Cenpc1 Cas9-KO Strategy

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Reviewer: Xueting Zhang

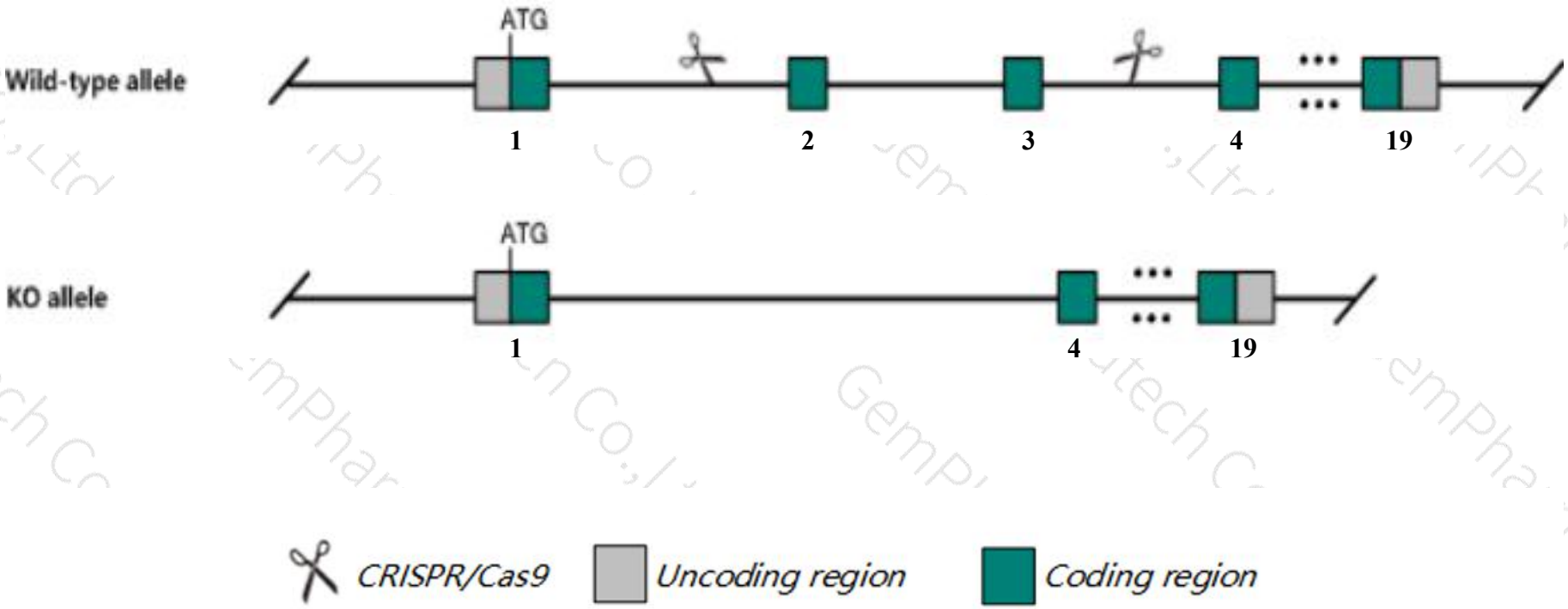
Design Date: 2020-5-6

Project Overview

Project Name	***Cenpc1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cenpc1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cenpc1* gene has 4 transcripts. According to the structure of *Cenpc1* gene, exon2-exon3 of *Cenpc1-201* (ENSMUST00000031170.9) transcript is recommended as the knockout region.The region contains 136bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cenpc1* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

- According to the existing MGI data,homozygous mutation of this gene results in early embryonic lethality and mitotic abnormalities.
- The *Cenpc1* 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）

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Cenpc1 centromere protein C1 [Mus musculus (house mouse)]

Gene ID: 12617, updated on 13-Mar-2020

Summary

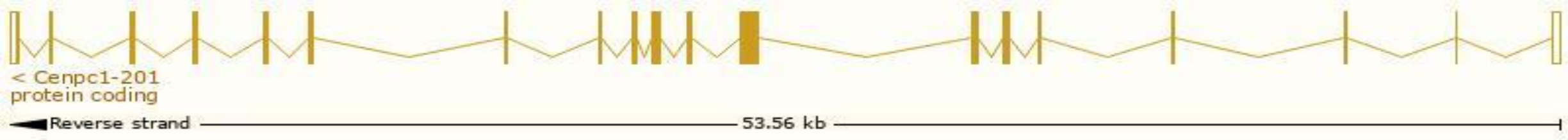
Official Symbol	Cenpc1 provided by MGI
Official Full Name	centromere protein C1 provided byMGI
Primary source	MGI:MGI:99700
See related	Ensembl:ENSMUSG00000029253
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CENP-C, Cenpc
Summary	This gene encodes a centromeric protein component of a nucleosome-associated complex that plays a central role in kinetochore protein assembly, mitotic progression and chromosome segregation. The human ortholog encodes a protein with DNA-binding activity, that associates constitutively to kinetochores throughout the cell cycle, as part of a prekinetochore complex, together with centromeric protein-A and centromeric protein-B. Multiple pseudogenes of this gene have been identified. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2016]
Expression	Broad expression in CNS E11.5 (RPKM 7.5), CNS E14 (RPKM 5.7) and 24 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

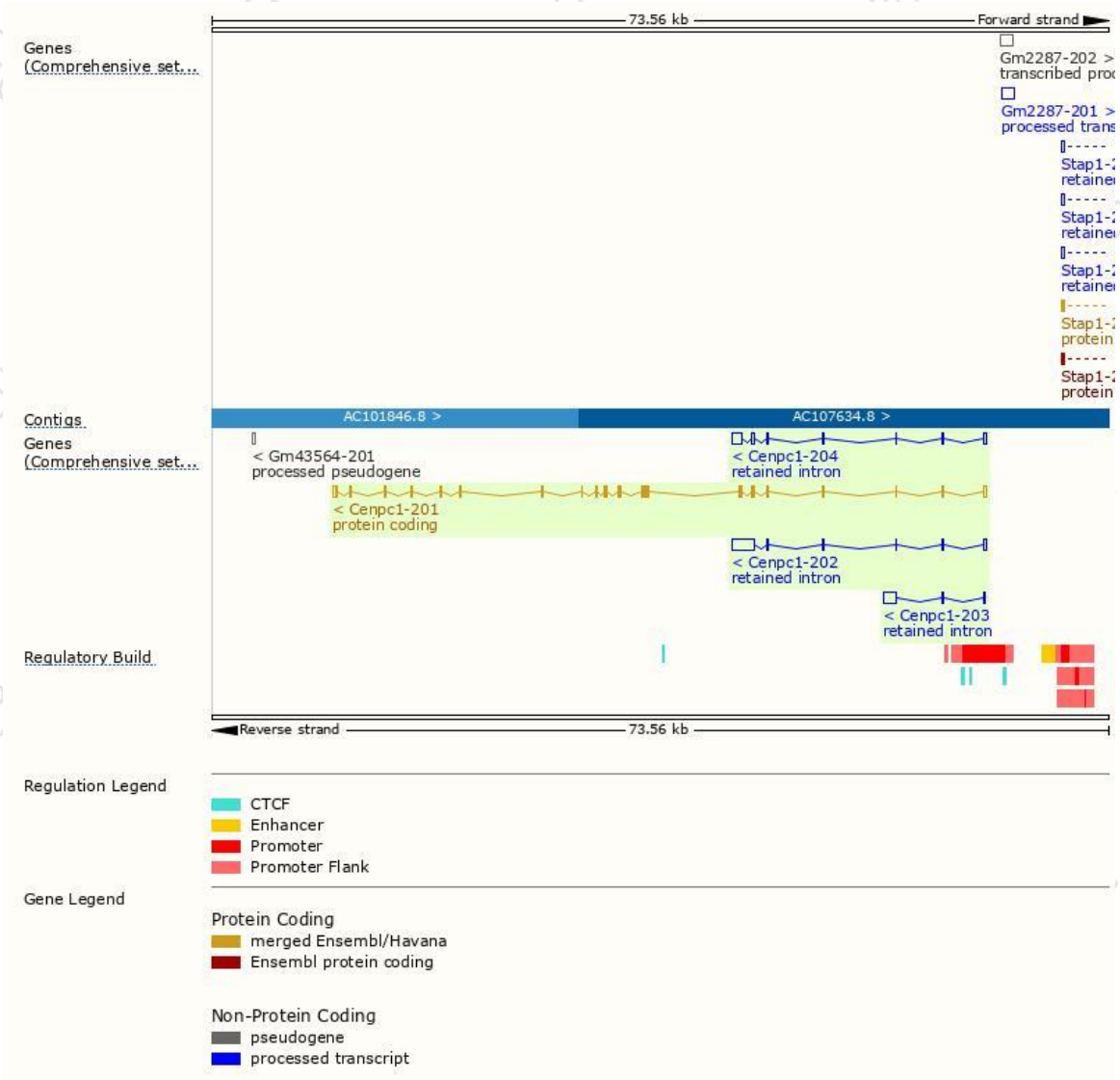
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cenpc1-201	ENSMUST00000031170.9	3192	906aa	Protein coding	CCDS39123	P49452	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
Cenpc1-202	ENSMUST00000198059.4	2341	No protein	Retained intron	-	-	TSL:2
Cenpc1-204	ENSMUST00000199392.4	1469	No protein	Retained intron	-	-	TSL:2
Cenpc1-203	ENSMUST00000199141.1	1370	No protein	Retained intron	-	-	TSL:2

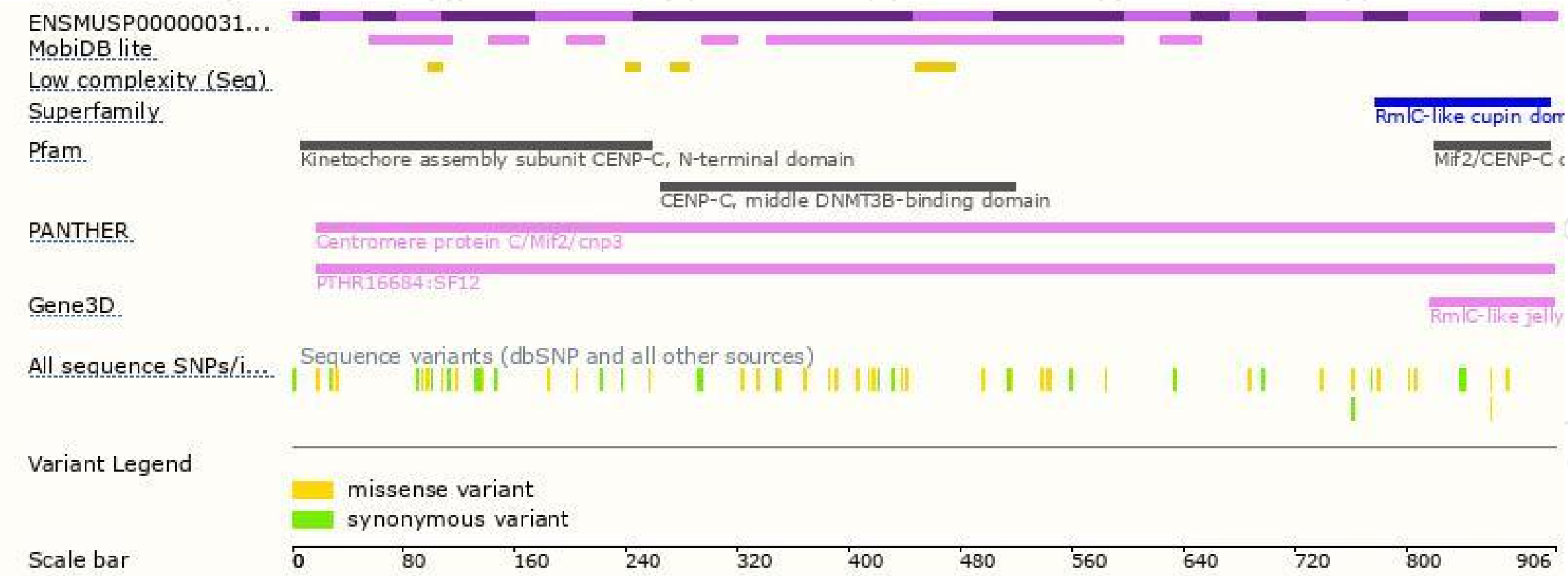
The strategy is based on the design of *Cenpc1-201* transcript,the transcription is shown below:



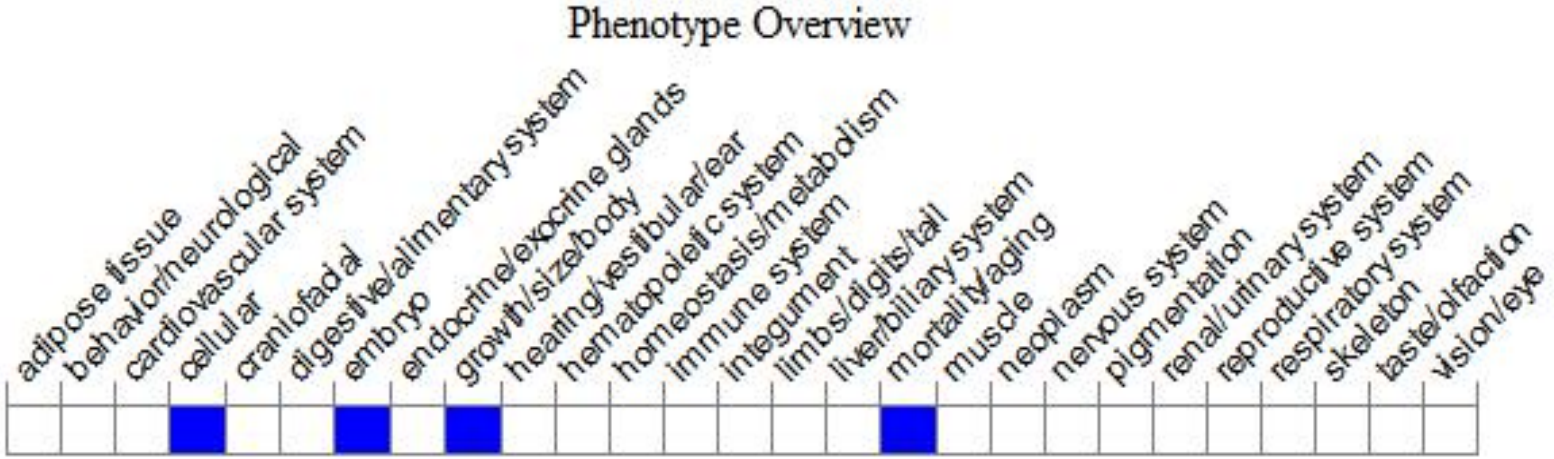
Genomic location distribution



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 early embryonic lethality and mitotic abnormalities.

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

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