|  |  |  |
| --- | --- | --- |
| **Taxa** | **Amount of Contaminant Sequences** | **Percent of Total Contaminant Sequences** |
| *Lycoperdon perlatum* | 714 | 16.38% |
| *Trichoderma harzianum* | 632 | 14.50% |
| *Mortierella minutissima* | 596 | 13.67% |
| *Trichoderma atroviride* | 454 | 10.42% |
| *Absidia cylindrospora* | 409 | 9.38% |
| *Gymnopus dryophilus* | 356 | 8.17% |
| *Ilyonectria destructans* | 339 | 7.78% |
| *Schwanniomyces polymorphus* | 554 | 12.71% |
| *Strobilurus trullisatus* | 305 | 7.00% |
| **Total**  | **4359** | **100%** |

## Supplementary Information

Article title: A rapid approach to profiling diverse fungal communities using Oxford's MinION™ nanopore sequencer

**Supplementary Table 1** The amount and percentage of contaminant sequences in the negative control that passed through quality filtering and clustered into operational taxonomic units (OTUs). The negative control contained trace contaminants from nine of the 16 mock community members. This is presumably due to cross-contamination during PCR and library preparation steps, despite surface sterilization and stringency in protocols.