

Appendix A Number of quality passing sequences for further analysis.

| Sample | Bacteria | | Fungi | |
|---------|-------------------|------|-------------------|------|
| | Passing sequences | OTUs | Passing sequences | OTUs |
| Si-P+_1 | 36195 | 2623 | 58414 | 618 |
| Si-P+_2 | 37243 | 2611 | 55853 | 781 |
| Si-P+_3 | 39301 | 2529 | 58731 | 774 |
| Si+P+_1 | 35519 | 2765 | 53954 | 544 |
| Si+P+_2 | 43305 | 2839 | 63370 | 942 |
| Si+P+_3 | 37878 | 2566 | 37101 | 551 |
| Si-P-_1 | 39429 | 3095 | 59131 | 818 |
| Si-P-_2 | 33844 | 2738 | 55328 | 786 |
| Si-P-_3 | 37300 | 2951 | 64598 | 601 |
| Si+P-_1 | 37614 | 3036 | 35728 | 685 |
| Si+P-_2 | 47635 | 3208 | 51768 | 660 |
| Si+P-_3 | 36864 | 2966 | 31389 | 600 |

Si-P+: no Si addition with the plant; Si+P+: 2.0 mmol L⁻¹ Si addition with the plant; Si-P-: no Si addition without the plant; Si+P-: 2.0 mmol L⁻¹ Si addition without the plant.

Appendix B Observed richness and diversity estimates based on 97 % OTU clusters

| Treatment | Bacteria | | | Fungi | | |
|-----------|-------------|-----------------|-----------------|------------|----------------|----------------|
| | Shannon | Chao1 | ACE | Shannon | Chao1 | ACE |
| Si-P+ | 8.97±0.11b | 2544.36±35.03c | 2578.55±37.32c | 4.38±0.41a | 794.25±68.44a | 821.81±68.35a |
| Si+P+ | 9.21±0.05ab | 2663.34±96.43bc | 2716.46±97.51bc | 4.21±0.35a | 663.73±104.64a | 690.23±115.75a |
| Si-P- | 9.23±0.16ab | 3178.9±191.07a | 3248.78±203.07a | 5.22±0.66a | 756.65±60.45a | 793.61±72.08a |
| Si+P- | 9.34±0.07a | 3026.22±64.17ab | 3104.6±97.26ab | 4.14±0.43a | 626.33±40.63a | 644.61±49.62a |

Si-P+: no Si addition with the plant; Si+P+: 2.0 mmol L⁻¹ Si addition with the plant; Si-P-: no Si addition without the plant; Si+P-: 2.0 mmol L⁻¹ Si addition without the plant. Different letters indicate statistically significant differences at the 0.05 probability level according to Duncan test