

# Cd276 Cas9-CKO Strategy

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#### Overview

#### Target Gene Name

• Cd276

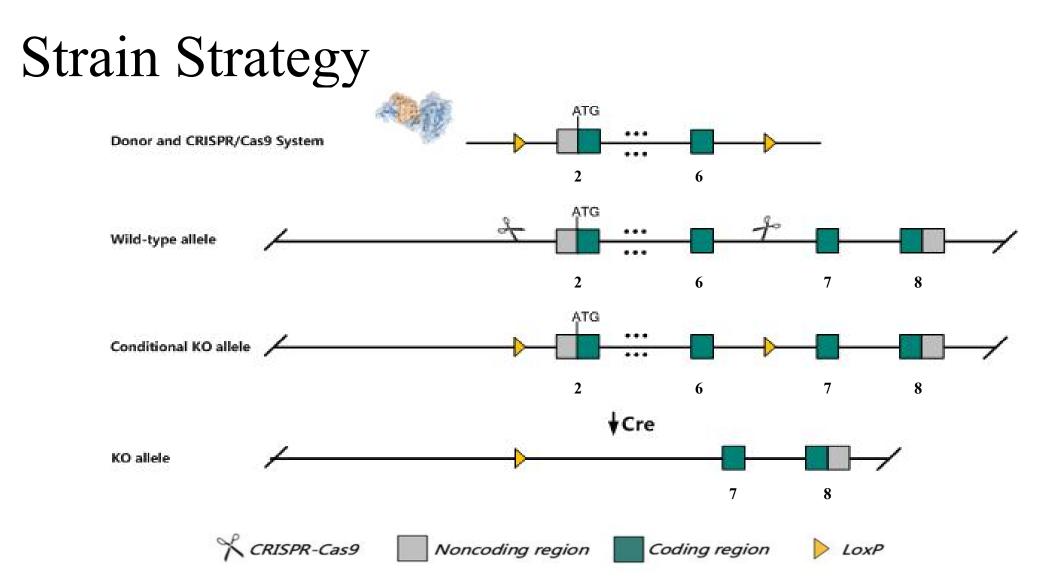
Project Type

• Cas9-CKO

Genetic Background

• C57BL/6JGpt





Schematic representation of CRISPR-Cas9 engineering used to edit the Cd276 gene.

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### **Technical Information**

- The *Cd276* gene has 4 transcripts. According to the structure of *Cd276* gene, exon2-exon6 of *Cd276*-202 (ENSMUST00000165365.3) transcript is recommended as the knockout region. The region contains start codon ATG. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Cd276* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

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#### Gene Information

#### Cd276 CD276 antigen [Mus musculus (house mouse)]

Gene ID: 102657, updated on 13-Mar-2020

Summary		\$
Official Symbol	Cd276 provided by MGI	
Official Full Name	CD276 antigen provided by MGI	
Primary source	MGI:MGI:2183926	
See related	Ensembl:ENSMUSG00000035914	
Gene type	protein coding	
<b>RefSeq status</b>	PROVISIONAL	
Organism	Mus musculus	
Lineage		
	Muroidea; Muridae; Murinae; Mus; Mus	
	6030411F23Rik, AU016588, B7RP-2, B7h3	
Expression	Broad expression in limb E14.5 (RPKM 25.4), CNS E14 (RPKM 11.9) and 22 other tissues See more	
Orthologs	human all	

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

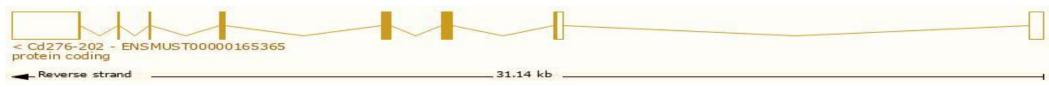


### **Transcript Information**

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

Name	Transcript ID	D bp Protein Biotype		Biotype CCDS		UniProt	Flags				
Cd276-202	ENSMUST00000165365.2	3603	<u>316aa</u>	Protein coding	CCDS23244	A6MDC5 Q8VE98	TSL1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1				
Cd276-201	ENSMUST00000039788.10	3186	<u>316aa</u>	Protein coding	<u>CCDS23244</u>	A6MDC5 Q8VE98	TSL1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1				
Cd276-203	ENSMUST00000213722.1	434	<u>145aa</u>	Protein coding		A0A1L1SUD4	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				
Cd276-204	ENSMUST00000216629.1	346	<u>94aa</u>	Protein coding	1	<u>A0A1L1SV51</u>	CDS 5' incomplete TSL3				

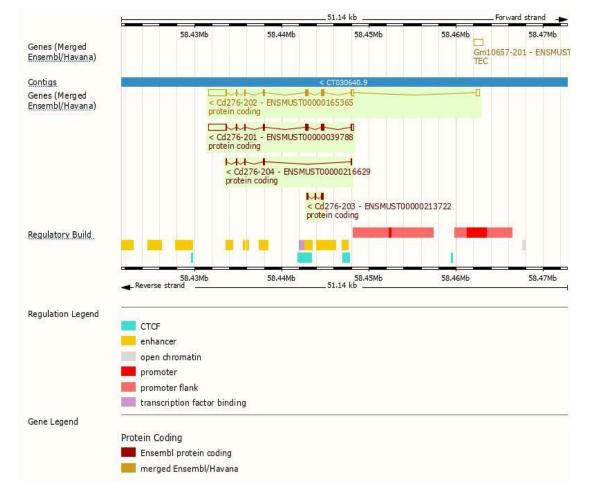
The strategy is based on the design of Cd276-202 transcript, the transcription is shown below:



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



#### Genomic Information



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

#### Protein Information

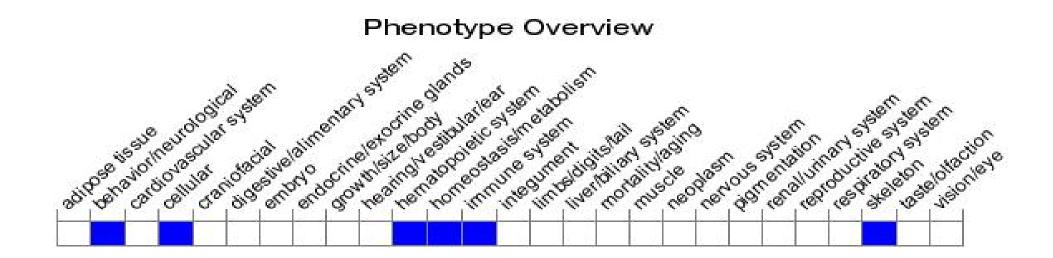
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ENSMUSP0000129418 Transmembrane helices PDB-ENSP mappings MobiDB lite Low complexity (Seg) Cleavage site (Sig AFDB-ENSP mappings Superfamily SMART	Immunogio Immu	bulin-like domain si inoglobulin V-set do lobulin subtype		-					
Pfam		oglobulin subtype 2 Iobulin V-set domai		PF13927					
PROSITE profiles PANTHER	Immunoglobulin-like PTHK241001SF2 PTHK24100	domain		20 20				_	
Gene3D	Immunogi	obulin-like told				_	-		
All sequence SNPs/	Sequence variants (E	VA and all other s	sources)	1 11			1.		
Variant Legend	stop gained frameshift varia missense varian stop retained va	t iriant							
Scale bar	<b>b</b> 40	80	120	160	200		240		316

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

## Mouse Phenotype Information (MGI)



• Inactivation of this locus results in abnormal T helper 1 physiology. Mutant mice have an increased susceptibility to inflammation and autoimmunity.

Source: https://www.informatics.jax.org

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### **Important Information**

- According to the existing MGI data, Inactivation of this locus results in abnormal T helper 1 physiology. Mutant mice have an increased susceptibility to inflammation and autoimmunity.
- The effect on transcript *Cd276*-203 is unknown.
- *Cd276* is located on Chr9. 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

