Table S1. Result of the BLAST analyses for the nucleotide sequence obtained in this study MicroBac 01. (QC: query cover; Idt: identity).

| Microsporidia                      | Acc. Number | Host                          | Taxonomy | QC    | Idt    |
|------------------------------------|-------------|-------------------------------|----------|-------|--------|
| Cucumispora sp. KKB15              | MG063425.1  | Brandtia latissima            | Crustacea| 99%   | 94.89% |
| Cucumispora sp. KK1B16             | MG063426.1  | Brandtia latissima            | Crustacea| 99%   | 94.81% |
| Microsporidium sp. MSCLHCY01       | HM800853.2  | Lepeophtheirus hospitalis     | Crustacea| 99%   | 94.86% |
| Hyperspora aquatica                | KX364284.1  | Marsella cochillia            | Paranyxida| 99%   | 94.72% |
| Microsporidium sp. Dhae17W         | KP699690.1  | Dikerogammarus haemobaphes    | Crustacea| 99%   | 94.01% |
| Microsporidium sp. 1049            | FN434092.1  | Gammarus duebeniduebeni       | Crustacea| 99%   | 93.93% |
| Microsporidium sp. JES2002G        | AJ438962.1  | Gammarus chevreuxi            | Crustacea| 99%   | 93.49% |
| Cucumispora ornata                 | KR190602.1  | Dikerogammarus haemobaphes    | Crustacea| 94%   | 93.58% |
| Cucumispora dikerogammarri         | GQ426188.1  | Dikerogammarus villosus       | Crustacea| 99%   | 91.86% |
| Cucumispora dikerogammarri         | GQ258752.1  | Dikerogammarus villosus       | Crustacea| 99%   | 91.85% |
| Cucumispora dikerogammarri (in GenBank: Microsporidium sp. RW-2009a) | KR871370.1  | Dikerogammarus haemobaphes    | Crustacea| 76%   | 91.97% |
| Microsporidium sp. CRANPA          | AJ966718.1  | Crangonyx pseudogracilis      | Crustacea| 65%   | 94.89% |
| Microsporidium sp. EC-3            | KT956054.1  | Eulimnogammarus cyaneus       | Crustacea| 69%   | 94.60% |
| Microsporidium sp. EC-1            | KR080135.1  | Eulimnogammarus cyaneus       | Crustacea| 69%   | 94.50% |
| Microsporidium sp. EC-2            | KT956053.1  | Eulimnogammarus cyaneus       | Crustacea| 68%   | 94.94% |
| Microsporidium sp. G               | KR871369.1  | Dikerogammarus haemobaphes    | Crustacea| 76%   | 94.37% |
|                                    |             | Gammarus pulex                |          |       |        |
|                                    |             | Gammarus roeseli              |          |       |        |
Table S2. Comparison of small subunit gene (SSU rDNA) sequences among microsporidia parasites. Pairwise distance (bottom diagonal) obtained by p-distance.

| Species (GenBank Acc. Number) | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
|-------------------------------|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|
| 1. Microsporidia sp. EC-1 (KR080135.1) | - |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |
| 2. Microsporidia sp. EC-2 (KT956053.1) | 0.006 | - |   |   |   |   |   |   |   |    |    |    |    |    |    |    |
| 3. Microsporidium sp. CRANPA (A966718.1) | 0.040 | 0.035 | - |   |   |   |   |   |   |    |    |    |    |    |    |    |
| 4. Microsporidium sp. Dhae17W (KX364284.1) | 0.053 | 0.047 | 0.043 | - |   |   |   |   |   |    |    |    |    |    |    |    |
| 5. Thelohania butleri (DQ417114.1) | 0.134 | 0.128 | 0.118 | 0.116 | 0.137 | - |   |   |   |    |    |    |    |    |    |    |
| 6. Potaspora morhaphis (EUS34408.1) | 0.274 | 0.266 | 0.268 | 0.274 | 0.263 | 0.238 | - |   |   |    |    |    |    |    |    |    |
| 7. Cucumispora ornata (KL1305) | 0.043 | 0.037 | 0.043 | 0.039 | 0.049 | 0.114 | 0.268 | - |   |    |    |    |    |    |    |    |
| 8. Cucumispora sp. KK18 (MG063426.1) | 0.009 | 0.004 | 0.035 | 0.052 | 0.021 | 0.125 | 0.266 | 0.041 | - |    |    |    |    |    |    |    |
| 9. Cucumispora sp. KK18 (MG063425.1) | 0.009 | 0.004 | 0.035 | 0.051 | 0.021 | 0.125 | 0.266 | 0.041 | 0.000 | - |    |    |    |    |    |    |
| 10. Microsporidium sp. MSCLHCY01 (H9680385.1) | 0.057 | 0.051 | 0.053 | 0.047 | 0.063 | 0.120 | 0.277 | 0.051 | 0.049 | 0.049 | - |    |    |    |    |    |
| 11. Hyperspora baccigeri (KK364284.1) | 0.055 | 0.049 | 0.055 | 0.049 | 0.065 | 0.123 | 0.274 | 0.053 | 0.047 | 0.047 | 0.002 | - |    |    |    |    |
| 12. Unikaryon legeri (X364285.1) | 0.263 | 0.255 | 0.267 | 0.246 | 0.258 | 0.230 | 0.250 | 0.252 | 0.255 | 0.255 | 0.239 | 0.239 | - |    |    |    |
| 13. Unikaryon panopei (MW377751.1) | 0.260 | 0.253 | 0.259 | 0.242 | 0.255 | 0.233 | 0.251 | 0.242 | 0.253 | 0.253 | 0.234 | 0.234 | 0.051 | - |    |    |
| 14. Unikaryon panopei (KK190602.1) | 0.023 | 0.017 | 0.049 | 0.049 | 0.000 | 0.137 | 0.263 | 0.049 | 0.021 | 0.021 | 0.063 | 0.065 | 0.258 | 0.255 | - |    |
| 15. Cucumispora dikerogammar (GQ258752.1) | 0.067 | 0.061 | 0.078 | 0.055 | 0.070 | 0.146 | 0.277 | 0.067 | 0.065 | 0.065 | 0.078 | 0.076 | 0.266 | 0.267 | 0.070 | - |