**Table S2.** Single nucleotide polymorphisms (SNPs) used for analyzing the cacao populations

|  |  |  |  |
| --- | --- | --- | --- |
| SNP ID | SNP form | Linkage group | Haboring sequences |
| Tcm001s00947643 | A/C | LG1 | TtCTTCAtAGCTGGTATTCTCTGATATTAGaGATATCGAGCTTGGCCGCTTtATTAATGG[A/C]AGAGATGGGCTCTCTAGCTGAGGAAGctCTACGAACTGATCAGAGTGGATGAAGTTTAGA |
| Tcm002s20575712 | A/G | LG2 | ATATGAATCATTAGCCTCTGAACCCCGACGGCATATGTGGTGCTTTACATGACTtCTTTT[A/G]ACTATATCATCATTGTCATCATTTGAAGAATCAAAAGATTCTAAATCTGATCTTGAATCA |
| Tcm003s01336581 | A/C | LG3 | TCTCTGCCcTCTtGTTtCTTGGATTGTTCTGCACTTGAGCATCATTCTTCACCTGTGGAG[A/C]AACAGACTCAACCACCAATTTGTGGCTGACTTCTTCAAAAGCCTCAGCTTtGTTATGTGA |
| Tcm003s34112745 | A/C | LG5 | GCtACCCTTTTGAaaTTYTGTCCCAATTTGCGAGAGATGTTGTAATTGTAGAATTGCATC[A/C]GCGGTGTCGTCGTTCTAAGGGGTTTCGAGATAAACGGTGAAGGTGAAGGTGAMGGTGGTG |
| Tcm006s26664133 | A/C | LG6 | TTGGAATTTAAACATTCATTTGGAAGCAAGAGGCAAAAgAAGGGGCAGTCTAATTCGATC[A/C]TATTCTACAGACCACGACCATTACAAGCCAGAAAAGGAAaGACCCATCAAGACTCCATAG |
| TcSNP23 | T/C | LG8 | AGGTTGTGGGTGCAAGGAAAGATGAATTGCAACAGAAAATAACCTCGCATTCTAGCATGC[T/C]TGCTTGATGCAGAGAAGCATGAATCAAGGTTTAGTTGTACTCCTTGAAGTCTGATTTCTG |
| TcSNP25 | C/G | LG9 | TTTATGTTACTAGTTTTTGTTGGGTGGTTGTCTGTTTCTTGTTTGCATTATTTTGTGGAC[C/G]GGACCTTAGTATATCCTGCTTGTTTGCTCTGTTTTTTGTTCAGTAGTCTGGGTTGTTAGT |
| TcSNP32 | A/T | LG4 | TTCCACTTTTGTCAATATAGATCAGTCATGGATGATATTGTGCAAAAATAATACCATAGT[A/T]CTAAGAAATCATGCACATTTTTGTAAATAGGAAGAATCTGCCATGGTAATGTTGTGTTGA |
| TcSNP42 | A/G | LG1 | TTCTTGGAGTCAAACCAACACCCAAGAAGGAACTTCTGGGTATTCCTGTTATAACACATG[A/G]CAAATCCTTAAAGGTGCCAACTAAGTTCGATGCTAGAACAGCTTGGCCACAATGTAGCAC |
| TcSNP122 | T/C | LG2 | AGATCAAAGAAGCTCCCAAACGTGAGGATGAGAAACAACAGTGAAGTCACTAATCCTCGT[T/C]GTAGTATTTTACTTCTCTGGTTGTTTTTGTATGGAGAAGTTGCTTCGTCCCMCAATCGCT |
| TcSNP144 | A/C | LG10 | ACCGACACAGGATTCACCGTGAATGGGGTCAACTATGAAGGCAGCTTGCTATGTGTGGGA[A/C]ATTTGCTCACTTCTTGGGTTCCCAATAAGTTTTCTCAAATTACTCCCGACAGCTTATCTA |
| TcSNP150 | T/G | LG5 | ATACCCTTCGACGACTACTGCTGACTTGGGAACACCCACCAGCGTTTTGCCGGCAACATC[T/G]GGTGACTGGTCTGATTTTTCCTCTAATTTTTATCTAGAACTTTGTCAAGCGTTTAAAATA |
| TcSNP172 | A/G | LG9 | TCTATCATAAGGTCTTTTTTCAGGTGACTCTTCTTTGGATGGACATTTGTCTTTTGTTAG[A/G]TGCTTTGATTTTGATCTTTATTAGTAGGTTTTACAATCTACTTGTGGATCAAACTCCAAA |
| TcSNP226 | C/G | LG9 | AAGCCCAAGGCCCAAGAGCTACGCGATCCGAAGGCAGTGAACCAGGCGCTGAGGTCGGGG[C/G]CACCGGTCCAGACTATCAAGAAATTCGATGCTGGTTCGAACAAGAAAACCGAGGGGCCGG |
| TcSNP230 | A/G | LG10 | CAGCAGAGGCCGAAGACAAAGAAGGGGAGAGGATGTGATCCATCCCCTCAAGGTTTCTTT[A/G]GAAGATCTCTACAACGGAACATCCAAAAAGCTTTCTCTTTCACGCAACATAATTTGCTTC |
| TcSNP242 | T/C | LG9 | AGCAATCTTCCTCCGCCAAACAAGCCATCAATCAAACCCTCGTTCCTCTGTCTTCGCCTT[T/C]CTCTTCGTTGCCGTCATCGTCATCGATCTCATCATCTCCATTTTCGGGTTCCTTGCCAAT |
| TcSNP288 | T/C | LG6 | TTTGGGGTACGATTATCAAGGAGTTGATGTTCCATGGCTTAAAACTAAGCCAGTTCCTCG[T/C]AAGTTTTCCAAGAAAGGGGGAAAGGGTCATGGTCAGGCAGTGGCAGCCGAGACAAAGAAC |
| TcSNP316 | A/T | LG2 | CAAGAGTCGGTTCAAGAAATCGTACGGGTCGCAGGAGGAGCACGATTACAGGTTCAAGGT[A/T]TTTCAGGATAACTTGAGACGTGCGGCGCGTCATCAGAAGCTTGACCCGTCTGCGAGTCAC |
| TcSNP372 | A/T | LG4 | GGAAATTCTGAAGATTGTGAAGGAGAACTTCGATTTCAGACCTGGAATGATTTCTATCAA[A/T]CTTGATCTTAAGAGGGGTGGCAATGGCAGGTTTTTGAAGACTGCTGCCTATGGGCATTTT |
| TcSNP375 | A/G | LG8 | CATTTCATTTGGAGTAAATCTGCTTCGACGATGATTTCTGACTTCAGACTACTGCAATCT[A/G]CTTTGCTACCTTCCTCTGCTTTTGCCTTTCGCTTTTGGTGTAGTTGACATAGGCAATAAA |
| TcSNP413 | T/C | LG3 | CGCAGTTTTCTCAGTTTCGGGCAATGATTCTAGTTATATCATGAAACTAAGTTCTTAGGT[T/C]GTTATTATGAGCCTATGCATACAGCATACGTAATGCGGAACTGTAGTTGATACTTTATGT |
| TcSNP418 | A/G | LG1 | CAATTCCCTTTCCGGAAAAATCCCACAACAGATAGGGAATCTCCAGAAGCTCACTGTCTT[A/G]AACCTCGCAGACAATAAGCTAAGTGGAGAGATCCCAAGCTCCTTAGTTCAACTCTCCAGT |
| TcSNP448 | C/G | LG4 | TTTGGCTGCAAGGAATTCTAGTTTGATTTTACCCGAGTTTTACAAGTTCTTGAAGGTACT[C/G]TATTACCTTTACTATCCTAGATTCTAAGGCTGCTGTTATTCTAATTCTACCCCAAGAAGA |
| TcSNP469 | A/G | LG7 | AGCCATGGCTCCGAGATCAAAAGCCAGCCCGGTTAACCCGATTTCCGACCCGACTTCCAG[A/G]GAGATCCGTTACCGCGGCGTTCGAAAGCGCCCATGGGGCCGTTACGCGGCGGAGATCCGG |
| TcSNP521 | A/C | LG2 | GATTCTGTGAACTATAGCACCAAGGAAAAGAAGGCCAACCTTAAAGAAAATCCTTTAATA[A/C]ATACTACTGACTGGTATATGTATCAGAAACAAAAAAAGAAATAGTAGAAATTCCAATGGC |
| TcSNP529 | A/C | LG1 | ATAGGCCTTGAATGACTTCATCTCCTCTGTCACCTTCACAAGCTCAACAAAAGGCTTCTC[A/C]AGAAAAATAGGCATGTATGGTCCTTGCACTTGGGTTGCAGTTGCAAGCTCCTCGGCAGTA |
| TcSNP534 | T/C | LG1 | TGTAAAGAGTGCCATTGTAAGTGGATGCAGCGCCTTTTAAGCAATGGTACCTAGCA[T/C]TATGGTGGACATTGGGAGGAAGAAGAAAACAGCAGCTAAGAAGGAAGCTACTGAGGAA |
| TcSNP547 | A/G | LG8 | AGAGCCTTTCGCTTCCTCATCTTTCTCTCTGCGACTGCGTTTCAGTGTTGGACTGAGTTG[A/G]AAGGAGGATGGCGGTTCGTAGGGACAAAGGGCAGTCAATCCGCGGATCTCGAATTGCTAT |
| TcSNP560 | T/G | LG10 | GAGGCAGAGAAATACAAGGCCGAGGATGAGGAGCACAAGAAGAAGGCGGAGGCCAAGAAT[T/G]CTTTGGAGAACTACGCCTATAACATGAGGAACACTGTCAAGGATGAGAAGATTGGCTCAA |
| TcSNP591 | A/C | LG1 | GGGCGTCGAGAAGACTTCGGCTGCTATTAAGGTCTTGAAACAGATCGGGGCTTATGCGGA[A/C]GTCGAGAAGGCGAAAGATAGCCAGGCCATTCGTCCCGGAAAGGGCAAAATGAGGAATCGC |
| TcSNP602 | T/C | LG6 | CCATGGTTTCCGTATGGCACTGTGGTATGAGCACCTTGGCATGCTTGATGATACCTTCCT[T/C]TTTCCAGAAAGTGAGGAGTGTGTCAGGAAGGTGAACCAGATTGCTGACAAATATTGGGAT |
| TcSNP606 | A/G | LG7 | ATGTGTACAAGTTCACATGTTGAGTGAAAACTAGAATTTCTGTGTGTTAAGCTTGTGCCT[A/G]CATAAAAAGGATAATTGTACAAAATGTTAAAAAGAATAATTTGTGCTTTGCAACGTTTAA |
| TcSNP619 | T/C | LG6 | GAACAAAAATTGTAAATTAATCTTATGCATGGAGTAATGACCCCACAGCTTTGCAACACC[T/C]CAAAAATGGTGGTTGTCCCTTTGTACATAATGATTCTGGGATGAATCATTTGTCTTTGTA |
| TcSNP645 | A/G | LG5 | TGAAGGCACTGGAGCCCTTTGTGAATTGGCTGGAGGAAGCAGAAGAAGAGGAATAAGTGC[A/G]ATAACAATAATATTATGATCACTTTGAAAAGAAAAGGGGTGAACCCTGTACTTGTTCCTT |
| TcSNP709 | T/C | LG1 | GGCATTTGCAGATGAAGTTGGCATACCTTTTATGGAAACCAGTGCAAAAGATGCCACAAA[T/C]GTGGAACAGGCTTTCATGGCCATGGCTGCTTCCATCAAGGATAGAATGGCAAGCCAACCA |
| TcSNP723 | T/G | LG10 | AAATTGGAACCCCACCTCAAACCATGCTCATGGCCATGGATACTAGCAATGATGCTGCTT[T/G]GTTACCTTGCTCAGGCTGCCTTGGCTGCTCTTCTAGTGTTTTCGACAATGCTAAATCAAC |
| TcSNP731 | A/G | LG10 | ATTTACAAGGCTAAGGTGAAGAAGAATGGCTCACACTATCGTTGCATTTGGGGAAAGGTT[A/G]CTAGACCTCATGGTAACAGTGGCGTTATTCGTGCTAAGTTCAAGTCTAACCTTCCCCCTA |
| TcSNP751 | T/G | LG5 | AGCATTTCACCATGGCCATTTTCTTGCTTCCTTGCTTGCTTAAGCAGCTTGAGGGGTTCC[T/G]TTCGTCTGTGGATGCAACTGGAGTTCCAAGTCATCTTTCCCGTCTTTCTCCCTAGCCTTT |
| TcSNP823 | A/C | LG5 | AGGTATTGAGGCTAAGCAGCCAAACTCTGCTATCCGTAAGTGTGCTAGAGTTCAACTGAT[A/C]AAAAATGGAAAGAAGATTGCTGCATTCGTTCCAAATGATGGTTGCTTAAACTACATTGAA |
| TcSNP836 | T/C | LG2 | AAGGGTAATCCCATGTGGAATCAGCTATCAGTGCCATCTTCCACCATGTACTCATGGGAC[T/C]CCAACTCAACCTACATTCATGAGCCTCCATACTTCAAGAGTATGACCATGGAGCCTCCTG |
| TcSNP872 | C/G | LG4 | AGTGATGTTGCACAGGTCACAAAGCTTCTCAACCTTGTTGCCAGTCAATCCAAGAGGTCG[C/G]AGATCCCAAAGAACAAGGTGGTTCTCAGTTCCCCCAGTTACAAGCTTGTATCCCTTGCTC |
| TcSNP878 | C/G | LG3 | CCTCGAGTCGACTCGGCCGACACGGGCTTCGACTCGCCCGAGTCTACTATCGTGGAACCC[C/G]ACCTGGATGACGGGAATGTTCAGTCGCCGGAGGTAAAGCGTATCCAGGAGGATTTGTTGA |
| TcSNP899 | A/G | LG8 | GGCGCTTATTTACAGTTACAAGACGGCTGCTAGCGGTTTCTCCGCCAAGCTTACTCCCGA[A/G]CAGGTTGCGGAAATCTCGAAGCAACCCGGCGTTCTTCAGGTTGTCCCGAGCAGGACTCTC |
| TcSNP917 | T/C | LG10 | TATGGAAACTGGGTAAAGGCTCAAGAATGGGCGGCAATTCCTGGTGGACAAGCCACTTAC[T/C]TGGGCAACCCTGTTCCATGGGGTACCCTCCCTATCATCTTGGTCATCGAATTCTTCGCCA |
| TcSNP929 | C/G | LG3 | TGAAATGGAAATGAAAATACAAAAAACCAAGTCATGTTCAATAGCAAGTGATGTCCTTTT[C/G]TCTGCTGATTATAACAGAAGTTGTGTTAATTTTACACTTAGTTGATGTGGTTTTAAAGGG |
| TcSNP944 | T/C | LG7 | TGACATGCCCCCACTGGAGGATGCTGATGCAGAGGCCGAGGGCAGCAAGATGGAGGAAGT[T/C]GACTAAGCCTGACATRTTTTAATGTTTGAACTTTATCTTTATGTAGTAGTCTCATTTTAA |
| TcSNP953 | A/T | LG4 | GGGTCTCTAAATGGCACTTGAGGTTGCCAGAGATAAAGCTTCATTCATGCTCCAAGCCAA[A/T]TCTTTGGGCATTCCAGGGTCAAACACCTCAAAAACAAGTTTCTTTATGGCTCAAATCATG |
| TcSNP994 | T/C | LG6 | AACAAACCGAAATATATTCTAGGGAAACTTTGCATTTGCAACCCCTATTTGACTTTCGAT[T/C]TGCTCAGATCTGCTTTTGAATCCTCAACTTCTGAATAGTCAAYATGGGAGGAGGGTTCAG |
| TcSNP998 | A/G | LG5 | AACAAGAACAAGGGAATGGGGACAATATGATCCCACTAGACATGATGGCTTTTCCTCCTC[A/G]TAGTAGTGAGAAAGGAATAACATAGAATCTAAGCTGTCACAGATGTCTCCACTGCAACCT |
| TcSNP999 | T/C | LG8 | ACTGGGAGTAAACAAAGCAAAATCCCAATCATTTATTGGAGTAAATTATGGGCAAGTGGC[T/C]GACAACCTACCGTCACCGGCAGCCACTGCAAAGCTTCTCCAGTCCACTTCAATCCAAAAG |
| TcSNP1034 | T/C | LG4 | CTTCAGCCAGCACTCAGCAACTAGGAAGTGAGCATTGCAGTTTTTGTTCTTCATTTTTCT[T/C]GCCTCCTGGTTTGAATTGCCCCGGTTTGCTTGTTGAGTCACTTCATCTTAAGTTCATAGA |
| TcSNP1038 | A/G | LG5 | GTCGACACCTTCAGACTTCAGGAGCAACCTGCTTTTGACAAGAAGCAGTTTGTAACCTTC[A/G]TGAAGAGGTACATCAAGAACTTGACACCCAAATTAGAGCCAGAGAAGCAAGAGTTGTTCA |
| TcSNP1041 | C/G | LG10 | CAATGTCCAGCCTGATGCAGTTCTGCAGACTGTTTCAAAGACTGGAAAGAAGACTACCTT[C/G]TGGGAAACAGAAGCTCCAGCAGAACCCGAGGCAAAGCCTGCGGAAGCTGTTGCCACAGCT |
| TcSNP1060 | T/C | LG2 | CAGTTCTTGATTTTGAGATTGAAGTCCTAACCTTGCACTGAGTACTTGGCACTTGGTAAC[T/C]GTTGGAAGAATATGTAGCCTGAATAAGTCACGTGCCATGAACATATATGGATATTATCGG |
| TcSNP1062 | A/G | LG3 | ATGCAAGAGGGAACTCTGGAGAGTTCAGTATGCTCTAAGCCGCATTCGAAATGCTGCAAG[A/G]GACCTTCTGACCCTTGATGAGAAGAACCCACGTCGGATCTTTGAGGGTGAGGCTCTTCTT |
| TcSNP1075 | A/T | LG1 | TTATGGCAGCATGCACTTATAATTTATGATTGCAACCCAACTGATACATAAATG[A/T]GTAGTAGGCCTGTATAGATGAATTACGAAACAAAGCATGAGAGTGCATGT |
| TcSNP1096 | T/C | LG1 | CATTATACTTAGGATCAATGTTAAGGCGGAAATGGGCTTCAGCTGACTCAACAAACTTTG[T/C]ACTTGTCATTTCCTTTAACAATGATATTGCTGTCTTTAGATCATACTCCTTTTTGTTTTC |
| TcSNP1111 | A/G | LG5 | CCATCAATGGTTGCTGCCTCGGCAGTGTATGCTGCTCGTTGCACACTGAACAAGACCCCA[A/G]CTTGGACTGACACACTAAAGTTTCACACTGGATACTCTGAAGCACAGCTAATGGAATGTG |
| TcSNP1126 | A/T | LG7 | CGTCTTCAAGGGAACTTACAAGAGTCTGAGGACATTGATATTGTGGCACTAAAGAACTAC[A/T]TGGATGCTCAGTACTTTGGTGAGATTGGTATTGGCACACCTCCACAGAACTTCACTGTGA |
| TcSNP1144 | T/C | LG6 | GGTTCGGACTTTGTGGATCGGAGATTTGCAGTATTATATGGATGAGAATTATCTCTTGGG[T/C]TGTTTTGCCCAAACTGGAGAGGTTGTTTCAGTGAAAGTTATCCGTAACAAGCAAACAGGC |
| TcSNP1165 | T/C | LG2 | GATCAATTGCTTAAACATATTTGCATAGCATTATAGATATTTTCAAAACCATGATGGAGG[T/C]TGCCAAGGTTTTCCTAGCTCTTACTTGTCTCATGGCCTTAGCCTTGGTCCTCCCCTCCCA |
| TcSNP1175 | T/G | LG4 | TAAGGCTACATTCGTGGTGTTTGTCACGGACGGATATGGGTACGCTCAAATGGCTTGCCC[T/G]CATCTCTCCAGACAGAGCCAGGGATCCCAAAGTGGAAGGCAAGACAGAAGAGAACAAGAA |
| TcSNP1253 | T/G | LG9 | CACTTGCCACTCAAGTTCCTCACTAAAGCATTGAAACCAGCATCAGAAGTCTGATTTCTA[T/G]ATTACCAGCACTTATCAAACTTCTTTCAATCAGGATAGGTGAGTAAAGAAATGAGGCGCT |
| TcSNP1414 | T/C | LG9 | TGTGACTTACGGTTACCCCAATCTCAAGAGCGTGAGGGAGTTGATTTACAAAAGAGGTTA[T/C]GGGAAGTTGAACAAGCAGCGTGTTGCTTTGACTGACAATGAAATCATTGAGCAGGCTCTG |
| TcSNP1442 | T/C | LG9 | AAAAGTGATGGAGGAAAGGGAAAGAGATGGGTGGGAGTAGAGATGGCCTTTGGTGTTTCC[T/C]TATGGATTTTCACTCTACATCAAAGCTTTGGTGTGTGATGGAATTTACAGCTACTGTTAT |
| TcSNP1458 | C/G | LG1 | TGGATCTGATCGTCAGCTAAATCAGTCAATTATCGAAGGAATCAATCGCAGTCATGGCGA[C/G]TCCAGAGTTTCTGCAAAGAGAAGCCGACCTTCTCCTTTCATCTCCCTTGATTGAGCTTCG |
| TcSNP1484 | A/G | LG6 | AAAACAGTCAAACGGGTCGTCTTGACTTCTTCAGCCGCAGCTGTGTCTATCAACACACTC[A/G]AGGGGACAGATCTGGTCCTGACTGAGAAAGACTGGACCGACGTTGAGTTCTTATCGTCGG |