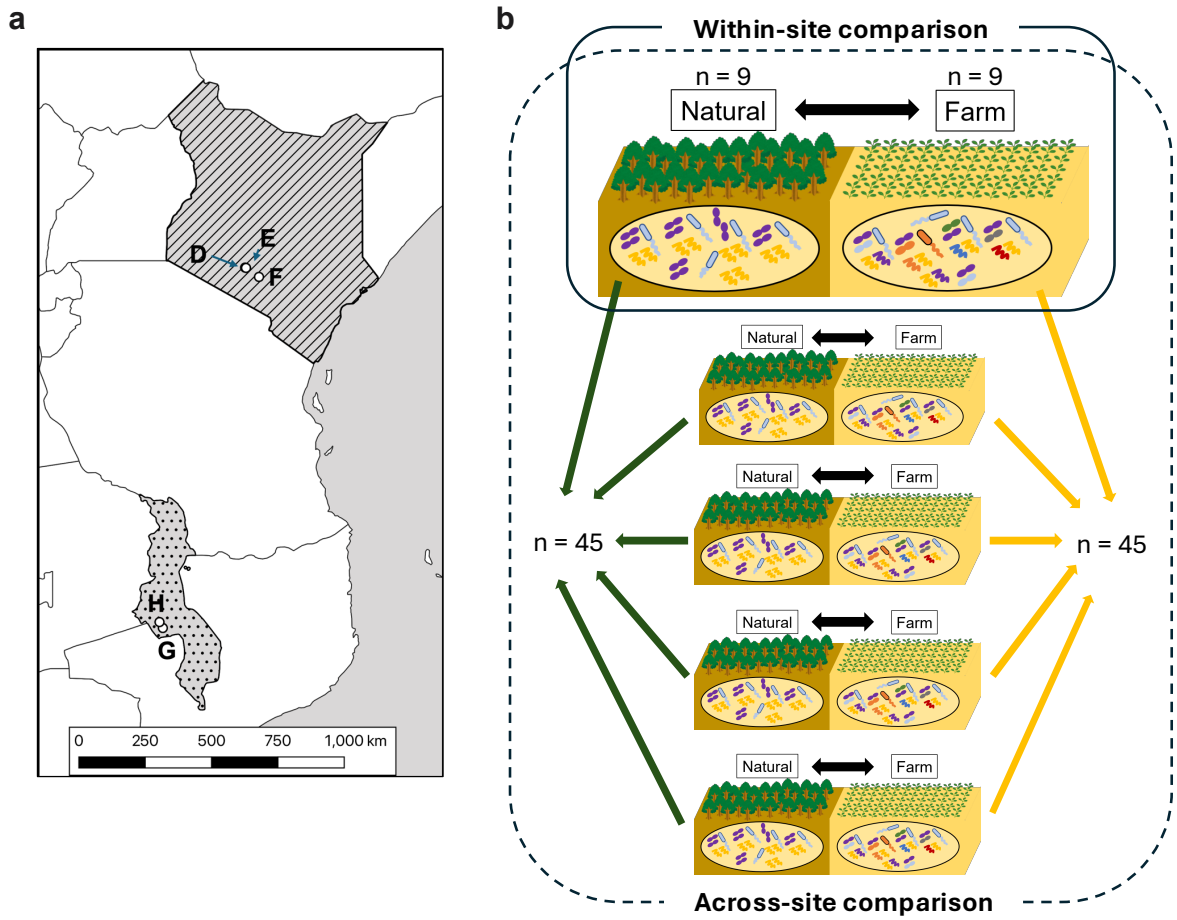

Figure 1. Location of sampling sites and concept of the analysis. (**a**) The sampling locations, Sites D—F in Kenya and Sites G and H in Malawi, are annotated in the map. (**b**) All sites had pairs of neighboring natural (unmanaged) lands and farmlands. Nine soil samples were collected at each land use at one site, resulting in 45 samples for each land use across five sites.

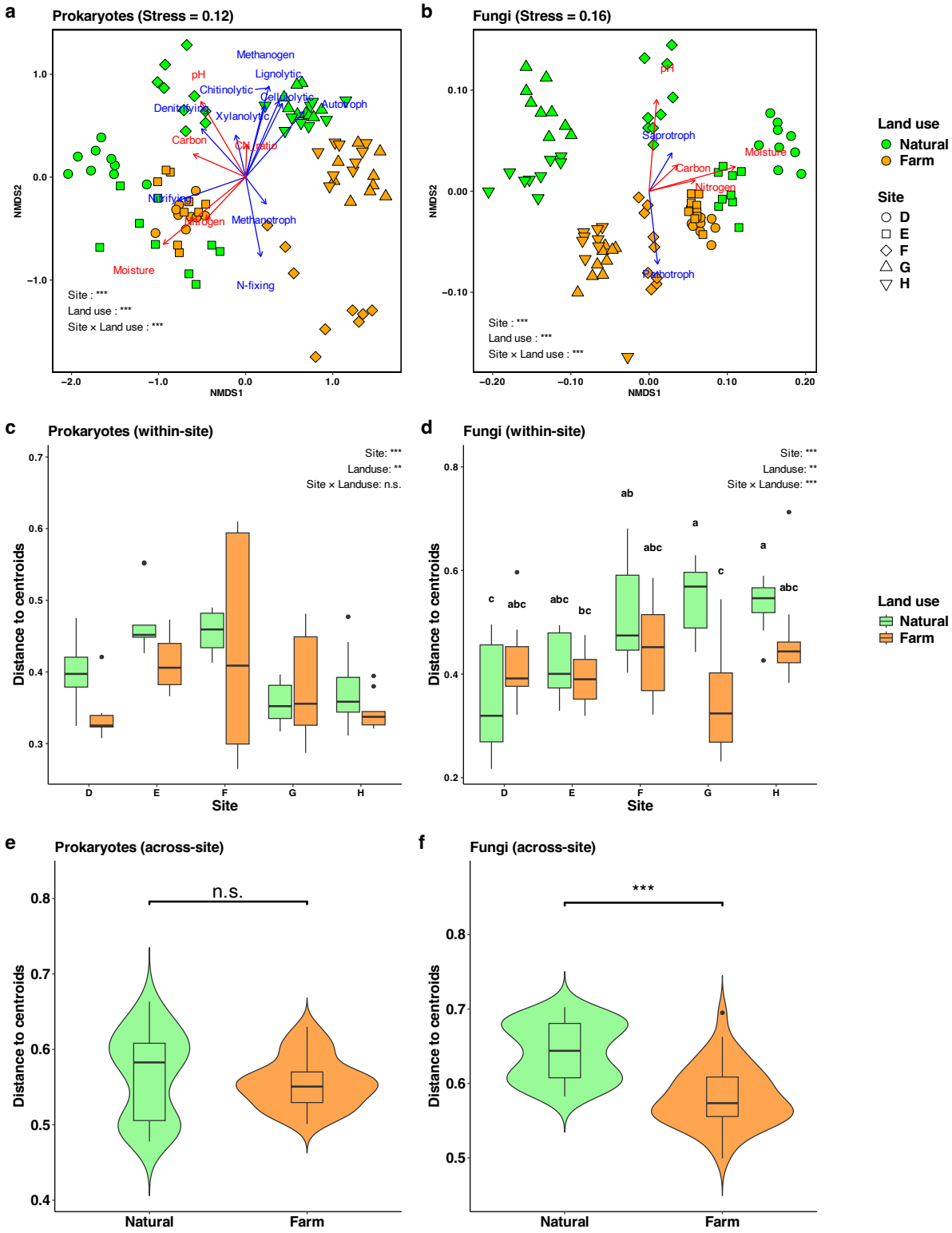

Figure 2. Dissimilarity of soil microbial communities in natural lands and farmlands. NMDS for (**a**) prokaryotes and (**b**) fungi are shown. Prokaryotic or fungal functions and the environmental variables that significantly correlated with the communities are illustrated with arrows, colored by red and blue, respectively. Distance to centroids of the communities in each land use in (**c, d**) within-site and (**e, f**) across-site scales are plotted, for prokaryotes (**c, e**) and fungi (**d, f**). The p-values in the PERMANOVA or two-way ANOVA on sites, land uses and their interaction, and those in the t-test on land uses are indicated with "*", "**", or "***", representing $p < 0.05$, $p < 0.01$, or $p < 0.001$, respectively.

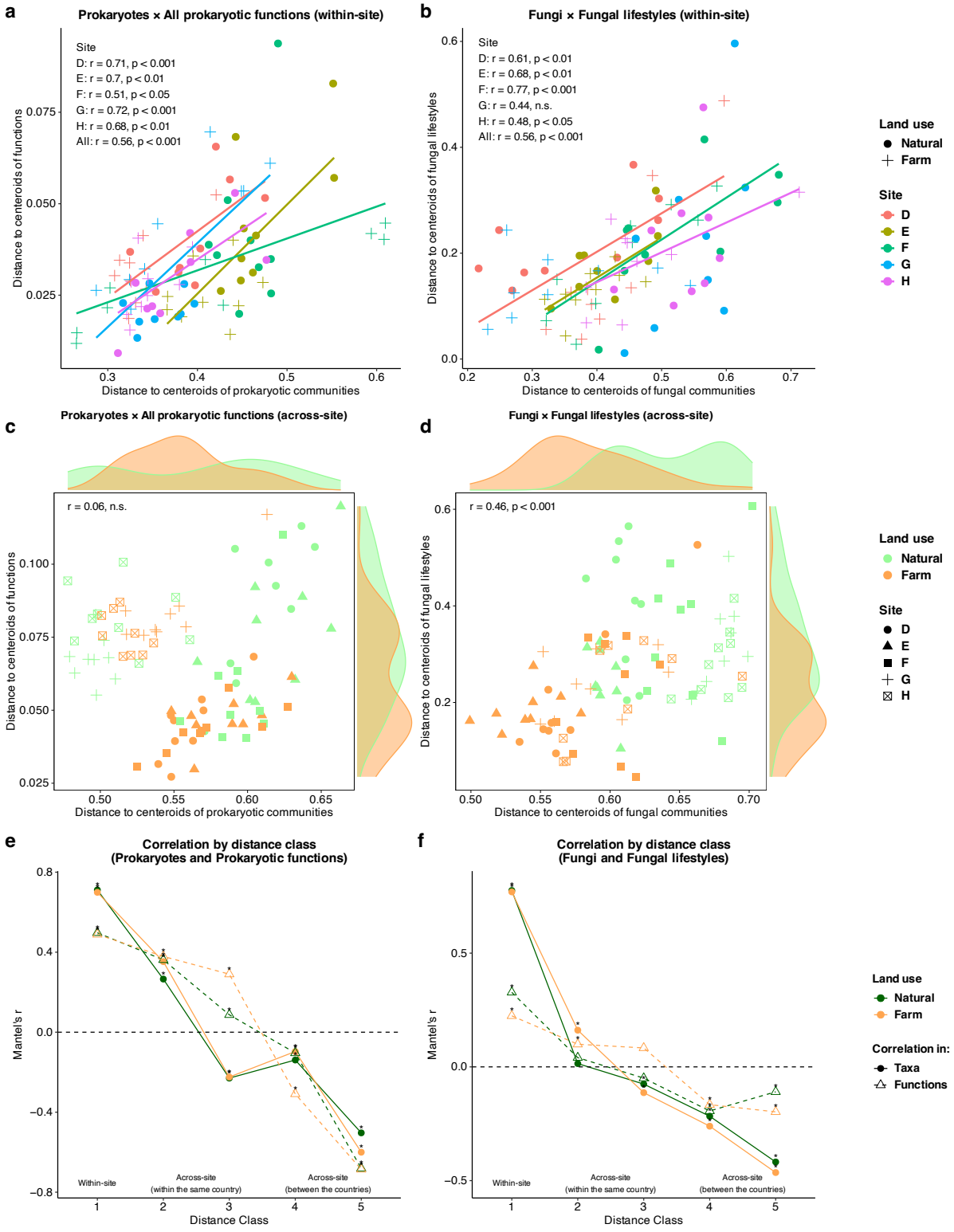

Figure 3. Relationships between heterogeneities of microbial communities and their functions. Correlations between distance to centroids of the microbial communities and that of their functions in each land use within site for (**a**) prokaryotes and (**b**) fungi, and across sites for (**c**) prokaryotes and (**d**) fungi are shown. The correlation coefficients and p-values in the Pearson's correlation tests are indicated with "*", "**", or "***", representing $p < 0.05$, $p < 0.01$, or $p < 0.001$, respectively. Mantel's correlograms of microbial communiitiy compositions and their functional compositions by distance class are plotted for (**e**) prokaryotes and prokaryotic functions and (**f**) fungi and fungal lifestyles. The significant autocorrelations Corrected $p < 0.05$) in each distance class tested by permutation is indicated with "*".

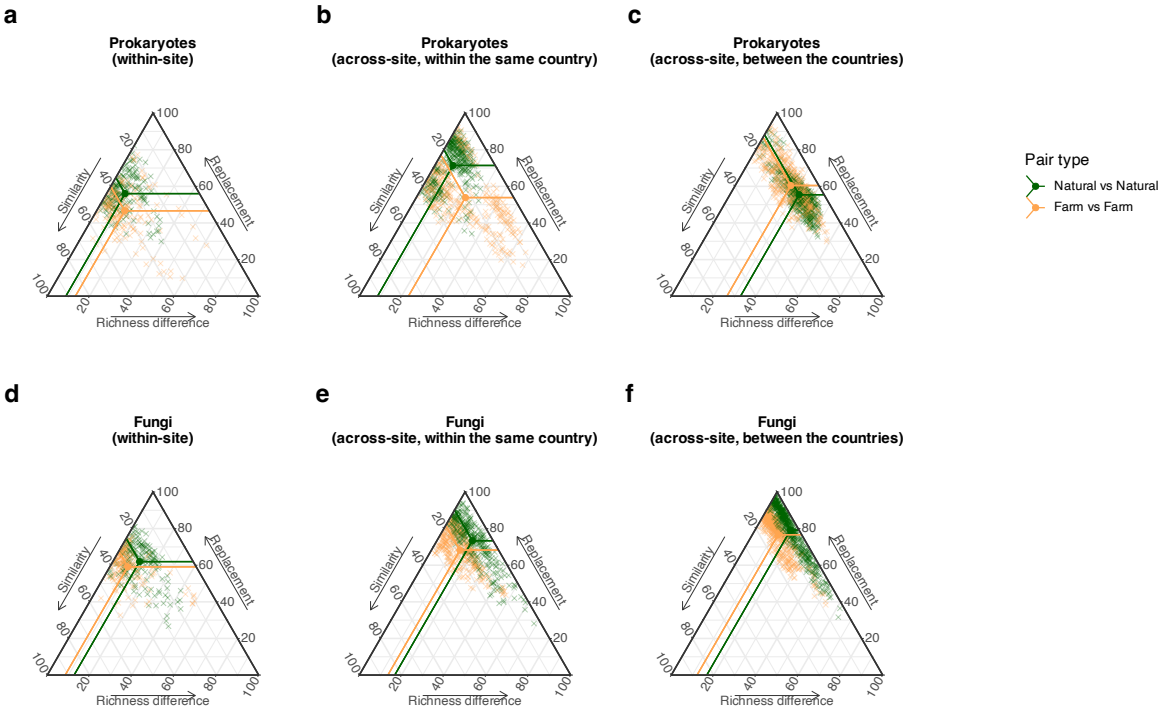

Figure 4. The components of dissimilarity of microbial communities. Sørensen's similarity for each pair of samples were decomposed into "Replacement" and "Richness difference". Ratios of these components are illustrated considering whether the pair of samples were from (**a, d**) within the same site, (**b, e**) across sites within the same country, and (**c, f**) across sites between the countries, for (**a, b, c**) prokaryotes and (**d, e, f**) fungi, respectively.

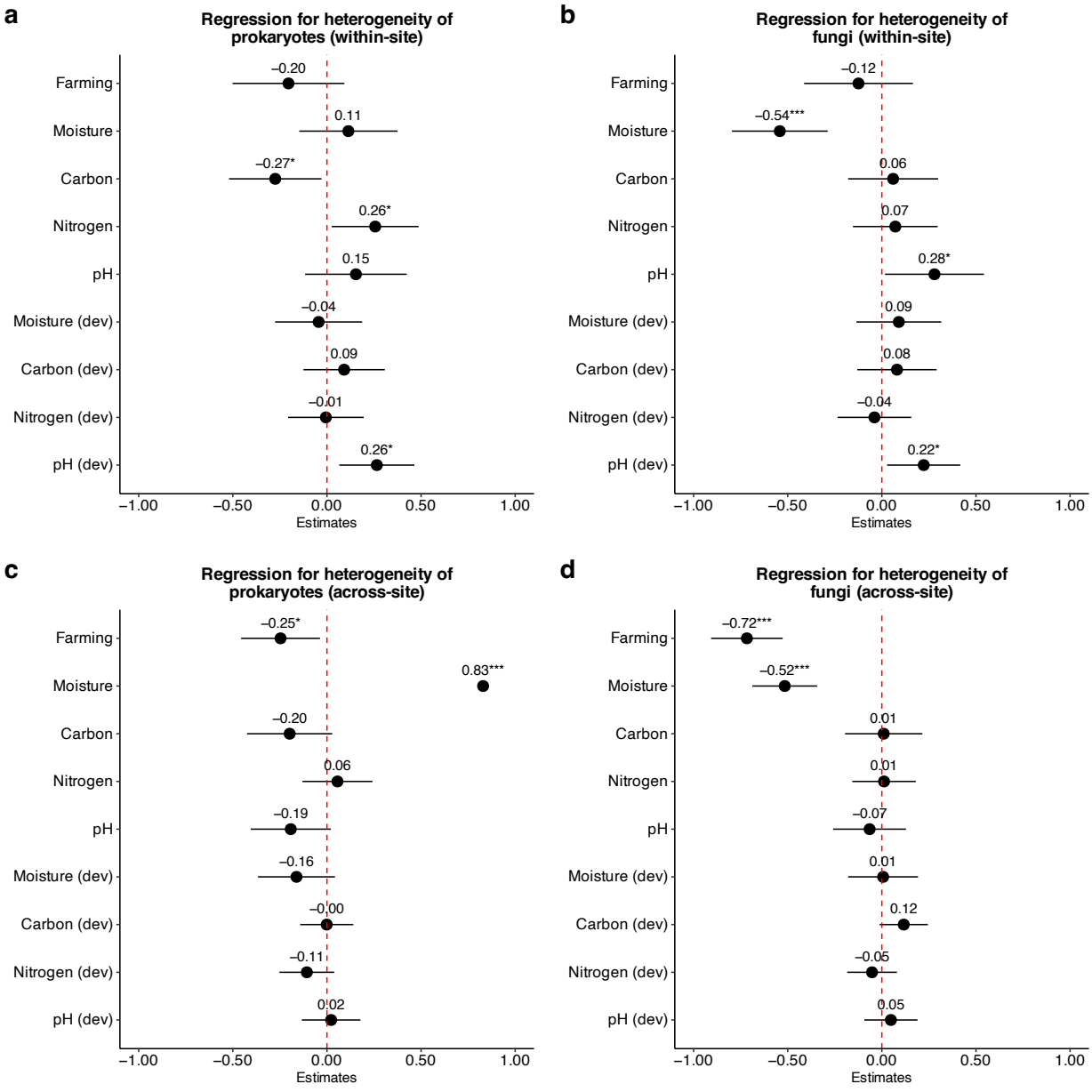

Figure 5. Contributions of farming activity and environmental variables to the heterogeneity of microbial community. The 95% confidence intervals of the regression coefficients, calculated in the multiple regression from farming activity, environmental variables, and absolute deviations of encironmental variables to the distance to centroids of (**a, c**) prokaryotes and (**b, d**) fungi in the (**a, b**) within-site and (**c, d**) across-site scales, are shown. The values of coefficients and significance as indicated with "*", "**", or "***", representing $p < 0.05$, $p < 0.01$, or $p < 0.001$, respectively, are noted above each point.

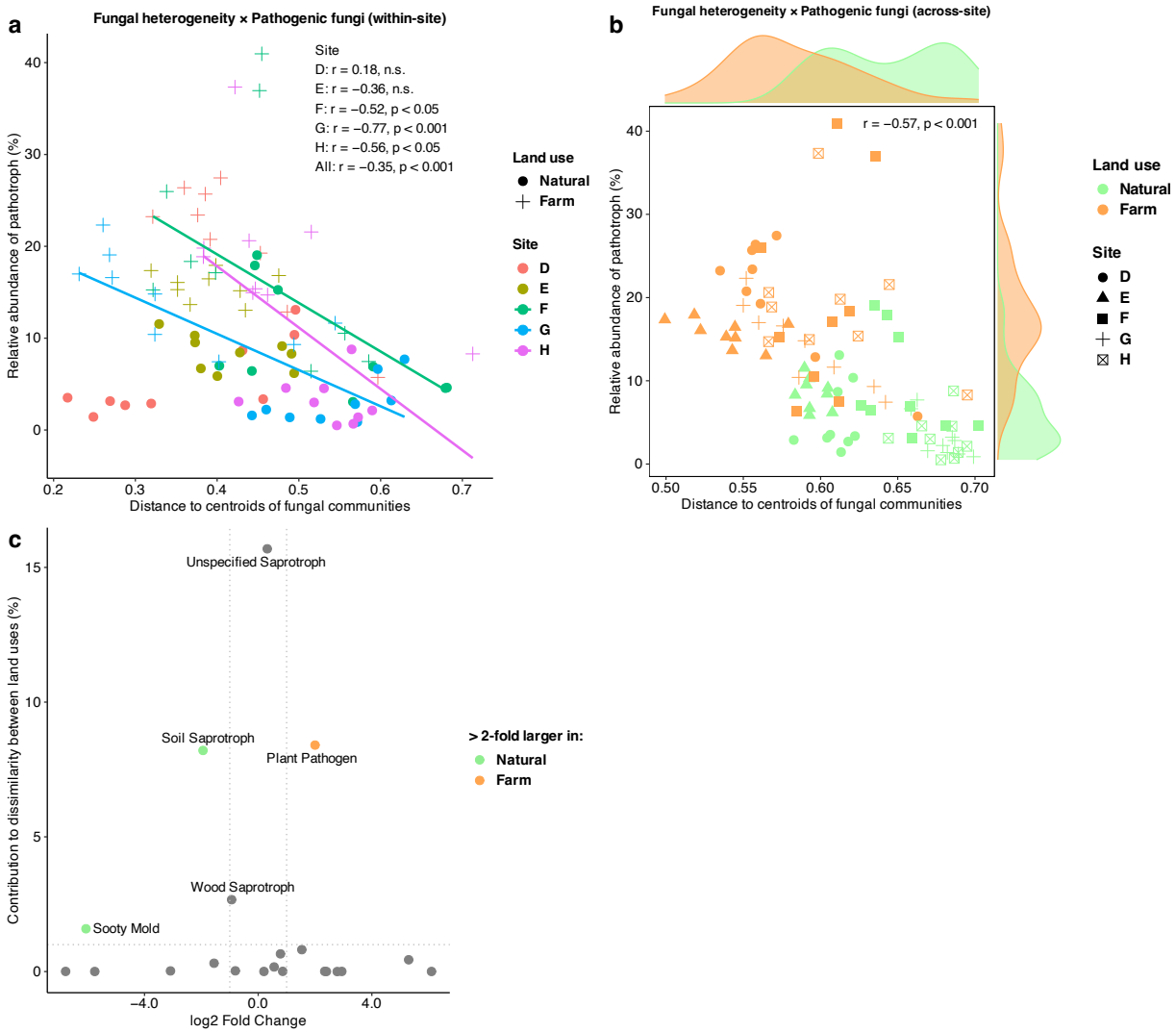

Figure 6. Relation between the heterogeneity of fungal communities and abundance of pathogenic fungi. Correlations between distance to centroids of the fungal communities and relative abundance of pathogenic fungi are plotted for the (**a**) within-site and (**b**) across-site scales. The correlation coefficients and p-values in the Pearson's correlation tests are indicated with "*", "**", or "***", representing $p < 0.05$, $p < 0.01$, or $p < 0.001$, respectively. (**c**) The contributions of each fungal ASV to the Bray-Curtis dissimilarity between the land uses were summed within each fungal lifestyle, and these are shown with log fold changes of their relative abundances between the land uses.