

Ccdc33 Cas9-KO Strategy

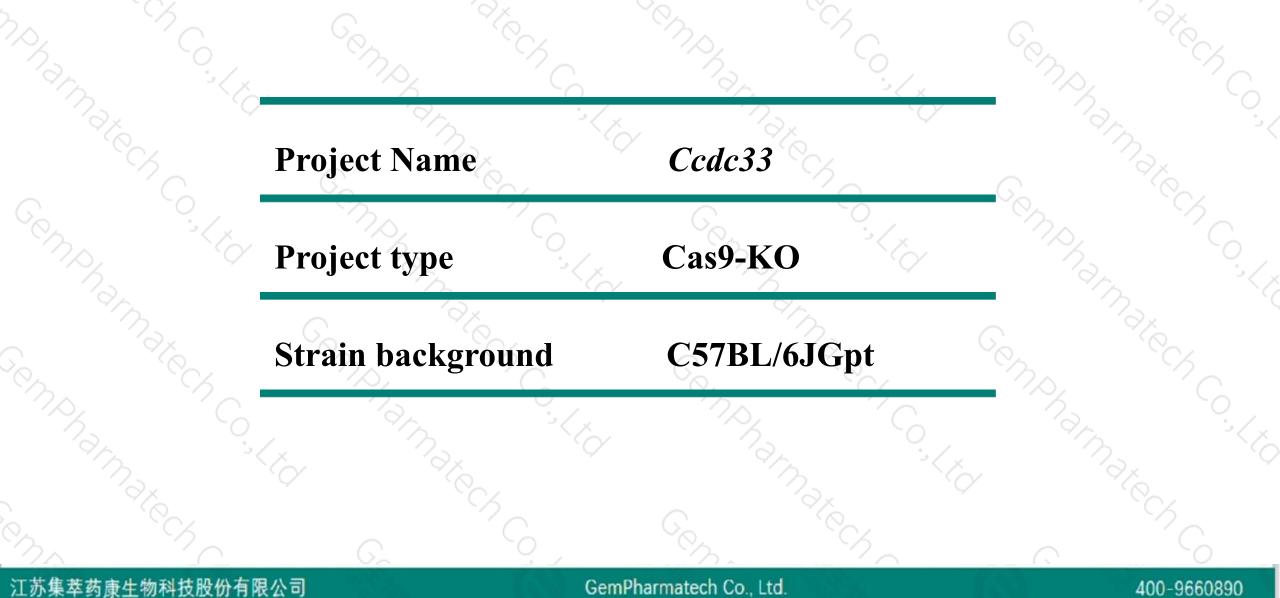
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Reviewer: Xiaojing Li

Design Date: 2020-10-21

Project Overview

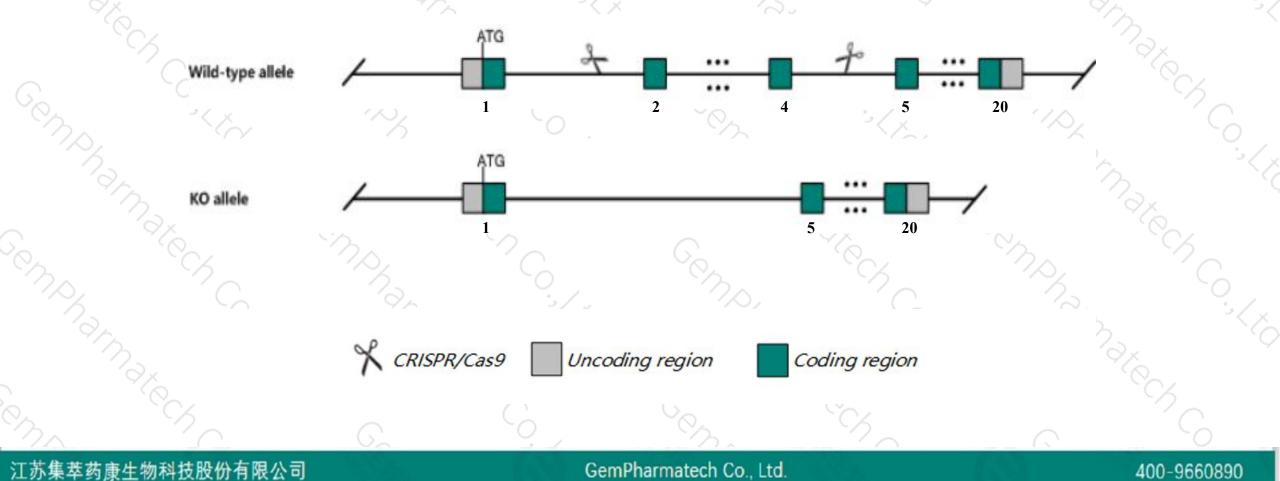




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Ccdc33 gene. The schematic diagram is as follows:





> The *Ccdc33* gene has 10 transcripts. According to the structure of *Ccdc33* gene, exon2-exon4 of *Ccdc33*-203(ENSMUST00000098682.9) transcript is recommended as the knockout region. The region contains 610bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Ccdc33* 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.

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The *Ccdc33* 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.
 The flox region is in the intron of the Stra6 gene, which may affect the regulation of this gene.
 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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Ccdc33 coiled-coil domain containing 33 [Mus musculus (house mouse)]

Gene ID: 382077, updated on 13-Mar-2020

Summary

Official Symbol	Ccdc33 provided by MGI
Official Full Name	coiled-coil domain containing 33 provided by MGI
Primary source	MGI:MGI:1922464
See related	Ensembl:ENSMUSG0000037716
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	4930535E21Rik, Gm1117, Tzip1
Expression	Biased expression in testis adult (RPKM 23.9) and ovary adult (RPKM 2.7)See more
Orthologs	human all

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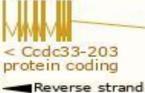
Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccdc33-203	ENSMUST0000098682.9	3117	<u>985aa</u>	Protein coding	CCD552811	E9QQ55	TSL:1 GENCODE basic APPRIS ALT2
Ccdc33-201	ENSMUST0000042205.12	2632	<u>731aa</u>	Protein coding	CCDS40654	A0A0R4J0H2	TSL:1 GENCODE basic APPRIS P3
Ccdc33-204	ENSMUST00000119665.1	2552	<u>730aa</u>	Protein coding	CCDS81006	D3YU68	TSL:1 GENCODE basic APPRIS ALT2
Ccdc33-210	ENSMUST00000215944.1	3012	<u>950aa</u>	Protein coding	-	A0A1L1SR74	TSL:5 GENCODE basic APPRIS ALT2
Ccdc33-202	ENSMUST0000098681.3	1093	<u>278aa</u>	Protein coding	-	Q3ULW6	TSL:1 GENCODE basic
Ccdc33-208	ENSMUST00000146741.1	747	No protein	Processed transcript	-	872	TSL:3
Ccdc33-206	ENSMUST00000143797.1	313	No protein	Processed transcript	-	-	TSL:5
Ccdc33-207	ENSMUST00000144887.1	922	No protein	Retained intron	12 12		TSL:2
Ccdc33-205	ENSMUST00000123746.1	893	No protein	Retained intron		1070	TSL:1
Ccdc33-209	ENSMUST00000151404.1	835	No protein	Retained intron	-	9 4 9	TSL:5
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The strategy is based on the design of *Ccdc33-203* transcript, the transcription is shown below:

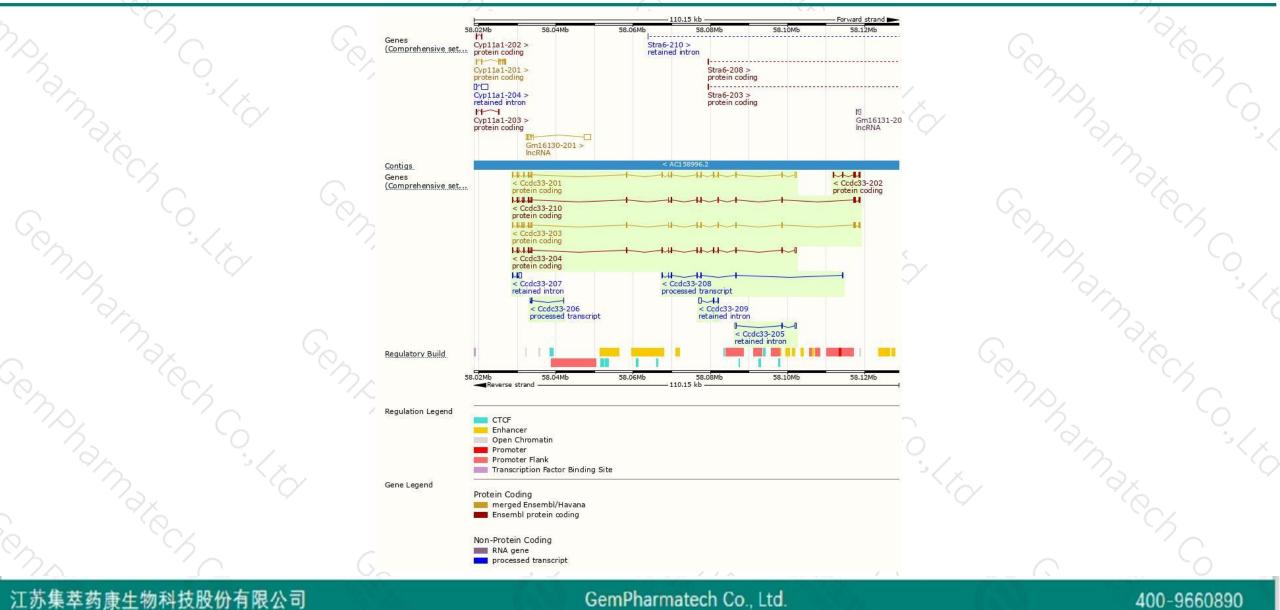


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Genomic location distribution





Protein domain



5	10			X	100				Go.		
9	ENSMUSP00000096 MobiDB lite Low complexity (Seg) Coiled-coils (Ncoils) Superfamily		SS	F49562		in constanti					6
	<u>Pfam</u>			C2 domain							
	PANTHER		Col	ed-coil domai	n-containing	protein 33					
2	Gene3D			C2 domain su	perfamily						0
	CDD			cd00030							~<
	All sequence SNPs/i	Sequence variants	dbSNP and a	other source	es)	1 1	1.1.1	11.1	П		
	Variant Legend	missense varia splice region v synonymous v	ariant							2	
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2	°°×	G.	2)	60%	5.	CC A		0	30	

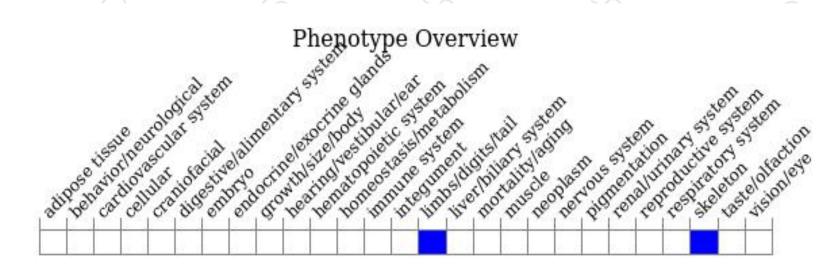
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Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).



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



