

Syt2 Cas9-CKO Strategy

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Project Overview



Project Name Syt2

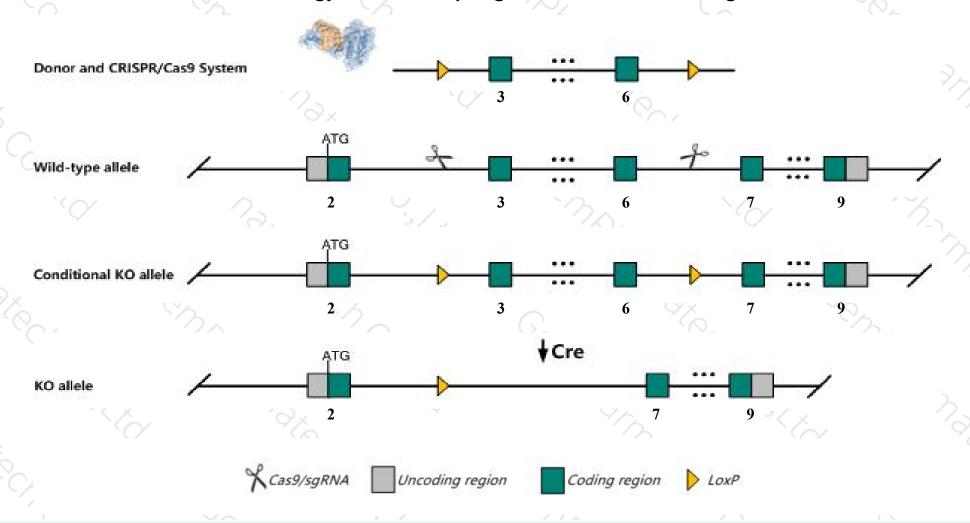
Project type Cas9-CKO

Strain background C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Syt2 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Syt2* gene has 4 transcripts. According to the structure of *Syt2* gene, exon3-exon6 of *Syt2*201(ENSMUST00000121990.1) transcript is recommended as the knockout region. The region contains 623bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Syt2* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was 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



- > According to the existing MGI data,mice homozygous for an ENU-induced allele are viable but sterile, weigh less and show ataxia and altered spontaneous and Ca2+-evoked neurotransmitter release. Mice homozygous for a null allele die at weaning showing growth arrest, motor dysfunction and impaired Ca2+-evoked neurotransmitter release.
- > The Syt2 gene is located on the Chr1. 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)



Syt2 synaptotagmin II [Mus musculus (house mouse)]

Gene ID: 20980, updated on 13-Mar-2020

Summary

↑ ?

Official Symbol Syt2 provided by MGI

Official Full Name synaptotagmin II provided by MGI

Primary source MGI:MGI:99666

See related Ensembl:ENSMUSG00000026452

Gene type protein coding
RefSeq status REVIEWED
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as IP4BP, R74640, mKIAA4194, sytll

Summary This gene encodes a member of the synaptotagmin protein family. Synaptotagmin proteins are involved in membrane trafficking and are

characterized by an N-terminal transmembrane region as well as tandem calcium binding domains. The encoded protein is able to bind inositol polyphosphate and is thought to be involved in synaptic function and neurotransmitter release. [provided by RefSeq, Sep 2017]

Expression Biased expression in cerebellum adult (RPKM 41.6) and cortex adult (RPKM 3.9)See more

Orthologs <u>human</u> all

Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

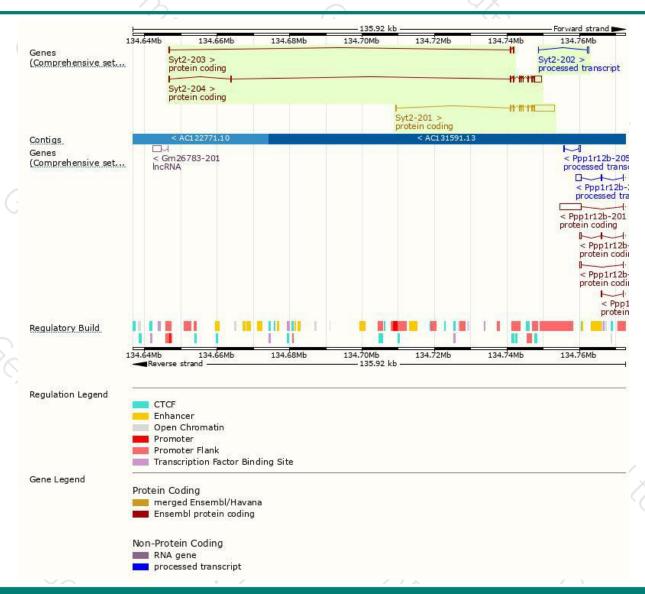
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syt2-201	ENSMUST00000121990.1	6879	422aa	Protein coding	CCDS15312	A0A0R4J2C2	TSL:1 GENCODE basic APPRIS P1
Syt2-204	ENSMUST00000188842.6	3386	<u>422aa</u>	Protein coding	CCDS15312	A0A0R4J2C2	TSL:1 GENCODE basic APPRIS P1
Syt2-203	ENSMUST00000187725.6	383	69aa	Protein coding	-20	Q9JM87	CDS 3' incomplete TSL:1
Syt2-202	ENSMUST00000187702.1	485	No protein	Processed transcript	20	2	TSL:3

The strategy is based on the design of *Syt2-201* transcript, the transcription is shown below:

Syt2-201 > protein coding

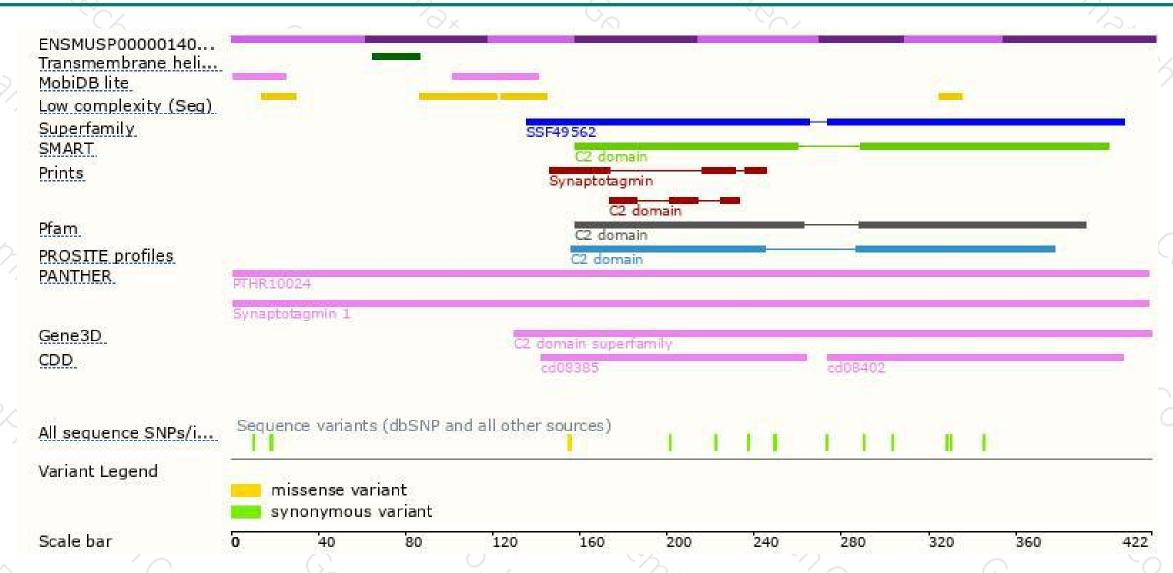
Genomic location distribution





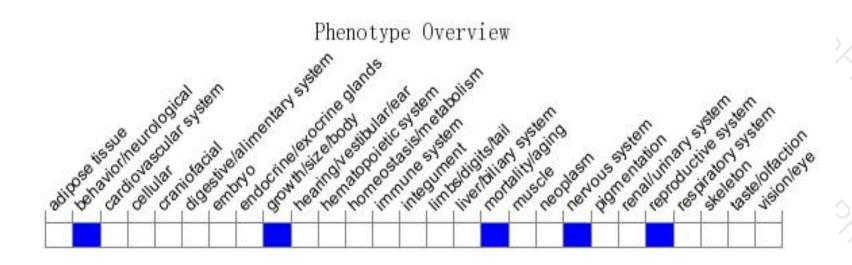
Protein domain





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 an ENU-induced allele are viable but sterile, weigh less and show ataxia and altered spontaneous and Ca2+-evoked neurotransmitter release. Mice homozygous for a null allele die at weaning showing growth arrest, motor dysfunction and impaired Ca2+-evoked neurotransmitter release.



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

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