

| Gene       | NCBI Reference Sequence | Primer sequence (5'-3')   | Amplicon size (bp) |
|------------|-------------------------|---|--------------------|
| VviIPT2    | XM_002263711            | F: CCCTCACATTCCCTTTCAGC<br>R: GGTCTACGGCAGGCTATTGG  | 108                |
| VviIPT9    | XM_002282976            | F: TTGTGCCAGTTCTGCAAGGT<br>R: AGGCATTCATCAACCGTGA   | 127                |
| VviIPT10   | XM_002279335            | F: GCGAGTCGATGAAATGCTTG<br>R: ACTTTCGGAAATGCCTGTCTG   | 140                |
| VviIPT11   | XM_002268812            | F: TGGACGCCACTGAAGTGTTT<br>R: GCGTTCCTCACCATCTCTT   | 152                |
| VviIPT12   | XM_002271926            | F: ATGCATATGCGCAAGCAAAC<br>R: CCCATTACCACCACCACCTT  | 110                |
| VviIPT13   | XM_003632592            | F: AGGGGTGGGCTAGTGGAAGA<br>R: GCCCTCAAGTAGGCGTCCAT  | 110                |
| VviIPT14   | XM_002277555            | F: AAGCACAGACGCCCTACTG<br>R: CCGGTGGCTCCTATCACGAA   | 100                |
| VviIPT15   | XM_002278900            | F: CACATATGCTCGATCCCACCG<br>R: ACCAAAACCTGACCATGGTTGC   | 95                 |
| VviCYP735A | XM_002280169            | F: GGCAGCTCTCGTCTCCAAAT<br>R: GGCAGCTCTCGTCTCCAAAT  | 112                |
| VviLOG5a   | XM_010665788            | F: CAAGCTGGGCCCATGTGATG<br>R: GGAGAGGTTTCGACCCGTAGC   | 136                |
| VviLOG5b   | XM_002281803            | F: TCAAGCCTTCACAGCGCCAT<br>R: CCTCGCCTTTGCAATGACCC  | 110                |
| VviLOG10   | XM_002276739            | F: CACATGGGCTCAGCTGGGTA<br>R: TGACGGCAGCTGCTGTTAT   | 134                |
| VviLOG11   | XM_002275378            | F: GTCCGCACCAACAGCCAAAG<br>R: GCCACACCAGGCTTCTCTGA  | 129                |
| VviLOG12   | XM_002276243            | F: TCATTAGTCCCAGTGCCCGC<br>R: GCTGCTCCATCTCCCAGCTC  | 129                |
| VviLOG13   | XM_002285210            | F: GGCAGTGGGGGCTGATACAA<br>R: TCCATGACAAACCGGTGGGA  | 132                |
| VviLOG14   | XM_002285680            | F: TATCAGGGCATGCGGTTGGG<br>R: TCCATACCCACCAGGAAGTGC   | 110                |
| VviLOG15   | XM_002274711            | F: TTTCAGCAACCACGGCAGAAG<br>R: TGGTCCACTTCCCAGGTTTG   | 97                 |
| VviLOG16   | XM_002277816            | F: CAGTGGGGCTATTGAATGTGGAC<br>R: AGTTCTTCTGCCGTGTCTGCTG   | 130                |
| VviLOG17   | XM_002278269            | F: AGCATGTGGGCTTCATGTCTT<br>R: CCAGTTGCGTGAAAGAGCGT   | 111                |
| VviCKX5    | XM_002280761            | F: TCTCAGCAATCAGAACCGTCAGA<br>R: GGGGTCTGAAGTCCATCTTTC  | 160                |
| VviCKX6a   | XM_002270805            | F: TTGTGGGAGGTTCCACACCC<br>R: GAATGGGGCCATTGCTGGTG  | 115                |
| VviCKX6b   | XM_002284524            | F: TGCAGAAATCCTGCTCCATGA<br>R: AAGTGGCAAGCGCACTTTGG   | 138                |
| VviCKX7    | XM_002279924            | F: TCCTCAAGCTAGGGTTGCCG<br>R: GGAAGGTTGGAAGCGCACT   | 132                |
| VviCKX8    | XM_002279483            | F: CATGGGCTGATGTCCTCCCC<br>R: GCAGCTGGGGTTTGTGGAC   | 127                |
| VviCKX9    | XM_003632356            | F: TCCTGCACAATTGTCCTCTAACA<br>R: TCTGAGACTTCATCAACTGTATGGC  | 160                |
| VviCKX10   | XM_002263610            | F1: TTGCACCAGTGTCTGGACT<br>R1: TGATCTGAGGACCATGGCGG<br>F2: ACTTCTCCACATTTTCTAGAGACCA<br>R2: ATTAGGAGGACTATTTTGCATGGAG | no product         |
| VviCKX11   | XM_002264409            | F: TCGCTCTAAAACCGGCACCA<br>R: TGCATCAAGAGTGAACCTTCCA  | 136                |
| VviCHK2    | XM_002269941            | F: ATTGTCACCTGCGTGGACAG<br>R: CCCATCCATCTCTGGCATTT  | 105                |
| VviCHK3    | XM_002276925            | F: GGAGCTGATGTCGTCTGTGC<br>R: GCTTCAAACCCGTCCATTTT  | 119                |
| VviCHK4    | XM_002285081            | F: AGCCATCCATCCCACATTTT<br>R: ACGGCTGCTCGAGAGTAAGG  | 158                |

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|----------|-------------------------|--|--------------------|
| VviRR11a | XM_002274637            | F: TTGAGAGCGCATAGGCGTGA<br>R: TGCAGTCTGCTCCACAGCAT   | 128                |
| VviRR11b | XM_002267580            | F: TGCCAAATGGTAAACCCTCAAGC<br>R: AGAGCTGACCCACTCCCTGA  | 140                |
| VviRR25  | XM_002269335            | F: TTGGCCAGGGAATGGTCTCC<br>R: GCCCGGCCTAGGCATACTTT   | 131                |
| VviRR26  | XM_002270082            | F: AGGATGCATTTGCCTGGGCT<br>R: ACCTTTGGCCCACTGAACTGT  | 95                 |
| VviRR27  | XM_002275106            | F: AGCTGCATGATATGCGAACGTG<br>R: TGCCCCATAACCAACACAACCT   | 129                |
| VviRR28  | XM_002281255            | F: ACCCAAGCACTGTCCAGAGA<br>R: GGCGCAAATTCTCAGTGCCT   | 120                |
| VviRR29  | XM_002270797            | F: TGGCGTCAGTGGTTCATCT<br>R: ACGGATCGCGATTGAGTGGT  | 114                |
| VviRR30  | XM_002282892            | F: GCGTCTTGCTCTGTTCCCTG<br>R: GTTGAAGCAAGTTGCCCT   | 137                |
| VviRR31  | FJ822980 (partial cds)  | F: CCGGGAAACTCCGGTGGTAA<br>R: CTTTCAGCCGCTTCACGTCC   | 128                |
| VviRR32  | XM_002283751            | F: CATAACCCTGTCATCCCAGGCA<br>R: ACGGCTGTGGAGAGTGGAAC   | 133                |
| VviRR33  | XM_002280710            | F: TCCTGCCCTAGGGATGGAT<br>R: AAGTGCCTGGAGGAAGGAGC  | 149                |
| VviRR34  | XM_002284468            | F: CCCGGGATGAGCGGTTATGA<br>R: TGCCCCTCCTTCCAAACACA   | 126                |
| VviRR35  | XM_002273954            | F: GCTAGCTGTTGATGACAGCCTT<br>R: ACGGAAGGTGTGTTTGGGTCA  | 147                |
| VviRR36  | XM_002266214            | F1: CCAGTTGTGATCATGTCCTCTGA<br>R1: GCGAGACCTCAACATCTACGAGT<br>F2: AATCATCACCAAGGAACGAAAGT<br>R2: TGATCACAACCTGGGATGCCT | no product         |
| VviRR37  | XM_002268316            | F: AGCTTCAAAGGCTGTTTCATGTCT<br>R: TCGATTGAAGACATTTTTGGAGGGT  | 116                |
| VviRR38  | XM_002267339            | F: AGCTGTTGATGACAGCCTCGT<br>R: TGCCTCTTGCAAACCCAGGA  | 124                |
| VviRR39  | XM_002267896            | F: TGGGTATTGCTGCAGAGACACAG<br>R: CCTACTCCCAGAATCCACAGCA  | 129                |
| VviRR40  | XM_003634849            | F: TCTAGCTGTTGATGACAGCCTCATT<br>R: CTTTCCTGTTCTGCCTCTTGAC  | 138                |
| VviRR41  | XM_002267368            | F: TGTTTGGGAAGAAGGAGCAGAA<br>R: CTTTTCCCTTCAGTAGATGGGG   | 91                 |