Dlg5 Cas9-KO Strategy

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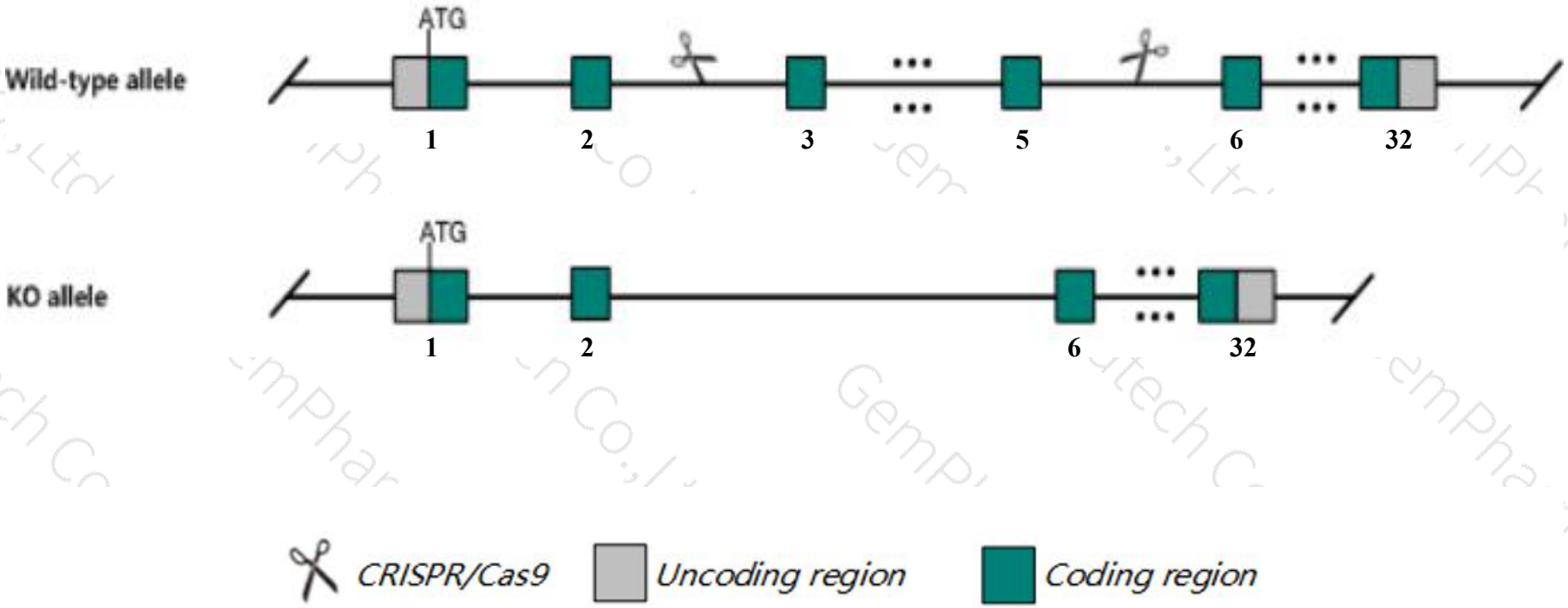
Project Overview

Project Name	***Dlg5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dlg5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Dlg5* gene has 8 transcripts. According to the structure of *Dlg5* gene, exon3-exon5 of *Dlg5-203*(ENSMUST00000090398.10) transcript is recommended as the knockout region.The region contains 491bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Dlg5* 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.

Notice

➢ According to the existing MGI data,mice homozygous for a null allele exhibit growth retardation, hydroencephaly, abnormal brain morphology, abnormal neurogenesis, kidney cysts, ureter defects, and abnormal kidney morphology.

➢ The *Dlg5* gene is located on the Chr14. 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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Dlg5 discs large MAGUK scaffold protein 5 [Mus musculus (house mouse)]

Gene ID: 71228, updated on 13-Mar-2020

Summary

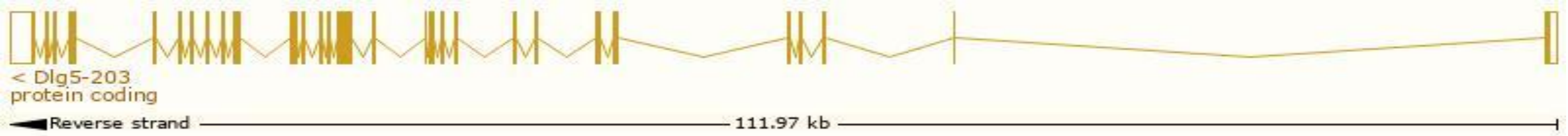
Official Symbol	Dlg5 provided by MGI
Official Full Name	discs large MAGUK scaffold protein 5 provided by MGI
Primary source	MGI:MGI:1918478
See related	Ensembl:ENSMUSG00000021782
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4933429D20Rik, T25557, mKIAA0583
Expression	Broad expression in limb E14.5 (RPKM 14.4), genital fat pad adult (RPKM 13.1) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

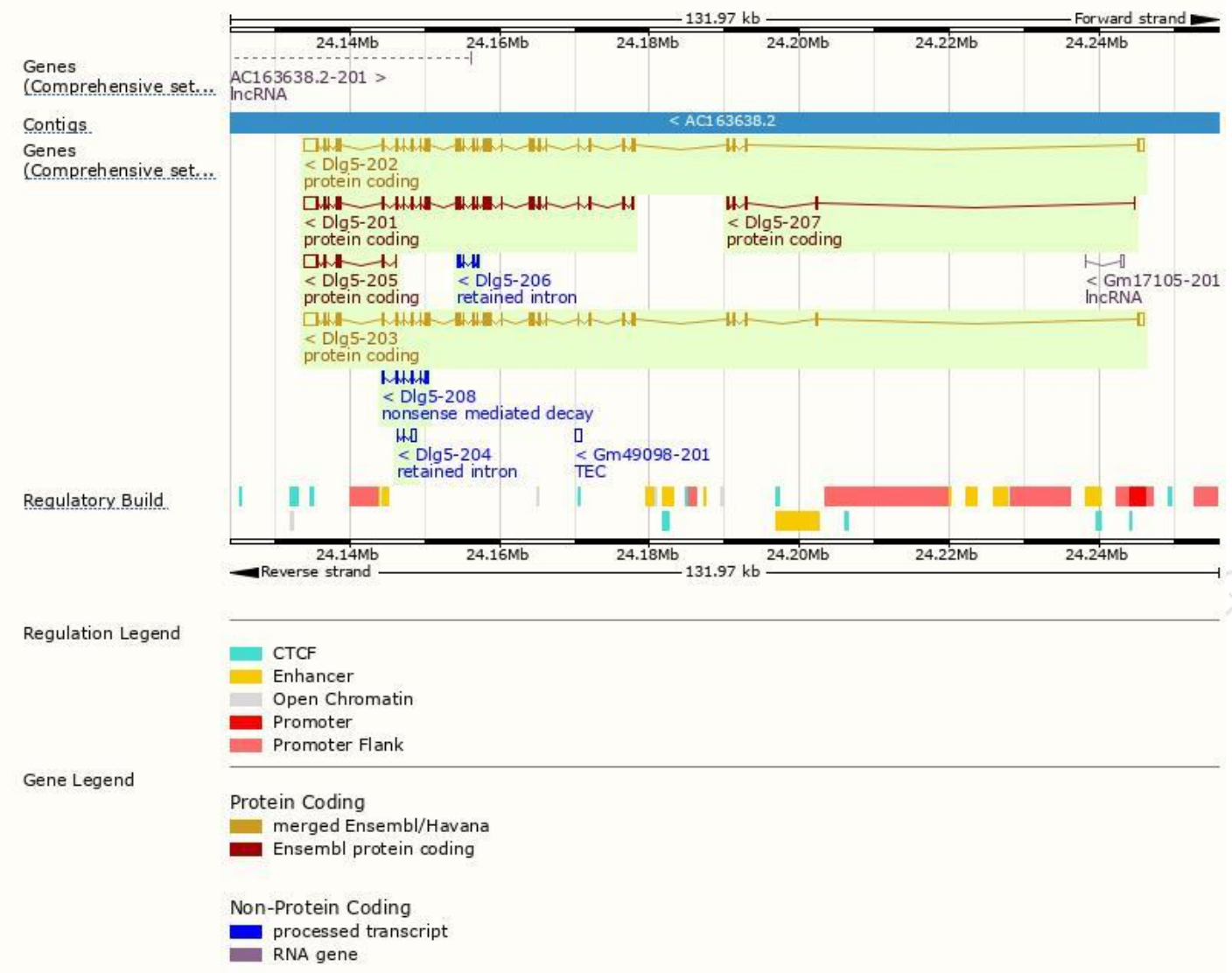
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dlg5-203	ENSMUST00000090398.10	7851	1921aa	Protein coding	CCDS49417	E9Q9R9	TSL:1 GENCODE basic APPRIS P1
Dlg5-202	ENSMUST00000073687.12	7784	1898aa	Protein coding	CCDS49416	E9Q9I2	TSL:1 GENCODE basic
Dlg5-201	ENSMUST00000042009.12	6336	1572aa	Protein coding	-	F6YZU5	CDS 5' incomplete TSL:1
Dlg5-205	ENSMUST00000166007.7	2334	228aa	Protein coding	-	F6VMK9	CDS 5' incomplete TSL:1
Dlg5-207	ENSMUST00000169880.2	614	205aa	Protein coding	-	F6Z115	CDS 5' and 3' incomplete TSL:3
Dlg5-208	ENSMUST00000170112.7	892	72aa	Nonsense mediated decay	-	F7BYL0	CDS 5' incomplete TSL:3
Dlg5-204	ENSMUST00000164638.1	748	No protein	Retained intron	-	-	TSL:5
Dlg5-206	ENSMUST00000167343.1	742	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Dlg5-203* transcript,the transcription is shown below:

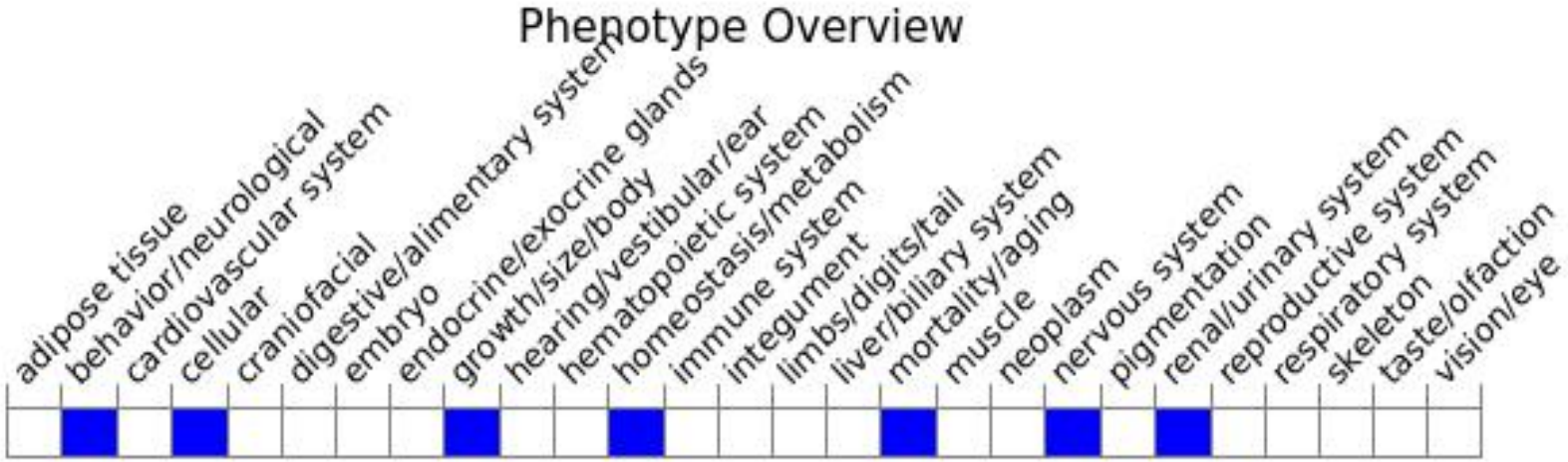


Genomic location distribution



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/).

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

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