

SUPPLEMENTARY MATERIAL TABLE S1 | Potential amplifiable microsatellite loci (PALs) described for the pacamã, forward and reverse primers, amplicon information (expected size), and repetitive motif. * Motifs are represented as the nucleotide repeats within parenthesis followed by the number of repeats observed in the amplicon.

| ID | Scaffold | Primer Forward | Primer Reverse | Size | Motif* |
|------|-----------|----------------------------|------------------------------|-------|---------|
| PM1 | C22028373 | TCGGCACTGACAAACAACAC | GAAGAGACAGTGGGTAGATATGTGA | 81bp | (ACA)6 |
| PM2 | C22131528 | TTCATGATGGTCCACCTTTG | GCTTGTGCATAAATCACTTGGGA | 80bp | (CCA)6 |
| PM3 | C22417400 | CTGAGGAGCGACAGCAGAG | GGGGCAGAGTGGAGGAAC | 62bp | (AGC)6 |
| PM4 | C22711680 | TCCTCAGTGGCCTTTCTTTT | GCACGAAGAGAGGGAGAAAAG | 83bp | (GC)8 |
| PM5 | C22724844 | GTGACCTGGCTCCACAAAAG | ACCCTCTGCTCTCGCTCAT | 93bp | (AAC)6 |
| PM6 | C23582443 | AAGAGACAGCCCCAACAGAC | GGAAGTGTCCGATTCCAGAC | 94bp | (AGG)6 |
| PM7 | C23610793 | GACAGGTCGCCACCTACT | AGCTCCCTCTCCCTGCTC | 102bp | (GCA)6 |
| PM8 | C23620145 | GCATCACAACCTTGATCCACCT | TGTCAGTAAAGCACCCATGC | 82bp | (TG)8 |
| PM9 | C23686366 | CCAATGTGAAAAATGACTGG | GCATTAAATTTACAGTAGCATTAAACAA | 71bp | (AT)8 |
| PM10 | C23737150 | TGAAAGTTCGAACCTGTTTGG | CAGGTTGTGGAAGATGGTGA | 95bp | (GCT)6 |
| PM11 | C23822591 | CCCGGCTCCATTTAACTACT | GACAGCTGCATAAGAGCTTCAG | 91bp | (TGA)6 |
| PM12 | C23858269 | TTGTTGAATGAAATTAAGAATGAAGA | GAGACAGGTGTTATTATGTGCTTTG | 78bp | (AG)8 |
| PM13 | C23878714 | AGACAGCTCATGGAGTGAAATG | AAGAGACAGATACTAACAAGGACTAAA | 99bp | (CCA)6 |
| PM14 | C23884028 | GGACGTCATACCTTCTCTGTCC | CTGAACACACTCAGAGGAAAGC | 106bp | (AT)8 |
| PM15 | C23924763 | CAGCACTCACACAGACTCAGAGA | TGAGTGAGTGAGACTATGAGTGAGG | 96bp | (AG)8 |
| PM16 | C23930391 | AGAGAATTTCAAAGCCAAACG | TTTTCACTGGGGTGGTAAT | 60bp | (CAC)6 |
| PM17 | C23930745 | CACCATTAACAGACTGAAGGAGAA | GCACATGTTTCATAAAGGAAGACA | 98bp | (TG)8 |
| PM18 | C23978623 | AGGATCTGAACAGAGGTACGG | AGATGACGGATGAGACATGC | 63bp | (TC)8 |
| PM19 | C24040009 | AGCAGTGAGTGGGAGTGTTA | TTTCCTGTCTCTTTTCACA | 78bp | (GA)8 |
| PM20 | C24045873 | ACCGTACGACTCCGTCATCT | TCCTCTCGAATCAAGAAACCA | 102bp | (CCT)6 |
| PM21 | C24079473 | TAACAATTAAGGGGAAAGG | ATGTCTGCTGCAGTCTCTCT | 94bp | (GCAG)5 |
| PM22 | C24109445 | TCAGCTGATTGAGCCAACAA | GGGGTTAAACAAGGCCAGAG | 96bp | (ATC)6 |
| PM23 | C24125823 | TTTGCTTGTCTTCTTTGTCAT | CGATTGTGAGCGAAACTGTA | 113bp | (TGA)6 |
| PM24 | C24184794 | CATAAAGGAGGTAATGATTAAA | GCTTCAGTGTTCATCTGACC | 81bp | (CAC)6 |
| PM25 | C24237809 | CGTGACGGGGATTTACTA | GGAGCGAAGCGAGTAATTCA | 96bp | (CCA)6 |
| PM26 | C24367025 | TCCTGGCACAGTGTAAAGAGAA | TGTGTGTGTGTGTTCATGC | 89bp | (AT)8 |
| PM27 | C24416107 | GTCAGTGGTTTTGTGGTTTT | CAGTGCTCATCTCATCTG | 101bp | (AC)8 |
| PM28 | C24463084 | TAGAAGAATGCTGCGGTCA | TCAGTCCATCAGTATTCTGTC | 97bp | (TCT)6 |
| PM29 | C24492749 | AGGTGTGAGTGAGCGTGTGA | GCTCGTCCCTACAAAGCTC | 92bp | (GAGC)5 |
| PM30 | C24518437 | ACCAACACACATCCTGTT | AAAACATTTGGACTAAGCAG | 107bp | (GT)8 |
| PM31 | C24529745 | CGAATAGGCATAGAACAGGTCA | TCCCTCTCATCTGCTTACTG | 101bp | (GA)8 |
| PM32 | C24543757 | AAGATTGTTATGGGGCATTAGC | CGGTGGTAATTGGCATTGTT | 97bp | (AG)8 |
| PM33 | C24579841 | ACAGCTCTCTTCTTTCCA | GAGCCTTTCACAGACCCAAG | 122bp | (GA)8 |
| PM34 | C24648821 | CAGTCTGCAGACAAGTCCA | ACCAGTTTGACCAGCTCCAC | 78bp | (GGCT)5 |
| PM35 | C24709698 | CCTACCTGCATGTTTCAGCA | TGGGTTAAATGCAGGGGTTA | 123bp | (AT)8 |
| PM36 | C24713072 | CTGCATGTTGTGTTGCTCACT | CCGATGAAAGCGTTAAGACA | 123bp | (GCT)7 |
| PM37 | C24736508 | TTATTAATGAGGCGCAGAA | GGTGCTGCACGTTCTTCTC | 98bp | (CA)8 |
| PM38 | C24748620 | AGAGACAGTTACTACTGAATGA | CTGATCAAAGCTGGAAACTCA | 114bp | (ACTA)5 |
| PM39 | C24781299 | CCGTAACAGGCTCGGTTTT | AGAGACAGGCTCGGGGAACA | 121bp | (CT)8 |
| PM40 | C24805186 | AAGGGTTAGCAATTTAGTTAACA | AAACCATCATGCGTGTGAGA | 117bp | (AT)8 |
| PM41 | C24835646 | TCATTAAGGCCCTCTCTTCC | ACAACAGAAGATGGCACTGG | 94bp | (CT)8 |
| PM42 | C24843358 | GAGACAGGGAAAACTGAGTAATG | AAGGCAAGAAGTCAGGATGG | 113bp | (CTG)6 |



TABLE S1 | (Continued)

| ID | Scaffold | Primer Forward | Primer Reverse | Size | Motif* |
|------|-----------|-----------------------------|-----------------------------|-------|---------|
| PM43 | C24847956 | TGAGATAAGTAAGTAATGGGTTTT | TCCATGGCAACATTAGCTTG | 93bp | (TA)8 |
| PM44 | C24855602 | TGTGTCTGAAGTCTTAAAGAGTAAAC | GCAAGATGGCAAACACAAGA | 81bp | (AG)8 |
| PM45 | C24879691 | CCGCTTCACACAAAAACACA | GGATGGAATGTGAAGGGTGT | 59bp | (CAG)6 |
| PM46 | C24895741 | CAGGCTTAATGACATAGATGTAACG | CCAGCATTTTATGCATTTTT | 91bp | (TA)8 |
| PM47 | C24912784 | GGAGCCAAGAGGAATTAGGG | AACCGACTGTTCACCTGCTG | 117bp | (TA)8 |
| PM48 | C24956419 | TCCTGAAGTGTGTTTTGTTTTG | GGAAAGCACCTGTTTTGTGC | 130bp | (AGT)6 |
| PM49 | C24957552 | TTGATACGAAAAAGTGGACACA | GTTACCGTGGCAACATCTGA | 100bp | (AT)8 |
| PM50 | C24981508 | GACAGTCAGAATTAGGACCAGACA | TGTGAACACAATCGTAGCTT | 125bp | (AC)8 |
| PM51 | C24996434 | TCTTAAGAACACAACCACATAAAAA | TCACAAATAATCAGTAAGCATGA | 72bp | (TA)8 |
| PM52 | C25078058 | CACACACACGCAGAACTGA | GCAGCCGATACATGATGTTG | 122bp | (CAA)6 |
| PM53 | C25097576 | TGTGTGCAAAGAAAGAGAGCA | GGGGTATTACACAACCTCTTTCC | 140bp | (TG)8 |
| PM54 | C25101964 | CACCTCATGGTCTGGCTTTG | CACTGAAAGCACTATTGACAGCA | 141bp | (AC)8 |
| PM55 | C25103136 | TCAGTATTGATGTGATTACCTTTTTGA | TTTTGTCCAGTTGTCTATTTTG | 124bp | (AT)9 |
| PM56 | C25121014 | TGATGGGGAGTACAGGTTTACG | GGCGTTAAACAAGTCCAGACC | 113bp | (GCT)6 |
| PM57 | C25130974 | TAAAAGGTGTGTGCGAATGC | CTTATCCCGCAACTTATC | 113bp | (AT)8 |
| PM58 | C25141490 | AACTGACCTCGTCCACATCC | AGAGGCAGCCAGGTTTCAGT | 114bp | (CAC)6 |
| PM59 | C25161988 | TCTTCTGTACGTCCACTGCT | CAGTCAATTGTTGGATTAAATAACA | 129bp | (TG)8 |
| PM60 | C25225336 | GAGACAGTCTTGGCTTTG | ACTCTGGGCCAGGCGTTTAT | 145bp | (CAG)6 |
| PM61 | C25228394 | AACTAGATGGCTGATTTCCCTTT | GATATGTGTCCCTGCTCCA | 73bp | (AC)8 |
| PM62 | C25278238 | TTTGACTCGCTGACTCATT | AAAGCAATGGGGTTAATTTTT | 83bp | (CTT)6 |
| PM63 | C25279688 | AGCAATTTTTACTATGAACACAAA | GATTTACGTACGCCCTGCTT | 81bp | (AT)8 |
| PM64 | C25292304 | AAAACAAGTTGTGAAACTGTATACCC | CAGCAGTTGTAGAACAACAGTTACAT | 145bp | (TA)9 |
| PM65 | C25303150 | TTTGGTTTCITTCACGATTCA | TTTGTCTGTCTGCTTGCTGTG | 114bp | (AG)8 |
| PM66 | C25310989 | TCAGCACATCAACAGTGCAA | CTTTGTGGGAGGCCTTAGT | 74bp | (TG)8 |
| PM67 | C25318456 | CTATTACGGCTGTTTCTTGG | CTCATCTTGAGGAAACGTTGG | 120bp | (CT)8 |
| PM68 | C25361238 | GACAAACACGCATACACAAAA | TCTCATCAACTTAGGTGCAGAA | 153bp | (TA)8 |
| PM69 | C25387478 | GGGGGTAAACCCATCATGTA | GCGTTATCCGTGCGTTAAT | 130bp | (GA)8 |
| PM70 | C25389218 | CAGGCTCTGTTCTGTGTGGA | GCACCACATATTGTTGATGAT | 147bp | (GT)8 |
| PM71 | C25397668 | CCATCTATCCATCCATCCAA | AGGTGGATAAGTGGTGGGTA | 135bp | (ACCT)5 |
| PM72 | C25435358 | AGAAGTGAATGAAAAATTGC | CAGTGACGGCATACTTGTG | 102bp | (GTT)6 |
| PM73 | C25438680 | AGCAAGAACTAGGTCAGTAGC | GCACAAAACACTGTGCCATA | 137bp | (CA)8 |
| PM74 | C25448220 | GTCCACGTGAGGGTCGTAAT | CGCGTGTGTTAGCAGTTTG | 143bp | (CA)8 |
| PM75 | C25457402 | TGACACAAGCTTTCTGTGAGA | CAGCAAGTCATCATGTGAAGG | 144bp | (AAG)6 |
| PM76 | C25465792 | TGTTGTGTGCTTGGCTCTG | GGGATTAATAAAGTTATCTATCGATCT | 147bp | (CAT)6 |
| PM77 | C25477203 | GAACCAAGGACTACATTGTTAAGG | GCTTTGAATCAATGAAAAGTTGC | 109bp | (TA)9 |
| PM78 | C25508043 | CCAAAGGGTTCAACCATCAT | AGCTGGTTCCACATCATCA | 111bp | (TAG)6 |
| PM79 | C25530725 | GGAGAGAGGACCTGCACAAC | GATGGTCACTATGCCGATCA | 161bp | (AC)8 |
| PM80 | C25557218 | GAAAATTAACACTGCCAGCA | GCTGATTAGGAGGAGGCTGA | 134bp | (CCT)6 |
| PM81 | C25573966 | AAAGCTAACTTTTGGCTTTTG | CCCACATGAGGAAACTGCAT | 87bp | (CAA)6 |
| PM82 | C25617962 | AAAGGAAGCAAAAAGTTACACACA | TGCAATGATGATATGTAACACACAC | 92bp | (GT)8 |
| PM83 | C25650429 | GACAGCTACACAGCAAACCTTA | TCCAATCACAGAACATAAATCAGG | 169bp | (TTA)6 |
| PM84 | C25650757 | AGTCCAGGTACAAACAAACG | CAGGTTCTAGGTTTTCATTTATTGC | 164bp | (TTC)6 |
| PM85 | C25653969 | CGTAGAATTTGCTGTGAGCAT | CTGTGTGTGTATGGCCGTGT | 141bp | (TG)8 |
| PM86 | C25655543 | TTTTTGCATGATGATGGATT | GCTATTTTCTCTTAATACAATACTAAA | 144bp | (ACA)6 |



TABLE S1 | (Continued)

| ID | Scaffold | Primer Forward | Primer Reverse | Size | Motif* |
|-------|-----------|--------------------------|-----------------------------|-------|---------|
| PM87 | C25669693 | CTCATTCTTGACAAATTGCTGA | GCCACACACACACAAGTACA | 106bp | (TG)8 |
| PM88 | C25672451 | CCCTAATGAACAAATCCAATGC | CAGCTTCCATGCTGTCTGTT | 158bp | (CT)8 |
| PM89 | C25693904 | GCAGTGCATGCCGATTAAA | GACTGCCTCTCAAATGTGCTC | 105bp | (CA)8 |
| PM90 | C25699156 | CCGTTACTCTGCAAGCTAGT | TGCTATAGGGCGTTTTCTCTC | 173bp | (AGCT)5 |
| PM91 | C25702614 | TTAGACATCCTCGAGCACCA | AAATCTATACAATTCATTGCCATT | 150bp | (TC)8 |
| PM92 | C25725018 | TCATGCATCCAAACATCTCC | GTTGTGAATGAGCCAGCAAA | 157bp | (CAA)6 |
| PM93 | C25729812 | ATCTTCTCCGCTCCCGAGT | CACAGCTACAGTACCCTTTTG | 137bp | (AC)8 |
| PM94 | C25737534 | TGAAGGAAAAGAAAAGGAGGAA | TATGCTCCGAGGCTGATCTT | 160bp | (AGA)6 |
| PM95 | C25746770 | AACCTCAAACCTCAAACATTACCG | GTGGCTACATGCAGACATGG | 149bp | (TTC)6 |
| PM96 | C25779040 | CGAATGTGTACCCTAGCCTGT | CAACATGGCAGCTTGGATTA | 121bp | (TA)8 |
| PM97 | C25789988 | TCTCAACCATTCCCACATTT | ATTGTGGCTGGGAATCAAAG | 123bp | (AG)8 |
| PM98 | C25795008 | ACTTGCGGCCTGTTTACG | GCGCTACCTTTCCGTGAC | 173bp | (GGC)6 |
| PM99 | C25816386 | AGCCACACCACAGAGTCACA | CAGGGCTAAAAATCCCTGAAA | 171bp | (CAT)6 |
| PM100 | C25823712 | CGGGGGAGTGTTAATCAGA | CCAGCTAGCACTCGACACCT | 195bp | (CA)8 |
| PM101 | C25824152 | GTGAGGAAGGGGAGGAGTCT | GACGAGGTTTAGAAATCCAGA | 179bp | (GAT)6 |
| PM102 | C25828544 | CGATTAAACTGAGGGAGACTCG | TCACGCTTAGATCAATTTTCCA | 158bp | (AGG)6 |
| PM103 | C25831970 | GTCCTTCTGAGGGAAAAGC | GAATCCGTCACGGGTAAAGA | 186bp | (CAG)6 |
| PM104 | C25838574 | TTCCTTGCACCTCTTGTCT | TTCAGTTGGGAAGTAGCTTAAA | 65bp | (GA)8 |
| PM105 | C25853757 | CACCGATTAGAACTGAAGG | ATGCAGAAAAATCGCAAACA | 177bp | (CG)8 |
| PM106 | C25858335 | GAGACAGGGAATAAGTTCTGCAA | TTTTTGTGGCAACCTGAGAA | 129bp | (AT)8 |
| PM107 | C25866791 | TTTCACATCTTCAGGGTCCA | TGAAAAGAACAGATCAAGTGAATG | 189bp | (AT)8 |
| PM108 | C25867901 | TGAAGAGGAGGCATATGGAA | CAACCCAACAAGGTATCAGTCT | 174bp | (GAT)6 |
| PM109 | C25893047 | AAGAGACAGGTTTTTATGTGTTCA | ATACCTGCCACCCCTGTA | 200bp | (TTC)6 |
| PM110 | C25893575 | AGCCATCTAGCTAGCTCTTG | GCGGGGCTAAAGACAAAAAT | 139bp | (CAA)6 |
| PM111 | C25925798 | TGTTTCAGGCTGGAGCAAC | CAGACCATAAATCTTTATTCTTATTC | 168bp | (TTC)6 |
| PM112 | C25951202 | CACCTAGAAAATGCCACCA | AAACATGAGGTTTATGCTATCC | 154bp | (CAAT)5 |
| PM113 | C25964882 | GGAGCCCACGCACTATAAAC | TTTCATCCACAATGGAAACAG | 127bp | (AG)8 |
| PM114 | C25965244 | GTGACCCCAAGCCAATAGAA | CATTGCTAGCTTGAAGAATGTCA | 148bp | (TA)8 |
| PM115 | C26002183 | CAAAGGAACCAGAAGTGGAAA | CCACAGAGTTGTTGCAATCG | 125bp | (CCT)6 |
| PM116 | C26009473 | GGTTATGCACAAAATATCCATT | TGAATTTGGTGTATTGGTGCTC | 160bp | (GAA)6 |
| PM117 | C26017003 | TGTGCTTGGTCTTCTAACCA | GGGGGTTTATAAGTTCTTTACGC | 187bp | (AG)8 |
| PM118 | C26022697 | TCCCTCTTTACAATCAGCATCA | AAGAGACAGGTTTACGGCTGA | 203bp | (CAC)6 |
| PM119 | C26026584 | GGAGATACGGAGCACGAATG | AGAGCCAGGTCTCATGTTCC | 207bp | (GA)8 |
| PM120 | C26047688 | TTTTTCCCTTCTAAGAGCAC | AGCGCATTAAAATCACAGCTT | 178bp | (GAT)6 |
| PM121 | C26049446 | AGAAAACGAAAAGCGCAAAG | GAAGTCAACACACACACATGA | 204bp | (TGA)6 |
| PM122 | C26069128 | GTGTGTGGGTGTGTGTGTA | GTGTTTGTGTGTGGTCAGCA | 206bp | (TG)8 |
| PM123 | C26077585 | TGACGACCTTATTCATGAGTTTC | ATGAGGTCAGCAACAACACG | 178bp | (GTT)6 |
| PM124 | C26080905 | GAGCCAGCACTCCTCACAGT | CAGTGCTTCTGAACAACATGC | 191bp | (TCA)6 |
| PM125 | C26094699 | ATCGGCCAATTACACAAAAGC | TTCAGATCACCCGAGAGAGTT | 204bp | (GGA)6 |
| PM126 | C26096281 | CTGTGACCATTACAGAAAACCTT | TTGCATAAAAAATGATGCATAATAAAA | 221bp | (TA)8 |
| PM127 | C26102265 | AGCCGTATGAATTGTTGAAA | GGGAAAAGGGAGAGGAAAAA | 210bp | (TCT)6 |
| PM128 | C26108233 | CTCTGTCACTCTCTCACCTCA | AAGAGATGGGGGCATAAAGC | 233bp | (CT)8 |
| PM129 | C26116593 | GAAATGAAACAGGCCAGGAA | TGTAGAAGAGTAGACCACGAACTGA | 186bp | (TC)8 |
| PM130 | C26136707 | AGACATGTTGCTGCCCTCCA | CTATAGAAAACAGAAGCGCTAA | 250bp | (TG)8 |



TABLE S1 | (Continued)

| ID | Scaffold | Primer Forward | Primer Reverse | Size | Motif* |
|-------|-----------|------------------------------|---------------------------|-------|---------|
| PM131 | C26152177 | TATAAGAGACAGCCTTGCT | AAGAGACAGGTGATGTTGCAG | 250bp | (CAA)6 |
| PM132 | C26158989 | ACCCTATGGTAAAAATATTAATTAGCTG | ACTAGGGTTAACTTGGTTAGCA | 250bp | (TGT)6 |
| PM133 | C26179896 | CACACTTCTCCTAAGCCGAAT | TCAGGCATGATATGCTTTGG | 250bp | (CA)8 |
| PM134 | C26184004 | CAACTGTATAAGAGATCAAATTTTC | GTGCTAACATATACATTGATAATCC | 250bp | (ACA)6 |
| PM135 | C26184142 | CTCGTCTCCATGTGTACCTCCT | CAGCTGATCACTCTGCCTGT | 250bp | (AAG)6 |
| PM136 | C26190892 | AACACTAAAGTGGCAATAACAG | CCAGACCAGACTAGAACAGGCTA | 257bp | (GCT)6 |
| PM137 | C26194819 | ACAGGCTTCGGACGTTCTTA | CTTCACAGGTCAAAGCTGAAG | 259bp | (AGG)6 |
| PM138 | C26197331 | AAGAGACAGGTGTAATCATAGACT | GTAGTGACCGTGGTGGCTTT | 262bp | (AT)8 |
| PM139 | C26221000 | GCCTTTAAACCCAAAAACCA | TGAAGCTCCTTCTGAGAAAACC | 254bp | (GTT)6 |
| PM140 | C26222656 | GGTTTTATCTGCAATTATTTAATGAGG | CCGTAACCTCATCACTTGACA | 276bp | (CAA)6 |
| PM141 | C26227738 | AAAAACCCCACTGAAAGCAT | GCCGTTGTTCTAACTAGTTTTGTTC | 269bp | (TACC)5 |
| PM142 | C26230062 | ACAGCTGCTTCTGTCTCCA | GTGGATGCCTCTGTTCTCGT | 250bp | (TC)8 |
| PM143 | C26231760 | GCAACAACATCAACAGCAAAA | CCACTGTGTAATCTCACTGCTG | 268bp | (GCA)6 |
| PM144 | C26232768 | AAGAGACAGGTGCAGGTTGAA | TTCCTAACATGATCAACAAAACG | 253bp | (GCT)6 |
| PM145 | C26240829 | TGGGTTAAACGCAAAACAATC | GAGACAGACACACTGGACTTTGA | 250bp | (CAG)6 |
| PM146 | C26242445 | TGTATTTACGAAAGGTGAAGG | TGATTTTACCACCTTTCTCG | 256bp | (GT)8 |
| PM147 | C26252131 | GCCCTGTGAATGAAATCCTAAT | CCAAGTACTTATAGACATCAATCAA | 274bp | (TAC)6 |
| PM148 | C26256787 | CACTGAACCAAATAAGGTCATTTAAA | TTTGGCTGTGTATTAGACTTACGG | 270bp | (TA)8 |
| PM149 | C26261641 | AGCTGGGTCCTGTCAGACC | TGCAGCTGCTTCAGACAAGT | 266bp | (AC)8 |
| PM150 | C26265867 | TATGACCGACTCCAGCATCA | CGAACAGAGAGACTGCGAGA | 284bp | (AG)8 |
| PM151 | C26266911 | TGATGTCCCTAAACCCCGTA | GAGAATGGATCATGCGCTTC | 261bp | (CGTG)5 |
| PM152 | C26268097 | TCCTCTCACACTGGAACAA | CATTGCAGTCATCCATCAGT | 276bp | (GA)8 |
| PM153 | C26274625 | CAGGTGTAGATTTGTGCGTCA | AAACAACAGCCTTTCATAAGTGTG | 258bp | (AC)8 |
| PM154 | C26277657 | CCATGTCTACAGATGAGATAGA | AAGAGACAGCCTTCAACCTCT | 305bp | (GT)8 |
| PM155 | C26279835 | CAGGTCTGAACGAAGGCTTTT | CAGCTTCTGCATAACGTTTC | 253bp | (AC)8 |
| PM156 | C26280433 | GACCTTCAGACATCTTAGGAACAGA | GTGCACCTTGCAGCCTTGTA | 250bp | (ACA)6 |
| PM157 | C26283585 | AGCTGGTCACTTTGATTAGGC | ACGTCAGCTAATGGCTCCTG | 277bp | (AGA)6 |
| PM158 | C26285877 | GAAGTCATGCCCTTCTACCG | CAGTGCAAGTGTGTTTGTGCT | 304bp | (AGA)6 |
| PM159 | C26287023 | GCTTGTGGAGGAAATGGAAC | CACAGCAAAGCAGATCAATCA | 266bp | (ACA)6 |
| PM160 | C26308317 | GGCTGATCAATGCATAAGCTG | GCATTGTCCACATGTCAGGA | 299bp | (TA)8 |
| PM161 | C26309243 | ACTAGCCTCTGGGCTTTCTG | GCCAATCAGGACAGACAGGT | 296bp | (GA)8 |
| PM162 | C26312417 | CAGAACCCTCCTGTTCAACC | CCAACACCGTCACTCCTAACT | 266bp | (TTC)6 |
| PM163 | C26318957 | GAGCTTGATAAAGATACAATTGCTGA | GACGCTCCGAAACCATTITAG | 274bp | (TTG)6 |
| PM164 | C26324223 | GGCTGGCACAGATTTACACC | CTGTGGCAAACGTGAGAAGA | 298bp | (AG)8 |
| PM165 | C26324305 | GCTGCCTAATATATCCACACCA | GTTATACTGCGGCAGGCTGT | 296bp | (TAA)6 |
| PM166 | C26324379 | TCAAACAAGAAAAGCAACAACA | CAGCAGCATGTCCATCCTTA | 301bp | (TGT)6 |
| PM167 | C26328399 | AGAGGAAAGGACCTCCAAA | TGGATCATCAGGTTTACACACA | 295bp | (ACC)6 |
| PM168 | C26336157 | GCGAAAATCGCAGGTTTCT | ACGCATATTCACGCACAAGA | 260bp | (AT)9 |
| PM169 | C26338609 | AAAGGGCAGACGTAATGGTG | CCCAGCTTGTGTCTAAAATTGG | 297bp | (AT)8 |
| PM170 | C26343581 | TGGCATCTTGGAGTCATGTG | TAAATTGTGTGCGAGCTGGA | 303bp | (TC)8 |
| PM171 | C26344461 | AACACGCATTAAGTGACCTG | CACGTATGAACTCACGTCTGC | 290bp | (TAG)6 |
| PM172 | C26349879 | TGGCAATGTGTCTCTTTGTT | ACCGTCCAGTTCTCTGACCT | 312bp | (AT)8 |
| PM173 | C26351741 | ATGCACATGGTCAGCAACAG | TCAGGCATGAAAAATGAAGC | 347bp | (AG)8 |
| PM174 | C26360957 | AACACGAACCAACACATGGA | TGCTTTACTGTTTGTTCGGAGA | 291bp | (CAA)6 |



TABLE S1 | (Continued)

| ID | Scaffold | Primer Forward | Primer Reverse | Size | Motif* |
|-------|---------------|-----------------------|----------------------|-------|--------|
| PM175 | C26364309 | AGCAGCTTATGGGTCTCTGC | AGCAGAGGGCCTTCTCTCTC | 336bp | (AT)8 |
| PM176 | scaffold10808 | AAGTCTGGTTTGGTTGTTGC | GCTGCAGCAGAAGAAATTGA | 310bp | (TA)8 |
| PM177 | scaffold10976 | CCATTACACAAAAGTGGCATT | CITTTCTTGGCTGCCATTTC | 314bp | (AT)8 |
| PM178 | scaffold8450 | CACATTCCACACAGACGA | CAGACCCGAAAAGTGTAGCA | 256bp | (TG)8 |

Neotropical Ichthyology



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- **Farias RS, Silva BCNR, Nascimento WVG, Silva GC, Luz RK, Prosdocimi F, Figueiredo RACR, Carvalho DC, Coimbra MRM.**
Genetic diversity and aquaculture conservation for a threatened Neotropical catfish. *Neotrop Ichthyol.* 2020; 18(3):e200028. <https://doi.org/10.1590/1982-0224-2020-0028>