

Cd276 Cas9-KO Strategy

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Design Date: 2019-9-5

Overview

Target Gene Name

- Cd276

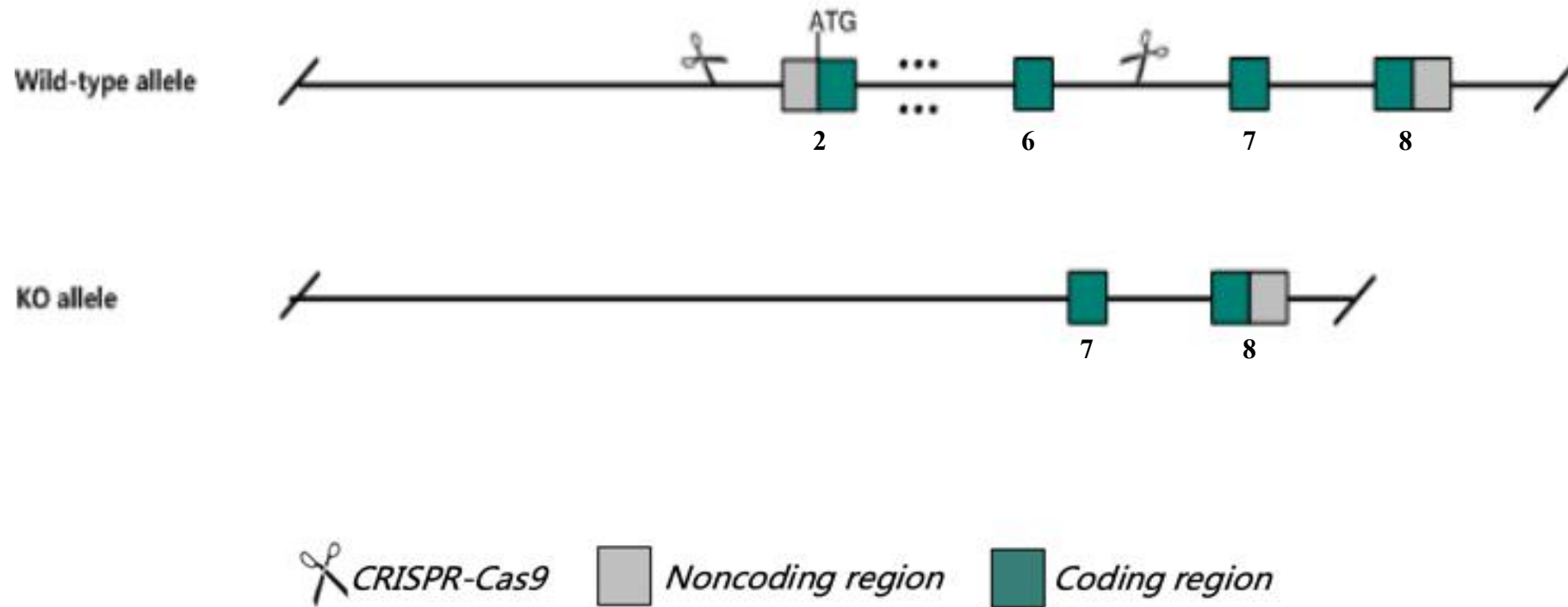
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



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: 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

Cd276 CD276 antigen [Mus musculus (house mouse)]

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

Summary

| | |
|---------------------------|---|
| Official Symbol | Cd276 <small>provided by MGI</small> |
| Official Full Name | CD276 antigen <small>provided by MGI</small> |
| Primary source | MGI:MGI:2183926 |
| See related | Ensembl:ENSMUSG00000035914 |
| Gene type | protein coding |
| RefSeq status | PROVISIONAL |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 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 |

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

Transcript Information

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

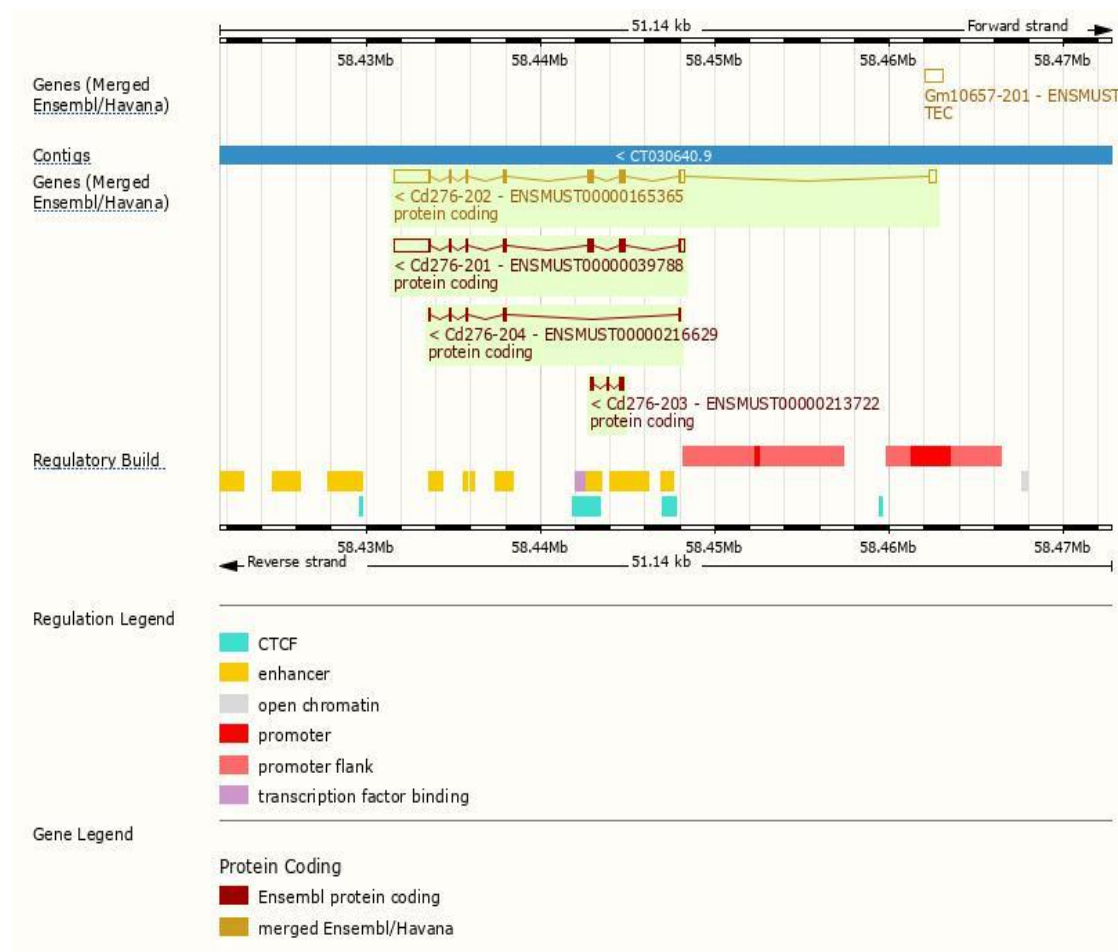
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|----------------|---------------------------|-------------------------------|--|
| Cd276-202 | ENSMUST00000165365.2 | 3603 | 316aa | Protein coding | 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 | 316aa | 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 |
| Cd276-203 | ENSMUST00000213722.1 | 434 | 145aa | 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 | 94aa | Protein coding | . | A0A1L1SV51 | CDS 5' incomplete TSL:3 |

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

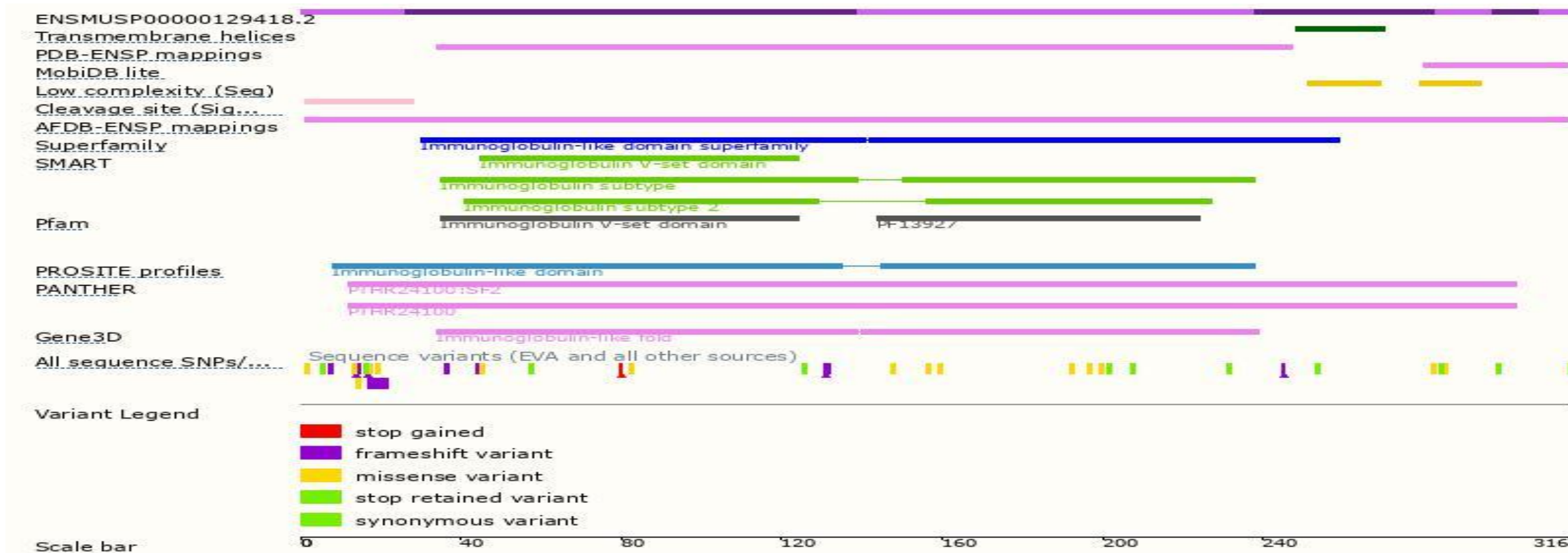


Source: <https://www.ensembl.org>

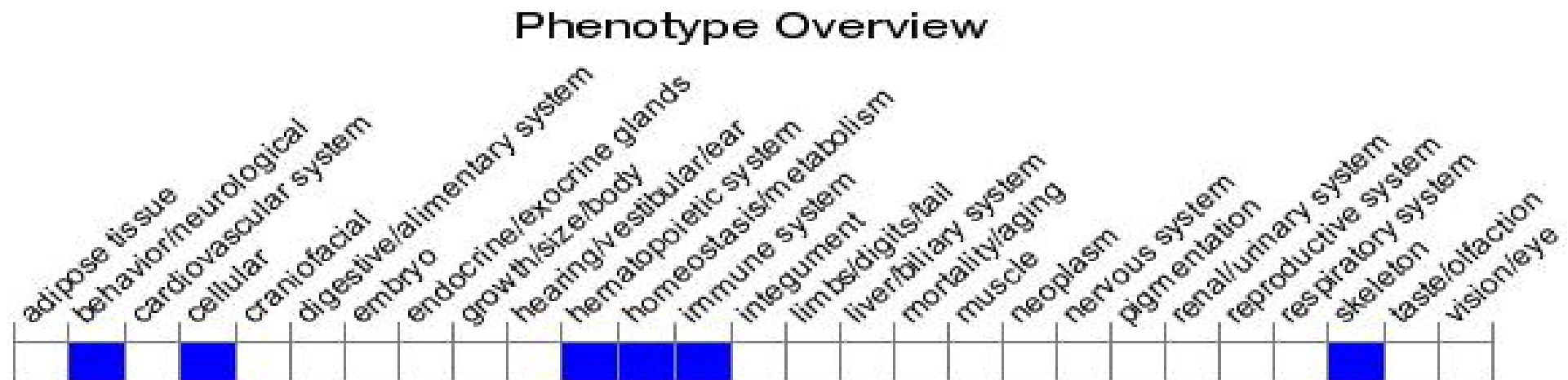
Genomic Information



Protein Information



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.

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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.