

Sptbn2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Sptbn2

Project type

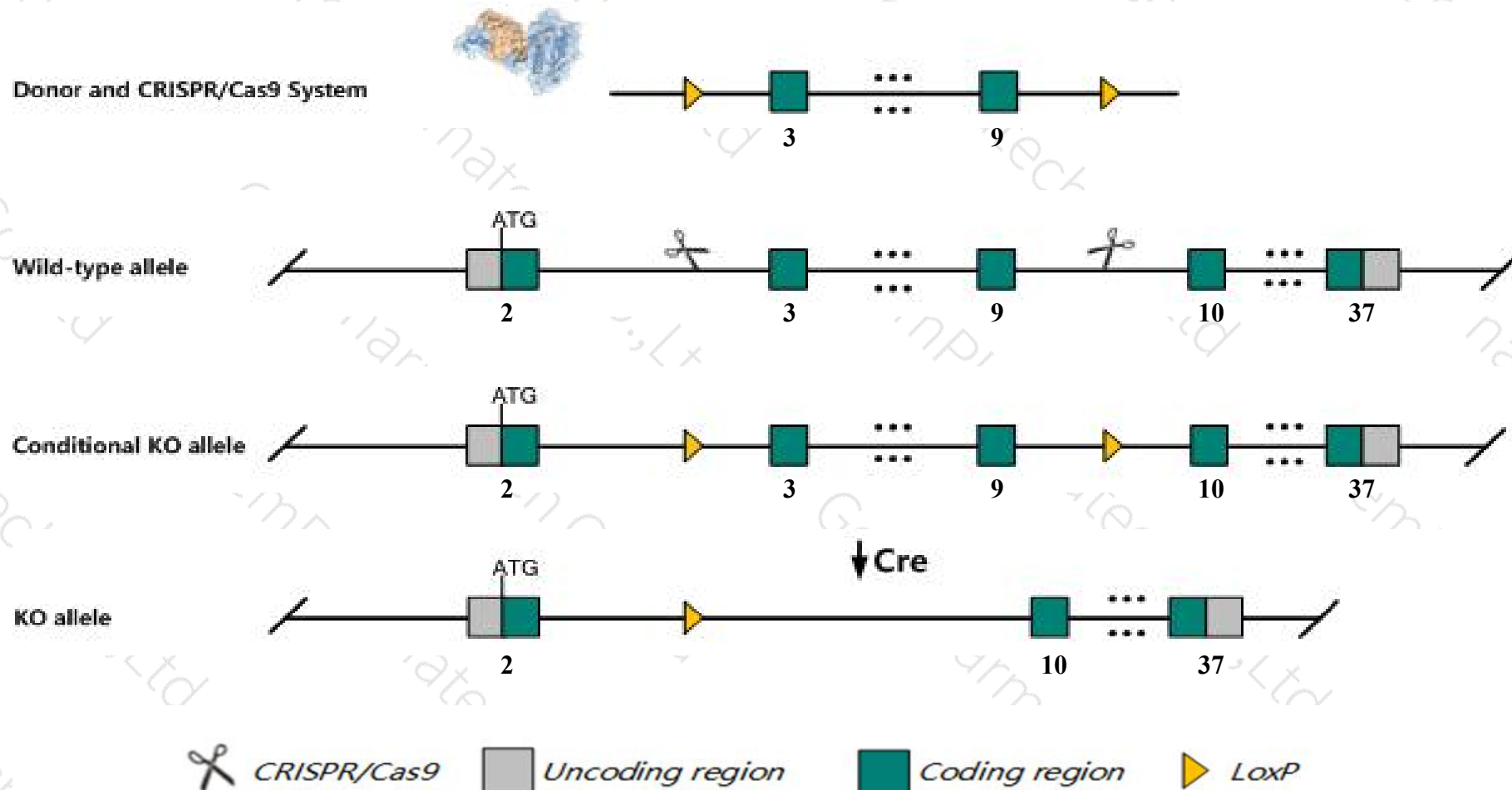
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sptbn2* gene. The schematic diagram is as follows:



Technical routes

- The *Sptbn2* gene has 3 transcripts. According to the structure of *Sptbn2* gene, exon3-exon9 of *Sptbn2-201* (ENSMUST00000008991.7) transcript is recommended as the knockout region. The region contains 916bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sptbn2* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be 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.

- According to the existing MGI data, Homozygous hypomorphic mutants exhibit a progressive ataxic phenotype with gait abnormalities, tremor, deteriorating motor coordination, Purkinje cell loss, and cerebellar atrophy (molecular layer thinning) and age-related reduction in simple firing rate in surviving Purkinje cells.
- The *Sptbn2* gene is located on the Chr19. 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)

Sptbn2 spectrin beta, non-erythrocytic 2 [Mus musculus (house mouse)]

Gene ID: 20743, updated on 7-Apr-2019

Summary



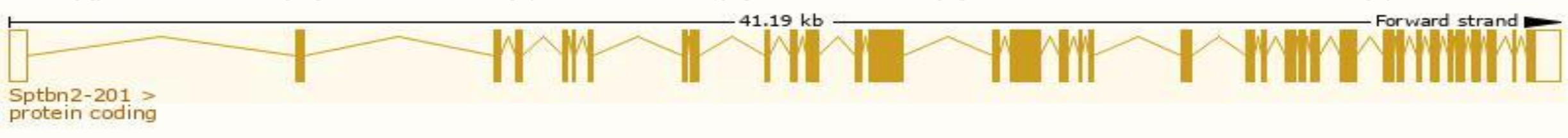
Official Symbol	Sptbn2 provided by MGI
Official Full Name	spectrin beta, non-erythrocytic 2 provided by MGI
Primary source	MGI:MGI:1313261
See related	Ensembl:ENSMUSG000000067889
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Spnb3
Expression	Biased expression in cortex adult (RPKM 49.2), frontal lobe adult (RPKM 46.9) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

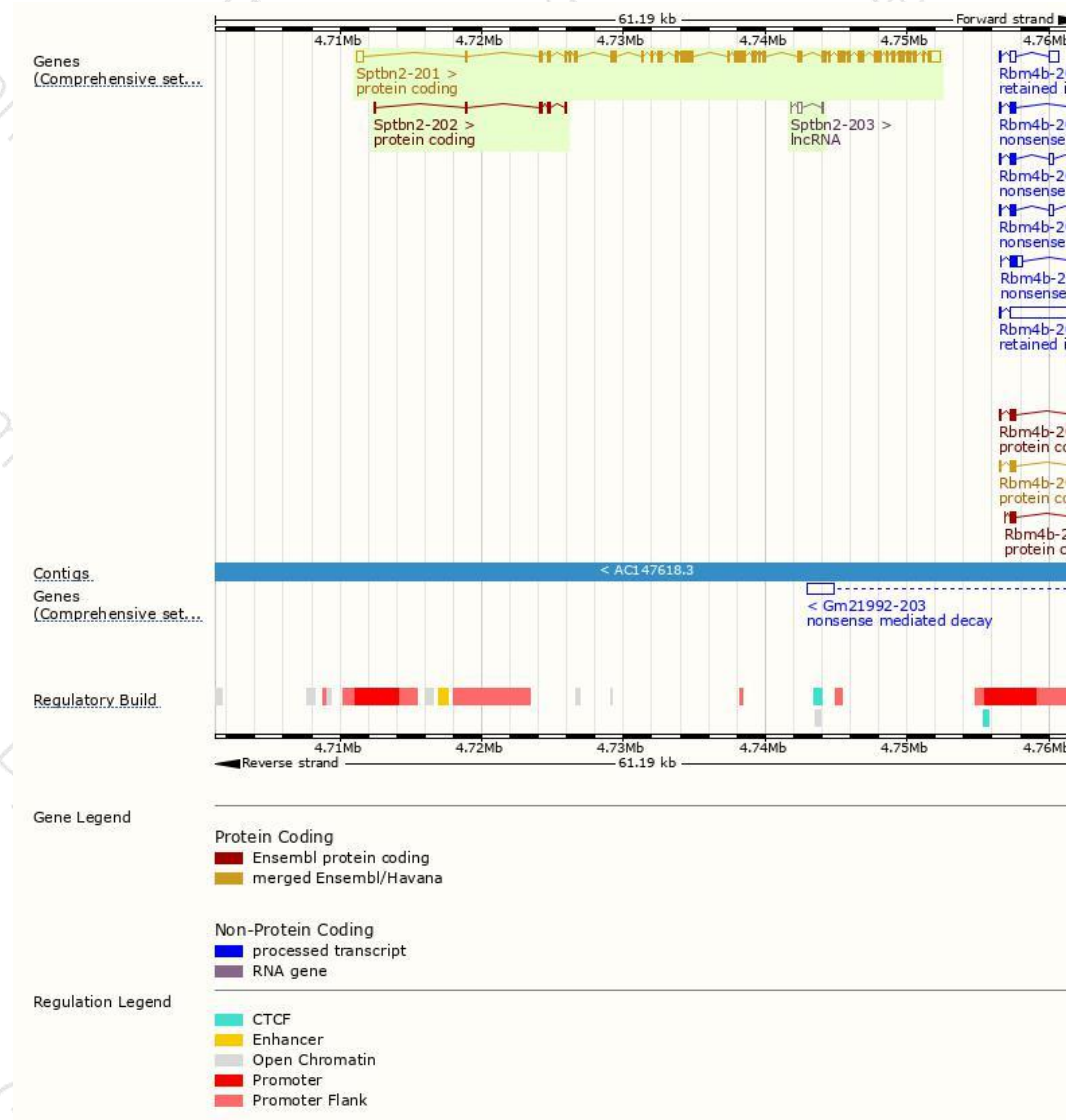
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sptbn2-201	ENSMUST00000008991.7	8299	2388aa	Protein coding	CCDS29434	Q68FG2	TSL:1 GENCODE basic APPRIS P1
Sptbn2-202	ENSMUST00000237694.1	626	175aa	Protein coding	-	-	CDS 3' incomplete
Sptbn2-203	ENSMUST00000238162.1	360	No protein	lncRNA	-	-	

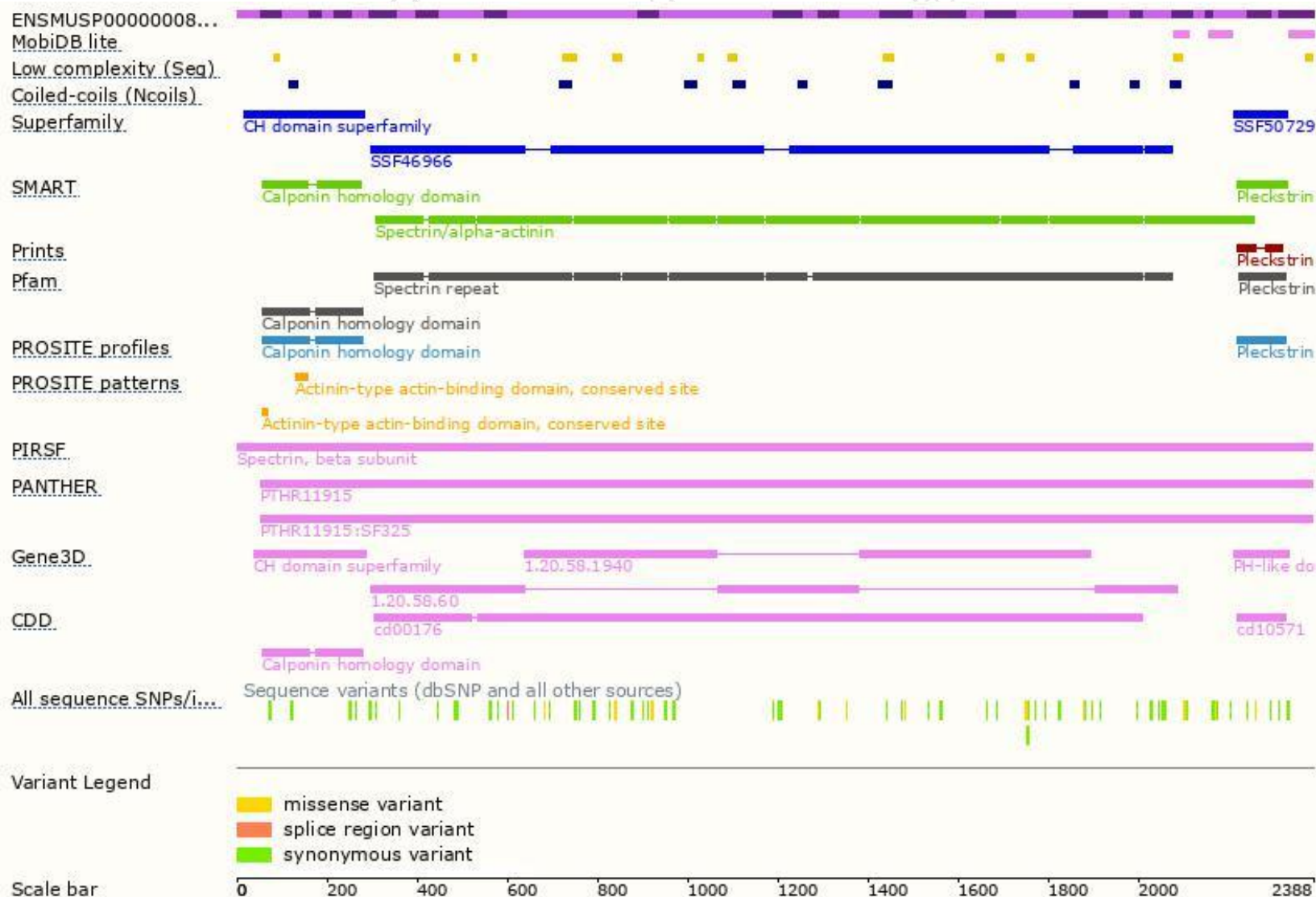
The strategy is based on the design of *Sptbn2-201* transcript,The transcription is shown below



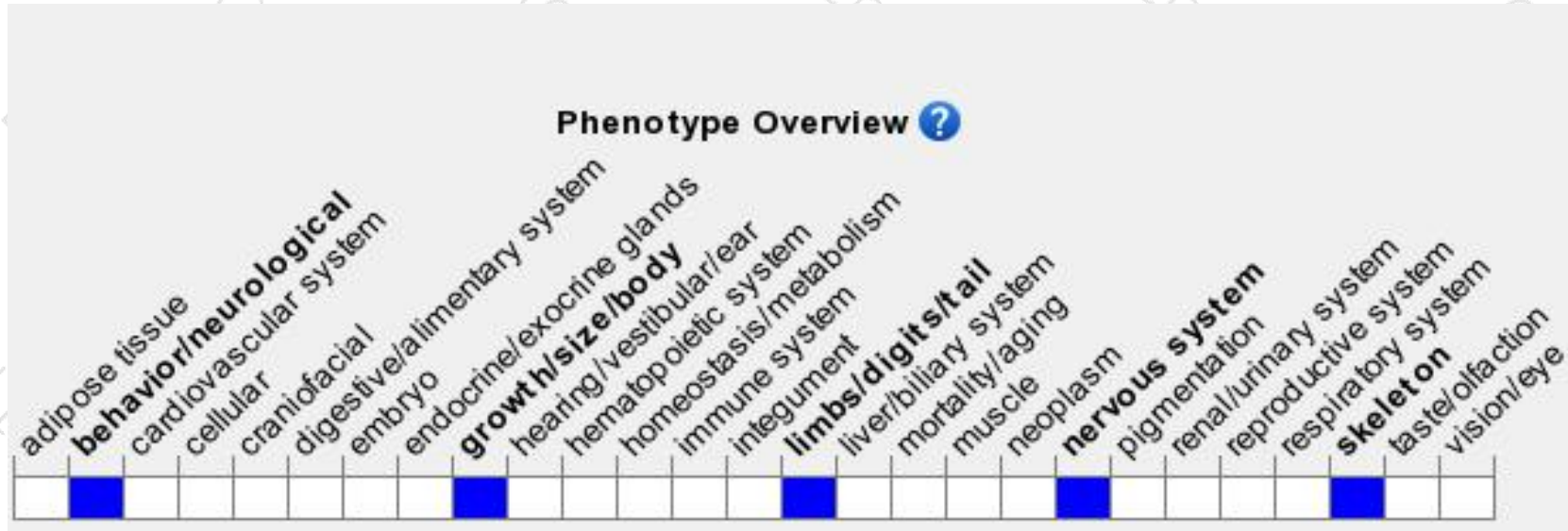
Genomic location distribution



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, Homozygous hypomorphic mutants exhibit a progressive ataxic phenotype with gait abnormalities, tremor, deteriorating motor coordination, Purkinje cell loss, and cerebellar atrophy (molecular layer thinning) and age-related reduction in simple firing rate in surviving Purkinje cells.

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

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