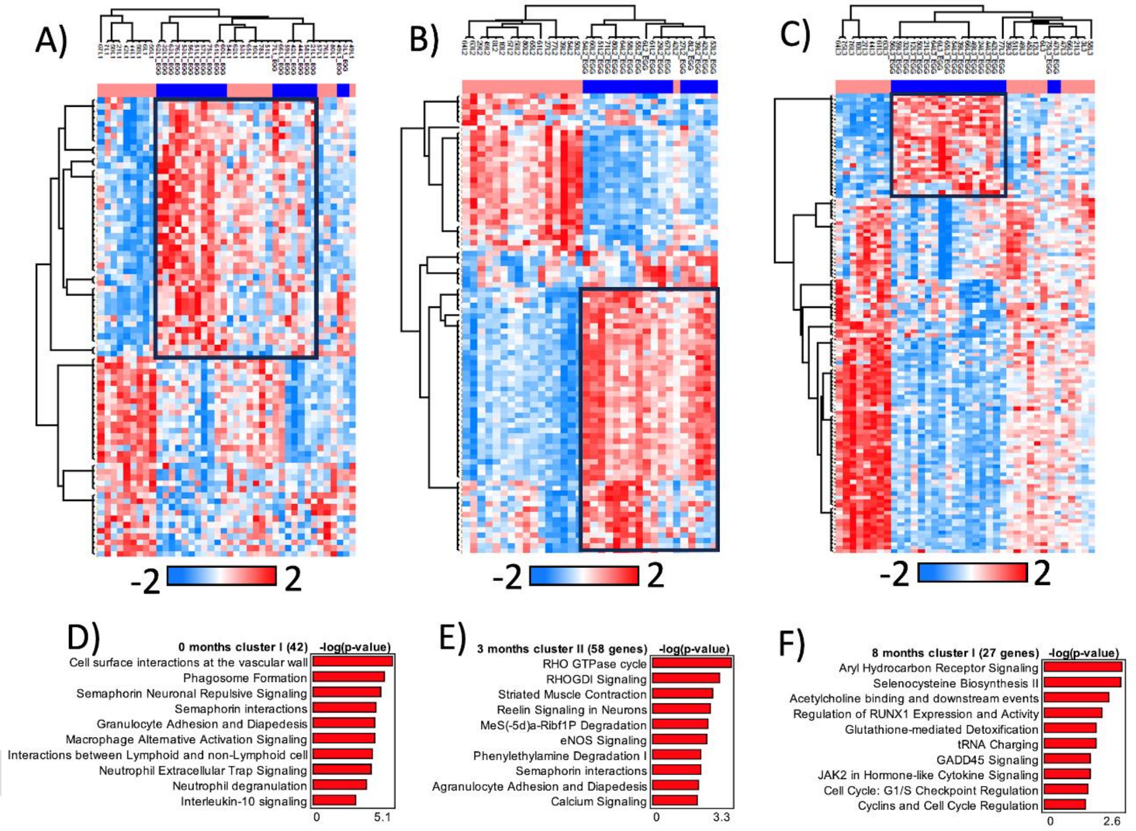
SUPPLEMENTARY MATERIAL

Figure S1. Egg-extract-stimulation changes gene expression of PMBCs during OIT at 0, 3 and 8 m. Heatmap of DEGs between egg-extract stimulated PBMCs (blue bar) and controls (peach bar). We included all DEGs from baseline (49 genes) and, for subsequent time points the top 50 DEGs based on the highest adjusted p-values. Heatmaps of the Anova positive genes are shown at A) baseline (0 m), B) 3 m and C) 8 m of OIT. The top ten Canonical pathways of egg-stimulation upregulated genes are shown atD) 0 m E) 3 m and F) 8 m. The negative logarithm of Fisher's exact test p-value is shown (IPA).



doi: 10.18176/jiaci.1079

Figure S2. Validation of three transcriptomic gene targets, S100A8, S100A9, and IL-1β in ELISA assays. A, Heterodimer, the biologically active form of antimicrobial S100A8/A9 followed the gene expressional changes of S100A8 and S100A9 along the OIT (0-8 m). B, OIT inhibited the expression of IL-1β from PBMCs after stimulation with egg-extract at 3 or 8 m. Statistics was done by Kruskal-Wallis test with Dunn's multiple comparison test in Graph Pad Prism. P-value * < 0.05, ** < 0.01, *** < 0.001, **** < 0.0001.

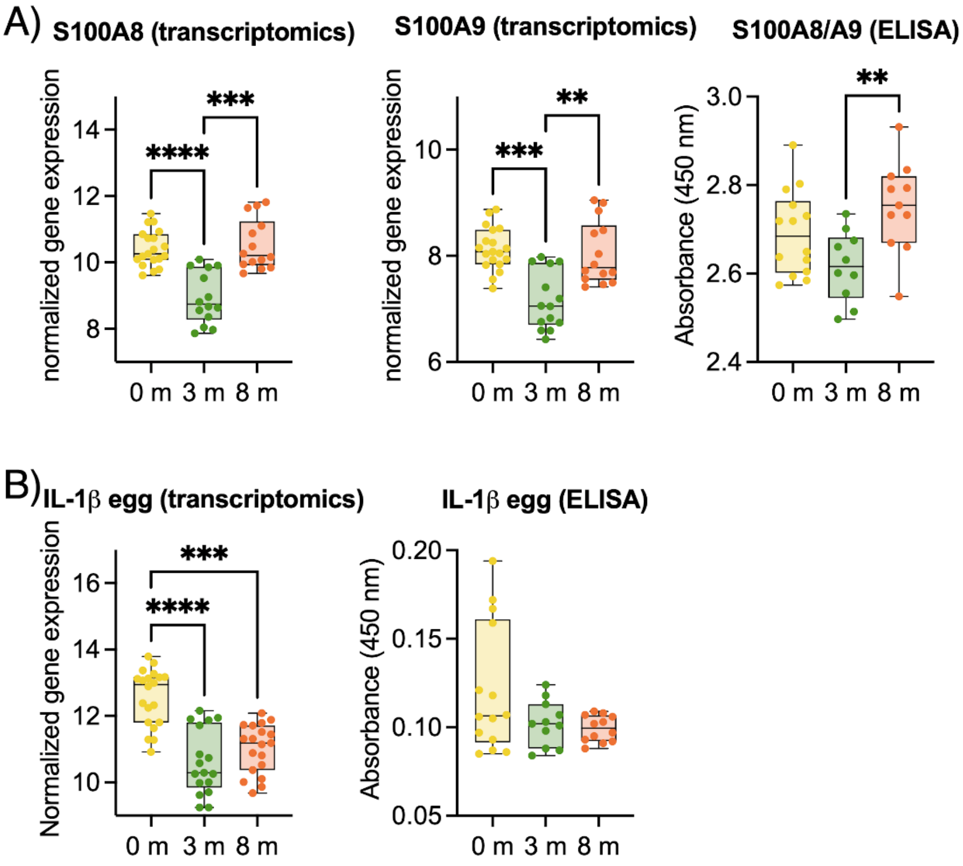


Figure S3. Shared DEGs in egg-extract-stimulated PMBCs vs unstimulated PBMCs at 0 m, 3 m and 8 m. Canonical pathway analysis of A) shared DEGs at 0 m and 3 m, B) shared DEGs at 3 m and 8 m, and D) shared DEGs at 0 m and 8 m are shown using Ingenuity pathway analysis (IPA). The negative logarithm of Fisher's exact p-value and associated z-scores are shown when available.

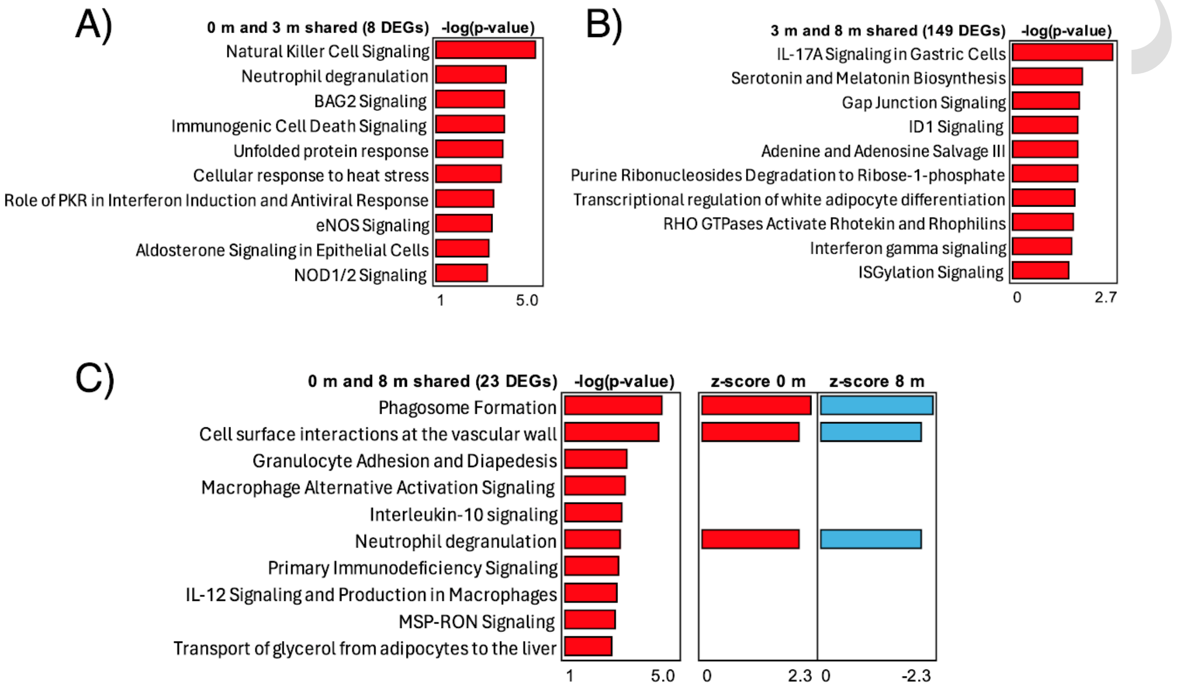


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Figure S4. Association of clinical parameters with DEGs during the OIT. A) Pearson correlation was calculated between DEGs and clinical parameters. They included variables at food challenge (FC) including symptom score (FC_symptom_score) and severity (FC_Severity), tolerated amount of egg (FC_tolerated_dose) and cumulative dose (FC_cumulative_dose). Additionally, variables of OIT length (OIT_m) and dose at 8 m (OIT_dose_8_m), as well as tolerance formation at 8 m (Tolerance_8_m) were studied. The canonical functions of the clusters B) I, C) II, and D) III were studied by IPA. The negative p-values of of Fisher's exact test are shown by bars.

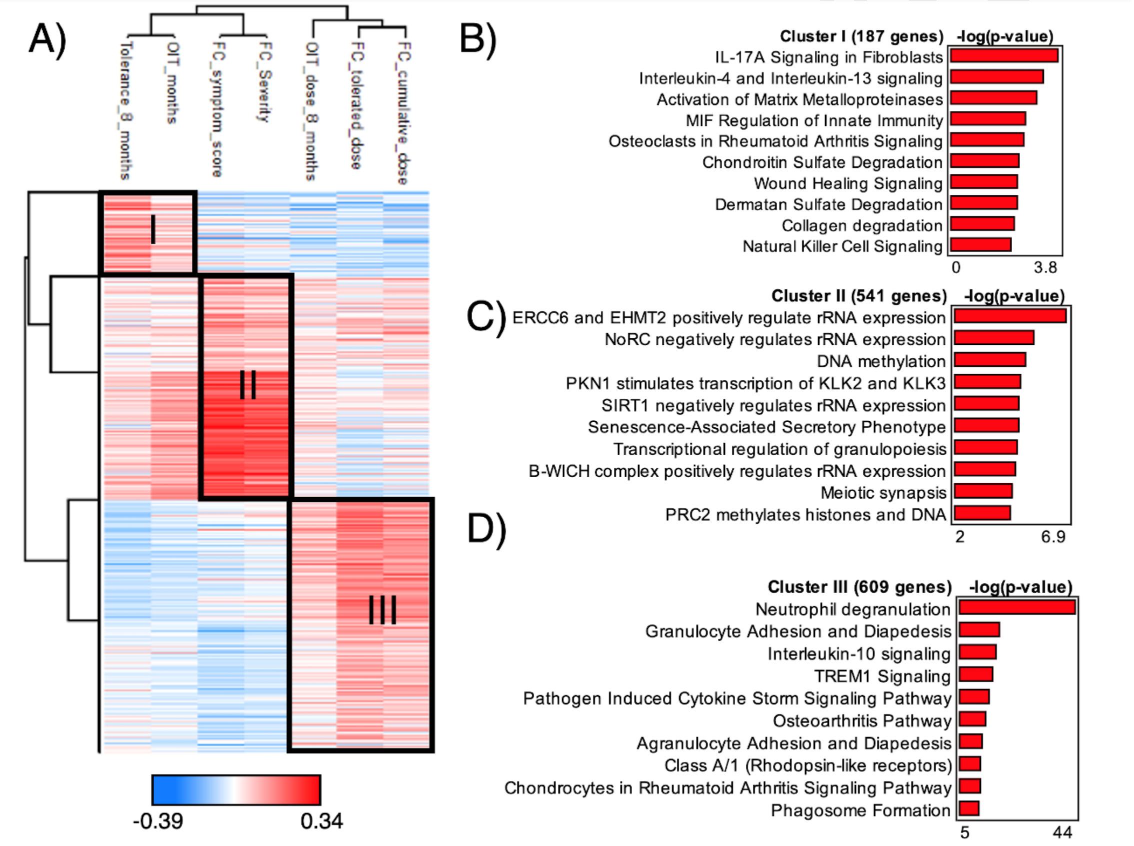

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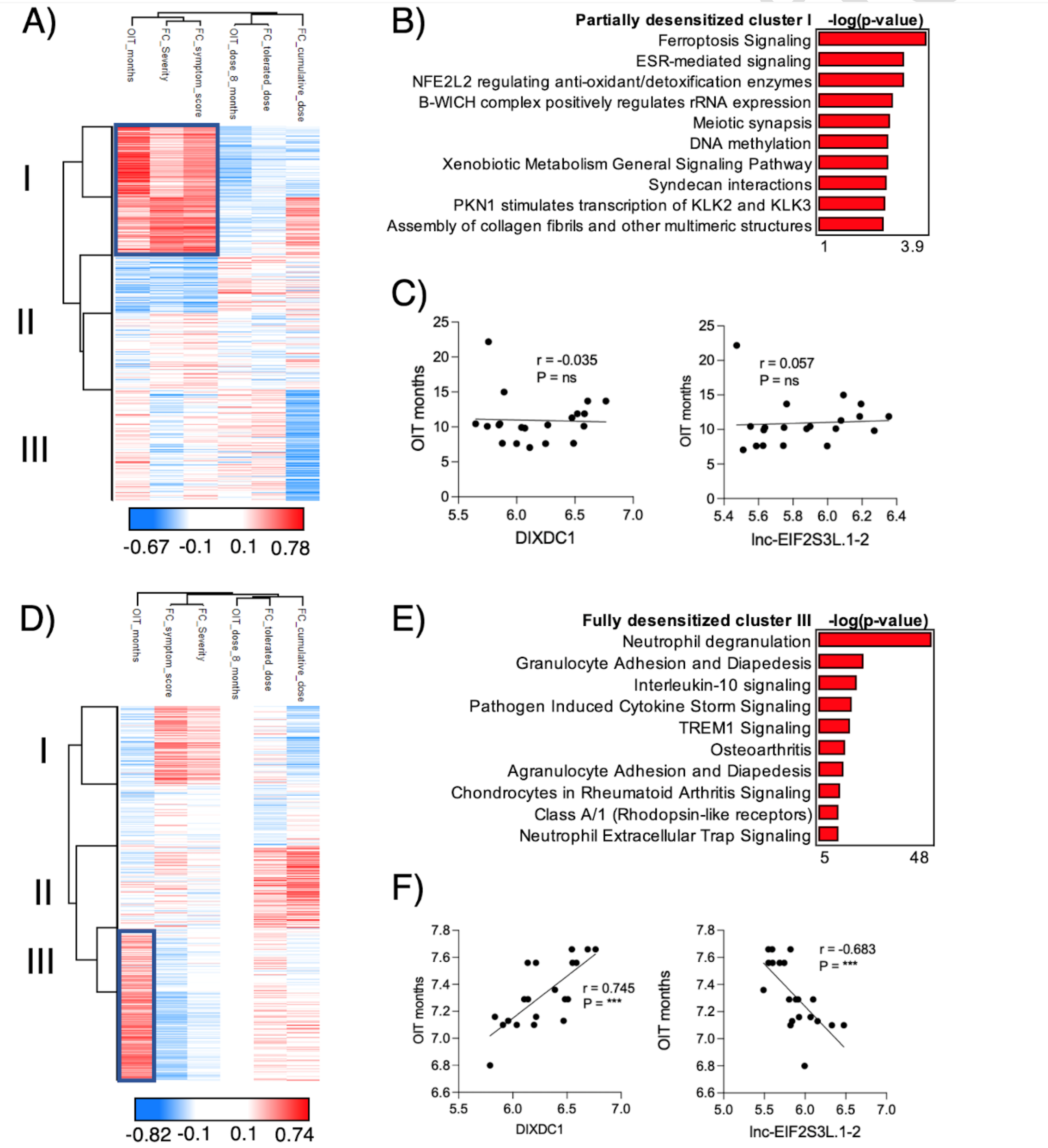
Figure S5. Correlation of PBMCs from part and full patients with clinical factors. A) Pearson correlation of clinical parameters and DEGs from partially desensitized (part) patients at the beginning of the OIT (0 m). B) The canonical pathways of part patients from cluster I of A). C) Pearson correlation of genes DIXDC1 and lnc-EIF2S3L.1-2 with the duration of OIT (OIT_months) in part patients. D) Similarly, pearson correlation of clinical parameters and DEGs from fully desensitized (full) patients, E) the canonical pathway analysis of its cluster III and F) correlations of desensitization speed with two example genes. The negative Log10 p-values of of Fisher's exact test are shown by bars.



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