

Sbf2 Cas9-KO Strategy

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Project Overview

Project Name

Sbf2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sbf2* gene. The schematic diagram is as follows:



- The *Sbf2* gene has 15 transcripts. According to the structure of *Sbf2* gene, exon2 of *Sbf2-201* (ENSMUST00000033058.13) transcript is recommended as the knockout region. The region contains 89bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sbf2* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for null alleles display progressive misfolding of myelin sheaths and abnormal nerve electrophysiology.
- Transcript 202,203,204,209 CDS 5' and 3' incomplete the influences is unknown.
- The *Sbf2* gene is located on the Chr7. 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)

Sbf2 SET binding factor 2 [Mus musculus (house mouse)]

Gene ID: 319934, updated on 19-Mar-2019

Summary



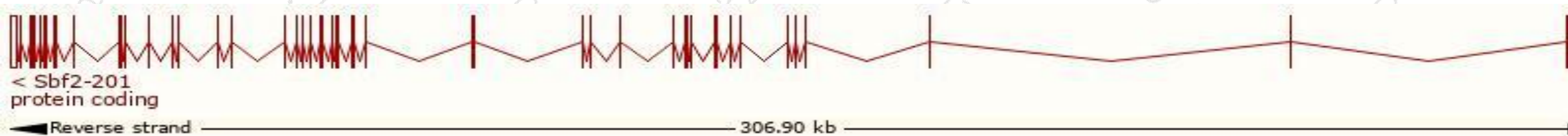
Official Symbol	Sbf2 provided by MGI
Official Full Name	SET binding factor 2 provided by MGI
Primary source	MGI:MGI:1921831
See related	Ensembl:ENSMUSG00000038371
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4833411B01Rik, AA414977, AI317167, B430219L04Rik, Mtmr13, mMTMH1
Expression	Ubiquitous expression in CNS E18 (RPKM 16.7), whole brain E14.5 (RPKM 16.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

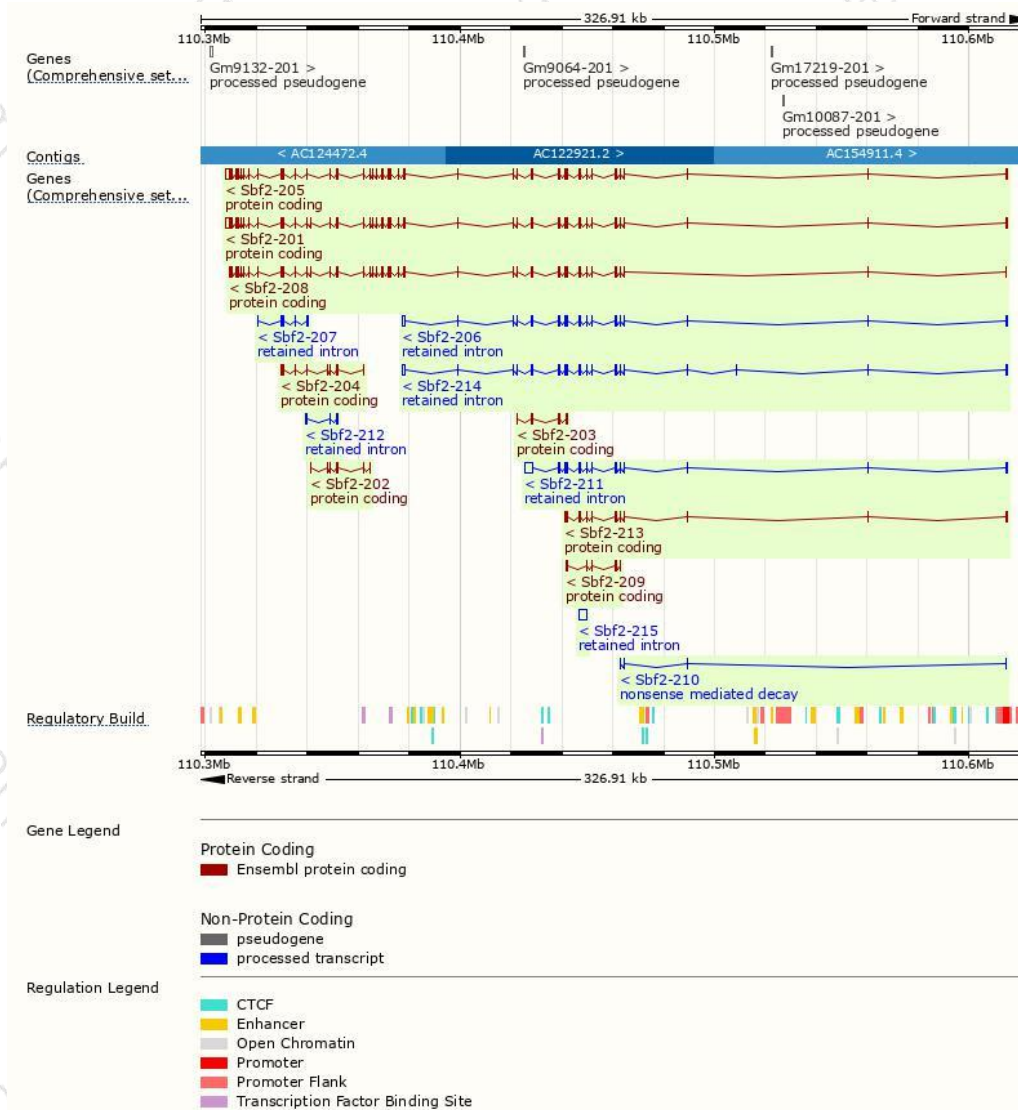
The gene has 15 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sbf2-201	ENSMUST00000033058.13	7154	1872aa	Protein coding	CCDS52361	E9PXF8	TSL:5 GENCODE basic APPRIS P2
Sbf2-205	ENSMUST00000164759.7	7090	1847aa	Protein coding	-	-	TSL:5 GENCODE basic APPRIS ALT2
Sbf2-208	ENSMUST00000166020.7	5481	1826aa	Protein coding	-	E9Q0D4	TSL:5 GENCODE basic APPRIS ALT2
Sbf2-213	ENSMUST00000171218.7	1476	408aa	Protein coding	-	E9Q372	TSL:1 GENCODE basic
Sbf2-204	ENSMUST00000164599.7	1018	339aa	Protein coding	-	F6ZDC5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sbf2-202	ENSMUST00000164525.1	733	245aa	Protein coding	-	F7BBM8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sbf2-209	ENSMUST00000166885.1	595	198aa	Protein coding	-	F6QZ02	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sbf2-203	ENSMUST00000164559.1	530	177aa	Protein coding	-	F6QG63	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sbf2-210	ENSMUST00000167652.1	404	44aa	Nonsense mediated decay	-	E9Q4I8	TSL:5
Sbf2-211	ENSMUST00000167880.7	4280	No protein	Retained intron	-	-	TSL:1
Sbf2-206	ENSMUST00000165449.7	2961	No protein	Retained intron	-	-	TSL:1
Sbf2-215	ENSMUST00000211732.1	2770	No protein	Retained intron	-	-	TSL:NA
Sbf2-214	ENSMUST00000171378.7	2694	No protein	Retained intron	-	-	TSL:1
Sbf2-212	ENSMUST00000169740.1	1681	No protein	Retained intron	-	-	TSL:1
Sbf2-207	ENSMUST00000165992.1	920	No protein	Retained intron	-	-	TSL:5

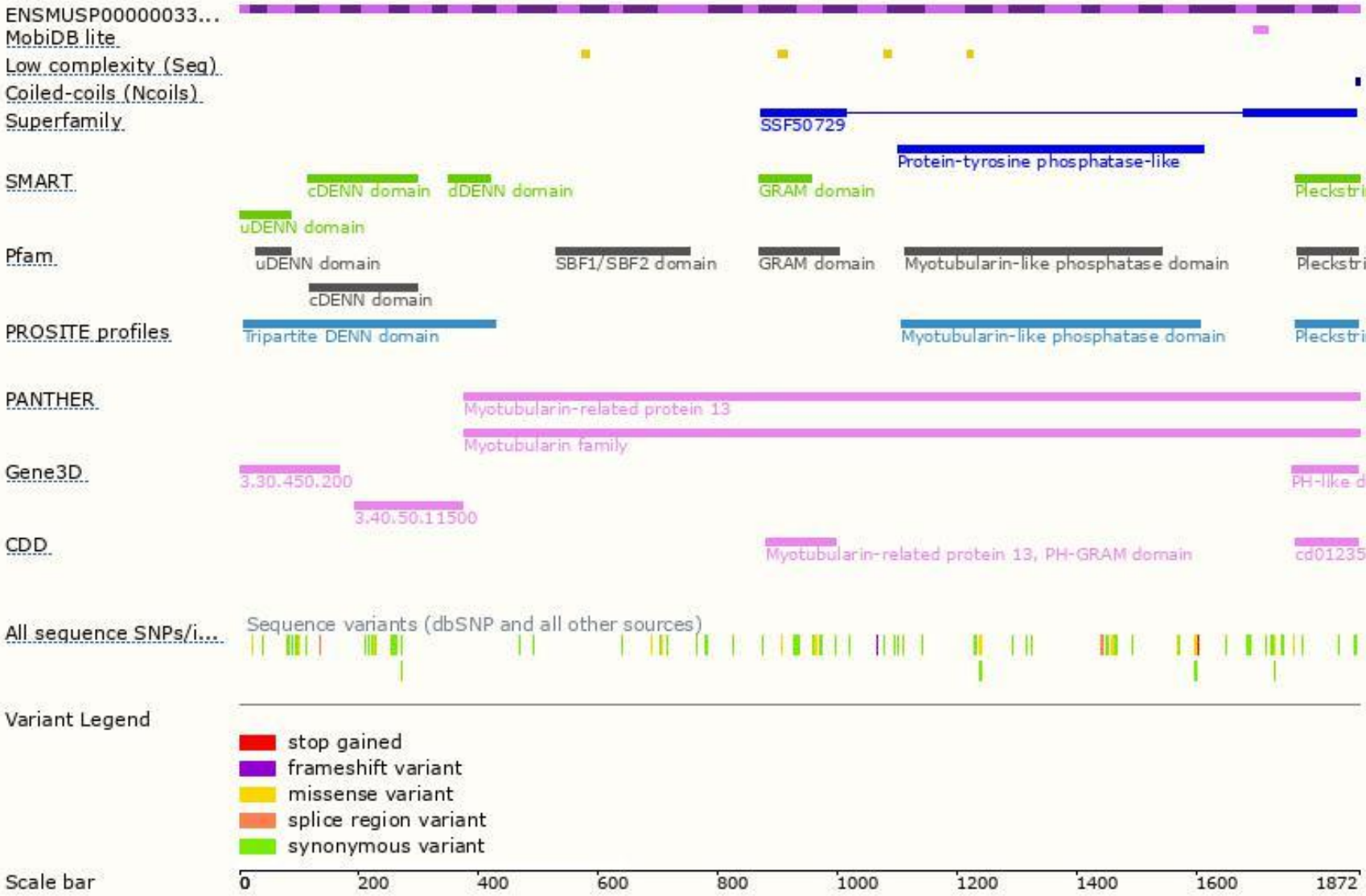
The strategy is based on the design of *Sbf2-201* transcript, The transcription is shown below



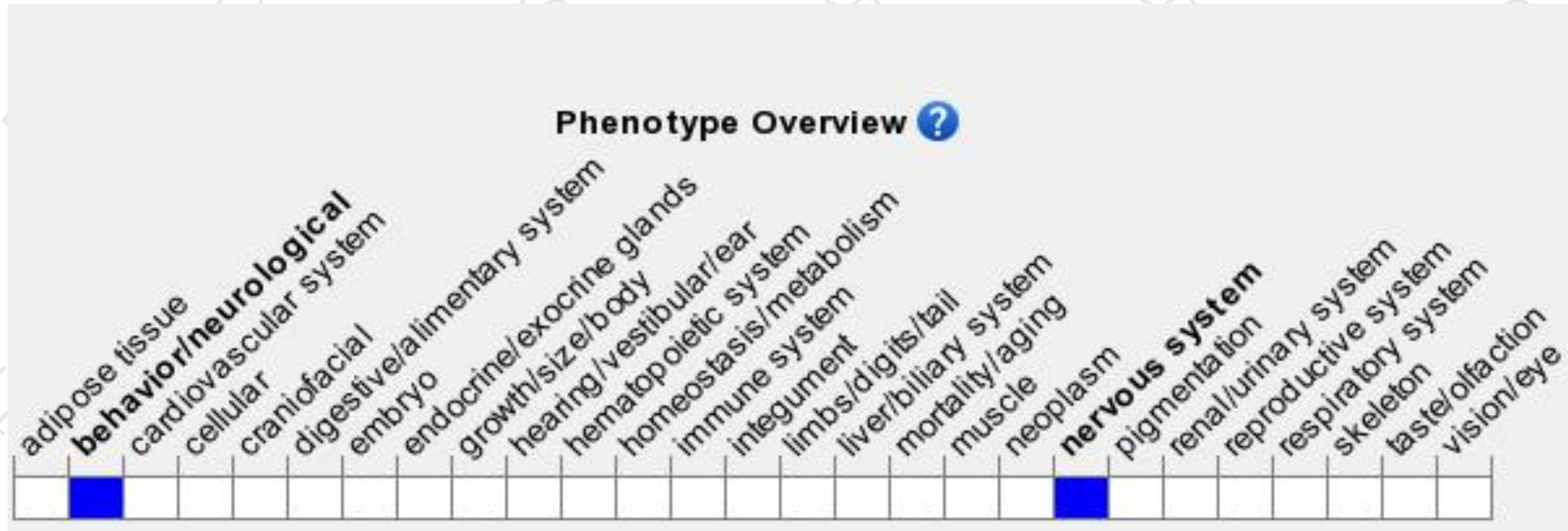
Genomic location distribution



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 null alleles display progressive misfolding of myelin sheaths and abnormal nerve electrophysiology.

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

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