

# Galnt16 Cas9-KO Strategy

**Designer:** 

**Reviewer:** 

**Design Date:** 

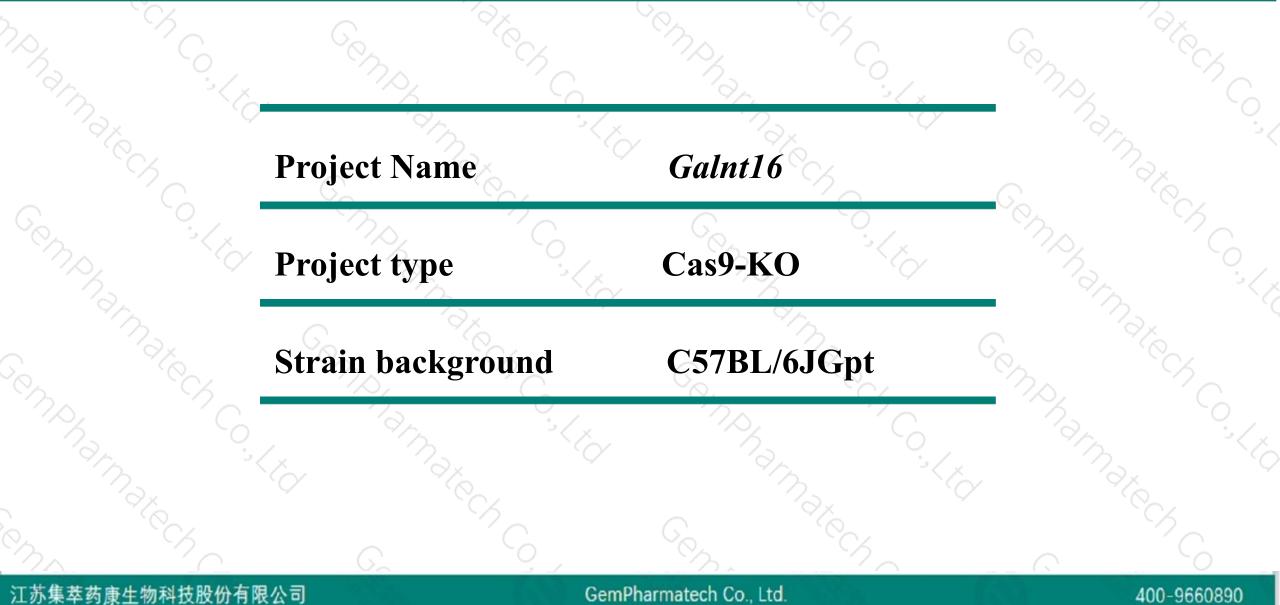
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2020-4-15

## **Project Overview**

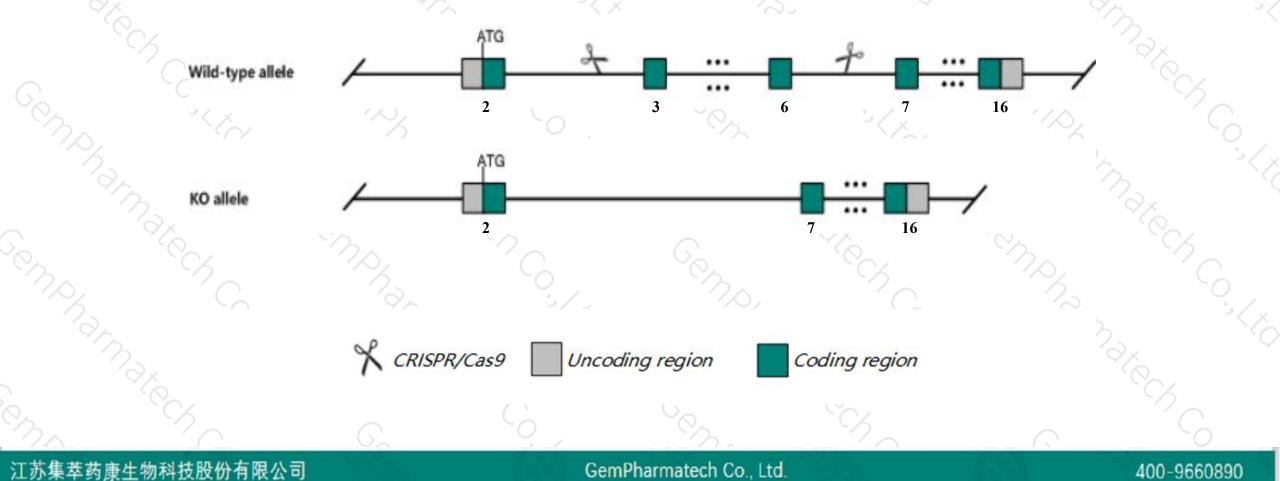




# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the Galnt16 gene. The schematic diagram is as follows:





The Galnt16 gene has 6 transcripts. According to the structure of Galnt16 gene, exon3-exon6 of Galnt16-206 (ENSMUST00000219993.1) transcript is recommended as the knockout region. The region contains 391bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify Galnt16 gene. The brief process is as follows: CRISPR/Cas9 syste

- > Some amino acids will remain at the N-terminus and some functions may be retained.
- ➤ The effect of transcripts 202,205 is unknown.
- ➤ Transcript 203 may not be affected.

Notice

- The Galnt16 gene is located on the Chr12. 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)**



\$ ?

### GaInt16 polypeptide N-acetylgalactosaminyltransferase 16 [Mus musculus (house mouse)]

Gene ID: 108760, updated on 13-Mar-2020

#### Summary

| Official Symbol      | Galnt16 provided by MGI  |
|----------------------|--|
|                      |  |
| Official Full Name   | polypeptide N-acetylgalactosaminyltransferase 16 provided by <u>MGI</u>  |
| Primary source       | MGI:MGI:1917754  |
| See related          | Ensembl:ENSMUSG00000021130   |
| 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        | 5730405L21Rik, Al415388, Galntl1, galNAc-T16, mpp-GalNAc-T16   |
| Expression           | Broad expression in frontal lobe adult (RPKM 9.5), cerebellum adult (RPKM 7.3) and 19 other tissues See more                         |
| Orthologs            | human all  |

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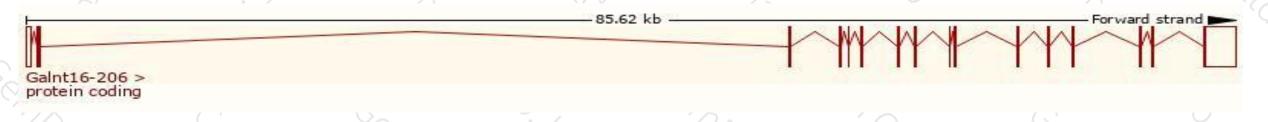
# **Transcript information (Ensembl)**



### The gene has 6 transcripts, all transcripts are shown below:

| Name        | Transcript ID        | bp   | Protein      | Biotype                 | CCDS      | UniProt       | Flags   |
|-------------|----------------------|------|--------------|-------------------------|-----------|---------------|---|
| Gaint16-206 | ENSMUST00000219993.1 | 4222 | <u>558aa</u> | Protein coding          | CCDS36482 | Q9JJ61        | 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 |
| Gaint16-201 | ENSMUST00000021558.7 | 3922 | <u>558aa</u> | Protein coding          | CCDS36482 | <u>Q9JJ61</u> | 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 |
| Gaint16-204 | ENSMUST00000218943.1 | 2047 | <u>558aa</u> | Protein coding          | CCDS36482 | Q9JJ61        | 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 |
| Gaint16-202 | ENSMUST00000217926.1 | 771  | <u>125aa</u> | Protein coding          | -         | A0A1W2P6P9    | CDS 5' incomplete TSL:2   |
| Gaint16-205 | ENSMUST00000219267.1 | 502  | <u>59aa</u>  | Nonsense mediated decay | -         | A0A1W2P7U3    | CDS 5' incomplete TSL:3   |
| Gaint16-203 | ENSMUST00000218648.1 | 2827 | No protein   | Retained intron         | -         | -             | TSLINA  |

The strategy is based on the design of Galnt16-206 transcript, The transcription is shown below



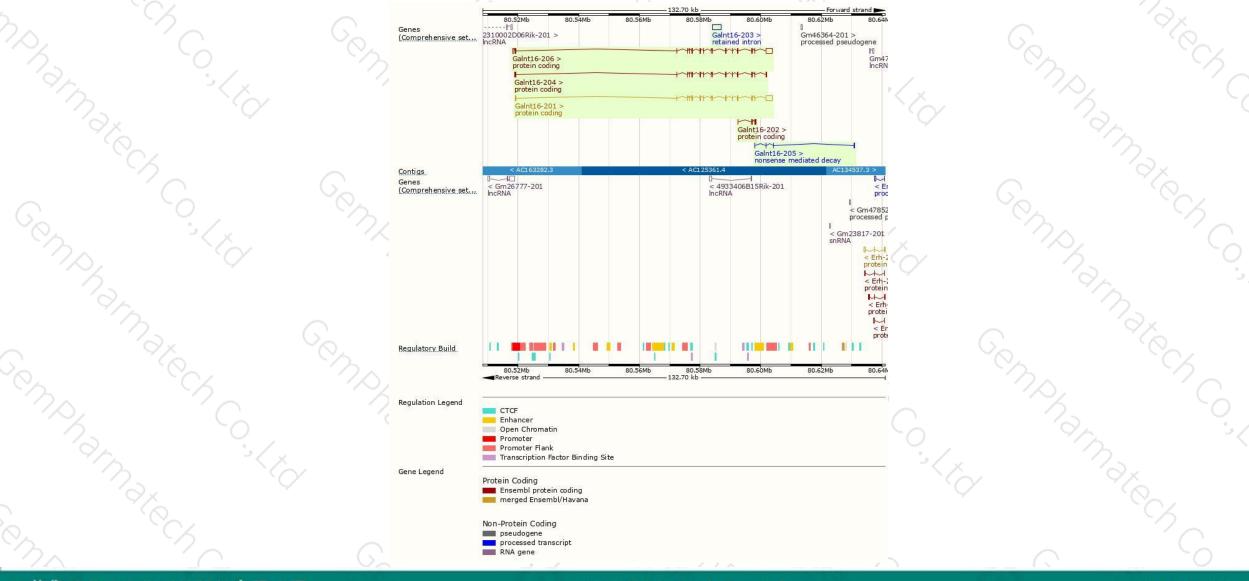
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### **Genomic location distribution**





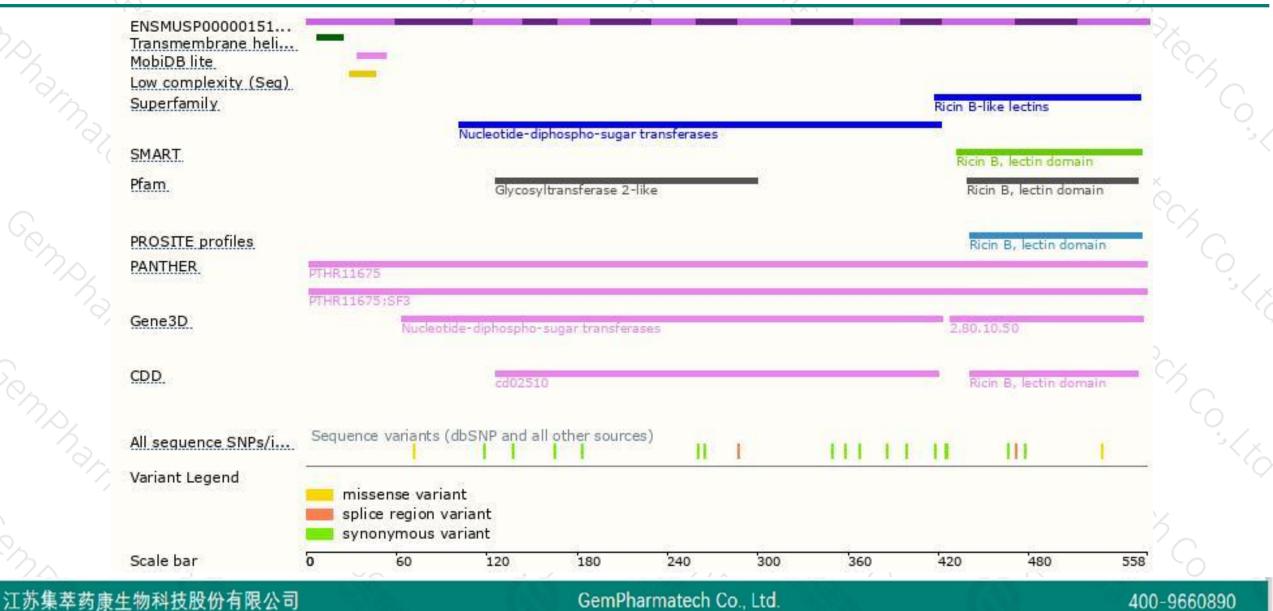
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### **Protein domain**







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



