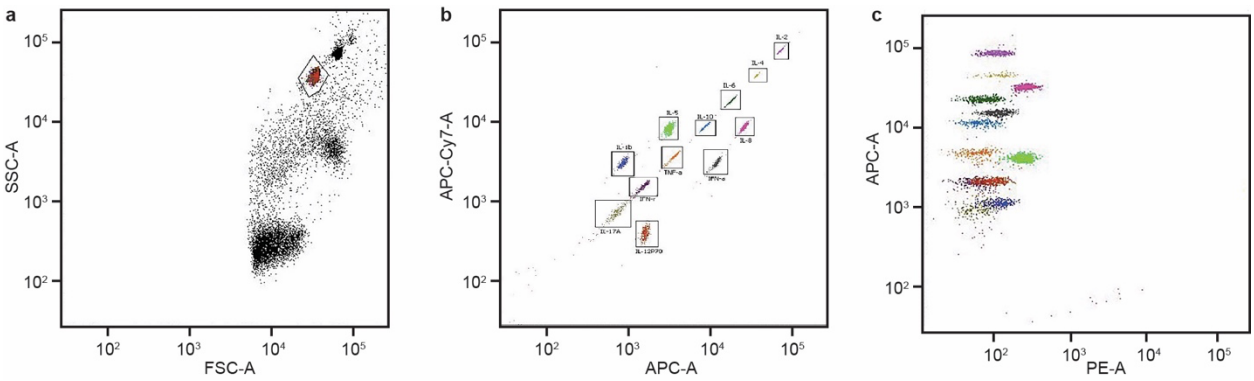
Supporting Table 1. Oligonucleotides used in this study.

Name	Sequence (5'-3')
For gene expression analysis by qRT-PCR	
mouse GAPDH -F	AGGTCGGTGTGAACGGATTTG
mouse GAPDH -R	TGTAGACCATGTAGTTGAGGTCA
mouse IL-25-F	ACAGGGACTTGAATCGGGTC
mouse IL-25-R	TGGTAAAGTGGGACGGAGTTG
mouse IL-1β-F	GAAATGCCACCTTTTGACAGTG
mouse IL-1β-R	TGGATGCTCTCATCAGGACAG
mouse Il-5-F	GCAATGAGACGATGAGGCTTC
mouse Il-5-R	GCCCCTGAAAGATTTCTCCAATG
mouse Il-6-F	CTGCAAGAGACTTCCATCCAG
mouse Il-6-R	AGTGGTATAGACAGGTCTGTTGG
mouse TNFα-F	CAGGCGGTGCCTATGTCTC
mouse TNFα-R	CGATCACCCCGAAGTTCAGTAG
human GAPDH-F	GGAGCGAGATCCCTCCAAAAT
human GAPDH-R	GGCTGTTGTCATACTTCTCATGG
human TSLP-F	ATGTTCGCCATGAAAACTAAGGC
human TSLP-R	GCGACGCCACAATCCTTGTA
human Eotaxin-F	ACACCTTCAGCCTCCAACAT
human Eotaxin-R	GGTCTTGAAGATCACAGCTT
human IL-8-F	ACTGAGAGTGATTGAGAGTGGAC
human IL-8-R	AACCCTCTGCACCCAGTTTTC
human IL-33-F	TCAGGTGACGGTGTTGATGG
human IL-33-R	GGAGCTCCACAGAGTGTTCC
human IL-6-F	ACTCACCTCTTCAGAACGAATTG
human IL-6-R	CCATCTTTGGAAGGTTCAGGTTG
human TNFα-F	CCTCTCTCTAATCAGCCCTCTG
human TNFα-R	GAGGACCTGGGAGTAGATGAG
For bacterial abundance analysis by qPCR	
16s-F	CGTCAGCTCGTGYCGTGAG
16s-R	CGTCRTCCCCRCCTTCC
16s-probe	TTAAGTCCCRYAACGAGCGCAACCC
tpi-F	CATCTGATAAACCTTCGACAGCTTT
tpi-R	TGCTATCTTCAATCACGGTATGACA
tpi-probe	CCAGCTTCACGTTCTTCATCAGATTCACC
gtf-F	CACGCCATGCTGGAAGTG
gtf-R	GCGATGAGCCAAGCTGAAG
gtf-probe	TTAGCTGCTGCGTAGACTTCGTCT
For construction of MUC5AC deletion	
sgRNA-1	GCACCTTTTTCATGCACCACTGG
sgRNA-2	CAGAACGTGGAGGGCATATCAGG
sgRNA-3	CAATAACCACCCGTGAGTCTGGG
sgRNA-4	AGTCTGGGGCAGTATTGGATGGG
For analysis of MUC5AC deletion	
oGN383	GGGAGTCGACTTCTGCTGAC
oGN384	ATCCTTTGCCCCATTTTACC
oGN385	GATGGACAGGTCTTCTACTTCCC
oGN386	AGTGGTGGTATTAGACTCCTGGA



Supporting Fig. 1. FACS gating strategy for cytokine measurement. The assay uses antibody-coated beads to capture analytes efficiently. Each bead has a unique fluorescence intensity that resolves as a unique population by Allophycocyanin (APC) and APC-CY7 on a flow cytometer. Analyte bound to a bead is detected by a second antibody with a phycoerythrin (PE) label. The PE signal is proportional to the amount of bound analyte. According to the kit instructions, we first adjusted the voltage of forward scatter (FSC) and side scatter (SSC) until the singlet bead populations fitted well. Singlet bead populations were gated by SSC-A versus FSC-A to exclude cell debris and platelets (**a**). A total of 3600 beads with around 300 in each cluster were analyzed. Different antibody-labeled bead populations were identified by APC and APC-CY7 according to their fluorescence intensities (**b**). Some serially diluted standards with known concentration were also analyzed to generate a standard curve for each analyte. After acquiring samples on a flow cytometer (**c**), the FCS files were analyzed by FCAP Array™ 3.0 software which identifies each bead population, generates a standard curve, and calculates the concentration of unknown samples.