

Syncrip Cas9-KO Strategy

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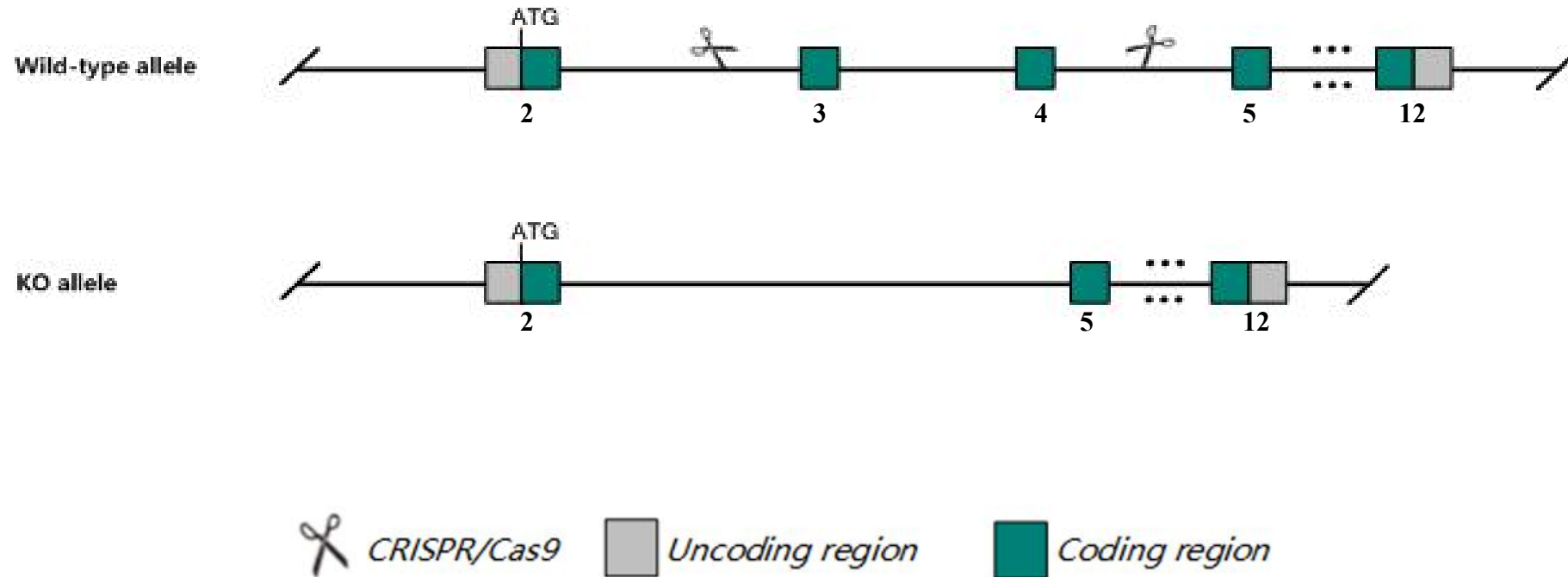


Project Overview

Project Name	<i>Syncrip</i>
Project type	Cas9-KO
Strain background	C57BL/6JGpt

Knockout strategy

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



The *Syncrip* gene has 12 transcripts. According to the structure of *Syncrip* gene, exon3-exon4 of *Syncrip-201* (ENSMUST00000069221.11) transcript is recommended as the knockout region. The region contains 227bp coding sequence. Knock out the region will result in disruption of protein function.

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

The *Syncrip* gene is located on the Chr9. 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.

Syncrip synaptotagmin binding, cytoplasmic RNA interacting protein [Mus musculus (house mouse)]

Gene ID: 56403, updated on 31-Jan-2019

Summary



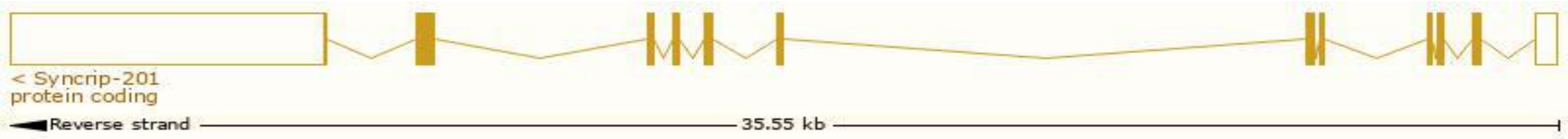
Official Symbol	Syncrip provided by MGI
Official Full Name	synaptotagmin binding, cytoplasmic RNA interacting protein provided by MGI
Primary source	MGI:MGI:1891690
See related	Ensembl:ENSMUSG000000032423
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610109K23Rik, 4632417O19Rik, GRY-RBP, Nsap1, Nsap1l, hnRNP Q, pp68
Expression	Broad expression in CNS E11.5 (RPKM 10.8), limb E14.5 (RPKM 9.0) and 21 other tissues See more
Orthologs	human all

Transcript information Ensembl

The gene has 12 transcripts,all transcripts are shown below:

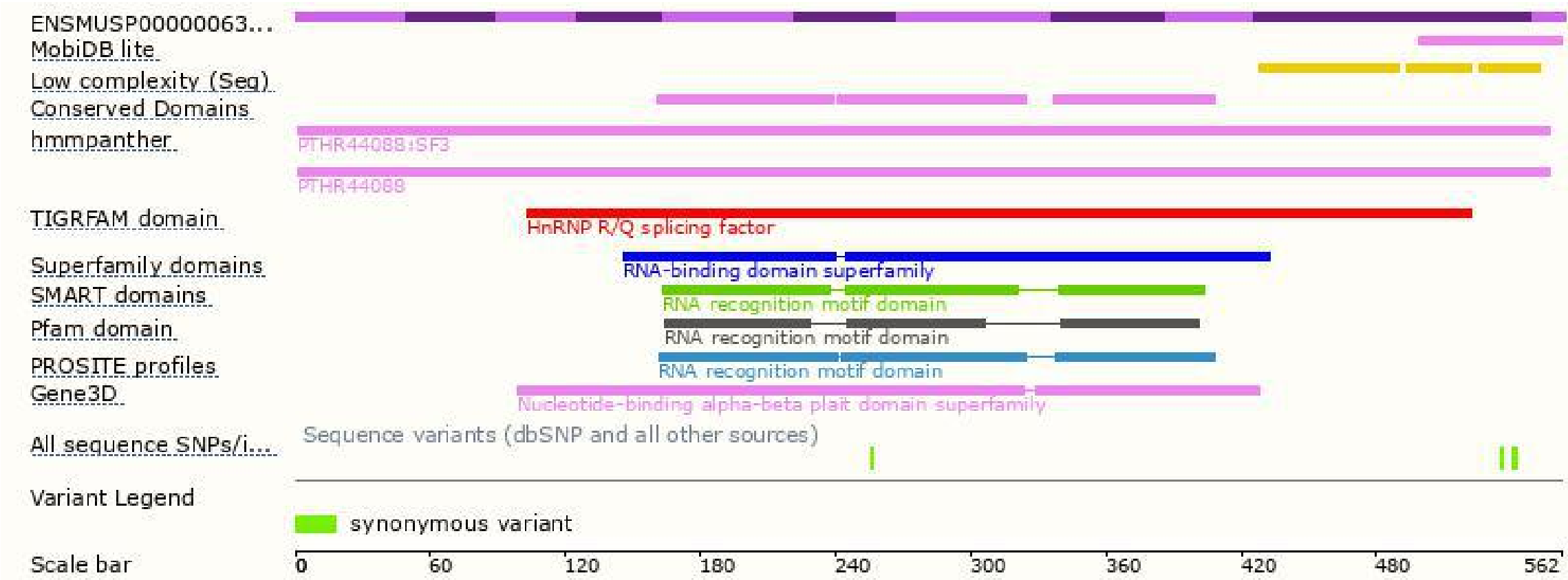
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Syncrip-201	ENSMUST00000069221.11	9450	562aa	Protein coding	CCDS23388	Q7TMK9	TSL:1 GENCODE basic APPRIS P3
Syncrip-210	ENSMUST00000174391.7	6257	464aa	Protein coding	CCDS81048	G3UZ48	TSL:1 GENCODE basic
Syncrip-208	ENSMUST00000174282.7	3404	561aa	Protein coding	CCDS72292	A0A0R4J259	TSL:1 GENCODE basic APPRIS ALT 1
Syncrip-205	ENSMUST00000173801.7	2944	623aa	Protein coding	CCDS57686	Q7TMK9	TSL:1 GENCODE basic APPRIS ALT 1
Syncrip-207	ENSMUST00000174269.7	3286	527aa	Protein coding	-	G3UZI2	TSL:5 GENCODE basic
Syncrip-211	ENSMUST00000174688.7	3176	448aa	Protein coding	-	G3UXJ6	TSL:5 GENCODE basic
Syncrip-209	ENSMUST00000174361.7	1767	588aa	Protein coding	-	G3V018	TSL:5 GENCODE basic
Syncrip-204	ENSMUST00000173405.7	766	196aa	Protein coding	-	G3UWM1	CDS 3' incomplete TSL:3
Syncrip-202	ENSMUST00000172508.1	473	94aa	Protein coding	-	G3XA76	CDS 3' incomplete TSL:5
Syncrip-203	ENSMUST00000172828.7	1925	67aa	Nonsense mediated decay	-	G3UXU5	TSL:5
Syncrip-212	ENSMUST00000187770.1	2387	No protein	Retained intron	-	-	TSL:1
Syncrip-206	ENSMUST00000174145.1	549	No protein	Retained intron	-	-	TSL:3

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



Genomic location distribution

Protein domain



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