Supplementary data Fig. S1. *MspI* generated OTU contribution to the overall faecal bacterial profile of individual rats within the healthy control and DSS-induced colitic groups. a) Rats from experimental set I. b) Rats from experimental set II. Legend shows OTU (n=29) in order of smallest to largest, which were identified in the faeces of individual rats. OTU identified by SIMPER analysis as being significantly different between healthy control and DSS-induced colitic rats are marked with an asterix. SIMPER analysis showed that OTU 118 and 188 were more abundant in the control group, while OTU 94 and 914 were more abundant in the DSS-induced colitic group.
Supplementary data Fig. S2. CfoI generated OTU contribution to the overall faecal bacterial profile of individual rats within the healthy control and DSS-induced colitic groups. a) Rats from experimental set I. b) Rats from experimental set II. Legend shows OTU (n=50) in order of smallest to largest, which were identified in the faeces of individual rats. OTU identified by SIMPER analysis as being significantly different between healthy control and DSS-induced colitic rats are marked with an asterix. SIMPER analysis showed that OTU 116, 226, 360 and 948 were more abundant in the control group, while OTU 94, 98, 174 and 384 were more abundant in the DSS-induced colitic group.