Supplementary Methods

Site-directed mutagenesis: The seed sequence of miR-133α on AFTPH 3' UTR luciferase reporter (AFTPH 3' UTR) plasmid (Switchgear Genomics, Menlo Park, CA, USA) was deleted by site-directed mutagenesis to generate AFTPH 3'UTR-ΔmiR-133α. The primers used were as follows: i) AFTPH-del198: (5'-atc agt atg att cag aga agg aca tta tat gaa tgt ctt aca atg g-3') and ii) AFTPH-del198-antisense (5'-cca ttg taa gac att cat ata atg tcc ttc tct gaa tca tac tga t-3'). Site-directed mutagenesis was done using QuikChange II XL site-directed mutagenesis Kit (Agilent Technologies, Santa Clara, CA, USA) according to the manufacturer's instructions.

Luciferase assay: AFTPH 3'UTR, AFTPH 3'UTR-ΔmiR-133α and the control plasmid, R01_3UTR (Switchgear Genomics, Carlsbad, CA, USA), were transfected to NCM460-NTR1 cells using lipofectamine 2000 in the presence of as-miR-133α or to HEK293 cells in the presence of miR-133α precursor and their controls. Two days after transfection, NCM460-NTR1 cells were exposed to NT (100 nM, 1 h) after overnight incubation in serum-free media, while luciferase activities in transfected HEK293 cells were measured without NT exposure. Firefly and Renilla luciferase cell activities were detected using Dual-luciferase reporter assays (Promega, Madison, WI, USA) according to manufacturer's instructions. The relative AFTPH 3' UTR-associated luciferase activities were calculated by normalizing AFTPH 3' UTR-associated luciferase activities with R01_3' UTR luciferase activity.

NF-κB p65 translocation: NCM460-NTR1 cells were transfected with miR-133α and its control and cell lysates were collected 48 h after transfection. Nuclei were collected using Nuclei EZ Prep (Sigma Aldrich) according to manufacturer's instructions. The nuclei were then lysed with RIPA buffer and total p65 was quantified using NF-κB/p65 ActivELISA ™ (Imgenex, San Diego, CA, USA).

Measurement of interleukin-8 (IL-8) production: NCM460-NTR1 cells were transfected with miR-133α and its control, and cultured in serum-free media overnight 48 h after transfection. Media were collected and IL-8 production was quantified using Human CXCL8/IL-8 Quantikine ELISA Kit (R&D Systems, Minneapolis, MN, USA).

Immunoblot analyses: NCM460-NTR1 cells were washed with ice-cold PBS and incubated with radiolabelled immunoprecipitation assay buffer containing the protease inhibitors phenylmethylsulfonyl fluoride and sodium orthovanadate (Santa Cruz) for 5 min. The insoluble debris were removed by centrifugation (12,000 rpm, 15 min, 4°C) and supernatants were analyzed by immunoblot analysis. Equal amount of cell lysates were loaded (~ 35 μg) and transferred to nitrocellulose membrane. The membrane was blocked with Odyssey ® Blocking Buffer (LI-COR, Lincoln, NE, USA). Appropriate antibodies were incubated with the membranes overnight at 4°C, washed with 0.1% Tween 20 in PBS (PBS-T) and incubated with appropriate IRDye ® secondary antibodies (LI-COR). Signals were detected with Odyssey ® Infrared Imaging System (LI-COR) and quantified using Image Studio (LI-COR).

Messenger RNA and miR expression analysis: NCM460-NTR1 cells were washed once with ice-cold phosphate-buffered saline (PBS) after various treatments. Total RNA were extracted by TRIzol (Life Technologies) and reverse-transcribed into first strand cDNAs using random decamers and reverse transcriptase (Life Technologies) for quantitative PCR (qPCR) analysis. Complementary DNAs for miRNA expression were prepared with Universal cDNA Synthesis kit II (Exiqon, Woburn, MA, USA) and detected by ExiLENT SYBR ® Green Master Mix (Exiqon) according to the manufacturer's instructions.

MicroRNA profiling in blood samples: Whole blood from UC patients and healthy donors (IRB#12-000420) was subjected to serum and peripheral blood mononuclear cells (PBMCs) isolation by centrifugation (1600g, 15 minutes, 4^{o}C) and Ficoll (Roche) gradient centrifugation

(1600g, 10 minutes, 4oC), respectively. RNA was isolated from serum samples using the miRNeasy Serum/Plasma Kit (Qiagen) and from PBMCs with the miRCURY Cell and Plant RNA Isolation Kit (Exiqon) according to the manufacturer's instructions. Eluted RNA from serum samples and PBMCs was further purified and concentrated by using Amicon Ultra YM-3 columns (3000 kDa MWCO, Millipore). RNAs following hybridization reactions were processed using the nCounter Prep Station and subsequently the nCounter Digital Analyzer and analyzed by nSolver software, v1.1 (Nanostring Technologies). Normalization was performed using the predominant microRNAs with coefficient of variation less than 70%.