

Shprh Cas9-KO Strategy

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Design Date: 2020-4-26

Project Overview

Project Name

Shprh

Project type

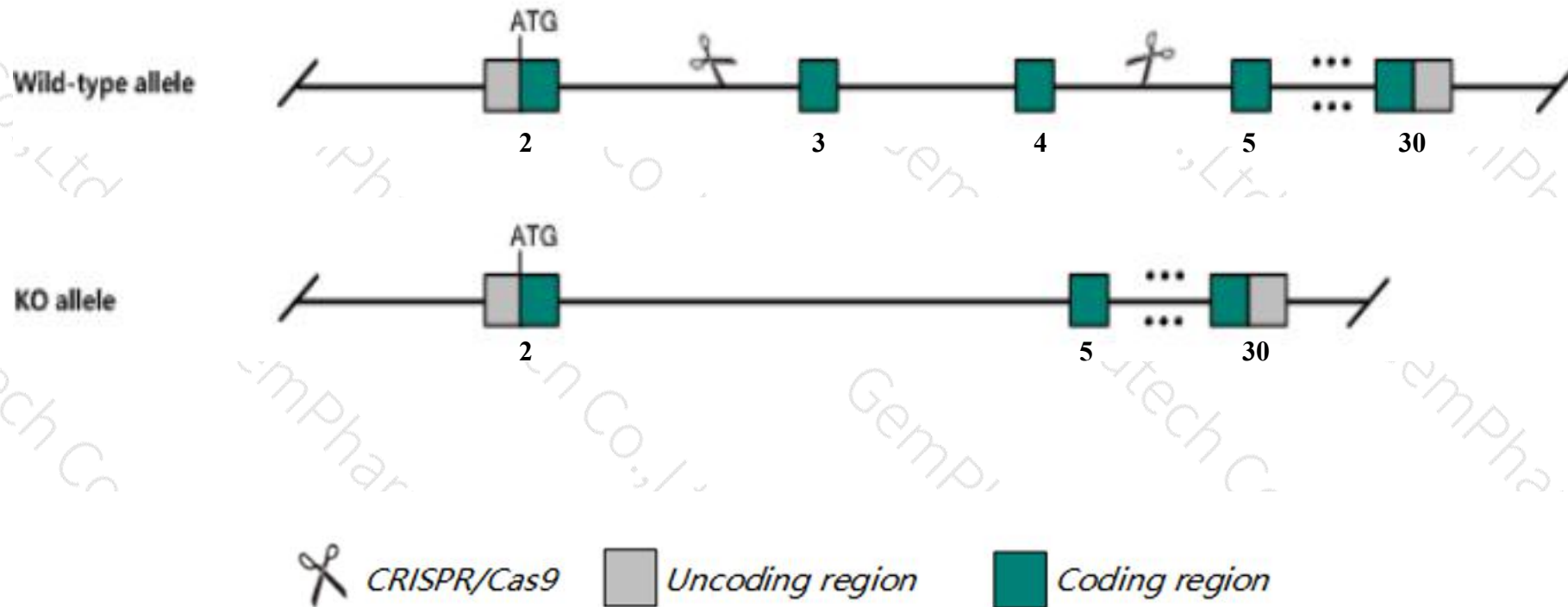
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Shprh* gene has 8 transcripts. According to the structure of *Shprh* gene, exon3-exon4 of *Shprh-201* (ENSMUST00000044053.12) transcript is recommended as the knockout region. The region contains 349bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Shprh* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, the gene product is an e3 ligase involved in poly-ubiquitination of
- The *Shprh* gene is located on the Chr10. 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)

Shprh SNF2 histone linker PHD RING helicase [Mus musculus (house mouse)]

Gene ID: 268281, updated on 13-Mar-2020

Summary



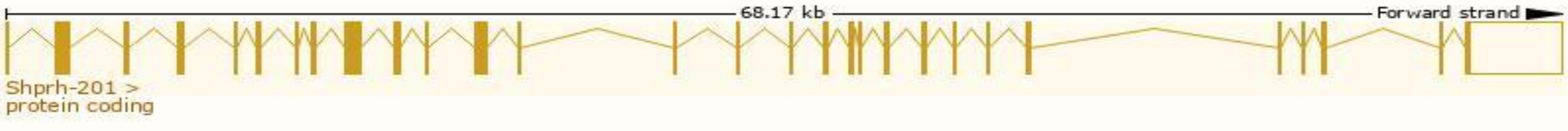
Official Symbol	Shprh provided by MGI
Official Full Name	SNF2 histone linker PHD RING helicase provided by MGI
Primary source	MGI:MGI:1917581
See related	Ensembl:ENSMUSG00000090112
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610103K11Rik, AA450458, AU024614, BC006883, D230017O13Rik, E130018M05
Expression	Broad expression in cerebellum adult (RPKM 3.8), CNS E18 (RPKM 3.8) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

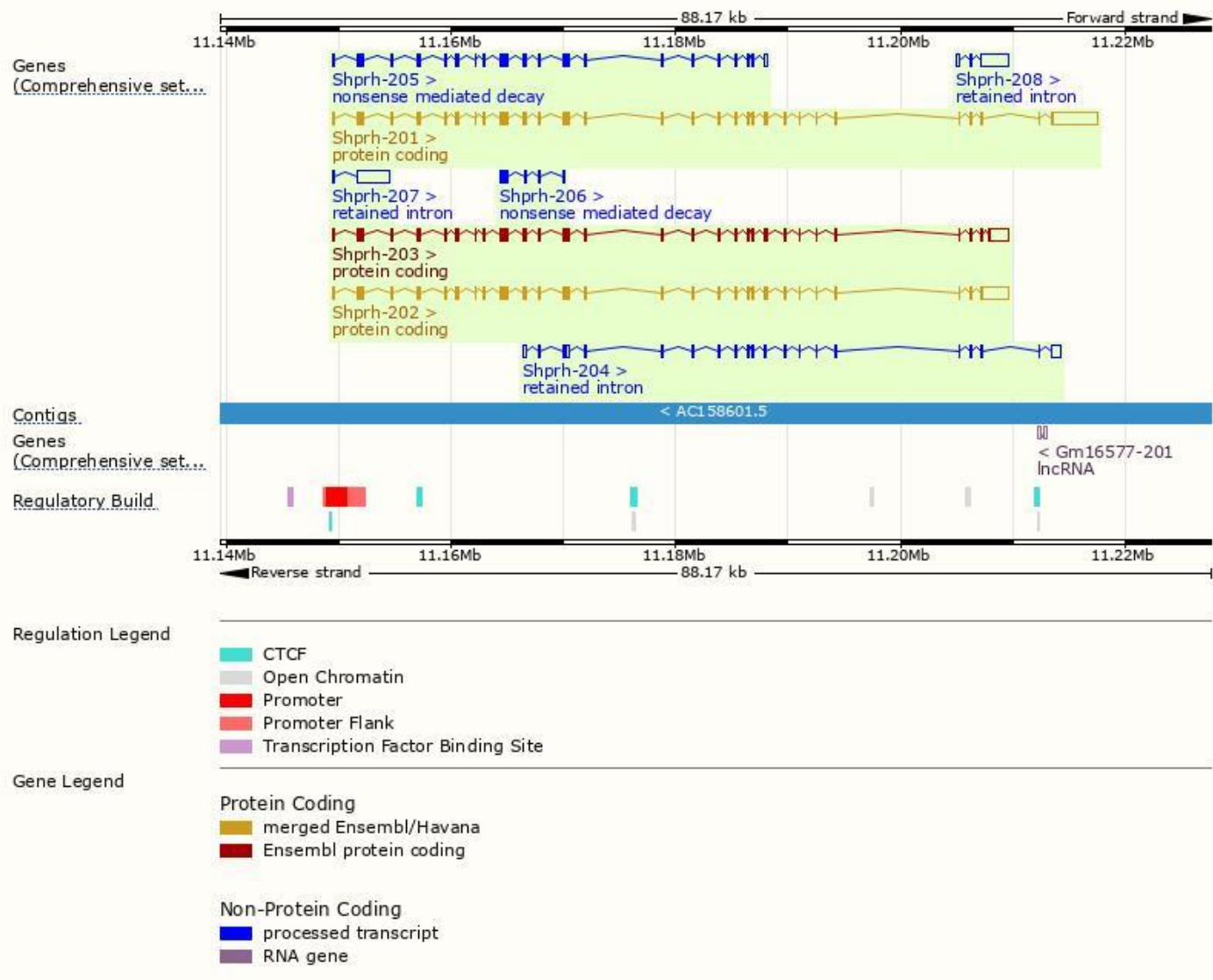
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Shprh-201	ENSMUST00000044053.12	9271	1674aa	Protein coding	CCDS35838	Q7TPQ3	TSL:1 GENCODE basic APPRIS P4
Shprh-202	ENSMUST00000054814.13	7225	1616aa	Protein coding	CCDS35839	Q7TPQ3	TSL:1 GENCODE basic APPRIS ALT2
Shprh-203	ENSMUST00000159541.7	6679	1646aa	Protein coding	CCDS70003	Q7TPQ3	TSL:1 GENCODE basic APPRIS ALT2
Shprh-205	ENSMUST00000159810.7	4171	1031aa	Nonsense mediated decay	-	Q7TPQ3	TSL:1
Shprh-206	ENSMUST00000160461.7	945	218aa	Nonsense mediated decay	-	F7D4T4	CDS 5' incomplete TSL:3
Shprh-204	ENSMUST00000159553.7	3467	No protein	Retained intron	-	-	TSL:1
Shprh-207	ENSMUST00000161858.1	3028	No protein	Retained intron	-	-	TSL:1
Shprh-208	ENSMUST00000161910.1	2857	No protein	Retained intron	-	-	TSL:1

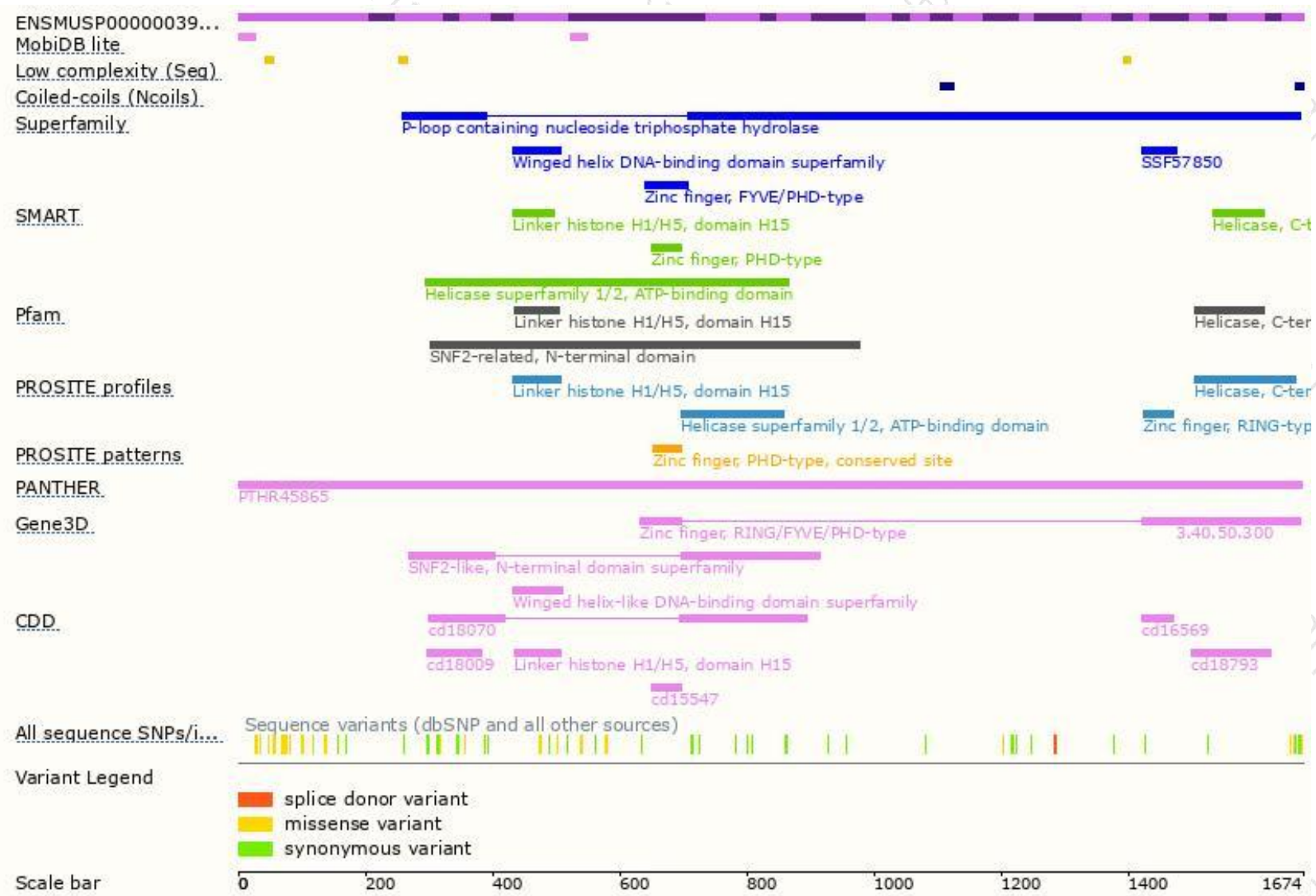
The strategy is based on the design of *Shprh-201* transcript,the transcription is shown below:



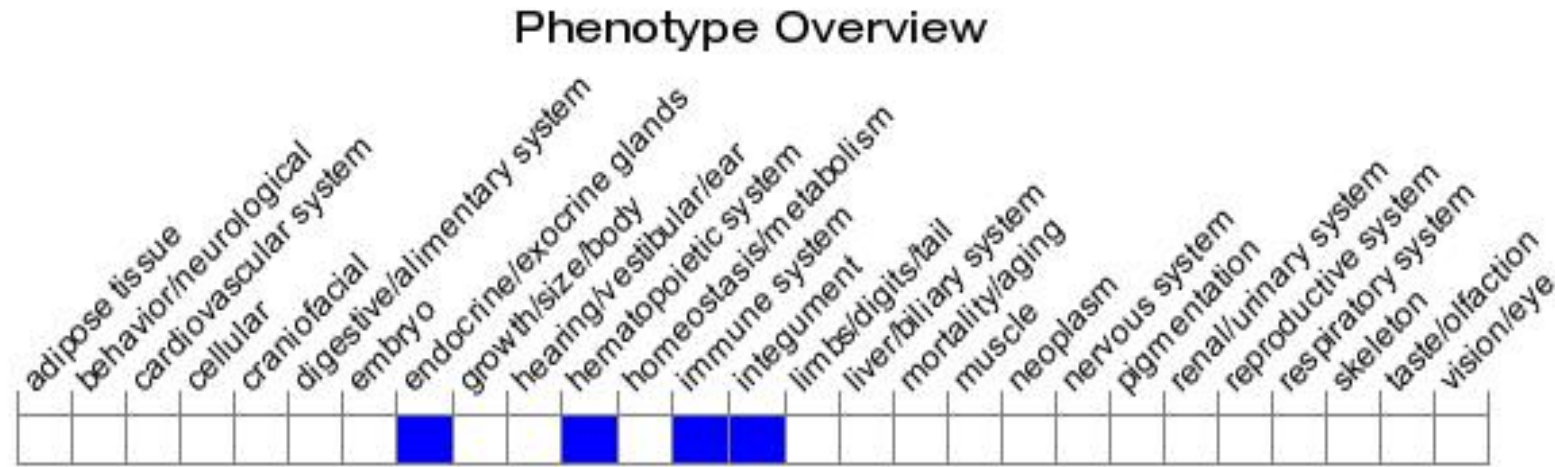
Genomic location distribution



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, the gene product is an E3 ligase involved in poly-ubiquitination of

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

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