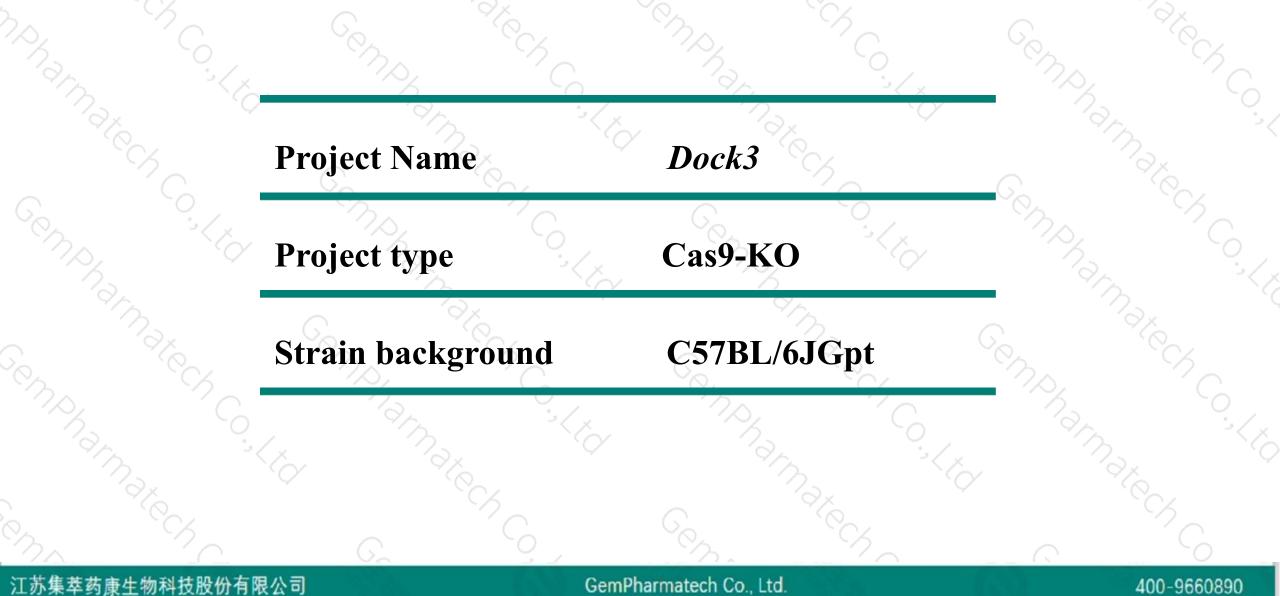


Dock3 Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-1-20

Project Overview

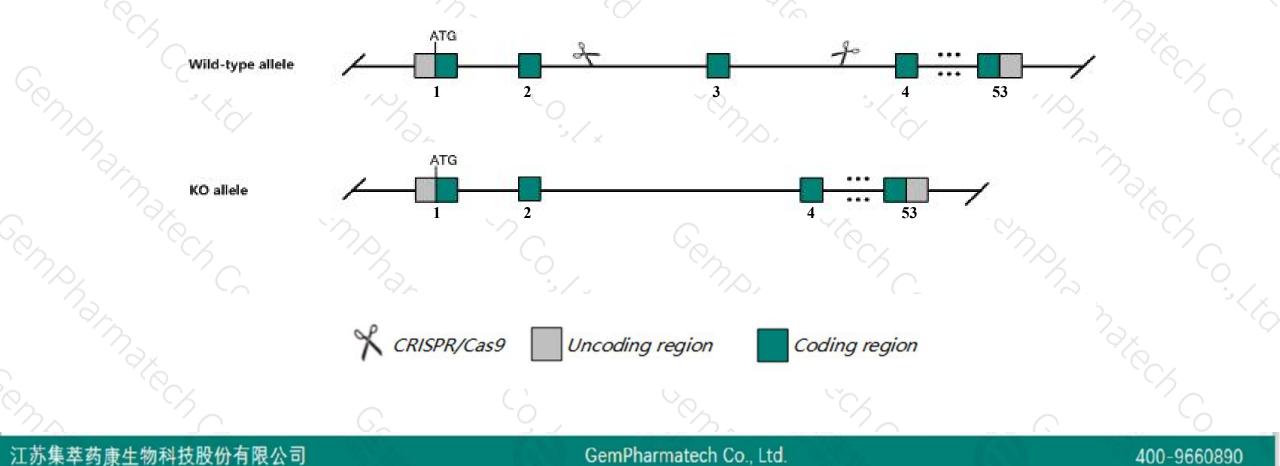




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Dock3 gene. The schematic diagram is as follows:





- The Dock3 gene has 11 transcripts. According to the structure of Dock3 gene, exon3 of Dock3-201 (ENSMUST00000044532.10) transcript is recommended as the knockout region. The region contains 41bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Dock3* gene. The brief process is as follows: CRISPR/Cas9 system

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- According to the existing MGI data, Mice homozygous for a null allele exhibit abnormal behaviors and muscular weakness associated with axonal dystrophy.
- Transcript 202,205,208,211 CDS 5' and 3' incomplete the influences is unknown.
- The Dock3 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.

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Gene information (NCBI)



☆ ?

Dock3 dedicator of cyto-kinesis 3 [Mus musculus (house mouse)]

Gene ID: 208869, updated on 31-Jan-2019

Summary

Official SymbolDock3 provided by MGIOfficial Full Namededicator of cyto-kinesis 3 provided by MGIPrimary sourceMGI:MG:2429763See relatedEnsembl:ENSMUSG0000039716Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusAlso knownasMOCA, PBP, mKIAA0299ExpressionBiased expression in frontal lobe adult (RPKM 24.4), cortex adult (RPKM 21.6) and 7 other tissues
See more
human all

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Transcript information (Ensembl)



The gene has 11 transcripts, all transcripts are shown below:

76150 ²⁰							
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
ENSMUST00000044532.10	9063	<u>2030aa</u>	Protein coding	CCDS40760	F8VPQ1	TSL:2 GENCODE basic APPRIS P1	
ENSMUST00000171095.7	3947	<u>552aa</u>	Protein coding	-3	F6VMI1	CDS 5' incomplete TSL:1	
ENSMUST00000165075.1	723	<u>241aa</u>	Protein coding	-12	F7CVM6	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3	
ENSMUST00000168759.1	723	<u>241aa</u>	Protein coding	20	<u>F6YXW9</u>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5	
ENSMUST00000166152.1	263	<u>87aa</u>	Protein coding	7.0	F7AGL4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5	
ENSMUST00000167053.7	5440	No protein	Retained intron	₹5	8	TSL:2	
ENSMUST00000169164.7	920	No protein	Retained intron	-	-	TSL:3	
ENSMUST00000166759.1	679	No protein	Retained intron	20	22	TSL:3	
ENSMUST00000165182.1	529	No protein	Retained intron	7.1	17	TSL:3	
ENSMUST00000170193.1	529	No protein	Retained intron	•6	8	TSL:5	
ENSMUST00000165562.1	453	No protein	IncRNA	-2	-	TSL:3	
	ENSMUST0000044532.10 ENSMUST0000171095.7 ENSMUST00000165075.1 ENSMUST00000166152.1 ENSMUST00000166152.1 ENSMUST00000167053.7 ENSMUST00000165182.1 ENSMUST00000165182.1	ENSMUST0000044532.10 9063 ENSMUST0000171095.7 3947 ENSMUST0000165075.1 723 ENSMUST0000166152.1 723 ENSMUST0000166152.1 263 ENSMUST0000167053.7 5440 ENSMUST0000167053.7 920 ENSMUST0000166759.1 679 ENSMUST0000165182.1 529	ENSMUST0000044532.00 9063 2030aa ENSMUST0000171095.7 3947 552aa ENSMUST0000165075.1 723 241aa ENSMUST0000166152.1 723 241aa ENSMUST0000166152.1 723 37aa ENSMUST0000166152.1 263 87aa ENSMUST0000167053.7 5440 No protein ENSMUST0000166759.1 920 No protein ENSMUST0000166152.1 679 No protein ENSMUST0000166158.1 529 No protein	ENSMUST0000044532.1090632030aaProtein codingENSMUST0000171095.73947552aaProtein codingENSMUST0000165075.1723241aaProtein codingENSMUST000016675.1723241aaProtein codingENSMUST0000166152.126387aaProtein codingENSMUST0000167053.75440No proteinRetained intronENSMUST0000167053.7540No proteinRetained intronENSMUST0000166759.1679No proteinRetained intronENSMUST0000165182.1529No proteinRetained intron	ENSMUST00000445321090632030aaProtein codingCCDS40760ENSMUST000017109573947552aaProtein coding-ENSMUST00001650751723241aaProtein coding-ENSMUST00001667591723241aaProtein coding-ENSMUST0000166152126387aaProtein coding-ENSMUST000016705375440No proteinRetained intron-ENSMUST00001667591920No proteinRetained intron-ENSMUST00001667591679No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST000016671821529No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST00001667591529No proteinRetained intron-ENSMUST000001667591529No proteinRetained intron-ENSMUST000001667591529No proteinRetained intron-ENSMUST000001667591529No proteinRetained intron-ENSMUST000001667591529No proteinRetained intron-ENSMUST000001667591 <td>ENSMUST0000044532.1090632030aaProtein codingCCDS40760F8VPQ1ENSMUST0000017109573947552aaProtein codingC<ds40760< td="">F6VM11ENSMUST00001650751723241aaProtein codingCF7CVM6ENSMUST00001667591723241aaProtein codingCF7AGL4ENSMUST0000166152126387aaProtein codingCF7AGL4ENSMUST000016675375440No proteinRetained intronCCENSMUST00001667591679No proteinRetained intronCCENSMUST00001667591679No proteinRetained intronCCENSMUST00001667591529No proteinRetained intronCCENSMUST00001667</ds40760<></td>	ENSMUST0000044532.1090632030aaProtein codingCCDS40760F8VPQ1ENSMUST0000017109573947552aaProtein codingC <ds40760< td="">F6VM11ENSMUST00001650751723241aaProtein codingCF7CVM6ENSMUST00001667591723241aaProtein codingCF7AGL4ENSMUST0000166152126387aaProtein codingCF7AGL4ENSMUST000016675375440No proteinRetained intronCCENSMUST00001667591679No proteinRetained intronCCENSMUST00001667591679No proteinRetained intronCCENSMUST00001667591529No proteinRetained intronCCENSMUST00001667</ds40760<>	

The strategy is based on the design of *Dock3-201* transcript, The transcription is shown below

< Dock3-201 protein coding

Reverse strand

- 339.08 kb -

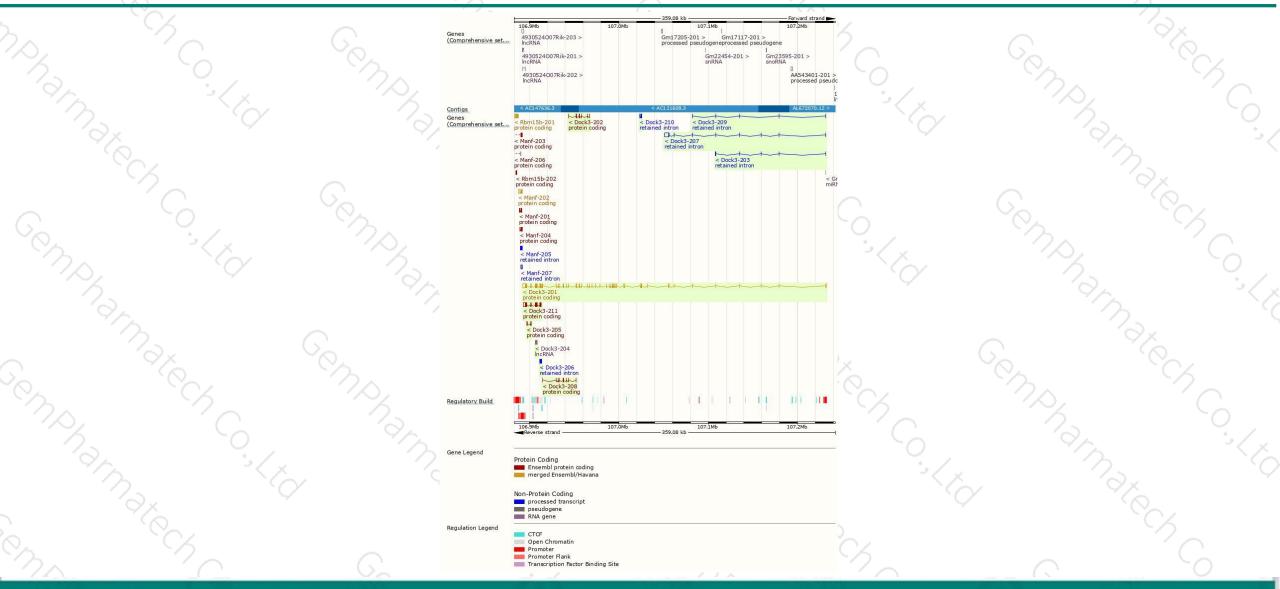
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Genomic location distribution





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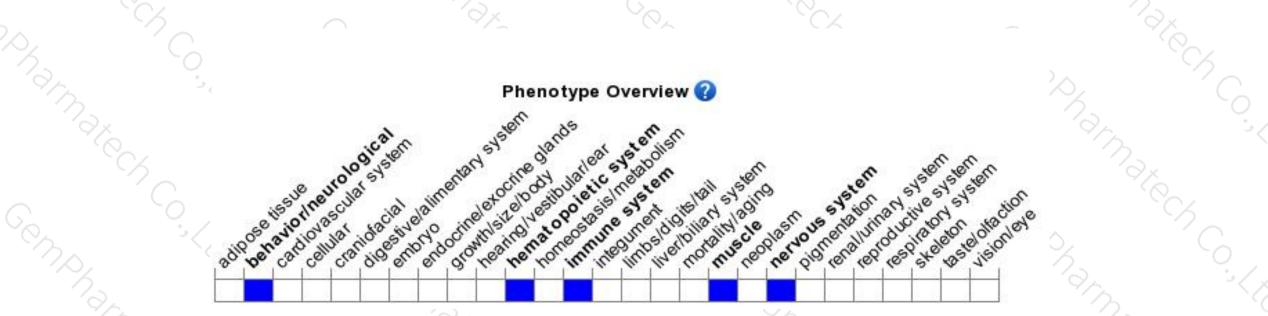
Protein domain



	ENSMUSP00000047 MobiDB lite Low complexity (Seg) Coiled-coils (Ncoils)		NOX Ch
annax	Superfamily	SH3-like domain superfamily Armadillo-type fold	í Co
12700	SMART	SH3 domain	3<
	Pfam.	Dedicator of cytokinesis, N-terminal domain Dedicator of cytokinesis, C-terminal	
C _C	PROSITE profiles	SH3 domain DHR-1 domain DHR-2 domain	° M
$\gamma_{\mathcal{O}_{\mathcal{L}}}$	PANTHER	Dedicator of cytokinesis	~0
narm.	Gene3D	Dedicator of cytokinesis 3 1,20,1270,350 C2 domain superfamily 1.25,40,410 1.20,58,740 2.30,30,40	
Go in	<u>CDD</u>	Dedicator of cytokinesis B, C2 domain cd11704	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
ma.		Dedicator of cytokinesis 3, SH3 domain	í C
The second	All sequence SNPs/i	Sequence variants (dbSNP and all other sources)	is/x
ALL ALL	Variant Legend	stop gained missense variant splice region variant synonymous variant	
	Scale bar	0 200 400 600 800 1000 1200 1400 1600 1800 2030	6
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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 null allele exhibit abnormal behaviors and muscular weakness associated with axonal dystrophy.



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



