

Syt17 Cas9-KO Strategy

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Project Overview

Project Name

Syt17

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Syt17* gene. The schematic diagram is as follows:



- The *Syt17* gene has 6 transcripts. According to the structure of *Syt17* gene, exon4 of *Syt17-201* (ENSMUST00000081574.7) transcript is recommended as the knockout region. The region contains 149bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Syt17* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Syt17* gene is located on the Chr7. 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)

Syt17 synaptotagmin XVII [Mus musculus (house mouse)]

Gene ID: 110058, updated on 31-Jan-2019

Summary



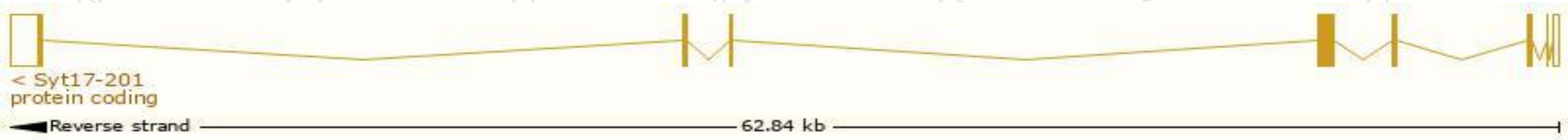
Official Symbol	Syt17 provided by MGI
Official Full Name	synaptotagmin XVII provided by MGI
Primary source	MGI:MGI:104966
See related	Ensembl:ENSMUSG00000058420
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bk, sytXVII
Expression	Biased expression in frontal lobe adult (RPKM 12.9), cortex adult (RPKM 9.9) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

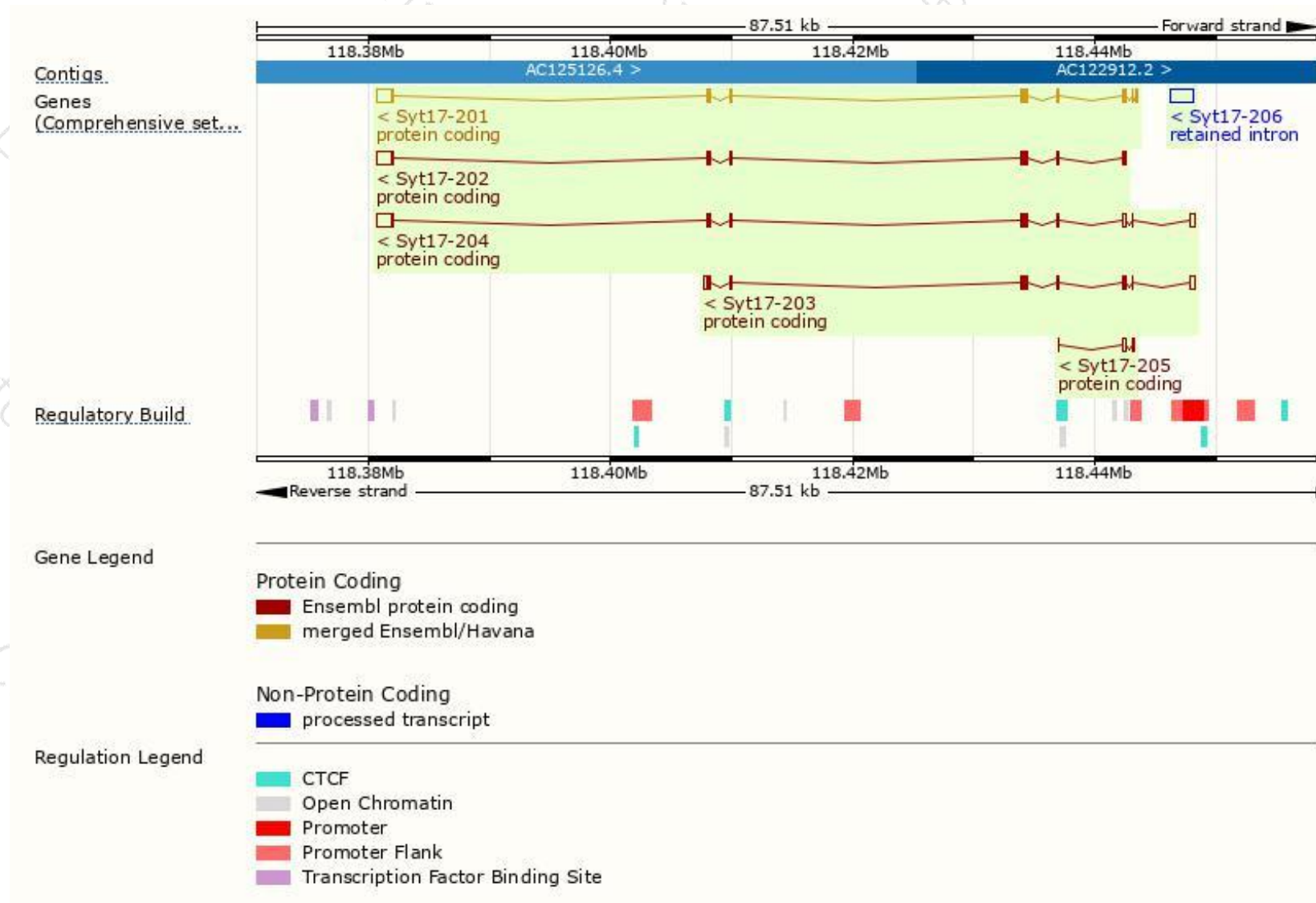
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syt17-201	ENSMUST00000081574.7	2764	470aa	Protein coding	CCDS40103	Q920M7	TSL:1 GENCODE basic APPRIS P1
Syt17-204	ENSMUST00000203796.3	2957	413aa	Protein coding	-	A0A0N4SVG2	TSL:1 GENCODE basic
Syt17-202	ENSMUST00000203465.1	2548	469aa	Protein coding	-	A0A140LJ89	CDS 5' incomplete TSL:1
Syt17-203	ENSMUST00000203485.2	1932	419aa	Protein coding	-	A0A0N4SV78	TSL:1 GENCODE basic
Syt17-205	ENSMUST00000207034.1	362	13aa	Protein coding	-	A0A140LHL3	CDS 3' incomplete TSL:5
Syt17-206	ENSMUST00000207650.1	1794	No protein	Retained intron	-	-	TSL:NA

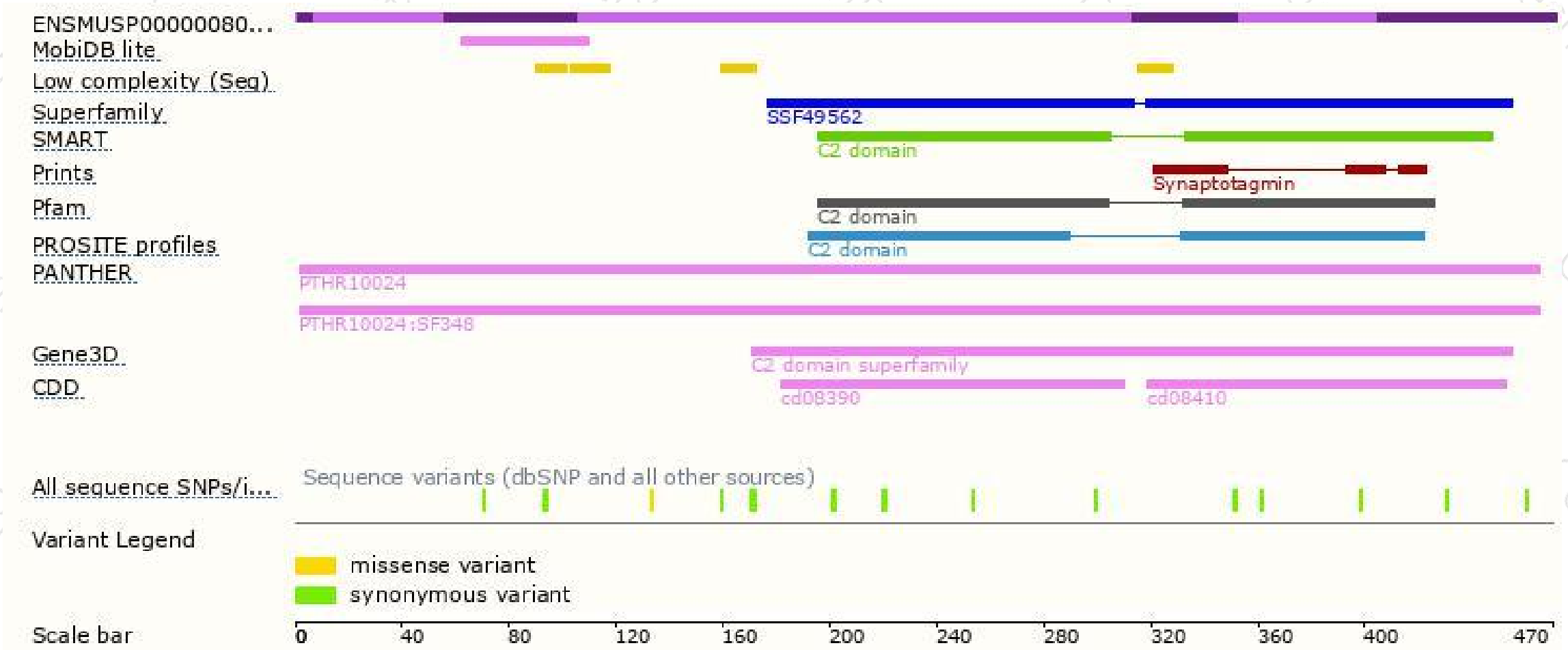
The strategy is based on the design of *Syt17-201* transcript,The transcription is shown below



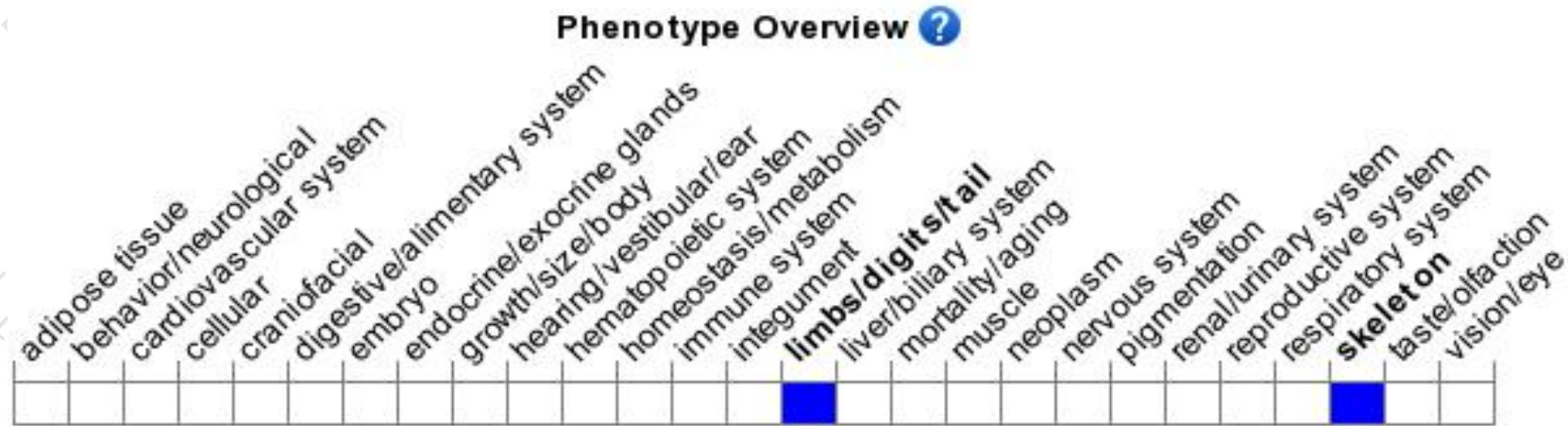
Genomic location distribution



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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