

| | 18S rRNA (PCR-amplified) | cDNA (MEGAN « default parameters ») | cDNA (MEGAN « stringent parameters ») |
|-----------------------|--------------------------|-------------------------------------|---------------------------------------|
| Fungi | 24 / 17 | 2365 / 1410 | 2455 / 1490 |
| Metazoa | 21 / 13 | 369 / 384 | 458 / 502 |
| Amoebozoa | 2 / 2 | 64 / 56 | 70 / 74 |
| Alveolata | 2 / 2 | 19 / 5 | 32 / 20 |
| Rhizaria | 2 / 0 | 0 / 0 | 1 / 1 |
| Heterokonta | 0 / 1 | 8 / 5 | 12 / 11 |
| Excavata | 1 / 0 | 11 / 8 | 17 / 9 |
| Plantae | 6 / 7 | 169 / 84 | 195 / 114 |
| Bacteria | 0 / 0 | 71 / 114 | 164 / 212 |
| Other Eukaryotes | 0 / 0 | 0 / 10 | 13 / 18 |
| Multiple affiliations | 0 / 0 | 885 / 849 | 879 / 843 |

Table S2: Taxonomic affiliation of the 18S rRNA and cDNA sequence datasets from the spruce (first figures) and beech (second figures) forest soils. Putative protein coding cDNA sequences were annotated using two different settings of the MEGAN software. Using the “default parameters”, the “Min. Support” value was set to five while it was set to one in the “stringent parameter” analysis.