

Stau1 Cas9-KO Strategy

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Date: 2020-1-22

Project Overview

Project Name

Stau1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stau1* gene. The schematic diagram is as follows:



- The *Stau1* gene has 11 transcripts. According to the structure of *Stau1* gene, exon3-exon5 of *Stau1*-202 (ENSMUST00000109235.7) transcript is recommended as the knockout region. The region contains 478bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stau1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a targeted allele exhibit hypoactivity and impaired dendrite outgrowth and spine formation.
- Transcript *Stau1*-207&209 may not be affected.
- The *Stau1* gene is located on the Chr2. 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)

Stau1 stauflen double-stranded RNA binding protein 1 [*Mus musculus* (house mouse)]

Gene ID: 20853, updated on 12-Aug-2019

Summary

- Official Symbol** Stau1 provided by [MGI](#)
- Official Full Name** stauflen double-stranded RNA binding protein 1 provided by [MGI](#)
- Primary source** [MGI:MGI:1338864](#)
- See related** [Ensembl:ENSMUSG00000039536](#)
- 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** Stau; C85792; AW549911; 5830401L18Rik
- Expression** Ubiquitous expression in CNS E14 (RPKM 16.8), adrenal adult (RPKM 16.1) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 2; 2 H3 See Stau1 in [Genome Data Viewer](#)

Exon count: 12

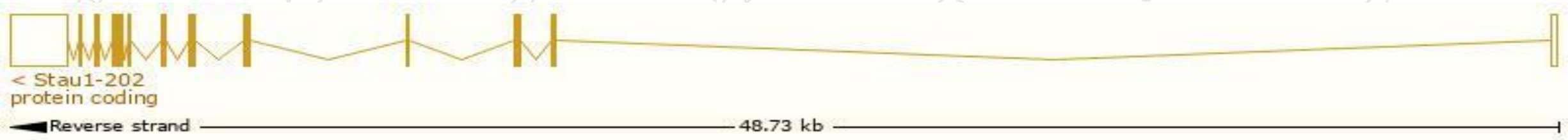
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (166947549..166996315, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (166773641..166821778, complement)

Transcript information (Ensembl)

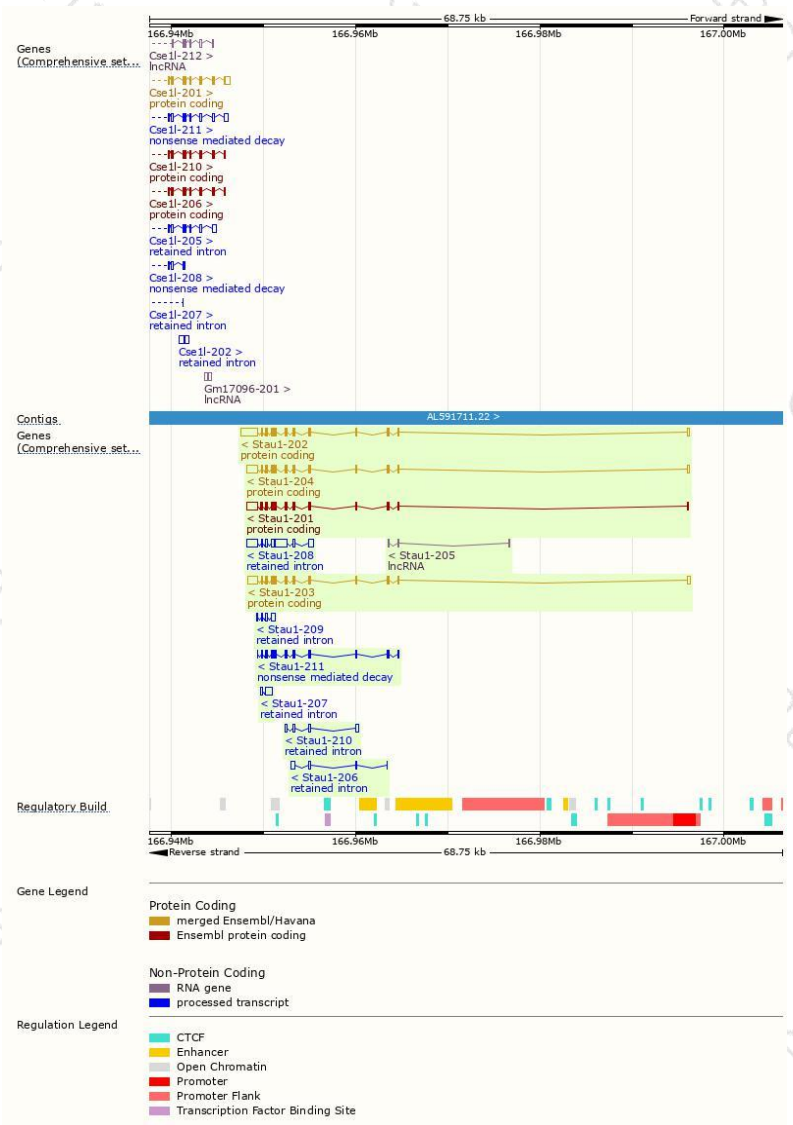
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stau1-202	ENSMUST00000109235.7	3569	489aa	Protein coding	CCDS50800	Q9DBE7	TSL:1 GENCODE basic APPRIS ALT2
Stau1-204	ENSMUST00000109238.8	2976	495aa	Protein coding	CCDS50801	A2A5S3	TSL:1 GENCODE basic APPRIS ALT2
Stau1-203	ENSMUST00000109236.8	2860	487aa	Protein coding	CCDS17093	Q9Z108	TSL:1 GENCODE basic APPRIS P3
Stau1-201	ENSMUST00000049412.11	2840	485aa	Protein coding	CCDS71197	A2A5R8	TSL:1 GENCODE basic APPRIS ALT2
Stau1-211	ENSMUST00000184390.1	1513	436aa	Nonsense mediated decay	-	V9GX87	TSL:1
Stau1-208	ENSMUST00000142481.7	3573	No protein	Retained intron	-	-	TSL:2
Stau1-207	ENSMUST00000134664.1	862	No protein	Retained intron	-	-	TSL:3
Stau1-210	ENSMUST00000154506.1	826	No protein	Retained intron	-	-	TSL:3
Stau1-206	ENSMUST00000130790.1	788	No protein	Retained intron	-	-	TSL:5
Stau1-209	ENSMUST00000149454.1	774	No protein	Retained intron	-	-	TSL:2
Stau1-205	ENSMUST00000130104.1	341	No protein	lncRNA	-	-	TSL:3

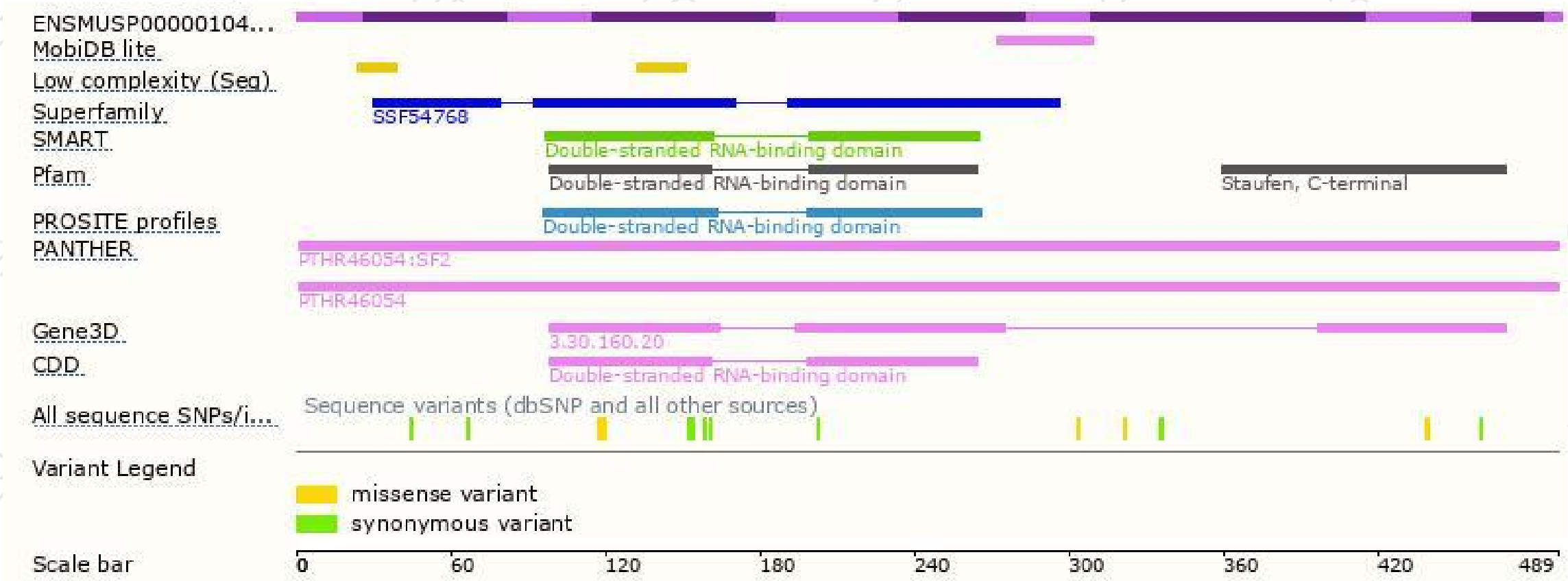
The strategy is based on the design of *Stau1-202* transcript,The transcription is shown below



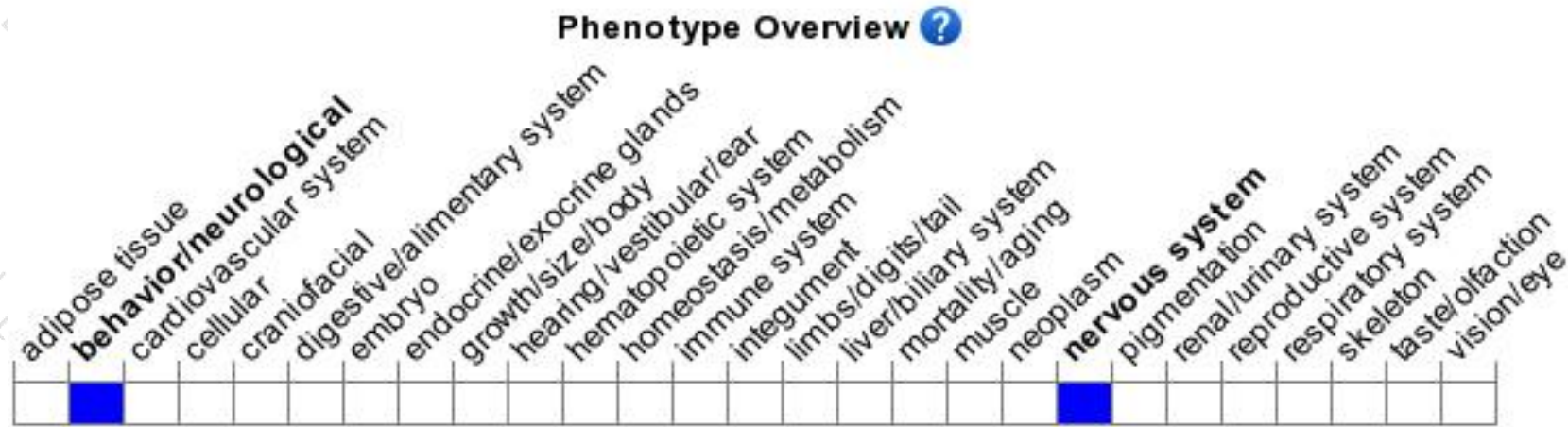
Genomic location distribution



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 targeted allele exhibit hypoactivity and impaired dendrite outgrowth and spine formation.

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

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