

***Ctnnd2* Cas9-KO Strategy**

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Project Overview

Project Name

Ctnnd2

Project type

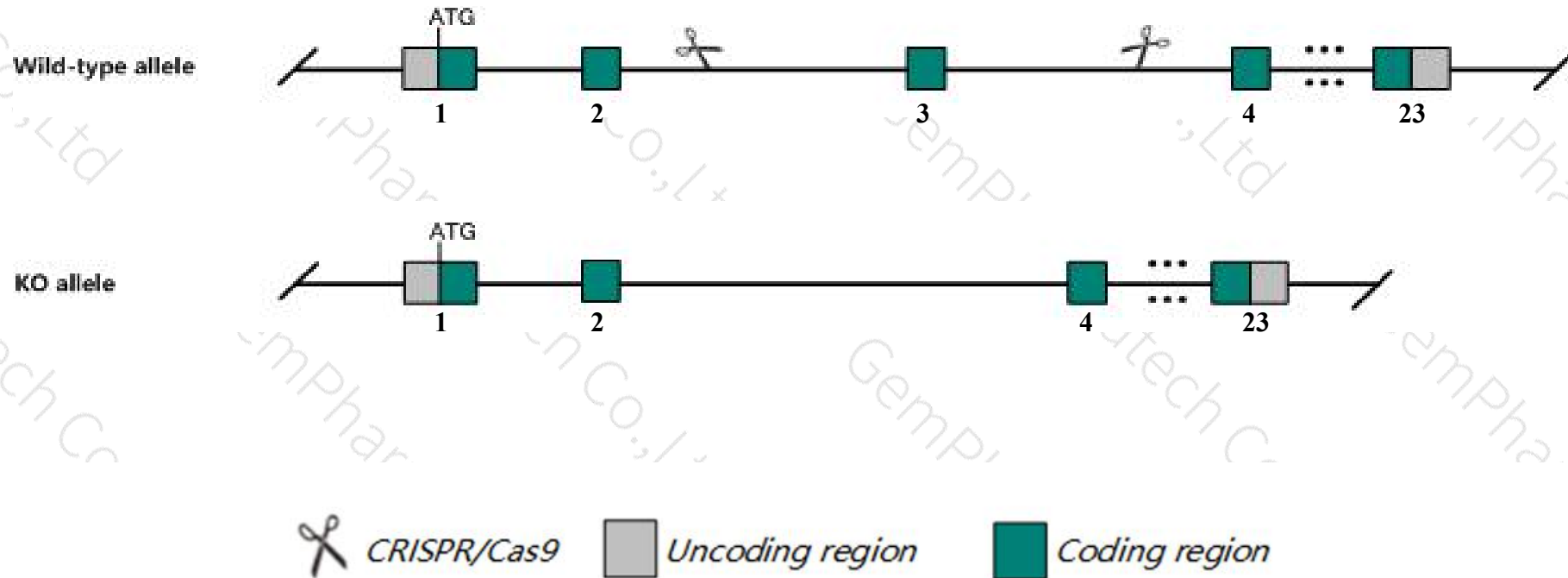
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ctnnd2* gene. The schematic diagram is as follows:



- The *Ctnnd2* gene has 12 transcripts. According to the structure of *Ctnnd2* gene, exon3 of *Ctnnd2-201* (ENSMUST00000081728.6) transcript is recommended as the knockout region. The region contains 113bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ctnnd2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a reporter allele exhibit abnormal conditioning, spatial learning and coordination behaviors and abnormal long term potentiation.
- The *Ctnnd2* gene is located on the Chr15. 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)

Ctnnd2 catenin (cadherin associated protein), delta 2 [Mus musculus (house mouse)]

Gene ID: 18163, updated on 26-Feb-2019

Summary



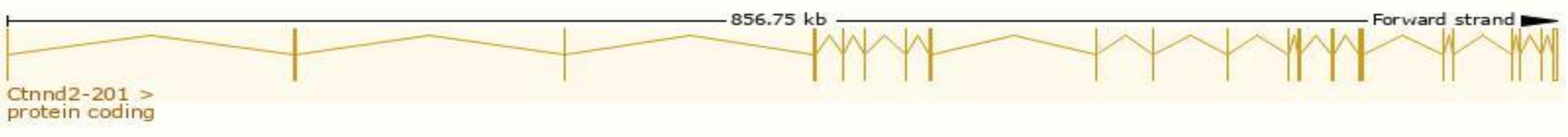
Official Symbol	Ctnnd2 provided by MGI
Official Full Name	catenin (cadherin associated protein), delta 2 provided by MGI
Primary source	MGI:MGI:1195966
See related	Ensembl:ENSMUSG00000022240
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Catnd2, Nprap, neurojugin
Expression	Biased expression in cortex adult (RPKM 25.6), frontal lobe adult (RPKM 25.1) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

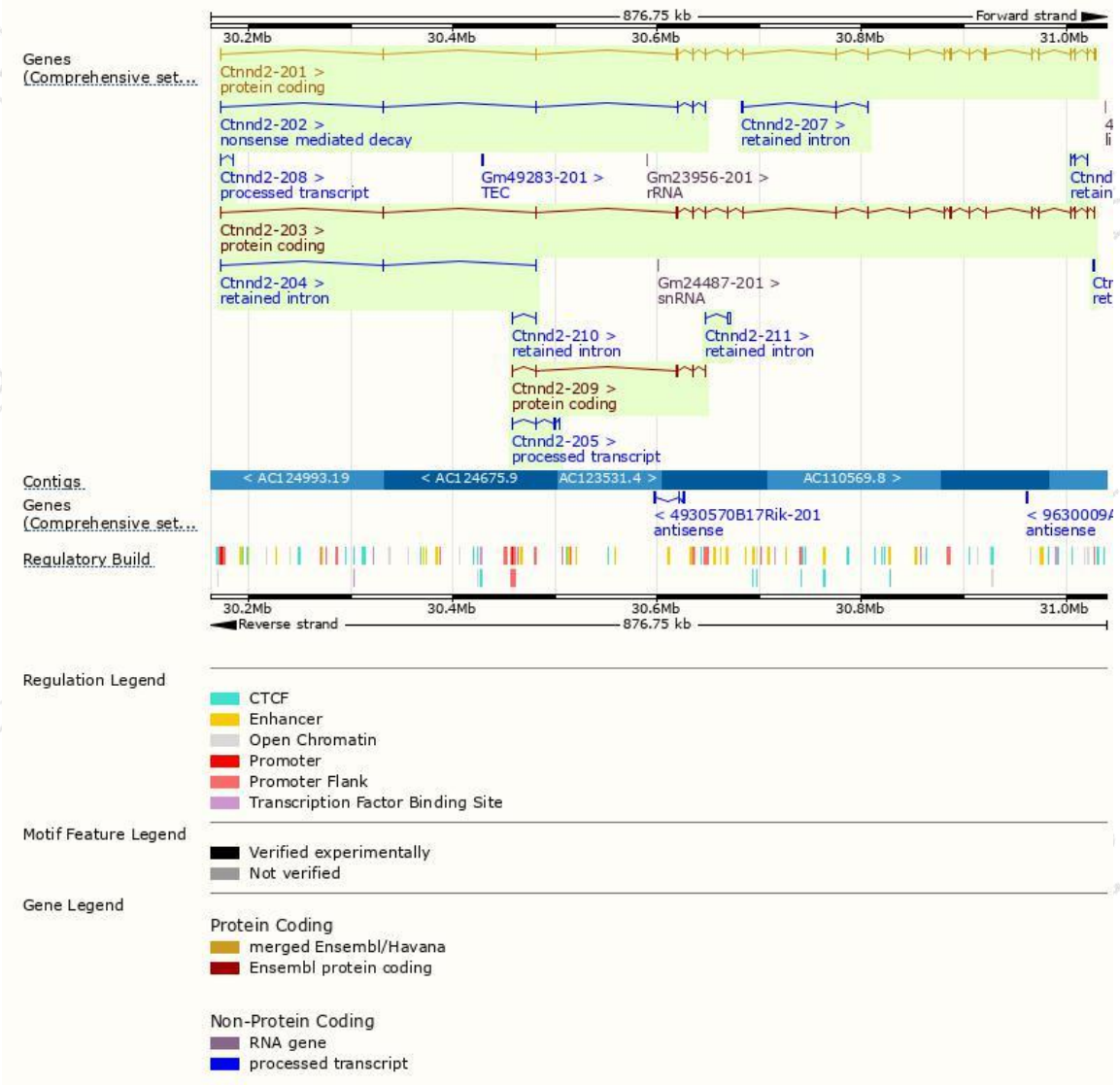
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ctnnd2-201	ENSMUST00000081728.6	5944	1246aa	Protein coding	CCDS27405	E9QKH8	TSL:1 GENCODE basic APPRIS P2
Ctnnd2-203	ENSMUST00000226119.1	4111	1221aa	Protein coding	-	B7ZNF6	GENCODE basic APPRIS ALT2
Ctnnd2-209	ENSMUST00000228282.1	847	145aa	Protein coding	-	A0A2I3BQV6	CDS 3' incomplete
Ctnnd2-202	ENSMUST00000226116.1	861	103aa	Nonsense mediated decay	-	A0A2I3BQV7	
Ctnnd2-208	ENSMUST00000227857.1	486	No protein	Processed transcript	-	-	
Ctnnd2-205	ENSMUST00000227004.1	476	No protein	Processed transcript	-	-	
Ctnnd2-211	ENSMUST00000228753.1	2506	No protein	Retained intron	-	-	
Ctnnd2-212	ENSMUST00000228827.1	2014	No protein	Retained intron	-	-	
Ctnnd2-204	ENSMUST00000226797.1	731	No protein	Retained intron	-	-	
Ctnnd2-207	ENSMUST00000227065.1	660	No protein	Retained intron	-	-	
Ctnnd2-206	ENSMUST00000227029.1	488	No protein	Retained intron	-	-	
Ctnnd2-210	ENSMUST00000228695.1	436	No protein	Retained intron	-	-	

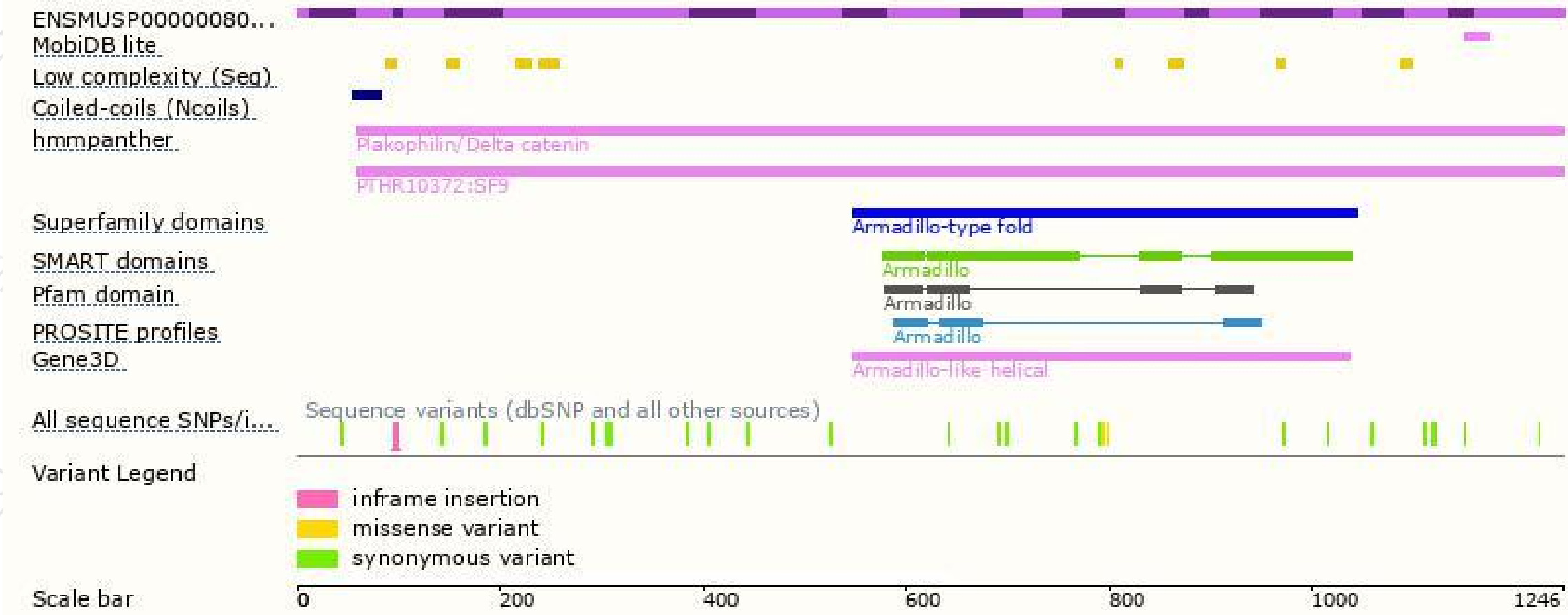
The strategy is based on the design of *Ctnnd2-201* transcript,The transcription is shown below



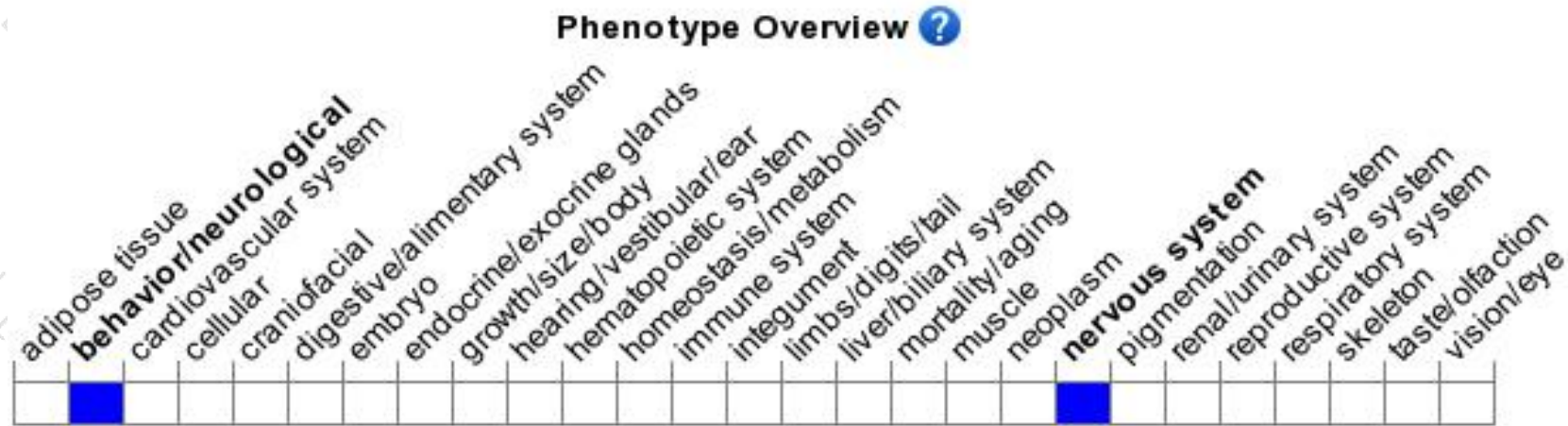
Genomic location distribution



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 reporter allele exhibit abnormal conditioning, spatial learning and coordination behaviors and abnormal long term potentiation.

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

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