

Fig. S1: Nonmetric multidimensional scaling (nMDS) ordination plot, based on Bray-Curtis similarity indices calculated from presence/absence data of 16S rDNA TRFs abundance from above water table (oxic) zones showing variation based on age of drainage.

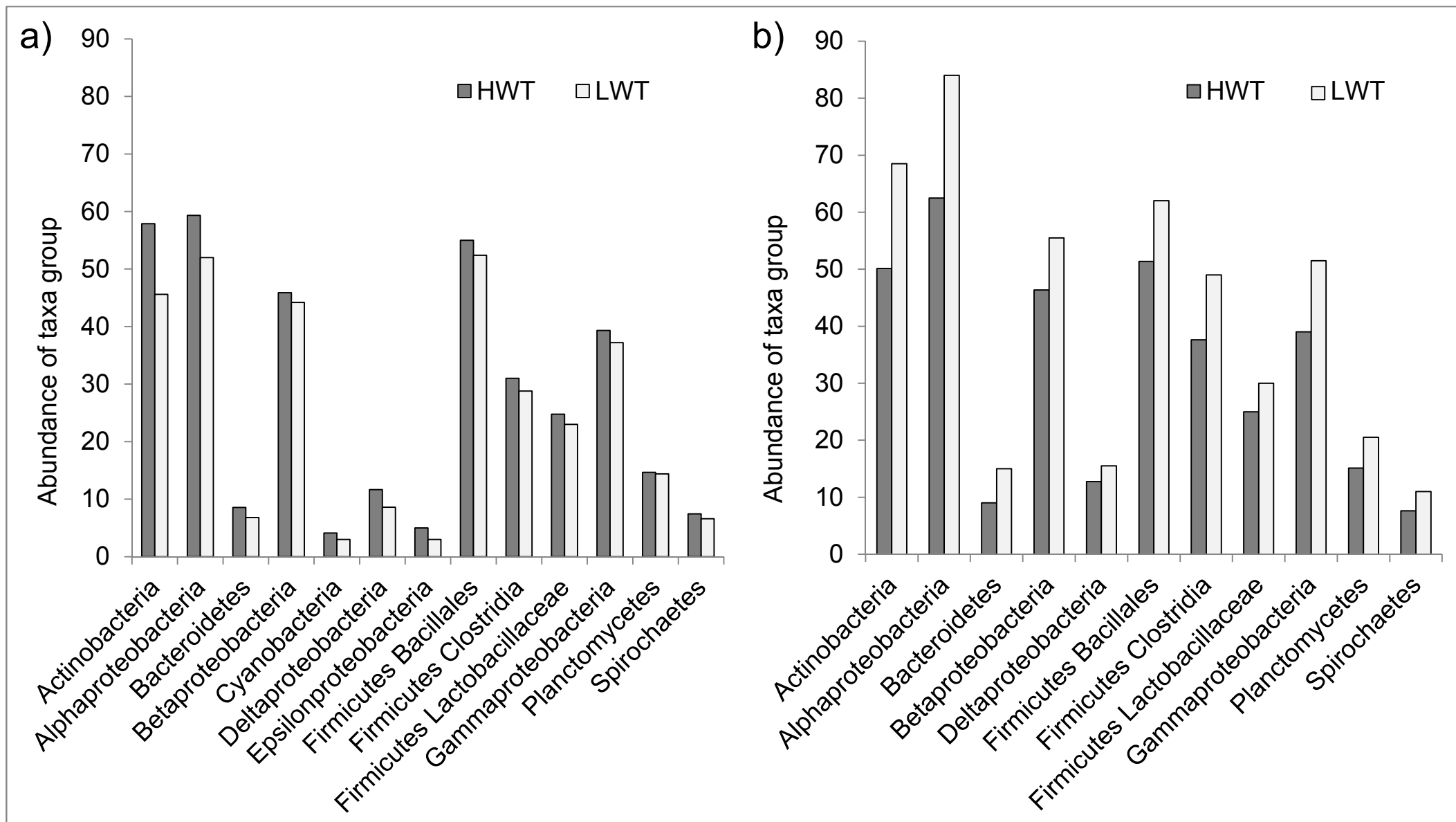


Figure S2: Relative abundance of bacterial population from all sites with high water table (HWT) and low watertable (LWT), based on phylogenetic assignment using FRAGSORT from a) above water table (oxic) zones and b) below water table (anoxic) zones. For oxic zones of LWT sites, average of predicted taxa from depths, 20-30 cm and 50 cm from water table, were taken

Table S1: Relationship between the bacterial community structure and geochemical parameters as revealed by canonical correspondence analyses and Monte Carlo permutation tests performed separately for 16S rDNA gene-based T-RFLP data sets and geochemical data.

Sampling zones	Monte Carlo permutation test (p-value) of first / all canonical axes	Percentage variance of bacterial community-environment relation		Bacterial community-environment correlation / Eigen values	
		Canonical axis 1	Canonical axis 2	Canonical axis 1	Canonical axis 2
Above water table (oxic) zones	0.03/0.05	21.1	14.7	0.978 / 0.366	0.945 / 0.256
Below water table (anoxic) zones	0.004/0.009	17.6	14	0.980 / 0.362	0.979 / 0.289