# *Dgkb* Cas9-KO Strategy

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# Project Overview

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

# Knockout strategy

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

# Technical routes

➢ The *Dgkb* gene has 8 transcripts. According to the structure of *Dgkb* gene, exon3 of *Dgkb-201* (ENSMUST00000040500.8) transcript is recommended as the knockout region.The region contains 77bp coding sequence. Knock out the region will result in disruption of protein function.

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

# Notice

- According to the existing MGI data,Mice homozygous for a transposon distruption have defects in long term potentiation, synapase morphology, and in spatial reference and working memory.

- Transcript 208  CDS 3' incomplete the influences is unknown.

- The *Dgkb* gene is located on the Chr12. 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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## Dgkb diacylglycerol kinase, beta [Mus musculus (house mouse)]

Gene ID: 217480, updated on 19-Mar-2019

### Summary

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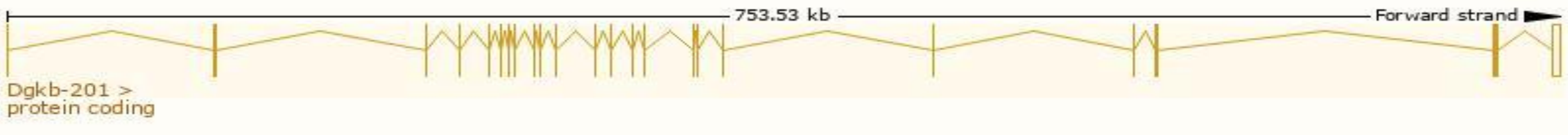
| **Official Symbol** | Dgkb provided by MGI |
| **Official Full Name** | diacylglycerol kinase, beta provided by MGI |
| **Primary source** | MGI:MGI:2442474 |
| **See related** | Ensembl:ENSMUSG00000036095 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | 6430574F24, 90kda, C630029D13Rik, DAGK2, DGK, DGK-beta, mKIAA0718 |
| **Expression** | Biased expression in frontal lobe adult (RPKM 12.9), cortex adult (RPKM 7.5) and 2 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

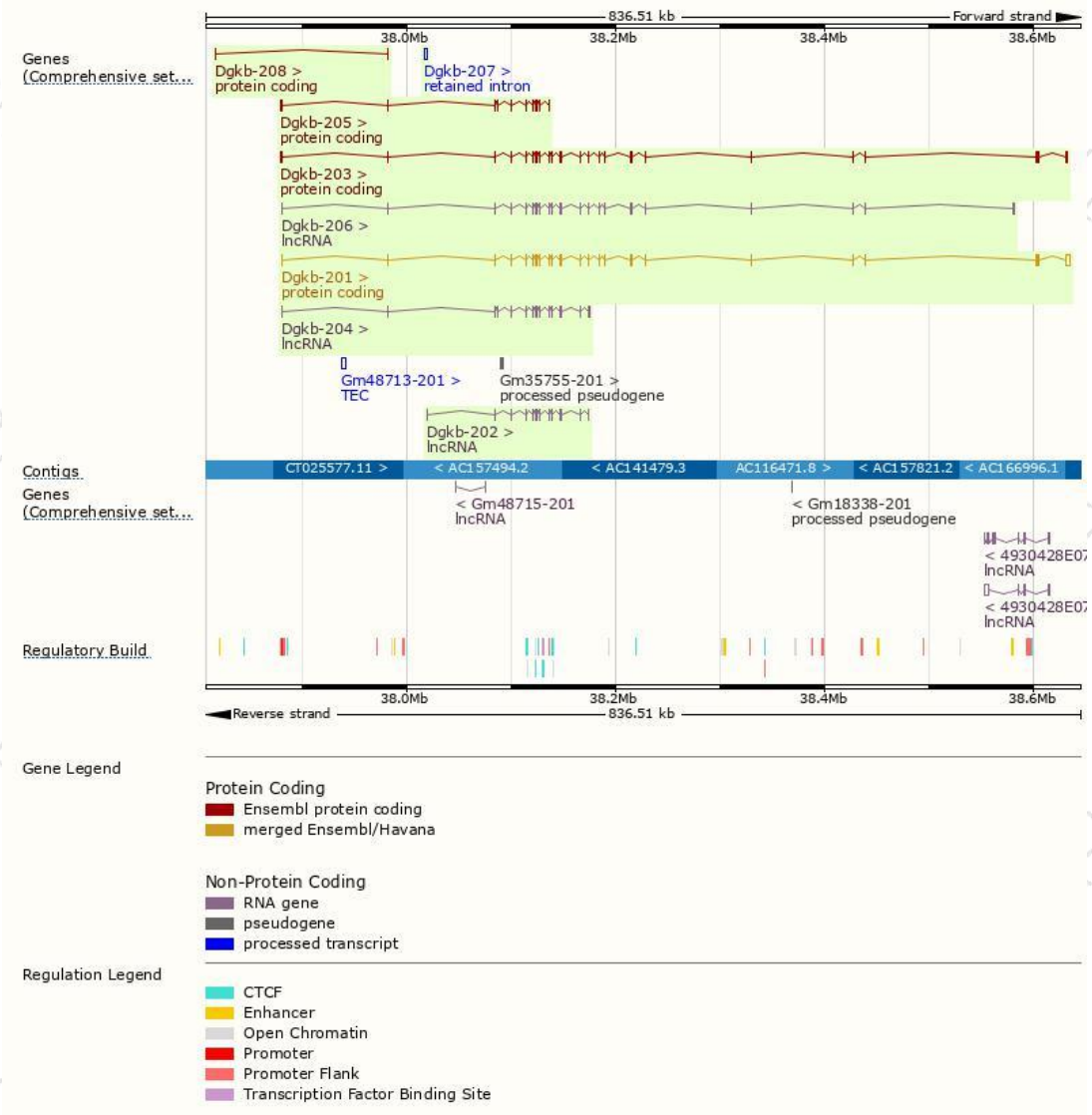
The gene has 8 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Dgkb-201 | ENSMUST00000040500.8 | 6373 | 795aa | Protein coding | CCDS25889 | Q6NS52 | TSL:1 GENCODE basic APPRIS P1 |
| Dgkb-203 | ENSMUST00000220990.1 | 4085 | 795aa | Protein coding | CCDS25889 | Q6NS52 | TSL:1 GENCODE basic APPRIS P1 |
| Dgkb-205 | ENSMUST00000221176.1 | 1439 | 282aa | Protein coding | - | Q3TSN3 | TSL:1 GENCODE basic |
| Dgkb-208 | ENSMUST00000222337.1 | 460 | 23aa | Protein coding | - | A0A1Y7VLG5 | CDS 3' incomplete TSL:5 |
| Dgkb-206 | ENSMUST00000221540.1 | 3472 | No protein | Processed transcript | - | - | TSL:1 |
| Dgkb-204 | ENSMUST00000221098.1 | 2947 | No protein | Processed transcript | - | - | TSL:1 |
| Dgkb-202 | ENSMUST00000220606.1 | 2240 | No protein | Processed transcript | - | - | TSL:1 |
| Dgkb-207 | ENSMUST00000221686.1 | 2061 | No protein | Retained intron | - | - | TSL:NA |

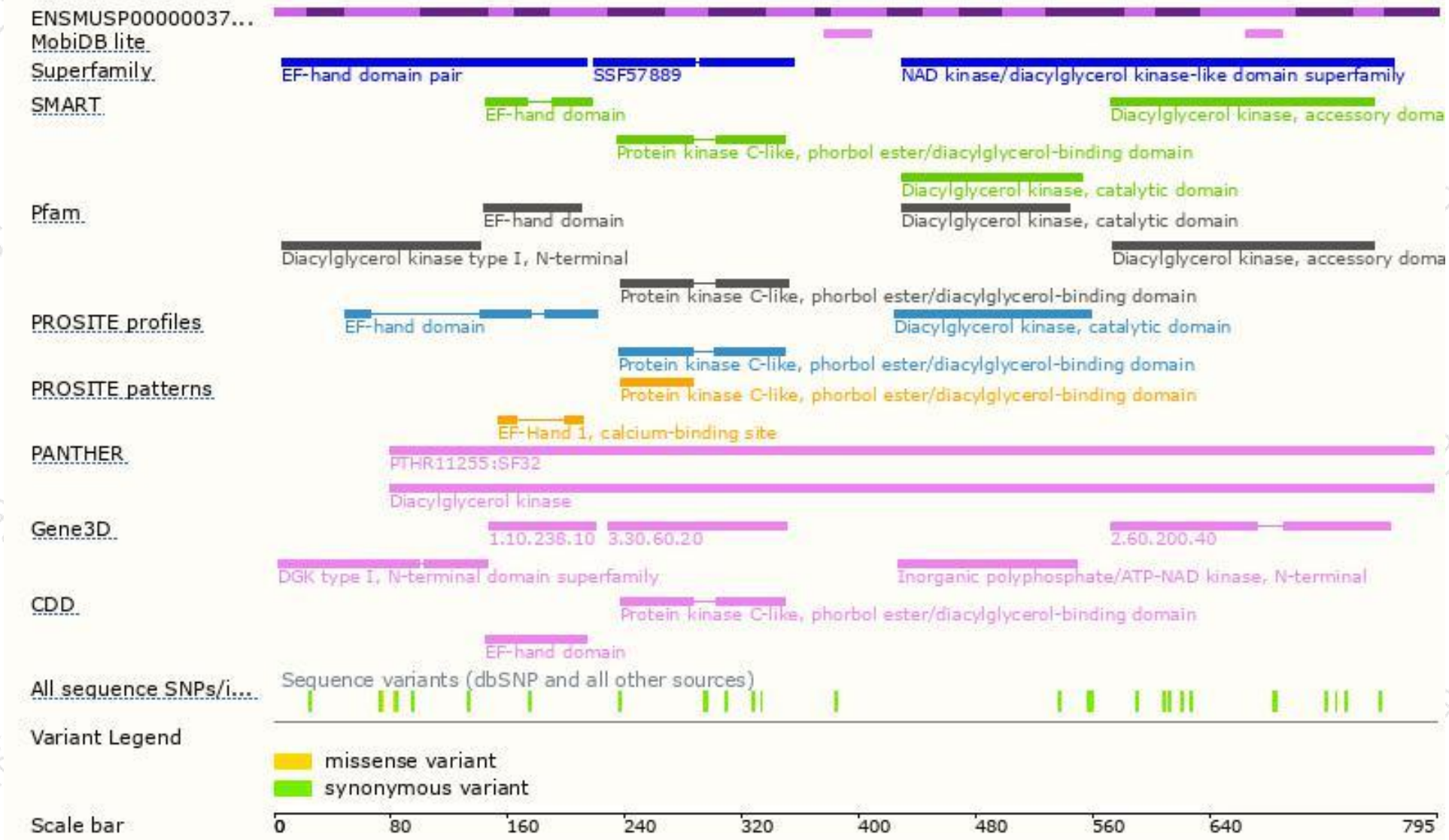
The strategy is based on the design of *Dgkb-201* transcript,The transcription is shown below



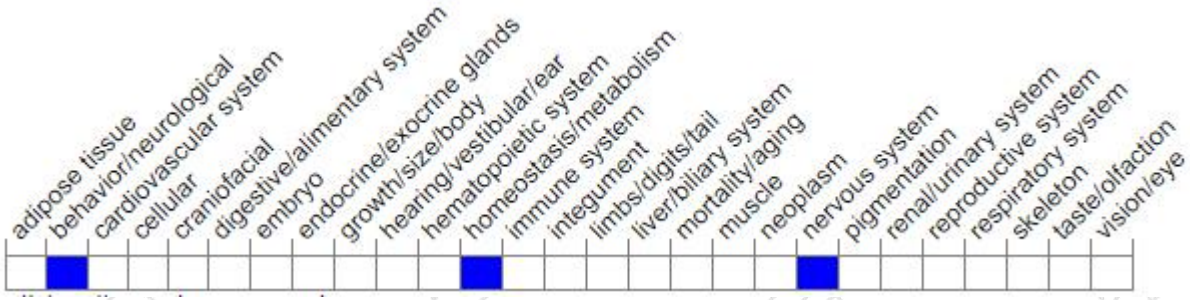
# Genomic location distribution



# 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,Mice homozygous for a transposon distruption have defects in long term potentiation, synapase morphology, and in spatial reference and working memory.

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

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