Cnst Cas9-KO Strategy

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Project Overview

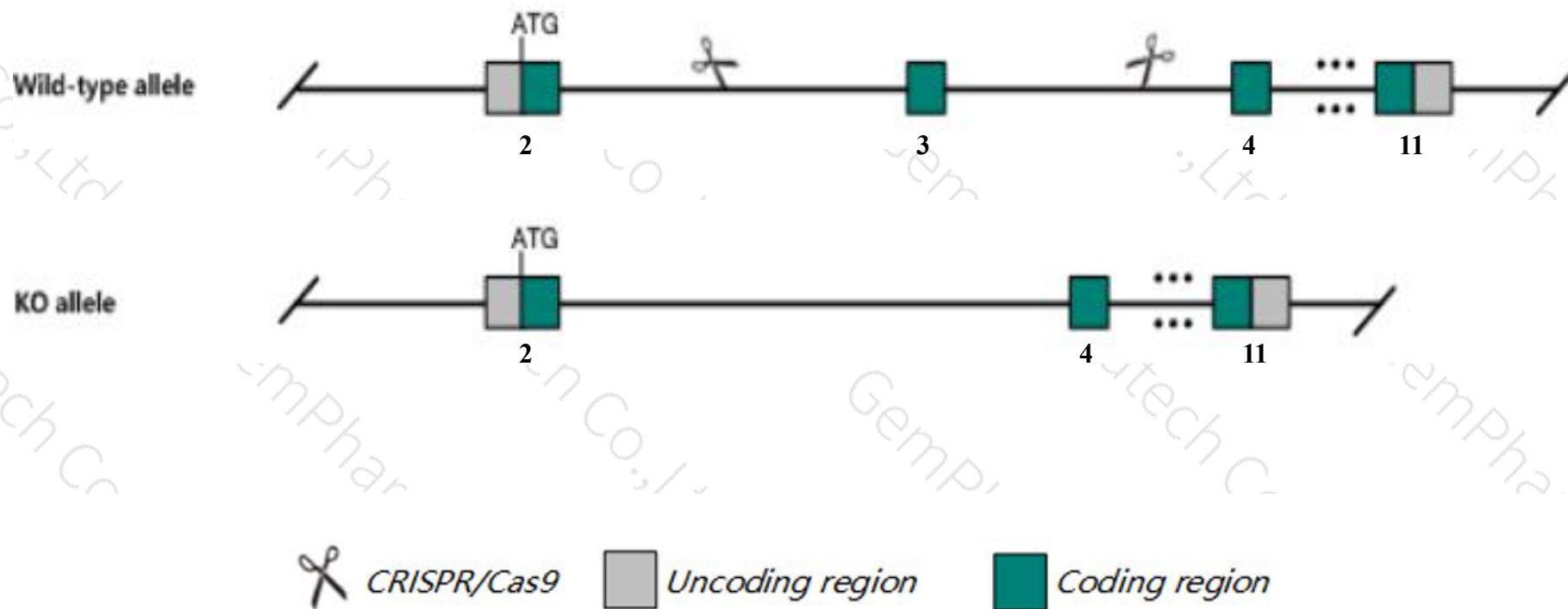|	
Project Name	*Cnst*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Cnst* gene has 4 transcripts. According to the structure of *Cnst* gene, exon3 of *Cnst-201* (ENSMUST00000040706.8) transcript is recommended as the knockout region.The region contains 182bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

➢ The *Cnst* gene is located on the Chr1. 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.

➢ Transcript *Cnst*-203 may not be affected.

➢ 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）

Cnst consortin, connexin sorting protein [Mus musculus (house mouse)]

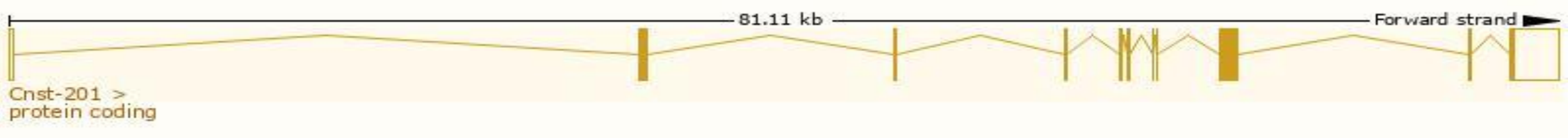Gene ID: 226744, updated on 13-Mar-2020

Summary

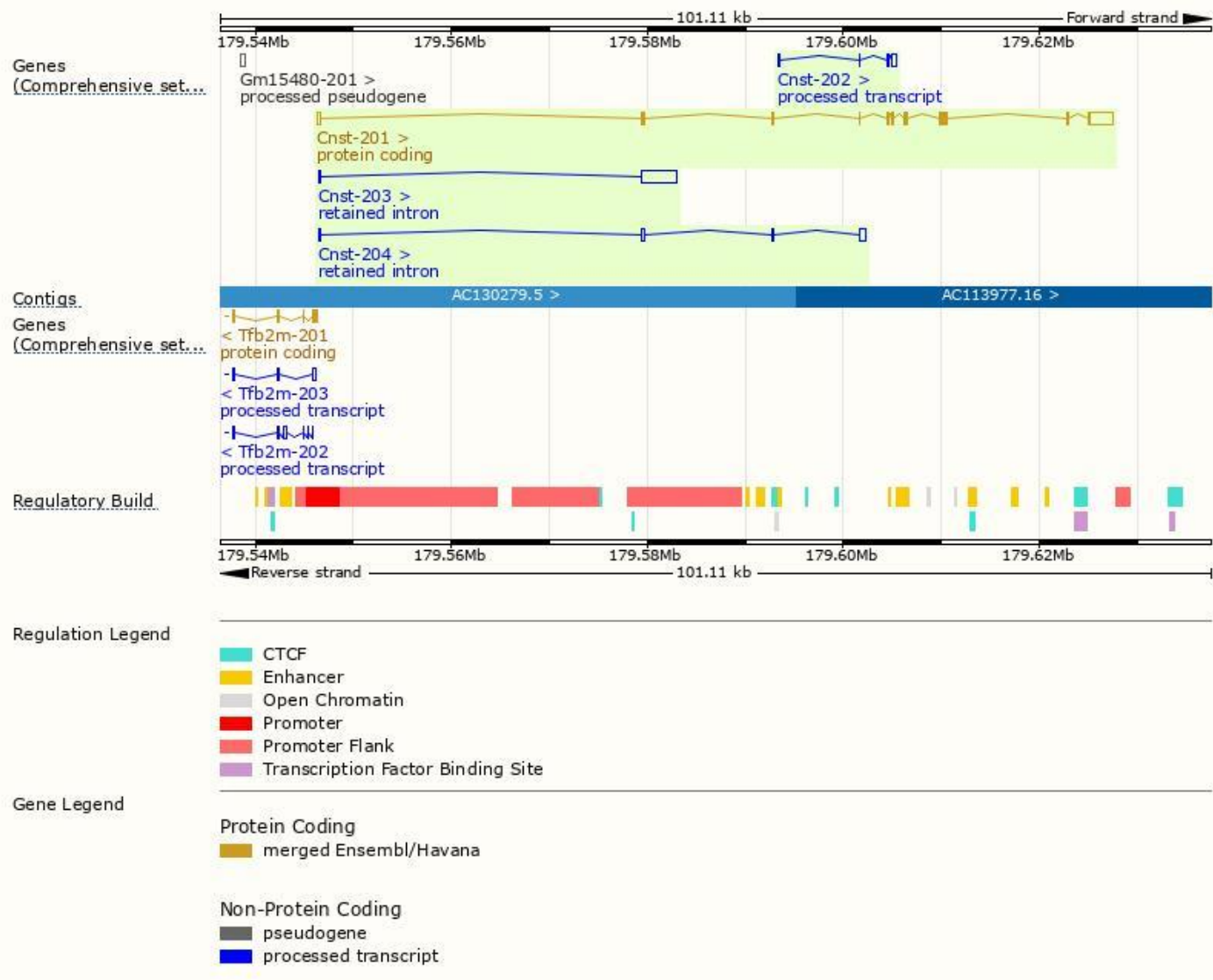|	
Official Symbol	Cnst provided by MGI
Official Full Name	consortin, connexin sorting protein provided by MGI
Primary source	MGI:MGI:2445141
See related	Ensembl:ENSMUSG00000038949
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9630058J23Rik
Expression	Ubiquitous expression in cerebellum adult (RPKM 11.4), heart adult (RPKM 11.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnst-201	ENSMUST00000040706.8	4709	711aa	Protein coding	CCDS15562	Q8CBC4	TSL:1 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
Cnst-202	ENSMUST00000143270.1	617	No protein	Processed transcript	-	-	TSL:3
Cnst-203	ENSMUST00000144370.1	3717	No protein	Retained intron	-	-	TSL:1
Cnst-204	ENSMUST00000153962.1	1350	No protein	Retained intron	-	-	TSL:1

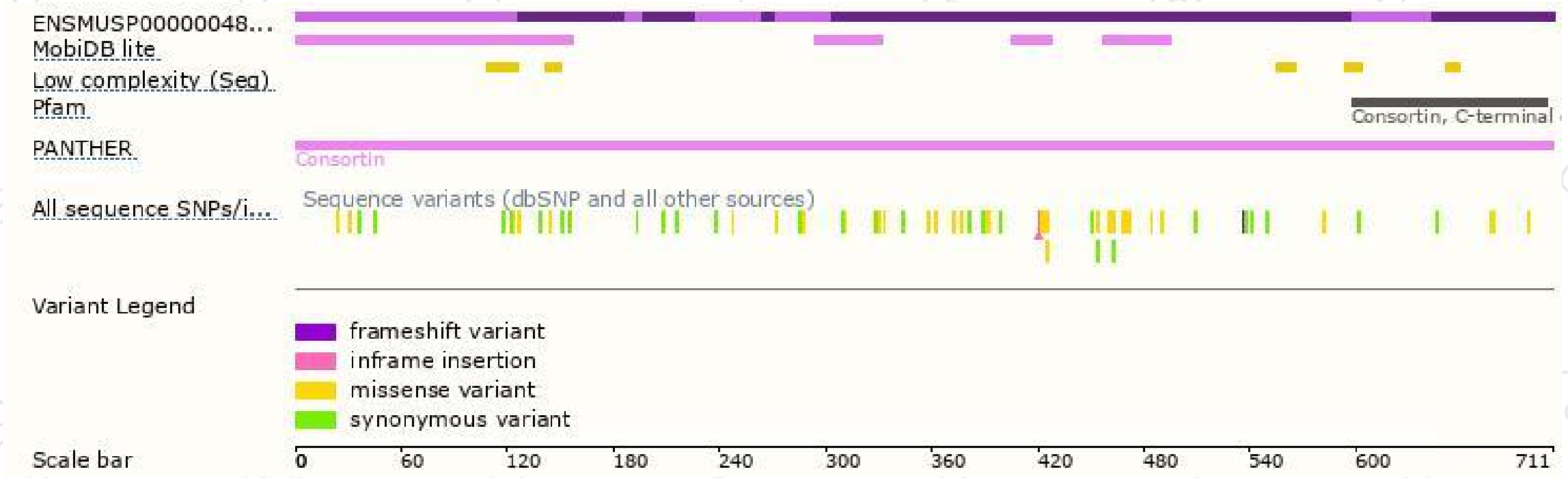The strategy is based on the design of *Cnst-201* transcript,the transcription is shown below:

Genomic location distribution

Protein domain

ENSMUSP00000048...	
MobiDB lite	
Low complexity (Seg)	
Pfam	Consortin, C-terminal
PANTHER	Consortin
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

- ■ frameshift variant
- ■ inframe insertion
- ■ missense variant
- ■ synonymous variant

Scale bar

0   60   120   180   240   300   360   420   480   540   600   711

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