Syp Cas9-KO Strategy

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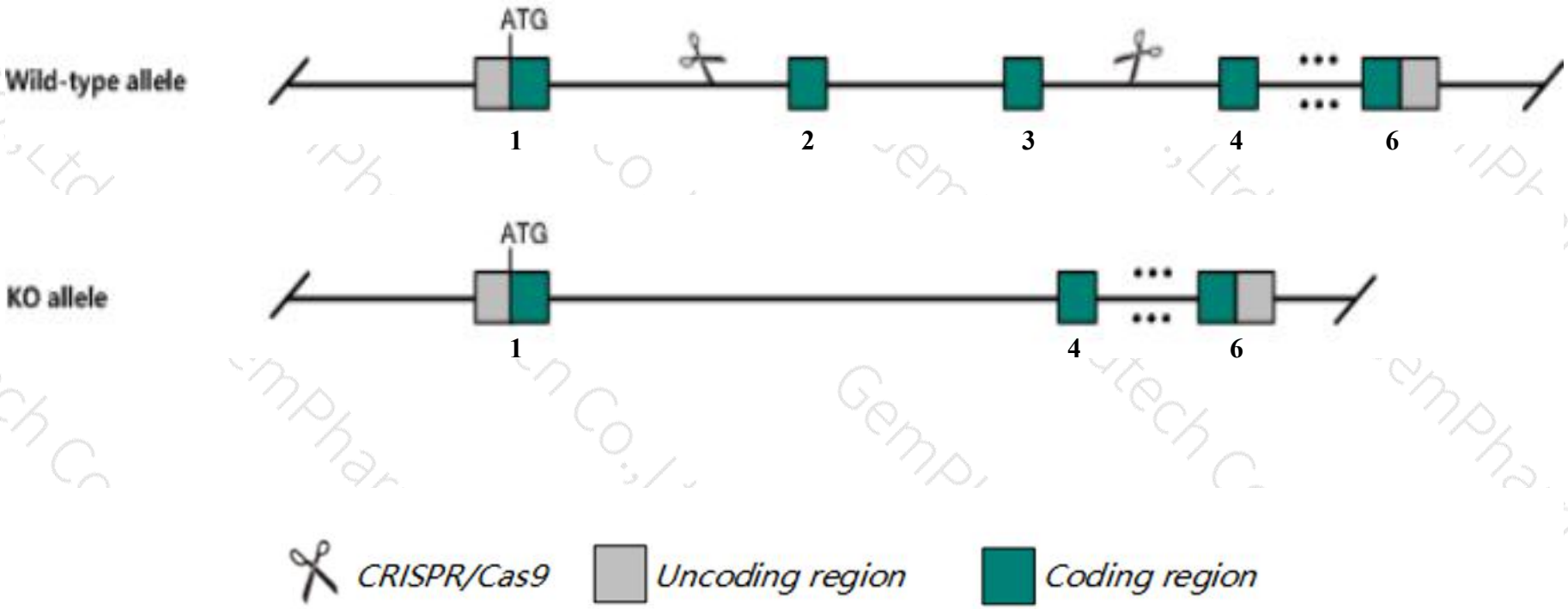
Project Overview

Project Name	***Syp***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Syp* gene has 6 transcripts. According to the structure of *Syp* gene, exon2-exon3 of *Syp-201* (ENSMUST00000069520.10) transcript is recommended as the knockout region.The region contains 191bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Syp* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,mice homozygous for either one of two independently generated knock-out mutations are viable and fertile and display normal central nervous system morphology and synaptic transmission with no detectable changes in synaptic plasticity or neurotransmitter release.
- The *Syp* gene is located on the ChrX. 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）

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Syp synaptophysin [Mus musculus (house mouse)]

Gene ID: 20977, updated on 13-Mar-2020

Summary

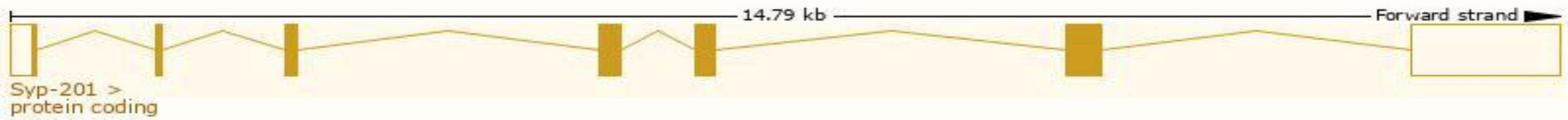
Official Symbol	Syp provided by MGI
Official Full Name	synaptophysin provided byMGI
Primary source	MGI:MGI:98467
See related	Ensembl:ENSMUSG00000031144
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A230093K24Rik, AI848995, Syn, p38
Expression	Biased expression in cortex adult (RPKM 270.0), frontal lobe adult (RPKM 246.0) and 4 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

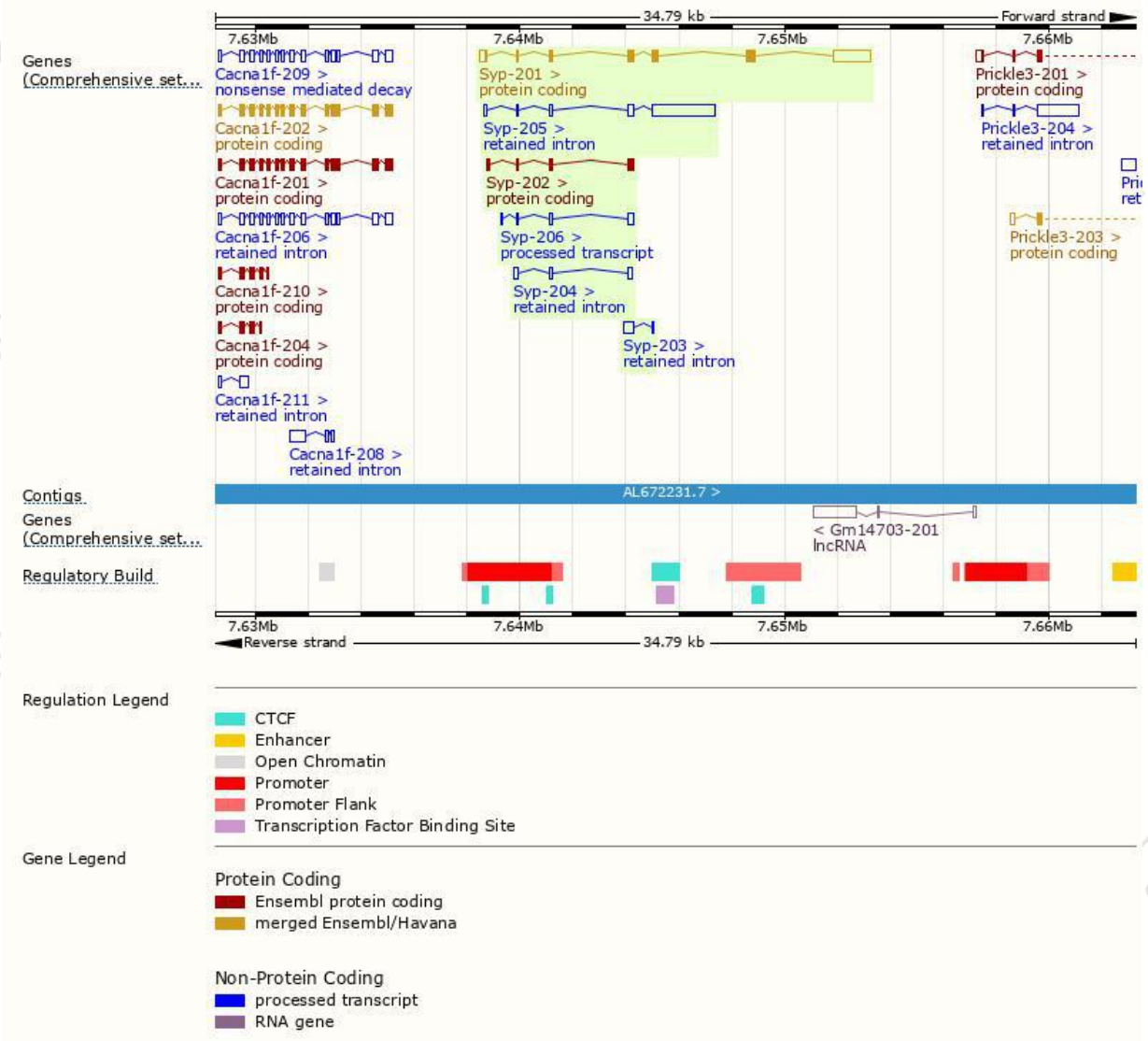
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syp-201	ENSMUST00000069520.10	2591	314aa	Protein coding	CCDS29967	Q62277	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
Syp-202	ENSMUST00000128890.1	494	165aa	Protein coding	-	F6VR28	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Syp-206	ENSMUST00000150572.7	433	No protein	Processed transcript	-	-	TSL:2
Syp-205	ENSMUST00000149795.7	2843	No protein	Retained intron	-	-	TSL:1
Syp-204	ENSMUST00000137515.1	430	No protein	Retained intron	-	-	TSL:2
Syp-203	ENSMUST00000134355.1	417	No protein	Retained intron	-	-	TSL:2

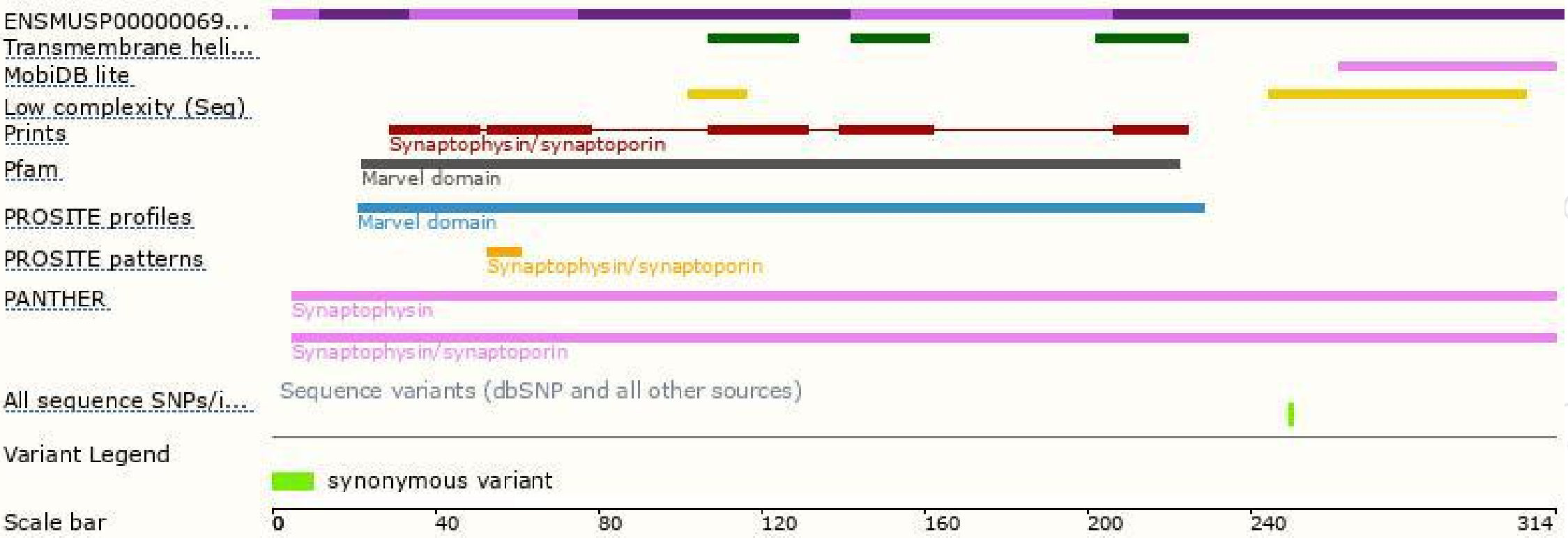
The strategy is based on the design of *Syp-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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