

Cetn3 Cas9-KO Strategy

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Project Overview

Project Name

Cetn3

Project type

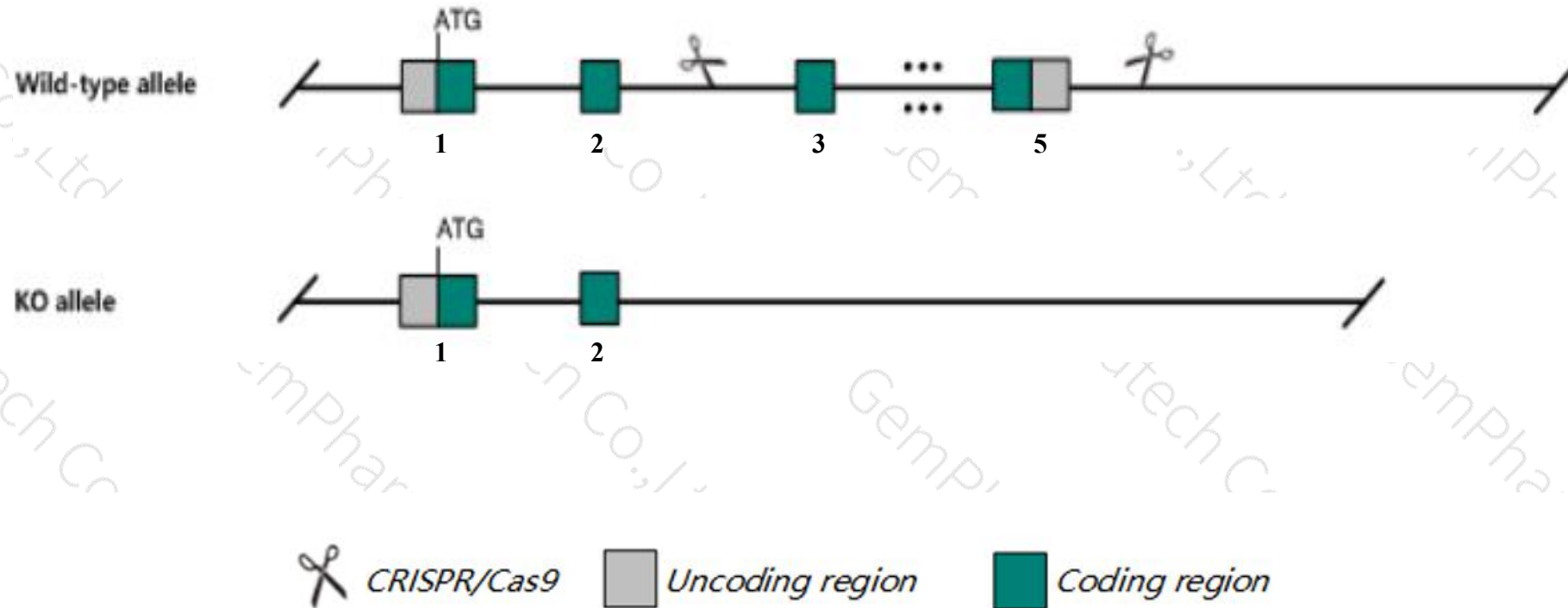
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cetn3* gene. The schematic diagram is as follows:



- The *Cetn3* gene has 8 transcripts. According to the structure of *Cetn3* gene, exon3-exon5 of *Cetn3-201* (ENSMUST00000022009.9) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cetn3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous null mice are viable and fertile with no signs of syndromic ciliopathy and no detectable defects in retinal photoreceptor development and function.
- The *Cetn3* gene is located on the Chr13. 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)

Cetn3 centrin 3 [Mus musculus (house mouse)]

Gene ID: 12626, updated on 13-Mar-2020

Summary



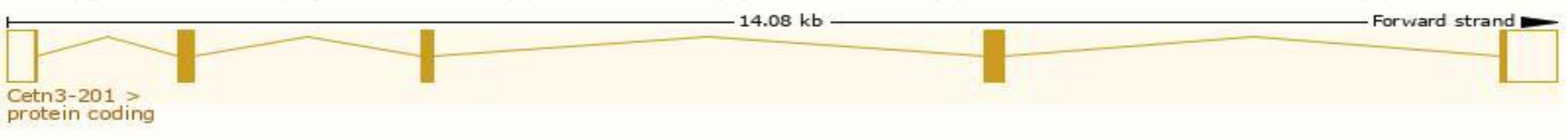
Official Symbol	Cetn3 provided by MGI
Official Full Name	centrin 3 provided by MGI
Primary source	MGI:MGI:1097706
See related	Ensembl:ENSMUSG00000021537
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MmCEN3
Expression	Biased expression in CNS E18 (RPKM 18.1), CNS E11.5 (RPKM 17.0) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

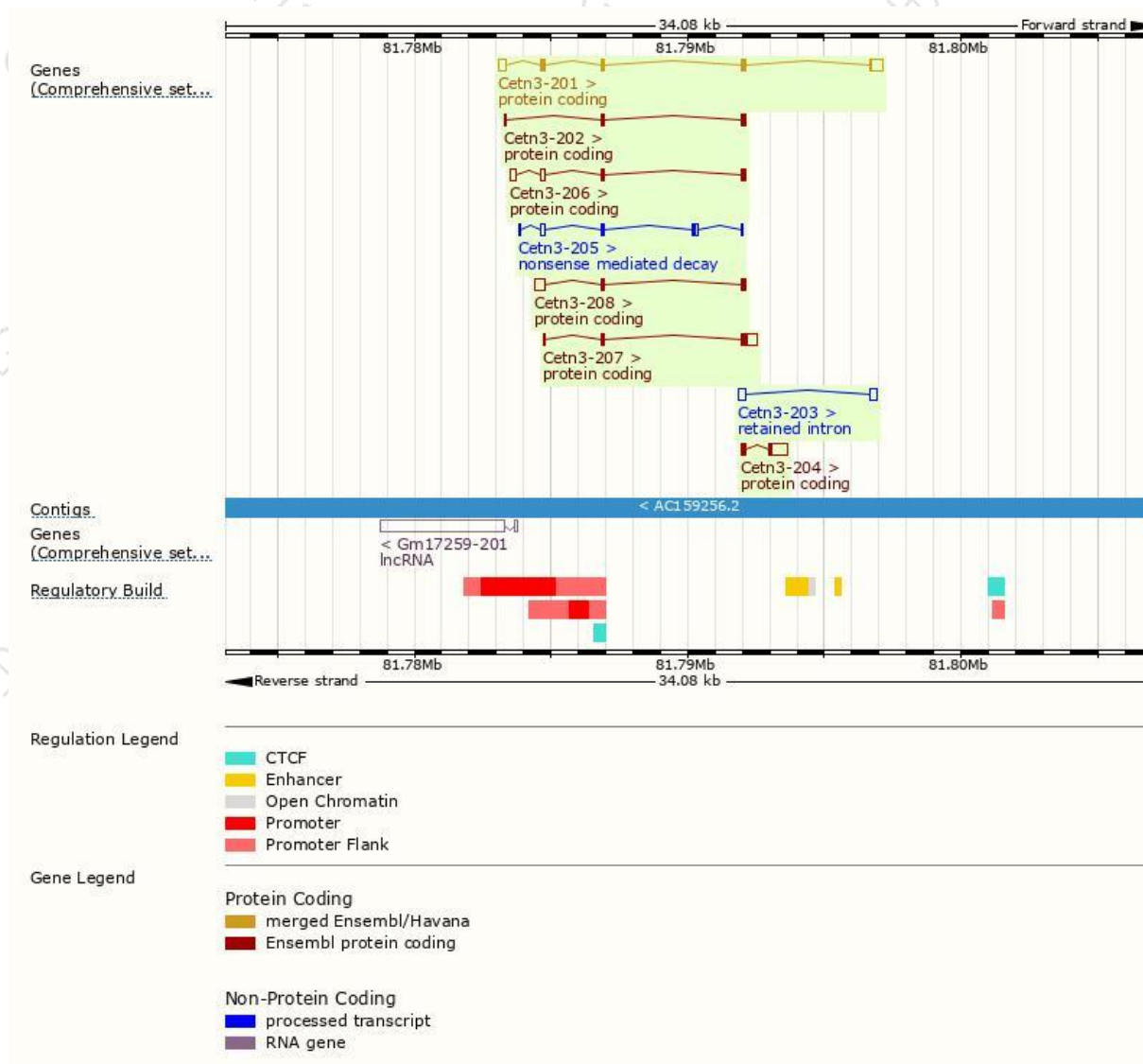
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cetn3-201	ENSMUST0000022009.9	1226	167aa	Protein coding	CCDS26663	Q35648 Q545L8	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
Cetn3-204	ENSMUST00000224168.1	876	87aa	Protein coding	-	A0A286YCB3	CDS 5' incomplete
Cetn3-207	ENSMUST00000224705.1	769	137aa	Protein coding	-	A0A286YDP0	CDS 5' incomplete
Cetn3-208	ENSMUST00000226007.1	697	100aa	Protein coding	-	A0A286YDS3	CDS 3' incomplete
Cetn3-206	ENSMUST00000224574.1	628	97aa	Protein coding	-	A0A286YD15	CDS 3' incomplete
Cetn3-202	ENSMUST00000223793.1	387	100aa	Protein coding	-	A0A286YDS3	CDS 3' incomplete
Cetn3-205	ENSMUST00000224433.1	598	62aa	Nonsense mediated decay	-	A0A286YCV3	
Cetn3-203	ENSMUST00000223858.1	529	No protein	Retained intron	-	-	

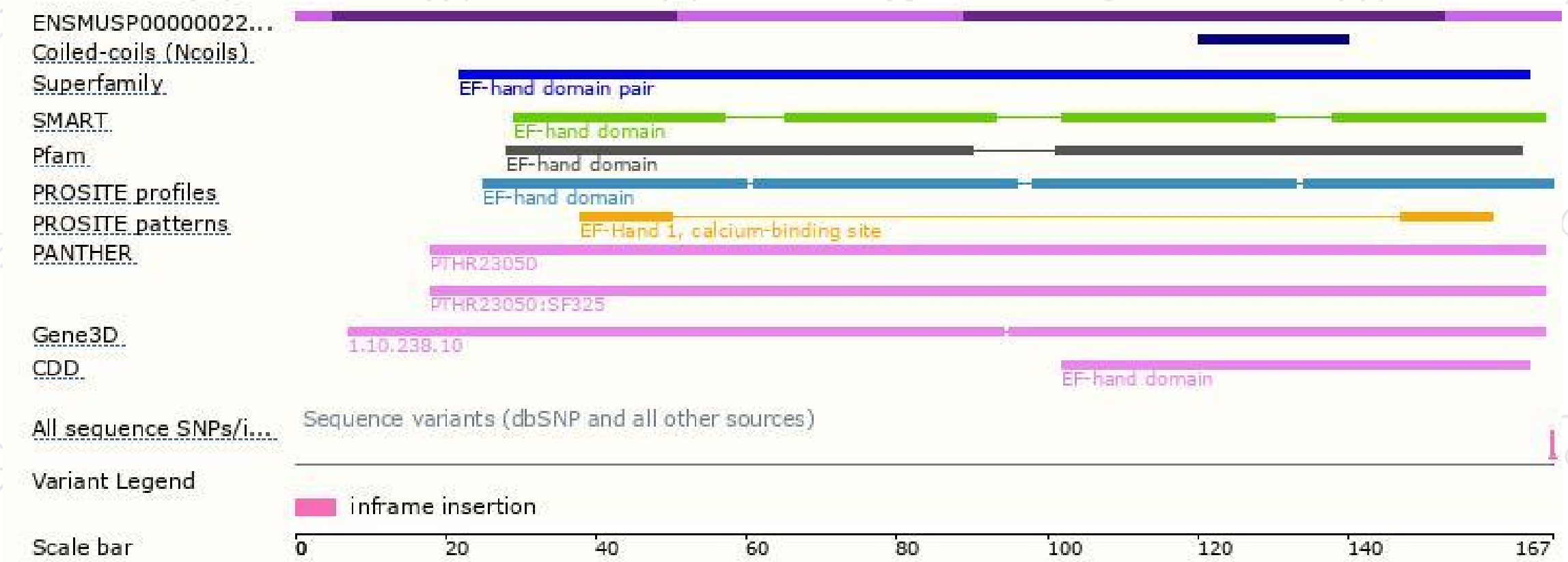
The strategy is based on the design of *Cetn3-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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