**Supplementary table S1**. Forward (F) and reverse (R) primers sequences for each marker locus designed for *Ilex paraguariensis* from whole-genome sequence data

|  |  |  |
| --- | --- | --- |
| Locus | Primer sequences (5′−3′)Forward | Primer sequences (5′−3′)Reverse |
| *Ip100.1* | AGTCGCCACTGTTCTGTTCG  | ACCACAGAGTACTTTACGGGC |
|  *Ip100.2\** |  CAACTTCATGCCTCCACGTC | CCAACTGCTTGCTAAGTCGC |
| *Ip100.3* |  GAGAGGTGGGTGGGTTTCTG | TGCCTTTCCATTCTTCTGCAC |
| *Ip100.4* | GGGTTTCAGGAATGTCAAGTGTC | GTACCGGCATCCACTAAGGC |
| *Ip100.5* | CTGTCACTCCCAATTACGTGC | TGGTTAACTTCTAGAAATGCTGGTG |
| *Ip100.6\** | GCGGAATAGTCATCCATTTCTGC | TTGCTCCGTCTGTGGTTAGG |
| *Ip100.7* | GCCTTCGATTGACTGACTGAC | TTCGCTCATCTCAGTGCCTC |
| *Ip100.8* | GACCACATTCCTATGCACACAC | AGAGCTTTCAATCAAATGGCCC |
| *Ip100.9* | AAGCAGTCTCCTTCAGTGGC | GTGGCCGAACTTTGAGAACC |
| *Ip100.10* | GGGTCAAAGTCGGGATTTAATCAAG | GCCTTCTCTCTCTACACTACTCC |
| *Ip100.11\** | ACACAATCTGATGCTGCGAAG | GTCATGTCATACAAGTGAGCCC |
| *Ip100.12* | ACATGAATAAATGACAGAGCCCG | GTTCGGAAGTTGCCATCTCAAG |
| *Ip100.13* | GGTCACTGCTCAGAGAGAAAGAG | CCATTGTATAGCTCACACACTGAC |
| *Ip100.14* | TGACACACTGTAGGGCCAAG | TGGCTCCCGAAGATCTGATTG |
| *Ip100.15* | TCCACCTCTACCTCCACCTC | CGCATGCCATCAAACAAAGC |
| *Ip100.16* | CTGCAGACAGTTTGAGCACAC | TTGTTCTTTGGGCTTGACTTTGC |
| *Ip100.17* |  ACCTCCACCTCTACCTCCAC | CGCATGCCATCAAACAAAGC |
| *Ip100.18* | TTCCTACCAGAAACACATTGCAC | TGCAGTATTTCCATGCACTTTCAG |
| *Ip100.19* | CACAAACACCCACCCAACAG | TTGAGCCAGAGATGGAAGCC |
| *Ip100.20\** |  ACCTTAACACTCCATCCATTTGC | TGGCAGGAAATTCGGGATCTC |
| *Ip200.1* | ATTCATATTTGTGTGTGTTGTGTGC | TCTGTTTCACTTATTCTCAACTGCC |
| *Ip200.3\** | AGGCTCTCTATGTCCGCTTG | TATGCCGCAGAGATGGGTTG |
| *Ip200.4* | CCTTGTTGCTTGACTAGACATGTG | AAGTGGCCAGTTTGCAAGTG |
| *Ip200.5* | CATGTTTCCCAGGTTTGCGC | TTGGGAAGAAGTGGCTGAGC |
| *Ip200.6* | TGAAGGCTCTCTATGTCCGC | TATGCCGCAGAGATGGGTTG |
| *Ip200.7* | CATCAGCTCACATAATCACTCCATC | GCCACGCACACATAACACAG |
| *Ip200.8\** | GCCTCACTTCTCTCCATCCC | ATGTGTGTGTGCATGCGTTG |
| *Ip200.9* | AACAAGGGAATCGCACTCAATG | ACCCAGCCATACTCAGGTTG |
| *Ip200.11* |  GGCTGAGCGAAGATTTGACG | GCGCCCATCAATGACACAAG |
| *Ip200.12* | TACAGAAGTGCTAACAACAGGGAG | ACCGAGGCCAATTATAGTTACTCC |
| *Ip200.13* | AATGAACTTTCCTTCCAACTCACC | CAGTAGTTGTAGCGTGACTTTCG |
| *Ip200.16* | GCTGAAAGGTGCATTGTCTCAC | ACAGATCATTTGAGAGGGAAAGGG |
| *Ip200.17\** |  GTAGCACGTTGTAGGCTAAGC | TTCGATCTTTGAGATTGTGGCG |
| *Ip200.20* | TACATTGACTCTGCCTCCGG | AGCCCTGTCCAAACCTAAGC |

\*Locus used in multiplex amplifications



**Supplementary Figure S1.** Map with the locations of the Uruguayan populations of yerba mate included in this study. The 12 populations included in the diverse panel (one individual per population) are represented by black circles. For the population level analysis, Population Demicheli (DM) is represented by a blue circle, population Gruta de los Helechos (GH) by a yellow circle and population Tapera de Ayala (TA) by a red circle. The scale bar represents 100 km. Samples were collected by Pablo Hernández, Joaquín Garrido, Gabriela Jolochin, Luis Rodríguez and Rodrigo Olano