

# *Cdc45* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Cdc45***

**Project type**

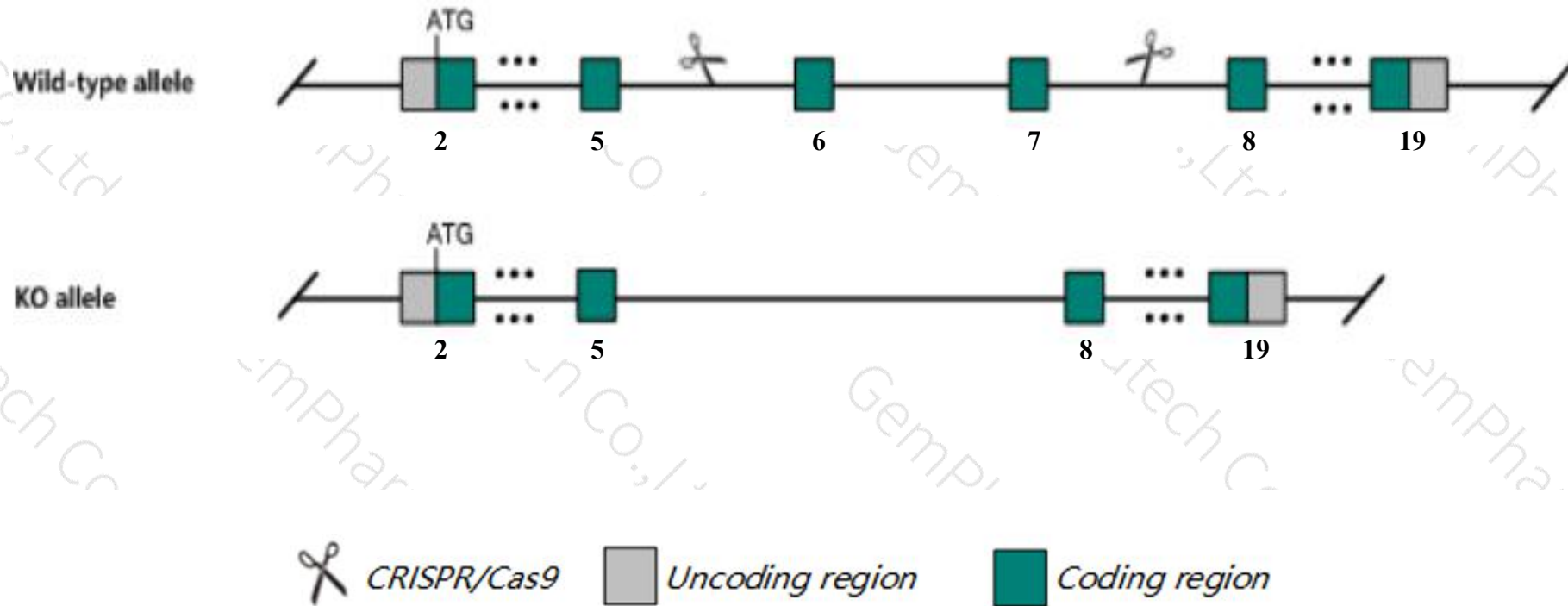
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cdc45* gene. The schematic diagram is as follows:



- The *Cdc45* gene has 4 transcripts. According to the structure of *Cdc45* gene, exon6-exon7 of *Cdc45-201*(ENSMUST00000000028.13) transcript is recommended as the knockout region. The region contains 200bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cdc45* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous mutant embryos do not develop after implantation, resulting in embryonic lethality between E4.5-E5.5. Heterozygous animals appear normal and fertile.
- The *Cdc45* gene is located on the Chr16. 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)

## Cdc45 cell division cycle 45 [Mus musculus (house mouse)]

Gene ID: 12544, updated on 13-Mar-2020

### Summary



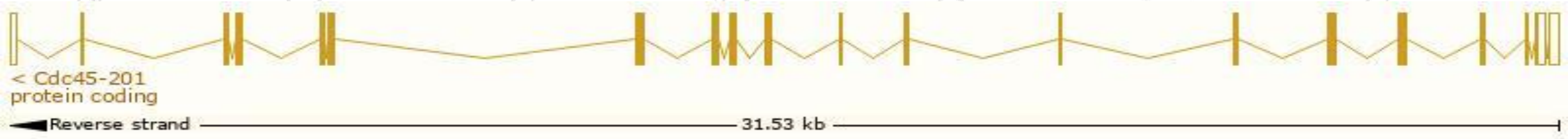
Official Symbol	Cdc45 provided by <a href="#">MGI</a>
Official Full Name	cell division cycle 45 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1338073</a>
See related	<a href="#">Ensembl:ENSMUSG000000000028</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cdc45l
Expression	Broad expression in liver E14.5 (RPKM 24.8), liver E14 (RPKM 24.1) and 20 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

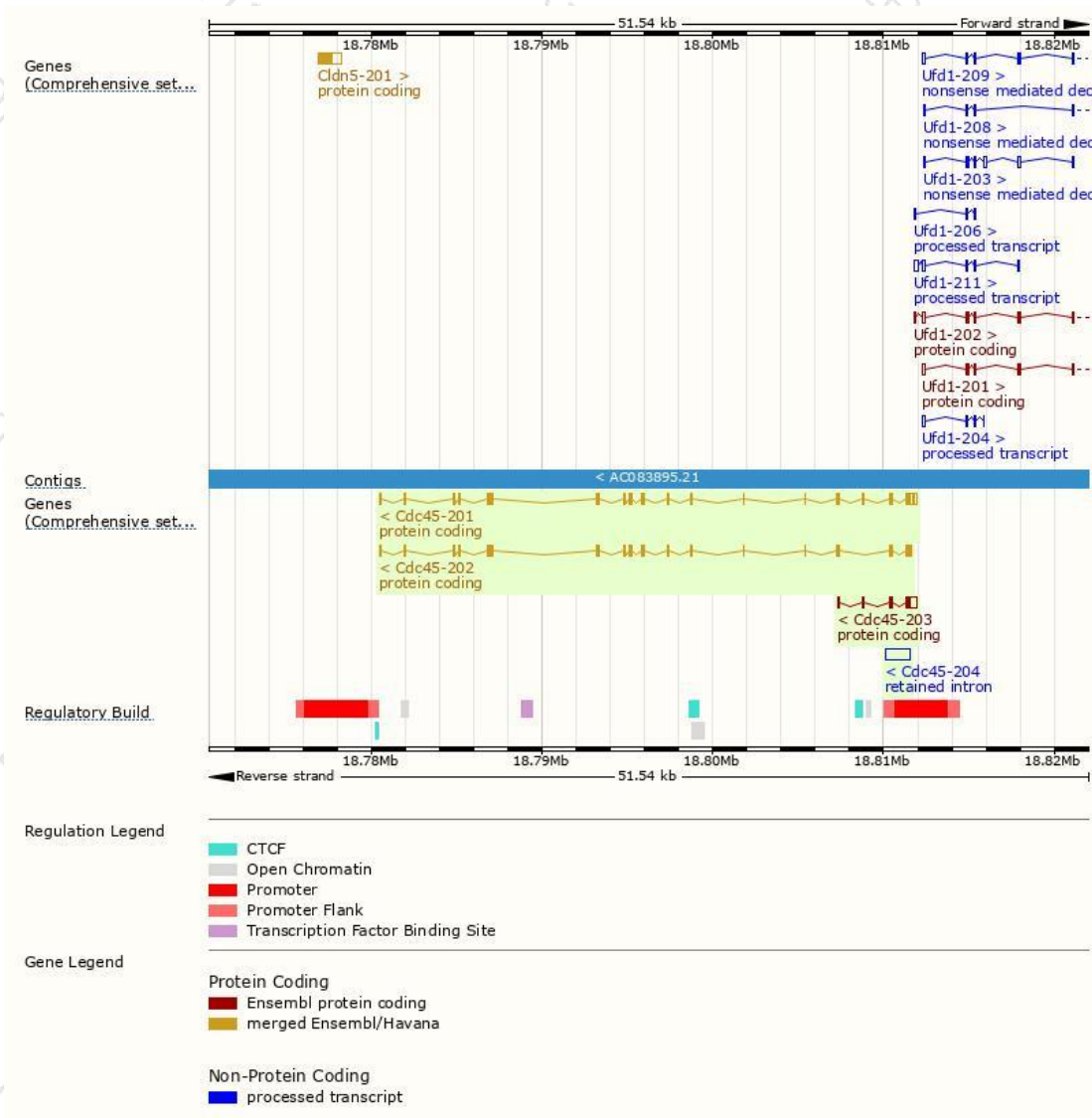
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cdc45-201	<a href="#">ENSMUST0000000028.13</a>	2143	<a href="#">566aa</a>	Protein coding	<a href="#">CCDS28027</a>	<a href="#">Q3UI99 Q9Z1X9</a>	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
Cdc45-202	<a href="#">ENSMUST00000096990.9</a>	1747	<a href="#">520aa</a>	Protein coding	<a href="#">CCDS49788</a>	<a href="#">F8WJ72</a>	TSL:1 GENCODE basic
Cdc45-203	<a href="#">ENSMUST00000115585.1</a>	832	<a href="#">136aa</a>	Protein coding	-	<a href="#">D3Z0L5</a>	CDS 3' incomplete TSL:2
Cdc45-204	<a href="#">ENSMUST00000231819.1</a>	1484	No protein	Retained intron	-	-	

The strategy is based on the design of *Cdc45-201* transcript,the transcription is shown below:

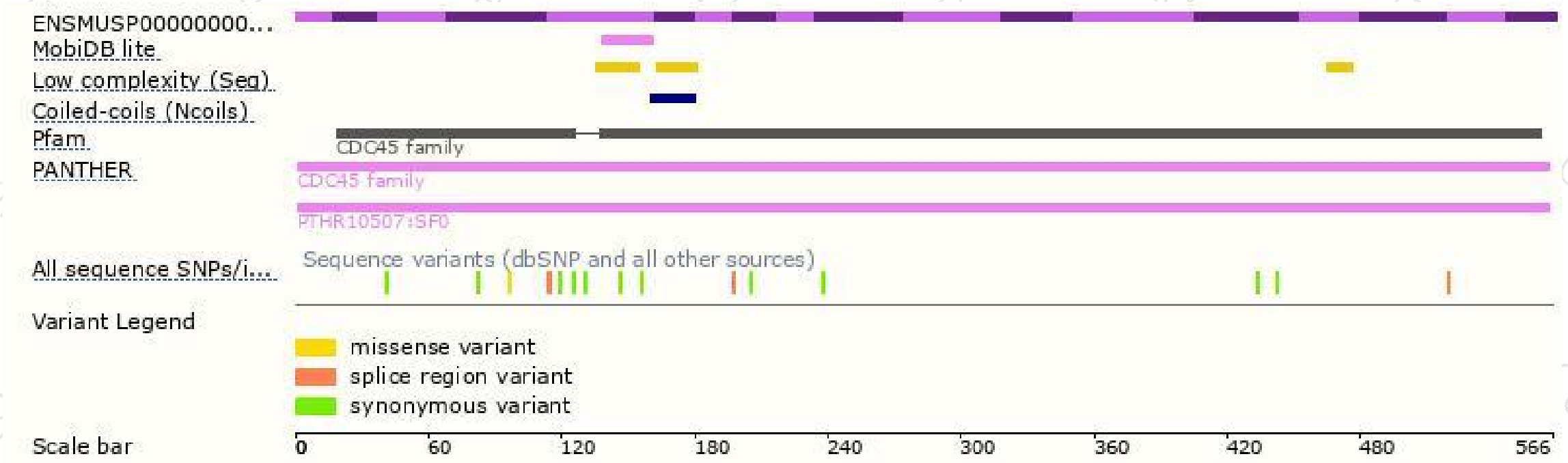


# Genomic location distribution

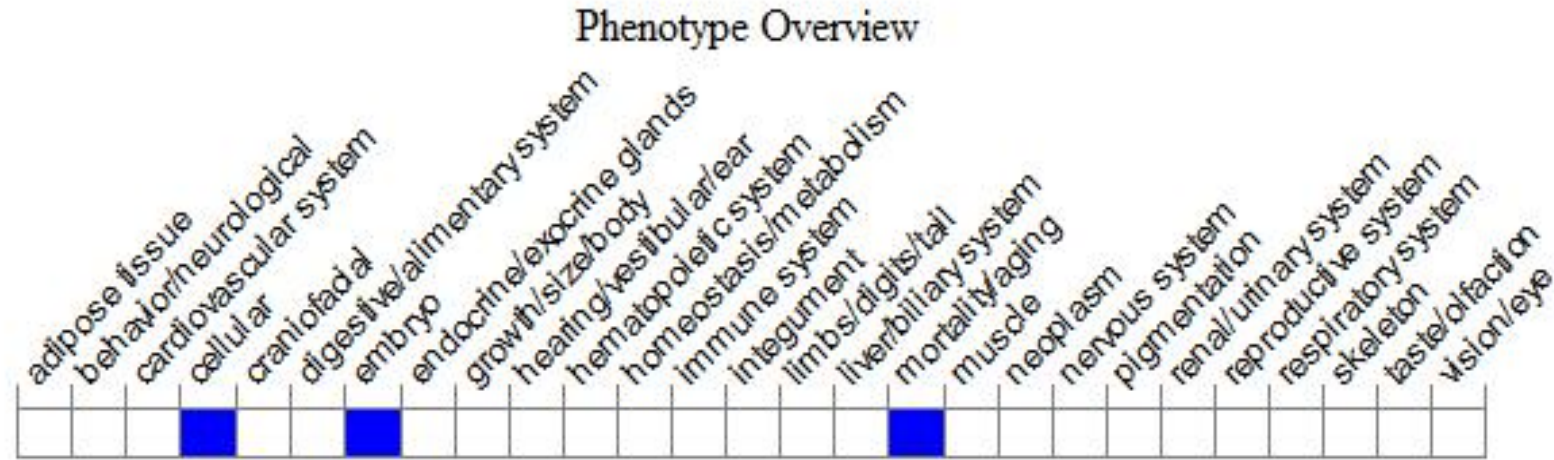




# Protein domain



# 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 do not develop after implantation, resulting in embryonic lethality between E4.5-E5.5. Heterozygous animals appear normal and fertile.

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

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