**S1 Table. Information on the fungal communities for soil samples. Diversity indices and Good’s coverage were calculated after normalization (570 reads) without *T. matsutake* reads. Because the number of G1D sequences without *T. matsutake* reads was too small, G1D was excluded for diversity measurement.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Soil type** | **Sample ID** | **Location** | **SR. No.\*** | ***Tm***† **Proportion (%)** | **Diversity measure** | | | **Good's coverage** |
| **Chao1** | **Shannon** | **Shannon’s equitability** |
| ***Tm*-dominant** | G1D | Gyeongju | 9284 | 98.1% | - | - | - | - |
| G2D | Gyeongju | 4448 | 87.2% | 14.00 | 0.81 | 0.23 | 0.99 |
| G3D | Gyeongju | 7240 | 84.8% | 9.50 | 0.88 | 0.28 | 0.99 |
| H2D | Hongcheon | 5956 | 88.7% | 25.00 | 2.70 | 0.63 | 0.98 |
| H5D | Hongcheon | 4500 | 83.6% | 34.14 | 2.72 | 0.56 | 0.98 |
|  |  |  |  |  |  |  |  |  |
| ***Tm*-minor** | G4m | Gyeongju | 11997 | 0.0% | 25.00 | 1.52 | 0.36 | 0.98 |
| G5m | Gyeongju | 2229 | 34.7% | 41.00 | 1.92 | 0.41 | 0.98 |
| G6m | Gyeongju | 9094 | 1.3% | 43.75 | 1.83 | 0.36 | 0.97 |
| H1m | Hongcheon | 4263 | 0.0% | 40.00 | 3.46 | 0.68 | 0.98 |
| H3m | Hongcheon | 7283 | 0.0% | 36.14 | 2.54 | 0.51 | 0.98 |
| H4m | Hongcheon | 4180 | 0.0% | 64.00 | 3.61 | 0.66 | 0.97 |
| H6m | Hongcheon | 5820 | 0.0% | 51.00 | 1.19 | 0.26 | 0.97 |

*\** SR. No: Sequence reads number  
†*Tm*: *Tricholoma matsutake*