

Syn1-IRES-EGFP Mouse Model Strategy

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Project Overview





Strategy



400-9660890

This model will use CRISPR/Cas9 technology to edit the Syn1 gene. The schematic diagram is as follows:



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➤ The Syn1 gene has 2 transcripts.

> According to the structure of *Syn1* gene, the element IRES-EGFP will be inserted at the translation stop codon of *Syn1-201*(ENSMUST00000081893.6), the length of inserted fragment is about 1.3kb.

➤ In this project we use CRISPR/Cas9 technology to modify Syn1 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.

Notice



> According to the existing MGI data, homozygous inactivation of this gene causes impaired CNS synapse formation and synaptic vesicle (SV) clustering, and may lead to altered SV recycling and inhibitory postsynaptic currents, convulsive seizures, increased response to electrical stimulation, and enhanced paired-pulse facilitation.

> It is necessary to introduce 1-2 synonymous mutation in exon13.

> The IERS-linked genes will be tarnscripted together and then be translated two protein separately, but the downstream protein is lower than the upstream protein.

> The *Syn1* gene is located on the ChrX. Please take the loci in consideration when breeding this knockin mice with other gene modified (e.g., Tg, iCre) strains, if the other gene is also on ChrX, it may be extremely hard to get double gene positive homozygotes.

> The scheme is designed according to the genetic information in the existing database. Inserting a foreign gene between the 3'UTR and the gene coding region may affect the expression of endogenous and foreign genes. Due to the complexity of biological processes, it cannot be predicted completely at the present technology level.

Gene information (NCBI)



☆ ?

Syn1 synapsin I [Mus musculus (house mouse)]

Gene ID: 20964, updated on 13-Mar-2020

- Summary

Official SymbolSyn1 provided by MGIOfficial Full Namesynapsin l provided by MGIPrimary sourceMGI:MGI:98460Primary sourceEnsembl:ENSMUSG00000037217Gene typeprotein codinggene typeprotein codingVALIDATEDVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Muriae; Mus; MusAlso known asSyn-1, Syn1-SExpressionBiased expression in frontal lobe adult (RPKM 77.1), cortex adult (RPKM 74.4) and 11 other tissues
See more
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Transcript information (Ensembl)



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The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syn1-202	ENSMUST00000115345.7	3261	<u>670aa</u>	Protein coding	CCDS53018	<u>088935</u>	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 ALT
Syn1-201	ENSMUST0000081893.6	3209	<u>706aa</u>	Protein coding	CCDS53017	<u>088935</u>	TSL:5 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

The strategy is based on the design of *Syn1-201* transcript, the transcription is shown below:



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Genomic location distribution





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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, homozygous inactivation of this gene causes impaired CNS synapse formation and synaptic vesicle (SV) clustering, and may lead to altered SV recycling and inhibitory postsynaptic currents, convulsive seizures, increased response to electrical stimulation, and enhanced paired-pulse facilitation.

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



