Clstn1 Cas9-KO Strategy

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Design Date: **2020-2-21**

Project Overview

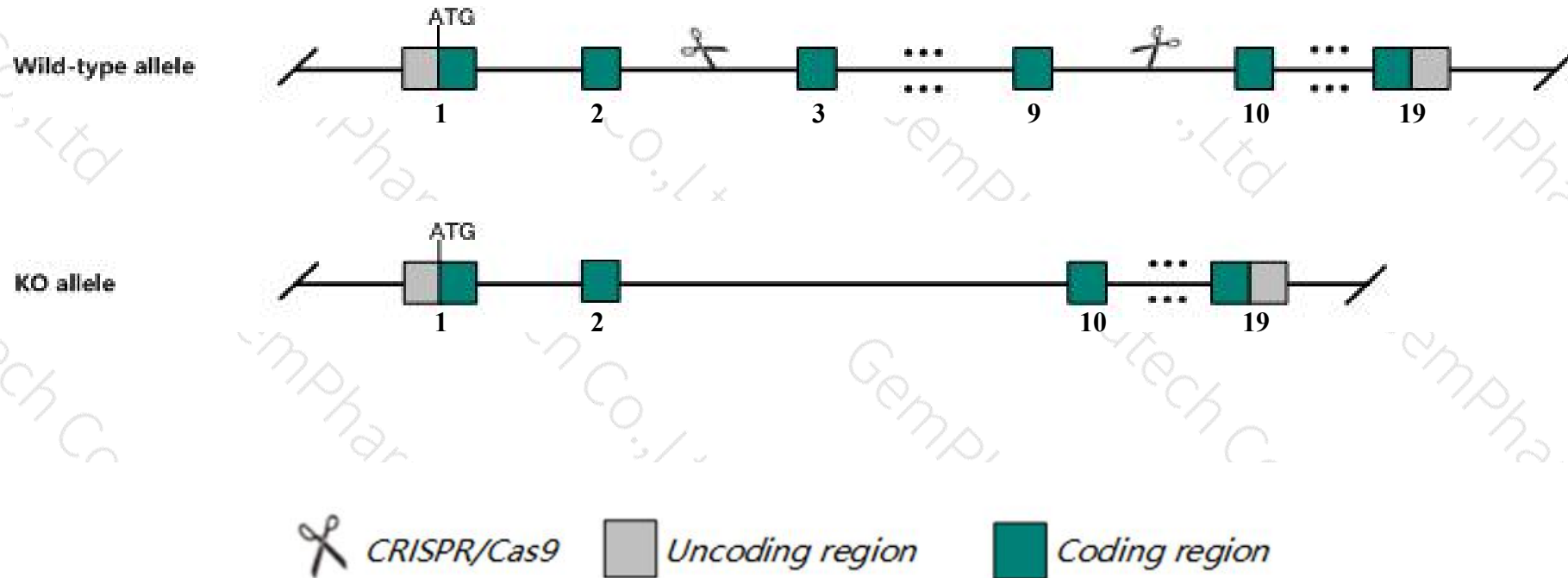|	
Project Name	*Clstn1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clstn1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Clstn1* gene has 4 transcripts. According to the structure of *Clstn1* gene, exon3-exon9 of *Clstn1-201* (ENSMUST00000039144.6) transcript is recommended as the knockout region.The region contains 1275bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Clstn1* gene. The brief process is as follows: CRISPR/Cas9 system w

➢ According to the existing MGI data,Juvenile mice homozygous for a null allele show reduced basal excitatory synaptic transmission, abnormal excitatory postsynaptic currents, enhanced NMDA receptor-dependent long term potentiation, and delayed dendritic spine maturation in CA1 hippocampal pyramidal cells.

➢ The *Clstn1* gene is located on the Chr4. 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）

Clstn1 calsyntenin 1 [*Mus musculus* (house mouse)]

Gene ID: 65945, updated on 5-Jan-2020

▲ Summary

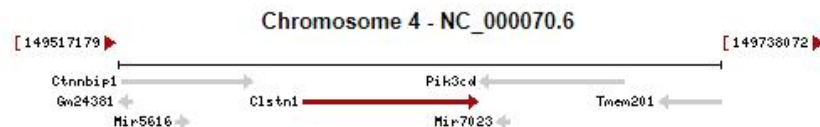|	
Official Symbol	Clstn1 provided by MGI
Official Full Name	calsyntenin 1 provided by MGI
Primary source	MGI:MGI:1929895
See related	Ensembl:ENSMUSG00000039953
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cst-1; Cstn1; 1810034E21Rik
Expression	Broad expression in cortex adult (RPKM 93.0), frontal lobe adult (RPKM 80.3) and 23 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 4; 4 E2

See Clstn1 in Genome Data Viewer

Exon count: 21

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (149585111..149648899)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (148960747..149022008)

Chromosome 4 - NC_000070.6

[149517179 ►

[149738072 ►

Ctnnbip1   Pik3cd
Gm24381   Clstn1   Tmem201
Mir5616   Mir7023

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Clstn1-202	ENSMUST00000105691.7	4459	969aa	Protein coding	CCDS71522	Q9EPL2	TSL:1	GENCODE basic	APPRIS ALT2
Clstn1-201	ENSMUST00000039144.6	3319	979aa	Protein coding	CCDS18963	Q9EPL2	TSL:1	GENCODE basic	APPRIS P3
Clstn1-203	ENSMUST00000137232.1	358	No protein	Processed transcript	-	-	TSL:3		
Clstn1-204	ENSMUST00000151895.1	822	No protein	Retained intron	-	-	TSL:2		

The strategy is based on the design of *Clstn1-201* transcript,The transcription is shown below
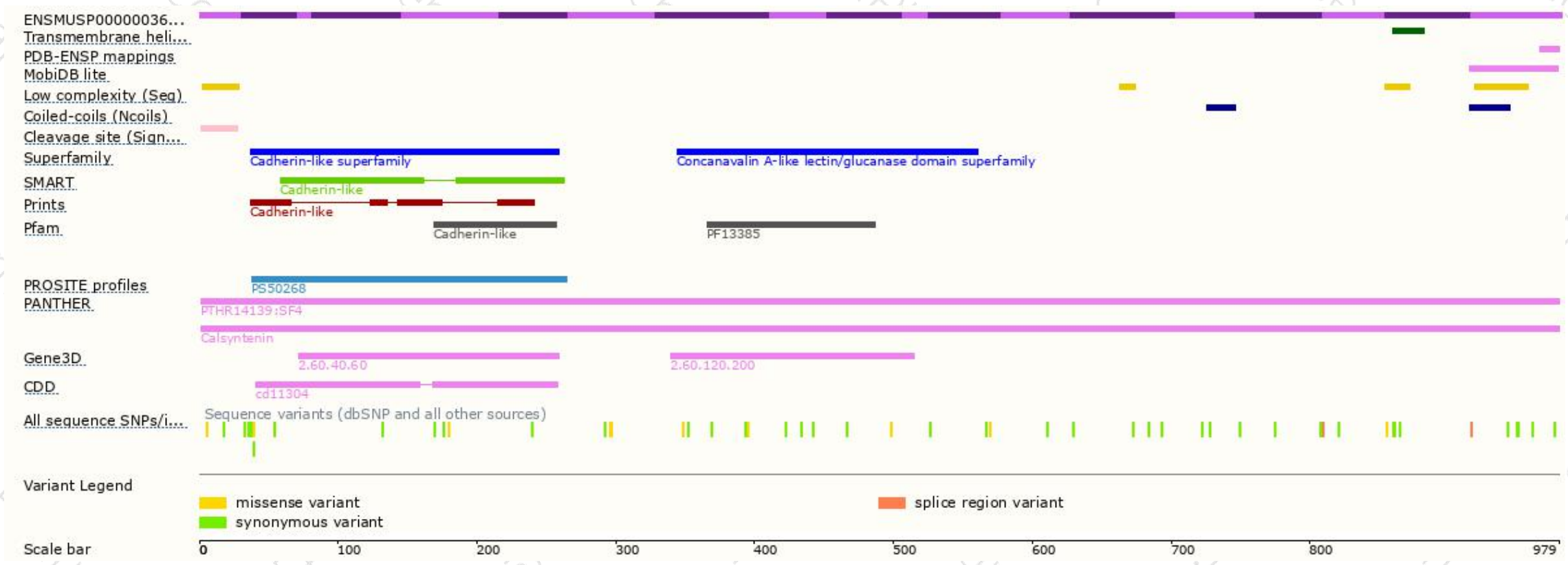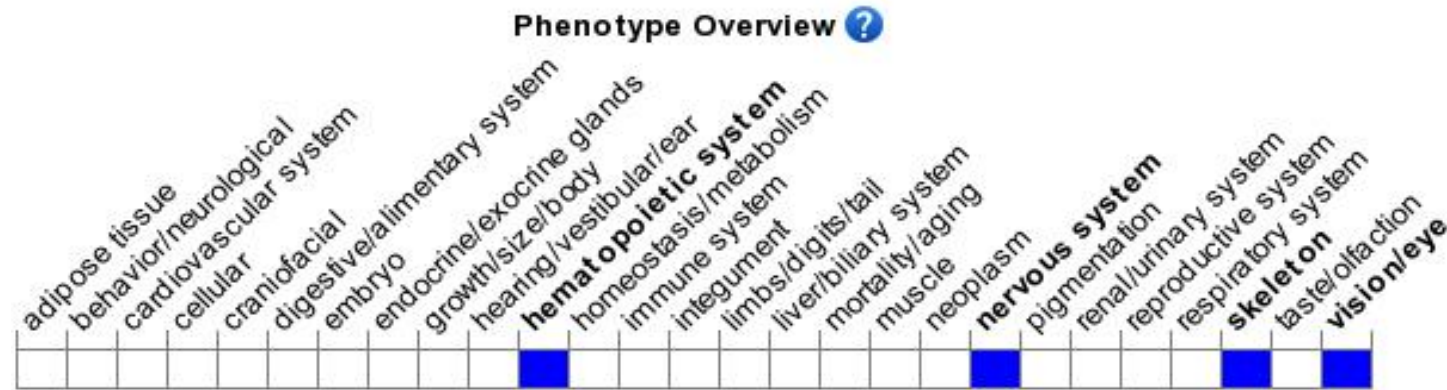
Genomic location distribution
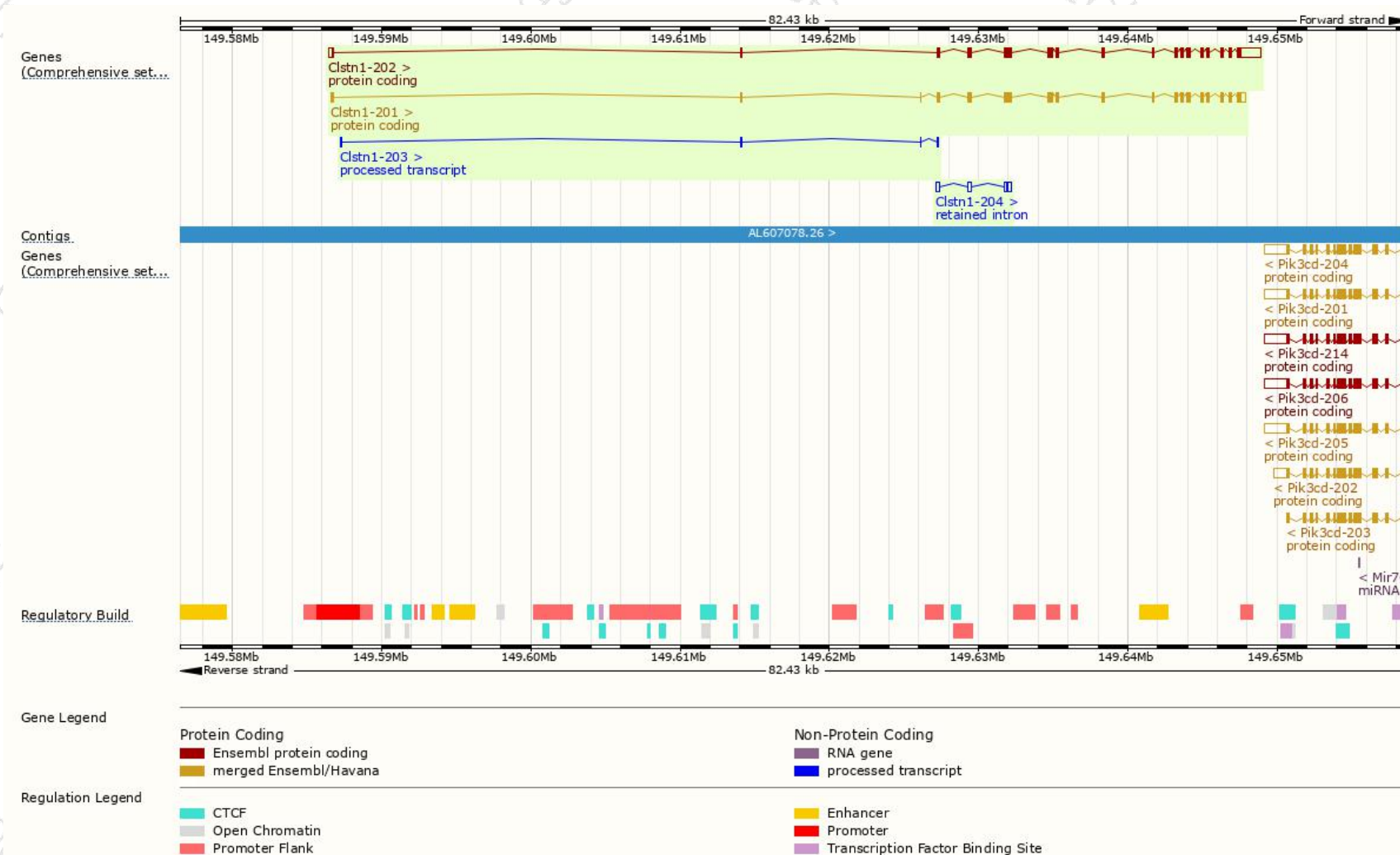
Protein domain

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,Juvenile mice homozygous for a null allele show reduced basal excitatory synaptic transmission, abnormal excitatory postsynaptic currents, enhanced NMDA receptor-dependent long term potentiation, and delayed dendritic spine maturation in CA1 hippocampal pyramidal cells.

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