

C2cd3 Cas9-KO Strategy

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Design Date: 2020-8-2

Project Overview



Project Name

C2cd3

Project type

Cas9-KO

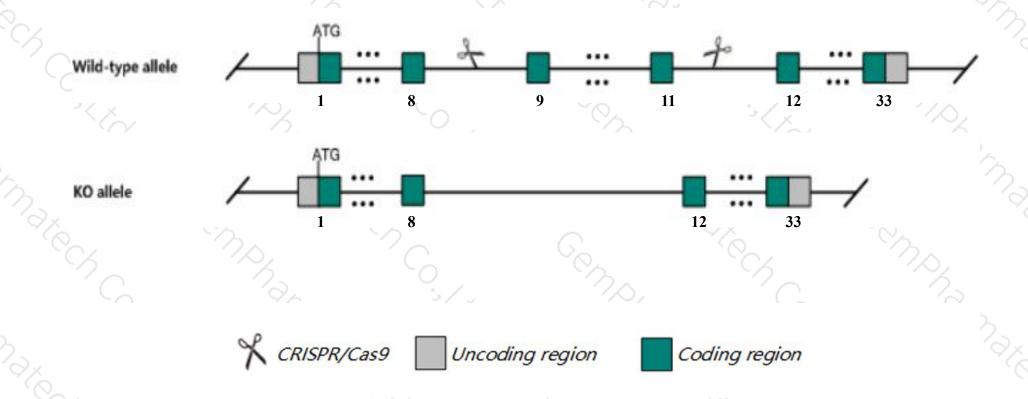
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the C2cd3 gene. The schematic diagram is as follows:



Technical routes



- The C2cd3 gene has 14 transcripts. According to the structure of C2cd3 gene, exon9-exon11 of C2cd3-201(ENSMUST00000051777.14) transcript is recommended as the knockout region. The region contains 472bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *C2cd3* 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.

Notice



- > According to the existing MGI data, homozygotes inactivating allele are embryonic lethal with pericardial edema and twisted body axis, abnormal patterning of brain and open neural tube defect.
- The *C2cd3* gene is located on the Chr7. 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)



C2cd3 C2 calcium-dependent domain containing 3 [Mus musculus (house mouse)]

Gene ID: 277939, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol C2cd3 provided by MGI

Official Full Name C2 calcium-dependent domain containing 3 provided by MGI

Primary source MGI:MGI:2142166

See related Ensembl: ENSMUSG00000047248

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 AU020772

Expression Ubiquitous expression in testis adult (RPKM 8.4), thymus adult (RPKM 7.8) and 28 other tissuesSee more

Orthologs <u>human all</u>

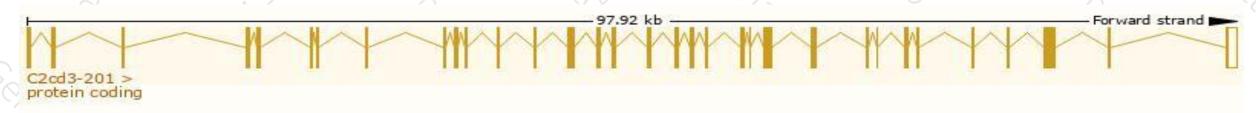
Transcript information (Ensembl)



The gene has 14 transcripts, all transcripts are shown below:

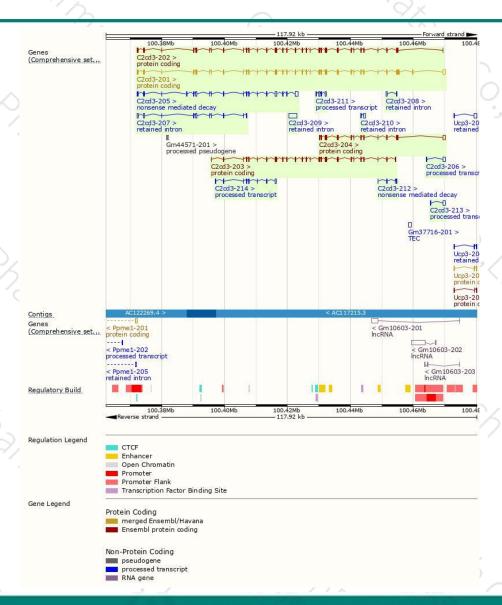
bp 4 7803 0 6602	2323aa 2130aa	Biotype Protein coding	CCDS CCDS57568	UniProt	Flags
0 6602	2000000	Protein coding	CCDS57568	OFDIER	
100	2130aa			Q52KB6	TSL:5 GENCODE basic APPRIS P2
	LIJUdd	Protein coding	-	E9Q526	TSL:5 GENCODE basic APPRIS ALT
4840	1566aa	Protein coding	29	D3Z640	CDS 5' incomplete TSL:1
3391	899aa	Protein coding	-	D3Z4D9	CDS 5' incomplete TSL:5
4167	250aa	Nonsense mediated decay	=	D6RH58	TSL:1
600	100aa	Nonsense mediated decay	-	V9GXB2	CDS 5' incomplete TSL:3
1 1304	No protein	Processed transcript	н ,	((- -))	TSL:5
925	No protein	Processed transcript	E	12.5	TSL:5
2 879	No protein	Processed transcript	-	155	TSL:1
788	No protein	Processed transcript	×	-	TSL:3
2576	No protein	Retained intron	8	023	TSL:NA
7 1909	No protein	Retained intron	=	0.00	TSL:1
660	No protein	Retained intron	=	(7 2 ()	TSL:2
1 639	No protein	Retained intron	5	653	TSL:2
	.8 3391 .7 4167 .1 600 .1 1304 .1 925 .2 879 .1 788 .1 2576 .7 1909 .1 660	8 3391 899aa .7 4167 250aa .1 600 100aa .1 1304 No protein .2 879 No protein .1 788 No protein .1 2576 No protein .7 1909 No protein .1 660 No protein	8 3391 899aa Protein coding 7 4167 250aa Nonsense mediated decay 1 600 100aa Nonsense mediated decay 1 1304 No protein Processed transcript 1 925 No protein Processed transcript 2 879 No protein Processed transcript 1 788 No protein Processed transcript 1 2576 No protein Processed transcript 1 2576 No protein Retained intron 1 1909 No protein Retained intron 1 660 No protein Retained intron	.8 3391 899aa Protein coding - .7 4167 250aa Nonsense mediated decay - .1 600 100aa Nonsense mediated decay - .1 1304 No protein Processed transcript - .1 925 No protein Processed transcript - .2 879 No protein Processed transcript - .1 788 No protein Processed transcript - .1 2576 No protein Retained intron - .7 1909 No protein Retained intron - .1 660 No protein Retained intron -	.8 3391 899aa Protein coding - D3Z4D9 .7 4167 250aa Nonsense mediated decay - D6RH58 .1 600 100aa Nonsense mediated decay - V9GXB2 .1 1304 No protein Processed transcript - - .1 925 No protein Processed transcript - - .2 879 No protein Processed transcript - - .1 788 No protein Retained intron - - .1 2576 No protein Retained intron - - .7 1909 No protein Retained intron - - .1 660 No protein Retained intron - -

The strategy is based on the design of *C2cd3-201* transcript, the transcription is shown below:



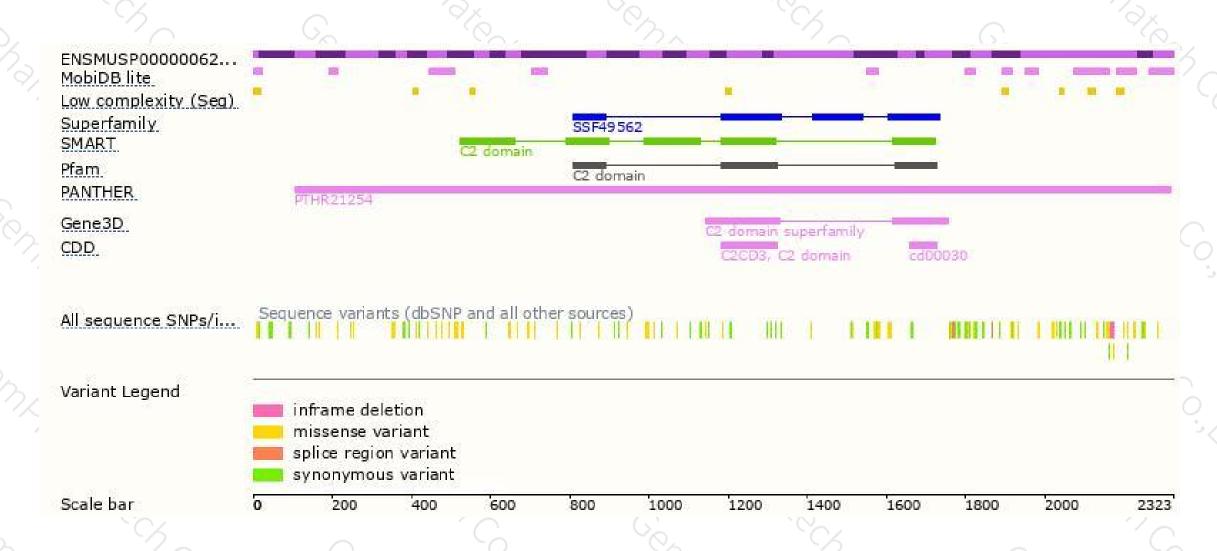
Genomic location distribution





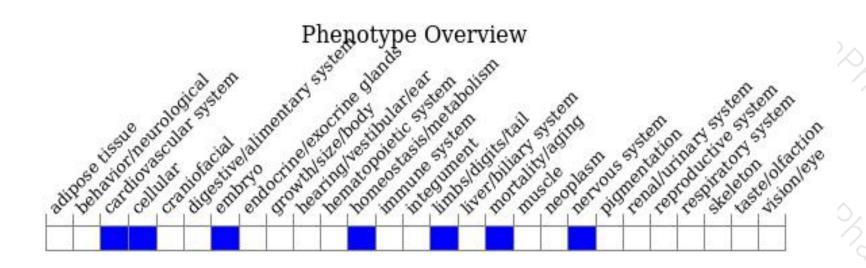
Protein domain





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, homozygotes inactivating allele are embryonic lethal with pericardial edema and twisted body axis, abnormal patterning of brain and open neural tube defect.



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





