**SUPPLEMENTARY MATERIAL**

**High-throughput sequencing of fungal communities across the perennial ice block of Scărișoara Ice Cave**

Antonio MONDINI1, Johanna DONHAUSER2, Corina ITCUS1, Constantin MARIN3, Aurel PERȘOIU1,4,5, Paris LAVIN6,7, Beat FREY2, Cristina PURCAREA1

**Table S2**. Illumina Miseq sequencing of ITS2 region applied to the triplicate ice samples from Scarisoara ice block

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample** | **Number of Reads** | **Number of Bases** | **Average Quality** | **Duplicate (%)** |
| 1-S.1 | 92,518 | 46,259,000 | 34 | 92.520 |
| 1-S.2 | 77,189 | 38,594,500 | 33 | 92.511 |
| 1-S.3 | 75,720 | 37,860,000 | 34 | 93.321 |
| 1-L.1 | 91,420 | 45,710,000 | 33 | 91.775 |
| 1-L.2 | 83,116 | 41,558,000 | 34 | 95.210 |
| 1-L.3 | 86,131 | 43,065,500 | 34 | 95.287 |
| 400-O.1 | 84,538 | 42,269,000 | 33 | 93.216 |
| 400-O.2 | 62,555 | 31,277,500 | 32 | 93.128 |
| 400-O.3 | 105,357 | 52,678,500 | 33 | 94.251 |
| 900-O.1 | 73,439 | 36,719,500 | 33 | 92.987 |
| 900-O.2 | 91,907 | 45,953,500 | 35 | 94.474 |
| 900-O.3 | 98,532 | 49,266,000 | 33 | 94.850 |
| 900-I.1 | 75,216 | 37,608,000 | 35 | 94.118 |
| 900-I.2 | 70,409 | 35,204,500 | 35 | 93.967 |
| 900-I.3 | 86,009 | 43,004,500 | 35 | 94.363 |
| 1200-I.1 | 68,411 | 34,205,500 | 34 | 93.413 |
| 1200-I.2 | 73,126 | 36,563,000 | 34 | 95.538 |
| 1200-I.3 | 77,914 | 38,957,000 | 33 | 94.435 |
| 1500-I.1 | 85,608 | 42,804,000 | 34 | 94.179 |
| 1500-I.2 | 92,131 | 46,065,500 | 34 | 94.967 |
| 1500-I.3 | 100,531 | 50,265,500 | 34 | 92.774 |