

Muc2 Cas9-CKO Strategy

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Overview

Target Gene Name

- Muc2

Project Type

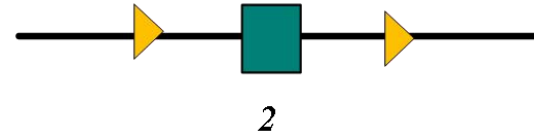
- Cas9-CKO

Genetic Background

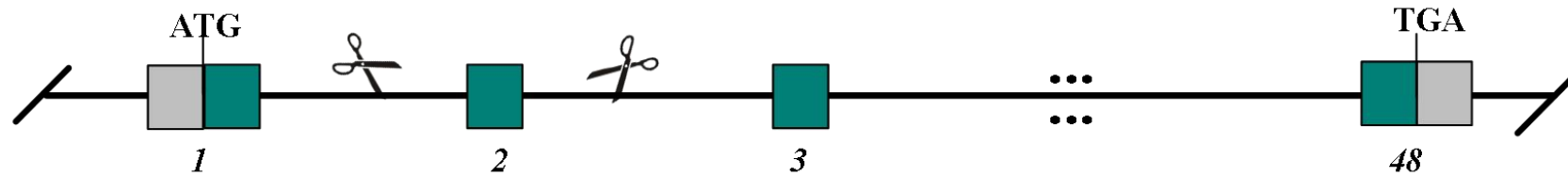
- C57BL/6JGpt

Strain Strategy

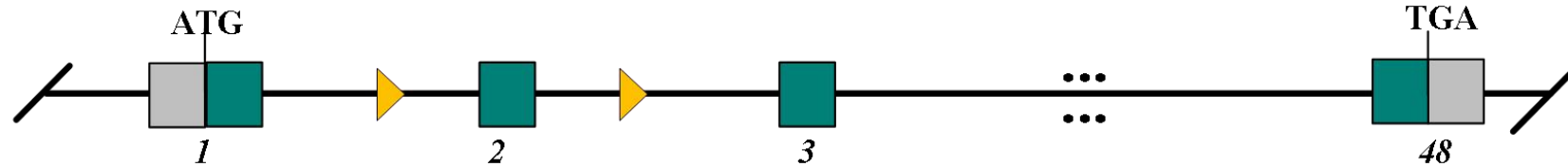
Donor and CRISPR-Cas9 System



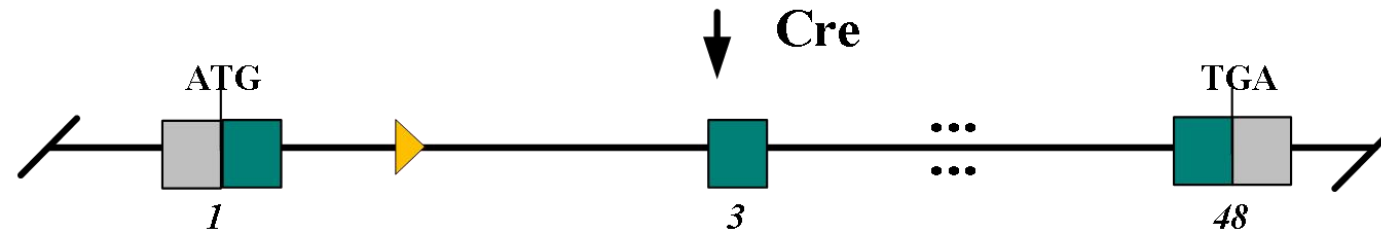
Wild-type allele



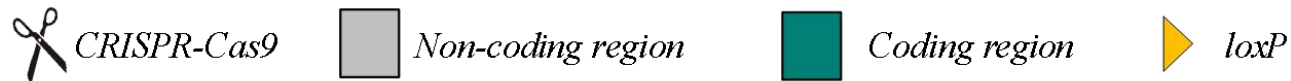
Conditional KO allele



KO allele



↓ Cre



Schematic representation of CRISPR-Cas9 engineering used to edit the *Muc2* gene.

Technical Information

- The *Muc2* gene has 1 transcript. According to the structure of *Muc2* gene, exon 2 of *Muc2*-201 (ENSMUST00000185406.8) transcript is recommended as the knockout region. The region contains 262 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Muc2* 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.

Gene Information

Muc2 mucin 2 [Mus musculus (house mouse)]

Gene ID: 17831, updated on 18-May-2023

Summary

Official Symbol	Muc2 provided by MGI
Official Full Name	mucin 2 provided by MGI
Primary source	MGI:MGI:1339364
See related	Ensembl:ENSMUSG00000025515
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	2010015E03Rik, MCM, wnn
Summary	Predicted to enable identical protein binding activity. Acts upstream of or within several processes, including epithelial cell development; negative regulation of cell migration; and positive regulation of apoptotic process. Located in extracellular matrix; inner mucus layer; and outer mucus layer. Is expressed in ileum and intestine. Used to study inflammatory bowel disease. Human ortholog(s) of this gene implicated in asthma. Orthologous to human MUC2 (mucin 2, oligomeric mucus/gel-forming). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Annotation category: partial on reference assembly See more
Orthologs	human all

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

Transcript Information

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

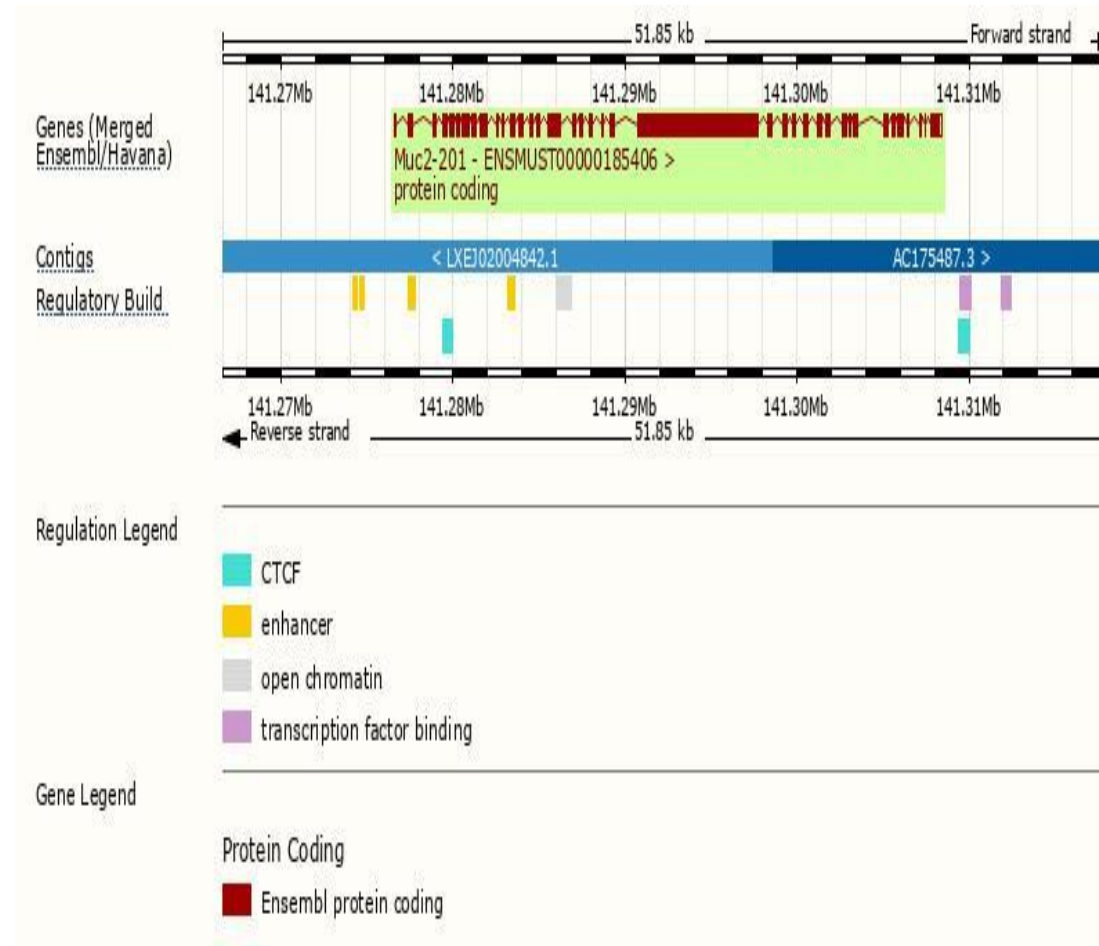
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000185406.8	Muc2-201	13916	4576aa	Protein coding		Q80Z19	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:5

The strategy is based on the design of *Muc2-201* transcript, the transcription is shown below:

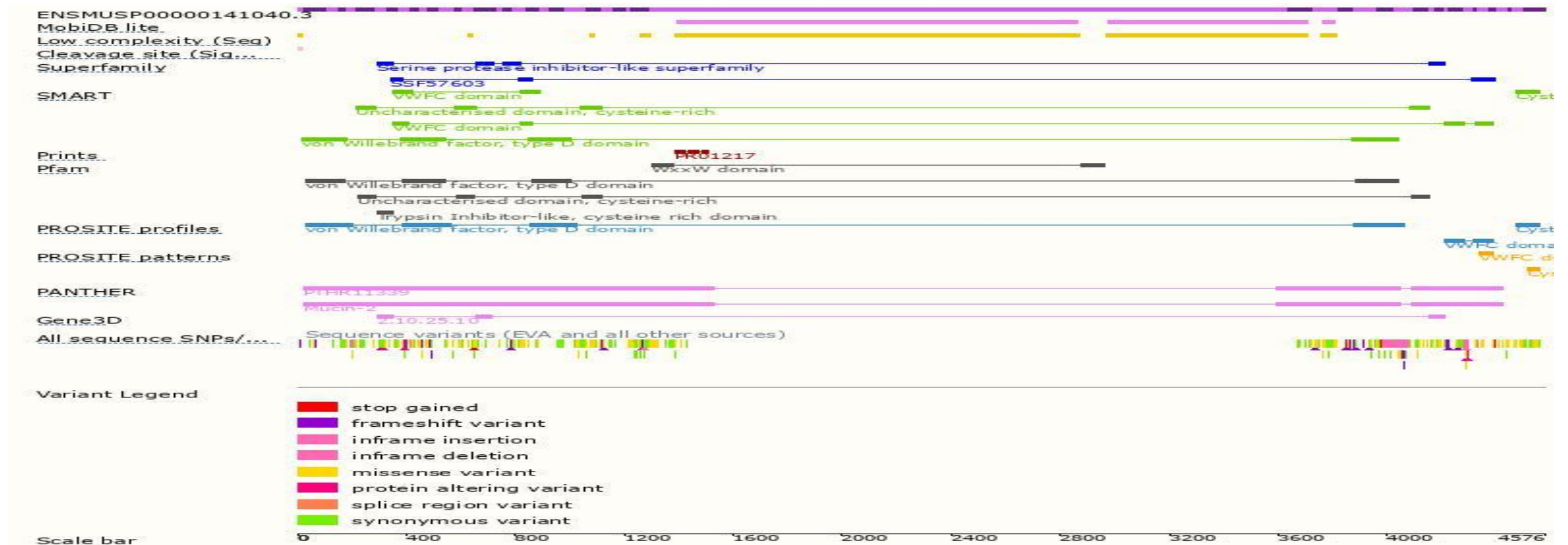


Source: <https://www.ensembl.org>

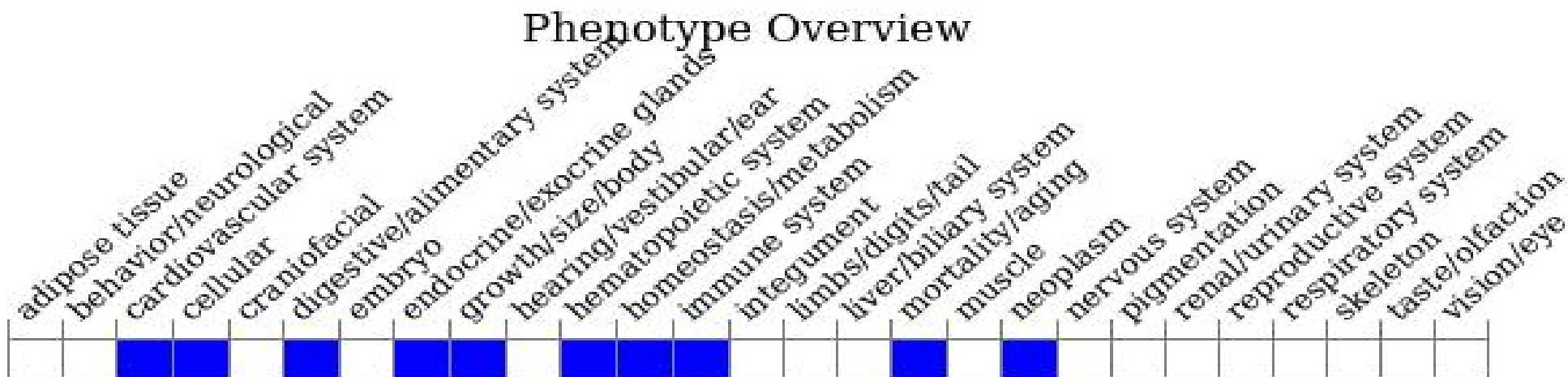
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Homozygotes for a point mutation have soft feces at weaning and develop diarrhea associated with malabsorption syndrome. Homozygous null mutants pass blood in their feces at 6 months, and 65% of null mutants have intestinal tumors at 1 year.

Important Information

- According to the existing MGI data, Homozygotes for a point mutation have soft feces at weaning and develop diarrhea associated with malabsorption syndrome. Homozygous null mutants pass blood in their feces at 6 months, and 65% of null mutants have intestinal tumors at 1 year.
- After cross cre, 25 amino acids remained at the N-terminus of this strategy, with unknown effects.
- *Muc2* 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.