

| Primer names                   | Primer sequences (5' -> 3')                              |
|--------------------------------|----------------------------------------------------------|
| Forward primers <sup>a</sup>   |                                                          |
| NC1_with_Illumina_Adapter_(0N) | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACGTCTGGTTCAGGGTTGTT    |
| NC1_with_Illumina_Adapter_(1N) | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNACGTCTGGTTCAGGGTTGTT   |
| NC1_with_Illumina_Adapter_(2N) | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNACGTCTGGTTCAGGGTTGTT  |
| NC1_with_Illumina_Adapter_(3N) | TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNACGTCTGGTTCAGGGTTGTT |
| Reverse primers <sup>a</sup>   |                                                          |
| NC2_with_Illumina_Adapter_(0N) | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTAGTTTCTTTTCTCCGCT    |
| NC2_with_Illumina_Adapter_(1N) | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGNTTAGTTTCTTTTCTCCGCT   |
| NC2_with_Illumina_Adapter_(2N) | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGNNTAGTTTCTTTTCTCCGCT   |
| NC2_with_Illumina_Adapter_(3N) | GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGNNNTTAGTTTCTTTTCTCCGCT |

**Table S1** Primers for amplification of internal transcribed spacer for Illumina sequencing

<sup>a</sup>In order to avoid problems with calculation of correction factors, which is not possible if the same base is detected for all positions on the Illumina Flow Cell during primer sequencing, zero to three random bases (N<sub>0-3</sub>) were inserted between the NC1/NC2 sequences and the Illumina adapters, as detailed by Avramenko, et al.<sup>23</sup>