Additional file 3. *Trachymyrmex septentrionalis* polymorphic microsatellite markers analyzed for *Trachymyrmex pomonae* ants/cross-amplification. Details include: marker information, primer sequences, repeat motif, annealing temperature (Tm), size range of observed alleles given in base pairs (bp), number of individuals genotyped (N), number of alleles observed (K), observed heterozygosity (Ho), expected heterozygosity (He), and probability of identity (PI). Superscript a indicates deviation from Hardy-Weinberg expectations after Bonferroni corrections, superscript b indicates no Hardy-Weinberg information, and superscript c indicates the marker shows evidence of null alleles.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Marker | Primer sequence 5' -> 3' | Repeat motif | Tm (°C) | Size (bp) | N | K | Ho | He | PI |
| Ts11 | F: GCAGATACAAACGTCCTACGTGC | TGCG | 66.4 | 278-294 | 6 | 2 | 0.83 | 0.49 | 0.38 |
|  | R: CGCACATTTGTGACGGACG | | |  |  |  |  |  |  |
| Ts13 | F: CGAGAGATAACGGACGTTGC | AACG | 64 | 432-452 | 6 | 3 | 0.67 | 0.49 | 0.33 |
|  | R: ACGTGTGTTCATTCGTTGCC | | |  |  |  |  |  |  |
| Ts21 | F: CCATCCCAACCATCCTGG | AGCC | 65.2 | 300-308 | 6 | 3 | 0.33 | 0.49 | 0.33 |
|  | R: TTACGATCAGGAGAGCGTGC | | |  |  |  |  |  |  |
| Ts32 | F: ATAACAAGCGGCAGCATCG | TTGG | 59.4 | 206-218 | 6 | 3 | 0.83 | 0.57 | 0.25 |
|  | R: ATTTCGAACTCGCCGGTAGC | | |  |  |  |  |  |  |
| Ts35 | F: TGCTCGATTCGGACACGG | ACCG | 60.5 | 196-288 | 6 | 3 | 1.00 | 0.57 | 0.28 |
|  | R: CTCACAGCGGAGACAAAGGC | | |  |  |  |  |  |  |
| Ts38 a,b | F: AGACTGCTGGCTACGCTCG | ATAC | 60.5 | 258-270 | 6 | 3 | 0.00 | 0.67 | 0.19 |
|  | R: CGTGGTGACACTCTCATTTCG | | |  |  |  |  |  |  |
| Ts39 | F: CTAACAAGATGCGCAGCCC | TGCG | 61.3 | 238-250 | 6 | 3 | 0.17 | 0.40 | 0.40 |
|  | R: TCGAATAATCCAGTCGTGTCG | | |  |  |  |  |  |  |
| Ts41 | F: TTAACGTCGGCATAATTTCGG | TGCC | 61.3 | 194-196 | 5 | 2 | 0.00 | 0.48 | 0.39 |
|  | R: CAATTGACTACGCAGGAGCG | | |  |  |  |  |  |  |
| Ts44 | F: GCGCGAAATTGAAGAGTAAGC | TGCC | 60.5 | 256-304 | 6 | 2 | 0.17 | 0.38 | 0.46 |
|  | R: GCGAACGATCGAGTATGACG | | |  |  |  |  |  |  |
| Ts45 | F: CGTGTCAAGTATGTTCCCGC | TGCG | 61.3 | 166-202 | 6 | 3 | 0.17 | 0.40 | 0.40 |
|  | R: AGTTTCAGGCGCAGGTAGC | | |  |  |  |  |  |  |
| Ts46 | F: GTACGCACATCGTGCTAAACG | ACCG | 60.5 | 314-338 | 6 | 4 | 0.67 | 0.65 | 0.17 |
|  | R: AGCGGTGGTGGTTTCACG | | |  |  |  |  |  |  |
| Ts7 b | F: GAACTTCCCTCCCTCGAACC | TGCG | 61.3 | 198-202 | 6 | 2 | 0.17 | 0.15 | 0.73 |
|  | R: TGAACGTGTAAAGATTGCATACAGC | | | |  |  |  |  |  |