

Table S5. Effect of treatment (unamended soil, amended soil with young maize plants or its neutral detergent fibre) and effect of soil (EC: 1.9 dS m⁻¹, 17.3 dS m⁻¹, 33.4 dS m⁻¹) on bacterial phyla or genera using a compositional approach, i.e. analysis of differential abundance taking sample variation into account (ALDEx2 package [39]).

Soil ^a		Treatment	
Phyla			
Acidobacteria	2.99×10 ⁻¹⁰ ^b	Verrucomicrobia	1.00×10 ⁻⁴
Firmicutes	9.63×10 ⁻⁸	Proteobacteria	1.00×10 ⁻⁴
Gemmatimonadetes	1.10×10 ⁻⁶	Planctomycetes	3.00×10 ⁻⁴
Bacteroidetes	5.77×10 ⁻⁷	Actinobacteria	5.00×10 ⁻⁴
[Thermi]	2.92×10 ⁻⁷	Chloroflexi	8.00×10 ⁻⁴
Proteobacteria	5.00×10 ⁻⁴	Gemmatimonadetes	3.10×10 ⁻³
Actinobacteria	3.00×10 ⁻⁴	Bacteroidetes	4.80×10 ⁻³
Armatimonadetes	1.00×10 ⁻⁴	Nitrospirae	9.20×10 ⁻³
Spirochaetes	1.70×10 ⁻³	NC10	3.62×10 ⁻²
Chloroflexi	1.30×10 ⁻³		
Genera			
<i>Halomonas</i>	9.35×10 ⁻⁹	<i>Acinetobacter</i>	3.14×10 ⁻⁷
<i>Lysobacter</i>	1.10×10 ⁻⁸	<i>Prauseria</i>	4.62×10 ⁻⁷
<i>KSA1</i>	1.14×10 ⁻⁸	<i>Variovorax</i>	4.32×10 ⁻⁶
<i>Euzebya</i>	1.36×10 ⁻⁸	<i>Streptomyces</i>	5.70×10 ⁻⁶
<i>Xylanimicrobium</i>	2.10×10 ⁻⁸	<i>Glycomyces</i>	6.60×10 ⁻⁶
<i>Alkaliphilus</i>	3.37×10 ⁻⁸	<i>Pseudomonas</i>	2.82×10 ⁻⁵
<i>Nocardioides</i>	6.98×10 ⁻⁸	<i>Marinobacter</i>	8.93×10 ⁻⁵
<i>Prauseria</i>	1.15×10 ⁻⁷	<i>Azorhizophilus</i>	2.00×10 ⁻³
<i>Pseudomonas</i>	6.74×10 ⁻⁷	<i>Williamsia</i>	1.00×10 ⁻³
<i>Anaerobacillus</i>	6.77×10 ⁻⁷	<i>Bacillus</i>	7.00×10 ⁻³
<i>Rhodobaca</i>	9.60×10 ⁻⁷	<i>Nitriliruptor</i>	4.70×10 ⁻³
<i>Steroidobacter</i>	1.12×10 ⁻⁶	<i>Nesterenkonia</i>	6.40×10 ⁻³
<i>Desulfonatronum</i>	1.30×10 ⁻⁶		
<i>Devosia</i>	1.53×10 ⁻⁶		
<i>B-42</i>	2.67×10 ⁻⁶		
<i>Rhodoplanes</i>	5.57×10 ⁻⁶		
<i>Dethiobacter</i>	1.40×10 ⁻⁵		
<i>Hyphomicrobium</i>	2.61×10 ⁻⁵		
<i>Pedomicrobium</i>	4.11×10 ⁻⁵		
<i>Adhaeribacter</i>	4.63×10 ⁻⁵		

^a Only ten phyla and twenty genera most significantly affected by soil EC $P < 0.001$ and with the lowest p values obtained are given, ^b The expected values of the Kruskal-Wallis test for each feature obtained with aldex.kw argument with converted sequence data using the centered log-ratio transform test returned by the aldex.clr argument ALDEx2 package.