Syt7 Cas9-KO Strategy

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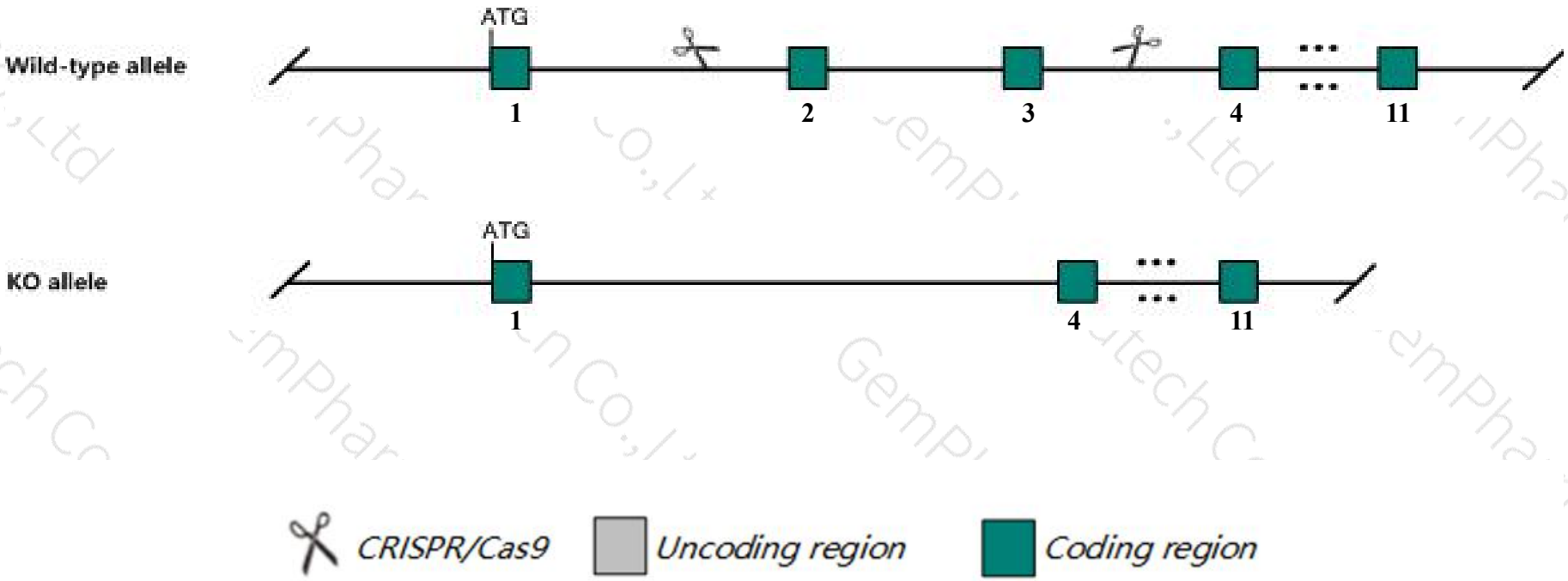
Project Overview

Project Name	***Syt7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Syt7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Syt7* gene has 15 transcripts. According to the structure of *Syt7* gene, exon2-exon3 of *Syt7-205* (ENSMUST00000224135.2) transcript is recommended as the knockout region.The region contains 184bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Syt7* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

➢ According to the existing MGI data,Mice homozygous for disruptions in this gene have no gross abnormalities or obvious neurological defects. They do develop fibrosis in the skin and skeletal muscle over time.

➢ The *Syt7* gene is located on the Chr19. 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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Syt7 synaptotagmin VII [Mus musculus (house mouse)]

Gene ID: 54525, updated on 19-Mar-2019

Summary

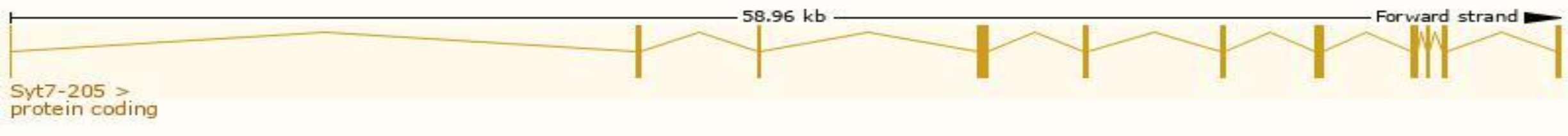
Official Symbol	Syt7 provided by MGI
Official Full Name	synaptotagmin VII provided by MGI
Primary source	MGI:MGI:1859545
See related	Ensembl:ENSMUSG00000024743
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI851541, B230112P13Rik
Expression	Biased expression in cortex adult (RPKM 37.8), frontal lobe adult (RPKM 34.9) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

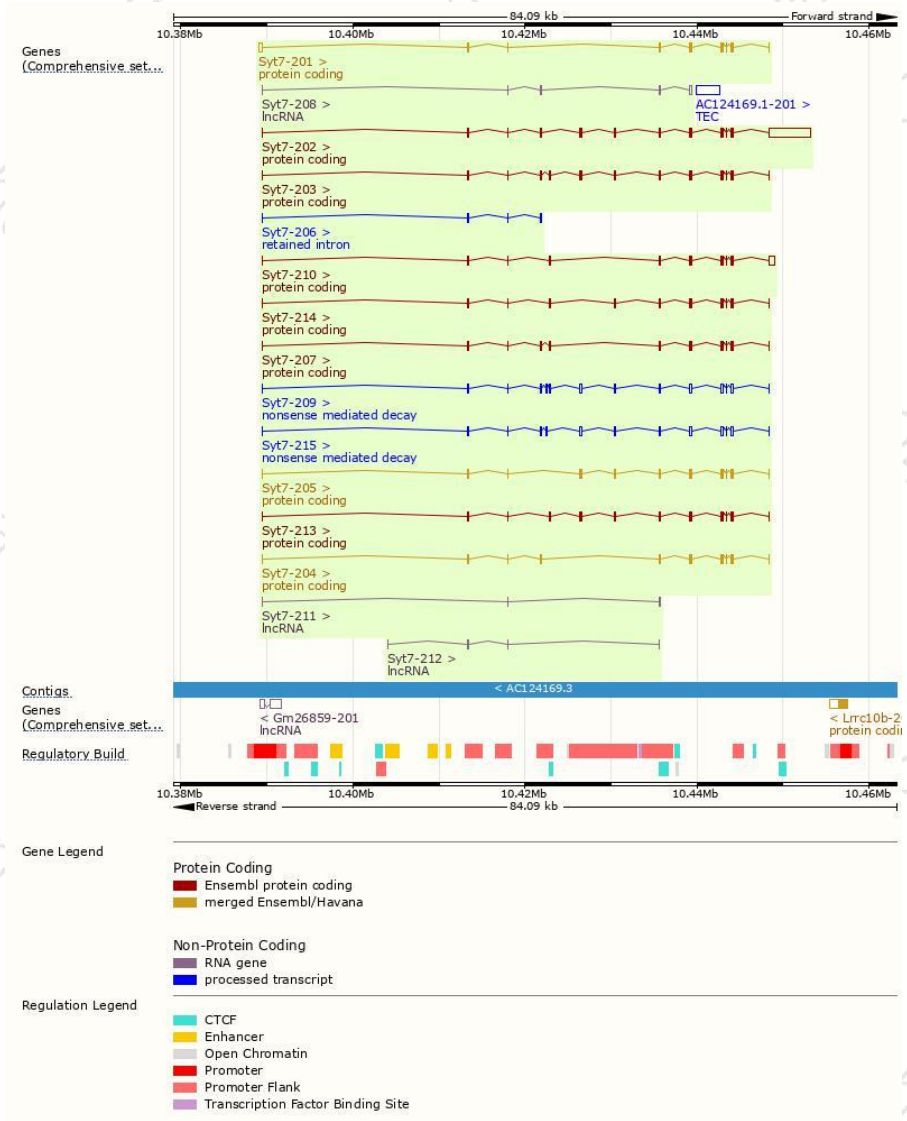
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syt7-205	ENSMUST00000224135.2	1704	567aa	Protein coding	CCDS50388	A0A286YCU4	GENCODE basic APPRIS ALT2
Syt7-201	ENSMUST00000073899.5	1605	403aa	Protein coding	CCDS29575	Q9R0N7	TSL:1 GENCODE basic APPRIS ALT1
Syt7-204	ENSMUST00000223586.1	1344	447aa	Protein coding	CCDS29576	Q9R0N7	GENCODE basic APPRIS P4
Syt7-202	ENSMUST00000076968.10	6624	611aa	Protein coding	-	A0A2C9F2C1	TSL:1 GENCODE basic
Syt7-203	ENSMUST00000169121.8	2116	687aa	Protein coding	-	Q9R0N7	TSL:5 GENCODE basic
Syt7-210	ENSMUST00000235479.1	2000	479aa	Protein coding	-	-	GENCODE basic APPRIS ALT1
Syt7-213	ENSMUST00000235784.1	1932	643aa	Protein coding	-	-	GENCODE basic
Syt7-207	ENSMUST00000225452.2	1572	523aa	Protein coding	-	A0A286YCR9	GENCODE basic
Syt7-214	ENSMUST00000237366.1	1563	520aa	Protein coding	-	-	GENCODE basic
Syt7-209	ENSMUST00000235303.1	2187	122aa	Nonsense mediated decay	-	-	
Syt7-215	ENSMUST00000237745.1	1959	122aa	Nonsense mediated decay	-	-	
Syt7-206	ENSMUST00000225019.1	479	No protein	Retained intron	-	-	
Syt7-208	ENSMUST00000225861.1	697	No protein	lncRNA	-	-	
Syt7-212	ENSMUST00000235717.1	393	No protein	lncRNA	-	-	
Syt7-211	ENSMUST00000235568.1	236	No protein	lncRNA	-	-	

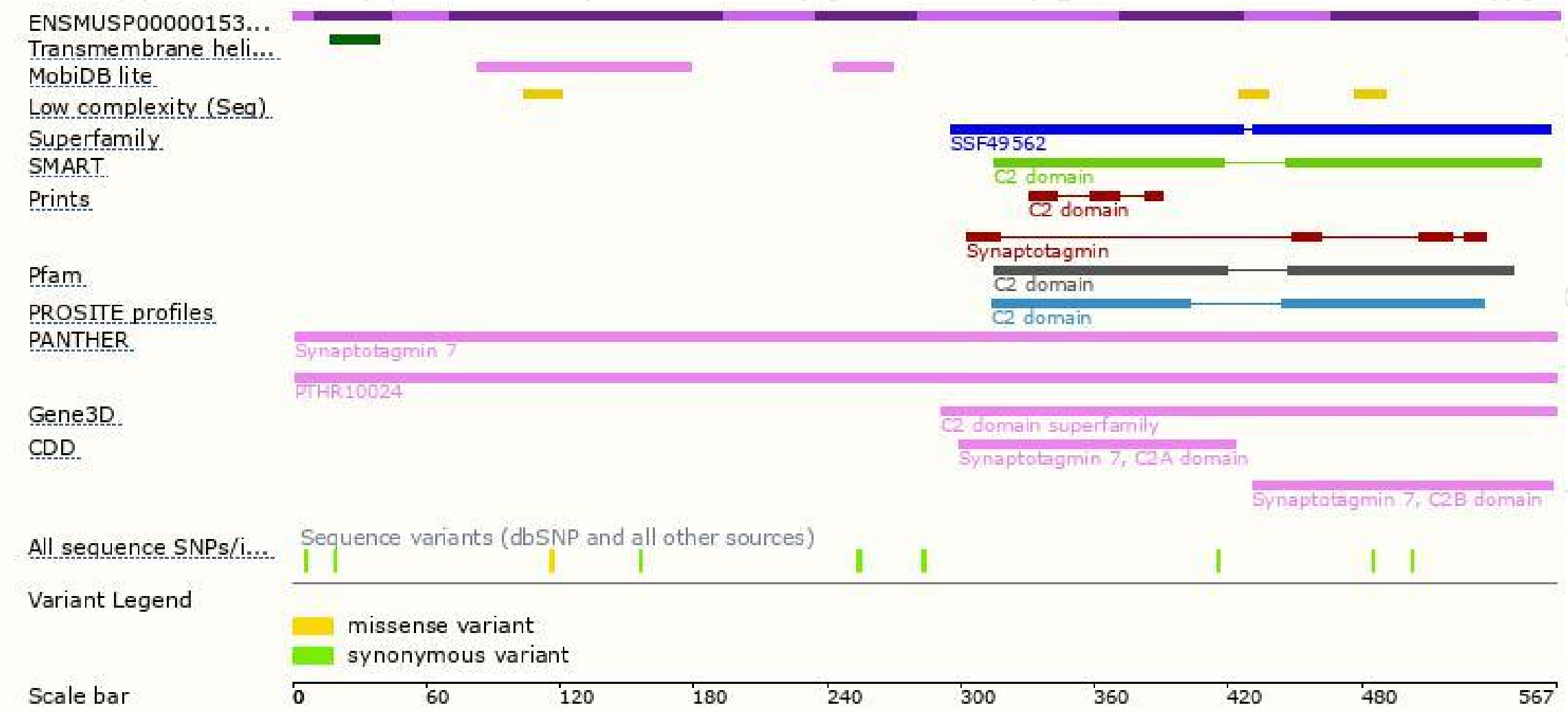
The strategy is based on the design of *Syt7-205* transcript,The transcription is shown below



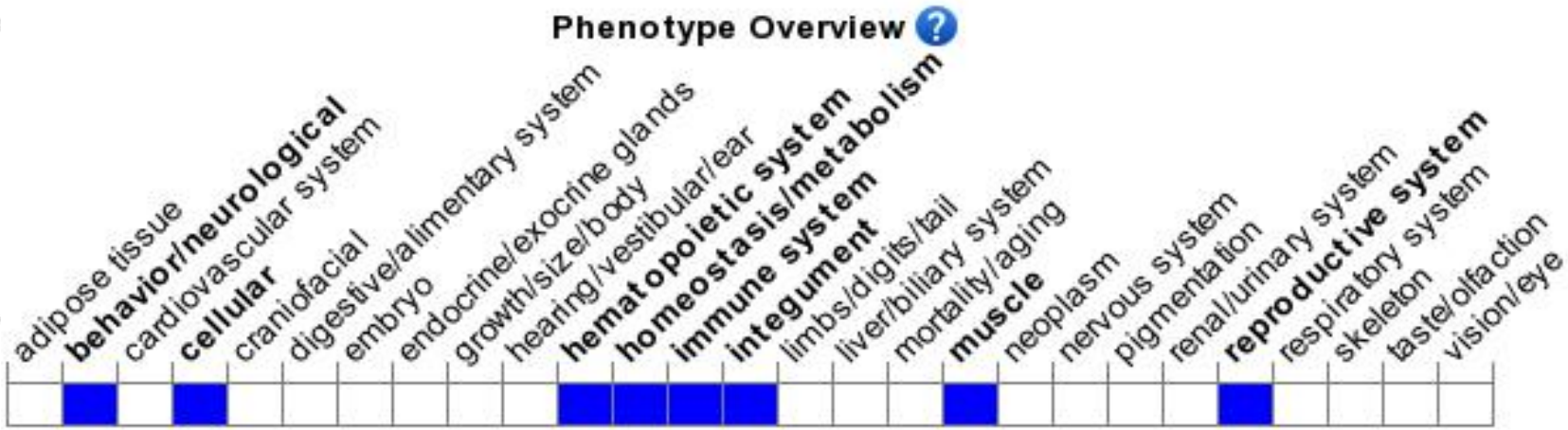
Genomic location distribution



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/).

According to the existing MGI data,Mice homozygous for disruptions in this gene have no gross abnormalities or obvious neurological defects. They do develop fibrosis in the skin and skeletal muscle over time.

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

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