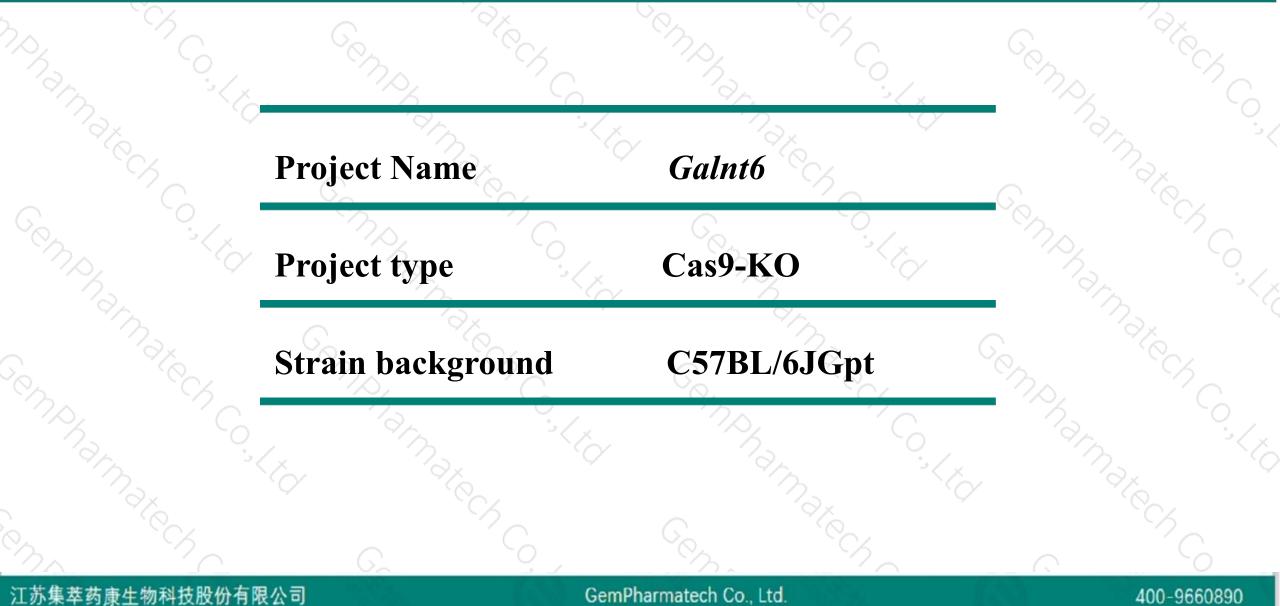


# Galnt6 Cas9-KO Strategy

Designer: Yanhua Shen Reviewer: Xueting Zhang Design Date: 2020-4-8

# **Project Overview**

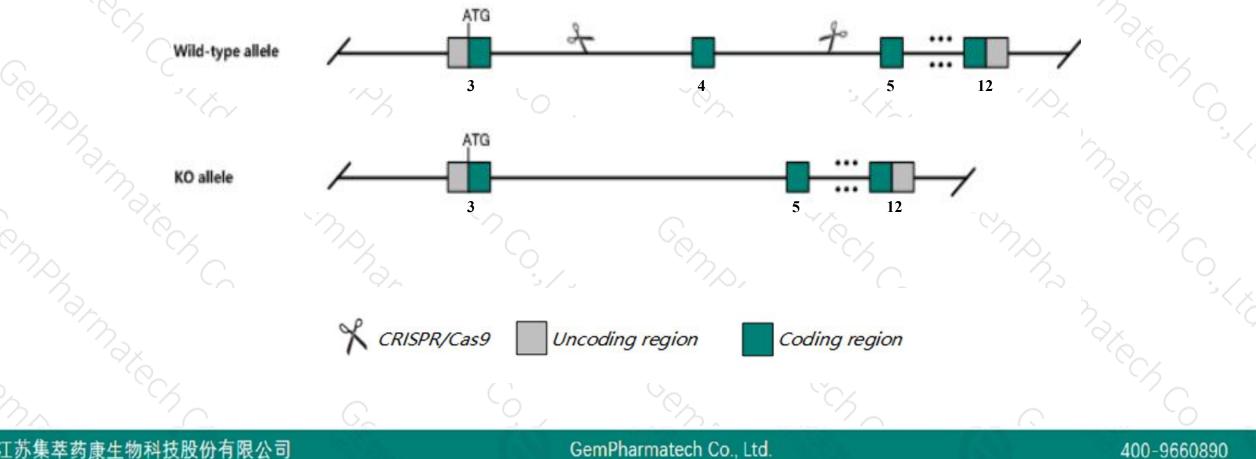




# **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the Galnt6 gene. The schematic diagram is as follows:



技股份有限公司 江苏集萃药康牛

GemPharmatech Co., Ltd.



- The Galnt6 gene has 3 transcripts. According to the structure of Galnt6 gene, exon4 of Galnt6-201 (ENSMUST00000052069.11) transcript is recommended as the knockout region. The region contains 173bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Galnt6 gene. The brief process is as follows: CRISPR/Cas9 system

- > Some amino acids will remain at the N-terminus and some functions may be retained.
- The Galnt6 gene is located on the Chr15. 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)**



\$ ?

### GaInt6 polypeptide N-acetylgalactosaminyltransferase 6 [Mus musculus (house mouse)]

Gene ID: 207839, updated on 13-Mar-2020

#### Summary

Official Symbol	Gaint6 provided by MGI
Official Full Name	polypeptide N-acetylgalactosaminyltransferase 6 provided byMGI
Primary source	MGI:MGI:1891640
See related	Ensembl:ENSMUSG00000037280
Gene type	protein coding
<b>RefSeq status</b>	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	4632410F13, AW047994, GalNAc-T6
Expression	Biased expression in large intestine adult (RPKM 18.2), small intestine adult (RPKM 15.4) and 11 other tissues See more
Orthologs	human all



# **Transcript information (Ensembl)**

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

25 170.						4	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gaint6-201	ENSMUST0000052069.11	3798	<u>622aa</u>	Protein coding	CCDS27843	Q8C7U7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Galnt6-202	ENSMUST00000159715.7	3796	<u>622aa</u>	Protein coding	CCDS27843	Q8C7U7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Gaint6-203	ENSMUST00000161514.1	2746	<u>622aa</u>	Protein coding	CCDS27843	Q8C7U7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of Galnt6-201 transcript, The transcription is shown below

< Galnt6-201 protein coding

Reverse strand

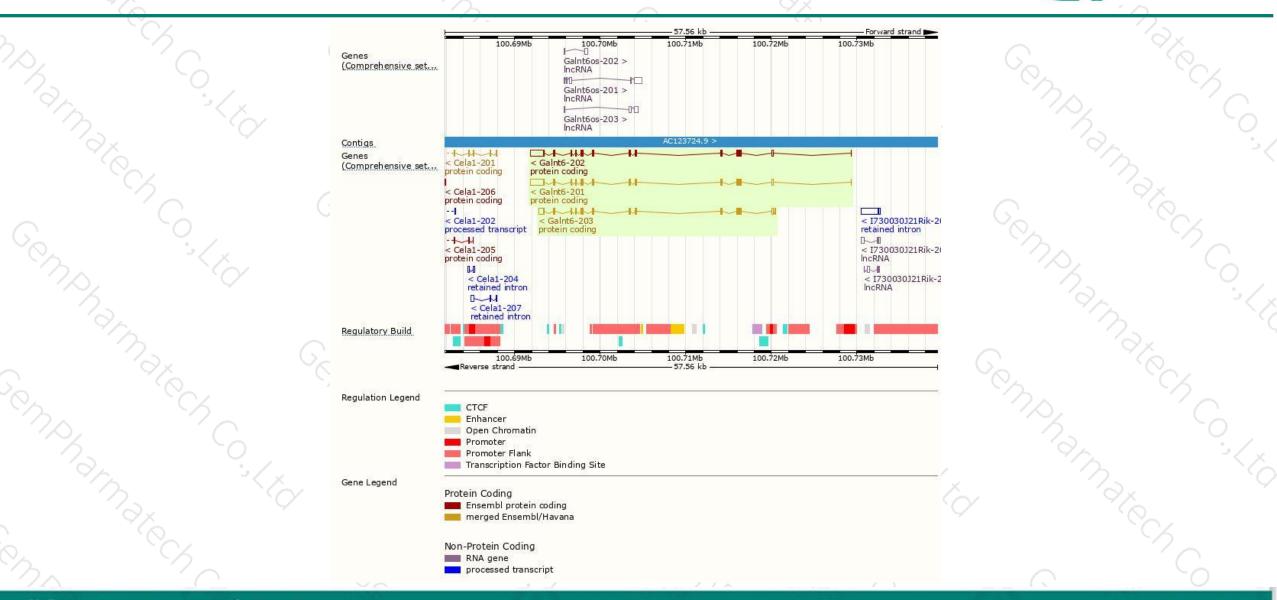
— 37.56 kb -

### 江苏集萃药康生物科技股份有限公司

### GemPharmatech Co., Ltd.

#### 400-9660890

### **Genomic location distribution**



**集萃药康** GemPharmatech

400-9660890

江苏集萃药康生物科技股份有限公司

GemPharmatech Co., Ltd.

# **Protein domain**

江苏



集萃药康	生物科技股份有限公司				Ge	mPharmat	ech Co., Lt	d.				40	0-9660890
	Scale bar	0	60	120	180	240	300	360	420	480	540	622	G
- <sup>-</sup> - <u>-</u>	Variant Legend	💼 spl	ssense var ice region nonymous	variant									5
	All sequence SINPS/I	<u>.</u>	1111			1 1 0	1.101	III.	¶.	111			~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	All sequence SNPs/i	Sequen	ce variants	(dbSNP an	d all other s	ources)							-7 C
	CDD				cd02510					Ric	in B, lectin domai	in	
- A	Gene3D	RUNKTIP	Nucleotide-diphospho-sugar transferases								0.10.50	-	
3	PANTHER	PTHR116 PTHR116											6
	PROSITE profiles									R	icin B, lectin dom	ain	202
~~	Pfam.				Glycosyl	transferase 2	-like			Ric	in B, lectin domai	n	
"m	SMART									Rici	n B, lectin domain	n	
	Superfamily			1	Nucleotide-di	Ricin		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~					
	ENSMUSP00000056 Low complexity (Seg)	-				-							200



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



