

Supplementary Figure S3

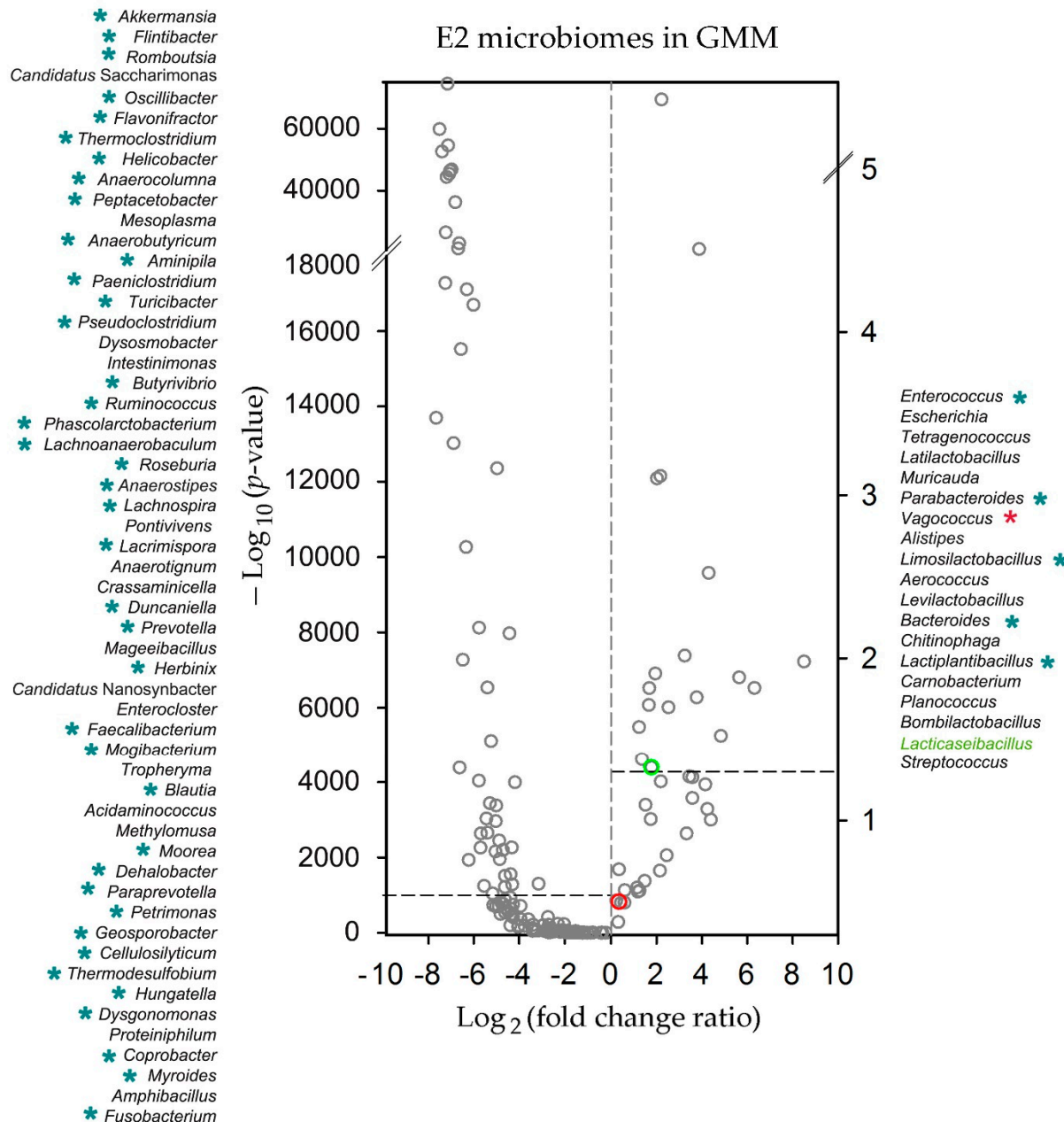


Figure S3. Transfer of the E2 fecal biota to MM and culturing during 48 hours significantly ($p < 0.05$) suppressed 126 tracked genera and activated the growth of 19 taxa. A total of 173 genera met the selection criteria for comparative evaluation. The volcano plot was constructed using paired samples 1s-1s_GM*, 3s-5s_GM*, 7s-7s_GM*, 8s-8s_GM* and 9s-9s_GM* (**Figure 1**). Red and green symbols correspond to bifidobacteria and lactobacilli, respectively. Genera with negative (left) and positive (right) reactions are listed in a descending order of effect caused by the changed environment. Only those taxa whose negative decimal logarithms of p-values exceeded the thresholds indicated by the dashed lines were included in the lists. Asterisks mark genera that showed a similar (cyan) or opposite (red) response in the model E1 microbiome ($p < 0.05$).