

Table 1 Primer sequences characteristics of 15 microsatellite loci resulting from the amplification of 30 individuals of *Hippopus hippopus*

| Locus | Primer sequence 5'-3' | Motif | Mix | Dye | Size (bp) | Na | H_O | H_E | F_{IS} | Accession no. |
|----------------------|---|---------------------|-----|-------|-----------|----|-------|-------|----------|---------------|
| <i>Hhiphip_04656</i> | F : TCCAGTAGTGGCAAACATCTC R : AGGCCTTGAAGAAGCTAAAGTTG | (TGT) ₈ | 1 | NED | 147 – 157 | 5 | 0.433 | 0.517 | 0.180 | xxx |
| <i>Hhiphip_04873</i> | F : ACAATATTTACGACGGCGG R : CAAGTGGACGCTGCACATAG | (GT) ₁₂ | 1 | PET | 081 – 092 | 8 | 0.733 | 0.791 | 0.091 | xxx |
| <i>Hhiphip_10072</i> | F : AGAAGAACAAGAAGTAGAGGATGG R : AGCCGGGGTTTACTGTATCTC | (TGA) ₇ | 2 | NED | 144 – 150 | 3 | 0.533 | 0.522 | -0.003 | xxx |
| <i>Hhiphip_11742</i> | F : TGCTAACACGGGAGAGAAGC R : ATTCCCACGTGCATAACCG | (GA) ₁₄ | 2 | PET | 126 – 140 | 7 | 0.800 | 0.810 | 0.030 | xxx |
| <i>Hhiphip_13326</i> | F : TCCCTGAAAGAGTAGCCTTG R : ACTTCTAACTGCAGATCGTTGC | (AGTA) ₇ | 2 | PET | 229 – 249 | 6 | 0.344 | 0.663 | 0.494* | xxx |
| <i>Hhiphip_14190</i> | F : AAGTTGCAATGAACCCACCG R : CCGGAAGTTGCGTTTTACATTC | (CA) ₁₆ | 2 | 6-FAM | 149 – 163 | 9 | 0.733 | 0.650 | -0.111 | xxx |
| <i>Hhiphip_14220</i> | F : GTGATAAACAGTGTGTGTGCG R : TGGCAAGAACAATGACAACCTG | (GT) ₂₁ | 1 | VIC | 101 – 113 | 11 | 0.346 | 0.835 | 0.598* | xxx |
| <i>Hhiphip_20250</i> | F : AACCCCGAAGCTTCATTCC R : GGCGAATCCAATGAGAACCAG | (CA) ₁₆ | 2 | VIC | 173 – 181 | 10 | 0.700 | 0.770 | 0.108 | xxx |
| <i>Hhiphip_22672</i> | F : TGTTTTTAGAAGCTATTCGCAGG R : AGCGGCGTAAAGCAACATTC | (TGAT) ₉ | 2 | VIC | 097 – 117 | 8 | 0.800 | 0.812 | 0.032 | xxx |
| <i>Hhiphip_23712</i> | F : TTTCCAAACGCCAAGTCTGC R : TCAAACAATAAACAACAACAACGC | (GT) ₁₂ | 2 | 6-FAM | 081 – 096 | 9 | 0.800 | 0.708 | -0.112 | xxx |
| <i>Hhiphip_24055</i> | F : TACCCGCTACCGTACATTCC R : GCGAAGCTCAACTACCAGTC | (CT) ₁₃ | 1 | VIC | 181 – 197 | 8 | 0.700 | 0.802 | 0.144 | xxx |
| <i>Hhiphip_25901</i> | F : ACTGAATGGAATGAAAAAGGGTG R : CCACTACACAACCTCGATCTG | (AC) ₁₇ | 1 | NED | 118 – 129 | 9 | 0.800 | 0.745 | -0.057 | xxx |
| <i>Hhiphip_27358</i> | F : TGCAGGGTACTGGTTAGGAG R : AGCTTGAACATGGCCAACC | (TGT) ₁₁ | 1 | PET | 151 – 173 | 8 | 0.800 | 0.807 | 0.027 | xxx |
| <i>Hhiphip_27369</i> | F : GCCATTGACCCGGATTTGAC R : CAGATCCGAGCGAAACACAC | (TCT) ₈ | 1 | 6-FAM | 123 – 134 | 2 | 0.300 | 0.495 | 0.408 | xxx |
| <i>Hhiphip_27960</i> | F : TGCGGAGTAGGGAACACATC R : TGCTGATTACGGAAGTAGGC | (ACA) ₈ | 2 | NED | 207 – 309 | 10 | 0.866 | 0.858 | 0.008 | xxx |

Mix multiplex in which it was amplified, *Dye* fluorescent dye used, *Size* amplified fragment size range in base pairs, *Na* number of alleles, H_O observed heterozygosity, H_E expected heterozygosity, F_{IS} Wright and Cockerham (1984) estimate, * Departure from HWE after Bonferroni corrections