

# ***Incenp*** Cas9-CKO Strategy

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# Project Overview

**Project Name**

***Incenp***

**Project type**

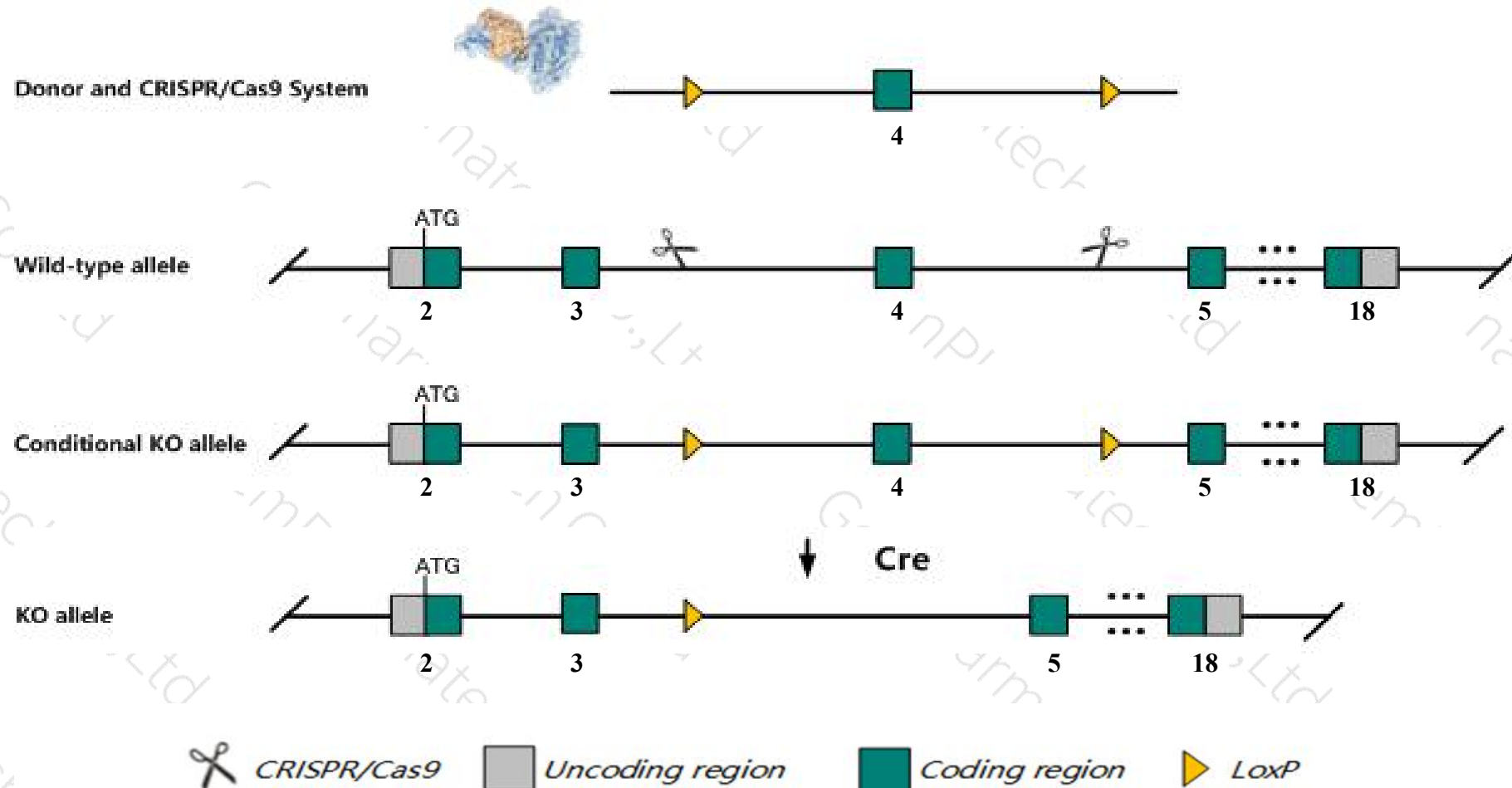
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Incenp* gene has 9 transcripts. According to the structure of *Incenp* gene, exon4 of *Incenp-201* (ENSMUST00000025562.8) transcript is recommended as the knockout region. The region contains 737bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Incenp* 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.

- According to the existing MGI data, Homozygous mutant embryos die before E8.5. Embryonic cells exhibit abnormal nuclei and aberrant mitosis.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- Transcript 202,203,206 may not be affected. The effect of transcripts 204,207,208 is unknown.
- The *Incenp* gene is located on the Chr19. 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)

## Incenp inner centromere protein [ *Mus musculus* (house mouse) ]

Gene ID: 16319, updated on 24-Oct-2019

### Summary



Official Symbol	Incenp provided by <a href="#">MGI</a>
Official Full Name	inner centromere protein provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1313288</a>
See related	<a href="#">Ensembl:ENSMUSG00000024660</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C77457; AU019509; C130081E20; 2700067E22Rik
Expression	Broad expression in liver E14 (RPKM 26.8), CNS E11.5 (RPKM 25.6) and 19 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context



Location: 19 A; 19 6.1 cM

Exon count: 20

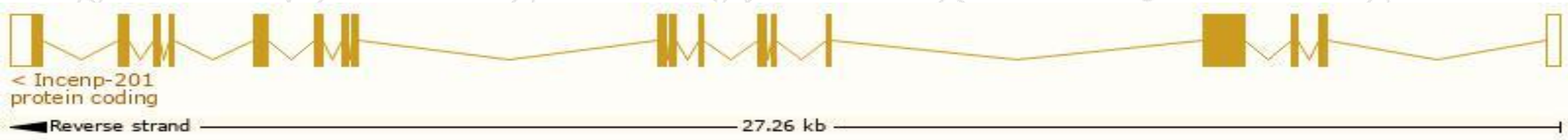
See Incenp in [Genome Data Viewer](#)

# Transcript information (Ensembl)

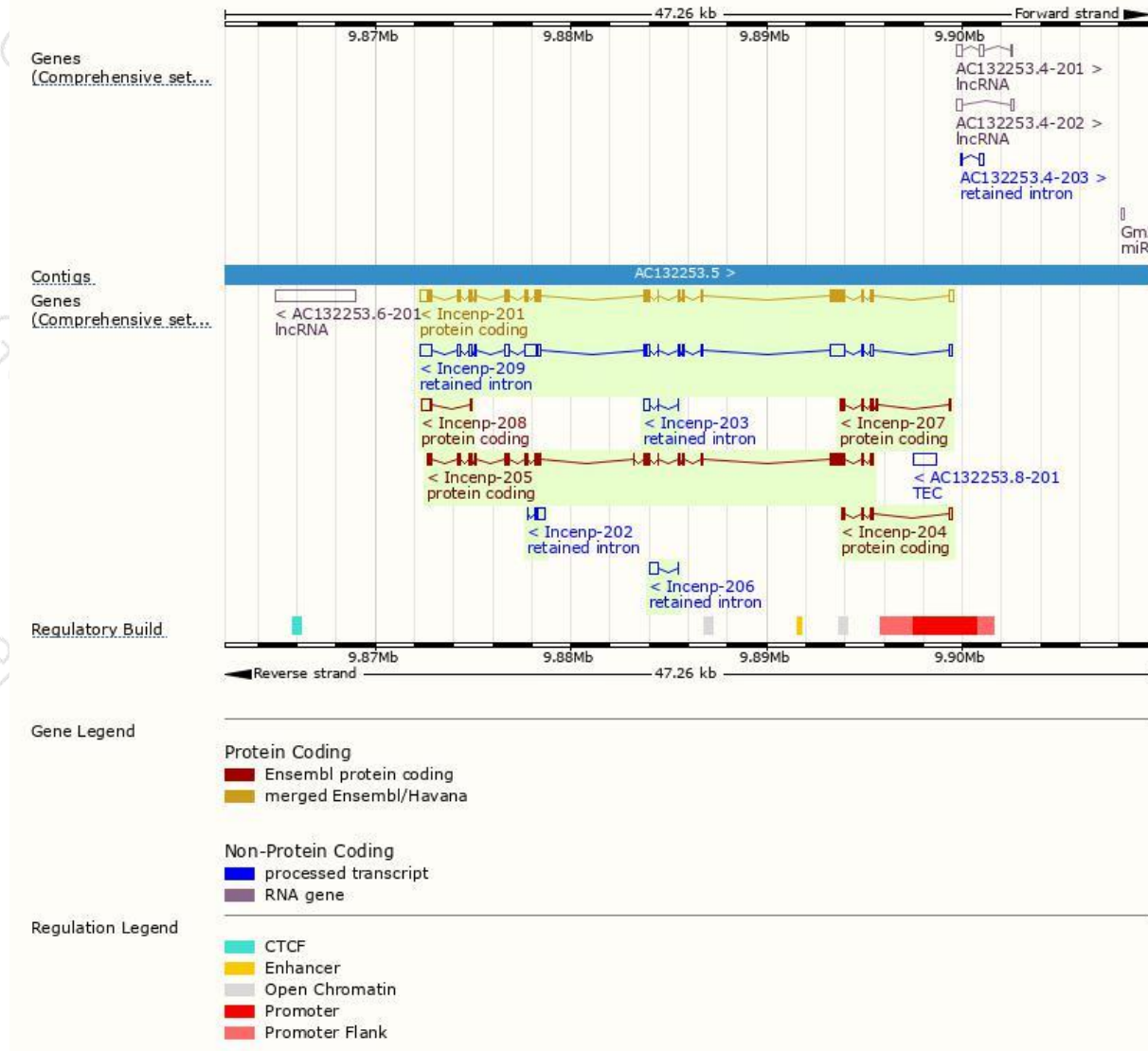
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Incenp-201	<a href="#">ENSMUST00000025562.8</a>	3236	<a href="#">876aa</a>	Protein coding	<a href="#">CCDS37912</a>	<a href="#">Q9WU62</a>	TSL:1 GENCODE basic APPRIS P2
Incenp-205	<a href="#">ENSMUST00000237439.1</a>	2643	<a href="#">880aa</a>	Protein coding	-	-	GENCODE basic APPRIS ALT2
Incenp-207	<a href="#">ENSMUST00000237725.1</a>	637	<a href="#">172aa</a>	Protein coding	-	-	CDS 3' incomplete
Incenp-208	<a href="#">ENSMUST00000238004.1</a>	577	<a href="#">33aa</a>	Protein coding	-	-	CDS 5' incomplete
Incenp-204	<a href="#">ENSMUST00000237147.1</a>	574	<a href="#">138aa</a>	Protein coding	-	-	CDS 3' incomplete
Incenp-209	<a href="#">ENSMUST00000238129.1</a>	3449	No protein	Retained intron	-	-	
Incenp-206	<a href="#">ENSMUST00000237655.1</a>	489	No protein	Retained intron	-	-	
Incenp-202	<a href="#">ENSMUST00000235358.1</a>	478	No protein	Retained intron	-	-	
Incenp-203	<a href="#">ENSMUST00000236533.1</a>	349	No protein	Retained intron	-	-	

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

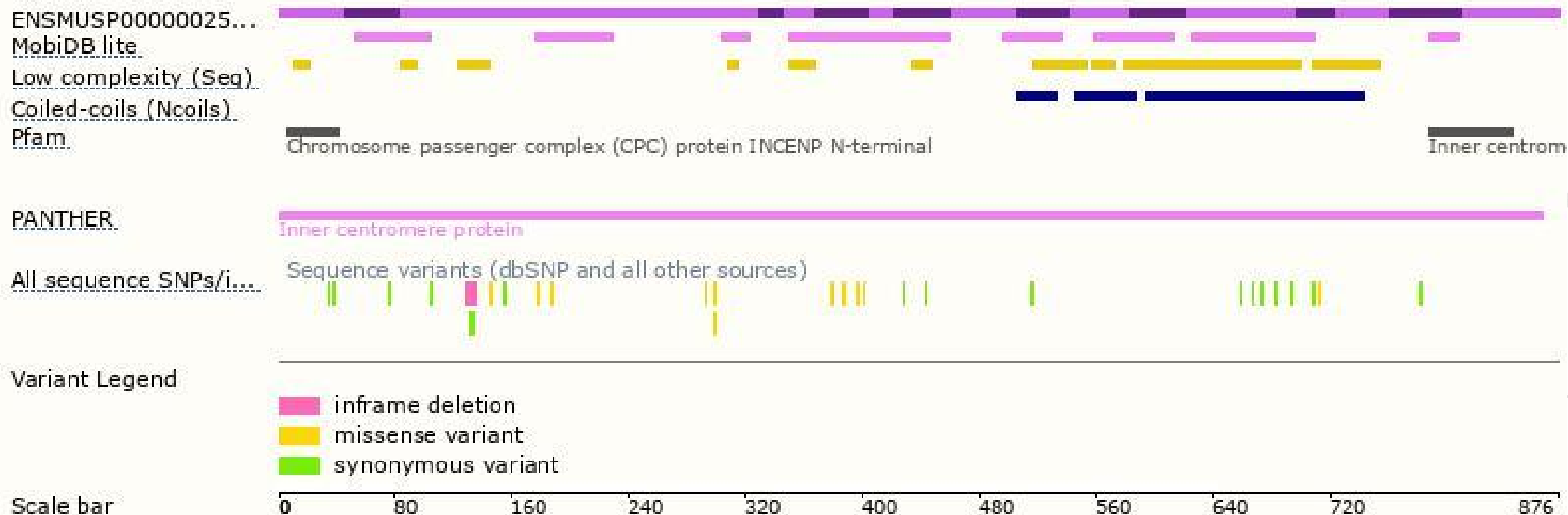


# Genomic location distribution

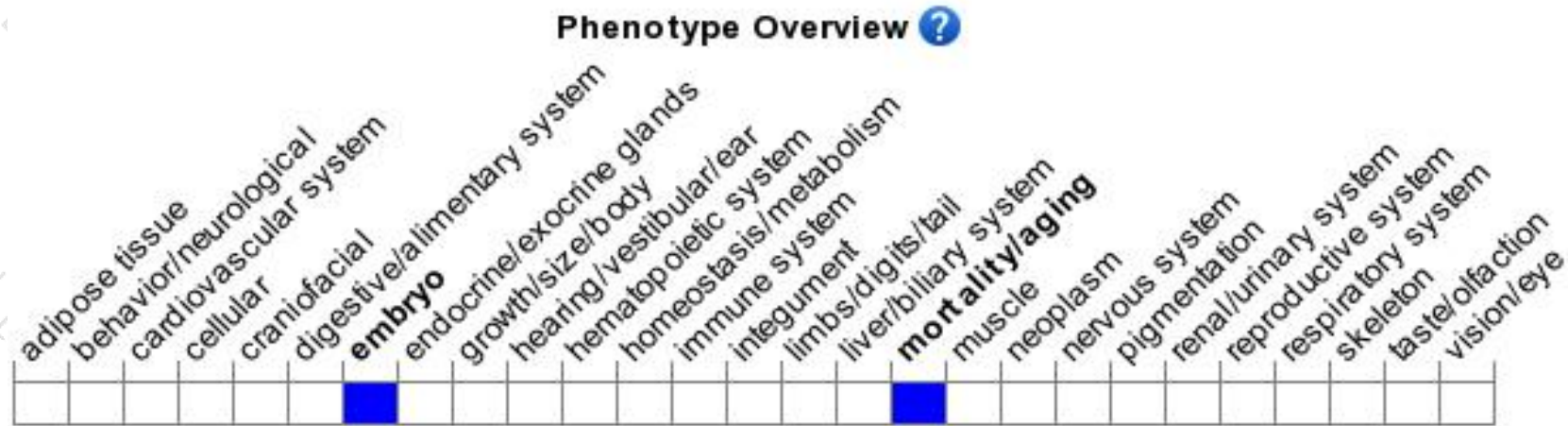




# Protein domain



# 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 mutant embryos die before E8.5. Embryonic cells exhibit abnormal nuclei and aberrant mitosis.

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

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