

Muc6 Cas9-KO Strategy

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Overview

Target Gene Name

• Muc6

Project Type

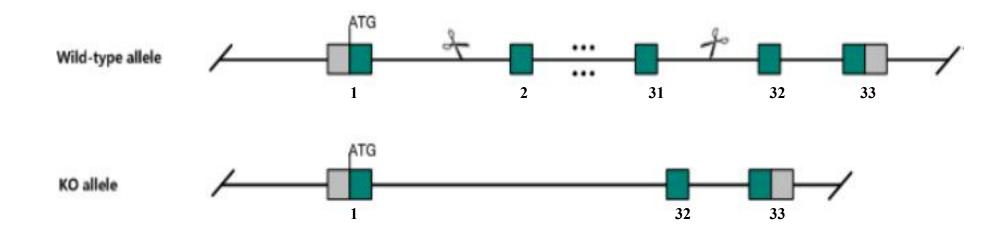
• Cas9-KO

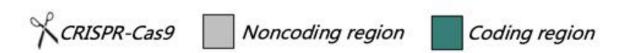
Genetic Background

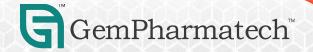
• C57BL/6JGpt



Strain Strategy







Technical Information

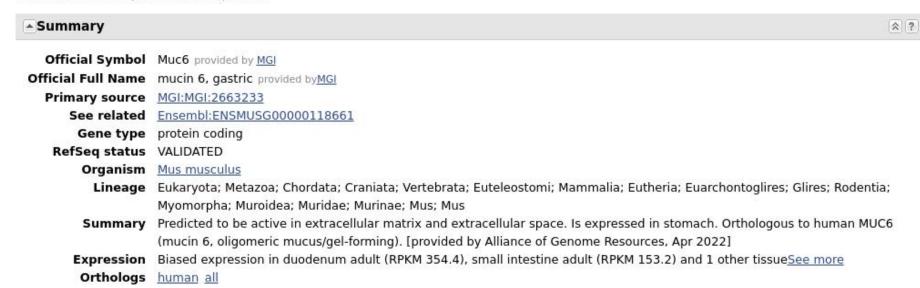
- The *Muc6* gene has 1 transcript. According to the structure of *Muc6* gene, exon2-exon31 of *Muc6*-201 (ENSMUST00000239500.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Muc6* 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 ontarget 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

Muc6 mucin 6, gastric [Mus musculus (house mouse)]

Gene ID: 353328, updated on 26-Apr-2023



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

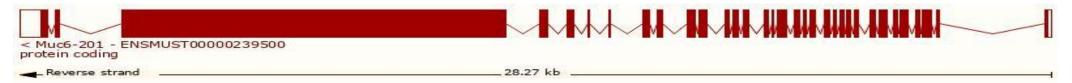


Transcript Information

The gene has 1 transcript, and the transcript is shown below:



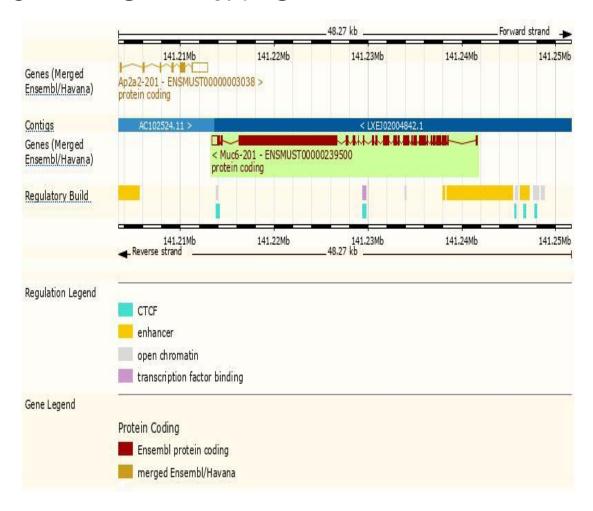
The strategy is based on the design of *Muc6*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



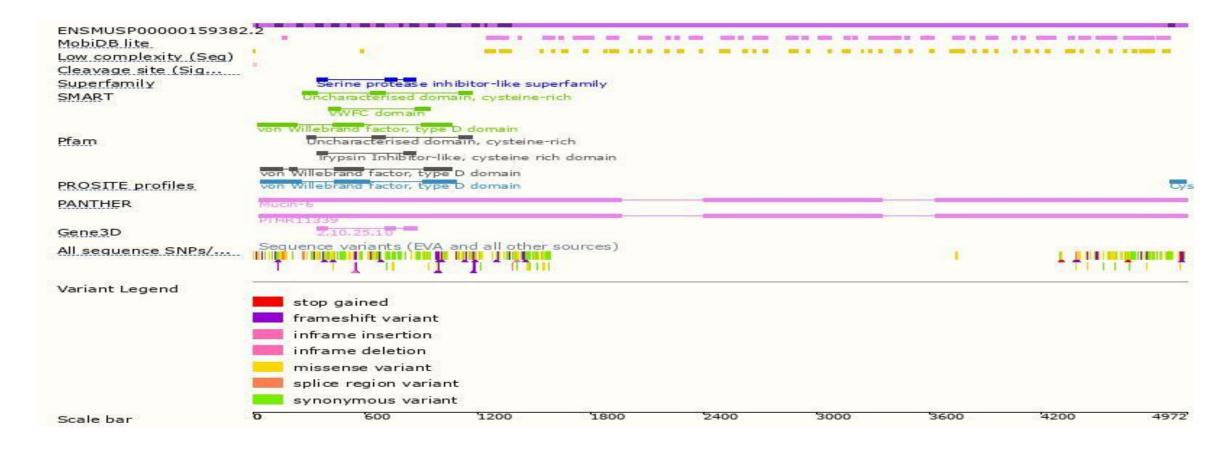
Genomic Information





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

Protein Information





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

Important Information

- *Muc6* is located on Chr7. 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.

