solute carrier family 27 (fatty acid transporter), member 4 provided by MGI
Primary source	MGI:MGI:1347347
See related	Ensembl:ENSMUSG0000059316
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	BB144259, FATP4
Expression	Biased expression in duodenum adult (RPKM 297.3), small intestine adult (RPKM 226.2) and 14 other tissues See more
Orthologs	human all

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Transcript information (Ensembl)



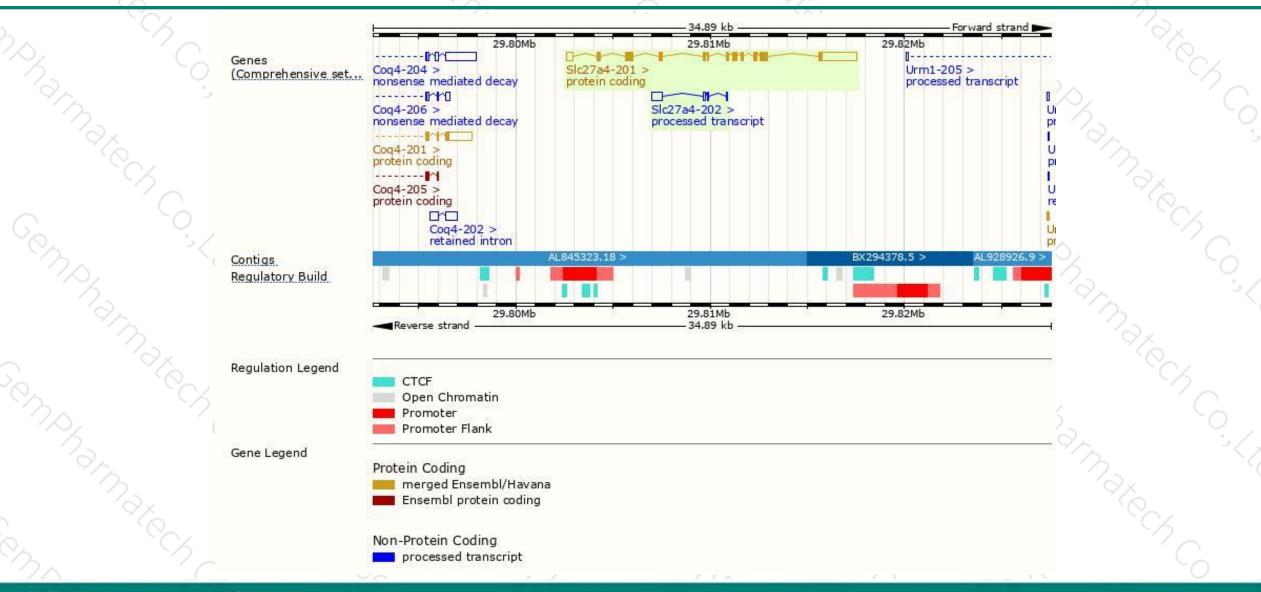
The gene has 2 transcripts, all transcripts are shown below:

Name 🍦	Transcript ID	bp 🖕	Protein 🖕	Biotype 🔺	CCDS 🖕	UniProt 🖕	Flags 🔶		
SIc27a4-201	ENSMUST0000080065.2	4054	<u>643aa</u>	Protein coding	CCDS15858	<u>Q91VE0</u> @	TSL:1	GENCODE basic	APPRIS P1
SIc27a4-202	ENSMUST00000136444.1	722	No protein	Processed transcript	2	12		TSL:5	

The strategy is based on the design of Slc27a4-201 transcript, The transcription is shown below



Genomic location distribution



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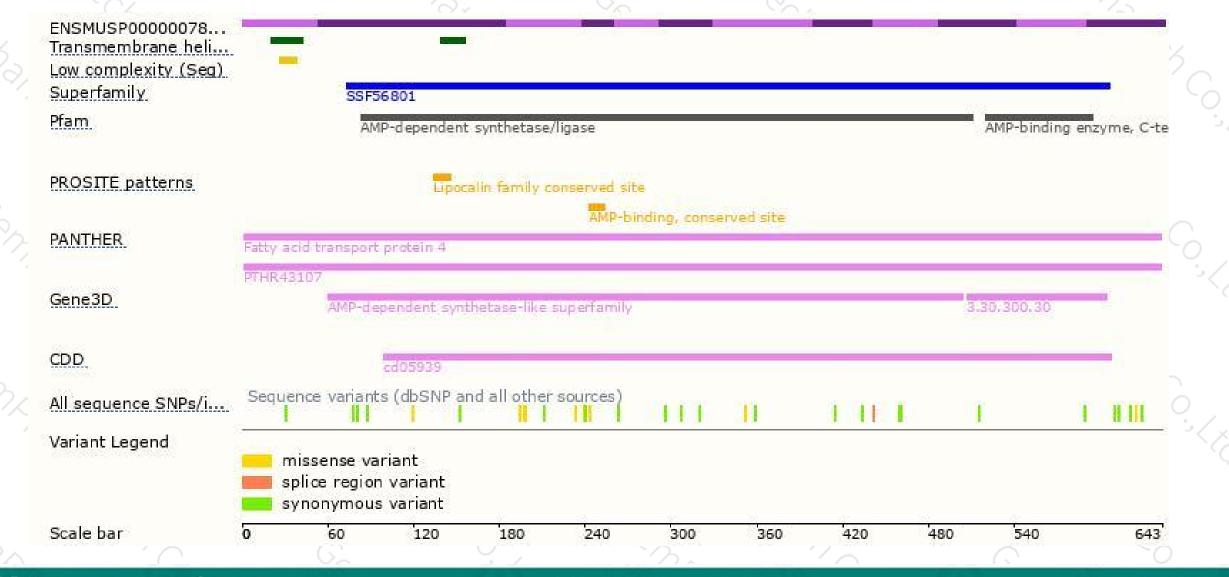
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Protein domain





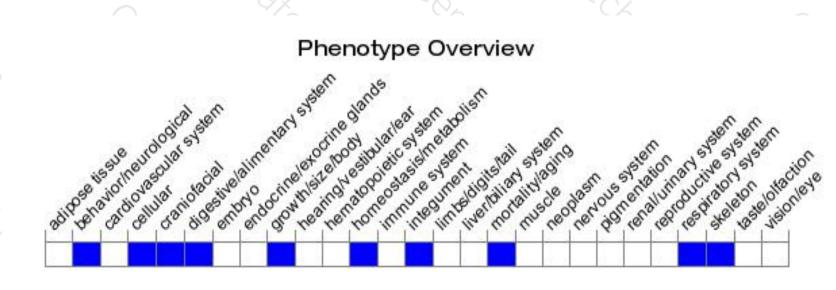
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Mouse phenotype description(MGI)





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, Homozygous mutant mice are not viable. While mice of one mutant line die during early development, mice of other mutant lines die at birth exhibiting abnormal skin.



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



