Cenpk Cas9-KO Strategy

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Project Overview

Project Name	*Cenpk*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Cenpk* gene has 8 transcripts. According to the structure of *Cenpk* gene, exon3-exon4 of *Cenpk-201* (ENSMUST00000022227.7) transcript is recommended as the knockout region.The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cenpk* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ Some amino acids will remain at the N-terminus and some functions may be retained.

➢ Transcripts 203,204 may not be affected.

➢ The *Cenpk* 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）

Cenpk centromere protein K [Mus musculus (house mouse)]

Gene ID: 60411, updated on 13-Mar-2020

Summary

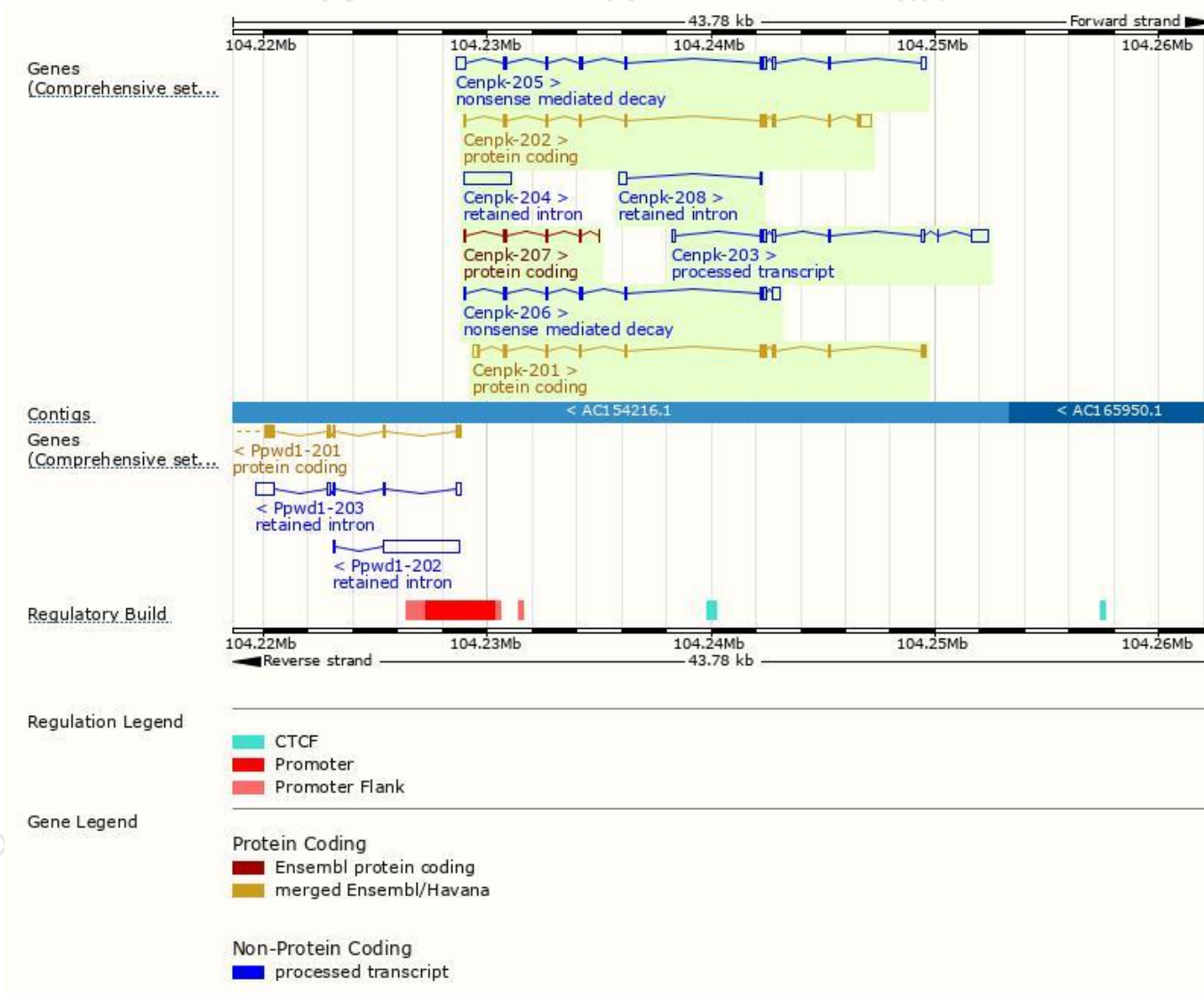|	
Official Symbol	Cenpk provided by MGI
Official Full Name	centromere protein K provided by MGI
Primary source	MGI:MGI:1926210
See related	Ensembl:ENSMUSG00000021714
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B130045K24Rik, BB232189, C530004N04Rik, Cenp-K, Solt, Solzt
Expression	Biased expression in liver E14 (RPKM 9.5), CNS E11.5 (RPKM 6.6) and 9 other tissuesSee 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
Cenpk-202	ENSMUST00000070761.9	1306	253aa	Protein coding	CCDS26750	Q9ESN5	TSL:1 GENCODE basic
Cenpk-201	ENSMUST00000022227.7	1217	306aa	Protein coding	CCDS26749	A0A0R4J037	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
Cenpk-207	ENSMUST00000225557.1	351	94aa	Protein coding	-	A0A286YDG4	CDS 3' incomplete
Cenpk-205	ENSMUST00000224500.1	1353	91aa	Nonsense mediated decay	-	A0A286YE26	
Cenpk-206	ENSMUST00000224857.1	856	91aa	Nonsense mediated decay	-	A0A286YE26	
Cenpk-203	ENSMUST00000224098.1	1404	No protein	Processed transcript	-	-	
Cenpk-204	ENSMUST00000224179.1	2077	No protein	Retained intron	-	-	
Cenpk-208	ENSMUST00000225939.1	409	No protein	Retained intron	-	-	

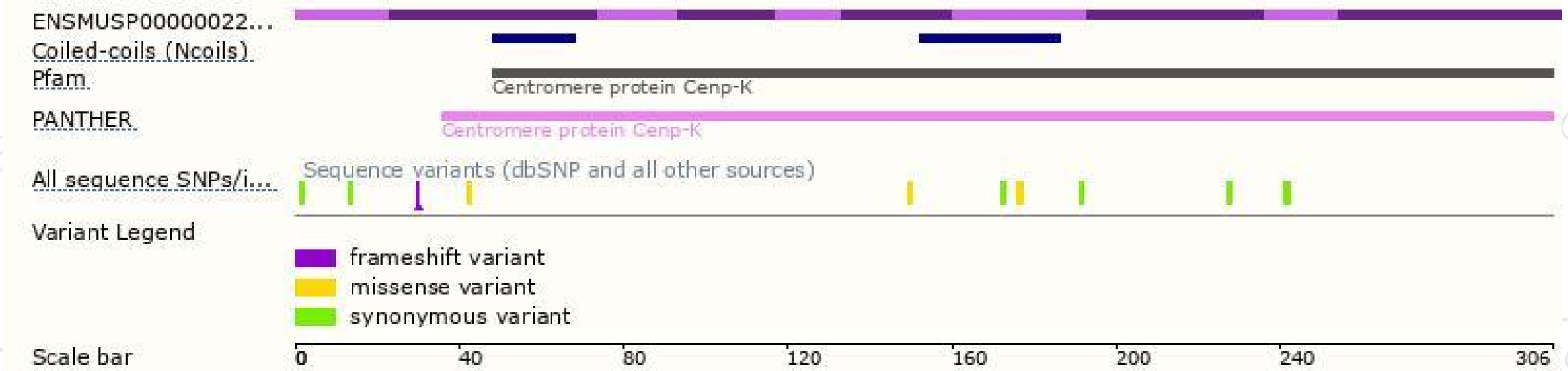The strategy is based on the design of *Cenpk-201* transcript,the transcription is shown below:

Genomic location distribution

Protein domain

ENSMUSP00000022...						
Coiled-coils (Ncoils)						
Pfam.	Centromere protein Cenp-K					
PANTHER	Centromere protein Cenp-K					
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)					
Variant Legend						

frameshift variant
missense variant
synonymous variant

Scale bar 0   40   80   120   160   200   240   306

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