

Supplementary Figures from the publication:

Baseline gut microbiome and metabolome profiles predict weight loss after a structured lifestyle intervention, Seethaler *et al.*

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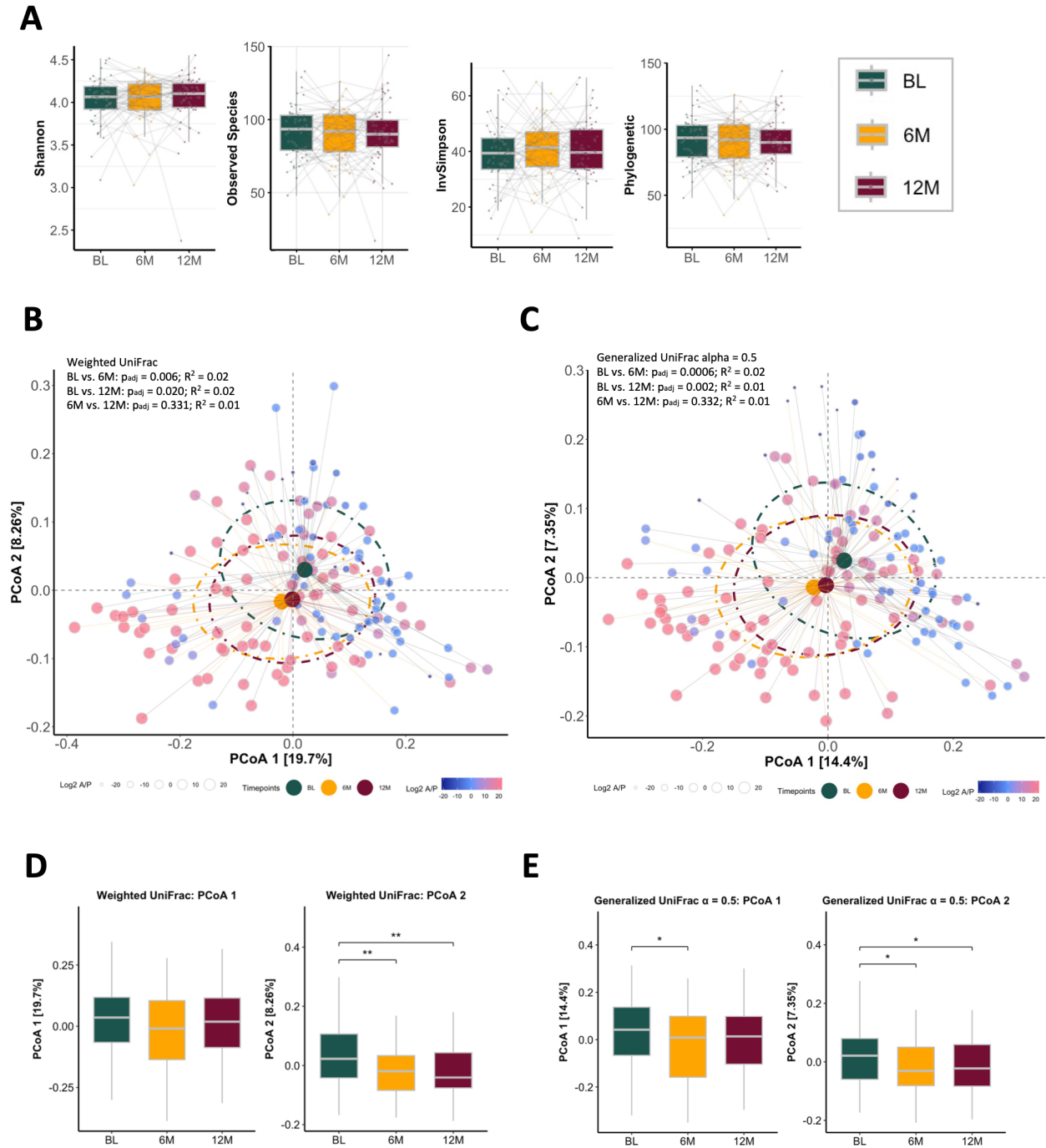


Figure S1. A, Using 16S rRNA sequencing, we found no effect of the intervention on gut microbial alpha diversity between baseline (BL) and month 6 (6M) as well as month 12 (12M) (all $p_{\text{adj}} > 0.1$, linear mixed models). **B,C**, Principal coordinate analysis (PCoA) plot depicting the beta diversity of the gut microbiome on the basis of weighted UniFrac (B) and generalized UniFrac (C) at baseline (BL), month 6 (6M), and month 12 (12M) ($n = 141$). An ordination analysis was performed using a permutational multivariate analysis of variance (PERMANOVA), adjusted for sex and individual variations. **D,E**, Boxplots showing PCoA1 and PCoA2 for each time point in detail (linear mixed models; * $p < 0.05$, ** $p < 0.01$).

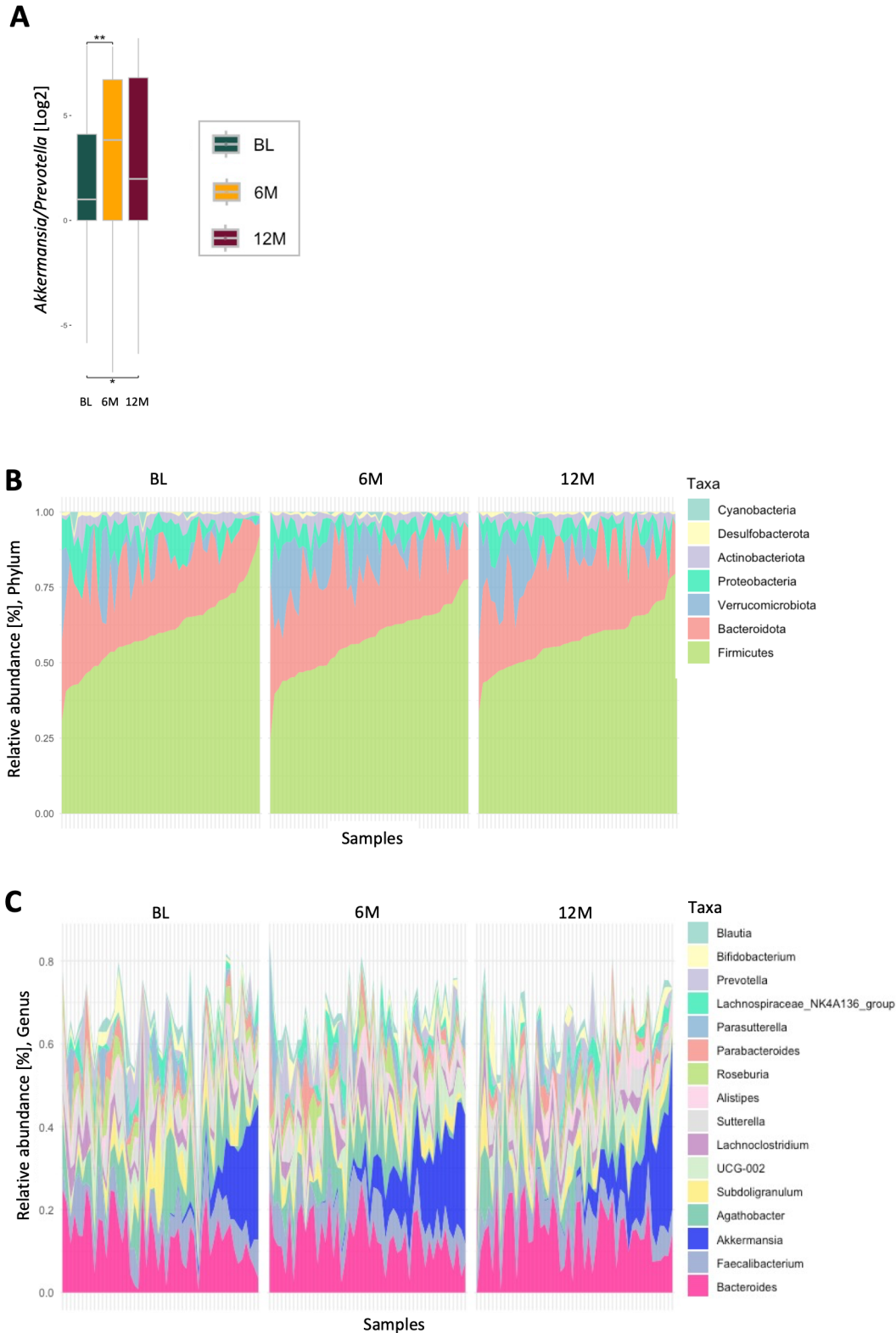


Figure S2. A, Boxplots showing the *Akkermansia/Prevotella* ratio at baseline (BL), month 6 (6M), and month 12 (12M) (linear mixed models; * $p < 0.05$, ** $p < 0.01$). **B**, Relative abundance of the phyla. There was a higher relative abundance of the phylum Verrucomicrobiota at 6M (padj < 0.001) and 12M (padj = 0.009), as compared to BL. **C**, Relative abundance of bacterial genera at three time points: BL, 6M, and 12M ($n = 141$).

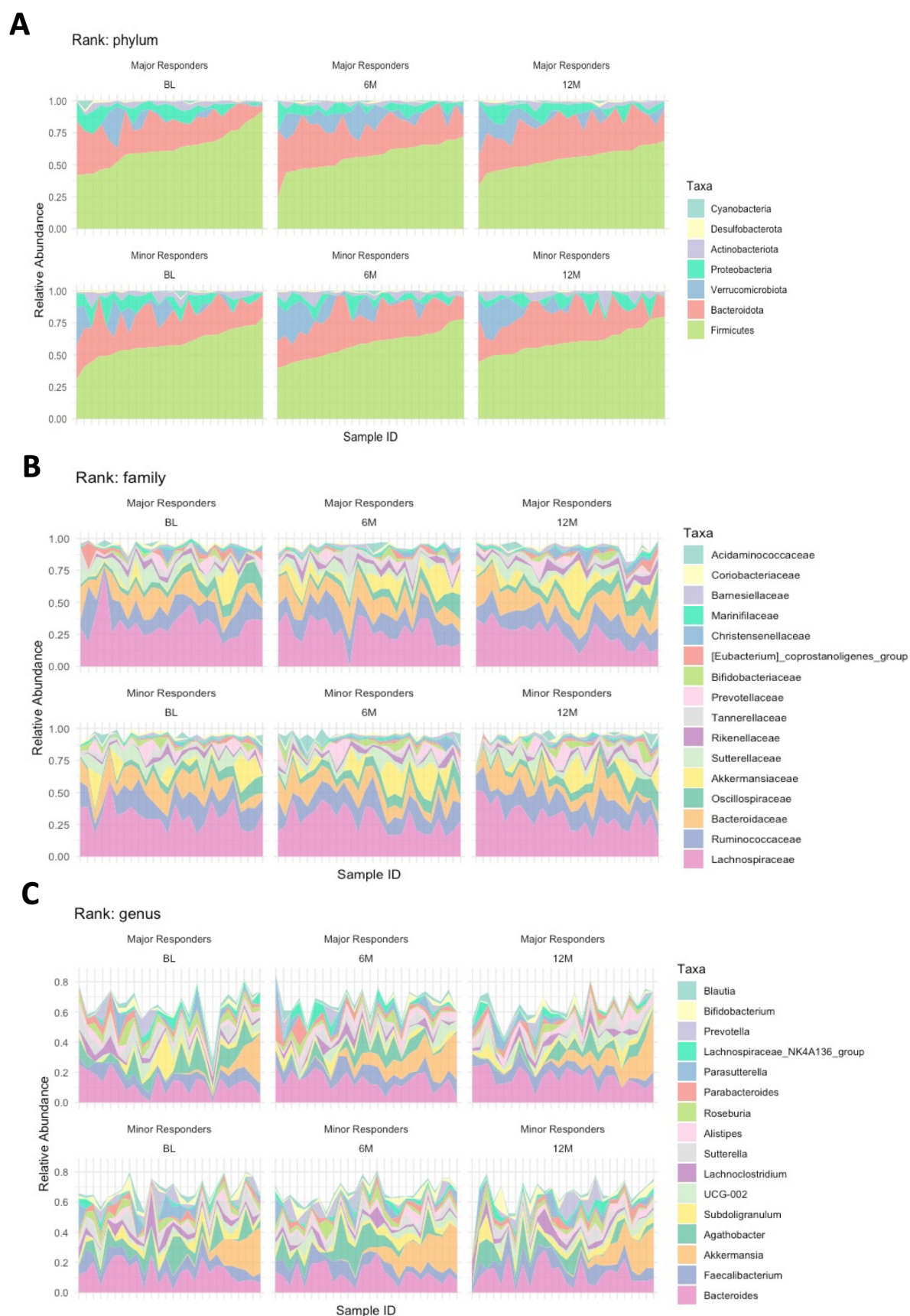


Figure S4. Relative abundance of bacterial taxa on different taxonomic levels (A, phylum; B, family; C, genus). Shown are the data for major and minor responders (see Figure 7) for baseline (BL), month 6 (6M), and month 12 (12M) (n = 141).