**Table S2 Phylotype coverage and diversity estimation based on the fungal ITS rRNA gene libraries for the samples from the MiSeq sequencing analysis. Sample names include the site (G, sandy grassland; S, semi-fixed sandy land) and nitrogen addition treatment: control (CK), no N addition; N5, 5 g N m−2 yr−1; N10, 10 g N m−2 yr−1; N15, 15 g N m−2 yr−1.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Samples | Valid sequences | Average length (bp) | OTUsa | ACEa | Chaoa | Shannona | Simpsona | Coverage |
| G1CK | 61950 | 250.127 | 268 | 278.237 | 295.143 | 3.773 | 0.048 | 0.99972 |
| G3CK | 69669 | 247.635 | 244 | 258.275 | 256.214 | 3.530 | 0.074 | 0.99974 |
| G5CK | 67161 | 240.780 | 276 | 289.095 | 294.071 | 3.482 | 0.061 | 0.99967 |
| G1N5 | 68303 | 247.160 | 203 | 210.425 | 214.143 | 3.322 | 0.068 | 0.99982 |
| G3N5 | 67904 | 239.774 | 241 | 252.984 | 252.333 | 3.684 | 0.057 | 0.99976 |
| G5N5 | 68954 | 245.224 | 235 | 253.304 | 252.250 | 3.275 | 0.096 | 0.99966 |
| G1N10 | 62859 | 244.185 | 264 | 273.895 | 273.130 | 2.934 | 0.119 | 0.99970 |
| G3N10 | 57367 | 239.727 | 281 | 292.088 | 298.769 | 3.522 | 0.066 | 0.99969 |
| G5N10 | 68327 | 242.764 | 314 | 318.141 | 318.500 | 4.037 | 0.046 | 0.99986 |
| G1N15 | 67792 | 240.302 | 292 | 300.548 | 301.000 | 3.547 | 0.062 | 0.99976 |
| G3N15 | 68431 | 249.070 | 242 | 247.397 | 248.000 | 2.669 | 0.249 | 0.99983 |
| G5N15 | 59879 | 240.757 | 243 | 251.083 | 258.111 | 3.518 | 0.061 | 0.99972 |
| S1CK | 56652 | 246.955 | 273 | 345.389 | 346.000 | 1.386 | 0.581 | 0.99871 |
| S3CK | 68076 | 244.892 | 373 | 384.353 | 384.040 | 4.081 | 0.039 | 0.99966 |
| S5CK | 73089 | 244.797 | 365 | 381.185 | 388.619 | 3.589 | 0.068 | 0.99957 |
| S1N5 | 70478 | 246.198 | 317 | 323.009 | 325.750 | 3.691 | 0.088 | 0.99979 |
| S3N5 | 72117 | 230.261 | 363 | 395.885 | 397.459 | 2.535 | 0.247 | 0.99931 |
| S5N5 | 68935 | 246.985 | 314 | 322.729 | 319.913 | 3.658 | 0.062 | 0.99976 |
| S1N10 | 60039 | 242.285 | 234 | 244.467 | 258.000 | 3.655 | 0.060 | 0.99978 |
| S3N10 | 66654 | 238.641 | 222 | 228.237 | 229.857 | 3.562 | 0.073 | 0.99985 |
| S5N10 | 72555 | 247.284 | 211 | 215.009 | 214.273 | 2.600 | 0.283 | 0.99988 |
| S1N15 | 70873 | 230.935 | 178 | 186.157 | 184.111 | 2.732 | 0.182 | 0.99985 |
| S3N15 | 69637 | 248.059 | 161 | 173.659 | 172.143 | 2.693 | 0.226 | 0.99982 |
| S5N15 | 67072 | 236.890 | 181 | 184.951 | 185.000 | 2.975 | 0.132 | 0.99989 |

a The operational taxonomic units (OTUs) were defined using a 97% similarity threshold. Abbreviations: ACE and Chao, richness estimators; Shannon and Simpson, diversity indices.