Shc2 Cas9-KO Strategy

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Reviewer: Huimin Su

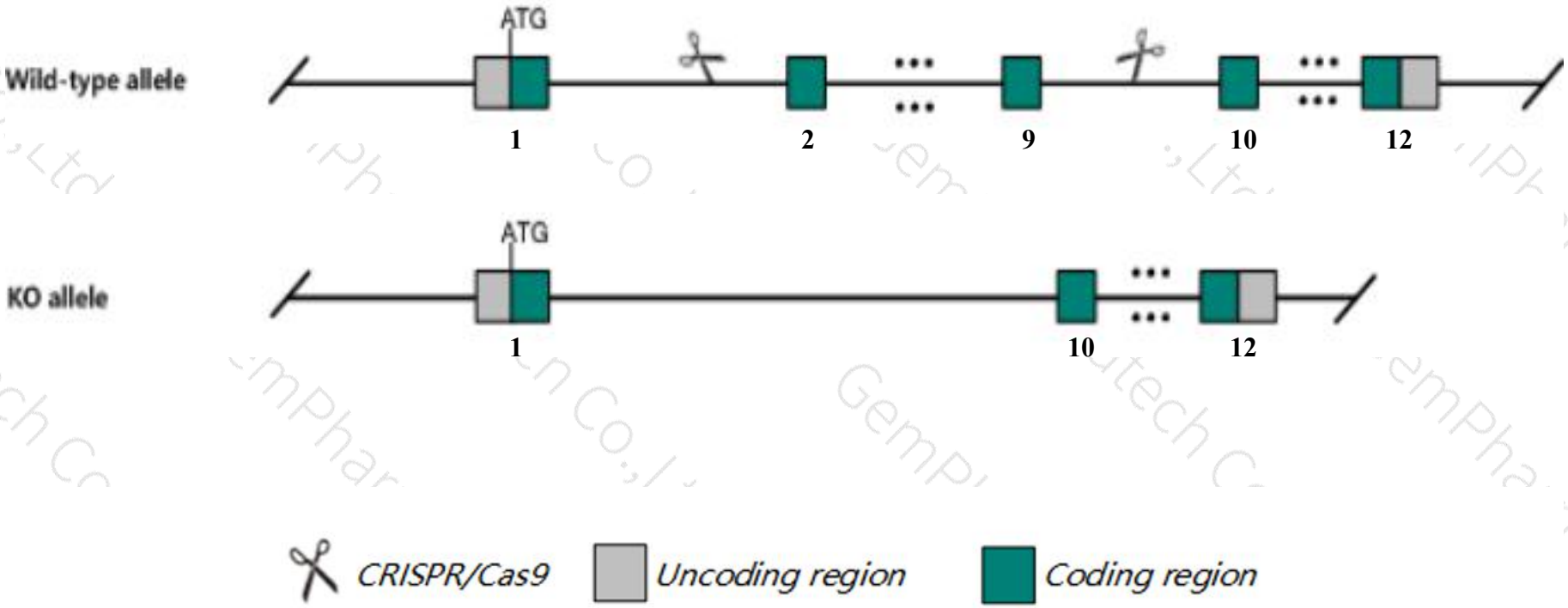
Design Date: 2020-4-20

Project Overview

Project Name	***Shc2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Shc2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Shc2* gene has 3 transcripts. According to the structure of *Shc2* gene, exon2-exon9 of *Shc2-201* (ENSMUST00000020564.6) transcript is recommended as the knockout region.The region contains 715bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Shc2* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,mice homozygous for disruptions in this gene display sensory nerve defects related to nociception.
- The *Shc2* 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）

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Shc2 SHC (Src homology 2 domain containing) transforming protein 2 [Mus musculus (house mouse)]

Gene ID: 216148, updated on 13-Mar-2020

Summary

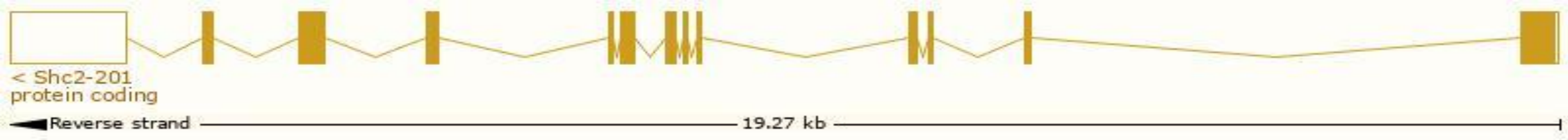
Official Symbol	Shc2 provided by MGI
Official Full Name	SHC (Src homology 2 domain containing) transforming protein 2 provided by MGI
Primary source	MGI:MGI:106180
See related	Ensembl:ENSMUSG00000020312
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6720466E06, SCK, ShcB, Sli
Expression	Broad expression in CNS E18 (RPKM 14.0), whole brain E14.5 (RPKM 11.3) and 19 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

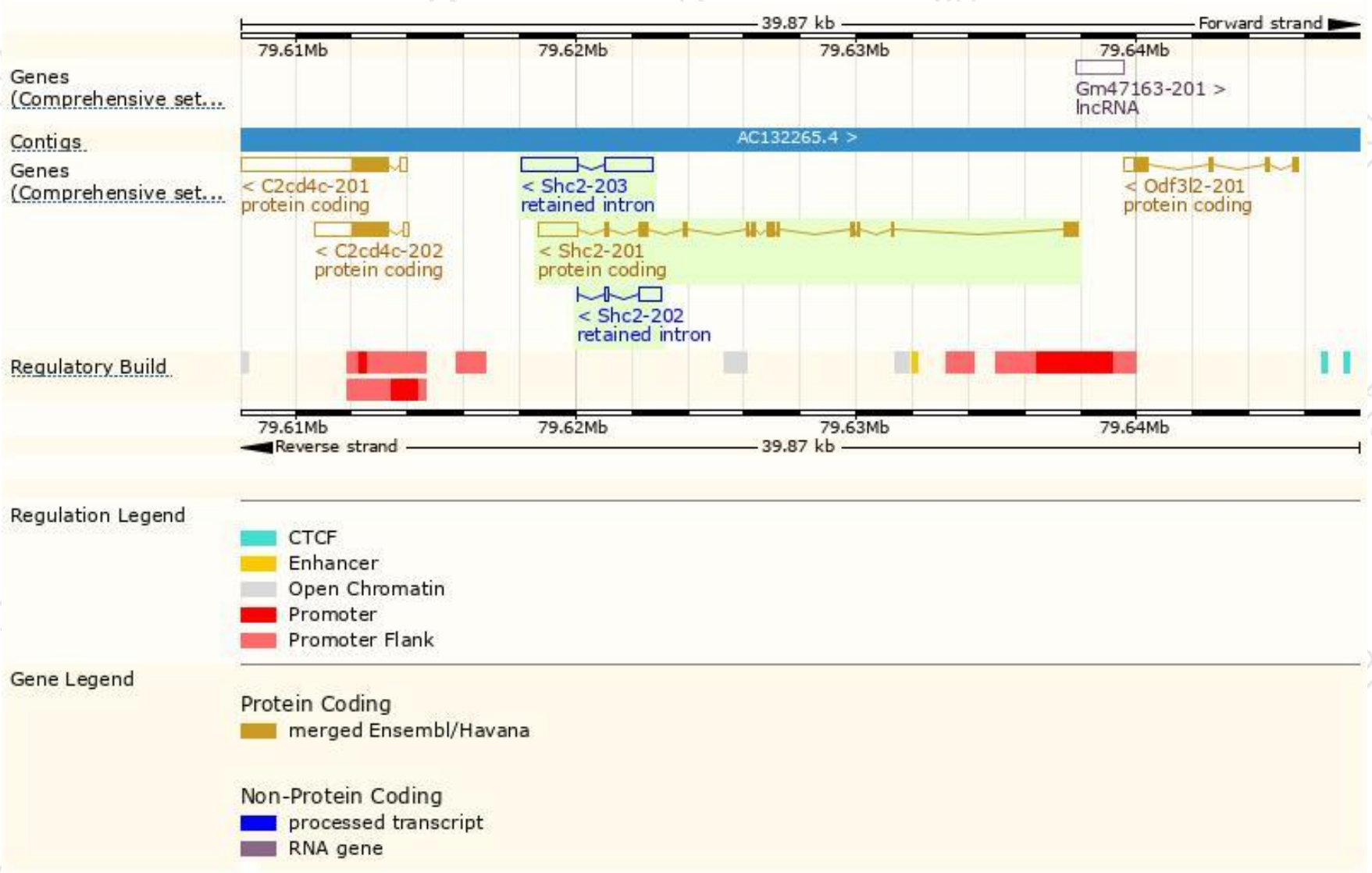
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Shc2-201	ENSMUST00000020564.6	3243	573aa	Protein coding	CCDS48620	E9QLZ0 Q8BMC3	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Shc2-203	ENSMUST00000168116.1	3720	No protein	Retained intron	-	-	TSL:1
Shc2-202	ENSMUST00000166450.1	969	No protein	Retained intron	-	-	TSL:3

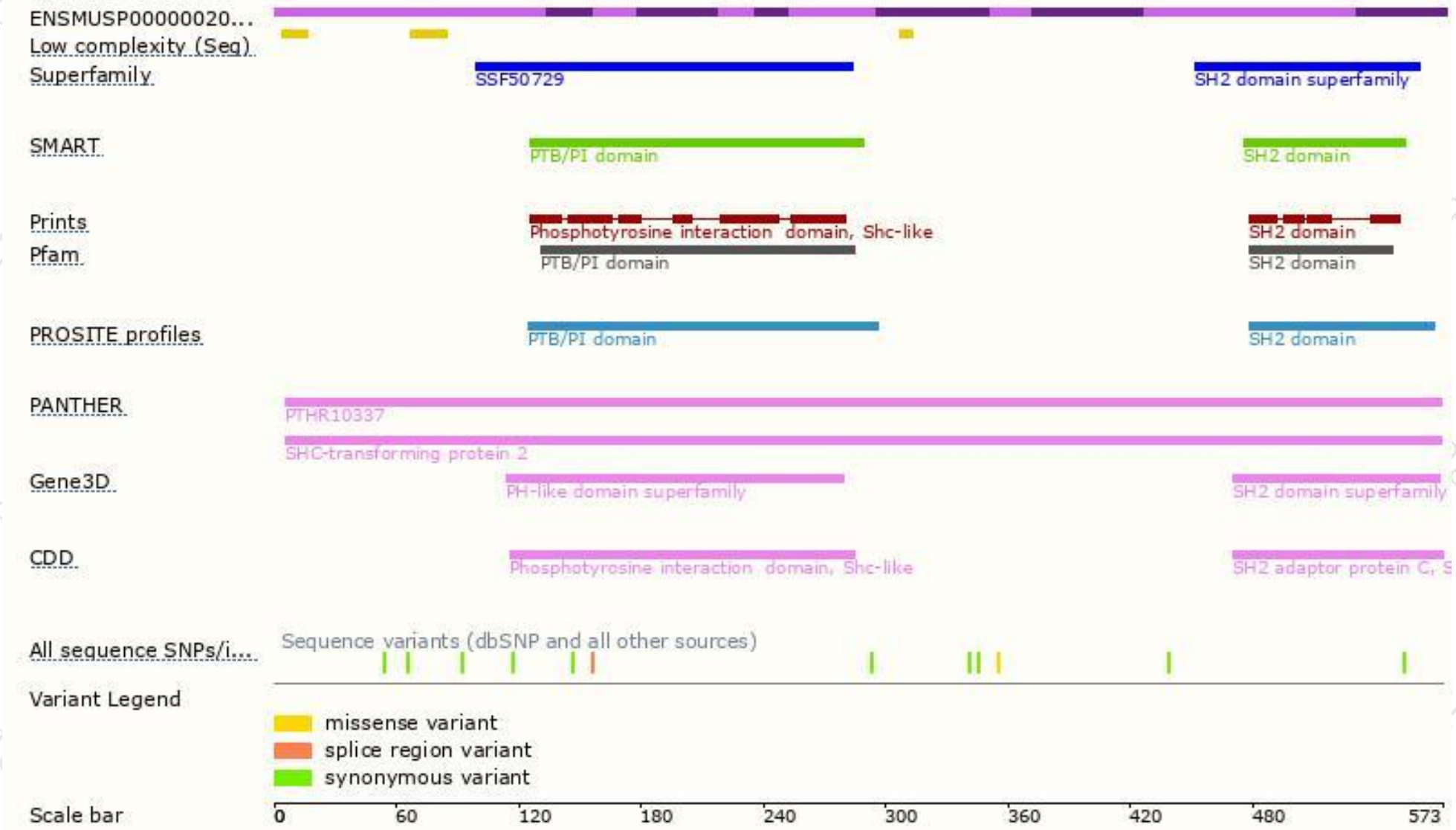
The strategy is based on the design of *Shc2-201* transcript,the transcription is shown below:



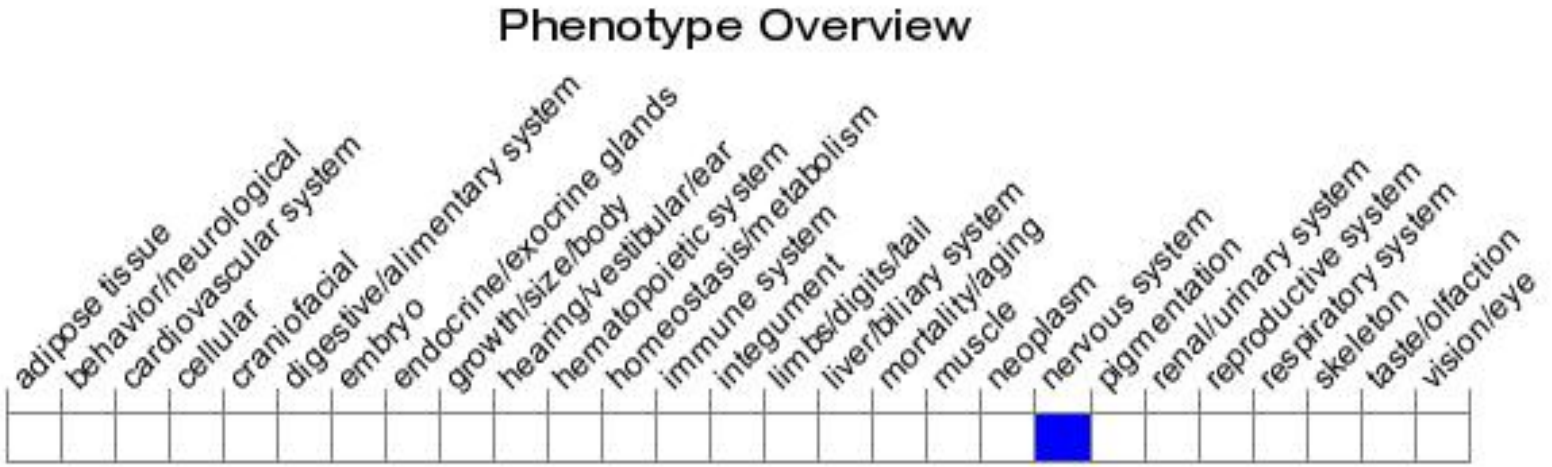
Genomic location distribution



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/).

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

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