

3686 differentially expressed genes between 3 groups (p -value <0.05 FDR <0.2)

Three pairwise comparisons between groups (FDR <0.05):
total of 2573 genes

E-CVID vs. Control

noE-CVID vs. Control

E-CVID vs. noE-CVID

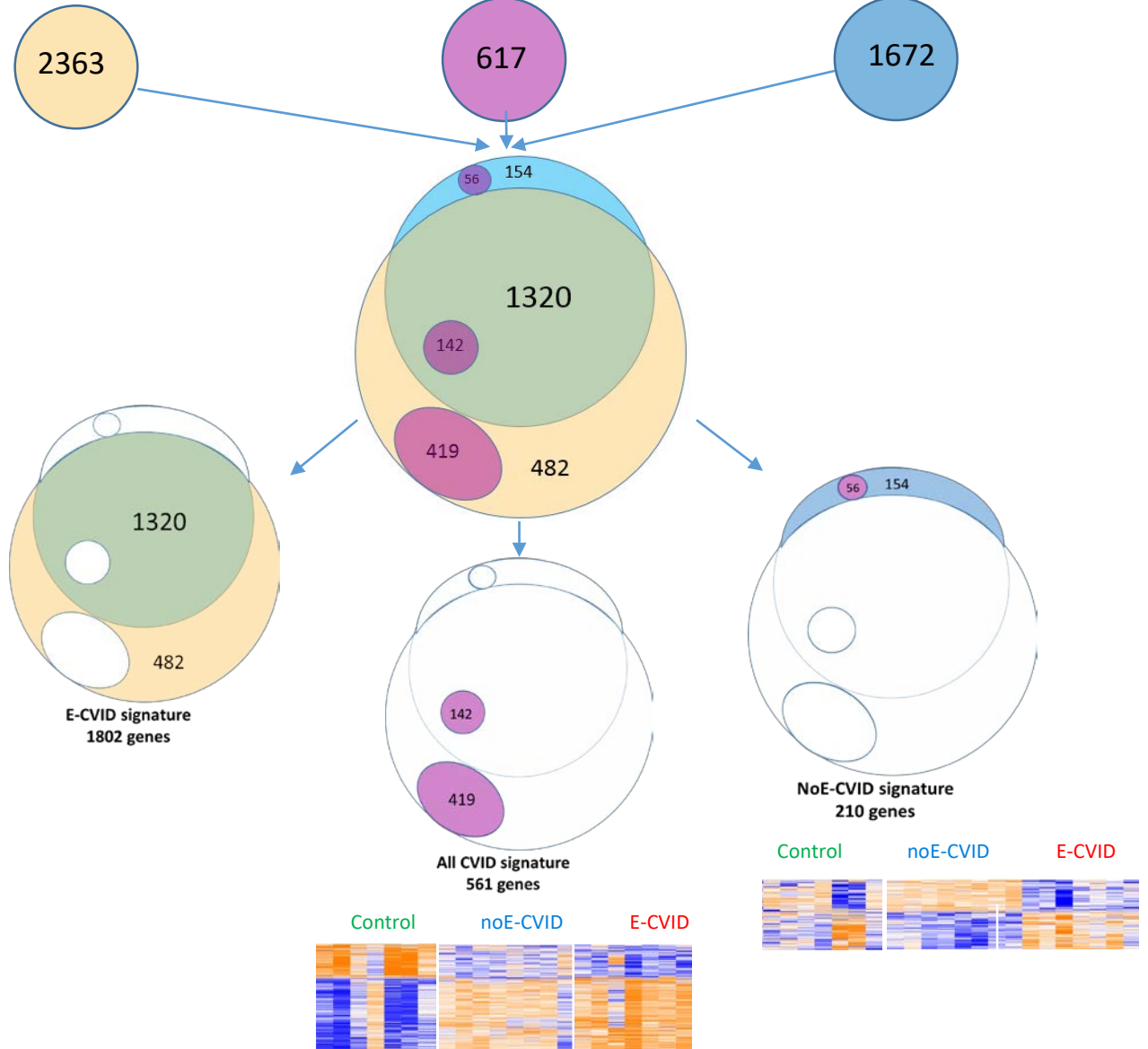


Figure S1. Establishing gene expression signature of CVID enteropathy (E-CVID), noE-CVID and all CVID(E-CVID and noE-CVID). Orange color in heatmap indicate high abundance, blue color indicate low abundance. In order to establish gene signatures we used two-step analysis: first step- using univariate test with a relaxed threshold (p -value <0.05 and FDR <0.2) we found 3686 differentially expressed genes among all three groups; second step: searching within this group of genes we selected 2573 differentially expressed genes that passed FDR <0.05 at least in one out of three pairwise comparisons. Next, by overlapping results of pairwise comparisons we have established gene expression signatures for E-CVID, All CVID, and NoE-CVID (Supplementary Table S1).

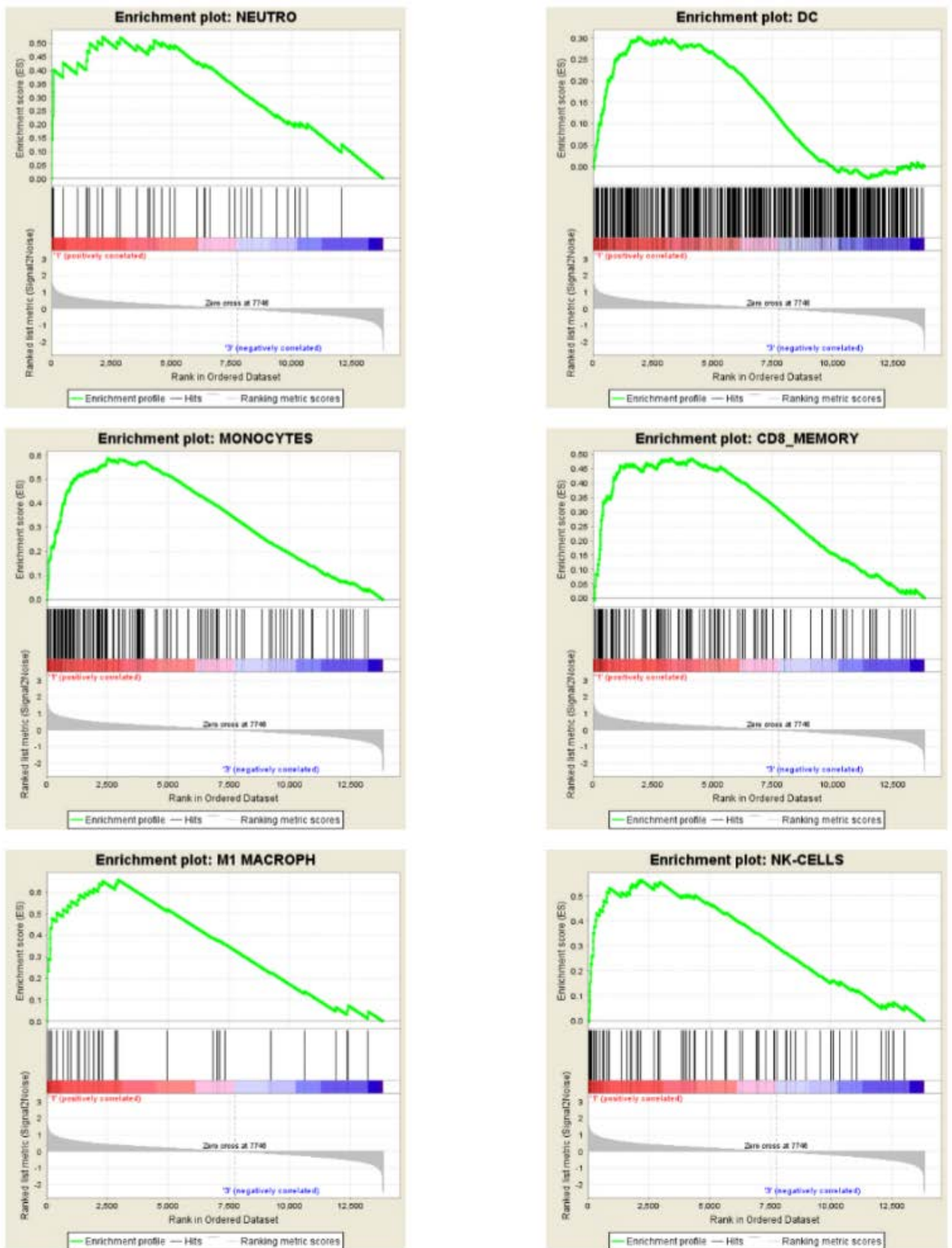


Figure S2. (a) Leading edge plots of cell type specific gene sets from GSEA analysis E-CVID compared to Control. Black lines between green curve panel and red-blue fold change panel represent the genes in each cell type signature set. Red color represents higher gene expression in E-CVID compared to Control.

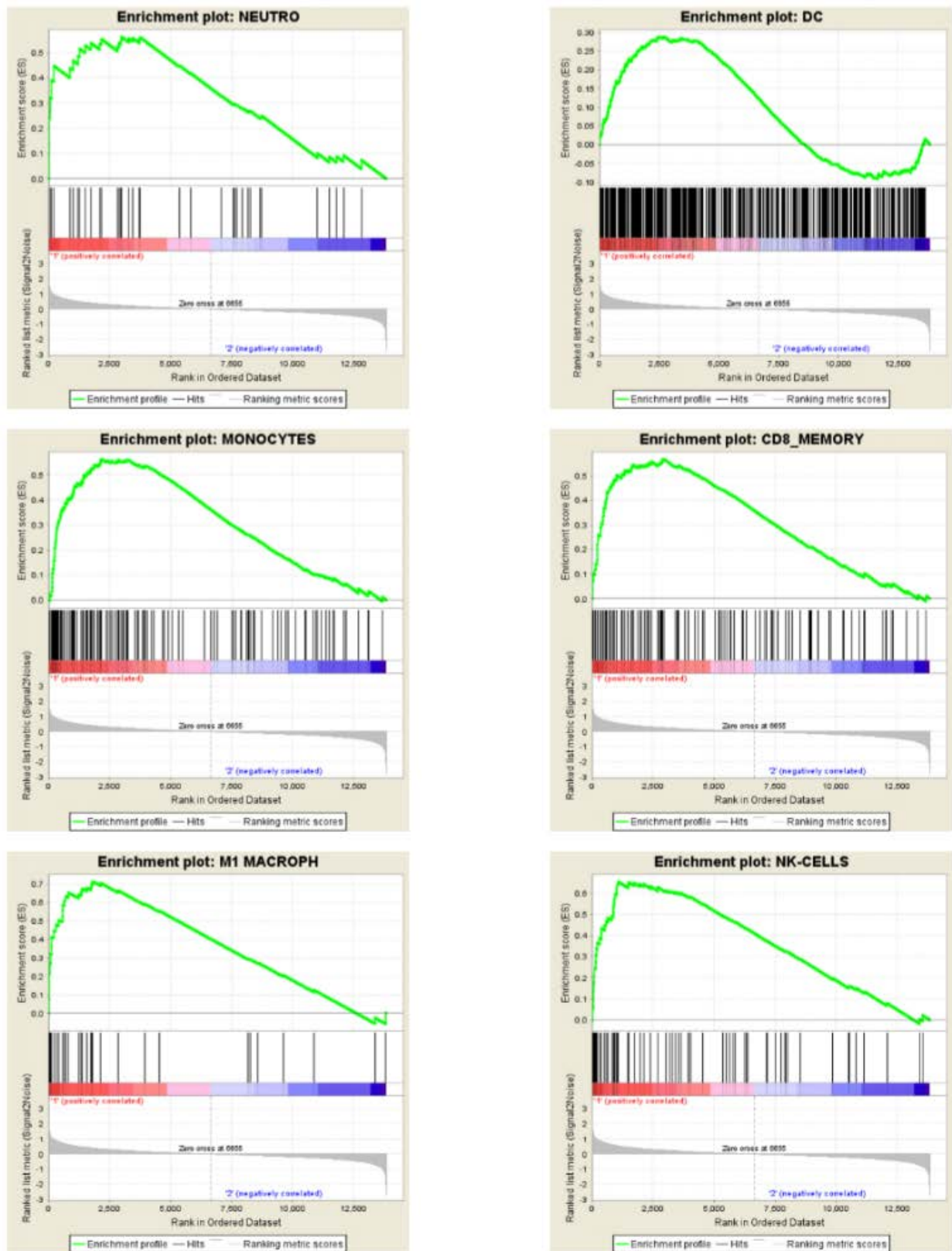


Figure S2. (b) Leading edge plots of cell type specific gene sets from GSEA analysis E-CVID compared to noE-CVID. Black lines between green curve panel and red-blue fold change panel represent the genes in each cell type signature set. Red color represents higher gene expression in E-CVID compared to noE-CVID.

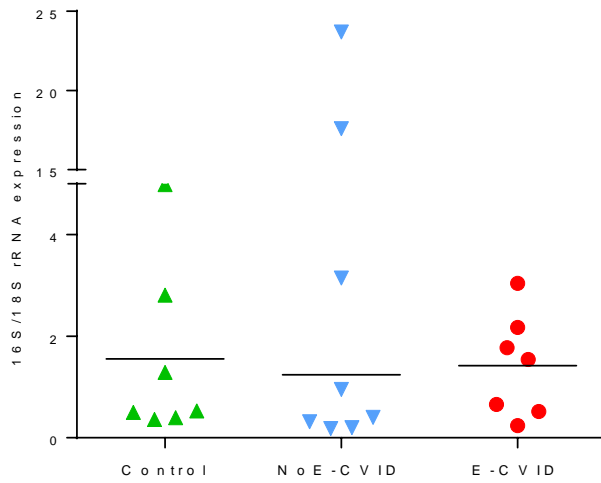


Figure S3. Amount of bacterial 16S RNA gene expression normalized by amount human 18S RNA measured by quantitative PCR. No significant difference detected between three groups: Control; no enteropathy CVID (noE-CVID), CVID enteropathy (E-CVID).

Number of reads in all samples: *Geobacillus* species

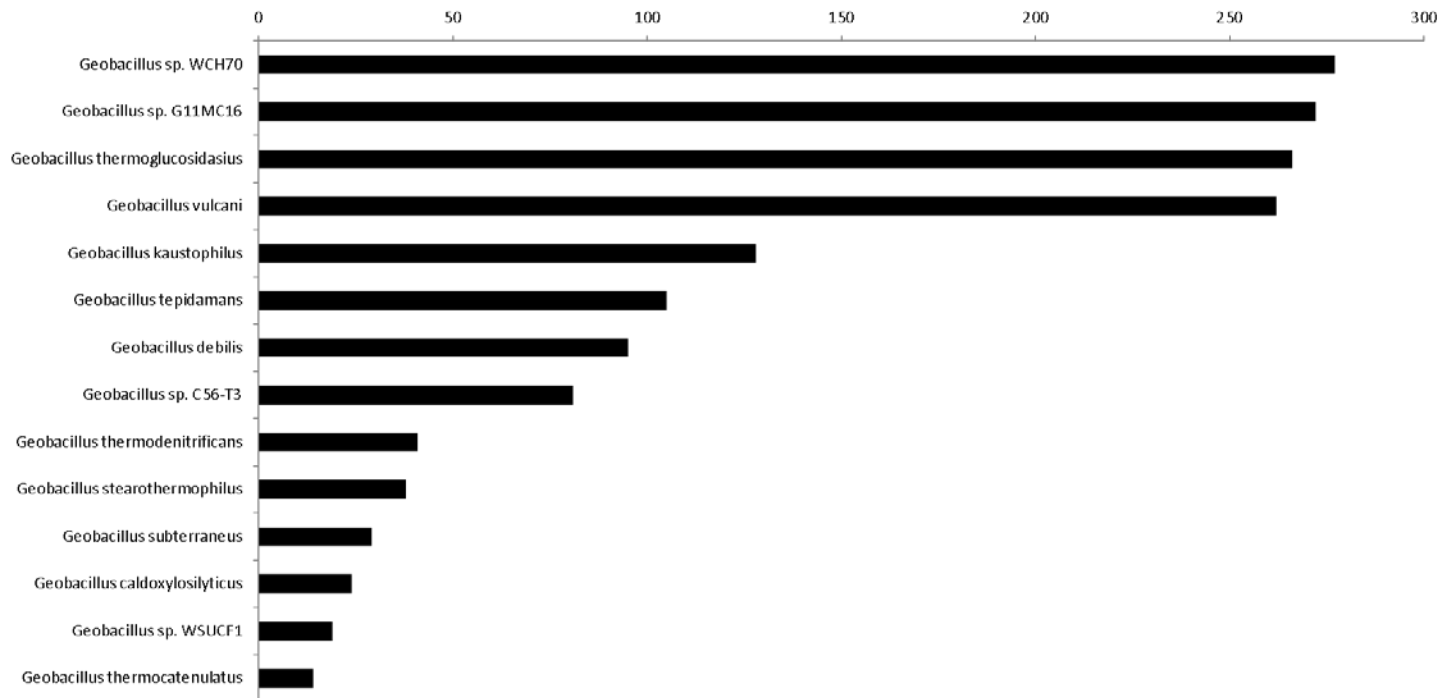


Figure S4. Number of shotgun RNA-SEQ reads assigned to each *Geobacillus* species. The number of reads shown was the total number of reads for a species in all samples in three groups (Control, E-CVID and noE-CVID)

correlation to OTU denovo 106733

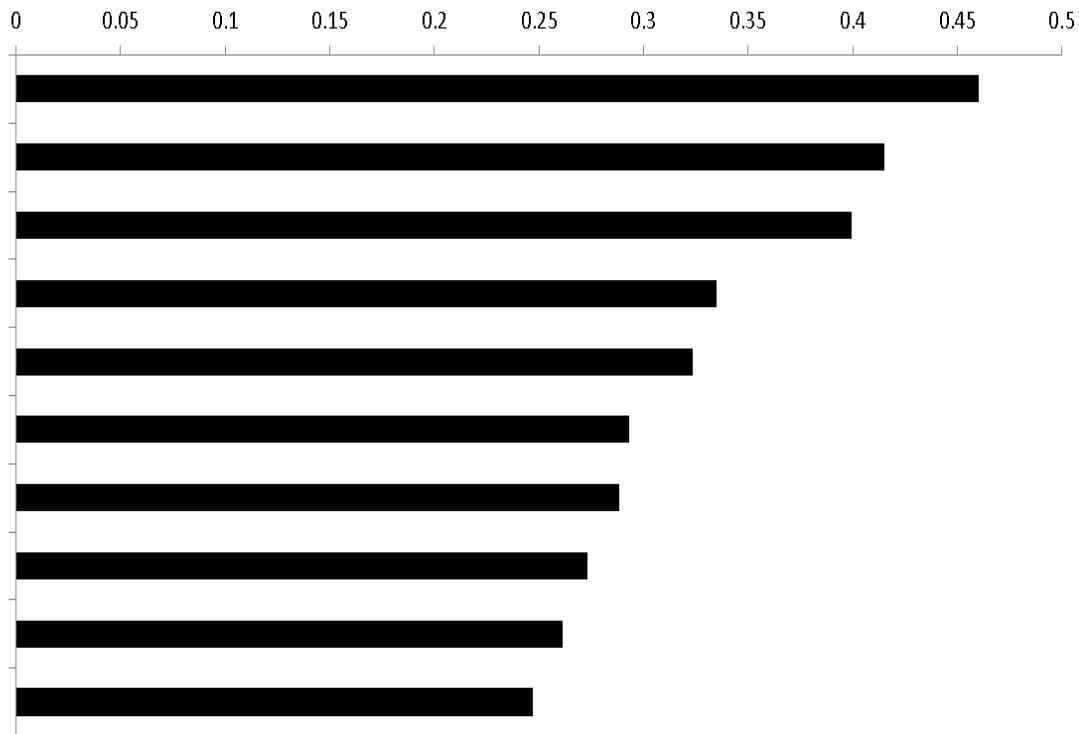


Figure S5. *Lactobacillus* species inferred from shotgun RNA sequencing in correlation to OTU denovo 106733.

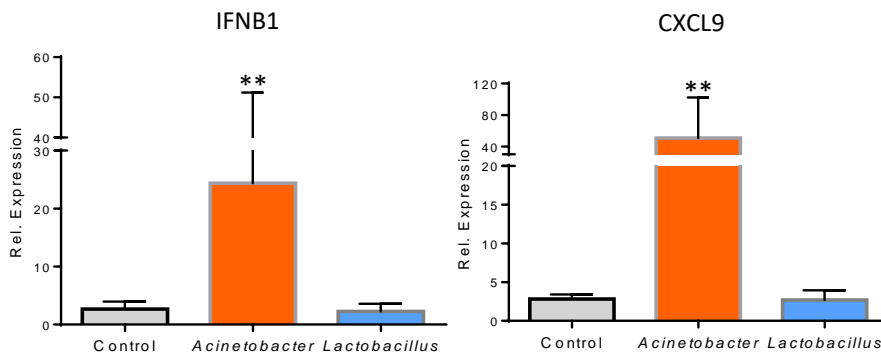


Figure S6. Gene expression of IFNB1 and CXCL9 (relative expression to control gene) in THP-1 cells after 6 h of incubation with *A. baumannii*, *L. plantarum* or no bacteria control; n=7 biological replicates per group, p<0.01, one-sided Wilcoxon test comparing *Acinetobacter*-treated to other groups.

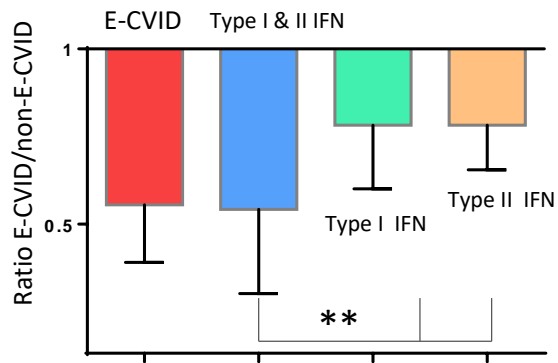


Figure S8. The degree of downregulation of lipid metabolism genes in epithelial cells in vitro by both interferons is higher than that by each one separately; $p < 0.01$, t test.

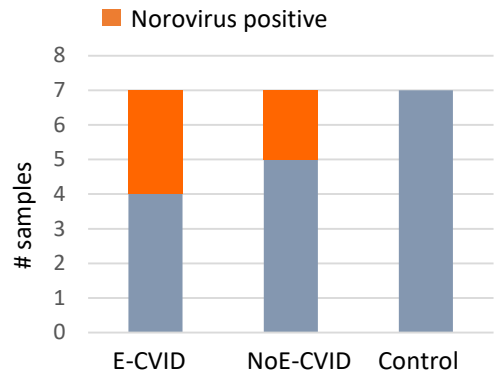


Figure S9. Number of duodenal biopsies positive for Norovirus as estimated by nested PCR described in methods section.