

St8sia5 Cas9-KO Strategy

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Project Overview



Project Name

St8sia5

Project type

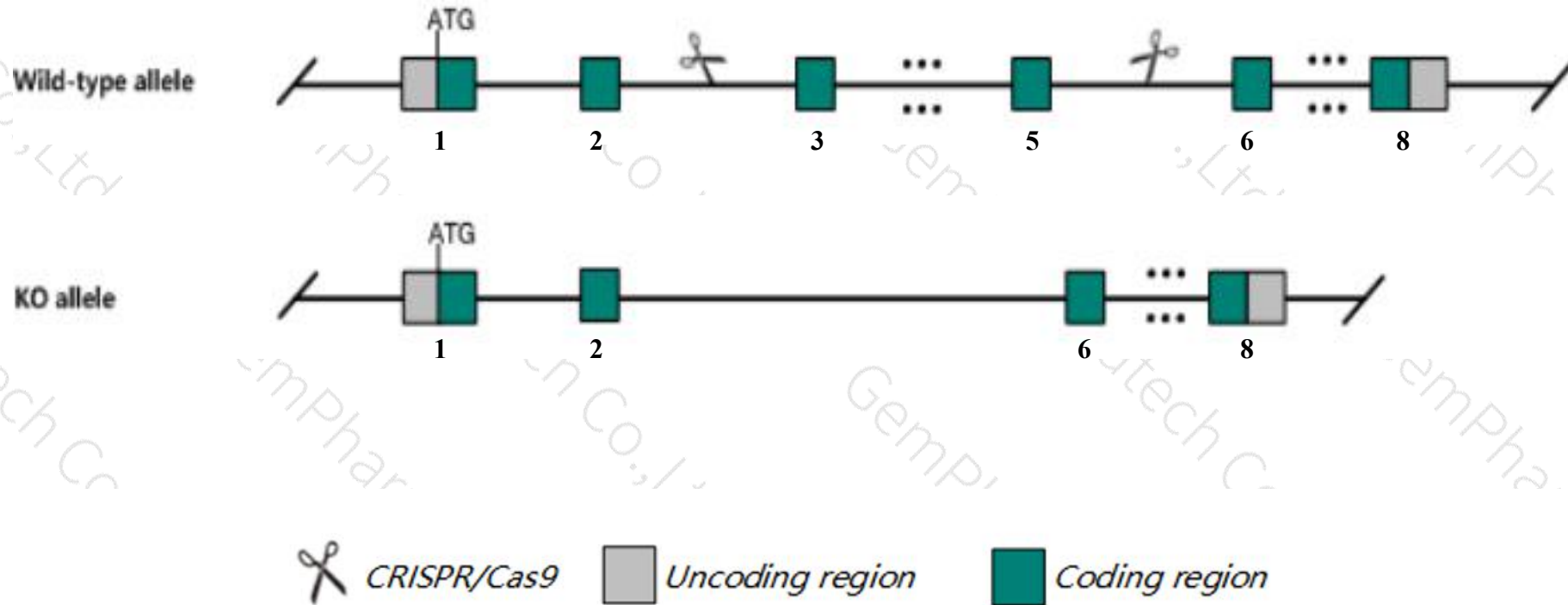
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *St8sia5* gene. The schematic diagram is as follows:



- The *St8sia5* gene has 3 transcripts. According to the structure of *St8sia5* gene, exon3-exon5 of *St8sia5-201* (ENSMUST00000075290.7) transcript is recommended as the knockout region. The region contains 325bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *St8sia5* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *St8sia5* gene is located on the Chr18. 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)

St8sia5 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 [Mus musculus (house mouse)]

Gene ID: 225742, updated on 13-Mar-2020

Summary



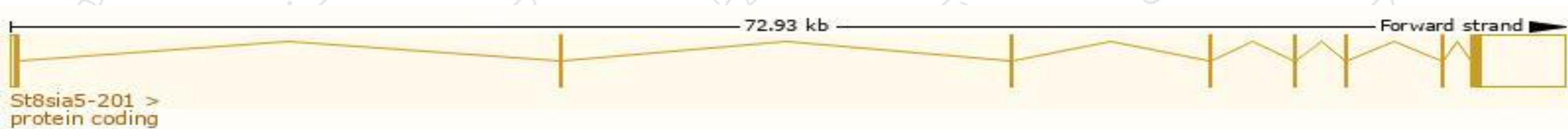
Official Symbol	St8sia5 provided by MGI
Official Full Name	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 provided by MGI
Primary source	MGI:MGI:109243
See related	Ensembl:ENSMUSG000000025425
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ST8SiaV, Siat8e
Expression	Biased expression in cerebellum adult (RPKM 39.0), cortex adult (RPKM 14.8) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

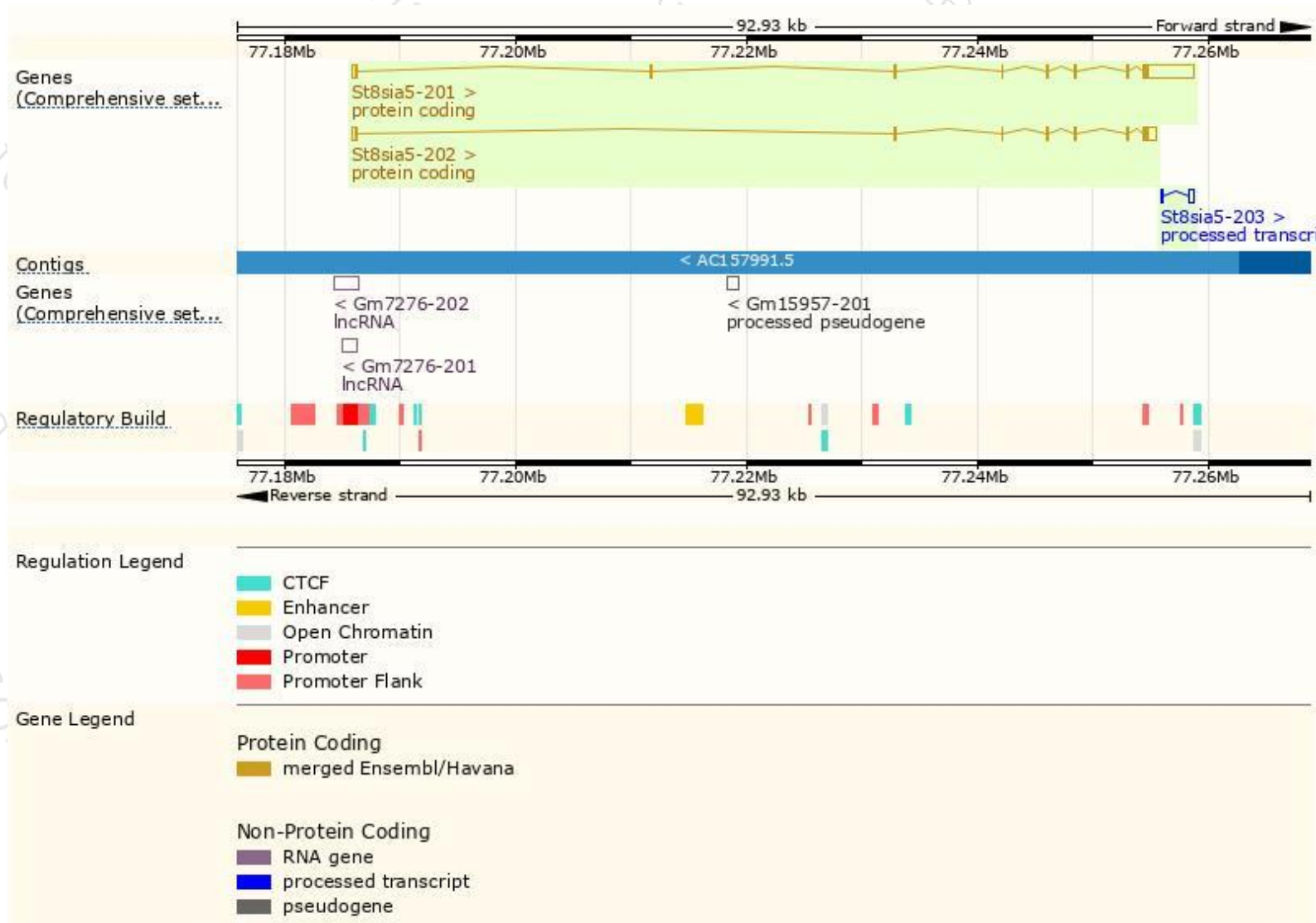
The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
St8sia5-201	ENSMUST00000075290.7	5432	412aa	Protein coding	CCDS50325	P70126	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 ALT 1
St8sia5-202	ENSMUST00000079618.10	1989	376aa	Protein coding	CCDS29353	P70126_Q3TRR3	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
St8sia5-203	ENSMUST00000236592.1	634	No protein	Processed transcript	-	-	

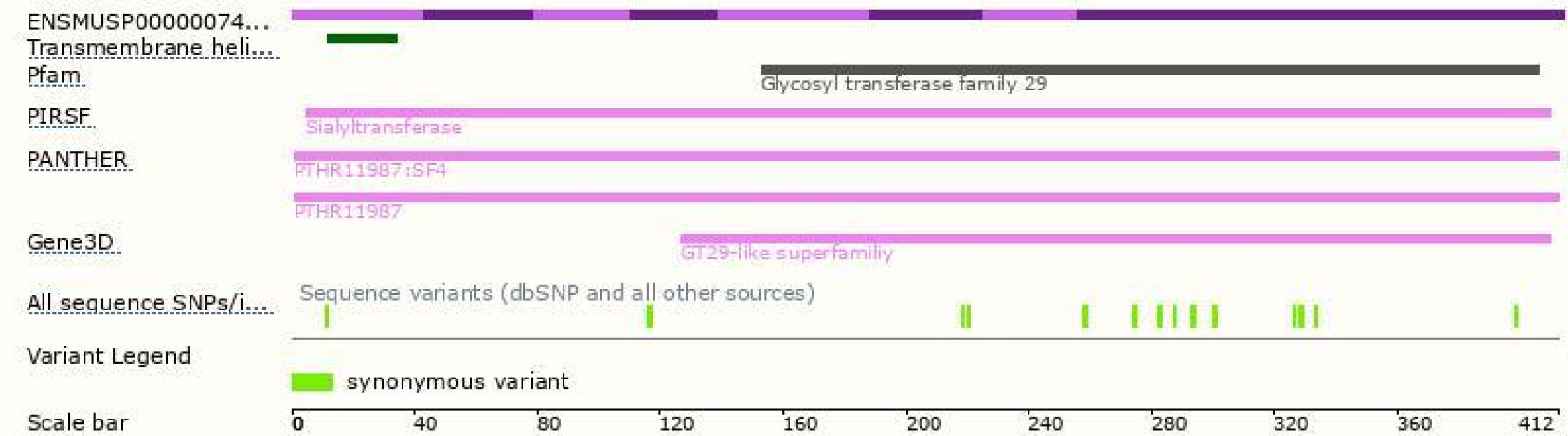
The strategy is based on the design of *St8sia5-201* transcript, The transcription is shown below



Genomic location distribution



Protein domain



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

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