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# QTL identification and candidate gene identification for monoterpene content in grape (*Vitis vinifera* L.) berries

Hong Lin1), 2), Yinshan Guo1), Xiaoxu Yang1), Satoru Kondo2), Yuhui Zhao1), Zhendong Liu1), Kun Li1) and Xiuwu Guo1)

1) College of Horticulture, Shenyang Agricultural University, Shenyang, China
2) Graduate School of Horticulture, Chiba University, Matsudo, Japan

Supplementary Table 1

New SSR primers used in this study

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 1 | VLG101 | Forward | TGGACACACACACACACACA | 212 |
| | | Reverse | GCATGTGCTCACTGATGCTT | |
| 2 | VLG102 | Forward | TATCAGGGCTTTGCGTAACC | 216 |
| | | Reverse | TGTGCAACACTGCAAACAAA | |
| 3 | VLG103 | Forward | GTTACCAAACAGGGCTAGGG | 175 |
| | | Reverse | CATGAAGAAGGGTTGCCAGT | |
| 4 | VLG104 | Forward | TGCTTCTCGAGTTCCCTTTT | 249 |
| | | Reverse | CCTGTTAGAACCAAAGAAGACCA | |
| 5 | VLG105 | Forward | TTCATTTGAGAACCGGAATC | 186 |
| | | Reverse | CTCCAAAGTCCCAATTTTCA | |
| 6 | VLG106 | Forward | TGGAATACGAGGGGAGTCTG | 147 |
| | | Reverse | CTGATGGTGGGAAGAAAAGC | |
| 7 | VLG107 | Forward | CCAGAGTGCCATCAGAATCC | 234 |
| | | Reverse | CATTGAAGTTTGGGGAGGAA | |
| 8 | VLG108 | Forward | CCCCTCAAAGAATCAATAGACC | 219 |
| | | Reverse | AGTGCAGTGACACCAGCAAC | |
| 9 | VLG109 | Forward | CATCAAAATATGCCCCAGCTA | 183 |
| | | Reverse | CCTGTCCACAGACCGTGTTT | |
| 10 | VLG110 | Forward | TAGACGGTCAGTGTGCAAGC | 139 |
| | | Reverse | CCGCAATTATGAAGCGTTCT | |
| 11 | VLG111 | Forward | CCCAGAAATATCTTAAGGGATGG | 172 |
| | | Reverse | ATGTGTGCGCCTGTACCATA | |
| 12 | VLG112 | Forward | ATTGCTTTTGTGTGGAGGAA | 133 |
| | | Reverse | CAGGGAGCCCTTTGCATTAT | |
| 13 | VLG113 | Forward | TCTGACTGACATTACACCGATTC | 196 |
| | | Reverse | TCTGTTCACATCACACCCAAT | |
| 14 | VLG114 | Forward | CCCATGGAGATTGATTGAGG | 194 |
| | | Reverse | TTCAAGTGGACAATGAAGCAAC | |
| 15 | VLG115 | Forward | CAAGTTGCAGAAGTGGCTGA | 184 |
| | | Reverse | CCTCTTCTTCCCCATCAACA | |
| 16 | VLG116 | Forward | TCAAGAACAGACGGAAACCA | 190 |
| | | Reverse | AGGGCCTTCAATGCTCTACA | |
| 17 | VLG117 | Forward | CCTGCCAATAAAGAACCCATT | 195 |
| | | Reverse | TCAAGTGCCAAATCATCAGG | |
| 18 | VLG1-A-1 | Forward | TCACATATGCCTTTTGTCAC | 167 |
| | | Reverse | CACACCAATATCATGAGCAA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 19 | VLG1-B-1 | Forward | GCTCTGTTTCTTCAGTTTCC | 206 |
| | | Reverse | CTCACATATGGCTCCTCCTA | |
| 20 | VLG1-C-1 | Forward | AAGGTTTCTTATCCCCTCAA | 194 |
| | | Reverse | GCGTTATTTGAAAGCACTCT | |
| 21 | VLG1-D-1 | Forward | AAAATCAGAGCAAGCAGAAG | 89 |
| | | Reverse | CATGCAGCAACTCTCTTACA | |
| 22 | VLG1-E-1 | Forward | GCCACAGTTGTGTTATTTTC | 191 |
| | | Reverse | AATATGGTGAAATGCTGTCC | |
| 23 | VLG1-F-1 | Forward | GGAGTCTGAATCAGTGGGTA | 96 |
| | | Reverse | CTCCAGCTTGTGTGGTAAGT | |
| 24 | VLG1-G-1 | Forward | TGATGGTGACATGAGCTAGA | 185 |
| | | Reverse | TCATCCTCATCACCACTACC | |
| 25 | VLG1-H-1 | Forward | TCCCCTATTTTCCCCTATT | 179 |
| | | Reverse | GAAATCCTGAGCAAAATCAG | |
| 26 | VLG1-I-1 | Forward | TGACGGTTCGACCAGGTA | 182 |
| | | Reverse | AAAAGAACAGGGTCCAAAAC | |
| 27 | VLG1-J-1 | Forward | GAACCATTCATAGCTGGGTA | 229 |
| | | Reverse | TCTTCAAAAGGAACTCCTGA | |
| 28 | VLG1-K-1 | Forward | ATTTGAGCATGTAAGCAACC | 235 |
| | | Reverse | GATTTCAAAAGGCCATCC | |
| 29 | VLG1-L-1 | Forward | GGCAATGAGATAGTGATGGT | 201 |
| | | Reverse | TATTGGTTCACCCACCTTTA | |
| 30 | VLG1-M-1 | Forward | GTGGGTGAATATGGAAAATG | 246 |
| | | Reverse | AGAGATCAGCTTGCGTTTAG | |
| 31 | VLG1-N-1 | Forward | ATAGCCAAACTTGCTCCTCT | 231 |
| | | Reverse | GAGCTCGAAACCAAGAAAAT | |
| 32 | VLG1-O-1 | Forward | GTGCATCAATATGTGCAAAG | 222 |
| | | Reverse | GAGCCTCCTATCCCTCTCTA | |
| 33 | VLG1-P-1 | Forward | CTATCCCACACTGCCTCTAC | 230 |
| | | Reverse | ATGAAGAATAGTGGGGAGGT | |
| 34 | VLG1-Q-1 | Forward | AACACATGTACACGCACAAC | 146 |
| | | Reverse | AGCAAGTGTTTGGTTTAGGA | |
| 35 | VLG1-R-1 | Forward | TTTTTCTTCCCCTTTCTCTC | 190 |
| | | Reverse | GGTATGTGGTGTGGAAAAAT | |
| 36 | VLG1-S-1 | Forward | CAAATCTTATGGTTCGGAAG | 93 |
| | | Reverse | TGACATGCACTCACACTTTT | |
| 37 | VLG1-T-1 | Forward | AGCCTACTCAACCAGCATAA | 157 |
| | | Reverse | TCCATGAGGAAGAAGAGAGA | |
| 38 | VLG1-U-1 | Forward | TTGCCTAGGTCCAGAAAATA | 186 |
| | | Reverse | TAAAACCAAACCCTTAGCTG | |
| 39 | VLG2-A-1 | Forward | TAATTTCGCTGTTCCTCAAG | 186 |
| | | Reverse | TAAGCGCATATCACAAGAAG | |
| 40 | VLG2-B-1 | Forward | GCTTAGACGATAGTGACAACAA | 249 |
| | | Reverse | TGTTGAAGAAAGACACTTGC | |
| 41 | VLG2-C-1 | Forward | GAATCCTCCCATCAAAGAA | 219 |
| | | Reverse | TGTGTGGAGTAAGGATTTGA | |
| 42 | VLG2-D-1 | Forward | ATGTCCTCTGGTTGCTTAAA | 120 |
| | | Reverse | AACCAAGGCTGACAAGTAAA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 43 | VLG2-E-1 | Forward | CCTTTGGCTCTAAATGTGAA | 217 |
| | | Reverse | GTAAGGTTGCCATGTCTGTT | |
| 44 | VLG2-F-1 | Forward | GAAACCACAAGGACATGATT | 139 |
| | | Reverse | CTTCCACCCCTTTTATCTCT | |
| 45 | VLG2-G-1 | Forward | ACAATGCTTCTTACCACACC | 245 |
| | | Reverse | CCCACACTTGCTTTTAGTTC | |
| 46 | VLG2-H-1 | Forward | CAAGGCTTTAGCTTTTTAGG | 237 |
| | | Reverse | AGATGGAACACATGCAAAGT | |
| 47 | VLG2-I-1 | Forward | CTCCTCCCCTATCCTTCTTA | 124 |
| | | Reverse | TGTCTATGGAGGGAGAGAGA | |
| 48 | VLG2-J-1 | Forward | TGGTATCGAAGAGGTAGTTTG | 148 |
| | | Reverse | GACTCAGCCAAACCTCATAG | |
| 49 | VLG2-K-1 | Forward | ATGGATATGTGCTTCGAGTT | 179 |
| | | Reverse | CAACAACAACAACACACACA | |
| 50 | VLG2-L-1 | Forward | AGCCTAAGGAAACCCTAAAA | 130 |
| | | Reverse | GCATCGAGTACTTTTGATCC | |
| 51 | VLG2-M-1 | Forward | ATCCTTTATTCCAAGCTTCC | 82 |
| | | Reverse | GCCAAATCCTCAAAGAACTA | |
| 52 | VLG2-N-1 | Forward | CAAAGCCTTCACTATGTTCC | 111 |
| | | Reverse | CTCCTCCTCTTGACTTTTCA | |
| 53 | VLG2-O-1 | Forward | TTTCTCTCTACGCCTTTTTC | 249 |
| | | Reverse | GTCACATAAGGTGAGGCAAT | |
| 54 | VLG2-P-1 | Forward | AGGCAGGTAAACCTTTCTTT | 178 |
| | | Reverse | GAAGACCATTGAACTCTGCT | |
| 55 | VLG2-Q-1 | Forward | GCAGGAGTGGAGATTATCAG | 219 |
| | | Reverse | GGAGGGGAGTAGTGTTTTCTA | |
| 56 | VLG2-R-1 | Forward | CTCGCCAAAAAGAAAGTG | 250 |
| | | Reverse | CATGGCCACCTTTCTGAG | |
| 57 | VLG2-S-1 | Forward | CCAATAGACAGGAAAATCCA | 202 |
| | | Reverse | GGCCGCAATACAATAGATAA | |
| 58 | VLG3-A-1 | Forward | TTCTGGAGGGATGTTTATTG | 138 |
| | | Reverse | GGCCAATTGACTAACTGAAG | |
| 59 | VLG3-B-1 | Forward | AGTTCAACTCCCTATTGCTG | 214 |
| | | Reverse | GGTGTAACATGCTTGGATTT | |
| 60 | VLG3-C-1 | Forward | CCCCTAGGTTCAAATTATGCAG | 248 |
| | | Reverse | GGGCCCTAGAGTTTGCACTA | |
| 61 | VLG3-D-1 | Forward | GAAGAGGTTCCCCAGAAAGG | 212 |
| | | Reverse | GACCTTCCAATCTCCCCAAT | |
| 62 | VLG3-E-1 | Forward | CCATGTGTCCTCCATCCTCT | 214 |
| | | Reverse | CACGCACCAGCACAAAGTTA | |
| 63 | VLG3-F-1 | Forward | ATGGCACCACCTCAACTCTC | 218 |
| | | Reverse | GTAGGCGTGGAGTGGAAAAG | |
| 64 | VLG3-G-1 | Forward | TGTGCAATCGACATTCAAAC | 119 |
| | | Reverse | CCAAATGCACCTGAAAAATG | |
| 65 | VLG3-H-1 | Forward | ACCTCCTGTCCACATGCTTC | 154 |
| | | Reverse | GTTCATCCACCAGCAAACCT | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 66 | VLG3-I-1 | Forward | CACTTGCATTTGGTTTGGAA | 180 |
| | | Reverse | TTTTTAGGACCACAAAGTGC | |
| 67 | VLG3-J-1 | Forward | CTTGGGGATGGAGTAACGAA | 183 |
| | | Reverse | TCACCTAACCCAATGCATCA | |
| 68 | VLG3-K-1 | Forward | CCGGTAATACAGAAAATGATGC | 174 |
| | | Reverse | ACTTCCTTTGCAGCCAAAAA | |
| 69 | VLG3-L-1 | Forward | TCCAGGTACGTCCTCAATCA | 218 |
| | | Reverse | AAGCGCTATCACAAGACATCAA | |
| 70 | VLG3-M-1 | Forward | CTAATGGGGTCCAAAGAAGG | 179 |
| | | Reverse | ATCAATCCGAGACCTCATGC | |
| 71 | VLG3-N-1 | Forward | TCTAAGCCAAGAACCCCAGA | 129 |
| | | Reverse | GGAGTGTTTCCCTTCTTTTT | |
| 72 | VLG3-O-1 | Forward | GGGTCAGAATTTAAGCTTGC | 250 |
| | | Reverse | CGACATTGGAAATGCGAATA | |
| 73 | VLG3-P-1 | Forward | CCTCCGGGATCATAACAAAA | 148 |
| | | Reverse | ATAAGGGCTCCCTCATGCTT | |
| 74 | VLG3-Q-1 | Forward | GGGTAGGAGATACCAAACATGAA | 188 |
| | | Reverse | TCGATATCGTAACTTTTCCCTCTC | |
| 75 | VLG3-R-1 | Forward | GGAAGGAAGGCATTGGAATA | 204 |
| | | Reverse | TCAAGACTATCCCCAAAACCA | |
| 76 | VLG4-A-1 | Forward | GGACGCAATCACATTTTGTT | 246 |
| | | Reverse | CTTGATTGAGTACATGCTATGATGC | |
| 77 | VLG4-B-1 | Forward | TCTTGCCCAACCTCTGATTC | 229 |
| | | Reverse | CTGGGAAGACAATGCATCAA | |
| 78 | VLG4-C-1 | Forward | AAACGAAGAGGACGAGACGA | 139 |
| | | Reverse | GACGTGGCAAAGACGAAAAT | |
| 79 | VLG4-D-1 | Forward | TCCTCTGGTGGGAGAGAGAA | 186 |
| | | Reverse | GAGACCCCCAAATGCAGTAA | |
| 80 | VLG4-E-1 | Forward | GGGAAGGCAAATCCCTCTAC | 117 |
| | | Reverse | GAGGTCCAGTCGAGAAGTGC | |
| 81 | VLG4-F-1 | Forward | AAAAGGAGCTAAAGCTAAGG | 140 |
| | | Reverse | CTCTGGTTGACCCCAACATT | |
| 82 | VLG4-G-1 | Forward | TCAGTCAATGTCCGTTCCAG | 241 |
| | | Reverse | CACATTTGCAGCAGGAAGAA | |
| 83 | VLG4-H-1 | Forward | TTCCCCCATCATCGAAATAA | 160 |
| | | Reverse | TCAAAAGAAGTGTCTCCATGCT | |
| 84 | VLG4-I-1 | Forward | CGTCCTTGGTGGAACCTTTA | 213 |
| | | Reverse | CCATGCTTTTCACTTTCAAC | |
| 85 | VLG4-J-1 | Forward | CTCTTTGGATCGGAGGAGTT | 190 |
| | | Reverse | CTCTACTGCTCCCCGTTCAG | |
| 86 | VLG4-K-1 | Forward | CCAATAATCTGTGCAAATGG | 237 |
| | | Reverse | AAGCATTTGAGAGCTCATACCA | |
| 87 | VLG4-L-1 | Forward | TGCTGGTGAATCAAGCAAAC | 173 |
| | | Reverse | TCTTAGCCATCCCAAAGGAA | |
| 88 | VLG4-M-1 | Forward | TGACCAACAAAGTAAGCCTTCA | 194 |
| | | Reverse | TTTTCCCTTGTCTTGGCATC | |
| 89 | VLG4-N-1 | Forward | TGCAAACCTACATTTTAGCC | 232 |
| | | Reverse | TTGGGCGGACCTATTAAAAA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 90 | VLG4-O-1 | Forward | AATTTCAACCCCAATCACCA | 107 |
| | | Reverse | GTTGGAGCCTATGCTACTTACTTT | |
| 91 | VLG4-P-1 | Forward | CCACGTTTCTTCCCAAACAT | 201 |
| | | Reverse | GAAAAGGCCCACGAAATTAAG | |
| 92 | VLG4-Q-1 | Forward | TGCCAAACACGATCAGAGAC | 91 |
| | | Reverse | CGGTCTAGTGGTCAGGGAAA | |
| 93 | VLG4-R-1 | Forward | GTGCAGACTCTGGAGGAAGC | 136 |
| | | Reverse | TGCCAATGAGCAAAAACTAGC | |
| 94 | VLG4-S-1 | Forward | TGGTTCCTCCAACAAACACA | 222 |
| | | Reverse | TTGAATACCTTGGCTGTTGC | |
| 95 | VLG4-T-1 | Forward | ACATATCTCCCTCCCCAACC | 169 |
| | | Reverse | CAGTTCTTTCCTGCCCAGTC | |
| 96 | VLG4-U-1 | Forward | ACTTGGGAGGAGGAGGAAAA | 119 |
| | | Reverse | ATCAACCCCGCTACAATCAC | |
| 97 | VLG4-V-1 | Forward | AGTCCACGCCAGCTGATATT | 171 |
| | | Reverse | TCCTTCTCGCTCAAAATAAAGG | |
| 98 | VLG4-W-1 | Forward | TAATTGGCATGTGACCGTTG | 196 |
| | | Reverse | GGAAGGGACCCTCATGTTTA | |
| 99 | VLG4-X-1 | Forward | TTGGGTTCAATGAGCTTTCC | 217 |
| | | Reverse | TGGGCTCACCCTAATTCACT | |
| 100 | VLG5-A-1 | Forward | GAGTCTAAATTGCCTAGGAT | 240 |
| | | Reverse | TGGAGACTTGTGACCCGACT | |
| 101 | VLG5-B-1 | Forward | TGGATCATCTCACCATCATTG | 165 |
| | | Reverse | TTGTCTTTGGCCCTGCTAAT | |
| 102 | VLG5-C-1 | Forward | GGTCCGTATCACCAAAATGC | 129 |
| | | Reverse | TCATGGCTGTAGGCTTTGAA | |
| 103 | VLG5-D-1 | Forward | TGCAATTGCTGCAACTCAAT | 173 |
| | | Reverse | CAGCCAACCTTTTTCCAGAG | |
| 104 | VLG5-E-1 | Forward | GCAAAATCAGAGGACCAGGA | 229 |
| | | Reverse | CCAGGGCTTGTATTCTTACACC | |
| 105 | VLG5-F-1 | Forward | GTTGAAAGGGCCTACCACAA | 191 |
| | | Reverse | TGATTTGAAAAGCCAGGTGA | |
| 106 | VLG5-G-1 | Forward | CTGAAGGATGGAGGGAATTG | 123 |
| | | Reverse | TCCCCCAGATTAAATGCCTA | |
| 107 | VLG5-H-1 | Forward | CCAGAGCAGAACATAACCAGAA | 206 |
| | | Reverse | TGAATGCTGAGCTACGAGGA | |
| 108 | VLG5-I-1 | Forward | CTTAGGTGTCGCATTGTCCA | 198 |
| | | Reverse | TAGCTTGGAGGTCGCTTGAT | |
| 109 | VLG5-J-1 | Forward | TTGGGATTGGCATCTTCAAT | 200 |
| | | Reverse | GGAGAAATTTGGCTAAGAAAGG | |
| 110 | VLG5-K-1 | Forward | CTCAACTCCCACACCCATCT | 106 |
| | | Reverse | GGGACGTGCGCAATATTTTA | |
| 111 | VLG5-L-1 | Forward | TATGGGAGGCATCCTAAAT | 235 |
| | | Reverse | TTGCATGGTGGTTATTGTCTTC | |
| 112 | VLG5-M-1 | Forward | TTTGTGTGTGAAAGACAGCAAC | 226 |
| | | Reverse | CGCAATGGTGGATTTAAAGG | |
| 113 | VLG5-N-1 | Forward | GTCACCAAACGGTCCCTAAA | 179 |
| | | Reverse | GTGCGTTCTCCGATCTTCTC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 114 | VLG5-O-1 | Forward | GAGTGCTTCGGGTTTAATGG | 168 |
| | | Reverse | AAAGGGACAAGTCAATGCAGA | |
| 115 | VLG5-P-1 | Forward | TGGCTTGTACGAGGCTTTCT | 223 |
| | | Reverse | CACGTGGATTGCTACAGAAAAA | |
| 116 | VLG5-Q-1 | Forward | AGGAAAGTGGCAGCAAAAGA | 184 |
| | | Reverse | CCACCTTGCCACACATCATA | |
| 117 | VLG5-R-1 | Forward | TCAATTTCAACCCCATGAGA | 214 |
| | | Reverse | TCTCCTAGCCCCTTGTATGG | |
| 118 | VLG5-S-1 | Forward | AATCACCCACCAATGTGAGC | 204 |
| | | Reverse | AGCAACCAAAACTCCAAACG | |
| 119 | VLG5-T-1 | Forward | CACTCCTGCCCATTTACCAC | 245 |
| | | Reverse | CGCTTCGGAATCGATCTTAG | |
| 120 | VLG5-U-1 | Forward | CCCCAACACACAAACAAAAC | 187 |
| | | Reverse | TTGTCGGATGGTTCTTGACA | |
| 121 | VLG6-A-1 | Forward | CAAAAGCTTCCTGGGCTTTA | 250 |
| | | Reverse | TTGCTTGTGAGAATGAGAGTGA | |
| 122 | VLG6-B-1 | Forward | TCCCACTTGGATCTTAGGTGT | 192 |
| | | Reverse | CGATCATGCAAGATGATGCT | |
| 123 | VLG6-C-1 | Forward | AGGACTGCATGCACAGTGG | 225 |
| | | Reverse | CCCCAGTTCCTGTAAATCCA | |
| 124 | VLG6-D-1 | Forward | GGAAGCACTCGATCGACAAT | 210 |
| | | Reverse | TTCACCCTCGCTGTAAATCC | |
| 125 | VLG6-E-1 | Forward | GGATGCATAAATAATGGGGTCA | 171 |
| | | Reverse | TTGTTGCAAAACCATGCCTA | |
| 126 | VLG6-F-1 | Forward | TTCAATGGGCAGTAATTCCA | 180 |
| | | Reverse | GGTCCGGTCCGGTTTTTA | |
| 127 | VLG6-G-1 | Forward | CCCACAAGCTCTATCCCTCA | 152 |
| | | Reverse | CCGCCCCTTTTATTTCATTT | |
| 128 | VLG6-H-1 | Forward | AACTTGTTTGCACACGCATC | 186 |
| | | Reverse | GTTGGGCTCATGGCTAGAGA | |
| 129 | VLG6-I-1 | Forward | GTGCTCTCTTTCTGGGTTGG | 194 |
| | | Reverse | GGTACGGCTTCTCAGACTGG | |
| 130 | VLG6-J-1 | Forward | CACTAAGGGCTTGGGTCACT | 140 |
| | | Reverse | CATAAGGTGACACAGGGGTAA | |
| 131 | VLG6-K-1 | Forward | TGGGGGTTATCATGAGGATG | 245 |
| | | Reverse | TGTAGACCCCCAAATTTGTCA | |
| 132 | VLG6-L-1 | Forward | ATGGTGCGAACATCTTAGGG | 196 |
| | | Reverse | GACACAGAATTCTTGGAAAG | |
| 133 | VLG6-M-1 | Forward | CAGAGCAATTCGTACTGATAACG | 228 |
| | | Reverse | AAGGCTTCTTACACCCCATGT | |
| 134 | VLG6-N-1 | Forward | TTGTGCCATCATTCAGCAAT | 219 |
| | | Reverse | TTGAAACGTCTTTGCAGCAG | |
| 135 | VLG6-O-1 | Forward | TTTACCCTACTACAAGGCTTTC | 230 |
| | | Reverse | TCTGGGCTTCCCCTATCTTT | |
| 136 | VLG6-P-1 | Forward | CATGGTCCAACAGCCATTTA | 223 |
| | | Reverse | TGTGCTATCACACCCCTTCA | |
| 137 | VLG6-Q-1 | Forward | ATGCACACGACTTTCCCATT | 193 |
| | | Reverse | TCATATGAGCGCAATGTTTACC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 138 | VLG6-R-1 | Forward | TGGGGAGGACTTCTCATGTT | 194 |
| | | Reverse | TCTGGTGTGTGTTACCTGGA | |
| 139 | VLG6-S-1 | Forward | TGGTGTTCACGCTTCTTGTG | 248 |
| | | Reverse | CCCTGTGCAAGGGAGTAATTT | |
| 140 | VLG6-T-1 | Forward | TGGTTATCCTGAATCTCTCTCACTC | 136 |
| | | Reverse | CCAACTGCCTCATGTGTTTG | |
| 141 | VLG7-A-1 | Forward | ACGCACTCCTCCTTCTCCTT | 221 |
| | | Reverse | AATGAACAGGCTCCAAAACG | |
| 142 | VLG7-B-1 | Forward | AGTGCCCACACAGCTTCATT | 166 |
| | | Reverse | GCCAACTGGGTCAGGTAAAA | |
| 143 | VLG7-C-1 | Forward | GGTAGCATCTTTTCATTCCCTA | 160 |
| | | Reverse | ATGCTTCTTTTCCACGGTTG | |
| 144 | VLG7-D-1 | Forward | AGAACAAGGACCATGGAACG | 212 |
| | | Reverse | TTTATGGCAACCCTCCAATC | |
| 145 | VLG7-E-1 | Forward | GCTGCTAGCTGGTCATCCTC | 221 |
| | | Reverse | GCAGCGCACTCTGAAAGTAA | |
| 146 | VLG7-F-1 | Forward | TCTTTCCCCATGGACATTTT | 128 |
| | | Reverse | AGTTGGGAAGCAATTGGATG | |
| 147 | VLG7-G-1 | Forward | CGTCAAAGCTTGTTTGATCTC | 188 |
| | | Reverse | AAAAACACACACACACACAC | |
| 148 | VLG7-H-1 | Forward | ACCTGTGGCCAGTCATGATA | 222 |
| | | Reverse | TCCTCCTCCAATGGAATCAG | |
| 149 | VLG7-I-1 | Forward | CATAACTCCATGCCACATGC | 217 |
| | | Reverse | GGTGACATCATTCCCCTCTG | |
| 150 | VLG7-J-1 | Forward | ATCCGAGTAGCTGCCTTGAA | 188 |
| | | Reverse | CCTGCTGCTTCTTCTTCCAT | |
| 151 | VLG7-K-1 | Forward | TGCTGCGTGGTGAATAATTT | 158 |
| | | Reverse | TCTTAGCATCCGAAGATTGA | |
| 152 | VLG7-L-1 | Forward | TTTCCCATATATAGCCCAAG | 148 |
| | | Reverse | GGATGGAACCCAAACATTCA | |
| 153 | VLG7-M-1 | Forward | AACCTTGGACACTTCACCTCAT | 171 |
| | | Reverse | TCTGTGACATATCTTCAGGT | |
| 154 | VLG7-N-1 | Forward | TCCCTCGTGGCTATCAATTT | 213 |
| | | Reverse | TGATGAATGGGATCAGGCTA | |
| 155 | VLG7-O-1 | Forward | GGCTGCCTACAAAGATTGTCA | 119 |
| | | Reverse | TTGAGATTTACCCCCAGGTT | |
| 156 | VLG7-P-1 | Forward | CCCAGAAACCCAAATTAACA | 205 |
| | | Reverse | TTTCCCATCTCATCCGTTTC | |
| 157 | VLG7-Q-1 | Forward | GCTGTTTTGGGGTGGATGTA | 170 |
| | | Reverse | AGGGGCCTCTTCATAGGTGT | |
| 158 | VLG7-R-1 | Forward | AGTGTATCAGGATTGTTTGG | 220 |
| | | Reverse | CCAGTCCATATAGGGGTCGTT | |
| 159 | VLG7-S-1 | Forward | TCTCGGACGAGATGTACACG | 147 |
| | | Reverse | AGAATGGAAAGGGAACAATG | |
| 160 | VLG7-T-1 | Forward | GCAGCGAGGATATGATCAGG | 247 |
| | | Reverse | GCAAATCGGACTGGTAGCTT | |
| 161 | VLG7-U-1 | Forward | TGAACTCCCACAAATCACCA | 194 |
| | | Reverse | AATGGGTGGTTGAAGGTGAA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 162 | VLG7-V-1 | Forward | GCTTGAGGCTTGGAAAACAG | 182 |
| | | Reverse | GGCAGGATATTCATGGTTGG | |
| 163 | VLG7-W-1 | Forward | AAGTGCCAACGGCTAACAAT | 166 |
| | | Reverse | ACACACCCTTAACCCATTCG | |
| 164 | VLG7-X-1 | Forward | ACCGTGTGTGCTCTCAACAG | 218 |
| | | Reverse | TGGGCTCACCCTAATTCACT | |
| 165 | VLG7-Y-1 | Forward | GTTCATTCAAGCCCCAACAT | 146 |
| | | Reverse | GCTTCATCACTGCCACTTGA | |
| 166 | VLG7-Z-1 | Forward | AACCCAAAAGCCTCAAAAGC | 235 |
| | | Reverse | GAGCAATGAGTGCTTCTTCTTG | |
| 167 | VLG18-A-1 | Forward | ATATTGCATGGGGATTGATG | 243 |
| | | Reverse | CGAATGCACACCAAATCTTA | |
| 168 | VLG18-B-1 | Forward | GATTGGATGCTTTGAATTGG | 255 |
| | | Reverse | GTTCTCACACAAGTCCTAAA | |
| 169 | VLG18-C-1 | Forward | AGCAAGCAAGCAAGAAACAT | 223 |
| | | Reverse | TCCATCATTCCCATATCTCC | |
| 170 | VLG18-D-1 | Forward | AGGCCATGTTATGGAGATGA | 167 |
| | | Reverse | GATGGCCGAGACAATGATAC | |
| 171 | VLG18-E-1 | Forward | GCGAGACTGTTTGGAGAAGA | 175 |
| | | Reverse | GGGCATAATGCAAATGGTTA | |
| 172 | VLG18-F-1 | Forward | GTGGTCCATAATGGGACTGA | 228 |
| | | Reverse | CCAAAATGCACACACATCTC | |
| 173 | VLG18-G-1 | Forward | GTAAGGACCTCTACTCCCTAA | 137 |
| | | Reverse | ATTCCTAAGCTGCACACCAG | |
| 174 | VLG18-H-1 | Forward | AAGGTGGTTTGTTCTCGAATC | 246 |
| | | Reverse | ATTCAACCAGCATGAGCTTT | |
| 175 | VLG18-I-1 | Forward | GCTGTCCTAAGAAGTGGGATT | 200 |
| | | Reverse | AAAACCGAAGACTGTTGTGC | |
| 176 | VLG18-J-1 | Forward | AGTTCCGAATTCAAACTAGGC | 117 |
| | | Reverse | TACATTGATGTGCCCCTTTT | |
| 177 | VLG18-K-1 | Forward | ATGAAAGGCCAGTTGGATCT | 235 |
| | | Reverse | GACAAAAACCGTTTCCCTTT | |
| 178 | VLG18-L-1 | Forward | AAAGTGCACAGGAACGAAAG | 208 |
| | | Reverse | TTCAACTTGGCAGGAAAAAG | |
| 179 | VLG18-M-1 | Forward | CCTAGCTTCAGTCGTGCAGT | 133 |
| | | Reverse | GCCTAACGGAAGGTATGTGA | |
| 180 | VLG18-N-1 | Forward | AAATCGGCCTTCCTTCTCT | 234 |
| | | Reverse | ATGCTCAGTTGCCATTTGAT | |
| 181 | VLG18-O-1 | Forward | TCCCACATCGGTTAAGAAAA | 161 |
| | | Reverse | TTGGTTCCCTCCTGTGTAAA | |
| 182 | VLG18-P-1 | Forward | GGCGCTTTGGTAATGTATGA | 177 |
| | | Reverse | CAACAATTGGCTGAGAGCTT | |
| 183 | VLG18-Q-1 | Forward | GGGATTTTGTAGAAGAAAGG | 183 |
| | | Reverse | CTCCAAAGAATTGTCTCCTTCA | |
| 184 | VLG18-R-1 | Forward | GATGCAACCACATCCTCTTC | 92 |
| | | Reverse | AAAAAGCCACCCAAGGTAAC | |
| 185 | VLG18-S-1 | Forward | TTGTGTTGCCATTTCACTGT | 134 |
| | | Reverse | TATTCCCGGAAAAAGAAACC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 186 | VLG18-T-1 | Forward | TTTAGCTACCCAAGGTTCCA | 205 |
| | | Reverse | TCCTAATGGCATGGATTGAT | |
| 187 | VLG18-U-1 | Forward | TATTGCGACCCTTAGCAGTC | 249 |
| | | Reverse | TCCCACCTTCCAAATATCAA | |
| 188 | VLG18-V-1 | Forward | TTGTTGGCATATGCTTCATC | 187 |
| | | Reverse | AAAACACTACCCTAAACGCAGT | |
| 189 | VLG18-W-1 | Forward | AAAAATGCGTCGTTGTGG | 107 |
| | | Reverse | TCCCCAACAATTCTCCATTA | |
| 190 | VLG18-X-1 | Forward | CTTGGGAAGAAGCAGAAAAA | 238 |
| | | Reverse | TGAGCCTTAGGCATCTTTTG | |
| 191 | VLG18-Y-1 | Forward | CGTTTGGTTGCTGAGAAAAT | 133 |
| | | Reverse | CGAGGAAGTGAGGAAATTGA | |
| 192 | VLG18-Z-1 | Forward | TACTGAAATCGGGTTGTTGG | 170 |
| | | Reverse | GTGGCCACAGTAAAAACACC | |
| 193 | VLG18-ZA-1 | Forward | CCAAAAAGTTGCACTTCCAC | 159 |
| | | Reverse | GCCCACACATGTTTCCTATG | |
| 194 | VLG19-A-1 | Forward | GCCATGCATGAAATGGTAAT | 192 |
| | | Reverse | GGGGATTCAAAAAGGACAGT | |
| 195 | VLG19-B-1 | Forward | TTTTCACCATTCACTCCTCAG | 232 |
| | | Reverse | CCTAGAATTCATCCTCATAGGTCT | |
| 196 | VLG19-C-1 | Forward | GGACATAGCTAGGGCATTCA | 182 |
| | | Reverse | GGTAATGAATCTGCCCAGTG | |
| 197 | VLG19-D-1 | Forward | TCTGGAACCTAAACCCCAAT | 200 |
| | | Reverse | TCCTAACACAAGGGTGCATT | |
| 198 | VLG19-E-1 | Forward | TGGAACCTCCAAGGATAACA | 180 |
| | | Reverse | AGGCTGTGCCATATCATTGT | |
| 199 | VLG19-F-2 | Forward | TGGGCATTACCCTTTAATCA | 188 |
| | | Reverse | CGCAATGAGAGACCACATTT | |
| 200 | VLG19-G-1 | Forward | GAGGCAATTAAACCAAAGGA | 162 |
| | | Reverse | GGGCTAAAGAGCCCTCATAC | |
| 201 | VLG19-H-1 | Forward | CAACCTGTTTGTTCCTTTGG | 158 |
| | | Reverse | GAACCTCCCTTCACTCCACT | |
| 202 | VLG19-I-1 | Forward | CCTTATCTTATCCCTGTCCTGA | 220 |
| | | Reverse | AGCTTCTGGGTTGGCTATG | |
| 203 | VLG19-J-1 | Forward | GGATGACGAATTCAGAGAGC | 236 |
| | | Reverse | ACTGACCATGGAACACCCTA | |
| 204 | VLG19-K-1 | Forward | TTGGCATTGAGATGATGATG | 167 |
| | | Reverse | GAAAGCAACAGTTTGGGAGA | |
| 205 | VLG19-L-1 | Forward | GACTTGTGTTAAAGTGTTCTACCC | 186 |
| | | Reverse | ATTCACACCCATCCATGTTC | |
| 206 | VLG19-M-1 | Forward | AACATTACGGGGGATTTCTC | 186 |
| | | Reverse | TGTCATGTGGATGGAGTGAG | |
| 207 | VLG19-N-1 | Forward | TTGAAAGAGGGCATTCAAAG | 179 |
| | | Reverse | CCTCATTGTCATCCCTATGC | |
| 208 | VLG19-O-1 | Forward | CTTGCTTCAATCATGGAGAA | 215 |
| | | Reverse | TTCAGTGCTCATTCATGTGG | |
| 209 | VLG19-P-1 | Forward | AACATAAGTGCCCAATGGAG | 147 |
| | | Reverse | TCTTTCCCATTGGAGTTTGA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 210 | VLG19-Q-1 | Forward | CCAGCCTGGCTTACTTACCT | 172 |
| | | Reverse | CCTCCATAGGAGAGCTGATG | |
| 211 | VLG19-R-1 | Forward | AGCAAGAAGGTGACATTTGC | 165 |
| | | Reverse | GGGTGGAGAGAGGAGAAGAG | |
| 212 | VLG19-S-1 | Forward | CAGAGTCCATCCCATCATGT | 215 |
| | | Reverse | CACACCAATCTTGCTTTTCC | |
| 213 | VLG19-T-1 | Forward | ACCTTGGATGCAAATGTTGT | 225 |
| | | Reverse | AGGGATGACAATGATCCAGA | |
| 214 | VLG19-U-1 | Forward | GATTTGGAGTGCTTATTTGAGG | 160 |
| | | Reverse | GCAAAATAGGTTTGATCCATGC | |
| 215 | VLG19-V-2 | Forward | AACGTGCTCTGATACCAAATG | 179 |
| | | Reverse | AATCGACTACAATGGCTGGA | |
| 216 | VLG19-W-1 | Forward | TGAGATCAACATGGGCAAAC | 229 |
| | | Reverse | GCCAAATTGTGTTTGATGGT | |
| 217 | VLG19-X-1 | Forward | GGCCTTGAAAGTGAAGATGA | 248 |
| | | Reverse | ATGTTGGGATGTGTTTGCTT | |
| 218 | VLG19-Y-1 | Forward | CAACGGACATTTTCCAAGTC | 238 |
| | | Reverse | GAAATGCAGGAACAAGATGG | |
| 219 | VLG13-A-1 | Forward | AAAATCGGGGCGGGAAAATT | |
| | | Reverse | CATGATATGCCTTCCACGTGG | |
| 220 | VLG13-F-1 | Forward | TGAAGTATCAGCGATTGTGGT | |
| | | Reverse | ATGATAACACCACCCTTCCG | |
| 221 | VLG13-H-1 | Forward | ACCAGGGTCCAAATAAGGTGA | |
| | | Reverse | GGAGTAGGAGGTTTTGTTGAACT | |
| 222 | VLG13-J-1 | Forward | TCCCTTAAACCAAAGACCATACA | |
| | | Reverse | AAGCAGTCCTAGTTTCTTGTGT | |
| 223 | VLG13-L-1 | Forward | AGCTATAGAACCATCCTCTACCT | |
| | | Reverse | ATTGCCAACATATGCGTGCA | |
| 224 | VLG13-N-1 | Forward | TGGCAAAGACTGTGCTCAAC | |
| | | Reverse | GCCCAAGAGATTAGATGTGCA | |
| 225 | VLG13-P-1 | Forward | AGGAGGGGTTTGTTGAGAGT | |
| | | Reverse | TGTTGCATGCCATCTCACAG | |
| 226 | VLG13-R-1 | Forward | GGTGGCCCTCATCCTCTTAT | |
| | | Reverse | TCTCTCCTATGGTATCTGACGT | |
| 227 | VLG13-T-1 | Forward | CGGGTGAGTGTAGAAAGGGA | |
| | | Reverse | CATGGCGCTTATATTAGGTGAC | |
| 228 | VLG13-V-1 | Forward | TTTGACTGCATACTAGGACAAGT | |
| | | Reverse | ATGGCCTGAGTCGAAAATATCT | |
| 229 | VLG12-A-1 | Forward | CGCTTGGCAAAGTGATAATG | |
| | | Reverse | TGGTGGATAGATTCCAAGCTC | |
| 230 | VLG12-C-1 | Forward | GGTCTACCTTCTTCCTTGGGA | |
| | | Reverse | TGGCTTGCAAATGAAGAAAGGA | |
| 231 | VLG12-E-1 | Forward | GTTTTGTGGTTGTGCATGCC | |
| | | Reverse | TCTTTCCCTACACAACACCCA | |
| 232 | VLG12-G-1 | Forward | GGGTTTCCATCTTGTTCCATCT | |
| | | Reverse | TGCCTCATGATGCATCCTACT | |
| 233 | VLG12-I-1 | Forward | CGTGGACGCAAAACATTTCC | |
| | | Reverse | TCAATGGCCCTGATTTTATCGT | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 234 | VLG12-M-1 | Forward | GCGTGATTTTCTAGAACGGTGA | |
| | | Reverse | TTCCTAGATGTCCACACGCA | |
| 235 | VLG12-N-1 | Forward | TCCCACGATGCTGGAAGTTA | |
| | | Reverse | AAAAGGAAGGCAAGGCTTTTC | |
| 236 | VLG12-P-1 | Forward | AGGTCAAGAAGGTAAAATCTGCA | |
| | | Reverse | TCCTTTACGTGGTGGCAGAT | |
| 237 | VLG12-R-1 | Forward | AGCCACCAACTACACCCATT | |
| | | Reverse | AGCGTGATTTTCTGTGAAGAGA | |
| 238 | VLG12-S-1 | Forward | GTATTGGGCCTTGAAGTGGG | |
| | | Reverse | CCTTCAAATTGTGTCACATGTCC | |
| 239 | VLG12-T-1 | Forward | TTCCCTCACTTCCCCATCAC | |
| | | Reverse | AGTCCAAACATAAGGCCACA | |
| 240 | VLG12-W-1 | Forward | TCACCCTTGGATTTGACTTCA | |
| | | Reverse | TTGGGGCTGCAATTGGTTAC | |
| 241 | VLG15-A-1 | Forward | CCTTCGTAAAGCCTTTTGTCCA | |
| | | Reverse | GCATTCAAGGAAGCAAAACAGT | |
| 242 | VLG15-C-1 | Forward | TCATCTCACCACCTTATCCTCTC | |
| | | Reverse | TGGAGATAGAAGTGGGTATGAGG | |
| 243 | VLG15-E-1 | Forward | AGCCATCCAACAACCCAAAA | |
| | | Reverse | CCTCGAGTAAGAACCGTTGC | |
| 244 | VLG15-G-1 | Forward | TGTGTCTCATGGATGTTGCT | |
| | | Reverse | ACCACATGCGTCTAGATTGC | |
| 245 | VLG15-K-1 | Forward | CCCACACACTTCATGGCTTT | |
| | | Reverse | AAGTAGGGAGGACACAAGCC | |
| 246 | VLG15-M-1 | Forward | GAACAACCCTACAACGCCAC | |
| | | Reverse | TCACCACCTCATTCACCACA | |
| 247 | VLG15-O-1 | Forward | ACAAAATTTCAAGCTTGGCACT | |
| | | Reverse | AACACACACACACACACACA | |
| 248 | VLG15-Q-1 | Forward | TCCTCCACATATATCAGCAGGA | |
| | | Reverse | TGCATTTCACAATCACGCCA | |
| 249 | VLG15-S-1 | Forward | GCATTTTCCCTCATCTTTCCCT | |
| | | Reverse | CGAATGGTTCTTTTGCCCCA | |
| 250 | VLG15-U-1 | Forward | TCCTCCCCAAACACTTTCCT | |
| | | Reverse | CACCAAGCCAAACCCAGTT | |
| 251 | VLG14-A-1 | Forward | CTGACCAGGGCAATGCATAC | |
| | | Reverse | ATCCAATTGTGTGCCGTGTC | |
| 252 | VLG14-B-1 | Forward | ATGAATGGGAAGGGAAACAGT | |
| | | Reverse | AGGGAGCACTTGGTTGTCAA | |
| 253 | VLG14-D-1 | Forward | TCCTGCTTTTGTGTGTGGAC | |
| | | Reverse | ACCACCATTGTAGCTCCCAA | |
| 254 | VLG14-F-1 | Forward | ACGTCACTCACAAACATCCA | |
| | | Reverse | AGTAGAGTTGGTGGGGTTGT | |
| 255 | VLG14-G-1 | Forward | ACAGCAAAACAAGAGATAGGGT | |
| | | Reverse | CCAAATACACTTGATGACGTGGA | |
| 256 | VLG14-H-1 | Forward | TGTCGTGTAGCAGAGGGTTT | |
| | | Reverse | TCTTTCCTAATCTTACCCTCCCT | |
| 257 | VLG14-I-1 | Forward | TGCGTTGTCTTGTGCGTTTA | |
| | | Reverse | GAGAGGGCATCATCCAGAGT | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 258 | VLG14-J-1 | Forward | GTGAACGGAACCAAACCAGG | |
| | | Reverse | TTAGTGTGGAGTCGAACCGA | |
| 259 | VLG14-K-1 | Forward | GCTTGTATGCATGTCCTAGGTG | |
| | | Reverse | GGACCAAAATCAAGGGACACC | |
| 260 | VLG14-L-1 | Forward | TGCAACGAATTTTCAGAAGGGA | |
| | | Reverse | TAGGGGTTTTCTCAGGCCAG | |
| 261 | VLG14-M-1 | Forward | ACCCCAGAGAGATTGTAGCA | |
| | | Reverse | ACACACAACGCACGAATACC | |
| 262 | VLG14-N-1 | Forward | TACCTCTCCCCTAACTCCCC | |
| | | Reverse | GCATTGTAGCTTGGTTTAGGGT | |
| 263 | VLG14-P-1 | Forward | TCACCTCACCCCACTTTTCA | |
| | | Reverse | CCTCTCATCCTTCCCTTGGT | |
| 264 | VLG14-Q-1 | Forward | ACCTTGATCTTGATACACTTCCA | |
| | | Reverse | TGGTGGGCTCAAGTCACTTA | |
| 265 | VLG14-R-1 | Forward | TGGGTGGTTTACATGTCCCA | |
| | | Reverse | TGGCTCCAACATTGCATCAA | |
| 266 | VLG14-S-1 | Forward | TGGGGTTCATGTATCCATCAGT | |
| | | Reverse | ACCCACAATGACAAATATACCCA | |
| 267 | VLG14-T-1 | Forward | TGTTCGGATGTTGTTCTCCA | |
| | | Reverse | TGGTATTGGGTCATGAAGAGAGA | |
| 268 | VLG14-Y-1 | Forward | ACTAGATTTGGTAGGTGCCCC | |
| | | Reverse | GCCTTGGTTATTCTGATTGCCA | |
| 269 | VLG14-AA-1 | Forward | CCTTCTCTCTTTTGGGCCCA | |
| | | Reverse | TGCAAGCATAAGGACACGTT | |
| 270 | VLG14-AC-1 | Forward | GTTGTGAATTTCATATGCCTGCT | |
| | | Reverse | CTGGCCCTCTCTTGGTTGTA | |
| 271 | VLG14-AD-1 | Forward | GGACATGGATTGGGGTTTCAC | |
| | | Reverse | AAACATATCCCAAACCCGGC | |
| 272 | VLG16-A-1 | Forward | CAAGGGGTTACTTTGGTTCC | 196 |
| | | Reverse | TAGCCTTAAGGTGCCCTTTT | |
| 273 | VLG16-B-1 | Forward | TGTGGTACATCCAAAATGTGAC | 195 |
| | | Reverse | GATGTCAAACAGGGATGGAA | |
| 274 | VLG16-C-1 | Forward | CCTTTTGCACGCAGTAAAAT | 238 |
| | | Reverse | TTTCCTAGGCTGTTGTGTCC | |
| 275 | VLG16-D-1 | Forward | CGTGTTACCACAGTATTGATGC | 214 |
| | | Reverse | GGTCTGAGTGGTACTTTCAGGA | |
| 276 | VLG16-E-1 | Forward | AGGCATGTTCTTGATTTTGG | 154 |
| | | Reverse | TGTCAAACTCAAACCCTCAA | |
| 277 | VLG16-F-1 | Forward | CCAATTTCCTCACCTAATGC | 222 |
| | | Reverse | CCCTTCAAGCTTTACAACCA | |
| 278 | VLG16-G-1 | Forward | TTTTTCAGATCCCTTGTGGA | 269 |
| | | Reverse | AGCACCAAGATGCAGAAAAC | |
| 279 | VLG16-H-1 | Forward | CTAAAAAGGGATGGGAGGTC | 162 |
| | | Reverse | TCTTCTAGCCAGTCCCCAAT | |
| 280 | VLG16-I-1 | Forward | GTGGAATTAGAGGAATTTAGGG | 216 |
| | | Reverse | TCATCAGCACTTATCAAGAC | |
| 281 | VLG16-J-1 | Forward | CTTGTTGGAGGAGTAAATCCAA | 99 |
| | | Reverse | CAGTCGGACAAATGGTTTTC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 282 | VLG16-K-1 | Forward | CAATCCTGAGGAAAATGGTG | 253 |
| | | Reverse | GGTGATCAACATTGGAGCAT | |
| 283 | VLG16-L-1 | Forward | CACCAAGGCTTAGTTTGTGC | 189 |
| | | Reverse | CGGGCTTCGAATCTTAAACT | |
| 284 | VLG16-M-1 | Forward | GCCACCACCTATATGGATAAAA | 261 |
| | | Reverse | GGAAGGATTCAATGGAAGGT | |
| 285 | VLG16-N-1 | Forward | GCAGAGAGAGGCAATACCAA | 258 |
| | | Reverse | ACCAAAATGGGAAATCTTCG | |
| 286 | VLG16-O-1 | Forward | TTGATGCTGGAAGCACATAA | 203 |
| | | Reverse | AAACCCGGGATAGGGTATATT | |
| 287 | VLG16-P-1 | Forward | GTGATATCTCACATTGGATTGG | 262 |
| | | Reverse | AGAGAGTAGGTGAACCCCAAA | |
| 288 | VLG16-Q-1 | Forward | CATGTCATCAACGCCAATTA | 169 |
| | | Reverse | CCCATTGAATGTTTGTTGAC | |
| 289 | VLG16-R-1 | Forward | ACCCAGCTAGAGAGCCACTT | 81 |
| | | Reverse | AAGTCAAGTGGTGGTCCAAA | |
| 290 | VLG16-S-1 | Forward | CGAGTTTGAATCCCCATTAT | 245 |
| | | Reverse | CCGGTTTTGGCTCTTTTAGT | |
| 291 | VLG17-A-1 | Forward | CCTCCTCCATCCCACTATTT | 159 |
| | | Reverse | GGGGCTAATGAAGGTTTGAT | |
| 292 | VLG17-B-1 | Forward | TTGCTTATCCCCCTCTTCTC | 237 |
| | | Reverse | CGCCAGACTGTAACCAATTC | |
| 293 | VLG17-C-1 | Forward | ACTGTGTCCGAGTGCTGTTT | 256 |
| | | Reverse | TGGACTTTTTGGTGGTGACT | |
| 294 | VLG17-D-1 | Forward | GAAGTGGTTTTTACGGATAG | 214 |
| | | Reverse | CAGCACTGATGAGCTGTGTC | |
| 295 | VLG17-E-1 | Forward | AAGCCGTATTCTTTCGAGGT | 219 |
| | | Reverse | GTTCTATCCCCAACCGTTTT | |
| 296 | VLG17-F-1 | Forward | CCCAGGGTTTCCATTTCTAT | 174 |
| | | Reverse | TTCCTCTCCCCATTCTCTCT | |
| 297 | VLG17-G-1 | Forward | CTTTTCTTTCCCTCGCATTT | 234 |
| | | Reverse | GGGATGGATTTCTTGATTACC | |
| 298 | VLG17-H-1 | Forward | GCTCTTTCCTCCATTCTTCC | 232 |
| | | Reverse | CTCACGATCTTGCCAATTTT | |
| 299 | VLG17-I-1 | Forward | TGGCTCGTCTTTTGTTACTTG | 203 |
| | | Reverse | CATCAGCAGTGTTTCCATCA | |
| 300 | VLG17-J-1 | Forward | AGGAAGAGGATTGATCACCA | 199 |
| | | Reverse | AATTCTTGGTAAGGTGCCAAC | |
| 301 | VLG17-K-1 | Forward | GGGATGGGTGTGTGTGTATT | 236 |
| | | Reverse | CATGCTCACCACTTTTCACA | |
| 302 | VLG17-L-1 | Forward | CGATGGATCCCATAGTTTGA | 270 |
| | | Reverse | GTTGCTTGAGGTGTTTGGTT | |
| 303 | VLG17-M-1 | Forward | CCAATGTCACTGATAACCAAAG | 270 |
| | | Reverse | GGTAAGGGTTAGTAATGCAA | |
| 304 | VLG17-N-1 | Forward | AACTACCAGAAGCAGCAACC | 244 |
| | | Reverse | CGAGTTACCAGGGAATGATTT | |
| 305 | VLG17-O-1 | Forward | ATTTCCCTTTTTCCCACATC | 220 |
| | | Reverse | TGGTTTTTGATGCCTAGCTC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 306 | VLG17-P-1 | Forward | CACCTCCTTGCTCTCAAAAA | 149 |
| | | Reverse | AGGAGAAGAGAATGGGTTGG | |
| 307 | VLG17-Q-1 | Forward | AGAATTAGTGTGGGGAACAA | 225 |
| | | Reverse | CTTGCAAATTAGACACATGG | |
| 308 | VLG17-R-1 | Forward | AAGTGCCAAACGAATTTCAG | 173 |
| | | Reverse | CGCAACCCTAAGAATGAGAA | |
| 309 | VLG17-S-1 | Forward | CCAACCCACTTAGGTTCACTT | 205 |
| | | Reverse | TGTTGTTGTTGTGTGCATGA | |
| 310 | VLG8-A-1 | Forward | AAGCAGAGCCATCACATGAC | 238 |
| | | Reverse | CCTTAAACCACATGTTCCAAAG | |
| 311 | VLG8-B-1 | Forward | ATTTTCGTGGGGATGAGCTA | 142 |
| | | Reverse | CAATGCCATTTCTCCTATCCA | |
| 312 | VLG8-C-1 | Forward | GTTCAGTTTGGTGCCCTTTT | 220 |
| | | Reverse | CCCATGTCAAACCTTGAAGC | |
| 313 | VLG8-D-1 | Forward | GAGGGACTAGGGGCTCAAAC | 175 |
| | | Reverse | AAAGGTTTAGGAGACGCAAAAG | |
| 314 | VLG8-E-1 | Forward | GATCGATCTGTCATCATCATCTTC | 216 |
| | | Reverse | GGACATATTTTCACCTGCAAGA | |
| 315 | VLG8-F-1 | Forward | CAAAAGCTGAGTTCCTTTGTTG | 163 |
| | | Reverse | GTACATTCACCTTTTTAGGG | |
| 316 | VLG8-G-1 | Forward | GATGGGTAGTCACTTGTTTGGA | 187 |
| | | Reverse | GGAGTGATGAGTTTGATTTG | |
| 317 | VLG8-H-1 | Forward | TCTCCAGGAAGTTTTACCAACA | 119 |
| | | Reverse | TCCTCTCATGGATAAGTTTCCCTA | |
| 318 | VLG8-I-1 | Forward | AACAAACTCAAGCTCACCATTG | 207 |
| | | Reverse | TTTCCTCTCAGCACCAGCTT | |
| 319 | VLG8-J-1 | Forward | CGACTTATGCATCTCAGTCAA | 213 |
| | | Reverse | TGTATCCACCAAACACAATGG | |
| 320 | VLG8-K-1 | Forward | GCCCACTTACATTTTCCCAAT | 196 |
| | | Reverse | TTGGAGCCTTTCAATGAAGC | |
| 321 | VLG9-A-1 | Forward | TGGTTAACAATGCCCTCACA | 170 |
| | | Reverse | TTCGGGGTATTTCCATGTGT | |
| 322 | VLG9-B-1 | Forward | CCTCCATGCCAATCCTAGTC | 209 |
| | | Reverse | CTCCGAGTCAATCCATTCAA | |
| 323 | VLG9-C-1 | Forward | TGCATGCTGAGAAAATCTGC | 245 |
| | | Reverse | CCATTTGGTTGCTAGGGAAA | |
| 324 | VLG9-D-1 | Forward | AGCACTCGTCTCGAATCCAT | 235 |
| | | Reverse | GGTCCAAGTCATCCCCATTT | |
| 325 | VLG9-E-1 | Forward | GTCTTCAAGCCTTGGTGCTC | 217 |
| | | Reverse | GCTCAAGTTTTCACCCAAGG | |
| 326 | VLG9-F-1 | Forward | TCGAACCAATTTGGAAGTGA | 221 |
| | | Reverse | GTCCAATAAAAGCGTACCCAAA | |
| 327 | VLG9-G-1 | Forward | TCCGCTGAGTACTTGTCGTG | 229 |
| | | Reverse | ATTGGGCCTCACGAGTCTTA | |
| 328 | VLG9-H-1 | Forward | AAGGTTGTGGCCTTTGAGTG | 240 |
| | | Reverse | CACAAATCATCCTGGGCTTT | |
| 329 | VLG9-I-1 | Forward | TTTAATGGGGGATGGGGTAT | 233 |
| | | Reverse | GGCGATGAAGATTGGGTTTA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 330 | VLG9-J-1 | Forward | GTGATCTTCATCACAAGTTTGG | 213 |
| | | Reverse | ATGGCATGCACAACTAGCAA | |
| 331 | VLG9-K-1 | Forward | GGCAGATCACAGCTGAAGGT | 165 |
| | | Reverse | GCAAGTTGTCCCCCTATCAA | |
| 332 | VLG9-L-1 | Forward | CCCAATACTAACAGCACAAA | 240 |
| | | Reverse | ATGCAAAATTTCCTGCCATC | |
| 333 | VLG9-M-1 | Forward | GCCAAACTTGGGGAGATTC | 247 |
| | | Reverse | CACCACACATAATGCTTACCG | |
| 334 | VLG9-N-1 | Forward | CGATGCCAGAGAATTCACAC | 221 |
| | | Reverse | ATCGATCCGGGAACAGAACT | |
| 335 | VLG9-O-1 | Forward | GATGTATTGGGTGTATCCCAAAG | 93 |
| | | Reverse | GGTCTCTATGCAGGAATAAACCA | |
| 336 | VLG10-A-1 | Forward | GTGGAGGTGGAGCAACTCAT | 194 |
| | | Reverse | CACCACCCCAGCTCTCTTTA | |
| 337 | VLG10-B-1 | Forward | CCCCACCACTACCAGACAAG | 249 |
| | | Reverse | AACCGAACAAAATGGAGTGC | |
| 338 | VLG10-C-1 | Forward | TCCACAACTCCATGAACAGC | 236 |
| | | Reverse | AGTTGCCCTTGGTTCTCCTT | |
| 339 | VLG10-D-1 | Forward | CTCAAGTCCAACCACCCAAC | 178 |
| | | Reverse | CTCCTACCCAAGTCCAGCTC | |
| 340 | VLG10-E-1 | Forward | CCCACCGTGGAAGATAAAAA | 212 |
| | | Reverse | TGAATGTTGTGTTCAAGGAG | |
| 341 | VLG10-F-1 | Forward | CAATAGGGGCGTCCTGTTTA | 155 |
| | | Reverse | AGGATTCCGGATTCTCTTCC | |
| 342 | VLG10-G-1 | Forward | AAAGGGCAACAAAAATGCAG | 211 |
| | | Reverse | TCGTGAAAGAGAAGGTTGCT | |
| 343 | VLG10-H-1 | Forward | TGTTGTGTCTCCTCTCTGTGG | 191 |
| | | Reverse | CAGGCATGCTTCATCTCTCA | |
| 344 | VLG10-I-1 | Forward | ATCAAAGGGGTGAAATGTGC | 248 |
| | | Reverse | TGATCATTTTGTTCGAGAGG | |
| 345 | VLG10-J-1 | Forward | TCCATCCTCACTTAATGGTGAA | 161 |
| | | Reverse | GGCCTCTATGCCTCCTCAAT | |
| 346 | VLG10-K-1 | Forward | ACCTGATCCCTGTGACTTGG | 197 |
| | | Reverse | GATTTCCACCCATCTTGTGG | |
| 347 | VLG10-L-1 | Forward | CAGAACCAGTGCTAGAAGCAT | 176 |
| | | Reverse | GAGATCCAGCTTGGATTGGA | |
| 348 | VLG10-M-1 | Forward | ATGGGGGCTAGACATACACG | 163 |
| | | Reverse | GTTGTCGCTCCCATTTTGTT | |
| 349 | VLG10-N-1 | Forward | TGATCGGAGGAGCCTAATTG | 183 |
| | | Reverse | AAGAGCGGGAAAAGGAAAAG | |
| 350 | VLG10-O-1 | Forward | GGGCAATGGAAAGAATGAAA | 175 |
| | | Reverse | AAATGACCCAAGCCTTGATG | |
| 351 | VLG10-P-1 | Forward | TGGCATTTACGCAACTCTTTC | 207 |
| | | Reverse | GTTCTCCCCTTCCATTGTCA | |
| 352 | VLG10-Q-1 | Forward | GAAGAATCCTCCCTGCTTCC | 197 |
| | | Reverse | ACCCACGTTTTCTAAGATCA | |
| 353 | VLG10-R-1 | Forward | GAAGGTTCGTAGCCCAATGA | 217 |
| | | Reverse | GATTCCAATCACTTTGCTCA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 354 | VLG10-S-1 | Forward | AAAGACACGAGTCCGTCTTCA | 187 |
| | | Reverse | TTCGACTGCCTCTCTCCAAT | |
| 355 | VLG10-T-1 | Forward | GCATGCCAATAAAGTTTCTGC | 170 |
| | | Reverse | TTGCAGCACCAGTAAATCCA | |
| 356 | VLG10-U-1 | Forward | TTTTCTCCGGATTTGCATTC | 155 |
| | | Reverse | TTGAGTTACCAACACCCAAGC | |
| 357 | VLG10-V-1 | Forward | TGAGGGGGCCTACCTAGTTT | 156 |
| | | Reverse | GGAGAGACCAAGTAAATGTCCAA | |
| 358 | VLG10-W-1 | Forward | GTCCTTGTGAGTGCTGGTTG | 175 |
| | | Reverse | CAACCCTGAGGACCCTAACA | |
| 359 | VLG10-X-1 | Forward | TTCCAATGGTATGCAACGTG | 236 |
| | | Reverse | TTAGCCCATGGATGTCACCT | |
| 360 | VLG10-Y-1 | Forward | GAGGAGGAAAGGAAGGGAAG | 181 |
| | | Reverse | TCCCTAAAACACCCTTTTCT | |
| 361 | VLG11-A-1 | Forward | TGTTTCCAGACATGCACCAT | 224 |
| | | Reverse | AAATTCCTGGACAGCACCAC | |
| 362 | VLG11-B-1 | Forward | AAAGGATTTGCTTGAAGTGCTC | 218 |
| | | Reverse | GCCCGAGGACCAATTACTTC | |
| 363 | VLG11-C-1 | Forward | AAAAGATTGCCCCCAAGTTT | 208 |
| | | Reverse | GTTTAAATCACGGTCAAACC | |
| 364 | VLG11-D-1 | Forward | TCCTGTTTGCTTGCTCTTTTC | 118 |
| | | Reverse | TGCCACAATTCTTCTCTCCA | |
| 365 | VLG11-E-1 | Forward | GTCTTTGCGGGTTGATTGAT | 170 |
| | | Reverse | TGAAGTTGGATAGCGACCAT | |
| 366 | VLG11-F-1 | Forward | TGGTTGCATTTTCTCAAGTCTG | 188 |
| | | Reverse | TTGCCATCATCCAACACATT | |
| 367 | VLG11-G-1 | Forward | AGGTATTGTTGGAGGGTGTTG | 152 |
| | | Reverse | CCCGTCATTTTGATCCTTGT | |
| 368 | VLG11-H-1 | Forward | CAAGGCTATGAGTCCTAACTACCA | 183 |
| | | Reverse | AAAAGGTTTGGGGATGGTTT | |
| 369 | VLG11-I-1 | Forward | TGGCTAAGGGGTCAAATGAT | 185 |
| | | Reverse | CCATCTGCCATGGTTTTCTT | |
| 370 | VLG11-J-1 | Forward | ATTTCTGCGCTCACACTCCT | 186 |
| | | Reverse | AAGCTAAGTGGCGAGCATGT | |
| 371 | VLG11-K-1 | Forward | TATGGAATGGTGCGAAGTGA | 167 |
| | | Reverse | GCGAAATAAGTGACCCTTCC | |
| 372 | VLG11-L-1 | Forward | CATCCTCCATGGGTCATTTC | 238 |
| | | Reverse | TGCTCAATACCACCATTTGC | |
| 373 | VLG11-M-1 | Forward | AACCCGGATTCACTTCAGC | 196 |
| | | Reverse | GGTTGGAAACTTGGAAGTGG | |
| 374 | VLG11-N-1 | Forward | TCTAGGGTCTGTTTGAGCTTCT | 242 |
| | | Reverse | TCTCATCCTGTTTCCAACTCTT | |
| 375 | VLG11-O-1 | Forward | TGCCAGGTCCTGATGTGTTA | 150 |
| | | Reverse | GGCATAGCATCAACCCCATA | |
| 376 | VLG11-P-1 | Forward | TGGGACACCTCATAAAGACCA | 128 |
| | | Reverse | ACCATGCTCAGGTTTCAAGG | |
| 377 | VLG11-Q-1 | Forward | ACGAGCAAAAGTCCATGTCC | 241 |
| | | Reverse | CGTTTTTGCCCAAAATCAAG | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 378 | VLG11-R-1 | Forward | ACCAGTTCACTAGCCGTTGG | 187 |
| | | Reverse | CGAGGTCTGGTCAAGAGGAG | |
| 379 | VLG11-S-1 | Forward | GGCAAATTGATGGAAGACTTG | 250 |
| | | Reverse | GGCAATGTTTTGCTTCCTCT | |
| 380 | VLG11-T-1 | Forward | TTTTTCAGGGCATATCAGGA | 209 |
| | | Reverse | AGGTTCAAAGGTGTGGGCTA | |
| 381 | Y-2-1A | Forward | TCCATGAGAGATGTAGATGTG | |
| | | Reverse | CTCCTGCGATGAGTAACC | |
| 382 | Y-2-1B | Forward | CTCCATTCTCTTATCCTAACCA | |
| | | Reverse | AACTCAACTCCTAGCCAAG | |
| 383 | Y-2-2A | Forward | AGCAGATGGACTGATGGA | |
| | | Reverse | ATCTTGACCACACTCTAACA | |
| 384 | Y-2-2B | Forward | CCAGTTGTAGACCGATCC | |
| | | Reverse | GCATAGTTAAGTGCTTGTGT | |
| 385 | Y-2-3A | Forward | CCTTCATTGAATGCTGGAAT | |
| | | Reverse | GCGAACTATACACCACAGA | |
| 386 | Y-2-3B | Forward | GGAGGTTCTAGGTTCATGTC | |
| | | Reverse | TAGGAAGTGTATCCCAATAGAC | |
| 387 | Y-2-4A | Forward | CCTCCTTCCACTTCCTCT | |
| | | Reverse | AATGTATCCGACTCAAATGC | |
| 388 | Y-2-4B | Forward | ATGAAACGAGTCCTTATCCA | |
| | | Reverse | ACATAGTTAGGCTACAACCA | |
| 389 | Y-2-5A | Forward | ACCTGACTAGGAGCTGAC | |
| | | Reverse | CCTCACACTTGGTATGCC | |
| 390 | Y-2-5B | Forward | CTTACGTCTCGCTGAGGT | |
| | | Reverse | GCCAGCAATTCGTTTATAGG | |
| 391 | Y-2-6A | Forward | ATGCCTCTTGTCTATCTTGG | |
| | | Reverse | CCTCCATTGAGACTTCCTAC | |
| 392 | Y-2-6B | Forward | ATGGTTCATTATGGGTAGCC | |
| | | Reverse | CTGTGATTGGATGGTATTTGG | |
| 393 | Y-2-6C | Forward | TACCTCCTGAGTGAGACAA | |
| | | Reverse | ACATGATCCCACTACTATCTG | |
| 394 | Y-2-7A | Forward | CACTATTCACTCACGAGATTAC | |
| | | Reverse | CTTACATGGTGAGAGGTAGG | |
| 395 | Y-2-7B | Forward | GGAATATTGGATTCTTTCAGGG | |
| | | Reverse | TTCGTCGTCGAGTGGAAG | |
| 396 | Y-2-8A | Forward | CCAAGTATGAGTGTTGTATCTC | |
| | | Reverse | GATTTCTCCATTCCCTATCCT | |
| 397 | Y-2-8B | Forward | TCTTGTTGTCTTCGTCTCC | |
| | | Reverse | AGAGCGAAAGGGTAGGAA | |
| 398 | Y-2-9A | Forward | TGTTCCTACCTCAATTCCTT | |
| | | Reverse | AAGTGACCTAAGCCTTTGTA | |
| 399 | Y-2-9B | Forward | GTATGTGAGGTTGAGATTGT | |
| | | Reverse | TAGGACTCGCATCCCAAA | |
| 400 | Y-2-10A | Forward | ATTCAATGGTCCTTCAGTGT | |
| | | Reverse | CGCAGATTGGTGGATTATG | |
| 401 | Y-2-10B | Forward | GTACACACAGCTACTCTCTC | |
| | | Reverse | GACAATCCGCTTCCCATC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 402 | Y-2-11A | Forward | AGCAACATCACCAACCAAT | |
| | | Reverse | GAGAAGAGAAGAACCTGAGAG | |
| 403 | Y-2-11B | Forward | GCAGCATCTTCCAGAAGT | |
| | | Reverse | AAATTCACACCCTCCACTT | |
| 404 | Y-2-12 | Forward | TTCCAAGTGCCTCTTATCTT | |
| | | Reverse | AAGCGGAGAAAGGAATGTT | |
| 405 | Y-2-13A | Forward | TGGCTACTAATTGTAAGACC | |
| | | Reverse | CCACTTGGTTAATGACTTCT | |
| 406 | Y-2-13B | Forward | CATGTGGCACTCATTGGG | |
| | | Reverse | GTCGGATTGCTATATGTAAGTG | |
| 407 | Y-2-14A | Forward | AAGAGTGGTATATCCTTCCC | |
| | | Reverse | TGCACCAATTGACATAACC | |
| 408 | Y-2-14B | Forward | GCATTAGTTGATCTGGATTG | |
| | | Reverse | GTGAAAGCACACAGAAGAT | |
| 409 | Y-2-15A | Forward | CGAACCAACAATAGGAGTAG | |
| | | Reverse | AGCCTTACCAACATCACAT | |
| 410 | Y-2-15B | Forward | GCTCCTTGTGGTGTAGAA | |
| | | Reverse | TCTGAAACCCTAATCCCTTC | |
| 411 | Y-2-16A | Forward | AACAAGGTCGGCAAGAAC | |
| | | Reverse | TGAGGAGTTGGTTACAGAGA | |
| 412 | Y-2-16B | Forward | GGTCAAGAACGCACCTATT | |
| | | Reverse | CCTTATGGTCGGGAGTCA | |
| 413 | Y-2-17A | Forward | GCTCAAACATAAAGTTCACC | |
| | | Reverse | CATCTTCCTACGGTCCTTC | |
| 414 | Y-2-17B | Forward | GGAGTCCTAACTACCATACAT | |
| | | Reverse | GTCTTGGACACTTGAGAATT | |
| 415 | Y-2-18A | Forward | TTGGGTTGGGTTCATCAAT | |
| | | Reverse | GCCAGATATGAGAACAAGGA | |
| 416 | Y-2-18B | Forward | TGGGAAACCTCAAGAAGTG | |
| | | Reverse | GCCTAATGGTGTCCTAATTG | |
| 417 | Y-7-1 | Forward | GGGTTTGAGTTGATCGTATATC | |
| | | Reverse | GGTTGATTAGATTTGGCTACAC | |
| 418 | Y-7-2 | Forward | AGGTGAGGTTGAGGTAGAT | |
| | | Reverse | GTAATGGACCAGTGAGTGA | |
| 419 | Y-7-3 | Forward | AACACATGACCTCTTGCTAA | |
| | | Reverse | AGTGGATGGCTTAGTTGAC | |
| 420 | Y-7-4 | Forward | CTGGTCCATTAAGTCAAGTG | |
| | | Reverse | TTCCTCTCCAAGATTCAGTC | |
| 421 | Y-7-5 | Forward | TTATCCTCGTTGGAAATCCC | |
| | | Reverse | GCTTGAGTTCACCAATGGA | |
| 422 | Y-7-6 | Forward | ATGCCATCTATCACAATGTG | |
| | | Reverse | TCATCCTTTAACCTCGTTTG | |
| 423 | Y-7-7 | Forward | ACCCTTTGTGTCTCCCTT | |
| | | Reverse | GTGACTCCAACCTTGAAGA | |
| 424 | Y-7-10 | Forward | TTGTGCTAGATGTTGCTGTA | |
| | | Reverse | TGGAATTGGTCGCTCTAAC | |
| 425 | Y-7-11 | Forward | TCCACCTCCTGATCTGTC | |
| | | Reverse | AGGACTCCTAGCCTTGTATA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 426 | Y-7-12 | Forward | GTCACATACTACAACAGTGT | |
| | | Reverse | CATGGGTTTCGATGATCTAT | |
| 427 | Y-7-13 | Forward | CTGAAGCACCAACTGAAGA | |
| | | Reverse | GGAATACAAGCAATCCCAAA | |
| 428 | Y-7-14 | Forward | CCCATACACATGACAATATACG | |
| | | Reverse | CTGGAAAGAAGACACCTCTAT | |
| 429 | Y-7-16 | Forward | GCAAATCCAAGGCACATAA | |
| | | Reverse | CTCGTCACTCACTCACTG | |
| 430 | Y-7-17 | Forward | GTAAGCACAAGAGCCATAGA | |
| | | Reverse | TTCGTCGTGACTGGAGTT | |
| 431 | Y-7-18 | Forward | GGACTGTCTTGATACTGTTCA | |
| | | Reverse | ATTAGGCATTCCAGTTGTGT | |
| 432 | Y-7-19 | Forward | AGTTGAATCCTCTTTCTCTC | |
| | | Reverse | GGTGAGACTATTGTGGATAA | |
| 433 | Y-7-20 | Forward | GAGACTCAGATAGAGATAGAGG | |
| | | Reverse | AAGGACGGAAACTGCTTT | |
| 434 | Y-7-21 | Forward | GTCATTGCATCACCTTCAT | |
| | | Reverse | CTATGTGTATGTTGATGTGC | |
| 435 | Y-11-3A | Forward | TCCGCACAATTCATATCATC | |
| | | Reverse | GTGACATGCTAAACAGTGAA | |
| 436 | Y-11-3B | Forward | GTTAGCCGTCTTATGAATAGC | |
| | | Reverse | AATATGAGAGACAAGAGGGTAG | |
| 437 | Y-11-4A | Forward | GGCGTGATTCAAGGAGAG | |
| | | Reverse | CCCTATGAATGATGCTTTCG | |
| 438 | Y-11-4B | Forward | CCAACAACCAAACAATTTCG | |
| | | Reverse | CTTCTTCTTCCTCTTCTTCTTC | |
| 439 | Y-11-5A | Forward | ACTAAGACTACCAACTCCTTC | |
| | | Reverse | GAATGAACTCTGGGATAATAGC | |
| 440 | Y-11-5B | Forward | CCTATATGCTTTGGGTCGG | |
| | | Reverse | TGTTCCATGAATTGCCTAAG | |
| 441 | Y-11-6A | Forward | GGACCACCATCTCAATATACC | |
| | | Reverse | GGAGCCACTGAAGAGACA | |
| 442 | Y-11-6B | Forward | TGCCCTTGAATCTATTGGAA | |
| | | Reverse | GTACTGTCACTGATGGAAGA | |
| 443 | Y-11-7 | Forward | TCTCGTGCTCCACACTATA | |
| | | Reverse | ACTAGAATTACGTGGCTGTA | |
| 444 | Y-11-8 | Forward | GATGTCTCTGCTGCTACTT | |
| | | Reverse | TTACTAGGTATCAGGAGGTTAC | |
| 445 | Y-11-9A | Forward | AAGGCAGGTAGACATAACAT | |
| | | Reverse | GTAATTCTGTGGATCGCTAT | |
| 446 | Y-11-9B | Forward | CACCTAACCACAAACAAGAA | |
| | | Reverse | AAGAGGTTGGGTGACATTT | |
| 447 | Y-11-10 | Forward | TTCTGAGTGTCACGAGGT | |
| | | Reverse | GTCCATTTCAACCCTATTCTG | |
| 448 | Y-11-11 | Forward | AAGGATAACCAGCGTTAGTT | |
| | | Reverse | CCTGATTGGAGTTGAACCTA | |
| 449 | Y-11-12 | Forward | ACTGGGATTGGAAGTATTAC | |
| | | Reverse | TGAGTGTATAGGAGGTATGG | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 450 | Y-11-13A | Forward | AGTCTGAGTGTATAGGAGGTA | |
| | | Reverse | GCAGAGCCATCACATGAT | |
| 451 | Y-11-13B | Forward | CCACTGTCTCTGATTATTAGTC | |
| | | Reverse | ACAATTCCTATGCTCACCAA | |
| 452 | Y-11-14 | Forward | CCTACTCCTTCTCAGGTTTG | |
| | | Reverse | CCTTTCTTGATATTGGGTTGG | |
| 453 | Y-11-15A | Forward | GAGACTTCCTCATGGATATTC | |
| | | Reverse | GGAACCTGAAGACAAGTTG | |
| 454 | Y-11-15B | Forward | TTAGGCTGGTTTGGTTTG | |
| | | Reverse | CAATTTCTCCTCTACATGAG | |
| 455 | Y-11-16 | Forward | GAGTGGAGTTGGGATACATC | |
| | | Reverse | GCTTAGGACATTAGGCTTCA | |
| 456 | Y-11-17 | Forward | GTGCAACGATCATAACTCAT | |
| | | Reverse | GCCATATCCTTATCCCAAGA | |
| 457 | Y-11-18 | Forward | TCTCAAGATAGCATGTGGAA | |
| | | Reverse | GTGGCAAATTCATTTAGACC | |
| 458 | Y-11-19 | Forward | CCTGTTAAGGTATTTAGGTGGA | |
| | | Reverse | CGTAAGGAACTCGCAATGA | |
| 459 | Y-11-20 | Forward | TGACAAGGATGATGCAACTA | |
| | | Reverse | AACATTAGGGCTAACACCAA | |
| 460 | Y-15-1A | Forward | CTACACATGGATCTTTCGTATG | |
| | | Reverse | GCACAAGACTAGAAGGACAT | |
| 461 | Y-15-1B | Forward | GGATGAGTGTAACAATCAAC | |
| | | Reverse | CTAATGGCTTAGCATCTAAG | |
| 462 | Y-15-2 | Forward | GCCTAATATCCACATGAGTT | |
| | | Reverse | ATTGCGAGTTCCACACAT | |
| 463 | Y-15-3A | Forward | ATGGATAAGTTTCCCTACTCTC | |
| | | Reverse | CGGAGCTTAGTTGCTTAATTC | |
| 464 | Y-15-3B | Forward | GAGACTTTAAGCTTGAGGAA | |
| | | Reverse | CTAGACCCGAACAAAGAAA | |
| 465 | Y-15-4 | Forward | TGGCTTCTTCATTCCTTGG | |
| | | Reverse | TGCTTATATCACCAGGACCT | |
| 466 | Y-15-5A | Forward | TCCATACACCTTAACGGTAA | |
| | | Reverse | ATGAGTCTTGCTTGTCTGT | |
| 467 | Y-15-5B | Forward | CTTTACGCACTTCAGCATTA | |
| | | Reverse | CTTCCATCCATAGCACTTCT | |
| 468 | Y-15-6 | Forward | AGTCAGTCTAAGAACGGATAC | |
| | | Reverse | ACCCTATTCTCTACTTCAAACC | |
| 469 | Y-15-7A | Forward | AGTATGTAAGGTTGAGATCG | |
| | | Reverse | AAGTGTAGGCGTAGGATG | |
| 470 | Y-15-7B | Forward | GAGCAAGACATTGTTCAAGA | |
| | | Reverse | TCTGAAGAGCATTGTTGTTG | |
| 471 | Y-15-8 | Forward | AACATTCTTGCCTCTTAACG | |
| | | Reverse | GGTGATAGTCGGTTGTGAA | |
| 472 | Y-15-9A | Forward | ACGGTAAGAGTCCATGTATTC | |
| | | Reverse | TCATCGCTAACCTCACAAC | |
| 473 | Y-15-9B | Forward | TACACCACCTTACTAGACTTG | |
| | | Reverse | GGCATTGTTTGTGAGCATT | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 474 | Y-15-10 | Forward | CACTCCATAAGAGACTTGTTG | |
| | | Reverse | TGTCCTCAAATCTGTTCCTT | |
| 475 | Y-15-11 | Forward | CTCTTCTTTCAATATGGTAGGC | |
| | | Reverse | AGTCGTCTAACCTATACTCCTA | |
| 476 | Y-15-12 | Forward | CCAATGCTTTCTTGCTCAT | |
| | | Reverse | CTCTTCACTAATCAGGTAGGA | |
| 477 | Y-15-13 | Forward | AGAGGAGAGAAATCGCATAC | |
| | | Reverse | CCAACACCAGGTCACTTC | |
| 478 | Y-15-14 | Forward | CAACACCTTCTCTTCTCTATG | |
| | | Reverse | CCAGAACTCTGATCTCAATC | |
| 479 | Y-15-15A | Forward | CTGCGTGACATCCATAGC | |
| | | Reverse | GGACCAACTCAACATTAGGA | |
| 480 | Y-15-15B | Forward | CCATCAATCTCAGTCTCATT | |
| | | Reverse | CCATGTCCAAAGGCAAAT | |
| 481 | Y-15-16 | Forward | CCAGTGGTCATAATAAGATGTC | |
| | | Reverse | TGCTTGCTTAGTAAGAAGGT | |
| 482 | Y-15-17A | Forward | CCTTGTAACGATAGATTCAGAG | |
| | | Reverse | TACCAACCAACCATACCATT | |
| 483 | Y-15-17B | Forward | GCACTGTAAGTCCTATTCTCT | |
| | | Reverse | GCTCTCGTTCAGATGATGG | |
| 484 | Y-15-18 | Forward | GATGAGGAATCTCTACTAAGGA | |
| | | Reverse | TCTCAACCAGGAAAGTGAAT | |
| 485 | Y-15-19A | Forward | AGCAACAGCAACAGTCTA | |
| | | Reverse | CCAGTTCCACAACATTCC | |
| 486 | Y-15-19B | Forward | GGTAACTCAGGAGAAACATTG | |
| | | Reverse | GTTGAACCTACGGGAAAGA | |
| 487 | Y-15-20 | Forward | AAGTCAAGTCGTCCAACTAA | |
| | | Reverse | TGGTCCGAGAACAAGAGA | |
| 488 | Y-17-1A | Forward | CGAACATAGACCAGTAGGAC | 300 |
| | | Reverse | GTAATCTTGAGAGGATGATAGC | |
| 489 | Y-17-1B | Forward | AATGAAGGTCGATTCGTGTT | 220 |
| | | Reverse | CGTCGTCACTGGGCTATA | |
| 490 | Y-17-2A | Forward | TACAGCCTTGAGACTATCG | 170 |
| | | Reverse | CAAAGCCCATTCAAACCAT | |
| 491 | Y-17-2B | Forward | CCGACAAAGAACTGGGAAA | 240 |
| | | Reverse | AGATTTAGGGCTACGAGAGT | |
| 492 | Y-17-3A | Forward | ACATCCACATCTGCTCTC | 170 |
| | | Reverse | GCCTCACATCATATACTACA | |
| 493 | Y-17-3B | Forward | TTCTTGCCTCTCTTCTTACTC | 280 |
| | | Reverse | GCTGGAAATAAGTCGTGATG | |
| 494 | Y-17-4A | Forward | TCTCTGTGTGCGTGTCTAT | 180 |
| | | Reverse | CCTCTTGGTGTTGGAATCG | |
| 495 | Y-17-4B | Forward | CCAGAGAACAGACGACTG | 270 |
| | | Reverse | AAGGACTCACAACTCCAATA | |
| 496 | Y-17-5A | Forward | AAGGCAAAGAGAGTATTCCA | 180 |
| | | Reverse | AGATTTACACCCATCAACAG | |
| 497 | Y-17-5B | Forward | AGACTTGTGTTACTCCTGTG | 230 |
| | | Reverse | ATCTTGCCTTGAATCATTGC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 498 | Y-17-6A | Forward | TTCTGTTGCTCCACATACC | 140 |
| | | Reverse | TCATTAGCGATCAACTCCAT | |
| 499 | Y-17-6B | Forward | GGGCCATTTCTTCTCTCT | 140 |
| | | Reverse | CTTTCAAATAAAGGCTCTCC | |
| 500 | Y-17-7A | Forward | GCTACTACTACTACTACTACTG | 210 |
| | | Reverse | GGAATCTGGTTGCATCATT | |
| 501 | Y-17-7B | Forward | AGTGCTTTGTGAGAGGATT | 220 |
| | | Reverse | GATACGCCATACTGTTGTG | |
| 502 | Y-17-8A | Forward | TCATGGTACAAGTCGTGAC | 190 |
| | | Reverse | GTTGATAAGTAGTTCTGTCTCC | |
| 503 | Y-17-8B | Forward | CCTTCCTAAGTCGGTCCTA | 150 |
| | | Reverse | GGCCCACAAACAAACATAA | |
| 504 | Y-17-9A | Forward | CCAACTTGCACATGAATAAC | 190 |
| | | Reverse | CCAAGGCTCTTGTAGGAA | |
| 505 | Y-17-9B | Forward | TCACAATGGTCTCGCTTAA | 190 |
| | | Reverse | GCTTTGTAAATGTGTTGGTC | |
| 506 | Y-17-12A | Forward | CAGATGTTCCACACCTTGA | 260 |
| | | Reverse | GCTCACTTAGACTGCTTGA | |
| 507 | Y-17-12B | Forward | TTGATGGACTTGATGACTGT | 210 |
| | | Reverse | AGGTTGAAAGGGTTACTGTT | |
| 508 | Y-17-13A | Forward | GTCACACTAAGTGGCTCAA | 210 |
| | | Reverse | TTGGAGATACATGGTTGGTT | |
| 509 | Y-17-13B | Forward | GATGGTGATGATGATGATGG | 130 |
| | | Reverse | GCCGCTATGTCTCCTAAC | |
| 510 | Y-17-14A | Forward | TTCACATTCCCACTACTCTC | 150 |
| | | Reverse | AATCTCCTCTTCTGCATCTC | |
| 511 | Y-17-14B | Forward | GAGGTTCCAGGTTAGAGTC | 110 |
| | | Reverse | CACCTTAAGTTCTTCCTACAC | |
| 512 | Y-17-15A | Forward | TAAGGTAAACACTCACATGC | 150 |
| | | Reverse | TTCCGCCAATTACCCTATT | |
| 513 | Y-17-15B | Forward | CAAGAATCCAATACCACTACC | 240 |
| | | Reverse | CTCTCAAGGAACTAGCATACT | |
| 514 | Y-17-16A | Forward | GCTTCTGTTGGAACTCTCA | 170 |
| | | Reverse | GGTTCTCTGTTTAGGGTTGT | |
| 515 | Y-17-16B | Forward | TGCTTAGAGTTCACTAGACA | 220 |
| | | Reverse | CCACTTAGGTTCACTTAGATAG | |
| 516 | Y-17-17A | Forward | GTGCCTTTGATAGGAAGC | 190 |
| | | Reverse | GCATATCTCTTACCACCATT | |
| 517 | Y-17-17B | Forward | GCCAATTACACCATAGACTAC | 180 |
| | | Reverse | GCTCTGTGATATGTATTGATCC | |
| 518 | Y-18-1A | Forward | GTGTTCCTTCCTCCATATCC | 270 |
| | | Reverse | GCCGTCTTGTATTACTCTCA | |
| 519 | Y-18-1B | Forward | GAAAGCACATAGGCATCAAA | 220 |
| | | Reverse | CGTTCTTCCCTCCATCATT | |
| 520 | Y-18-2A | Forward | ATAGTTGATGCCGCTGTT | 190 |
| | | Reverse | GTATGCCATTGGATACTGTC | |
| 521 | Y-18-2B | Forward | GATGTCATATCAACGGTCCTA | 200 |
| | | Reverse | CTCACTTCTAGTTCGAGTCTTA | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 522 | Y-18-3A | Forward | CTGTTTGGTGCTCTTAATCA | 250 |
| | | Reverse | GATGTCTCGTCCTTCTTGA | |
| 523 | Y-18-3B | Forward | TTGTCACATCTCCCAGTTG | 220 |
| | | Reverse | ATGGCGGGTGTATAGGTT | |
| 524 | Y-18-4A | Forward | TTGAATGAGACCAGATCCAT | 160 |
| | | Reverse | GCATGAAGATGTGAGAAGTT | |
| 525 | Y-18-4B | Forward | GGCAATAGAAGGTTGTGAAT | 240 |
| | | Reverse | AGGAATAGGTCAATCGTCTT | |
| 526 | Y-18-5A | Forward | ATCTCCATCTCCATCTCACT | 170 |
| | | Reverse | TTCTCGCTCTCCACTCTC | |
| 527 | Y-18-5B | Forward | GGAAGGTCAATCCTGATAATG | 160 |
| | | Reverse | ACCGACCAATCTGATATGG | |
| 528 | Y-18-6A | Forward | CTCCTTACTTCCCGCATC | 210 |
| | | Reverse | AGTACCCGAGGCATTGAT | |
| 529 | Y-18-6B | Forward | GTTAGCACTCCATTCATAGG | 200 |
| | | Reverse | ACGGTTGTGTTCTATATGTG | |
| 530 | Y-18-7A | Forward | TGATTGCCTATTGGTGTCTA | 200 |
| | | Reverse | AAGCCTTGTTGTGATTCTG | |
| 531 | Y-18-7B | Forward | CCTTGGCTCTGAGAACAG | 140 |
| | | Reverse | TGAAACCCTAATCCCTTATGG | |
| 532 | Y-18-8A | Forward | TTGTCCTCTGAGCATCTTC | 200 |
| | | Reverse | CCGCGTTGTGATCTGTAA | |
| 533 | Y-18-8B | Forward | GCTGCCTGATGGAGATTA | 200 |
| | | Reverse | ACCATACATTGACCATTACC | |
| 534 | Y-18-9A | Forward | TTCCTTCTTCCCTCTTCCA | 170 |
| | | Reverse | GGTTGCTCGCATTAATATGA | |
| 535 | Y-18-9B | Forward | GGATCTCATGCTCCTTAGTAA | 160 |
| | | Reverse | TGACATGGCATTCTTCTTTG | |
| 536 | Y-18-10A | Forward | GCCTGCTGATAATTGAGATAG | 180 |
| | | Reverse | CAACCAACATGGAGAACCT | |
| 537 | Y-18-10B | Forward | CTCTCCAGTGATGATTCCTT | 210 |
| | | Reverse | GAGTTGCTCACATGATTGC | |
| 538 | Y-18-12A | Forward | GGTTACTACGGTTGCTGAG | 250 |
| | | Reverse | TCTGTTTGGTTGCTGGAAA | |
| 539 | Y-18-12B | Forward | TGTGCTTGTAGTGCTCTC | 160 |
| | | Reverse | CCTAATTCACTTGACTGACC | |
| 540 | Y-18-13A | Forward | TCTTCAAGAGACGAGTTCC | 120 |
| | | Reverse | GAGACGAGTTCCGTTAGG | |
| 541 | Y-18-13B | Forward | CTGGACGACAACGGAATT | 190 |
| | | Reverse | TTGTGTGTTGATGAAGGGTA | |
| 542 | Y-18-15A | Forward | GCAATACAAGCAATCCCAAA | 200 |
| | | Reverse | ATGCCACACTCTCATCCA | |
| 543 | Y-18-15B | Forward | CCTAGCCACTCATCTTCTAA | 240 |
| | | Reverse | CCTTGTAATCCACCAACCA | |
| 544 | Y-18-16A | Forward | CACTAAATCAAAGGAAGAGG | 220 |
| | | Reverse | GTGTTCTTTATTCCTCGTTC | |
| 545 | Y-18-16B | Forward | CCACACTATCTTGTTGTTGT | 150 |
| | | Reverse | AGGACAATGATCTCCATCTC | |

Suppl. Tab. 1, continued

| No. | Primer name | Primer sequence (5'--3') | | Size |
|---|---|---|---|---|
| 546 | Y-18-17A | Forward | TCTAGCCACTCATTCTCTAAG | 160 |
| | | Reverse | CTCAGACGCATCCTTTGT | |
| 547 | Y-18-17B | Forward | TCACCTTCACCTTCACCTT | 170 |
| | | Reverse | GGGAAAGCGACTCAGAGA | |
| 548 | Y-18-19A | Forward | ATCCACCTCATCCTTCCAT | 180 |
| | | Reverse | ACCGTGATTAACGCTGTC | |
| 549 | Y-18-19B | Forward | CGTATATGGGTTTGTATGGATC | 180 |
| | | Reverse | GAAGGAAGAAGGAACAGAGAT | |
| 550 | Y-18-20A | Forward | TCCACTTACAAAGAGAAACC | 110 |
| | | Reverse | TAGCATGGCGACAACTAA | |
| 551 | Y-18-20B | Forward | TGAGACGCTCCGAGATAG | 170 |
| | | Reverse | GGTGAGGAGAGTCTTCTGA | |
| 552 | Y-18-21A | Forward | CAAACATAAGGCCCACAAA | 120 |
| | | Reverse | CTCACTTTCCCATCACACT | |
| 553 | Y-18-21B | Forward | GGTGTACTGTCCTTGTCTC | 140 |
| | | Reverse | GGTAGAAGAGCCAACAGAA | |
| 554 | Y-18-22A | Forward | GATTACGCTCAACTTTGTGT | 130 |
| | | Reverse | ATGCTTCCATGTGTCTGTA | |
| 555 | Y-18-22B | Forward | GGATATGTGGATCTCATCTCT | 180 |
| | | Reverse | CCAAGTTTCCAACCATCATT | |
| 556 | Y-18-23A | Forward | CACTAGACAGTCGCCATC | 190 |
| | | Reverse | CAATGTGGAATAAGGGATAAGG | |
| 557 | Y-18-23B | Forward | GCAAATGATAGGCACTCTG | 270 |
| | | Reverse | TGTCATTCTCATTAGGAGGTC | |
| 558 | Y-18-25A | Forward | CTAGGATGGTCAAAGGTTTATC | 200 |
| | | Reverse | GCTTTGAACTTCCCTTATGG | |
| 559 | Y-18-25B | Forward | ACCAAGAAGAGAAGACTACTG | 150 |
| | | Reverse | GGCTAACCGACTCAACTG | |
| 560 | Y-18-26A | Forward | GAACACATCGTACCTCCAT | 180 |
| | | Reverse | GACATCCTCACCACCATC | |
| 561 | Y-18-26B | Forward | TCGCTTTCCAACCTTTAACT | 200 |
| | | Reverse | CATGCACCATTATTCCTTATCC | |
| 562 | Y-18-27A | Forward | AGGGTTCTATCCTAACAACT | 160 |
| | | Reverse | CTAAGATAAGGTCCAGTCACT | |
| 563 | Y-18-27B | Forward | TGAACCTTAGGCAAATCTCT | 140 |
| | | Reverse | AAGAAAGGACGTGTGTGG | |
| 564 | Y-18-28A | Forward | CAGTATCAACACAATCCTCA | 170 |
| | | Reverse | TTTCTGGGCTACCAAGCA | |
| 565 | Y-18-28B | Forward | CACCAGCAGTAGAAGTCAA | 150 |
| | | Reverse | GTCTATGCAAGCCAGTAGT | |
| 566 | Y-18-29A | Forward | TTGCTTGTCGTAGGATTGT | 250 |
| | | Reverse | GATGTGTCTGATTTGTGTGT | |
| 567 | Y-18-29B | Forward | ATCTGAAGTCACCCTTACAT | 170 |
| | | Reverse | CCTGCTCCATCCATTAGTT | |

## Supplementary Table 2

Broad sense heritability of free linalool, nerol and α-terpineol in the 87-1 × 9-22 population

| Trait | 2011 | 2012 | 2013 | 2014 | 2015 |
|---|---|---|---|---|---|
| Free linalool | 0.966 | 0.988 | 0.989 | 0.973 | 0.971 |
| Free α-terpineol | 0.986 | 0.968 | 0.983 | 0.944[a] | 0.967 |
| Free nerol | 0.992[a] | 0.972 | 0.964 | 0.955 | 0.978 |

[a] The green and red color indicate minimum and maximum values respectively.

## Supplementary Table 3

List of the candiate genes underlying the focused QTL intervals

| Chromosome | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr5 | 4367851 | 4384523 | VIT_205s0020g02660 | tvp38 tmem64 family membrane protein slr0305-like |
| chr5 | 4385273 | 4386103 | VIT_205s0020g02670 | uncharacterized protein |
| chr5 | 4388697 | 4407780 | VIT_205s0020g02680 | ring u-box domain-containing protein |
| chr5 | 4417324 | 4421347 | VIT_205s0020g02690 | heavy metal transport detoxification domain-containing protein |
| chr5 | 4441484 | 4442745 | VIT_205s0020g02700 | transcription factor mute |
| chr5 | 4446556 | 4451040 | VIT_205s0020g02710 | dual specificity protein phosphatase 1 |
| chr5 | 4453502 | 4455917 | VIT_205s0020g02720 | basic 7s globulin 2 precursor small |
| chr5 | 4456371 | 4457690 | VIT_205s0020g02730 | basic 7s globulin 2 precursor small |
| chr5 | 4462134 | 4463569 | VIT_205s0020g02740 | mip nip subfamily |
| chr5 | 4471944 | 4478093 | VIT_205s0020g02760 | signal peptidase complex subunit 3b |
| chr5 | 4483940 | 4487917 | VIT_205s0020g02770 | aluminum-induced protein |
| chr5 | 4488819 | 4490843 | VIT_205s0020g02780 | hypothetical protein |
| chr5 | 4490987 | 4495658 | VIT_205s0020g02790 | nuclear transcription factor y subunit c-9 |
| chr5 | 4495689 | 4502807 | VIT_205s0020g02800 | pfkb-like carbohydrate kinase family protein |
| chr5 | 4509982 | 4514468 | VIT_205s0020g02810 | uncharacterized protein |
| chr5 | 4515511 | 4529146 | VIT_205s0020g02820 | nedd8-activating enzyme e1 catalytic subunit |
| chr5 | 4531089 | 4531963 | VIT_205s0020g02830 | hypothetical protein |
| chr5 | 4535578 | 4539184 | VIT_205s0020g02840 | rossmann-fold nad -binding domain-containing protein |
| chr5 | 4539926 | 4546777 | VIT_205s0020g02850 | type iif peroxiredoxin |
| chr5 | 4549590 | 4553901 | VIT_205s0020g02860 | e3 ubiquitin-protein ligase rhf1a |
| chr5 | 4554200 | 4560076 | VIT_205s0020g02870 | dead-box atp-dependent rna helicase 58 |
| chr5 | 4559039 | 4563814 | VIT_205s0020g02880 | adp-glucose pyrophosphorylase large subunit |
| chr5 | 4600767 | 4604280 | VIT_205s0020g02890 | glycoprotein membrane precursor gpi-anchored protein |
| chr5 | 4607220 | 4617288 | VIT_205s0020g02900 | peroxisomal membrane protein |
| chr5 | 4619125 | 4633396 | VIT_205s0020g02910 | mitogen activated protein kinase kinase kinase |
| chr5 | 4640855 | 4642204 | VIT_205s0020g02920 | hypothetical protein |
| chr5 | 4651037 | 4670494 | VIT_205s0020g02930 | rna polymerase iii subunit rpc82 family protein |
| chr5 | 4673443 | 4694685 | VIT_205s0020g02940 | protein phosphatase 2c 70 |
| chr5 | 4695286 | 4703436 | VIT_205s0020g02950 | protein |
| chr5 | 4705744 | 4730333 | VIT_205s0020g02960 | chromatin remodeling complex subunit |
| chr5 | 4728395 | 4730152 | VIT_205s0020g02970 | ran gtpase activating protein 2 |
| chr5 | 4733971 | 4738431 | VIT_205s0020g02980 | hypothetical protein |
| chr5 | 4738910 | 4739540 | VIT_205s0020g02990 | protein |
| chr5 | 4744289 | 4745805 | VIT_205s0020g03000 | 2-hydroxyisoflavanone dehydratase |
| chr5 | 4745806 | 4746810 | VIT_205s0020g03010 | 2-hydroxyisoflavanone dehydratase |
| chr5 | 4747460 | 4764728 | VIT_205s0020g03020 | arm repeat protein interacting with abf2-like |
| chr5 | 4768424 | 4774376 | VIT_205s0020g03030 | serine-threonine protein plant- |
| chr5 | 4775429 | 4776350 | VIT_205s0020g03040 | uncharacterized protein |
| chr5 | 4782960 | 4784781 | VIT_205s0020g03050 | hypothetical protein |
| chr5 | 4794345 | 4798018 | VIT_205s0020g03060 | cyclin t1 |
| chr5 | 4800109 | 4802663 | VIT_205s0020g03070 | cyclin family protein |
| chr5 | 4804040 | 4828331 | VIT_205s0020g03080 | annotation was added to scaffolds in november 2011~long chain fatty acid- ligase |
| chr5 | 4830549 | 4846815 | VIT_205s0020g03090 | chloride channel protein clc-d |
| chr5 | 4851647 | 4854507 | VIT_205s0020g03100 | hexose transporter |
| chr5 | 4860808 | 4865320 | VIT_205s0020g03130 | protein |
| chr5 | 4868566 | 4873580 | VIT_205s0020g03140 | hexose transporter |
| chr5 | 4894124 | 4901725 | VIT_205s0020g03150 | protein time for coffee |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr5 | 4912150 | 4920596 | VIT_205s0020g03160 | snare associated golgi protein |
| chr5 | 4934698 | 4939578 | VIT_205s0020g03170 | lipoxygenase |
| chr5 | 4942932 | 4943720 | VIT_205s0020g03180 | psi reaction center subunit ii |
| chr5 | 4947640 | 4950458 | VIT_205s0020g03190 | protein |
| chr5 | 4962281 | 4965973 | VIT_205s0020g03200 | spermine synthase |
| chr5 | 4973604 | 4975974 | VIT_205s0020g03210 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1-like |
| chr5 | 4977347 | 4978110 | VIT_205s0020g03220 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1-like |
| chr5 | 5000885 | 5003269 | VIT_205s0020g03240 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1 |
| chr5 | 5018464 | 5019799 | VIT_205s0020g03250 | alpha- -glucan-protein synthase |
| chr5 | 5040289 | 5043665 | VIT_205s0020g03260 | amine oxidase |
| chr5 | 5047205 | 5049693 | VIT_205s0020g03270 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1 |
| chr5 | 5055636 | 5059157 | VIT_205s0020g03280 | amine oxidase |
| chr5 | 5059966 | 5061410 | VIT_205s0020g03290 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1-like |
| chr5 | 5065463 | 5066922 | VIT_205s0020g03300 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1-like |
| chr5 | 5082857 | 5085083 | VIT_205s0020g03310 | primary amine oxidase |
| chr5 | 5085522 | 5088671 | VIT_205s0020g03320 | amine oxidase |
| chr5 | 5092609 | 5096914 | VIT_205s0020g03330 | heat shock 70 kda protein |
| chr5 | 5098458 | 5099384 | VIT_205s0020g03340 | hypothetical protein |
| chr5 | 5108036 | 5111493 | VIT_205s0020g03350 | random slug protein |
| chr5 | 5118933 | 5120313 | VIT_205s0020g03360 | uncharacterized protein loc100852693 |
| chr5 | 5121028 | 5134133 | VIT_205s0020g03370 | 5 -nucleotidase sure |
| chr5 | 5145035 | 5149267 | VIT_205s0020g03380 | with no lysine kinase |
| chr5 | 5162320 | 5163551 | VIT_205s0020g03390 | uncharacterized protein loc100245548 |
| chr5 | 5165690 | 5166307 | VIT_205s0020g03400 | hypothetical protein |
| chr5 | 5175156 | 5176331 | VIT_205s0020g03410 | hypothetical protein VITISV_008647 [Vitis vinifera] |
| chr5 | 5188583 | 5201108 | VIT_205s0020g03420 | acyl- n-acyltransferase with ring fyve phd-type zinc finger protein |
| chr5 | 5203487 | 5212585 | VIT_205s0020g03430 | imidazoleglycerol-phosphate dehydratase |
| chr5 | 5209074 | 5212739 | VIT_205s0020g03440 | low psii accumulation 19 protein |
| chr5 | 5212636 | 5215888 | VIT_205s0020g03450 | pointed first leaf |
| chr5 | 5228835 | 5252996 | VIT_205s0020g03460 | uncharacterized protein |
| chr5 | 5253759 | 5260539 | VIT_205s0020g03470 | frigida-like protein |
| chr5 | 5261959 | 5263242 | VIT_205s0020g03480 | structural constituent of |
| chr5 | 5264210 | 5264834 | VIT_205s0020g03490 | ferredoxin |
| chr5 | 5267459 | 5277004 | VIT_205s0020g03500 | prefoldin subunit 2 |
| chr5 | 5277293 | 5277996 | VIT_205s0020g03510 | transposon protein |
| chr5 | 5284997 | 5285845 | VIT_205s0020g03520 | protein |
| chr5 | 5290176 | 5291777 | VIT_205s0020g03530 | seed maturation protein |
| chr5 | 5292061 | 5292467 | VIT_205s0020g03540 | hypothetical protein |
| chr5 | 5292468 | 5294489 | VIT_205s0020g03550 | lactoylglutathione lyase glyoxalase i-like protein |
| chr5 | 5297910 | 5298444 | VIT_205s0020g03560 | protein |
| chr5 | 5302968 | 5305900 | VIT_205s0020g03570 | pentatricopeptide repeat-containing protein |
| chr5 | 5307187 | 5307921 | VIT_205s0020g03580 | pre-rrna-processing protein tsr2 homolog |
| chr5 | 5310663 | 5317171 | VIT_205s0020g03590 | uncharacterized protein |
| chr5 | 5318159 | 5333991 | VIT_205s0020g03600 | uncharacterized protein |
| chr5 | 5335769 | 5337658 | VIT_205s0020g03610 | protein |
| chr5 | 5339130 | 5347529 | VIT_205s0020g03620 | hypothetical protein |
| chr5 | 5347757 | 5350624 | VIT_205s0020g03630 | pentatricopeptide repeat-containing protein |
| chr5 | 5352030 | 5353849 | VIT_205s0020g03640 | c-8 sterol isomerase |
| chr5 | 5357586 | 5358363 | VIT_205s0020g03650 | hypothetical protein |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr5 | 5363109 | 5383808 | VIT_205s0020g03660 | major facilitator protein |
| chr5 | 5384867 | 5389068 | VIT_205s0020g03670 | hypothetical protein |
| chr5 | 5399165 | 5399892 | VIT_205s0020g03680 | uncharacterized n-acetyltransferase p20-like |
| chr5 | 5401299 | 5402084 | VIT_205s0020g03690 | gcn5-related n-acetyltransferase-like protein |
| chr5 | 5407600 | 5407857 | VIT_205s0020g03700 | uncharacterized n-acetyltransferase p20 |
| chr5 | 5408291 | 5409013 | VIT_205s0020g03710 | gcn5-related n-acetyltransferase-like protein |
| chr5 | 5426416 | 5436841 | VIT_205s0020g03720 | paf1 complex component |
| chr5 | 5436365 | 5437832 | VIT_205s0020g03730 | protein |
| chr5 | 5438841 | 5440757 | VIT_205s0020g03740 | non-specific lipid-transfer protein at2g13820-like |
| chr5 | 5441226 | 5442384 | VIT_205s0020g03750 | protein |
| chr5 | 5444081 | 5449731 | VIT_205s0020g03760 | atp-dependent helicase |
| chr5 | 5466136 | 5469485 | VIT_205s0020g03770 | type i inositol- -trisphosphate 5-phosphatase cvp2-like |
| chr5 | 5481021 | 5483477 | VIT_205s0020g03780 | atp-dependent rna helicase mitochondrial-like |
| chr5 | 5485064 | 5492412 | VIT_205s0020g03790 | atp-dependent rna helicase mitochondrial-like |
| chr5 | 5492723 | 5493771 | VIT_205s0020g03800 | pentatricopeptide repeat-containing protein mitochondrial-like |
| chr5 | 5499719 | 5500905 | VIT_205s0020g03810 | hypothetical protein |
| chr5 | 5501527 | 5502959 | VIT_205s0020g03820 | atp-dependent rna helicase mitochondrial-like |
| chr5 | 5503547 | 5505344 | VIT_205s0020g03830 | pentatricopeptide repeat-containing |
| chr5 | 5505726 | 5511939 | VIT_205s0020g03840 | protein |
| chr5 | 5509389 | 5511899 | VIT_205s0020g03850 | pentatricopeptide repeat-containing protein |
| chr5 | 5513689 | 5518278 | VIT_205s0020g03860 | homocysteine s-methyltransferase |
| chr5 | 5521448 | 5528679 | VIT_205s0020g03870 | protein kinase |
| chr5 | 5537279 | 5545365 | VIT_205s0020g03880 | lin-54-like protein |
| chr5 | 5552870 | 5561700 | VIT_205s0020g03890 | centromere protein |
| chr5 | 5562325 | 5566729 | VIT_205s0020g03900 | 40s ribosomal protein |
| chr5 | 5569568 | 5570952 | VIT_205s0020g03910 | protein |
| chr5 | 5577800 | 5594684 | VIT_205s0020g03920 | heat shock protein 70 -interacting |
| chr5 | 5595826 | 5599901 | VIT_205s0020g03930 | sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| chr5 | 5622461 | 5627345 | VIT_205s0020g03970 | sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| chr5 | 5650192 | 5654115 | VIT_205s0020g03980 | calmodulin binding |
| chr5 | 5688624 | 5690324 | VIT_205s0020g04000 | ring u-box domain-containing protein |
| chr5 | 5691983 | 5695681 | VIT_205s0020g04010 | hypothetical protein |
| chr10 | 1181039 | 1181707 | VIT_210s0523g00010 | heat shock protein 70 -interacting |
| chr10 | 1185495 | 1188247 | VIT_210s0523g00020 | tyrosine specific protein phosphatase family protein |
| chr10 | 1189941 | 1199180 | VIT_210s0523g00030 | e3 ubiquitin-protein ligase cop1-like |
| chr10 | 1199998 | 1208459 | VIT_210s0523g00040 | alternative oxidase |
| chr10 | 1211148 | 1214353 | VIT_210s0523g00050 | at3g20300 mqc12_5 |
| chr10 | 1216991 | 1220185 | VIT_210s0405g00010 | protein |
| chr10 | 1228810 | 1236087 | VIT_210s0405g00020 | mo25-like protein |
| chr10 | 1236382 | 1242362 | VIT_210s0405g00030 | l-galactose-1-phosphate phosphatase |
| chr10 | 1242431 | 1244597 | VIT_210s0405g00040 | auxin-responsive protein |
| chr10 | 1253851 | 1257687 | VIT_210s0405g00050 | inositol transporter |
| chr10 | 1262013 | 1262151 | VIT_210s0405g00060 | hypothetical protein |
| chr10 | 1265392 | 1267196 | VIT_210s0405g00070 | hypothetical protein |
| chr10 | 1276150 | 1277523 | VIT_210s0597g00010 | tsjt1-like protein |
| chr10 | 1279171 | 1288041 | VIT_210s0597g00020 | hypothetical protein |
| chr10 | 1288396 | 1295559 | VIT_210s0597g00030 | glutaredoxin s17 |
| chr10 | 1296255 | 1298947 | VIT_210s0597g00040 | pentatricopeptide repeat-containing protein |
| chr10 | 1299756 | 1301763 | VIT_210s0597g00050 | protein |

Suppl. Tab. 3, continued

| Chromosome | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr10 | 1304377 | 1305587 | VIT_210s0003g00010 | 30s ribosomal protein s5 |
| chr10 | 1305946 | 1307011 | VIT_210s0003g00020 | late embryo abundance protein |
| chr10 | 1317314 | 1320277 | VIT_210s0003g00030 | f-box family protein |
| chr10 | 1334689 | 1337916 | VIT_210s0003g00040 | dof zinc finger protein |
| chr10 | 1345902 | 1349046 | VIT_210s0003g00050 | squamosa promoter binding-like protein |
| chr10 | 1349086 | 1357129 | VIT_210s0003g00060 | mitochondrial substrate carrier family protein s-like |
| chr10 | 1357464 | 1366051 | VIT_210s0003g00070 | trypsin domain-containing |
| chr10 | 1391485 | 1397847 | VIT_210s0003g00080 | e3 ubiquitin-protein ligase ring1a-like |
| chr10 | 1397043 | 1399568 | VIT_210s0003g00090 | dormancy-associated 1 |
| chr10 | 1403637 | 1406467 | VIT_210s0003g00100 | hypothetical protein |
| chr10 | 1407224 | 1411356 | VIT_210s0003g00110 | hypothetical protein |
| chr10 | 1418944 | 1428870 | VIT_210s0003g00120 | leucine-rich repeat receptor-like serine threonine-protein kinase at2g14440-like |
| chr10 | 1429982 | 1431021 | VIT_210s0003g00130 | ap2 erf domain-containing transcription factor |
| chr10 | 1442862 | 1444120 | VIT_210s0003g00140 | ethylene response factor 3 |
| chr10 | 1447873 | 1454918 | VIT_210s0003g00150 | mac perforin domain-containing protein |
| chr11 | 3173940 | 3179558 | VIT_211s0016g03890 | chlorophyll b reductase |
| chr11 | 3182349 | 3186809 | VIT_211s0016g03900 | protein chromosomal-like |
| chr11 | 3186960 | 3190875 | VIT_211s0016g03910 | uncharacterized protein |
| chr11 | 3191296 | 3193086 | VIT_211s0016g03920 | polyol transporter 5-like |
| chr11 | 3196791 | 3198228 | VIT_211s0016g03923 | hypothetical protein |
| chr11 | 3202822 | 3204402 | VIT_211s0016g03926 | atp-dependent rna helicase chl1 |
| chr11 | 3212646 | 3215223 | VIT_211s0016g03930 | flavine-containing monoxygenase |
| chr11 | 3223827 | 3225994 | VIT_211s0016g03940 | heat stress transcription factor c-1 |
| chr11 | 3234658 | 3236304 | VIT_211s0016g03950 | dehydration-responsive protein rd22 |
| chr11 | 3236265 | 3243936 | VIT_211s0016g03960 | kinesin-like protein kif2a-like |
| chr11 | 3245946 | 3247926 | VIT_211s0016g03970 | ubiquitin-conjugating enzyme |
| chr11 | 3249496 | 3250787 | VIT_211s0016g03980 | uncharacterized protein |
| chr11 | 3250267 | 3255173 | VIT_211s0016g03990 | rpi-vnt1-like protein |
| chr11 | 3255550 | 3256739 | VIT_211s0016g04000 | hypothetical protein |
| chr11 | 3262818 | 3270343 | VIT_211s0016g04010 | ist1-like protein |
| chr11 | 3270669 | 3276683 | VIT_211s0016g04020 | gtp binding protein |
| chr11 | 3276161 | 3276314 | VIT_211s0016g04030 | hypothetical protein |
| chr11 | 3286424 | 3287791 | VIT_211s0016g04035 | hypothetical protein |
| chr11 | 3289439 | 3295150 | VIT_211s0016g04040 | late embryogenesis abundant hydroxyproline-rich glycoprotein |
| chr11 | 3298356 | 3299653 | VIT_211s0016g04050 | hypothetical protein |
| chr11 | 3304574 | 3323536 | VIT_211s0016g04060 | protein kinase-like protein |
| chr11 | 3325351 | 3326466 | VIT_211s0016g04065 | hypothetical protein |
| chr11 | 3329763 | 3336953 | VIT_211s0016g04070 | protein frigida |
| chr11 | 3340651 | 3341251 | VIT_211s0016g04080 | ethylene-responsive transciptional coactivator-like protein |
| chr11 | 3341776 | 3358113 | VIT_211s0016g04090 | dna mismatch repair protein msh6-2 |
| chr11 | 3358818 | 3363084 | VIT_211s0016g04100 | pattern formation protein emb30 |
| chr11 | 3365564 | 3366469 | VIT_211s0016g04110 | hypothetical protein |
| chr11 | 3367410 | 3370853 | VIT_211s0016g04120 | hypothetical protein |
| chr11 | 3376824 | 3378266 | VIT_211s0016g04130 | pinus taeda anonymous locus umn_3517_01 genomic sequence |
| chr11 | 3379988 | 3380598 | VIT_211s0016g04140 | hypothetical protein |
| chr11 | 3381452 | 3385726 | VIT_211s0016g04150 | sulfate transporter |
| chr11 | 3394662 | 3399230 | VIT_211s0016g04160 | sulfate transporter |
| chr11 | 3413268 | 3417781 | VIT_211s0016g04170 | sulfate transporter |
| chr11 | 3426961 | 3452667 | VIT_211s0016g04180 | coatomer subunit beta -2-like |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr11 | 3457655 | 3460515 | VIT_211s0016g04190 | protein |
| chr11 | 3476713 | 3483990 | VIT_211s0016g04200 | serinc-domain containing serine and sphingolipid biosynthesis protein |
| chr11 | 3485660 | 3494158 | VIT_211s0016g04210 | arf-gap domain and fg repeats-containing protein |
| chr11 | 3504347 | 3510279 | VIT_211s0016g04215 | hypothetical protein |
| chr11 | 3513588 | 3516208 | VIT_211s0016g04220 | chloroplast-targeted copper |
| chr11 | 3521290 | 3524451 | VIT_211s0016g04230 | uncharacterized protein |
| chr11 | 3525357 | 3539575 | VIT_211s0016g04240 | protein vernalization insensitive 3-like |
| chr11 | 3539829 | 3550442 | VIT_211s0016g04250 | protein mrp homolog |
| chr11 | 3553407 | 3555050 | VIT_211s0016g04260 | alpha beta fold family protein |
| chr11 | 3557159 | 3557696 | VIT_211s0016g04265 | alpha beta fold family protein |
| chr11 | 3566176 | 3569299 | VIT_211s0016g04270 | alpha beta fold family protein |
| chr11 | 3571380 | 3572024 | VIT_211s0016g04280 | zinc finger ccch domain-containing protein 14-like |
| chr11 | 3577637 | 3590813 | VIT_211s0016g04290 | 3-hydroxyisobutyryl- hydrolase-like protein |
| chr11 | 3591311 | 3596486 | VIT_211s0016g04300 | nudix hydrolase 24 |
| chr11 | 3603704 | 3604592 | VIT_211s0016g04310 | dioxygenase domain-containing protein |
| chr11 | 3605912 | 3611360 | VIT_211s0016g04320 | nudix hydrolase 24 |
| chr11 | 3616755 | 3617721 | VIT_211s0016g04330 | dihydrofolate reductase |
| chr11 | 3621060 | 3638739 | VIT_211s0016g04340 | protein |
| chr11 | 3655490 | 3663699 | VIT_211s0016g04350 | low quality protein: trna (guanine-n -)-methyltransferase-like |
| chr11 | 3664518 | 3666568 | VIT_211s0016g04360 | glucan endo- -beta-glucosidase |
| chr11 | 3667294 | 3672435 | VIT_211s0016g04370 | syntaxin 32 |
| chr11 | 3684539 | 3689260 | VIT_211s0016g04380 | protein |
| chr11 | 3689789 | 3695685 | VIT_211s0016g04390 | hypothetical protein |
| chr11 | 3695730 | 3697125 | VIT_211s0016g04400 | taxadien-5-alpha-ol o- |
| chr11 | 3703145 | 3706939 | VIT_211s0016g04410 | cid5 ipd1 |
| chr11 | 3708009 | 3733519 | VIT_211s0016g04420 | dnaj homolog subfamily c member 13-like |
| chr11 | 3734115 | 3734920 | VIT_211s0016g04430 | pentatricopeptide repeat-containing protein |
| chr11 | 3748747 | 3749448 | VIT_211s0016g04440 | lipid binding |
| chr11 | 3757752 | 3762574 | VIT_211s0016g04450 | e3 ubiquitin-protein ligase at4g11680-like |
| chr11 | 3768892 | 3770348 | VIT_211s0016g04460 | ornithine decarboxylase |
| chr11 | 3771950 | 3773188 | VIT_211s0016g04470 | ornithine decarboxylase |
| chr11 | 3786018 | 3793029 | VIT_211s0016g04480 | acyl acp-thioesterase |
| chr11 | 3793962 | 3798589 | VIT_211s0016g04490 | auxin-responsive protein iaa7 |
| chr11 | 3799268 | 3803891 | VIT_211s0016g04500 | serine threonine protein phosphatase 2a 57 kda regulatory subunit b iota isoform |
| chr11 | 3804692 | 3805164 | VIT_211s0016g04510 | hypothetical protein |
| chr11 | 3805508 | 3809677 | VIT_211s0016g04520 | uncharacterized protein |
| chr11 | 3810986 | 3816594 | VIT_211s0016g04530 | uncharacterized protein |
| chr11 | 3826617 | 3837079 | VIT_211s0016g04540 | abc transporter g family member 32 |
| chr11 | 3839749 | 3853158 | VIT_211s0016g04550 | transcriptional corepressor leunig-like isoform 2 |
| chr11 | 3854966 | 3862819 | VIT_211s0016g04560 | bile acid na+ symporter family protein |
| chr11 | 3880574 | 3884136 | VIT_211s0016g04570 | inactive receptor kinase |
| chr11 | 3888012 | 3891011 | VIT_211s0016g04580 | chlororespiratory reduction partial |
| chr11 | 3891251 | 3899059 | VIT_211s0016g04590 | pleiotropic drug resistance protein 1-like |
| chr11 | 3913460 | 3916375 | VIT_211s0016g04600 | myb family transcription factor |
| chr11 | 3916747 | 3928165 | VIT_211s0016g04610 | glycine-rich rna-binding |
| chr11 | 3942400 | 3949091 | VIT_211s0016g04620 | protein argonaute pnh1-like |
| chr11 | 3959481 | 3961177 | VIT_211s0016g04630 | della protein |
| chr11 | 3966116 | 3971982 | VIT_211s0016g04650 | gdp-mannose transporter |
| chr11 | 3966363 | 3968501 | VIT_211s0016g04640 | organelle transcript processing partial |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr11 | 3972559 | 3974547 | VIT_211s0016g04660 | pentatricopeptide repeat-containing protein |
| chr11 | 3975392 | 3976209 | VIT_211s0016g04670 | hypothetical protein |
| chr11 | 3983718 | 3983983 | VIT_211s0016g04680 | hypothetical protein |
| chr11 | 3983984 | 3988224 | VIT_211s0016g04690 | soul heme-binding protein |
| chr11 | 3988735 | 3992060 | VIT_211s0016g04700 | beta-ketoacyl-coa synthase family protein |
| chr11 | 3989722 | 4003000 | VIT_211s0016g04710 | serine-threonine kinase receptor-associated |
| chr11 | 4011782 | 4017044 | VIT_211s0016g04720 | hypothetical protein |
| chr11 | 4024220 | 4034033 | VIT_211s0016g04730 | e3 ubiquitin-protein ligase march3 |
| chr11 | 4037062 | 4042168 | VIT_211s0016g04740 | anion exchanger family protein |
| chr11 | 4045856 | 4052296 | VIT_211s0016g04750 | potassium channel |
| chr11 | 4071996 | 4073115 | VIT_211s0016g04760 | uncharacterized protein |
| chr11 | 4077449 | 4082074 | VIT_211s0016g04770 | protein |
| chr11 | 4088564 | 4093081 | VIT_211s0016g04780 | gtp-binding nuclear protein ran-3-like |
| chr11 | 4093242 | 4093418 | VIT_211s0016g04790 | hypothetical protein |
| chr11 | 4094051 | 4095808 | VIT_211s0016g04800 | hypothetical protein |
| chr11 | 4100613 | 4105250 | VIT_211s0016g04810 | cytochrome p450 |
| chr11 | 4109153 | 4119816 | VIT_211s0016g04820 | tudor-like rna-binding protein |
| chr11 | 4124248 | 4146175 | VIT_211s0016g04830 | protein arginine n-methyltransferase |
| chr11 | 4152701 | 4154110 | VIT_211s0016g04840 | probable receptor-like protein kinase at5g20050-like |
| chr11 | 4157149 | 4179239 | VIT_211s0016g04850 | phospholipase carboxylesterase family protein |
| chr11 | 4178515 | 4183972 | VIT_211s0016g04860 | hypothetical protein |
| chr11 | 4184324 | 4188764 | VIT_211s0016g04870 | protein |
| chr11 | 4194812 | 4202353 | VIT_211s0016g04880 | serine threonine protein |
| chr11 | 4209741 | 4211787 | VIT_211s0016g04890 | g-type lectin s-receptor-like serine threonine-protein kinase ces101-like |
| chr11 | 4212374 | 4212886 | VIT_211s0016g04900 | uncharacterized protein loc100261115 |
| chr11 | 4223647 | 4225409 | VIT_211s0016g04910 | protein kinase pinoid 2-like |
| chr11 | 4233399 | 4234829 | VIT_211s0016g04920 | early nodulin 93 |
| chr11 | 4243133 | 4244564 | VIT_211s0016g04930 | ran bp2 nzf zinc finger-like protein |
| chr11 | 4251492 | 4256225 | VIT_211s0016g04940 | zinc finger ccch domain-containing protein |
| chr11 | 4261111 | 4267327 | VIT_211s0016g04950 | nudix hydrolase chloroplastic-like |
| chr11 | 4271013 | 4273874 | VIT_211s0016g04960 | racemase and acting on amino acids and |
| chr11 | 4286562 | 4295477 | VIT_211s0016g04970 | nadh-cytochrome b5 reductase-like protein |
| chr11 | 4296131 | 4304338 | VIT_211s0016g04980 | zinc finger c-x8-c-x5-c-x3-h type family protein |
| chr11 | 4305018 | 4306207 | VIT_211s0016g04990 | hypothetical protein |
| chr11 | 4310749 | 4313543 | VIT_211s0016g05000 | dynein light chain |
| chr11 | 4317116 | 4320611 | VIT_211s0016g05010 | metallothiol transferase fosb |
| chr11 | 4327782 | 4333251 | VIT_211s0016g05020 | protein |
| chr11 | 4334317 | 4334409 | VIT_211s0016g05030 | hypothetical protein |
| chr11 | 4336832 | 4342397 | VIT_211s0016g05040 | protein |
| chr11 | 4345774 | 4350298 | VIT_211s0016g05050 | f-box kelch-repeat protein |
| chr11 | 4350402 | 4357913 | VIT_211s0016g05060 | choline ethanolamine |
| chr11 | 4357981 | 4360345 | VIT_211s0016g05070 | probable ethanolamine kinase a-like |
| chr11 | 4364300 | 4373478 | VIT_211s0016g05080 | binding protein |
| chr11 | 4374336 | 4380476 | VIT_211s0016g05090 | dead-box atp-dependent rna helicase 37-like |
| chr11 | 4381945 | 4385875 | VIT_211s0016g05100 | alba dna rna-binding protein |
| chr11 | 4386076 | 4390843 | VIT_211s0016g05110 | protein brittle- chloroplastic amyloplastic-like |
| chr11 | 4399603 | 4404298 | VIT_211s0016g05120 | protein |
| chr11 | 4403537 | 4419303 | VIT_211s0016g05130 | signal peptidase complex catalytic subunit sec11c |
| chr11 | 4421194 | 4424137 | VIT_211s0016g05140 | protein |

Suppl. Tab. 3, continued

| Chromosome | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr11 | 4424880 | 4427726 | VIT_211s0016g05150 | pentatricopeptide repeat-containing protein |
| chr11 | 4444362 | 4448840 | VIT_211s0016g05170 | nitrate transporter |
| chr11 | 4466615 | 4469928 | VIT_211s0016g05180 | nitrate transporter |
| chr11 | 4478590 | 4479964 | VIT_211s0016g05190 | nucleotide-sugar transporter family protein |
| chr11 | 4486303 | 4486583 | VIT_211s0016g05200 | hypothetical protein |
| chr11 | 4492987 | 4499927 | VIT_211s0016g05210 | xylosyltransferase 1-like |
| chr11 | 4500664 | 4502689 | VIT_211s0016g05220 | pentatricopeptide repeat-containing protein |
| chr11 | 4503132 | 4505121 | VIT_211s0016g05230 | alcohol dehydrogenase superfamily protein |
| chr11 | 4508216 | 4590861 | VIT_211s0016g05240 | nuclear pore complex protein nup205-like |
| chr11 | 4591464 | 4601816 | VIT_211s0016g05250 | uncharacterized protein |
| chr11 | 4602154 | 4606833 | VIT_211s0016g05260 | uncharacterized protein loc100254186 |
| chr11 | 4607033 | 4609819 | VIT_211s0016g05270 | bundle-sheath defective protein 2 family |
| chr11 | 4611416 | 4626713 | VIT_211s0016g05280 | peroxidase |
| chr11 | 4628147 | 4628995 | VIT_211s0016g05290 | hypothetical protein |
| chr11 | 4630221 | 4635343 | VIT_211s0016g05300 | heme oxygenase 1 protein 1 |
| chr11 | 4636943 | 4651752 | VIT_211s0016g05310 | peroxidase 25-like |
| chr11 | 4651872 | 4654043 | VIT_211s0016g05320 | peroxidase |
| chr11 | 4656604 | 4659824 | VIT_211s0016g05330 | spx domain-containing protein 2 |
| chr11 | 4677731 | 4680660 | VIT_211s0016g05340 | ethylene-responsive transcription factor win1-like |
| chr11 | 4690140 | 4694983 | VIT_211s0016g05350 | protein |
| chr11 | 4695215 | 4699274 | VIT_211s0016g05360 | phospholipase d |
| chr11 | 4700957 | 4708076 | VIT_211s0016g05370 | phospholipase d |
| chr11 | 4710737 | 4712979 | VIT_211s0016g05380 | hypothetical protein |
| chr11 | 4716009 | 4723644 | VIT_211s0016g05390 | ribosomal protein l36 |
| chr11 | 4724294 | 4734437 | VIT_211s0016g05400 | hypothetical protein |
| chr11 | 4745252 | 4749243 | VIT_211s0016g05410 | ein3-binding f-box protein 1-like |
| chr11 | 4753080 | 4787687 | VIT_211s0016g05420 | cbl-interacting serine threonine-protein |
| chr11 | 4812500 | 4814306 | VIT_211s0016g05430 | tetratricopeptide repeat domain-containing protein |
| chr11 | 4815485 | 4818469 | VIT_211s0016g05440 | g-type lectin s-receptor-like serine threonine-protein kinase sd2-5-like |
| chr11 | 4818752 | 4820843 | VIT_211s0016g05450 | equilibrative nucleoside transporter 4-like |
| chr11 | 4831814 | 4836663 | VIT_211s0016g05460 | tpx2 (targeting protein for xklp2) protein family |
| chr11 | 4837129 | 4857892 | VIT_211s0016g05470 | nucleoporin-related protein |
| chr18 | 24595027 | 24596218 | VIT_218s0041g00210 | tmv resistance protein n-like |
| chr18 | 24597285 | 24598025 | VIT_218s0041g00220 | tmv resistance protein n-like |
| chr18 | 24598305 | 24599846 | VIT_218s0041g00230 | tmv resistance protein n-like |
| chr18 | 24609787 | 24626801 | VIT_218s0041g00240 | hypothetical protein |
| chr18 | 24631635 | 24635997 | VIT_218s0041g00250 | tmv resistance protein n-like |
| chr18 | 24652979 | 24653491 | VIT_218s0041g00260 | disease resistance protein at3g14460-like |
| chr18 | 24653492 | 24658740 | VIT_218s0041g00270 | disease resistance protein at3g14460-like |
| chr18 | 24686246 | 24707066 | VIT_218s0041g00280 | t-complex protein 11 |
| chr18 | 24707099 | 24716985 | VIT_218s0041g00290 | c3hc4-type ring finger protein |
| chr18 | 24717744 | 24718545 | VIT_218s0041g00303 | hypothetical protein |
| chr18 | 24759581 | 24777617 | VIT_218s0041g00330 | atp-dependent protease la domain-containing protein |
| chr18 | 24785424 | 24788576 | VIT_218s0041g00340 | receptor-like protein kinase |
| chr18 | 24806056 | 24810149 | VIT_218s0041g00350 | alpha beta-hydrolase domain-containing protein |
| chr18 | 24811408 | 24819016 | VIT_218s0041g00360 | uncharacterized protein |
| chr18 | 24821729 | 24822234 | VIT_218s0041g00370 | cysteine proteinase inhibitor 1-like |
| chr18 | 24825861 | 24826369 | VIT_218s0041g00380 | dna repair protein xrcc4 |
| chr18 | 24839099 | 24839594 | VIT_218s0041g00390 | cysteine proteinase inhibitor 1-like |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr18 | 24849485 | 24851219 | VIT_218s0041g00400 | tmv resistance protein n-like |
| chr18 | 24854521 | 24856451 | VIT_218s0041g00410 | uncharacterized protein loc100256342 |
| chr18 | 24871290 | 24875309 | VIT_218s0041g00420 | sec14 cytosolic factor family protein |
| chr18 | 24888829 | 24892272 | VIT_218s0041g00430 | patellin-5 isoform 1 |
| chr18 | 24924640 | 24927094 | VIT_218s0041g00440 | hypothetical protein |
| chr18 | 24928359 | 24930210 | VIT_218s0041g00450 | protein acclimation of photosynthesis to environment |
| chr18 | 24941524 | 24944093 | VIT_218s0041g00465 | probable peptide nitrate transporter at1g22540 |
| chr18 | 24949976 | 24953370 | VIT_218s0041g00480 | low quality protein: probable peptide nitrate transporter at1g22540-like |
| chr18 | 24955903 | 24960190 | VIT_218s0041g00490 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 24961108 | 24961708 | VIT_218s0041g00500 | low quality protein: probable peptide nitrate transporter at1g22540-like |
| chr18 | 24962005 | 24963721 | VIT_218s0041g00510 | low quality protein: probable peptide nitrate transporter at1g22540-like |
| chr18 | 24964693 | 24968480 | VIT_218s0041g00520 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 24994025 | 24994306 | VIT_218s0041g00530 | hypothetical protein |
| chr18 | 25007145 | 25015336 | VIT_218s0041g00540 | low quality protein: probable peptide nitrate transporter at1g22540-like |
| chr18 | 25018968 | 25023066 | VIT_218s0041g00550 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25024777 | 25027475 | VIT_218s0041g00560 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25031517 | 25037565 | VIT_218s0041g00570 | low quality protein: probable peptide nitrate transporter at1g22540-like |
| chr18 | 25040486 | 25046631 | VIT_218s0041g00580 | probable peptide nitrate transporter at1g22540 |
| chr18 | 25051862 | 25055614 | VIT_218s0041g00590 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25056287 | 25063928 | VIT_218s0041g00600 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25081402 | 25084411 | VIT_218s0041g00605 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25092653 | 25094575 | VIT_218s0041g00610 | proton-dependent oligopeptide transporter |
| chr18 | 25113725 | 25122191 | VIT_218s0041g00630 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25128931 | 25133105 | VIT_218s0041g00640 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25134747 | 25139428 | VIT_218s0041g00650 | probable peptide nitrate transporter at1g22540 |
| chr18 | 25163239 | 25167281 | VIT_218s0041g00660 | probable peptide nitrate transporter at1g22540-like |
| chr18 | 25170119 | 25173850 | VIT_218s0041g00670 | probable peptide nitrate transporter at1g22540 |
| chr18 | 25182672 | 25183368 | VIT_218s0041g00675 | hypothetical protein |
| chr18 | 25188028 | 25199839 | VIT_218s0041g00680 | transmembrane 9 superfamily member 3-like |
| chr18 | 25210586 | 25217152 | VIT_218s0041g00690 | basic helix-loop-helix family protein |
| chr18 | 25246440 | 25247384 | VIT_218s0041g00700 | nac domain-containing protein 90-like |
| chr18 | 25251228 | 25252798 | VIT_218s0041g00710 | udp-glycosyltransferase 88a1-like |
| chr18 | 25256563 | 25257046 | VIT_218s0041g00720 | hypothetical protein |
| chr18 | 25257047 | 25260217 | VIT_218s0041g00730 | eukaryotic peptide chain release factor subunit 1-3-like |
| chr18 | 25261198 | 25262924 | VIT_218s0041g00740 | udp-glycosyltransferase 88a1-like |
| chr18 | 25267326 | 25267822 | VIT_218s0041g00750 | xyloglucan endotransglycosylase |
| chr18 | 25288567 | 25288797 | VIT_218s0041g00770 | hypothetical protein |
| chr18 | 25300595 | 25302062 | VIT_218s0041g00790 | udp-glycosyltransferase 88a1-like |
| chr18 | 25305678 | 25310682 | VIT_218s0041g00800 | udp-glycosyltransferase 88a1-like |
| chr18 | 25313205 | 25314864 | VIT_218s0041g00810 | udp-glycosyltransferase 88a1-like |
| chr18 | 25326336 | 25327956 | VIT_218s0041g00830 | udp-glycosyltransferase 88a1-like |
| chr18 | 25334386 | 25335895 | VIT_218s0041g00840 | udp-glycosyltransferase 88a1-like |
| chr18 | 25337994 | 25339009 | VIT_218s0041g00850 | low quality protein: hemoglobin-2-like |
| chr18 | 25344562 | 25344903 | VIT_218s0041g00860 | hypothetical protein |
| chr18 | 25352280 | 25354050 | VIT_218s0041g00865 | udp-glycosyltransferase 88a1-like |
| chr18 | 25358676 | 25361391 | VIT_218s0041g00870 | low quality protein: replication factor a protein 1-like |
| chr18 | 25380525 | 25381024 | VIT_218s0041g00890 | anthocyanidin -o-glucosyltransferase-like |
| chr18 | 25392821 | 25394502 | VIT_218s0041g00900 | udp-glycosyltransferase 88a1-like |
| chr18 | 25406239 | 25407741 | VIT_218s0041g00910 | udp-glycosyltransferase 88a1-like |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr18 | 25418409 | 25420003 | VIT_218s0041g00920 | udp-glycosyltransferase 88a1-like |
| chr18 | 25436532 | 25437710 | VIT_218s0041g00930 | udp-glycosyltransferase 88a1-like |
| chr18 | 25438458 | 25439474 | VIT_218s0041g00940 | low quality protein: hemoglobin-2-like |
| chr18 | 25452274 | 25453819 | VIT_218s0041g00950 | udp-glycosyltransferase 88a1-like |
| chr18 | 25457608 | 25460537 | VIT_218s0041g00960 | low quality protein: replication factor a protein 1-like |
| chr18 | 25480999 | 25482066 | VIT_218s0041g00970 | udp-glycosyltransferase 88a1-like |
| chr18 | 25499849 | 25501966 | VIT_218s0041g00980 | udp-glycosyltransferase 88a1-like |
| chr18 | 25522586 | 25524045 | VIT_218s0041g01000 | udp-glycosyltransferase 88a1-like |
| chr18 | 25542317 | 25543132 | VIT_218s0041g01010 | udp-glycosyltransferase 88a1-like |
| chr18 | 25544863 | 25545437 | VIT_218s0041g01020 | hypothetical protein |
| chr18 | 25545438 | 25545728 | VIT_218s0041g01030 | low quality protein: hemoglobin-2-like |
| chr18 | 25565515 | 25567075 | VIT_218s0041g01040 | udp-glycosyltransferase 88a1-like |
| chr18 | 25580877 | 25581151 | VIT_218s0041g01050 | hypothetical protein |
| chr18 | 25602787 | 25604114 | VIT_218s0041g01065 | protein |
| chr18 | 25604405 | 25605856 | VIT_218s0041g01080 | udp-glycosyltransferase 88a1-like |
| chr18 | 25645181 | 25647652 | VIT_218s0041g01090 | f-box kelch-repeat protein |
| chr18 | 25655818 | 25656549 | VIT_218s0041g01100 | f-box kelch-repeat protein |
| chr18 | 25669617 | 25672961 | VIT_218s0041g01110 | pentatricopeptide repeat-containing protein |
| chr18 | 25750956 | 25751986 | VIT_218s0041g01130 | protein rrp5 homolog |
| chr18 | 25769243 | 25771054 | VIT_218s0041g01140 | probable l-type lectin-domain containing receptor kinase -like |
| chr18 | 25780512 | 25781205 | VIT_218s0041g01150 | acyl- n-acyltransferases-like protein |
| chr18 | 25797007 | 25799964 | VIT_218s0041g01160 | probable l-type lectin-domain containing receptor kinase -like |
| chr18 | 25805856 | 25807616 | VIT_218s0041g01170 | probable l-type lectin-domain containing receptor kinase -like |
| chr18 | 25815319 | 25820332 | VIT_218s0041g01180 | hypothetical protein |
| chr18 | 25820370 | 25821085 | VIT_218s0041g01190 | gcn5-related n-acetyltransferase family-like protein |
| chr18 | 25830848 | 25832659 | VIT_218s0041g01210 | probable l-type lectin-domain containing receptor kinase -like |
| chr18 | 25837986 | 25840078 | VIT_218s0041g01220 | acyl- n-acyltransferases-like protein |
| chr18 | 25847065 | 25853638 | VIT_218s0041g01230 | stromal 70 kda heat shock-related chloroplastic-like |
| chr18 | 25876273 | 25883232 | VIT_218s0041g01240 | amino acid permease 2-like |
| chr18 | 25886238 | 25888623 | VIT_218s0041g01250 | amino acid permease 2-like |
| chr18 | 25896478 | 25897018 | VIT_218s0041g01260 | protein phosphatase 1 regulatory subunit inhibitor-3 |
| chr18 | 25899437 | 25904421 | VIT_218s0041g01270 | amino acid permease 2-like |
| chr18 | 25909353 | 25934857 | VIT_218s0041g01280 | adenylate kinase |
| chr18 | 25936364 | 25938905 | VIT_218s0041g01290 | serine threonine-protein kinase-like protein ccr4-like |
| chr18 | 25945643 | 25946775 | VIT_218s0041g01300 | hypothetical protein |
| chr18 | 25972659 | 25974524 | VIT_218s0041g01310 | tmv resistance protein n-like |
| chr18 | 25972962 | 25973198 | VIT_218s0041g01320 | hypothetical protein |
| chr18 | 25979007 | 26000298 | VIT_218s0041g01330 | tmv resistance protein n-like |
| chr18 | 26016813 | 26021251 | VIT_218s0041g01340 | tmv resistance protein n-like |
| chr18 | 26025830 | 26031990 | VIT_218s0041g01350 | leucine-rich receptor-like protein kinase |
| chr18 | 26047294 | 26077101 | VIT_218s0041g01360 | translocon tic40 |
| chr18 | 26112969 | 26116153 | VIT_218s0041g01370 | tmv resistance protein n-like |
| chr18 | 26121589 | 26124946 | VIT_218s0041g01380 | tmv resistance protein n-like |
| chr18 | 26155193 | 26155303 | VIT_218s0041g01390 | hypothetical protein |
| chr18 | 26159230 | 26160354 | VIT_218s0041g01400 | tmv resistance protein n-like |
| chr18 | 26165569 | 26165946 | VIT_218s0041g01410 | tmv resistance protein n-like |
| chr18 | 26170918 | 26174628 | VIT_218s0041g01420 | hypothetical protein |
| chr18 | 26187569 | 26190602 | VIT_218s0041g01430 | tmv resistance protein n-like |
| chr18 | 26217053 | 26223822 | VIT_218s0041g01440 | tmv resistance protein n-like |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr18 | 26227551 | 26229511 | VIT_218s0041g01450 | uncharacterized protein loc100266406 |
| chr18 | 26247825 | 26251181 | VIT_218s0041g01460 | tmv resistance protein n-like |
| chr18 | 26257432 | 26262353 | VIT_218s0041g01470 | tmv resistance protein n-like |
| chr18 | 26286935 | 26296593 | VIT_218s0041g01480 | hypothetical protein |
| chr18 | 26310641 | 26319306 | VIT_218s0041g01500 | cytochrome p450 |
| chr18 | 26340185 | 26341510 | VIT_218s0041g01510 | cytochrome p450 716b2 |
| chr18 | 26355144 | 26361843 | VIT_218s0041g01520 | tmv resistance protein n-like |
| chr18 | 26365667 | 26366158 | VIT_218s0041g01530 | cytochrome p450 716b2 |
| chr18 | 26391778 | 26396402 | VIT_218s0041g01550 | beta chain |
| chr18 | 26399782 | 26401436 | VIT_218s0041g01560 | hypothetical protein |
| chr18 | 26402820 | 26405256 | VIT_218s0041g01570 | tmv resistance protein n-like |
| chr18 | 26414629 | 26416346 | VIT_218s0041g01580 | cytochrome p450 |
| chr18 | 26421154 | 26422968 | VIT_218s0041g01590 | cytochrome p450 |
| chr18 | 26433783 | 26446631 | VIT_218s0041g01600 | hypothetical protein |
| chr18 | 26470822 | 26471450 | VIT_218s0041g01610 | hypothetical protein |
| chr18 | 26481427 | 26487339 | VIT_218s0041g01620 | tmv resistance protein n-like |
| chr18 | 26487340 | 26488435 | VIT_218s0041g01630 | hypothetical protein |
| chr18 | 26502442 | 26503608 | VIT_218s0041g01640 | tmv resistance protein n-like |
| chr18 | 26507474 | 26508098 | VIT_218s0041g01650 | tmv resistance protein n-like |
| chr18 | 26551666 | 26552962 | VIT_218s0041g01680 | tmv resistance protein n-like |
| chr18 | 26556338 | 26557232 | VIT_218s0041g01690 | hypothetical protein |
| chr18 | 26557233 | 26558253 | VIT_218s0041g01700 | hypothetical protein |
| chr18 | 26562393 | 26562908 | VIT_218s0041g01710 | tmv resistance protein n-like |
| chr18 | 26566758 | 26572084 | VIT_218s0041g01720 | tmv resistance protein n-like |
| chr18 | 26572450 | 26573443 | VIT_218s0041g01730 | hypothetical protein |
| chr18 | 26573497 | 26574595 | VIT_218s0041g01740 | unnamed protein product [Vitis vinifera] |
| chr18 | 26576621 | 26586665 | VIT_218s0041g01750 | tmv resistance protein n-like |
| chr18 | 26610910 | 26614456 | VIT_218s0041g01770 | tmv resistance protein n-like |
| chr18 | 26622176 | 26622859 | VIT_218s0041g01773 | src2-like protein |
| chr18 | 26632986 | 26633564 | VIT_218s0041g01776 | src2 homolog |
| chr18 | 26650350 | 26650869 | VIT_218s0041g01780 | aspartic proteinase |
| chr18 | 26685498 | 26687218 | VIT_218s0041g01790 | tmv resistance protein n-like |
| chr18 | 26702176 | 26702766 | VIT_218s0041g01795 | src2 homolog |
| chr18 | 26733761 | 26735477 | VIT_218s0041g01800 | cytochrome p450 |
| chr18 | 26756577 | 26758590 | VIT_218s0041g01810 | cytochrome p450 716b2 |
| chr18 | 26762452 | 26767772 | VIT_218s0041g01820 | hypothetical protein |
| chr18 | 26772834 | 26795752 | VIT_218s0041g01830 | d-3-phosphoglycerate dehydrogenase |
| chr18 | 26803571 | 26810156 | VIT_218s0041g01840 | f-box family protein |
| chr18 | 26814674 | 26824192 | VIT_218s0041g01850 | polyneuridine-aldehyde esterase |
| chr18 | 26843038 | 26849429 | VIT_218s0041g01860 | aig1 domain-containing protein |
| chr18 | 26856807 | 26873199 | VIT_218s0041g01870 | phosphopantetheine adenylyltransferase |
| chr18 | 26888662 | 26896754 | VIT_218s0041g01880 | mads-box transcription factor |
| chr18 | 26908223 | 26916825 | VIT_218s0041g01890 | hypothetical protein |
| chr18 | 26917336 | 26938218 | VIT_218s0041g01900 | elongation factor 1-gamma |
| chr18 | 26948961 | 26954668 | VIT_218s0041g01910 | potassium channel kor2-like |
| chr18 | 27006644 | 27007495 | VIT_218s0041g01920 | atp binding microtubule motor |
| chr18 | 27010620 | 27014657 | VIT_218s0041g01930 | pentatricopeptide repeat-containing protein |
| chr18 | 27015568 | 27023764 | VIT_218s0041g01940 | membrane fusion protein use1 |
| chr18 | 27027226 | 27030397 | VIT_218s0041g01960 | hypothetical protein |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr18 | 27102063 | 27102260 | VIT_218s0041g01980 | hypothetical protein |
| chr18 | 27121758 | 27179917 | VIT_218s0041g02010 | 12-oxophytodienoate reductase |
| chr18 | 27135095 | 27138019 | VIT_218s0041g02020 | 12-oxophytodienoate reductase |
| chr18 | 27158318 | 27161921 | VIT_218s0041g02040 | 12-oxophytodienoate reductase |
| chr18 | 27186796 | 27189275 | VIT_218s0041g02060 | 12-oxophytodienoate reductase |
| chr18 | 27197974 | 27199869 | VIT_218s0041g02070 | 12-oxophytodienoate reductase |
| chr18 | 27211258 | 27214786 | VIT_218s0041g02080 | 12-oxophytodienoate reductase |
| chr18 | 27216525 | 27217681 | VIT_218s0041g02090 | 12-oxophytodienoate reductase 2 isoform 1 |
| chr18 | 27223834 | 27224243 | VIT_218s0041g02100 | histidine kinase osmosensor protein |
| chr18 | 27236706 | 27243125 | VIT_218s0041g02110 | hypothetical protein |
| chr18 | 27244797 | 27249772 | VIT_218s0041g02120 | tmv resistance protein n-like |
| chr18 | 27252795 | 27252944 | VIT_218s0041g02130 | hypothetical protein |
| chr18 | 27268849 | 27284583 | VIT_218s0041g02140 | mads-box protein agl12 |
| chr18 | 27298746 | 27301498 | VIT_218s0041g02150 | gdsl esterase lipase |
| chr18 | 27303881 | 27305844 | VIT_218s0041g02160 | gdsl esterase lipase |
| chr18 | 27308684 | 27314821 | VIT_218s0041g02170 | uncharacterized protein |
| chr18 | 27318562 | 27327449 | VIT_218s0041g02180 | protein da1-related 1-like |
| chr18 | 27324161 | 27325815 | VIT_218s0041g02190 | protein da1-related 1-like |
| chr18 | 27337565 | 27339377 | VIT_218s0041g02200 | hypothetical protein |
| chr18 | 27341122 | 27342959 | VIT_218s0041g02210 | tmv resistance protein n-like |
| chr18 | 27344025 | 27347748 | VIT_218s0041g02220 | uncharacterized protein |
| chr18 | 27357687 | 27357962 | VIT_218s0041g02230 | hypothetical protein |
| chr18 | 27366984 | 27386055 | VIT_218s0041g02260 | 12-oxophytodienoate reductase 2 isoform 1 |
| chr18 | 27367072 | 27377291 | VIT_218s0041g02240 | abc transporter cholesterol phospholipid flippase |
| chr18 | 27377308 | 27377568 | VIT_218s0041g02250 | hypothetical protein |
| chr18 | 27386056 | 27387315 | VIT_218s0041g02270 | 12-oxophytodienoate reductase |
| chr18 | 27402303 | 27404654 | VIT_218s0041g02290 | hypothetical protein |
| chr18 | 27404735 | 27411603 | VIT_218s0041g02300 | hypothetical protein |
| chr18 | 27418792 | 27419826 | VIT_218s0041g02310 | hypothetical protein |
| chr18 | 27421750 | 27424327 | VIT_218s0041g02315 | e3 ubiquitin-protein ligase upl2-like |
| chr18 | 27426691 | 27430888 | VIT_218s0041g02320 | and hydrolase domain-containing protein |
| chr18 | 27435043 | 27435406 | VIT_218s0041g02330 | hypothetical protein |
| chr18 | 27443467 | 27445912 | VIT_218s0041g02350 | tmv resistance protein n-like |
| chr18 | 27461823 | 27467042 | VIT_218s0041g02360 | uncharacterized protein loc100251634 |
| chr18 | 27468331 | 27468644 | VIT_218s0041g02370 | hypothetical protein |
| chr18 | 27478624 | 27483830 | VIT_218s0041g02380 | tmv resistance protein n-like |
| chr18 | 27491474 | 27505772 | VIT_218s0041g02390 | aldehyde oxidase 4-like |
| chr18 | 27505773 | 27508138 | VIT_218s0041g02400 | aldehyde oxidase 4-like |
| chr18 | 27514537 | 27525639 | VIT_218s0041g02410 | aldehyde oxidase 4-like |
| chr18 | 27565853 | 27577170 | VIT_218s0041g02430 | aldehyde oxidase 4-like |
| chr18 | 27596011 | 27600885 | VIT_218s0041g02440 | tmv resistance protein n-like |
| chr18 | 27605080 | 27608932 | VIT_218s0041g02450 | probable disease resistance protein at5g63020-like |
| chr18 | 27641256 | 27643249 | VIT_218s0041g02470 | tmv resistance protein n-like |
| chr18 | 27668094 | 27672912 | VIT_218s0089g00010 | leucine-rich repeat-containing protein |
| chr18 | 27674896 | 27678176 | VIT_218s0089g00020 | phosphatidylinositol n-acetylglucosaminyltransferase subunit p |
| chr18 | 27682632 | 27701978 | VIT_218s0089g00030 | kinase family protein |
| chr18 | 27705194 | 27707866 | VIT_218s0089g00040 | tmv resistance protein n-like |
| chr18 | 27713911 | 27721484 | VIT_218s0089g00050 | tmv resistance protein n-like |
| chr18 | 27729875 | 27733818 | VIT_218s0089g00060 | tmv resistance protein n-like |

Suppl. Tab. 3, continued

| Chromo-some | Position start | Position stop | ID | Annotation |
|---|---|---|---|---|
| chr18 | 27762784 | 27764096 | VIT_218s0089g00070 | hypothetical protein |
| chr18 | 27764434 | 27770111 | VIT_218s0089g00080 | tmv resistance protein n-like |
| chr18 | 27778809 | 27785781 | VIT_218s0089g00090 | tmv resistance protein n-like |
| chr18 | 27828676 | 27849058 | VIT_218s0089g00100 | tmv resistance protein n-like |
| chr18 | 27859383 | 27862326 | VIT_218s0089g00110 | tmv resistance protein n-like |
| chr18 | 27867278 | 27871145 | VIT_218s0089g00120 | hypothetical protein |
| chr18 | 27892542 | 27903415 | VIT_218s0089g00140 | mannan endo- -beta-mannosidase 5 |
| chr18 | 27911708 | 27913748 | VIT_218s0089g00160 | mannan endo- -beta-mannosidase 5 |
| chr18 | 27919134 | 27921047 | VIT_218s0089g00170 | mannan endo- -beta-mannosidase 5 |
| chr18 | 27922457 | 27924039 | VIT_218s0089g00180 | mannan endo- -beta-mannosidase 5 |
| chr18 | 27926186 | 27927923 | VIT_218s0089g00190 | mannan endo- -beta-mannosidase 5 |
| chr18 | 27936394 | 27938714 | VIT_218s0089g00200 | mannan endo- -beta-mannosidase 5 |
| chr18 | 27952489 | 27956544 | VIT_218s0089g00210 | endo- -beta-glucanase |
| chr18 | 27953423 | 27965061 | VIT_218s0089g00220 | rna recognition motif-containing protein |
| chr18 | 27982615 | 27983482 | VIT_218s0089g00250 | hypothetical protein |
| chr18 | 27983868 | 27985625 | VIT_218s0089g00260 | pentatricopeptide repeat-containing protein |
| chr18 | 27994460 | 27995057 | VIT_218s0089g00270 | tmv resistance protein n-like |
| chr18 | 28008743 | 28018133 | VIT_218s0089g00280 | tmv resistance protein n-like |
| chr18 | 28032472 | 28032720 | VIT_218s0089g00290 | hypothetical protein |
| chr18 | 28032837 | 28034687 | VIT_218s0089g00300 | hypothetical protein |
| chr18 | 28036802 | 28045466 | VIT_218s0089g00305 | protein transport protein sec61 subunit beta |
| chr18 | 28049383 | 28051640 | VIT_218s0089g00310 | uncharacterized protein loc100854344 |
| chr18 | 28113470 | 28119368 | VIT_218s0089g00340 | membrane protein |
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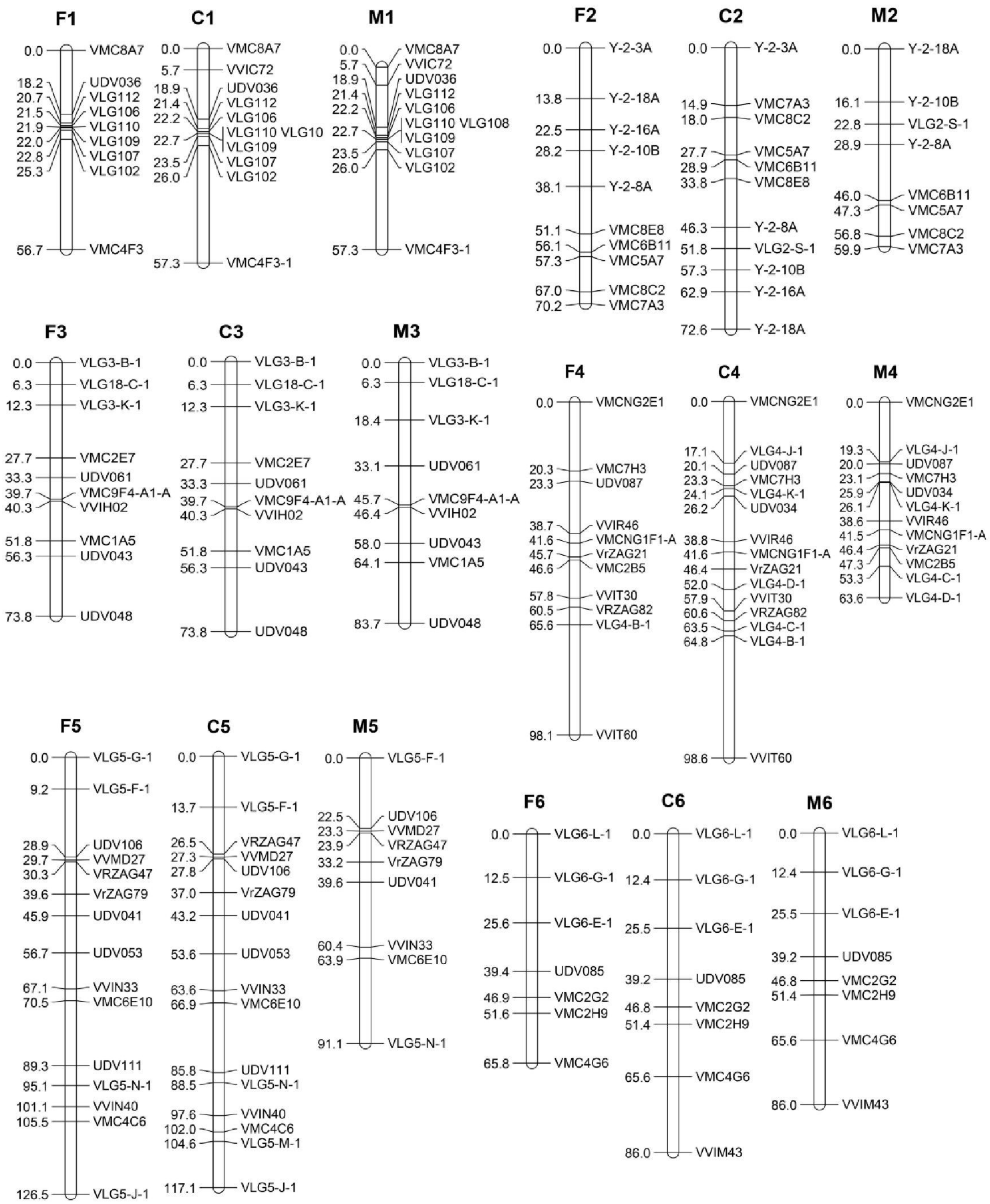
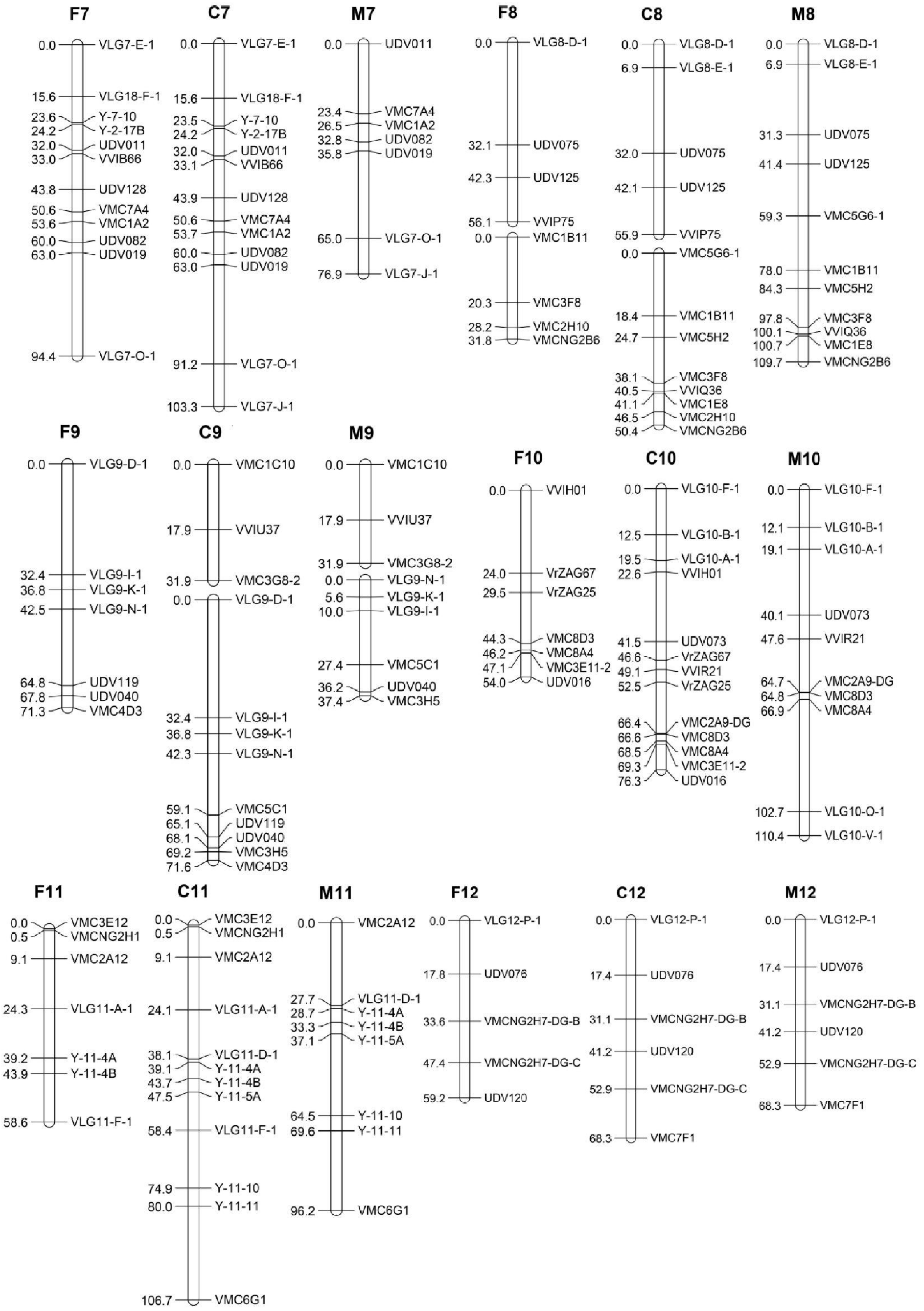


Supplementary Figure: The female parent 87-1, male parent 9-22 and consensus maps. Linkage groups of the maternal, paternal and consensus maps are numbered from 1 to 19 with the prefixes **F**, **M** and **C**, respectively. Distances are in cM Kosambi.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15.6 VLG18-F-1
23.6 Y-7-10
24.2 Y-2-17B
32.0 UDV011
33.0 VVIB66
43.8 UDV128
50.6 VMC7A4
53.6 VMC1A2
60.0 UDV082
63.0 UDV019
94.4 VLG7-O-1
C7
0.0 VLG7-E-1
15.6 VLG18-F-1
23.5 Y-7-10
24.2 Y-2-17B
32.0 UDV011
33.1 VVIB66
43.9 UDV128
50.6 VMC7A4
53.7 VMC1A2
60.0 UDV082
63.0 UDV019
91.2 VLG7-O-1
103.3 VLG7-J-1
M7
0.0 UDV011
23.4 VMC7A4
26.5 VMC1A2
32.8 UDV082
35.8 UDV019
65.0 VLG7-O-1
76.9 VLG7-J-1
F8
0.0 VLG8-D-1
32.1 UDV075
42.3 UDV125
56.1 VVIP75
0.0 VMC1B11
20.3 VMC3F8
28.2 VMC2H10
31.8 VMCNG2B6
C8
0.0 VLG8-D-1
6.9 VLG8-E-1
32.0 UDV075
42.1 UDV125
55.9 VVIP75
0.0 VMC5G6-1
18.4 VMC1B11
24.7 VMC5H2
38.1 VMC3F8
40.5 VVIQ36
41.1 VMC1E8
46.5 VMC2H10
50.4 VMCNG2B6
M8
0.0 VLG8-D-1
6.9 VLG8-E-1
31.3 UDV075
41.4 UDV125
59.3 VMC5G6-1
78.0 VMC1B11
84.3 VMC5H2
97.8 VMC3F8
100.1 VVIQ36
100.7 VMC1E8
109.7 VMCNG2B6
F9
0.0 VLG9-D-1
32.4 VLG9-I-1
36.8 VLG9-K-1
42.5 VLG9-N-1
64.8 UDV119
67.8 UDV040
71.3 VMC4D3
C9
0.0 VMC1C10
17.9 VVIU37
31.9 VMC3G8-2
0.0 VLG9-D-1
32.4 VLG9-I-1
36.8 VLG9-K-1
42.3 VLG9-N-1
59.1 VMC5C1
65.1 UDV119
68.1 UDV040
69.2 VMC3H5
71.6 VMC4D3
M9
0.0 VMC1C10
17.9 VVIU37
31.9 VMC3G8-2
0.0 VLG9-N-1
5.6 VLG9-K-1
10.0 VLG9-I-1
27.4 VMC5C1
36.2 UDV040
37.4 VMC3H5
F10
0.0 VVIH01
24.0 VrZAG67
29.5 VrZAG25
44.3 VMC8D3
46.2 VMC8A4
47.1 VMC3E11-2
54.0 UDV016
C10
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12.5 VLG10-B-1
19.5 VLG10-A-1
22.6 VVIH01
41.5 UDV073
46.6 VrZAG67
49.1 VVIR21
52.5 VrZAG25
66.4 VMC2A9-DG
66.6 VMC8D3
68.5 VMC8A4
69.3 VMC3E11-2
76.3 UDV016
M10
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12.1 VLG10-B-1
19.1 VLG10-A-1
40.1 UDV073
47.6 VVIR21
64.7 VMC2A9-DG
64.8 VMC8D3
66.9 VMC8A4
102.7 VLG10-O-1
110.4 VLG10-V-1
F11
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0.5 VMCNG2H1
9.1 VMC2A12
24.3 VLG11-A-1
39.2 Y-11-4A
43.9 Y-11-4B
58.6 VLG11-F-1
C11
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0.5 VMCNG2H1
9.1 VMC2A12
24.1 VLG11-A-1
38.1 VLG11-D-1
39.1 Y-11-4A
43.7 Y-11-4B
47.5 Y-11-5A
58.4 VLG11-F-1
74.9 Y-11-10
80.0 Y-11-11
106.7 VMC6G1
M11
0.0 VMC2A12
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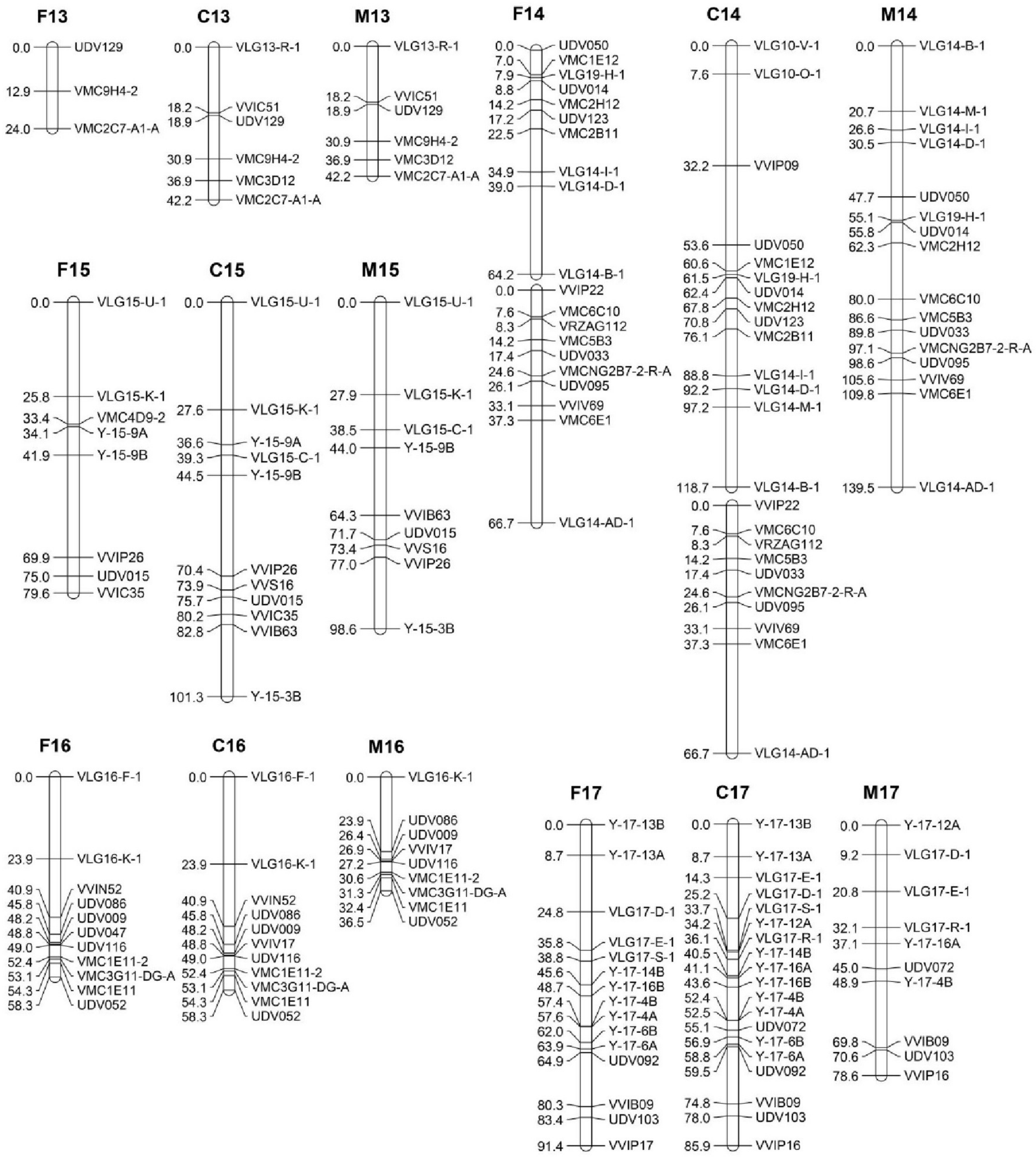
28.7 Y-11-4A
33.3 Y-11-4B
37.1 Y-11-5A
64.5 Y-11-10
69.6 Y-11-11
96.2 VMC6G1
F12
0.0 VLG12-P-1
17.8 UDV076
33.6 VMCNG2H7-DG-B
47.4 VMCNG2H7-DG-C
59.2 UDV120
C12
0.0 VLG12-P-1
17.4 UDV076
31.1 VMCNG2H7-DG-B
41.2 UDV120
52.9 VMCNG2H7-DG-C
68.3 VMC7F1
M12
0.0 VLG12-P-1
17.4 UDV076
31.1 VMCNG2H7-DG-B
41.2 UDV120
52.9 VMCNG2H7-DG-C
68.3 VMC7F1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12.9 VMC9H4-2
24.0 VMC2C7-A1-A
C13
0.0 VLG13-R-1
18.2 VVIC51
18.9 UDV129
30.9 VMC9H4-2
36.9 VMC3D12
42.2 VMC2C7-A1-A
M13
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18.2 VVIC51
18.9 UDV129
30.9 VMC9H4-2
36.9 VMC3D12
42.2 VMC2C7-A1-A
F14
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7.0 VMC1E12
7.9 VLG19-H-1
8.8 UDV014
14.2 VMC2H12
17.2 UDV123
22.5 VMC2B11
34.9 VLG14-I-1
39.0 VLG14-D-1
64.2 VLG14-B-1
0.0 VVIP22
7.6 VMC6C10
8.3 VRZAG112
14.2 VMC5B3
17.4 UDV033
24.6 VMCNG2B7-2-R-A
26.1 UDV095
33.1 VVIV69
37.3 VMC6E1
66.7 VLG14-AD-1
C14
0.0 VLG10-V-1
7.6 VLG10-O-1
32.2 VVIP09
53.6 UDV050
60.6 VMC1E12
61.5 VLG19-H-1
62.4 UDV014
67.8 VMC2H12
70.8 UDV123
76.1 VMC2B11
88.8 VLG14-I-1
92.2 VLG14-D-1
97.2 VLG14-M-1
118.7 VLG14-B-1
0.0 VVIP22
7.6 VMC6C10
8.3 VRZAG112
14.2 VMC5B3
17.4 UDV033
24.6 VMCNG2B7-2-R-A
26.1 UDV095
33.1 VVIV69
37.3 VMC6E1
66.7 VLG14-AD-1
M14
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20.7 VLG14-M-1
26.6 VLG14-I-1
30.5 VLG14-D-1
47.7 UDV050
55.1 VLG19-H-1
55.8 UDV014
62.3 VMC2H12
80.0 VMC6C10
86.6 VMC5B3
89.8 UDV033
97.1 VMCNG2B7-2-R-A
98.6 UDV095
105.6 VVIV69
109.8 VMC6E1
139.5 VLG14-AD-1
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25.8 VLG15-K-1
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41.9 Y-15-9B
69.9 VVIP26
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C15
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27.6 VLG15-K-1
36.6 Y-15-9A
39.3 VLG15-C-1
44.5 Y-15-9B
70.4 VVIP26
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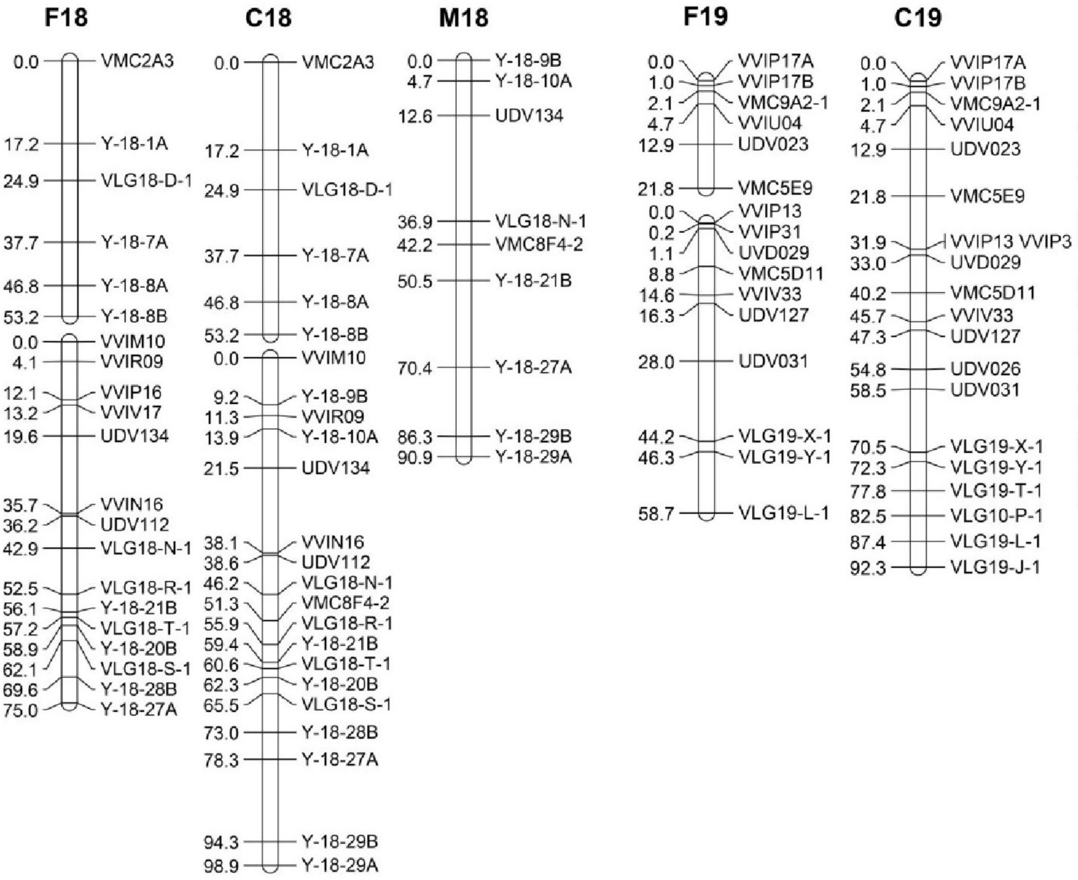
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