

**miRNAs in the alga *Chlamydomonas reinhardtii* are not phylogenetically conserved and play a limited role in responses to nutrient deprivation**

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Supplemental Figure 1: miRNA clusters for all conditions examined

miRNAs identified in TAP only :

Table with columns: miRNA, chromosome, start, end, condition, and conservation scores. miR-18 is highlighted in red.

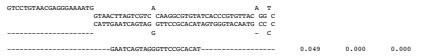


Table of miRNA clusters for miR-18, including genomic coordinates and conservation scores.

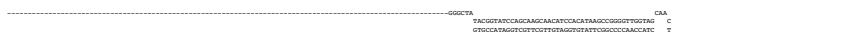


Table of miRNA clusters for miR-136, including genomic coordinates and conservation scores.

Table of miRNA clusters for miR-134, including genomic coordinates and conservation scores.

Table of miRNA clusters for miR-134, including genomic coordinates and conservation scores.









Sequence alignment table with 4 columns: sequence, 0.097, 0.203, 0.151. Includes sequences like ATTCGAAAATTGACAGGG and ATTCGAAAATTGACAGG.

miR181a miR\_1120 chromosome\_16 table. 4 columns: sequence, 0.049, 0.114, 0.075. Includes sequences like GATTCGAGGAGGAGAGGAGAGG and GATTCGAGGAGGAGAGGAGAGG.

miR181a identified in HSN only table. 4 columns: sequence, 0.129, 2.538, 0.904. Includes sequences like TGGAGACTACAGAGGAGGAGG and TGGAGACTACAGAGGAGGAGG.

miR181a miR\_11 chromosome\_3 table. 4 columns: sequence, 0.049, 0.038, 0.038. Includes sequences like TCAACCTCTCCGAGAGGAGG and TCAACCTCTCCGAGAGGAGG.

miR181a miR\_11 table. 4 columns: sequence, 0.466, 0.189, 0.478. Includes sequences like AGGCTATCGGACTGATTTAT and AGGCTATCGGACTGATTTAT.

Genomic coordinates and sequence alignments for chr16:34762. Includes sequence reads and their corresponding quality scores.

Genomic coordinates and sequence alignments for chr16:241546. Includes sequence reads and their corresponding quality scores.

Genomic coordinates and sequence alignments for chr16:241546 (continued). Includes sequence reads and their corresponding quality scores.

Genomic coordinates and sequence alignments for chr16:241546 (continued). Includes sequence reads and their corresponding quality scores.



-----CCTATGCTTCGCCCCGGT----- 0.874 0.114 0.753

mir181 chr19 chromosome\_9 Start: 194647 End: 194808 Condition: BFBH
-----AGATATATGAGGCGTATAC----- 0.000 0.014 0.838

-----TCCATGCGGATCAGTCACAT----- 2.914 1.289 0.828

mir181 chr127 chromosome\_7 Start: 1922440 End: 1923085 Condition: BFBH
-----TACTATTGAACCTGAGCCTCA----- 324.327 697.104 443.760 mir\_127
-----TACTATTGAACCTGAGCCTCA----- 0.097 0.303 0.113

-----TACTATTGAACCTGAGCCTCA----- 2.186 3.561 1.995

mir181 chr18 chromosome\_15 Start: 109972 End: 110410 Condition: BFBH
-----CAGACAGCTCCAGGCAATTC----- 247.455 35.286 91.868 mir\_1181\*
-----CAGACAGCTCCAGGCAATTC----- 0.000 0.075 0.875

-----TATGAGATATGAGGCGTATAC----- 0.000 0.014 0.838





miRSeq mir\_138, mir\_1116 chromosome\_15 Start: 199972 End: 119418 Condition: HS-H

Sequence	0.000	0.038	0.038
.....TGGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	16.445	0.758	11.044
.....GCGTCAC-AGCGGGG.....TG.....	0.097	0.038	0.038
.....GGGTCAC-AGCGGGG.....T.....	0.709	0.245	1.205
.....GGGTCAC-AGCGGGG.....T.....	0.097	0.038	0.038
.....GCGTCAC-AGCGGGG.....T.....	0.649	0.114	0.113
.....GCGTCAC-AGCGGGG.....T.....	0.649	0.075	0.075

miRSeq mir\_138, mir\_1116 scaffold\_21 Start: 47228 End: 47408 Condition: HS-H

Sequence	0.000	0.076	0.075
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.076<td>0.075</td></td>	0.076 <td>0.075</td>	0.075
.....GGGTCAC-AGCGGGG.....TG.....	1.457 <td>0.189<td>0.189</td></td>	0.189 <td>0.189</td>	0.189
.....GGGTCAC-AGCGGGG.....TG.....	0.294 <td>0.076<td>0.113</td></td>	0.076 <td>0.113</td>	0.113
.....GGGTCAC-AGCGGGG.....TG.....	2.477 <td>0.265</td> <td>0.527</td>	0.265	0.527
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.076<td>0.075</td></td>	0.076 <td>0.075</td>	0.075
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.076<td>0.075</td></td>	0.076 <td>0.075</td>	0.075
.....GGGTCAC-AGCGGGG.....TG.....	0.437 <td>0.076<td>0.038</td></td>	0.076 <td>0.038</td>	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.260 <td>0.038</td> <td>0.075</td>	0.038	0.075
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.076<td>0.038</td></td>	0.076 <td>0.038</td>	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.464 <td>0.071</td> <td>0.489</td>	0.071	0.489
.....GGGTCAC-AGCGGGG.....TG.....	0.049 <td>0.075</td> <td>0.075</td>	0.075	0.075
.....GGGTCAC-AGCGGGG.....TG.....	1.748 <td>0.114<td>0.189</td></td>	0.114 <td>0.189</td>	0.189
.....GGGTCAC-AGCGGGG.....TG.....	0.009 <td>1.446</td> <td>1.242</td>	1.446	1.242
.....GGGTCAC-AGCGGGG.....TG.....	0.049 <td>0.038</td> <td>0.038</td>	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.243 <td>0.265</td> <td>0.151</td>	0.265	0.151
.....GGGTCAC-AGCGGGG.....TG.....	25.451	48.040	34.074
.....GGGTCAC-AGCGGGG.....TG.....	1.566	0.417	0.339
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.038</td> <td>0.038</td>	0.038	0.038

miRSeq mir\_118 scaffold\_21 Start: 47228 End: 47408 Condition: HS-H

Sequence	0.000	0.113	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.113<td>0.113</td></td>	0.113 <td>0.113</td>	0.113
.....GGGTCAC-AGCGGGG.....TG.....	1.700	0.417	2.108
.....GGGTCAC-AGCGGGG.....TG.....	0.194	0.264	0.244
.....GGGTCAC-AGCGGGG.....TG.....	0.389	0.038	0.241
.....GGGTCAC-AGCGGGG.....TG.....	14.842	5.531	11.220
.....GGGTCAC-AGCGGGG.....TG.....	5.137	0.009	11.549
.....GGGTCAC-AGCGGGG.....TG.....	0.000 <td>0.113<td>0.113</td></td>	0.113 <td>0.113</td>	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.194	0.548	1.130
.....GGGTCAC-AGCGGGG.....TG.....	28.518	10.457	190.114
.....GGGTCAC-AGCGGGG.....TG.....	0.243	0.076	0.652
.....GGGTCAC-AGCGGGG.....TG.....	1.311	0.758	5.535
.....GGGTCAC-AGCGGGG.....TG.....	4.464	14.113	11.512
.....GGGTCAC-AGCGGGG.....TG.....	87.416	33.404	390.175
.....GGGTCAC-AGCGGGG.....TG.....	29.421	12.839	80.862
.....GGGTCAC-AGCGGGG.....TG.....	4.917	1.985	55.761
.....GGGTCAC-AGCGGGG.....TG.....	0.291	0.379	0.863
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.114	0.408
.....GGGTCAC-AGCGGGG.....TG.....	262.511	94.913	371.451
.....GGGTCAC-AGCGGGG.....TG.....	0.049	0.152	0.791
.....GGGTCAC-AGCGGGG.....TG.....	0.097	0.188	0.188
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.075	0.075
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.076	0.226
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.049	0.440	0.640
.....GGGTCAC-AGCGGGG.....TG.....	0.194	0.227	0.294
.....GGGTCAC-AGCGGGG.....TG.....	0.389	0.303	3.577
.....GGGTCAC-AGCGGGG.....TG.....	4.323	2.993	4.929
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	4.711	2.155	3.640
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.076	1.355
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.389	0.341	1.167
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.076	1.770
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.264	0.244
.....GGGTCAC-AGCGGGG.....TG.....	0.049	0.565	0.565

miRSeq identified in HS-H Only:

miRSeq mir\_111 chromosome\_6 Start: 654237 End: 654272 Condition: HS-H

Sequence	0.777	0.076	0.301
.....GGGTCAC-AGCGGGG.....TG.....	0.777	0.076	0.301
.....GGGTCAC-AGCGGGG.....TG.....	1.457	0.033	0.188
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.097	0.114	0.114
.....GGGTCAC-AGCGGGG.....TG.....	0.243	0.152	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.076	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.097	0.076	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.826	0.417	0.377
.....GGGTCAC-AGCGGGG.....TG.....	3.446	0.379	4.929
.....GGGTCAC-AGCGGGG.....TG.....	0.340	0.417	0.828
.....GGGTCAC-AGCGGGG.....TG.....	0.049	0.227	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.631	0.976	0.226
.....GGGTCAC-AGCGGGG.....TG.....	0.314	14.662	15.663
.....GGGTCAC-AGCGGGG.....TG.....	0.680	1.819	0.864
.....GGGTCAC-AGCGGGG.....TG.....	0.340	0.303	0.151
.....GGGTCAC-AGCGGGG.....TG.....	79.943	26.448	26.017
.....GGGTCAC-AGCGGGG.....TG.....	39.729	36.787	85.882
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	2.477	3.637	0.828
.....GGGTCAC-AGCGGGG.....TG.....	71.076	127.411	164.149
.....GGGTCAC-AGCGGGG.....TG.....	122.663	21.785	20.934
.....GGGTCAC-AGCGGGG.....TG.....	0.389	0.076	0.189
.....GGGTCAC-AGCGGGG.....TG.....	31.132	3.410	7.944
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.109	0.189
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.076	0.076
.....GGGTCAC-AGCGGGG.....TG.....	2.326	0.038	0.244
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.194	0.241	0.244
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.114	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.114	0.113
.....GGGTCAC-AGCGGGG.....TG.....	10.296	1.137	2.033
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.076	0.038
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.189	0.075
.....GGGTCAC-AGCGGGG.....TG.....	0.146	0.076	0.076
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.226
.....GGGTCAC-AGCGGGG.....TG.....	0.243	0.038	0.113
.....GGGTCAC-AGCGGGG.....TG.....	1.198	3.978	4.130
.....GGGTCAC-AGCGGGG.....TG.....	0.097	0.076	0.244
.....GGGTCAC-AGCGGGG.....TG.....	1.453	5.180	4.939
.....GGGTCAC-AGCGGGG.....TG.....	25.838	7.501	11.295
.....GGGTCAC-AGCGGGG.....TG.....	81.708	21.934	35.450
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.076	0.226
.....GGGTCAC-AGCGGGG.....TG.....	0.631	0.076	0.038
.....GGGTCAC-AGCGGGG.....TG.....	4.857	0.133	1.958
.....GGGTCAC-AGCGGGG.....TG.....	5.783	0.227	1.989
.....GGGTCAC-AGCGGGG.....TG.....	2.040	0.985	1.954
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.379	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.226
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.152	0.113
.....GGGTCAC-AGCGGGG.....TG.....	0.000	0.038	0.038
.....GGGTCAC-AGCGGGG.....TG.....	15.882	14.965	8.321

















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-----CCTAGACTCTTGAGACGTT-----CCTAGACTCTTGAGACGTT-----0.146 0.152 0.452
-----GGGCGGCGGCGGCGGCGT-----GGGCGGCGGCGGCGGCGT-----0.097 0.076 0.076
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----CACGGCGGCGGCGGCGGCGT-----CACGGCGGCGGCGGCGGCGT-----0.777 0.455 0.941
-----GCGGGCGGCGGCGGCGGCGT-----GCGGGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.631 0.076 0.151
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.049 0.038 0.038
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.090 0.038 0.113
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.049 0.076 0.076
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.068 0.114 0.151
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.340 1.226 1.183
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.146 0.114 0.114
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.146 0.068 0.715
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.146 0.038 0.113
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----0.729 1.328 4.064
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----34.378 159.540 192.107 mir_1103
-----CGGGCGGCGGCGGCGGCGT-----CGGGCGGCGGCGGCGGCGT-----26.181 28.263 29.181
-----GGGCGGCGGCGGCGGCGGCGT-----GGGCGGCGGCGGCGGCGGCGT-----0.680 1.743 1.054
-----GGGCGGCGGCGGCGGCGGCGT-----GGGCGGCGGCGGCGGCGGCGT-----0.243 0.038 0.038
-----GGGCGGCGGCGGCGGCGGCGT-----GGGCGGCGGCGGCGGCGGCGT-----0.146 0.038 0.038
-----AGGCGGCGGCGGCGGCGGCGT-----AGGCGGCGGCGGCGGCGGCGT-----0.049 0.038 0.038

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mir_1106 chrX:991164-991170:454641-4546397 Condition: HS-B
-----GTTGCGGCGGCGGCGGCGT-----10.199 32.317 32.719
-----GTTGCGGCGGCGGCGGCGT-----1.194 0.076 0.864
-----GTTGCGGCGGCGGCGGCGT-----0.629 0.114 0.038
-----GTTGCGGCGGCGGCGGCGT-----0.729 0.227 0.151
-----GTTGCGGCGGCGGCGGCGT-----19.016 3.940 2.078
-----GTTGCGGCGGCGGCGGCGT-----10.879 22.504 19.503
-----GTTGCGGCGGCGGCGGCGT-----1.211 0.023 0.755
-----GTTGCGGCGGCGGCGGCGT-----0.597 0.114 0.114
-----GTTGCGGCGGCGGCGGCGT-----0.263 0.076 0.228
-----GTTGCGGCGGCGGCGGCGT-----0.597 0.038 0.038
-----GTTGCGGCGGCGGCGGCGT-----0.309 0.379 0.028
-----GTTGCGGCGGCGGCGGCGT-----0.049 0.114 0.038
-----GTTGCGGCGGCGGCGGCGT-----1.748 0.379 0.791
-----GTTGCGGCGGCGGCGGCGT-----0.049 0.076 0.076
-----GTTGCGGCGGCGGCGGCGT-----1.506 0.241 4.452
-----GTTGCGGCGGCGGCGGCGT-----2.040 3.940 4.431
-----GTTGCGGCGGCGGCGGCGT-----1.051 0.265 0.715
-----GTTGCGGCGGCGGCGGCGT-----0.049 0.038 0.075
-----GTTGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----GTTGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----GTTGCGGCGGCGGCGGCGT-----1.117 0.303 0.284
-----GTTGCGGCGGCGGCGGCGT-----0.049 0.303 0.284
-----GTTGCGGCGGCGGCGGCGT-----0.923 0.038 0.038
-----GTTGCGGCGGCGGCGGCGT-----0.000 0.076 0.038
-----GTTGCGGCGGCGGCGGCGT-----0.000 0.303 0.303
-----GTTGCGGCGGCGGCGGCGT-----0.000 0.152 0.152
-----GTTGCGGCGGCGGCGGCGT-----12.045 0.138 3.078
-----GTTGCGGCGGCGGCGGCGT-----0.184 0.114 0.075
-----GTTGCGGCGGCGGCGGCGT-----0.729 0.076 0.076

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C TGA A CCAAGATGCGACCTAC CTACAGTCGGAGATGACGACGCTCC ACCCTGTCGCGA GTCCTCCATCTGATGGGCGCCGCGCCGCGAC C CGCC CACCTCAGCAGAGTTCC A CACCTCTCTCTTGGTGGCC G TAA

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-----CCTAGACTCTTGAGACGTT-----0.000 0.038 0.038
-----GGTACGCTGCTTGAGAGTCTCT-----10.025 24.097 21.095 mir_1106
-----AGTGTCTCTGAGAGTCTCT-----26.081 3.713 2.523
-----GATGCTGCTTGAGAGTCTCT-----10.291 0.720 0.301
-----GATGCTGCTTGAGAGTCTCT-----10.529 2.740 2.456
-----GATGCTGCTTGAGAGTCTCT-----2.866 8.297 4.807
-----GATGCTGCTTGAGAGTCTCT-----0.000 0.038 0.038
-----GATGCTGCTTGAGAGTCTCT-----1.506 0.530 0.828
-----GATGCTGCTTGAGAGTCTCT-----0.486 0.038 0.038
-----GATGCTGCTTGAGAGTCTCT-----0.486 0.038 0.038
-----GATGCTGCTTGAGAGTCTCT-----0.486 0.038 0.038
-----GATGCTGCTTGAGAGTCTCT-----23.147 0.549 1.629
-----GATGCTGCTTGAGAGTCTCT-----199.984 8.797 6.965
-----GATGCTGCTTGAGAGTCTCT-----0.680 3.402 1.393
-----GATGCTGCTTGAGAGTCTCT-----0.680 0.189 0.189
-----GATGCTGCTTGAGAGTCTCT-----0.146 0.076 0.151
-----GATGCTGCTTGAGAGTCTCT-----0.000 0.114 0.114
-----GATGCTGCTTGAGAGTCTCT-----0.000 0.076 0.076
-----GATGCTGCTTGAGAGTCTCT-----0.000 0.114 0.114
-----CGGCGGCGGCGGCGGCGGCGT-----0.800 0.076 0.440
-----CGGCGGCGGCGGCGGCGGCGT-----0.751 0.114 0.038
-----ATATCTGCTCTTGAGAGTCTCT-----0.000 0.152 0.152
-----ATATCTGCTCTTGAGAGTCTCT-----1.051 0.411 0.339
-----CGAGCGCTACTATCTCTCTCT-----0.971 0.303 0.113
-----GATGCTGCTTGAGAGTCTCT-----0.194 0.076 0.038
-----GATGCTGCTTGAGAGTCTCT-----0.289 0.038 0.038
-----GATGCTGCTTGAGAGTCTCT-----1.844 0.114 0.113
-----GATGCTGCTTGAGAGTCTCT-----1.651 0.152 0.602
-----GATGCTGCTTGAGAGTCTCT-----3.091 1.819 1.206
-----GATGCTGCTTGAGAGTCTCT-----0.049 0.265 0.265
-----GATGCTGCTTGAGAGTCTCT-----0.000 0.038 0.038
-----GATGCTGCTTGAGAGTCTCT-----7.188 1.478 1.286

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mir_1119 chrX:991164-991170:454641-4546397 Condition: HS-B
-----TPTGAGAG-----ACCTFPAAGCGG-----0.826 0.833 0.904
-----TPTGAGAG-----ACCTFPAAGCGG-----0.129 1.124 1.083
-----TPTGAGAG-----ACCTFPAAGCGG-----1.894 5.797 2.614
-----TPTGAGAG-----ACCTFPAAGCGG-----0.437 0.076 0.076
-----TPTGAGAG-----ACCTFPAAGCGG-----0.049 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.076 0.076
-----TPTGAGAG-----ACCTFPAAGCGG-----3.203 1.623 1.242
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.152 0.152
-----TPTGAGAG-----ACCTFPAAGCGG-----1.117 0.227 0.113
-----TPTGAGAG-----ACCTFPAAGCGG-----0.049 0.241 0.241
-----TPTGAGAG-----ACCTFPAAGCGG-----0.097 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.114 0.228
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----2.671 2.311 0.246
-----TPTGAGAG-----ACCTFPAAGCGG-----0.146 1.127 0.565
-----TPTGAGAG-----ACCTFPAAGCGG-----1.514 0.379 0.379 mir_1119
-----TPTGAGAG-----ACCTFPAAGCGG-----51.482 46.197 64.400
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----0.449 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----1.263 0.038 0.038
-----TPTGAGAG-----ACCTFPAAGCGG-----0.000 0.076 0.209
-----TPTGAGAG-----ACCTFPAAGCGG-----4.460 4.433 7.116

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-----CA GCGGCGGCGGCGGCGGCGT-----0.000 0.076 0.038
-----GATGCTGCTTGAGAGTCTCT-----0.923 0.379 0.075
-----GATGCTGCTTGAGAGTCTCT-----0.340 0.114 0.038

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mir_1121 chrX:991164-991170:454641-4546397 Condition: HS-B
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----TCCGCGGCGGCGGCGGCGT-----0.097 0.076 0.075
-----TCCGCGGCGGCGGCGGCGT-----0.049 0.141 0.241
-----TCCGCGGCGGCGGCGGCGT-----0.291 0.227 0.151
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.038 0.038
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.038 0.113
-----TCCGCGGCGGCGGCGGCGT-----0.146 0.076 0.075
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.114 0.114
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.076 0.075
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.114 0.114
-----TCCGCGGCGGCGGCGGCGT-----0.049 0.076 0.113
-----TCCGCGGCGGCGGCGGCGT-----0.000 0.303 0.492

```











Sequence	0.049	2.008	0.904
.....	0.144	0.388	0.451
.....	0.000	0.038	0.038
.....	0.000	0.038	0.038
.....	0.097	0.038	0.113
.....	0.583	0.341	0.452
.....	0.000	0.114	0.075
.....	31.424	11.693	25.527
.....	6.097	25.620	35.384
.....	1.700	2.841	3.500
.....	38.127	61.113	101.002
.....	0.000	0.076	0.113
.....	0.291	0.182	1.205
.....	0.000	0.530	0.414
.....	0.417	0.114	0.264
.....	0.049	0.076	0.038
.....	0.049	0.038	0.038

Sequence	0.000	0.075	0.075
.....	0.194	0.181	0.194
.....	0.583	0.493	0.151
.....	0.146	0.076	0.038
.....	2.186	0.985	1.205
.....	0.000	0.038	0.038
.....	4.420	1.212	0.391
.....	0.000	0.227	0.075
.....	0.431	0.038	0.038
.....	2.224	0.227	0.339
.....	434.108	221.211	264.016
.....	0.194	0.189	0.038
.....	11.414	2.965	1.958
.....	1.048	0.189	0.188
.....	0.291	0.075	0.075
.....	6.071	3.031	4.593
.....	0.000	0.075	0.075

Sequence	0.000	0.076	0.038
.....	0.097	0.303	0.103
.....	2.803	1.056	1.144
.....	0.144	0.455	0.455
.....	0.097	0.152	0.492
.....	0.000	0.038	0.038
.....	1.748	0.831	0.038
.....	0.000	0.038	0.264
.....	0.000	0.076	0.076
.....	0.000	0.038	0.038
.....	11.016	0.682	2.071
.....	0.000	0.038	0.038
.....	1.556	0.227	0.226
.....	0.000	0.038	0.038
.....	0.243	0.602	1.200
.....	0.097	0.114	0.151
.....	0.000	0.038	0.113
.....	0.389	0.152	0.038

Sequence	0.000	0.038	0.038
.....	0.488	0.038	0.188
.....	0.291	0.076	0.038
.....	0.194	0.076	0.076
.....	0.049	0.038	0.038
.....	0.291	0.038	0.391
.....	0.631	0.114	0.114
.....	0.049	0.076	0.076
.....	0.000	0.038	0.038
.....	0.049	0.038	0.038
.....	21.807	211.070	125.415
.....	5.956	5.721	2.184
.....	0.097	0.076	0.076
.....	1.291	1.705	1.147
.....	0.000	0.038	0.038
.....	0.097	0.038	0.188

Sequence	0.000	0.038	0.038
.....	0.049	0.076	0.151
.....	1.146	1.591	1.109
.....	0.389	0.265	0.151
.....	0.000	0.038	0.038
.....	1.748	0.833	0.038
.....	0.000	0.038	0.038
.....	0.000	0.038	0.038

Sequence	0.049	0.493	0.377
.....	0.729	1.623	0.188
.....	4.211	48.115	21.373
.....	0.000	0.075	0.075

Sequence	0.000	0.038	0.038
.....	0.291	0.114	0.075
.....	0.000	0.038	0.038
.....	0.000	0.038	0.038
.....	0.146	0.114	0.692

Sequence	0.000	0.132	0.113
.....	0.000	0.241	0.341
.....	0.000	0.241	0.341
.....	0.000	0.076	0.076
.....	0.000	0.871	0.871
.....	0.049	0.038	0.038
.....	0.049	1.932	0.075
.....	0.000	1.553	0.261
.....	0.000	0.152	0.152
.....	0.000	0.038	0.038
.....	0.000	0.265	0.151
.....	0.000	3.940	3.940
.....	0.000	0.038	0.038
.....	0.114	0.114	0.114
.....	12.725	27.940	2.765
.....	0.189	0.189	0.189
.....	0.146	0.417	0.075
.....	0.000	0.189	0.189
.....	0.000	0.152	0.152
.....	0.000	0.114	0.114
.....	0.097	0.245	0.452
.....	0.265	0.265	0.265
.....	0.049	0.265	0.265
.....	0.000	0.568	0.568
.....	1.797	34.416	0.753
.....	0.000	0.038	0.038
.....	0.000	0.530	0.530
.....	0.000	0.038	0.038
.....	0.000	0.076	0.076
.....	0.049	0.038	0.038
.....	0.000	0.189	0.189
.....	1.991	5.493	0.828
.....	0.049	0.038	0.075
.....	0.000	0.114	0.114
.....	0.000	0.038	0.038
.....	0.000	0.038	0.038
.....	0.243	0.243	0.113
.....	1.603	13.828	1.205
.....	0.097	0.466	0.038
.....	5.440	51.222	16.077
.....	0.000	0.758	0.758
.....	0.000	0.379	0.113
.....	0.000	0.038	0.038



Table with multiple columns showing sequence motifs and associated numerical values. Motifs include 'CGAAGGCCTG', 'GGAACACCTG', and various combinations of 'GAG', 'GAA', 'GAC'. Values range from 0.000 to 3.203. Some rows are marked with 'mir\_133'.

Table with 5 columns: 'MIRNA mir\_133\_mir\_196 chromosome\_17 Start: 1972737 End: 1972997 Condition: HSFF'. Lists motifs like 'GAGAGGCCTG', 'GGAACACCTG', and 'GGAAGGCCTG' with corresponding values.

Table with 5 columns: 'mir\_133\_mir\_196 chromosome\_17 Start: 1972737 End: 1972997 Condition: HSFF'. Lists motifs like 'GAGAGGCCTG', 'GGAACACCTG', and 'GGAAGGCCTG' with corresponding values.

Table with 5 columns: 'MIRNA mir\_137\_mir\_139 chromosome\_10 Start: 6282575 End: 6282576 Condition: HSFF'. Lists motifs like 'GAGAGGCCTG', 'GGAACACCTG', and 'GGAAGGCCTG' with corresponding values.

Table with 5 columns: 'MIRNA mir\_137\_mir\_139 chromosome\_10 Start: 6282575 End: 6282576 Condition: HSFF'. Lists motifs like 'GAGAGGCCTG', 'GGAACACCTG', and 'GGAAGGCCTG' with corresponding values.









Table with 4 columns: sequence, score, and two other numerical values. It is divided into sections for miR-193 and miR-194, each showing sequence alignments and associated scores.

Table with 4 columns: sequence, score, and two other numerical values. It is divided into sections for miR-198 and miR-199, each showing sequence alignments and associated scores.

Table with 4 columns: sequence, score, and two other numerical values. It is divided into sections for miR-199 and miR-200, each showing sequence alignments and associated scores.

Table with 4 columns: sequence, score, and two other numerical values. It is divided into sections for miR-200 and miR-201, each showing sequence alignments and associated scores.







-----TGGAGCGCGATGATGAGAG----- 2.283 7.274 4.593  
 -----TGGAGCGCGATGATGAGAG----- 0.243 1.174 0.688  
 -----TGGAGCGCGATGATGAGAG----- 0.341 0.301 0.301  
 -----TGGAGCGCGATGATGAGAG----- 2.730 11.025 1.619  
 -----TGGAGCGCGATGATGAGAG----- 0.097 0.189 0.618  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.075 0.075  
 -----TGGAGCGCGATGATGAGAG----- 0.097 0.227 0.264  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.038 0.038  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.075 0.075  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.038 0.038  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.114 0.188  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.227 0.226  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.038 0.038  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.114 0.188  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.038 0.151  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.103 0.224  
 -----TGGAGCGCGATGATGAGAG----- 0.146 0.227 0.038  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.144 0.452  
 -----TGGAGCGCGATGATGAGAG----- 0.097 1.478 1.883  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.144 0.188  
 -----TGGAGCGCGATGATGAGAG----- 0.049 0.038 0.038  
 -----TGGAGCGCGATGATGAGAG----- 0.146 0.227 0.440  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.417 0.753  
 -----TGGAGCGCGATGATGAGAG----- 0.049 0.644 0.688  
 -----TGGAGCGCGATGATGAGAG----- 0.184 1.094 2.372  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.038 0.075  
 -----TGGAGCGCGATGATGAGAG----- 0.049 1.440 2.749  
 -----TGGAGCGCGATGATGAGAG----- 0.146 0.682 0.188  
 -----TGGAGCGCGATGATGAGAG----- 0.000 0.492 0.866

TGAGACCTTGGGCGTGAAGACTTGGCGGCACATGAG G C G C ACCGTGGAGCGCGATGAGATGAT T GA TG  
 AT AGAG TTGGCGGCGTGAAGCGGAG GAGCGCGATGAGATGAGAG TTGGCGGCGTGAAGACTG AGAGCTTGGCGGCGTGAAGCA A AGCT C  
 TG TGTTC AACGGCGGCGCTTCTGGCTTT TGGCGGCTACTACTACTG AACGGCGGCGTGAAGCA TTGGAGACCGGCGGACTTCTCT T TGAG /  
 ---AGG G T A T C AC AG GC

-----GCTTCTTACCGCGGACTT----- 0.000 0.038 0.038  
 -----GCTTCTTACCGCGGACTT----- 11.456 1.174 1.995  
 -----GCTTCTTACCGCGGACTT----- 6.145 0.796 1.242  
 -----GCTTCTTACCGCGGACTT----- 0.129 0.038 0.075  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.075 0.075  
 -----GCTTCTTACCGCGGACTT----- 0.049 0.038 0.188  
 -----GCTTCTTACCGCGGACTT----- 0.194 0.076 0.151  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.075 0.075  
 -----GCTTCTTACCGCGGACTT----- 0.486 1.099 0.226  
 -----GCTTCTTACCGCGGACTT----- 0.097 0.038 0.038  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.114 0.075  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.076 0.075  
 -----GCTTCTTACCGCGGACTT----- 0.243 0.038 0.151  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.038 0.038  
 -----GCTTCTTACCGCGGACTT----- 1.166 0.985 0.462  
 -----GCTTCTTACCGCGGACTT----- 0.971 0.833 0.602  
 -----GCTTCTTACCGCGGACTT----- 35.358 15.079 152.900  
 -----GCTTCTTACCGCGGACTT----- 0.074 2.084 1.732  
 -----GCTTCTTACCGCGGACTT----- 0.437 0.189 0.462  
 -----GCTTCTTACCGCGGACTT----- 0.289 0.406 0.319  
 -----GCTTCTTACCGCGGACTT----- 0.097 0.038 0.038  
 -----GCTTCTTACCGCGGACTT----- 0.097 0.189 0.151  
 -----GCTTCTTACCGCGGACTT----- 2.234 0.227 0.188  
 -----GCTTCTTACCGCGGACTT----- 0.486 0.152 0.113  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.075 0.075  
 -----GCTTCTTACCGCGGACTT----- 11.456 1.174 1.995  
 -----GCTTCTTACCGCGGACTT----- 6.145 0.796 1.242  
 -----GCTTCTTACCGCGGACTT----- 0.729 0.638 0.075  
 -----GCTTCTTACCGCGGACTT----- 96.242 4.979 12.462  
 -----GCTTCTTACCGCGGACTT----- 0.074 0.076 0.113  
 -----GCTTCTTACCGCGGACTT----- 0.486 0.152 0.075  
 -----GCTTCTTACCGCGGACTT----- 2.180 0.265 0.075  
 -----GCTTCTTACCGCGGACTT----- 0.391 0.038 0.038  
 -----GCTTCTTACCGCGGACTT----- 0.184 0.655 0.678  
 -----GCTTCTTACCGCGGACTT----- 38.932 6.024 7.869  
 -----GCTTCTTACCGCGGACTT----- 0.146 0.038 0.075  
 -----GCTTCTTACCGCGGACTT----- 19.767 4.471 10.467  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.038 0.038

miR181 miR\_125 chromosome\_12 Start: 609837 End: 601216 Condition: BS-H

-----TGGGCACGGCTTCTGTAC----- 0.000 0.038 0.038  
 AC CAGAGCGGGTTC GA A C GATGATGGC C T CC-- A TGCGCCGGAATGCTTGCTGCTCAT T A  
 TTGGGGAGCGGCTCTTCTACTCAATGTCTA GAGGATGCTGTGCGA CCG GAGGAGTTC C GGGCT GC GAGG A  
 AACCGCTGGCGAGGACGACTTTCACATG TC-----ATGCA AAGGATGATGAGT GCG GCGATCTA C GGGCT GC GAGG A  
 -----TGGGCACGGCTTCTGTAC----- AC G G G C CATT T C

-----GAGGCTTTCACAGTTGCT----- 0.340 0.758 0.678  
 -----GAGGCTTTCACAGTTGCT----- 0.000 0.038 0.038  
 -----GAGGCTTTCACAGTTGCT----- 1.000 2.397 5.810  
 -----GAGGCTTTCACAGTTGCT----- 0.000 0.189 0.489  
 -----GAGGCTTTCACAGTTGCT----- 0.194 0.038 0.151  
 -----GAGGCTTTCACAGTTGCT----- 0.000 0.151 0.151  
 -----GAGGCTTTCACAGTTGCT----- 1.311 1.705 2.786  
 -----GAGGCTTTCACAGTTGCT----- 0.184 0.230 0.115  
 -----GAGGCTTTCACAGTTGCT----- 0.000 0.038 0.038  
 -----GAGGCTTTCACAGTTGCT----- 2.331 7.312 4.518  
 -----GAGGCTTTCACAGTTGCT----- 0.049 0.038 0.038  
 -----GAGGCTTTCACAGTTGCT----- 31.104 91.448 93.227 miR\_125  
 -----GAGGCTTTCACAGTTGCT----- 0.923 1.264 0.866

miR181 miR\_127 chromosome\_5 Start: 2264251 End: 2264412 Condition: BS-H

-----TTAAAGAGTGGGGCGGAAA----- 0.000 0.075 0.075  
 -----TTAAAGAGTGGGGCGGAAA----- 0.097 0.113 0.113  
 -----TTAAAGAGTGGGGCGGAAA----- 0.000 0.038 0.038  
 -----TTAAAGAGTGGGGCGGAAA----- 0.194 0.038 0.151  
 -----TTAAAGAGTGGGGCGGAAA----- 0.049 0.038 0.188  
 -----TTAAAGAGTGGGGCGGAAA----- 0.486 0.189 0.715  
 -----TTAAAGAGTGGGGCGGAAA----- 1.993 1.993 1.993  
 -----TTAAAGAGTGGGGCGGAAA----- 26.664 25.156 34.865 miR\_127  
 -----TTAAAGAGTGGGGCGGAAA----- 1.993 1.993 1.993  
 -----TTAAAGAGTGGGGCGGAAA----- 0.000 0.075 0.075

G G A C- TGTCT  
 TCTCTTGGGTGCTGTAAACA GTGGGG TA CTTG- TGC C T  
 CAAGCACTGTTGCGAGGCTTCTT GAGCTG G T GAC AGTG G /  
 A G - AA C TTTTT  
 -----GCTTCTTACCGCGGACTT----- 0.000 0.075 0.075

miR181 identified in TAP and BS-H :

miR181 miR\_190 chromosome\_16 Start: 185984 End: 185184 Condition: TAP  
 -----TAAAGCGGCTGTTGAG----- 14.238 4.167 1.017  
 -----TAAAGCGGCTGTTGAG----- 0.097 0.000 0.000  
 -----TAAAGCGGCTGTTGAG----- 0.146 0.000 0.000  
 -----TAAAGCGGCTGTTGAG----- 0.486 0.076 0.188  
 -----TAAAGCGGCTGTTGAG----- 0.049 0.000 0.000  
 -----TAAAGCGGCTGTTGAG----- 0.049 0.000 0.000  
 -----TAAAGCGGCTGTTGAG----- 1.030 0.114 0.188  
 -----TAAAGCGGCTGTTGAG----- 0.049 0.000 0.000  
 -----TAAAGCGGCTGTTGAG----- 0.194 0.000 0.000  
 -----TAAAGCGGCTGTTGAG----- 5.093 0.985 1.242  
 -----TAAAGCGGCTGTTGAG----- 0.777 0.241 0.224  
 -----TAAAGCGGCTGTTGAG----- 1.457 0.530 0.377  
 -----TAAAGCGGCTGTTGAG----- 0.097 0.000 0.000 miR\_190  
 -----TAAAGCGGCTGTTGAG----- 0.291 0.189 0.377  
 -----TAAAGCGGCTGTTGAG----- 4.420 1.478 2.347  
 -----TAAAGCGGCTGTTGAG----- 0.049 0.075 0.075

ATS  
 AGCTGATCCAGACACATCCATCCATAGCGGGGCTGTTGAG T  
 TGCATAGCTCTCTTCTGTTAGTGTATATPCCGCCCAACATC G  
 GGG

-----ATAGTCTCTCTGTTGAG----- 0.049 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 0.097 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 11.705 2.917 1.995  
 -----ATAGTCTCTCTGTTGAG----- 30.501 4.357 8.283  
 -----ATAGTCTCTCTGTTGAG----- 102.770 98.448 186.540  
 -----ATAGTCTCTCTGTTGAG----- 0.049 0.076 0.038  
 -----ATAGTCTCTCTGTTGAG----- 0.486 0.168 0.602  
 -----ATAGTCTCTCTGTTGAG----- 0.097 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 0.049 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 44.204 42.460 57.756  
 -----ATAGTCTCTCTGTTGAG----- 0.049 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 0.289 0.400 0.800  
 -----ATAGTCTCTCTGTTGAG----- 4879.810 846.444 1013.513  
 -----ATAGTCTCTCTGTTGAG----- 0.486 0.568 0.188  
 -----ATAGTCTCTCTGTTGAG----- 817.791 703.446 1314.140 miR\_190  
 -----ATAGTCTCTCTGTTGAG----- 1537.231 334.913 189.645  
 -----ATAGTCTCTCTGTTGAG----- 2.380 1.061 0.527  
 -----ATAGTCTCTCTGTTGAG----- 6.262 5.153 4.330  
 -----ATAGTCTCTCTGTTGAG----- 0.049 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 5.245 5.001 3.189  
 -----ATAGTCTCTCTGTTGAG----- 1.748 0.152 0.152  
 -----ATAGTCTCTCTGTTGAG----- 0.049 0.000 0.000  
 -----ATAGTCTCTCTGTTGAG----- 27.546 1.888 1.581  
 -----ATAGTCTCTCTGTTGAG----- 3.594 0.152 0.478  
 -----ATAGTCTCTCTGTTGAG----- 0.146 0.114 0.114  
 -----ATAGTCTCTCTGTTGAG----- 363.784 263.120 371.007  
 -----ATAGTCTCTCTGTTGAG----- 1.166 3.599 0.075

















-----GCCTTCCGCTACTGCTCG-----	0.146	0.227	0.075
-----CPTTCCGCTACTGCTCG-----	0.146	0.038	0.110
-----CCTTCCGCTACTGCTCG-----	0.128	0.122	0.639
-----GPTTCCGCTACTGCTCG-----	5.285	0.909	1.280
-----CTTCCGCTACTGCTCG-----	4.714	0.774	3.770
-----TTCCGCTACTGCTCG-----	0.049	0.000	0.000
-----TCCGCTACTGCTCG-----	0.049	0.000	0.000
-----TCGCTACTGCTCG-----	0.049	0.000	0.000
-----TCCGCTACTGCTCG-----	0.971	0.114	0.414
-----CTCCTACTGCTCG-----	2.168	0.462	1.431
-----CTCCGCTACTGCTCG-----	413.461	144.725	116.303 mir_513
-----CTCCCCTACTGCTCG-----	133.551	1.284	1.189

MIRNA: mir_146_mir_1113 chromosome_13 Start: 2001058 End: 2001210 Condition: TAP			
-----TAATTCAGACAGCACTGAG-----	0.049	0.265	0.377
-----ACTTCAGACAGCACTGAG-----	0.049	0.141	0.452
-----ATTCAGACAGCACTGAG-----	0.194	2.193	0.753
-----TTTCAGACAGCACTGAG-----	0.049	0.114	0.114
-----TTCAGACAGCACTGAG-----	1.991	3.902	2.974
-----TTCAGACAGCACTGAG-----	16.410	50.192	16.388
-----TTTCAGACAGCACTGAG-----	0.146	0.303	0.038
-----TTCAGACAGCACTGAG-----	2.485	3.889	3.889
-----ATTCAGACAGCACTGAG-----	0.049	0.241	0.341
-----ACTTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----TTCAGACAGCACTGAG-----	0.243	1.894	0.779
-----ATTCAGACAGCACTGAG-----	0.194	1.326	1.488
-----ACTTCAGACAGCACTGAG-----	0.049	0.219	0.219
-----TTTCAGACAGCACTGAG-----	0.049	0.189	0.188
-----TTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----ATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----TTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----TTTCAGACAGCACTGAG-----	15.736	3.220	5.346
-----TTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----TTCAGACAGCACTGAG-----	0.729	0.000	0.000
-----TTCAGACAGCACTGAG-----	5.424	1.978	2.937
-----TTCAGACAGCACTGAG-----	0.140	1.440	2.673
-----TTCAGACAGCACTGAG-----	1.740	0.190	15.405
-----TTCAGACAGCACTGAG-----	0.146	0.758	0.941
-----TTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----TTCAGACAGCACTGAG-----	0.146	0.076	0.112
-----TTCAGACAGCACTGAG-----	0.194	0.038	0.038
-----TTCAGACAGCACTGAG-----	0.049	0.189	1.265
-----TTCAGACAGCACTGAG-----	0.291	0.038	0.075
-----TTCAGACAGCACTGAG-----	13.211	46.373	54.707
-----TTCAGACAGCACTGAG-----	0.146	0.114	0.038
-----TTCAGACAGCACTGAG-----	0.146	0.265	0.753

-----CGG T A A-----  
 C AATTCAGACAGCACTGAG GAGCGCGGATGAGGATGAGGATG GGGATATATAGG CT  
 G CATTTCAGACAGCACTGAG CTTCGGGCTGATCTCTCCTCCTCATC CCGCATATATAGG GA  
 T A T A  
 C T A  
 A

-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.049	0.075	0.075
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.243	0.303	0.753
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.583	0.076	0.301
-----CTCCCATATATATAGGATG-----	2.423	4.887	5.405
-----CTCCCATATATATAGGATG-----	0.194	0.000	0.000
-----CTCCCATATATATAGGATG-----	24.430	12.222	1.830
-----CTCCCATATATATAGGATG-----	8.448	4.257	3.878
-----CTCCCATATATATAGGATG-----	13.256	4.887	1.154
-----CTCCCATATATATAGGATG-----	1884.833	2599.440	3531.718 mir_146
-----CTCCCATATATATAGGATG-----	0.146	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.076	0.113	0.113
-----CTCCCATATATATAGGATG-----	0.777	0.227	0.301
-----CTCCCATATATATAGGATG-----	1.131	0.203	0.201
-----CTCCCATATATATAGGATG-----	27.781	31.673	75.282
-----CTCCCATATATATAGGATG-----	5.400	0.076	0.482
-----CTCCCATATATATAGGATG-----	0.194	0.113	0.113
-----CTCCCATATATATAGGATG-----	0.049	0.114	0.038
-----CTCCCATATATATAGGATG-----	0.194	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	1.214	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.437	0.189	0.189
-----CTCCCATATATATAGGATG-----	0.243	0.138	0.038
-----CTCCCATATATATAGGATG-----	5.000	1.448	3.727
-----CTCCCATATATATAGGATG-----	0.049	0.076	0.076
-----CTCCCATATATATAGGATG-----	0.389	0.038	0.038
-----CTCCCATATATATAGGATG-----	2.414	4.257	2.407
-----CTCCCATATATATAGGATG-----	0.923	3.296	2.523
-----CTCCCATATATATAGGATG-----	0.146	0.038	0.400
-----CTCCCATATATATAGGATG-----	0.140	1.440	4.452
-----CTCCCATATATATAGGATG-----	38.355	10.911	6.739
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	661.274	109.491	38.893 mir_1113
-----CTCCCATATATATAGGATG-----	0.049	0.076	0.076
-----CTCCCATATATATAGGATG-----	10.236	2.046	0.753
-----CTCCCATATATATAGGATG-----	0.389	0.132	0.038
-----CTCCCATATATATAGGATG-----	0.049	0.455	0.188
-----CTCCCATATATATAGGATG-----	2.088	0.076	0.904
-----CTCCCATATATATAGGATG-----	0.049	0.189	0.189
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.174	2.993	0.941
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	1.020	0.038	0.038
-----CTCCCATATATATAGGATG-----	0.049	0.038	0.038
-----CTCCCATATATATAGGATG-----	0.049	0.000	0.000
-----CTCCCATATATATAGGATG-----	0.291	0.241	0.341
-----CTCCCATATATATAGGATG-----	0.049	0.227	0.227

MIRNA: mir_146 chromosome_17 Start: 3137537 End: 3137719 Condition: TAP			
-----TTCCCTTTTCTACTGCTT-----	0.049	0.075	0.075
-----TTCCTTTTCTACTGCTT-----	0.146	0.038	0.038
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.631	1.174	1.657
-----TTCCCTTTTCTACTGCTT-----	0.049	0.076	0.076
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.049	0.227	0.227
-----TTCCCTTTTCTACTGCTT-----	0.146	0.264	0.264
-----TTCCCTTTTCTACTGCTT-----	0.486	0.417	0.414
-----TTCCCTTTTCTACTGCTT-----	0.049	0.038	0.131
-----TTCCCTTTTCTACTGCTT-----	0.194	0.038	0.113
-----TTCCCTTTTCTACTGCTT-----	0.049	0.530	1.139
-----TTCCCTTTTCTACTGCTT-----	2.914	3.940	7.130
-----TTCCCTTTTCTACTGCTT-----	0.583	0.720	0.075
-----TTCCCTTTTCTACTGCTT-----	0.194	0.203	0.264
-----TTCCCTTTTCTACTGCTT-----	0.631	0.227	0.038
-----TTCCCTTTTCTACTGCTT-----	0.289	0.201	0.201
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.777	0.227	0.377
-----TTCCCTTTTCTACTGCTT-----	0.194	0.075	0.075
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.049	0.038	0.038
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000
-----TTCCCTTTTCTACTGCTT-----	1.214	0.303	0.301
-----TTCCCTTTTCTACTGCTT-----	0.049	0.000	0.000

MIRNA: mir_146_mir_145 chromosome_11 Start: 1442246 End: 1442394 Condition: TAP			
-----TTCTTACCAAGCTTGCGGCG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.146	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.038	0.038
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.291	0.038	0.113
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.189	0.189
-----AAATTCAGACAGCACTGAG-----	0.049	0.038	0.038
-----AAATTCAGACAGCACTGAG-----	0.049	0.227	0.227
-----AAATTCAGACAGCACTGAG-----	0.146	1.212	0.489
-----AAATTCAGACAGCACTGAG-----	0.049	0.038	0.038
-----AAATTCAGACAGCACTGAG-----	0.923	0.189	0.038
-----AAATTCAGACAGCACTGAG-----	0.194	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.777	10.243	4.819
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.000	0.000
-----AAATTCAGACAGCACTGAG-----	0.049	0.076	0.075
-----AAATTCAGACAGCACTGAG-----	2.137	1.440	0.224
-----AAATTCAGACAGCACTGAG-----	0.437	0.265	0.038

-----GTTTTCAGACAGCACTGAG-----	0.049	0.000	0.000
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Table with 4 columns showing sequence motifs, counts, and values. Motifs include CTTTTCACAGTGCGAGG, TTTCACAGTGCGAGG, TTTTCACAGTGCGAGG, and TTTTCACAGTGCGAGGCT. Values range from 0.000 to 1.167.

Table with 4 columns showing motifs like TTGACAAAGTGCGAGGACT, TTTTCACAGTGCGAGGACT, and TTTTCACAGTGCGAGGACTTT. Values range from 0.000 to 5.185.

Table with 4 columns showing motifs like TTTTCACAGTGCGAGGACTTT, TTTTCACAGTGCGAGGACTTT, and TTTTCACAGTGCGAGGACTTTT. Values range from 0.000 to 5.185.

Table with 4 columns showing motifs like TTTTCACAGTGCGAGGACTTTT, TTTTCACAGTGCGAGGACTTTT, and TTTTCACAGTGCGAGGACTTTTT. Values range from 0.000 to 5.185.

Table with 4 columns showing motifs like TTTTCACAGTGCGAGGACTTTTT, TTTTCACAGTGCGAGGACTTTTT, and TTTTCACAGTGCGAGGACTTTTTT. Values range from 0.000 to 5.185.

Table with 4 columns showing motifs like TTTTCACAGTGCGAGGACTTTTTT, TTTTCACAGTGCGAGGACTTTTTT, and TTTTCACAGTGCGAGGACTTTTTTT. Values range from 0.000 to 5.185.





-----AAAGCAGCCAGAT----- 0.340 0.000 0.000  
 -----GCAAGAGCCAGAT----- 2.331 3.486 2.372  
 -----AGCAGAGCCAGAT----- 0.045 0.078 0.038  
 -----GAAAGCCAGAT----- 0.293 0.000 0.000  
 -----AATCAAGCCAGAT----- 0.045 0.000 0.000  
 -----TACGAAAGCCAGATC----- 0.194 0.038 0.038

mir381 mir\_199\_mir\_1104 chromosome\_4 Start: 310617 End: 310762 Condition: TAP  
 -----TACAGGGCGCATAGCCTC----- 0.049 0.000 0.000  
 -----TCTTACGCACTACAG----- 0.777 1.364 0.791  
 -----GCTCTTACGCACTACAG----- 0.049 0.076 0.076  
 -----CTCTCTTACGCACTACAG----- 0.146 0.000 0.000  
 -----GCTCTCTTACGCACTACAG----- 0.231 0.508 0.606  
 -----CTCTCTTACGCACTACAGCC----- 1.402 17.731 12.877  
 -----CTCTCTTACGCACTACAG----- 15.745 3.706 1.934  
 -----TCTCTTACGCACTACAG----- 1.457 0.909 0.565  
 -----TCTCTTACGCACTACAGGG----- 11.796 171.655 0.113  
 -----TCTCTTACGCACTACAG----- 454.418 303.543 142.772  
 -----TCTCTTACGCACTACAGGG----- 275.736 1042.322 407.323  
 -----GCTCTTACGCACTACAG----- 0.049 0.038 0.038  
 -----AGTCTCTTACGCACTACAG----- 0.097 0.076 0.038  
 -----AGTCTCTTACGCACTACAGGG----- 0.049 0.000 0.000  
 -----AGTCTCTTACGCACTACAG----- 0.046 0.038 0.038  
 -----AGTCTCTTACGCACTACAGGG----- 0.049 0.000 0.000  
 -----CAPTCTCTTACGCACTACAG----- 0.097 0.000 0.000  
 -----TCTCTTACGCACTACAG----- 0.146 0.152 0.075  
 -----GTTTACTACTACAG----- 0.049 0.000 0.000  
 -----TCTTACTACTACAG----- 0.049 0.000 0.000  
 -----ACTTACTACTACAG----- 0.049 0.000 0.000  
 -----CATCTTACTACTACAG----- 0.049 0.000 0.000  
 -----CATCTTACTACTACAG----- 0.340 0.038 0.527  
 -----CATCTTACTACTACAG----- 0.049 0.038 0.188  
 -----GGCAGCTTACTACTACAG----- 0.826 0.038 0.038  
 -----GGCAGCTTACTACTACAG----- 10.286 0.108 0.000  
 -----GGCAGCTTACTACTACT----- 1.020 1.174 1.544  
 -----GGCAGCTTACTACTAG----- 0.049 0.205 0.640  
 -----GGCAGCTTACTACTA----- 0.049 0.038 0.038  
 -----GGCAGCTTACTACTAG----- 49.085 23.677 34.613  
 -----GGCAGCTTACTACTACAG----- 291.020 65.202 105.046  
 -----GGCAGCTTACTACTA----- 12.746 1.932 4.744  
 -----GGCAGCTTACTACT----- 0.049 0.000 0.000  
 -----GGCAGCTTACTACTACAG----- 1833.241 4046.203 5636.241 mir\_199  
 -----GGCAGCTTACTACT----- 10.553 23.262 36.228  
 -----GGCAGCTTACTACT----- 2499.267 1009.421 1328.283  
 -----GGCAGCTTACTACTA----- 8.742 4.947 9.979  
 -----GGCAGCTTACTACTACT----- 693.893 118.354 175.340  
 -----GGCAGCTTACTACTAG----- 0.049 0.935 1.081  
 -----GGCAGCTTACTACTACTGCTC----- 0.049 0.000 0.000  
 -----GGCAGCTTACTACTACTC----- 0.049 0.038 0.038  
 -----AATGGCAGCTTACTACTACT----- 0.049 0.000 0.000

T G A C G T G  
 CGAAGGGCGCATGTATTAGTATCTCTCTCTG GAG TACAGGGCGCATGCAAGCTGCTTAT A  
 CTTTACTCTGCTAGCGTATG TAGTCAAGCAT G CTTT ATGTTCTGGCCTG CTTCACTCGATG C  
 CGAAGGC T C C A A C C

-----ACCGCTTACTCTGCTAGCT----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATG----- 0.291 0.076 0.038  
 -----TCTACTCTGCTAGCTATAT----- 1.066 0.444 0.904  
 -----GTTTACTCTGCTAGCTATGTT----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTT----- 1.408 11.797 4.062  
 -----TCTACTCTGCTAGCTATGT----- 0.671 1.124 4.419  
 -----TCTACTCTGCTAGCTATGTT----- 0.049 0.076 0.076  
 -----TCTACTCTGCTAGCTATGTT----- 48.228 111.028 87.764  
 -----TCTACTCTGCTAGCTATGTT----- 0.146 0.000 0.000  
 -----ACTCTGCTAGCTATGTTAG----- 0.146 0.227 0.151  
 -----ACTCTGCTAGCTATGTTAG----- 0.049 0.000 0.000  
 -----ACTCTGCTAGCTATGTTAG----- 9.422 16.291 10.203  
 -----ACTCTGCTAGCTATGTTAG----- 1.506 3.466 2.937  
 -----GTTACTGCTAGCTATGTTAG----- 0.049 0.000 0.000  
 -----CTGCTGCTAGCTATGTTAG----- 5.585 5.304 4.066  
 -----TCTACTCTGCTAGCTATGTTAG----- 0.049 0.000 0.000  
 -----ACTCTGCTAGCTATGTTAGCC----- 0.097 0.341 0.038  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 1.117 1.042 0.339  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.049 0.152 0.152  
 -----ACTCTGCTAGCTATGTTAGCC----- 0.146 0.458 0.351  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.097 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.291 0.455 0.264  
 -----ACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----ACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.049 0.114 0.038  
 -----ACTCTGCTAGCTATGTTAGCC----- 0.309 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.097 0.227 0.227  
 -----ACTCTGCTAGCTATGTTAGCC----- 0.088 0.728 0.715  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.194 0.151 0.151  
 -----GTTACTCTGCTAGCTATGTTAGCC----- 0.309 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 3.303 1.705 1.807  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.100 10.332 0.000  
 -----CTACTCTGCTAGCTATGTTAGCC----- 0.049 0.152 0.113  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 1.991 2.500 1.893  
 -----GTTACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----ATGCTCTGCTAGCTATGTTAGCC----- 12.045 4.187 2.274  
 -----ATGCTCTGCTAGCTATGTTAGCC----- 140.556 70.886 65.437 mir\_1104  
 -----GTTACTCTGCTAGCTATGTTAGCC----- 0.049 0.000 0.000  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 1.166 2.993 2.993  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 60.218 23.378 28.615  
 -----GTTACTCTGCTAGCTATGTTAGCC----- 0.440 32.544 28.125  
 -----ATGCTCTGCTAGCTATGTTAGCC----- 122.877 45.091 40.173  
 -----ATGCTCTGCTAGCTATGTTAGCC----- 0.340 0.000 0.000  
 -----CTACTCTGCTAGCTATGTTAGCC----- 3.108 3.523 2.221  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.585 1.991 0.852  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.971 6.205 3.351  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 334.722 166.437 144.984  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.923 0.114 0.226  
 -----TCTACTCTGCTAGCTATGTTAGCC----- 0.049 0.075 0.075  
 -----GTTACTCTGCTAGCTATGTTAGCC----- 0.486 0.152 0.377

mir381 mir\_108 chromosome\_6 Start: 304745 End: 304749 Condition: BSN  
 -----GGCTACTTACTGAGCAGAG----- 3.993 1.023 0.527  
 -----TACAGACACTGAGCAGAG----- 3.837 0.947 0.941  
 -----TACAGACACTGAGCAGAG----- 0.008 0.038 0.038

-----GC A C G C C C G T A AG  
 CTACAC GAGTGGGGGCGC GG GATAATFACTAGCAGCC CC CC CCGAGGG A  
 GAGTCT GATGGGGGCGC CG GATATGTAGATGTTGTC CC CC CCGTCCC /  
 TTTCT C C T C C A C C T

-----TGCAGTGGGTCGGCTGGCT----- 0.097 0.038 0.038  
 -----GCAGTGGGTCGGCTGGCT----- 0.205 0.174 2.050  
 -----GAGTGGGTCGGCTGGCT----- 0.000 0.113 1.113  
 -----GGCTGGGTCGGCTGGCTATG----- 1.603 0.303 0.828  
 -----GGCTGGGTCGGCTGGCTATG----- 0.486 0.016 0.075  
 -----CTGGCTGGGTCGGCTGGCTAG----- 0.194 0.227 0.188  
 -----GCTGGCTGGGTCGGCTGGCTAG----- 0.437 0.152 0.075  
 -----CTGGCTGGGTCGGCTGGCTATG----- 0.097 0.038 0.038  
 -----CTGGCTGGGTCGGCTGGCTATG----- 1.748 1.402 0.489  
 -----CTGGCTGGGTCGGCTGGCTATG----- 2.963 0.568 1.167  
 -----CTGGCTGGGTCGGCTGGCTATG----- 231.050 67.475 124.921  
 -----TCCGATTTGATGATGTT----- 0.049 0.189 0.301  
 -----TCCGATTTGATGATGTT----- 101.012 18.402 11.021  
 -----CTCCGATTTGATGATGTT----- 1497.093 7820.560 8621.621 mir\_1108  
 -----CTCCGATTTGATGATGTT----- 3.004 2.307 1.410  
 -----GCTGATTTGATGATGTT----- 3.400 1.402 1.205  
 -----GCTGATTTGATGATGTT----- 1.283 1.243 5.235  
 -----CTCCGATTTGATGATGTT----- 434.345 122.599 154.740  
 -----TCCGATTTGATGATGTTCTC----- 0.049 0.075 0.075  
 -----GTTATGTTCCCGCAGTACT----- 0.486 0.152 0.377

mir381 mir\_109 chromosome\_10 Start: 319970 End: 340011 Condition: BSN  
 -----CCGGCGCGGGAGGGCGAG----- 0.000 0.038 0.038  
 -----CCGGCGCGGGAGGGCGAG----- 0.000 0.038 0.038  
 -----CCGGCGCGGGAGGGCGAG----- 0.000 0.075 0.075  
 -----ACCGCGCGGGAGGGCGAG----- 0.194 0.076 0.904  
 -----ACCGCGCGGGAGGGCGAG----- 0.049 0.038 0.113  
 -----TACCGCGCGGGAGGGCGAG----- 25.207 16.367 27.749  
 -----TACCGCGCGGGAGGGCGAG----- 0.049 0.038 0.038  
 -----TACCGCGCGGGAGGGCGAG----- 0.049 0.075 0.075  
 -----TACCGCGCGGGAGGGCGAG----- 0.049 0.038 0.038  
 -----TACCGCGCGGGAGGGCGAG----- 0.097 0.414 0.414  
 -----TACCGCGCGGGAGGGCGAG----- 0.000 0.075 0.075  
 -----AAGAGAGCCCGTAGTT----- 0.049 0.075 0.075  
 -----AAGAGAGCCCGTAGTT----- 0.000 0.113 0.113  
 -----AAGAGAGCCCGTAGTT----- 0.179 2.448 8.597  
 -----AAGAGAGCCCGTAGTT----- 0.023 0.062 0.355  
 -----AAGAGAGCCCGTAG----- 2.137 1.539 17.422  
 -----AAGAGAGCCCGTAGTT----- 2.837 11.394 36.785  
 -----AAGAGAGCCCGTAGTT----- 0.000 0.076 0.151  
 -----AAGAGAGCCCGTAGTT----- 0.097 0.038 0.038







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-----AATGCAAGAAGCAATGGG----- 2,129 4,561 6,360
-----AAATGCAAGAAGCAATGGG----- 0,220 0,500 1,086
-----AAATGCAAGAAGCAATGGG----- 0,514 1,100 1,712
-----AAATGCAAGAAGCAATGGG----- 0,220 0,200 0,082
-----AGSCAAATGCAAGAAGGC----- 0,073 0,100 0,082
-----AGSCAAATGCAAGAAGGC----- 1,489 7,802 2,935
-----AGSCAAATGCAAGAAGGC----- 0,147 1,700 1,222
-----ACACGCGGAAGAATGCAAG----- 0,073 1,300 0,489
-----ACACGCGGAAGAATGCAAG----- 0,073 0,200 0,226
-----ACACGCGGAAGAATGCAAG----- 0,073 0,000 0,000
-----ACACGCGGAAGAATGCAAG----- 0,000 0,000 0,000
-----ACACGCGGAAGAATGCAAG----- 0,147 0,100 0,163
-----ACACGCGGAAGAATGCAAG----- 0,073 0,100 0,000
-----AGSCCTACGCAAGCAGGCA----- 0,073 0,100 0,163

          G C A      G G      G A      C T      C C      C A      T A C A A C T
          A A C A      A G      A C      C A      C G      T G      T G      G T      G G      G G      G C      G C
GDTTGTTCAC-----ATGCAGGCAATGGG-----ACAGCAGCTTCAGGCTTC-----ATGCAGGCAATGGG-----
-----AATGCAGGCAATGGG----- 0,073 0,000 0,000
-----AATGCAGGCAATGGG----- 0,147 0,300 0,326
-----AATGCAGGCAATGGG----- 0,294 0,300 0,571
-----AATGCAGGCAATGGG----- 0,073 0,100 0,163
-----AGCTTGTTCAGGCTTC----- 0,073 0,000 0,000
-----AGCTTGTTCAGGCTTC----- 0,073 0,000 0,000
-----AGCTTGTTCAGGCTTC----- 0,294 0,300 0,000
-----AGCTTGTTCAGGCTTC----- 0,073 0,000 0,000
-----AGCTTGTTCAGGCTTC----- 0,147 1,200 0,897
-----AGCTTGTTCAGGCTTC----- 0,147 0,200 0,326
-----ATACGCTTCATATAGAGCTTC----- 0,073 0,000 0,082
-----ATACGCTTCATATAGAGCTTC----- 0,073 0,100 0,000
-----ATACGCTTCATATAGAGCTTC----- 0,261 0,600 1,223
-----ATACGCTTCATATAGAGCTTC----- 0,073 0,000 0,000
-----ATACGCTTCATATAGAGCTTC----- 0,147 0,000 0,082
-----ATACGCTTCATATAGAGCTTC----- 3,204 4,001 5,463
-----ATACGCTTCATATAGAGCTTC----- 0,220 0,100 0,571
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,063 3,801 2,987
-----ATATGCTTCAGCAGCGGAG----- 0,147 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,163
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,082
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,147 0,700 0,082
-----ATATGCTTCAGCAGCGGAG----- 0,147 1,300 0,163
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,147 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,220 0,100 0,245
-----ATATGCTTCAGCAGCGGAG----- 0,073 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,147 0,000 0,000
-----ATATGCTTCAGCAGCGGAG----- 0,147 0,000 0,000

miR8 miR_1117_mir_155_mir_14 chromosome_5_start: 327762 End: 327766 Condition: Nutrient-replete
-----CCACTTCAGCAGGCTTC----- 0,073 0,000 0,000
-----CCACTTCAGCAGGCTTC----- 0,147 0,000 0,000
-----CCACTTCAGCAGGCTTC----- 0,147 0,000 0,000
-----CCACTTCAGCAGGCTTC----- 0,247 0,000 0,000
-----CCACTTCAGCAGGCTTC----- 1,939 0,200 0,489
-----CCACTTCAGCAGGCTTC----- 0,734 0,000 0,082
-----CCACTTCAGCAGGCTTC----- 1,174 0,300 1,060
-----CCACTTCAGCAGGCTTC----- 1,468 0,600 0,632
-----CCACTTCAGCAGGCTTC----- 16,768 0,002 4,492 miR_1112
-----CCACTTCAGCAGGCTTC----- 0,147 0,000 0,000
-----CCACTTCAGCAGGCTTC----- 0,514 0,100 0,082
-----CCACTTCAGCAGGCTTC----- 0,147 0,100 0,000
-----CCACTTCAGCAGGCTTC----- 3,030 0,400 1,223
-----CCACTTCAGCAGGCTTC----- 0,220 0,400 0,245
-----CCACTTCAGCAGGCTTC----- 0,073 0,000 0,000

          AGT
          C C G C G A G T G C A G T T C C C C A G C A G C A G C A G C
          C C G C T A G C T T C C A A T T C G A A G C G C G C T C C C G C T C
TCCCACAGC / CCC
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,100 0,000
-----AGCGGGTAAAGTTCAGAA----- 1,232 0,200 0,489
-----AGCGGGTAAAGTTCAGAA----- 0,954 0,200 0,815
-----AGCGGGTAAAGTTCAGAA----- 0,220 0,200 0,082
-----AGCGGGTAAAGTTCAGAA----- 1,939 0,300 0,815
-----AGCGGGTAAAGTTCAGAA----- 1,615 0,700 0,978
-----AGCGGGTAAAGTTCAGAA----- 0,147 0,100 0,126
-----AGCGGGTAAAGTTCAGAA----- 0,147 0,000 0,082
-----AGCGGGTAAAGTTCAGAA----- 0,367 0,000 0,082
-----AGCGGGTAAAGTTCAGAA----- 0,220 0,100 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,147 0,100 0,163
-----AGCGGGTAAAGTTCAGAA----- 15,712 11,302 15,085 miR_154
-----AGCGGGTAAAGTTCAGAA----- 0,267 0,500 0,489
-----AGCGGGTAAAGTTCAGAA----- 0,220 0,000 0,082
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,267 0,400 0,245
-----AGCGGGTAAAGTTCAGAA----- 0,367 0,700 0,371
-----AGCGGGTAAAGTTCAGAA----- 1,542 0,900 0,408
-----AGCGGGTAAAGTTCAGAA----- 0,220 0,100 0,082
-----AGCGGGTAAAGTTCAGAA----- 7,109 1,801 1,794
-----AGCGGGTAAAGTTCAGAA----- 18,125 12,161 11,578
-----AGCGGGTAAAGTTCAGAA----- 0,954 2,000 1,549
-----AGCGGGTAAAGTTCAGAA----- 0,463 0,200 0,566
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 15,712 265,054 244,742 miR_1117
-----AGCGGGTAAAGTTCAGAA----- 41,923 88,614 48,108
-----AGCGGGTAAAGTTCAGAA----- 7,280 1,200 1,390
-----AGCGGGTAAAGTTCAGAA----- 0,461 0,801 0,180
-----AGCGGGTAAAGTTCAGAA----- 0,367 0,900 0,163
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 1663,813 770,554 1259,199 miR_14
-----AGCGGGTAAAGTTCAGAA----- 16,813 1,401 7,911
-----AGCGGGTAAAGTTCAGAA----- 123,475 46,311 109,814
-----AGCGGGTAAAGTTCAGAA----- 16,373 0,300 0,218
-----AGCGGGTAAAGTTCAGAA----- 1,615 0,200 0,632
-----AGCGGGTAAAGTTCAGAA----- 0,284 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,641 0,300 0,978
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 1,449 0,800 1,468
-----AGCGGGTAAAGTTCAGAA----- 1,248 0,300 0,632
-----AGCGGGTAAAGTTCAGAA----- 0,220 0,100 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,073 0,000 0,000
-----AGCGGGTAAAGTTCAGAA----- 0,441 0,000 0,082

miR8 miR_18_miR_140_miR_172_miR_542 chromosome_14_start: 195055 End: 195059 Condition: Nutrient-replete
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,147 0,200 0,371
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 1,181 0,600 0,082
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,220 0,000 0,082
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,147 0,100 0,163
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,954 0,500 1,384
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,384 0,900 0,489
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,082
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,147 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,082
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 2,117 3,101 1,448
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,220 0,100 0,245
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,220 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 1,248 1,000 0,978
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,147 0,400 0,082
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,100 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,147 0,200 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,100 0,245
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,000
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,590 0,802 10,111
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,267 0,800 0,324
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,214 0,200 0,000 miR_142
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 1611,116 2393,563 2450,640 miR_118
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 11,454 20,664 48,108
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 52,289 181,837 156,880
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 36,930 36,907 45,825
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,220 0,000 0,163
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,500 0,571
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,000 0,163
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,220 0,200 0,082
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,734 0,500 1,448
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 1,248 1,400 2,772
-----TTGCGCTTCAGCAGGCTTCAGAGC----- 0,073 0,100 0,163

```

Table with 5 columns: sequence, position, and three numerical values. The table contains multiple rows of sequence alignments and associated numerical data.

Table with 5 columns: sequence, position, and three numerical values. This section includes a header 'MIR41: miR\_19, miR\_1104 chromosome\_4' and a list of sequences with their corresponding positions and values.







```

-----CTGGTGCGGCATATTC----- 0.073  5.700  0.326
-----CTGGTGCGGCATATTCAGAGA----- 0.220  0.100  0.000
-----CTGGTGCGGCATATTCAGAGA----- 1.455  11.402  -1.772
-----CTGGTGCGGCATATTCAGAG----- 0.000  0.200  0.000
-----TGGTGCGGCATATTCAGAGAT----- 0.267  0.100  0.734
-----TGGTGCGGCATATTCAGAGAT----- 5.066  6.501  13.209
-----TGGTGCGGCATATTCAGAGAT----- 0.000  0.100  0.002
-----TGGTGCGGCATATTCAGAGAT----- 0.147  0.400  0.245
-----TGGTGCGGCATATTCAGAGAT----- 0.441  0.400  1.631
-----TGGTGCGGCATATTCAGAGAT----- 0.294  0.200  0.408
-----CTGGTGCGGCATATTCAGAGAT----- 0.000  0.100  0.000
-----TGGTGCGGCATATTCAGAGAT----- 1.909  1.200  7.420
-----TGGTGCGGCATATTCAGAGAT----- 0.000  0.100  0.104
-----TGGTGCGGCATATTCAGAGAT----- 2.863  1.900  8.317
-----ATGCAGAGATATTCAGAGAT----- 1.762  1.300  1.712
-----ATGCAGAGATATTCAGAGAT----- 0.367  0.800  1.349
-----ATGCAGAGATATTCAGAGAT----- 0.000  0.200  0.582
-----TGCAGAGATATTCAGAGAT----- 13.216  5.401  18.102
-----TGCAGAGATATTCAGAGAT----- 0.147  0.100  0.245
-----ATGCAGATATTCAGAGAT----- 0.000  0.100  0.000
-----ATGCAGATATTCAGAGAT----- 0.073  0.100  0.000
-----ATGCAGATATTCAGAGAT----- 0.587  1.200  0.815
-----ATGCAGATATTCAGAGAT----- 19.970  17.404  19.732
-----ATGCAGATATTCAGAGAT----- 0.314  0.000  0.408
-----ATGCAGATATTCAGAGAT----- 0.881  4.101  3.262
-----ATGCAGATATTCAGAGAT----- 1.393  1.100  1.528
-----ATGCAGATATTCAGAGAT----- 0.000  0.100  0.002
-----ATGCAGATATTCAGAGAT----- 0.000  0.100  0.002
-----ATGCAGATATTCAGAGAT----- 0.000  0.200  0.245
-----ATGCAGATATTCAGAGAT----- 0.294  0.100  0.326
-----ATGCAGATATTCAGAGAT----- 0.147  0.100  0.002
-----ATGCAGATATTCAGAGAT----- 0.073  0.100  0.104
-----ATGCAGATATTCAGAGAT----- 0.881  1.000  0.452
-----ATGCAGATATTCAGAGAT----- 5.433  10.902  12.535
-----TGCAGAGATATTCAGAGAT----- 0.000  0.100  0.326

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      AG      A      AA      STAGS      C---      ACA      A      T      G      A      A      G
      GTCAGTACATC  CGGKCT  TC  CAGGAG  CG  GGGAGAG  CG  TCGCTTTC  AGCCCTCCGCTGGAGAT  CAGAGATATTCAGATCTGGAGAGCC  GGCC  TCAAGTC  T
      CCAGGTAGAC  GGGCAG  AG  GCGTCCG  TGCCCTCTG  CC  AGATTAGAG  TGCCGAGCAGCTATTA  GTCCTCTCTCATATAGATCCGGCT  CGG  AGTACCA  C
      GGCACCTCGTTATCGCA  C  CG  CCTG  TCCC  GCA  C  T  G  G  C  A

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-----AGAACTCGGTTCCCGCAGT----- 0.220  0.400  0.002
-----AGAACTCGGTTCCCGCAGT----- 1.982  2.400  2.528
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 2.889  0.600
-----AGAACTCGGTTCCCGCAGT----- 0.220  0.300  0.571
-----AGAACTCGGTTCCCGCAGT----- 295.684  74.113  276.972
-----AGAACTCGGTTCCCGCAGT----- 0.734  0.100  0.326
-----AGAACTCGGTTCCCGCAGT----- 0.973  0.200  10.028
-----AGAACTCGGTTCCCGCAGT----- 3.765  4.201  12.038
-----AGAACTCGGTTCCCGCAGT----- 0.294  0.400  1.024
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 2.863  0.400  2.083
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.409  1.500  2.751
-----AGAACTCGGTTCCCGCAGT----- 0.147  0.100  0.326
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.200  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.200  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.147  0.000  1.142
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.073  0.000  0.245
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.200  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.073  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.147  0.200  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.220  0.900  0.815
-----AGAACTCGGTTCCCGCAGT----- 2.700  0.302  2.184
-----AGAACTCGGTTCCCGCAGT----- 5.580  8.802  8.806
-----AGAACTCGGTTCCCGCAGT----- 0.207  13.701  11.905
-----AGAACTCGGTTCCCGCAGT----- 140.505 280.342 218.540 mir_191
-----AGAACTCGGTTCCCGCAGT----- 2.496  0.402  5.282
-----AGAACTCGGTTCCCGCAGT----- 0.073  0.400  0.002
-----AGAACTCGGTTCCCGCAGT----- 41.155  71.314  64.995
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.200  0.245
-----AGAACTCGGTTCCCGCAGT----- 0.073  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.734  1.900  1.205
-----AGAACTCGGTTCCCGCAGT----- 0.147  1.600  0.245
-----AGAACTCGGTTCCCGCAGT----- 0.073  0.200  0.163
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.061  1.700  0.714
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.300  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.441  3.000  0.489
-----AGAACTCGGTTCCCGCAGT----- 0.220  0.200  0.408
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.367  0.300  0.408
-----AGAACTCGGTTCCCGCAGT----- 1.762  0.400  0.452
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----AGAACTCGGTTCCCGCAGT----- 0.000  0.100  0.002
-----AGAACTCGGTTCCCGCAGT----- 0.294  0.300  0.245

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mirlet_mir_191_mir_198 chromosome_3_start: 657285 End: 657432 Orientation: 5' to 3'
-----GGGAGCACACAGACAG----- 0.465  0.303  0.326
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.100  0.000
-----TGCACCGGGAGCACACAGACAG----- 1.148  0.100  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.147  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.220  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.147  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.147  0.100  0.000
-----TGCACCGGGAGCACACAGACAG----- 2.717  2.901  2.245
-----TGCACCGGGAGCACACAGACAG----- 1.248  0.500  0.002
-----TGCACCGGGAGCACACAGACAG----- 0.061  1.500  0.000
-----TGCACCGGGAGCACACAGACAG----- 8.084  8.001  0.002
-----TGCACCGGGAGCACACAGACAG----- 1.982  2.601  0.408
-----TGCACCGGGAGCACACAGACAG----- 5.453  9.102  0.304
-----TGCACCGGGAGCACACAGACAG----- 8.150  18.104  0.163
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 4.038  3.101  0.326
-----TGCACCGGGAGCACACAGACAG----- 41.099  293.160  271.560
-----TGCACCGGGAGCACACAGACAG----- 2.790  2.400  0.326
-----TGCACCGGGAGCACACAGACAG----- 4.099  3.901  2.245
-----TGCACCGGGAGCACACAGACAG----- 6.481  6.901  0.452
-----TGCACCGGGAGCACACAGACAG----- 0.314  0.500  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.147  0.100  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.100  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.147  0.300  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.147  0.000  0.000
-----TGCACCGGGAGCACACAGACAG----- 0.073  0.000  0.000

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-----T----- A
-----AAATACGGCATTATTCAGATCAAGGATTCACCGGAGCACACAGACAG----- G
-----TTCACCTCGGTTCCCGCAGTATTCAGATCAAGGATTCACCGGAGCACACAGACAG----- T
-----TTCACCTCGGTTCCCGCAGT----- 0.220  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.220  0.200  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.441  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 4.332  2.361  4.488
-----TTCACCTCGGTTCCCGCAGT----- 1.028  0.200  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.367  0.000  0.002
-----TTCACCTCGGTTCCCGCAGT----- 0.000  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 3.991  2.801  0.408
-----TTCACCTCGGTTCCCGCAGT----- 0.167  0.000  0.002
-----TTCACCTCGGTTCCCGCAGT----- 10.426  3.601  0.408
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.200  0.000
-----TTCACCTCGGTTCCCGCAGT----- 15.071  5.801  2.365
-----TTCACCTCGGTTCCCGCAGT----- 0.287  0.200  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 44.566  31.105  3.343
-----TTCACCTCGGTTCCCGCAGT----- 0.734  0.200  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.441  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 1.322  0.800  0.163
-----TTCACCTCGGTTCCCGCAGT----- 20.137  8.102  1.468
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.000  0.002
-----TTCACCTCGGTTCCCGCAGT----- 0.073  0.100  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.000  0.000
-----TTCACCTCGGTTCCCGCAGT----- 0.147  0.000  0.000

```

Table with 4 columns: sequence, count, and two values. Rows include motifs like -TGGGTAGTAAAGTAAAGG- and -ATATATATATATATATATAT-.

Table with 4 columns: motif, count, and two values. Rows include motifs like -TATCCAGAGCAGCAGCAGC- and -ATCCAGAGCAGCAGCAGC-.

Table with 4 columns: motif, count, and two values. Rows include motifs like -TATCCAGAGCAGCAGCAGC- and -ATCCAGAGCAGCAGCAGC-.

Table with 4 columns: motif, count, and two values. Rows include motifs like -TGGGTAGTAAAGTAAAGG- and -ATATATATATATATATATAT-.



Table with 5 columns: sequence, score, 1.100, 1.305, 1.400. Row 1: -----CGAGCCAGCTGGGTCGCA----- 0.461 1.100 1.305

miR: mir\_18 chromosome\_4 start: 369473 End: 369593 Condition: Phosphate-deficient

Table with 5 columns: sequence, score, 0.220, 0.100, 0.082. Row 1: -----CTTATGTCCTCAGAGGCGT----- 0.220 0.100 0.082

ATCA C GGGAAATGTAATTAATGCTGCG GAGGGGTTATACCTCCGTTGAG GG G  
ACAT C GCTTTTACATTAATGCTAGT GTTCCGACATATGTTGATACAG CC /  
A G C G C

AGTCTGTCAGAGGGGGGGCTGATACGGGGTCCGAGGCGGCTCCAGGGGAGGAGACCTCCCTGGACAGCCGAGCAGCCGAGCCGCGGAGCCAGCCGCGGCTCCCTCCCTCCGAGCTCCACGCCAGCAGGAGCGCT /

-----CGTCCAGAAAGGGGCGCGT----- 0.000 0.000 0.002

miR: mir\_113\_mir\_119 chromosome\_10 start: 339964 End: 340007 Condition: Nutrient-replete

Table with 5 columns: sequence, score, 0.367, 2.400, 0.326. Row 1: -----CGATATAGAGAGGCGTATAG----- 0.073 0.000 0.000

-----CA----- GS  
TGGGATATAGAGAGGCGTATAGTACGGGCGTGGGAGGCGGAGCGAGCGGATAG G  
AGGGTATATCTCTGGGATGATGATGAGGGGGGGTCCCTCTCCCGTCCGCTCAATG G  
GGAG----- GS

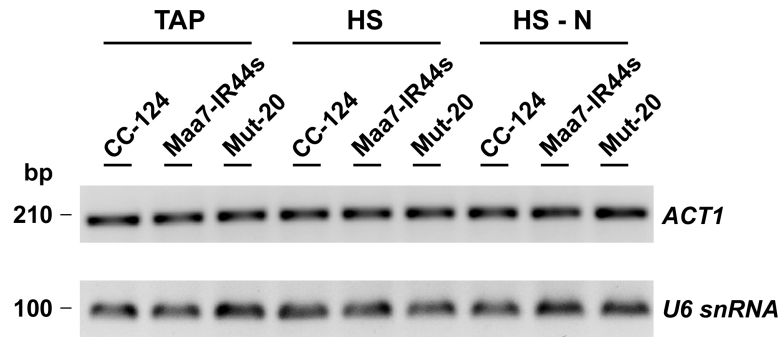
Table with 5 columns: sequence, score, 1.213, 3.201, 1.631 mir\_113. Row 1: -----TCAATCTCTGGGATCCAT----- 0.073 0.000 0.163

miR: mir\_112\_mir\_170 chromosome\_9 start: 6518812 End: 6519983 Condition: Nutrient-replete

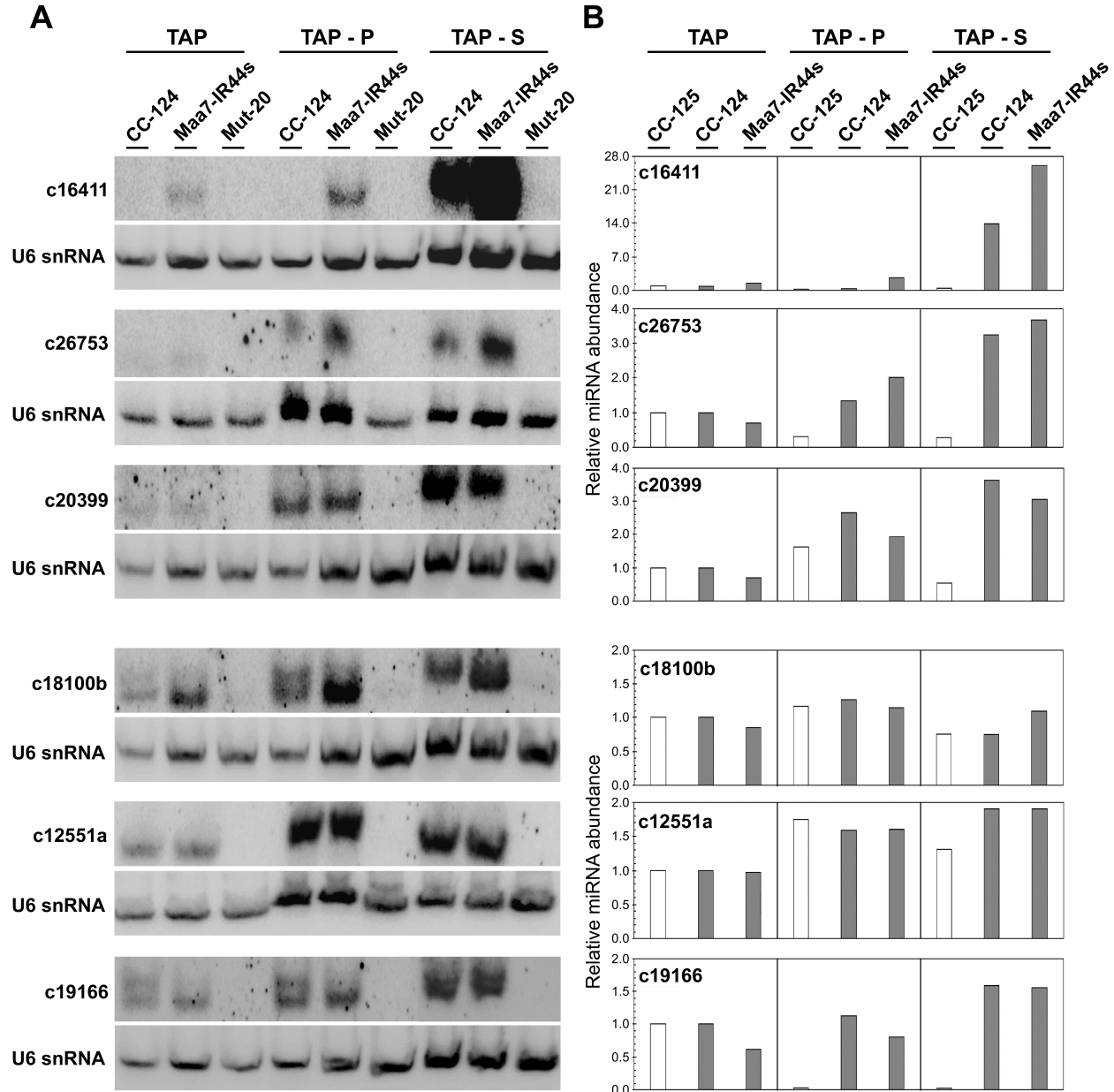
Table with 5 columns: sequence, score, 0.073, 0.100, 0.000. Row 1: -----TGGGACAGCCCTTAGAGCGT----- 0.073 0.100 0.000



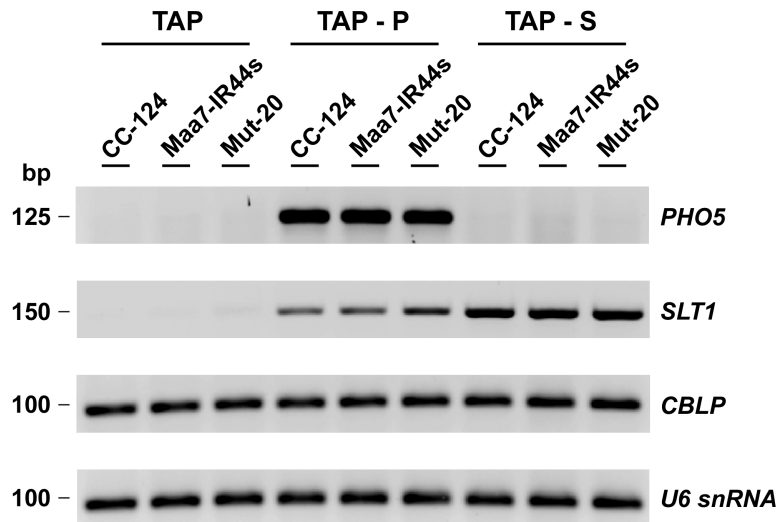
**Figure S1. Secondary structure plots of predicted miRNA precursor loci and frequency of reads from the *Chlamydomonas* AGO3-associated sRNA libraries or from the total sRNA libraries prepared by Chávez Montes *et al.*<sup>25</sup>.** For AGO3-associated sRNAs, the first column indicates read abundance (Counts Per Million mapped reads) in libraries prepared from cells grown mixotrophically (TAP), the second column indicates read abundance in libraries prepared from cells grown photoautotrophically in nitrogen depleted minimal medium (HS-N) and the third column indicates read abundance in libraries prepared from cells grown photoautotrophically in nutrient replete minimal medium (HS+N). For the miRNAs identified in the libraries prepared by Chávez Montes *et al.*<sup>25</sup>, the first column indicates read abundance (CPM) in the libraries from cells grown in nutrient replete medium, the second column indicates read abundance in the libraries from cells grown in sulfur deprived medium and the third column indicates read abundance in the libraries from cells grown in phosphate deprived medium. Mature miRNAs are indicated in red and passenger strands (miRNA\*), when detected, are indicated in blue. Each plot is annotated with the locus ID (miR\_#), the chromosome, the chromosomal position (start and end), and the trophic condition(s) under which the miRNA was preferentially identified. Loci with long hairpins may code for more than one candidate miRNA. Additionally, some loci code for more than one hairpin in a tandem arrangement (clustered miRNA precursor loci) and, in these cases, the folding of each hairpin is shown separately.



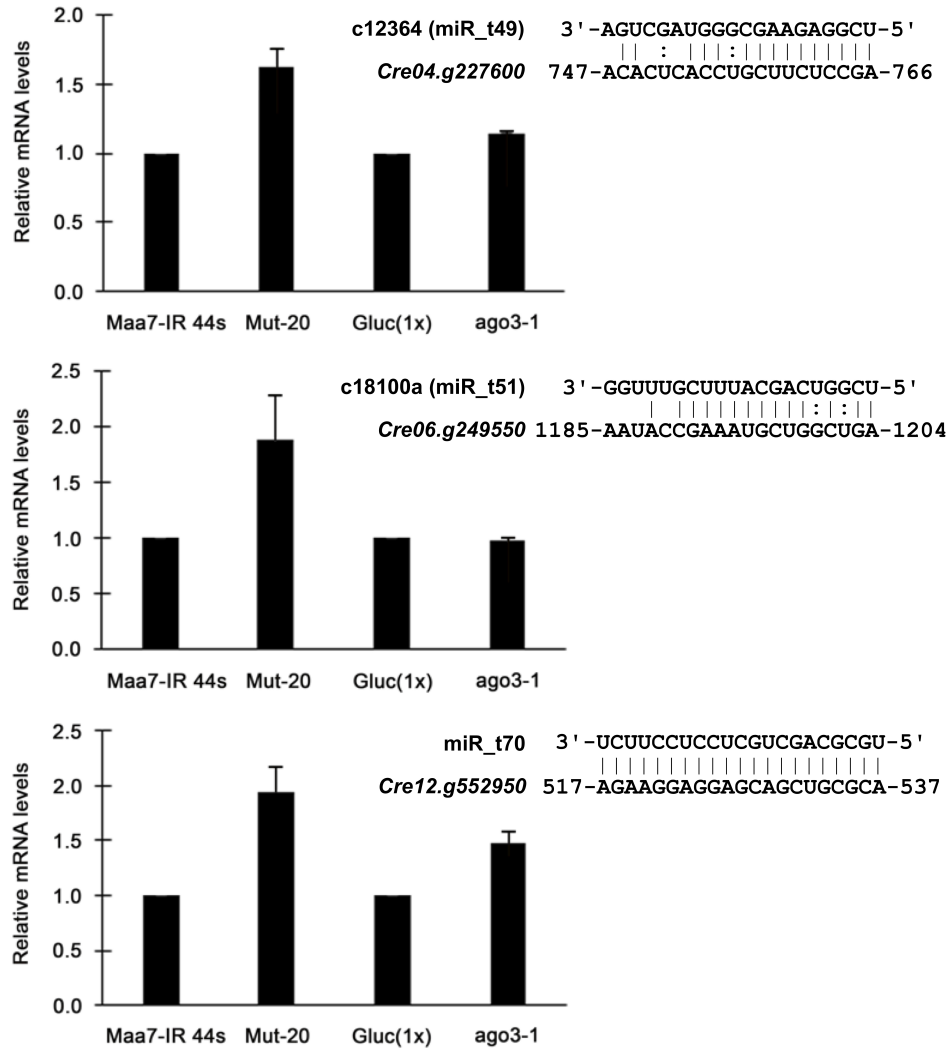
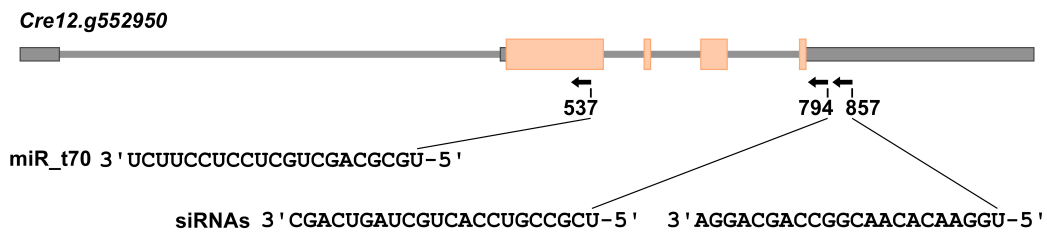
**Figure S2. U6 small nuclear RNA abundance in *Chlamydomonas* cells grown under the denoted trophic conditions.** Transcript abundance was examined by semi-quantitative RT-PCR. The panels show representative reverse images of agarose resolved RT-PCR products stained with ethidium bromide. CC-124, wild type strain (mt); Maa7-IR44s, CC-124 containing a transgene expressing FLAG-tagged AGO3; Mut-20, *TSNI* deletion mutant, in the Maa7-IR44s background, defective in sRNA biogenesis<sup>14</sup>. Amplification of the mRNA corresponding to *ACT1* (encoding actin) was used as a control for equivalent amounts of input RNA and for the efficiency of the RT-PCRs [Msanne, J. *et al. Phytochemistry* **75**, 50-59 (2012)].



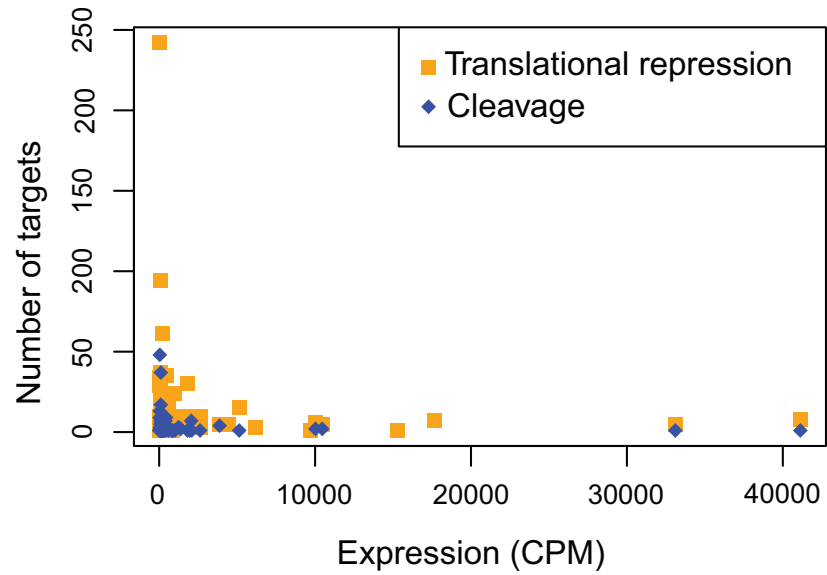
**Figure S3. Northern blot analysis of miRNA expression in *Chlamydomonas* cells grown under the denoted trophic conditions.** (A) Small RNAs were detected with probes specific for the indicated miRNAs. The same filters were reprobated with the U6 small nuclear RNA sequence as a control for lane loading. CC-124, wild type strain ( $mt^-$ ); CC-125, wild type strain ( $mt^+$ ); Maa7-IR44s, CC-124 containing a transgene expressing FLAG-tagged AGO3; Mut-20, *TSN1* deletion mutant, in the Maa7-IR44s background, defective in sRNA biogenesis<sup>14</sup>. (B) Relative miRNA levels in the indicated strains under the different trophic conditions. Values shown are the average of two independent experiments and are normalized to those of the CC-124 strain (the CC-125 strain for read counts) grown mixotrophically in nutrient replete medium (TAP). The relative standard deviation, as percentage of the mean, was in no case higher than 34.7%. Data corresponds to phosphorimager measurements of sRNA signals on northern blots (gray bars) or normalized read counts from the total sRNA libraries prepared by Chávez Montes *et al.*<sup>25</sup> (white bars).



**Figure S4. Gene expression in *Chlamydomonas* cells grown under the denoted trophic conditions.** Transcript abundance was examined by semi-quantitative RT-PCR. The panels show representative reverse images of agarose resolved RT-PCR products stained with ethidium bromide. CC-124, wild type strain (*mt*); Maa7-IR44s, CC-124 containing a transgene expressing FLAG-tagged AGO3; Mut-20, *TSN1* deletion mutant, in the Maa7-IR44s background, defective in sRNA biogenesis<sup>14</sup>. Examined genes included *PHO5*, encoding a phosphate-repressible alkaline phosphatase, *SLT1* (*SAC1-LIKE TRANSPORTER1*), encoding a sodium/sulfate cotransporter, and the *U6* small nuclear RNA. Amplification of the mRNA corresponding to *CBLP* (also known as *RECEPTOR OF ACTIVATED PROTEIN KINASE C1*, *RCK1*) was used as a control for equivalent amounts of input RNA and for the efficiency of the RT-PCRs [Aksoy, M. *et al. Plant Physiol* **162**, 195-211 (2013)].

**A****B**

**Figure S5. Quantitative RT-PCR analysis of predicted miRNA-target transcript abundance. (A)** Relative transcript levels of *Cre04.g227600* (target of c12364), *Cre06.g249550* (target of c18100a) and *Cre12.g552950* (target of miR\_t70) in the indicated strains. Maa7-IR44s, CC-124 strain containing a transgene expressing FLAG-tagged AGO3; Mut-20, *TSN1* deletion mutant, in the Maa7-IR44s background, defective in sRNA biogenesis<sup>14</sup>; Gluc(1x), wild type strain derived from CC-124; ago3-1, *AGO3* disrupted mutant, in the Gluc(1x) background, defective in RNAi<sup>28</sup>. Values, normalized to those in the wild type strains, are means  $\pm$  SD of three independent experiments. **(B)** Diagram of the *Cre12.g552950* gene (from Phytozome v11, coding region shown in orange), indicating the binding sites for miR\_t70 and two putative, perfectly complementary, siRNAs.



**Figure S6. Relationship between miRNA expression level and number of predicted targets in *C. reinhardtii*.** The expression level and the number of predicted targets (blue diamonds for cleavage targets and orange squares for translational repression targets) are plotted for each miRNA identified in the AGO3-pulldown libraries from *C. reinhardtii*.