

Srgap3 Cas9-KO Strategy

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Project Overview

Project Name

Srgap3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srgap3* gene. The schematic diagram is as follows:



- The *Srgap3* gene has 5 transcripts. According to the structure of *Srgap3* gene, exon2-exon3 of *Srgap3-202* (ENSMUST00000088373.10) transcript is recommended as the knockout region. The region contains 356bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Srgap3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit a reduction in spine density in the brain CA1 and cortical layers IV/V. Mice homozygous for a different knock-out allele exhibit a neurodevelopment disorder with schizophrenia-related intermediate phenotypes.
- The *Srgap3* gene is located on the Chr6. 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)

Srgap3 SLIT-ROBO Rho GTPase activating protein 3 [Mus musculus (house mouse)]

Gene ID: 259302, updated on 31-Jan-2019

Summary



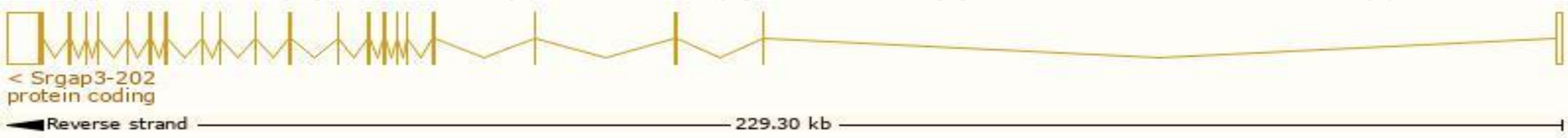
Official Symbol	Srgap3 provided by MGI
Official Full Name	SLIT-ROBO Rho GTPase activating protein 3 provided by MGI
Primary source	MGI:MGI:2152938
See related	Ensembl:ENSMUSG00000030257
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI452337, Arhgap14, D130026O08Rik, Gbi, MEGAP, WRP, mKIAA0411
Expression	Biased expression in frontal lobe adult (RPKM 27.6), CNS E18 (RPKM 23.8) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srgap3-202	ENSMUST00000088373.10	8887	1099aa	Protein coding	CCDS39590	F8VPQ4	TSL:1 GENCODE basic APPRIS P2
Srgap3-203	ENSMUST00000113169.8	8300	1075aa	Protein coding	-	E9QN14	TSL:5 GENCODE basic APPRIS ALT1
Srgap3-204	ENSMUST00000131835.1	841	102aa	Nonsense mediated decay	-	F6QZR7	CDS 5' incomplete TSL:3
Srgap3-201	ENSMUST00000060215.11	2482	No protein	Retained intron	-	-	TSL:1
Srgap3-205	ENSMUST00000143475.1	600	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Srgap3-202* transcript,The transcription is shown below



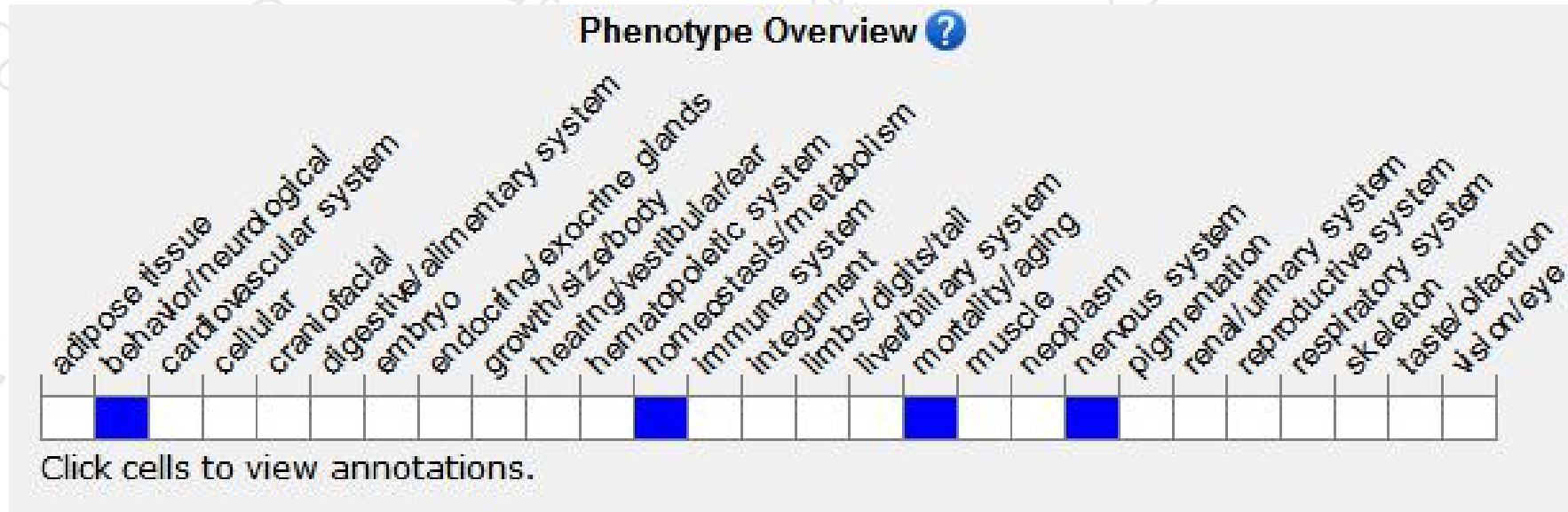
Genomic location distribution



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 a knock-out allele exhibit a reduction in spine density in the brain CA1 and cortical layers IV/V. Mice homozygous for a different knock-out allele exhibit a neurodevelopment disorder with schizophrenia-related intermediate phenotypes.

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

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