

# Cdc42bpa Cas9-KO Strategy

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### Overview

#### Target Gene Name

• Cdc42bpa

#### Project Type

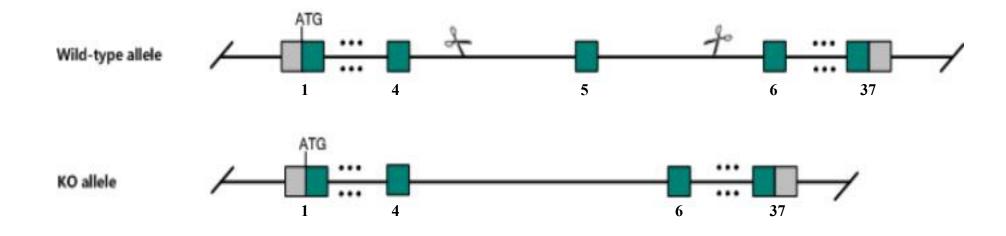
• Cas9-KO

#### Genetic Background

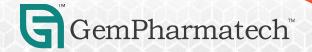
• C57BL/6JGpt



## Strain Strategy







#### **Technical Information**

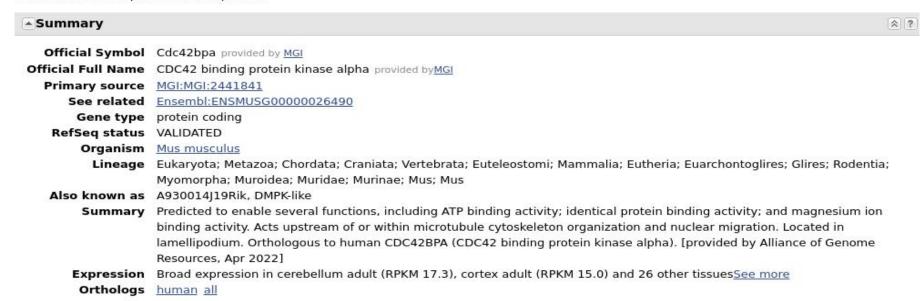
- The *Cdc42bpa* gene has 18 transcripts. According to the structure of *Cdc42bpa* gene, exon5 of *Cdc42bpa*-204 (ENSMUST00000111117.8) transcript is recommended as the knockout region. The region contains 149bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Cdc42bpa* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



#### Gene Information

#### Cdc42bpa CDC42 binding protein kinase alpha [Mus musculus (house mouse)]

Gene ID: 226751, updated on 12-Apr-2023



Source: https://www.ncbi.nlm.nih.gov/

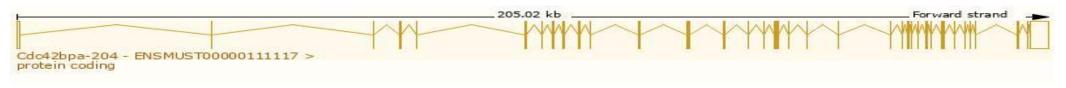


### Transcript Information

The gene has 18 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
dc42bpa-218	ENSMUST00000212756.	2 5247	1748aa	Protein coding			A single transcript chosen for a gene which is the most conserved, most highly expressed, has the longest coding sequence and is represented in other key resources, such as NCBI and UniProt. This is defined in detail on http://www.ersembl.org/info/genome/gene-build/canonical.html Ensembl Caronical. The GENCOOE set is the gene set for human and mouse. GENCODE basic. TSL5
dc42bpa-204	ENSMUST00000111117.	8 9161	<u>1732aa</u>	Protein coding	CCDS48466		The GENCODE set is the gene set for human and mouse. CENCODE basic, APPRIS ALTI., TSL-1,
dc42bpa-203	ENSMUST00000097453.	9 6704	1691aa	Protein coding			The GENCODE set is the gene set for human and mouse. GENCODE basic, TSLS ,
dc42bpa-212	ENSMUST00000143176.	8 6389	984aa	Protein coding			TSL5 , CDS 5' incomplete ,
dc42bpa-202	ENSMUST00000097450.1	5160	<u>1719aa</u>	Protein coding	CCDS83649		The GENCODE set is the gene set for human and mouse. GENCODE basic , APPRIS P4 , TSL1 ,
dc42bpa-201	ENSMUST00000076687.1	4917	1638aa	Protein coding	CCDS83650		The GENCODE set is the gene set for human and mouse. GENCODE basic, TSLS ,
dc42bpa-207	ENSMUST00000133890.	8 3567	1048aa	Protein coding			TSL-5 , CDS 5' incomplete ,
dc42bpa-209	ENSMUST00000135056.	8 2197	732aa	Protein coding			TSL5, CDS 5' and 3' incomplete,
dc42bpa-214	ENSMUST00000145181.	2 554	185aa	Protein coding			TSL2 , CDS 5' and 3' incomplete ,
dc42bpa-208	ENSMUST00000134959.	8 2892	93aa	Nonsense mediated decay			TSL5,
dc42bpa-213	ENSMUST00000143350.	8 1298	No protein	Protein coding CDS not defined			TSL1.
dc42bpa-215	ENSMUST00000145274.	2 645	No protein	Protein coding CDS not defined			TSL3,
dc42bpa-216	ENSMUST00000152582.	8 3900	No protein	Retained intron			TSL1,
dc42bpa-217	ENSMUST00000194974.	2 3175	No protein	Retained intron			TSLNA,
dc42bpa-211	ENSMUST00000143161.	2 2447	No protein	Retained intron			TSL1.
dc42bpa-206	ENSMUST00000132894.	3 2129	No protein	Retained intron			15.1.
dc42bpa-205	ENSMUST00000129754.	2 951	No protein	Retained intron			151.2
dc42bpa-210	ENSMUST00000139002.	2 732	No protein	Retained intron			TSLS.

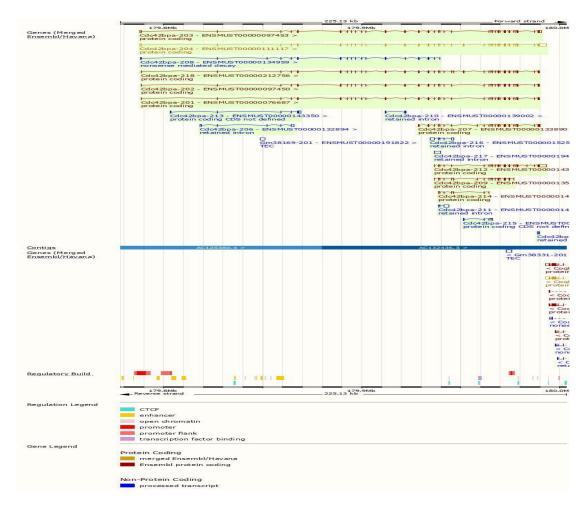
The strategy is based on the design of *Cdc42bpa*-204 transcript, the transcription is shown below



Source: https://www.ensembl.org



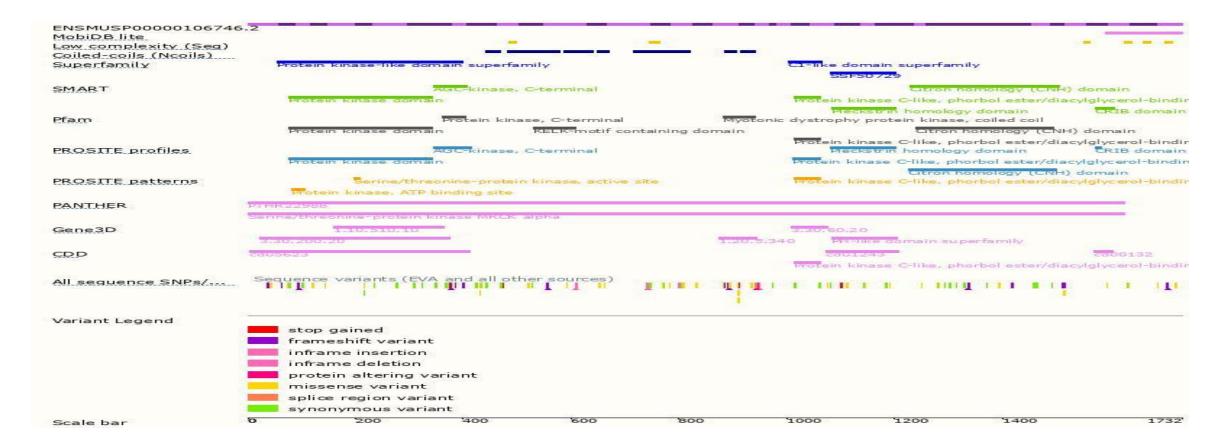
### Genomic Information





Source: : https://www.ensembl.org

#### Protein Information





### Important Information

- *Cdc42bpa* is located on Chr1. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

