St6galnac6 Cas9-CKO Strategy

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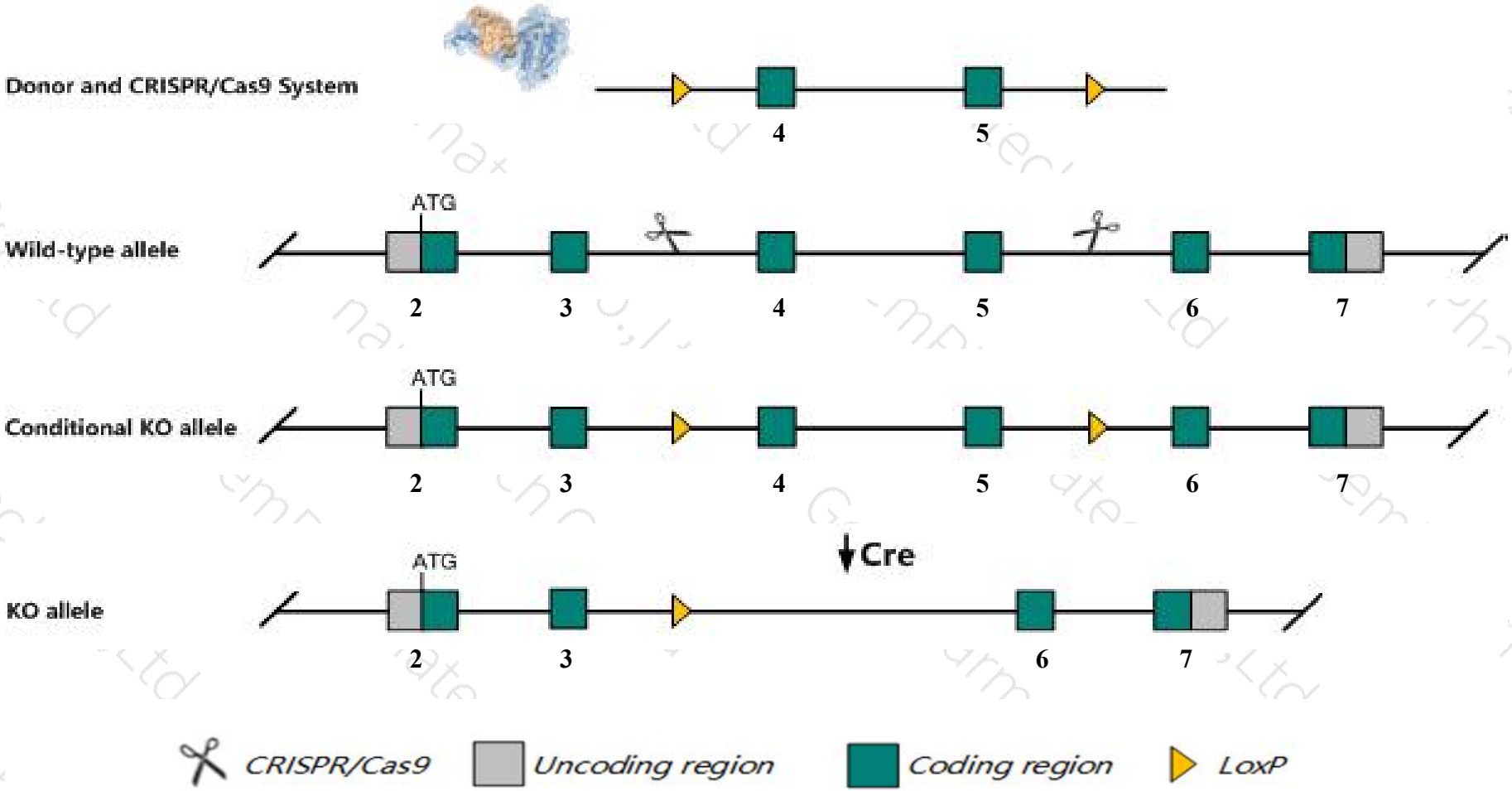
Project Overview

Project Name	***St6galnac6***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *St6galnac6* gene. The schematic diagram is as follows:



Technical routes

- The *St6galnac6* gene has 13 transcripts. According to the structure of *St6galnac6* gene, exon4-exon5 of *St6galnac6-203* (ENSMUST00000095044.9) transcript is recommended as the knockout region.The region contains 587bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *St6galnac6* 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.

Notice

- Some amino acids will remain at the N-terminus and some functions may be retained.
- The effect of transcripts 206,207,208,210,211 is unknown.
- The *St6galnac6* gene is located on the Chr2. 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）

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St6galnac6 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 [Mus musculus (house mouse)]

Gene ID: 50935, updated on 13-Mar-2020

Summary

Official Symbol	St6galnac6 provided by MGI
Official Full Name	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 provided byMGI
Primary source	MGI:MGI:1355316
See related	Ensembl:ENSMUSG00000026811
Gene type	protein coding
RefSeq status	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	ST6GalNAcVI, Siat7f
Expression	Biased expression in colon adult (RPKM 299.0), adrenal adult (RPKM 26.2) and 6 other tissuesSee more
Orthologs	human all

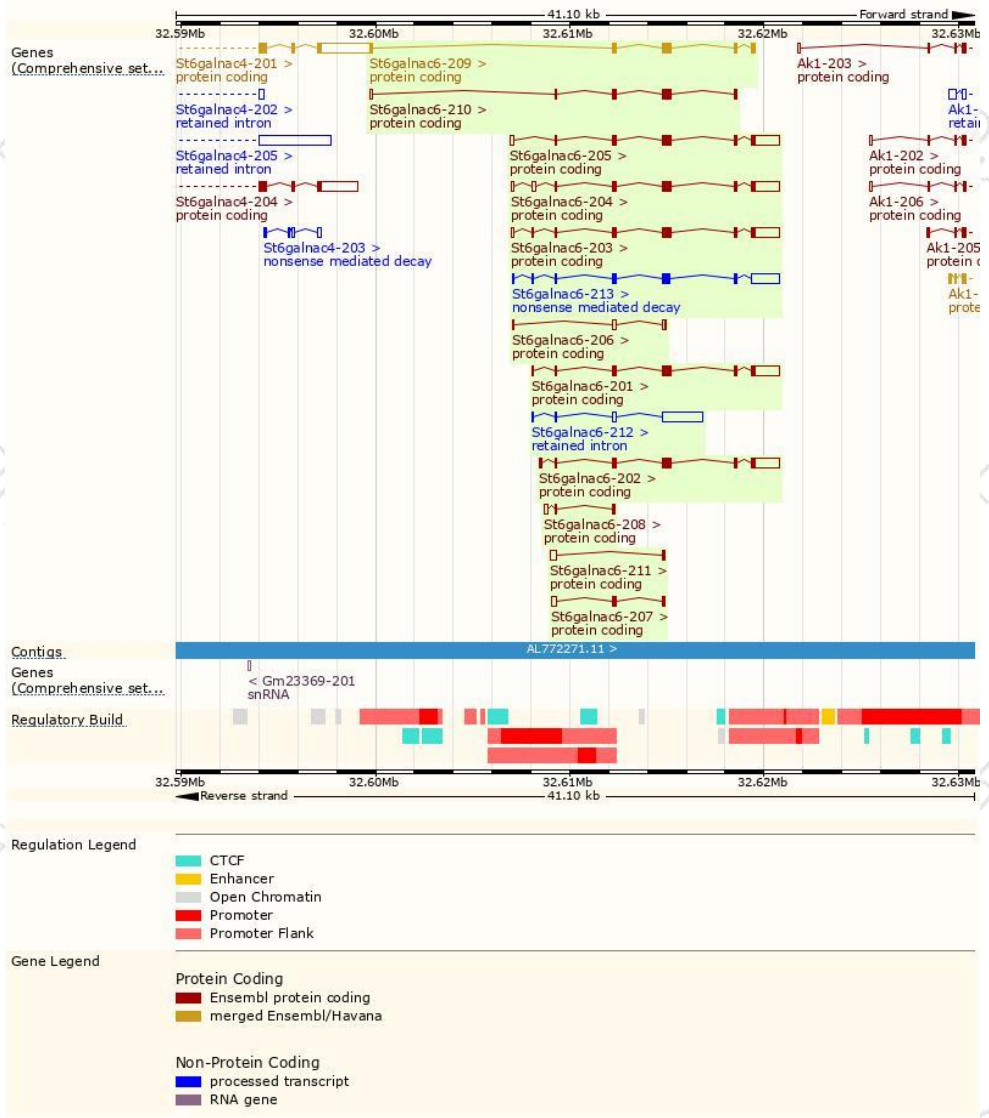
Transcript information（Ensembl）

The gene has 13 transcripts,all transcripts are shown below:

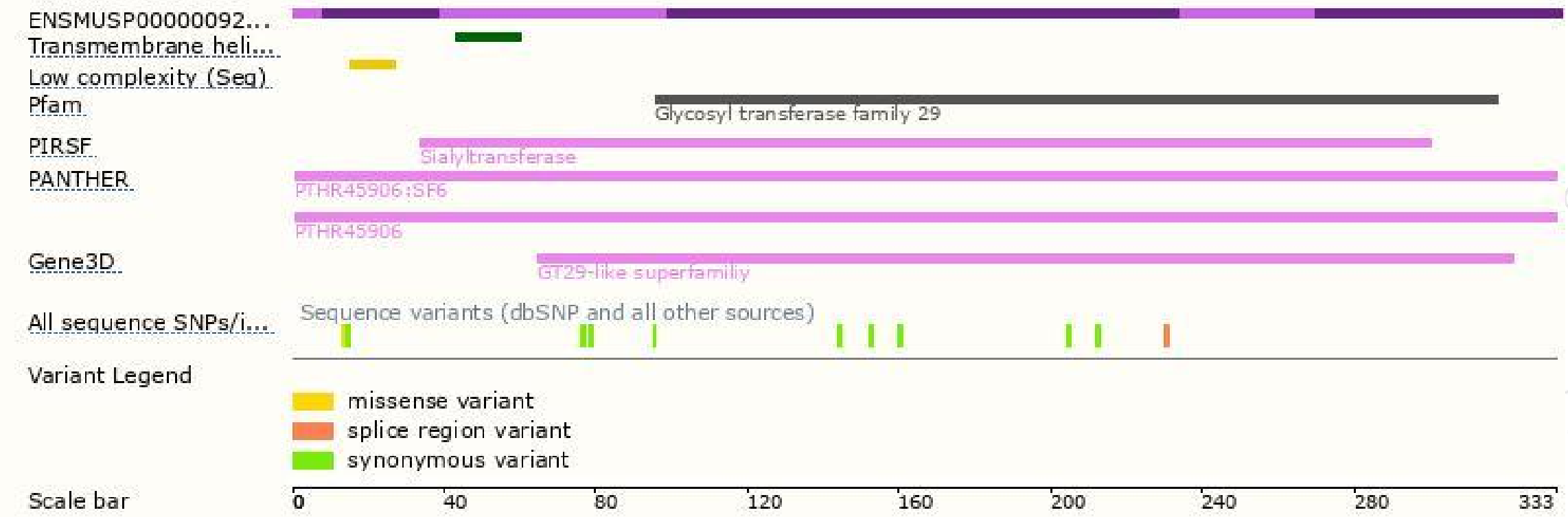
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
St6galnac6-204	ENSMUST00000095045.8	2536	299aa	Protein coding	CCDS38105	E9PUI0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
St6galnac6-205	ENSMUST00000113290.7	2402	299aa	Protein coding	CCDS38105	E9PUI0	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 ALT1
St6galnac6-203	ENSMUST00000095044.9	2394	333aa	Protein coding	CCDS15923	Q9JM95	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 P3
St6galnac6-201	ENSMUST00000072111.7	2277	333aa	Protein coding	CCDS15923	Q9JM95	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 P3
St6galnac6-209	ENSMUST00000131229.7	1013	313aa	Protein coding	CCDS15922	Z4YLR0	TSL:2 GENCODE basic
St6galnac6-202	ENSMUST00000081879.11	2345	335aa	Protein coding	-	Q9JM95	TSL:1 GENCODE basic
St6galnac6-210	ENSMUST00000140983.7	875	229aa	Protein coding	-	Z4YLN2	CDS 3' incomplete TSL:5
St6galnac6-207	ENSMUST00000128811.1	584	108aa	Protein coding	-	Z4YMI1	CDS 3' incomplete TSL:2
St6galnac6-206	ENSMUST00000126636.7	438	28aa	Protein coding	-	A0A0A6YW64	CDS 3' incomplete TSL:2
St6galnac6-211	ENSMUST00000143625.1	414	41aa	Protein coding	-	A0A0A6YW84	CDS 3' incomplete TSL:2
St6galnac6-208	ENSMUST00000129165.1	355	39aa	Protein coding	-	Z4YN31	CDS 3' incomplete TSL:2
St6galnac6-213	ENSMUST00000183538.7	2361	235aa	Nonsense mediated decay	-	Q9JM95	TSL:1
St6galnac6-212	ENSMUST00000149220.1	2322	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *St6galnac6-203* transcript,The transcription is shown below

Genomic location distribution



Protein domain



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