

Dclk2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Dclk2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

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

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

Summary

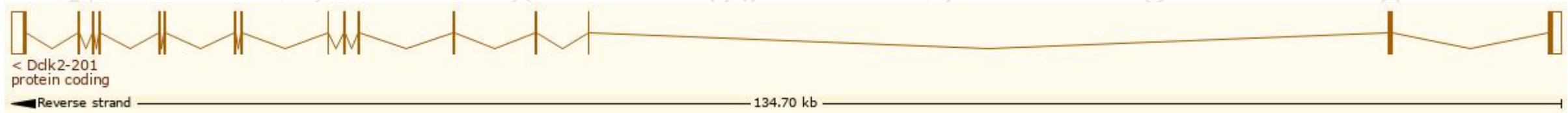
Official Symbol	Dclk2 provided by MGI
Official Full Name	doublecortin-like kinase 2 provided by MGI
Primary source	MGI:MGI:1918012
See related	Ensembl:ENSMUSG00000028078
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 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 ²⁺ /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)

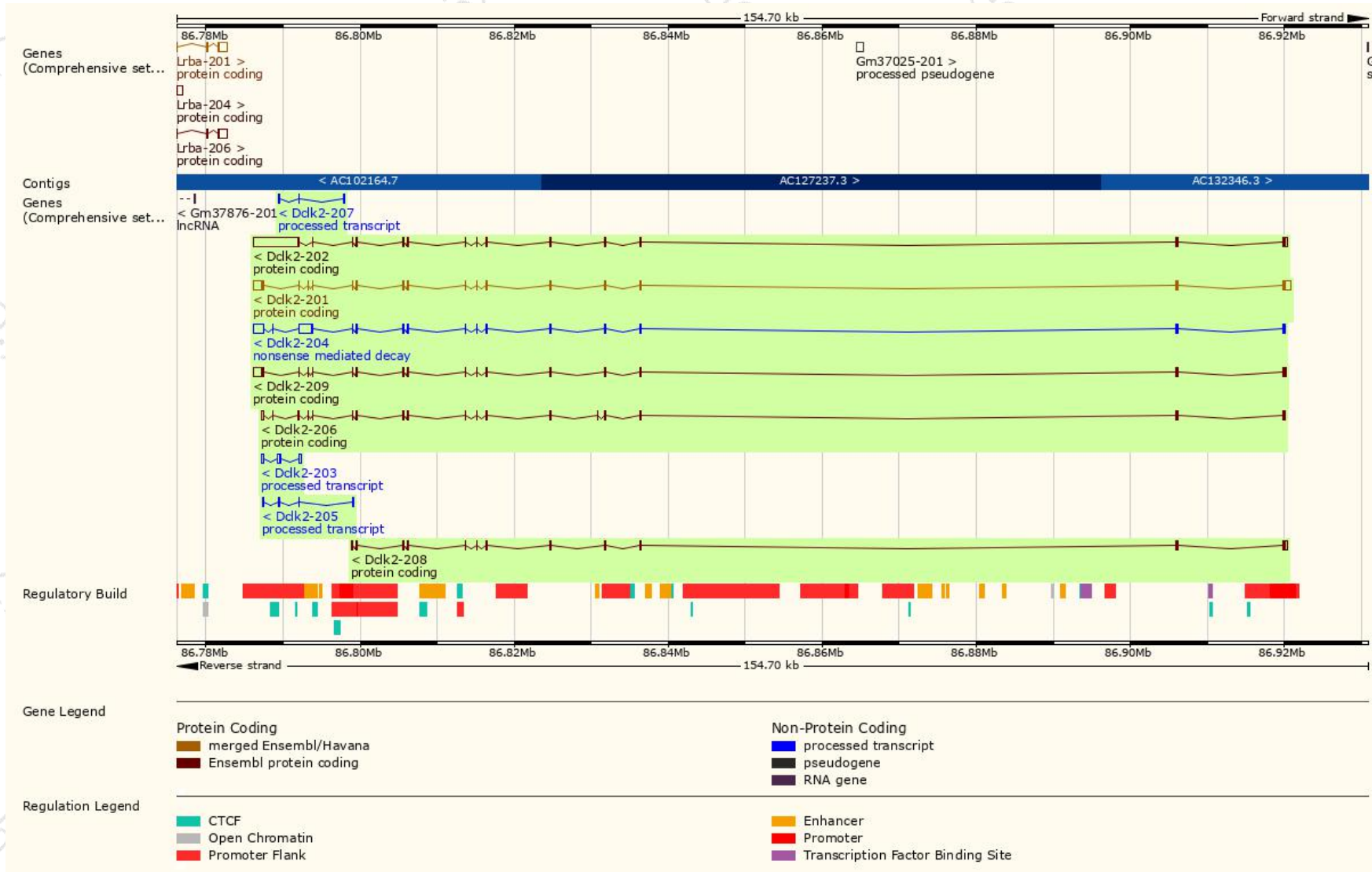
The gene has 9 transcripts,all transcripts are shown below:

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

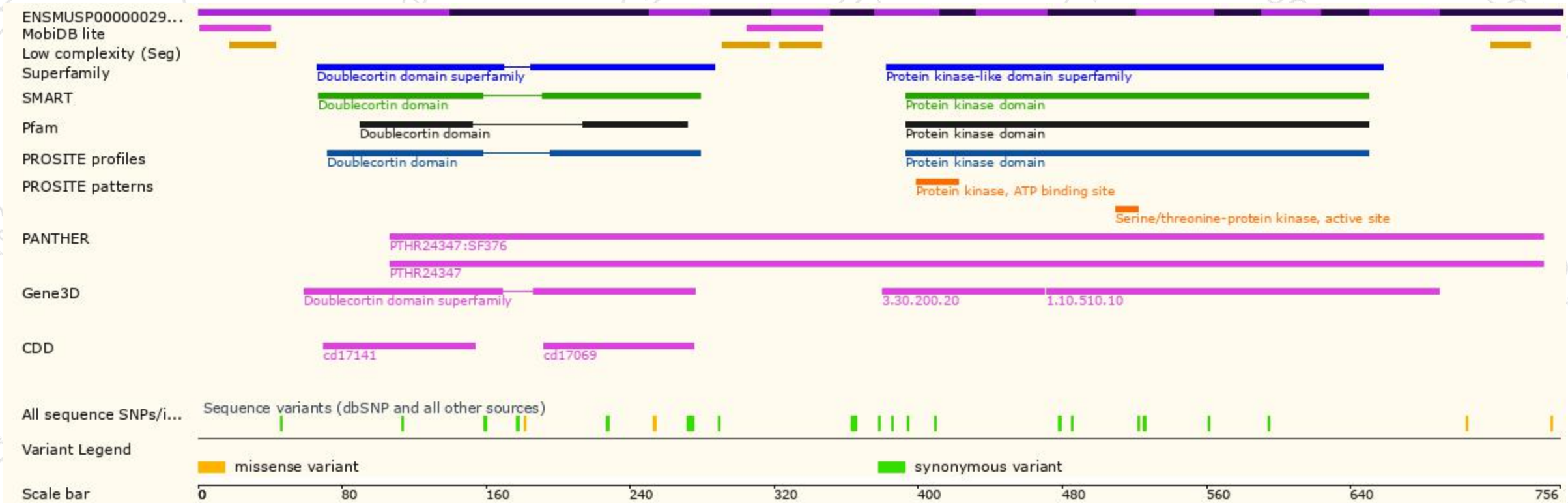
The strategy is based on the design of *Dclk2-201* transcript, the transcription is shown below:



Genomic location distribution



Protein domain



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

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