Supplemental Figure 1: Secondary structure of 31 identified sorghum miRNAs.
Mature miRNA sequences are shaded by red color

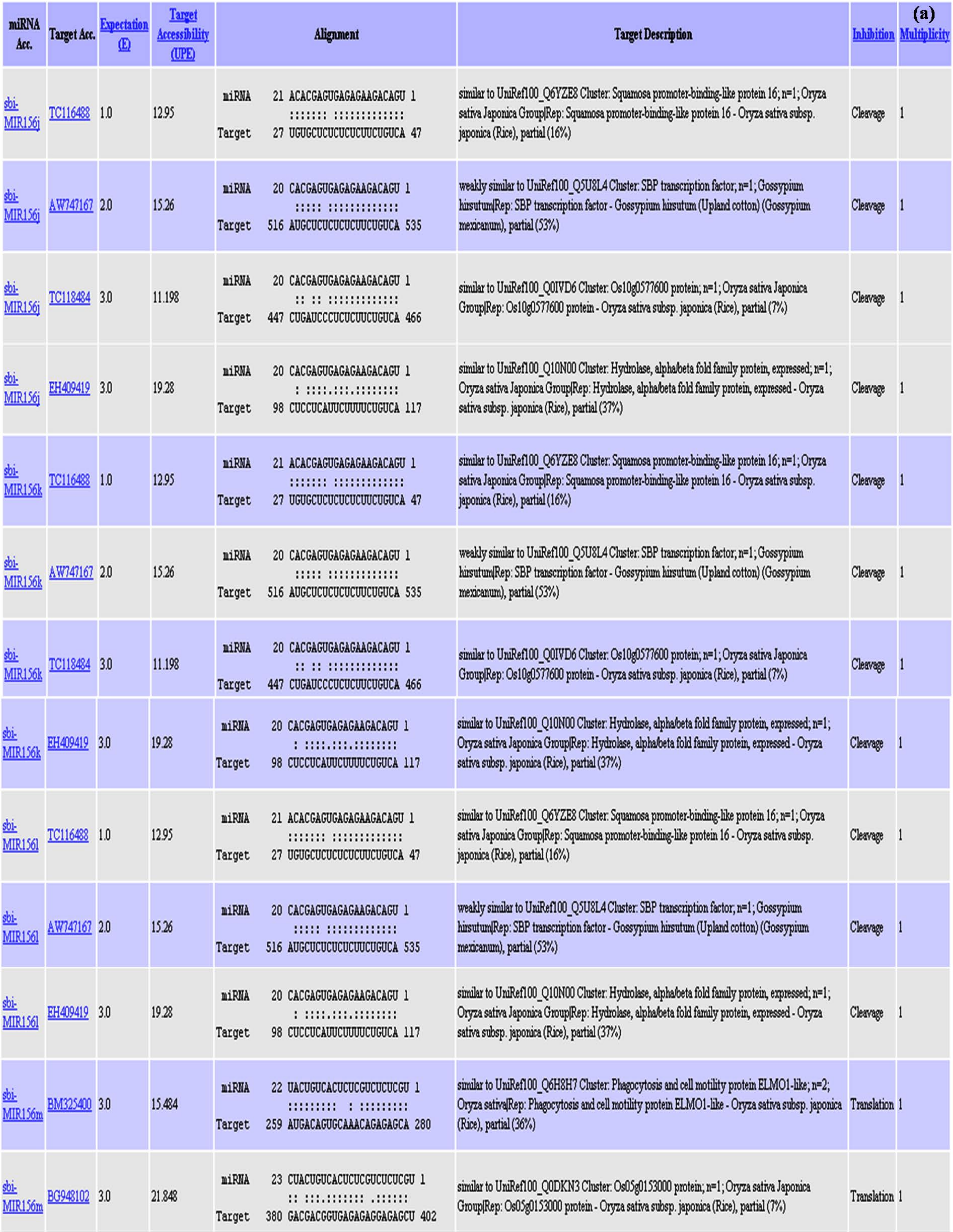
MIR168b MIR390b MIR168c MIR167j MIR166l MIR399l MIR398b MIR396f

MIR396g MIR396k MIR396h MIR396i MIR166o MIR166n MIR166m MIR166r

MIR166p MIR166q MIR166s MIR166t MIR396j MIR167k MIR156j MIR156k

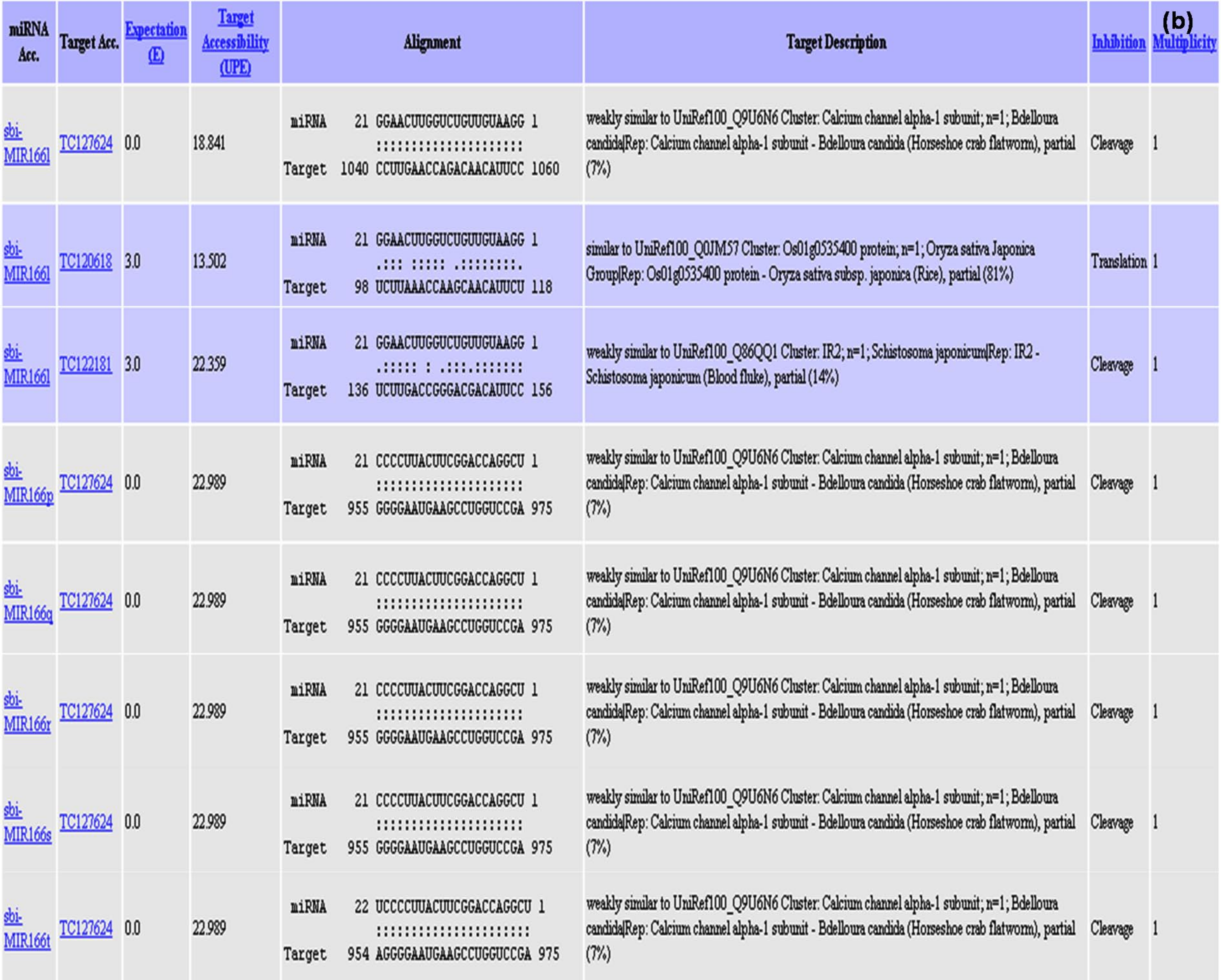
MIR156l MIR444a MIR156m MIR171l MIR171m MIR444c MIR444b

Supplemental Figure 2a-e: Sequence alignments of 31 putative microRNAs and their corresponding targets in sorghum



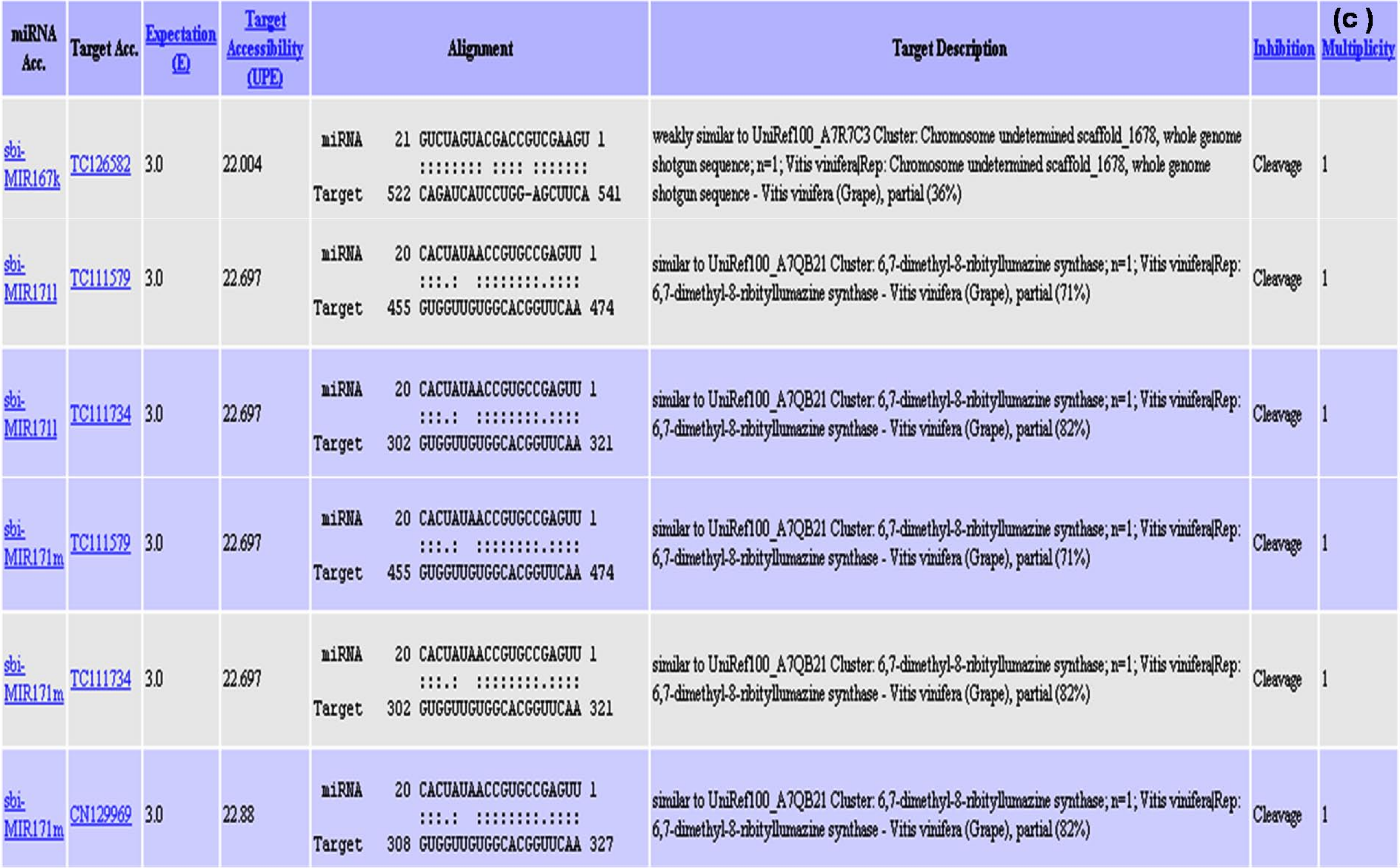
(a)

| miRNA Acc. | Target Acc. | Expectation (E) | Target Accessibility (UPE) | Alignment | Target Description | Inhibition | Multiplicity |
|---|---|---|---|---|---|---|---|
| sbi-MIR156j | TC116488 | 1.0 | 12.95 | miRNA 21 ACACGAGUGAGAGAAGACAGU 1<br>::::::: :::::::::::::<br>Target 27 UGUGCUCUCUCUCUUCUGUCA 47 | similar to UniRef100_Q6YZE8 Cluster: Squamosa promoter-binding-like protein 16; n=1; Oryza sativa Japonica Group\|Rep: Squamosa promoter-binding-like protein 16 - Oryza sativa subsp. japonica (Rice), partial (16%) | Cleavage | 1 |
| sbi-MIR156j | AW747167 | 2.0 | 15.26 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>::::: :::::::::::::<br>Target 516 AUGCUCUCUCUCUUCUGUCA 535 | weakly similar to UniRef100_Q5U8L4 Cluster: SBP transcription factor; n=1; Gossypium hirsutum\|Rep: SBP transcription factor - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum), partial (53%) | Cleavage | 1 |
| sbi-MIR156j | TC118484 | 3.0 | 11.198 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>:: :: :::::::::::::<br>Target 447 CUGAUCCCUCUCUUCUGUCA 466 | similar to UniRef100_Q0IVD6 Cluster: Os10g0577600 protein; n=1; Oryza sativa Japonica Group\|Rep: Os10g0577600 protein - Oryza sativa subsp. japonica (Rice), partial (7%) | Cleavage | 1 |
| sbi-MIR156j | EH409419 | 3.0 | 19.28 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>: ::::.:::.::::::::<br>Target 98 CUCCUCAUUCUUUUCUGUCA 117 | similar to UniRef100_Q10N00 Cluster: Hydrolase, alpha/beta fold family protein, expressed; n=1; Oryza sativa Japonica Group\|Rep: Hydrolase, alpha/beta fold family protein, expressed - Oryza sativa subsp. japonica (Rice), partial (37%) | Cleavage | 1 |
| sbi-MIR156k | TC116488 | 1.0 | 12.95 | miRNA 21 ACACGAGUGAGAGAAGACAGU 1<br>::::::: :::::::::::::<br>Target 27 UGUGCUCUCUCUCUUCUGUCA 47 | similar to UniRef100_Q6YZE8 Cluster: Squamosa promoter-binding-like protein 16; n=1; Oryza sativa Japonica Group\|Rep: Squamosa promoter-binding-like protein 16 - Oryza sativa subsp. japonica (Rice), partial (16%) | Cleavage | 1 |
| sbi-MIR156k | AW747167 | 2.0 | 15.26 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>::::: :::::::::::::<br>Target 516 AUGCUCUCUCUCUUCUGUCA 535 | weakly similar to UniRef100_Q5U8L4 Cluster: SBP transcription factor; n=1; Gossypium hirsutum\|Rep: SBP transcription factor - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum), partial (53%) | Cleavage | 1 |
| sbi-MIR156k | TC118484 | 3.0 | 11.198 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>:: :: :::::::::::::<br>Target 447 CUGAUCCCUCUCUUCUGUCA 466 | similar to UniRef100_Q0IVD6 Cluster: Os10g0577600 protein; n=1; Oryza sativa Japonica Group\|Rep: Os10g0577600 protein - Oryza sativa subsp. japonica (Rice), partial (7%) | Cleavage | 1 |
| sbi-MIR156k | EH409419 | 3.0 | 19.28 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>: ::::.:::.::::::::<br>Target 98 CUCCUCAUUCUUUUCUGUCA 117 | similar to UniRef100_Q10N00 Cluster: Hydrolase, alpha/beta fold family protein, expressed; n=1; Oryza sativa Japonica Group\|Rep: Hydrolase, alpha/beta fold family protein, expressed - Oryza sativa subsp. japonica (Rice), partial (37%) | Cleavage | 1 |
| sbi-MIR156l | TC116488 | 1.0 | 12.95 | miRNA 21 ACACGAGUGAGAGAAGACAGU 1<br>::::::: :::::::::::::<br>Target 27 UGUGCUCUCUCUCUUCUGUCA 47 | similar to UniRef100_Q6YZE8 Cluster: Squamosa promoter-binding-like protein 16; n=1; Oryza sativa Japonica Group\|Rep: Squamosa promoter-binding-like protein 16 - Oryza sativa subsp. japonica (Rice), partial (16%) | Cleavage | 1 |
| sbi-MIR156l | AW747167 | 2.0 | 15.26 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>::::: :::::::::::::<br>Target 516 AUGCUCUCUCUCUUCUGUCA 535 | weakly similar to UniRef100_Q5U8L4 Cluster: SBP transcription factor; n=1; Gossypium hirsutum\|Rep: SBP transcription factor - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum), partial (53%) | Cleavage | 1 |
| sbi-MIR156l | EH409419 | 3.0 | 19.28 | miRNA 20 CACGAGUGAGAGAAGACAGU 1<br>: ::::.:::.::::::::<br>Target 98 CUCCUCAUUCUUUUCUGUCA 117 | similar to UniRef100_Q10N00 Cluster: Hydrolase, alpha/beta fold family protein, expressed; n=1; Oryza sativa Japonica Group\|Rep: Hydrolase, alpha/beta fold family protein, expressed - Oryza sativa subsp. japonica (Rice), partial (37%) | Cleavage | 1 |
| sbi-MIR156m | BM325400 | 3.0 | 15.484 | miRNA 22 UACUGUCACUCUCGUCUCUCGU 1<br>:::::::::  : :::::::::<br>Target 259 AUGACAGUGCAAACAGAGAGCA 280 | similar to UniRef100_Q6H8H7 Cluster: Phagocytosis and cell motility protein ELMO1-like; n=2; Oryza sativa\|Rep: Phagocytosis and cell motility protein ELMO1-like - Oryza sativa subsp. japonica (Rice), partial (36%) | Translation | 1 |
| sbi-MIR156m | BG948102 | 3.0 | 21.848 | miRNA 23 CUACUGUCACUCUCGUCUCUCGU 1<br>:: :::.::::::: .::::::<br>Target 380 GACGACGGUGAGAGAGGAGAGCU 402 | similar to UniRef100_Q0DKN3 Cluster: Os05g0153000 protein; n=1; Oryza sativa Japonica Group\|Rep: Os05g0153000 protein - Oryza sativa subsp. japonica (Rice), partial (7%) | Translation | 1 |



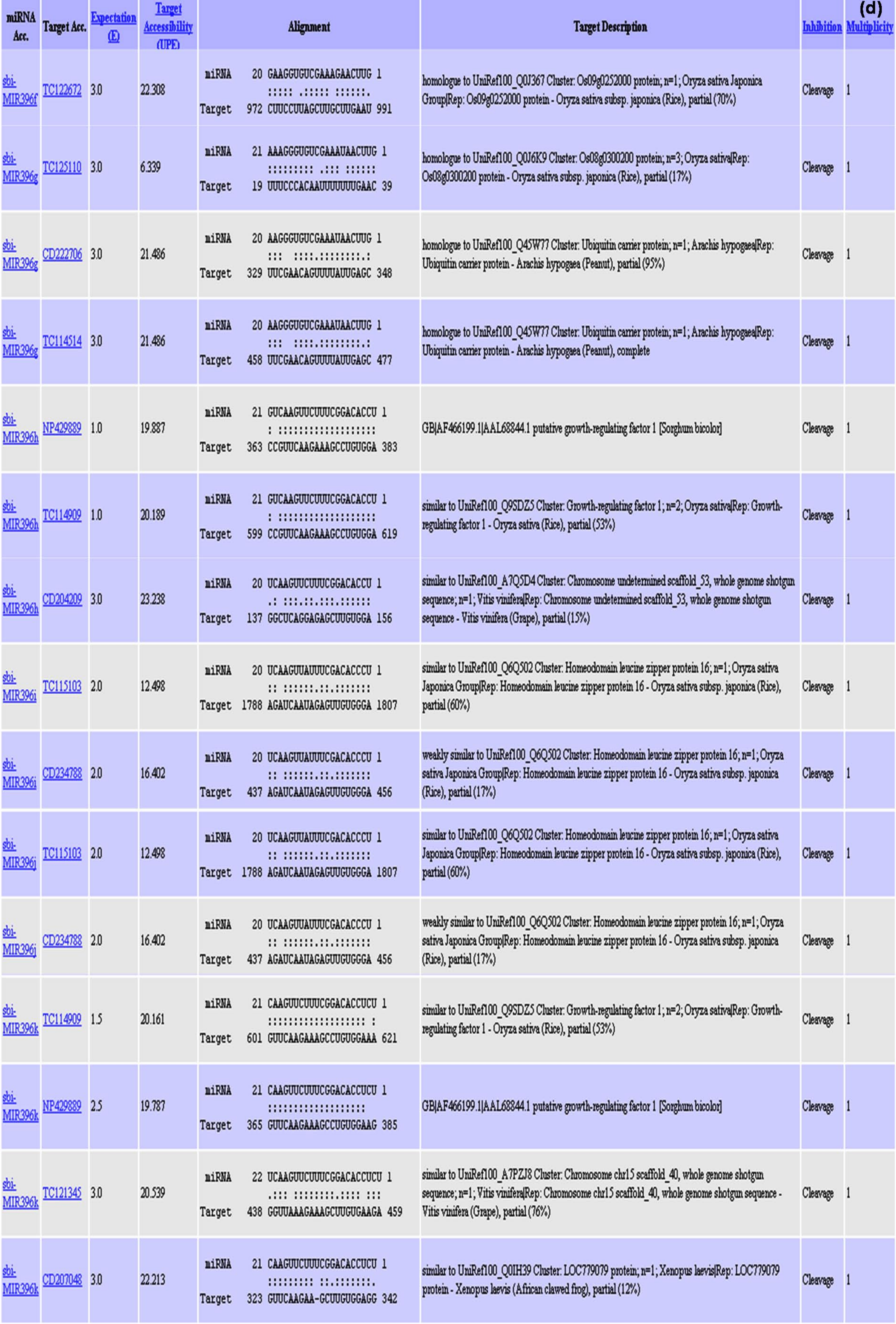
(b)

| miRNA Acc. | Target Acc. | Expectation (E) | Target Accessibility (UPE) | Alignment | Target Description | Inhibition | Multiplicity |
|---|---|---|---|---|---|---|---|
| sbi-MIR1661 | TC127624 | 0.0 | 18.841 | miRNA 21 GGAACUUGGUCUGUUGUAAGG 1<br>:::::::::::::::::::::<br>Target 1040 CCUUGAACCAGACAACAUUCC 1060 | weakly similar to UniRef100_Q9U6N6 Cluster: Calcium channel alpha-1 subunit; n=1; Bdelloura candida\|Rep: Calcium channel alpha-1 subunit - Bdelloura candida (Horseshoe crab flatworm), partial (7%) | Cleavage | 1 |
| sbi-MIR1661 | TC120618 | 3.0 | 13.502 | miRNA 21 GGAACUUGGUCUGUUGUAAGG 1<br>.::: ::::: .::::::::.<br>Target 98 UCUUAAACCAAGCAACAUUCU 118 | similar to UniRef100_Q0JM57 Cluster: Os01g0535400 protein; n=1; Oryza sativa Japonica Group\|Rep: Os01g0535400 protein - Oryza sativa subsp. japonica (Rice), partial (81%) | Translation | 1 |
| sbi-MIR1661 | TC122181 | 3.0 | 22.359 | miRNA 21 GGAACUUGGUCUGUUGUAAGG 1<br>.::::: : .:::.:::::::<br>Target 136 UCUUGACCGGGACGACAUUCC 156 | weakly similar to UniRef100_Q86QQ1 Cluster: IR2; n=1; Schistosoma japonicum\|Rep: IR2 - Schistosoma japonicum (Blood fluke), partial (14%) | Cleavage | 1 |
| sbi-MIR166p | TC127624 | 0.0 | 22.989 | miRNA 21 CCCCUUACUUCGGACCAGGCU 1<br>:::::::::::::::::::::<br>Target 955 GGGGAAUGAAGCCUGGUCCGA 975 | weakly similar to UniRef100_Q9U6N6 Cluster: Calcium channel alpha-1 subunit; n=1; Bdelloura candida\|Rep: Calcium channel alpha-1 subunit - Bdelloura candida (Horseshoe crab flatworm), partial (7%) | Cleavage | 1 |
| sbi-MIR166q | TC127624 | 0.0 | 22.989 | miRNA 21 CCCCUUACUUCGGACCAGGCU 1<br>:::::::::::::::::::::<br>Target 955 GGGGAAUGAAGCCUGGUCCGA 975 | weakly similar to UniRef100_Q9U6N6 Cluster: Calcium channel alpha-1 subunit; n=1; Bdelloura candida\|Rep: Calcium channel alpha-1 subunit - Bdelloura candida (Horseshoe crab flatworm), partial (7%) | Cleavage | 1 |
| sbi-MIR166r | TC127624 | 0.0 | 22.989 | miRNA 21 CCCCUUACUUCGGACCAGGCU 1<br>:::::::::::::::::::::<br>Target 955 GGGGAAUGAAGCCUGGUCCGA 975 | weakly similar to UniRef100_Q9U6N6 Cluster: Calcium channel alpha-1 subunit; n=1; Bdelloura candida\|Rep: Calcium channel alpha-1 subunit - Bdelloura candida (Horseshoe crab flatworm), partial (7%) | Cleavage | 1 |
| sbi-MIR166s | TC127624 | 0.0 | 22.989 | miRNA 21 CCCCUUACUUCGGACCAGGCU 1<br>:::::::::::::::::::::<br>Target 955 GGGGAAUGAAGCCUGGUCCGA 975 | weakly similar to UniRef100_Q9U6N6 Cluster: Calcium channel alpha-1 subunit; n=1; Bdelloura candida\|Rep: Calcium channel alpha-1 subunit - Bdelloura candida (Horseshoe crab flatworm), partial (7%) | Cleavage | 1 |
| sbi-MIR166t | TC127624 | 0.0 | 22.989 | miRNA 22 UCCCCUUACUUCGGACCAGGCU 1<br>::::::::::::::::::::::<br>Target 954 AGGGGAAUGAAGCCUGGUCCGA 975 | weakly similar to UniRef100_Q9U6N6 Cluster: Calcium channel alpha-1 subunit; n=1; Bdelloura candida\|Rep: Calcium channel alpha-1 subunit - Bdelloura candida (Horseshoe crab flatworm), partial (7%) | Cleavage | 1 |



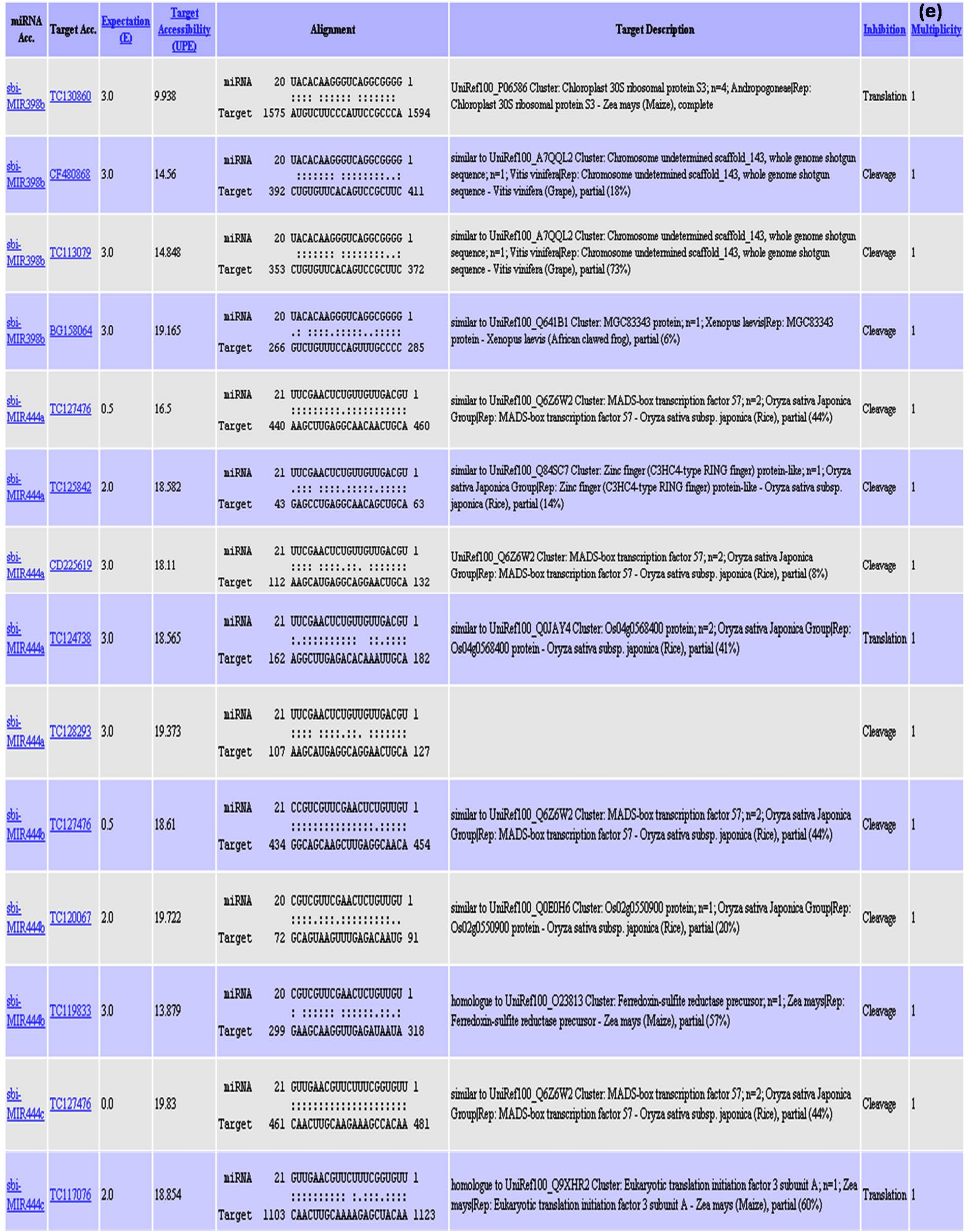
**(c)**

| miRNA Acc. | Target Acc. | Expectation (E) | Target Accessibility (UPE) | Alignment | Target Description | Inhibition | Multiplicity |
|---|---|---|---|---|---|---|---|
| sbi-MIR167k | TC126582 | 3.0 | 22.004 | miRNA 21 GUCUAGUACGACCGUCGAAGU 1<br>:::::::: :::: :::::::<br>Target 522 CAGAUCAUCCUGG-AGCUUCA 541 | weakly similar to UniRef100_A7R7C3 Cluster: Chromosome undetermined scaffold_1678, whole genome shotgun sequence; n=1; Vitis vinifera\|Rep: Chromosome undetermined scaffold_1678, whole genome shotgun sequence - Vitis vinifera (Grape), partial (36%) | Cleavage | 1 |
| sbi-MIR171l | TC111579 | 3.0 | 22.697 | miRNA 20 CACUAUAACCGUGCCGAGUU 1<br>:::.:  ::::::::.::::<br>Target 455 GUGGUUGUGGCACGGUUCAA 474 | similar to UniRef100_A7QB21 Cluster: 6,7-dimethyl-8-ribityllumazine synthase; n=1; Vitis vinifera\|Rep: 6,7-dimethyl-8-ribityllumazine synthase - Vitis vinifera (Grape), partial (71%) | Cleavage | 1 |
| sbi-MIR171l | TC111734 | 3.0 | 22.697 | miRNA 20 CACUAUAACCGUGCCGAGUU 1<br>:::.:  ::::::::.::::<br>Target 302 GUGGUUGUGGCACGGUUCAA 321 | similar to UniRef100_A7QB21 Cluster: 6,7-dimethyl-8-ribityllumazine synthase; n=1; Vitis vinifera\|Rep: 6,7-dimethyl-8-ribityllumazine synthase - Vitis vinifera (Grape), partial (82%) | Cleavage | 1 |
| sbi-MIR171m | TC111579 | 3.0 | 22.697 | miRNA 20 CACUAUAACCGUGCCGAGUU 1<br>:::.:  ::::::::.::::<br>Target 455 GUGGUUGUGGCACGGUUCAA 474 | similar to UniRef100_A7QB21 Cluster: 6,7-dimethyl-8-ribityllumazine synthase; n=1; Vitis vinifera\|Rep: 6,7-dimethyl-8-ribityllumazine synthase - Vitis vinifera (Grape), partial (71%) | Cleavage | 1 |
| sbi-MIR171m | TC111734 | 3.0 | 22.697 | miRNA 20 CACUAUAACCGUGCCGAGUU 1<br>:::.:  ::::::::.::::<br>Target 302 GUGGUUGUGGCACGGUUCAA 321 | similar to UniRef100_A7QB21 Cluster: 6,7-dimethyl-8-ribityllumazine synthase; n=1; Vitis vinifera\|Rep: 6,7-dimethyl-8-ribityllumazine synthase - Vitis vinifera (Grape), partial (82%) | Cleavage | 1 |
| sbi-MIR171m | CN129969 | 3.0 | 22.88 | miRNA 20 CACUAUAACCGUGCCGAGUU 1<br>:::.:  ::::::::.::::<br>Target 308 GUGGUUGUGGCACGGUUCAA 327 | similar to UniRef100_A7QB21 Cluster: 6,7-dimethyl-8-ribityllumazine synthase; n=1; Vitis vinifera\|Rep: 6,7-dimethyl-8-ribityllumazine synthase - Vitis vinifera (Grape), partial (82%) | Cleavage | 1 |



(d)

| miRNA Acc. | Target Acc. | Expectation (E) | Target Accessibility (UPE) | Alignment | Target Description | Inhibition | Multiplicity |
|---|---|---|---|---|---|---|---|
| sbi-MIR396f | TC122672 | 3.0 | 22.308 | miRNA 20 GAAGGUGUCGAAAGAACUUG 1<br>::::: .::::: ::::::.<br>Target 972 CUUCCUUAGCUUGCUUGAAU 991 | homologue to UniRef100_Q0J367 Cluster: Os09g0252000 protein; n=1; Oryza sativa Japonica Group\|Rep: Os09g0252000 protein - Oryza sativa subsp. japonica (Rice), partial (70%) | Cleavage | 1 |
| sbi-MIR396g | TC125110 | 3.0 | 6.339 | miRNA 21 AAAGGGUGUCGAAAUAACUUG 1<br>::::::::: .::: ::::::<br>Target 19 UUUCCCACAAUUUUUUUGAAC 39 | homologue to UniRef100_Q0J6K9 Cluster: Os08g0300200 protein; n=3; Oryza sativa\|Rep: Os08g0300200 protein - Oryza sativa subsp. japonica (Rice), partial (17%) | Cleavage | 1 |
| sbi-MIR396g | CD222706 | 3.0 | 21.486 | miRNA 20 AAGGGUGUCGAAAUAACUUG 1<br>:::  ::::.::::::::.:<br>Target 329 UUCGAACAGUUUUAUUGAGC 348 | homologue to UniRef100_Q45W77 Cluster: Ubiquitin carrier protein; n=1; Arachis hypogaea\|Rep: Ubiquitin carrier protein - Arachis hypogaea (Peanut), partial (95%) | Cleavage | 1 |
| sbi-MIR396g | TC114514 | 3.0 | 21.486 | miRNA 20 AAGGGUGUCGAAAUAACUUG 1<br>:::  ::::.::::::::.:<br>Target 458 UUCGAACAGUUUUAUUGAGC 477 | homologue to UniRef100_Q45W77 Cluster: Ubiquitin carrier protein; n=1; Arachis hypogaea\|Rep: Ubiquitin carrier protein - Arachis hypogaea (Peanut), complete | Cleavage | 1 |
| sbi-MIR396h | NP429889 | 1.0 | 19.887 | miRNA 21 GUCAAGUUCUUUCGGACACCU 1<br>: ::::::::::::::::::<br>Target 363 CCGUUCAAGAAAGCCUGUGGA 383 | GB\|AF466199.1\|AAL68844.1 putative growth-regulating factor 1 [Sorghum bicolor] | Cleavage | 1 |
| sbi-MIR396h | TC114909 | 1.0 | 20.189 | miRNA 21 GUCAAGUUCUUUCGGACACCU 1<br>: ::::::::::::::::::<br>Target 599 CCGUUCAAGAAAGCCUGUGGA 619 | similar to UniRef100_Q9SDZ5 Cluster: Growth-regulating factor 1; n=2; Oryza sativa\|Rep: Growth-regulating factor 1 - Oryza sativa (Rice), partial (53%) | Cleavage | 1 |
| sbi-MIR396h | CD204209 | 3.0 | 23.238 | miRNA 20 UCAAGUUCUUUCGGACACCU 1<br>.: :::.::.:::.::::::<br>Target 137 GGCUCAGGAGAGCUUGUGGA 156 | similar to UniRef100_A7Q5D4 Cluster: Chromosome undetermined scaffold_53, whole genome shotgun sequence; n=1; Vitis vinifera\|Rep: Chromosome undetermined scaffold_53, whole genome shotgun sequence - Vitis vinifera (Grape), partial (15%) | Cleavage | 1 |
| sbi-MIR396i | TC115103 | 2.0 | 12.498 | miRNA 20 UCAAGUUAUUUCGACACCCU 1<br>:: ::::::.::.:::::::<br>Target 1788 AGAUCAAUAGAGUUGUGGGA 1807 | similar to UniRef100_Q6Q502 Cluster: Homeodomain leucine zipper protein 16; n=1; Oryza sativa Japonica Group\|Rep: Homeodomain leucine zipper protein 16 - Oryza sativa subsp. japonica (Rice), partial (60%) | Cleavage | 1 |
| sbi-MIR396i | CD234788 | 2.0 | 16.402 | miRNA 20 UCAAGUUAUUUCGACACCCU 1<br>:: ::::::.::.:::::::<br>Target 437 AGAUCAAUAGAGUUGUGGGA 456 | weakly similar to UniRef100_Q6Q502 Cluster: Homeodomain leucine zipper protein 16; n=1; Oryza sativa Japonica Group\|Rep: Homeodomain leucine zipper protein 16 - Oryza sativa subsp. japonica (Rice), partial (17%) | Cleavage | 1 |
| sbi-MIR396j | TC115103 | 2.0 | 12.498 | miRNA 20 UCAAGUUAUUUCGACACCCU 1<br>:: ::::::.::.:::::::<br>Target 1788 AGAUCAAUAGAGUUGUGGGA 1807 | similar to UniRef100_Q6Q502 Cluster: Homeodomain leucine zipper protein 16; n=1; Oryza sativa Japonica Group\|Rep: Homeodomain leucine zipper protein 16 - Oryza sativa subsp. japonica (Rice), partial (60%) | Cleavage | 1 |
| sbi-MIR396j | CD234788 | 2.0 | 16.402 | miRNA 20 UCAAGUUAUUUCGACACCCU 1<br>:: ::::::.::.:::::::<br>Target 437 AGAUCAAUAGAGUUGUGGGA 456 | weakly similar to UniRef100_Q6Q502 Cluster: Homeodomain leucine zipper protein 16; n=1; Oryza sativa Japonica Group\|Rep: Homeodomain leucine zipper protein 16 - Oryza sativa subsp. japonica (Rice), partial (17%) | Cleavage | 1 |
| sbi-MIR396k | TC114909 | 1.5 | 20.161 | miRNA 21 CAAGUUCUUUCGGACACCUCU 1<br>:::::::::::::::::: :<br>Target 601 GUUCAAGAAAGCCUGUGGAAA 621 | similar to UniRef100_Q9SDZ5 Cluster: Growth-regulating factor 1; n=2; Oryza sativa\|Rep: Growth-regulating factor 1 - Oryza sativa (Rice), partial (53%) | Cleavage | 1 |
| sbi-MIR396k | NP429889 | 2.5 | 19.787 | miRNA 21 CAAGUUCUUUCGGACACCUCU 1<br>::::::::::::::::::<br>Target 365 GUUCAAGAAAGCCUGUGGAAG 385 | GB\|AF466199.1\|AAL68844.1 putative growth-regulating factor 1 [Sorghum bicolor] | Cleavage | 1 |
| sbi-MIR396k | TC121345 | 3.0 | 20.539 | miRNA 22 UCAAGUUCUUUCGGACACCUCU 1<br>.::: ::::::::.:::: :::<br>Target 438 GGUUAAAGAAAGCUUGUGAAGA 459 | similar to UniRef100_A7PZJ8 Cluster: Chromosome chr15 scaffold_40, whole genome shotgun sequence; n=1; Vitis vinifera\|Rep: Chromosome chr15 scaffold_40, whole genome shotgun sequence - Vitis vinifera (Grape), partial (76%) | Cleavage | 1 |
| sbi-MIR396k | CD207048 | 3.0 | 22.213 | miRNA 21 CAAGUUCUUUCGGACACCUCU 1<br>::::::::: ::.:::::::.<br>Target 323 GUUCAAGAA-GCUUGUGGAGG 342 | similar to UniRef100_Q0IH39 Cluster: LOC779079 protein; n=1; Xenopus laevis\|Rep: LOC779079 protein - Xenopus laevis (African clawed frog), partial (12%) | Cleavage | 1 |



(e)

| miRNA Acc. | Target Acc. | Expectation (E) | Target Accessibility (UPE) | Alignment | Target Description | Inhibition | Multiplicity |
|---|---|---|---|---|---|---|---|
| sbi-MIR398b | TC130860 | 3.0 | 9.938 | miRNA 20 UACACAAGGGUCAGGCGGGG 1<br>:::: :::::: :::::::<br>Target 1575 AUGUCUUCCCAUUCCGCCCA 1594 | UniRef100_P06586 Cluster: Chloroplast 30S ribosomal protein S3; n=4; Andropogoneae\|Rep: Chloroplast 30S ribosomal protein S3 - Zea mays (Maize), complete | Translation | 1 |
| sbi-MIR398b | CF480868 | 3.0 | 14.56 | miRNA 20 UACACAAGGGUCAGGCGGGG 1<br>::::::: ::::::::..:<br>Target 392 CUGUGUUCACAGUCCGCUUC 411 | similar to UniRef100_A7QQL2 Cluster: Chromosome undetermined scaffold_143, whole genome shotgun sequence; n=1; Vitis vinifera\|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequence - Vitis vinifera (Grape), partial (18%) | Cleavage | 1 |
| sbi-MIR398b | TC113079 | 3.0 | 14.848 | miRNA 20 UACACAAGGGUCAGGCGGGG 1<br>::::::: ::::::::..:<br>Target 353 CUGUGUUCACAGUCCGCUUC 372 | similar to UniRef100_A7QQL2 Cluster: Chromosome undetermined scaffold_143, whole genome shotgun sequence; n=1; Vitis vinifera\|Rep: Chromosome undetermined scaffold_143, whole genome shotgun sequence - Vitis vinifera (Grape), partial (73%) | Cleavage | 1 |
| sbi-MIR398b | BG158064 | 3.0 | 19.165 | miRNA 20 UACACAAGGGUCAGGCGGGG 1<br>.: ::::.:::::..:::::<br>Target 266 GUCUGUUUCCAGUUUGCCCC 285 | similar to UniRef100_Q641B1 Cluster: MGC83343 protein; n=1; Xenopus laevis\|Rep: MGC83343 protein - Xenopus laevis (African clawed frog), partial (6%) | Cleavage | 1 |
| sbi-MIR444a | TC127476 | 0.5 | 16.5 | miRNA 21 UUCGAACUCUGUUGUUGACGU 1<br>:::::::::.:::::::::::<br>Target 440 AAGCUUGAGGCAACAACUGCA 460 | similar to UniRef100_Q6Z6W2 Cluster: MADS-box transcription factor 57; n=2; Oryza sativa Japonica Group\|Rep: MADS-box transcription factor 57 - Oryza sativa subsp. japonica (Rice), partial (44%) | Cleavage | 1 |
| sbi-MIR444a | TC125842 | 2.0 | 18.582 | miRNA 21 UUCGAACUCUGUUGUUGACGU 1<br>.::: ::::.:::::.:::::<br>Target 43 GAGCCUGAGGCAACAGCUGCA 63 | similar to UniRef100_Q84SC7 Cluster: Zinc finger (C3HC4-type RING finger) protein-like; n=1; Oryza sativa Japonica Group\|Rep: Zinc finger (C3HC4-type RING finger) protein-like - Oryza sativa subsp. japonica (Rice), partial (14%) | Cleavage | 1 |
| sbi-MIR444a | CD225619 | 3.0 | 18.11 | miRNA 21 UUCGAACUCUGUUGUUGACGU 1<br>:::: ::::.::. :::::::<br>Target 112 AAGCAUGAGGCAGGAACUGCA 132 | UniRef100_Q6Z6W2 Cluster: MADS-box transcription factor 57; n=2; Oryza sativa Japonica Group\|Rep: MADS-box transcription factor 57 - Oryza sativa subsp. japonica (Rice), partial (8%) | Cleavage | 1 |
| sbi-MIR444a | TC124738 | 3.0 | 18.565 | miRNA 21 UUCGAACUCUGUUGUUGACGU 1<br>:.:::::::::  ::.::::<br>Target 162 AGGCUUGAGACACAAAUUGCA 182 | similar to UniRef100_Q0JAY4 Cluster: Os04g0568400 protein; n=2; Oryza sativa Japonica Group\|Rep: Os04g0568400 protein - Oryza sativa subsp. japonica (Rice), partial (41%) | Translation | 1 |
| sbi-MIR444a | TC128293 | 3.0 | 19.373 | miRNA 21 UUCGAACUCUGUUGUUGACGU 1<br>:::: ::::.::. :::::::<br>Target 107 AAGCAUGAGGCAGGAACUGCA 127 |  | Cleavage | 1 |
| sbi-MIR444b | TC127476 | 0.5 | 18.61 | miRNA 21 CCGUCGUUCGAACUCUGUUGU 1<br>::::::::::::::::.:::::<br>Target 434 GGCAGCAAGCUUGAGGCAACA 454 | similar to UniRef100_Q6Z6W2 Cluster: MADS-box transcription factor 57; n=2; Oryza sativa Japonica Group\|Rep: MADS-box transcription factor 57 - Oryza sativa subsp. japonica (Rice), partial (44%) | Cleavage | 1 |
| sbi-MIR444b | TC120067 | 2.0 | 19.722 | miRNA 20 CGUCGUUCGAACUCUGUUGU 1<br>::::.:::.:::::::::..<br>Target 72 GCAGUAAGUUUGAGACAAUG 91 | similar to UniRef100_Q0E0H6 Cluster: Os02g0550900 protein; n=1; Oryza sativa Japonica Group\|Rep: Os02g0550900 protein - Oryza sativa subsp. japonica (Rice), partial (20%) | Cleavage | 1 |
| sbi-MIR444b | TC119833 | 3.0 | 13.879 | miRNA 20 CGUCGUUCGAACUCUGUUGU 1<br>: :::::: ::::::.::.:<br>Target 299 GAAGCAAGGUUGAGAUAAUA 318 | homologue to UniRef100_O23813 Cluster: Ferredoxin-sulfite reductase precursor; n=1; Zea mays\|Rep: Ferredoxin-sulfite reductase precursor - Zea mays (Maize), partial (57%) | Cleavage | 1 |
| sbi-MIR444c | TC127476 | 0.0 | 19.83 | miRNA 21 GUUGAACGUUCUUUCGGUGUU 1<br>:::::::::::::::::::::<br>Target 461 CAACUUGCAAGAAAGCCACAA 481 | similar to UniRef100_Q6Z6W2 Cluster: MADS-box transcription factor 57; n=2; Oryza sativa Japonica Group\|Rep: MADS-box transcription factor 57 - Oryza sativa subsp. japonica (Rice), partial (44%) | Cleavage | 1 |
| sbi-MIR444c | TC117076 | 2.0 | 18.854 | miRNA 21 GUUGAACGUUCUUUCGGUGUU 1<br>:::::::::: :.:::.::::<br>Target 1103 CAACUUGCAAAAGAGCUACAA 1123 | homologue to UniRef100_Q9XHR2 Cluster: Eukaryotic translation initiation factor 3 subunit A; n=1; Zea mays\|Rep: Eukaryotic translation initiation factor 3 subunit A - Zea mays (Maize), partial (60%) | Translation | 1 |

**Supplemental Table 1:** miRNAs expression in differen

| miRNA Family | Target Gene Acc. | Gene Synonym | Callus | Embryo | Leaf | Ovary | Panicle |
|---|---|---|---|---|---|---|---|
| sbi-MIR156j | BG947367 | Sb02g029300 | [redacted] | | | | |
| sbi-MIR156j | EH409419 | Sb01g038620 | | | | [redacted] | |
| sbi-MIR156j | CF756128 | Sb01g027940 | | | | | |
| sbi-MIR156k | BG947367 | Sb02g029300 | [redacted] | | | | |
| sbi-MIR156k | CF756053 | Sb01g027940 | | | | | |
| sbi-MIR156l | BG947367 | Sb02g029300 | [redacted] | | | | |
| sbi-MIR156m | BG948102 | Sb09g004120 | | | | | [redacted] |
| sbi-MIR156m | BM325400 | Sb04g033230 | | | [redacted] | [redacted] | [redacted] |
| sbi-MIR166m | CF074035 | Sb08g005200 | | | | | |
| sbi-MIR166o | CF074035 | Sb08g005200 | | | | | |
| sbi-MIR166p | CF074035 | Sb08g005200 | | | | | |
| sbi-MIR166q | CF074035 | Sb08g005200 | | | | | |
| sbi-MIR166r | CF074035 | Sb08g005200 | | | | | |
| sbi-MIR167j | CX614408 | Sb04g033320 | | | | | |
| sbi-MIR167k | CD423596 | Sb08g021460 | | | | [redacted] | [redacted] |
| sbi-MIR168c | CD209773 | Sb04g030860 | | | [redacted] | | |
| sbi-MIR171l | CN129969 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR171l | CN142205 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR171l | AW747132 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR171l | CN131513 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR171 | CN131513 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR171m | CN129969 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR171m | BM317608 | Sb06g031050 | | | [redacted] | [redacted] | |
| sbi-MIR390b | BE363723 | Sb08g002760 | | | | [redacted] | |
| sbi-MIR396f | CF480198 | Sb09g022550 | | | [redacted] | | |
| sbi-MIR396g | CB927788 | NTMC2T2.2 | | | [redacted] | | [redacted] |
| sbi-MIR396h | CD204209 | Sb09g019370 | | | [redacted] | | |
| sbi-MIR396k | AW676947 | Sb04g034800 | | | | | |
| sbi-MIR396k | BM329506 | Sb10g004460 | | | [redacted] | | |
| sbi-MIR398b | CF480868 | Sb08g001790 | | | | | |
| sbi-MIR398b | CF487358 | Sb08g001790 | | | | | |
| sbi-MIR444a | CD224118 | Sb03g012810 | [redacted] | | | [redacted] | |
| sbi-MIR444a | CN125113 | Sb06g025690 | | [redacted] | | [redacted] | |
| sbi-MIR444b | AW564049 | Sb09g024840 | [redacted] | [redacted] | [redacted] | | |
| sbi-MIR444c | BM325378 | Sb03g007840 | | | [redacted] | [redacted] | |

*Transcript per million (TPM)

t tissues and developmental stages

| Pollen | Root | Shoot | TPM* | Gene EST | Total EST in Pool |
|---|---|---|---|---|---|
| | | | 206 | 2 | 9689 |
| | ● | | 218/55 | 2/1 | 9137/17945 |
| ● | | | 221 | 2 | 26 |
| | | | 206 | 2 | 9689 |
| ● | | | 221 | 2 | 9026 |
| | | | 206 | 2 | 9689 |
| | ● | | 232/55 | 2/1 | 8617/17945 |
| | | | 103/218/232 | 2/2/2/ | 19261/9137/8617 |
| | | ● | 188 | 2 | 10613 |
| | | ● | 188 | 2 | 10613 |
| | | ● | 188 | 2 | 10613 |
| | | ● | 188 | 2 | 10613 |
| | | ● | 188 | 2 | 10613 |
| | ● | ● | 111/659 | 2/7/ | 17945/10613 |
| | ● | | 218/232/55 | 2/2/1 | 9137/8617/17945 |
| | | | 103 | 2 | 19261 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| ● | ● | | 155/218/221/501 | 3/2/2/9 | 19261/9137/9026/17945 |
| | | | 218 | 2 | 9137 |
| ● | | | 103/221 | 2/2 | 19261/9026 |
| | ● | | 155/464/111 | 3/4/2 | 19261/8617/17945 |
| | | | 103 | 2 | 19261 |
| | ● | | 55 | 1 | 17945 |
| ● | ● | | 259/221/55 | 5/2/1 | 19261/9026/17945 |
| ● | ● | | 664/111 | 6/2/ | 9026/17945 |
| ● | ● | | 664/111 | 6/2/ | 9026/17945 |
| | | | 206/328 | 2/3 | 9689/9137 |
| | ● | | 231/218/111 | 2/2/2/ | 4648/9137/17945 |
| ● | | | 309/578/726/110 | 3/5/14/1 | 9689/8648/19261/9026 |
| | | | 51/109 | 1/1/ | 19261/9137 |