Supplementary Table 1 Dye swap design of 2D-DIGE profiling

	Cy2	Cy3	Cy5
gel 01*	STANDARD	HC.6	CD.6
gel 02*	STANDARD	CD.3	HC.3
gel 03*	STANDARD	HC.3	CD.3
gel 04	STANDARD	HC.5	CD.5
gel 05	STANDARD	HC.1	CD.1
gel 06	STANDARD	CD.6	HC.6
gel 07*	STANDARD	HC.2	CD.2
gel 08*	STANDARD	HC.4	CD.4
gel 09*	STANDARD	CD.4	HC.4
gel 10*	STANDARD	CD.1	HC.1
gel 11*	STANDARD	CD.2	HC.2
gel 12*	STANDARD	CD.5	HC.5

*Gels used for spot excision and protein identifications. Microbial fractions were extracted in duplicate for each participant, giving 24 protein samples in total, which were analyzed in a dye swap design. Typically, the two protein samples (50 µg each) from a given patient-control pair were differentially labeled with Cy3 or Cy5, respectively (for instance, HC.6-Cy3 and CD.6-Cy5, top row of the table) and their replicates were reversely labeled with Cy5 or Cy3 (HC.6-Cy5 and CD.6-Cy3, row 6 of the table). They were combined in pairs, and each pair was run in the same first- and second-dimension gel (gels 01 and 06 in the example), together with 50 µg of a Cy2-labeled internal standard made of a pool of equal protein amounts from each of the 24 samples included in the study. The 12 gels in total were scanned with a Typhoon imager 9410 (GE Healthcare) and the multiplexed DIGE images were analyzed using Progenesis SameSpots software (Nonlinear Dynamics) (online supplementary method 3).