

Cenpw Cas9-KO Strategy

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Project Overview

Project Name

Cenpw

Project type

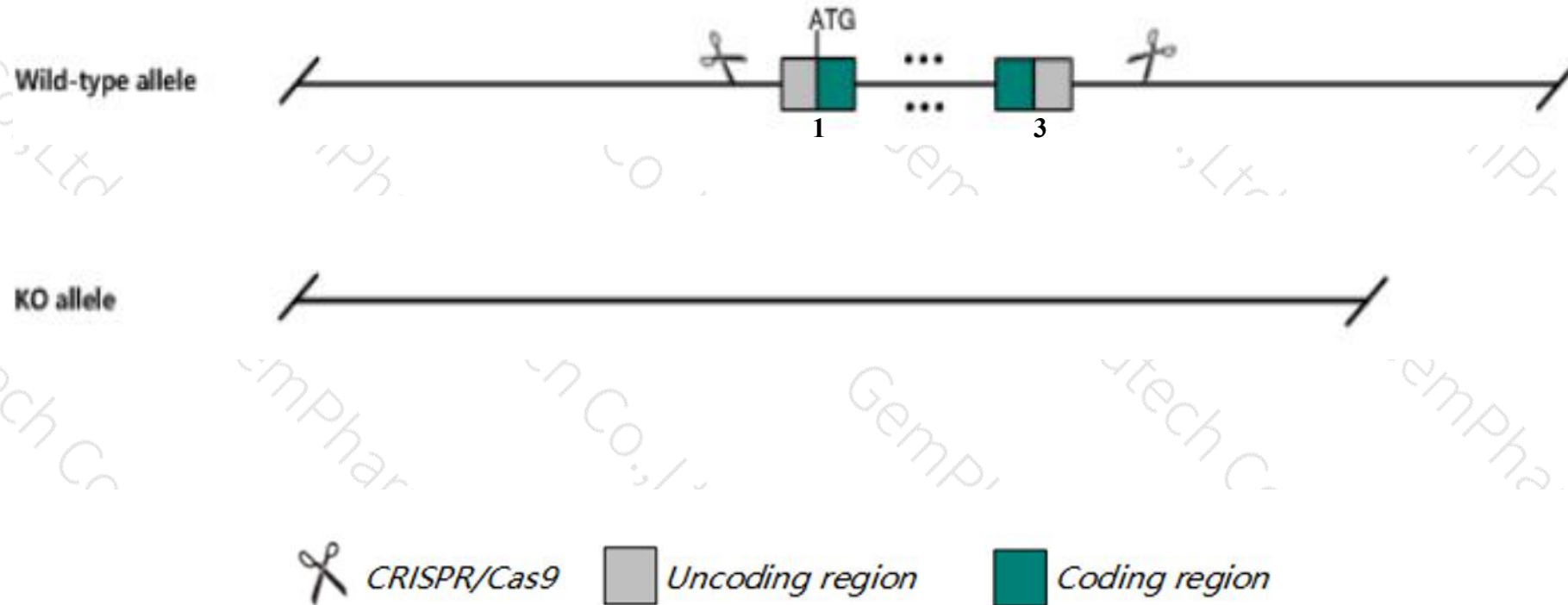
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Cenpw* gene has 2 transcripts. According to the structure of *Cenpw* gene, exon1-exon3 of *Cenpw-201* (ENSMUST00000099985.5) transcript is recommended as the knockout region. The region contains all 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 *Cenpw* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Cenpw* gene is located on the Chr10. 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)

Cenpw centromere protein W [Mus musculus (house mouse)]

Gene ID: 66311, updated on 13-Mar-2020

Summary



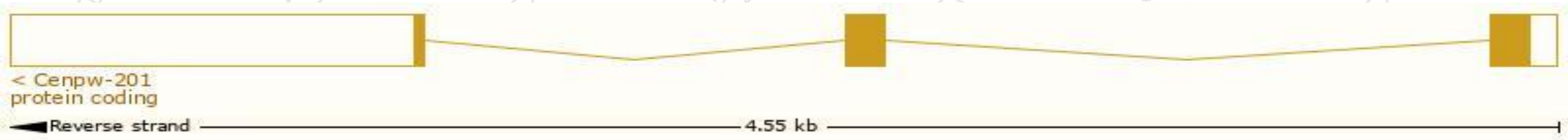
Official Symbol	Cenpw provided by MGI
Official Full Name	centromere protein W provided by MGI
Primary source	MGI:MGI:1913561
See related	Ensembl:ENSMUSG00000075266
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610036L11Rik, Cug2
Expression	Broad expression in liver E14 (RPKM 9.7), CNS E11.5 (RPKM 8.7) and 20 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

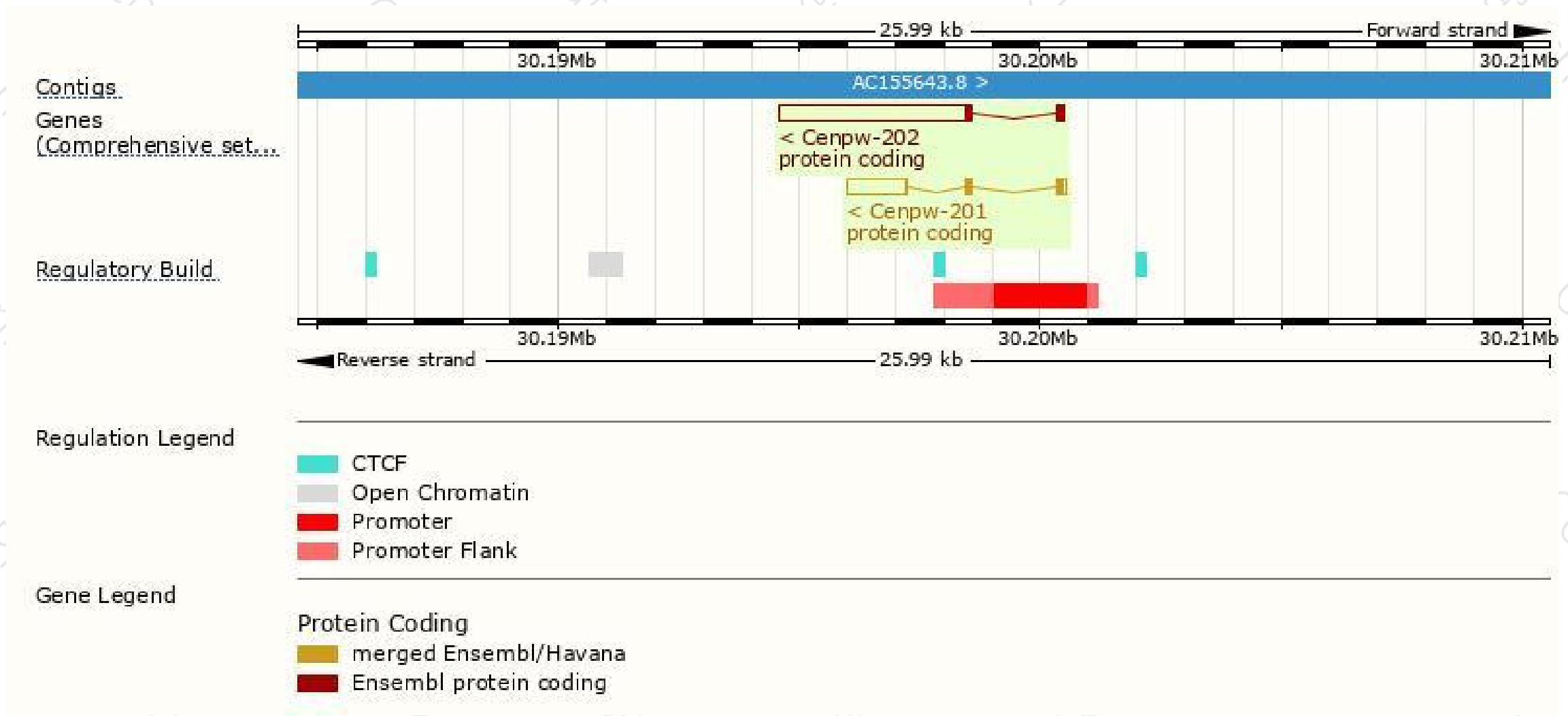
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cenpw-201	ENSMUST00000099985.5	1532	86aa	Protein coding	CCDS35876	B2RVH1_Q3URR0	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 P2
Cenpw-202	ENSMUST00000216853.1	4143	84aa	Protein coding	-	A0A1L1SQB9	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 ALT1

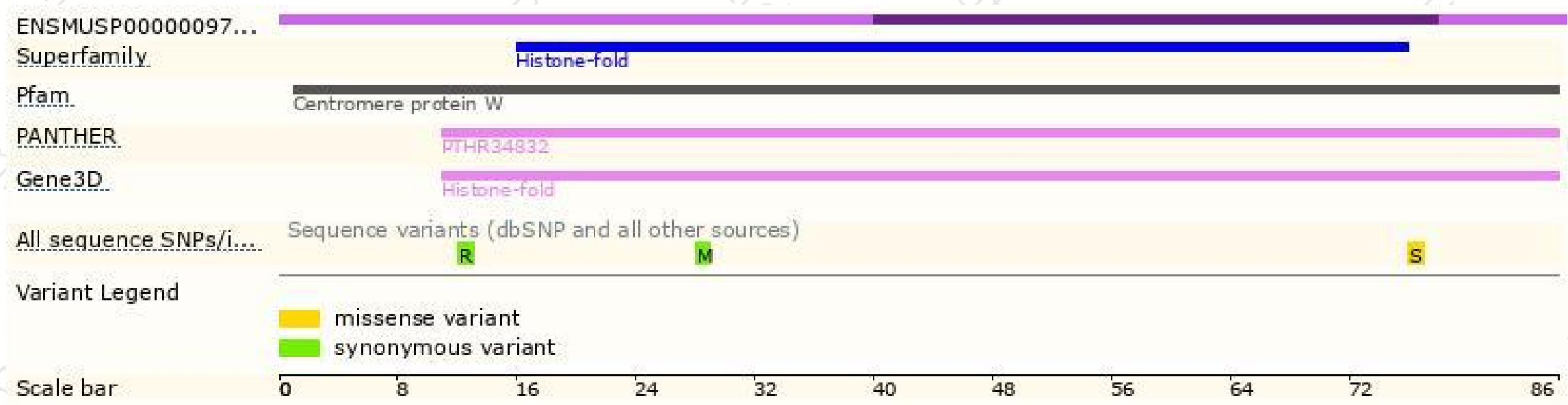
The strategy is based on the design of *Cenpw-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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