

St6gal1 Cas9-KO Strategy

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Reviewer: Huan Fan
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Project Overview

Project Name

St6gal1

Project type

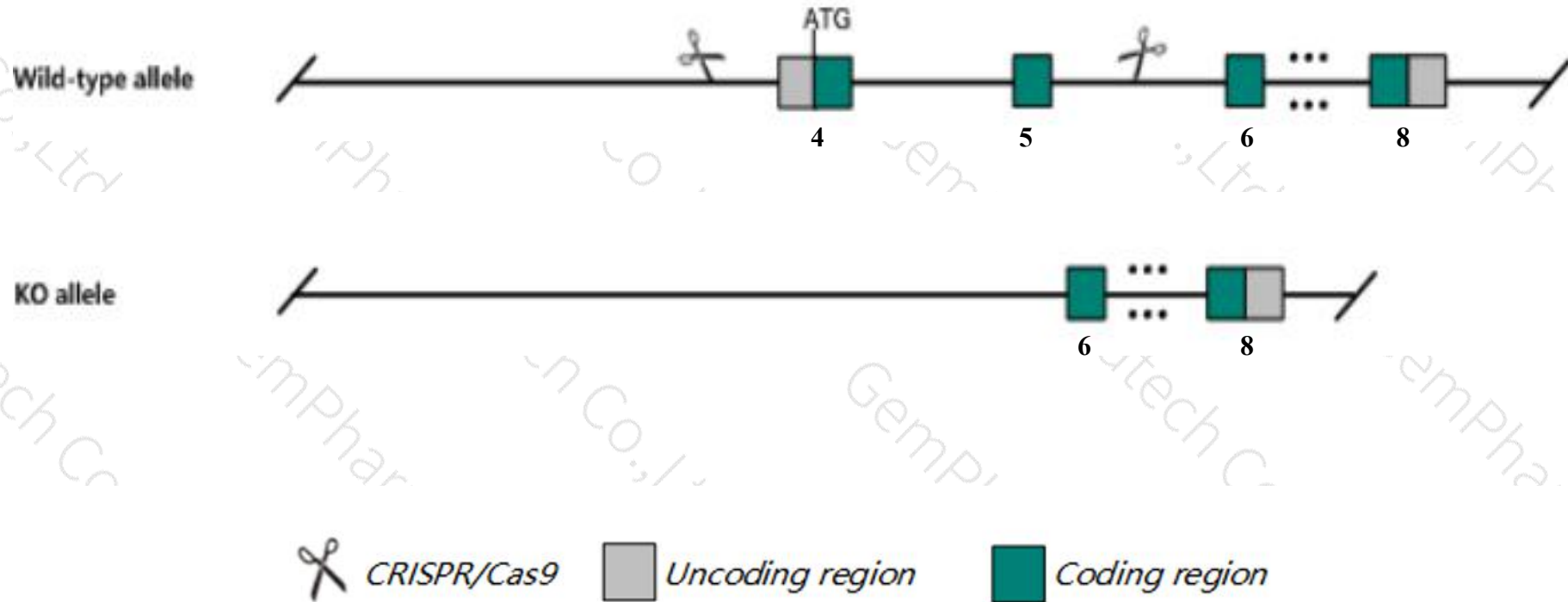
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *St6gal1* gene. The schematic diagram is as follows:



➤ The *St6gal1* gene has 5 transcripts. According to the structure of *St6gal1* gene, exon4-exon5 of *St6gal1-201* (ENSMUST00000023601.13) 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 *St6gal1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous mutation of this gene results in altered terminal glycosylation.
- The *St6gal1* gene is located on the Chr16. 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)

St6gal1 beta galactoside alpha 2,6 sialyltransferase 1 [Mus musculus (house mouse)]

Gene ID: 20440, updated on 13-Mar-2020

Summary

Official Symbol St6gal1 provided by [MGI](#)

Official Full Name beta galactoside alpha 2,6 sialyltransferase 1 provided by [MGI](#)

Primary source [MGI:MGI:108470](#)

See related [Ensembl:ENSMUSG00000022885](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AW742324, Siat1, St6Gal-I, St6gal, St6gall

Summary This gene encodes a member of glycosyltransferase family 29. The encoded protein is a type II membrane protein that catalyzes the transfer of sialic acid from CMP-sialic acid to galactose-containing substrates. The protein, which is normally found in the Golgi but can be proteolytically processed to a soluble form, is involved in the generation of the cell-surface carbohydrate determinants and differentiation antigens HB-6, CD75, and CD76. This gene has been incorrectly referred to as CD75. Alternatively spliced transcript variants have been observed for this gene, and a pseudogene of this gene is located on chromosome 15. [provided by RefSeq, Nov 2011]

Expression Broad expression in genital fat pad adult (RPKM 48.2), liver E18 (RPKM 29.4) and 22 other tissues [See more](#)

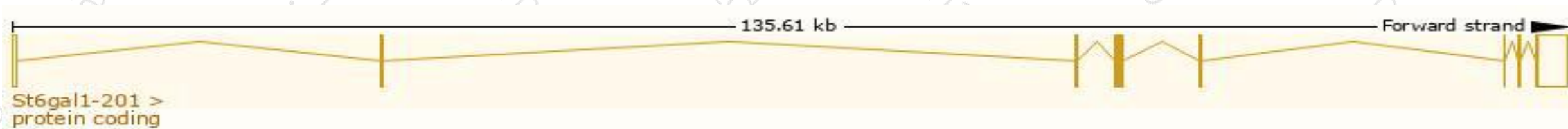
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
St6gal1-201	ENSMUST00000023601.13	4506	403aa	Protein coding	CCDS28077	Q64685	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
St6gal1-205	ENSMUST00000178797.7	4177	403aa	Protein coding	CCDS28077	Q64685	TSL:5 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
St6gal1-202	ENSMUST00000115335.1	2289	403aa	Protein coding	CCDS28077	Q64685	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
St6gal1-203	ENSMUST00000128050.7	362	33aa	Protein coding	-	D3Z1Z5	CDS 3' incomplete TSL:3
St6gal1-204	ENSMUST00000152449.7	476	No protein	Processed transcript	-	-	TSL:2

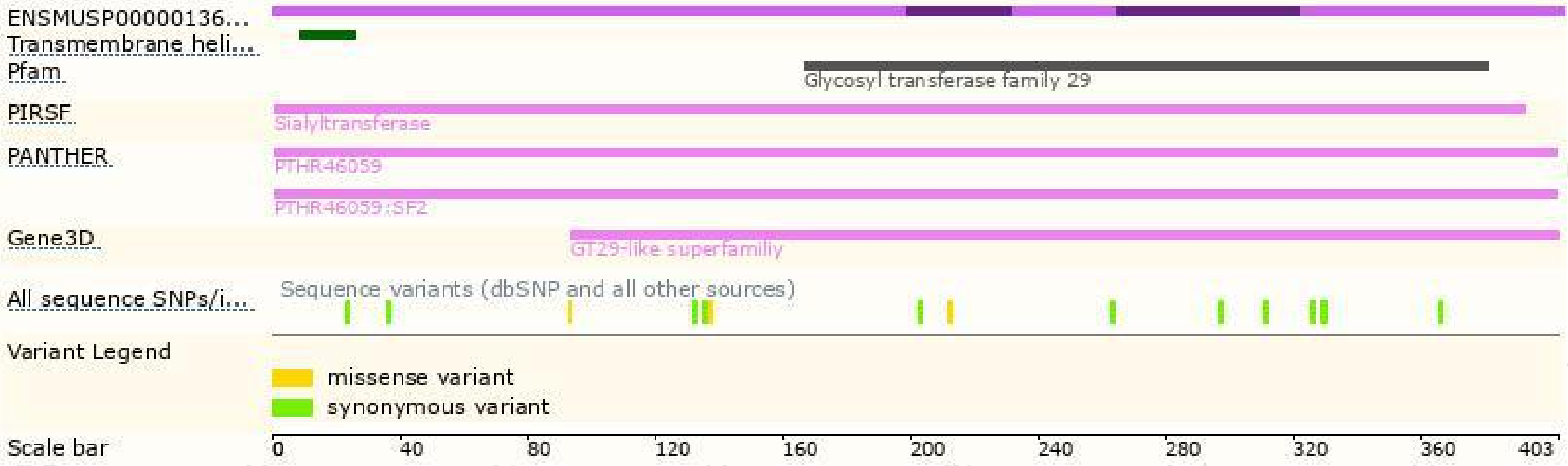
The strategy is based on the design of *St6gal1-201* transcript, the transcription is shown below



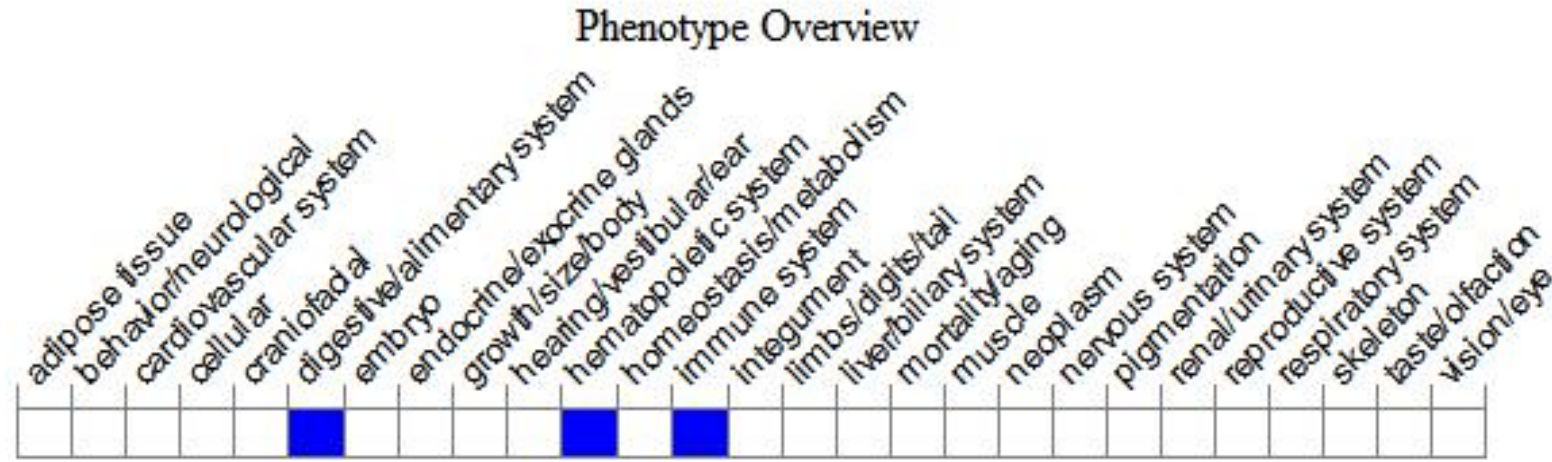
Genomic location distribution



Protein domain



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 mutation of this gene results in altered terminal glycosylation.

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

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