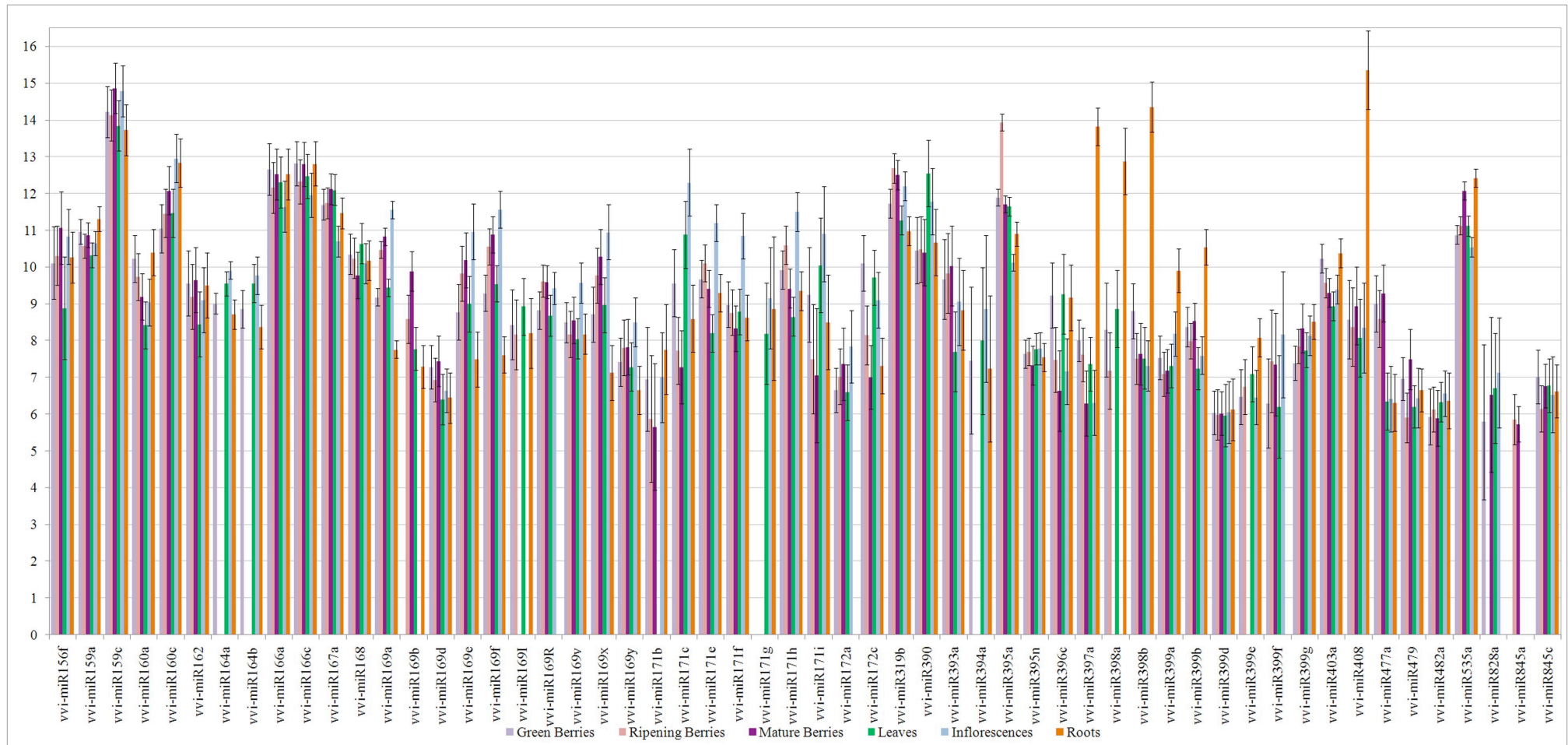


Supplemental Table S1: Frequencies of mapped small RNA reads by size and locus.

<u>length</u>	<u># loci</u>	<u># reads</u>	<u>mean reads/locus</u>
19	146612	1466320	10,001364
20	212166	2464169	11,614344
21	664229	6143363	9,248863
22	376958	2474858	6,565341
23	330553	674605	2,040838
24	896304	2038037	2,273823

Supplemental Figure S2: Log Expression levels of all predicted miRNAs in all tissues tested by oligonucleotide array. Error bars represent confidence intervals. Y axis represents Log2 of the normalized median of spot intensities





CTGACAGAAGAGACTGAGCACA 4  
TGACAGAAGAGACTGAGCACAC 4  
CTGACAGAAGAGACTGA 3  
CTGACAGAAGAGACTGAG 3  
ACAGAAGAGAGTGAACA 2  
ACTGACAGAAGAGACTGAGC 1  
GACAGAAGAGAGTGAACA 1  
ACTGACAGAAGAGACTGAGCA 1  
TGACAGAAGAGACTGAGCACACA 1

---

>vvi-MIR156c [sc:6 - 841232 841335] [chr:4 - 850300 850403]  
.....(((((.....))).....))..... (-60.20)  
AAGGAATAGGTGACAGAAGAGAGTGAACACATGGTCTTGCATGGGTCATGCTTGAAGCTCTGGGTGCTCACTCTCATCTGCTCCTCTCTCT  
TGACAGAAGAGACTGAGCAC 835876

TGACAGAAGAGACTGAGCACA 4751  
TGACAGAAGAGACTGAGCA 3092  
TGACAGAAGAGACTGAGC 1409  
GACAGAAGAGACTGAGCAC 475  
ACAGAAGAGACTGAGCAC 162  
GTGACAGAAGAGACTGAGCAC 112  
TGACAGAAGAGACTGAG 97  
GTGACAGAAGAGACTGAGCA 95  
GACAGAAGAGACTGAGCACA 90  
ACAGAAGAGACTGAGCACACA 42  
ACAGAAGAGACTGAGCACAC 30  
CAGAAGAGAGTGAACA 9  
GGTGACAGAAGAGACTGAGCAC 8  
ACAGAAGAGACTGAGCACACA 6  
TGACAGAAGAGACTGAGCACAC 4  
GTGACAGAAGAGACTGAGC 2  
ACAGAAGAGACTGAGCA 2  
GACAGAAGAGAGTGAACA 1  
GGTGACAGAAGAGACTGAGCA 1  
TGACAGAAGAGACTGAGCACACA 1  
TGACAGAAGAGACTGAGCACACATGG1

---

>vvi-MIR156d [sc:14 + 5411513 5411615] [chr:11 - 5633893 5633995]  
.....(((((.....))).....))..... (-47.50)  
AGAGAGAGACTGACAGAAGAGACTGACACATGCAGGCATTTGTATAAGGGTATACCTATGCCGGTGCCTGCCTCCTCTTTTGTGACAGTTAGGTCCT  
TGACAGAAGAGACTGAGCAC 835876

CTGACAGAAGAGACTGAGCAC 9068  
TGACAGAAGAGACTGAGCACACA 4751  
TGACAGAAGAGACTGAGCA 3092  
TGACAGAAGAGACTGAGC 1409  
GACAGAAGAGACTGAGCAC 475  
ACAGAAGAGACTGAGCAC 162  
CTGACAGAAGAGACTGAGCA 102  
TGACAGAAGAGACTGAG 97  
GACAGAAGAGACTGAGCACACA 90  
ACAGAAGAGACTGAGCACACA 42  
CTGACAGAAGAGACTGAGC 17  
TGACAGAAGAGACTGAGCACAT 12  
CAGAAGAGAGTGAACA 9  
ACTGACAGAAGAGACTGAGCAC 7  
ACAGAAGAGACTGAGCACAT 6  
AGACTGACAGAAGAGACTGAGCAC 5  
CTGACAGAAGAGACTGAGCACACA 4  
CTGACAGAAGAGACTGAG 3  
CTGACAGAAGAGACTGA 3



>vvi-MIR160a [sc:47 + 660403 660505] [chr:12 + 8539030 8539132]  
(((((((((.....)))))))))..... (-52.30)  
GGGGTTGATCTGGCTGGCTCCCTGAAATGCCATTAAGAAGCTTGTCAAGGTGTTGACTCTCTCCCTAGTTGGCATCAGAGGATCATGCAGGCCCAACATTT  
TGGCTGGCTCCCTGAAATGCCA 276  
TGCTGGCTCCCTGAAATGC 4  
CTGGCTCCCTGAAATGCCA 2

>vvi-MIR160b [sc:383 + 36508 36611] [chr:Un\_random + 78660926 78661029]  
..... ((-47.00)  
AATATTGTTCTGGCTGGCTCCCTGAAATGCCATTAAGAAGCTTGTAAAGAGTGTGACAACCTTCCTATTGGCATGAGGGGAGTCAAGCAGCGGAACACTT  
TGGCTGGCTCCCTGAAATGCCA 276  
TGCTGGCTCCCTGAAATGC 4  
CTGGCTCCCTGAAATGCCA 2

>vvi-MIR160c [sc:76 + 752851 752956] [chr:10 - 8894085 8894190]  
...(((.....)))..... (-58.30)  
AAATGGTTGGCTGGCTCCCTGAAATGCCACACAGTACAGACCACTCCCTTTCCCGGATGGCTATTGGCGGGTGGCGTGGAGGACCAAGCATACCCACCATTC  
TGGCTGGCTCCCTGAAATGCCA 130  
CTGGCTCCCTGAAATGCCA 1

>vvi-MIR160d [sc:29 - 1349764 1349865] [chr:8 + 11902361 11902462]  
..... ((-49.30)  
CATACTTACATGCTGGCTGGCTCCCTGAAATGCCATTTGCAAGCTCCACCGAGGATGGTAGCCTTCGCGGATGGCGTGGAGGACCATGCATGATCTGCTT  
TGGCTGGCTCCCTGAAATGCCA 130  
ATGCTGGCTCCCTGAAATGCCA 2  
CTGGCTCCCTGAAATGCCA 1  
TGCTGGCTCCCTGAAATGCCA 1

>vvi-MIR160e [sc:1809 - 11818 1192] [scaffold not incorporated in genome assembly]  
..... ((-47.00)  
AATATTGTTCTGGCTGGCTCCCTGAAATGCCATTAAGAAGCTTGTAAAGAGTGTGACAACCTTCCTATTGGCATGAGGGGAGTCAAGCAGCGGAACACTT  
TGGCTGGCTCCCTGAAATGCCA 276  
TGCTGGCTCCCTGAAATGC 4  
CTGGCTCCCTGAAATGCCA 2

>vvi-MIR160f [sc:17 - 2195098 2195199] [chr:13 + 5553097 5553198]  
..... ((-51.10)  
TAAGCATATATGCTGGCTGGCTCCCTGAAATGCCATTTGCAAGCTCCACCGGACATCGATGGCTTCGCGGATGGCGTGGAGGACCATGCATATGCCCATCT  
TGGCTGGCTCCCTGAAATGCCA 130  
ATGCTGGCTCCCTGAAATGCCA 2  
CTGGCTCCCTGAAATGCCA 1  
TGCTGGCTCCCTGAAATGCCA 1

>vvi-MIR162 [sc:16 - 630729 630831] [chr:17 + 4714987 4715089]  
..... ((-41.70)  
TGAAGTCACTGGATGCAGCGGTTTCATCGATCTCTCCCTGAAATGTTGTGAAAAAGCAGATCAAGAATCGGTGCGTAAACCTCTGCATCCAGCGTTCACTCC  
TCGATAAACCTCTGCATCCAG 1

>vvi-MIR164a [sc:42 - 451600 451720] [chr:7 - 3651395 3651515]  
..... ((-45.00)  
AGTCCCTTGGTGGAGAAGCAGGGCACGTGCAGATTTGGCTCAGTTTTTCOCCTTTTCTCCTTTACTCCACCACCGCCACAGGGTTGACAGTGCCTCCCTTCCCAACATGGGTTCCT  
TGGAGAAGCAGGGCACCTGC 13841  
TGGAGAAGCAGGGCACCTGC 19  
TGGAGAAGCAGGGCACCTGC 19  
TGGAGAAGCAGGGCACCTGC 13  
GGAGAAGCAGGGCACCTGCA 8  
TGGAGAAGCAGGGCACCTGC 5  
GTTGGAGAAGCAGGGCACCTGCA 1  
GAGAAGCAGGGCACCTGCA 1

>vvi-MIR164b [sc:7 - 511008 511100] [chr:9 - 511008 511100]  
..... ((-38.80)  
TAAACCATGCTGGAGAAGCAGGGCACATGCTGGATCAATCAGCACCTGGATCTGAGATTTTACATGTCCTGGCTCCTCCACTTGATCTCTTA  
TGGAGAAGCAGGGCACATGC 1  
TGGAGAAGCAGGGCACATGC 1

>vvi-MIR164c [sc:88 + 655651 655747] [chr:8 + 8981162 8981258]  
..... ((-25.61)  
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TGGAGAAGCAGGGCACCTGC 13841  
TGGAGAAGCAGGGCACCTGC 99  
TGGAGAAGCAGGGCACCTGCAT 20  
TGGAGAAGCAGGGCACCTGC 19



GAAATGTTGTCTGGCTCGAGG 1  
AGGGGAATGTTGTCTGGCTC 1  
GAGGGGAATGTTGTCTGGCTC 1

GACCAGGCTTCATTCCCC 1  
CGGACCAGGCTTCATTCC 1  
TCGGACCAGGCTTCATTCCCCCAAT 1  
TCGGACCAGGCTTCATTCCCCCA 1

>vvi-MIR166d [sc:86 - 899379 899538] [chr:16 - 7520920 7521079]  
.....(((((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(.....)) ..... (-50.99)  
CTGCTTTGAGGGGATTGTGTCTGGCTCGAGGCCACCAACCACTTTGATTGATTCAAATACCTTGATCAGCTTCAACCCACTTCTCCCTCAATTCAATTCCACCCTTGATTATGTGTAGTGCCTCGGACCAGGCTTCATTCCCTCAATCACTGC

TCGGACCAGGCTTCATTCC 219273  
TCGGACCAGGCTTCATTCC 1496  
TCGGACCAGGCTTCATTCC 1281  
GGACCAGGCTTCATTCC 791  
TCGGACCAGGCTTCATT 529  
TCGGACCAGGCTTCATTCCCC 180  
CGGACCAGGCTTCATTCC 128  
TCGGACCAGGCTTCATT 118  
CTGGACCAGGCTTCATTCC 118  
GGACCAGGCTTCATTCC 103  
CTGGACCAGGCTTCATTCC 38  
CGGACCAGGCTTCATTCC 10  
GGACCAGGCTTCATTCC 8  
CGGACCAGGCTTCATTCCCT 7  
CCTCGGACCAGGCTTCATTCC 5  
CGGACCAGGCTTCATTCC 2  
CCTCGGACCAGGCTTCATTCC 2  
CTGGACCAGGCTTCATT 1  
CGGACCAGGCTTCATT 1  
CTGGACCAGGCTTCATTCC 1  
GACCAGGCTTCATTCC 1  
GGACCAGGCTTCATTCCCT 1

>vvi-MIR166e [sc:105 - 1099967 1100132] [chr:2 + 2180274 2180439]  
(((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(.....)) ..... (-71.80)  
GTGTTTGAAGGGGATGTTGTCTGGCTCGAGGCCACCAACTAGATCTATGATCTGCTGTAATTTGTAATGGTGTATGCTCTCAGTTTTGAAGGAGAGATTTGAGTGTATTTGATCGTGGTGGTGTGCTCGGACCAGGCTTCATTCCCCCAATTATTTG

TCGGACCAGGCTTCATTCC 219273  
TCGGACCAGGCTTCATTCC 1496  
TCGGACCAGGCTTCATTCC 1281  
GGACCAGGCTTCATTCC 791  
TCGGACCAGGCTTCATT 529  
CGGACCAGGCTTCATTCC 128  
TCGGACCAGGCTTCATT 118  
GGACCAGGCTTCATTCC 103  
TCGGACCAGGCTTCATTCCCC 89  
CGGACCAGGCTTCATTCC 10  
GGACCAGGCTTCATTCC 8  
GTGGACCAGGCTTCATTCC 5  
CGGACCAGGCTTCATTCC 2  
TCGGACCAGGCTTCATTCCCC 2

TTTGAAGGGGATGTTGTCTGG 51  
  
GAGGGGAATGTTGTCTGGCTC 1  
AGGGGAATGTTGTCTGGCTC 1  
GGAATGTTGTCTGGCTCGAGG 1

CGGACCAGGCTTCATT 1  
GACCAGGCTTCATTCC 1  
TCGGACCAGGCTTCATTCCCCCA 1  
TCGGACCAGGCTTCATTCCCCCAAT 1

>vvi-MIR166f [sc:20 - 663678 663777] [chr:7 + 14569971 14570070]  
(((((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(((((.....(.....)) ..... (-49.50)  
TGTAGTTGTGGGGAATGTTGGCTGGCTCGAGGCTTTCTTGAGTATTTATGTATACCTCAAAAAGCTTCGGACCAGGCTTCATTCCCTCAACACACT

TCGGACCAGGCTTCATTCC 219273  
TTCGGACCAGGCTTCATTCC 44209  
TCGGACCAGGCTTCATTCC 1496  
TCGGACCAGGCTTCATTCC 1281  
GGACCAGGCTTCATTCC 791  
TTCGGACCAGGCTTCATT 529  
TTCGGACCAGGCTTCATTCC 237  
TTCGGACCAGGCTTCATTCCCC 180  
TTCGGACCAGGCTTCATT 170  
CGGACCAGGCTTCATTCC 128  
TCGGACCAGGCTTCATT 118  
GGACCAGGCTTCATTCC 103  
TTCGGACCAGGCTTCATT 47  
TTCGGACCAGGCTTCATT 27  
CTTCGGACCAGGCTTCATTCC 22  
CGGACCAGGCTTCATTCC 10  
TTCGGACCAGGCTTCATTCC 9  
GGACCAGGCTTCATTCC 8













>vvi-MIR169y [sc:180 - 169908 170155] [chr:1 + 14661042 14661289] ...  
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TGATGGCCTC  
TAGCGAAGGATGACTTGCCTA 0

>vvi-MIR171a [sc:9 + 461317 461415] [chr:14 - 14693988 14694086] (-47.80)  
TGGTGGGAAGCGTGATGTGGGACGGCTCAATCAAACCAAGATCTCAATGGTTGAGTCCTTTAATCTGATTGAGCCGTGCCAATATCATGTTCAAATAC  
TTGAGCCCGTGCCAAATATCATG 0  
TGATTGAGCCCGTGCCAAATATC 637  
TGATTGAGCCCGTGCCAAATA 43  
TGATTGAGCCCGTGCCAAATAT 4  
TGATTGAGCCCGTGCCAAAT 4  
TGATTGAGCCCGTGCCAA 1  
CTGATTGAGCCCGTGCCAAATATC 1

>vvi-MIR171b [sc:36 - 591211 591309] [chr:12 + 7277319 7277417] (-46.90)  
TGGGGGGGAGGATTTGGCGGCTCAAATTTAAAGACATGGTTAGATTGAAGAGATATTAGCCATGTGATTTGATTGAGCCCGCTCAATATCTCCTTTTGCA  
TGATTGAGCCCGCTCAATATC 0

>vvi-MIR171c [sc:36 - 536559 536661] [chr:12 + 7331967 7332069] (-48.00)  
TGGATTTACGGGATATTTGGTCGGCTCAATAAGAAAGCAGTGCTCGCAATCTTTTTGAGTTCTGGTTTTGATTGAGCCGTGCCAATATCACGTGTCATTTGCT  
TGATTGAGCCCGTGCCAAATATC 637  
TGATTGAGCCCGTGCCAAATA 43  
TGATTGAGCCCGTGCCAAAT 4  
TGATTGAGCCCGTGCCAAAT 4  
TTGAGCCCGTGCCAAATATCAG 4  
TTGAGCCCGTGCCAAATATC 2  
TGATTGAGCCGTGCCAA 1

>vvi-MIR171d [sc:795 - 2155 2254] [scaffold not incorporated in genome assembly] (-38.60)  
TAGATACACGAGATATTTGATACGGTTCAATTAGAAAGCTGTGTCTAAGTTAAGAACTCTGTGTTGATTGAGCCGTGCCAATATCACGTCTACTTCT  
TGATTGAGCCCGTGCCAAATATC 637  
TGATTGAGCCCGTGCCAAATA 43  
TGATTGAGCCCGTGCCAAAT 4  
TGATTGAGCCCGTGCCAAAT 4  
TTGAGCCCGTGCCAAATATCAG 4  
TTGAGCCCGTGCCAAATATCAC 2  
TGATTGAGCCGTGCCAA 1

>vvi-MIR171e [sc:13 + 5162582 5162684] [chr:11 + 5162582 5162684] (-44.70)  
GGAAAGTAAGCGATTTGGTGAAGTTCAATCCGAAAGCAGATTTACGAAGAGCCGTAAAGAAATCACTCAGATTTTGGTTGAGCCCGTGCCAATATCACACTTTCTGTAAAG  
TGATTGAGCCCGTGCCAAATATC 53  
TGATTGAGCCCGTGCCAAATA 4  
TGATTGAGCCCGTGCCAA 1

>vvi-MIR171f [sc:104 - 699397 699499] [chr:9 + 7000493 7000595] (-45.90)  
TTGAAAGAAGCGATTTGGTGAAGTTCAATCTGAAGATTTGATTTATGCTTGAATGTAAAACATGATCTCAGATTGAGCCCGTGCCAATATCACACTTTCTGTGGC  
TTGAGCCCGTGCCAAATATCACT 0

>vvi-MIR171g [sc:1 - 10508015 10508090] [chr:18 + 3212869 3212944] (-21.70)  
GCCAGCCTTCCATGTTGGTTCCATCGGTGGGGACACCAACTCTTGAGCCGAACCAATATCACCCGAGCCAAAT  
TTGAGCCGAACCAATATCAC 0

>vvi-MIR171h [sc:16 + 3531871 3531966] [chr:17 - 1813852 1813947] (-47.30)  
TTPCCAGAGATGTGGTGCGGTTCAACCTAACCTGATGTCATGAAATGATCGACTCTGATGTTGGTTGAGCCCGTGCCAATATCCCGCTCAATC  
TGGTTGAGCCCGTGCCAAATATC 0



>vvi-MIR319b [sc:5 + 4170832 4171025] [chr:1 + 4170832 4171025] (-102.82)  
..(((((((.....)))))).....)  
TTGGAAGAAGGAGCTCTCTTAGTCCAATCCGAGACAGCTCAAGGCTGATACCTGGCTGCTGACTCGTTGCTTCAAGAACATCATACATAGGCCGGAAGAAGATGGATGGTTTGTGATCCAACAGATGCGAGAGCTGCGTTTATGCTGTCACGTCCTGGACTGAAGGGAGCTCCCTTGTATCCACA  
CTTGGACTGAAGGGAGCTCCCT 0  
TTGGACTGAAGGGAGCTCCCT 1

>vvi-MIR319c [sc:132 + 439049 439230] [chr:2 - 661750 661931] (-83.40)  
...(((((((.....)))))).....)  
TTACATTGAAGAGAGCTTTCTTCACTCCACTCATGGTGGCAGTAGGATGAATTAGCTGCCGACTCATTCATCCAAATACCTGTGTTAAGACTACCCGATAAATGATGAATGATGCGGGAGACAAATGGATCTTAAAGCTCCCTGTGCTTGGACTGAAGGGAGCTCCCTTCACTGCAATC  
CTTGGACTGAAGGGAGCTCCCT 0  
AGCTGCCGACTCATTATCCCA 3  
TTGGACTGAAGGGAGCTCCCT 1

>vvi-MIR319e [sc:13 + 4274222 4274328] [chr:11 + 4274222 4274328] (-40.40)  
..(((((((.....)))))).....)  
TGCAGAAATGGGGTTCCTTTGACGCCAAAACAACCTCCATCGCTGAAGAAGATGATGAATCTCATGCTCCTGTGTTTGGACTGAAGGGAGCTCCCTTCACTGCTCTCT  
TTGGACTGAAGGGAGCTCCCT 0  
TTGGACTGAAGGGAGCT 1

>vvi-MIR319f [sc:3 - 409791 409983] [chr:6 + 9069150 9069342] (-88.70)  
..(((((((.....)))))).....)  
AGTGGTTTAAAGAGAGCTTCCCTCAGTCCACTCATGGATGGTTAGGGTTGGATTAGCTGCCGACTCATTCATCAACACAGTAGAATGGAATGGATTACTACTGTGATGTTGATGATGCGGGAGGTAATTCATCCTTTTCTGCTGTGGACTGAAGGGAGCTCCCTTCACTGCTTCT  
CTTGGACTGAAGGGAGCTCCCT 0  
TTGGACTGAAGGGAGCTCCCT 1

>vvi-MIR319g [sc:16 + 1677842 1678063] [chr:17 - 3667755 3667976] (-96.00)  
..(((((((.....)))))).....)  
GAACAGCTGAAGAGCTCCTTTAGTCCAATAAAGAGGGCTGAGGGGGCGCCAGAGCTGCCATCTCATGCACTTGGCTATGCTTATTCTTCTCAATCAATTGCTGCGAGTATGGCTGGAGTGACAAATGCTAAGTTTTCCTGATGATGACATGGGACAACTCCTCCGACGCTTTGCCACTCATTGGACTGAAGGGAGCTCCAGGGCAGATCT  
ATTGGACTGAAGGGAGCTCCCT 0

>vvi-MIR390 [sc:3 - 1385305 1385444] [chr:6 + 8093689 8093828] (-62.30)  
..(((((((.....)))))).....)  
AGAATCTGTAAAGCTCAGGAGGGATAGCCCATGAGCCATGAGAAAATGATGTTGAGTTGAAAATTTTCTAGCTGTTTGTGGCTCATCATTTTGTGTGTGGCCCTATCTATCCCTGAGTTTCAAGGGTCTCTC  
AAGCTCAGGAGGATAGCCGC 141  
AAGCTCAGGAGGATAGCCCA 5  
AAGCTCAGGAGGATAGCCG 4  
AAGCTCAGGAGGATAGCCG 1  
AAGCTCAGGAGGATAGCCGC 1  
TCAGGAGGATAGCCGC 1

>vvi-MIR393a [sc:222 - 104163 104288] [chr:Un\_random - 54807498 54807623] (-53.90)  
..(((((((.....)))))).....)  
GGTGGACAGTTCCAAGGGATCGCATTTGATCCCAACTGCTTCCACCTCTCTTACCAGACTATCATAAACAAGCTGGCCCTTTTCCCATTGGATCATGCTATCCCTTAGGAACCTCCCATCAG  
TCCAAGGGATCGCATTGATCC 0  
TTCCAAGGGATCGCATTGAT 14983  
TCCAAGGGATCGCATTGATC 398  
TCCAAGGGATCGCATTGA 136  
TTCCAAGGGATCGCATTGATC 127  
CAAAGGGATCGCATTGAT 46  
TCCAAGGGATCGCATTGAT 30  
TCCAAGGGATCGCATTGA 19  
CAAAGGGATCGCATTGATC 7  
TTCCAAGGGATCGCAT 5  
TCCAAGGGATCGCAT 4  
TTCCAAGGGATCGCATTG 4  
AAAGGGATCGCATTGAT 2  
TCCAAGGGATCGCATTG 1  
CAAAGGGATCGCATTGA 1

>vvi-MIR393b [sc:17 - 3375224 3375306] [chr:13 + 4372990 4373072] (-45.70)  
..(((((((.....)))))).....)  
GGAGGAGGATCCAAGGGATCGCATTTGATCCCAACTGCTTCCATGCTTGGATCATGCTATCCCTTTGGATTCCCTCCTTTGG  
TCCAAGGGATCGCATTGATCC 0  
TTCCAAGGGATCGCATTGATC 398  
CAAAGGGATCGCATTGAT 46  
TCCAAGGGATCGCATTGAT 30  
TCCAAGGGATCGCATTGA 19  
CAAAGGGATCGCATTGATC 7  
ATCCAAGGGATCGCATTGAT 4  
AAAGGGATCGCATTGAT 2  
TCCAAGGGATCGCAT 1  
CAAAGGGATCGCATTGA 1

>vvi-MIR394a [sc:38 + 1925563 1925651] [chr:12 - 14925943 14926031]



(((.....)))))).. (-51.01)  
CAGAGCCATTGGCATTCTGCCACCTCCATGCACATCATGGGTCTATATCTTTGGAGGTGGCCAGCATGCCAARGTGGCTCTGTA  
TTGGCATTCTGCCACCTCC 748  
TTGGCATTCTGCCACCTCCA 9  
GGCATTCTGCCACCTCC 3  
TTGGCATTCTGCCACCTC 3  
TTGGCATTCTGCCACCT 2  
TTGGCATTCTGCCACC 1

>vvi-MIR394b [sc:1 + 12335062 12335154] [chr:18 - 1385805 1385897] ((.....)).. (-42.60)  
ACAGAGTTATTGGCATTCTGCCACCTCCCATCTCTTGAAAATCTCTTTTCTCTCTGTGGAGGTGGGCATACTGCCAACCAAGCTCTGTT  
TTGGCATTCTGCCACCTCC 748  
GGCATTCTGCCACCTCC 3  
TTGGCATTCTGCCACCTC 3  
TTGGCATTCTGCCACCT 2  
TTGGCATTCTGCCACC 1  
ATTGGCATTCTGCCACCTCC 1

>vvi-MIR394c [sc:1 + 10217177 10217278] [chr:18 - 3503681 3503782] ((.....)).. (-59.50)  
CAGAGCCATTGGCATTCTGCCACCTCCATATATACCAATCTTCTGAATGGCGCCACAAAGCTTTGGAGGGCCAGGATGCCAATGGCTCTGTA  
TTGGCATTCTGCCACCTCC 748  
TTGGCATTCTGCCACCTCCA 9  
GGCATTCTGCCACCTCC 3  
TTGGCATTCTGCCACCTC 3  
TTGGCATTCTGCCACCT 2  
TTGGCATTCTGCCACC 1

>vvi-MIR395a [sc:5 + 6669509 6669600] [chr:1 + 6669509 6669600] ..... (-40.86)  
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TGAAGTGTGGGGGAAC 198  
TGAAGTGTGGGGGAAC 3  
CTGAAGTGTGGGGGAAC 2  
AAGTGTGGGGGAAC 1  
GAAGTGTGGGGGAAC 1  
TGAAGTGTGGGGGAAC 1

>vvi-MIR395b [sc:5 + 6643441 6643530] [chr:1 + 6643441 6643530] ..... (-34.90)  
GTCCCTTAGAGTTCCCTTACCACCTTCACTGGGATCTCTCTAATGAATGCCTACGTACTGAAAGTGTGGGGGAACCTGGTGCAT  
TGAAGTGTGGGGGAAC 198  
TGAAGTGTGGGGGAAC 3  
CTGAAGTGTGGGGGAAC 2  
AAGTGTGGGGGAAC 1  
GAAGTGTGGGGGAAC 1  
TGAAGTGTGGGGGAAC 1

>vvi-MIR395c [sc:5 - 6640691 6640782] [chr:1 - 6640691 6640782] ..... (-37.80)  
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TGAAGTGTGGGGGAAC 198  
TGAAGTGTGGGGGAAC 3  
CTGAAGTGTGGGGGAAC 2  
TGAAGTGTGGGGGAAC 1  
GAAGTGTGGGGGAAC 1  
AAGTGTGGGGGAAC 1

>vvi-MIR395d [sc:5 + 6653540 6653625] [chr:1 + 6653540 6653625] ..... (-40.80)  
GCCCTTAGAGTTCCCTTACCACCTTCACTGGGATCTCTCTAATGACTTCCCTACTGAAAGTGTGGGGGAACCTGGTGCAT  
TGAAGTGTGGGGGAAC 198  
TGAAGTGTGGGGGAAC 3  
CTGAAGTGTGGGGGAAC 2  
AAGTGTGGGGGAAC 1  
GAAGTGTGGGGGAAC 1  
TGAAGTGTGGGGGAAC 1

>vvi-MIR395e [sc:5 + 6646025 6646116] [chr:1 + 6646025 6646116] ..... (-37.30)  
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TGAAGTGTGGGGGAAC 198  
TGAAGTGTGGGGGAAC 3  
CTGAAGTGTGGGGGAAC 2





AGTGCAGCGTTGATGAA 6  
ATTGAGTGCAGCGTTGATGA 6  
TTGAGTGCAGCGTTGATG 3  
TCATTGAGTGCAGCGTTGATG 2  
TTGAGTGCAGCGTTGAT 1  
ATTGAGTGCAGCGTTGATGAAA 1  
ATTGAGTGCAGCGTTGATG 1  
ATTGAGTGCAGCGTTGA 1  
CATTGAGTGCAGCGTTGATGA 1

>vvi-MIR397b [sc:1477 - 246 363] [chr:Un\_random - 146568042 146568159] (-46.40)  
.....(((.(((((((((((((((((((((((((.....)))))))))...)))...)))...))).....)))).  
GAAGAAAACATCATTGAGTGCAGCGTTGATGAACTGAAGTATCCATTTTTCAGCTCTCTTGAAGTCCCGCAAGATGGGTTCTGGTGTATCCATTGGCCGCTGCCTCAATCATGTG

ATTGAGTGCAGCGTTGATGAA 714  
TTGAGTGCAGCGTTGATGAA 96  
TTGAGTGCAGCGTTGATGAAA 88  
TTGAGTGCAGCGTTGATGA 15  
TTGAGTGCAGCGTTGATGAAA 13  
ATTGAGTGCAGCGTTGATGA 6  
AGTGCAGCGTTGATGAA 6  
TTGAGTGCAGCGTTGATG 3  
TCATTGAGTGCAGCGTTGATG 2  
ATTGAGTGCAGCGTTGA 1  
TTGAGTGCAGCGTTGATG 1  
ATTGAGTGCAGCGTTGATG 1  
CATTGAGTGCAGCGTTGATGA 1  
ATTGAGTGCAGCGTTGATGAAA 1

>vvi-MIR398a [sc:5 + 717225 717327] [chr:1 + 717225 717327] (-55.60)  
.....(((.(((((((((((((((((((((((((.....)))))))))...)))...)))...))).....)))).  
ACACCCCAAGGAGTGCAGCGTTGAGAAACACCGGTTGTGTGGCTGCACAAAGCTCTGCTAGCTAATGCATTTGTGTTCTCAGGTCACCCCTTGGGGCACCA

TTCTCAGGTCACCCCTTGGG 13  
TGTGTTCTCAGGTCACCCCT 6  
TGTGTTCTCAGGTCACC 1  
TGTGTTCTCAGGTCACCC 1

>vvi-MIR398b [sc:25 + 3324549 3324636] [chr:6 - 20660658 20660745] (-44.70)  
.....(((.(((((((((((((((((((((((((.....)))))))))...)))...)))...))).....)))).  
GTGTCCACAGGTGAGACTGAGAATCACATGCCCGCACACCCTCTTTGCTCTCATGTGTTCTCAGGTCGCCCTGCTGACTCCC

TGTGTTCTCAGGTCGCCCTG 0  
CTCATGTGTTCTCAGGTCGCC 15  
TGTGTTCTCAGGTCGCC 5  
GTGTTCTCAGGTCGCCCTGC 1  
TGTGTTCTCAGGTCGCC 1  
ATGTTCTCAGGTCGCC 1  
CATGTGTTCTCAGGTCGCC 1  
TCATGTGTTCTCAGGTCGCC 1

>vvi-MIR398c [sc:15 - 78481 78568] [chr:6 + 14851882 14851969] (-45.80)  
.....(((.(((((((((((((((((((((((((.....)))))))))...)))...)))...))).....)))).  
GTGTCCACAGGAGTACCTGAGAATCACATGCCCGCATCACCCTCTTTGCTCTCATGTGTTCTCAGGTCGCCCTGCTGACTCCC

TGTGTTCTCAGGTCGCCCTG 0  
CTCATGTGTTCTCAGGTCGCC 15  
TGTGTTCTCAGGTCGCC 5  
TCATGTGTTCTCAGGTCGCC 1  
CATGTGTTCTCAGGTCGCC 1  
ATGTTCTCAGGTCGCC 1  
TGTGTTCTCAGGTCGCC 1  
GTGTTCTCAGGTCGCCCTGC 1

>vvi-MIR399a [sc:81 - 819715 819811] [chr:10 + 1853461 1853557] (-51.32)  
.....(((.(((((((((((((((((((((((((.....)))))))))...)))...)))...))).....)))).  
GAGAATAACAGTGTGATTTCTCCTTTGGCAGAGATATCAGCATGGAGTAGAGGCCGTAGTCTGCTGCCAAGGAGAATTGCCCTGTTAATCAATT

TGCCAAGGAGAATTGCCCTG 106  
TGCCAAGGAGAATTGCC 4  
TGCCAAGGAGAATTGCCCTGTT 3  
TGCCAAGGAGAATTGCC 2  
CAAAGGAGAATTGCCCTG 1  
TGCCAAGGAGAATTGCCCTGT 1  
AAAGGAGAATTGCCCTGT 1  
AAAGGAGAATTGCCCTGTT 1

>vvi-MIR399b [sc:376 + 84186 84302] [chr:Un\_random + 77999653 77999769] (-48.22)  
.....(((.(((((((((((((((((((((((((.....)))))))))...)))...)))...))).....)))).





TATAAAGTTTCTTGTCAAATGAGTATTCCAACAACAGCTTGTGAAGCAATGATTACTGTCTATAGTCTCTGATGTGGATTGTTGTTGAGATGCTCATTGAGGAAGCAACCTTAAAAATG  
TCTTGTCTCAAATGAGTATTCCA 0

>vvi-MIR828b [sc:5 + 2945837 2945908] [chr:1 + 2945837 2945908] ..... (-21.00)  
...(((((((.....)))))).....  
GCTCTGGTTTCTTGTCAAATGAGTATTCCAACAACAGCTTGTGAAGCAATGATTACTGTCTATAGTCTCTGATGTGGATTGTTGTTGAGATGCTCATTGAGGAAGCAACCTTAAAAATG  
TCTTGTCTCAAATGAGTATTCCA 0

>vvi-MIR845a [sc:86 + 3156 3597] [chr:16 + 6624697 6625138]  
.....(((((((.....)))))).....  
TTTCACTTGATTAGTTCCTTCAATGAGTATTGCAAGTAATCTCCAAATTTCCCTTAGCGGATTACATTGACATATTCTATTATATTCATTCCATAGCACATTGCAAAAGTAAAAACGACTTAGCATTTAATTGAAAATTTCTCTATCAAGCTCATCCATTCTGCTTGGGTTTTGGAAACCAAATTCATCAACTAAATTTAGTGGGTAAGTTGGCCATCTCAATGGCA  
TCCCATACATCAAAATCAGTTGATTGTAAGTACCAAGTCATTTAGCTTTCCAATAGGGATAGTCGGTTCGCCATAAAGAAATGGAGCTCTATGTTTGAACAATTTTCAGTTTGAGATGAGCTTGATGGAAATAGCCATTTTCCTCTAGATGATTAAGTCTTAAGCAAGAGGTCTAGCTCTGATACCAATTTGATAAAACAAAGGC  
TAGCTCTGATACCAATTGATA 0

>vvi-MIR845b [sc:216 + 313861 314302] [chr:Un\_random + 53496712 53497153]  
.....(((((((.....)))))).....  
TTTCACTTGATTAGTTCCTTCAATGAGTATTGCAAGTAATCTCCAAATTTCCCTTAGCGGATTACATTGACATATTCTATTATATTCATTCCATAGCACATTGCAAAAGTAAAAACGACTTAGCATTTAATTGAAAATTTCTCTATCAAGCTCATCCATTCTGCTTGGGTTTTGGAAACCAAATTCATCAACTAAATTTAGTGGGTAAGTTGGCCATCTCAATGGCA  
TCCCATACATCAAAATCAGTTGATTGTAAGTACCAAGTCATTTAGCTTTCCAATAGGGATAGTCGGTTCGCCATAAAGAAATGGAGCTCTATGTTTGAACAATTTTCAGTTTGAGATGAGCTTGATGGAAACAAACCTTTTCCTCTAGATGATTAAGTCTTAAGCAAGAGGTCTAGCTCTGATACCAATTTGATAAAACAAAGGC  
TAGCTCTGATACCAATTGATA 0

>vvi-MIR845c [sc:31 - 2686178 2686267] [chr:7 + 503529 503618] ..... (-30.30)  
...(((((((.....)))))).....  
CAATTTAGTGGTTTTGTTGCTGAGTTCATGTTGGCAATTTCTTAATGATTAAACATGAGGCTCTGATACCAATTTGATGCATAAAACCAT  
AGGCTCTGATACCAATTGATG 0

>vvi-MIR845d [sc:30 - 551951 552081] [chr:Un\_random - 108642758 108642888] ..... (-32.25)  
.....(((((((.....)))))).....  
ATAACCAACATTAATTATCCCTAGGGCCATGGGATAAACAAAACCTTCGAAAACCAAGTTAGCACACCTTAGAATGGTCTAGACAAATTAACCTATGGCTCTGATACCAATTTGATGGGAAAAACCT  
TGGCTCTGATACCAATTGATG 0

>vvi-MIR845e [sc:168 + 268220 268350] [chr:Un\_random + 37572078 37572208] ..... (-31.30)  
.....(((((((.....)))))).....  
AGAACGCACATTAATTATCCCTAGGGCCATGGGATAAACAAAACCTTCGAAAACCAAGTTAGCACACCTTAGAATGGTCTAGCACGATTAACTAACCCTATGGCTCTGATACCAATTTGATGGGAAAAACCTC  
TGGCTCTGATACCAATTGATG 0

**Supplemental Figure S4: predicted transcript and intron coordinates for 25 *Vitis vinifera* pri-miRNAs.** For each miRNA genomic locus showing extensive coverage with Illumina RNAseq reads, Transcription start and (where possible) stop coordinates were estimated from read coverage. Introns were predicted as explained in the main text. The table shows transcript coordinates estimated from different tissues, frequencies of support for introns(by tissue), splice site scores, promoter coordinates estimated by TSS-TCM, and notes showing additional support obtained for introns and transcript coordinates



icroRNA	Chr	strand	TSS(TSSP-TCM)	TATA(TSSP-TCM)	Leaf start	Stem start	Root start	Callus start	Leaf Stop	Stem stop	Root stop	Callus stop	donor	donor score	donor support	acceptor acceptor score	acceptor support	leaf	stem	root	callus	f reads	Additional Info (support for introns, RACE start/stop)					
iiR156d	chr11	-	5634584	TATA-less	5634380	5634415	5634364	5634353	5631341	5631328	5633903	nd	5633555 5633512 5633184 5632979 5632655 5631801	0.571000 0.389000 0.370000 0.593000 0.606000 0.328000	stem	5633474 5631712 5631712 5632856 5632529 5631712	0.330000 0.164000 0.164000 0.392000 0.426000 0.164000	leaf callus leaf callus stem leaf stem leaf callus	0 2 1 0 7 2 1	2 0 0 0 0 17 0	0 0 0 0 0 1 0	0 0 0 0 0 1 0	2 1 3 0 1 10 1					
iiR156g	chr17	-	No pred	no	3038168	3037793	nd	3038273	3036995	3037004	nd	3037013	3038152 3037895 3037783 3037711 3037596 3037392	0.355000 0.524000 0.430000 0.555000 0.401000 0.503000	stem callus	3037280 3037280 3037280 3037280 3037280 3037280	0.490000 0.490000 0.490000 0.490000 0.490000 0.490000	stem callus stem callus stem callus stem callus stem callus stem callus	2 1 3 12 1 0	0 0 1 0 0 4	0 0 0 0 0 0	0 1 0 0 0 1	1 2 2 8 1 4	2 454 leaf				
miR156i iiR159c	chrUn_random chr17	+ -	36776661 No pred	36776634 no	36776678 2610336	36776678 2610326	36776742 2610317	36776743 2610317	nd 2609123	nd 2609131	nd nd	nd 2609196	2610173	0.508000		2609343	0.374000	leaf stem root	22	8	0	2	8					
iiR160c	chr10	-	8894350	8894374	8894318	8894386	8894350	8894371	nd	nd	nd	nd	8893990	0.577000		8893881	0.505000	leaf stem root callus	0	3	1	0	4					
miR162	chr17	+	4714318	TATA-less	4714680	4714686	4714687	4714687	4717308	4717340	4717273	4717307	4716567 4715520 4715520 4715520 4715510 4715507 4715476 4715350 4714863 4714768 4714759 4714759 4714740 4714729	0.501000 0.504000 0.504000 0.504000 0.471000 0.501000 0.449000 0.373000 0.390000 0.407000 0.377000 0.377000 0.470000 0.426000		4716673 4716673 4716420 4716673 4716673 4716573 4715429 4716240 4715429 4716673 4715429 4715429 4714740 4715429	0.490000 0.490000 0.366000 0.490000 0.490000 0.490000 0.490000 0.481000 0.244000 0.481000 0.490000 0.481000 0.481000 0.481000 0.481000	leaf stem root callus	4 0 0 0 0 1 1 3 0 0 0 3 3 3	1 2 1 0 0 0 0 0 1 1 0 3 1 2	0 1 1 0 0 0 0 0 0 0 0 0 0 0 0	0 1 1 0 0 0 0 0 0 1 1 0 0 0	0 2 1 0 0 1 0 0 0 0 0 0 0 0	2 1 1 1 0 0 0 0 0 0 0 0 0 0	0 1 1 0 0 0 0 0 0 1 1 0 0 1	2 3 2 1 1 1 4 5 6		RACE STOP: 4717237/4715594/4715751/4717045/4716530
iiR167a iiR167d	chr1 chr7	+ -	No pred 845566	no 845597	1563294 845542	nd 845545	1563320 nd	1563291 nd	1563916 844270	nd 844250	1563933 nd	1563912 nd	844837	0.489000	leaf	844632	0.370000	stem	0	1	0	0	1					
miR168	chr2	-	16750258	16750282	16750255	16750240	16750225	16750239	16747427	16747408	nd	16747419	16750027 16750019 16748088	0.467000 0.448000 0.482000		16748197 16748197 16747680	0.506000 0.506000 0.448000	leaf root leaf root leaf stem callus	2 4 0	0 8 1	0 1 0	0 5 0	0 1 0	1 5 1	1 454 berry 6 454 berry			
iiR169g iiR171a iiR319c iiR393b	chr8 chr14 chr2 chr13	+ - - +	No pred No pred No pred No pred	no no no no	20118544 14694238 662167 4372918	nd 14694267 662167 4372919	nd 14694292 nd nd	nd 14694236 nd 4373963	20119875 nd 660898 4373978	nd nd nd nd	nd nd nd nd	nd nd nd nd	4373255	0.551000		4373664	0.402000		1	0	0	0	1					
iiR394b	chr18	-	1386133	TATA-less	1386084	1386013	nd	nd	1385071	1384873	nd	nd	1385724	0.510000		1385362	0.467000	leaf stem callus	3	11	0	1	7	RACE STOP 1385081/1385085/1385121/1385102/1385108 7 RACE				
iiR396b	chr11	+	No pred	no	5205873	5205921	5205886	5205883	5208124	5208135	5208011	5208094	5206245 5206451 5206513 5207688 5207750	0.545000 0.542000 0.439000 0.409000 0.538000	leaf	5206387 5207749 5207086 5207749 5207816	0.369000 0.404000 0.171000 0.404000 0.363000	stem callus stem callus leaf leaf	3 0 0 0 0	1 1 0 0 1	1 0 0 0 0	0 0 0 0 0	5 2 1 1 1					
iiR397a	chrUn_random	+	No pred	no	85971353	85971349	85971353	85971342	nd	nd	nd	nd	85971560 85972847 85973070	0.435000 0.571000 0.598000		85971702 85972917 85973212	0.385000 0.439000 0.454000	stem root callus stem callus	0 0 0	1 5 2	0 0 0	0 40 0	0 11 2					
iiR397b	chrUn_random	-	No pred	no	146568205	146568210	146568207	146568217	nd	nd	nd	nd	146567996	0.435000		146567862	0.385000		0	1	0	2	2					
iiR398a	chr1	+	No pred	no	717331	717187	717264	717248	719184	717198	719188	719200	717390 717390 717390 717855 718282 718500	0.499000 0.499000 0.499000 0.510000 0.533000 0.479000		717577 717687 718148 718148 718370 719049	0.314000 0.351000 0.353000 0.353000 0.390000 0.363000	leaf stem root callus leaf stem root callus leaf stem root callus leaf stem root callus leaf stem root callus leaf stem root callus	0 0 0 2 2 0	2 1 1 15 8 0	1 0 0 2 0 0	1 0 0 4 4 1	4 1 1 11 8 1					
iiR398b iiR398c iiR403a	chr6 chr6 chr5	- + -	No pred No pred 1835411	no no 1835441	20660773 14851851 nd	20660783 14851857 1835395	20660768 14851856 1835420	20660767 14851858 1835389	20660459 14852180 nd	20660448 14852215 nd	nd nd nd	nd 14852186 nd	1834959 1835273	0.568000 0.431000		1834086 1835195	0.411000 0.349000		0 0	4 2	0 0	0 0	2 2	2 454 leaf				
iiR403c	chr5	-	1302236	1302265	1302234	1302219	1302219	1302232	1301756	1301756	1301760	1301760	1302097	0.365000		1302012	0.349000		0	2	0	0	2					
iiR403e	chr5	-	No pred	no	1738240	1738247	1738248	1738231	nd	nd	nd	nd	1737325 1738206	0.632000 0.568000		1737240 1737402	0.404000 0.303000		1 1	2 1	0 1	8 1	8 3					
miR408	chr7	+	No pred	no	5372904	5372907	5372907	5372896	5374243	5374226	5374255	5374207	5373063 5373063 5373063 5373063	0.555000 0.555000 0.555000 0.555000		5373688 5373709 5373745 5373858	0.179000 0.261000 0.303000 0.327000	leaf root root	2 0	1 0	0 0	0 0	2 1 0 2					
iiR482a	chr17	+	No pred	no	5579315	5579315	5579315	5579315	5580798	5580493	5580438	5581255	5579322 5579346 5579360	0.514000 0.367000 0.390000	leaf stem root callus leaf stem root callus stem callus	5579599 5579599 5579599	0.482000 0.482000 0.482000	leaf stem root callus leaf stem root callus leaf stem root callus	1 5 0	0 0 1	0 0 0	0 0 0	1 2 1		RACE START: 5579321 RACE STOP: 5580180			

**Supplemental Figure S5: RNAseq reads Supporting predicted splice junctions for *Vitis vinifera* pri-miRNAs shown in Figure 4**

Vvi-MIR162	chr17	+	4716567		4716673		
CCCCAGGCAGCAA	AAATTTAGTGT	TTCCACAGG	TTGCATTTTTG	.....	TTTCTTGAGCAGG	TATCTGGAATCGGAAAGTTGTTTCTTGTTT	
	CAA	AAATTTAGTGT	TTCCACAG			GTATCTGGA	3
	GCAA	AAATTTAGTGT	TTCCACAG			GTATCTGG	2
Vvi-MIR162	chr17	+	4715520		4716673		
GCCAAATTC	TGCTGAATGT	AGTAATTTCC	AGTAAATTTAAT	.....	TTTCTTGAGCAGG	TATCTGGAATCGGAAAGTTGTTTCTTGTTT	
	CTTGCTGAAT	GTAGTAATTTCC				GTATCTGGA	1
	GAATGTAG	TAATTTCC				GTATCTGGAATCG	1
	GCTGAATGT	AGTAATTTCC				GTATCTGGAA	2
Vvi-MIR162	chr17	+	4715520		4716420		
GCCAAATTC	TGCTGAATGT	AGTAATTTCC	AGTAAATTTAAT	.....	GTTCTTGAGTAG	GGGGGATAAAGGCTGCTGGTTTTGCGAAGTGC	
	TCTTGCTGAAT	GTAGTAATTTCC				GGGGG	1
	AATGTAG	TAATTTCC				GGGGGATAAAGGCTG	1
Vvi-MIR162	chr17	+	4715510		4716673		
GCATCACAACG	CCAAATTC	TGCTGAATGT	AGTAATTTCCAGT	.....	TTTCTTGAGCAGG	TATCTGGAATCGGAAAGTTGTTTCTTGTTT	
	TCTTGCTGAAT	GTA				GTATCTGGAATCGGAA	1
Vvi-MIR162	chr17	+	4715507		4716673		
GTAGCATCACAAC	GCCAAATTC	TGCTGAATGT	AGTAATTTCC	.....	TTTCTTGAGCAGG	TATCTGGAATCGGAAAGTTGTTTCTTGTTT	
	CACAACGCC	AAATTC	TGCTGAAT			GTATCT	1
Vvi-MIR162	chr17	+	4715476		4716673		
CTGTGTTCTTCT	GTGTTTCGAAC	AGACTCTGG	TAGCATCACAA	.....	TTTCTTGAGCAGG	TATCTGGAATCGGAAAGTTGTTTCTTGTTT	
	CAGACTCTG					GTATCTGGAATCGGAAAGTTG	1
Vvi-MIR162	chr17	+	4715350		4715429		
AGACCATGTTCA	CAAATAGTCT	TGTAAGCTG	TAAACAGCCTGA	.....	AGTTTATTGCAG	GGAAGGAGATCCGCCCTGTGTTCTTCTGTGT	
	AATAGTCT	TGTAAGCT				GGAAGGAGATCCG	3

Vvi-MIR162	chr17	+	4714863		4716240	
TCATTTGGTCAGATCTGTGGTTTTT	GATTTTGTGTTTTT	GAAA	.....	ACACTCCATAAGGTTTTTTA	ATTGGGTTAACTTCTATTCTCAT	
GTCAGATCTGTGGTTTTT	GATTTT			GTTTTT		1
Vvi-MIR162	chr17	+	4714768		4715429	
ATGGTGACCCTTCAGATTCCTGGTTCACGCTGTTACTCTTTCT	.....	AGTTTATTGCAGGGAAGGAGATCCGCCCTGTGTTCTTCTGTGT				
TCCTGGTTCACGCT		GGAAGGAGATCCGCC				1
GATTCCTGGTTCACGCT		GGAAGGAGATCCG				3
Vvi-MIR162	chr17	+	4714759		4716673	
CGTACGGCAATGGTGACCCTTCAGATTCCTGGTTCACGCTGTT	.....	TTTCTTGAGCAGGTATCTGGAATCGGAAAGTTGTTTCTTGTTT				
TCAGATTCCTG		GTATCTGGAATCGGAAAGTTG				1
Vvi-MIR162	chr17	+	4714759		4715429	
CGTACGGCAATGGTGACCCTTCAGATTCCTGGTTCACGCTGTT	.....	AGTTTATTGCAGGGAAGGAGATCCGCCCTGTGTTCTTCTGTGT				
CAGATTCCTG		GGAAGGAGATCCGCCCTGTG				2
GACCTTCAGATTCCTG		GGAAGGAGATCCG				3
GTGACCTTCAGATTCCTG		GGAAGGAGATC				1
TGACCTTCAGATTCCTG		GGAAGGAGATCC				2
Vvi-MIR162	chr17	+	4714740		4715429	
AGAGAGAGAGGGAGAAAAACGTACGGCAATGGTGACCCTTCAG	.....	AGTTTATTGCAGGGAAGGAGATCCGCCCTGTGTTCTTCTGTGT				
GAAAAACGTACGGCAATG		GGAAGGAGATCC				1
CGTACGGCAATG		GGAAGGAGATCCGCCCTG				1
AGAAAAACGTACGGCAATG		GGAAGGAGATC				2
Vvi-MIR162	chr17	+	4714729		4715429	
ATAGAGAAGGGAGAGAGAGAGGGAGAAAAACGTACGGCAATGG	.....	AGTTTATTGCAGGGAAGGAGATCCGCCCTGTGTTCTTCTGTGT				
GGGAGAGAGAGAGGGAGAAAAAC		GGAAGGAGA				1
GAAAAAC		GGAAGGAGATCCGCCCTGTGTTCT				1
GAGAGGGAGAAAAAC		GGAAGGAGATCCGCC				1
AGAGAGAGGGAGAAAAAC		GGAAGGAGATCC				1
GAGAGAGGGAGAAAAAC		GGAAGGAGATCCG				1
GAGAGAGGGAGAAAAAC		GGAAGGAGATC				1

Vvi-MIR168 chr2 - 16750027 16748197  
 ATGTGATGATGAAAGACTACTTCGATCTCAGGTTTCTAGGTTG ..... GCTTGTTTTTCAGGTGCGGGGGCTCAACAAATTTGTTGCAGGGC  
 GAAAGACTACTTCGATCTCAG GTGCGGGGG 2

Vvi-MIR168 chr2 - 16750019 16748197  
 ATGAAAGACTACTTCGATCTCAGGTTTCTAGGTTGAAAAATT ..... GCTTGTTTTTCAGGTGCGGGGGCTCAACAAATTTGTTGCAGGGC  
 CTTCGATCTCAGGTTTCTAG GTGCGGGGGC 5  
 GTTTCTAG GTGCGGGGGCTCAACAAATTTG 3  
 CTA CTACTTCGATCTCAGGTTTCTAG GTGCGGG 4  
 ATCTCAGGTTTCTAG GTGCGGGGGCTCAAC 1  
 GATCTCAGGTTTCTAG GTGCGGGGGCTCAACA 2  
 AGGTTTCTAG GTGCGGGGGCTCAACAAATT 3

Vvi-MIR168 chr2 - 16748088 16747680  
 TCAACCCTAACAATTATTGTCACATGCCAGGTTTCTTGGTAA ..... TTTATTCTGTAGATCATTGTCATGATTGGCCCATTCCTCCTCTCT  
 CATGCCAG ATCATTGTCATGATTGGCCCAT 1

Vvi-MIR394B chr18 - 1385724 1385362  
 CTCTCTCGTCTTCCACTCTAGAGCATCAAGGTGAAAACCCCA ..... CTTGTGTTGCAGGGGTTTCATCAACTCCTCCTCTTTGCCTCTT  
 CTAGAGCATCAAG GGGTTTCATCAACTCCT 1  
 TCTTCCACTCTAGAGCATCAAG GGGTTTCATC 1  
 GAGCATCAAG GGGTTTCATCAACTCCTCCT 2  
 TCCACTCTAGAGCATCAAG GGGTTTCATCA 1  
 CATCAAG GGGTTTCATCAACTCCTCCTCTT 2  
 TTCCACTCTAGAGCATCAAG GGGTTTCATC 5  
 AGAGCATCAAG GGGTTTCATCAACTCCTCC 3