

Muc5ac Cas9-KO Strategy

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Project Overview

Project Name

Muc5ac

Project type

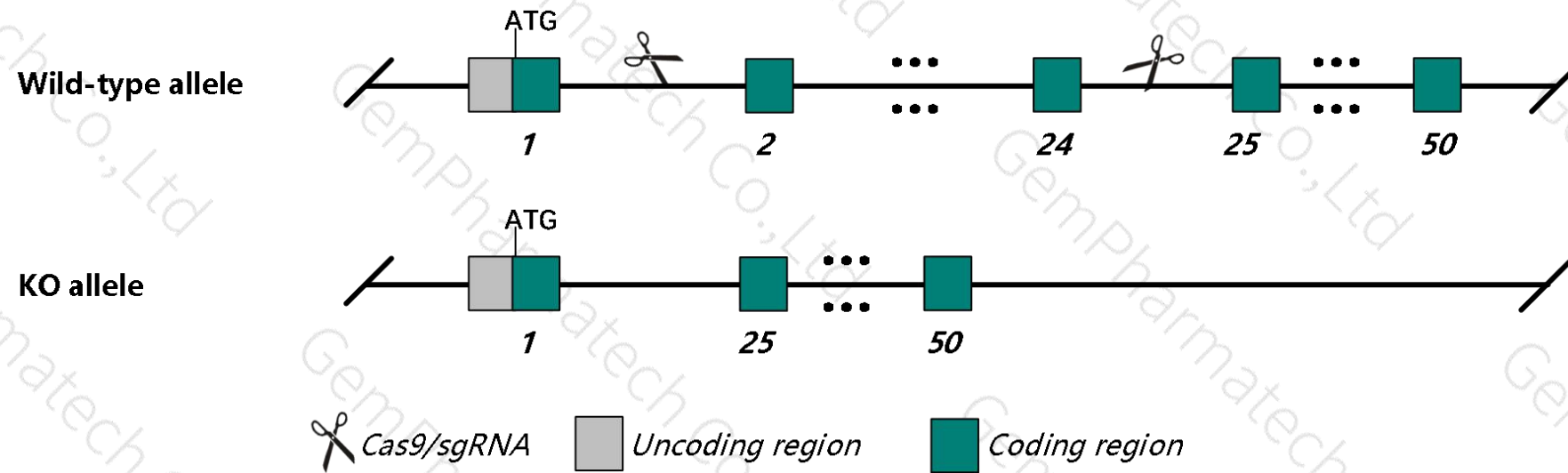
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 v

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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

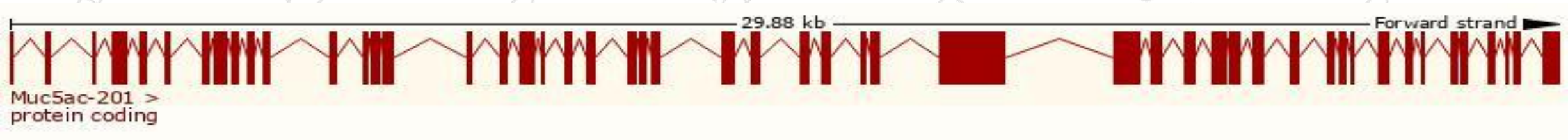
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (141788958..141819227)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (148974916..149005040)

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



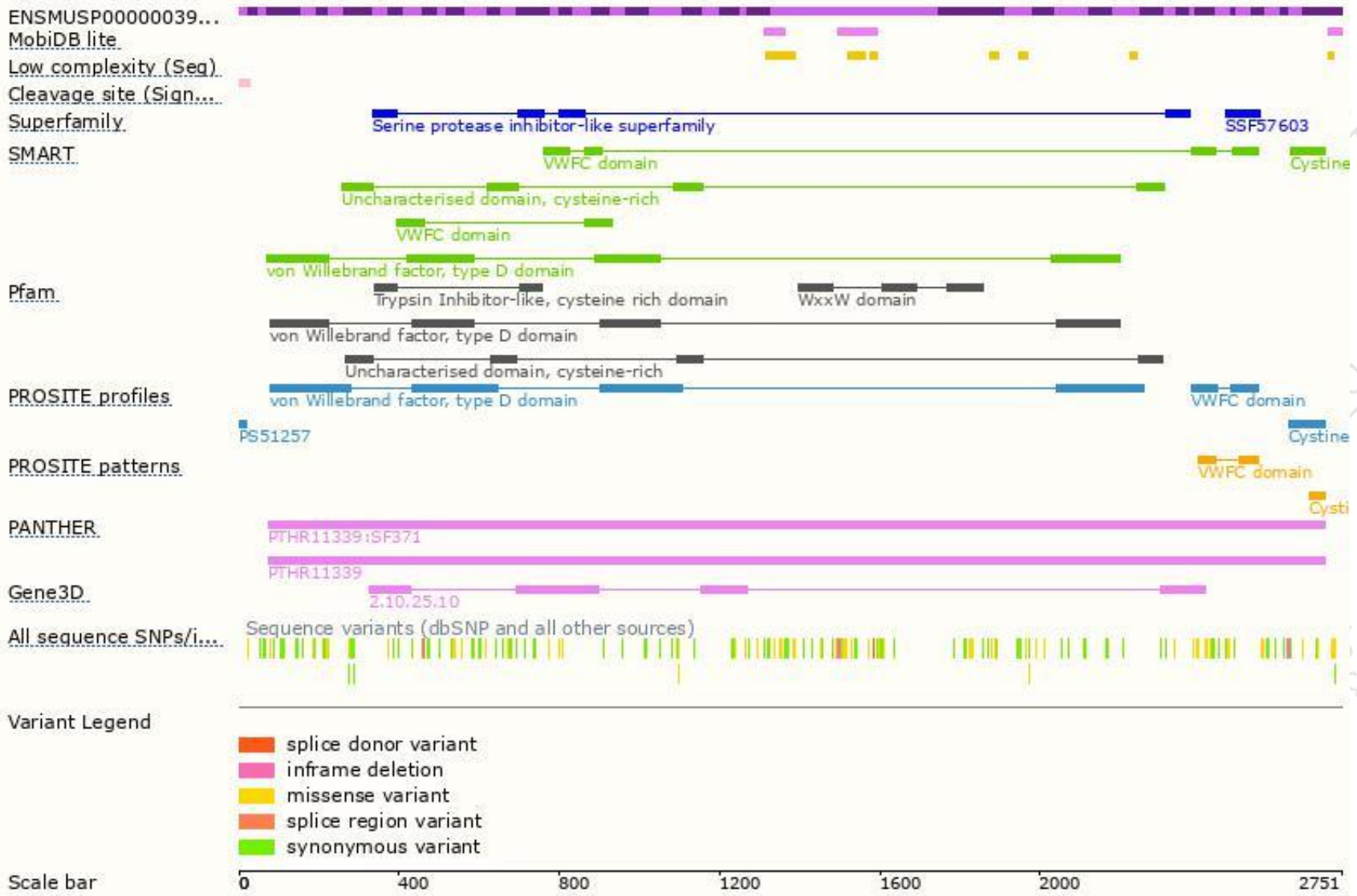
Genomic location distribution



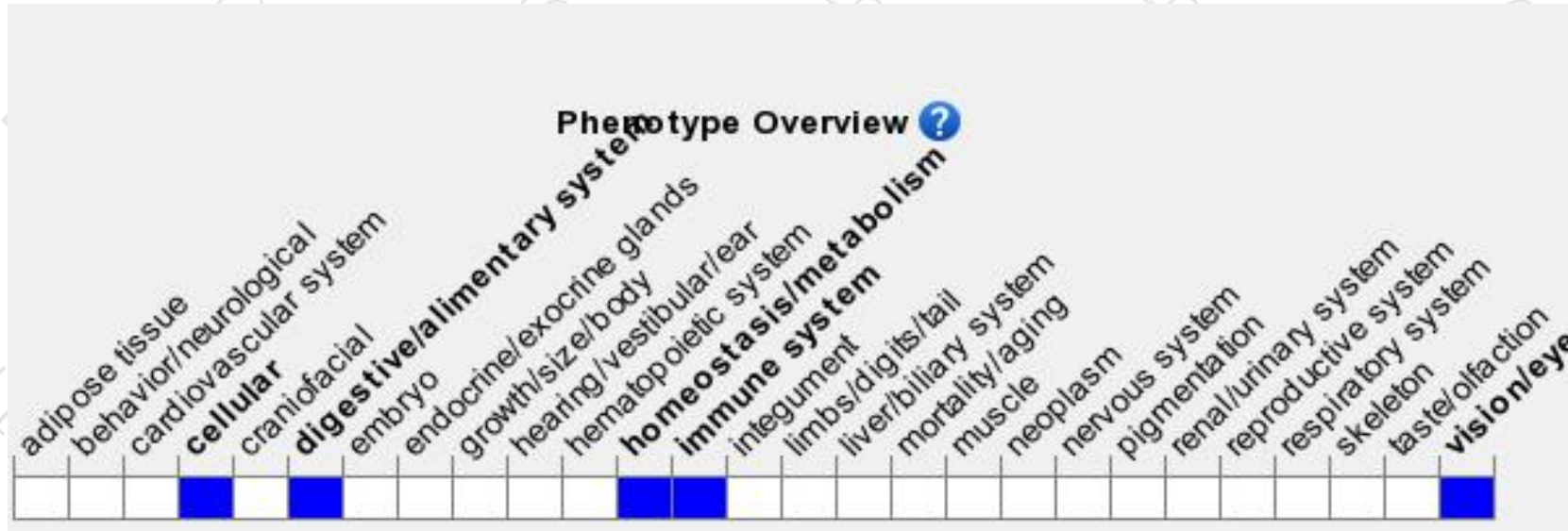
Protein domain



集萃药康
GemPharmatech



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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