



Muc5ac Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-4-14

Project Overview

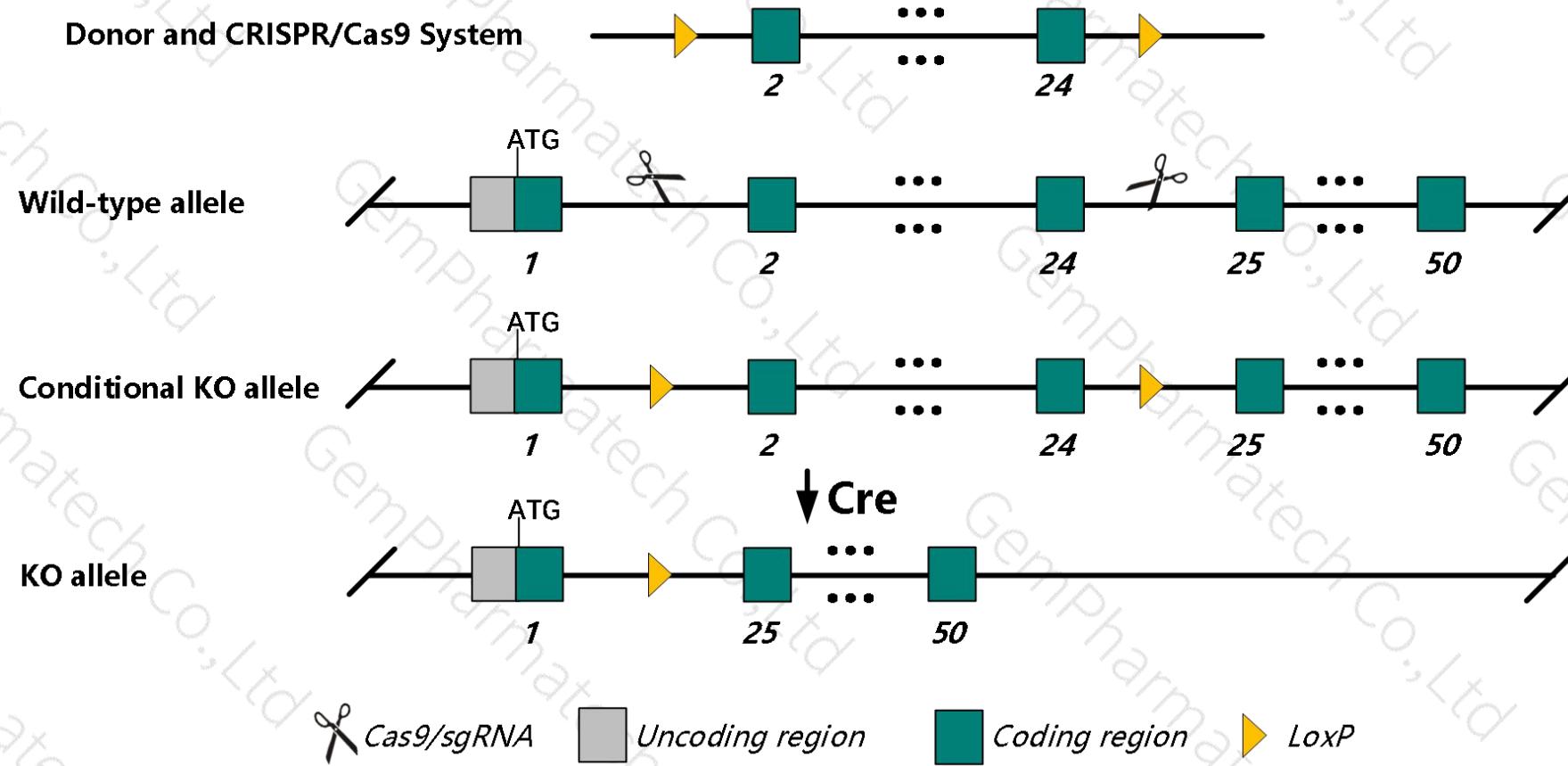
Project Name***Muc5ac***

Project type**Cas9-CKO**

Strain background**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Muc5ac* gene. The schematic diagram is as follows:



Technical routes

- The *Muc5ac* gene has 3 transcripts. According to the structure of *Muc5ac* gene, exon2-exon24 of *Muc5ac-201* (ENSMUST00000041924.13) transcript is recommended as the knockout region. The region contains 3008bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Muc5ac* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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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Notice

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased susceptibility to *T. muris* infection with persistent worm burden, goblet cell hyperplasia, and increased serum IFN-gamma despite a normal TH2-type immune response. A portion of mice show corneal opacity and poor tear quality.
- The *Muc5ac* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Muc5ac mucin 5, subtypes A and C, tracheobronchial/gastric [*Mus musculus* (house mouse)]

Gene ID: 17833, updated on 10-Sep-2019

Summary

Official Symbol Muc5ac provided by [MGI](#)

Official Full Name mucin 5, subtypes A and C, tracheobronchial/gastric provided by [MGI](#)

Primary source [MGI:MGI:104697](#)

See related [Ensembl:ENSMUSG00000037974](#)

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 MGM; 2210005L13Rik

Expression Restricted expression toward stomach adult (RPKM 445.3) [See more](#)

Orthologs [human](#) [all](#)

Genomic context

Location: 7 F5; 7 87.23 cM

See Muc5ac in [Genome Data Viewer](#)

Exon count: 49

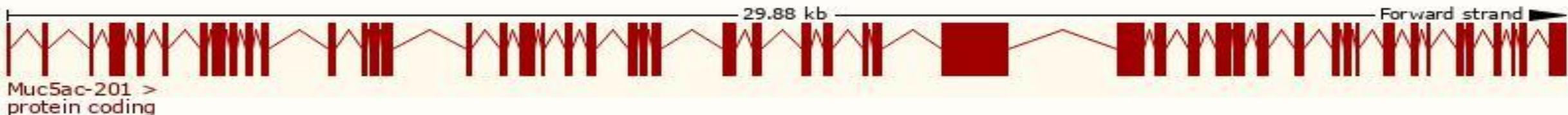
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (141788958..141819227)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (148974916..149005040)

Transcript information (Ensembl)

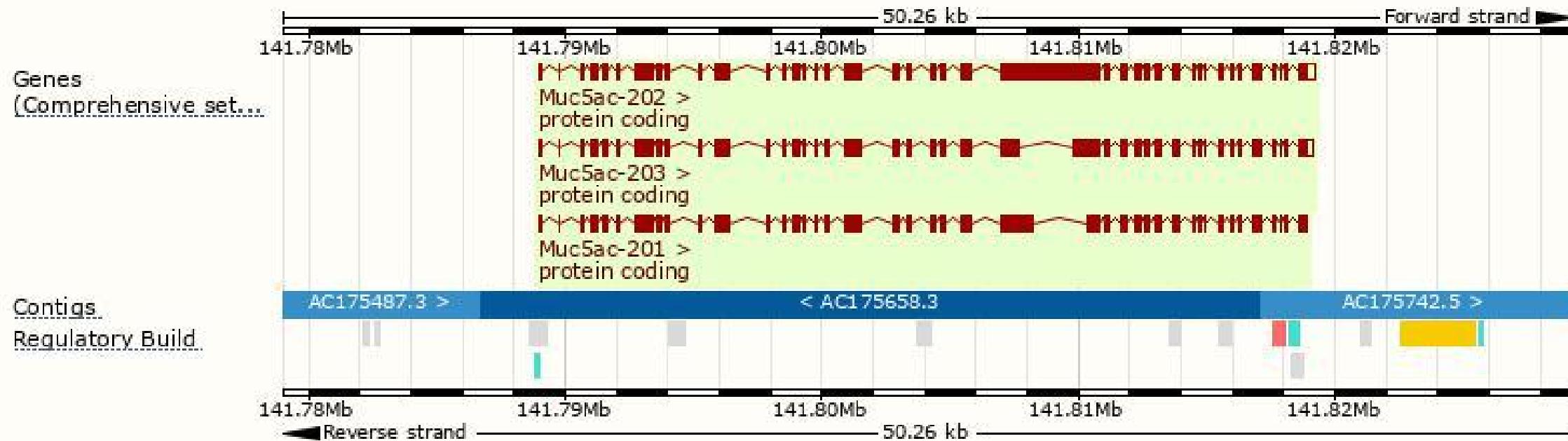
The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Muc5ac-201	ENSMUST00000041924.13	8256	2751aa	Protein coding	CCDS40189	E9PWB6	TSL:5 GENCODE basic APPRIS P2
Muc5ac-202	ENSMUST00000155534.8	10752	3455aa	Protein coding	-	E9QAQ8	TSL:5 GENCODE basic APPRIS ALT2
Muc5ac-203	ENSMUST00000163321.2	8505	2751aa	Protein coding	-	E9PWB6	TSL:5 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Muc5ac-201* transcript, the transcription is shown below



Genomic location distribution



Gene Legend

Protein Coding

Ensembl protein coding

Regulation Legend

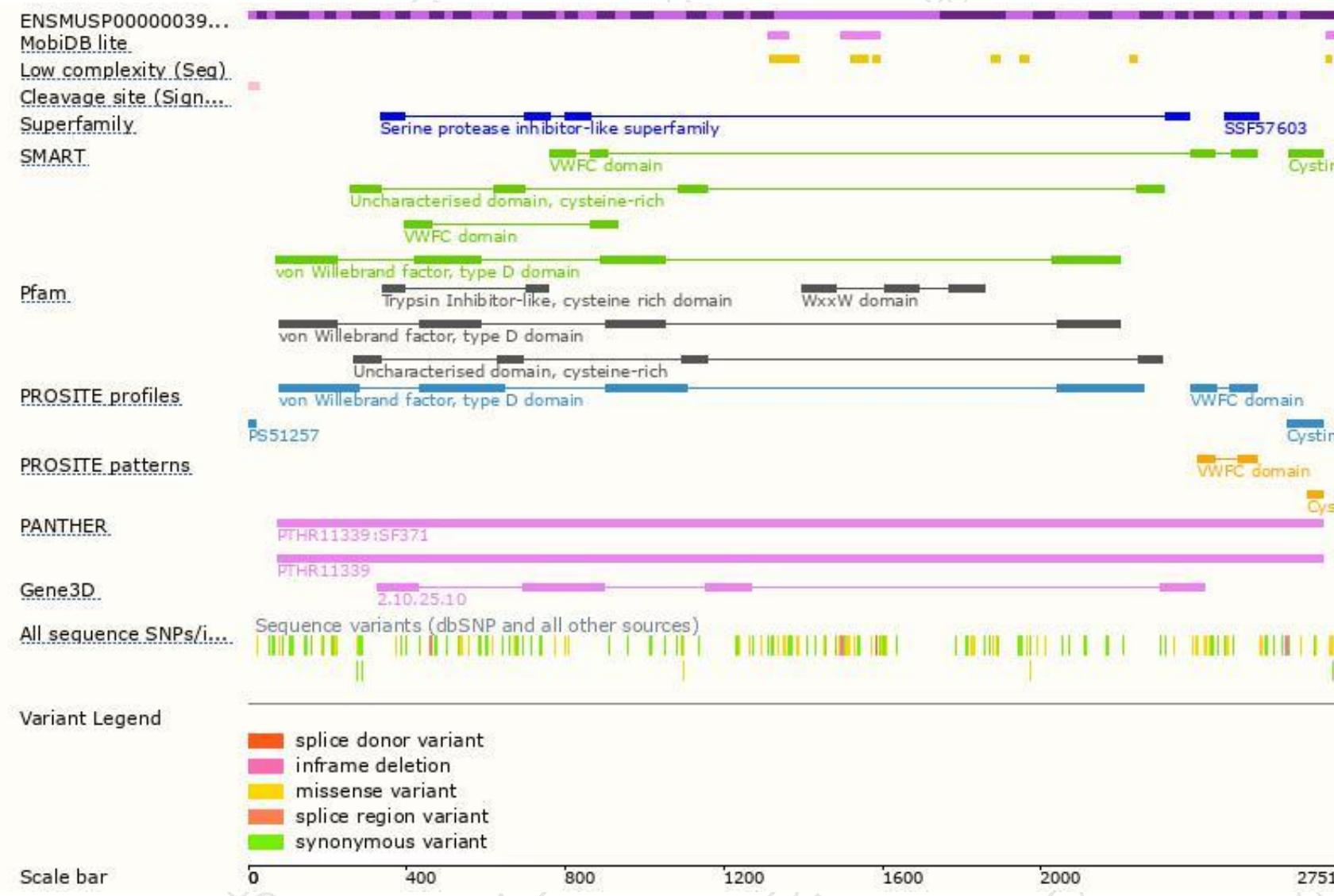
CTCF

Enhancer

Open Chromatin

Promoter Flank

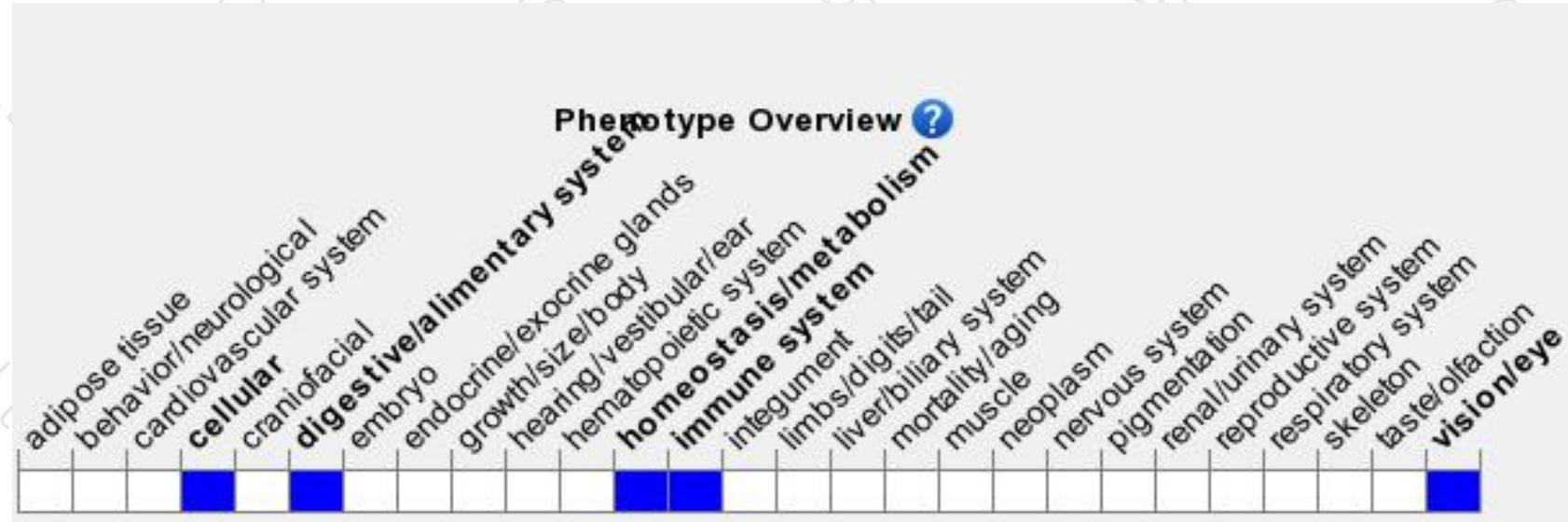
Protein domain





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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, Mice homozygous for a knock-out allele exhibit increased susceptibility to *T. muris* infection with persistent worm burden, goblet cell hyperplasia, and increased serum IFN-gamma despite a normal TH2-immune response. A portion of mice show corneal opacity and poor tear quality.



If you have any questions, you are welcome to inquire.

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