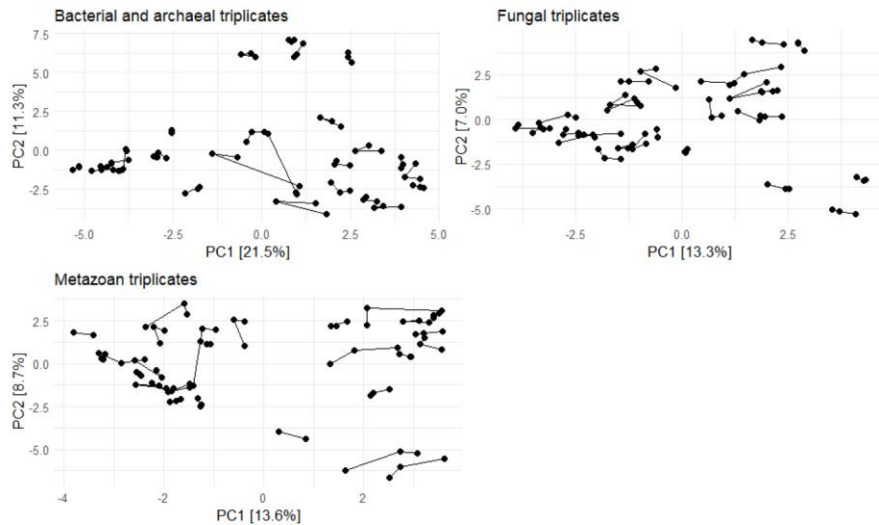
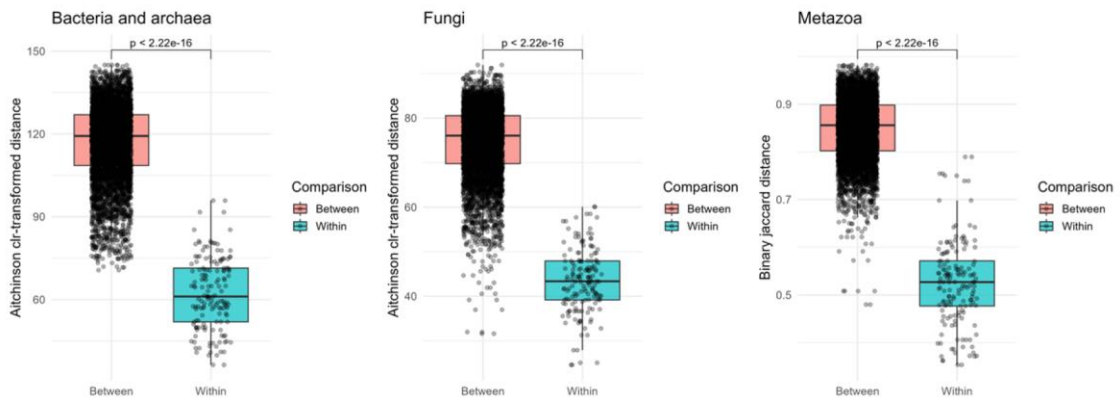


Supplementary figure 1

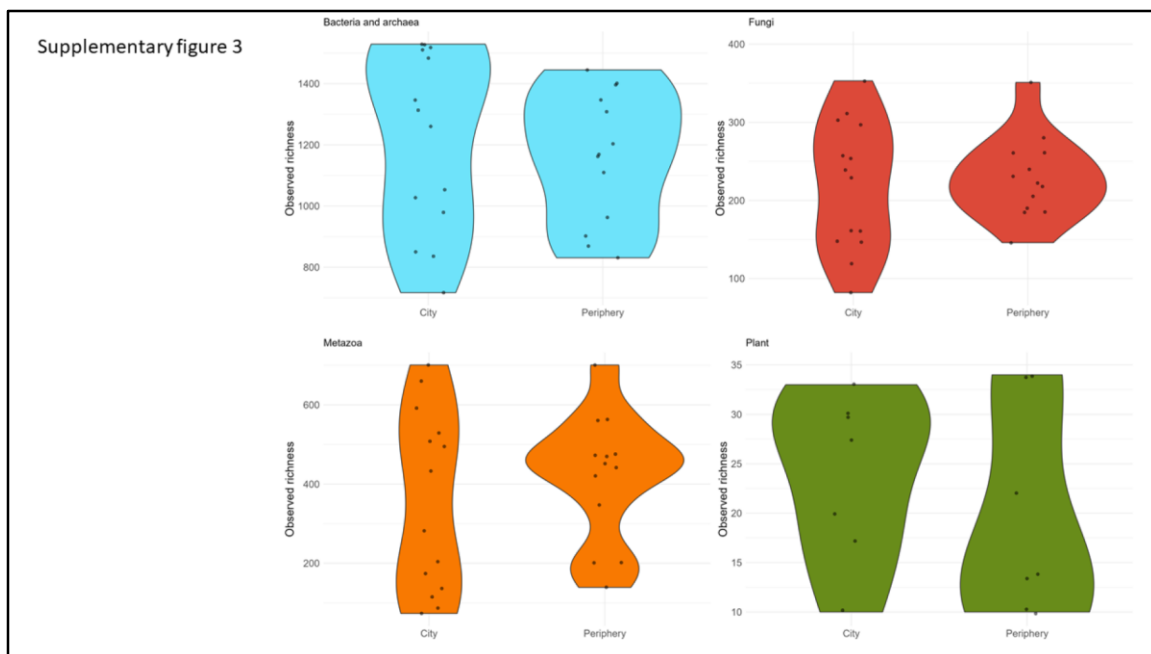


Supplementary figure 1. PCA plots of BFM communities show triplicate samples from each sampling set, with points representing individual samples. Triplicates from the same site are connected by lines to illustrate within-site variation. Percentages explaining principle components 1 and 2 are indicated in brackets.

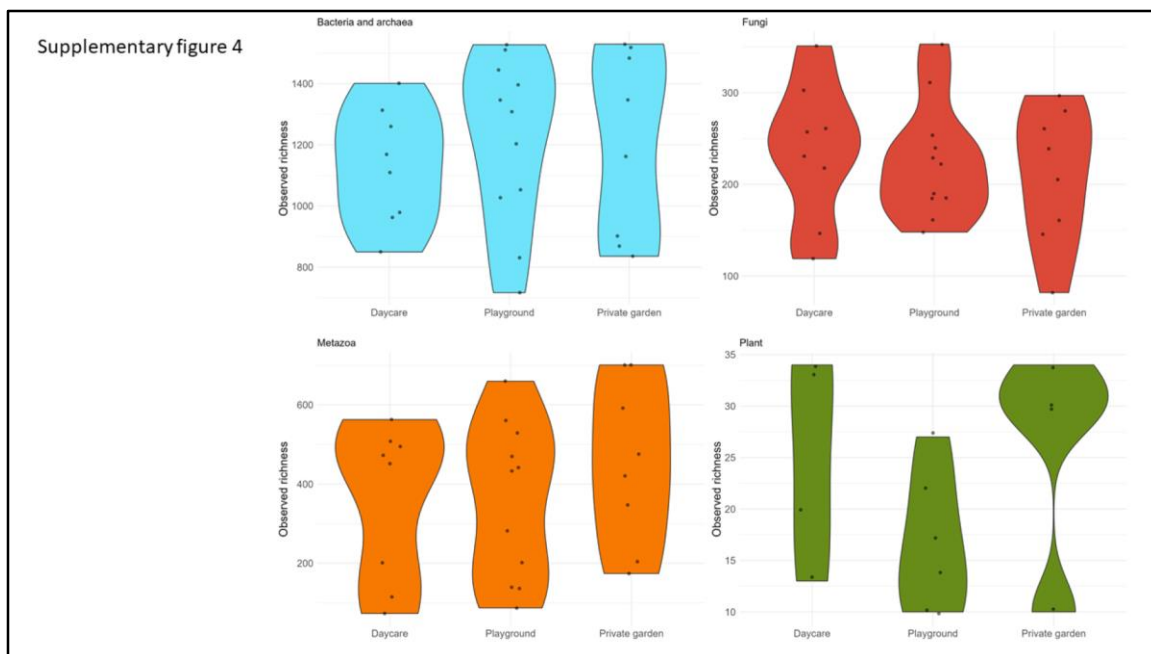
Supplementary figure 2



Supplementary figure 2. Beta diversity within and between triplicates, calculated using Aitchison distance for Bacteria and Archaea and for Fungi, and binary Jaccard distance for Metazoa. Wilcoxon test p values are shown above the brackets.

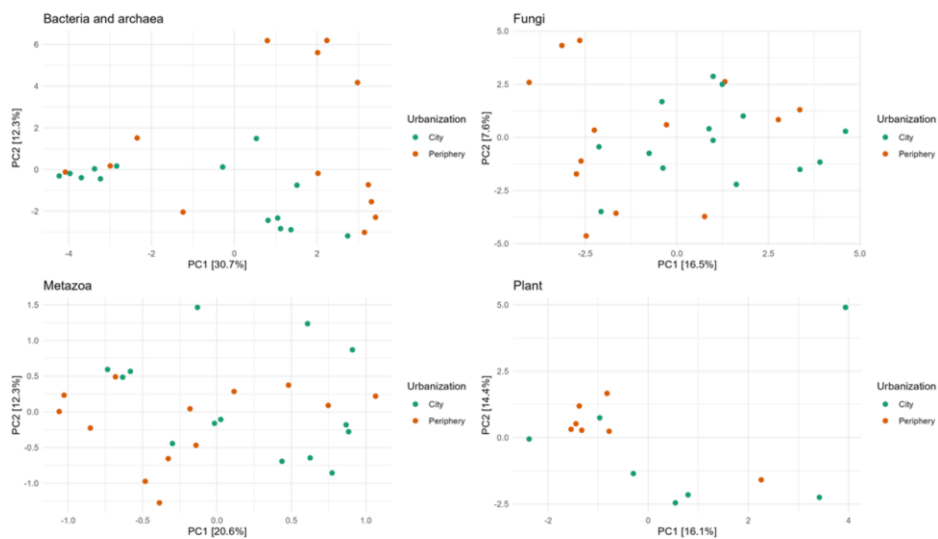


Supplementary figure 3. Observed richness difference between city and periphery for BFMP.



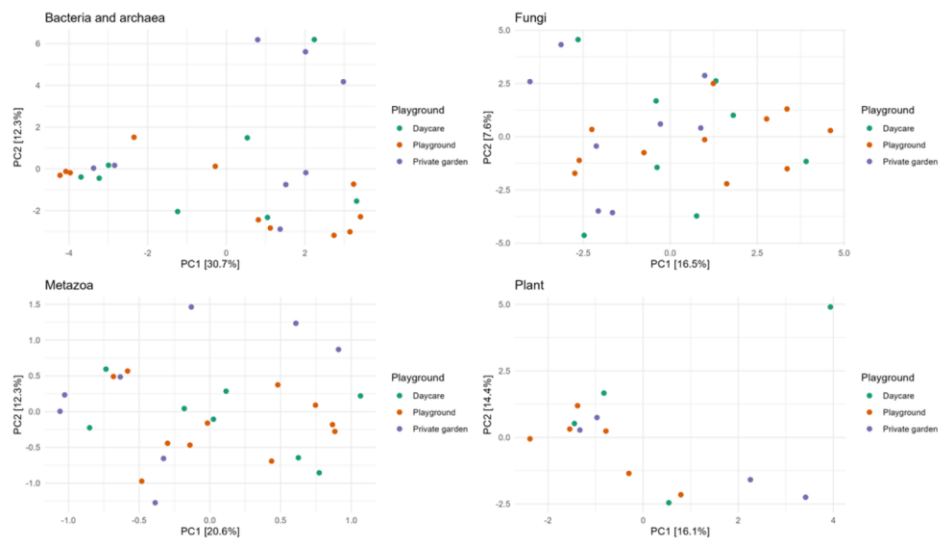
Supplementary figure 4. Observed richness difference between playgrounds for BFMP.

Supplementary figure 5

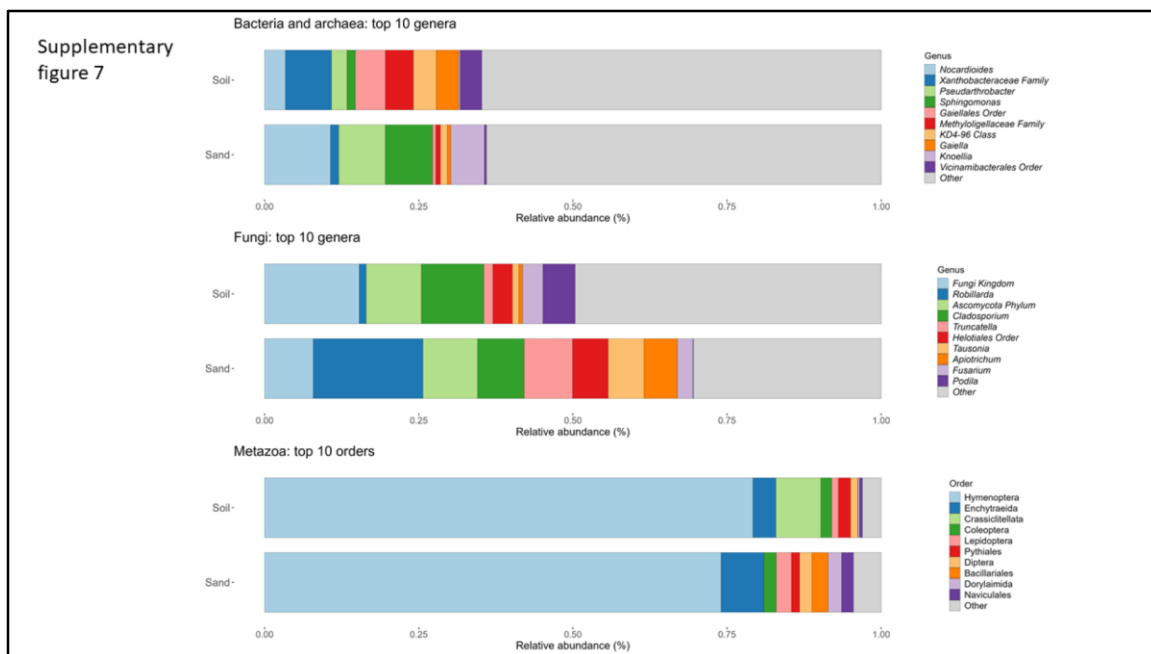


Supplementary figure 5. PCA plots for BFMP. Urbanization levels are color coded. Percentages explaining principle components 1 and 2 are indicated in brackets.

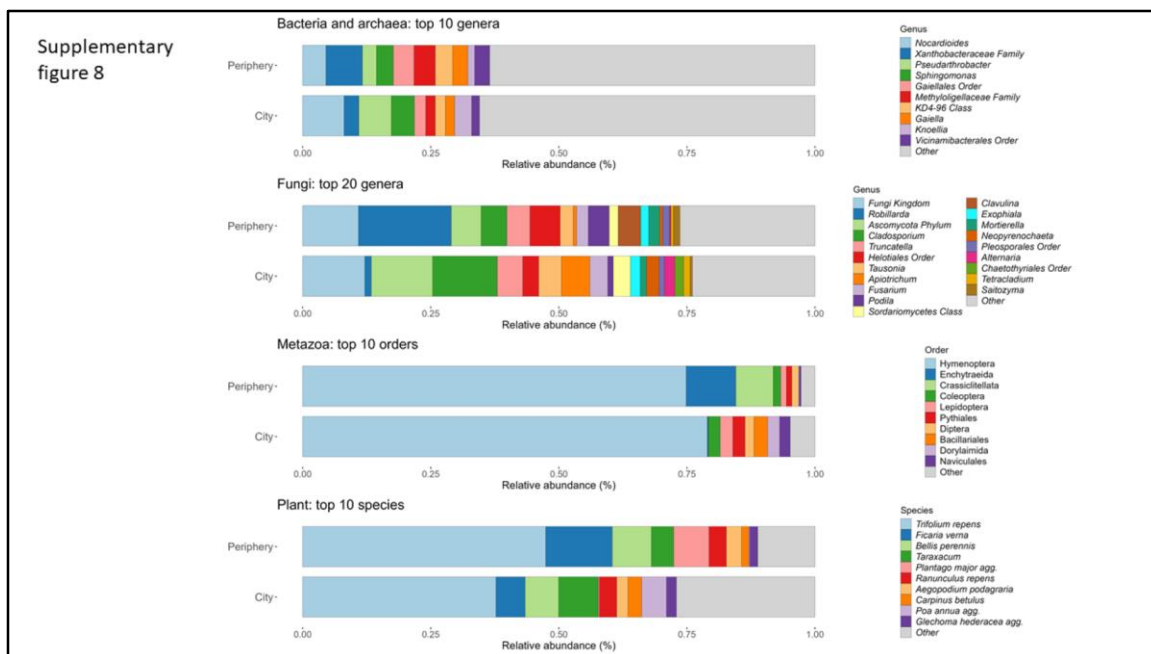
Supplementary figure 6



Supplementary figure 6. PCA for BFMP. Playgrounds are color coded. Percentages explaining principle components 1 and 2 are indicated in brackets.



Supplementary figure 7. Taxonomical compositions between soil types for BFM. Top 10 most abundant taxa are shown.



Supplementary figure 8. Taxonomical compositions between city and periphery for BFMP. Top 10 (for BMP) and top 20 (for F) most abundant taxa are shown.



Supplementary figure 9. Univariate PERMANOVA. Only significant variables are shown and indicated with a stars: “***” indicates p-values < 0.001, “**” indicates p-values between 0.001 and 0.01, and “*” indicates p-values between 0.01 and 0.05. Bars show explained variance (R²).