| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m0033 | VIT_212s0034g02556.1 | target 5' GGTCTA-TAATTTAGTTCTTG 3'<br>:::::: .::::::::.:::.<br>miRNA 3' CCAGATGGTTAAATCAGGAAT 5' | 3 | 222-241 | Protein |
| grape-m0033 | VIT_212s0035g00003.1 | target 5' GGTCTA-TAATTTAGTTCTTG 3'<br>:::::: .::::::::.:::.<br>miRNA 3' CCAGATGGTTAAATCAGGAAT 5' | 3 | 222-241 | Protein |
| grape-m0073 | VIT_204s0008g06230.1 | target 5' ACTCTAGCAGACAGCAACCTAA 3'<br>:::::  ::.::::::::::::<br>miRNA 3' TGAGA-GGTTTGTCGTTGGATT 5' | 3 | 557-578 | Large proline-rich protein bat3 |
| grape-m0073 | VIT_204s0008g06230.2 | target 5' ACTCTAGCAGACAGCAACCTAA 3'<br>:::::  ::.::::::::::::<br>miRNA 3' TGAGA-GGTTTGTCGTTGGATT 5' | 3 | 509-530 | Large proline-rich protein bat3 |
| grape-m0073 | VIT_204s0008g06230.3 | target 5' ACTCTAGCAGACAGCAACCTAA 3'<br>:::::  ::.::::::::::::<br>miRNA 3' TGAGA-GGTTTGTCGTTGGATT 5' | 3 | 557-578 | Large proline-rich protein bat3 |
| grape-m0073 | VIT_204s0008g06230.4 | target 5' ACTCTAGCAGACAGCAACCTAA 3'<br>:::::  ::.::::::::::::<br>miRNA 3' TGAGA-GGTTTGTCGTTGGATT 5' | 3 | 557-578 | Large proline-rich protein bat3 |
| grape-m0256 | VIT_200s0375g00020.1 | target 5' GACTGGTCGGACTTTGTAAA 3'<br>:::.:.::::::::.:::::<br>miRNA 3' CTGGCTAGCCTGAGACATTG 5' | 3 | 478-497 | Tmv resistance protein n |
| grape-m0423 | VIT_206s0004g06795.1 | target 5' AAGATG-GCTATTGGAGCTG 3'<br>:: ::. :::::::::::::<br>miRNA 3' TTATATGCGATAACCTCGAC 5' | 2.5 | 693-711 | Polynucleotidyl ribonuclease h fold |
| grape-m0423 | VIT_217s0000g08870.1 | target 5' AAGAT-CGCTATTGGGGCTG 3'<br>:: :: :::::::::.::::<br>miRNA 3' TTATATGCGATAACCTCGAC 5' | 3 | 934-952 | Protein |
| grape-m0423 | VIT_217s0000g08870.2 | target 5' AAGAT-CGCTATTGGGGCTG 3'<br>:: :: :::::::::.::::<br>miRNA 3' TTATATGCGATAACCTCGAC 5' | 3 | 934-952 | Protein |
| grape-m0423 | VIT_218s0001g03430.1 | target 5' CAGATACGCTATTGGAGCTG 3'<br> : :::::::::::::::::<br>miRNA 3' TTATATGCGATAACCTCGAC 5' | 2 | 500-519 | Flavonol synthase |
| grape-m0423 | VIT_218s0001g03430.2 | target 5' CAGATACGCTATTGGAGCTG 3'<br> : :::::::::::::::::<br>miRNA 3' TTATATGCGATAACCTCGAC 5' | 2 | 500-519 | Flavonol synthase |
| grape-m0423 | VIT_218s0001g04730.1 | target 5' GGT-TGTGCTATTGGAGCTG 3'<br>..: :..:::::::::::::<br>miRNA 3' TTATATGCGATAACCTCGAC 5' | 3 | 520-538 | F-box kelch-repeat protein at1g22040-like |
| grape-m0693 | VIT_206s0004g07800.1 | target 5' TTTTCAAGATCAAAAATCCCAA 3'<br>: :::::  :::::::::::::<br>miRNA 3' ACAAGTT-AAGTTTTTAGGGTT 5' | 3 | 16-37 | Pentatricopeptide repeat-containing protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m1203 | VIT_214s0060g00250.1 | target 5' TACTG-AAAGTTGAGGAAGTG 3'<br>.::.: ::::::.::::::::<br>miRNA 3' GTGGCTTTTCAATTCCTTCAC 5' | 3 | 1682-1701 | Grip and coiled-coil domain-containing |
| grape-m1354 | VIT_205s0049g02250.1 | target 5' TGGAAAGAAGAAAAAGAGGAA 3'<br>:::::::::.: :::::::::<br>miRNA 3' ACCTTTCTTTTATTTCTCCTT 5' | 3 | 663-683 | Surfeit locus protein 6 |
| grape-m1354 | VIT_209s0002g06590.1 | target 5' TGGAGAAGAAAATAAAGAAGAA 3'<br>:::: ::::::::::::: :::<br>miRNA 3' ACCT-TTCTTTTATTTCTCCTT 5' | 3 | 939-960 | Udp-glycosyltransferase 75d1-like |
| grape-m1458 | VIT_216s0100g00490.1 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.2 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.3 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.4 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.5 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.6 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.7 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.8 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m1458 | VIT_216s0100g00490.9 | target 5' CAGTTTTCGGCGAAACCCCG 3'<br>:: . :.:::::::::::::<br>miRNA 3' GTGGCAGGCCGCTTTGGGGC 5' | 3 | 24-43 | Uncharacterized protein |
| grape-m2136 | VIT_213s0067g01040.1 | target 5' AGTCAATCCTCGACCTTGGTA 3'<br>:::::::::::::::::::::<br>miRNA 3' TCAGTTAGGAGCTGGAACCAT 5' | 1 | 179-199 | Hypothetical protein |
| grape-m2483 | VIT_201s0011g02270.1 | target 5' TTCAACATCTGCATCCTCATCA 3'<br>: ::::: ::.:::::::::::<br>miRNA 3' ACGTTGTCGATGTAGGAGTAGT 5' | 3 | 1521-1542 | Serine threonine-protein kinase sepa-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m2483 | VIT_201s0011g02270.2 | target 5' TTCAACATCTGCATCCTCATCA 3'<br>: ::::: ::.:::::::::::<br>miRNA 3' ACGTTGTCGATGTAGGAGTAGT 5' | 3 | 945-966 | Serine threonine-protein kinase sepa-like |
| grape-m2483 | VIT_211s0016g00160.1 | target 5' TGCCACAGCTACCTCCTCATCA 3'<br>::: :::::::: :::::::::<br>miRNA 3' ACGTTGTCGATGTAGGAGTAGT 5' | 3 | 1793-1814 | Formin 2b |
| grape-m2616 | VIT_206s0061g00330.1 | target 5' GAAGTAGACCTTCTGAAGCAA 3'<br>::::::.::::::.:::::::<br>miRNA 3' CTTCATTTGGAAGGCTTCGTT 5' | 1.5 | 176-196 | Uncharacterized protein |
| grape-m2616 | VIT_206s0061g00330.2 | target 5' GAAGTAGACCTTCTGAAGCAA 3'<br>::::::.::::::.:::::::<br>miRNA 3' CTTCATTTGGAAGGCTTCGTT 5' | 1.5 | 269-289 | Uncharacterized protein loc100258439 |
| grape-m2616 | VIT_206s0061g00330.3 | target 5' GAAGTAGACCTTCTGAAGCAA 3'<br>::::::.::::::.:::::::<br>miRNA 3' CTTCATTTGGAAGGCTTCGTT 5' | 1.5 | 269-289 | Uncharacterized protein |
| grape-m3245-3p | VIT_218s0072g01090.1 | target 5' GGAATAGGAGGGGTAGGAAAGA 3'<br>::::: :::::.::::::::::<br>miRNA 3' CCTTACCCTCCTCATCCTTTCT 5' | 1 | 154-175 | Hypothetical protein |
| grape-m3245-5p | VIT_211s0016g05880.1 | target 5' GAGCAGTTCTACTCTCCAATT 3'<br>.:::  :.:::::::::::::<br>miRNA 3' TTCGAAAGGATGAGAGGTTAA 5' | 3 | 1728-1748 | Cgs1 mrna stability |
| grape-m3453 | VIT_213s0019g02810.1 | target 5' CCCTCTTCACCTTCCATTCA 3'<br> ::::::: :::::::::::<br>miRNA 3' AGGAGAAGCGGAAGGTAAGT 5' | 3 | 179-198 | Udp-glycosyltransferase 76g1 |
| grape-m3453 | VIT_213s0019g02860.1 | target 5' CCCTCTTCACCTTCCATTCA 3'<br> ::::::: :::::::::::<br>miRNA 3' AGGAGAAGCGGAAGGTAAGT 5' | 3 | 1502-1521 | Udp-glycosyltransferase-like protein |
| grape-m3778 | VIT_205s0029g00750.1 | target 5' CCATCTATTGGAGATCTCAAG 3'<br>:::::.::::::: :::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2.5 | 1474-1494 | Tmv resistance protein n-like |
| grape-m3778 | VIT_205s0029g00750.2 | target 5' CCATCTATTGGAGATCTCAAG 3'<br>:::::.::::::: :::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2.5 | 1474-1494 | Tmv resistance protein n-like |
| grape-m3778 | VIT_205s0029g00750.3 | target 5' CCATCTATTGGAGATCTCAAG 3'<br>:::::.::::::: :::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2.5 | 436-456 | Tmv resistance protein n-like |
| grape-m3778 | VIT_205s0029g00870.1 | target 5' CCATCTATTGGAGATCTCAAG 3'<br>:::::.::::::: :::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2.5 | 2032-2052 | Tmv resistance protein n-like |
| grape-m3778 | VIT_212s0034g00280.1 | target 5' CCATCTGTTGGAGTTCTCAAG 3'<br>:::::..::::::.:::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2 | 631-651 | Tmv resistance protein n-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m3778 | VIT_212s0034g00850.1 | target 5' CCATCTGTTGGAGATCTCAAG 3'<br>:::::..:::::: :::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 3 | 2146-2166 | Tmv resistance protein n-like |
| grape-m3778 | VIT_212s0142g00590.1 | target 5' CCATCTCTTGGAGTTCTCAAG 3'<br>:::::. ::::::.:::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2.5 | 1672-1692 | Tmv resistance protein n-like |
| grape-m3778 | VIT_215s0045g00440.1 | target 5' CCATCCATTGGAGCTCTCCAG 3'<br>:::::::::::::::::: ::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 2 | 802-822 | Tmv resistance protein n-like |
| grape-m3778 | VIT_218s0041g00200.1 | target 5' CCATCTATTGGAGCTCTCAAG 3'<br>:::::.:::::::::::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 0.5 | 1561-1581 | Tmv resistance protein n-like |
| grape-m3778 | VIT_218s0041g00250.1 | target 5' CCATCTATTGGAGCTCTCAAG 3'<br>:::::.:::::::::::::::<br>miRNA 3' GGTAGGTAACCTCGAGAGTTC 5' | 0.5 | 1630-1650 | Tmv resistance protein n-like |
| grape-m3816 | VIT_212s0034g00280.1 | target 5' CTTTAGATTTTTTACCATCAA 3'<br>::::::: :.:.:::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 3 | 407-427 | Tmv resistance protein n-like |
| grape-m3816 | VIT_212s0034g00910.1 | target 5' CTTTAGATTTTTTACCATCAA 3'<br>::::::: :.:.:::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 3 | 1865-1885 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0001g05050.1 | target 5' CTTTAGAATCTTTACCAACAA 3'<br>:::::::::::.::::: :::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 3 | 1760-1780 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0072g01230.1 | target 5' CATTAGAATCTTTGCCATCAA 3'<br>: :::::::::.:.:::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 3 | 1781-1801 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00060.1 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>:::::::::::::::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1847-1867 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00060.2 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>:::::::::::::::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1847-1867 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00060.3 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>:::::::::::::::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1847-1867 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00090.1 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>:::::::::::::::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1772-1792 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00090.2 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>:::::::::::::::::::::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1772-1792 | Tmv resistance protein n-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m3816 | VIT_218s0089g00090.4 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>::::::::::::::::::::: <br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1772-1792 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00090.5 | target 5' CTTTAGAATCTCTACCATCAA 3'<br>::::::::::::::::::::: <br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 0 | 1772-1792 | Tmv resistance protein n-like |
| grape-m3816 | VIT_218s0089g00100.1 | target 5' CTTTAGAATCTCTACCACCAA 3'<br>::::::::::::::::: :::<br>miRNA 3' GAAATCTTAGAGATGGTAGTT 5' | 2 | 1250-1270 | Tmv resistance protein n-like |
| grape-m4051 | VIT_204s0069g00560.1 | target 5' TATGAAAATAGAGATATCTTA 3'<br>.:::  :::::::::::::::<br>miRNA 3' GTACGGTTATCTCTATAGAAT 5' | 2.5 | 2476-2496 | Glutamate receptor -like |
| grape-m4250 | VIT_211s0118g00150.1 | target 5' TCTTC-CATTTCTCATACCCA 3'<br>::::: :::::::::.::::<br>miRNA 3' AGAAGTGTAAAGAGTGTGGGA 5' | 1 | 37-56 | Hypothetical protein |
| grape-m4269 | VIT_204s0008g02560.1 | target 5' CCTTGAAGCAATTTTCAG-CA 3'<br>:::::::::::::.:::: ::<br>miRNA 3' GGAACTTCGTTAAGAGTCTGT 5' | 3 | 603-622 | Uncharacterized aarf domain-containing protein kinase chloroplastic-like |
| grape-m4269 | VIT_204s0008g02560.2 | target 5' CCTTGAAGCAATTTTCAG-CA 3'<br>:::::::::::::.:::: ::<br>miRNA 3' GGAACTTCGTTAAGAGTCTGT 5' | 3 | 237-256 | Uncharacterized aarf domain-containing protein kinase chloroplastic-like |
| grape-m4277 | VIT_211s0118g00150.1 | target 5' TCTTC-CATTTCTCATACCCA 3'<br>::::: :::::::::.::::<br>miRNA 3' AGAAGTGTAAAGAGTGTGGGA 5' | 1 | 37-56 | Hypothetical protein |
| grape-m4553-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| grape-m4553-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| grape-m4560 | VIT_203s0091g00850.1 | target 5' TTTTTCAGAATCACTGCCAAG 3'<br>:::.. ::::::::::::::.<br>miRNA 3' AAAGGATCTTAGTGACGGTTT 5' | 2.5 | 238-258 | Protein |
| grape-m4560 | VIT_203s0091g00850.2 | target 5' TTTTTCAGAATCACTGCCAAG 3'<br>:::.. ::::::::::::::.<br>miRNA 3' AAAGGATCTTAGTGACGGTTT 5' | 2.5 | 238-258 | Protein |
| grape-m4560 | VIT_214s0068g00250.1 | target 5' TCTCC-AAAATCACTGCCAAA 3'<br>: ::: : :::::::::::::<br>miRNA 3' AAAGGATCTTAGTGACGGTTT 5' | 3 | 1924-1943 | Exocyst complex component 7 |
| grape-m4560 | VIT_214s0068g00250.2 | target 5' TCTCC-AAAATCACTGCCAAA 3'<br>: ::: : :::::::::::::<br>miRNA 3' AAAGGATCTTAGTGACGGTTT 5' | 3 | 1924-1943 | Exocyst complex component 7 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m4846 | VIT_213s0067g01490.1 | target  5' GGTGGAATTTCAAATTGATGG 3'<br>:.::.:::::::::..:::::<br>miRNA   3' CTACTTTAAAGTTTGGCTACC 5' | 3 | 1176-1196 | Disease resistance protein at3g14460-like |
| grape-m4912 | VIT_208s0007g00660.1 | target  5' CAGAGAGCCACCCACTTCATC 3'<br> ::: :: :::::::::::::<br>miRNA   3' CTCTGTC-GTGGGTGAAGTAG 5' | 3 | 419-439 | Laccase 110c |
| grape-m4912 | VIT_218s0072g00510.1 | target  5' GAAACTGACACCCACTTCATC 3'<br>:: :: : :::::::::::::<br>miRNA   3' CTCTGTC-GTGGGTGAAGTAG 5' | 3 | 43-63 | Kda class i heat shock protein |
| grape-m5176 | VIT_205s0029g00780.1 | target  5' CGGCCTTCCTTTAGCTCTAAA 3'<br> ::::::::::::::::: ::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 3 | 741-761 | Tmv resistance protein n-like |
| grape-m5176 | VIT_205s0029g00870.1 | target  5' TGGCCTTCCTTTAGCTCTAAA 3'<br> ::::::::::::::::: ::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 3 | 1167-1187 | Tmv resistance protein n-like |
| grape-m5176 | VIT_208s0056g00770.1 | target  5' AGTCCTTCCTTTAGCTCTCAA 3'<br>:: ::::::::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 1 | 381-401 | Regulation of nuclear pre-mrna domain-containing protein 1b |
| grape-m5176 | VIT_208s0056g00770.2 | target  5' AGTCCTTCCTTTAGCTCTCAA 3'<br>:: ::::::::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 1 | 255-275 | Regulation of nuclear pre-mrna domain-containing protein 1b |
| grape-m5176 | VIT_208s0056g00770.3 | target  5' AGTCCTTCCTTTAGCTCTCAA 3'<br>:: ::::::::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 1 | 255-275 | Regulation of nuclear pre-mrna domain-containing protein 1b |
| grape-m5176 | VIT_208s0056g00770.4 | target  5' AGTCCTTCCTTTAGCTCTCAA 3'<br>:: ::::::::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 1 | 255-275 | Regulation of nuclear pre-mrna domain-containing protein 1b |
| grape-m5176 | VIT_208s0056g00770.5 | target  5' AGTCCTTCCTTTAGCTCTCAA 3'<br>:: ::::::::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 1 | 255-275 | Regulation of nuclear pre-mrna domain-containing protein 1b |
| grape-m5176 | VIT_214s0128g00050.1 | target  5' AGCTCTATCTTTAGCTCTCAA 3'<br>:: .:: .:::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 3 | 225-245 | Thylakoid lumen kda protein |
| grape-m5176 | VIT_214s0128g00050.2 | target  5' AGCTCTATCTTTAGCTCTCAA 3'<br>:: .:: .:::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 3 | 225-245 | Thylakoid lumen kda protein |
| grape-m5176 | VIT_214s0128g00050.3 | target  5' AGCTCTATCTTTAGCTCTCAA 3'<br>:: .:: .:::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 3 | 225-245 | Protein |
| grape-m5176 | VIT_214s0128g00050.4 | target  5' AGCTCTATCTTTAGCTCTCAA 3'<br>:: .:: .:::::::::::::<br>miRNA   3' TCCGGAAGGAAATCGAGAGTT 5' | 3 | 225-245 | Thylakoid lumen kda protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m5176 | VIT_218s0001g03900.1 | `target  5' GGGTCATCCTTTAGCTCTTAA 3'`<br>`           .::.: ::::::::::::.::`<br>`miRNA   3' TCCGGAAGGAAATCGAGAGTT 5'` | 3 | 1104-1124 | Tmv resistance protein n-like |
| grape-m5176 | VIT_218s0001g10420.1 | `target  5' ATTCCTTCTCTTTAGCTCTCAA 3'`<br>`           :  ::::: :::::::::::::`<br>`miRNA   3' TCCGGAAG-GAAATCGAGAGTT 5'` | 3 | 236-257 | Dna binding |
| grape-m5176 | VIT_218s0001g11250.1 | `target  5' AGGGCTTCCTTTGGCTCTTAA 3'`<br>`           ::: ::::::::.:::::.::`<br>`miRNA   3' TCCGGAAGGAAATCGAGAGTT 5'` | 3 | 1101-1121 | Nbs-lrr resistance protein |
| grape-m5380 | VIT_200s1313g00010.1 | `target  5' CCATCCACAACATAATCTCC 3'`<br>`           ::::::::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 0 | 240-259 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_200s1313g00010.2 | `target  5' CCATCCACAACATAATCTCC 3'`<br>`           ::::::::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 0 | 240-259 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_205s0049g00330.1 | `target  5' CCATCCACAACATAATCTCC 3'`<br>`           ::::::::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 0 | 111-130 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_205s0049g00340.1 | `target  5' CCATCCACAACATAATCTCC 3'`<br>`           ::::::::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 0 | 138-157 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_205s0049g00340.2 | `target  5' CCATCCACAACATAATCTCC 3'`<br>`           ::::::::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 0 | 138-157 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_205s0049g00350.1 | `target  5' CCATCCACAGCATTATCTCC 3'`<br>`           :::::::::.::: ::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 3 | 132-151 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_205s0049g00350.2 | `target  5' CCATCCACAGCATTATCTCC 3'`<br>`           :::::::::.::: ::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 3 | 132-151 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_205s0049g00370.1 | `target  5' CCATCCACAACATAATCTCT 3'`<br>`           :::::::::::::::::::.`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 0.5 | 132-151 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m5380 | VIT_216s0022g02420.1 | `target  5' CCA-CTACAACATAATCTCT 3'`<br>`           ::: :.:::::::::::::.`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 2 | 1470-1488 | Protein |
| grape-m5380 | VIT_216s0022g02450.1 | `target  5' CCA-ATACAACATAATCTCC 3'`<br>`           :::  .::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 2.5 | 2439-2457 | Protein |
| grape-m5380 | VIT_216s0100g00030.1 | `target  5' CCA-ATACAACATAATCTCC 3'`<br>`           :::  .::::::::::::::`<br>`miRNA   3' GGTAGGTGTTGTATTAGAGG 5'` | 2.5 | 1245-1263 | Cucumisin-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m6251 | VIT_211s0016g01760.1 | `target  5' TCGTACCAAAAAACCTAAAAT 3'`<br>`           : . :::::::::::::::::`<br>`miRNA   3' ATTTTGGTTTTTTGGATTTTA 5'` | 2.5 | 743-763 | Pre-mrna cleavage factor 25kd |
| grape-m6251 | VIT_211s0016g01760.2 | `target  5' TCGTACCAAAAAACCTAAAAT 3'`<br>`           : . :::::::::::::::::`<br>`miRNA   3' ATTTTGGTTTTTTGGATTTTA 5'` | 2.5 | 743-763 | Pre-mrna cleavage factor 25kd |
| grape-m6580 | VIT_201s0127g00500.1 | `target  5' AACA-AACATCTTATGAACA 3'`<br>`            :::  ::::::::::::::`<br>`miRNA   3' GTGTAGTGTAGAATACTTGT 5'` | 3 | 869-887 | Uncharacterized protein |
| grape-m6580 | VIT_201s0127g00500.2 | `target  5' AACA-AACATCTTATGAACA 3'`<br>`            :::  ::::::::::::::`<br>`miRNA   3' GTGTAGTGTAGAATACTTGT 5'` | 3 | 809-827 | Uncharacterized protein |
| grape-m6580 | VIT_205s0102g00460.1 | `target  5' TATATT-CATCTTATGAACA 3'`<br>`           .:.::. :::::::::::::`<br>`miRNA   3' GTGTAGTGTAGAATACTTGT 5'` | 2.5 | 1066-1084 | Ubiquitin carboxyl-terminal hydrolase-like protein |
| grape-m6580 | VIT_205s0102g00460.2 | `target  5' TATATT-CATCTTATGAACA 3'`<br>`           .:.::. :::::::::::::`<br>`miRNA   3' GTGTAGTGTAGAATACTTGT 5'` | 2.5 | 1066-1084 | Ubiquitin carboxyl-terminal hydrolase-like protein |
| grape-m6580 | VIT_209s0002g04070.1 | `target  5' CACAGAACATTTTATGAACA 3'`<br>`           ::::  ::::.:::::::::`<br>`miRNA   3' GTGTAGTGTAGAATACTTGT 5'` | 3 | 1041-1060 | Uncharacterized protein |
| grape-m6580 | VIT_216s0013g00774.1 | `target  5' TATATT-CATCTTATGAACA 3'`<br>`           .:.::. :::::::::::::`<br>`miRNA   3' GTGTAGTGTAGAATACTTGT 5'` | 2.5 | 487-505 | Ubiquitin carboxyl-terminal hydrolase-like protein |
| grape-m6905 | VIT_203s0110g00350.1 | `target  5' AAGCTCCTGCTCCAACGCGGC 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' TTCGAGGACGAGGTTGCGCCG 5'` | 0 | 67-87 | Cinnamoyl reductase-like protein |
| grape-m6905 | VIT_213s0047g00540.1 | `target  5' AAGCTCCTTCTCCAACGCGGC 3'`<br>`           :::::::: ::::::::::::`<br>`miRNA   3' TTCGAGGACGAGGTTGCGCCG 5'` | 2 | 67-87 | Low quality protein: bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like |
| grape-m6905 | VIT_213s0047g00940.1 | `target  5' AAGCTCCTGCTCCAACGCGGC 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' TTCGAGGACGAGGTTGCGCCG 5'` | 0 | 67-87 | Low quality protein: bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like |
| grape-m6905 | VIT_213s0047g00990.1 | `target  5' AAGCTCTTGCTCCAACGCGGC 3'`<br>`           ::::::.::::::::::::::`<br>`miRNA   3' TTCGAGGACGAGGTTGCGCCG 5'` | 0.5 | 67-87 | Low quality protein: bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like |
| grape-m6905 | VIT_213s0064g00290.1 | `target  5' AAGCTCCTGCTCCAACGCGGC 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' TTCGAGGACGAGGTTGCGCCG 5'` | 0 | 67-87 | Low quality protein: bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like |
| grape-m6905 | VIT_213s0064g00340.1 | `target  5' AAGCTCCTGCTCCAACGTGGC 3'`<br>`           :::::::::::::::::.:::`<br>`miRNA   3' TTCGAGGACGAGGTTGCGCCG 5'` | 1 | Nov-31 | Phenylacetaldehyde reductase |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m6905 | VIT_213s0067g00460.1 | target 5' AAGCTCCTGCTCCAACGTGGT 3'<br>:::::::::::::::::.::.<br>miRNA 3' TTCGAGGACGAGGTTGCGCCG 5' | 1.5 | 70-90 | Low quality protein: bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like |
| grape-m6905 | VIT_213s0067g00530.1 | target 5' AAGCTCCTGCTCCAACGTGGT 3'<br>:::::::::::::::::.::.<br>miRNA 3' TTCGAGGACGAGGTTGCGCCG 5' | 1.5 | 70-90 | Low quality protein: bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like |
| grape-m7192 | VIT_219s0090g01460.1 | target 5' CAG-ATCCATCTCTTCTTCC 3'<br> :: :: :::::::::::::<br>miRNA 3' CTCGTACGTAGAGAAGAAGG 5' | 3 | 151-169 | Brg-1 associated |
| grape-m7484 | VIT_205s0102g00030.1 | target 5' AGATGGCACTTAACAGCCAA 3'<br>::  ..::::::::::::::<br>miRNA 3' TCACTTGTGAATTGTCGGTT 5' | 3 | 1148-1167 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7484 | VIT_205s0165g00290.1 | target 5' AGATGATACTTAACAGCCAA 3'<br>::  .:.:::::::::::::<br>miRNA 3' TCACTTGTGAATTGTCGGTT 5' | 3 | 1172-1191 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_203s0110g00030.1 | target 5' AATGACACAGTCCTCCATATG 3'<br>:: .::::::::::::::::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 2.5 | 139-159 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_205s0124g00345.1 | target 5' AAGAACACAGTCCTCCATATT 3'<br>:::::::::::::::::::::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 0 | 385-405 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_205s0124g00697.1 | target 5' GAGAACACAGTCCTCCACATT 3'<br>.:::::::::::::::: :::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 2.5 | 208-228 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_205s0124g00720.1 | target 5' AAGAACACAGTTCTCCATGTT 3'<br>:::::::::::.::::::.::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 2 | 220-240 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_205s0124g00720.2 | target 5' AAGAACACAGTTCTCCATGTT 3'<br>:::::::::::.::::::.::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 2 | 220-240 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_205s0165g00080.1 | target 5' CAGAACACTGTCCTCCATATT 3'<br> ::::::: ::::::::::::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 3 | 220-240 | Ankyrin repeat-containing protein at3g12360-like |
| grape-m7644 | VIT_219s0014g05330.1 | target 5' AAGAACACAGCCCTTCATATT 3'<br>:::::::::: :::.::::::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 3 | 133-153 | Ankyrin repeat-containing |
| grape-m7644 | VIT_219s0085g00470.1 | target 5' AAGAACACAGTCCTCCATATT 3'<br>:::::::::::::::::::::<br>miRNA 3' TTCTTGTGTCAGGAGGTATAA 5' | 0 | 179-199 | Uncharacterized protein loc100854011 |
| grape-m7774 | VIT_200s1313g00010.1 | target 5' CCATCCACAACATAATCTCC 3'<br>::::::::::::::::::::<br>miRNA 3' GGTAGGTGTTGTATTAGAGG 5' | 0 | 240-259 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m7774 | VIT_200s1313g00010.2 | target  5' CCATCCACAACATAATCTCC 3'<br>           ::::::::::::::::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 0 | 240-259 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_205s0049g00330.1 | target  5' CCATCCACAACATAATCTCC 3'<br>           ::::::::::::::::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 0 | 111-130 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_205s0049g00340.1 | target  5' CCATCCACAACATAATCTCC 3'<br>           ::::::::::::::::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 0 | 138-157 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_205s0049g00340.2 | target  5' CCATCCACAACATAATCTCC 3'<br>           ::::::::::::::::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 0 | 138-157 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_205s0049g00350.1 | target  5' CCATCCACAGCATTATCTCC 3'<br>           :::::::::.::: ::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 3 | 132-151 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_205s0049g00350.2 | target  5' CCATCCACAGCATTATCTCC 3'<br>           :::::::::.::: ::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 3 | 132-151 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_205s0049g00370.1 | target  5' CCATCCACAACATAATCTCT 3'<br>           :::::::::::::::::::.<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 0.5 | 132-151 | 1-aminocyclopropane-1-carboxylate oxidase homolog 1 |
| grape-m7774 | VIT_216s0022g02420.1 | target  5' CCA-CTACAACATAATCTCT 3'<br>           ::: :.:::::::::::::.<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 2 | 1470-1488 | Protein |
| grape-m7774 | VIT_216s0022g02450.1 | target  5' CCA-ATACAACATAATCTCC 3'<br>           :::  .::::::::::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 2.5 | 2439-2457 | Protein |
| grape-m7774 | VIT_216s0100g00030.1 | target  5' CCA-ATACAACATAATCTCC 3'<br>           :::  .::::::::::::::<br>miRNA   3' GGTAGGTGTTGTATTAGAGG 5' | 2.5 | 1245-1263 | Cucumisin-like |
| grape-m7969 | VIT_212s0034g01000.1 | target  5' GATCTATGTTTTCTCTTTTGA 3'<br>            :::.:..:::::::::::::<br>miRNA   3' GTAGGTGTAAAAGAGAAAACT 5' | 2.5 | 117-137 | Mrna turnover protein 4 |
| grape-m8278-5p | VIT_201s0010g02270.1 | target  5' ATATTGGAAGCCTTTGAGGGA 3'<br>           : :::::::::::::::::::<br>miRNA   3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| grape-m8278-5p | VIT_217s0000g10300.1 | target  5' ATATTGGAAGCCTTTGAGGGA 3'<br>           : :::::::::::::::::::<br>miRNA   3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| grape-m8937-5p | VIT_207s0005g00700.1 | target  5' TCCTCTCCCTCTCCTCCCTCGG 3'<br>           ::::::: :::: :::::::::<br>miRNA   3' AGGAGAGCGAGA-GAGGGAGCC 5' | 3 | 131-152 | Epoxide hydrolase 2-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| grape-m8937-5p | VIT_209s0002g04913.1 | target 5' TCCTCT-GCTCTTTCCCTCGC 3'<br>:::::: :::::.:::::::<br>miRNA 3' AGGAGAGCGAGAGAGGGAGCC 5' | 3 | 2325-2344 | Disease resistance protein rps5-like |
| grape-m8937-5p | VIT_209s0002g05000.2 | target 5' TCCTCT-GCTCTTTCCCTCGC 3'<br>:::::: :::::.:::::::<br>miRNA 3' AGGAGAGCGAGAGAGGGAGCC 5' | 3 | 2481-2500 | Disease resistance protein rps5-like |
| grape-m8937-5p | VIT_209s0002g05070.1 | target 5' TCCTCT-GCTCTTTCCCTCGC 3'<br>:::::: :::::.:::::::<br>miRNA 3' AGGAGAGCGAGAGAGGGAGCC 5' | 3 | 2484-2503 | Disease resistance protein rps5-like |
| grape-m8937-5p | VIT_218s0001g02870.1 | target 5' TCCTCTCTCTCTCTCCCTCTG 3'<br>::::::: ::::::::::: :<br>miRNA 3' AGGAGAGCGAGAGAGGGAGCC 5' | 3 | 92-112 | Unnamed protein product [Vitis vinifera] |
| grape-m8937-5p | VIT_219s0085g00680.1 | target 5' TCCTC-CTCTCTCTCTCTCGG 3'<br>::::: : :::::::.:::::<br>miRNA 3' AGGAGAGCGAGAGAGGGAGCC 5' | 3 | 56-75 | Uncharacterized protein |
| grape-m8943 | VIT_210s0003g03070.1 | target 5' CGACTCCCAAGGTTACATTGA 3'<br>:. ::::::::::::::::::<br>miRNA 3' GTCGAGGGTTCCAATGTAACT 5' | 1.5 | 312-332 | Beta-ketoacyl-acp synthase i |
| grape-m8960 | VIT_214s0030g00650.1 | target 5' AGTCAAACAATCTCC-TTTG 3'<br>::::::::::::::: :::.<br>miRNA 3' TCAGTTTGTTAGAGGCAAAT 5' | 2.5 | 216-234 | Bifunctional 3-dehydroquinate dehydratase shikimate chloroplastic-like |
| grape-m8960 | VIT_214s0030g00650.2 | target 5' AGTCAAACAATCTCC-TTTG 3'<br>::::::::::::::: :::.<br>miRNA 3' TCAGTTTGTTAGAGGCAAAT 5' | 2.5 | 216-234 | Bifunctional 3-dehydroquinate dehydratase shikimate chloroplastic-like |
| grape-m8993 | VIT_208s0007g08500.1 | target 5' GGAGCTGTCGCAGCCACTACGA 3'<br>::::::::::::::::::::::<br>miRNA 3' CCTCGACAGCGTCGGTGATGCT 5' | 0 | 788-809 | 60s ribosomal export protein nmd3-like |
| grape-m9163 | VIT_200s2579g00010.1 | target 5' GCGTTAATGTCTTCAATCTCA 3'<br>.:.:.:: :::::::::::::<br>miRNA 3' TGTAGTTTCAGAAGTTAGAGT 5' | 2.5 | 92-112 | Phosphoserine aminotransferase |
| grape-m9163 | VIT_206s0004g04000.1 | target 5' ACATCAAAGCCTTCAATCTCA 3'<br>::::::::: :::::::::::<br>miRNA 3' TGTAGTTTCAGAAGTTAGAGT 5' | 2 | 470-490 | 3-ketoacyl- synthase |
| grape-m9269 | VIT_208s0007g05240.1 | target 5' GTGGAGAAGACGGTGAGAAGAA 3'<br>:. ::::: :::::::::::::<br>miRNA 3' CGACTCTT-TGCCACTCTTCTT 5' | 2.5 | 1762-1783 | Phosphatidylinositol-4-phosphate 5-kinase |
| vvi-miR156a | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156a | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1208-1228 | Squamosa promoter-binding-like protein 2 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156a | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156a | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156a | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1208-1228 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156a | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156a | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156a | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156a | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156a | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCAG 3'<br>::::::.:::::::::::::.<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156a | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCAG 3'<br>::::::.:::::::::::::.<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156a | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 788-808 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156a | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156a | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156a | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156a | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156a | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156a | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::.::::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 0.5 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156a | VIT_214s0068g01780.1 | target 5' GTGCTTTCTCTCTTCTGTCAT 3'<br>:::::..:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 2 | 866-886 | Squamosa promoter-binding-like protein 16-like |
| vvi-miR156a | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 797-817 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156a | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 953-973 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156a | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156a | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156a | VIT_217s0000g05020.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::.:::::::::::::<br>miRNA 3' CACGAGGGAGAGAAGACAGTT 5' | 1.5 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156b-5p | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156b-5p | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156b-5p | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156b-5p | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156b-5p | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156b-5p | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156b-5p | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156b-5p | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156b-5p | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156b-5p | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156b-5p | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156b-5p | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 788-807 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156b-5p | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156b-5p | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156b-5p | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156b-5p | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156b-5p | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156b-5p | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156b-5p | VIT_214s0068g01780.1 | target 5' GTGCTTTCTCTCTTCTGTCA 3'<br>:::::. :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1.5 | 866-885 | Squamosa promoter-binding-like protein 16-like |
| vvi-miR156b-5p | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 797-816 | Squamosa promoter-binding-like protein 7-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156b-5p | VIT_215s0046g01020.1 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156b-5p | VIT_215s0046g01020.2 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156b-5p | VIT_215s0046g01020.3 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156b-5p | VIT_215s0046g01020.4 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156b-5p | VIT_215s0046g01020.5 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 836-856 | Uncharacterized protein loc100241322 |
| vvi-miR156b-5p | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 953-972 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156b-5p | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156b-5p | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156b-5p | VIT_217s0000g05020.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156b-5p | VIT_219s0090g01180.4 | target 5' ATGCTCACTCTTTTCTGTCA 3'<br>::::::::::.::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 2 | 161-180 | Uncharacterized protein |
| vvi-miR156b-5p | VIT_219s0090g01180.7 | target 5' ATGCTCACTCTTTTCTGTCA 3'<br>::::::::::.::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 2 | 161-180 | Uncharacterized protein |
| vvi-miR156c-5p | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156c-5p | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156c-5p | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156c-5p | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156c-5p | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156c-5p | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156c-5p | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156c-5p | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156c-5p | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156c-5p | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156c-5p | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156c-5p | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 788-807 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156c-5p | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156c-5p | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156c-5p | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156c-5p | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156c-5p | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156c-5p | VIT_211s0065g00170.7 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`            :::::: :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156c-5p | VIT_214s0068g01780.1 | `target  5' GTGCTTTCTCTCTTCTGTCA 3'`<br>`            :::::. :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1.5 | 866-885 | Squamosa promoter-binding-like protein 16-like |
| vvi-miR156c-5p | VIT_215s0021g02290.1 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`            :::::: :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1 | 797-816 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156c-5p | VIT_215s0046g01020.1 | `target  5' GTGATCAACTTTCTTCTGTCA 3'`<br>`            ::: :: :::.::::::::::`<br>`miRNA   3' CACGAG-TGAGAGAAGACAGT 5'` | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156c-5p | VIT_215s0046g01020.2 | `target  5' GTGATCAACTTTCTTCTGTCA 3'`<br>`            ::: :: :::.::::::::::`<br>`miRNA   3' CACGAG-TGAGAGAAGACAGT 5'` | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156c-5p | VIT_215s0046g01020.3 | `target  5' GTGATCAACTTTCTTCTGTCA 3'`<br>`            ::: :: :::.::::::::::`<br>`miRNA   3' CACGAG-TGAGAGAAGACAGT 5'` | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156c-5p | VIT_215s0046g01020.4 | `target  5' GTGATCAACTTTCTTCTGTCA 3'`<br>`            ::: :: :::.::::::::::`<br>`miRNA   3' CACGAG-TGAGAGAAGACAGT 5'` | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156c-5p | VIT_215s0046g01020.5 | `target  5' GTGATCAACTTTCTTCTGTCA 3'`<br>`            ::: :: :::.::::::::::`<br>`miRNA   3' CACGAG-TGAGAGAAGACAGT 5'` | 3 | 836-856 | Uncharacterized protein loc100241322 |
| vvi-miR156c-5p | VIT_217s0000g01260.1 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`            :::::: :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1 | 953-972 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156c-5p | VIT_217s0000g05020.1 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`            :::::: :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156c-5p | VIT_217s0000g05020.2 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`            :::::: :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156c-5p | VIT_217s0000g05020.3 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`            :::::: :::::::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156c-5p | VIT_219s0090g01180.4 | `target  5' ATGCTCACTCTTTTCTGTCA 3'`<br>`             :::::::::::.::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 2 | 161-180 | Uncharacterized protein |
| vvi-miR156c-5p | VIT_219s0090g01180.7 | `target  5' ATGCTCACTCTTTTCTGTCA 3'`<br>`             :::::::::::.::::::::`<br>`miRNA   3' CACGAGTGAGAGAAGACAGT 5'` | 2 | 161-180 | Uncharacterized protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156d-5p | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156d-5p | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156d-5p | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156d-5p | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156d-5p | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156d-5p | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156d-5p | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156d-5p | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156d-5p | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156d-5p | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156d-5p | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156d-5p | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 788-807 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156d-5p | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156d-5p | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156d-5p | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156d-5p | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156d-5p | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156d-5p | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156d-5p | VIT_214s0068g01780.1 | target 5' GTGCTTTCTCTCTTCTGTCA 3'<br>:::::. :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1.5 | 866-885 | Squamosa promoter-binding-like protein 16-like |
| vvi-miR156d-5p | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 797-816 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156d-5p | VIT_215s0046g01020.1 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156d-5p | VIT_215s0046g01020.2 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156d-5p | VIT_215s0046g01020.3 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156d-5p | VIT_215s0046g01020.4 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 1781-1801 | Uncharacterized protein loc100241322 |
| vvi-miR156d-5p | VIT_215s0046g01020.5 | target 5' GTGATCAACTTTCTTCTGTCA 3'<br>::: :: :::.::::::::::<br>miRNA 3' CACGAG-TGAGAGAAGACAGT 5' | 3 | 836-856 | Uncharacterized protein loc100241322 |
| vvi-miR156d-5p | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 953-972 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156d-5p | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156d-5p | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156d-5p | VIT_217s0000g05020.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 1 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156d-5p | VIT_219s0090g01180.4 | target 5' ATGCTCACTCTTTTCTGTCA 3'<br> ::::::::::.::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 2 | 161-180 | Uncharacterized protein |
| vvi-miR156d-5p | VIT_219s0090g01180.7 | target 5' ATGCTCACTCTTTTCTGTCA 3'<br> ::::::::::.::::::::<br>miRNA 3' CACGAGTGAGAGAAGACAGT 5' | 2 | 161-180 | Uncharacterized protein |
| vvi-miR156e | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156e | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156e | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156e | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156e | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1208-1227 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156e | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1145-1164 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156e | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156e | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156e | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 881-900 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156e | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156e | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1250-1269 | Squamosa promoter-binding-like protein 6-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156e | VIT_204s0008g02640.1 | target 5' GTGCTC-TTCTCCTCTGTCA 3'<br>:::::: .::::::::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 16-34 | Plastid-lipid-associated protein 8 |
| vvi-miR156e | VIT_204s0008g02640.2 | target 5' GTGCTC-TTCTCCTCTGTCA 3'<br>:::::: .::::::::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 16-34 | Plastid-lipid-associated protein 8 |
| vvi-miR156e | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 788-807 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156e | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156e | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156e | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156e | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156e | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156e | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1124-1143 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156e | VIT_214s0068g01780.1 | target 5' GTGCTTTCTCTCTTCTGTCA 3'<br>:::::. :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2.5 | 866-885 | Squamosa promoter-binding-like protein 16-like |
| vvi-miR156e | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 797-816 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156e | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 953-972 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156e | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156e | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCA 3'<br>:::::: :::::.:::::::<br>miRNA 3' CACGAGTGAGAGGAGACAGT 5' | 2 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156e | VIT_217s0000g05020.3 | `target  5' GTGCTCTCTCTCTTCTGTCA 3'`<br>`           :::::: :::::.:::::::`<br>`miRNA   3' CACGAGTGAGAGGAGACAGT 5'` | 2 | 1232-1251 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156e | VIT_219s0090g01180.4 | `target  5' ATGCTCACTCTTTTCTGTCA 3'`<br>`            ::::::::::..:::::::`<br>`miRNA   3' CACGAGTGAGAGGAGACAGT 5'` | 3 | 161-180 | Uncharacterized protein |
| vvi-miR156e | VIT_219s0090g01180.7 | `target  5' ATGCTCACTCTTTTCTGTCA 3'`<br>`            ::::::::::..:::::::`<br>`miRNA   3' CACGAGTGAGAGGAGACAGT 5'` | 3 | 161-180 | Uncharacterized protein |
| vvi-miR156f | VIT_201s0010g03710.1 | `target  5' GTGCTCTCTCTCTTCTGTCAA 3'`<br>`           ::::::::: :::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156f | VIT_201s0010g03710.2 | `target  5' GTGCTCTCTCTCTTCTGTCAA 3'`<br>`           ::::::::: :::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2 | 1208-1228 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156f | VIT_201s0010g03710.3 | `target  5' GTGCTCTCTCTCTTCTGTCAA 3'`<br>`           ::::::::: :::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156f | VIT_201s0010g03710.4 | `target  5' GTGCTCTCTCTCTTCTGTCAA 3'`<br>`           ::::::::: :::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156f | VIT_201s0010g03710.5 | `target  5' GTGCTCTCTCTCTTCTGTCAA 3'`<br>`           ::::::::: :::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2 | 1208-1228 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156f | VIT_201s0010g03710.6 | `target  5' GTGCTCTCTCTCTTCTGTCAA 3'`<br>`           ::::::::: :::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156f | VIT_201s0010g03910.1 | `target  5' GTGCTCTCTCTCTTCTGTCAT 3'`<br>`           ::::::::: ::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156f | VIT_201s0010g03910.2 | `target  5' GTGCTCTCTCTCTTCTGTCAT 3'`<br>`           ::::::::: ::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156f | VIT_201s0010g03910.3 | `target  5' GTGCTCTCTCTCTTCTGTCAT 3'`<br>`           ::::::::: ::::::::::`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156f | VIT_201s0011g00130.1 | `target  5' GTGCTCTCTCTCTTCTGTCAG 3'`<br>`           ::::::::: ::::::::::.`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2.5 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156f | VIT_201s0011g00130.2 | `target  5' GTGCTCTCTCTCTTCTGTCAG 3'`<br>`           ::::::::: ::::::::::.`<br>`miRNA   3' CACGAGAGATAGAAGACAGTT 5'` | 2.5 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156f | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 788-808 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156f | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156f | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156f | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156f | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156f | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156f | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156f | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 797-817 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156f | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 953-973 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156f | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156f | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156f | VIT_217s0000g05020.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156g-5p | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156g-5p | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1208-1228 | Squamosa promoter-binding-like protein 2 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156g-5p | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156g-5p | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156g-5p | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1208-1228 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156g-5p | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156g-5p | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156g-5p | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156g-5p | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156g-5p | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCAG 3'<br>::::::::: ::::::::::.<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2.5 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156g-5p | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCAG 3'<br>::::::::: ::::::::::.<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2.5 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156g-5p | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 788-808 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156g-5p | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156g-5p | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156g-5p | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156g-5p | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156g-5p | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156g-5p | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156g-5p | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 797-817 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156g-5p | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 953-973 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156g-5p | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156g-5p | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156g-5p | VIT_217s0000g05020.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156i | VIT_201s0010g03710.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156i | VIT_201s0010g03710.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1208-1228 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156i | VIT_201s0010g03710.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156i | VIT_201s0010g03710.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156i | VIT_201s0010g03710.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1208-1228 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156i | VIT_201s0010g03710.6 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1145-1165 | Squamosa promoter-binding-like protein 2 |
| vvi-miR156i | VIT_201s0010g03910.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156i | VIT_201s0010g03910.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156i | VIT_201s0010g03910.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 881-901 | Squamosa promoter-binding-like protein 13-like |
| vvi-miR156i | VIT_201s0011g00130.1 | target 5' GTGCTCTCTCTCTTCTGTCAG 3'<br>::::::::: ::::::::::.<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2.5 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156i | VIT_201s0011g00130.2 | target 5' GTGCTCTCTCTCTTCTGTCAG 3'<br>::::::::: ::::::::::.<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2.5 | 1250-1270 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156i | VIT_208s0007g06270.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 788-808 | Squamosa promoter-binding-like protein 9-like |
| vvi-miR156i | VIT_211s0065g00170.1 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156i | VIT_211s0065g00170.2 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156i | VIT_211s0065g00170.3 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156i | VIT_211s0065g00170.4 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156i | VIT_211s0065g00170.5 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156i | VIT_211s0065g00170.7 | target 5' GTGCTCTCTCTCTTCTGTCAA 3'<br>::::::::: :::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 2 | 1124-1144 | Squamosa promoter-binding-like protein 12-like |
| vvi-miR156i | VIT_215s0021g02290.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 797-817 | Squamosa promoter-binding-like protein 7-like |
| vvi-miR156i | VIT_217s0000g01260.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 953-973 | Squamosa promoter-binding-like protein 13 |
| vvi-miR156i | VIT_217s0000g05020.1 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR156i | VIT_217s0000g05020.2 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR156i | VIT_217s0000g05020.3 | target 5' GTGCTCTCTCTCTTCTGTCAT 3'<br>::::::::: ::::::::::<br>miRNA 3' CACGAGAGATAGAAGACAGTT 5' | 3 | 1232-1252 | Squamosa promoter-binding-like protein 6-like |
| vvi-miR159a | VIT_200s0226g00070.1 | target 5' CAGAACTCTCTTCACTCCAA 3'<br>::: :::.:::::::::::<br>miRNA 3' CTCTCGAGGGAAGTGAGGTT 5' | 3 | 25-Jun | Gras family transcription factor |
| vvi-miR159a | VIT_202s0025g04120.1 | target 5' GAGAGGTCCCTTCACTCCCA 3'<br>::::: :::::::::::: :<br>miRNA 3' CTCTCGAGGGAAGTGAGGTT 5' | 3 | 1143-1162 | Calmodulin binding |
| vvi-miR159a | VIT_203s0038g01150.1 | target 5' GA-AGCACCCTTCATTCCAA 3'<br>:: ::: :::::::.:::::<br>miRNA 3' CTCTCGAGGGAAGTGAGGTT 5' | 3 | 153-171 | Auxin-induced protein 10a5 |
| vvi-miR159a | VIT_213s0067g01630.1 | target 5' TGGAGCTCCCTTCACTCCAA 3'<br>.::::::::::::::::::<br>miRNA 3' CTCTCGAGGGAAGTGAGGTT 5' | 1.5 | 956-975 | Transcription factor gamyb-like |
| vvi-miR159c.1-3p | VIT_219s0014g01700.1 | target 5' TAGAGCCCCCTTCAAACCAAA 3'<br>:::::: :::::::: :::::<br>miRNA 3' ATCTCGAGGGAAGTTAGGTTT 5' | 3 | 659-679 | Uncharacterized protein loc100505457 |
| vvi-miR159c.1-5p | VIT_201s0011g06470.1 | target 5' CTATTGGCCTACAAGGAGCTC 3'<br>::::::: :: ::::::::::<br>miRNA 3' GATAACCTGAAGTTCCTCGAG 5' | 3 | 336-356 | Probable nad h-dependent oxidoreductase 1 |
| vvi-miR159c.1-5p | VIT_201s0011g06470.2 | target 5' CTATTGGCCTACAAGGAGCTC 3'<br>::::::: :: ::::::::::<br>miRNA 3' GATAACCTGAAGTTCCTCGAG 5' | 3 | 336-356 | Probable nad h-dependent oxidoreductase 1 |
| vvi-miR159c.1-5p | VIT_201s0011g06470.3 | target 5' CTATTGGCCTACAAGGAGCTC 3'<br>::::::: :: ::::::::::<br>miRNA 3' GATAACCTGAAGTTCCTCGAG 5' | 3 | 336-356 | Probable nad h-dependent oxidoreductase 1 |
| vvi-miR159c.1-5p | VIT_201s0011g06470.4 | target 5' CTATTGGCCTACAAGGAGCTC 3'<br>::::::: :: ::::::::::<br>miRNA 3' GATAACCTGAAGTTCCTCGAG 5' | 3 | 336-356 | Probable nad h-dependent oxidoreductase 1 |
| vvi-miR159c.1-5p | VIT_201s0011g06470.5 | target 5' CTATTGGCCTACAAGGAGCTC 3'<br>::::::: :: ::::::::::<br>miRNA 3' GATAACCTGAAGTTCCTCGAG 5' | 3 | 336-356 | Probable nad h-dependent oxidoreductase 1 |
| vvi-miR159c.2-3p | VIT_207s0031g00480.1 | target 5' GTAGCTCCTGA-ATATGCAAG 3'<br>:.::::::::: :::::::::<br>miRNA 3' CGTCGAGGACTCTATACGTTC 5' | 2.5 | 1027-1046 | Probable serine threonine-protein kinase at1g01540-like |
| vvi-miR160c | VIT_206s0004g02750.1 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR160c | VIT_206s0004g02750.2 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160c | VIT_206s0004g02750.3 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160c | VIT_206s0004g02750.4 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160c | VIT_206s0004g02750.5 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160c | VIT_208s0040g01810.1 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160c | VIT_208s0040g01810.2 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160c | VIT_208s0040g01810.3 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160c | VIT_208s0040g01810.4 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160c | VIT_213s0019g04380.1 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160c | VIT_213s0019g04380.2 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160c | VIT_213s0019g04380.3 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160c | VIT_213s0019g04380.4 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160c | VIT_218s0001g04180.1 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1293-1313 | Auxin response |
| vvi-miR160c | VIT_218s0001g04180.2 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1293-1313 | Auxin response |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR160d | VIT_206s0004g02750.1 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160d | VIT_206s0004g02750.2 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160d | VIT_206s0004g02750.3 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160d | VIT_206s0004g02750.4 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160d | VIT_206s0004g02750.5 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160d | VIT_208s0040g01810.1 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160d | VIT_208s0040g01810.2 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160d | VIT_208s0040g01810.3 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160d | VIT_208s0040g01810.4 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160d | VIT_213s0019g04380.1 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160d | VIT_213s0019g04380.2 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160d | VIT_213s0019g04380.3 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160d | VIT_213s0019g04380.4 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160d | VIT_218s0001g04180.1 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1293-1313 | Auxin response |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR160d | VIT_218s0001g04180.2 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1293-1313 | Auxin response |
| vvi-miR160e | VIT_206s0004g02750.1 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160e | VIT_206s0004g02750.2 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160e | VIT_206s0004g02750.3 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160e | VIT_206s0004g02750.4 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160e | VIT_206s0004g02750.5 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1320-1340 | Auxin response factor 18-like |
| vvi-miR160e | VIT_208s0040g01810.1 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160e | VIT_208s0040g01810.2 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160e | VIT_208s0040g01810.3 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160e | VIT_208s0040g01810.4 | target 5' TGGCATGCAGGGAGCCAGGCA 3'<br>::::::.::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 0.5 | 1353-1373 | Auxin response factor 18-like |
| vvi-miR160e | VIT_213s0019g04380.1 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160e | VIT_213s0019g04380.2 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160e | VIT_213s0019g04380.3 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |
| vvi-miR160e | VIT_213s0019g04380.4 | target 5' AGGCATACAGGGAGCCAGGCA 3'<br>::::::::::::::::::::<br>miRNA 3' ACCGTATGTCCCTCGGTCCGT 5' | 1 | 1326-1346 | Protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR160e | VIT_218s0001g04180.1 | `target  5' TGGCATGCAGGGAGCCAGGCA 3'`<br>`           ::::::.::::::::::::::`<br>`miRNA   3' ACCGTATGTCCCTCGGTCCGT 5'` | 0.5 | 1293-1313 | Auxin response |
| vvi-miR160e | VIT_218s0001g04180.2 | `target  5' TGGCATGCAGGGAGCCAGGCA 3'`<br>`           ::::::.::::::::::::::`<br>`miRNA   3' ACCGTATGTCCCTCGGTCCGT 5'` | 0.5 | 1293-1313 | Auxin response |
| vvi-miR162-3p | VIT_206s0009g03510.1 | `target  5' TTGGGT-CAGAGGTTTATTGA 3'`<br>`           .:::.: :::::::::::.::`<br>`miRNA   3' GACCTACGTCTCCAAATAGCT 5'` | 3 | 337-356 | Pentatricopeptide repeat-containing protein |
| vvi-miR162-3p | VIT_215s0048g02380.1 | `target  5' CTGGATGCAGAGGTGTTATCGA 3'`<br>`           :::::::::::::: :::::::`<br>`miRNA   3' GACCTACGTCTCCA-AATAGCT 5'` | 2 | 3250-3271 | Endoribonuclease dicer homolog 1-like |
| vvi-miR162-3p | VIT_215s0048g02380.2 | `target  5' CTGGATGCAGAGGTGTTATCGA 3'`<br>`           :::::::::::::: :::::::`<br>`miRNA   3' GACCTACGTCTCCA-AATAGCT 5'` | 2 | 3250-3271 | Endoribonuclease dicer homolog 1-like |
| vvi-miR162-3p | VIT_215s0048g02380.3 | `target  5' CTGGATGCAGAGGTGTTATCGA 3'`<br>`           :::::::::::::: :::::::`<br>`miRNA   3' GACCTACGTCTCCA-AATAGCT 5'` | 2 | 2005-2026 | Endoribonuclease dicer homolog 1-like |
| vvi-miR164a-5p | VIT_217s0000g06400.1 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 644-664 | Nac domain ipr003441 |
| vvi-miR164a-5p | VIT_217s0000g06400.2 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 740-760 | Nac domain ipr003441 |
| vvi-miR164a-5p | VIT_217s0000g06400.3 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 467-487 | Nac domain ipr003441 |
| vvi-miR164a-5p | VIT_219s0014g02200.1 | `target  5' AGCACGTGCCCTGGTTCTCCA 3'`<br>`            :::::::::::: :::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 3 | 722-742 | No apical meristem |
| vvi-miR164a-5p | VIT_219s0027g00230.1 | `target  5' AGCAAGTGCCCTGCTTCTCCG 3'`<br>`            ::: :::::::::::::::.`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2.5 | 623-643 | Nac domain protein |
| vvi-miR164a-5p | VIT_219s0027g00230.2 | `target  5' AGCAAGTGCCCTGCTTCTCCG 3'`<br>`            ::: :::::::::::::::.`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2.5 | 488-508 | Nac domain protein |
| vvi-miR164c-3p | VIT_214s0036g01400.1 | `target  5' GAAGGAGAAGAGGGGCACATC 3'`<br>`           :: :: ::::::::::::::`<br>`miRNA   3' CTACCCCTTCTCCCCGTGTAC 5'` | 3 | 36-56 | Protein |
| vvi-miR164c-5p | VIT_217s0000g06400.1 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 644-664 | Nac domain ipr003441 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR164c-5p | VIT_217s0000g06400.2 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 740-760 | Nac domain ipr003441 |
| vvi-miR164c-5p | VIT_217s0000g06400.3 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 467-487 | Nac domain ipr003441 |
| vvi-miR164c-5p | VIT_219s0014g02200.1 | `target  5' AGCACGTGCCCTGGTTCTCCA 3'`<br>`            :::::::::::: :::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 3 | 722-742 | No apical meristem |
| vvi-miR164c-5p | VIT_219s0027g00230.1 | `target  5' AGCAAGTGCCCTGCTTCTCCG 3'`<br>`            ::: :::::::::::::::.`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2.5 | 623-643 | Nac domain protein |
| vvi-miR164c-5p | VIT_219s0027g00230.2 | `target  5' AGCAAGTGCCCTGCTTCTCCG 3'`<br>`            ::: :::::::::::::::.`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2.5 | 488-508 | Nac domain protein |
| vvi-miR164d-5p | VIT_217s0000g06400.1 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 644-664 | Nac domain ipr003441 |
| vvi-miR164d-5p | VIT_217s0000g06400.2 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 740-760 | Nac domain ipr003441 |
| vvi-miR164d-5p | VIT_217s0000g06400.3 | `target  5' CTCACGTGCCCTGCTTCTCCA 3'`<br>`             :::::::::::::::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2 | 467-487 | Nac domain ipr003441 |
| vvi-miR164d-5p | VIT_219s0014g02200.1 | `target  5' AGCACGTGCCCTGGTTCTCCA 3'`<br>`            :::::::::::: :::::::`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 3 | 722-742 | No apical meristem |
| vvi-miR164d-5p | VIT_219s0027g00230.1 | `target  5' AGCAAGTGCCCTGCTTCTCCG 3'`<br>`            ::: :::::::::::::::.`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2.5 | 623-643 | Nac domain protein |
| vvi-miR164d-5p | VIT_219s0027g00230.2 | `target  5' AGCAAGTGCCCTGCTTCTCCG 3'`<br>`            ::: :::::::::::::::.`<br>`miRNA   3' ACGTGCACGGGACGAAGAGGT 5'` | 2.5 | 488-508 | Nac domain protein |
| vvi-miR166a-3p | VIT_218s0075g00480.1 | `target  5' GGAATGAAGTATGGTCCGAGA 3'`<br>`           :::::::::. ::::::::::`<br>`miRNA   3' CCTTACTTCGGACCAGGCTCT 5'` | 3 | 2612-2632 | Tmv resistance protein n-like |
| vvi-miR166a-3p | VIT_218s0075g00480.2 | `target  5' GGAATGAAGTATGGTCCGAGA 3'`<br>`           :::::::::. ::::::::::`<br>`miRNA   3' CCTTACTTCGGACCAGGCTCT 5'` | 3 | 2612-2632 | Tmv resistance protein n-like |
| vvi-miR166a-3p | VIT_218s0075g00480.3 | `target  5' GGAATGAAGTATGGTCCGAGA 3'`<br>`           :::::::::. ::::::::::`<br>`miRNA   3' CCTTACTTCGGACCAGGCTCT 5'` | 3 | 1988-2008 | Tmv resistance protein n-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166a-3p | VIT_218s0075g00480.4 | target  5' GGAATGAAGTATGGTCCGAGA 3'<br>:::::::::. ::::::::::<br>miRNA   3' CCTTACTTCGGACCAGGCTCT 5' | 3 | 950-970 | Tmv resistance protein n-like |
| vvi-miR166a-3p | VIT_218s0075g00480.5 | target  5' GGAATGAAGTATGGTCCGAGA 3'<br>:::::::::. ::::::::::<br>miRNA   3' CCTTACTTCGGACCAGGCTCT 5' | 3 | 2612-2632 | Tmv resistance protein n-like |
| vvi-miR166a-3p | VIT_218s0075g00480.6 | target  5' GGAATGAAGTATGGTCCGAGA 3'<br>:::::::::. ::::::::::<br>miRNA   3' CCTTACTTCGGACCAGGCTCT 5' | 3 | 479-499 | Tmv resistance protein n-like |
| vvi-miR166a-3p | VIT_218s0075g00480.7 | target  5' GGAATGAAGTATGGTCCGAGA 3'<br>:::::::::. ::::::::::<br>miRNA   3' CCTTACTTCGGACCAGGCTCT 5' | 3 | 950-970 | Tmv resistance protein n-like |
| vvi-miR166b-3p | VIT_204s0008g03250.1 | target  5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miR166b-3p | VIT_204s0008g03250.2 | target  5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166b-3p | VIT_206s0004g02800.1 | target  5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166b-3p | VIT_206s0004g02800.2 | target  5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166b-3p | VIT_206s0004g02800.3 | target  5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166b-3p | VIT_209s0002g03740.1 | target  5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miR166b-3p | VIT_210s0003g04670.1 | target  5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166b-3p | VIT_210s0003g04670.2 | target  5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166b-3p | VIT_210s0003g04670.3 | target  5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166b-3p | VIT_213s0019g04320.1 | target  5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA   3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166b-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166b-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166b-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166b-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166b-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166b-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CTCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miR166c-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166c-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166c-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166c-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166c-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miR166c-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166c-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166c-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166c-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166c-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miR166d-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166d-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166d-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166d-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166d-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166d-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166d-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166d-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166d-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166d-5p | VIT_208s0056g01350.1 | target 5' GCCTCAGACCAGACAACAATC 3'<br>::::: . :::::::::::::<br>miRNA 3' CGGAGCTCGGTCTGTTGTTAG 5' | 2.5 | 1750-1770 | Protein |
| vvi-miR166e-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miR166e-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166e-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166e-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166e-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166e-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miR166e-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166e-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166e-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166e-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166e-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166e-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166e-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166e-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166e-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166e-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166f-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166f-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166f-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166f-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166f-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166f-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miR166f-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166f-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166f-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166f-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166f-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166f-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166f-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166f-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166f-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166f-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166g-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miR166g-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166g-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166g-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166g-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166g-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miR166g-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166g-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166g-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166g-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166g-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166g-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166g-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166g-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166g-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166g-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166h-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miR166h-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miR166h-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166h-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166h-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miR166h-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miR166h-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166h-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166h-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miR166h-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166h-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR166h-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166h-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166h-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166h-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR166h-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miR168-3p | VIT_208s0007g07890.1 | target 5' GTTTAGGTGATGCAAGGCGGG 3'<br>.::.:: ::::::::::::::<br>miRNA 3' TAAGTCAACTACGTTCCGCCC 5' | 2 | 347-367 | Pentatricopeptide repeat-containing protein mitochondrial-like |
| vvi-miR169k-3p | VIT_206s0004g00450.1 | target 5' GGTGGTCTAGGACAACCTGCT 3'<br>:::.:.: ::::::::::::.<br>miRNA 3' CCATCGGTTCCTGTTGGACGG 5' | 2.5 | 5188-5208 | Rna polymerase ii transcription mediator |
| vvi-miR169k-3p | VIT_206s0004g00450.2 | target 5' GGTGGTCTAGGACAACCTGCT 3'<br>:::.:.: ::::::::::::.<br>miRNA 3' CCATCGGTTCCTGTTGGACGG 5' | 2.5 | 5188-5208 | Rna polymerase ii transcription mediator |
| vvi-miR169w-3p | VIT_204s0008g03660.1 | target 5' GATGAGAAGAATGAGGCAGAAA 3'<br> :::::::: ::::::::::::<br>miRNA 3' GTACTCTTC-TACTCCGTCTTT 5' | 3 | 118-139 | Embyo flowering 1-like protein |
| vvi-miR169w-3p | VIT_204s0008g03660.2 | target 5' GATGAGAAGAATGAGGCAGAAA 3'<br> :::::::: ::::::::::::<br>miRNA 3' GTACTCTTC-TACTCCGTCTTT 5' | 3 | 118-139 | Embyo flowering 1-like protein |
| vvi-miR169w-3p | VIT_212s0028g03940.1 | target 5' TATG-GAGGATGAGGCAGAAC 3'<br>.::: ::.::::::::::::<br>miRNA 3' GTACTCTTCTACTCCGTCTTT 5' | 3 | 933-952 | Histone acetyltransferase |
| vvi-miR169w-3p | VIT_212s0028g03940.2 | target 5' TATG-GAGGATGAGGCAGAAC 3'<br>.::: ::.::::::::::::<br>miRNA 3' GTACTCTTCTACTCCGTCTTT 5' | 3 | 933-952 | Histone acetyltransferase |
| vvi-miR169w-3p | VIT_212s0028g03940.3 | target 5' TATG-GAGGATGAGGCAGAAC 3'<br>.::: ::.::::::::::::<br>miRNA 3' GTACTCTTCTACTCCGTCTTT 5' | 3 | 933-952 | Histone acetyltransferase |
| vvi-miR169w-3p | VIT_212s0028g03940.4 | target 5' TATG-GAGGATGAGGCAGAAC 3'<br>.::: ::.::::::::::::<br>miRNA 3' GTACTCTTCTACTCCGTCTTT 5' | 3 | 834-853 | Histone acetyltransferase |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR169w-3p | VIT_212s0028g03940.5 | `target  5' TATG-GAGGATGAGGCAGAAC 3'`<br>`           .::: ::.::::::::::::`<br>`miRNA   3' GTACTCTTCTACTCCGTCTTT 5'` | 3 | 738-757 | Histone acetyltransferase |
| vvi-miR169w-3p | VIT_212s0028g03940.6 | `target  5' TATG-GAGGATGAGGCAGAAC 3'`<br>`           .::: ::.::::::::::::`<br>`miRNA   3' GTACTCTTCTACTCCGTCTTT 5'` | 3 | 465-484 | Histone acetyltransferase |
| vvi-miR169w-3p | VIT_217s0053g00583.1 | `target  5' CTTGGAAGGATGAGGCAGAAA 3'`<br>`           : ::. :.:::::::::::::`<br>`miRNA   3' GTACTCTTCTACTCCGTCTTT 5'` | 3 | 41-61 | Cullin 3-like protein |
| vvi-miR171b | VIT_202s0154g00400.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`            :.:::::::.::::::::::`<br>`miRNA   3' CCTCTATAACTGCGCCGAGTT 5'` | 2.5 | 1218-1238 | Gras family transcription factor |
| vvi-miR171b | VIT_204s0023g01380.1 | `target  5' GGCGATATTGGCGCGGCTCAA 3'`<br>`           :: :::::::.::::::::::`<br>`miRNA   3' CCTCTATAACTGCGCCGAGTT 5'` | 2 | 585-605 | Gras family transcription factor |
| vvi-miR171b | VIT_215s0048g00270.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`            :.:::::::.::::::::::`<br>`miRNA   3' CCTCTATAACTGCGCCGAGTT 5'` | 2.5 | 1230-1250 | Gras family transcription factor |
| vvi-miR171e-3p | VIT_202s0154g00400.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`           :: ::::::::::::::::::`<br>`miRNA   3' TCACTATAACCGCGCCGAGTT 5'` | 1 | 1218-1238 | Gras family transcription factor |
| vvi-miR171e-3p | VIT_204s0023g01380.1 | `target  5' GGCGATATTGGCGCGGCTCAA 3'`<br>`           .: ::::::::::::::::::`<br>`miRNA   3' TCACTATAACCGCGCCGAGTT 5'` | 1.5 | 585-605 | Gras family transcription factor |
| vvi-miR171e-3p | VIT_215s0048g00270.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`           :: ::::::::::::::::::`<br>`miRNA   3' TCACTATAACCGCGCCGAGTT 5'` | 1 | 1230-1250 | Gras family transcription factor |
| vvi-miR171f-3p | VIT_202s0154g00400.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`           :: ::::::::::::::::::`<br>`miRNA   3' TCACTATAACCGCGCCGAGTT 5'` | 1 | 1218-1238 | Gras family transcription factor |
| vvi-miR171f-3p | VIT_204s0023g01380.1 | `target  5' GGCGATATTGGCGCGGCTCAA 3'`<br>`           .: ::::::::::::::::::`<br>`miRNA   3' TCACTATAACCGCGCCGAGTT 5'` | 1.5 | 585-605 | Gras family transcription factor |
| vvi-miR171f-3p | VIT_215s0048g00270.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`           :: ::::::::::::::::::`<br>`miRNA   3' TCACTATAACCGCGCCGAGTT 5'` | 1 | 1230-1250 | Gras family transcription factor |
| vvi-miR171h | VIT_202s0154g00400.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`            ::::::::::::::::::::`<br>`miRNA   3' GCCCTATAACCGCGCCGAGTT 5'` | 1 | 1218-1238 | Gras family transcription factor |
| vvi-miR171h | VIT_204s0023g01380.1 | `target  5' GGCGATATTGGCGCGGCTCAA 3'`<br>`            : ::::::::::::::::::`<br>`miRNA   3' GCCCTATAACCGCGCCGAGTT 5'` | 2 | 585-605 | Gras family transcription factor |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR171h | VIT_212s0059g00650.1 | `target  5' CGGGATATTGGTGCGGTTCAA 3'`<br>`           :::::::::::.::::.::::`<br>`miRNA   3' GCCCTATAACCGCGCCGAGTT 5'` | 1 | 142-166 | Hypothetical protein |
| vvi-miR171h | VIT_215s0048g00270.1 | `target  5' AGGGATATTGGCGCGGCTCAA 3'`<br>`            ::::::::::::::::::::`<br>`miRNA   3' GCCCTATAACCGCGCCGAGTT 5'` | 1 | 1230-1250 | Gras family transcription factor |
| vvi-miR172c-3p | VIT_206s0004g03590.1 | `target  5' CTGCAGCATCATCAGGATTCT 3'`<br>`           ::::::::::::::.:::::.`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1.5 | 1334-1354 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miR172c-3p | VIT_206s0004g03590.3 | `target  5' CTGCAGCATCATCAGGATTCT 3'`<br>`           ::::::::::::::.:::::.`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1.5 | 1289-1309 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miR172c-3p | VIT_207s0031g00220.1 | `target  5' CTGCAGCATCATCAGGATTCC 3'`<br>`           ::::::::::::::.::::::`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1 | 1430-1450 | Transcription factor apetala2 |
| vvi-miR172c-3p | VIT_207s0031g00220.2 | `target  5' CTGCAGCATCATCAGGATTCC 3'`<br>`           ::::::::::::::.::::::`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1 | 1442-1462 | Transcription factor apetala2 |
| vvi-miR172c-3p | VIT_208s0040g03180.1 | `target  5' CTGCAGCATCATCAGGATTCT 3'`<br>`           ::::::::::::::.:::::.`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1.5 | 1331-1351 | Ap2 domain-containing transcription factor |
| vvi-miR172c-3p | VIT_213s0019g03550.1 | `target  5' CTGCAGCATCATCAGGATTCC 3'`<br>`           ::::::::::::::.::::::`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1 | 1304-1324 | Ap2 domain-containing transcription factor |
| vvi-miR172c-3p | VIT_213s0019g03550.2 | `target  5' CTGCAGCATCATCAGGATTCC 3'`<br>`           ::::::::::::::.::::::`<br>`miRNA   3' GACGTCGTAGTAGTTCTAAGG 5'` | 1 | 1259-1279 | Ap2 domain-containing transcription factor |
| vvi-miR172c-5p | VIT_207s0191g00170.1 | `target  5' TGTAAAACTTGATGATGCTCA 3'`<br>`           ::: :: :::::::::::::`<br>`miRNA   3' ACACTTAGAACTACTACGAGG 5'` | 3 | 573-593 | Lmbr1 domain-containing protein 2 homolog a-like |
| vvi-miR172c-5p | VIT_207s0191g00170.2 | `target  5' TGTAAAACTTGATGATGCTCA 3'`<br>`           ::: :: :::::::::::::`<br>`miRNA   3' ACACTTAGAACTACTACGAGG 5'` | 3 | 183-203 | Lmbr1 domain-containing protein 2 homolog a-like |
| vvi-miR172c-5p | VIT_207s0191g00170.3 | `target  5' TGTAAAACTTGATGATGCTCA 3'`<br>`           ::: :: :::::::::::::`<br>`miRNA   3' ACACTTAGAACTACTACGAGG 5'` | 3 | 573-593 | Lmbr1 domain-containing protein 2 homolog a-like |
| vvi-miR172c-5p | VIT_207s0191g00170.6 | `target  5' TGTAAAACTTGATGATGCTCA 3'`<br>`           ::: :: :::::::::::::`<br>`miRNA   3' ACACTTAGAACTACTACGAGG 5'` | 3 | 573-593 | Lmbr1 domain-containing protein 2 homolog a-like |
| vvi-miR172c-5p | VIT_207s0191g00170.7 | `target  5' TGTAAAACTTGATGATGCTCA 3'`<br>`           ::: :: :::::::::::::`<br>`miRNA   3' ACACTTAGAACTACTACGAGG 5'` | 3 | 573-593 | Lmbr1 domain-containing protein 2 homolog a-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR172c-5p | VIT_207s0191g00170.8 | target 5' TGTAAAACTTGATGATGCTCA 3'<br>::: :: :::::::::::::<br>miRNA 3' ACACTTAGAACTACTACGAGG 5' | 3 | 183-203 | Lmbr1 domain-containing protein 2 homolog a-like |
| vvi-miR172c-5p | VIT_208s0007g05895.1 | target 5' TGTGAGTGTTGATGATGCTCT 3'<br>:::::.: ::::::::::::.<br>miRNA 3' ACACTTAGAACTACTACGAGG 5' | 2 | 702-722 | F-box family protein |
| vvi-miR172d | VIT_200s0184g00102.1 | target 5' GCATTCATGATCAAGATTCTCA 3'<br>:::  ::: :::::::::::::<br>miRNA 3' CGT-CGTAGTAGTTCTAAGAGT 5' | 3 | 215-236 | Ap2 erf and b3 domain-containing transcription factor rav2 |
| vvi-miR172d | VIT_206s0004g03590.1 | target 5' GCAGCATCATCAGGATTCTCA 3'<br>::::::::::::.::::::::<br>miRNA 3' CGTCGTAGTAGTTCTAAGAGT 5' | 1 | 1336-1356 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miR172d | VIT_206s0004g03590.3 | target 5' GCAGCATCATCAGGATTCTCA 3'<br>::::::::::::.::::::::<br>miRNA 3' CGTCGTAGTAGTTCTAAGAGT 5' | 1 | 1291-1311 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miR172d | VIT_207s0031g00220.1 | target 5' GCAGCATCATCAGGATTCCCA 3'<br>::::::::::::.::::: ::<br>miRNA 3' CGTCGTAGTAGTTCTAAGAGT 5' | 3 | 1432-1452 | Transcription factor apetala2 |
| vvi-miR172d | VIT_207s0031g00220.2 | target 5' GCAGCATCATCAGGATTCCCA 3'<br>::::::::::::.::::: ::<br>miRNA 3' CGTCGTAGTAGTTCTAAGAGT 5' | 3 | 1444-1464 | Transcription factor apetala2 |
| vvi-miR172d | VIT_208s0040g03180.1 | target 5' GCAGCATCATCAGGATTCTTG 3'<br>::::::::::::.::::::..<br>miRNA 3' CGTCGTAGTAGTTCTAAGAGT 5' | 2.5 | 1333-1353 | Ap2 domain-containing transcription factor |
| vvi-miR2111-3p | VIT_209s0002g02550.1 | target 5' AGTAAT-TGCAACCAGAGGAT 3'<br>:::::: :::::::::::::.<br>miRNA 3' TCATTAGACGTTGGTCTCCTG 5' | 1.5 | 955-974 | Tudor pwwp mbt superfamily protein |
| vvi-miR2111-3p | VIT_209s0002g02550.2 | target 5' AGTAAT-TGCAACCAGAGGAT 3'<br>:::::: :::::::::::::.<br>miRNA 3' TCATTAGACGTTGGTCTCCTG 5' | 1.5 | 1399-1418 | Tudor pwwp mbt superfamily protein |
| vvi-miR2111-3p | VIT_209s0002g02550.3 | target 5' AGTAAT-TGCAACCAGAGGAT 3'<br>:::::: :::::::::::::.<br>miRNA 3' TCATTAGACGTTGGTCTCCTG 5' | 1.5 | 955-974 | Tudor pwwp mbt superfamily protein |
| vvi-miR2111-3p | VIT_209s0002g02550.4 | target 5' AGTAAT-TGCAACCAGAGGAT 3'<br>:::::: :::::::::::::.<br>miRNA 3' TCATTAGACGTTGGTCTCCTG 5' | 1.5 | 955-974 | Tudor pwwp mbt superfamily protein |
| vvi-miR2111-3p | VIT_209s0002g02550.5 | target 5' AGTAAT-TGCAACCAGAGGAT 3'<br>:::::: :::::::::::::.<br>miRNA 3' TCATTAGACGTTGGTCTCCTG 5' | 1.5 | 955-974 | Tudor pwwp mbt superfamily protein |
| vvi-miR2111-3p | VIT_209s0002g02550.6 | target 5' AGTAAT-TGCAACCAGAGGAT 3'<br>:::::: :::::::::::::.<br>miRNA 3' TCATTAGACGTTGGTCTCCTG 5' | 1.5 | 955-974 | Tudor pwwp mbt superfamily protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR2111-5p | VIT_214s0068g02150.1 | target 5' TAGATACTCAGGATGCAGATTA 3'<br>::::. ::::::::::::::::<br>miRNA 3' ATCTG-GAGTCCTACGTCTAAT 5' | 1.5 | 239-260 | F-box kelch-repeat protein at3g27150-like |
| vvi-miR2111-5p | VIT_214s0068g02150.2 | target 5' TAGATACTCAGGATGCAGATTA 3'<br>::::. ::::::::::::::::<br>miRNA 3' ATCTG-GAGTCCTACGTCTAAT 5' | 1.5 | 239-260 | F-box kelch-repeat protein at3g27150-like |
| vvi-miR2111-5p | VIT_214s0068g02150.3 | target 5' TAGATACTCAGGATGCAGATTA 3'<br>::::. ::::::::::::::::<br>miRNA 3' ATCTG-GAGTCCTACGTCTAAT 5' | 1.5 | 410-431 | F-box kelch-repeat protein at3g27150-like |
| vvi-miR2111-5p | VIT_214s0068g02150.4 | target 5' TAGATACTCAGGATGCAGATTA 3'<br>::::. ::::::::::::::::<br>miRNA 3' ATCTG-GAGTCCTACGTCTAAT 5' | 1.5 | 239-260 | F-box kelch-repeat protein at3g27150-like |
| vvi-miR2111-5p | VIT_214s0068g02150.5 | target 5' TAGATACTCAGGATGCAGATTA 3'<br>::::. ::::::::::::::::<br>miRNA 3' ATCTG-GAGTCCTACGTCTAAT 5' | 1.5 | 239-260 | F-box kelch-repeat protein at3g27150-like |
| vvi-miR2950-5p | VIT_209s0002g01600.1 | target 5' CAACTTTGCAAGAGATGGAAT 3'<br>: : : :::::::::::::::<br>miRNA 3' GGTCACACGTTCTCTACCTTA 5' | 3 | 234-254 | Dna binding |
| vvi-miR319b-3p | VIT_210s0003g00870.1 | target 5' GGGAAC-CCCTTCAGTCCAC 3'<br>:::: : :::::::::::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 926-944 | Transcription factor tcp4-like |
| vvi-miR319b-3p | VIT_213s0067g01630.1 | target 5' TGGAGCTCCCTTCACTCCAA 3'<br>::::::::::::: :::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 956-975 | Transcription factor gamyb-like |
| vvi-miR319c-3p | VIT_210s0003g00870.1 | target 5' GGGAAC-CCCTTCAGTCCAC 3'<br>:::: : :::::::::::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 926-944 | Transcription factor tcp4-like |
| vvi-miR319c-3p | VIT_213s0067g01630.1 | target 5' TGGAGCTCCCTTCACTCCAA 3'<br>::::::::::::: :::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 956-975 | Transcription factor gamyb-like |
| vvi-miR319c-5p | VIT_214s0081g00480.1 | target 5' GAATGCACTGAAGAAAGCTCA 3'<br>:: :: ::::::::::::::<br>miRNA 3' CTCACCTGACTTCTTTCGAGA 5' | 3 | 322-342 | Protein |
| vvi-miR319f-3p | VIT_210s0003g00870.1 | target 5' GGGAAC-CCCTTCAGTCCAC 3'<br>:::: : :::::::::::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 926-944 | Transcription factor tcp4-like |
| vvi-miR319f-3p | VIT_213s0067g01630.1 | target 5' TGGAGCTCCCTTCACTCCAA 3'<br>::::::::::::: :::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 956-975 | Transcription factor gamyb-like |
| vvi-miR319g | VIT_210s0003g00870.1 | target 5' GGGAAC-CCCTTCAGTCCAC 3'<br>:::: : :::::::::::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 926-944 | Transcription factor tcp4-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR319g | VIT_213s0067g01630.1 | target 5' TGGAGCTCCCTTCACTCCAA 3'<br> ::::::::::::: :::::<br>miRNA 3' CCCTCGAGGGAAGTCAGGTT 5' | 3 | 956-975 | Transcription factor gamyb-like |
| vvi-miR3623-5p | VIT_218s0041g02180.2 | target 5' TGGTGCTTGGAGGAGCTTGTGA 3'<br>::::::::::: ::.:::::::<br>miRNA 3' ACCACGAACCTACTTGAACACT 5' | 3 | 115-136 | Protein da1-related 1-like |
| vvi-miR3623-5p | VIT_218s0041g02180.3 | target 5' TGGTGCTTGGAGGAGCTTGTGA 3'<br>::::::::::: ::.:::::::<br>miRNA 3' ACCACGAACCTACTTGAACACT 5' | 3 | 271-292 | Protein da1-related 1-like |
| vvi-miR3624-3p | VIT_200s0194g00300.1 | target 5' AGTAGTATGCTGCTGCCCTGA 3'<br>:::::::::::::::::::::<br>miRNA 3' TCATCATACGACGACGGGACT 5' | 0 | 141-161 | Uncharacterized protein loc100260893 |
| vvi-miR3624-3p | VIT_200s0194g00340.1 | target 5' AGTAGTATGCTGCTGCCCTGA 3'<br>:::::::::::::::::::::<br>miRNA 3' TCATCATACGACGACGGGACT 5' | 0 | 29-Sep | Uncharacterized protein loc100852467 |
| vvi-miR3624-3p | VIT_200s0194g00340.2 | target 5' AGTAGTATGCTGCTGCCCTGA 3'<br>:::::::::::::::::::::<br>miRNA 3' TCATCATACGACGACGGGACT 5' | 0 | 123-143 | Metal ion binding protein |
| vvi-miR3629a-5p | VIT_208s0040g01510.1 | target 5' TTTGGTTGCTGAGAAAAT-CG 3'<br>.::::.:::::::::::: ::<br>miRNA 3' GAACCGACGACTCTTTTACGC 5' | 3 | 48-67 | Uncharacterized protein loc100853283 |
| vvi-miR3629a-5p | VIT_212s0028g01350.1 | target 5' ATTGG-TGCTGAGAAAATGCT 3'<br> :::: ::::::::::::::<br>miRNA 3' GAACCGACGACTCTTTTACGC 5' | 3 | 834-853 | Lrr receptor-like serine threonine-protein kinase |
| vvi-miR3629a-5p | VIT_212s0028g01350.2 | target 5' ATTGG-TGCTGAGAAAATGCT 3'<br> :::: ::::::::::::::<br>miRNA 3' GAACCGACGACTCTTTTACGC 5' | 3 | 834-853 | Lrr receptor-like serine threonine-protein kinase |
| vvi-miR3629a-5p | VIT_212s0028g01350.3 | target 5' ATTGG-TGCTGAGAAAATGCT 3'<br> :::: ::::::::::::::<br>miRNA 3' GAACCGACGACTCTTTTACGC 5' | 3 | 447-466 | Lrr receptor-like serine threonine-protein kinase |
| vvi-miR3629a-5p | VIT_212s0028g01350.4 | target 5' ATTGG-TGCTGAGAAAATGCT 3'<br> :::: ::::::::::::::<br>miRNA 3' GAACCGACGACTCTTTTACGC 5' | 3 | 621-640 | Lrr receptor-like serine threonine-protein kinase |
| vvi-miR3629a-5p | VIT_212s0028g01350.5 | target 5' ATTGG-TGCTGAGAAAATGCT 3'<br> :::: ::::::::::::::<br>miRNA 3' GAACCGACGACTCTTTTACGC 5' | 3 | 834-853 | Lrr receptor-like serine threonine-protein kinase |
| vvi-miR3632-3p | VIT_213s0067g00790.1 | target 5' ATGGTATGGGGGGTCTGGGAAA 3'<br> :::::: ::::::::::::::<br>miRNA 3' AACCATAACCCCCAGACCCTTT 5' | 2 | 575-596 | Disease resistance protein |
| vvi-miR3632-3p | VIT_213s0067g00830.1 | target 5' ATGGTATGGGGGGTCTGGGAAA 3'<br> :::::: ::::::::::::::<br>miRNA 3' AACCATAACCCCCAGACCCTTT 5' | 2 | 578-599 | Probable disease resistance rpp8-like protein 2-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR3632-3p | VIT_213s0067g00830.2 | `target  5' ATGGTATGGGGGGTCTGGGAAA 3'`<br>`            :::::: ::::::::::::::`<br>`miRNA   3' AACCATAACCCCCAGACCCTTT 5'` | 2 | 578-599 | Probable disease resistance rpp8-like protein 2-like |
| vvi-miR3632-3p | VIT_213s0067g00830.3 | `target  5' ATGGTATGGGGGGTCTGGGAAA 3'`<br>`            :::::: ::::::::::::::`<br>`miRNA   3' AACCATAACCCCCAGACCCTTT 5'` | 2 | 578-599 | Probable disease resistance rpp8-like protein 2-like |
| vvi-miR3632-3p | VIT_213s0067g00830.4 | `target  5' ATGGTATGGGGGGTCTGGGAAA 3'`<br>`            :::::: ::::::::::::::`<br>`miRNA   3' AACCATAACCCCCAGACCCTTT 5'` | 2 | 578-599 | Probable disease resistance rpp8-like protein 2-like |
| vvi-miR3633b-5p | VIT_203s0180g00280.1 | `target  5' GGAT-CCAGCCATCCATTCT 3'`<br>`           .::: :::::::.::::::.`<br>`miRNA   3' TCTAGGGTCGGTGGGTAAGG 5'` | 3 | 431-449 | Limonoid udp-glucosyltransferase |
| vvi-miR3633b-5p | VIT_210s0003g03540.1 | `target  5' AGATTTCAGCCACCCATTAC 3'`<br>`           ::::..:::::::::::: :`<br>`miRNA   3' TCTAGGGTCGGTGGGTAAGG 5'` | 3 | 633-652 | Beta-amyrin synthase |
| vvi-miR3633b-5p | VIT_212s0034g02470.1 | `target  5' AGATCCCA-CCATCCATTCC 3'`<br>`           :::::::: :::.:::::::`<br>`miRNA   3' TCTAGGGTCGGTGGGTAAGG 5'` | 3 | 1081-1099 | Disease resistance protein at3g14460-like |
| vvi-miR3634-3p | VIT_219s0085g00430.1 | `target  5' ATGGCATGAGTG-GAGTCGGAAA 3'`<br>`           :.:::::::::: ::::::::::`<br>`miRNA   3' TGCCGTACTCACGCTCAGCCTTT 5'` | 2.5 | 86-107 | Uncharacterized protein loc100855287 |
| vvi-miR3634-3p | VIT_219s0085g00470.1 | `target  5' ATGGCATGAGTG-GAGTCGGAAA 3'`<br>`           :.:::::::::: ::::::::::`<br>`miRNA   3' TGCCGTACTCACGCTCAGCCTTT 5'` | 2.5 | 116-137 | Uncharacterized protein loc100854011 |
| vvi-miR3635-3p | VIT_217s0000g05850.1 | `target  5' GAGGCATGTGTGGGACATAAT 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' CTCCGTACACACCCTGTATTA 5'` | 0 | 2097-2117 | Abc transporter retinal flippase subfamily |
| vvi-miR3635-3p | VIT_217s0000g05850.2 | `target  5' GAGGCATGTGTGGGACATAAT 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' CTCCGTACACACCCTGTATTA 5'` | 0 | 2097-2117 | Abc transporter retinal flippase subfamily |
| vvi-miR3635-3p | VIT_217s0000g05850.3 | `target  5' GAGGCATGTGTGGGACATAAT 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' CTCCGTACACACCCTGTATTA 5'` | 0 | 2175-2195 | Abc transporter retinal flippase subfamily |
| vvi-miR3635-3p | VIT_217s0000g05850.4 | `target  5' GAGGCATGTGTGGGACATAAT 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' CTCCGTACACACCCTGTATTA 5'` | 0 | 2175-2195 | Abc transporter retinal flippase subfamily |
| vvi-miR3635-3p | VIT_217s0000g05850.5 | `target  5' GAGGCATGTGTGGGACATAAT 3'`<br>`           :::::::::::::::::::::`<br>`miRNA   3' CTCCGTACACACCCTGTATTA 5'` | 0 | 2175-2195 | Abc transporter retinal flippase subfamily |
| vvi-miR3635-5p | VIT_219s0015g00010.1 | `target  5' CCGCTATGCCCCACACATGCC 3'`<br>`           : . :::::::::::::::::`<br>`miRNA   3' GATAATACGGGGTGTGTACGG 5'` | 2.5 | 3417-3437 | Abc transporter c family member 3-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR3635-5p | VIT_219s0015g00020.1 | target 5' CCGCTATGCCCCACACATGCC 3'<br>: . :::::::::::::::::<br>miRNA 3' GATAATACGGGGTGTGTACGG 5' | 2.5 | 2208-2228 | Abc transporter c family member 3-like |
| vvi-miR3635-5p | VIT_219s0015g00050.1 | target 5' CCGCTATGCCCCACACATGCC 3'<br>: . :::::::::::::::::<br>miRNA 3' GATAATACGGGGTGTGTACGG 5' | 2.5 | 3753-3773 | Abc transporter c family member 3-like |
| vvi-miR3635-5p | VIT_219s0015g00060.1 | target 5' CCGCTATGCCCCACACATGCC 3'<br>: . :::::::::::::::::<br>miRNA 3' GATAATACGGGGTGTGTACGG 5' | 2.5 | 3486-3506 | Multidrug resistance protein abc transporter family |
| vvi-miR390-5p | VIT_210s0003g01890.1 | target 5' GGCGTTCTTCCTCCTGAGCTT 3'<br>::::.: :.::::::::::::<br>miRNA 3' CCGCGATAGGGAGGACTCGAA 5' | 2.5 | 319-339 | Lrr receptor-like serine threonine-protein kinase rfk1 |
| vvi-miR390-5p | VIT_216s0098g01090.1 | target 5' GGCTCTATACCTCCTGAGCTT 3'<br>::: :::: ::::::::::::<br>miRNA 3' CCGCGATAGGGAGGACTCGAA 5' | 3 | 1621-1641 | Leucine-rich repeat receptor-like protein kinase pepr1 |
| vvi-miR393a-5p | VIT_207s0104g01320.1 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393a-5p | VIT_207s0104g01320.2 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393a-5p | VIT_214s0030g01240.1 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393a-5p | VIT_214s0030g01240.2 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393a-5p | VIT_214s0030g01240.3 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393a-5p | VIT_214s0030g01240.4 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393a-5p | VIT_214s0068g01330.1 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1503-1522 | F-box family protein |
| vvi-miR393b | VIT_207s0104g01320.1 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393b | VIT_207s0104g01320.2 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: ::::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR393b | VIT_214s0030g01240.1 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: :::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393b | VIT_214s0030g01240.2 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: :::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393b | VIT_214s0030g01240.3 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: :::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393b | VIT_214s0030g01240.4 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: :::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1506-1525 | Transport inhibitor response 1 |
| vvi-miR393b | VIT_214s0068g01330.1 | target 5' GA-CAATGCGATCCCTTTGGA 3'<br>:: :::::::::::::::::<br>miRNA 3' CTAGTTACGCTAGGGAAACCT 5' | 1 | 1503-1522 | F-box family protein |
| vvi-miR394c | VIT_201s0010g03730.1 | target 5' GGAGGTTGACAGAATGCCAA 3'<br>:::::: :::::::::::::<br>miRNA 3' CCTCCACCTGTCTTACGGTT 5' | 1 | 939-958 | F-box family protein |
| vvi-miR394c | VIT_201s0010g03730.2 | target 5' GGAGGTTGACAGAATGCCAA 3'<br>:::::: :::::::::::::<br>miRNA 3' CCTCCACCTGTCTTACGGTT 5' | 1 | 1131-1150 | F-box family protein |
| vvi-miR395a | VIT_207s0031g00940.1 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br>:::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395a | VIT_207s0031g00940.2 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br>:::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395c-3p | VIT_207s0031g00940.1 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br>:::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395c-3p | VIT_207s0031g00940.2 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br>:::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395c-5p | VIT_214s0066g00910.1 | target 5' TGGTGAAGTGTTCAAGGGAAC 3'<br>..:::::::: :::::::::<br>miRNA 3' GTCACTTCACCAGTTCCCTTG 5' | 3 | 1101-1121 | Protein |
| vvi-miR395d | VIT_207s0031g00940.1 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br>:::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395d | VIT_207s0031g00940.2 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br>:::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR395e-3p | VIT_207s0031g00940.1 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395e-3p | VIT_207s0031g00940.2 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395e-5p | VIT_214s0066g00910.1 | `target  5' TGGTGAAGTGTTCAAGGGAAC 3'`<br>`           ..:::::::: ::::::::::   `<br>`miRNA   3' GTCACTTCACCAGTTCCCTTG 5'` | 3 | 1101-1121 | Protein |
| vvi-miR395f-3p | VIT_207s0031g00940.1 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395f-3p | VIT_207s0031g00940.2 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395g-3p | VIT_207s0031g00940.1 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395g-3p | VIT_207s0031g00940.2 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395h-3p | VIT_207s0031g00940.1 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395h-3p | VIT_207s0031g00940.2 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395h-5p | VIT_214s0066g00910.1 | `target  5' TGGTGAAGTGTTCAAGGGAAC 3'`<br>`           ..:::::::: ::::::::::   `<br>`miRNA   3' GTCACTTCACCAGTTCCCTTG 5'` | 3 | 1101-1121 | Protein |
| vvi-miR395i-3p | VIT_207s0031g00940.1 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395i-3p | VIT_207s0031g00940.2 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395j-3p | VIT_207s0031g00940.1 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395j-3p | VIT_207s0031g00940.2 | `target  5' AAGTTCTCCCAAACACTTCAA 3'`<br>`            :::::.:::::::::::::   `<br>`miRNA   3' CTCAAGGGGGTTTGTGAAGTC 5'` | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR395k-3p | VIT_207s0031g00940.1 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br> :::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395k-3p | VIT_207s0031g00940.2 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br> :::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395k-5p | VIT_214s0066g00910.1 | target 5' TGGTGAAGTGTTCAAGGGAAC 3'<br>..:::::::: ::::::::::<br>miRNA 3' GTCACTTCACCAGTTCCCTTG 5' | 3 | 1101-1121 | Protein |
| vvi-miR395l-3p | VIT_207s0031g00940.1 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br> :::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395l-3p | VIT_207s0031g00940.2 | target 5' AAGTTCTCCCAAACACTTCAA 3'<br> :::::.:::::::::::::<br>miRNA 3' CTCAAGGGGGTTTGTGAAGTC 5' | 2.5 | 37-57 | Sulfate bicarbonate oxalate exchanger and transporter sat-1 |
| vvi-miR395n | VIT_205s0020g04210.1 | target 5' CGAGTTCCTCCAAACTCTTCA 3'<br> ::::::::::: ::::::::<br>miRNA 3' TCTCAAGGAGGTCTGAGAAGT 5' | 3 | 339-359 | Atp sulfurylase |
| vvi-miR396a-3p | VIT_200s0208g00090.1 | target 5' CTGTCCACCAGCTTTCTTGAGC 3'<br>:. .::: ::::::::::::::<br>miRNA 3' GGAGGGT-GTCGAAAGAACTCG 5' | 3 | Dec-33 | Protein trichome birefringence-like 16 |
| vvi-miR396a-3p | VIT_207s0031g02320.1 | target 5' CCGTCCACCAGCTTTCTTGAGC 3'<br>:: .::: ::::::::::::::<br>miRNA 3' GGAGGGT-GTCGAAAGAACTCG 5' | 2.5 | 837-858 | Protein |
| vvi-miR396a-3p | VIT_207s0031g02320.2 | target 5' CCGTCCACCAGCTTTCTTGAGC 3'<br>:: .::: ::::::::::::::<br>miRNA 3' GGAGGGT-GTCGAAAGAACTCG 5' | 2.5 | 648-669 | Duf231 domain containing family protein |
| vvi-miR396a-3p | VIT_207s0031g02320.3 | target 5' CCGTCCACCAGCTTTCTTGAGC 3'<br>:: .::: ::::::::::::::<br>miRNA 3' GGAGGGT-GTCGAAAGAACTCG 5' | 2.5 | 501-522 | Protein trichome birefringence-like 16 |
| vvi-miR396a-5p | VIT_200s0494g00010.1 | target 5' CGTTCAAGAAAGCCTGTGGAA 3'<br> ::::::::::: ::::::::<br>miRNA 3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 781-801 | Transcription activator |
| vvi-miR396a-5p | VIT_202s0025g02680.1 | target 5' CGTTCAAGAAAGCCTGTGGAA 3'<br> ::::::::::: ::::::::<br>miRNA 3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 307-327 | Uncharacterized protein loc100258227 |
| vvi-miR396a-5p | VIT_202s0025g04910.1 | target 5' CGTTCAAGAAAGCATGTGGAA 3'<br> :::::::::::: :::::::<br>miRNA 3' TCAAGTTCTTTCG-ACACCTT 5' | 3 | 445-465 | Growth-regulating factor |
| vvi-miR396a-5p | VIT_207s0191g00220.1 | target 5' AACTCAAGGAAGCTGTGGAA 3'<br>:  :::::.:::::::::::<br>miRNA 3' TCAAGTTCTTTCGACACCTT 5' | 3 | 494-513 | Uncharacterized protein loc100251922 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR396a-5p | VIT_207s0191g00220.2 | target  5' AACTCAAGGAAGCTGTGGAA 3'<br>           :  :::::.:::::::::::<br>miRNA   3' TCAAGTTCTTTCGACACCTT 5' | 3 | 494-513 | Uncharacterized protein loc100251922 |
| vvi-miR396a-5p | VIT_208s0007g03760.1 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 538-558 | Growth-regulating factor 4 |
| vvi-miR396a-5p | VIT_209s0002g01350.1 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 334-354 | Growth-regulating factor 5 |
| vvi-miR396a-5p | VIT_210s0597g00040.1 | target  5' AGATGGAGAAAGCTGTGGAG 3'<br>           :: : .:::::::::::::.<br>miRNA   3' TCAAGTTCTTTCGACACCTT 5' | 3 | 1202-1221 | Pentatricopeptide repeat-containing protein |
| vvi-miR396a-5p | VIT_211s0016g01250.1 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 343-363 | Growth-regulating factor 5 |
| vvi-miR396a-5p | VIT_215s0048g01740.1 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 439-459 | Growth-regulating factor |
| vvi-miR396a-5p | VIT_215s0048g01740.2 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 460-480 | Growth-regulating factor |
| vvi-miR396a-5p | VIT_215s0048g01740.4 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 115-135 | Growth-regulating factor |
| vvi-miR396a-5p | VIT_215s0048g01740.5 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 115-135 | Growth-regulating factor |
| vvi-miR396a-5p | VIT_215s0048g01740.7 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 115-135 | Growth-regulating factor |
| vvi-miR396a-5p | VIT_216s0039g01450.1 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 361-381 | Growth-regulating factor 1 |
| vvi-miR396a-5p | VIT_216s0039g01450.2 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 361-381 | Growth-regulating factor 1 |
| vvi-miR396a-5p | VIT_216s0039g01450.3 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 361-381 | Growth-regulating factor 1 |
| vvi-miR396a-5p | VIT_216s0039g01450.4 | target  5' CGTTCAAGAAAGCCTGTGGAA 3'<br>            ::::::::::: ::::::::<br>miRNA   3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 172-192 | Growth-regulating factor 1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR396a-5p | VIT_216s0039g01450.5 | target 5' CGTTCAAGAAAGCCTGTGGAA 3'<br> ::::::::::: ::::::::<br>miRNA 3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 172-192 | Growth-regulating factor 1 |
| vvi-miR396a-5p | VIT_216s0098g01080.1 | target 5' CGTTCAAGAAAGCCTGTGGAA 3'<br> ::::::::::: ::::::::<br>miRNA 3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 322-342 | Protein |
| vvi-miR396a-5p | VIT_218s0001g08650.1 | target 5' CGTTCAAGAAAGCCTGTGGAA 3'<br> ::::::::::: ::::::::<br>miRNA 3' TCAAGTTCTTTC-GACACCTT 5' | 3 | 766-786 | Uncharacterized protein loc100260890 |
| vvi-miR396b-3p | VIT_201s0011g01220.1 | target 5' TTTCCAGCAGCTTTCTTGAAT 3'<br>::::: .:::::::::::::.<br>miRNA 3' AAAGGGTGTCGAAAGAACTTG 5' | 2 | 230-250 | Double top |
| vvi-miR396b-5p | VIT_207s0191g00220.1 | target 5' AAACTCAAGGAAGCTGTGGAA 3'<br>::  :::::.:::::::::::<br>miRNA 3' TTCAAGTTCTTTCGACACCTT 5' | 3 | 493-513 | Uncharacterized protein loc100251922 |
| vvi-miR396b-5p | VIT_207s0191g00220.2 | target 5' AAACTCAAGGAAGCTGTGGAA 3'<br>::  :::::.:::::::::::<br>miRNA 3' TTCAAGTTCTTTCGACACCTT 5' | 3 | 493-513 | Uncharacterized protein loc100251922 |
| vvi-miR396c-3p | VIT_205s0077g02140.1 | target 5' TGTT-CAGAATTTTCCTGAGC 3'<br>:::: :: ::.::::::::::<br>miRNA 3' ACAAGGTGTTGAAAGGACTCG 5' | 3 | 1659-1678 | Glyoxysomal fatty acid beta-oxidation multifunctional protein mfp-a |
| vvi-miR396c-5p | VIT_202s0025g02680.1 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 306-327 | Uncharacterized protein loc100258227 |
| vvi-miR396c-5p | VIT_208s0007g03760.1 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 537-558 | Growth-regulating factor 4 |
| vvi-miR396c-5p | VIT_209s0002g01350.1 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 333-354 | Growth-regulating factor 5 |
| vvi-miR396c-5p | VIT_211s0016g01250.1 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 342-363 | Growth-regulating factor 5 |
| vvi-miR396c-5p | VIT_216s0039g01450.1 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 360-381 | Growth-regulating factor 1 |
| vvi-miR396c-5p | VIT_216s0039g01450.2 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 360-381 | Growth-regulating factor 1 |
| vvi-miR396c-5p | VIT_216s0039g01450.3 | target 5' CCGTTCAAGAAAGCCTGTGGAA 3'<br>: ::::::::::: ::::::::<br>miRNA 3' GTCAAGTTCTTTC-GACACCTT 5' | 3 | 360-381 | Growth-regulating factor 1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR396c-5p | VIT_216s0039g01450.4 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 171-192 | Growth-regulating factor 1 |
| vvi-miR396c-5p | VIT_216s0039g01450.5 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 171-192 | Growth-regulating factor 1 |
| vvi-miR396c-5p | VIT_216s0098g01080.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 321-342 | Protein |
| vvi-miR396d-3p | VIT_215s0024g00350.1 | `target  5' CTTTCCATAGTTTTGTTGAAC 3'`<br>`           :::.:::.::.:::.::::::`<br>`miRNA   3' GAAGGGTGTCGAAATAACTTG 5'` | 3 | 617-637 | Tata box binding protein associated factor-like protein |
| vvi-miR396d-5p | VIT_202s0025g02680.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 306-327 | Uncharacterized protein loc100258227 |
| vvi-miR396d-5p | VIT_208s0007g03760.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 537-558 | Growth-regulating factor 4 |
| vvi-miR396d-5p | VIT_209s0002g01350.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 333-354 | Growth-regulating factor 5 |
| vvi-miR396d-5p | VIT_211s0016g01250.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 342-363 | Growth-regulating factor 5 |
| vvi-miR396d-5p | VIT_216s0039g01450.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 360-381 | Growth-regulating factor 1 |
| vvi-miR396d-5p | VIT_216s0039g01450.2 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 360-381 | Growth-regulating factor 1 |
| vvi-miR396d-5p | VIT_216s0039g01450.3 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 360-381 | Growth-regulating factor 1 |
| vvi-miR396d-5p | VIT_216s0039g01450.4 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 171-192 | Growth-regulating factor 1 |
| vvi-miR396d-5p | VIT_216s0039g01450.5 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 171-192 | Growth-regulating factor 1 |
| vvi-miR396d-5p | VIT_216s0098g01080.1 | `target  5' CCGTTCAAGAAAGCCTGTGGAA 3'`<br>`           : ::::::::::: ::::::::`<br>`miRNA   3' GTCAAGTTCTTTC-GACACCTT 5'` | 3 | 321-342 | Protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR397a-3p | VIT_204s0008g06470.1 | target 5' CAT-ATTGAGTGCAGTGCCAT 3'<br>:::  :::::::::::.::::<br>miRNA 3' GTACTAACTCACGTCGCGGTT 5' | 3 | 541-560 | Cysteinyl-trna synthetase |
| vvi-miR397a-3p | VIT_204s0008g06470.2 | target 5' CAT-ATTGAGTGCAGTGCCAT 3'<br>:::  :::::::::::.::::<br>miRNA 3' GTACTAACTCACGTCGCGGTT 5' | 3 | 832-851 | Cysteinyl-trna synthetase |
| vvi-miR397a-3p | VIT_204s0008g06470.3 | target 5' CAT-ATTGAGTGCAGTGCCAT 3'<br>:::  :::::::::::.::::<br>miRNA 3' GTACTAACTCACGTCGCGGTT 5' | 3 | 373-392 | Cysteinyl-trna synthetase |
| vvi-miR397a-5p | VIT_204s0069g00950.1 | target 5' TGTCAATGCTGCACTCAATGA 3'<br>..::::.::::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 1.5 | 243-263 | Laccase (diphenol oxidase)-like protein |
| vvi-miR397a-5p | VIT_204s0069g00950.2 | target 5' TGTCAATGCTGCACTCAATGA 3'<br>..::::.::::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 1.5 | 243-263 | Laccase (diphenol oxidase)-like protein |
| vvi-miR397a-5p | VIT_206s0004g03760.1 | target 5' CATCAATGCGGCACTCAATGA 3'<br>::::::.:: ::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 2.5 | 705-725 | Protein |
| vvi-miR397a-5p | VIT_206s0004g03760.2 | target 5' CATCAATGCGGCACTCAATGA 3'<br>::::::.:: ::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 2.5 | 705-725 | Protein |
| vvi-miR397a-5p | VIT_206s0004g06090.1 | target 5' CATCAACGCTGCGCTGAATGA 3'<br>::::::::::::.:: :::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 3 | 663-683 | Laccase 1a |
| vvi-miR397a-5p | VIT_208s0007g00600.1 | target 5' GATCAACGCTGCACTCAACGA 3'<br> ::::::::::::::::: ::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 3 | 693-713 | Laccase 110b |
| vvi-miR397a-5p | VIT_208s0007g00600.2 | target 5' GATCAACGCTGCACTCAACGA 3'<br> ::::::::::::::::: ::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 3 | 192-212 | Laccase 110b |
| vvi-miR397a-5p | VIT_208s0007g00670.1 | target 5' AATCAATGCTGCACTCAATGA 3'<br> :::::.::::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 1.5 | 687-707 | Laccase 110c |
| vvi-miR397a-5p | VIT_208s0007g01910.1 | target 5' CATTAACGCTGCACTCAATGA 3'<br>:::.:::::::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 0.5 | 666-686 | Laccase 1a |
| vvi-miR397a-5p | VIT_208s0007g01910.2 | target 5' CATTAACGCTGCACTCAATGA 3'<br>:::.:::::::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 0.5 | 666-686 | Laccase 1a |
| vvi-miR397a-5p | VIT_208s0040g01790.1 | target 5' CGTCAATGCTGCACTCAATGA 3'<br>:.::::.::::::::::::::<br>miRNA 3' GTAGTTGCGACGTGAGTTACT 5' | 1 | 684-704 | Laccase (diphenol oxidase)-like protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR397a-5p | VIT_208s0040g01790.2 | `target  5' CGTCAATGCTGCACTCAATGA 3'`<br>`           :.::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1 | 198-218 | Laccase (diphenol oxidase)-like protein |
| vvi-miR397a-5p | VIT_208s0040g01790.3 | `target  5' CGTCAATGCTGCACTCAATGA 3'`<br>`           :.::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1 | 684-704 | Laccase (diphenol oxidase)-like protein |
| vvi-miR397a-5p | VIT_208s0040g01790.4 | `target  5' CGTCAATGCTGCACTCAATGA 3'`<br>`           :.::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1 | 447-467 | Laccase (diphenol oxidase)-like protein |
| vvi-miR397a-5p | VIT_208s0040g01790.5 | `target  5' CGTCAATGCTGCACTCAATGA 3'`<br>`           :.::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1 | 39-59 | Laccase (diphenol oxidase)-like protein |
| vvi-miR397a-5p | VIT_213s0019g01930.1 | `target  5' GATCAACGCTGCACTCAATGA 3'`<br>`            ::::::::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1 | 696-716 | PREDICTED: laccase-17-like [Vitis vinifera] |
| vvi-miR397a-5p | VIT_213s0019g01940.1 | `target  5' GATCAATGCTGCACTCAATGA 3'`<br>`            :::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1.5 | 699-719 | Laccase-17 |
| vvi-miR397a-5p | VIT_213s0019g02150.1 | `target  5' GATCAATGCTGCACTCAATGA 3'`<br>`            :::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1.5 | 699-719 | Laccase-17 |
| vvi-miR397a-5p | VIT_213s0019g02160.1 | `target  5' GATCAATGCTGCACTCAATGA 3'`<br>`            :::::.::::::::::::::`<br>`miRNA   3' GTAGTTGCGACGTGAGTTACT 5'` | 1.5 | 699-719 | Laccase-17 |
| vvi-miR398a-3p | VIT_201s0127g00520.1 | `target  5' GGCAAAGGGGTGGCCTGAGAA 3'`<br>`             ::::::::::.::::::::`<br>`miRNA   3' GGGTTTCCCCACTGGACTCTT 5'` | 3 | 1458-1478 | Probable nucleoredoxin 1-like |
| vvi-miR398a-3p | VIT_201s0127g00540.1 | `target  5' GGCAAAGGGGTGGCCTGAGAA 3'`<br>`             ::::::::::.::::::::`<br>`miRNA   3' GGGTTTCCCCACTGGACTCTT 5'` | 3 | 213-233 | Probable nucleoredoxin 1-like |
| vvi-miR398a-3p | VIT_201s0127g00560.1 | `target  5' GGCAAAGGGGTGGCCTGAGAA 3'`<br>`             ::::::::::.::::::::`<br>`miRNA   3' GGGTTTCCCCACTGGACTCTT 5'` | 3 | 1461-1481 | Probable nucleoredoxin 1-like |
| vvi-miR399b-3p | VIT_213s0067g03280.1 | `target  5' CTGGGCAACTCTTCTTTGGCT 3'`<br>`           : ::::::::::.:::::::`<br>`miRNA   3' GTCCCGTTGAGAGGAAACCGT 5'` | 3 | 248-268 | High affinity inorganic phosphate transporter |
| vvi-miR399c | VIT_213s0067g03280.1 | `target  5' CTGGGCAACTCTTCTTTGGCT 3'`<br>`           : ::::::::::.:::::::`<br>`miRNA   3' GTCCCGTTGAGAGGAAACCGT 5'` | 3 | 248-268 | High affinity inorganic phosphate transporter |
| vvi-miR399i | VIT_213s0067g03280.1 | `target  5' CTGGGCAACTCTTCTTTGGCT 3'`<br>`           : ::::::::::.:::::::`<br>`miRNA   3' GTCCCGTTGAGAGGAAACCGC 5'` | 3 | 248-268 | High affinity inorganic phosphate transporter |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR403a-3p | VIT_207s0005g01690.1 | target 5' GGAGTTTGTGCGTGACTCTAA 3'<br> :::::::::::::: :::::<br>miRNA 3' GCTCAAACACGCACTTAGATT 5' | 3 | 149-169 | Unnamed protein product [Vitis vinifera] |
| vvi-miR403b | VIT_207s0005g01690.1 | target 5' GGAGTTTGTGCGTGACTCTAA 3'<br> :::::::::::::: :::::<br>miRNA 3' GCTCAAACACGCACTTAGATT 5' | 3 | 149-169 | Unnamed protein product [Vitis vinifera] |
| vvi-miR403d | VIT_207s0005g01690.1 | target 5' GGAGTTTGTGCGTGACTCTAA 3'<br> :::::::::::::: :::::<br>miRNA 3' GCTCAAACACGCACTTAGATT 5' | 3 | 149-169 | Unnamed protein product [Vitis vinifera] |
| vvi-miR403e-3p | VIT_207s0005g01690.1 | target 5' GGAGTTTGTGCGTGACTCTAA 3'<br> :::::::::::::: :::::<br>miRNA 3' GCTCAAACACGCACTTAGATT 5' | 3 | 149-169 | Unnamed protein product [Vitis vinifera] |
| vvi-miR403f-3p | VIT_207s0005g01690.1 | target 5' GGAGTTTGTGCGTGACTCTAA 3'<br> :::::::::::::: :::::<br>miRNA 3' GCTCAAACACGCACTTAGATT 5' | 3 | 149-169 | Unnamed protein product [Vitis vinifera] |
| vvi-miR403f-5p | VIT_207s0005g01690.1 | target 5' TCTTAGATTCACGCACAAACT 3'<br>: ::::: :::::::::::::<br>miRNA 3' AAAATCTCAGTGCGTGTTTGA 5' | 2 | 216-236 | Unnamed protein product [Vitis vinifera] |
| vvi-miR408-3p | VIT_212s0034g01140.1 | target 5' GCTGTGGGAAGAGGCAGTGCAG 3'<br>::.. ::::::::::::::::<br>miRNA 3' CGGT-CCCTTCTCCGTCACGTA 5' | 3 | 25-Apr | Basic blue protein |
| vvi-miR408-3p | VIT_218s0001g15240.1 | target 5' GTGAGGGAAGAGGCAGTGCAG 3'<br>:. :::::::::::::::::<br>miRNA 3' CGGTCCCTTCTCCGTCACGTA 5' | 2.5 | 146-166 | Basic blue protein |
| vvi-miR477 | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miR477 | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| vvi-miR477b-5p | VIT_201s0010g02270.1 | target 5' TGGAAGCCTTTGAGGGAGAGA 3'<br>..::::::.:::::::::::<br>miRNA 3' GTCTTCGGGAACTCCCTCTCA 5' | 3 | 782-802 | Gras family transcription factor |
| vvi-miR477b-5p | VIT_217s0000g10300.1 | target 5' TGGAAGCCTTTGAGGGAGAGA 3'<br>..::::::.:::::::::::<br>miRNA 3' GTCTTCGGGAACTCCCTCTCA 5' | 3 | 752-772 | Gras family transcription factor |
| vvi-miR479-3p | VIT_218s0001g03310.1 | target 5' GGGTGATATTGGTTCGGCTCA 3'<br>:.::::::::::::::::::<br>miRNA 3' CTCACTATAACCAAGCCGAGC 5' | 1.5 | 374-394 | Gras family protein |
| vvi-miR535a-3p | VIT_200s0358g00010.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>  ::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miR535a-3p | VIT_207s0104g00030.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>  ::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miR535a-5p | VIT_200s0358g00010.1 | target 5' GCGTGCTCTCTCTCGCTGTCA 3'<br>::::::::::::::: :::::<br>miRNA 3' CGCACGAGAGAGAGCAACAGT 5' | 2 | 132-152 | Unnamed protein product [Vitis vinifera] |
| vvi-miR535b-3p | VIT_200s0358g00010.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>  ::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miR535b-3p | VIT_207s0104g00030.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>  ::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miR535b-5p | VIT_200s0358g00010.1 | target 5' GCGTGCTCTCTCTCGCTGTCA 3'<br>::::::::::::::: :::::<br>miRNA 3' CGCACGAGAGAGAGCAACAGT 5' | 2 | 132-152 | Unnamed protein product [Vitis vinifera] |
| vvi-miR535c-5p | VIT_200s0358g00010.1 | target 5' GCGTGCTCTCTCTCGCTGTCA 3'<br>::::::::::::::: :::::<br>miRNA 3' CGCACGAGAGAGAGCAACAGT 5' | 2 | 132-152 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC159d | VIT_201s0127g00480.1 | target 5' AGAGCTACCTTCAAAACCAAA 3'<br>:::::: ::::: ::::::::<br>miRNA 3' TCTCGAGGGAAG-TTTGGTTT 5' | 3 | 261-281 | Uncharacterized protein |
| vvi-miRC159d | VIT_201s0127g00480.2 | target 5' AGAGCTACCTTCAAAACCAAA 3'<br>:::::: ::::: ::::::::<br>miRNA 3' TCTCGAGGGAAG-TTTGGTTT 5' | 3 | 261-281 | Uncharacterized protein |
| vvi-miRC159d | VIT_201s0127g00480.3 | target 5' AGAGCTACCTTCAAAACCAAA 3'<br>:::::: ::::: ::::::::<br>miRNA 3' TCTCGAGGGAAG-TTTGGTTT 5' | 3 | 261-281 | Uncharacterized protein |
| vvi-miRC159d | VIT_210s0003g00840.1 | target 5' AACGCACCCTTCAAACCAAA 3'<br>:  :: ::::::::::::::<br>miRNA 3' TCTCGAGGGAAGTTTGGTTT 5' | 3 | 588-607 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC159d | VIT_219s0014g01700.1 | target 5' AGAGCCCCCTTCAAACCAAA 3'<br>::::: ::::::::::::::<br>miRNA 3' TCTCGAGGGAAGTTTGGTTT 5' | 1 | 660-679 | Uncharacterized protein loc100505457 |
| vvi-miRC159d | VIT_219s0090g00590.1 | target 5' AGAGCTCCCTTCAAGCCAAT 3'<br>::::::::::::::.::::<br>miRNA 3' TCTCGAGGGAAGTTTGGTTT 5' | 2 | 846-865 | R2r3-myb transcription |
| vvi-miRC159e | VIT_201s0127g00480.1 | target 5' AGAGCTACCTTCAAAACCAAA 3'<br>:::::: ::::: ::::::::<br>miRNA 3' TCTCGAGGGAAG-TTTGGTTT 5' | 3 | 261-281 | Uncharacterized protein |
| vvi-miRC159e | VIT_201s0127g00480.2 | target 5' AGAGCTACCTTCAAAACCAAA 3'<br>:::::: ::::: ::::::::<br>miRNA 3' TCTCGAGGGAAG-TTTGGTTT 5' | 3 | 261-281 | Uncharacterized protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC159e | VIT_201s0127g00480.3 | target 5' AGAGCTACCTTCAAAACCAAA 3'<br>:::::: ::::: ::::::::<br>miRNA 3' TCTCGAGGGAAG-TTTGGTTT 5' | 3 | 261-281 | Uncharacterized protein |
| vvi-miRC159e | VIT_210s0003g00840.1 | target 5' AACGCACCCTTCAAACCAAA 3'<br>:  :: ::::::::::::::<br>miRNA 3' TCTCGAGGGAAGTTTGGTTT 5' | 3 | 588-607 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC159e | VIT_219s0014g01700.1 | target 5' AGAGCCCCCTTCAAACCAAA 3'<br>::::: ::::::::::::::<br>miRNA 3' TCTCGAGGGAAGTTTGGTTT 5' | 1 | 660-679 | Uncharacterized protein loc100505457 |
| vvi-miRC159e | VIT_219s0090g00590.1 | target 5' AGAGCTCCCTTCAAGCCAAT 3'<br>::::::::::::::.::::<br>miRNA 3' TCTCGAGGGAAGTTTGGTTT 5' | 2 | 846-865 | R2r3-myb transcription |
| vvi-miRC159f | VIT_200s0226g00070.1 | target 5' CAGAACTCTCTTCACTCCAA 3'<br> ::: :::.:::::::::::<br>miRNA 3' ATCTCGAGGGAAGTGAGGTT 5' | 3 | 25-Jun | Gras family transcription factor |
| vvi-miRC159f | VIT_206s0009g02480.1 | target 5' TGGAGCTCCCTTCTCTCCAA 3'<br>:.::::::::::: ::::::<br>miRNA 3' ATCTCGAGGGAAGTGAGGTT 5' | 2.5 | 959-978 | Transcription factor gamyb-like |
| vvi-miRC159f | VIT_206s0009g02480.2 | target 5' TGGAGCTCCCTTCTCTCCAA 3'<br>:.::::::::::: ::::::<br>miRNA 3' ATCTCGAGGGAAGTGAGGTT 5' | 2.5 | 959-978 | Transcription factor gamyb-like |
| vvi-miRC159f | VIT_206s0009g02480.3 | target 5' TGGAGCTCCCTTCTCTCCAA 3'<br>:.::::::::::: ::::::<br>miRNA 3' ATCTCGAGGGAAGTGAGGTT 5' | 2.5 | 524-543 | Transcription factor gamyb-like |
| vvi-miRC159f | VIT_206s0009g02480.4 | target 5' TGGAGCTCCCTTCTCTCCAA 3'<br>:.::::::::::: ::::::<br>miRNA 3' ATCTCGAGGGAAGTGAGGTT 5' | 2.5 | 959-978 | Transcription factor gamyb-like |
| vvi-miRC159f | VIT_213s0067g01630.1 | target 5' TGGAGCTCCCTTCACTCCAA 3'<br>:.::::::::::::::::::<br>miRNA 3' ATCTCGAGGGAAGTGAGGTT 5' | 0.5 | 956-975 | Transcription factor gamyb-like |
| vvi-miRC166i-3p | VIT_204s0008g03250.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Protein |
| vvi-miRC166i-3p | VIT_204s0008g03250.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 557-577 | Class iii hd-zip protein 8 |
| vvi-miRC166i-3p | VIT_206s0004g02800.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miRC166i-3p | VIT_206s0004g02800.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>  ::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC166i-3p | VIT_206s0004g02800.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 563-583 | Homeobox leucine-zipper protein |
| vvi-miRC166i-3p | VIT_209s0002g03740.1 | target 5' CTGGAATGAAGCCTGGTCCGG 3'<br>::::::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 2.5 | 551-571 | Homeobox-leucine zipper protein athb-15 |
| vvi-miRC166i-3p | VIT_210s0003g04670.1 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 566-586 | Homeobox-leucine zipper protein hox32-like |
| vvi-miRC166i-3p | VIT_210s0003g04670.2 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 293-313 | Homeobox-leucine zipper protein hox32-like |
| vvi-miRC166i-3p | VIT_210s0003g04670.3 | target 5' TTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 25-May | Homeobox-leucine zipper protein hox32-like |
| vvi-miRC166i-3p | VIT_213s0019g04320.1 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC166i-3p | VIT_213s0019g04320.2 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC166i-3p | VIT_213s0019g04320.3 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC166i-3p | VIT_213s0019g04320.4 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC166i-3p | VIT_213s0019g04320.5 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 173-193 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC166i-3p | VIT_213s0019g04320.6 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC166i-3p | VIT_213s0019g04320.7 | target 5' CTGGGATGAAGCCTGGTCCGG 3'<br>::.:::::::::::::::.<br>miRNA 3' CCCCTTACTTCGGACCAGGCT 5' | 3 | 263-283 | Homeobox-leucine zipper protein revoluta |
| vvi-miRC171h-3p | VIT_202s0154g00400.1 | target 5' GATATTGGCGCGGCTCAATCA 3'<br>:::::::::.:::::::::::<br>miRNA 3' CTATAACCGTGCCGAGTTAGT 5' | 1 | 1221-1241 | Gras family transcription factor |
| vvi-miRC171h-3p | VIT_204s0023g01380.1 | target 5' GATATTGGCGCGGCTCAATCA 3'<br>:::::::::.:::::::::::<br>miRNA 3' CTATAACCGTGCCGAGTTAGT 5' | 1 | 588-608 | Gras family transcription factor |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC171h-3p | VIT_215s0048g00270.1 | target  5' GATATTGGCGCGGCTCAATCA 3'<br>           :::::::::.:::::::::::<br>miRNA   3' CTATAACCGTGCCGAGTTAGT 5' | 1 | 1233-1253 | Gras family transcription factor |
| vvi-miRC171j | VIT_202s0154g00400.1 | target  5' GATATTGGCGCGGCTCAATCA 3'<br>           :::::::::.:::::::::::<br>miRNA   3' CTATAACCGTGCCGAGTTAGT 5' | 1 | 1221-1241 | Gras family transcription factor |
| vvi-miRC171j | VIT_204s0023g01380.1 | target  5' GATATTGGCGCGGCTCAATCA 3'<br>           :::::::::.:::::::::::<br>miRNA   3' CTATAACCGTGCCGAGTTAGT 5' | 1 | 588-608 | Gras family transcription factor |
| vvi-miRC171j | VIT_215s0048g00270.1 | target  5' GATATTGGCGCGGCTCAATCA 3'<br>           :::::::::.:::::::::::<br>miRNA   3' CTATAACCGTGCCGAGTTAGT 5' | 1 | 1233-1253 | Gras family transcription factor |
| vvi-miRC172e-3p | VIT_200s0184g00102.1 | target  5' GCATTCATGATCAAGATTCTCA 3'<br>           :::  ::: :::::::::::::<br>miRNA   3' CGT-CGTAGTAGTTCTAAGAGT 5' | 3 | 215-236 | Ap2 erf and b3 domain-containing transcription factor rav2 |
| vvi-miRC172e-3p | VIT_206s0004g03590.1 | target  5' GCAGCATCATCAGGATTCTCA 3'<br>           :::::::::::::.:::::::<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 1 | 1336-1356 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miRC172e-3p | VIT_206s0004g03590.3 | target  5' GCAGCATCATCAGGATTCTCA 3'<br>           :::::::::::::.:::::::<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 1 | 1291-1311 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miRC172e-3p | VIT_207s0031g00220.1 | target  5' GCAGCATCATCAGGATTCCCA 3'<br>           :::::::::::::.:::: ::<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 3 | 1432-1452 | Transcription factor apetala2 |
| vvi-miRC172e-3p | VIT_207s0031g00220.2 | target  5' GCAGCATCATCAGGATTCCCA 3'<br>           :::::::::::::.:::: ::<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 3 | 1444-1464 | Transcription factor apetala2 |
| vvi-miRC172e-3p | VIT_208s0040g03180.1 | target  5' GCAGCATCATCAGGATTCTTG 3'<br>           :::::::::::::.:::::..<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 2.5 | 1333-1353 | Ap2 domain-containing transcription factor |
| vvi-miRC172e-5p | VIT_216s0050g00455.1 | target  5' TATGAAGCTTGATGATGCTAT 3'<br>           : :::: :::::::::::::.<br>miRNA   3' ACACTTAGAACTACTACGATG 5' | 2.5 | 249-269 | Rna polymerase iii subunit rpc82 family protein |
| vvi-miRC172f-3p | VIT_200s0184g00102.1 | target  5' GCATTCATGATCAAGATTCTCA 3'<br>           :::  ::: :::::::::::::<br>miRNA   3' CGT-CGTAGTAGTTCTAAGAGT 5' | 3 | 215-236 | Ap2 erf and b3 domain-containing transcription factor rav2 |
| vvi-miRC172f-3p | VIT_206s0004g03590.1 | target  5' GCAGCATCATCAGGATTCTCA 3'<br>           :::::::::::::.:::::::<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 1 | 1336-1356 | Ethylene-responsive transcription factor rap2-7-like |
| vvi-miRC172f-3p | VIT_206s0004g03590.3 | target  5' GCAGCATCATCAGGATTCTCA 3'<br>           :::::::::::::.:::::::<br>miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5' | 1 | 1291-1311 | Ethylene-responsive transcription factor rap2-7-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC172f-3p | VIT_207s0031g00220.1 | `target  5' GCAGCATCATCAGGATTCCCA 3'`<br>`            ::::::::::::.::::: ::`<br>`miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5'` | 3 | 1432-1452 | Transcription factor apetala2 |
| vvi-miRC172f-3p | VIT_207s0031g00220.2 | `target  5' GCAGCATCATCAGGATTCCCA 3'`<br>`            ::::::::::::.::::: ::`<br>`miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5'` | 3 | 1444-1464 | Transcription factor apetala2 |
| vvi-miRC172f-3p | VIT_208s0040g03180.1 | `target  5' GCAGCATCATCAGGATTCTTG 3'`<br>`            ::::::::::::.::::::..`<br>`miRNA   3' CGTCGTAGTAGTTCTAAGAGT 5'` | 2.5 | 1333-1353 | Ap2 domain-containing transcription factor |
| vvi-miRC172f-5p | VIT_216s0050g00455.1 | `target  5' TATGAAGCTTGATGATGCTAT 3'`<br>`            : :::: :::::::::::::.`<br>`miRNA   3' ACACTTAGAACTACTACGATG 5'` | 2.5 | 249-269 | Rna polymerase iii subunit rpc82 family protein |
| vvi-miRC2275 | VIT_210s0003g02830.1 | `target  5' GGAGAAATTGGAGGAAACTGAA 3'`<br>`             :::: :::::::::::::.::`<br>`miRNA   3' ACTCTATAACCTCCTTTGATTT 5'` | 3 | 531-552 | O-acetyltransferase-like protein |
| vvi-miRC2275 | VIT_210s0003g02830.2 | `target  5' GGAGAAATTGGAGGAAACTGAA 3'`<br>`             :::: :::::::::::::.::`<br>`miRNA   3' ACTCTATAACCTCCTTTGATTT 5'` | 3 | 531-552 | O-acetyltransferase-like protein |
| vvi-miRC2275 | VIT_210s0003g02830.3 | `target  5' GGAGAAATTGGAGGAAACTGAA 3'`<br>`             :::: :::::::::::::.::`<br>`miRNA   3' ACTCTATAACCTCCTTTGATTT 5'` | 3 | 399-420 | Cas1 domain-containing protein 1-like |
| vvi-miRC3627a | VIT_209s0018g02130.1 | `target  5' GGCGCCATCTCTCGTGCGGCAG 3'`<br>`            :: ::::::::::::::::::.`<br>`miRNA   3' CCACGGTAGAGAGCACGCCGTT 5'` | 1.5 | 149-170 | Calcium-transporting atpase plasma membrane-type-like |
| vvi-miRC3629e | VIT_200s0524g00010.1 | `target  5' CAGTTTCTCGGCAACCAAACA 3'`<br>`            :: :::::::.::::::::::`<br>`miRNA   3' GTAAAAGAGCTGTTGGTTTGT 5'` | 2 | 280-300 | Protein |
| vvi-miRC3629e | VIT_208s0007g00890.1 | `target  5' CATGTTCTCG-CAACCAAACA 3'`<br>`            ::: :::::: ::::::::::`<br>`miRNA   3' GTAAAAGAGCTGTTGGTTTGT 5'` | 3 | 86-105 | Tropinone reductase homolog at1g07440 |
| vvi-miRC3629e | VIT_215s0048g02420.1 | `target  5' AGTTTTCTCGGCAACCAAACG 3'`<br>`             .::::::::.:::::::::.`<br>`miRNA   3' GTAAAAGAGCTGTTGGTTTGT 5'` | 1 | 62-82 | Hypothetical protein |
| vvi-miRC3629e | VIT_217s0000g07510.3 | `target  5' TATTTCCTCGGCAACCAAACG 3'`<br>`            .:::: ::::.:::::::::.`<br>`miRNA   3' GTAAAAGAGCTGTTGGTTTGT 5'` | 3 | 598-618 | Myb transcription factor |
| vvi-miRC390a-5p | VIT_210s0003g01890.1 | `target  5' GGCGTTCTTCCTCCTGAGCTT 3'`<br>`            ::::.: :.::::::::::::`<br>`miRNA   3' CCGCGATAGGGAGGACTCGAA 5'` | 2.5 | 319-339 | Lrr receptor-like serine threonine-protein kinase rfk1 |
| vvi-miRC390a-5p | VIT_216s0098g01090.1 | `target  5' GGCTCTATACCTCCTGAGCTT 3'`<br>`            ::: :::: ::::::::::::`<br>`miRNA   3' CCGCGATAGGGAGGACTCGAA 5'` | 3 | 1621-1641 | Leucine-rich repeat receptor-like protein kinase pepr1 |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC396e-5p | VIT_200s0179g00260.1 | target 5' GGGGTCAAGAGAGCCGTGGAA 3'<br>..: ::::::.::::::::::<br>miRNA 3' TTCAAGTTCTTTCGGCACCTT 5' | 3 | 1978-1998 | Calcium-transporting atpase plasma membrane-type-like |
| vvi-miRC477c-3p | VIT_217s0000g02070.1 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477c-3p | VIT_217s0000g02070.2 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477c-3p | VIT_217s0000g02070.3 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477c-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miRC477c-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| vvi-miRC477d-3p | VIT_217s0000g02070.1 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477d-3p | VIT_217s0000g02070.2 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477d-3p | VIT_217s0000g02070.3 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477d-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miRC477d-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| vvi-miRC477e-3p | VIT_217s0000g02070.1 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477e-3p | VIT_217s0000g02070.2 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477e-3p | VIT_217s0000g02070.3 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC477e-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miRC477e-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| vvi-miRC477f-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miRC477f-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| vvi-miRC477g-3p | VIT_217s0000g02070.1 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.:::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477g-3p | VIT_217s0000g02070.2 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.:::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477g-3p | VIT_217s0000g02070.3 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.:::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477g-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miRC477g-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |
| vvi-miRC477h-3p | VIT_217s0000g02070.1 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.:::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477h-3p | VIT_217s0000g02070.2 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.:::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477h-3p | VIT_217s0000g02070.3 | target 5' GGT-CTCCACCGGCTTCCAAG 3'<br>::: :.:::::::::::::::<br>miRNA 3' CCAGGGGGTGGCCGAAGGTTG 5' | 2.5 | 135-154 | Deoxyhypusine synthase |
| vvi-miRC477h-5p | VIT_201s0010g02270.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 778-798 | Gras family transcription factor |
| vvi-miRC477h-5p | VIT_217s0000g10300.1 | target 5' ATATTGGAAGCCTTTGAGGGA 3'<br>: :::::::::::::::::::<br>miRNA 3' TTTAACCTTCGGAAACTCCCT 5' | 1 | 748-768 | Gras family transcription factor |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC530-3p | VIT_200s0267g00060.1 | `target  5' TCTTCACCTTCACCT-CACCT 3'`<br>`           ::: ::::::::::: :::::`<br>`miRNA   3' AGACGTGGAAGTGGACGTGGA 5'` | 3 | 31-Dec | Unnamed protein product [Vitis vinifera] |
| vvi-miRC530-3p | VIT_201s0011g03410.1 | `target  5' ACTGCACCTGCACCTGCACCT 3'`<br>`            :::::::: :::::::::::`<br>`miRNA   3' AGACGTGGAAGTGGACGTGGA 5'` | 3 | 262-282 | Uv excision repair protein |
| vvi-miRC530-3p | VIT_201s0011g03410.2 | `target  5' ACTGCACCTGCACCTGCACCT 3'`<br>`            :::::::: :::::::::::`<br>`miRNA   3' AGACGTGGAAGTGGACGTGGA 5'` | 3 | 262-282 | Dna repair protein rad23-3 |
| vvi-miRC530-3p | VIT_201s0011g03410.3 | `target  5' ACTGCACCTGCACCTGCACCT 3'`<br>`            :::::::: :::::::::::`<br>`miRNA   3' AGACGTGGAAGTGGACGTGGA 5'` | 3 | 340-360 | Dna repair protein rad23-3 |
| vvi-miRC530-3p | VIT_201s0011g03410.4 | `target  5' ACTGCACCTGCACCTGCACCT 3'`<br>`            :::::::: :::::::::::`<br>`miRNA   3' AGACGTGGAAGTGGACGTGGA 5'` | 3 | 340-360 | Dna repair protein rad23-3 |
| vvi-miRC530-3p | VIT_202s0025g01250.1 | `target  5' TCTTCATCCTTCACTTGCACCT 3'`<br>`           ::: :: :::::::.:::::::`<br>`miRNA   3' AGACGT-GGAAGTGGACGTGGA 5'` | 3 | 69-90 | Nucleoporin seh1-like |
| vvi-miRC530-3p | VIT_202s0025g01250.2 | `target  5' TCTTCATCCTTCACTTGCACCT 3'`<br>`           ::: :: :::::::.:::::::`<br>`miRNA   3' AGACGT-GGAAGTGGACGTGGA 5'` | 3 | 127-148 | Nucleoporin seh1-like |
| vvi-miRC530-3p | VIT_213s0067g01550.1 | `target  5' TCTTCACCTTCACCTTCACCT 3'`<br>`           ::: ::::::::::: :::::`<br>`miRNA   3' AGACGTGGAAGTGGACGTGGA 5'` | 3 | 670-690 | Probable lrr receptor-like serine threonine-protein kinase mrh1-like |
| vvi-miRC530-5p | VIT_202s0012g02510.1 | `target  5' AGGT-CAGGTGCAAATGCAGG 3'`<br>`           :::: :::::::::::::::.`<br>`miRNA   3' TCCACGTCCACGTTTACGTCT 5'` | 1.5 | 268-287 | Protein |
| vvi-miRC530-5p | VIT_205s0020g04860.1 | `target  5' AGGTGCAGGTGCAAATGCAGG 3'`<br>`           ::::::::::::::::::::.`<br>`miRNA   3' TCCACGTCCACGTTTACGTCT 5'` | 0.5 | 99-119 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530-5p | VIT_205s0020g04860.2 | `target  5' AGGTGCAGGTGCAAATGCAGG 3'`<br>`           ::::::::::::::::::::.`<br>`miRNA   3' TCCACGTCCACGTTTACGTCT 5'` | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530-5p | VIT_205s0020g04860.3 | `target  5' AGGTGCAGGTGCAAATGCAGG 3'`<br>`           ::::::::::::::::::::.`<br>`miRNA   3' TCCACGTCCACGTTTACGTCT 5'` | 0.5 | 168-188 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530-5p | VIT_205s0020g04860.4 | `target  5' AGGTGCAGGTGCAAATGCAGG 3'`<br>`           ::::::::::::::::::::.`<br>`miRNA   3' TCCACGTCCACGTTTACGTCT 5'` | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530-5p | VIT_205s0020g04860.6 | `target  5' AGGTGCAGGTGCAAATGCAGG 3'`<br>`           ::::::::::::::::::::.`<br>`miRNA   3' TCCACGTCCACGTTTACGTCT 5'` | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC530-5p | VIT_205s0020g04860.7 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530-5p | VIT_206s0080g00400.1 | target 5' AGGTGCAGGTGCAGATGCAGG 3'<br>:::::::::::::.::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 1.5 | 143-163 | Ribosomal protein l1 |
| vvi-miRC530a | VIT_202s0012g02510.1 | target 5' AGGT-CAGGTGCAAATGCAGG 3'<br>:::: :::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 1.5 | 268-287 | Protein |
| vvi-miRC530a | VIT_205s0020g04860.1 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 99-119 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530a | VIT_205s0020g04860.2 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530a | VIT_205s0020g04860.3 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 168-188 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530a | VIT_205s0020g04860.4 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530a | VIT_205s0020g04860.6 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530a | VIT_205s0020g04860.7 | target 5' AGGTGCAGGTGCAAATGCAGG 3'<br>::::::::::::::::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 0.5 | 258-278 | Zinc knuckle (cchc-type) family protein |
| vvi-miRC530a | VIT_206s0080g00400.1 | target 5' AGGTGCAGGTGCAGATGCAGG 3'<br>:::::::::::::.::::::.<br>miRNA 3' TCCACGTCCACGTTTACGTCT 5' | 1.5 | 143-163 | Ribosomal protein l1 |
| vvi-miRC535f-3p | VIT_200s0358g00010.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>  ::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC535f-3p | VIT_207s0104g00030.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>  ::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC535f-5p | VIT_201s0011g00130.1 | target 5' ATTGTGCTCTCTCTCTTCTGTCA 3'<br>: ::::::::::::::: :::::<br>miRNA 3' TCACACGAGAGAGAGAA-ACAGT 5' | 3 | 1247-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miRC535f-5p | VIT_201s0011g00130.2 | target 5' ATTGTGCTCTCTCTCTTCTGTCA 3'<br>: ::::::::::::::: :::::<br>miRNA 3' TCACACGAGAGAGAGAA-ACAGT 5' | 3 | 1247-1269 | Squamosa promoter-binding-like protein 6-like |

| miRNA | Target id | Alignment | Score | Range | Target gene functional annotation |
|---|---|---|---|---|---|
| vvi-miRC535f-5p | VIT_217s0000g01260.1 | target 5' ATTGTGCTCTCTCTCTTCTGTCA 3'<br>: ::::::::::::::: :::::<br>miRNA 3' TCACACGAGAGAGAGAA-ACAGT 5' | 3 | 950-972 | Squamosa promoter-binding-like protein 13 |
| vvi-miRC535g-3p | VIT_200s0358g00010.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC535g-3p | VIT_207s0104g00030.1 | target 5' CTTGACAACGAGAGAGAGCAC 3'<br>::::: :::::::::::::<br>miRNA 3' ATACTGTCGCTCTCTCTCGTG 5' | 3 | 72-92 | Unnamed protein product [Vitis vinifera] |
| vvi-miRC535g-5p | VIT_201s0011g00130.1 | target 5' ATTGTGCTCTCTCTCTTCTGTCA 3'<br>: ::::::::::::::: :::::<br>miRNA 3' TCACACGAGAGAGAGAA-ACAGT 5' | 3 | 1247-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miRC535g-5p | VIT_201s0011g00130.2 | target 5' ATTGTGCTCTCTCTCTTCTGTCA 3'<br>: ::::::::::::::: :::::<br>miRNA 3' TCACACGAGAGAGAGAA-ACAGT 5' | 3 | 1247-1269 | Squamosa promoter-binding-like protein 6-like |
| vvi-miRC535g-5p | VIT_217s0000g01260.1 | target 5' ATTGTGCTCTCTCTCTTCTGTCA 3'<br>: ::::::::::::::: :::::<br>miRNA 3' TCACACGAGAGAGAGAA-ACAGT 5' | 3 | 950-972 | Squamosa promoter-binding-like protein 13 |
| vvi-miRC827-3p | VIT_204s0008g05050.1 | target 5' TGTTT-TTGTTGATCATCTAA 3'<br>::::: ::: ::::::::::<br>miRNA 3' ACAAACAACTACTAGTAGATT 5' | 3 | 393-412 | Pentatricopeptide repeat-containing protein |
| vvi-miRC827-5p | VIT_201s0026g01490.1 | target 5' CAC-AGAAGACCAGCAACAAAA 3'<br>:: ::: :::::::::::::<br>miRNA 3' CTGATCTACTGGTCGTTGTTTT 5' | 3 | 465-485 | Nitrate transporter |
| vvi-miRC827-5p | VIT_201s0026g01490.2 | target 5' CAC-AGAAGACCAGCAACAAAA 3'<br>:: ::: :::::::::::::<br>miRNA 3' CTGATCTACTGGTCGTTGTTTT 5' | 3 | 54-74 | Nitrate transporter |

[a] Score refers to values given by Target Finder using a plant-based scoring metric.

[b] Complementary site of the microRNA with the target gene.