

Syt14 Cas9-KO Strategy

Designer: Yumeng wang

Reviewer: Huan wang

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Project Overview

Project Name

Syt14

Project type

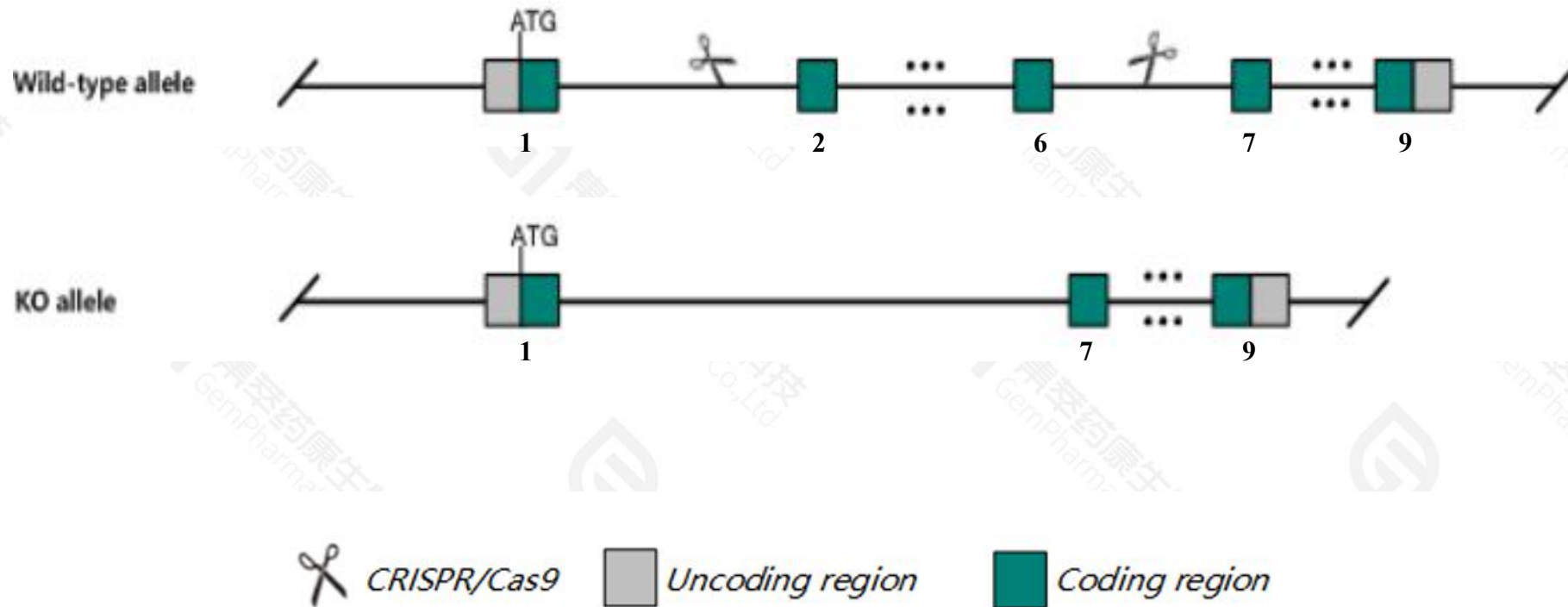
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Syt14* gene. The schematic diagram is as follows:



- The *Syt14* gene has 5 transcripts. According to the structure of *Syt14* gene, exon2-exon6 of *Syt14-201*(ENSMUST00000016344.9) transcript is recommended as the knockout region. The region contains 1151bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Syt14* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Syt14* gene is located on the Chr1. 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.

Syt14 synaptotagmin XIV [Mus musculus (house mouse)]

Gene ID: 329324, updated on 17-Dec-2020

Summary



Official Symbol Syt14 provided by [MGI](#)

Official Full Name synaptotagmin XIV provided by [MGI](#)

Primary source [MGI:MGI:2444490](#)

See related [Ensembl:ENSMUSG00000016200](#)

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 B230320I09Rik, sytXIV

Summary This gene encodes a member of the synaptotagmin family. The encoded protein may be involved in membrane trafficking. Disruption of a similar gene in human has been associated with autosomal recessive spinocerebellar ataxia. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2014]

Expression Broad expression in liver E14 (RPKM 2.1), liver E14.5 (RPKM 1.9) and 16 other tissues [See more](#)

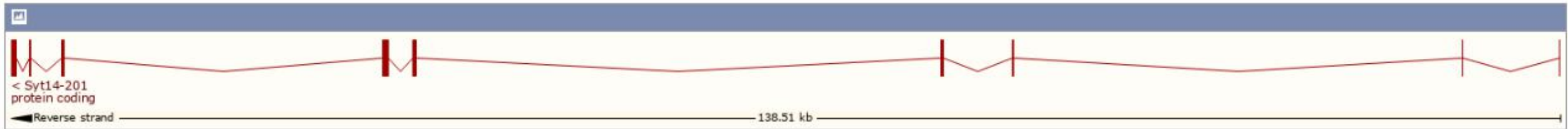
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

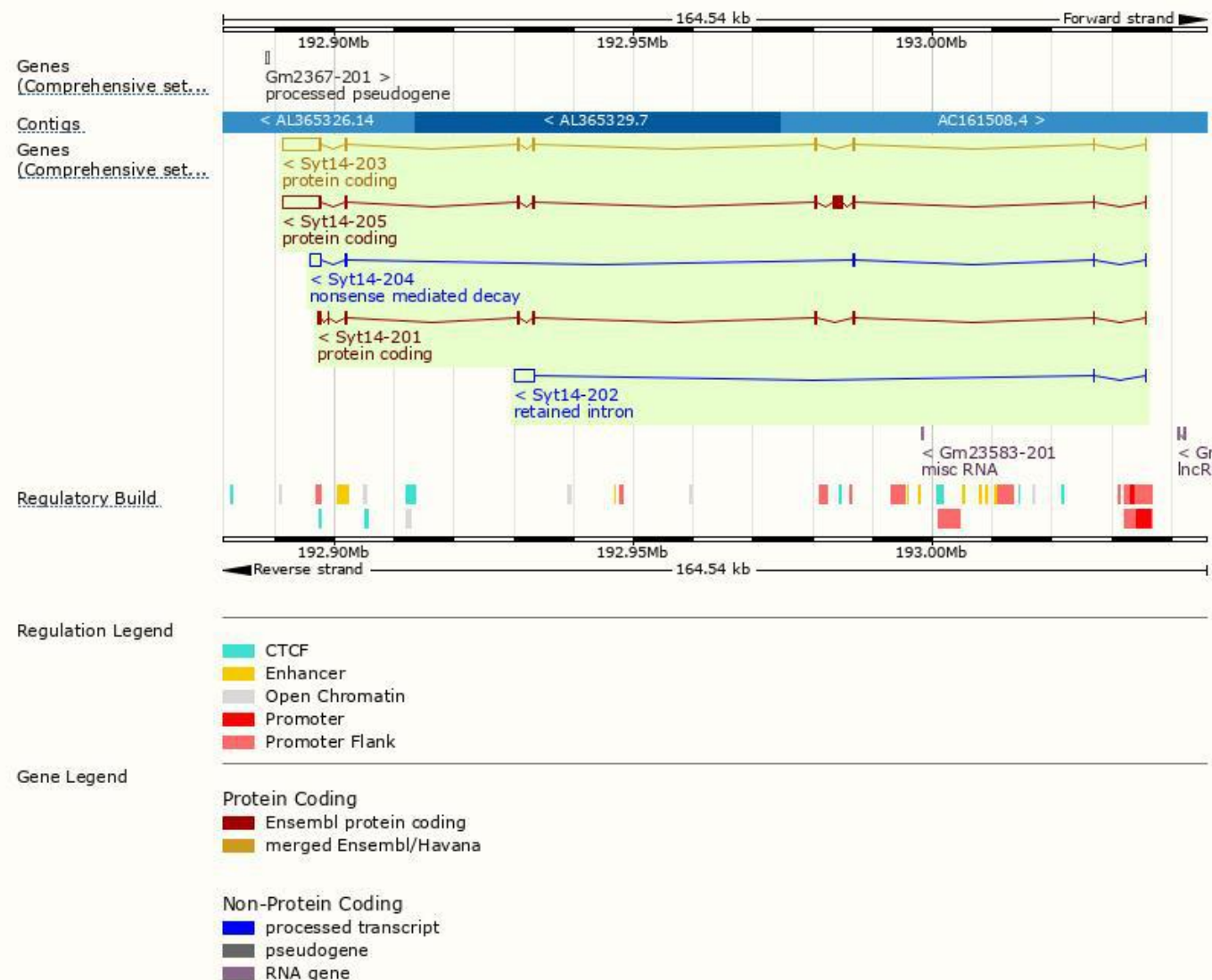
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syt14-203	ENSMUST00000195354.6	7882	555aa	Protein coding	CCDS48489		TSL:1 , GENCODE basic , APPRIS P1 ,
Syt14-201	ENSMUST00000016344.9	1904	574aa	Protein coding	CCDS78780		TSL:1 , GENCODE basic ,
Syt14-205	ENSMUST00000215093.2	9274	838aa	Protein coding	-		TSL:5 , GENCODE basic ,
Syt14-204	ENSMUST00000195530.6	2078	77aa	Nonsense mediated decay	-		TSL:5 ,
Syt14-202	ENSMUST00000191907.2	3393	No protein	Retained intron	-		TSL:1 ,

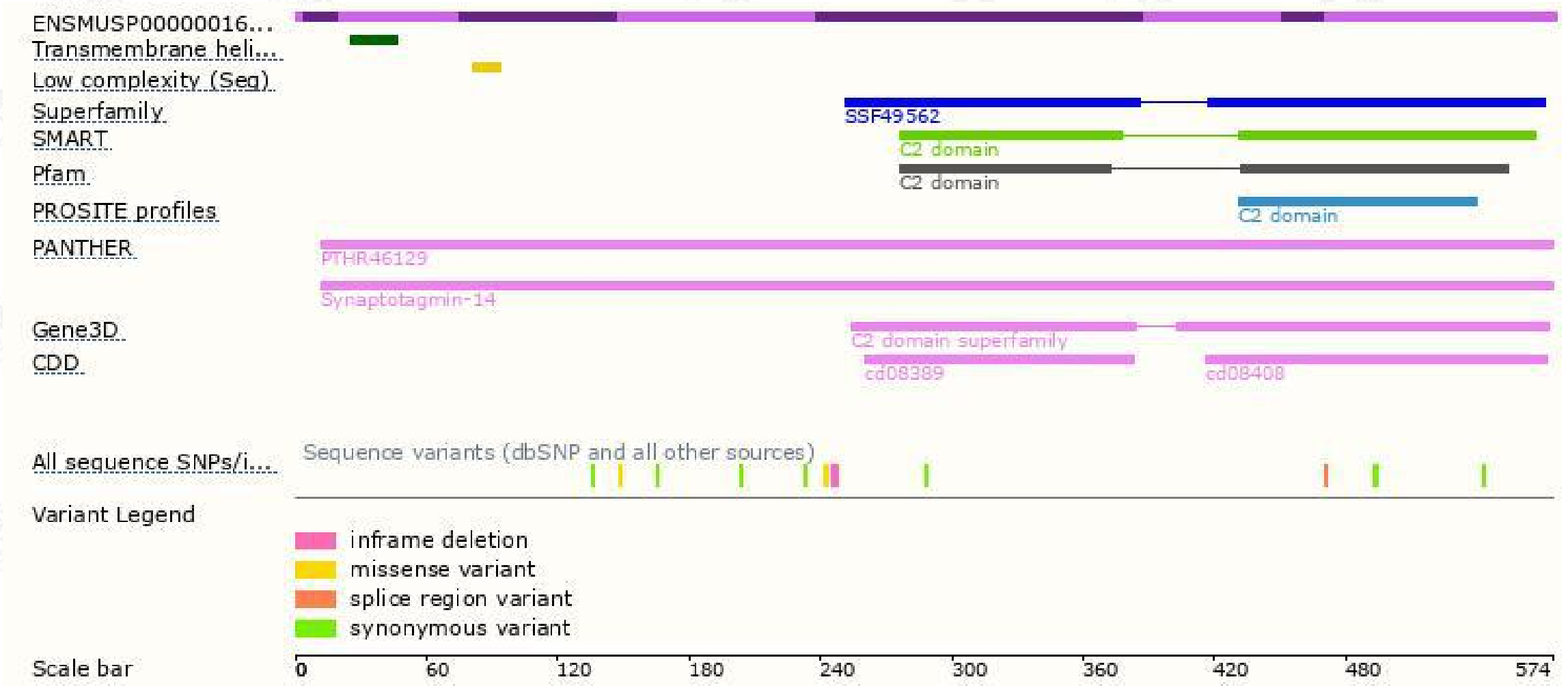
The strategy is based on the design of *Syt14-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



If you have any questions, you are welcome to inquire.
Tel: 400-9660890

