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

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| --- | --- | --- | --- |
| SNP ID | SNP form | Linkage group | Haboring sequences |
| Tcm001s00947643 | A/C | LG1 | TtCTTCAtAGCTGGTATTCTCTGATATTAGaGATATCGAGCTTGGCCGCTTtATTAATGG[A/C]AGAGAT  GGGCTCTCTAGCTGAGGAAGctCTACGAACTGATCAGAGTGGATGAAGTTTAGA |
| Tcm002s20575712 | A/G | LG2 | ATATGAATCATTAGCCTCTGAACCCCGACGGCATATGTGGTGCTTTACATGACTtCTTTT[A/G]ACTAT  ATCATCATTGTCATCATTTGAAGAATCAAAAGATTCTAAATCTGATCTTGAATCA |
| Tcm003s01336581 | A/C | LG3 | TCTCTGCCcTCTtGTTtCTTGGATTGTTCTGCACTTGAGCATCATTCTTCACCTGTGGAG[A/C]AACAGA  CTCAACCACCAATTTGTGGCTGACTTCTTCAAAAGCCTCAGCTTtGTTATGTGA |
| Tcm003s34112745 | A/C | LG5 | GCtACCCTTTTGAaaTTYTGTCCCAATTTGCGAGAGATGTTGTAATTGTAGAATTGCATC[A/C]GCGGT  GTCGTCGTTCTAAGGGGTTTCGAGATAAACGGTGAAGGTGAAGGTGAMGGTGGTG |
| Tcm006s26664133 | A/C | LG6 | TTGGAATTTAAACATTCATTTGGAAGCAAGAGGCAAAAgAAGGGGCAGTCTAATTCGATC[A/C]TAT  TCTACAGACCACGACCATTACAAGCCAGAAAAGGAAaGACCCATCAAGACTCCATAG |
| TcSNP23 | T/C | LG8 | AGGTTGTGGGTGCAAGGAAAGATGAATTGCAACAGAAAATAACCTCGCATTCTAGCATGC[T/C]TG  CTTGATGCAGAGAAGCATGAATCAAGGTTTAGTTGTACTCCTTGAAGTCTGATTTCTG |
| TcSNP25 | C/G | LG9 | TTTATGTTACTAGTTTTTGTTGGGTGGTTGTCTGTTTCTTGTTTGCATTATTTTGTGGAC[C/G]GGACC  TTAGTATATCCTGCTTGTTTGCTCTGTTTTTTGTTCAGTAGTCTGGGTTGTTAGT |
| TcSNP32 | A/T | LG4 | TTCCACTTTTGTCAATATAGATCAGTCATGGATGATATTGTGCAAAAATAATACCATAGT[A/T]CTA  AGAAATCATGCACATTTTTGTAAATAGGAAGAATCTGCCATGGTAATGTTGTGTTGA |
| TcSNP42 | A/G | LG1 | TTCTTGGAGTCAAACCAACACCCAAGAAGGAACTTCTGGGTATTCCTGTTATAACACATG[A/G]CA  AATCCTTAAAGGTGCCAACTAAGTTCGATGCTAGAACAGCTTGGCCACAATGTAGCAC |
| TcSNP122 | T/C | LG2 | AGATCAAAGAAGCTCCCAAACGTGAGGATGAGAAACAACAGTGAAGTCACTAATCCTCGT[T/C]GT  AGTATTTTACTTCTCTGGTTGTTTTTGTATGGAGAAGTTGCTTCGTCCCMCAATCGCT |
| TcSNP144 | A/C | LG10 | ACCGACACAGGATTCACCGTGAATGGGGTCAACTATGAAGGCAGCTTGCTATGTGTGGGA[A/C]AT  TTGCTCACTTCTTGGGTTCCCAATAAGTTTTCTCAAATTACTCCCGACAGCTTATCTA |
| TcSNP150 | T/G | LG5 | ATACCCTTCGACGACTACTGCTGACTTGGGAACACCCACCAGCGTTTTGCCGGCAACATC[T/G]GGT  GACTGGTCTGATTTTTCCTCTAATTTTTATCTAGAACTTTGTCAAGCGTTTAAAATA |
| TcSNP172 | A/G | LG9 | TCTATCATAAGGTCTTTTTTCAGGTGACTCTTCTTTGGATGGACATTTGTCTTTTGTTAG[A/G]TGCT  TTGATTTTGATCTTTATTAGTAGGTTTTACAATCTACTTGTGGATCAAACTCCAAA |
| TcSNP226 | C/G | LG9 | AAGCCCAAGGCCCAAGAGCTACGCGATCCGAAGGCAGTGAACCAGGCGCTGAGGTCGGGG[C/G]C  ACCGGTCCAGACTATCAAGAAATTCGATGCTGGTTCGAACAAGAAAACCGAGGGGCCGG |
| TcSNP230 | A/G | LG10 | CAGCAGAGGCCGAAGACAAAGAAGGGGAGAGGATGTGATCCATCCCCTCAAGGTTTCTTT[A/G]G  AAGATCTCTACAACGGAACATCCAAAAAGCTTTCTCTTTCACGCAACATAATTTGCTTC |
| TcSNP242 | T/C | LG9 | AGCAATCTTCCTCCGCCAAACAAGCCATCAATCAAACCCTCGTTCCTCTGTCTTCGCCTT[T/C]CTCT  TCGTTGCCGTCATCGTCATCGATCTCATCATCTCCATTTTCGGGTTCCTTGCCAAT |
| TcSNP288 | T/C | LG6 | TTTGGGGTACGATTATCAAGGAGTTGATGTTCCATGGCTTAAAACTAAGCCAGTTCCTCG[T/C]AAG  TTTTCCAAGAAAGGGGGAAAGGGTCATGGTCAGGCAGTGGCAGCCGAGACAAAGAAC |
| TcSNP316 | A/T | LG2 | CAAGAGTCGGTTCAAGAAATCGTACGGGTCGCAGGAGGAGCACGATTACAGGTTCAAGGT[A/T]TT  TCAGGATAACTTGAGACGTGCGGCGCGTCATCAGAAGCTTGACCCGTCTGCGAGTCAC |
| TcSNP372 | A/T | LG4 | GGAAATTCTGAAGATTGTGAAGGAGAACTTCGATTTCAGACCTGGAATGATTTCTATCAA[A/T]CTT  GATCTTAAGAGGGGTGGCAATGGCAGGTTTTTGAAGACTGCTGCCTATGGGCATTTT |
| TcSNP375 | A/G | LG8 | CATTTCATTTGGAGTAAATCTGCTTCGACGATGATTTCTGACTTCAGACTACTGCAATCT[A/G]CTT  TGCTACCTTCCTCTGCTTTTGCCTTTCGCTTTTGGTGTAGTTGACATAGGCAATAAA |
| TcSNP413 | T/C | LG3 | CGCAGTTTTCTCAGTTTCGGGCAATGATTCTAGTTATATCATGAAACTAAGTTCTTAGGT[T/C]GTT  ATTATGAGCCTATGCATACAGCATACGTAATGCGGAACTGTAGTTGATACTTTATGT |
| TcSNP418 | A/G | LG1 | CAATTCCCTTTCCGGAAAAATCCCACAACAGATAGGGAATCTCCAGAAGCTCACTGTCTT[A/G]AA  CCTCGCAGACAATAAGCTAAGTGGAGAGATCCCAAGCTCCTTAGTTCAACTCTCCAGT |
| TcSNP448 | C/G | LG4 | TTTGGCTGCAAGGAATTCTAGTTTGATTTTACCCGAGTTTTACAAGTTCTTGAAGGTACT[C/G]TAT  TACCTTTACTATCCTAGATTCTAAGGCTGCTGTTATTCTAATTCTACCCCAAGAAGA |
| TcSNP469 | A/G | LG7 | AGCCATGGCTCCGAGATCAAAAGCCAGCCCGGTTAACCCGATTTCCGACCCGACTTCCAG[A/G]G  AGATCCGTTACCGCGGCGTTCGAAAGCGCCCATGGGGCCGTTACGCGGCGGAGATCCGG |
| TcSNP521 | A/C | LG2 | GATTCTGTGAACTATAGCACCAAGGAAAAGAAGGCCAACCTTAAAGAAAATCCTTTAATA[A/C]A  TACTACTGACTGGTATATGTATCAGAAACAAAAAAAGAAATAGTAGAAATTCCAATGGC |
| TcSNP529 | A/C | LG1 | ATAGGCCTTGAATGACTTCATCTCCTCTGTCACCTTCACAAGCTCAACAAAAGGCTTCTC[A/C]AG  AAAAATAGGCATGTATGGTCCTTGCACTTGGGTTGCAGTTGCAAGCTCCTCGGCAGTA |
| TcSNP534 | T/C | LG1 | TGTAAAGAGTGCCATTGTAAGTGGATGCAGCGCCTTTTAAGCAATGGTACCTAGCA[T/C]TATGGT  GGACATTGGGAGGAAGAAGAAAACAGCAGCTAAGAAGGAAGCTACTGAGGAA |
| TcSNP547 | A/G | LG8 | AGAGCCTTTCGCTTCCTCATCTTTCTCTCTGCGACTGCGTTTCAGTGTTGGACTGAGTTG[A/G]AAG  GAGGATGGCGGTTCGTAGGGACAAAGGGCAGTCAATCCGCGGATCTCGAATTGCTAT |
| TcSNP560 | T/G | LG10 | GAGGCAGAGAAATACAAGGCCGAGGATGAGGAGCACAAGAAGAAGGCGGAGGCCAAGAAT[T/G]  CTTTGGAGAACTACGCCTATAACATGAGGAACACTGTCAAGGATGAGAAGATTGGCTCAA |
| TcSNP591 | A/C | LG1 | GGGCGTCGAGAAGACTTCGGCTGCTATTAAGGTCTTGAAACAGATCGGGGCTTATGCGGA[A/C]GT  CGAGAAGGCGAAAGATAGCCAGGCCATTCGTCCCGGAAAGGGCAAAATGAGGAATCGC |
| TcSNP602 | T/C | LG6 | CCATGGTTTCCGTATGGCACTGTGGTATGAGCACCTTGGCATGCTTGATGATACCTTCCT[T/C]TTT  CCAGAAAGTGAGGAGTGTGTCAGGAAGGTGAACCAGATTGCTGACAAATATTGGGAT |
| TcSNP606 | A/G | LG7 | ATGTGTACAAGTTCACATGTTGAGTGAAAACTAGAATTTCTGTGTGTTAAGCTTGTGCCT[A/G]CA  TAAAAAGGATAATTGTACAAAATGTTAAAAAGAATAATTTGTGCTTTGCAACGTTTAA |
| TcSNP619 | T/C | LG6 | GAACAAAAATTGTAAATTAATCTTATGCATGGAGTAATGACCCCACAGCTTTGCAACACC[T/C]CA  AAAATGGTGGTTGTCCCTTTGTACATAATGATTCTGGGATGAATCATTTGTCTTTGTA |
| TcSNP645 | A/G | LG5 | TGAAGGCACTGGAGCCCTTTGTGAATTGGCTGGAGGAAGCAGAAGAAGAGGAATAAGTGC[A/G]A  TAACAATAATATTATGATCACTTTGAAAAGAAAAGGGGTGAACCCTGTACTTGTTCCTT |
| TcSNP709 | T/C | LG1 | GGCATTTGCAGATGAAGTTGGCATACCTTTTATGGAAACCAGTGCAAAAGATGCCACAAA[T/C]GT  GGAACAGGCTTTCATGGCCATGGCTGCTTCCATCAAGGATAGAATGGCAAGCCAACCA |
| TcSNP723 | T/G | LG10 | AAATTGGAACCCCACCTCAAACCATGCTCATGGCCATGGATACTAGCAATGATGCTGCTT[T/G]GT  TACCTTGCTCAGGCTGCCTTGGCTGCTCTTCTAGTGTTTTCGACAATGCTAAATCAAC |
| TcSNP731 | A/G | LG10 | ATTTACAAGGCTAAGGTGAAGAAGAATGGCTCACACTATCGTTGCATTTGGGGAAAGGTT[A/G]CT  AGACCTCATGGTAACAGTGGCGTTATTCGTGCTAAGTTCAAGTCTAACCTTCCCCCTA |
| TcSNP751 | T/G | LG5 | AGCATTTCACCATGGCCATTTTCTTGCTTCCTTGCTTGCTTAAGCAGCTTGAGGGGTTCC[T/G]TTCG  TCTGTGGATGCAACTGGAGTTCCAAGTCATCTTTCCCGTCTTTCTCCCTAGCCTTT |
| TcSNP823 | A/C | LG5 | AGGTATTGAGGCTAAGCAGCCAAACTCTGCTATCCGTAAGTGTGCTAGAGTTCAACTGAT[A/C]AA  AAATGGAAAGAAGATTGCTGCATTCGTTCCAAATGATGGTTGCTTAAACTACATTGAA |
| TcSNP836 | T/C | LG2 | AAGGGTAATCCCATGTGGAATCAGCTATCAGTGCCATCTTCCACCATGTACTCATGGGAC[T/C]CCA  ACTCAACCTACATTCATGAGCCTCCATACTTCAAGAGTATGACCATGGAGCCTCCTG |
| TcSNP872 | C/G | LG4 | AGTGATGTTGCACAGGTCACAAAGCTTCTCAACCTTGTTGCCAGTCAATCCAAGAGGTCG[C/G]AG  ATCCCAAAGAACAAGGTGGTTCTCAGTTCCCCCAGTTACAAGCTTGTATCCCTTGCTC |
| TcSNP878 | C/G | LG3 | CCTCGAGTCGACTCGGCCGACACGGGCTTCGACTCGCCCGAGTCTACTATCGTGGAACCC[C/G]AC  CTGGATGACGGGAATGTTCAGTCGCCGGAGGTAAAGCGTATCCAGGAGGATTTGTTGA |
| TcSNP899 | A/G | LG8 | GGCGCTTATTTACAGTTACAAGACGGCTGCTAGCGGTTTCTCCGCCAAGCTTACTCCCGA[A/G]CA  GGTTGCGGAAATCTCGAAGCAACCCGGCGTTCTTCAGGTTGTCCCGAGCAGGACTCTC |
| TcSNP917 | T/C | LG10 | TATGGAAACTGGGTAAAGGCTCAAGAATGGGCGGCAATTCCTGGTGGACAAGCCACTTAC[T/C]T  GGGCAACCCTGTTCCATGGGGTACCCTCCCTATCATCTTGGTCATCGAATTCTTCGCCA |
| TcSNP929 | C/G | LG3 | TGAAATGGAAATGAAAATACAAAAAACCAAGTCATGTTCAATAGCAAGTGATGTCCTTTT[C/G]TC  TGCTGATTATAACAGAAGTTGTGTTAATTTTACACTTAGTTGATGTGGTTTTAAAGGG |
| TcSNP944 | T/C | LG7 | TGACATGCCCCCACTGGAGGATGCTGATGCAGAGGCCGAGGGCAGCAAGATGGAGGAAGT[T/C]G  ACTAAGCCTGACATRTTTTAATGTTTGAACTTTATCTTTATGTAGTAGTCTCATTTTAA |
| TcSNP953 | A/T | LG4 | GGGTCTCTAAATGGCACTTGAGGTTGCCAGAGATAAAGCTTCATTCATGCTCCAAGCCAA[A/T]TC  TTTGGGCATTCCAGGGTCAAACACCTCAAAAACAAGTTTCTTTATGGCTCAAATCATG |
| TcSNP994 | T/C | LG6 | AACAAACCGAAATATATTCTAGGGAAACTTTGCATTTGCAACCCCTATTTGACTTTCGAT[T/C]TGC  TCAGATCTGCTTTTGAATCCTCAACTTCTGAATAGTCAAYATGGGAGGAGGGTTCAG |
| TcSNP998 | A/G | LG5 | AACAAGAACAAGGGAATGGGGACAATATGATCCCACTAGACATGATGGCTTTTCCTCCTC[A/G]TA  GTAGTGAGAAAGGAATAACATAGAATCTAAGCTGTCACAGATGTCTCCACTGCAACCT |
| TcSNP999 | T/C | LG8 | ACTGGGAGTAAACAAAGCAAAATCCCAATCATTTATTGGAGTAAATTATGGGCAAGTGGC[T/C]GA  CAACCTACCGTCACCGGCAGCCACTGCAAAGCTTCTCCAGTCCACTTCAATCCAAAAG |
| TcSNP1034 | T/C | LG4 | CTTCAGCCAGCACTCAGCAACTAGGAAGTGAGCATTGCAGTTTTTGTTCTTCATTTTTCT[T/C]GCCT  CCTGGTTTGAATTGCCCCGGTTTGCTTGTTGAGTCACTTCATCTTAAGTTCATAGA |
| TcSNP1038 | A/G | LG5 | GTCGACACCTTCAGACTTCAGGAGCAACCTGCTTTTGACAAGAAGCAGTTTGTAACCTTC[A/G]TGA  AGAGGTACATCAAGAACTTGACACCCAAATTAGAGCCAGAGAAGCAAGAGTTGTTCA |
| TcSNP1041 | C/G | LG10 | CAATGTCCAGCCTGATGCAGTTCTGCAGACTGTTTCAAAGACTGGAAAGAAGACTACCTT[C/G]TG  GGAAACAGAAGCTCCAGCAGAACCCGAGGCAAAGCCTGCGGAAGCTGTTGCCACAGCT |
| TcSNP1060 | T/C | LG2 | CAGTTCTTGATTTTGAGATTGAAGTCCTAACCTTGCACTGAGTACTTGGCACTTGGTAAC[T/C]GTT  GGAAGAATATGTAGCCTGAATAAGTCACGTGCCATGAACATATATGGATATTATCGG |
| TcSNP1062 | A/G | LG3 | ATGCAAGAGGGAACTCTGGAGAGTTCAGTATGCTCTAAGCCGCATTCGAAATGCTGCAAG[A/G]G  ACCTTCTGACCCTTGATGAGAAGAACCCACGTCGGATCTTTGAGGGTGAGGCTCTTCTT |
| TcSNP1075 | A/T | LG1 | TTATGGCAGCATGCACTTATAATTTATGATTGCAACCCAACTGATACATAAATG[A/T]GTAGTAGG  CCTGTATAGATGAATTACGAAACAAAGCATGAGAGTGCATGT |
| TcSNP1096 | T/C | LG1 | CATTATACTTAGGATCAATGTTAAGGCGGAAATGGGCTTCAGCTGACTCAACAAACTTTG[T/C]AC  TTGTCATTTCCTTTAACAATGATATTGCTGTCTTTAGATCATACTCCTTTTTGTTTTC |
| TcSNP1111 | A/G | LG5 | CCATCAATGGTTGCTGCCTCGGCAGTGTATGCTGCTCGTTGCACACTGAACAAGACCCCA[A/G]CT  TGGACTGACACACTAAAGTTTCACACTGGATACTCTGAAGCACAGCTAATGGAATGTG |
| TcSNP1126 | A/T | LG7 | CGTCTTCAAGGGAACTTACAAGAGTCTGAGGACATTGATATTGTGGCACTAAAGAACTAC[A/T]T  GGATGCTCAGTACTTTGGTGAGATTGGTATTGGCACACCTCCACAGAACTTCACTGTGA |
| TcSNP1144 | T/C | LG6 | GGTTCGGACTTTGTGGATCGGAGATTTGCAGTATTATATGGATGAGAATTATCTCTTGGG[T/C]TG  TTTTGCCCAAACTGGAGAGGTTGTTTCAGTGAAAGTTATCCGTAACAAGCAAACAGGC |
| TcSNP1165 | T/C | LG2 | GATCAATTGCTTAAACATATTTGCATAGCATTATAGATATTTTCAAAACCATGATGGAGG[T/C]TG  CCAAGGTTTTCCTAGCTCTTACTTGTCTCATGGCCTTAGCCTTGGTCCTCCCCTCCCA |
| TcSNP1175 | T/G | LG4 | TAAGGCTACATTCGTGGTGTTTGTCACGGACGGATATGGGTACGCTCAAATGGCTTGCCC[T/G]C  ATCTCTCCAGACAGAGCCAGGGATCCCAAAGTGGAAGGCAAGACAGAAGAGAACAAGAA |
| TcSNP1253 | T/G | LG9 | CACTTGCCACTCAAGTTCCTCACTAAAGCATTGAAACCAGCATCAGAAGTCTGATTTCTA[T/G]A  TTACCAGCACTTATCAAACTTCTTTCAATCAGGATAGGTGAGTAAAGAAATGAGGCGCT |
| TcSNP1414 | T/C | LG9 | TGTGACTTACGGTTACCCCAATCTCAAGAGCGTGAGGGAGTTGATTTACAAAAGAGGTTA[T/C]G  GGAAGTTGAACAAGCAGCGTGTTGCTTTGACTGACAATGAAATCATTGAGCAGGCTCTG |
| TcSNP1442 | T/C | LG9 | AAAAGTGATGGAGGAAAGGGAAAGAGATGGGTGGGAGTAGAGATGGCCTTTGGTGTTTCC[T/C]T  ATGGATTTTCACTCTACATCAAAGCTTTGGTGTGTGATGGAATTTACAGCTACTGTTAT |
| TcSNP1458 | C/G | LG1 | TGGATCTGATCGTCAGCTAAATCAGTCAATTATCGAAGGAATCAATCGCAGTCATGGCGA[C/G]TC  CAGAGTTTCTGCAAAGAGAAGCCGACCTTCTCCTTTCATCTCCCTTGATTGAGCTTCG |
| TcSNP1484 | A/G | LG6 | AAAACAGTCAAACGGGTCGTCTTGACTTCTTCAGCCGCAGCTGTGTCTATCAACACACTC[A/G]AG  GGGACAGATCTGGTCCTGACTGAGAAAGACTGGACCGACGTTGAGTTCTTATCGTCGG |