Muc2 Cas9-KO Strategy

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Design Date: 2020-11-3

Project Overview



Project Name

Muc2

Project type

Cas9-KO

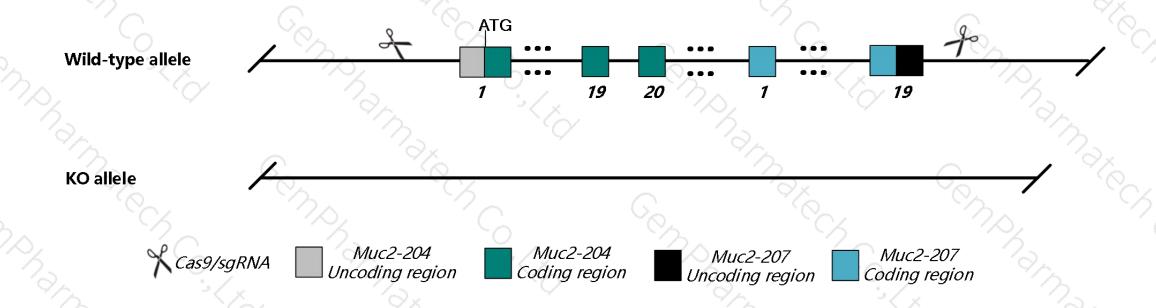
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Muc2 gene. The schematic diagram is as follows:



Technical routes



- The *Muc2* gene has 8 transcripts. According to the structure of *Muc2* gene, exon1 of *Muc2*-204 (ENSMUST00000185406.6) -exon19 of *Muc2-207* (
 - ENSMUST00000187945.6) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock 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: sgRNA was transcribed in vitro.Cas9, sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice



- According to the existing MGI data, homozygotes for a point mutation have soft feces at weaning and develop diarrhea associated with malapsorption syndrome. Homozygous null mutants pass blood in their feces at 6 months, and 65% of null mutants have intestinal tumors at 1 year.
- ➤ The *Muc2* gene is located on the Chr7. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

(NCBI) Gene information



Muc2 mucin 2 [Mus musculus (house mouse)]

Gene ID: 17831, updated on 27-Oct-2020

Summary

Official Symbol Muc2 provided by MGI

Official Full Name mucin 2 provided by MGI

Primary source MGI:MGI:1339364

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 MCM; wnn; 2010015E03Rik

Annotation information Annotation category: suggests misassembly

Expression Biased expression in colon adult (RPKM 1294.7), large intestine adult (RPKM 306.2) and 2 other tissues See more

Orthologs human all

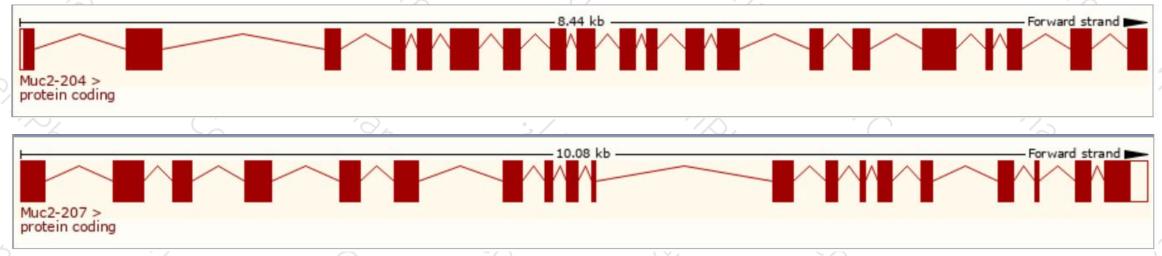
Transcript information (Ensembl)



The gene has 8 transcripts, and all transcripts are shown below:

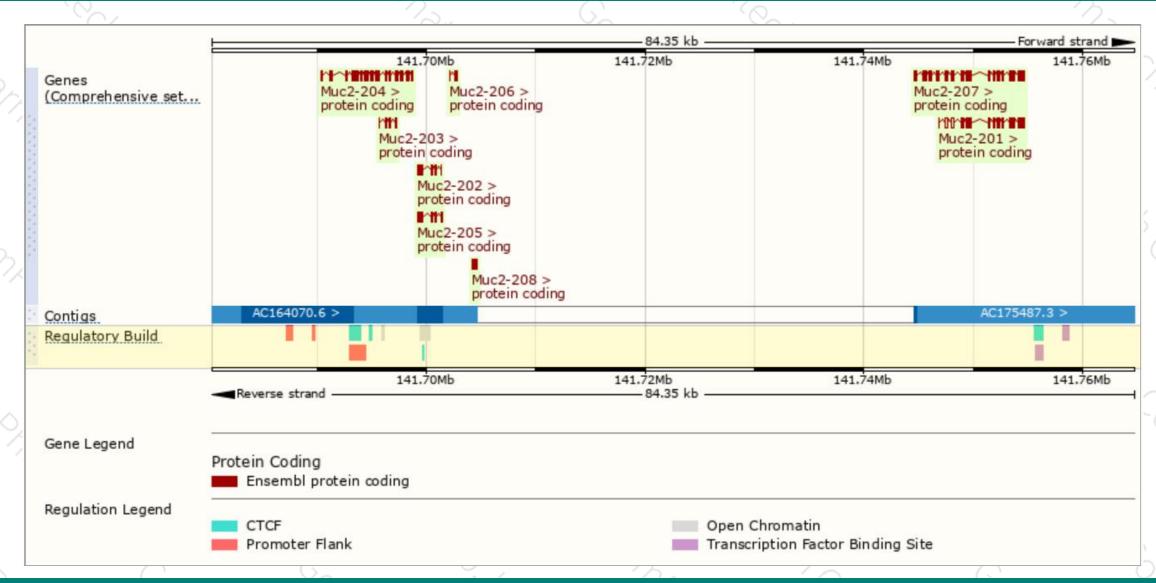
| Name 🍦 | Transcript ID 🛊 | bp 🛊 | Protein | Biotype 🍦 | CCDS | UniProt | Flags |
|----------|----------------------|------|--------------|----------------|---------------|-------------|---------------------------------|
| Muc2-207 | ENSMUST00000187945.6 | 2926 | <u>923aa</u> | Protein coding | 37.7 | A0A087WSP1 | CDS 5' incomplete TSL:1 |
| Muc2-204 | ENSMUST00000185406.6 | 2690 | <u>887aa</u> | Protein coding | - | A0A087WSG8& | CDS 3' incomplete TSL:5 |
| Muc2-201 | ENSMUST00000026590.8 | 2032 | 483aa | Protein coding | | A0A140T8I8& | TSL:1 GENCODE basic APPRIS P1 |
| Muc2-205 | ENSMUST00000185823.6 | 823 | 274aa | Protein coding | - | A0A087WS13& | CDS 5' and 3' incomplete TSL:3 |
| Muc2-202 | ENSMUST00000167366.2 | 711 | 237aa | Protein coding | 7 - 02 | F6QGV1& | TSL:5 GENCODE basic |
| Muc2-208 | ENSMUST00000191587.1 | 447 | 149aa | Protein coding | - | A0A087WP72& | CDS 5' and 3' incomplete TSL:NA |
| Muc2-203 | ENSMUST00000179227.1 | 399 | <u>132aa</u> | Protein coding | - | Q9R1L0& | TSL:1 GENCODE basic |
| Muc2-206 | ENSMUST00000187789.1 | 241 | 80aa | Protein coding | - | A0A087WQU6函 | CDS 5' and 3' incomplete TSL:5 |

The strategy is based on the design of *Muc2*-204&*Muc2*-207 transcript, The transcription is shown below:



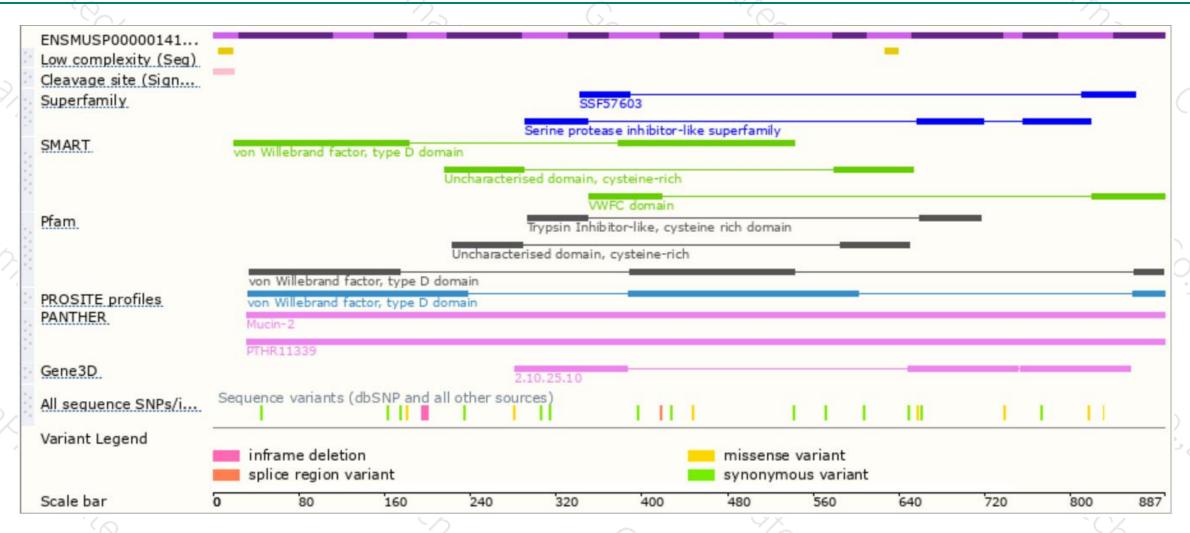
Genomic location distribution





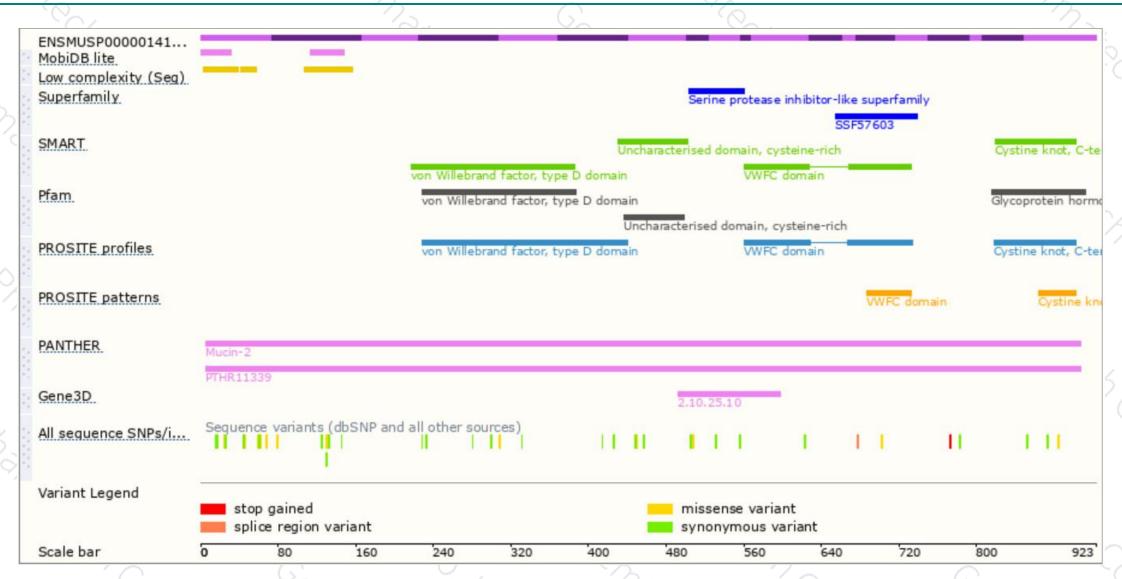
Protein domain





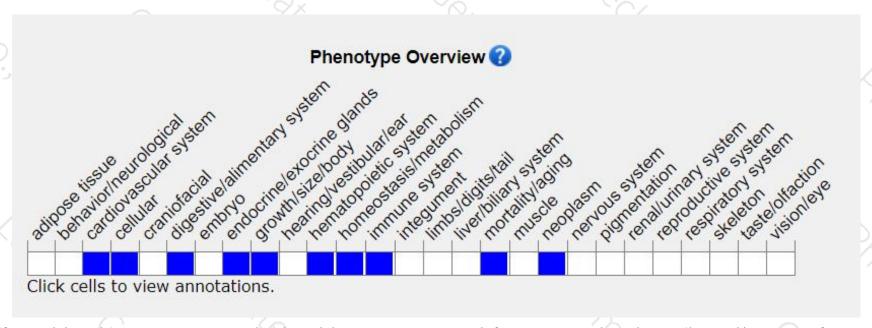
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/) .

According to the existing MGI data, homozygotes for a point mutation have soft feces at weaning and develop diarrhea associated with malapsorption syndrome. Homozygous null mutants pass blood in their feces at 6 months, and 65% of null mutants have intestinal tumors at 1 year.

If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





