

# *Cetn3* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Cetn3*

**Project type**

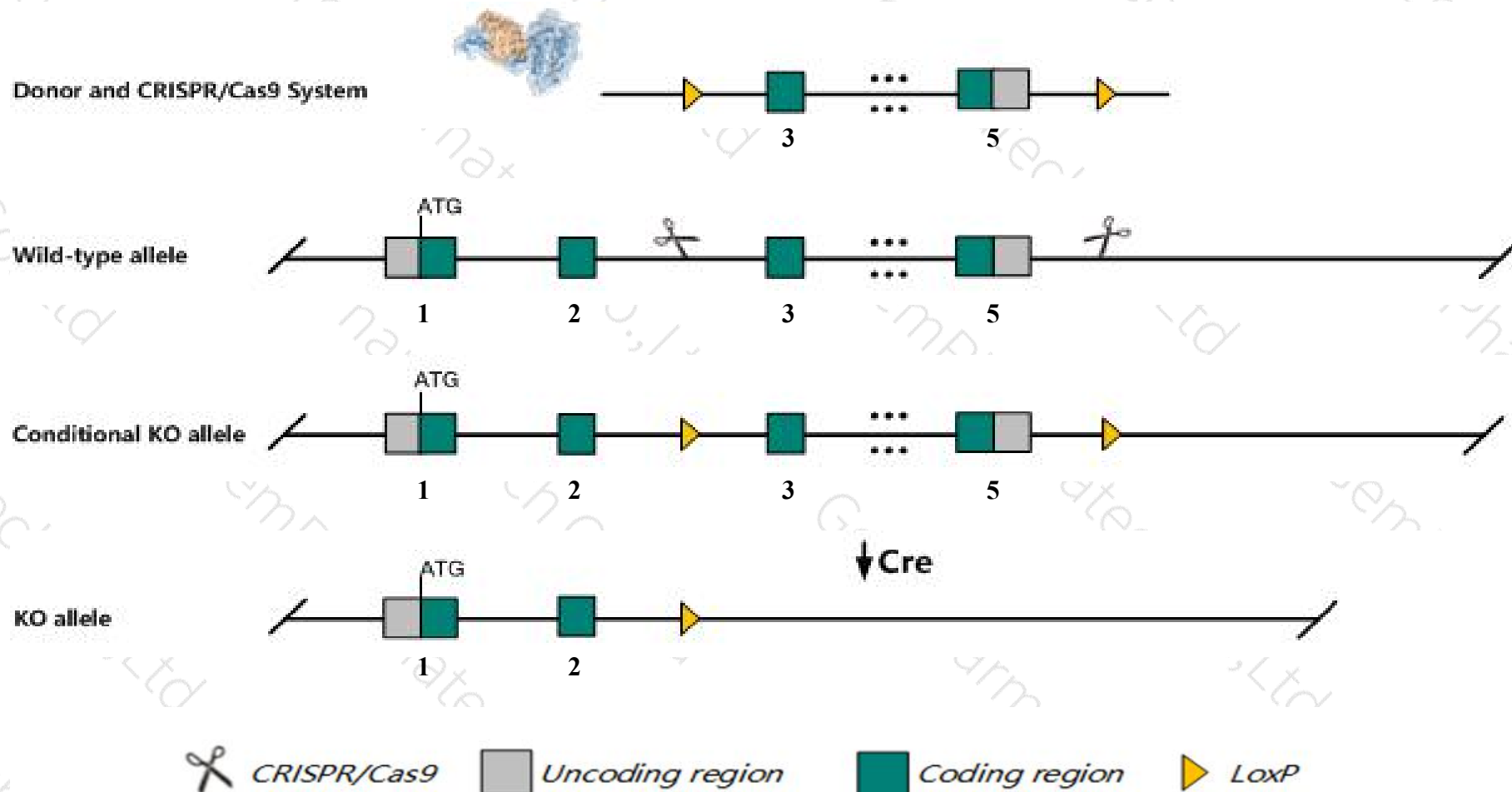
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



# Technical routes

- 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 and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Cetn3 centrin 3 [Mus musculus (house mouse)]

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

### Summary



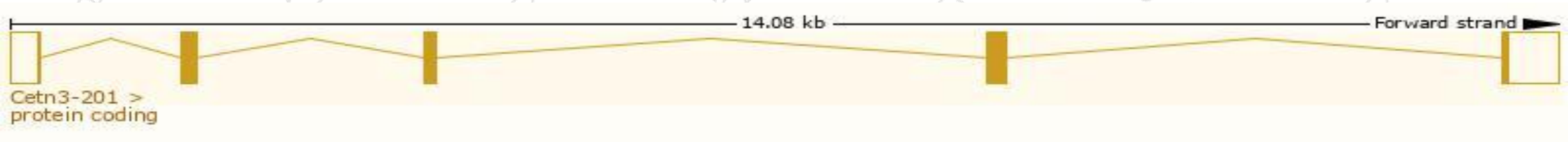
Official Symbol	Cetn3 provided by <a href="#">MGI</a>
Official Full Name	centrin 3 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1097706</a>
See related	<a href="#">Ensembl:ENSMUSG00000021537</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
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 <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

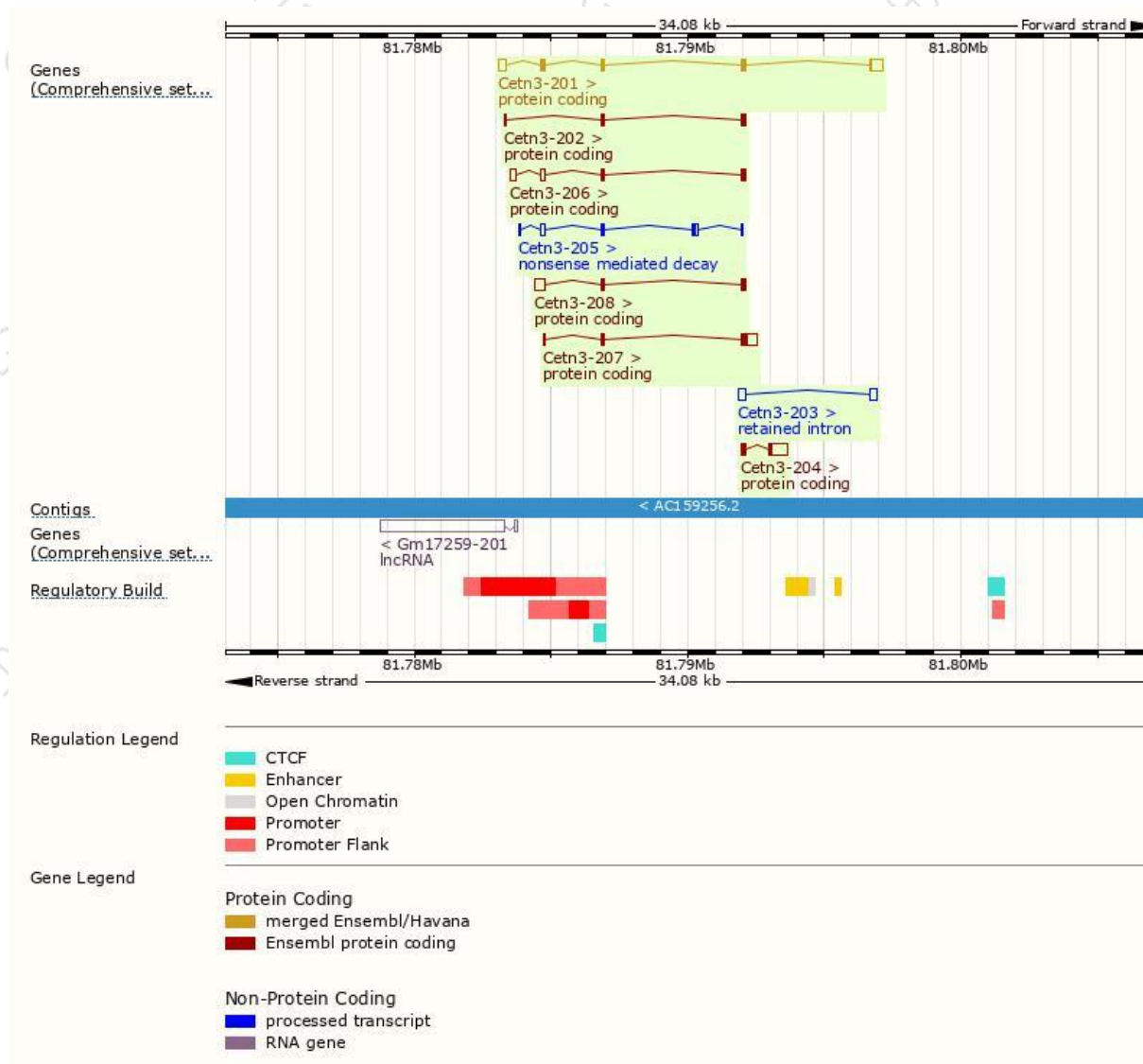
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cetn3-201	<a href="#">ENSMUST00000022009.9</a>	1226	<a href="#">167aa</a>	Protein coding	<a href="#">CCDS26663</a>	<a href="#">Q35648 Q545L8</a>	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	<a href="#">ENSMUST000000224168.1</a>	876	<a href="#">87aa</a>	Protein coding	-	<a href="#">A0A286YCB3</a>	CDS 5' incomplete
Cetn3-207	<a href="#">ENSMUST000000224705.1</a>	769	<a href="#">137aa</a>	Protein coding	-	<a href="#">A0A286YDP0</a>	CDS 5' incomplete
Cetn3-208	<a href="#">ENSMUST000000226007.1</a>	697	<a href="#">100aa</a>	Protein coding	-	<a href="#">A0A286YDS3</a>	CDS 3' incomplete
Cetn3-206	<a href="#">ENSMUST000000224574.1</a>	628	<a href="#">97aa</a>	Protein coding	-	<a href="#">A0A286YD15</a>	CDS 3' incomplete
Cetn3-202	<a href="#">ENSMUST000000223793.1</a>	387	<a href="#">100aa</a>	Protein coding	-	<a href="#">A0A286YDS3</a>	CDS 3' incomplete
Cetn3-205	<a href="#">ENSMUST000000224433.1</a>	598	<a href="#">62aa</a>	Nonsense mediated decay	-	<a href="#">A0A286YCV3</a>	
Cetn3-203	<a href="#">ENSMUST000000223858.1</a>	529	No protein	Retained intron	-	-	

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

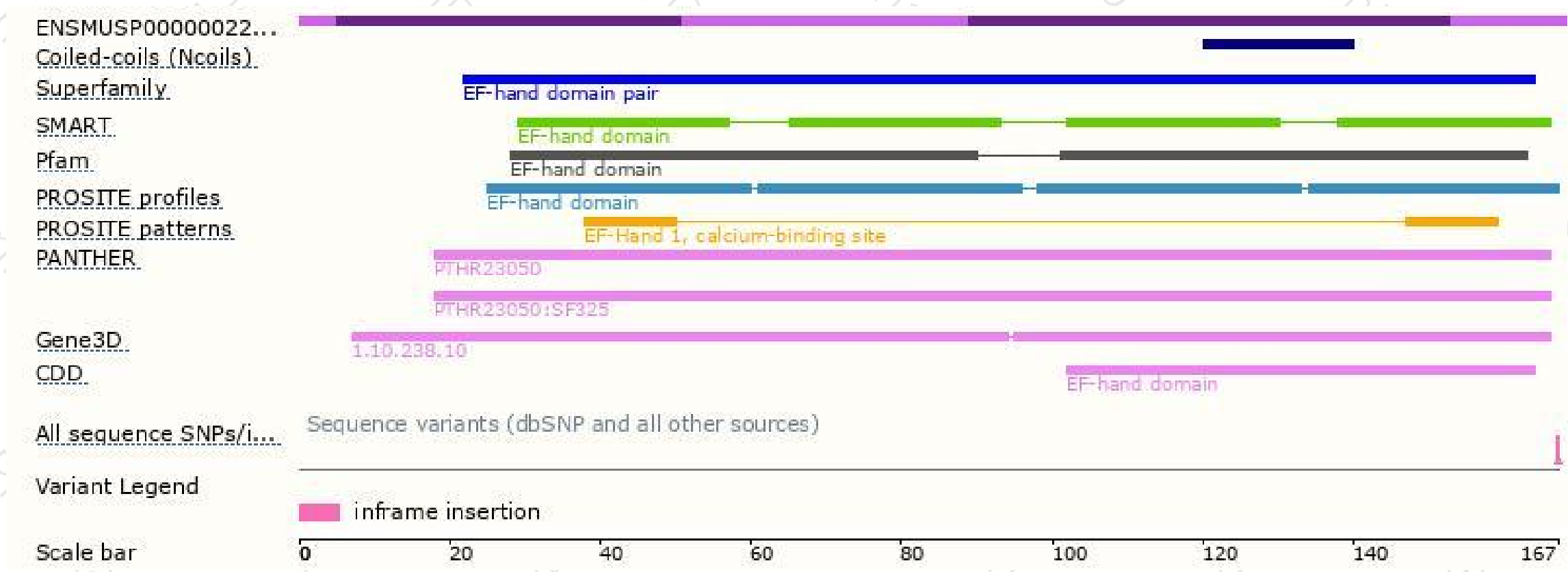


# Genomic location distribution





# Protein domain



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

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