

Supporting Information Table S6

PrimerProspector [34] results for all primers investigated in this study and investigated by Ihrmark et al. [35] and Toju et al. [36]

| Primer binding site and orientation | Primer name | Primer sequence (5' - 3') | 3' mismatch (%) | Average Primer Prospector Score | Standard Error on Score | Reference |
|-------------------------------------|-------------|---------------------------|-----------------|---------------------------------|-------------------------|-----------|
| 5.8S (forward) | ITS86F | GTGAATCATCGAATCTTTGAA | 3 | 0.00 | 0.00 | [27] |
| | ITS3 | GCATCGATGAAGAACGCAGC | 4 | 0.58 | 0.03 | [18] |
| | gITS9 | GAACGCAGCRAAIIGYGA | 4 | 0.41 | 0.02 | [35] |
| | fITS7 | GTGARTCATCGAATCTTTG | 4 | 0.49 | 0.02 | [35] |
| | gITS7 | GTGARTCATCGARTCTTTG | 4 | 0.49 | 0.02 | [35] |
| | ITS3_KYO1 | AHCGATGAAGAACRYAG | 5 | 0.42 | 0.02 | [36] |
| | ITS3_KYO2 | GATGAAGAACGYAGYRAA | 2 | 0.40 | 0.02 | [36] |
| | 58A1F | GCATCGATGAAGAACGC | 5 | 0.51 | 0.02 | [37] |
| | 58A2F | ATCGATGAAGAACGCAG | 6 | 0.52 | 0.02 | [37] |
| 5.8S (reverse) | ITS2 | GCTGCGTTCTTCATCGATGC | 9 | 0.70 | 0.03 | [18] |
| | ITS10mun | GCTGCGTTCTTCATCGAT | 3 | 0.48 | 0.02 | [38] |
| | ITS2_KYO1 | CTRYGTTCTTCATCGDT | 2 | 0.37 | 0.02 | [36] |
| | ITS2_KYO2 | TTYRCTRRCGTTCTTCATC | 5 | 0.49 | 0.02 | [36] |
| | 58A2R | CTGCGTTCTTCATCGAT | 3 | 0.47 | 0.02 | [37] |

| Primer binding site and orientation | Primer name | Primer sequence (5' - 3') | 3' mismatch (%) | Average Primer Prospector Score | Standard Error on Score | Reference |
|-------------------------------------|-------------------------|---------------------------|-----------------|---------------------------------|-------------------------|-----------|
| 28S (reverse) | ITS4B | CAGGAGACTTGTACACGGTCCAG | 41 | 5.75 | 0.03 | [19] |
| | ITS4_KYO1 | TCCTCCGCTTWTGWTWTGC | 23 | 3.71 | 0.04 | [36] |
| | ITS4_KYO2 | RBTTTCTTTTCCTCCGCT | 44 | 4.39 | 0.03 | [36] |
| | ITS4_KYO3 | CTBTTVCCCKCTTCACTCG | 42 | 3.47 | 0.04 | [36] |
| | ITS4 | TCCTCCGCTTATTGATATGC | 16 | 3.96 | 0.04 | [18] |
| | ITS8mun | CTTCACTCGCCGTTACTA | 61 | 4.07 | 0.03 | [38] |
| | NL6Amun | CAAGTGCTTCCCTTTCAACA | 10 | 3.49 | 0.03 | [38] |
| | NL6Bmun | CAAGCGTTTCCCTTTCAACA | 9 | 3.32 | 0.03 | [38] |
| | NLB3 | GGATTCTCACCTCTATGA | 13 | 3.04 | 0.03 | [37] |
| | NLB4 | GGATTCTCACCTCTATGAC | 53 | 4.17 | 0.04 | [37] |
| NLC2 | GAGCTGCATTCCCAAACAACCTC | 25 | 3.90 | 0.04 | [37] | |

| Primer binding site and orientation | Primer name | Primer sequence (5' - 3') | 3' mismatch (%) | Average Primer Prospector Score | Standard Error on Score | Reference |
|-------------------------------------|-------------|---------------------------|-----------------|---------------------------------|-------------------------|-----------|
| 18S (forward) | ITS1 | TCCGTAGGTGAACCTGCGG | 12 | 2.29 | 0.04 | [18] |
| | ITS1F | CTTGGTCATTTAGAGGAAGTAA | 44 | 4.55 | 0.05 | [19] |
| | ITS1F_KYO1 | CTHGGTCATTTAGAGGAASTAA | 36 | 4.11 | 0.05 | [36] |
| | ITS1F_KYO2 | TAGAGGAAGTAAAAGTCGTAA | 15 | 3.43 | 0.04 | [36] |
| | ITS5 | GGAAGTAAAAGTCGTAAACAAGG | 8 | 2.96 | 0.04 | [18] |
| | ITS9mun | TGTACACACCGCCCGTCG | 27 | 3.34 | 0.04 | [38] |
| | NSI1 | GATTGAATGGCTTAGTGAGG | 36 | 4.11 | 0.04 | [37] |
| | NSA3 | AAACTCTGTCGTGCTGGGGATA | 40 | 4.66 | 0.04 | [37] |