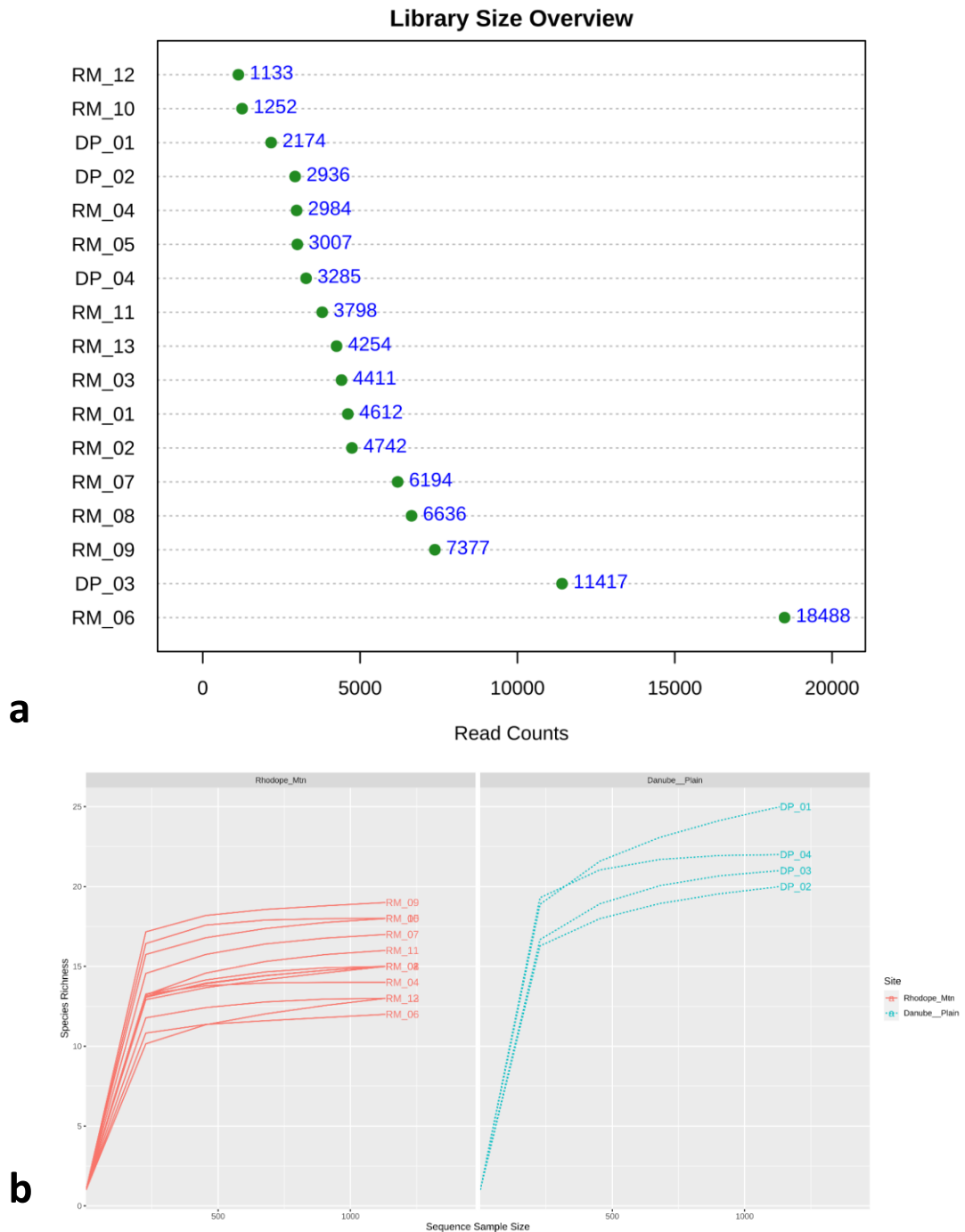


Diversity and composition of bacterial communities associated with honey bee foragers from two contrasting environments

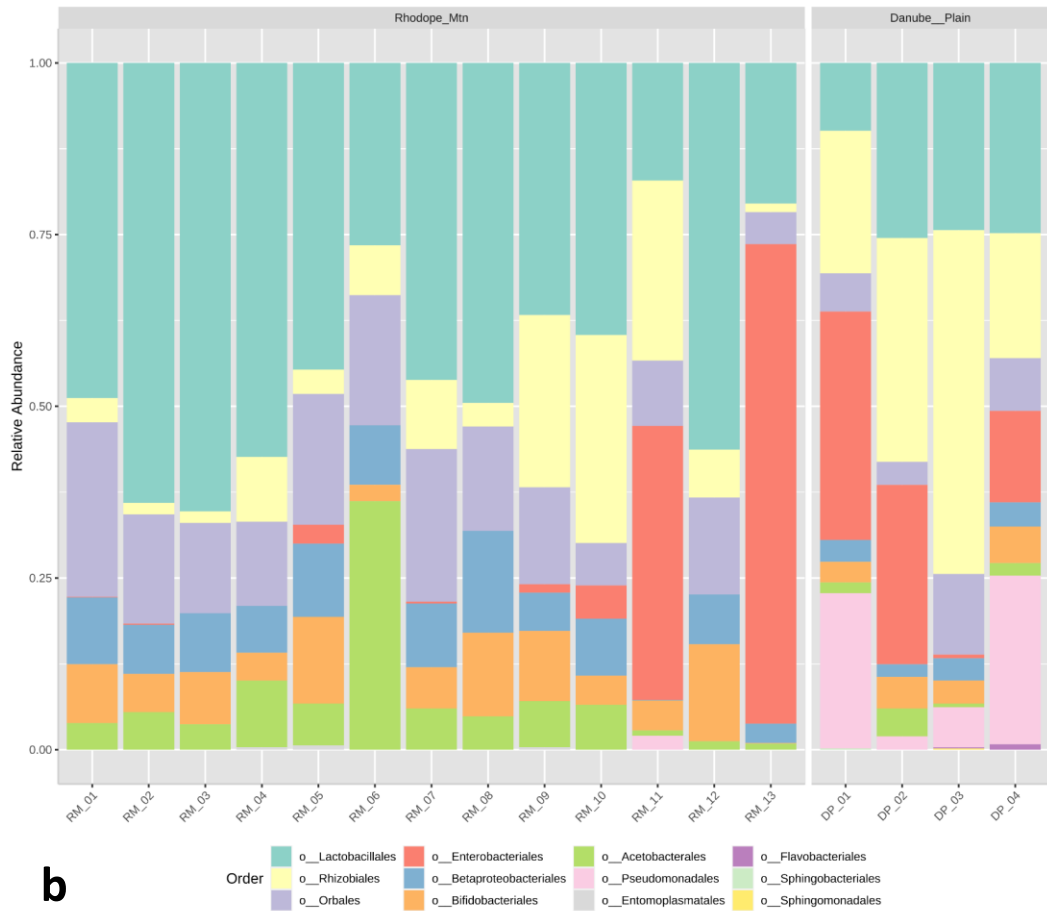
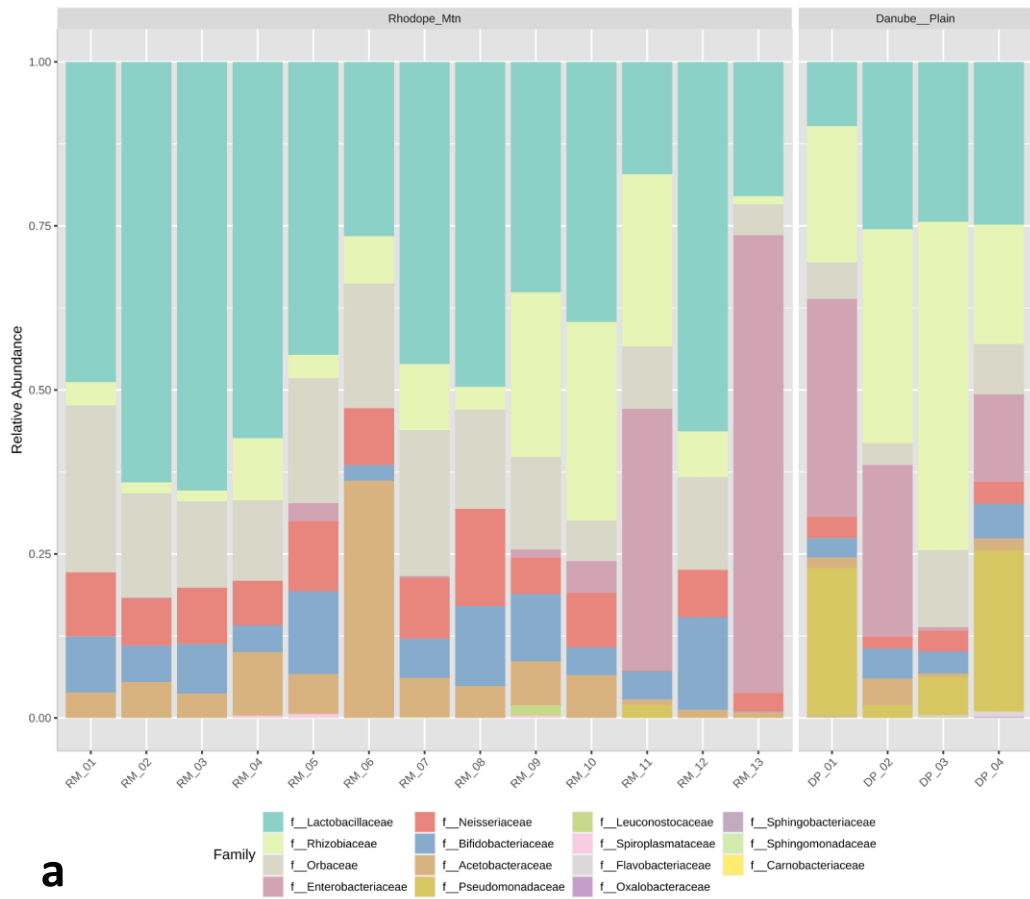
Stela Lazarova, Lyudmila Lozanova, Boyko Neov, Rositsa Shumkova, Ralitsa Balkanska, Nadezhda Pavlova, Delka Salkova, Georgi Radoslavov, Peter Hristov

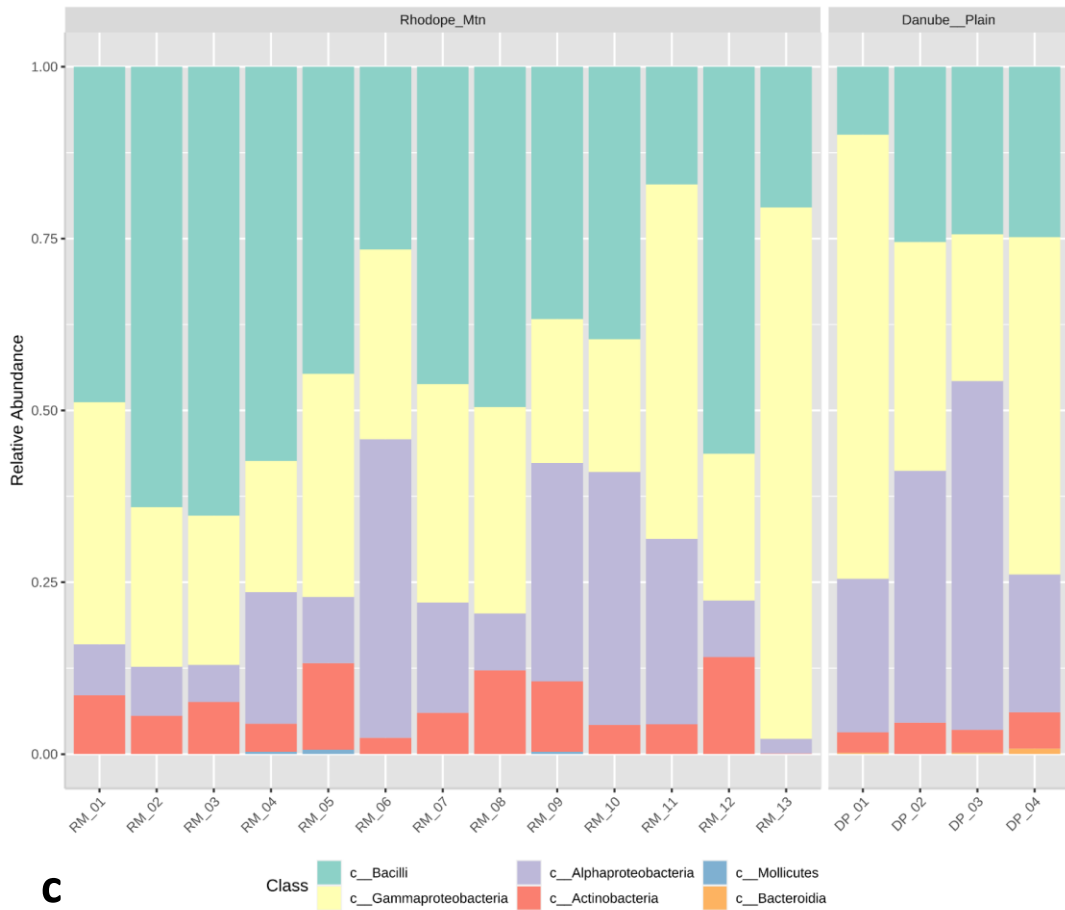
Supplementary figure S1



Supplementary figure S1. Information for sample characteristics: a) library size overview for each honey bee specimen; b) rarefaction curves using filtered dataset. Abbreviations: RM: Rhodope Mountains; DP: Danube plain

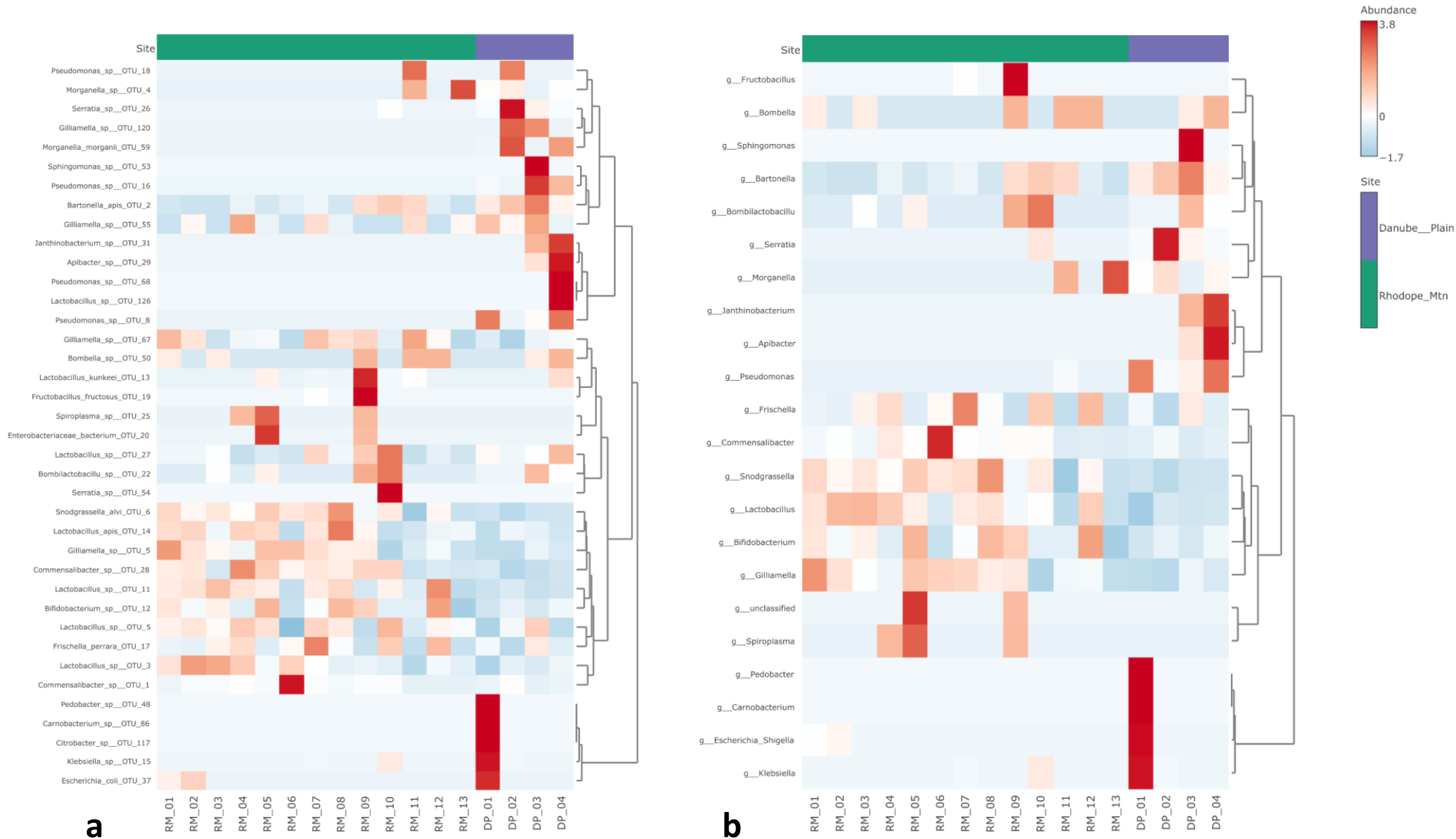
Supplementary figure S2





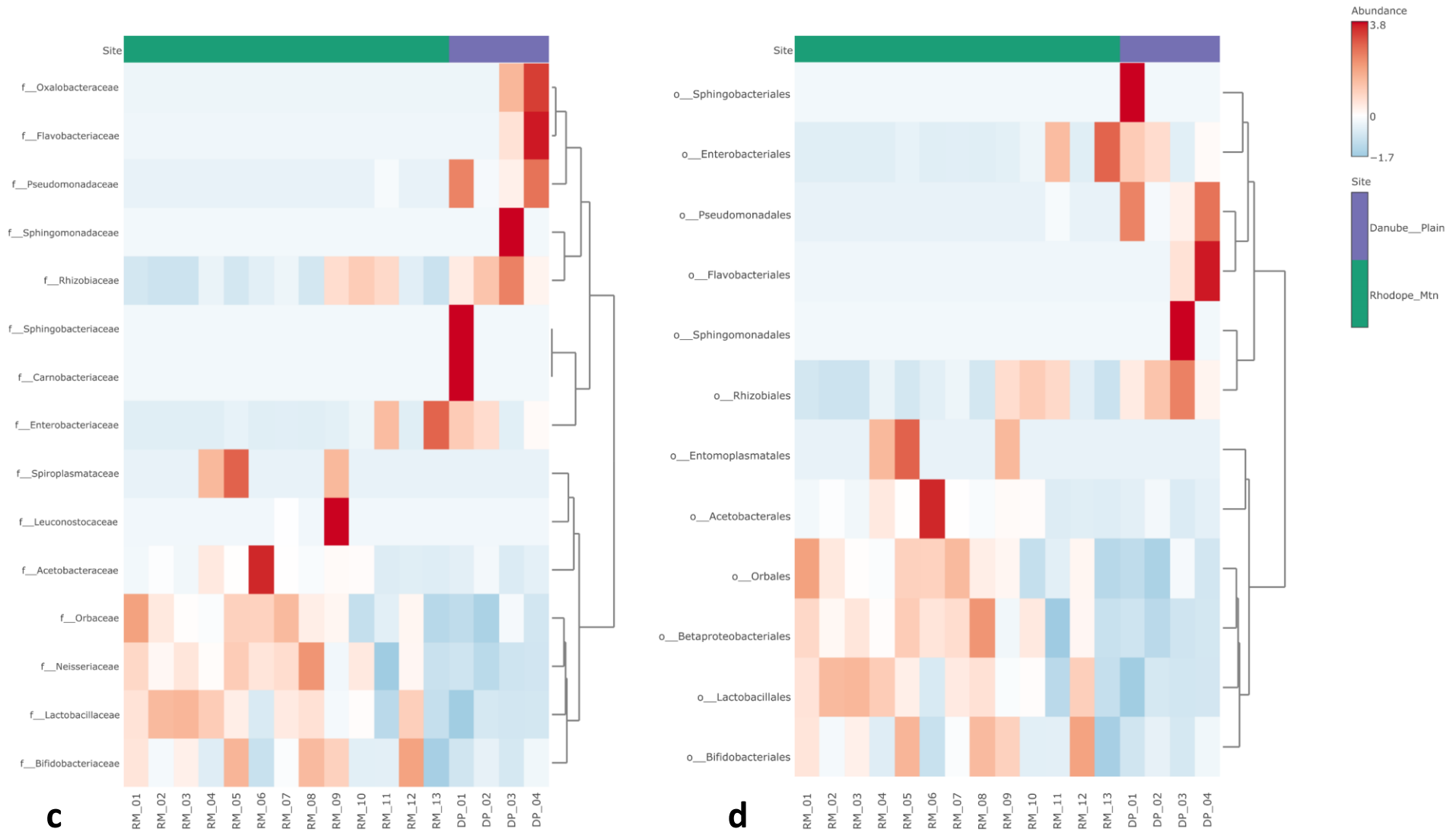
Supplementary figure S2. Bar charts illustrating the distribution and relative abundances of bacterial families (a), orders (b) and classes (c). Data are represented for each honey bee specimen and locality (abbreviations: RM: Rhodope Mountains; DP: Danube plain).

Supplementary figure S3



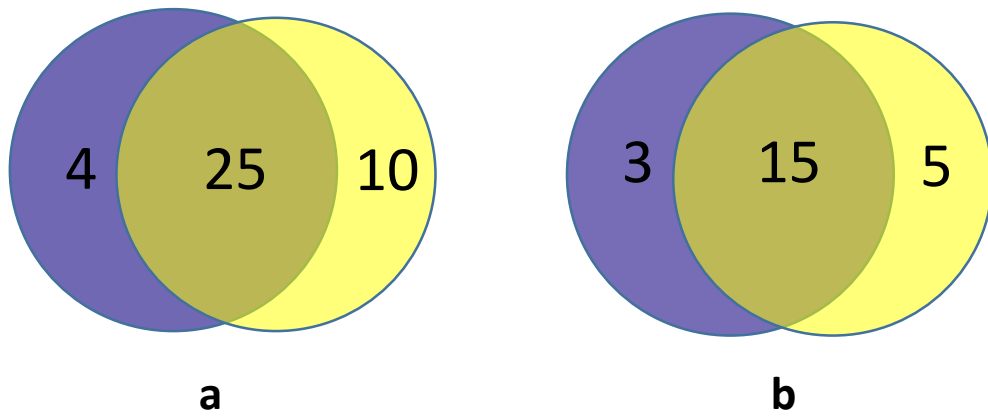
Supplementary figure S3. Heatmaps visualizing bacterial taxa composition - species (**a**) and genera (**b**), and their relative abundances indicated by a color gradient from blue (low) to red (high). Data presented per each bee specimen and locality; regions colored in green and purple for the Rhodope Mountains and Danube plain, respectively.

Supplementary figure S3



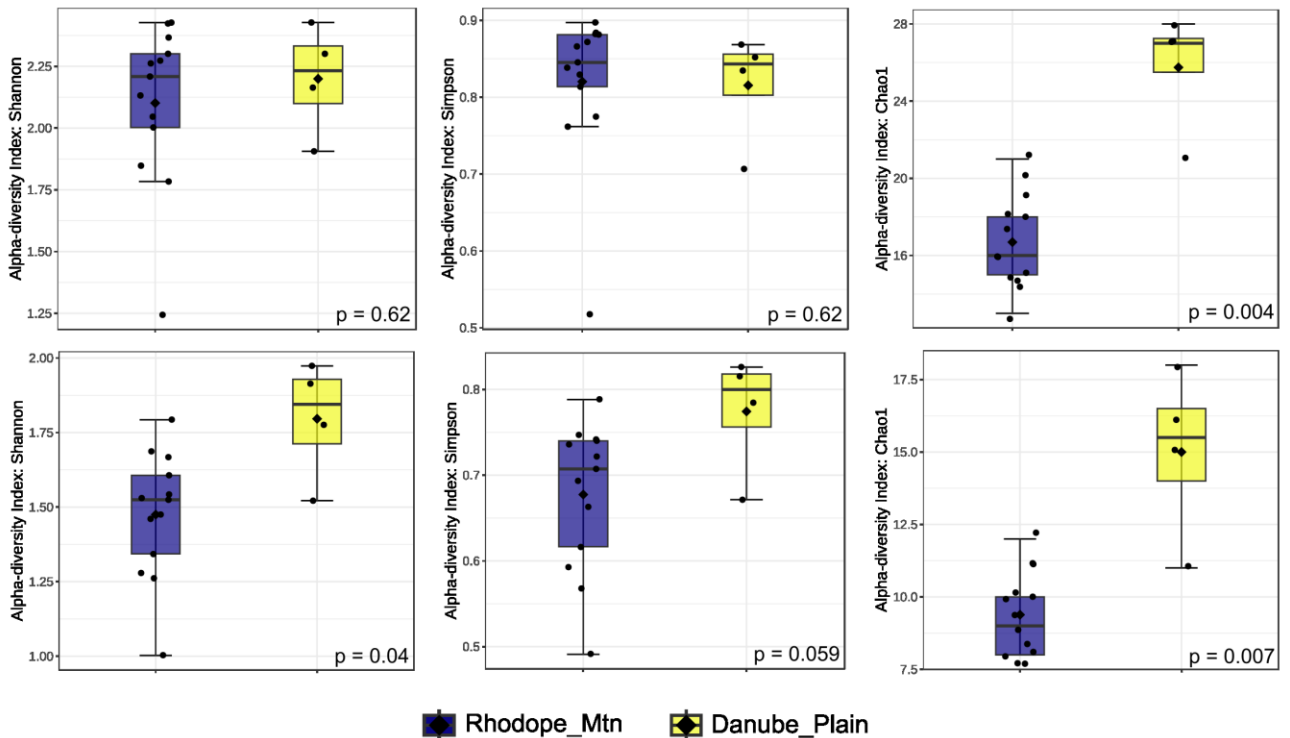
Supplementary figure S3. Heatmaps visualizing bacterial taxa composition - families (**c**) and orders (**d**), and their relative abundances indicated by a color gradient from blue (low) to red (high). Data presented per each bee specimen and locality; regions colored in green and purple for the Rhodope Mountains and Danube plain, respectively.

Supplementary figure S4



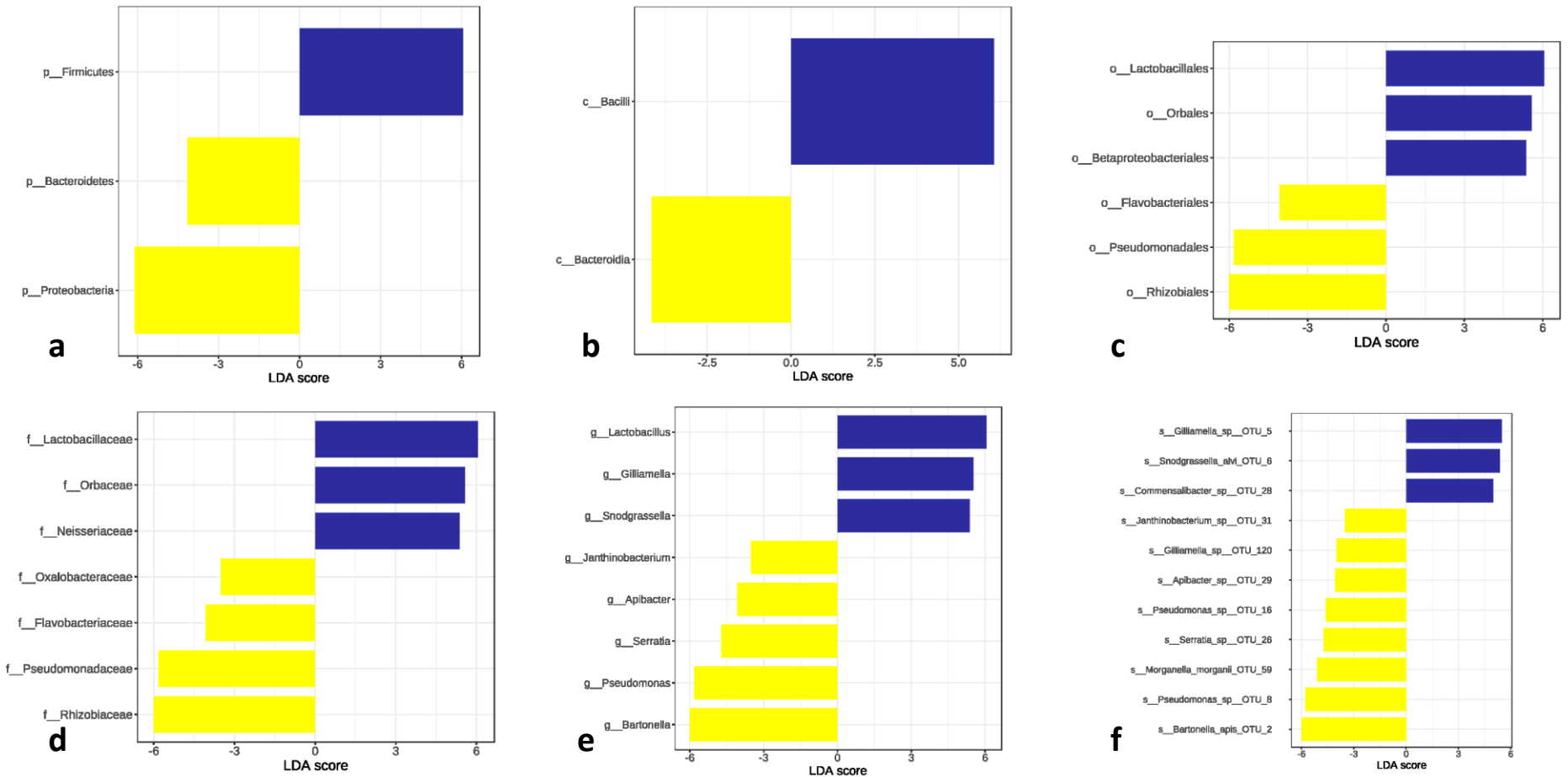
Supplementary figure S4. Venn diagrams show the presence of unique and shared bacterial OTUs (a) and genera (b) in the bacterial communities from both localities. Violet represents communities from the Rhodope Mountains, and yellow – the Danube plain.

Supplementary figure S5



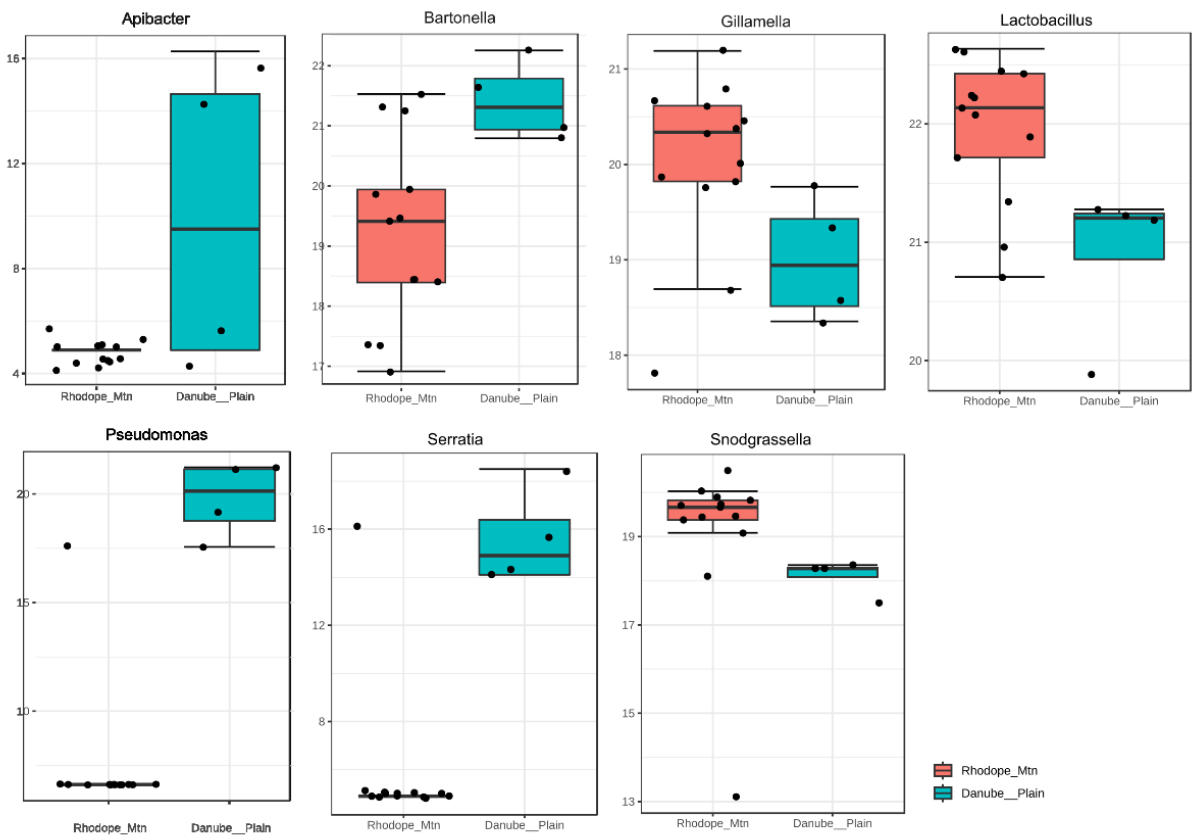
Supplementary figure S5. Box plots of alpha diversity measures showing the variation of Shannon (a, d), Simpson (b, e), and Chao1 (c, f) indices at OTUs (a, b, c) and genus (d, e, f) levels. Mann-Whitney U test statistic: 21, p-values given within the frame of each graph.

Supplementary figure S6



Supplementary figure S6. Linear discriminant analysis (LDA) effect size (LEfSe) showing the differential bacterial taxa of honey bee communities from both localities. Violet and yellow bars represent the Rhodope Mountains and Danube plain taxa, respectively. Data are presented at different taxonomic levels: phylum (**a**), class (**b**), order (**c**), family (**d**), genus (**e**) and OTUs (**f**). Features are considered significant based on their adjusted p-value with a cutoff level ≤ 0.05 . Statistically significant values are presented in the supplementary table S2.

Supplementary figure S7



Supplementary figure S7. Box plots of log-transformed abundances of seven bacterial genera associated with the honey bees, showing different distributions in both geographical regions: *Apibacter*, *Bartonella*, *Gilliamella*, *Lactobacillus*, *Pseudomonas*, *Serratia*, *Snodgrassella* (dark orange: the Rhodope Mountains, green: the Danube plain).