Table S2. Summary of pre- and post-assembly and post-QC metagenome sequences

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Field bulk | Field rhizosphere | Forest bulk | Forest rhizosphere |
| Total # of reads | 44,641,544 | 70,129,920 | 19,394,324 | 29,124,986 |
| GC content | 59.9%A | 51.5%B | 59.7%A | 48.9%B |
| Total # of reads after QC | 9,412,563 | 9,245,366 | 2,864,804 | 3,756,327 |
| GC content after QC | 59.3%A | 56.9%A | 59.0%A | 52.2%B |
| Average genome coverage | 41 | 32 | 31 | 34 |
| KOs | 4,233 | 4,434 | 3,661 | 4,372 |
| Pathways | 165 | 189 | 150 | 186 |
| Modules | 274 | 280 | 287 | 268 |

For each variable, data followed by different letters are significantly different according to Tukey’s test (P < 0.05).