

SUPPLEMENTARY INFORMATION
FOR
**Microbial and Metabolic Succession on Common Building
Materials Under High Humidity Conditions**

Lax et al.

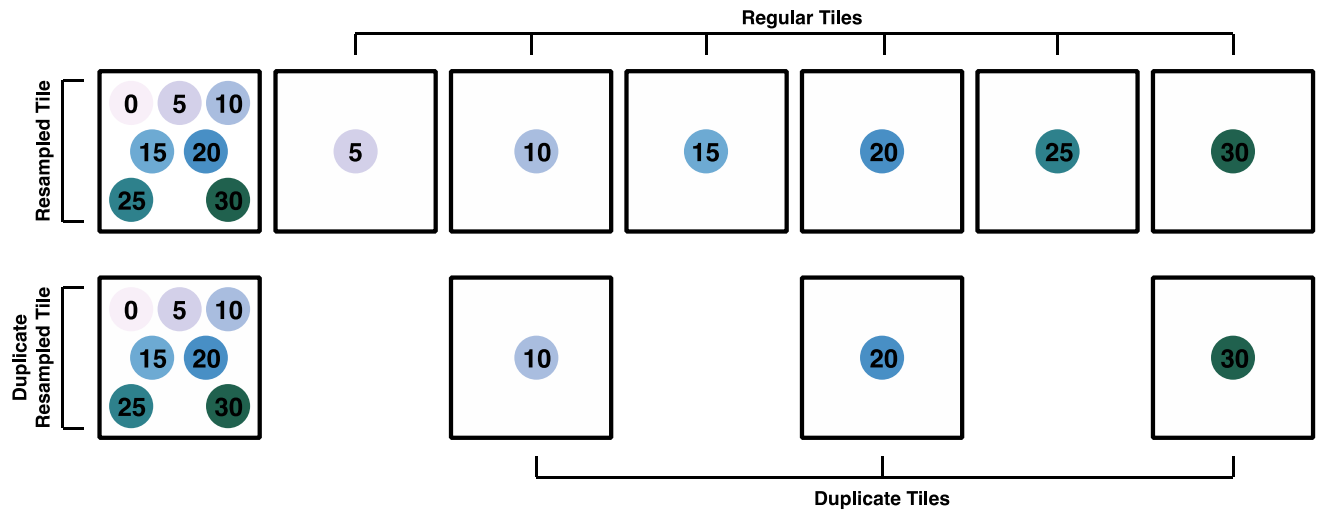


Figure S1: Experimental setup of project. Illustration of the experimental setup and coupon sampling procedures. Numbers indicate the day of study on which the tile was sampled.

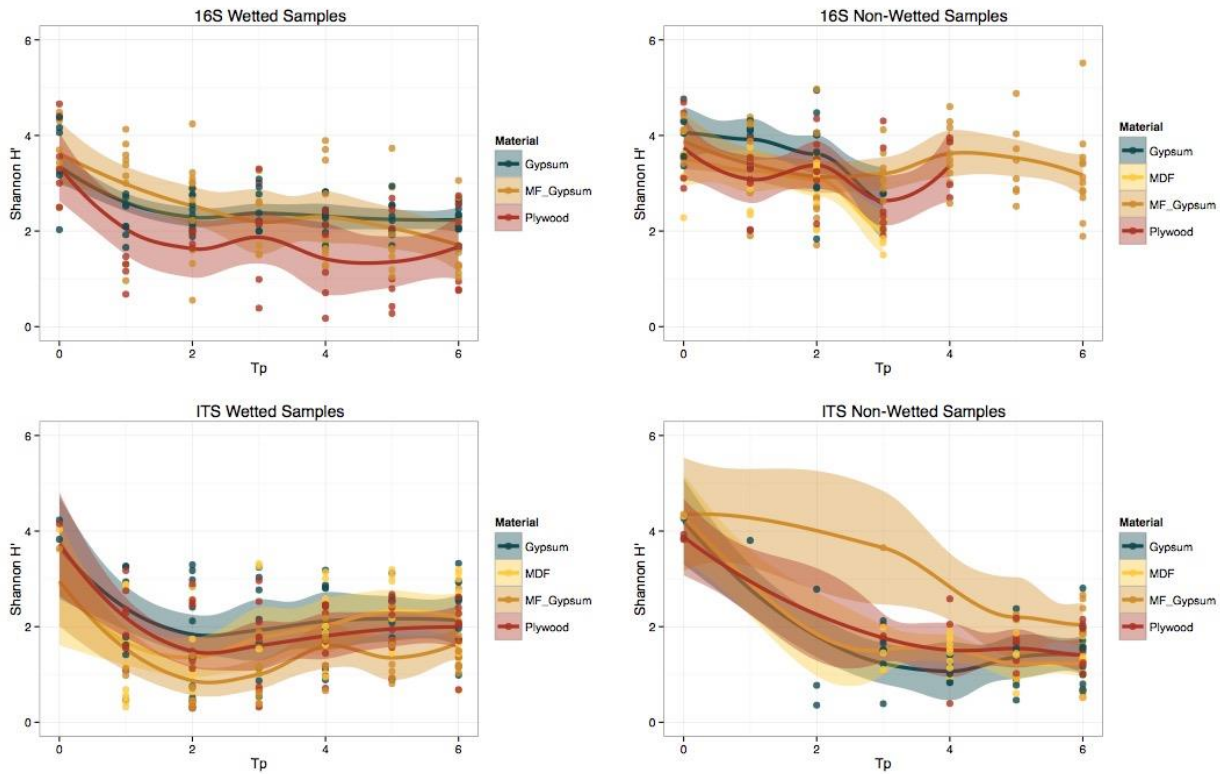


Figure S2: Change in the Shannon Index by material over time. Points represent individual samples ($n=338$, 330 samples for 16S and ITS, respectively) and the trend lines are a smoothed moving-average of the mean and shaded regions indicate the standard error

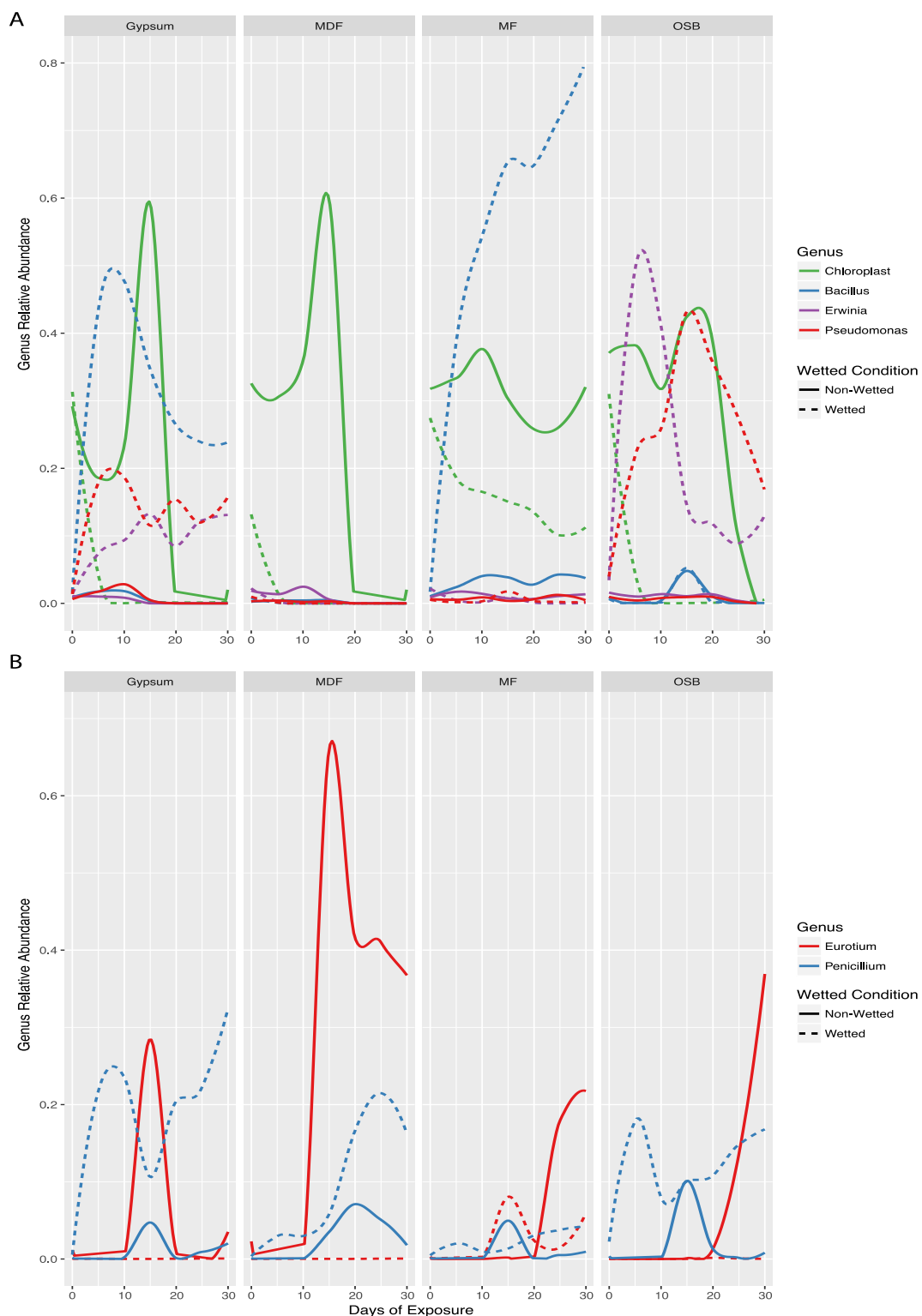


Figure S3: Microbial succession by material over time Changes in the relative abundance of selected microbial genera for each material over the course of succession. (n=338, 330 samples for 16S and ITS, respectively). (A) Lines represent a smoothed moving average of the mean. Genus is indicated by color and wetting condition is indicated by line style. (B) Changes in the relative abundance of selected fungal genera over the course of succession. Formatting is as in (A)

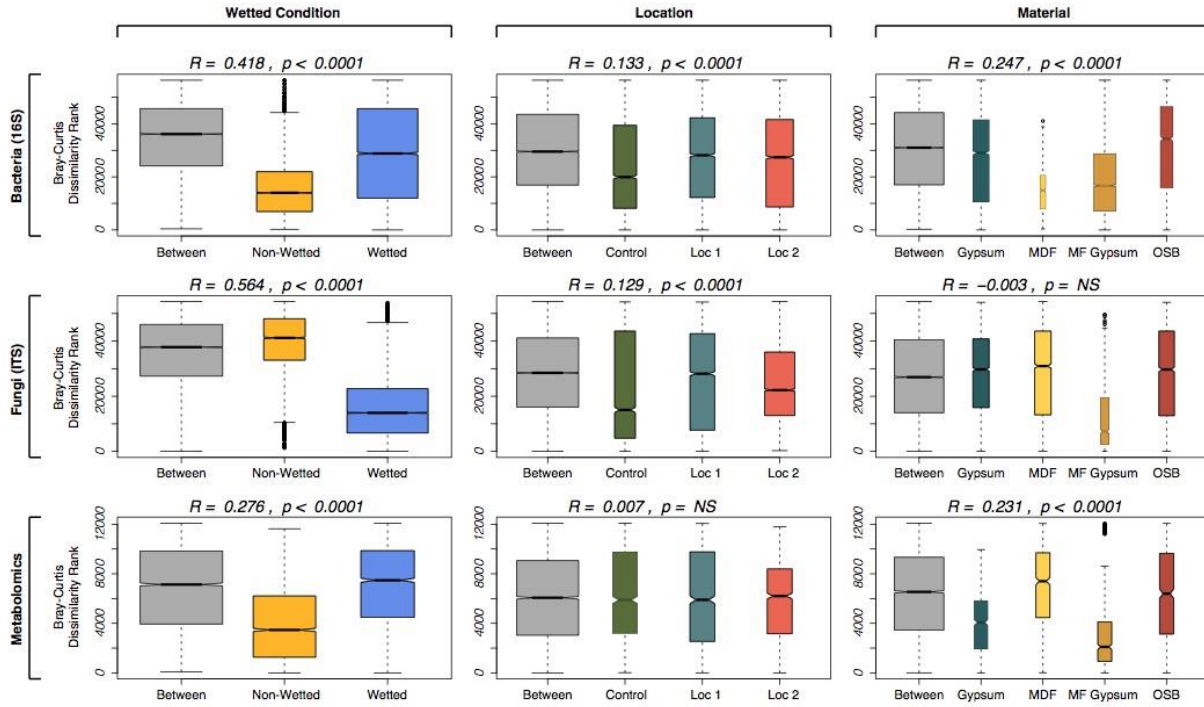


Figure S4: ANOSIM quantifies the influence of metadata factors on the dissimilarity between samples. Columns represent different metadata factors and rows represent the three datasets in this study (n=338, 330 samples for 16S and ITS, respectively). Boxplots depict the range of ranked Bray-Curtis dissimilarities within and between factors (lower rank = lower dissimilarity). Boxplot width indicates the number of samples represented by the boxplot

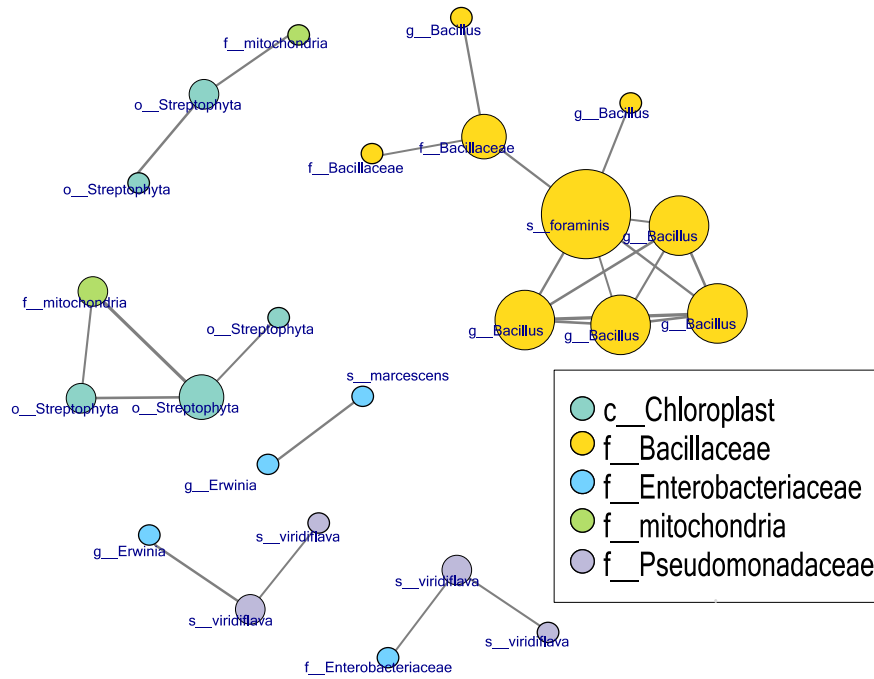


Figure S5: Bacteria-Bacteria co-occurrence network. Co-occurrence network (from n=83 bacteria samples) shows highly correlated bacteria form monophyletic clusters for samples containing more abundant taxa

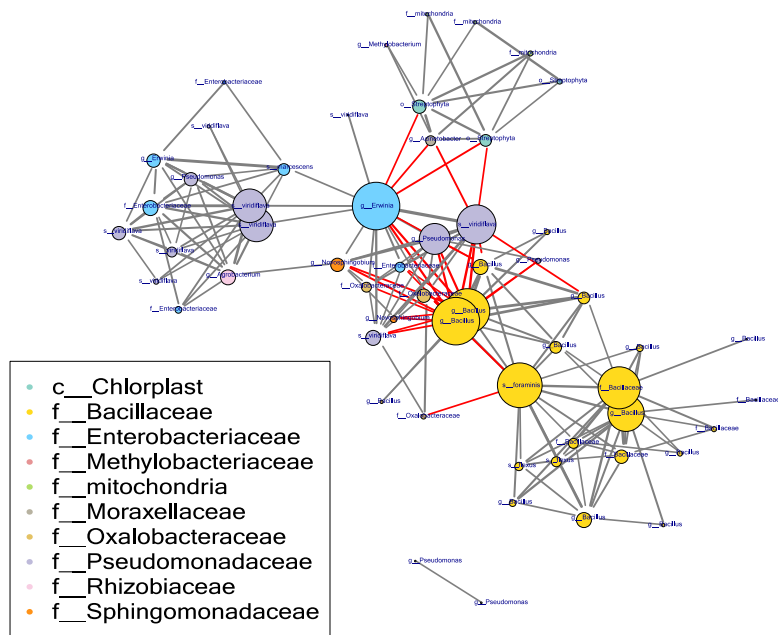


Figure S6: Bacteria-Bacteria co-occurrence network on wet samples. Co-occurrence network (from n=39 wet samples) shows how *Pseudomonas* and *Bacillus* are anticorrelated on wet samples for samples containing more abundant taxa

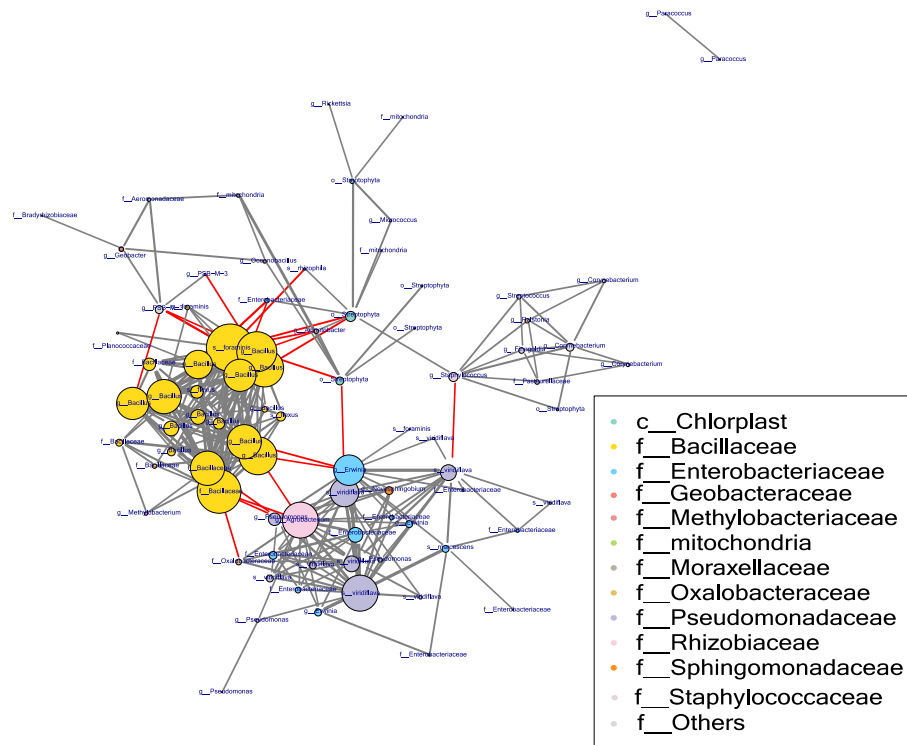


Figure S7: Bacteria-Bacteria co-occurrence network on gypsum samples. Co-occurrence network (from n=24 gypsum samples) shows how *Pseudomonas* and *Bacillus* are anticorrelated on all gypsum samples

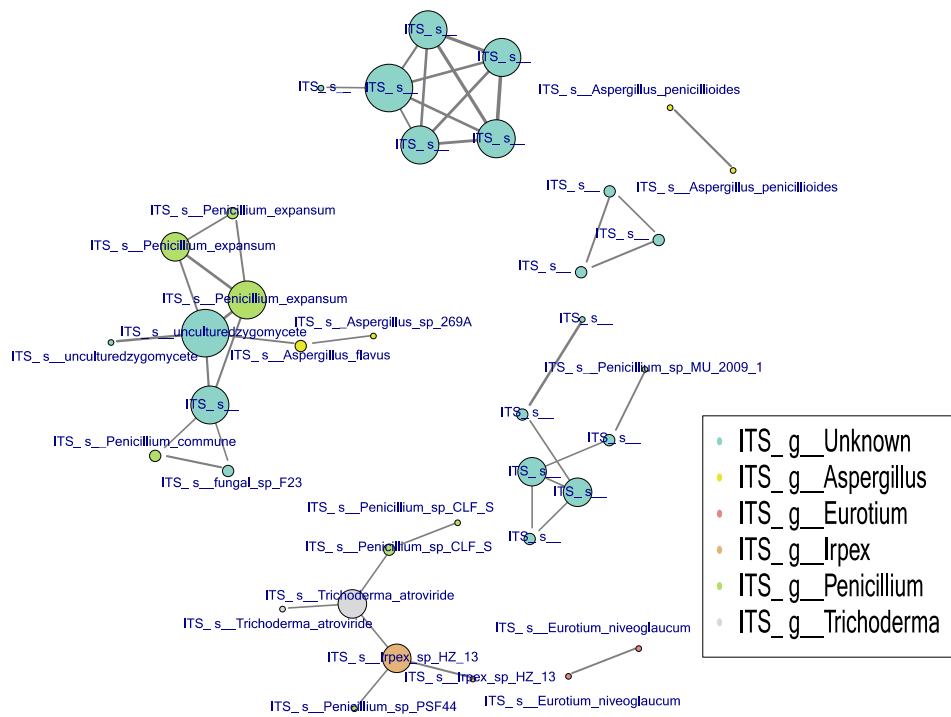


Figure S8: Fungi-Fungi co-occurrence network. Co-occurrence network (from n=91 fungi samples) shows highly correlated fungi forms mostly monophyletic clusters

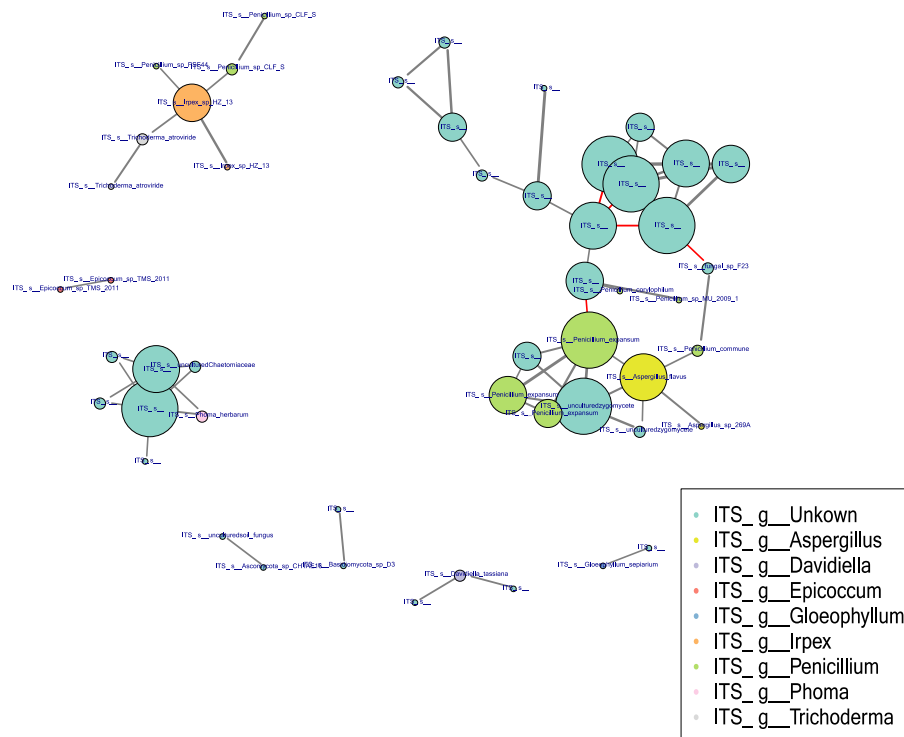


Figure S9: Fungi-Fungi co-occurrence network on wet samples. Co-occurrence network (from n=58 wet samples) shows how certain Fungi OTUs are anticorrelated on wet samples

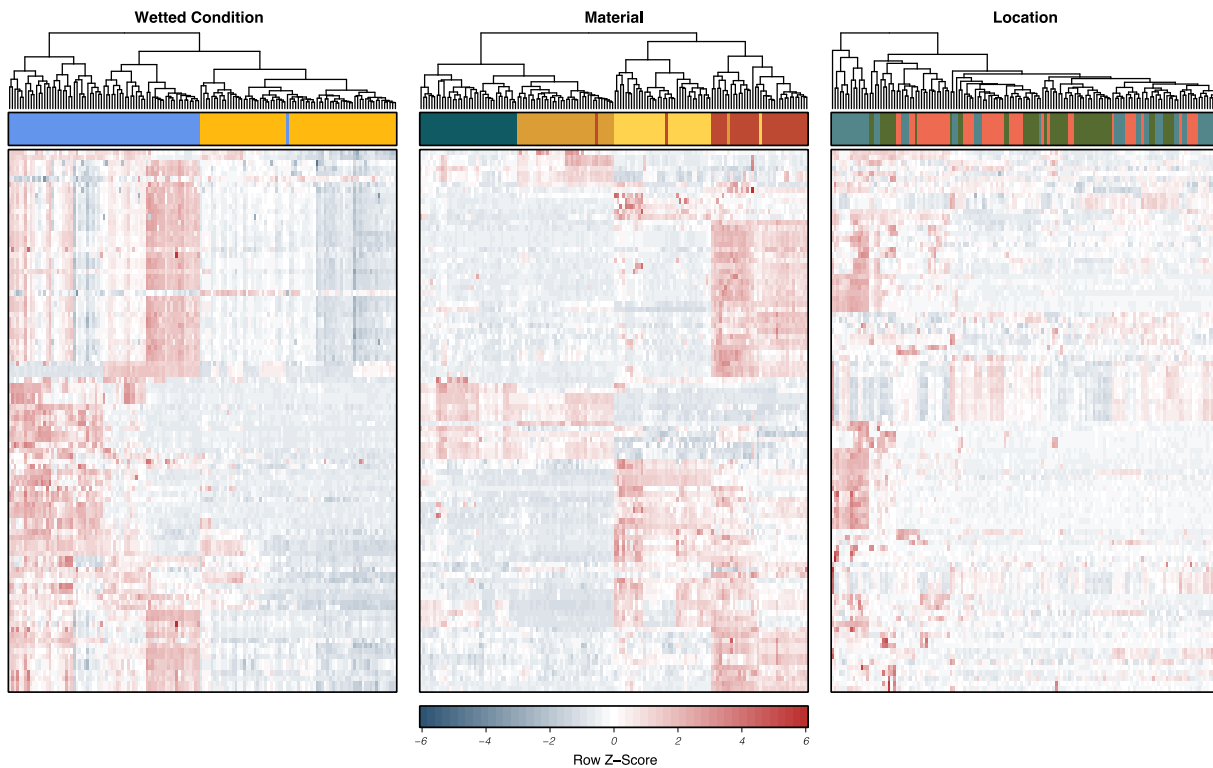


Figure S10: Random forest metabolite selection heatmap. Random forest learning was used to select the metabolites that most distinctly identify each environmental condition, wetted or non-wetted, wood material type and inoculation location (n=144 samples and 3187 metabolites), the 100 highest-scoring metabolite features for each condition where selected for further examination.

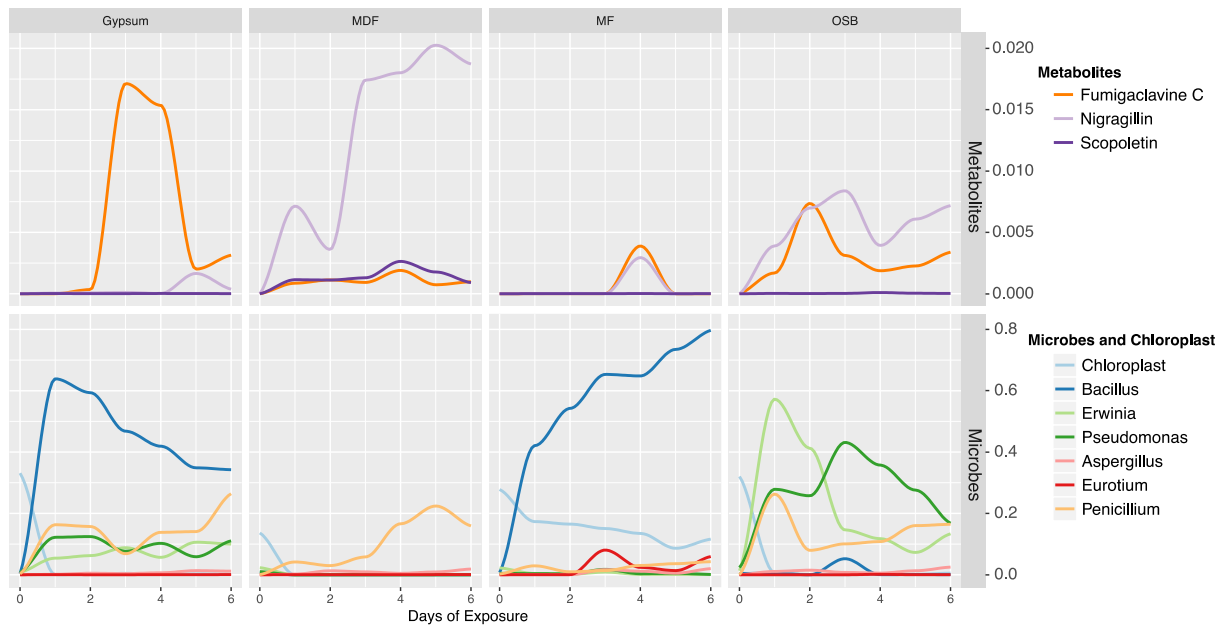


Figure S11: Metabolite and microbial succession on wet samples by material over time. Changes in the relative abundance of selected bacterial genera for each material, respectively. Lines represent a smoothed moving average of the mean. Genus and metabolites are indicated by different colors

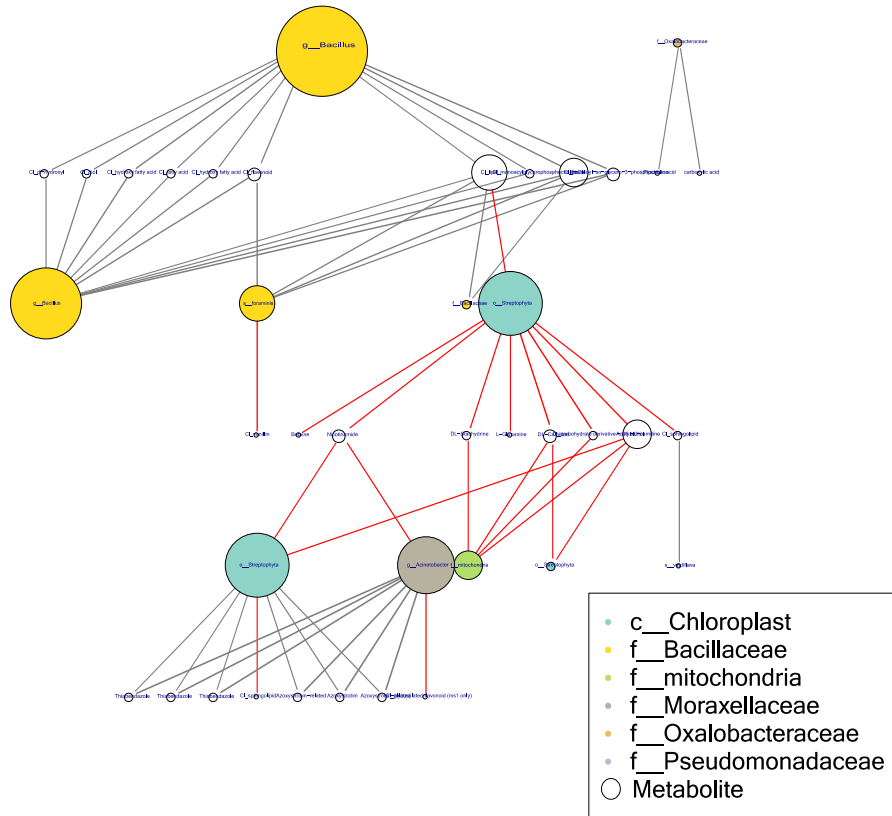


Figure S12: Bacteria-Metabolite co-occurrence network. Bacteria and Metabolite paired co-occurrences suggesting biochemical exchanges (from n=83, 144 samples, respectively). Lipid and hydroxyl compounds are strongly connected to *Bacillaceae* groups. Some specific lipids correlate positively with bacteria and negatively with wood material (plants). Vitamins and small carbon compounds negatively correlate with the wood material (plants).

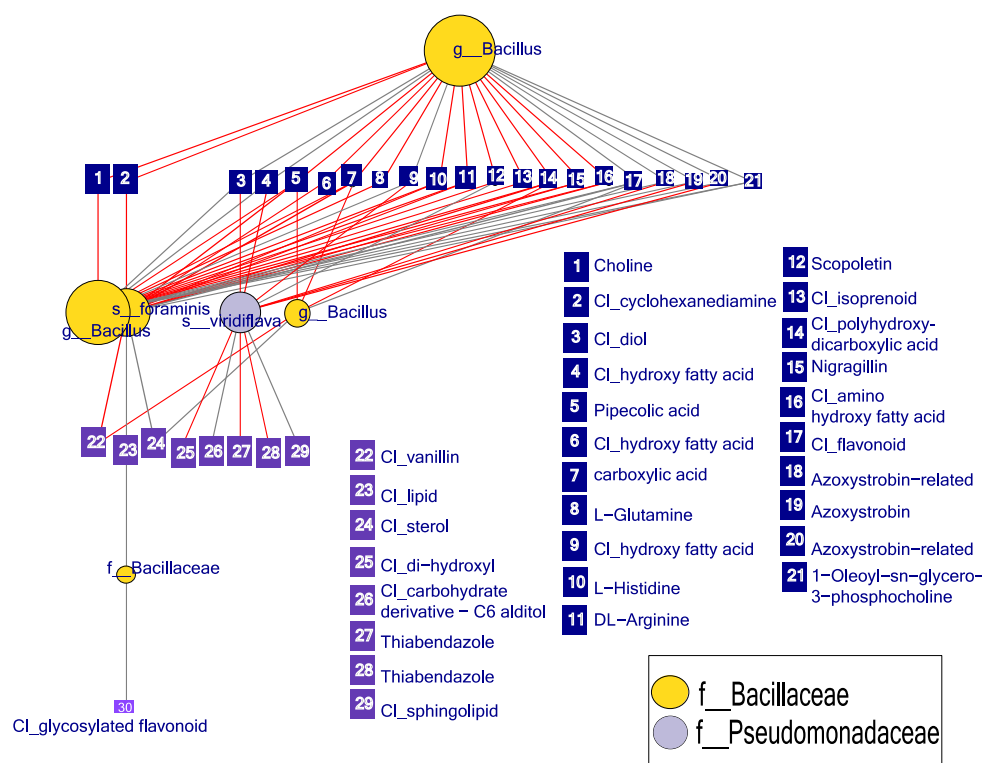
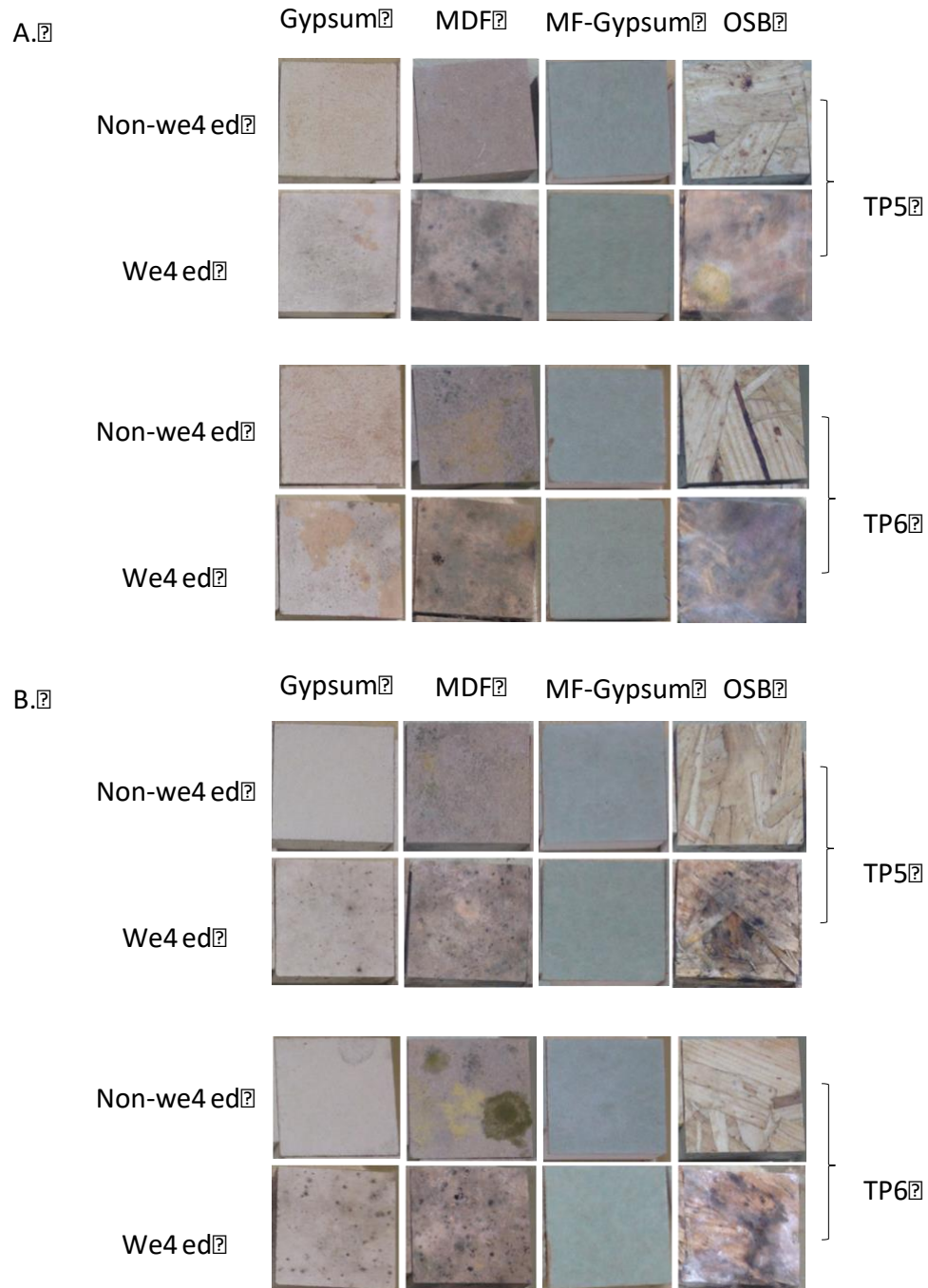


Figure S13: Bacteria-Metabolite co-occurrence network for *Bacillus* and *Pseudomonas* interactions only. Bacteria and Metabolite paired co-occurrences suggesting biochemical exchanges (from n=83, 144 samples, respectively). *Nigragillin* is negatively correlated with both *Pseudomonas* and *Bacillus*. *Azoxystrobin* correlates negatively with *Pseudomonas*, but positively with *Bacillus*. Hydroxyl compounds correlates negatively with *Pseudomonas* but positively with *Bacillus*



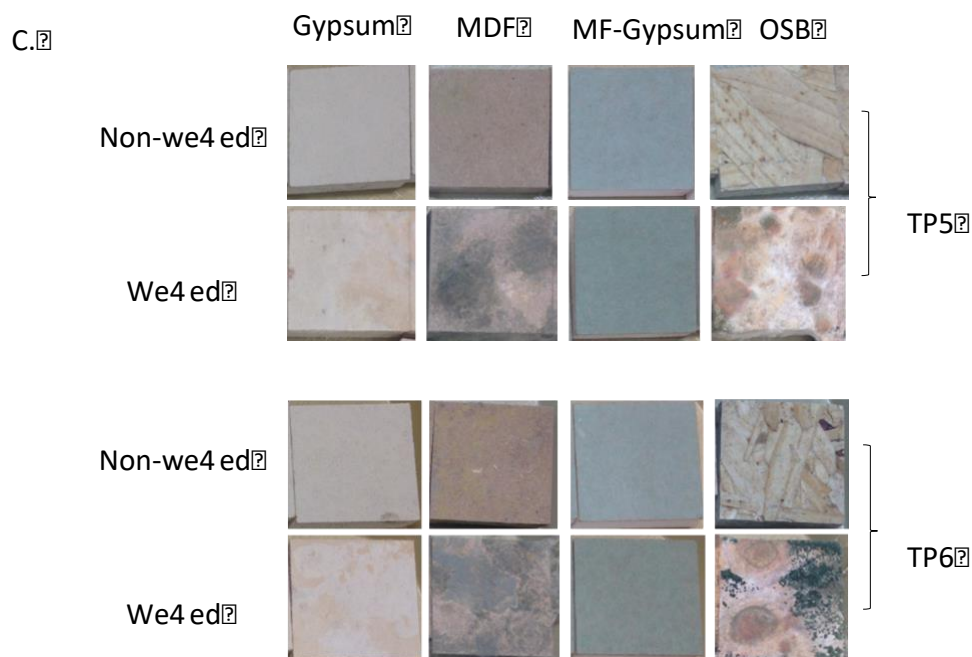


Figure S14: Photographs of wood coupons from different materials and wetting conditions at TP5 and TP6. Bacterial and Fungal growth on coupons surface photographs for (A) location 1 (B) location 2 and (C) control location.

| | <u>Bacteria (16S)</u> | | <u>Fungi (ITS)</u> | | <u>Metabolomics</u> | |
|--------------------|-----------------------|----------|----------------------|----------|----------------------|----------|
| | R² | p | R² | p | R² | p |
| Wetted | 0.374 | < 0.0001 | 0.450 | < 0.0001 | 0.204 | < 0.0001 |
| Timepoint | 0.130 | < 0.0001 | 0.094 | < 0.0001 | 0.178 | < 0.0001 |
| Control | 0.074 | < 0.0001 | 0.107 | < 0.0001 | 0.001 | 0.983 |
| Location 1 | 0.045 | 0.0006 | 0.076 | 0.0006 | 0.009 | 0.502 |
| Location 2 | 0.214 | < 0.0001 | 0.303 | < 0.0001 | 0.007 | 0.603 |
| Gypsum | 0.085 | < 0.0001 | 0.022 | 0.0271 | 0.141 | < 0.0001 |
| MDF | 0.108 | < 0.0001 | 0.009 | 0.2399 | 0.238 | < 0.0001 |
| MF Gypsum | 0.027 | 0.0095 | 0.008 | 0.2720 | 0.209 | < 0.0001 |
| OSB | 0.041 | 0.0015 | 0.002 | 0.762 | 0.503 | < 0.0001 |
| <i>Bacillus</i> | 0.259 | < 0.0001 | NA | NA | NA | NA |
| <i>Pseudomonas</i> | 0.088 | < 0.0001 | NA | NA | NA | NA |
| <i>Erwinia</i> | 0.098 | < 0.0001 | NA | NA | NA | NA |
| Chloroplast | 0.196 | < 0.0001 | NA | NA | NA | NA |
| <i>Penicillium</i> | NA | NA | 0.106 | < 0.0001 | NA | NA |
| <i>Eurotium</i> | NA | NA | 0.185 | < 0.0001 | NA | NA |

Table S1: ANOSIM results calculate the factors significantly correlated with differences in the microbial communities across our three datasets, Bacteria, fungi, Metabolomics

| | REG | | | RE | | | RE.DUP | | | DUP | | |
|--------|--------|--------------|----|--------|--------------|----|--------|--------------|----|--------|--------------|----|
| | mantel | significance | n | mantel | significance | n | mantel | significance | n | mantel | significance | n |
| REG | <NA> | | | 0.67 | 1E-05 | 74 | 0.71 | 1E-05 | 79 | 0.81 | 1E-05 | 44 |
| RE | 0.67 | 1E-05 | 74 | <NA> | | | 0.85 | 1E-05 | 77 | 0.75 | 1E-05 | 40 |
| RE.DUP | 0.71 | 1E-05 | 79 | 0.85 | 1E-05 | 77 | <NA> | | | 0.79 | 1E-05 | 39 |
| DUP | 0.81 | 1E-05 | 44 | 0.75 | 1E-05 | 40 | 0.79 | 1E-05 | 39 | <NA> | | |

Table S2: Mantel test results calculate the correlation among fungi samples across different sampling strategies.

| | REG | | | RE | | | RE.DUP | | | DUP | | |
|--------|--------|--------------|----|--------|--------------|----|--------|--------------|----|--------|--------------|----|
| | mantel | significance | n | mantel | significance | n | mantel | significance | n | mantel | significance | n |
| REG | <NA> | | | 0.62 | 1E-05 | 75 | 0.56 | 1E-05 | 75 | 0.60 | 1E-05 | 35 |
| RE | 0.62 | 1E-05 | 75 | <NA> | | | 0.72 | 1E-05 | 80 | 0.53 | 1E-05 | 36 |
| RE.DUP | 0.56 | 1E-05 | 75 | 0.72 | 1E-05 | 80 | <NA> | | | 0.50 | 1E-05 | 35 |
| DUP | 0.63 | 1E-05 | 56 | 0.53 | 1E-05 | 36 | 0.50 | 1E-05 | 35 | <NA> | | |

Table S3: Mantel test results calculate the correlation among bacteria samples across different sampling strategies.