SUPPLEMENTAL INFORMATION

Long-term Cu exposure selects for Cu-tolerant bacterial communities with altered composition, but unaltered richness

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Includes 5 pages and 4 figures (S1-S4).

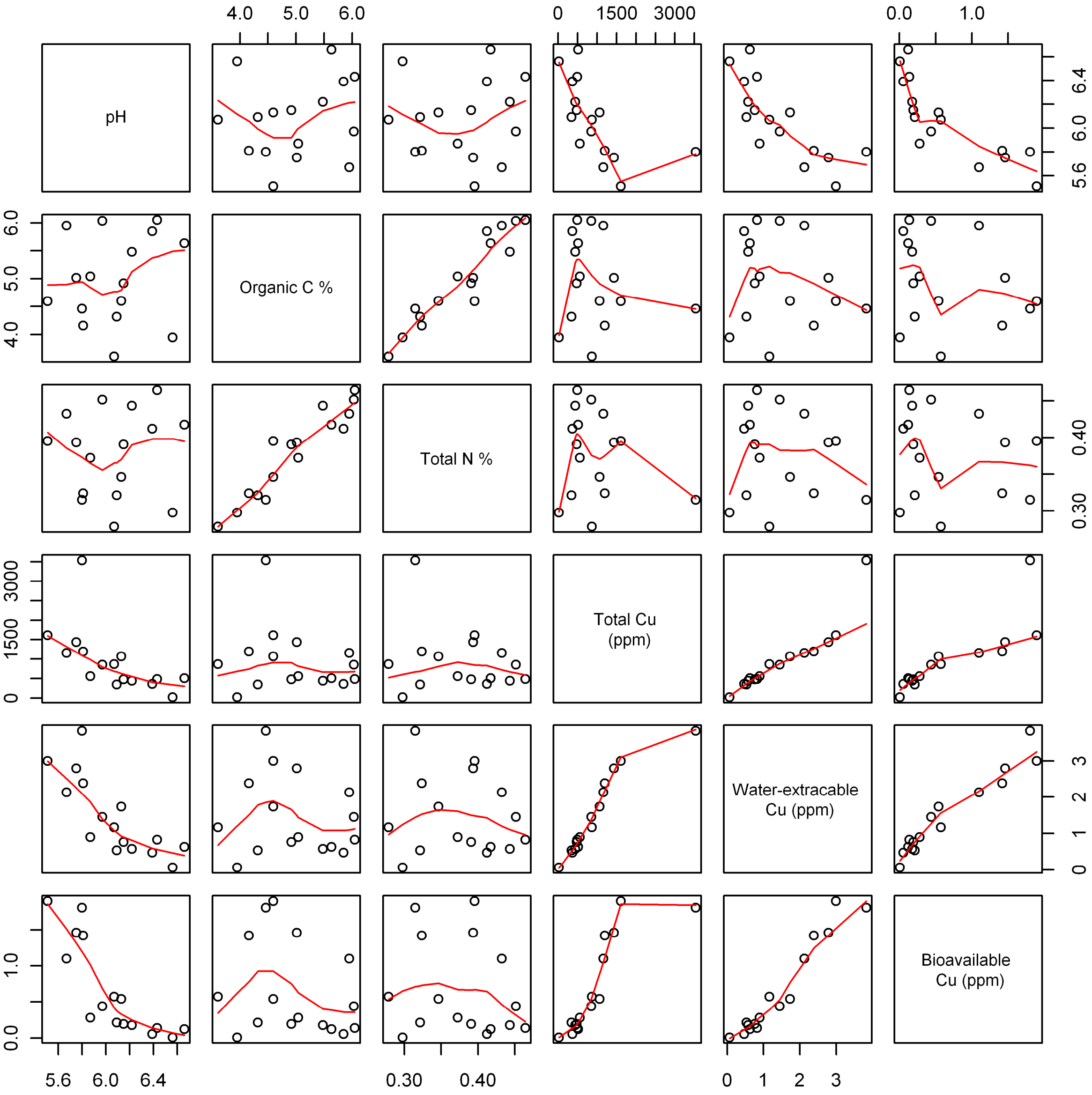

Figure S1 Pair wise correlation plots for the 16 Cu gradient soil samples with the explanatory variables named in the columns and the response variables named in the rows.

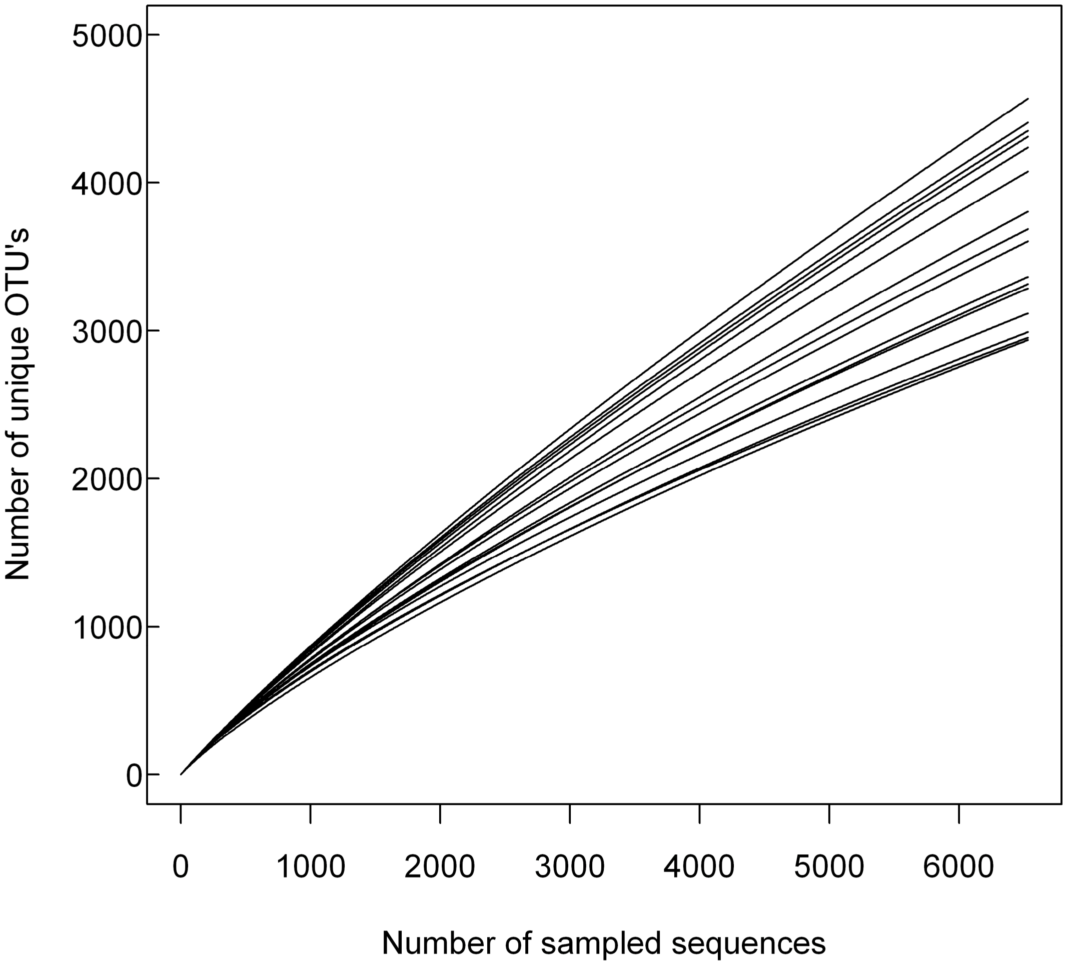

Figure S2 Rarefaction plot showing numbers of unique operational taxonomic units (OTUs) defined at the ≥ 97 % sequence similarity level for a sampling effort of 6538 sequences for the 16 soil samples.

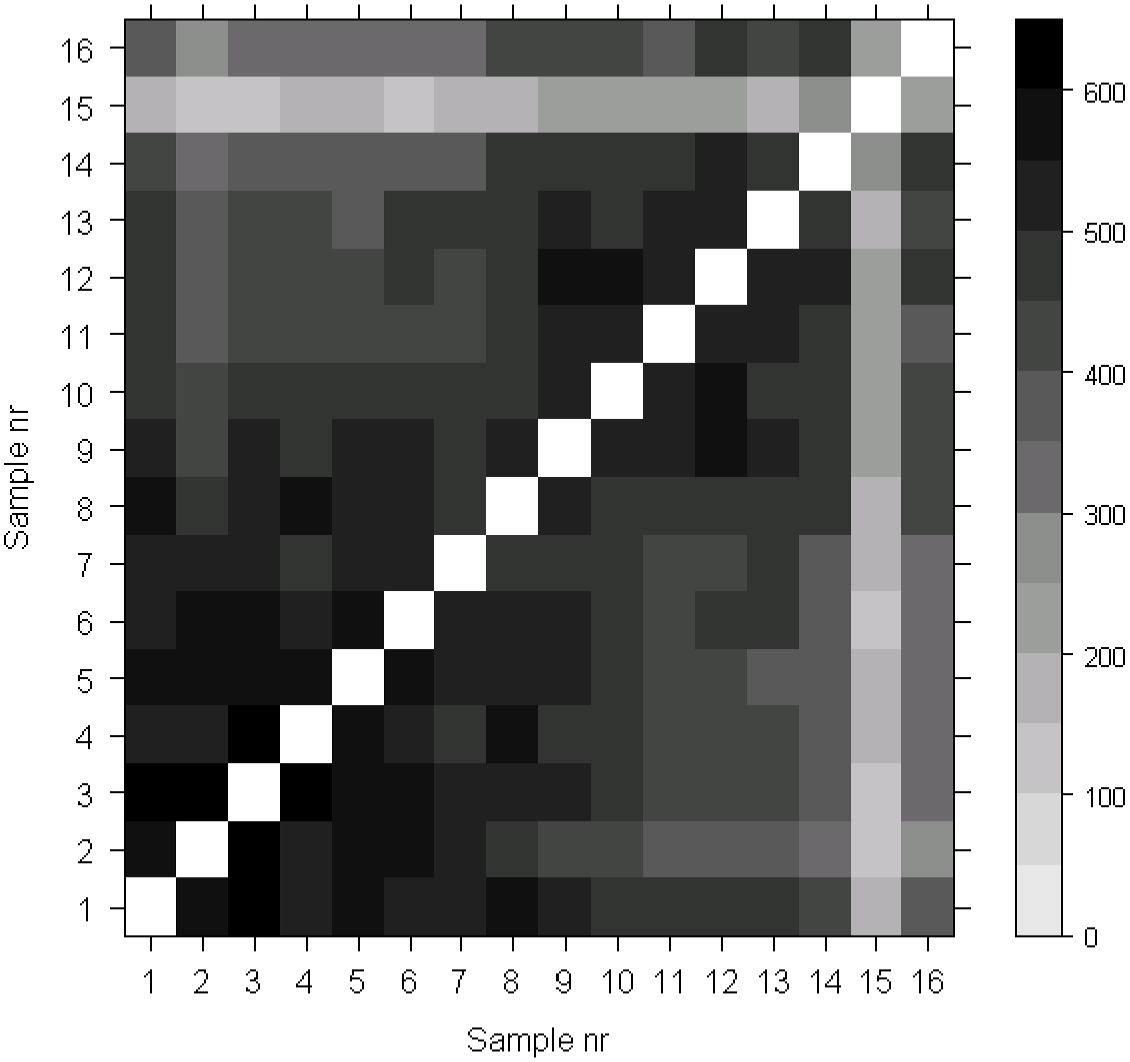

Figure S3 Number of shared operational taxonomic units among 6538 randomly selected 16S rRNA gene sequences per Cu gradient soil sample.

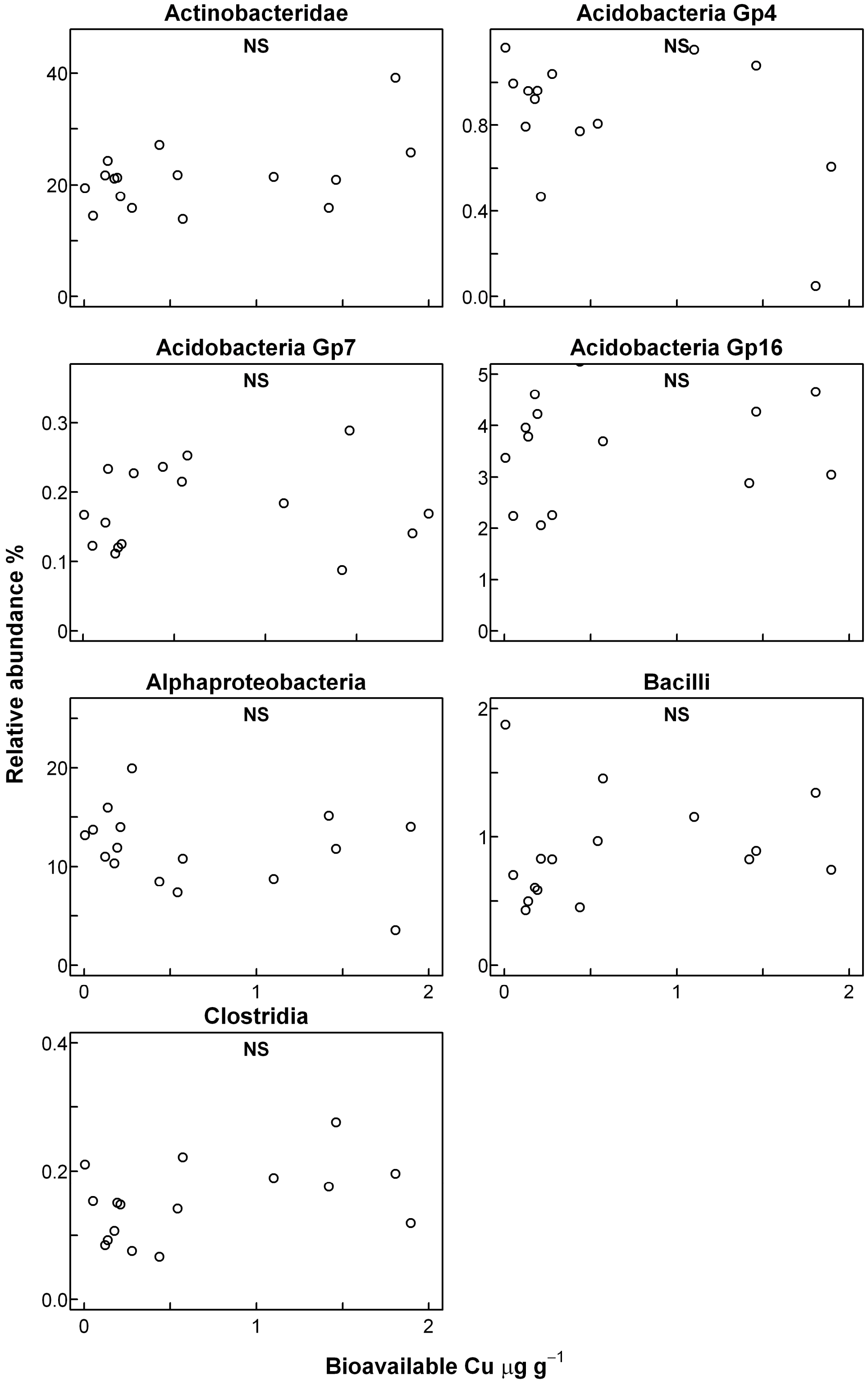

Figure S4 Relative abundance of high-abundant classes showing no significant correlation (Spearman rank correlation test) to bioavailable Cu in the 16 Cu gradient soil samples. NS = Not Significant.