Figure S1 Dendrogram of grouped samples from patients (FMT [n = 15] and sham [n = 16]) in red colours and sex and age-matched healthy controls (n = 31) and FMT donors (n = 4) in blue colours, respectively. The figure shows that the majority of PsA patients divide into one cluster (22 out of 31 [70.97%]) whereas the healthy controls divide into another (25 out of 31 [80.65%]). Two of the four stool donors (dark blue) are found in each of the two clusters.

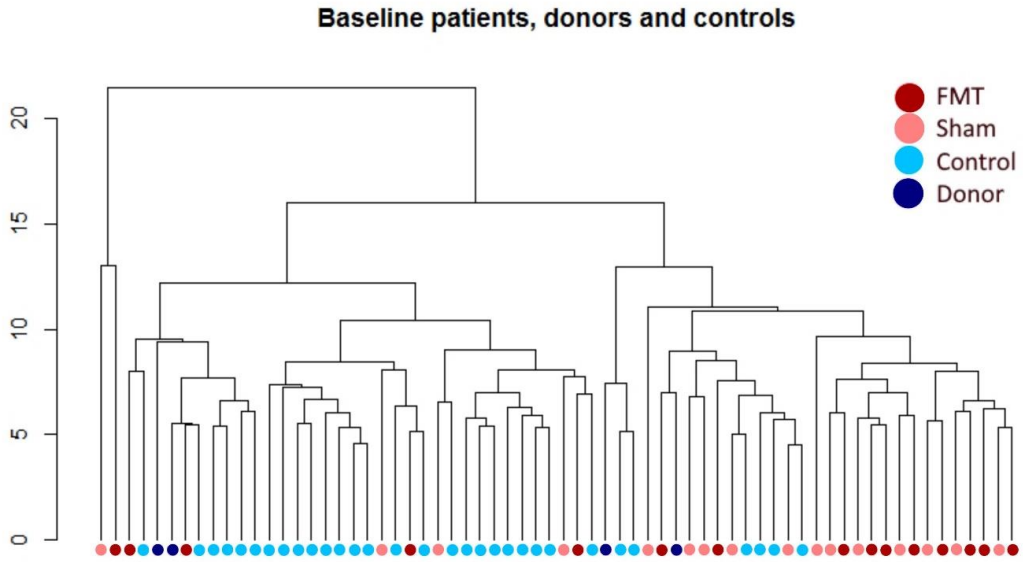


Figure S2 Heatmap showing profiles of inflammation-associated plasma protein levels of patients, faecal microbiota transplantation (FMT) donors and healthy controls (HC) at baseline using hierarchical clustering.

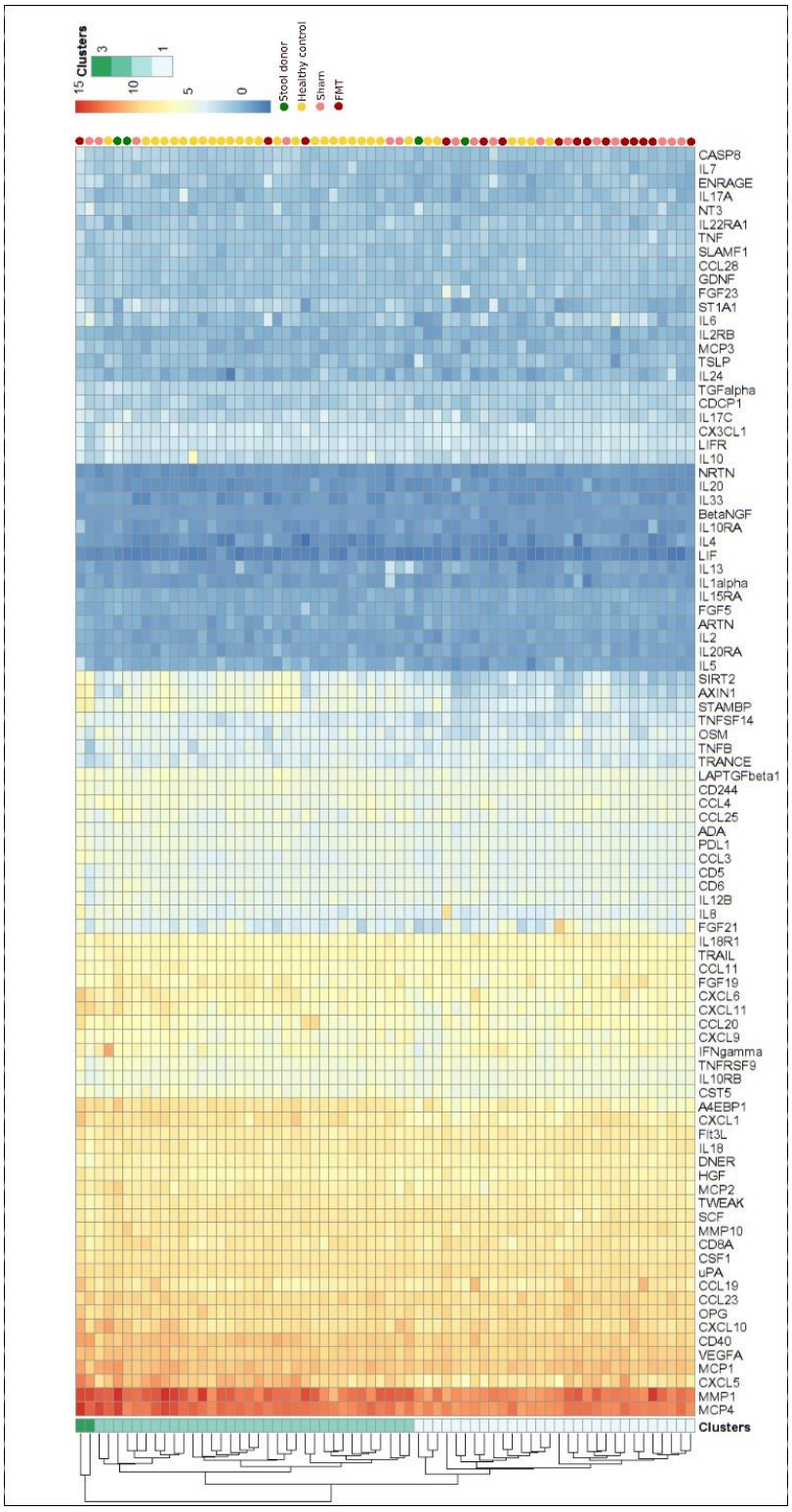


Figure S3 Dynamics of inflammation-associated proteins that changed significantly in FMT-treated patients across all time points (baseline, week 4, week 12, week 26). P-values were obtained from repeated measures ANOVA.

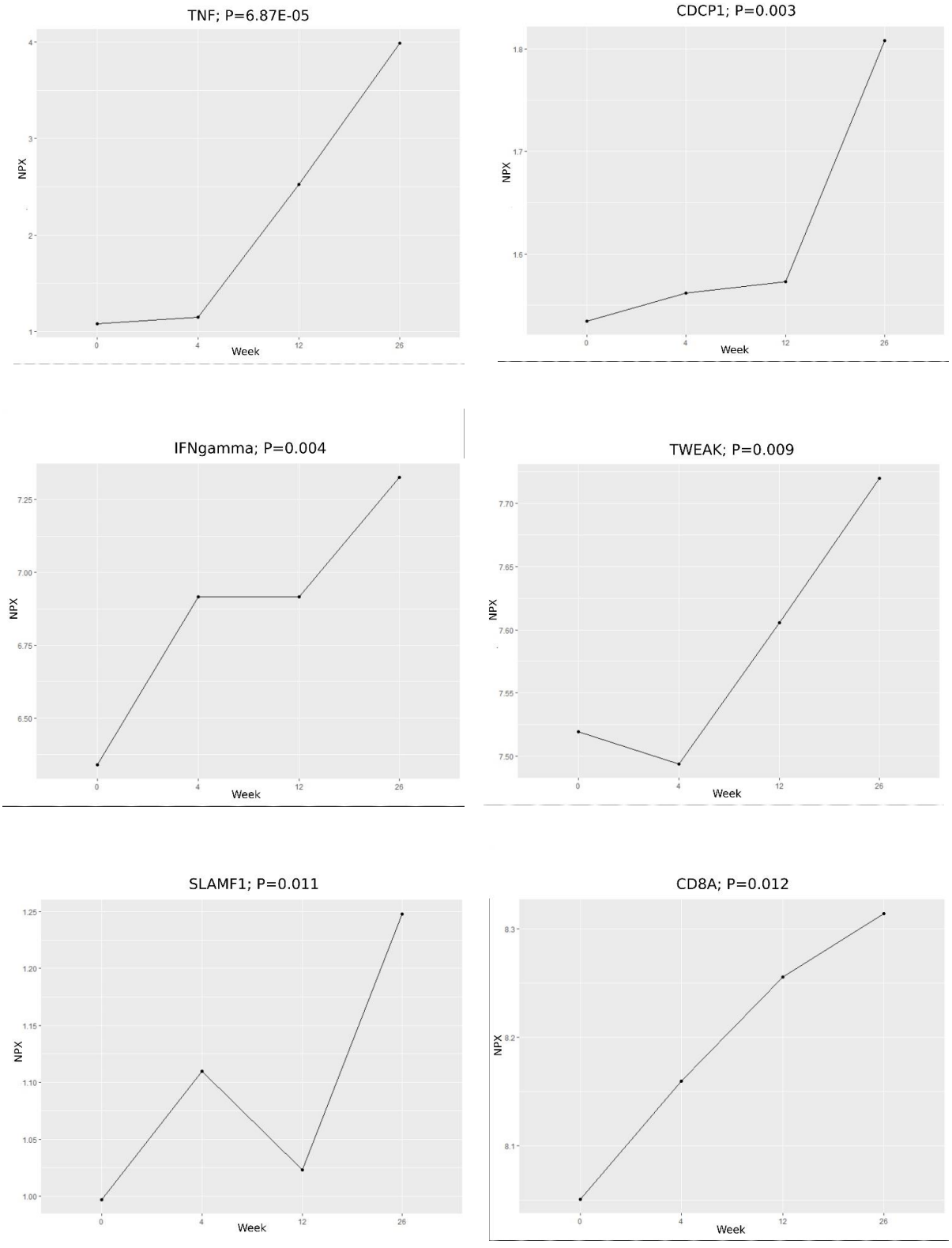
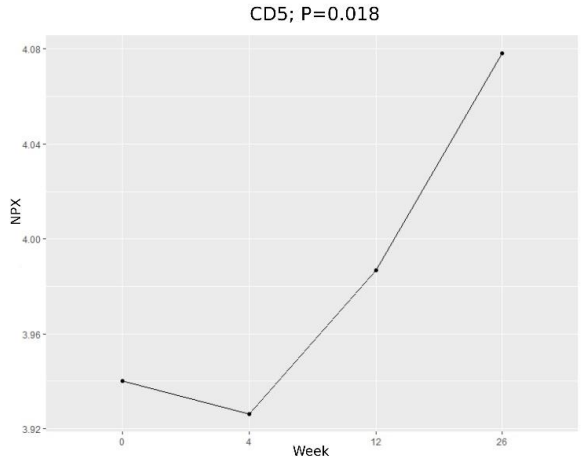
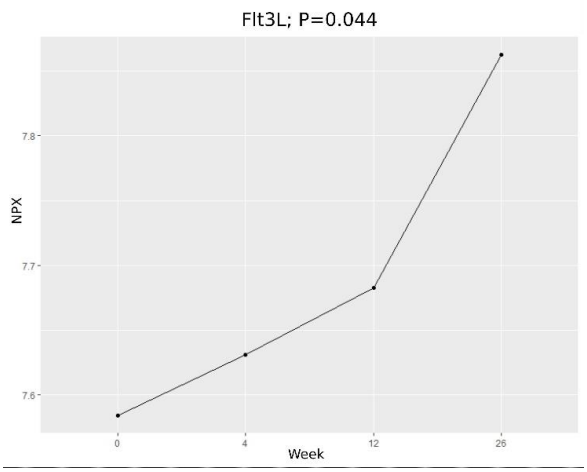
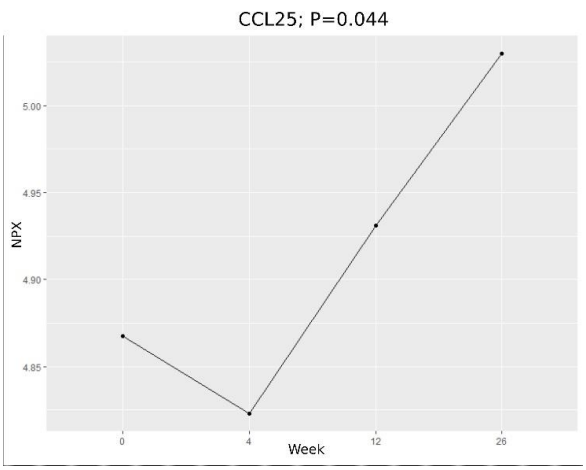
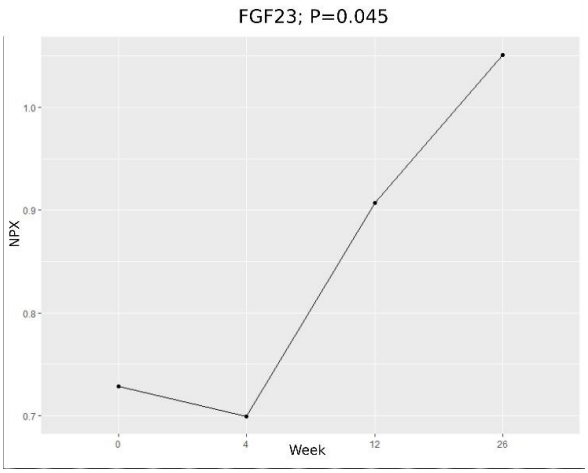


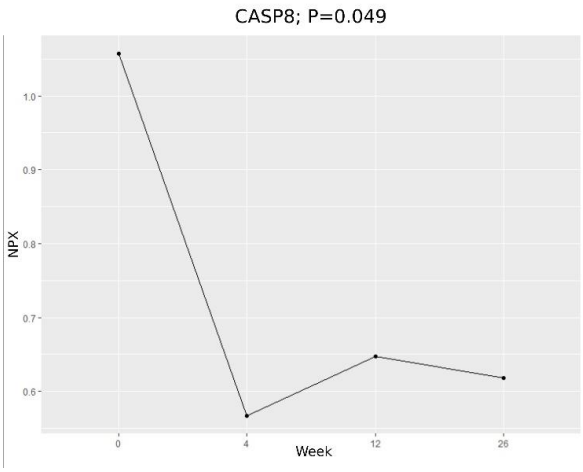
Figure S3 (continued)











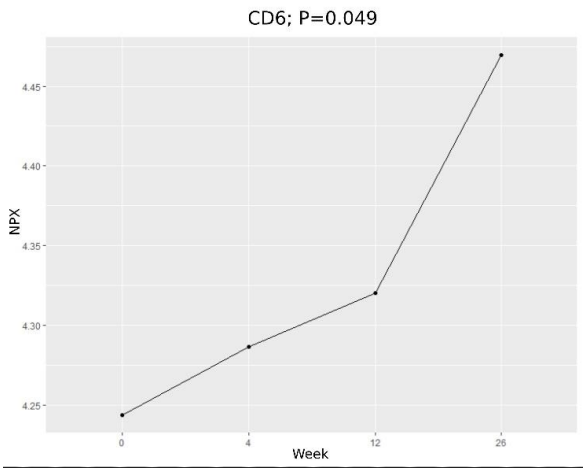
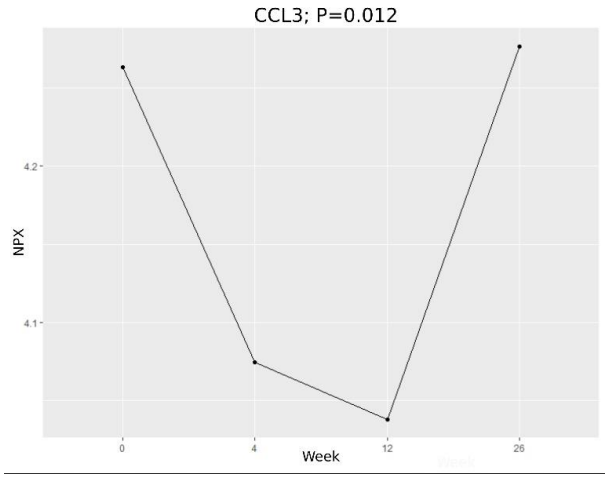
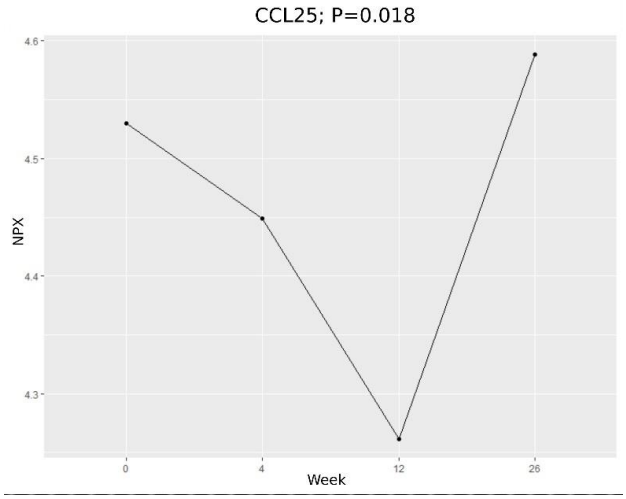
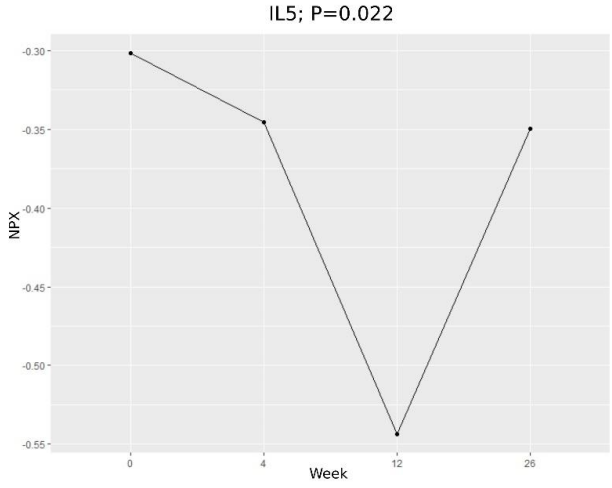
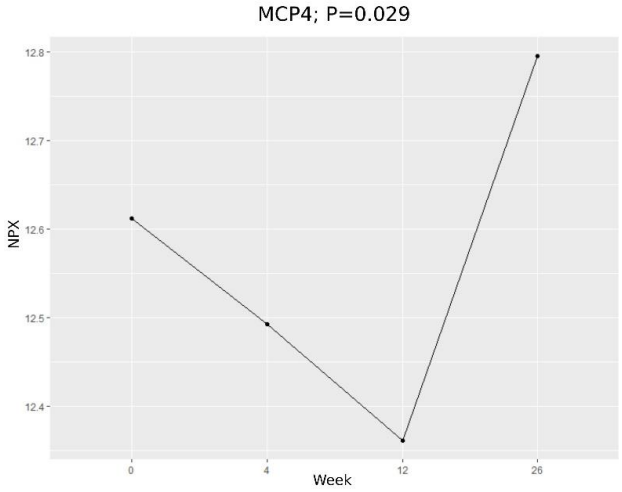


Figure S4 Dynamics of selected inflammation-associated proteins that changed significantly in sham-treated patients across all timepoints (baseline, week 4, week 12, week 26). P-values were obtained from repeated measures ANOVA.









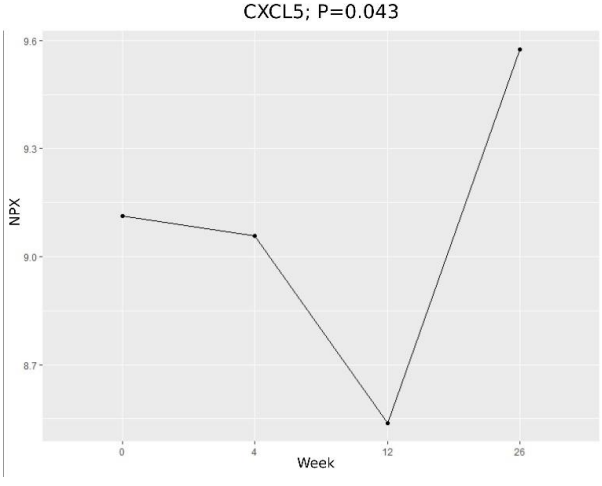


Figure S5 Visualization of dynamics/changes in protein expressions across all time points including baseline, week 4, week 12 and week 26 between patients receiving faecal microbiota transplantation (FMT) and sham treatment. FMT-treated patients are shown in red whereas sham-treated patients are shown in green with 95% confidence intervals. P values were obtained from mixed ANOVA.

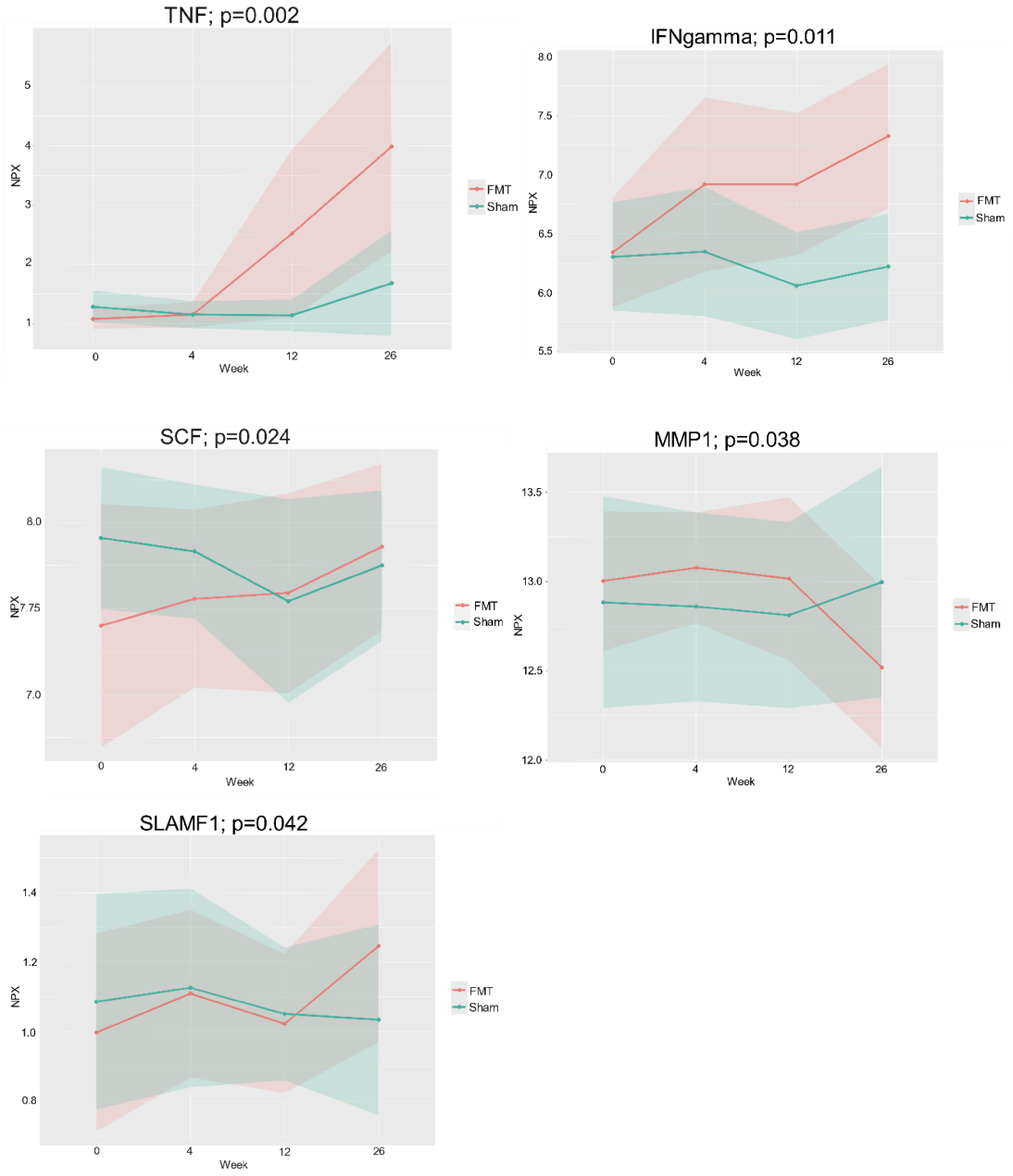
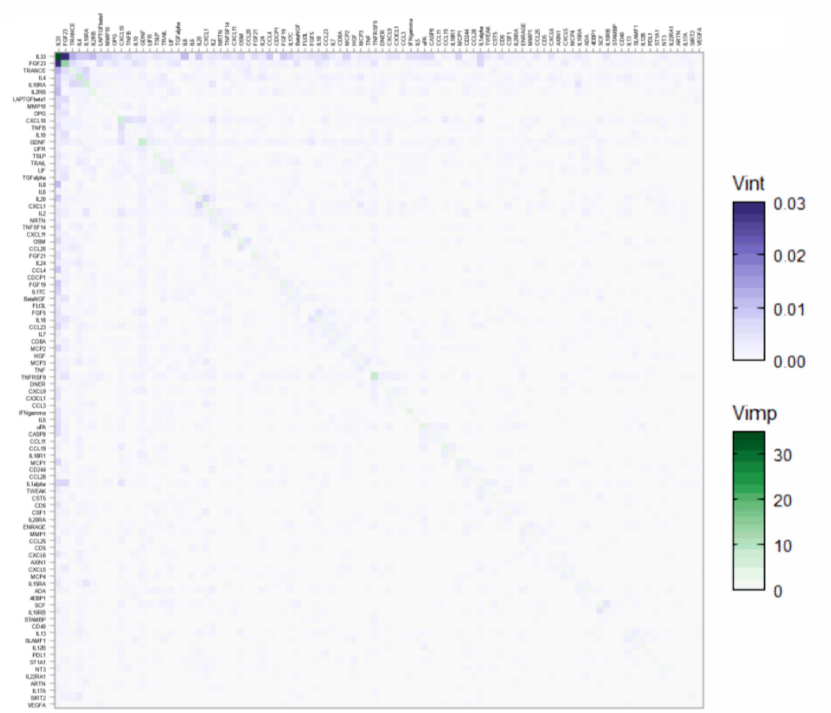
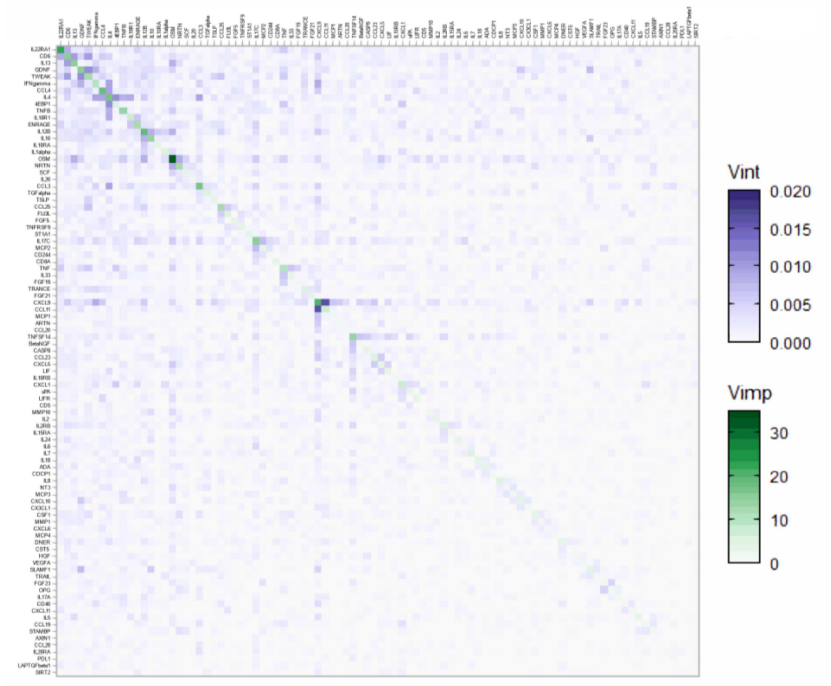


Figure S6 Heatmap of the random forest models with leaf sorting showing the variable importance (VImp) values and variable interaction (VInt) values of the 92 proteins measured at baseline in relation to the following disease activity measures: (A) Swollen joint count; (B) SPARCC enthesitis score; (C) HAQ-DI score; and (D) tender point count. From this analysis, the VImp and VInt for all proteins were low. For swollen joints, IL-33 was the protein with the highest value of VImp (0.514). For enthesitis score, the proteins with the highest VImp values were OSM (0.347) and CXCL9 (0.118). For tender point count, the proteins with the highest VImp values were IL-10 (0.396) and TNF-β (0.425). For HAQ-DI, IL-10 was the protein with the highest VImp value (0.0345).

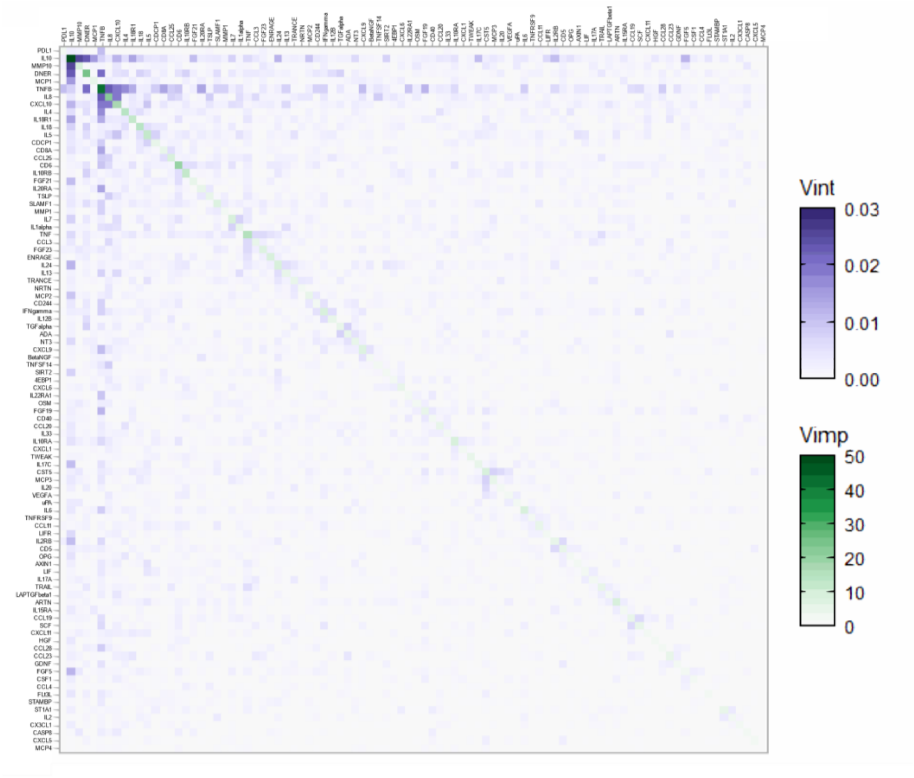
(A) Swollen joint count



(B) Enthesitis score



(C) HAQ-DI score



(D) Tender point count

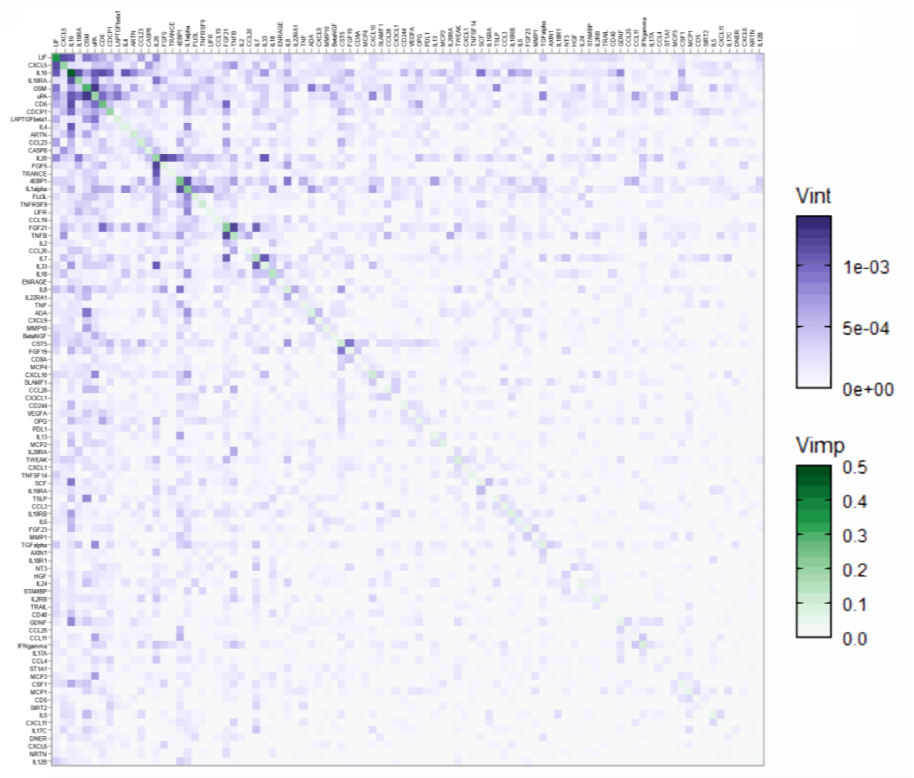


Figure S7 Post-intervention changes in levels of interleukin-6 between FMT and sham-treated patients. P values were obtained from mixed ANOVA (sham vs FMT). To visualise the influence of TNF inhibitor (TNFi) treatment given to the majority of treatment failures, we have divided the groups accordingly, when the first patient received TNFi treatment. Week 12: sham (n = 16); sham + TNFi (n = 0); FMT (n = 10); FMT + TNFi (n = 5). Week 26: sham (n = 15); sham + TNFi (n = 1); FMT (n = 9); FMT + TNFi (n = 6).