

Ctnna2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Ctnna2

Project type

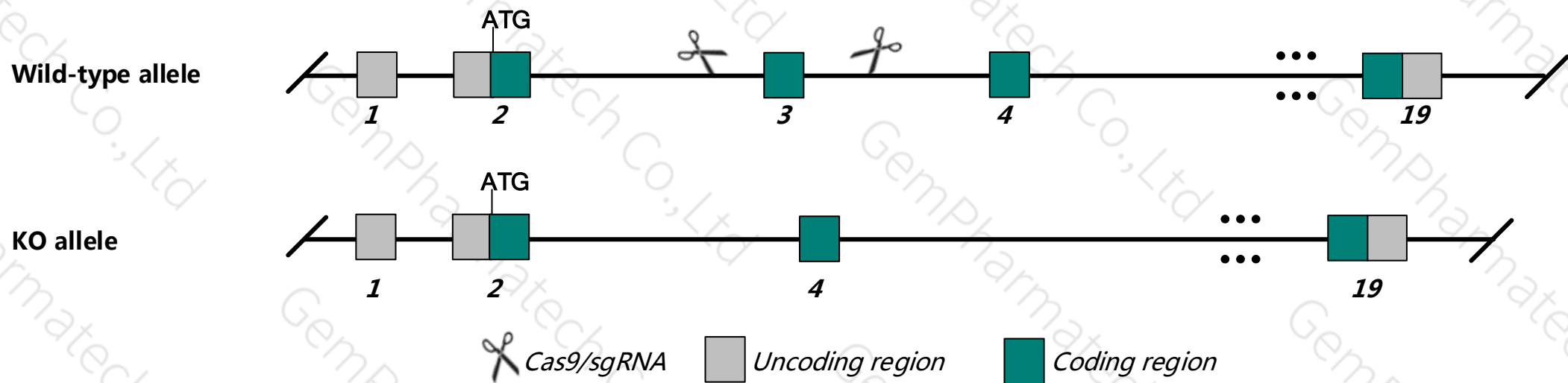
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ctnna2* gene. The schematic diagram is as follows:



Technical routes

- The *Ctnna2* gene has 8 transcripts. According to the structure of *Ctnna2* gene, exon3 of *Ctnna2*-202 (ENSMUST00000159626.7) transcript is recommended as the knockout region. The region contains 196bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ctnna2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating Positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data , animals homozygous for a mutation of this gene exhibit ataxia, reduced body weight, reduced male fertility, and abnormalities of the brain which include a hypoplastic cerebellum, abnormal foliation pattern, ectopic Purkinje cells, and abnormal pyramidal cells in the hippocampus.
- The *Ctnna2* gene is located on the Chr6. 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)

Ctnna2 catenin (cadherin associated protein), alpha 2 [*Mus musculus* (house mouse)]

Gene ID: 12386, updated on 24-Oct-2019

Summary

Official Symbol Ctnna2 provided by [MGI](#)

Official Full Name catenin (cadherin associated protein), alpha 2 provided by [MGI](#)

Primary source [MGI:MGI:88275](#)

See related [Ensembl:ENSMUSG00000063063](#)

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 cdf; chp; Catna; Catna2; AI481747

Expression Biased expression in CNS E18 (RPKM 45.0), CNS E14 (RPKM 36.8) and 5 other tissues [See more](#)

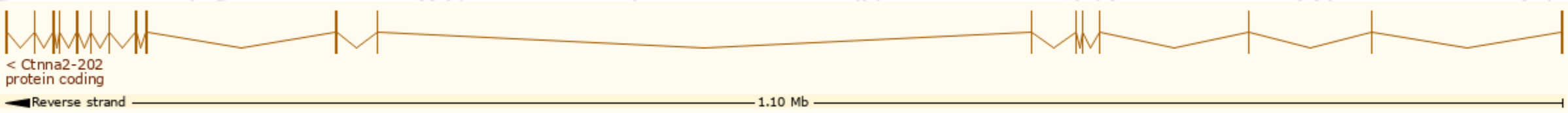
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

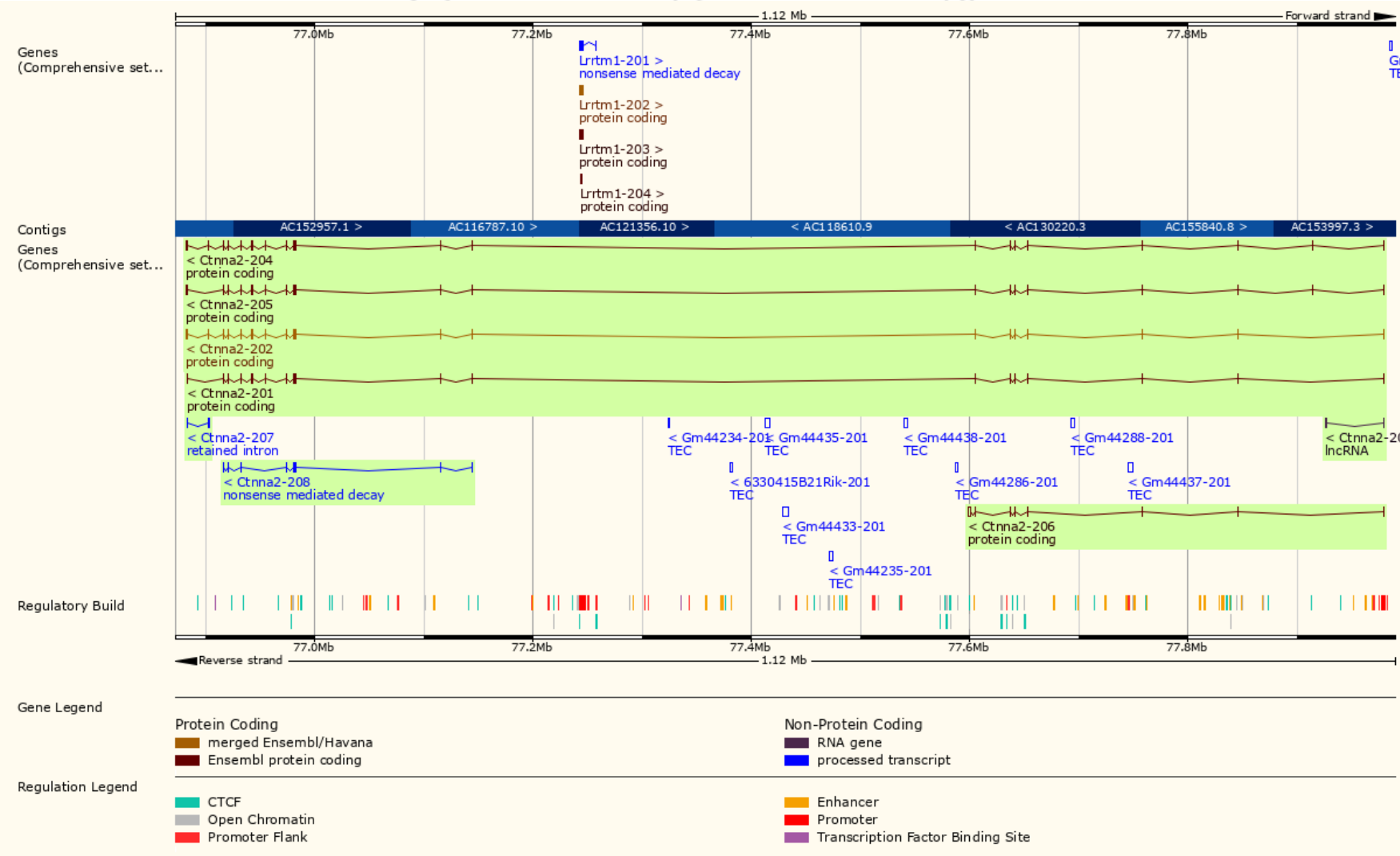
The gene has 8 transcripts, and all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Ctnna2-201	ENSMUST00000075340.11	2864	905aa	Protein coding	CCDS39521	Q61301	TSL:5 GENCODE basic APPRIS ALT1
Ctnna2-202	ENSMUST00000159626.7	3908	953aa	Protein coding	CCDS20250	Q61301	TSL:1 GENCODE basic APPRIS P3
Ctnna2-203	ENSMUST00000160252.1	418	No protein	lncRNA	-	-	TSL:3
Ctnna2-204	ENSMUST00000160894.7	4162	966aa	Protein coding	-	E0CXB9	TSL:1 GENCODE basic
Ctnna2-205	ENSMUST00000161846.7	4018	918aa	Protein coding	-	Q61301	TSL:1 GENCODE basic
Ctnna2-206	ENSMUST00000162273.1	3277	356aa	Protein coding	-	Q8BS72	TSL:1 GENCODE basic
Ctnna2-207	ENSMUST00000162991.1	684	No protein	Retained intron	-	-	TSL:3
Ctnna2-208	ENSMUST00000204527.1	1105	243aa	Nonsense mediated decay	-	A0A0N4SUZ7	CDS 5' incomplete TSL:5

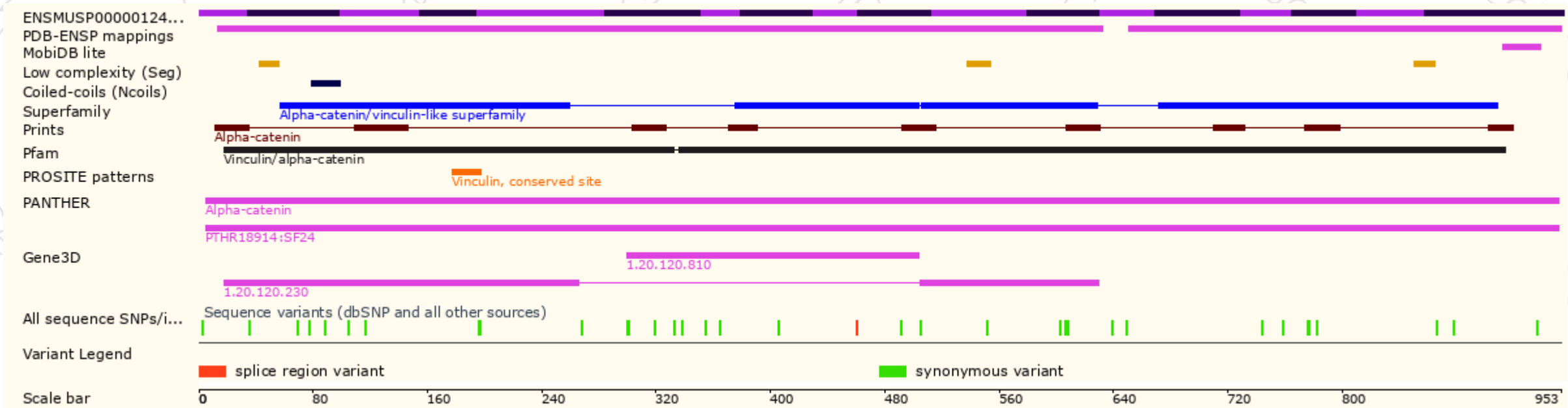
The strategy is based on the design of *Ctnna2*-202 transcript,the transcription is shown below:



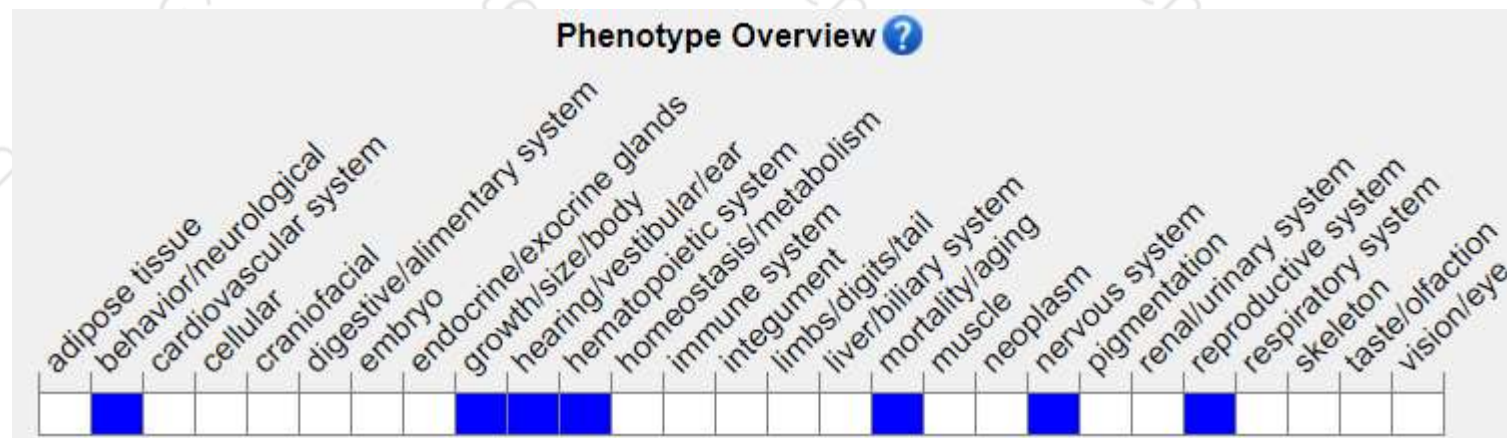
Genomic location (Ensembl)



Protein domain (Ensembl)



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, animals homozygous for a mutation of this gene exhibit ataxia, reduced body weight, reduced male fertility, and abnormalities of the brain which include a hypoplastic cerebellum, abnormal foliation pattern, ectopic Purkinje cells, and abnormal pyramidal cells in the hippocampus.

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