Supporting Information Table S2. Comparison of gene regions in rDNA sequences of isolate FD01 *Amoeboaphelidium protococcarum* and strain X-5 (Karpov et al. 2012).

| | strain X-5 | isolate FD01 | Sequence similarity |
|---|---|---|---|
| rDNA | 1-5774 bases | 1-4667 bases | |
| Ø region | 1-98 | | |
| 18S | 99-1890 | 1-2271 | 67%/86%[1] |
| ITS1 | 1891-2086 | 2272-2630 | 35% |
| 5.8S | 2087-2241 | 2631-2798 | 84% |
| ITS2 | 2242-2407 | 2799-3140 | 30% |
| 28S | 2408-5774 | 3142-4667 | 78%[2] |

[1] The 18S region of isolate FD01 has regions (bases 1156-1522 and 1528-1651 from the 5′ end)) that are absent in strain X-5. When sequences are compared without removing the regions, sequence similarity is 67%; when the regions are removed, sequence similarity is 86%.

[2] The 28S region of strain X-5 is complete, at 3367 bases; the 28S region of isolate FD01 is partial, at 1527 bases. When the 3’ end of the strain X-5 sequence is shortened to the length of the isolate FD01 sequence, similarity is 78%.