Supplemental Methods:

*RNA sequencing*

Only RNA samples that had RNA integrity numbers (RIN) ≥7.0 were used. RNA was amplified using the NuGEN Technologies Ovation RNA-Seq System V2 kit (Part # 7102-08) using manufacturer's instructions. Approximately, 2.5 µg of amplified DNA from each sample was sheared on a Covaris S200 focused-ultrasonicator (Woburn, MA, USA) with a target yield of an average 200bp fragment size. The fragmented DNA was taken into standard library preparation protocol using NEBNext® DNA Library Prep Master Mix Set for Illumina® (New England BioLabs Inc., Ipswich, MA, USA) with slight modifications. Briefly, end-repair was done followed by polyA addition and custom adapter ligation. Post-ligated materials were individually barcoded with unique in-house genomics service lab (GSL) primers and amplified through 8 cycles of PCR using KAPA HiFi HotStart Ready Mix (Kapa Biosystems, Inc., Woburn, MA, USA). The quantity of the libraries were assessed by Qubit® 2.0 Fluorometer, and the quality of the libraries was estimated by utilizing a DNA 1000 chip on an Agilent 2100 Bioanalyzer, respectively. Accurate quantification for sequencing applications was determined using the qPCR-based KAPA Biosystems Library Quantification kit (Kapa Biosystems, Inc., Woburn, MA, USA). Each library was then diluted to a final concentration of 12.5 nM and pooled equimolar prior to clustering. Paired End (PE) sequencing was performed on an Illumina HiSeq2500 following the manufacturer's protocols. Raw reads were

demultiplexed using a bcl2fastq conversion software v1.8.3 (Illumina, Inc., San Diego, CA, USA) with default settings.

Post processing of the sequencing reads from RNA-seq experiments from each sample was performed as per our unique in-house pipeline. Briefly, quality control checks on raw sequence data from each sample were performed using FastQC (Babraham Bioinformatics, London, UK). Raw reads were mapped to the reference mouse genome mm9 using TopHat v1.4 [1, 2] with two mismatches allowed and other default parameters. The alignment metrics of the mapped reads was estimated using SAMtools [3]. Aligned reads were then imported onto the commercial data analysis platform, Avadis NGS (Strand Scientifics, CA, USA). After quality inspection, the aligned reads were filtered on the basis of read quality metrics where reads with a base quality score less than 30, alignment score less than 95, and mapping quality less than 40 were removed. Remaining reads were then filtered on the basis of their read statistics, where missing mates, translocated, unaligned and flipped reads were removed. The reads list was then filtered to remove duplicates. All of the RNA sequencing data has been deposited in GEO (GSE77195). Samples were then grouped as treatment and control identifiers and quantification of transcript abundance was done on this final read list using Trimmed Means of M-values (TMM) [4] as the normalization method. Differential expression of genes was calculated on the basis of fold change (using default cut-off ≥ ±2.0) observed between defined conditions, and the p-value of the differentially expressed gene list was estimated by z-score calculations with Benjamini Hochberg False discovery rate (FDR)

correction of 0.05 [5]. Differentially expressed genes underwent gene ontology (GO) analysis and pathway analysis using DAVID and Ingenuity Pathway Analysis tool.

*Cytokine Array*

RNA from whole corpus was used to assess 84 genes in the Qiagen Mouse Cytokines and Chemokines Array (PAMM-150ZC). RNA was transcribed into cDNA using the $RT^2$ First Strand Kit (Qiagen) for the RT2 Profiler PCR Array (Qiagen) using RT SYBR Green ROX qPCR Mastermix (Qiagen). An ABI StepOnePlus machine was used for the real time PCR experiment and data was uploaded to the Qiagen website at http://www.qiagen.com/geneglobe for analysis. Alterations in cytokines and chemiokines were analyzed by a Mann-Whitney U 1-tailed test.

*Western Blot*

Samples of stomach corpus mucosa were lysed in RIPA buffer. 80 µg of protein for each sample was resolved on a 10% SDS-PAGE gel and proteins were transferred onto Odyssey nitrocellulose for 1 hr at 75 V. Blots were dried 1 hr at room temperature, and then blocked 1 hour in Odyssey TBS Blocking Buffer. The blot was probed with goat anti-hIL-33 (Research and Development Systems, AF3625, 1:2000) and rabbit anti-VDAC (Abcam ab15895, 1:2000) diluted in 2.5 mL 0.2% Tween-20/Odyssey TBS Blocking Buffer and incubated overnight at 4 C. The blot was washed 3 times in TBS-Tween, and was first probed with anti-

goat 800 nm secondary diluted 1:15,000 in the same solution as the primary antibody. The blot was incubated for 1 hr in secondary at room temp, washed 3 times in TBS-Tween, and then visualized on an Odyssey Imager (Licor). Subsequently, the blot was probed with anti-rabbit 680 nm secondary and visualized in the same way. Finally, the blot was probed with mouse anti-beta actin (Sigma A5316, 1:11,000) as for the other primaries, then probed with anti-mouse 680 nm secondary and imaged as above.

References


1 Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome biology 2009;**10**:R25.

2 Trapnell C, Pachter L, Salzberg SL. TopHat: discovering splice junctions with RNA-Seq. Bioinformatics (Oxford, England) 2009;**25**:1105-11.

3 Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N*, et al.* The Sequence Alignment/Map format and SAMtools. Bioinformatics 2009;**25**:2078-9.

4 Robinson MD, Oshlack A. A scaling normalization method for differential expression analysis of RNA-seq data. Genome biology 2010;**11**:R25.

5 Benjamini YaH, Y. Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. Journal of the Royal Statistical Society Series B (Methodological) 1995;**57**:12.