

Dcafl Cas9-KO Strategy

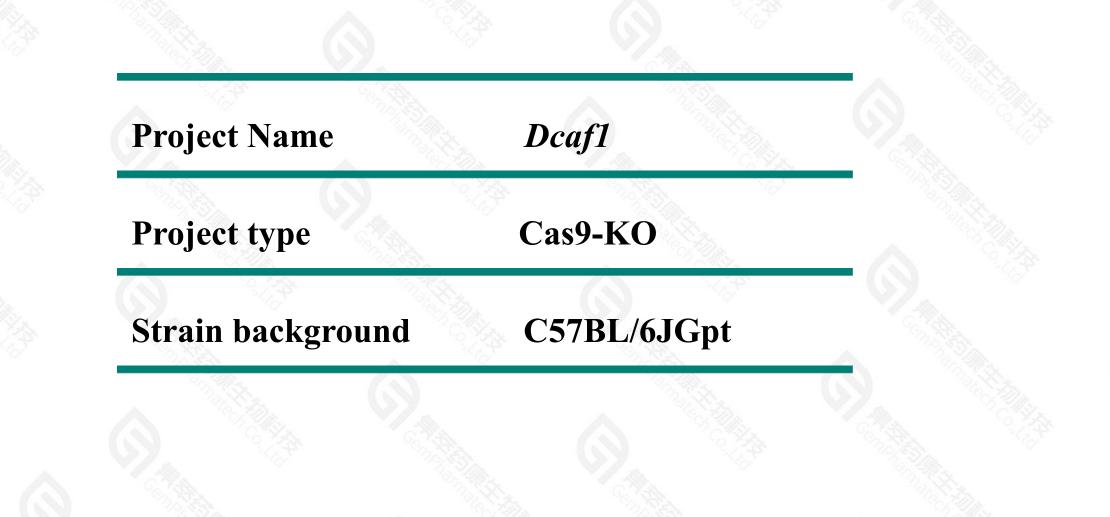
Designer: Miaomiao Cui

Reviewer: LingyanWu

Design Date: 2021-8-24

Project Overview





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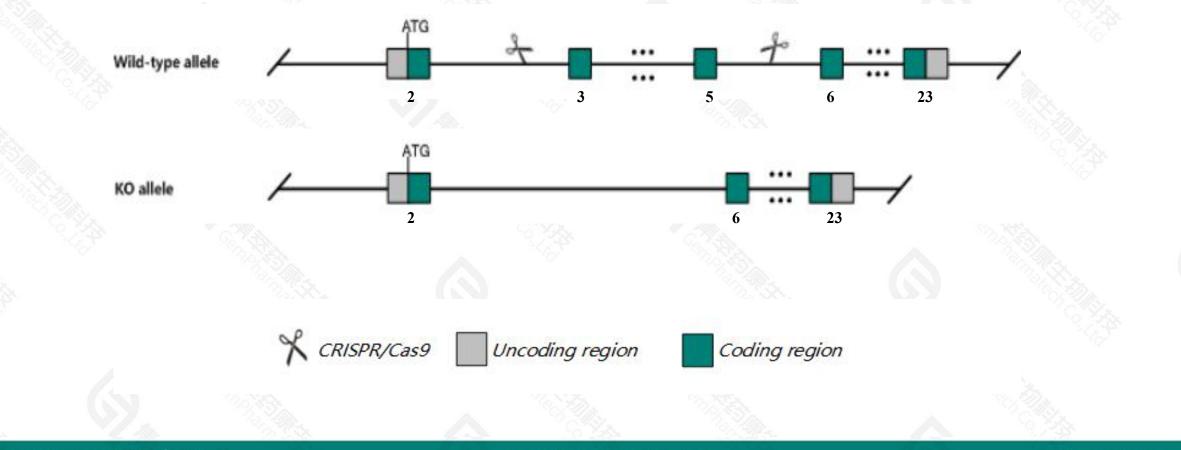
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Knockout strategy



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This model will use CRISPR/Cas9 technology to edit the *Dcaf1* gene. The schematic diagram is as follows:



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> The *Dcaf1* gene has 5 transcripts. According to the structure of *Dcaf1* gene, exon3-exon5 of *Dcaf1*-202(ENSMUST00000159645.8) transcript is recommended as the knockout region. The region contains 265bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Dcaf1* 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, embryos homozygous for a knock-out allele die prior to E7.5.
- Transcript *Dcaf1*-204 may not be affected.
- > The *Dcaf1* gene is located on the Chr9. 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.

Dcaf1 DDB1 and CUL4 associated factor 1 [Mus musculus (house mouse)] Gene ID: 321006, updated on 21-Feb-2021

Summary

Official Symbol	Dcaf1 provided by MGI
Official Full Name	DDB1 and CUL4 associated factor 1 provided by MGI
Primary source	MGI:MGI:2445220
See related	Ensembl:ENSMUSG0000040325
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	AI447437, B930007L02Rik, V, Vprbp, mKIAA0800
Expression	Ubiquitous expression in testis adult (RPKM 24.0), CNS E11.5 (RPKM 10.7) and 28 other tissuesSee more
Orthologs	human all

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Gene information (NCBI)



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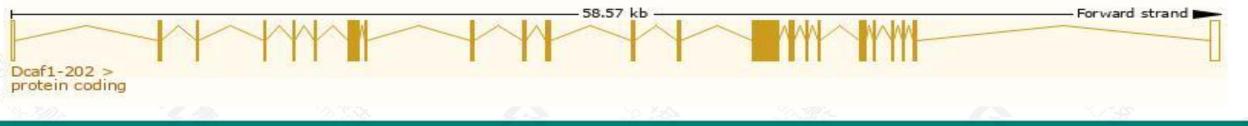
Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

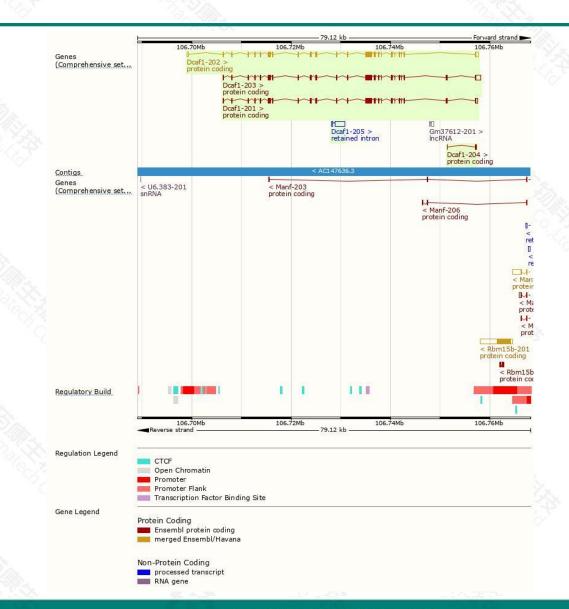
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dcaf1-202	ENSMUST00000159645.8	4945	<u>1419aa</u>	Protein coding	CCD523485		TSL:1 , GENCODE basic ,
Dcaf1-203	ENSMUST00000161758.3	5539	<u>1512aa</u>	Protein coding	848		TSL:5 , GENCODE basic ,
Dcaf1-201	ENSMUST0000055009.15	4967	<u>1506aa</u>	Protein coding	-		TSL:5, GENCODE basic, APPRIS P1,
Dcaf1-204	ENSMUST00000163657.2	275	<u>36aa</u>	Protein coding	-		CDS 5' incomplete , TSL:5 ,
Dcaf1-205	ENSMUST00000188343.2	2191	No protein	Retained intron	145		TSL:5,

The strategy is based on the design of *Dcaf1-202* transcript, the transcription is shown below:



Genomic location distribution





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Protein domain



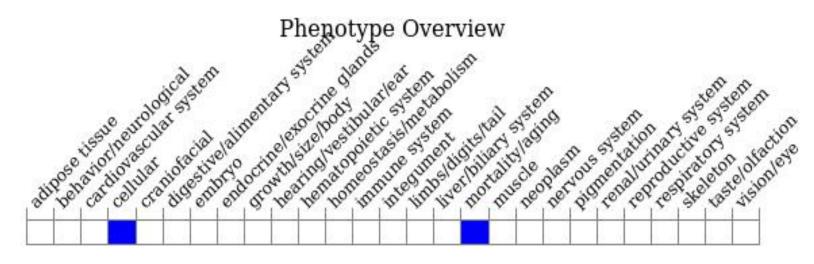
ENSMUSP00000123 MobiDB lite Low complexity (Seg) Superfamily Armadillo-type fold MD40-repeat-containing SMART. SMART. SMART. PROSITE profiles PANTHER. PROSITE profiles PANTHER. VPRBP/DCAF1 family PTHR13129:SF4 Gene 3D. All sequence SNPs/i Variant Legend missense variant synonymous variant Scale bar 0 200 400 600 800 1000 1200	
SMART. IIS1 hemology motif PROSITE profiles IIS1 hemology motif PANTHER. VPRBP/DCAF1 family. PTHR13129:SF4 WD40/YVTN repeat-like Gene3D. WD40/YVTN repeat-like All sequence SNPs/i Sequence variants (dbSNP and all other sources) Variant Legend missense variant synonymous variant	
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	1419

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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, embryos homozygous for a knock-out allele die prior to E7.5.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



