

Table S3. Effect of soil with EC 1.9 dS⁻¹ (low), 17.3 dS⁻¹ (medium), 33.4 dS⁻¹ (high) on bacterial phyla and genera in the unamended soil, soil amended with neutral detergent fibre (NDF) and soil amended with young maize plants using a compositional approach, i.e. analysis of differential abundance taking sample variation into account ALDEEx2 package [39].

| Unamended ^a | | NDF treatment | | Young maize plants |
|------------------------|----------------------|------------------------|--------|-------------------------------|
| <i>Prauseria</i> | 0.00009 ^b | <i>Xylanimicrobium</i> | 0.0360 | <i>KSA1</i> 0.0070 |
| <i>Rhodoplanes</i> | 0.0001 | | | <i>Prauseria</i> 0.0084 |
| <i>KSA1</i> | 0.0001 | | | <i>Lysobacter</i> 0.0089 |
| <i>Lysobacter</i> | 0.0001 | | | <i>Alkaliphilus</i> 0.0094 |
| <i>Pseudomonas</i> | 0.0001 | | | <i>Euzebya</i> 0.0121 |
| <i>Steroidobacter</i> | 0.0001 | | | <i>Nocardioides</i> 0.0121 |
| <i>Halomonas</i> | 0.0001 | | | <i>Halomonas</i> 0.0137 |
| <i>Euzebya</i> | 0.0001 | | | <i>Devosia</i> 0.0156 |
| <i>B-42</i> | 0.0002 | | | <i>B-42</i> 0.0160 |
| <i>Acinetobacter</i> | 0.0002 | | | <i>Anaerobacillus</i> 0.0171 |
| <i>Rhodobaca</i> | 0.0002 | | | <i>Pseudomonas</i> 0.0198 |
| <i>Devsosia</i> | 0.0003 | | | <i>Desulfonatronum</i> 0.0230 |
| <i>Desulfonatronum</i> | 0.0003 | | | <i>Steroidobacter</i> 0.0240 |
| <i>Nocardioides</i> | 0.0003 | | | <i>Dethiobacter</i> 0.0322 |
| <i>Cobetia</i> | 0.0003 | | | <i>Bacillus</i> 0.0359 |
| <i>Pedomicrobium</i> | 0.0003 | | | <i>Bradyrhizobium</i> 0.0360 |
| <i>Marinimicrobium</i> | 0.0004 | | | |
| <i>Alkaliphilus</i> | 0.0005 | | | |
| <i>Balneimonas</i> | 0.0005 | | | |
| <i>Adhaeribacter</i> | 0.0005 | | | |

^a Only the twenty bacterial genera in the unamended soil most highly significantly affected $p < 0.001$. ^b Significance was measured using ALDEEx2 and based on the Benjamini-Hochberg corrected p value of the Kruskal-Wallis test (significance threshold, $p < 0.05$).