

Table 1

| A total of 25 MS markers were tested flanking the K13 gene. In bold are MS markers (8.6kb and 31.5kb) that were informative and separated the C580Y haplotypes by geography. In green are MS markers = successful amplification. <i>Please refer to Table S1 for final raw data.</i> | | |
|---|---------|---|
| Number | Locus | Primer seq (5' to 3') |
| 1 | 0.1kb | ATGAAGAAATTTTAAATGTTC |
| | | ATTTATAGCTAATAAGTAATATC |
| 2 | 0.5kb | TATGATAATATAAATTCTCATG |
| | | TATTAATAGAATTGTTCAAACAT |
| 3 | 0.1kb | CTTTAATATTTATTTTCATGCAC |
| | | GAACAATTCTATTAATATTTTAAG |
| 4 | 3.4kb | TCTACAGCGGTAAGATGAATAG |
| | | TCCTTGGCATGTCCCGGCTGC |
| 5 | 8.6kb | ACGGGTTTCTGTACGCCTCAC |
| | | CTAAATTAGTGGCTTCTTCAT |
| 6 | 15.1kb | CTTACTTCTAGGAGAATCCT |
| | | GATAACTACTCATCTCCACA |
| 7 | 20.0kb | CTAAACCAAATGAGATAAGG |
| | | GTTATACTATTATACATATGTATAGG |
| 8 | 21.0kb | TCCTATACATATGTATAATAGTATAAC |
| | | AAGGATTCTTCGTACCTATG |
| 9 | 31.0kb | GAAGATGTAGATATTACTTGTA |
| | | TATAAGATTCGTTATTACATG |
| 10 | 31.5kb | GTACAAATGAACCTCTTCC |
| | | AATAATTCACCATGTCATGC |
| 11 | 42.0kb | TGTTAAGCATCCATTCTCTC |
| | | CATCTTAAATGTACAAATATGTCC |
| 12 | 43.0kb | CATCTTAAATGTACAAATATGTCC |
| | | TGTTAAGCATCCATTCTCTC |
| 13* | 72.3kb | TGTTAAGCATCCATTCTCTC |
| | | TGTTAAGCATCCATTCTCTC |
| 14 | -0.1kb | ACAAGGCGTAAATATTCGTGT |
| | | GATCCCTATCATACGTCATAG |
| 15 | -0.15kb | GATCCCTATCATACGTCATAG |
| | | ACAAGGCGTAAATATTCGTG |
| 16 | -0.4kb | CGAAAAATAATTTATTATTCATAC |
| | | TATATATACATTTACATATGG |
| 17 | -2.5kb | TGAAAACATATACATAGAATG |
| | | TTCACAAATATATCACTGC |
| 18 | -2.0kb | GCAGTGATATATTTGTGAACAG |
| | | TCCTTCATATTACATAAAGTCC |
| 19 | -3.0kb | GTTAATTATTGGGCTTACATTC |
| | | GTCAATATTTATAATTTAGATGAG |
| 20 | -3.74kb | GTCAATATTTATAATTTAGATGAG |
| | | GTCAATATTTATAATTTAGATGAG |
| 21 | -6.36kb | AATTAGACAGGACTTGTTAATG |
| | | GGATATGTTATCCAAAATGCA |
| 23* | -31.9kb | AATCAATCATGGAAATTATG |
| | | TTGTTCAATTAAGGGTATTT |
| 24 | -36.0kb | ACATATTATTATGTGTGGATGTC |
| | | ATAACAAATCAATAAATGAACTC |
| 25 | -40.0kb | TTAACGAGAATCGCTTCAT |
| | | TAATTATCACTTAATTATATTG |
| 26 | -45.5kb | AGCACAATAAAGTTGGC |
| | | TCTACCAGTATTAATATTTGAG |
| 27 | -50.0kb | ATGACGAGGATAACCATG |
| | | AATATGTACGATCATTACAGT |
| 28 | -56.0kb | TCCTTCTATTTGTGTGAGTACAG |
| | | TATTGTAATGCATGCACTG |
| | | *Cheeseman, I.H., et al., A major genome region underlying artemisinin resistance in malaria. Science, p. 79-82. 2012. 336(6077): |