

# ***Galnt6* Cas9-KO Strategy**

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Reviewer: Xueting Zhang

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# Project Overview

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**Project Name**

***Galnt6***

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**Project type**

**Cas9-KO**

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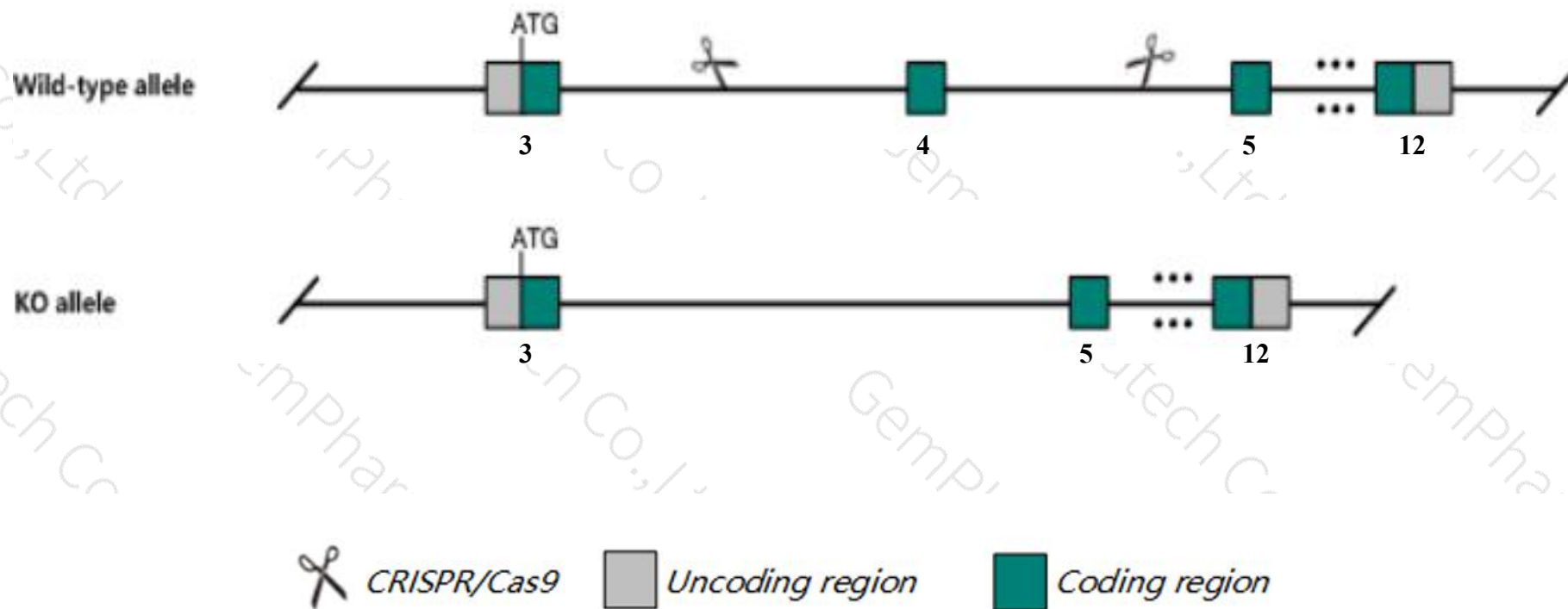
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- 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.



# Gene information (NCBI)

## Galnt6 polypeptide N-acetylgalactosaminyltransferase 6 [Mus musculus (house mouse)]

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

### Summary



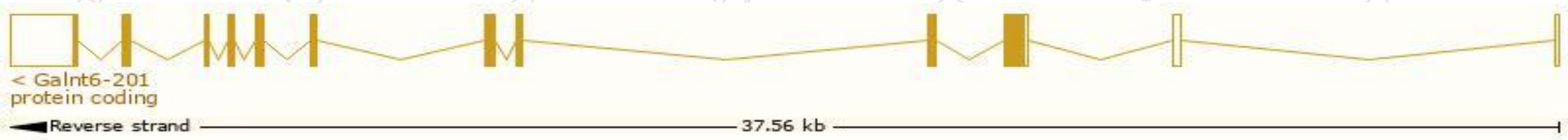
<b>Official Symbol</b>	Galnt6 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	polypeptide N-acetylgalactosaminyltransferase 6 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1891640</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000037280</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	4632410F13, AW047994, GalNAc-T6
<b>Expression</b>	Biased expression in large intestine adult (RPKM 18.2), small intestine adult (RPKM 15.4) and 11 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

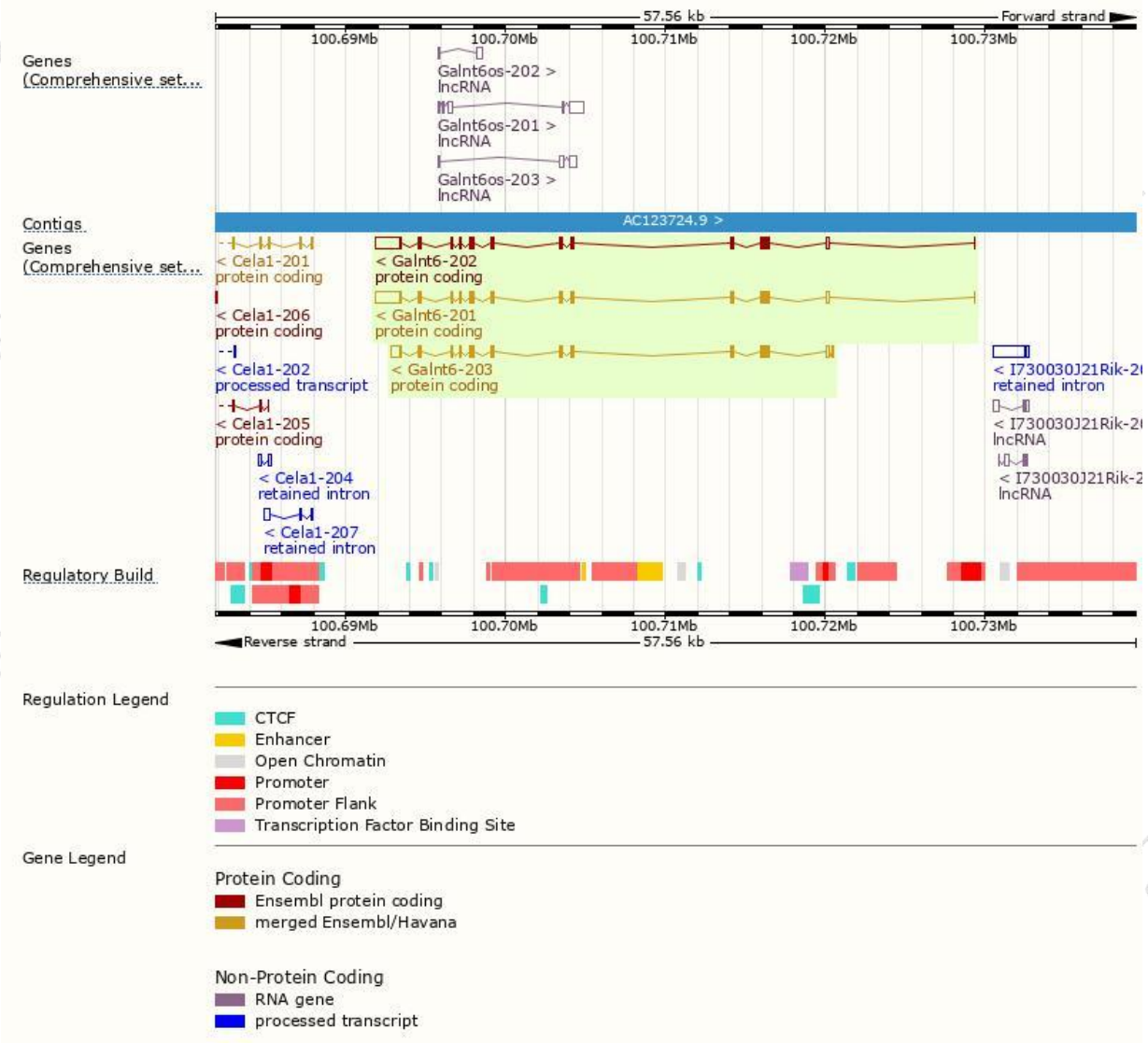
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Galnt6-201	<a href="#">ENSMUST00000052069.11</a>	3798	<a href="#">622aa</a>	Protein coding	<a href="#">CCDS27843</a>	<a href="#">Q8C7U7</a>	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	<a href="#">ENSMUST00000159715.7</a>	3796	<a href="#">622aa</a>	Protein coding	<a href="#">CCDS27843</a>	<a href="#">Q8C7U7</a>	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
Galnt6-203	<a href="#">ENSMUST00000161514.1</a>	2746	<a href="#">622aa</a>	Protein coding	<a href="#">CCDS27843</a>	<a href="#">Q8C7U7</a>	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

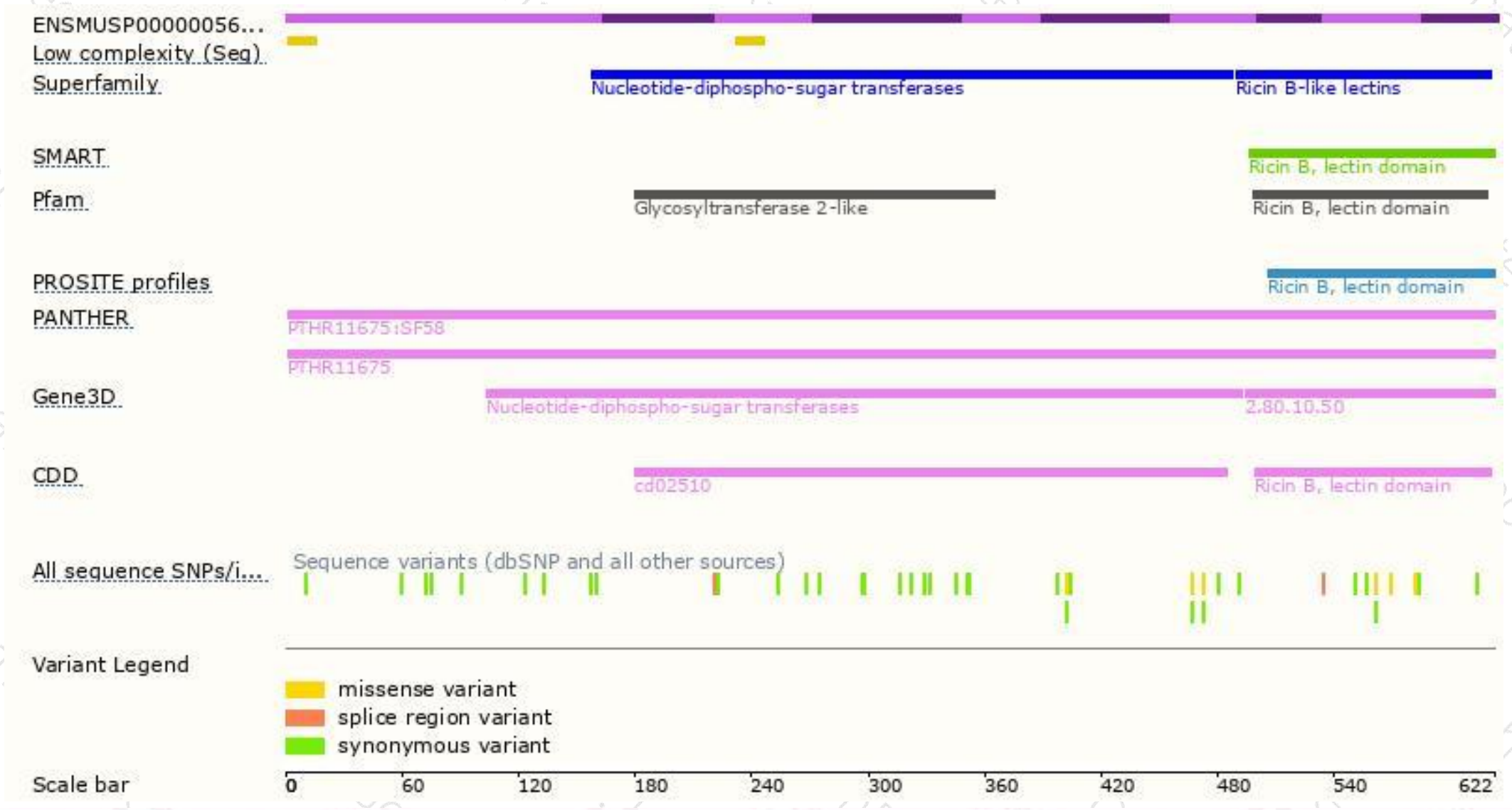


# Genomic location distribution





# Protein domain



If you have any questions, you are welcome to inquire.

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