

Sp9 Cas9-KO Strategy

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Project Overview

Project Name

Sp9

Project type

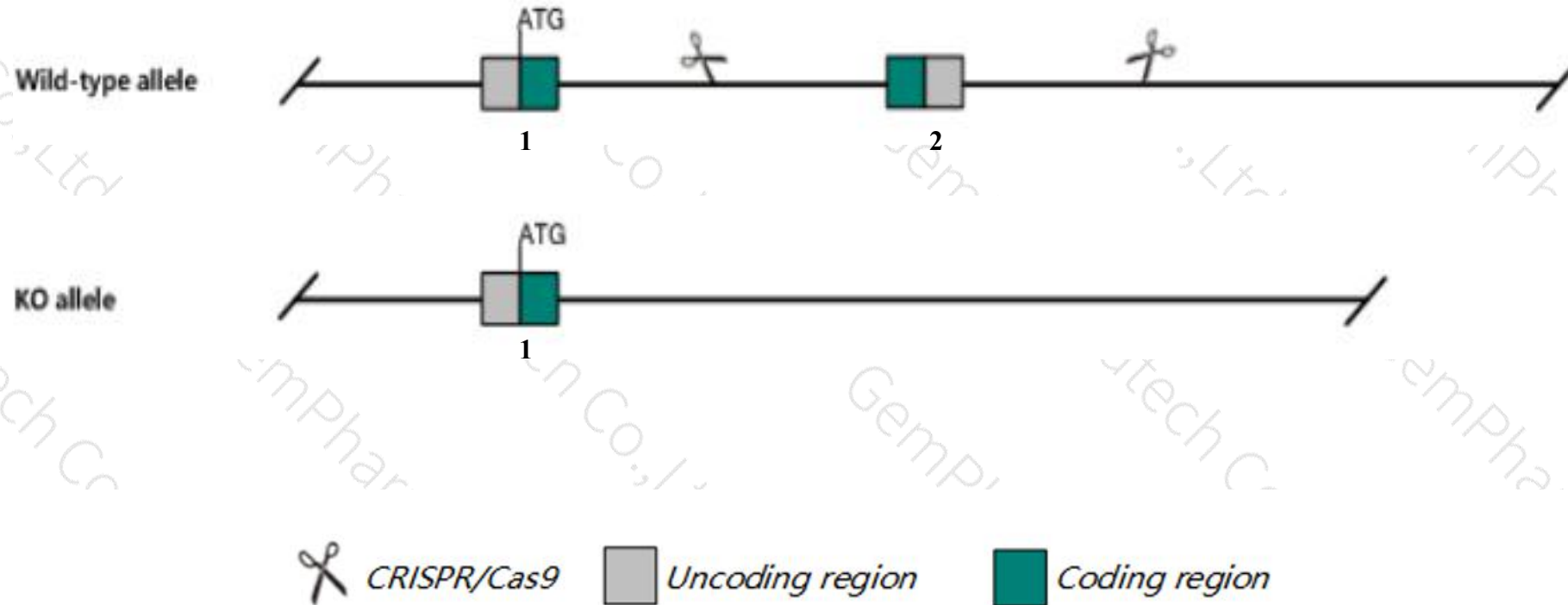
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sp9* gene. The schematic diagram is as follows:



- The *Sp9* gene has 2 transcripts. According to the structure of *Sp9* gene, exon2 of *Sp9-201* (ENSMUST00000090813.5) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sp9* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, mice homozygous for a knock-out allele fail to thrive and exhibit general weakness and postnatal lethality associated with striatum atrophy and loss of striatopallidal medium-sized spiny neurons (msns) due to decreased proliferation of striatopallidal msn progenitors and increased apoptosis.
- The *Sp9* 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)

Sp9 trans-acting transcription factor 9 [Mus musculus (house mouse)]

Gene ID: 381373, updated on 13-Mar-2020

Summary



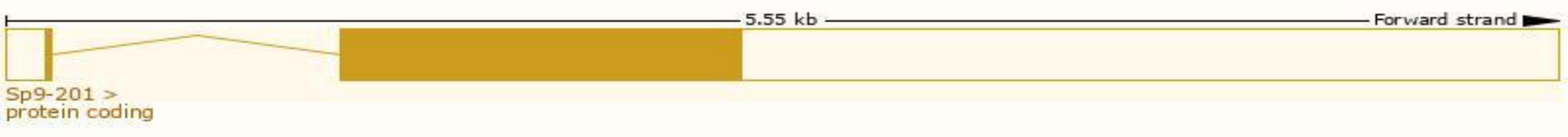
Official Symbol	Sp9 provided by MGI
Official Full Name	trans-acting transcription factor 9 provided by MGI
Primary source	MGI:MGI:3574660
See related	Ensembl:ENSMUSG00000068859
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in whole brain E14.5 (RPKM 7.9), frontal lobe adult (RPKM 7.8) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

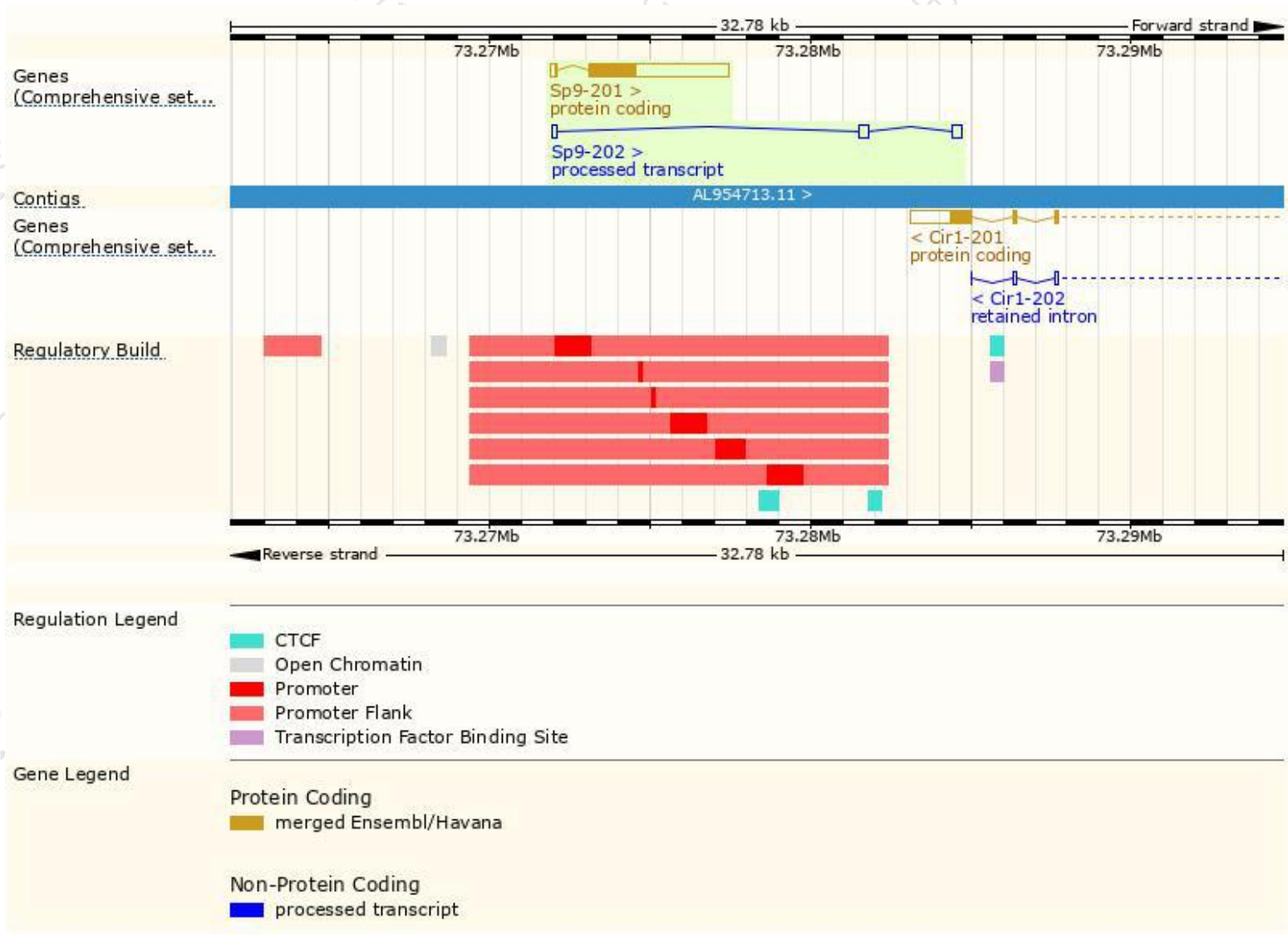
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sp9-201	ENSMUST00000090813.5	4514	484aa	Protein coding	CCDS16126	Q64HY3	TSL:1 GENCODE basic APPRIS P1
Sp9-202	ENSMUST00000147133.1	656	No protein	Processed transcript	-	-	TSL:2

The strategy is based on the design of *Sp9-201* transcript,the transcription is shown below:



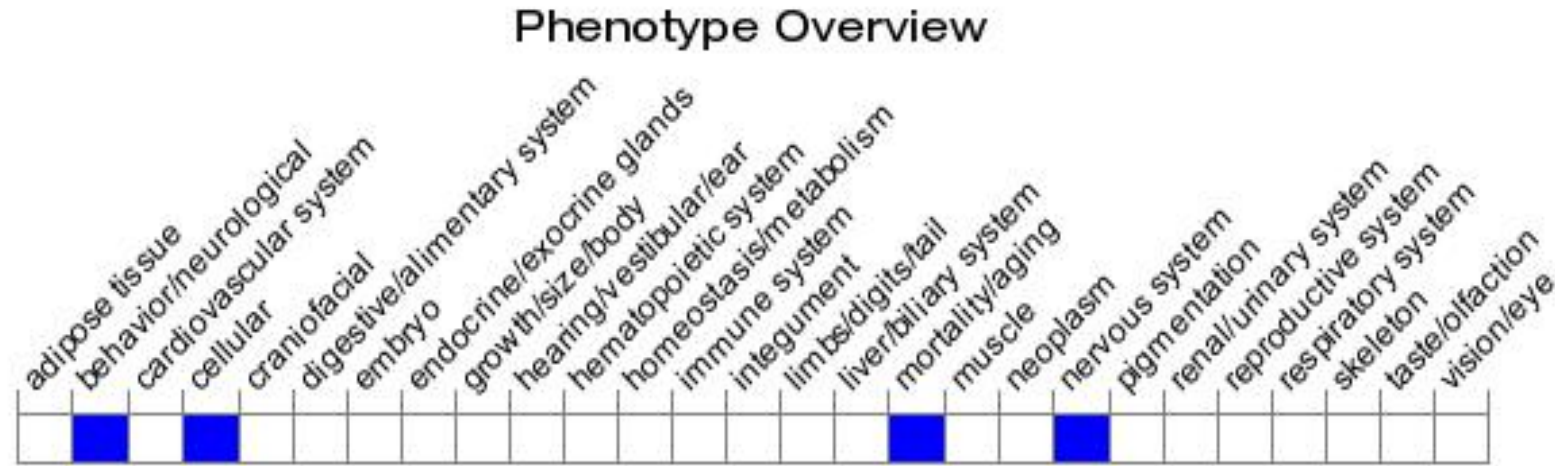
Genomic location distribution



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 a knock-out allele fail to thrive and exhibit general weakness and postnatal lethality associated with striatum atrophy and loss of striatopallidal medium-sized spiny neurons (MSNs) due to decreased proliferation of striatopallidal MSN progenitors and increased apoptosis.

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

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