

Cenpa Cas9-KO Strategy

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Project Overview

Project Name

Cenpa

Project type

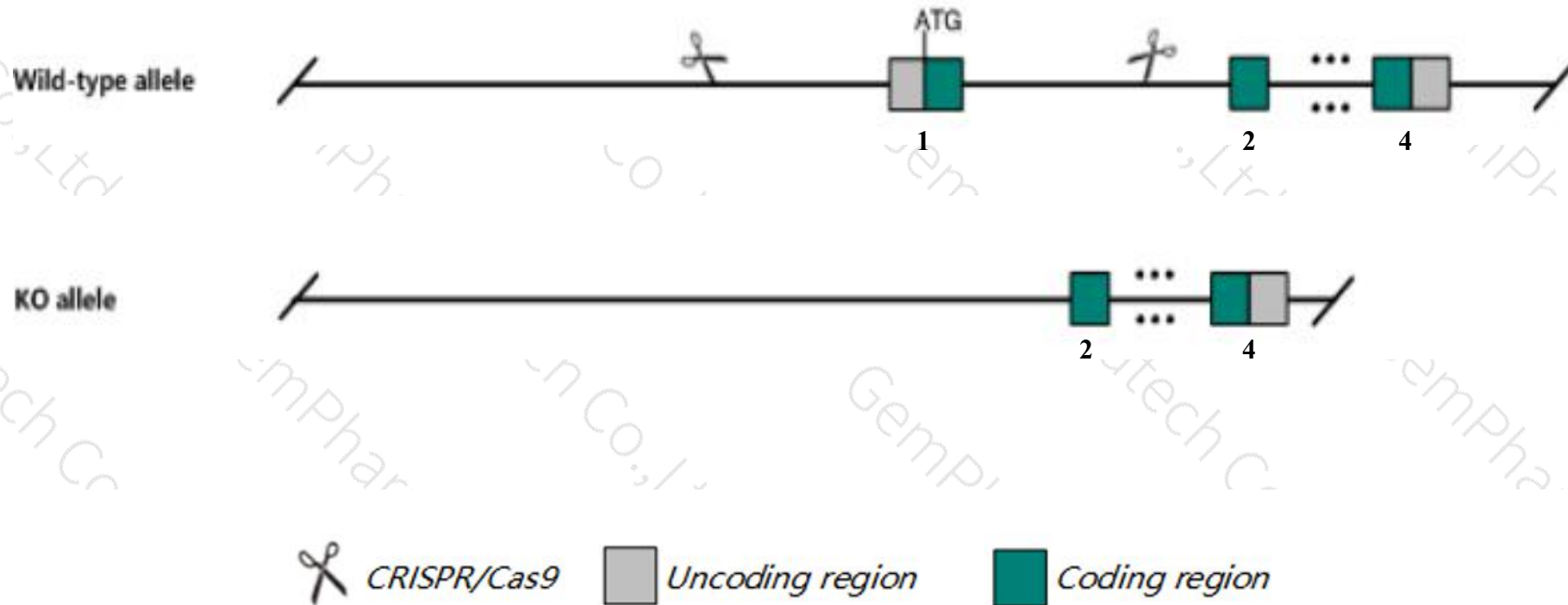
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Cenpa* gene has 10 transcripts. According to the structure of *Cenpa* gene, exon1 of *Cenpa-205* (ENSMUST00000144742.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cenpa* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous mutation of this gene results in embryonic lethality between e3.5 and e10.5. embryogenesis is impaired due to chromosomal missegregation, aneuploidy, and apoptosis.
- The *Cenpa* gene is located on the Chr5. 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)

Cenpa centromere protein A [Mus musculus (house mouse)]

Gene ID: 12615, updated on 13-Mar-2020

Summary

Official Symbol Cenpa provided by [MGI](#)

Official Full Name centromere protein A provided by [MGI](#)

Primary source [MGI:MGI:88375](#)

See related [Ensembl:ENSMUSG00000029177](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Cenp-A

Summary Centromeres are the differentiated chromosomal domains that specify the mitotic behavior of chromosomes. This gene encodes a centromere protein which contains a histone H3 related histone fold domain that is required for targeting to the centromere. Centromere protein A is proposed to be a component of a modified nucleosome or nucleosome-like structure in which it replaces 1 or both copies of conventional histone H3 in the (H3-H4)₂ tetrameric core of the nucleosome particle. The protein is a replication-independent histone that is a member of the histone H3 family. Alternative splicing results in multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Nov 2015]

Expression Broad expression in CNS E11.5 (RPKM 43.5), liver E14.5 (RPKM 41.9) and 20 other tissues [See more](#)

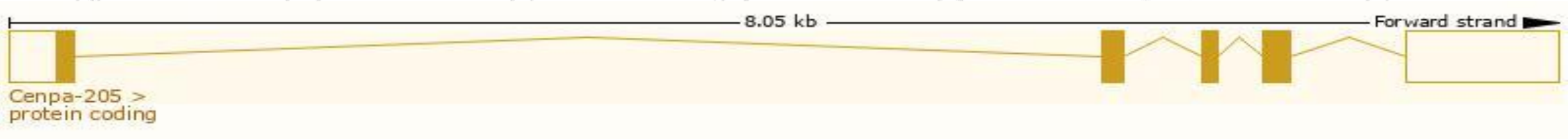
Orthologs [human](#) [all](#)

Transcript information（Ensembl）

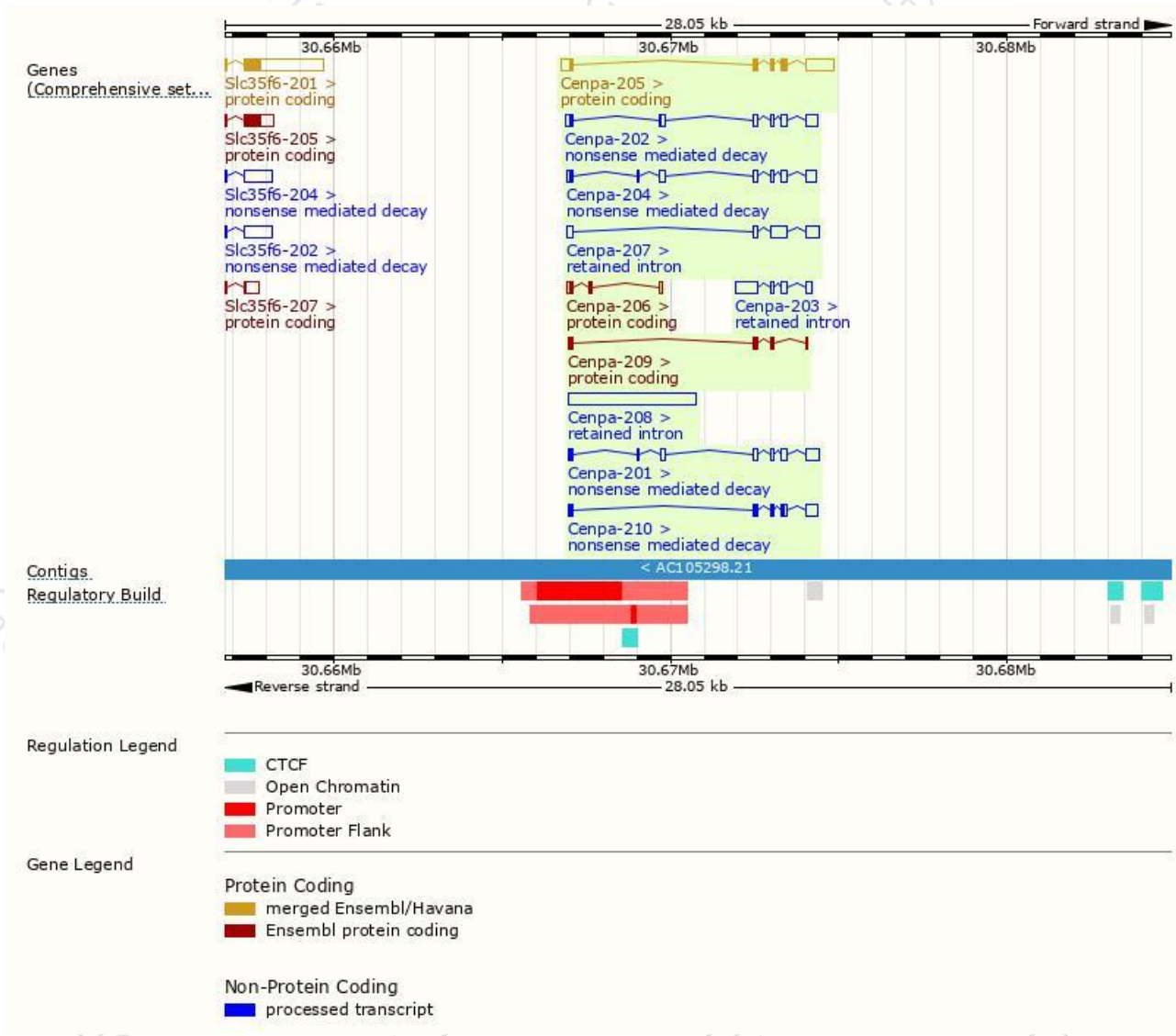
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cenpa-205	ENSMUST00000144742.5	1466	134aa	Protein coding	CCDS19162	Q35216	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
Cenpa-209	ENSMUST00000199320.4	369	99aa	Protein coding	-	A0A0G2JGI2	CDS 3' incomplete TSL:3
Cenpa-206	ENSMUST00000149759.1	346	59aa	Protein coding	-	A0A0G2JEV0	TSL:3 GENCODE basic
Cenpa-202	ENSMUST00000133316.7	1031	42aa	Nonsense mediated decay	-	D6RCV6	TSL:1
Cenpa-204	ENSMUST00000134846.7	1007	39aa	Nonsense mediated decay	-	D6RJ71	TSL:2
Cenpa-201	ENSMUST0000031073.9	993	39aa	Nonsense mediated decay	-	D6RJ71	TSL:1
Cenpa-210	ENSMUST00000199617.1	827	130aa	Nonsense mediated decay	-	A0A0G2JEV2	TSL:3
Cenpa-208	ENSMUST00000197962.1	3806	No protein	Retained intron	-	-	TSL:NA
Cenpa-207	ENSMUST00000150810.7	1120	No protein	Retained intron	-	-	TSL:5
Cenpa-203	ENSMUST00000134372.1	1010	No protein	Retained intron	-	-	TSL:2

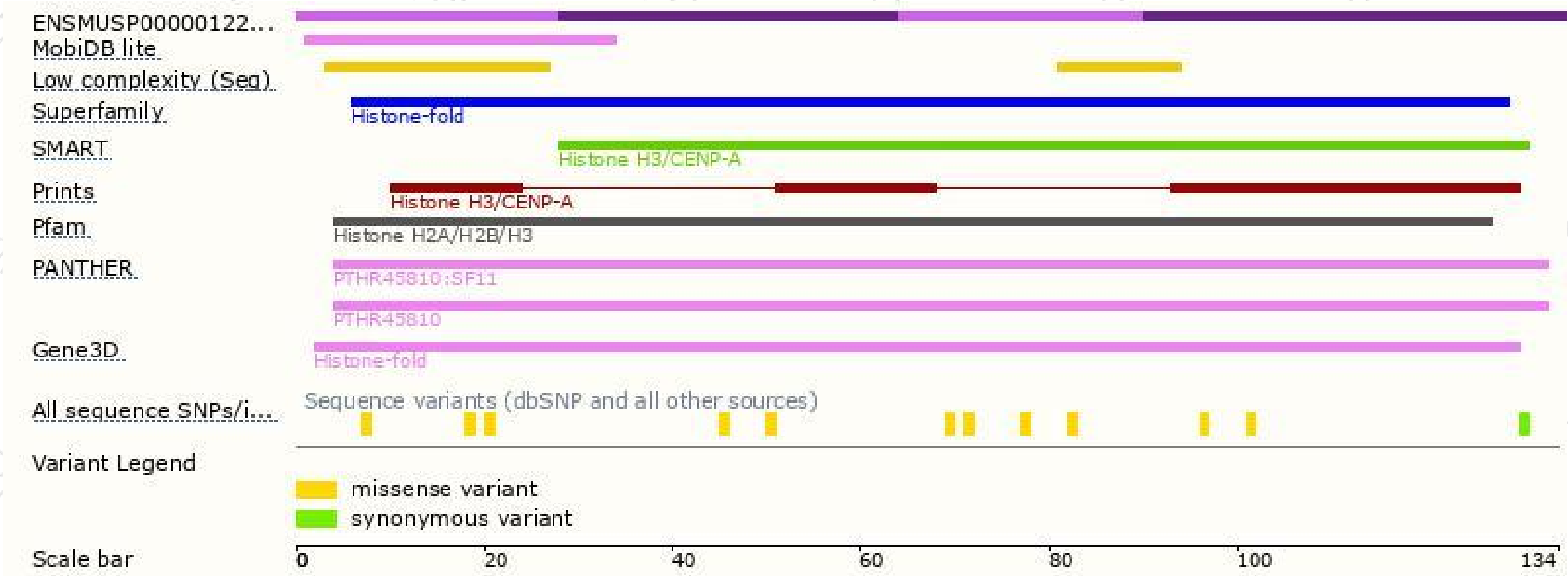
The strategy is based on the design of *Cenpa-205* transcript,the transcription is shown below:



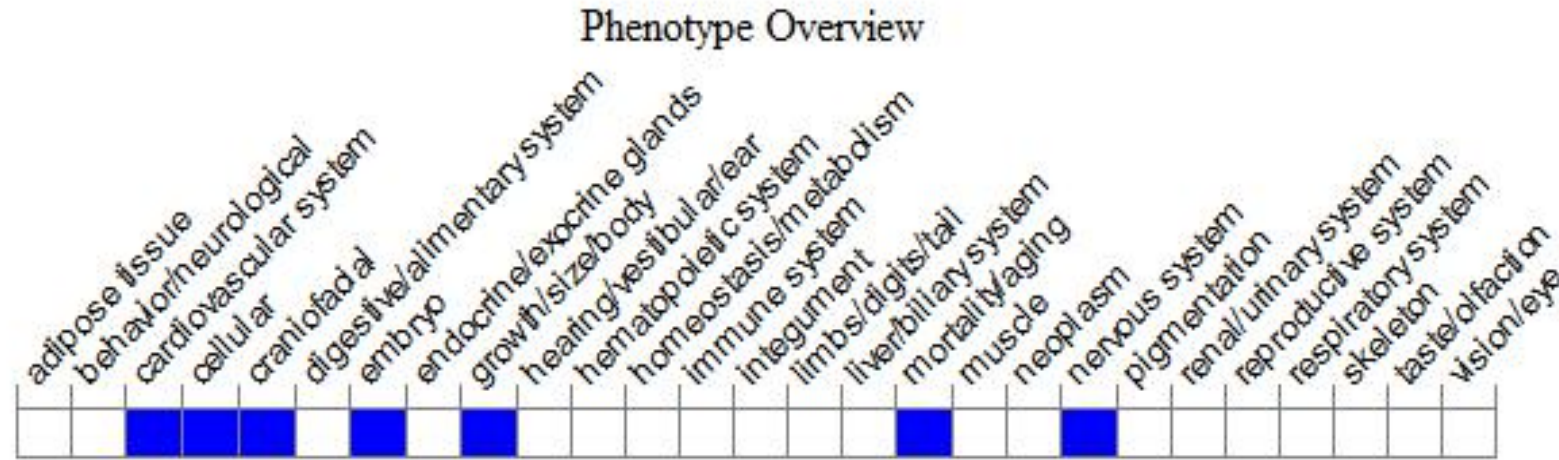
Genomic location distribution



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, homozygous mutation of this gene results in embryonic lethality between E3.5 and E10.5. Embryogenesis is impaired due to chromosomal missegregation, aneuploidy, and apoptosis.

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

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