

Dcaf13 Cas9-KO Strategy

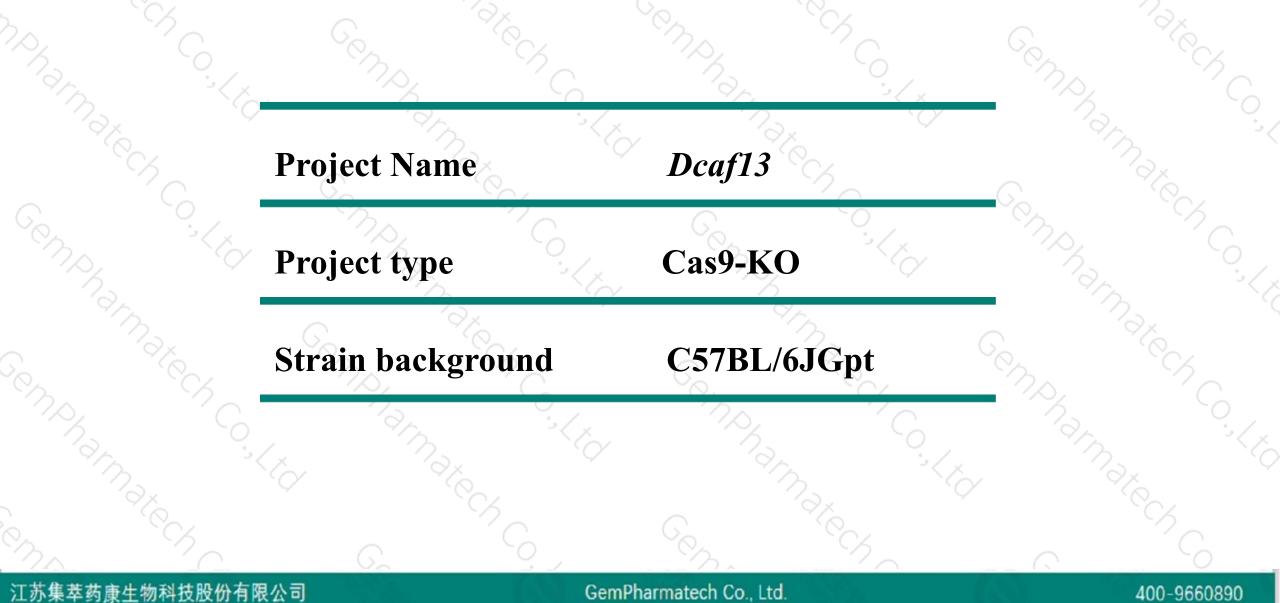
Designer: Reviewer:

Design Date:

Huan Wang Huan Fan 2020-3-9

Project Overview

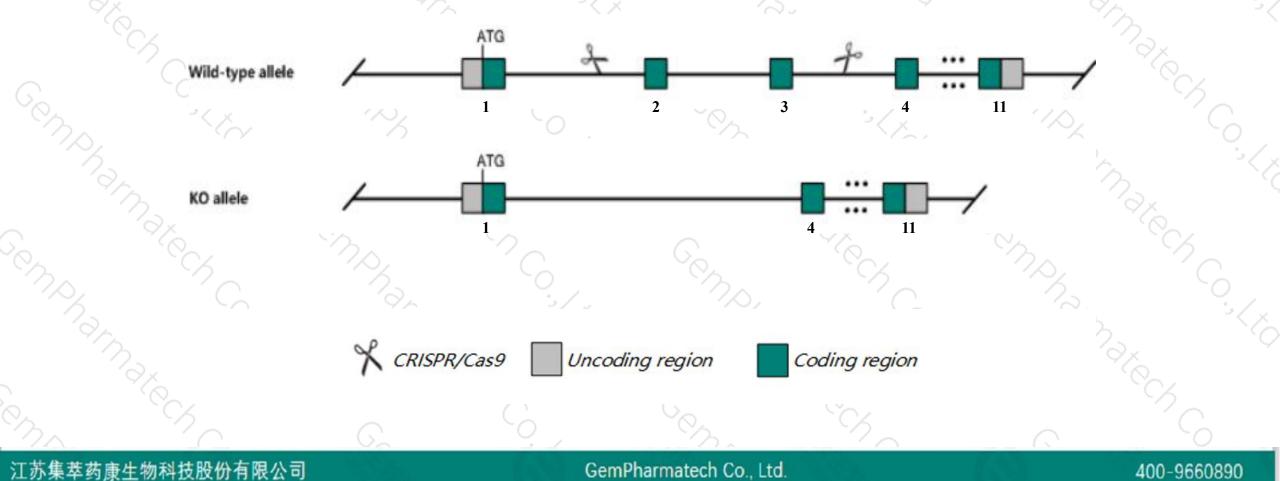




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Dcaf13* gene. The schematic diagram is as follows:





- The Dcaf13 gene has 4 transcripts. According to the structure of Dcaf13 gene, exon2-exon3 of Dcaf13-201 (ENSMUST0000022909.9) transcript is recommended as the knockout region. The region contains 308bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Dcaf13* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit pre-implantation lethality with failure of morula compaction.
- The Dcaf13 gene is located on the Chr15. 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.

Notice

Gene information (NCBI)



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Dcaf13 DDB1 and CUL4 associated factor 13 [Mus musculus (house mouse)]

Gene ID: 223499, updated on 31-Jan-2019

Summary

Official Symbol	Dcaf13 provided by MGI
Official Full Name	DDB1 and CUL4 associated factor 13 provided by MGI
Primary source	MGI:MGI:2684929
See related	Ensembl:ENSMUSG0000022300
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	Gm83, Wdsof1
Expression	Broad expression in placenta adult (RPKM 20.4), CNS E11.5 (RPKM 18.9) and 21 other tissues See more
Orthologs	human all

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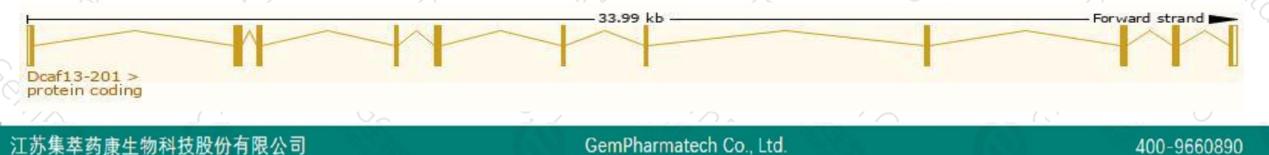
Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dcaf13-201	ENSMUST00000022909.9	1551	<u>445aa</u>	Protein coding	CCDS37066	Q6PAC3	TSL:1 GENCODE basic APPRIS P1
Dcaf13-202	ENSMUST00000226224.1	6477	No protein	Retained intron	*	-	
Dcaf13-204	ENSMUST00000228436.1	3389	No protein	Retained intron	<u>.</u>	-	
Dcaf13-203	ENSMUST00000227219.1	480	No protein	Retained intron	22	-	
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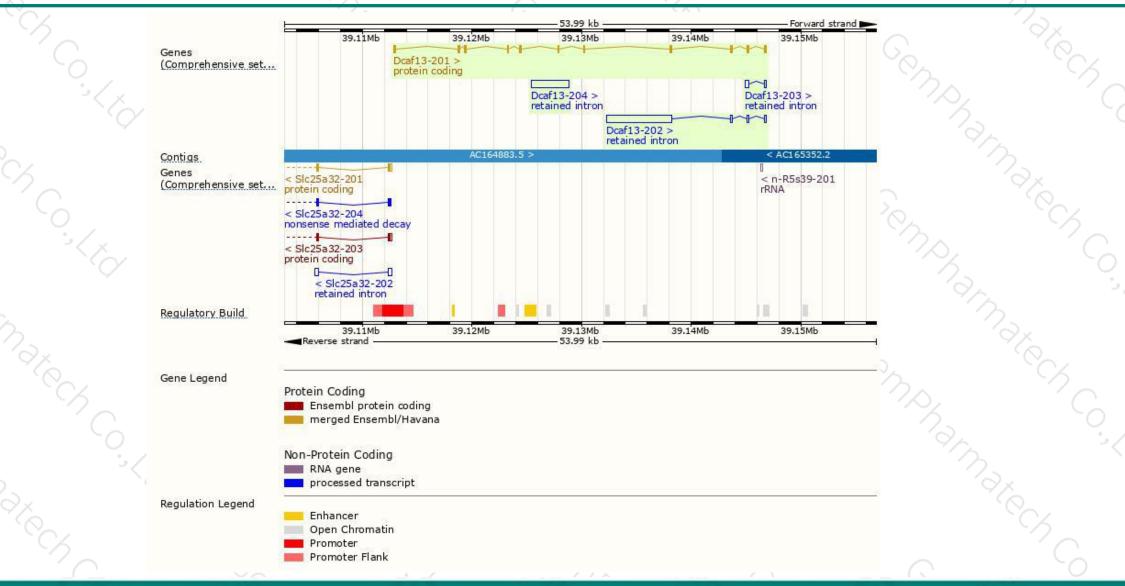
The strategy is based on the design of *Dcaf13-201* transcript, The transcription is shown below



Genomic location distribution



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Protein domain



10	<u>Gh</u>	(Ch	`^}_	<u>`</u> ?	2		No.
ENSMUSP00000022 Low complexity (Seg)					1.2		
Superfamily	WD40-repeat-o	ontaining domain super	rfamily				
SMART	and the second se	040 repeat					
Pfam.		VD40 repeat			Soft	1-like protein	
PROSITE profiles		WD40-repeat-containing	g domain				
		WD40 repeat					
PROSITE patterns		WD40 repeat, con	served site				
PANTHER	PTHR22851						
	PTHR22051:SF0						
Gene3D	WD40/	YVTN repeat-like-conta	aining domain superfamily	1			
CDD		d00200					
All sequence SNPs/i	Sequence varian	ts (dbSNP and all oth	ner sources)	n it	- A	4	10
Variant Legend	missense va						
Scale bar	0 40	80 120	160 200	240 280	320 36	50 400	445
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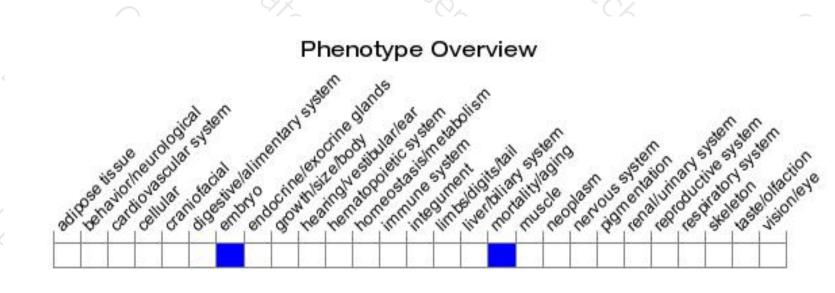
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Mouse phenotype description(MGI)





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, Mice homozygous for a knock-out allele exhibit pre-implantation lethality with failure of morula compaction.



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



