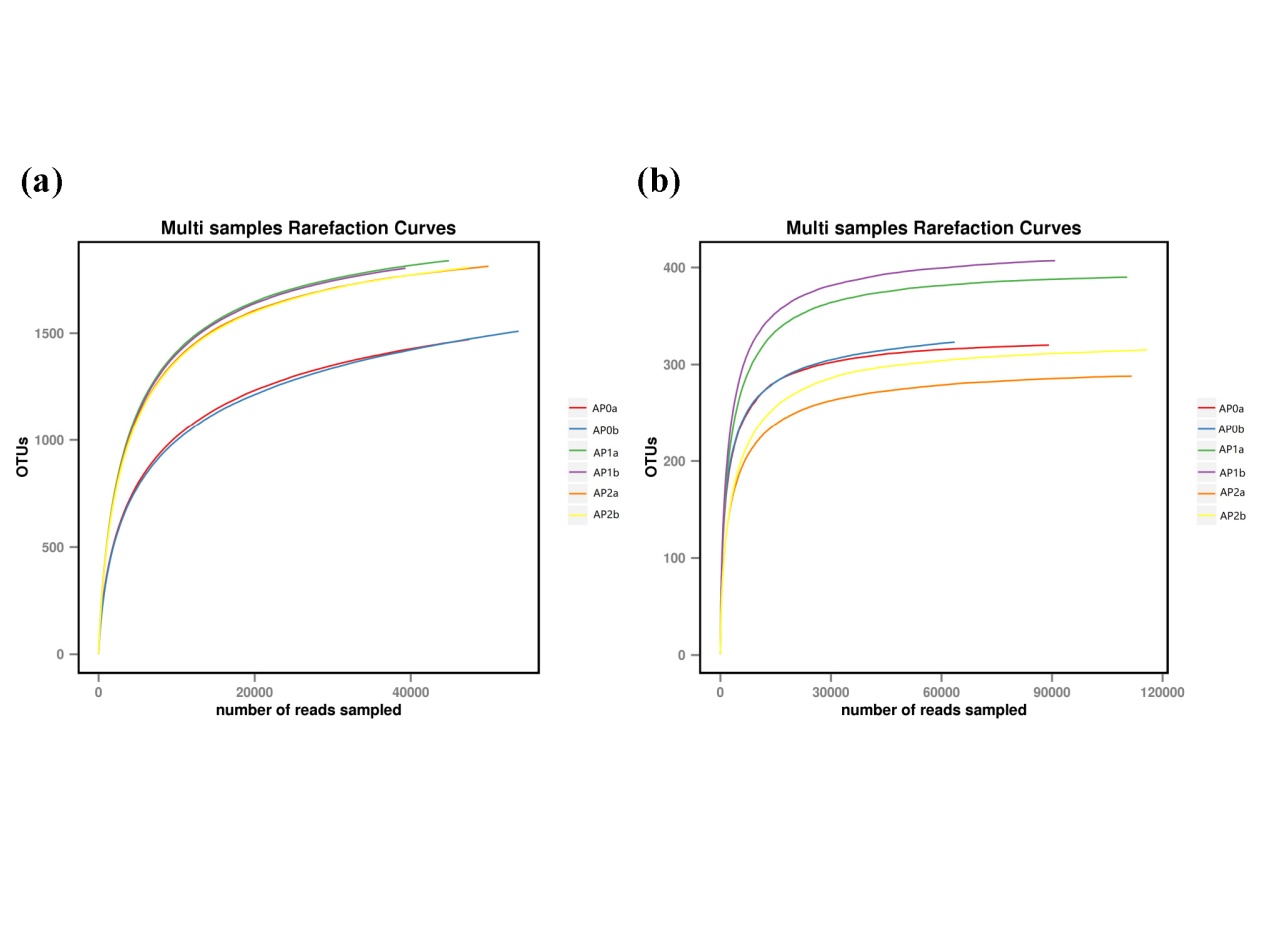
**Table S1.** Sequencing output of soil bacterial sequences

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample\_ID | PE\_Reads | Raw\_Tags | Clean\_Tags | AvgLen(bp) | GC(%) | Q20(%) | Q30(%) | Effective(%) |
| AP0-1 | 66685 | 63779 | 56461 | 454 | 54.6 | 96.47 | 93.29 | 84.67 |
| AP0-2 | 79106 | 77333 | 68166 | 453 | 54.96 | 97.86 | 95.89 | 86.17 |
| AP1-1 | 71436 | 67914 | 59218 | 456 | 55.57 | 96.17 | 92.69 | 82.9 |
| AP1-2 | 66788 | 65154 | 57857 | 456 | 55.91 | 97.71 | 95.57 | 86.63 |
| AP2-1 | 77642 | 73823 | 64672 | 457 | 56.01 | 96.45 | 93.18 | 83.3 |
| AP2-2 | 79522 | 77684 | 69089 | 456 | 56.43 | 97.74 | 95.57 | 86.88 |

**Table S2.** Sequencing output of soil fungal sequences

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample\_ID | PE\_Reads | Raw\_Tags | Clean\_Tags | AvgLen(bp) | GC(%) | Q20(%) | Q30(%) | Effective(%) |
| AP0-1 | 101723 | 93697 | 92107 | 345 | 41.75 | 97.82 | 96.09 | 90.55 |
| AP0-2 | 72639 | 66856 | 65607 | 345 | 42.75 | 98.6 | 97.67 | 90.32 |
| AP1-1 | 118767 | 114501 | 113433 | 306 | 44.26 | 98.31 | 96.92 | 95.51 |
| AP1-2 | 97751 | 94381 | 93624 | 313 | 44.17 | 98.82 | 98 | 95.78 |
| AP2-1 | 118437 | 114789 | 114088 | 292 | 44.56 | 98.86 | 97.95 | 96.33 |
| AP2-2 | 99496 | 97363 | 96996 | 302 | 49.73 | 99.11 | 98.7 | 97.49 |



**Fig. S1.** Rarefaction curves of soil microbial communities based on OTUs at the 97% similarity cut-off level for individual samples. (a) and (b) are the rarefaction curves of OTU for bacterial and fungal communities, respectively. AP0, AP1 and AP2 represent soil with continuously cropping histories of *A. paniculata* for 0, 1 and 2 years. “a” and “b” mean the two replicates.