

# ***Dclk2 Cas9-CKO Strategy***

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**Reviewer:**

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**Design Date:**

**2020-2-13**

# Project Overview

**Project Name**

***Dclk2***

**Project type**

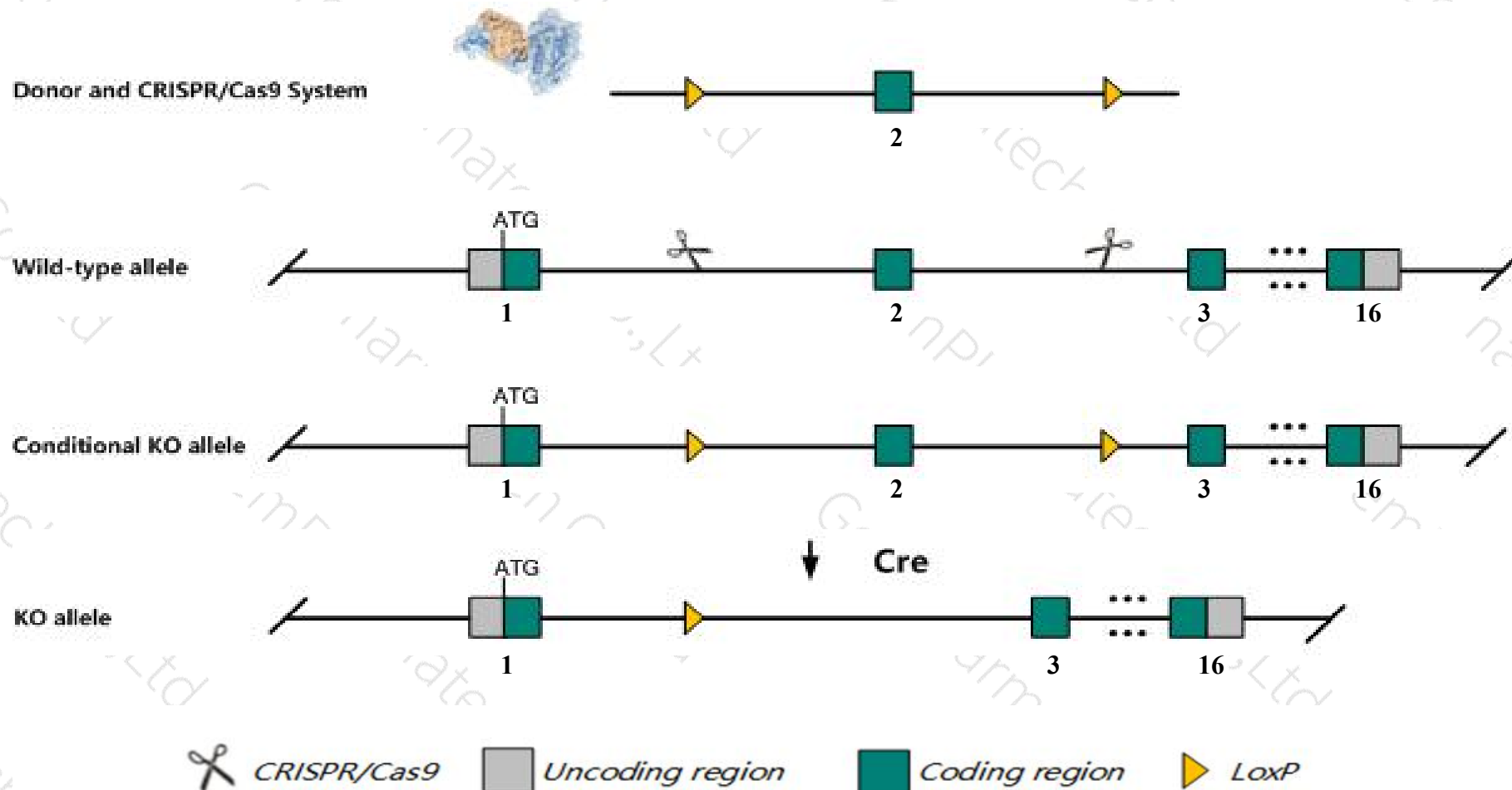
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dclk2* gene. The schematic diagram is as follows:



- The *Dclk2* gene has 9 transcripts. According to the structure of *Dclk2* gene, exon2 of *Dclk2-201* (ENSMUST00000029719.13) transcript is recommended as the knockout region. The region contains 332bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dclk2* 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.

# Notice

- The *Dclk2* gene is located on the Chr3. 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)

## Dclk2 doublecortin-like kinase 2 [ *Mus musculus* (house mouse) ]

Gene ID: 70762, updated on 9-Feb-2020

### Summary

**Official Symbol** Dclk2 provided by [MGI](#)

**Official Full Name** doublecortin-like kinase 2 provided by [MGI](#)

**Primary source** [MGI:MGI:1918012](#)

**See related** [Ensembl:ENSMUSG00000028078](#)

**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** CL2; CLICK2; Dcamk2; AU044875; Click-II; 6330415M09Rik

**Summary** This gene encodes a member of the protein kinase superfamily and the doublecortin family. The protein encoded by this gene contains two N-terminal doublecortin domains, which bind microtubules and regulate microtubule polymerization, a C-terminal serine/threonine protein kinase domain, which shows substantial homology to Ca<sup>2+</sup>/calmoduline-dependent protein kinase, and a serine/proline-rich domain in between the doublecortin and the protein kinase domains, which mediates multiple protein-protein interactions. The microtubule-polymerizing activity of the encoded protein is independent of its protein kinase activity. This gene and the DCX gene, another family member, share function in the establishment of hippocampal organization and their absence results in a severe epileptic phenotype and lethality, as described in human patients with lissencephaly. Multiple alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Sep 2010]

**Expression** Biased expression in whole brain E14.5 (RPKM 41.0), CNS E14 (RPKM 37.3) and 11 other tissues [See more](#)

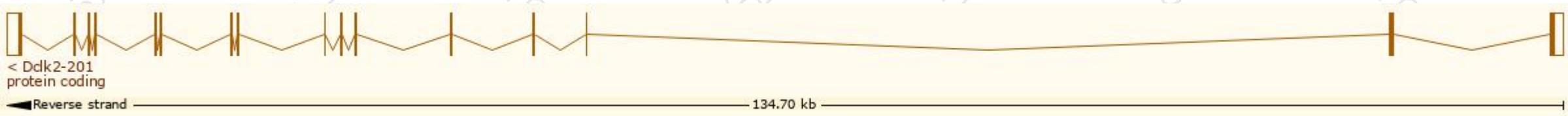
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

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

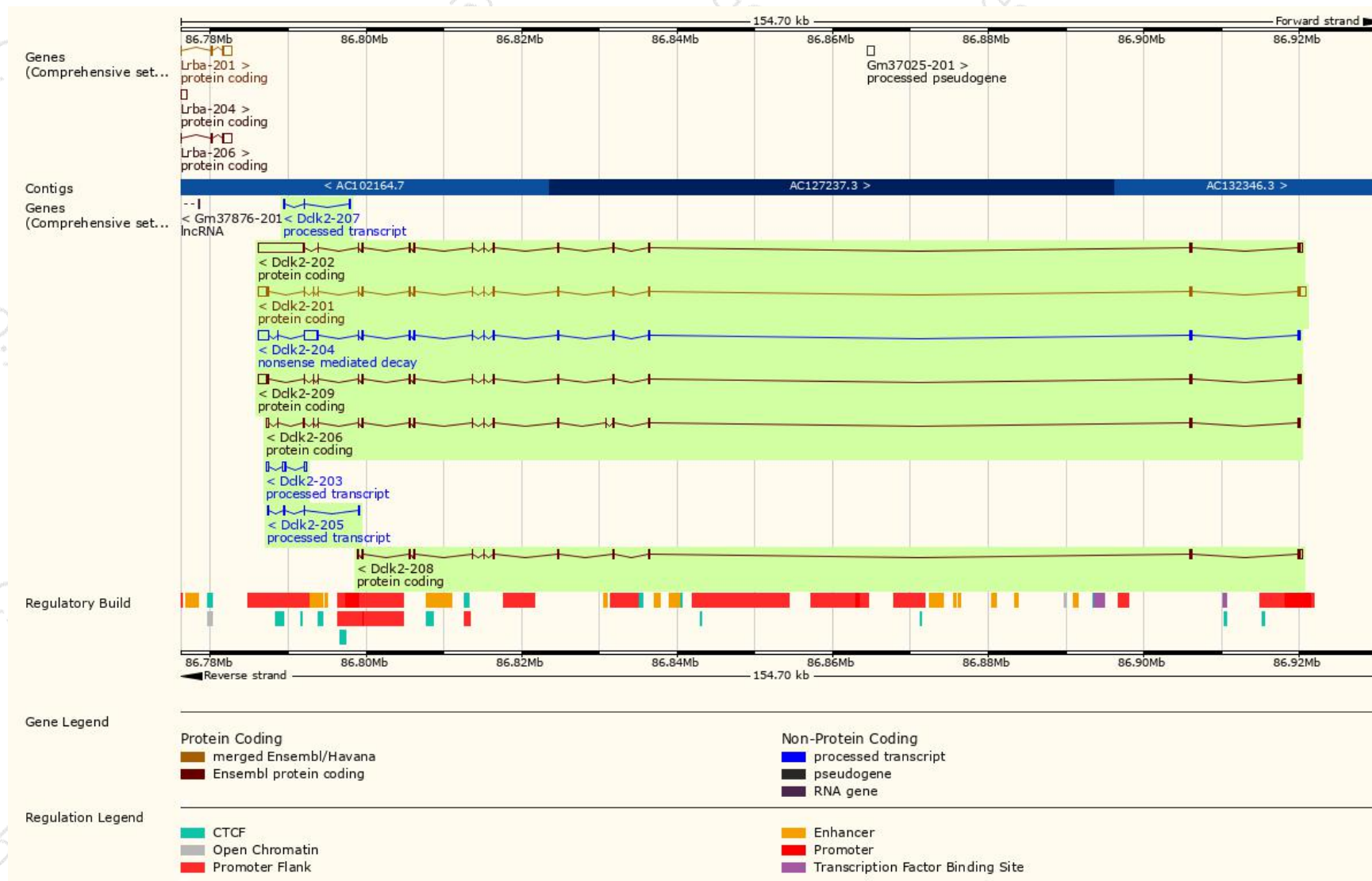
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dclk2-201	<a href="#">ENSMUST00000029719.13</a>	4012	<a href="#">756aa</a>	Protein coding	<a href="#">CCDS17448</a>	<a href="#">Q6PGN3</a>	TSL:1 GENCODE basic APPRIS P3
Dclk2-209	<a href="#">ENSMUST00000195561.5</a>	3486	<a href="#">755aa</a>	Protein coding	<a href="#">CCDS79936</a>	<a href="#">Q6PGN3</a>	TSL:1 GENCODE basic APPRIS ALT2
Dclk2-208	<a href="#">ENSMUST00000194452.1</a>	2066	<a href="#">591aa</a>	Protein coding	<a href="#">CCDS79935</a>	<a href="#">A0A0A6YX33</a>	TSL:1 GENCODE basic
Dclk2-202	<a href="#">ENSMUST00000191752.5</a>	8042	<a href="#">708aa</a>	Protein coding	-	<a href="#">Q6PGN3</a>	TSL:1 GENCODE basic APPRIS ALT2
Dclk2-206	<a href="#">ENSMUST00000193632.5</a>	2336	<a href="#">711aa</a>	Protein coding	-	<a href="#">A0A0A6YX71</a>	TSL:5 GENCODE basic APPRIS ALT2
Dclk2-204	<a href="#">ENSMUST00000192773.5</a>	4908	<a href="#">641aa</a>	Nonsense mediated decay	-	<a href="#">A0A0A6YWI6</a>	TSL:2
Dclk2-203	<a href="#">ENSMUST00000192260.1</a>	715	No protein	Processed transcript	-	-	TSL:3
Dclk2-205	<a href="#">ENSMUST00000193400.5</a>	413	No protein	Processed transcript	-	-	TSL:3
Dclk2-207	<a href="#">ENSMUST00000193769.1</a>	385	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Dclk2-201* transcript, the transcription is shown below:



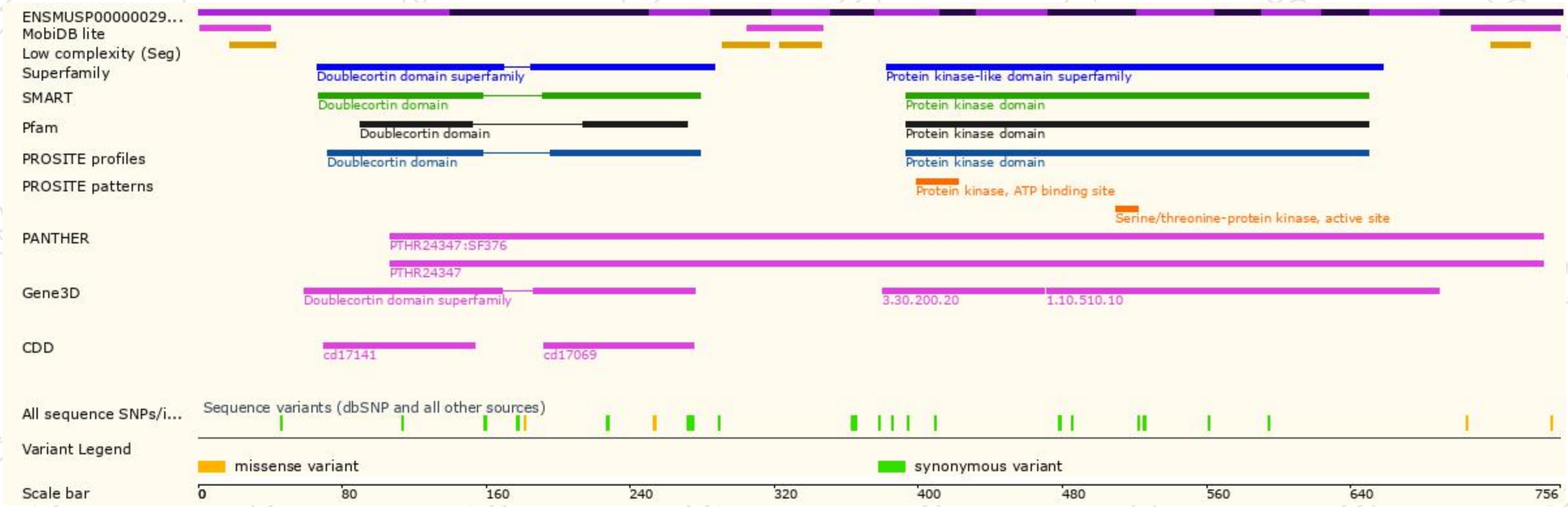


# Genomic location distribution





# Protein domain



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

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