Supplementary Methods

DNA was extracted from the samples using a phenol: chloroform extraction procedure as previously reported (1). The microbiota was analysed using bacterial tag-encoded FLX amplicon pyrosequencing as described in Dowd *et al*. (2). Generation of the sequencing library and was performed by MRDNA (www.mrdnalab.com, Shallowater, TX, USA) along with the pyrosequencing analysis, clean-up and operational taxonomic unit (OTU) identification. Identification was provided using BLASTn database with genus taxonomy given for > 95% sequence identity of the OTU to an appropriate reference sequence. Random resampling was performed to adjust the data for potential biasing caused by differences in the number of reads within a sample. Resampling was achieved by the random selection of a uniform number (n = 426) of reads from each sample. The uniform number corresponded to the smallest sample size. Resampling was repeated 1000 times with diversity indices calculated at each sampling event and the mean values recorded. Comparisons between the diversity measures were achieved using non-parametric analyses due to the small sample sizes. A significance difference was reported if the P-value was below the 0.05 threshold ($P < 0.05$). All statistical analyses and visualisations were performed in the statistical computing environment R (v.3.0.1; R Core Team, 2013). Richness was given by the mean count of the number of unique genera present in each sample after reshuffling. The Shannon's diversity index was calculated using the diversity command in the vegan (v.2.0-7) package.

Gender	**Height (cm)**	**Age (years)**	**Weight (kg)**	**Smoking**	**Treatment**
M	164	51	75	Never	Carbocysteine, Salbutamol, Symbicort, Montelukast
M	177	63	78	Never	Prednisolone, Salbutamol, Seretide
F	165	58	92	Never	Phyllocontin, prednisolone, Montelukast, Symbicort, Terbutaline
F	168	57	102	Never	Salbutamol, Seretide, Montelukast
F	168	18	82	Never	Salbutamol, Seretide, Montelukast

Supplementary Table 1 Patient Demographics

Figure 1: Characteristics of the microbiota in patients prior to and after azithromycin treatment.

Each data point represents a single sample with horizontal lines indicating the mean number of genera detected (a) and Shannon's index rank (b). Near significant differences were reported between groups for both measures ($\chi 2 = 3.15$, $P = 0.076$). Dotted lines are shown to indicate the change in measure for each patient.

References

1. Rogers GB, Cuthbertson L, Hoffman LR, et al. Reducing bias in bacterial community analysis of lower respiratory infections. *Journal of the International Society for Microbial Ecology* 2013 7:697-706.

2. Dowd SE, Wolcott RD, Sun Y, et al. Polymicrobial Nature of Chronic Diabetic Foot Ulcer Biofilm Infections Determined Using Bacterial Tag Encoded FLX Amplicon Pyrosequencing (bTEFAP). *PloS one*. 2008;3(10):e3326.