

Siglec1 Cas9-KO Strategy

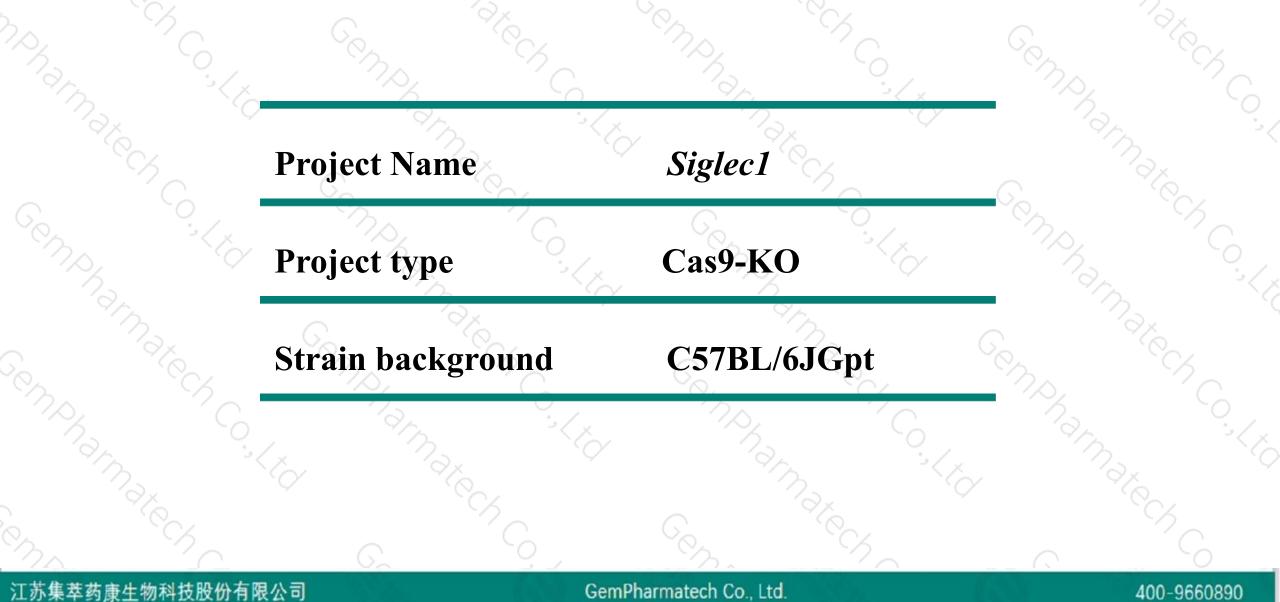
Designer: Reviewer:

Design Date:

Daohua Xu Huimin Su 2019-12-18

Project Overview

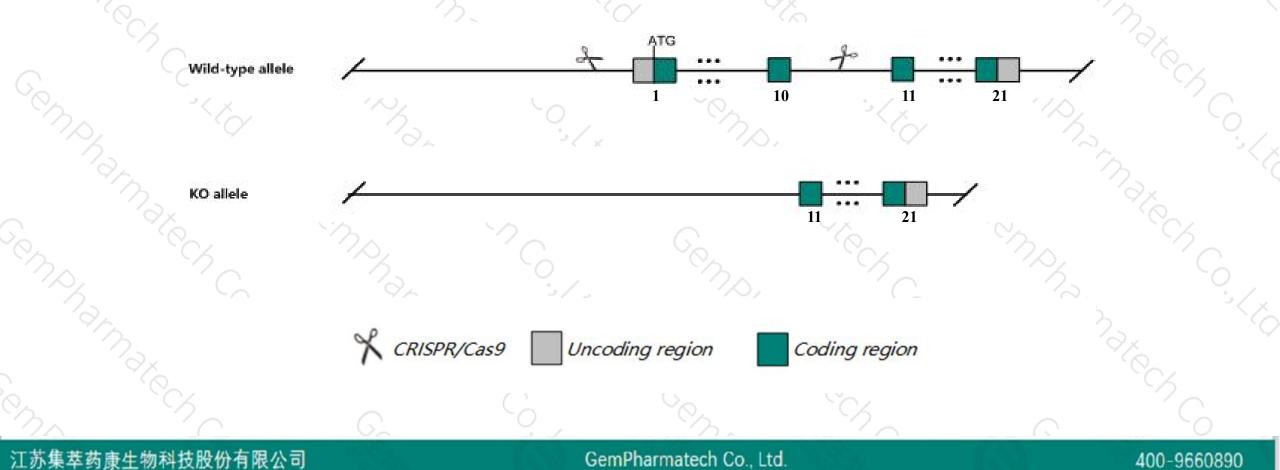




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Siglec1 gene. The schematic diagram is as follows:





- The Siglec1 gene has 3 transcripts. According to the structure of Siglec1 gene, exon1-exon10 of Siglec1-201 (ENSMUST00000028794.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Siglec1 gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Mice homozygous for a disruption in this gene display subtle changes in B- and T-cell populations and decreased IgM levels. Mice homozygous for a knock-out or knock-in allele exhibit impaired phagocytosis of sialylated C. jejuni.
- The Siglec1 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.

Gene information (NCBI)



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Siglec1 sialic acid binding Ig-like lectin 1, sialoadhesin [Mus musculus (house mouse)]

Gene ID: 20612, updated on 12-Mar-2019

Summary

Official Symbol	Siglec1 provided by MGI								
Official Full Name	sialic acid binding Ig-like lectin 1, sialoadhesin provided by MGI								
Primary source	MGI:MGI:99668								
See related	Ensembl:ENSMUSG00000027322								
Gene type	protein coding								
RefSeq status	VALIDATED								
Organism	Mus musculus								
Lineage									
	Muroidea; Muridae; Murinae; Mus; Mus								
Also known as	Cd169, Siglec-1, Sn								
Expression	Biased expression in mammary gland adult (RPKM 31.7), spleen adult (RPKM 18.9) and 11 other tissues See more								
Orthologs	human all								

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Transcript information (Ensembl)



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

Name 🍦	Transcript ID ENSMUST0000028794.9	Contractor	Protein <u>1701aa</u>	Biotype 🝦	CCDS 🝦 CCDS16754 &	UniProt <u>G3X8X6</u> ₪	Flags			
Siglec1-201							TSL:1 GENCODE basic APPRIS P2			
Siglec1-203	ENSMUST00000110227.7	5790	<u>1605aa</u>	Protein coding		H9KUZ3@	TSL:1	GENC	ODE basic	APPRIS ALT2
Siglec1-202	ENSMUST00000110226.1	1861	<u>346aa</u>	Protein coding		H9KUZ2@		TSL:1	GENCODE	basic

The strategy is based on the design of Siglec1-201 transcript, The transcription is shown below

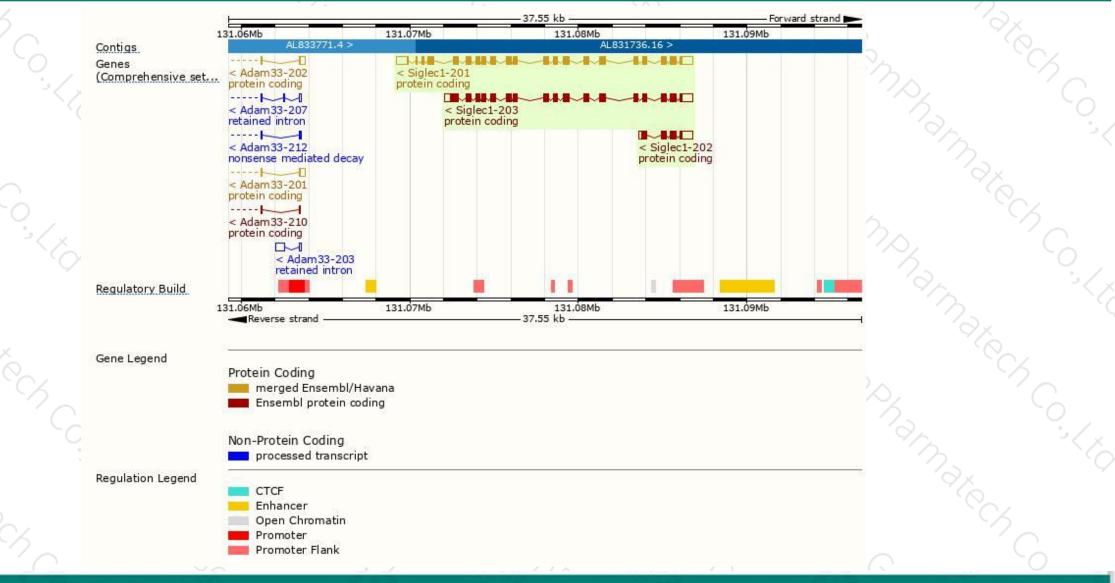


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Genomic location distribution





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Protein domain





Mouse phenotype description(MGI)

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nematopoletic

nomeostaste

Click cells to view annotations.

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Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

Phenotype Overview 🕜

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



