

St6galnac2 Cas9-CKO Strategy

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Project Overview

Project Name

St6galnac2

Project type

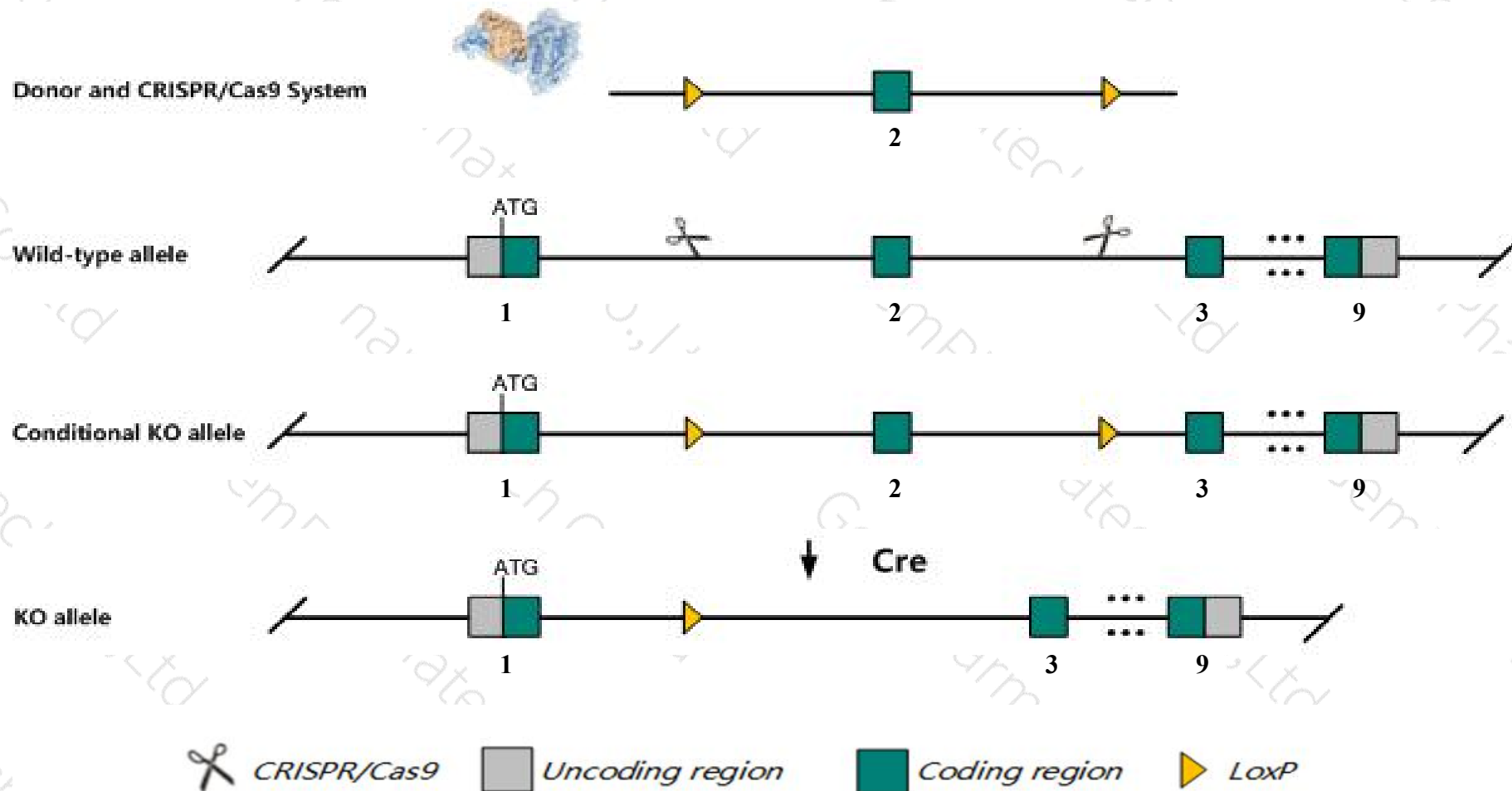
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *St6galnac2* gene. The schematic diagram is as follows:



- The *St6galnac2* gene has 5 transcripts. According to the structure of *St6galnac2* gene, exon2 of *St6galnac2-201* (ENSMUST00000079545.5) transcript is recommended as the knockout region. The region contains 61bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *St6galnac2* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knockout allele exhibit decreased body weight, decreased IgQ, increased B cell proliferation, increased pre-B cell number, abnormal erythropoiesis, increased ALT, decreased creatinine level and prominent spleen germinal center.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The transcript 202,203,204 may not be affected.
- The effect of transcript 206 is unknown.
- The *St6galnac2* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

St6galnac2 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 [*Mus musculus* (house mouse)]

Gene ID: 20446, updated on 13-Mar-2020

Summary

Official Symbol	St6galnac2 provided by MGI
Official Full Name	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 provided by MGI
Primary source	MGI:MGI:107553
See related	Ensembl:ENSMUSG00000057286
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	II; Siat7; Siat7b; ST6GalNAc
Expression	Biased expression in testis adult (RPKM 210.6), kidney adult (RPKM 42.3) and 9 other tissues See more
Orthologs	human all

Genomic context

Location: 11; 11 E2

Exon count: 9

See St6galnac2 in [Genome Data Viewer](#)

Transcript information (Ensembl)

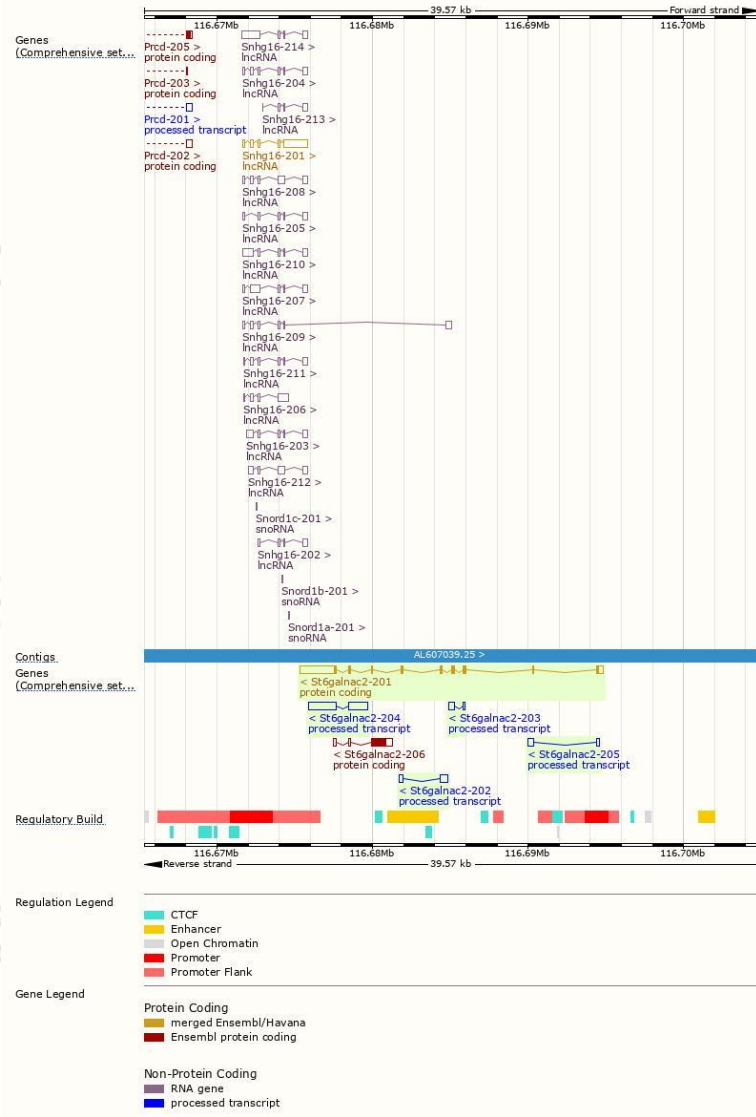
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
St6galnac2-201	ENSMUST00000079545.5	3643	373aa	Protein coding	CCDS36379	P70277	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
St6galnac2-204	ENSMUST00000135771.1	3006	No protein	Processed transcript	-	-	TSL:1
St6galnac2-202	ENSMUST00000123236.1	751	No protein	Processed transcript	-	-	TSL:3
St6galnac2-205	ENSMUST00000145441.1	579	No protein	Processed transcript	-	-	TSL:2
St6galnac2-203	ENSMUST00000129236.1	432	No protein	Processed transcript	-	-	TSL:3

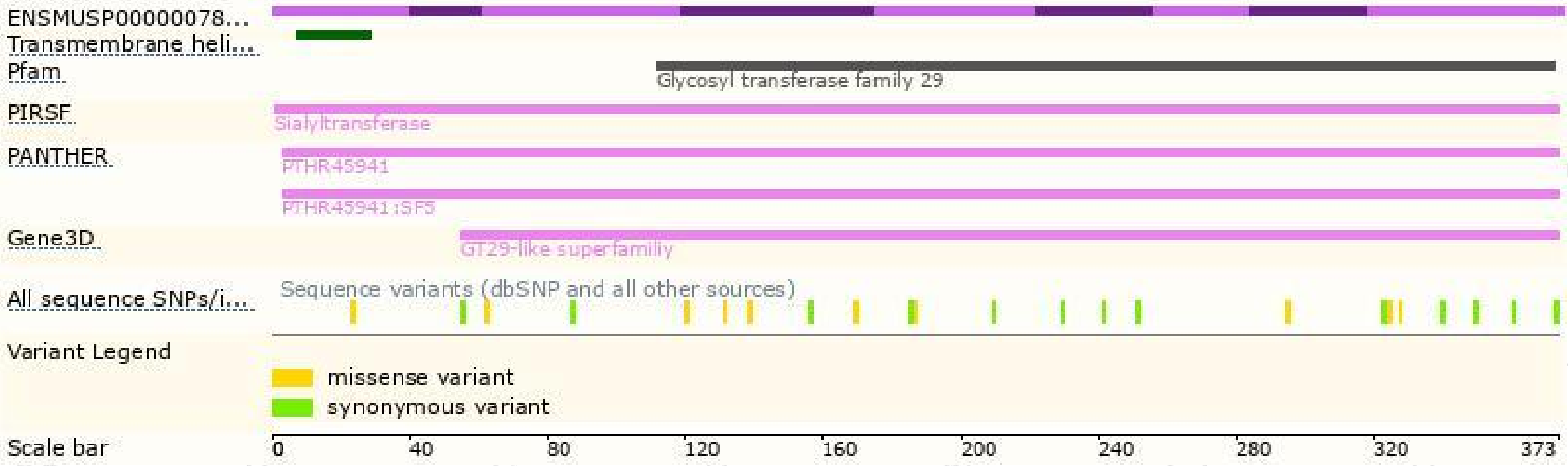
The strategy is based on the design of *St6galnac2-201* transcript, The transcription is shown below



Genomic location distribution

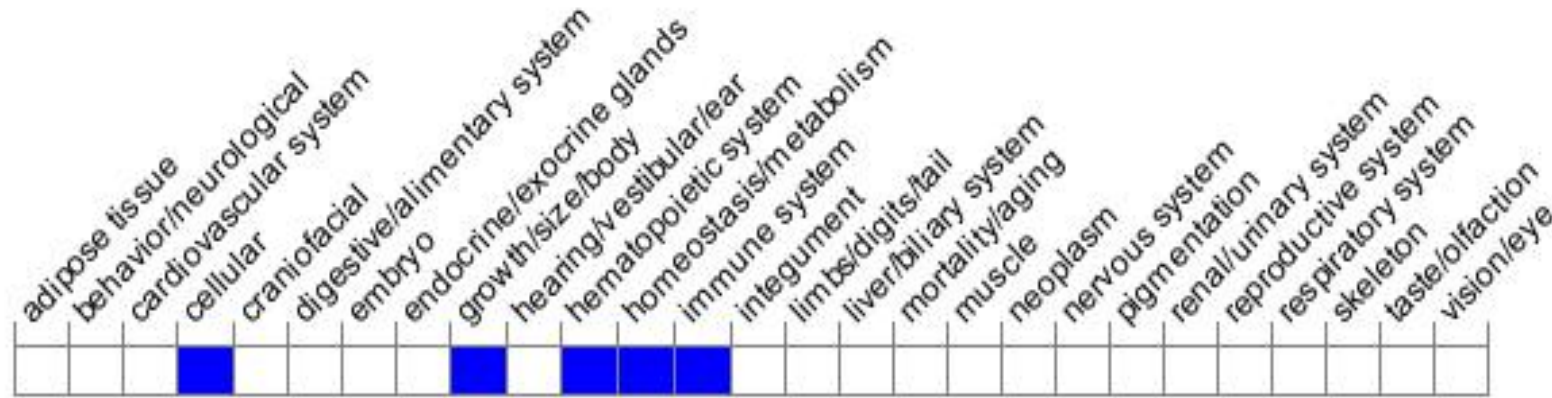


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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

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

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