Supporting Information for
Antimicrobial chemicals are associated with elevated antibiotic resistance genes in the indoor dust microbiome

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Summary
Three SI pages containing 2 figures.

Supplementary Tables

1. Metadata, including total mass collected, for all samples.
2. Target times and masses for analytes.
3. Mapping file containing architectural metadata and all measured chemical concentrations (ng/g) used in sequence data analysis.
4. A complete listing of all antibiotic resistance gene markers identified in this study and their ontologies.

Supplementary Figures

1. Heatmap of the 25 most abundant genera, as determined by 16S rDNA amplicon sequencing.
2. Community composition correlates with space type but not antimicrobial chemical profile. a) Principal coordinates analysis (PCoA) plot based on Canberra distance of 16S rRNA taxonomic composition. Points represent individual samples and are painted according to space type (point color). The R^2 and p values reported are from a PERMANOVA. b) Plot of community beta diversity by chemical profile distance. The R and p values reported are from the Mantel test.

Figure S1. Heatmap of the 25 most abundant genera, as determined by 16S rDNA amplicon sequencing.

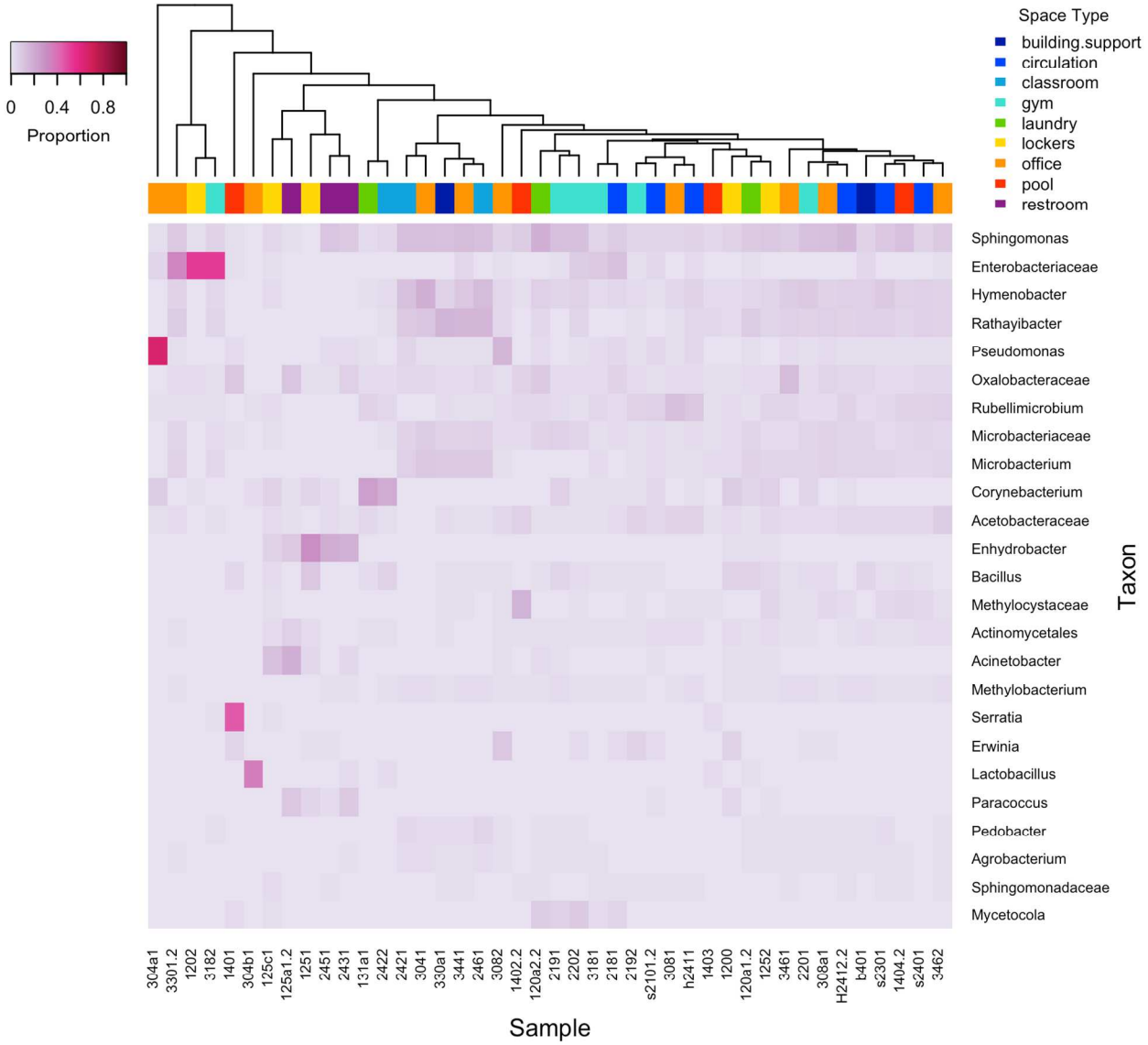
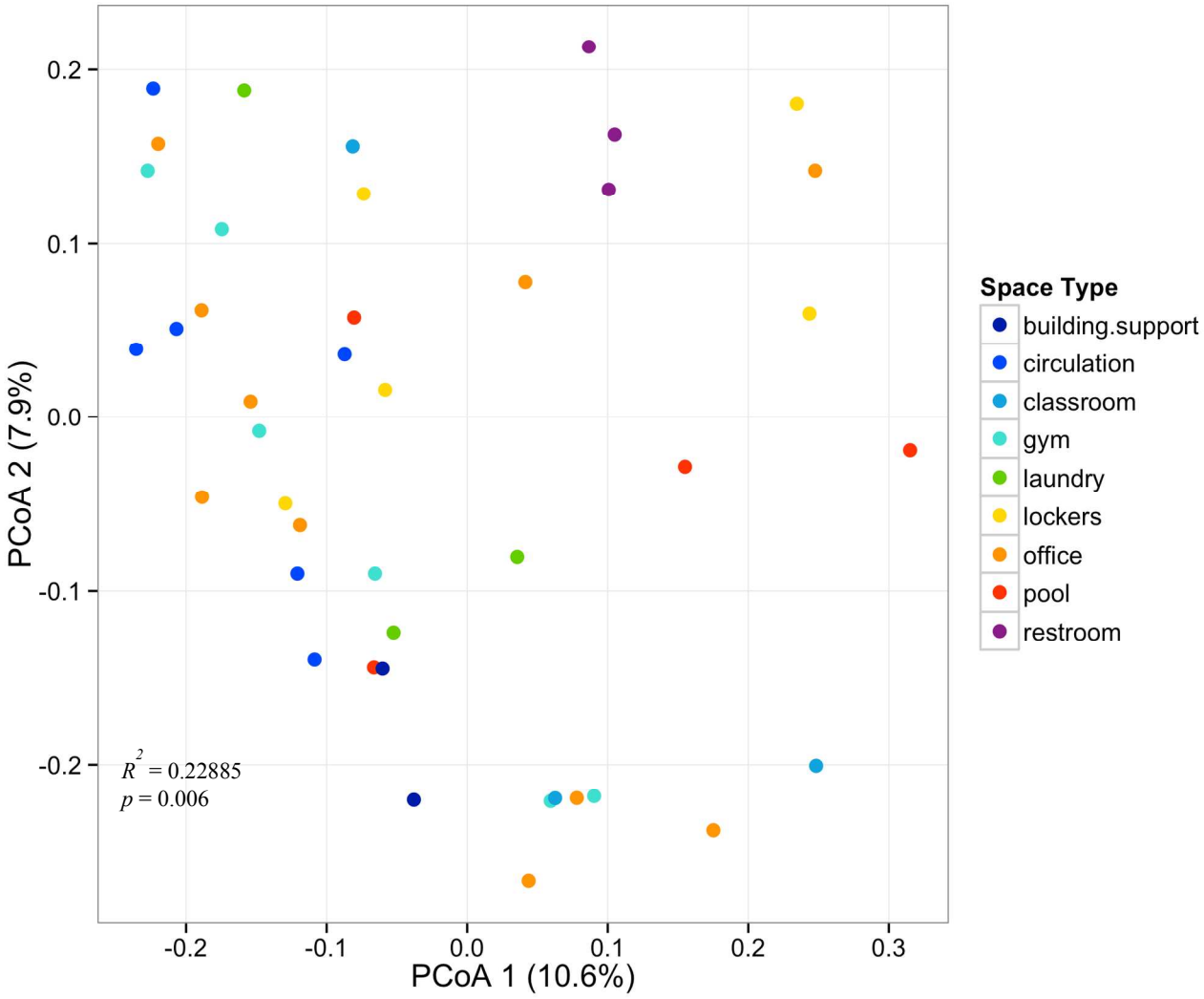
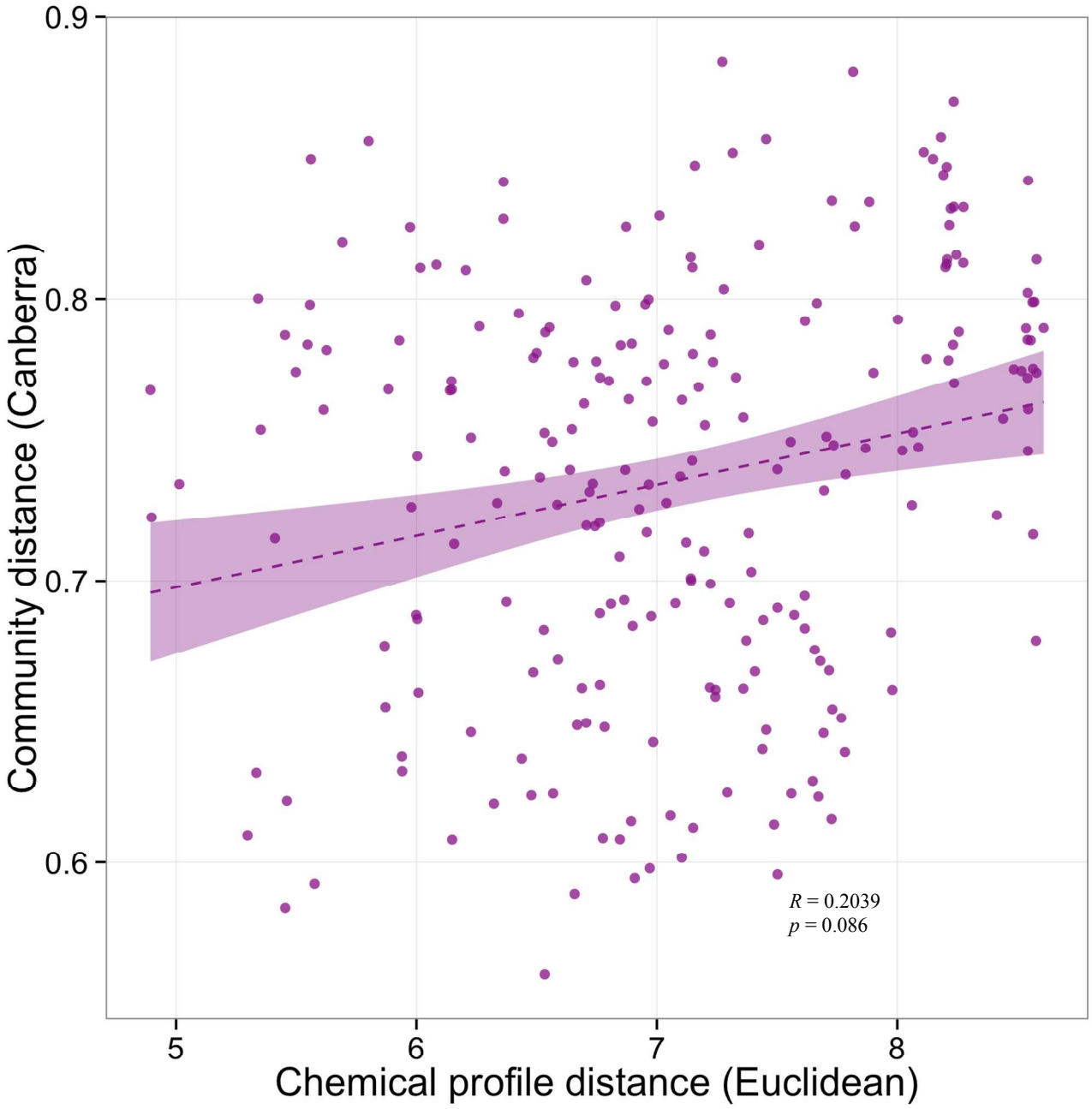


Figure S2. Community composition correlates with space type but not antimicrobial chemical profile. a) Principal coordinates analysis (PCoA) plot based on Canberra distance of 16S rRNA taxonomic composition. Points represent individual samples and are painted according to space type (point color). The R^2 and p values reported are from a PERMANOVA. b) Plot of community beta diversity by chemical profile distance. The R and p values reported are from the Mantel test.

a)



b)


0.9
0.8
0.7
0.6
Community distance (Canberra)
5
6
7
8
Chemical profile distance (Euclidean)
R = 0.2039
p = 0.086