

# *Dlg3* Cas9-KO Strategy

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# Project Overview



**Project Name**

***Dlg3***

**Project type**

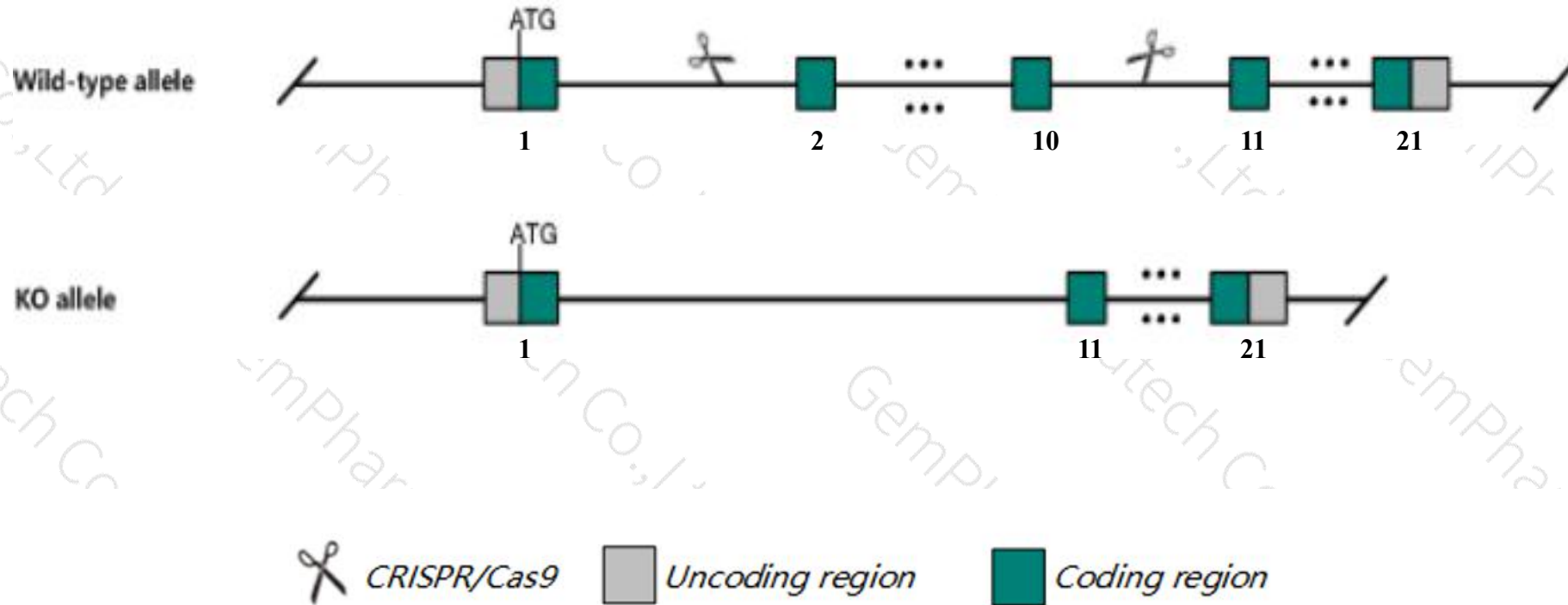
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dlg3* gene. The schematic diagram is as follows:



- The *Dlg3* gene has 8 transcripts. According to the structure of *Dlg3* gene, exon2-exon10 of *Dlg3*-202(ENSMUST00000087984.10) transcript is recommended as the knockout region. The region contains 1102bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dlg3* 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, male mice hemizygous for a knock-out allele show alterations in spatial learning, locomotor activation, LTP, and spike-timing-dependent plasticity. A portion of chimeras hemizygous for a gene trapped allele display forebrain deletion, posterior truncation, and failure to initiate embryo turning.
- The *Dlg3* gene is located on the ChrX. 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)

Dlg3 discs large MAGUK scaffold protein 3 [Mus musculus (house mouse)]

Gene ID: 53310, updated on 20-Mar-2020

## Summary



Official Symbol [Dlg3](#) provided by [MGI](#)

Official Full Name [discs large MAGUK scaffold protein 3](#) provided by [MGI](#)

Primary source [MGI:MGI:1888986](#)

See related [Ensembl:ENSMUSG00000000881](#)

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 [Dlg3](#), [SAP102](#), [mKIAA1232](#)

Expression Broad expression in frontal lobe adult (RPKM 16.8), cortex adult (RPKM 13.9) and 24 other tissues [See more](#)

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

# Transcript information (Ensembl)

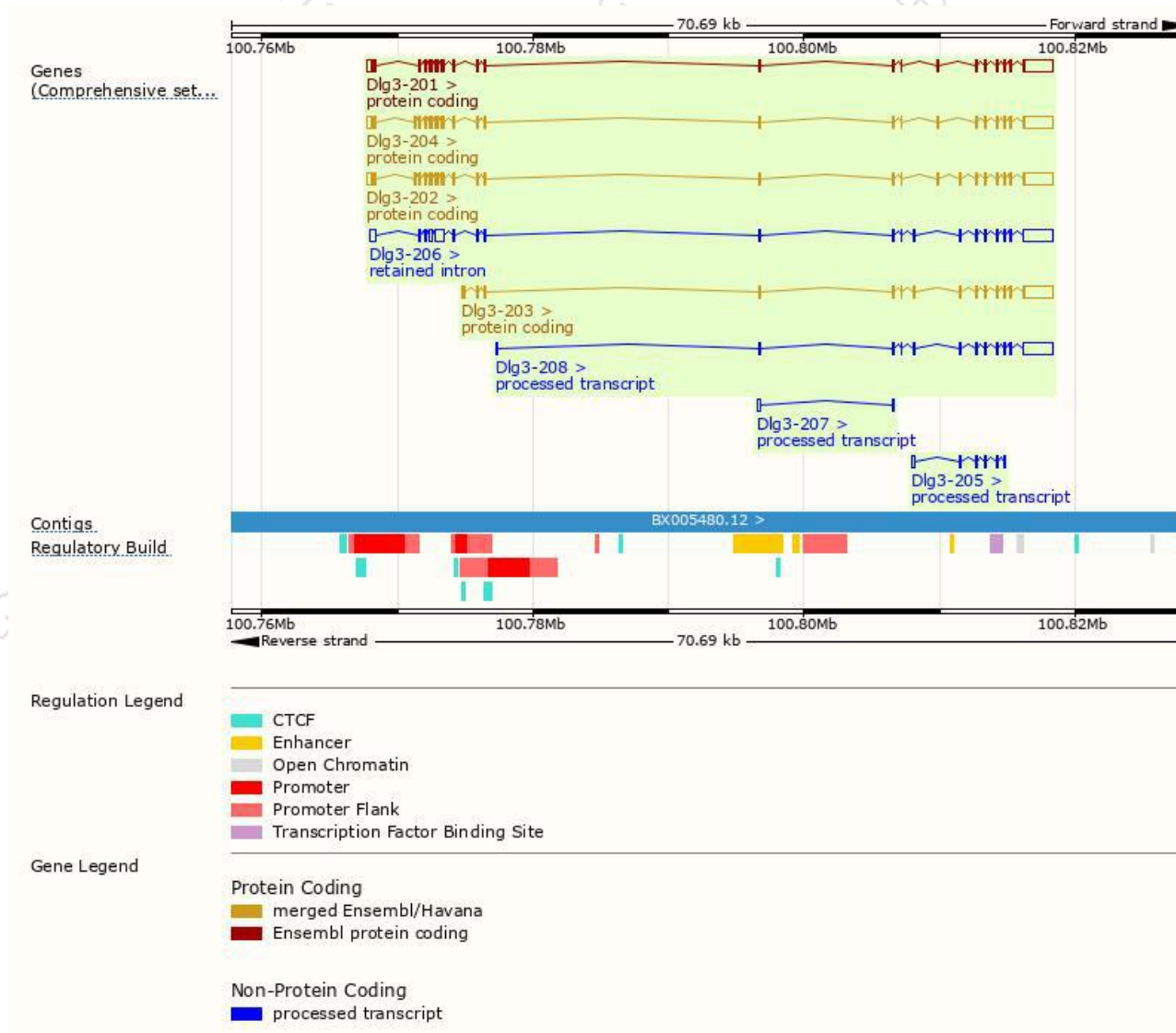
The gene has 8 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
<b>Dlg3-202</b>	<a href="#">ENSMUST00000087984.10</a>	4956	<a href="#">849aa</a>	Protein coding	<a href="#">CCDS30307</a>	<a href="#">P70175</a>	TSL:1 GENCODE basic
<b>Dlg3-204</b>	<a href="#">ENSMUST00000113736.8</a>	4940	<a href="#">835aa</a>	Protein coding	<a href="#">CCDS53148</a>	<a href="#">A2BEE9</a>	TSL:1 GENCODE basic
<b>Dlg3-201</b>	<a href="#">ENSMUST00000000901.12</a>	4885	<a href="#">817aa</a>	Protein coding	<a href="#">CCDS72413</a>	<a href="#">Q52KF7</a>	TSL:1 GENCODE basic APPRIS P1
<b>Dlg3-203</b>	<a href="#">ENSMUST00000113735.2</a>	3692	<a href="#">512aa</a>	Protein coding	<a href="#">CCDS53149</a>	<a href="#">A2BEF2</a>	TSL:1 GENCODE basic
<b>Dlg3-208</b>	<a href="#">ENSMUST00000151020.7</a>	3316	No protein	Processed transcript	-	-	TSL:1
<b>Dlg3-205</b>	<a href="#">ENSMUST00000146772.1</a>	559	No protein	Processed transcript	-	-	TSL:3
<b>Dlg3-207</b>	<a href="#">ENSMUST00000148076.1</a>	326	No protein	Processed transcript	-	-	TSL:2
<b>Dlg3-206</b>	<a href="#">ENSMUST00000147863.7</a>	5017	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Dlg3-202* transcript, the transcription is shown below:

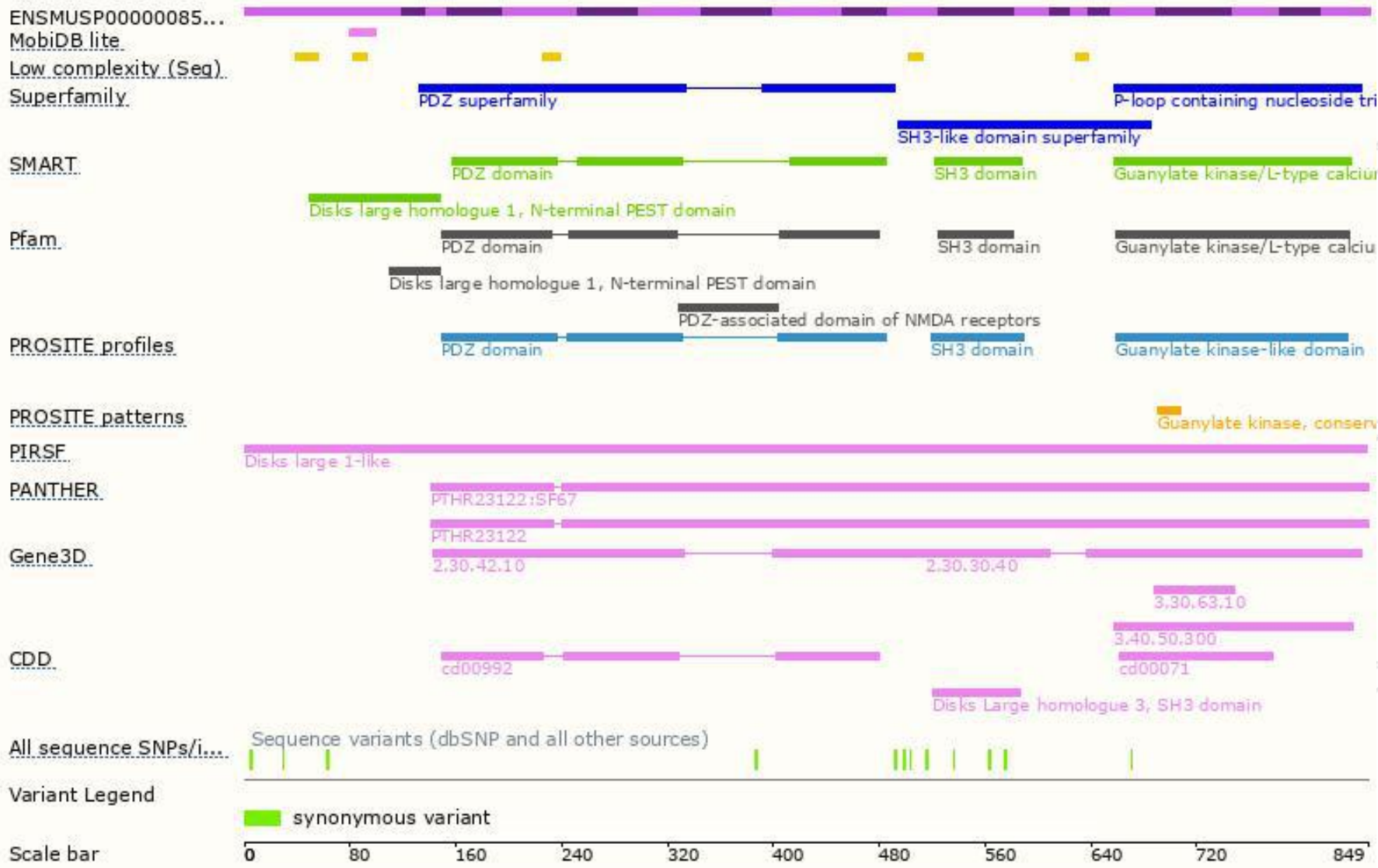


# Genomic location distribution

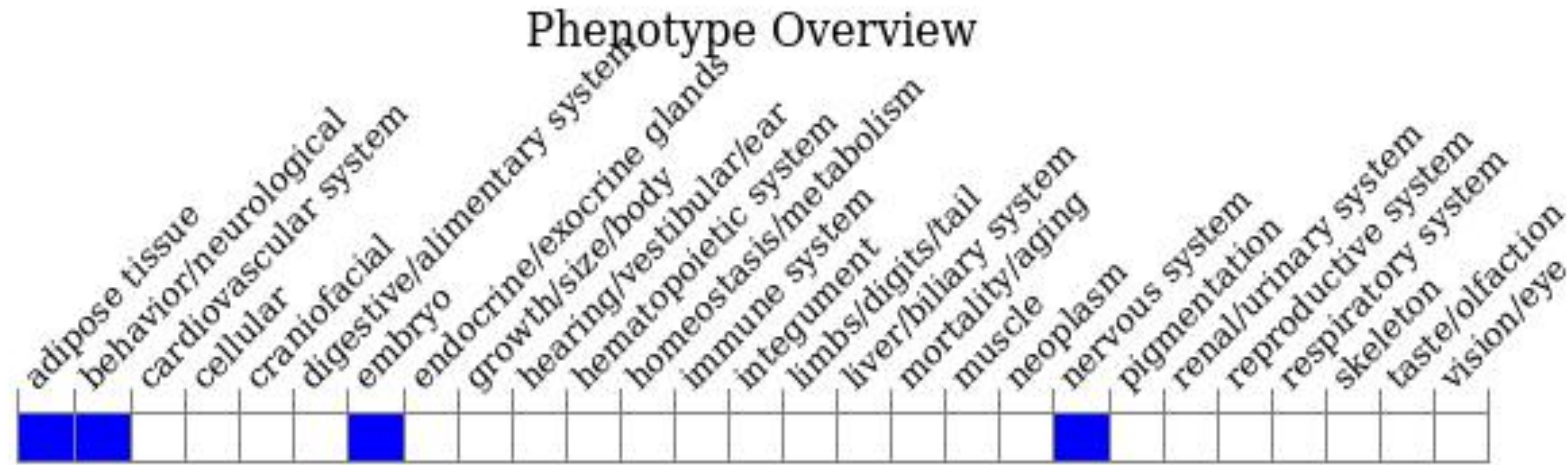




# Protein domain



# 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, male mice hemizygous for a knock-out allele show alterations in spatial learning, locomotor activation, LTP, and spike-timing-dependent plasticity. A portion of chimeras hemizygous for a gene trapped allele display forebrain deletion, posterior truncation, and failure to initiate embryo turning.

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

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