

Cenpi Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Cenpi

Project type

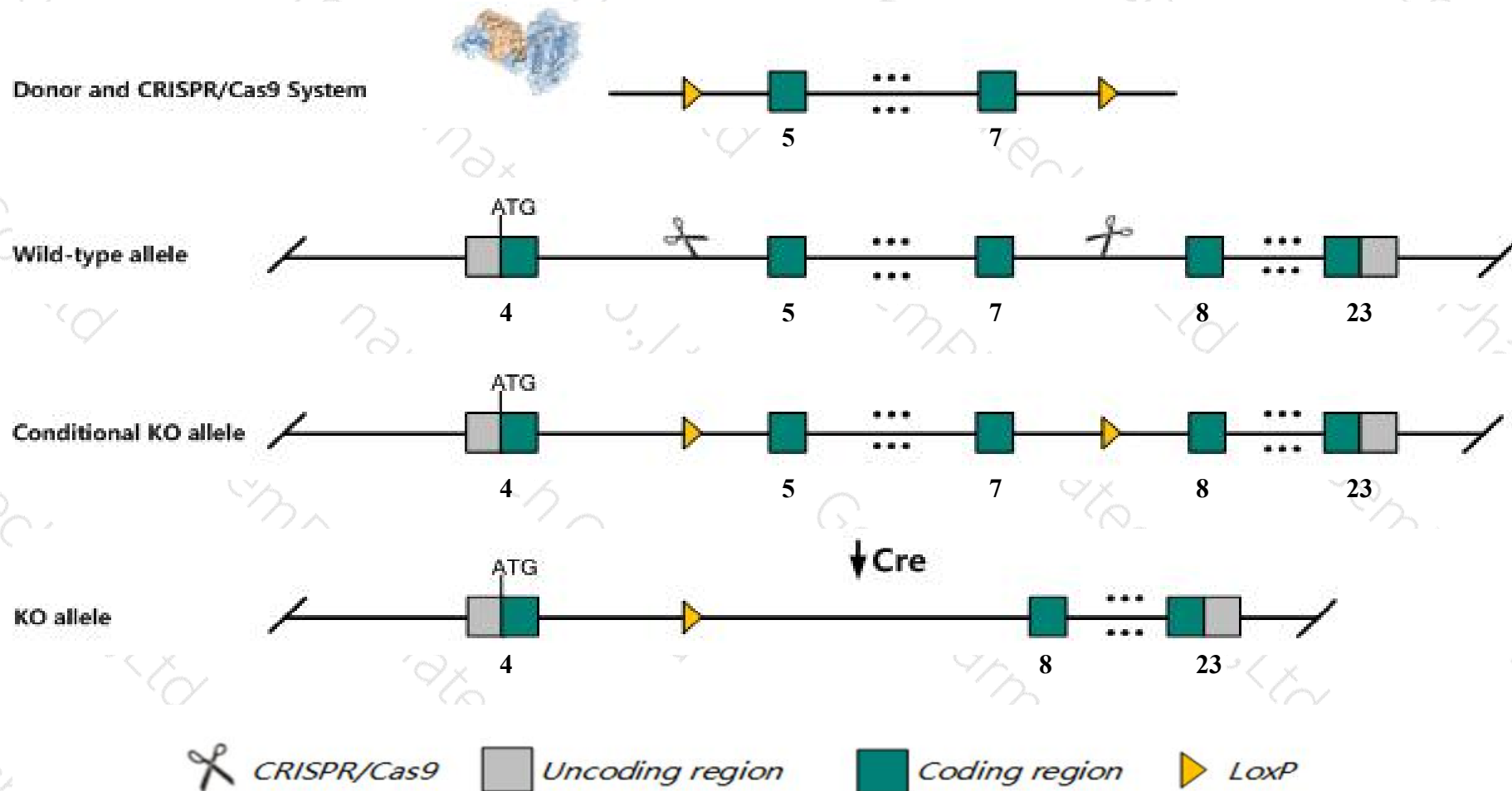
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Cenpi* gene has 5 transcripts. According to the structure of *Cenpi* gene, exon5-exon7 of *Cenpi*-201 (ENSMUST00000081064.11) transcript is recommended as the knockout region. The region contains 365bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cenpi* 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.

- Transcript 203 may not be affected. The effect of transcript 204 is unknown.
- The *Cenpi* gene is located on the ChrX. 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)

Cenpi centromere protein I [Mus musculus (house mouse)]

Gene ID: 102920, updated on 13-Mar-2020

Summary



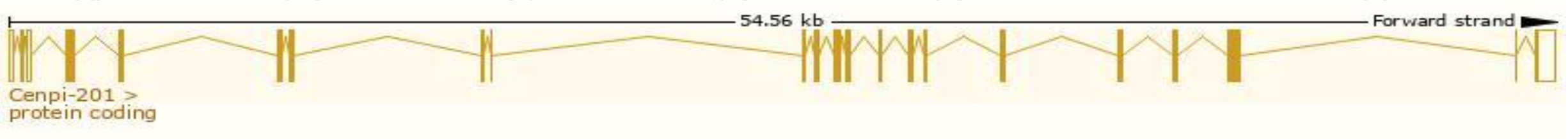
Official Symbol	Cenpi provided by MGI
Official Full Name	centromere protein I provided by MGI
Primary source	MGI:MGI:2147897
See related	Ensembl:ENSMUSG000000031262
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CENP-I, Fshprh1
Summary	This gene encodes a protein that may be constitutively associated with centromeres and might be involved in recruiting centromere protein A to the centromere for kinetochore assembly. A similar gene in human is involved in the response of gonadal tissues to follicle-stimulating hormone. Alternatively spliced transcript variants have been identified. [provided by RefSeq, Mar 2015]
Expression	Biased expression in liver E14 (RPKM 5.1), liver E14.5 (RPKM 4.7) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

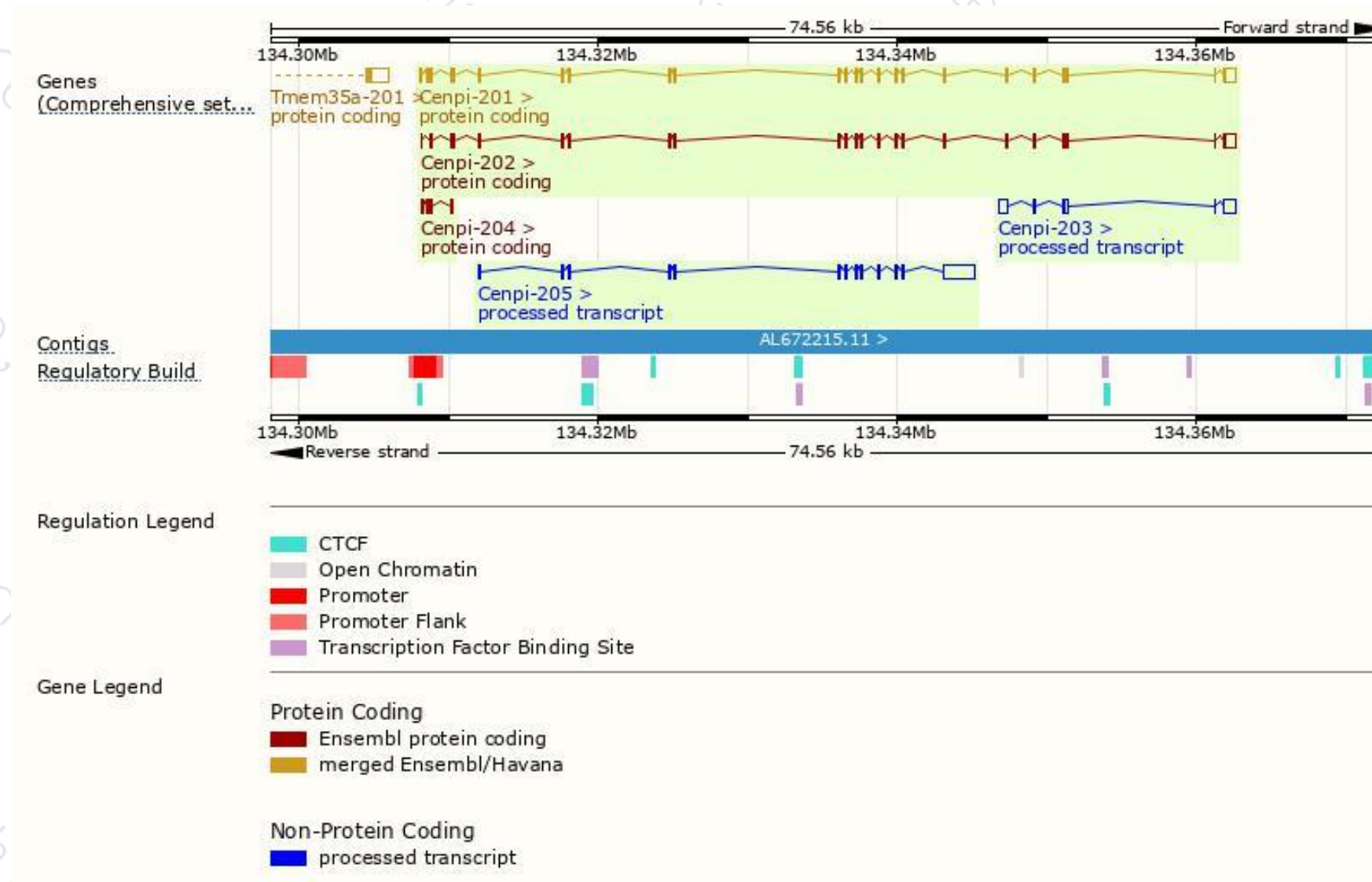
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cenpi-201	ENSMUST00000081064.11	3227	746aa	Protein coding	CCDS30393	Q8K1K4	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
Cenpi-202	ENSMUST00000101251.7	3085	746aa	Protein coding	CCDS30393	Q8K1K4	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
Cenpi-204	ENSMUST00000129782.1	398	31aa	Protein coding	-	B1AV88	CDS 3' incomplete TSL:2
Cenpi-205	ENSMUST00000144678.1	3309	No protein	Processed transcript	-	-	TSL:1
Cenpi-203	ENSMUST00000125604.1	1728	No protein	Processed transcript	-	-	TSL:1

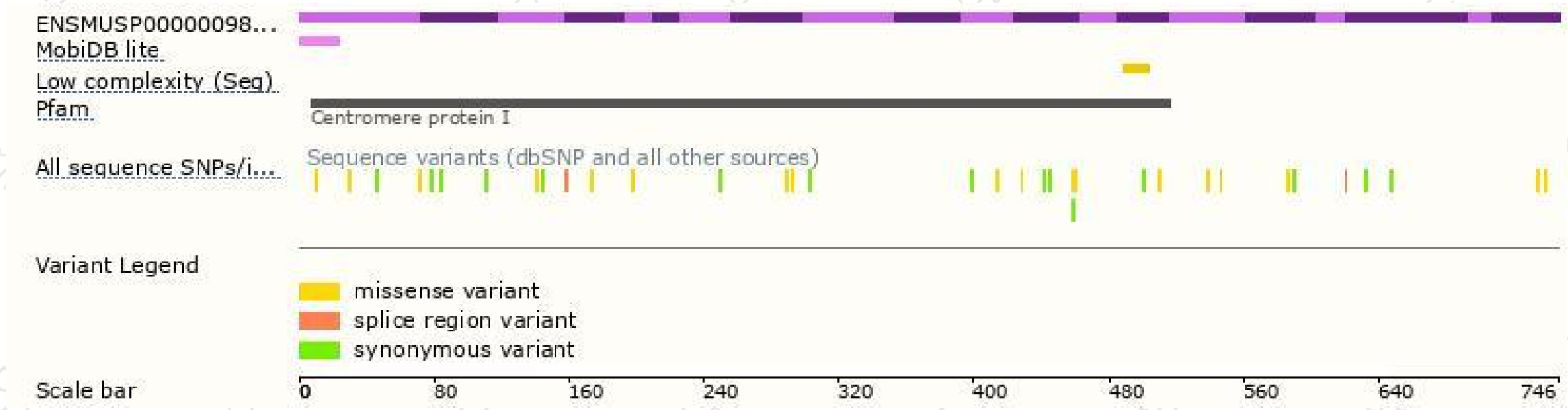
The strategy is based on the design of *Cenpi-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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