

## Supplementary Material

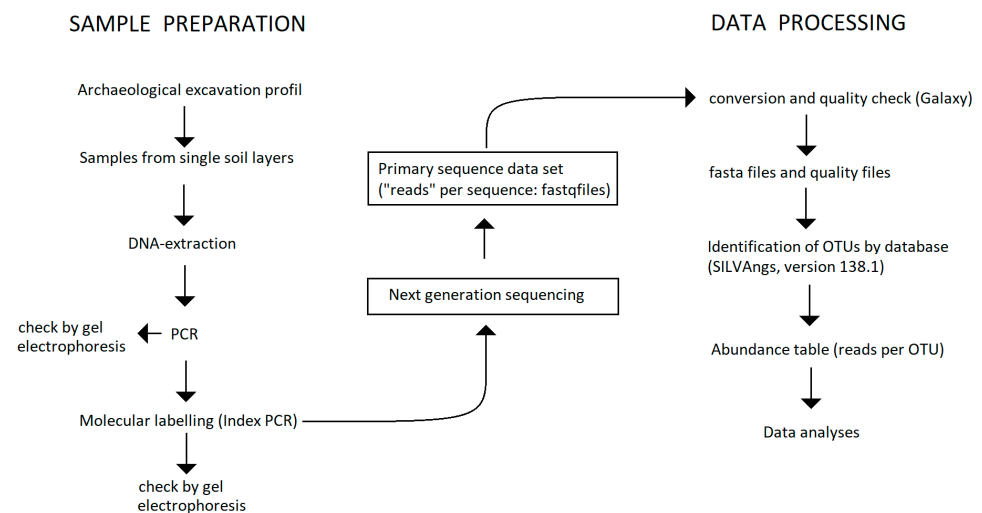
### Low Abundant Bacteria Reflect Soil Specificity—Analysis of Bacterial Communities from Archaeological Investigation of Pre-Industrial Saline Ash Deposits of Bad Dürrenberg (Germany)

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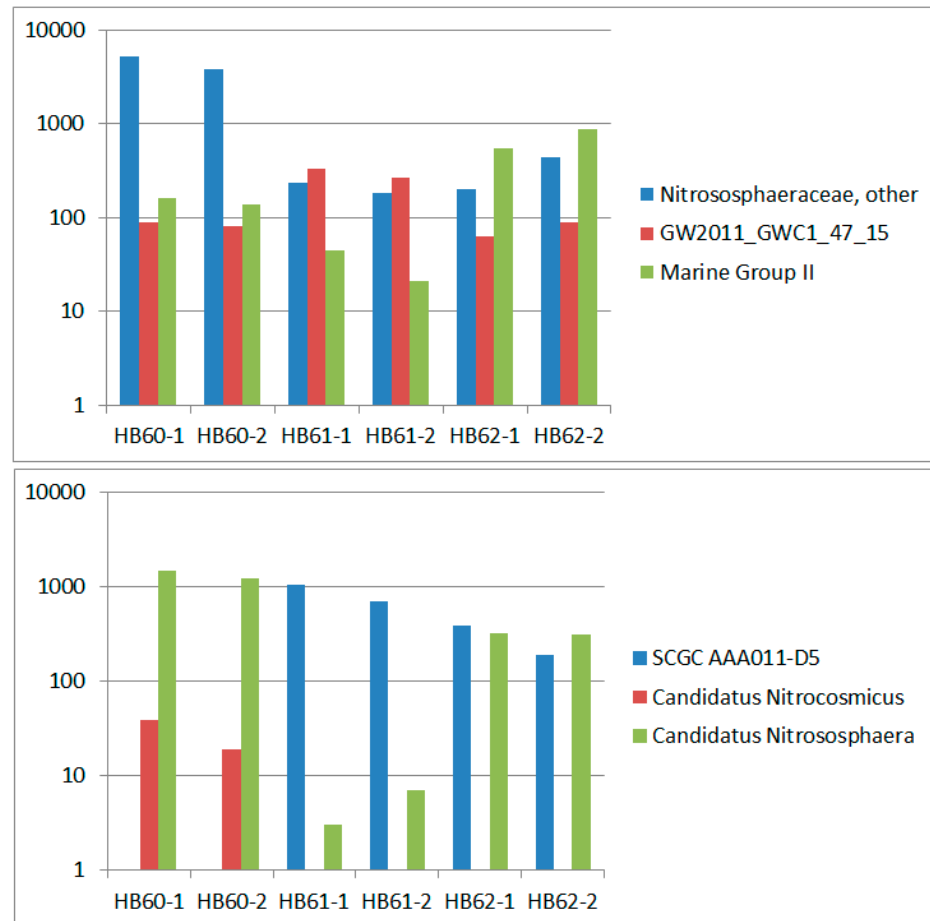
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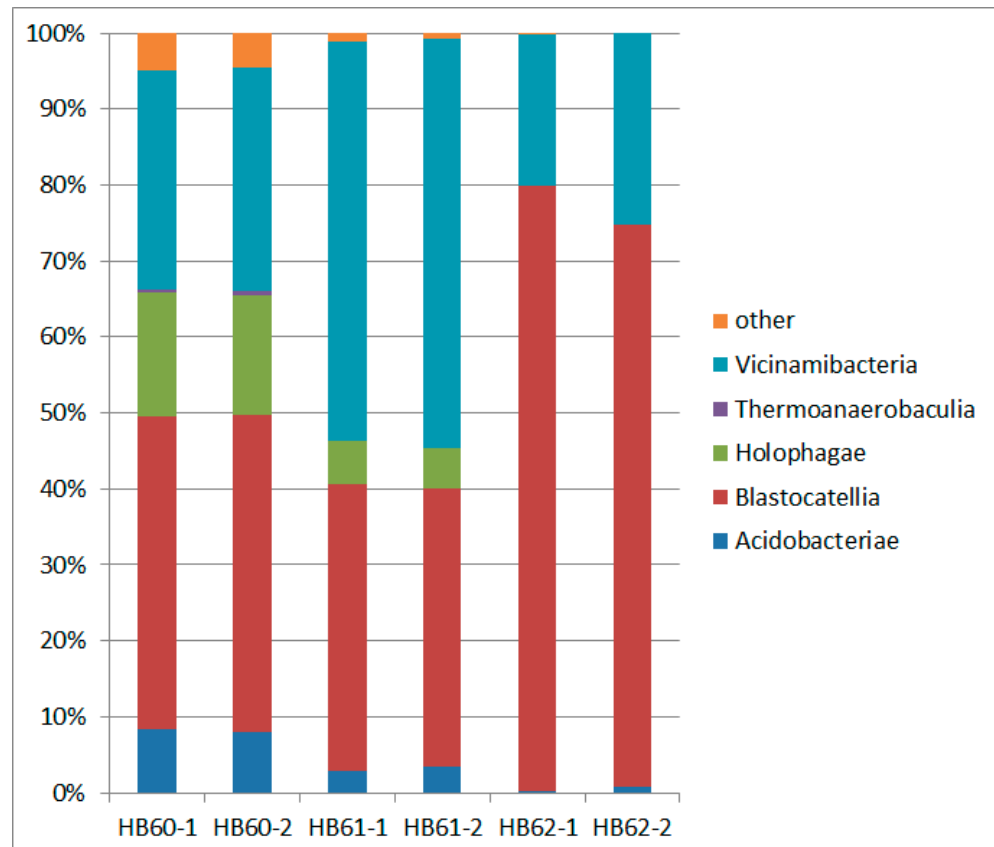
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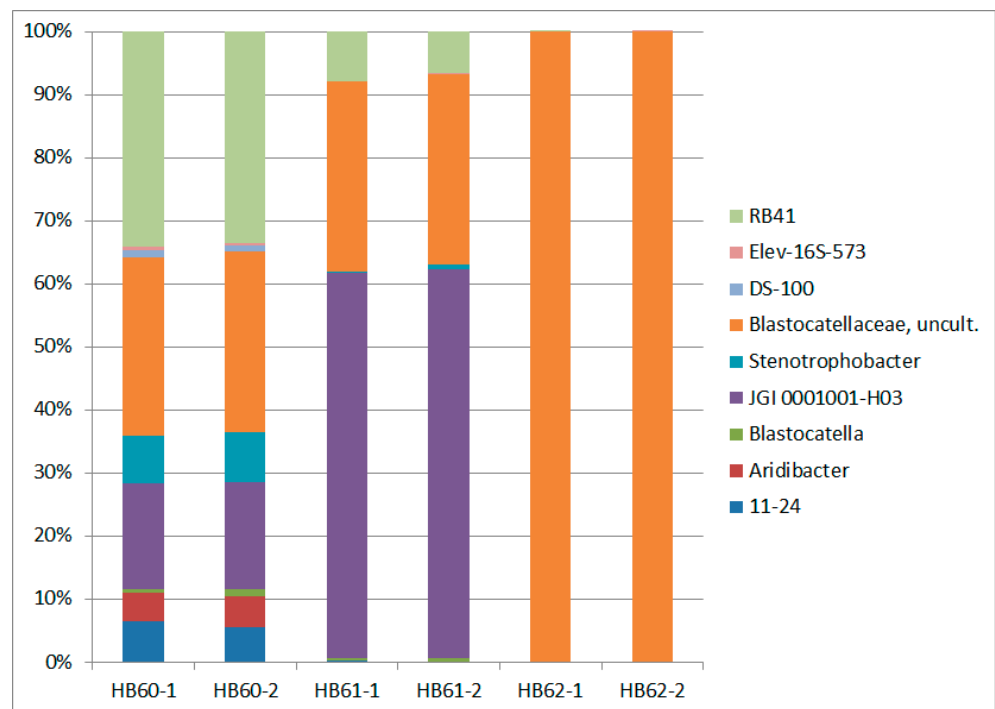
**Figure S1.** Scheme of process steps from archaeological excavation to data analysis.



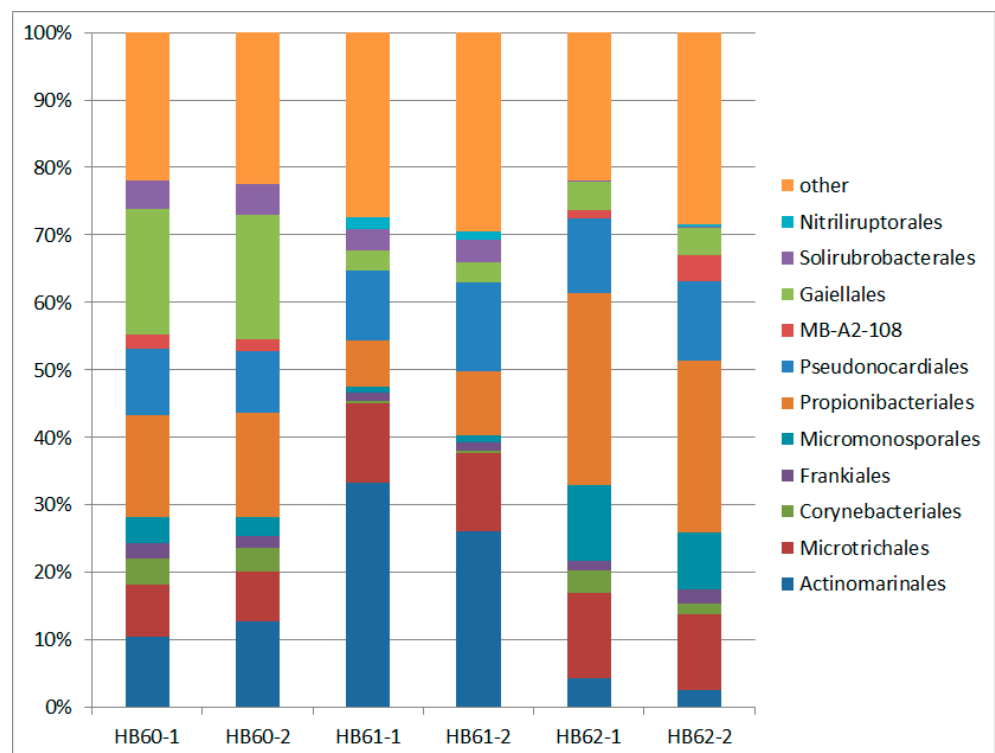
**Figure S2.** Relative abundances of selected *Archaea* in the samples from Bad Dürrenberg.



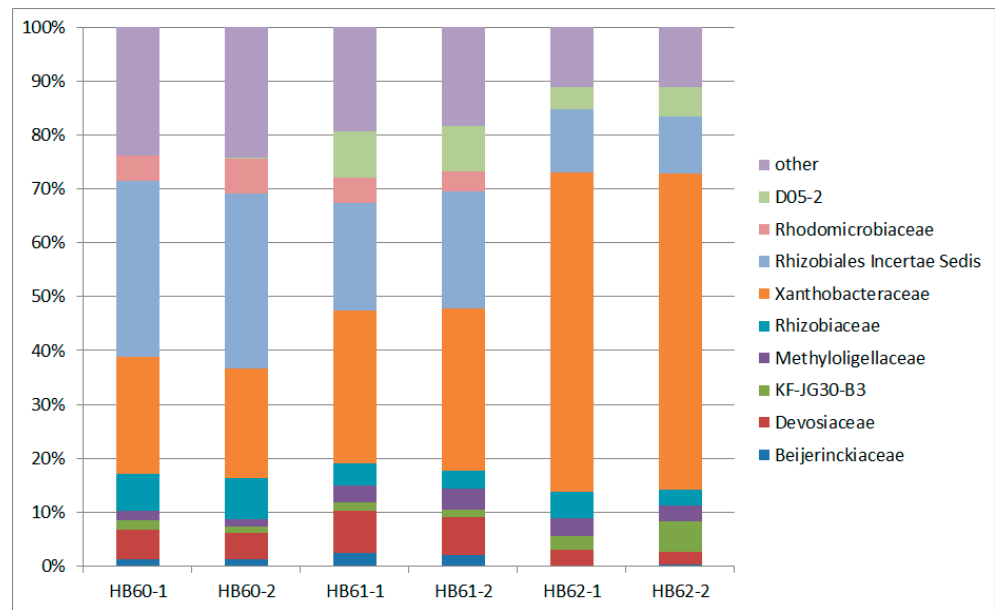
**Figure S3.** Relative abundances of dominating families/orders of *Actinobacteriota*.



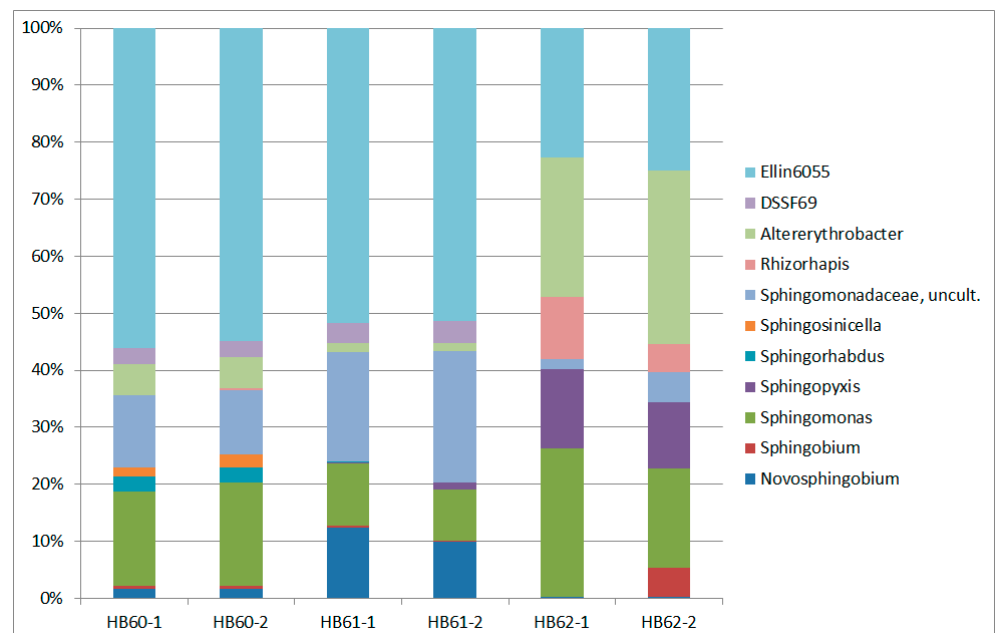
**Figure S4.** Relative abundances of selected OTUs inside the class *Blastocatellia*.



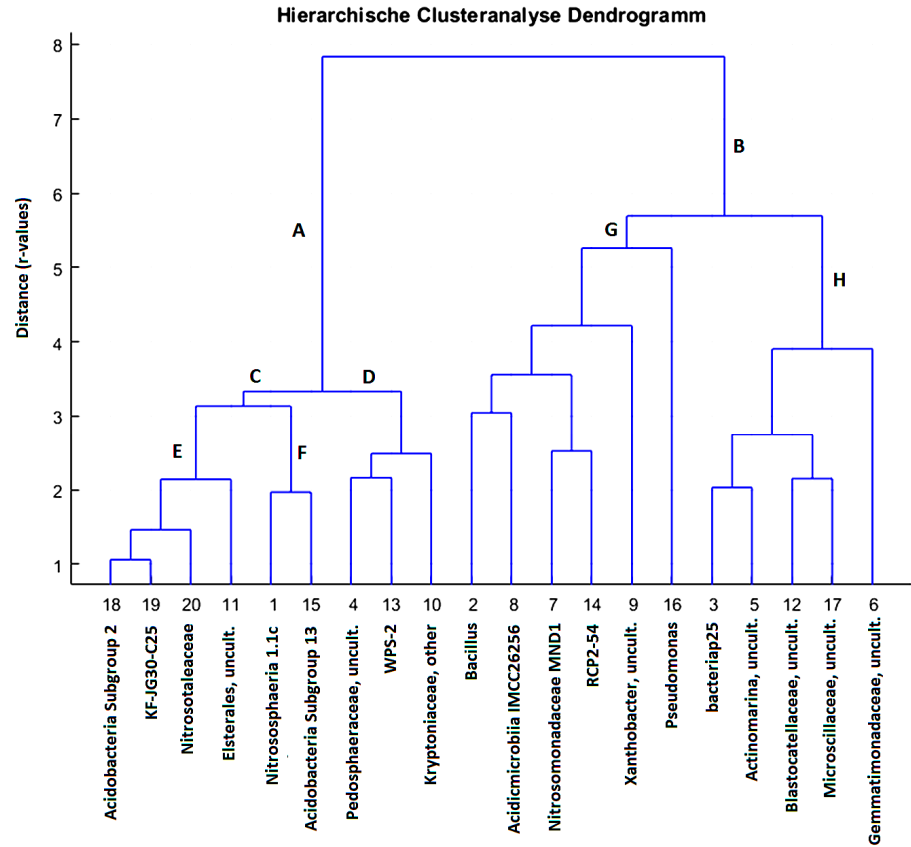
**Figure S5.** Relative abundances of most abundant orders in the phylum *Actinobacteriota*.



**Figure S6.** Relative abundances of families in the order *Rhizobiales*.



**Figure S7.** Relative abundances of OTUs in the family *Sphingomonadaceae*.



**Figure S8.** Result of hierarchical clustering (dendrogram) applied for all 12 sampling places and related to the 20 most abundant OTUs in total; The left hand branch of the tree (A) contains the OTUs which are most frequent in the samples of Bennstedt (low soil pH). The right hand branch (B) relates to the most abundant bacteria in the samples from Bad Dürrenberg.