

Sypl Cas9-CKO Strategy

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Project Overview

Project Name

Sypl

Project type

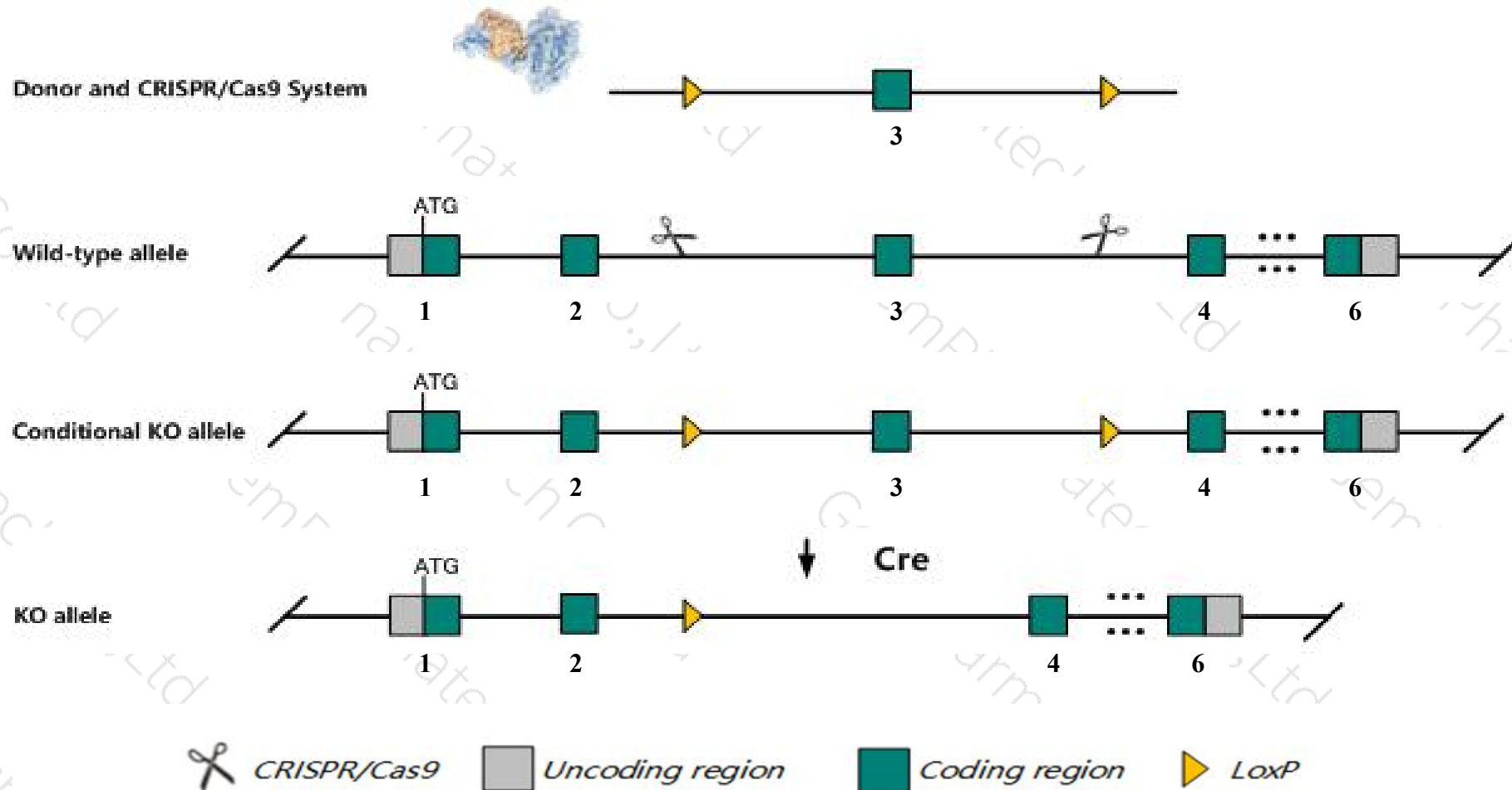
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Sypl* gene has 7 transcripts. According to the structure of *Sypl* gene, exon3 of *Sypl*-202(ENSMUST00000076698.12) transcript is recommended as the knockout region. The region contains 128bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sypl* 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

- The *Sypl* gene is located on the Chr12. 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)

Sypl synaptophysin-like protein [Mus musculus (house mouse)]

Gene ID: 19027, updated on 13-Mar-2020

Summary

Official Symbol Sypl provided by [MGI](#)

Official Full Name synaptophysin-like protein provided by [MGI](#)

Primary source [MGI:MGI:108081](#)

See related [Ensembl:ENSMUSG00000020570](#)

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 AI314763, AI604763, D12Ert446e, Panl, Pphn, Sypl1

Expression Ubiquitous expression in bladder adult (RPKM 15.7), testis adult (RPKM 11.1) and 28 other tissues [See more](#)

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

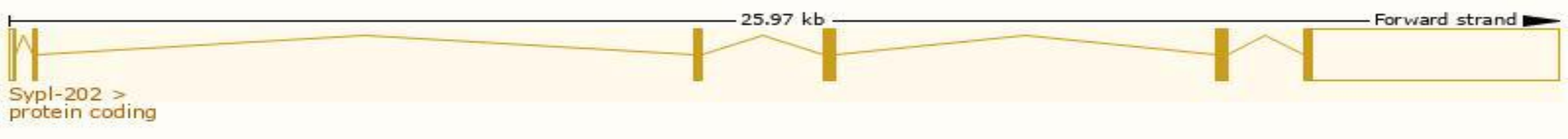
Transcript information (Ensembl)



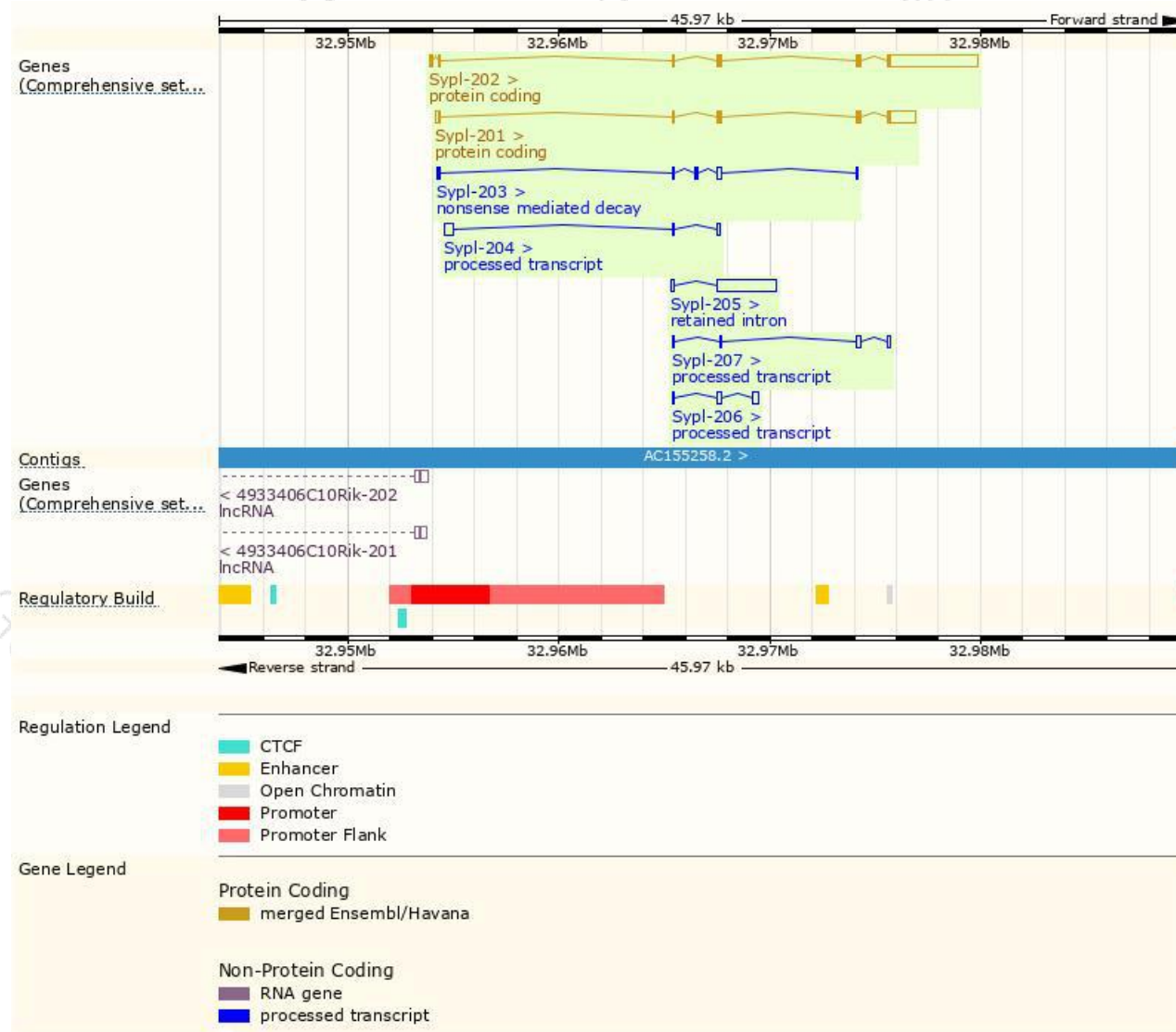
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sypl-202	ENSMUST00000076698.12	4999	261aa	Protein coding	CCDS25872	Q09117	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 P4
Sypl-201	ENSMUST00000020885.12	2019	243aa	Protein coding	CCDS25873	O09117_Q3TVX7	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 ALT2
Sypl-203	ENSMUST00000122861.7	646	79aa	Nonsense mediated decay	-	D6RFU9	TSL:3
Sypl-204	ENSMUST00000129592.1	696	No protein	Processed transcript	-	-	TSL:3
Sypl-206	ENSMUST00000139339.1	569	No protein	Processed transcript	-	-	TSL:3
Sypl-207	ENSMUST00000218816.1	529	No protein	Processed transcript	-	-	TSL:3
Sypl-205	ENSMUST00000131562.1	2982	No protein	Retained intron	-	-	TSL:1

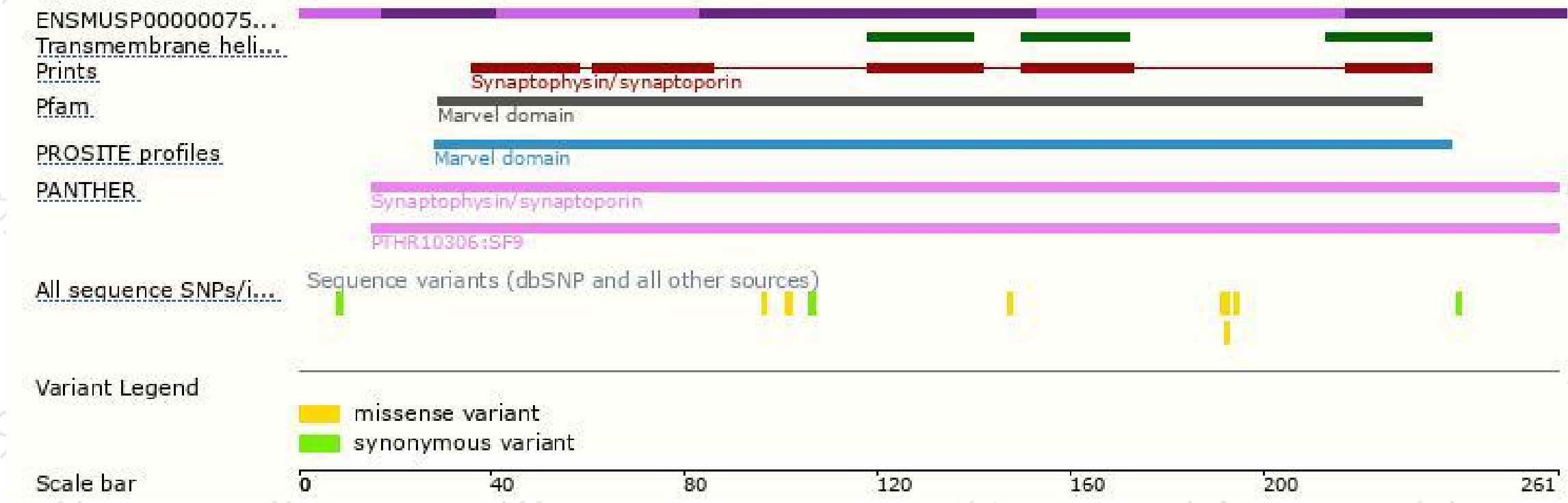
The strategy is based on the design of *Sypl-202* transcript,the transcription is shown below:



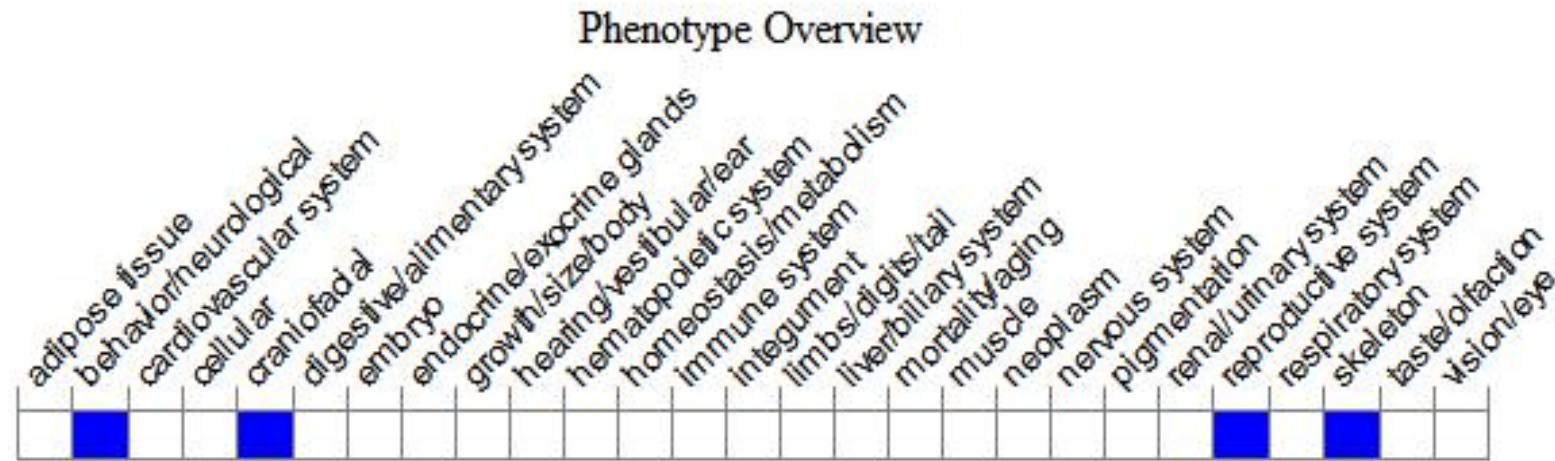
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



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

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

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