

***Dctn1* Cas9-KO Strategy**

Designer: Huan Fan

Reviewer: Wenjing Li

Design Date: 2018/11/7

Project Overview

Project Name

Dctn1

Project type

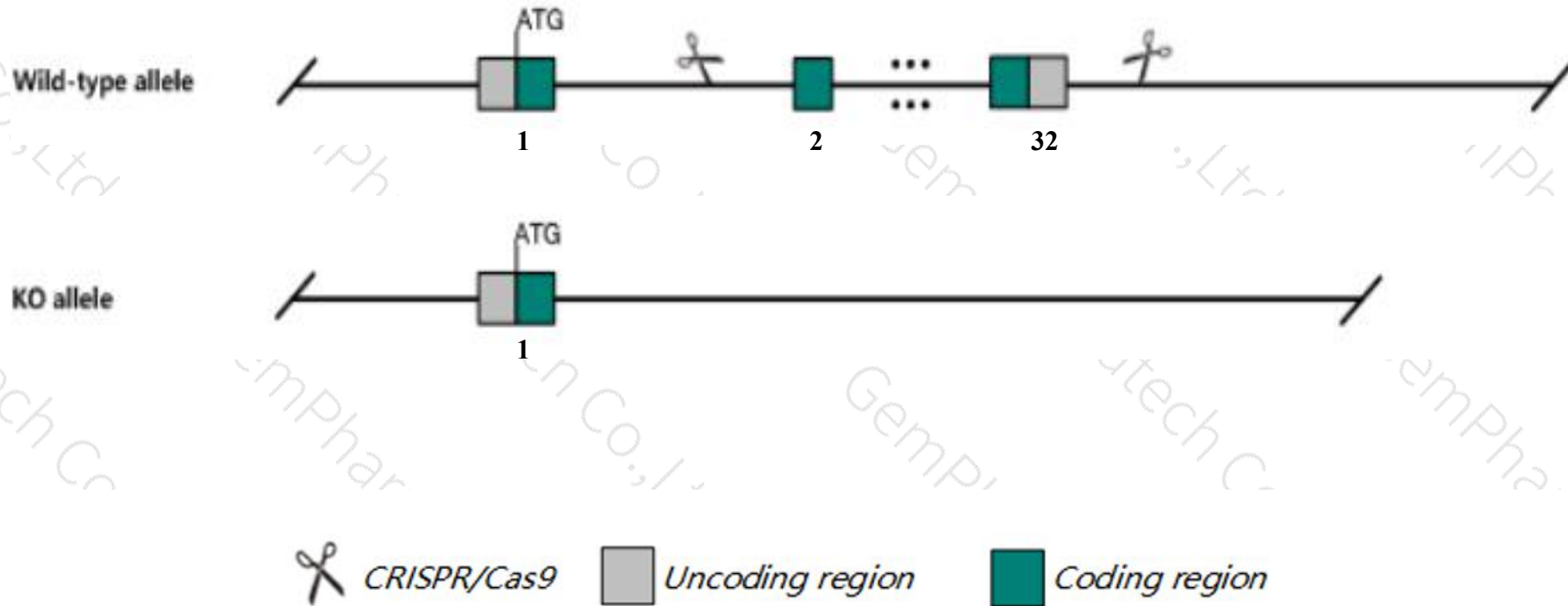
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dctn1* gene. The schematic diagram is as follows:



- The *Dctn1* gene has 12 transcripts. According to the structure of *Dctn1* gene, exon2-exon32 of *Dctn1*-205(ENSMUST00000113919.9) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dctn1* 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, mice homozygous for a null allele exhibit embryonic lethality and developmental arrest at E7.5 associated with increased apoptosis.
- The *Dctn1* gene is located on the Chr6. 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)

Dctn1 dynactin 1 [Mus musculus (house mouse)]

Gene ID: 13191, updated on 13-Mar-2020

Summary



Official Symbol Dctn1 provided by [MGI](#)

Official Full Name dynactin 1 provided by [MGI](#)

Primary source [MGI:MGI:107745](#)

See related [Ensembl:ENSMUSG000000031865](#)

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 AL022633, DAP-150, DP-150, Glued, p150, p150-glued, p150

Expression Ubiquitous expression in cerebellum adult (RPKM 36.9), frontal lobe adult (RPKM 32.3) and 28 other tissues [See more](#)

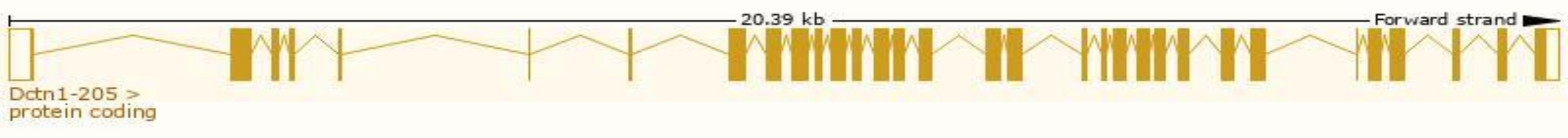
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

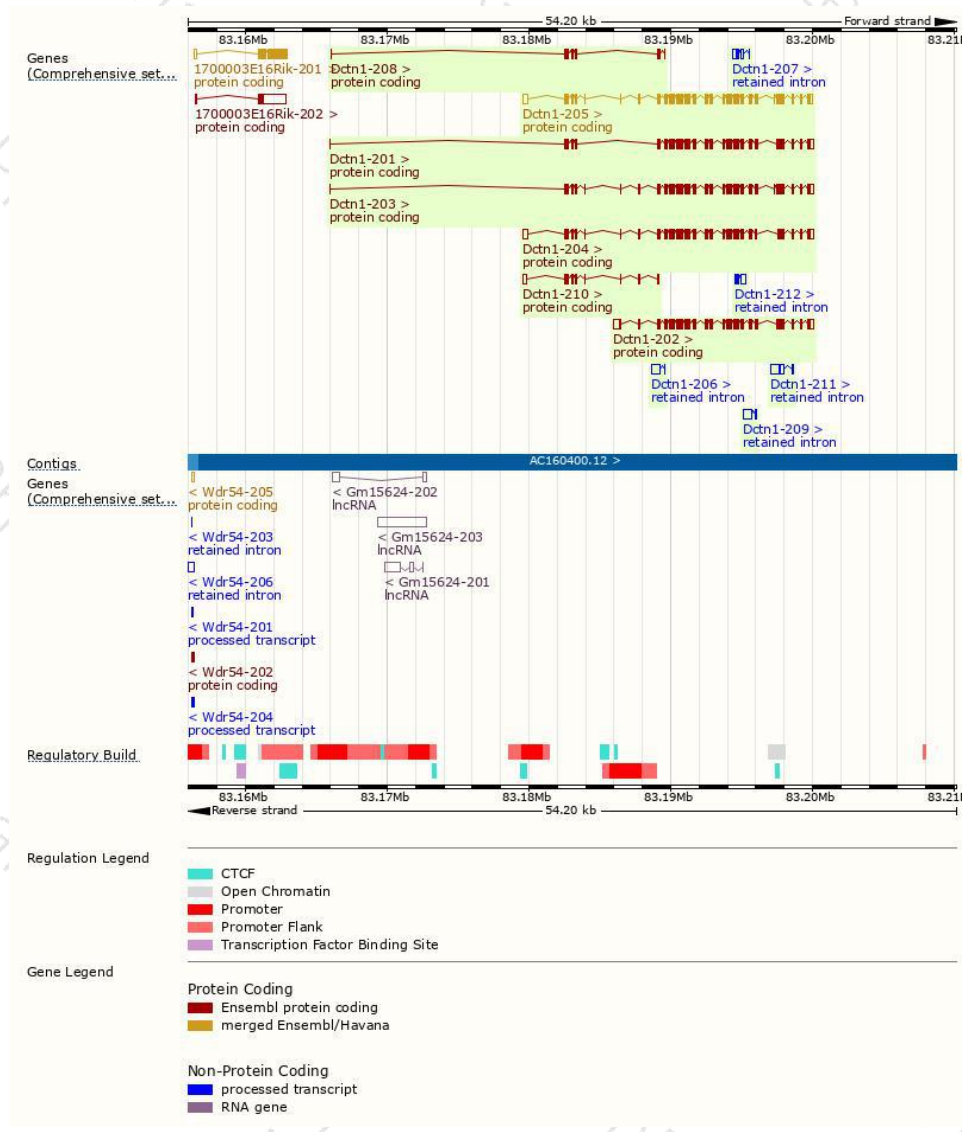
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dctn1-205	ENSMUST00000113919.9	4292	1281aa	Protein coding	CCDS39532	O08788	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Dctn1-203	ENSMUST00000113913.7	4163	1264aa	Protein coding	CCDS57432	E9Q3M3	TSL:1 GENCODE basic
Dctn1-201	ENSMUST00000077407.11	4118	1239aa	Protein coding	CCDS57433	E9Q586	TSL:1 GENCODE basic
Dctn1-204	ENSMUST00000113918.7	4321	1243aa	Protein coding	-	O08788	TSL:5 GENCODE basic
Dctn1-202	ENSMUST00000113907.1	4205	1142aa	Protein coding	-	D3YX34	TSL:5 GENCODE basic
Dctn1-210	ENSMUST00000141680.7	696	159aa	Protein coding	-	D3Z2M9	CDS 3' incomplete TSL:5
Dctn1-208	ENSMUST00000130212.7	652	189aa	Protein coding	-	D3YYG9	CDS 3' incomplete TSL:3
Dctn1-211	ENSMUST00000153793.1	839	No protein	Retained intron	-	-	TSL:3
Dctn1-206	ENSMUST00000123313.1	718	No protein	Retained intron	-	-	TSL:1
Dctn1-209	ENSMUST00000130917.1	717	No protein	Retained intron	-	-	TSL:1
Dctn1-207	ENSMUST00000127824.7	539	No protein	Retained intron	-	-	TSL:2
Dctn1-212	ENSMUST00000154420.1	481	No protein	Retained intron	-	-	TSL:1

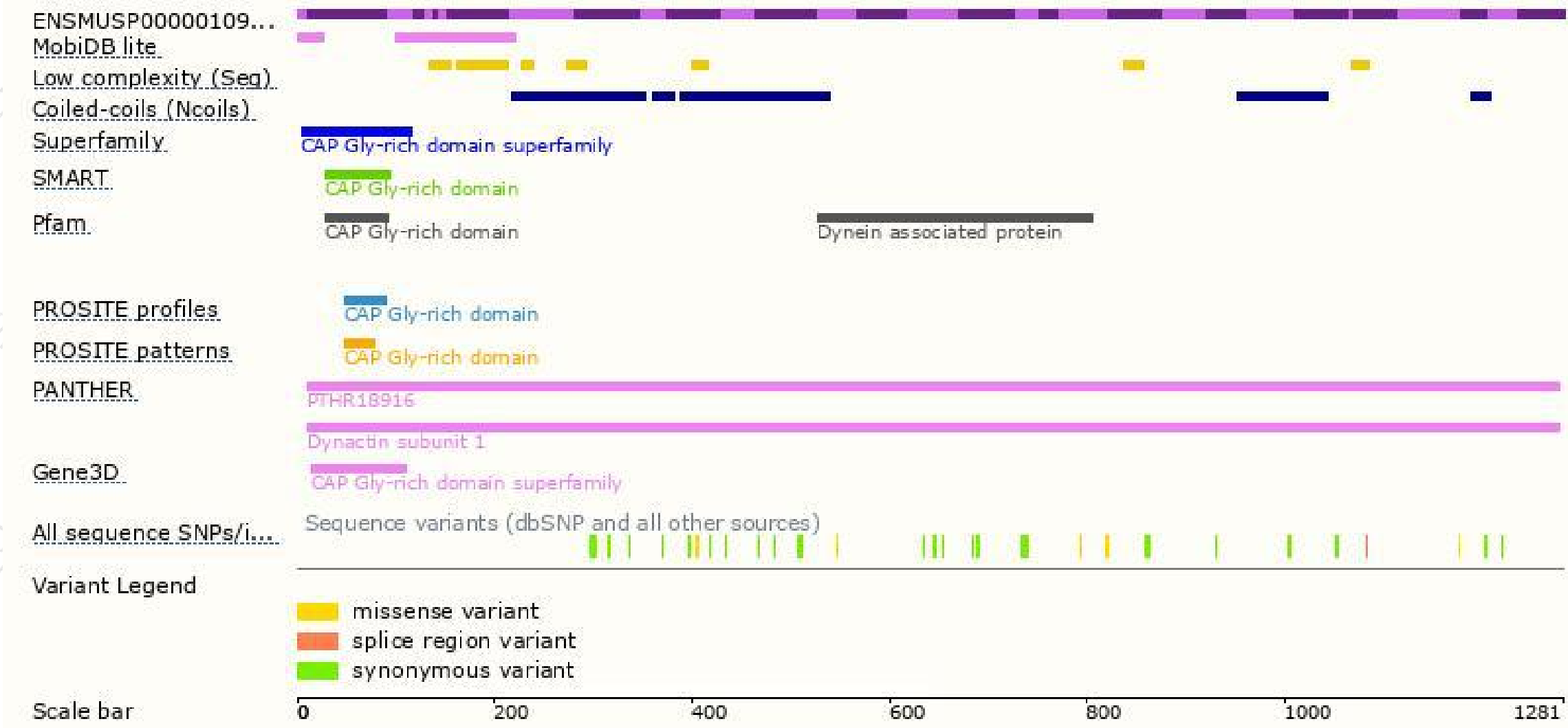
The strategy is based on the design of *Dctn1-205* transcript,the transcription is shown below:



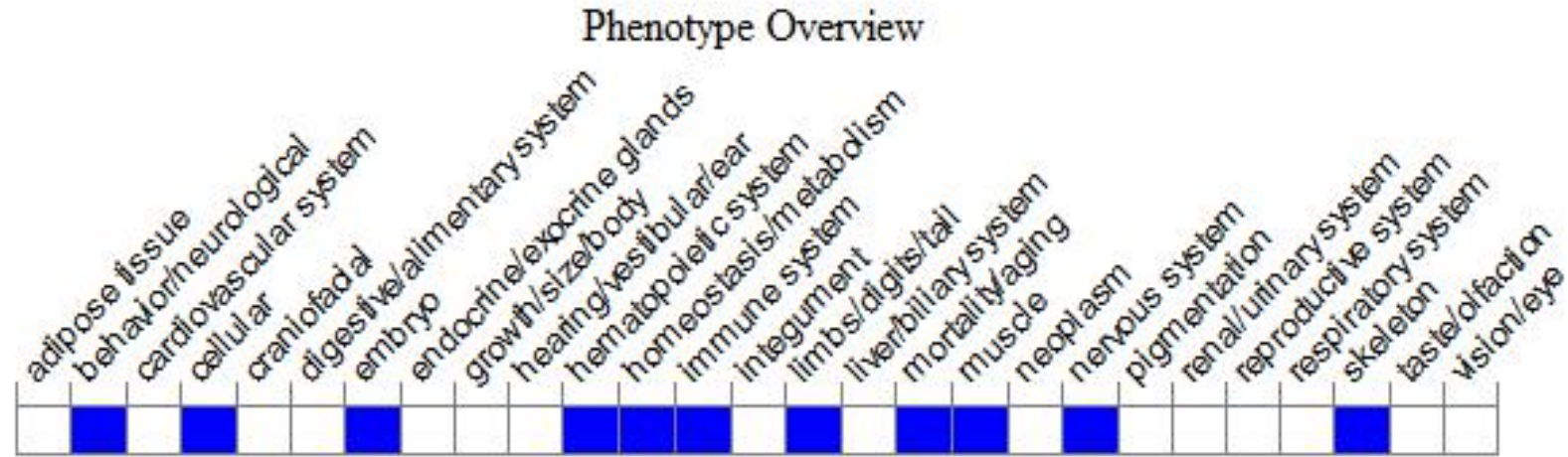
Genomic location distribution



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 null allele exhibit embryonic lethality and developmental arrest at E7.5 associated with increased apoptosis.

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

Tel: 400-9660890

