Appendix 1. Sequencing Result for Six egu-pre-miR172

Description: sequencing result of precursor miR172 in oil palm tissues (root, shoot, leaf, mature and immature flowers). Underlined italicized bases indicate mature miR172 location.

egu-pre-miR172a:

5'-UGUGCAGCAUCAUCAAGAUUCACAUCTGUUAAUCACUGCCAAAUUCTGU
UUAGUUAUUGAUCCUGAGCCUUCAACAUCUGCGUUGUCUCAGGAGGUGAAU
GAAGGAAUGCAGGUGCGACAACAAGGCGUACGGUCUGGGAGAUAUGCCAAA
GAAGUCUACAGGGACAAAGGAUG*AGAAUCUUGAUGAUGCUGCAU*-3'

egu-pre-miR172b:

5'-GUGCAGCAUCAUCAAGAUUCACAUCCUUUUCAGCUUCUGAUACCAAUAA
ACCCUUACAUGAUAACAAAGAUGUGCCUUCAGUGCUAGGCUUCUCAUUUUG
GUUAUUACUAUUAUCGUAAUUGUCCCUGCAACCCUUGCUAUCCAACAGAUG*A*
GAAUCUUGAUGAUGCUGCAU-3'

egu-pre-miR172c:

5'-GUGCAGCAUCAUCAAGAUUCACAUCCUUCGCCCAUCUCUGCUUGUGCCCC
CCAGGAGAAGGGUAUUUCAGGAUUUCUUAUAGAUUUUCUUAUGGGAGGAGU
UUCUGCUGCUGUCUCGAAAACAGCAGCUGCUCCAAUUGAGCGGGUGAAGCU
CUUAAUUCAGAACCAGGAUG*AGAAUCUUGAUGAUGCUGCAU*-3'

egu-pre-miR172d:

5'-GUGCAGCAUCAUCAAGAUUCACAUCGUUCCCAUCUCUGGGUUUGAAGGU

GAUAACAUGAUUGACAGGUCCACCAACCUUGAUUGGUACAAGGGCCCGACCC

UUCUUGAGGCUCUUGACUUGAUACAGGAGCCCAAGAGGCCCUCAGACAAGCC

CCUCCGUCUUCCACUUCAGGAUG*UGAAUCUUGAUGAUGCUGCAC*-3'

egu-pre-miR172e:

5'-AUGCAGCAUCAUCAAGAUUCUCAUCCUGGUUCUGAAUUAAGAGCUUCAC

CCGCUCAAUUGGAGCAGCUGCTGUUUUCGAGACAGCAGCAGAAACUCCUCCC

AUAAGAAAAUCUAUAAGAAAUCCUGAAAUACCCUUCUCCUGGGGGGGCACAA

GCAGAGAUGGGCGAUGGAUG*UGAAUCUUGAUGAUGCUGCAC*-3'

egu-pre-miR172f:

5'-AUGCAGCAUCAUCAAGAUUCUCAUCUUCUGUGCCUUUGACUUGUCGUAG

CGAGGAUGAGAUCUUGCAGUGCUCCAAACUGAGGUGCUUCGCCUUCAGCGA

UCUCAAAACCGCCACCAGGAAUUUCCGUCUCGAUAGCGUAUUGGGAGAGGG

GGGCUUCGGUUCUGUCUUCAAGGGAUG*UGAAUCUUGAUGAUGCUGCAC*-3'

Appendix 2. Sequence Reference Points in pGEM-T Easy Vector (Promega, USA)

Description: The insert sequences of egu-pre-miR172 in pGEM-T Easy vector was sequenced using the M13 forward primer (-20), which is located at the 2941-2957bp of the vector.

pGEM®-T Easy Vector Map and Sequence Reference Points
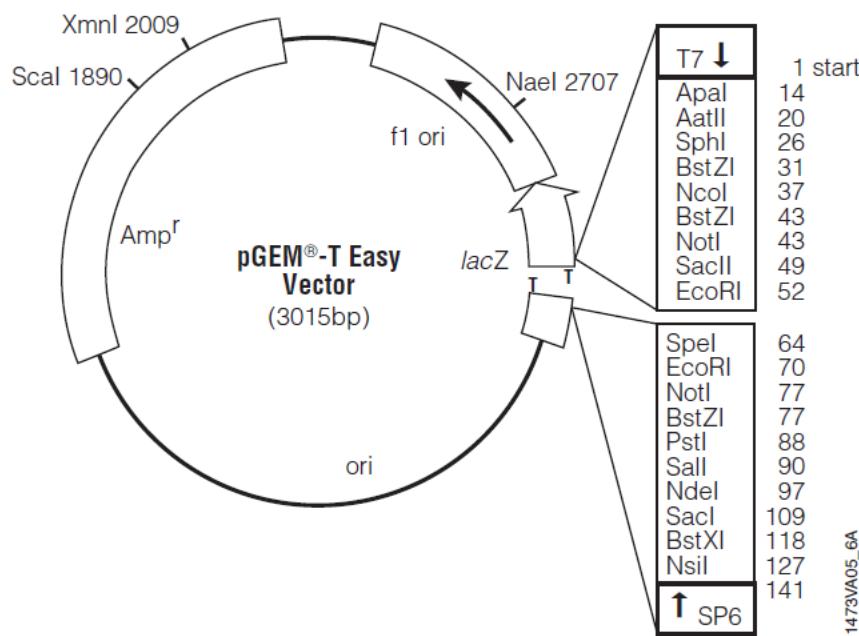
Appendix 3. Alignment of Three miR172 Paralogs with Same Isoforms

Description: ClustalW alignment of three paralogs with the same isoforms, also confirmed that the most highly conserved regions of the egu-miR172 in oil palm were mature and "star" sequences.

```
CLUSTAL 2.0.12 multiple sequence alignment


egu-pre-miR172e     ---AUGCAGCAUCAUCAAGAUUCUCAUC----CUG-GUUCU--GAAU--UAAG-AGCUUC 47
egu-pre-miR172f     ---AUGCAGCAUCAUCAAGAUUCUCAUCUU--CUGUG-CCUUUGACU----UGUCGU--A 48
egu-pre-miR172d     ---GUGCAGCAUCAUCAAGAUUCACAUCGUUCCCAUCUCU---GGGUUUGAAGGUGAU-A 53
                       .****************** ****    * .         *. *     * *    .

egu-pre-miR172e     ACCCGCUCAAUUGGAGCAG-CU-GCTGUUUUCGAGACAGCAG---------CAGAAACUC 96
egu-pre-miR172f     GCGAGG--AU---GAGAU--CUUGCAGU----GCUCCAAACU---------GAGGUGCUU 88
egu-pre-miR172d     ACAUGAU-----UGACAGGUC---CA---------CCAACCUUGAUUGGUACAAGGGCCC 96
                    .*  *         **  .   *   *:          .**...        *.. .*

egu-pre-miR172e     CUCCCAUAAGAAAAU-CUAUAAGAAAUCCUGAAAU-ACCCUUCUCCU-GGGG-G--GCAC 150
egu-pre-miR172f     CGCCUU-CAGCGAUCUCAAAACCGCCACCAGGAAUUUCCGU-CUCGAUAGCGUAUUGGGA 146
egu-pre-miR172d     GACCCUUCUUGAGGCUCUUGACUUGAUACAGGAG----CC----CAAGAGGCCCUCAGAC 148
                         **   .   ..   *    *.   . .* *.*.    *      *   .*     . ..

egu-pre-miR172e     AAGCAGAGAU--GG----G----CGAU----GGAUGUGAAUCUUGAUGAUGCUGCAC 193
egu-pre-miR172f     GAGGGGGGCUUCGGUUCUGUCUUCAAG----GGAUGUGAAUCUUGAUGAUGCUGCAC 199
egu-pre-miR172d     AAGCCCCUC--CGU------CUUCCACUUCAGGAUGUGAAUCUUGAUGAUGCUGCAC 197
                    .**    .   *        * *    *************************


CLUSTAL 2.0.12 multiple sequence alignment


egu-miR172e     AUGCAGCAUCAUCAAGAUUCUCAUC----CUG-GUUCU--GAAU--UAAG-AGCUUCACC 50
egu-miR172f     AUGCAGCAUCAUCAAGAUUCUCAUCUU--CUGUG-CCUUUGACU----UGUCGU--AGCG 51
egu-miR172d     GUGCAGCAUCAUCAAGAUUCACAUCGUUCCCAUCUCU---GGGUUUGAAGGUGAU-AACA 56
                .****************** ****    * .         *. *     * *    ..*

egu-miR172e     CGCUCAAUUGGAGCAG-CU-GCTGUUUUCGAGACAGCAG---------CAGAAACUCCUC 99
egu-miR172f     AGG--AU---GAGAU--CUUGCAGU----GCUCCAAACU---------GAGGUGCUUCGC 91
egu-miR172d     UGAU-----UGACAGGUC---CA---------CCAACCUUGAUUGGUACAAGGGCCCGAC 99
                  *        **  .   *   *:          .**...        *.. .*    *

egu-miR172e     CCAUAAGAAAAU-CUAUAAGAAAUCCUGAAAU-ACCCUUCUCCU-GGGG-G--GCACAAG 153
egu-miR172f     CUU-CAGCGAUCUCAAAACCGCCACCAGGAAUUUCCGU-CUCGAUAGCGUAUUGGGAGAG 149
egu-miR172d     CCUUCUUGAGGCUCUUGACUUGAUACAGGAG----CC----CAAGAGGCCCUCAGACAAG 151
                *   .   ..   *    *.   . .* *.*.    *      *   .*     . ...**

egu-miR172e     CAGAGAU--GG----G----CGAU----GGAUGUGAAUCUUGAUGAUGCUGCAC 193
egu-miR172f     GGGGGCUUCGGUUCUGUCUUCAAG----GGAUGUGAAUCUUGAUGAUGCUGCAC 199
egu-miR172d     CCCCUC--CGU------CUUCCACUUCAGGAUGUGAAUCUUGAUGAUGCUGCAC 197
                  .   *        * *    *************************
```

Appendix 4. Dissociation Curve and Raw Data Values for Quantitative Real-time PCR of six pre-egu-miR172 paralogs.

Description: (A) The dissociation curve showed a single peak for all the six egu-miR172 precursors and β-actin, indicating that all the six pair of the Nested miR172 and internal control primers used in this study were specific (B) RQ value indicates mean concentration level from 3 samples replicates while Ct value (cycle threshold) is defined as the number of cycles required for the fluorescent signal to cross the threshold.

egu-pre-miR172a:

(A)

(B)
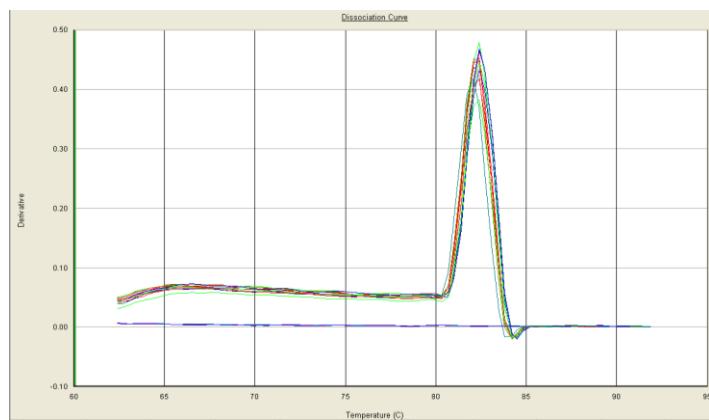
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	25.077	-4.230	0.000	1.000	0.966	1.035	0.03451	0.01992
Sh	24.671	-3.363	0.867	0.548	0.392	0.767	0.19527	0.11274
L	27.406	-2.096	2.134	0.228	0.178	0.291	0.05761	0.03326
R	27.965	-1.741	2.489	0.178	0.155	0.204	0.02463	0.01422
IF	25.364	-3.129	1.101	0.466	0.312	0.696	0.20296	0.11718

egu-pre-miR172b:

(A)

(B)
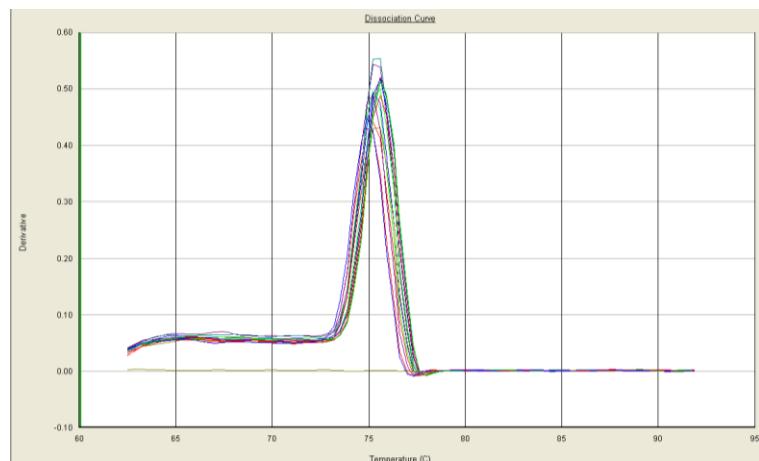
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	19.490	-9.205	0.000	1.000	0.877	1.140	0.13232	0.0764
Sh	23.290	-6.213	2.992	0.126	0.104	0.152	0.02424	0.014
L	31.307	1.377	10.581	6.53E-04	2.90E-04	0.001	0.00035	0.0002
R	21.114	-7.231	1.974	0.255	0.228	0.284	0.02805	0.0162
IF	18.935	-9.388	-0.183	1.135	0.851	1.514	0.34155	0.1972

egu-pre-miR172c:

(A)

(B)
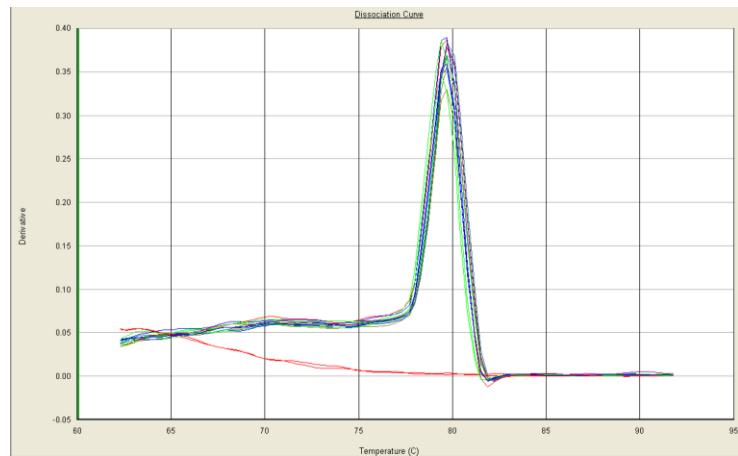
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	18.430	-11.539	0.000	1.000	0.909	1.100	0.09581	0.0553
Sh	25.992	-3.504	8.036	0.004	0.002	0.009	0.00435	0.00251
L	22.570	-7.579	3.961	0.064	0.052	0.080	0.01442	0.00832
R	21.456	-8.195	3.344	0.098	0.071	0.137	0.03459	0.01997
IF	18.708	-10.255	1.285	0.410	0.341	0.494	0.07759	0.0448

egu-pre-miR172d:

(A)

(B)
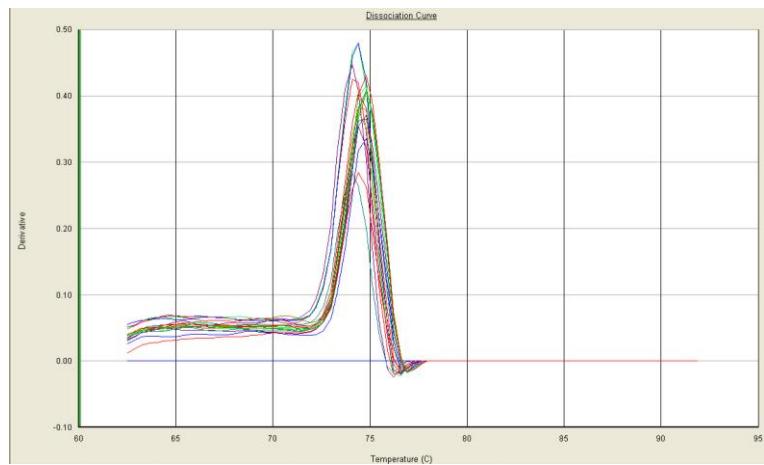
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	18.617	-10.718	0.000	1.000	0.912	1.097	0.09282	0.05359
Sh	23.267	-6.125	4.594	0.041	0.030	0.057	0.01417	0.00818
L	23.394	-7.440	3.278	0.103	0.071	0.149	0.04084	0.02358
R	21.027	-6.421	4.297	0.051	0.036	0.072	0.01873	0.01081
IF	19.189	-9.085	1.633	0.322	0.293	0.355	0.03119	0.01800

egu-pre-miR172e:

(A)

(B)
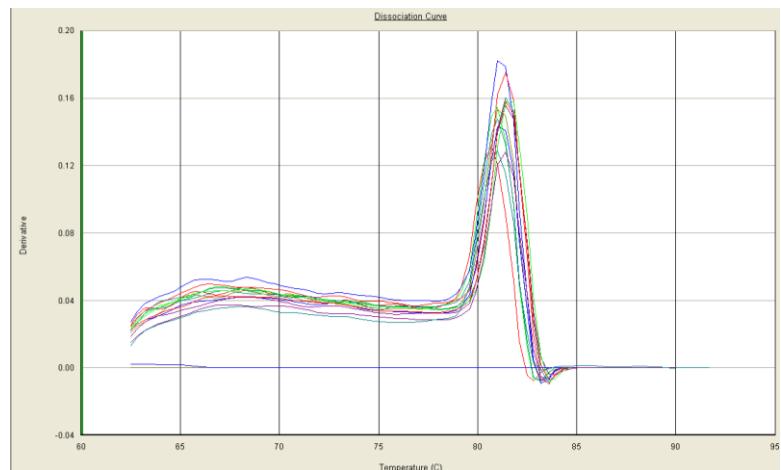
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	22.858	-5.836	0.000	1.000	0.899	1.112	0.10692	0.06173
Sh	27.874	-1.628	4.208	0.054	0.041	0.071	0.01539	0.00888
L	31.588	0.555	6.391	0.012	0.007	0.020	0.007	0.00404
R	25.234	-3.166	2.670	0.157	0.143	0.172	0.01452	0.00838
IF	24.132	-3.943	1.893	0.269	0,230	0.315	0.04293	0.02478

egu-pre-miR172f:

(A)

(B)
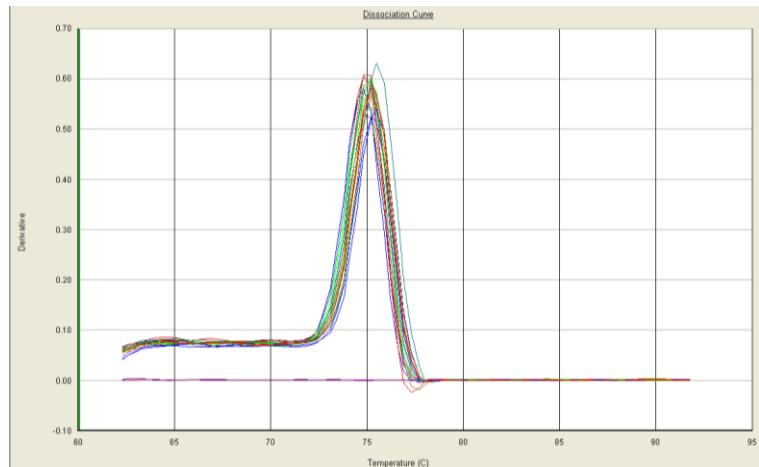
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	22.862	-5.833	0.000	1.000	0.802	1.246	0.22585	0.13039
Sh	25.987	-3.405	2.428	0.186	0.125	0.275	0.07882	0.04550
L	28.586	-1.563	4.270	0.052	0.027	0.100	0.04158	0.02400
R	25.846	-3.805	2.028	0.245	0.131	0.460	0.18630	0.10756
IF	22.316	-6.007	-0.174	1.129	0.913	1.395	0.24485	0.14136

β-actin:

(A)

(B)
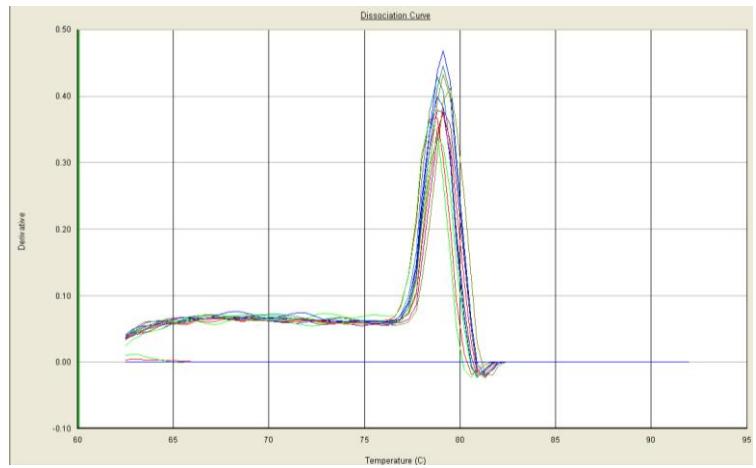
Sample	Avg Ct	Avg dCt	ddCt	RQ	RQ Min	RQ Max	StDev	std err
MF	22.862	30.148						
Sh	25.987	28.963						
L	28.586	29.496						
R	25.846	29.651						
IF	22.316	29.969						

Appendix 5. Clustal W Alignment of the EY408858.1 and EL692343.1from Oil Palm EST

Description: EY408858.1 is a truncated version of EST EL692343.1 with two nucleotides difference which, are outside of the predicted miR172 target region.

```
gi|161970769|gb|EL692343.1    ATACAATACTTGCGTGCAGGTACATATATCTTGGGCTATTCGACAGCGAA 50
gi|191194297|gb|EY408858.1    -------------------GTACATATATCTTGGGCTATTCGACAGCGAA 31
                                                 **************************

gi|161970769|gb|EL692343.1    ATAGAAGCTGCAAGGGCTTATGACAAGGCAGCTATAAAATGTAATGGAAG 100
gi|191194297|gb|EY408858.1    ATAGAAGCTGCAAGGGCTTATGACAAGGCAGCTATAAAATGTAATGGAAG 81
                              **************************************************

gi|161970769|gb|EL692343.1    GGATGCTGTTACCAATTTTGAGCCCAGCACCTATGAAGGAGAACTGCTTA 150
gi|191194297|gb|EY408858.1    GGATGCTGTTACCAATTTTGAGCCCAGCACCTATGAAGGAGAACTGCTTA 131
                              **************************************************

gi|161970769|gb|EL692343.1    CTGAGGCTAATAGTGAAGCAACTGGCCATGATGTTGATCTGAACTTGAGG 200
gi|191194297|gb|EY408858.1    CTGAGGCTAATAGTGAAGCAACTGGCCATGATGTTGATCTGAACTTGAGG 181
                              **************************************************

gi|161970769|gb|EL692343.1    ATTTCTCAACCTGTTGCCCATAGTCCAAAGAAGGATCACAATTCAATAGG 250
gi|191194297|gb|EY408858.1    ATTTCTCAACCTGTTGCCCATAGTCCAAAGAAGGATCACAATTCAATAGG 231
                              **************************************************

gi|161970769|gb|EL692343.1    CATCCAATTCCACTATGGCTTGCTTGAATCTTGGGATGCCAAGAAAGTAA 300
gi|191194297|gb|EY408858.1    CATCCAATTCCACTATGGCTTGCTTGAATCTTCTGATGCCAAGAAAGTAA 281
                              ********************************* ****************

gi|161970769|gb|EL692343.1    CGATTGACAGCACGTCTTCCCAATTGGCTGGTCAGCCGCATCATGTATGG 350
gi|191194297|gb|EY408858.1    CGATTGACAGCACGTCTTCCCAATTGGCTGGTCAGCCGCATCATGTATGG 331
                              **************************************************

gi|161970769|gb|EL692343.1    ACTGCTCAACGCCCAGCTCTCTTTCCTACCATTGAGGAAGGAGCAAGAGA 400
gi|191194297|gb|EY408858.1    ACTGCTCAACGCCCAGCTCTCTTTCCTACCATTGAGGAAGGAGCAAGAGA 381
                              **************************************************

gi|161970769|gb|EL692343.1|   GAAGAGGCTTGAGGTTGGTTCTCAAGCTCTACCCGCCTGGGCGTGGCAGA 450
gi|191194297|gb|EY408858.1|   GAAGAGGCTTGAGGTTGGTTCTCAAGCTCTACCCGCCTGGGCGTGGCAGA 431
                              **************************************************

gi|161970769|gb|EL692343.1|   TGCATGGCCCTACTCCATTGCCGCTGTTCTCTTCTGCAGCATCATCAGGA 500
gi|191194297|gb|EY408858.1|   TGCATGGCCCTACTCCATTGCCGCTGTTCTCTTCTGCAGCATCATCAGGA 481
                              **************************************************

gi|161970769|gb|EL692343.1|   TTCTCAACTACTGCTGTGACATCTGCCCATCCTTCCTCGCTGCCTCCTCC 550
gi|191194297|gb|EY408858.1|   TTCTCAACTACTGCTGTTACATCTGCCCATCCTTCCTCGCTGCCTCCTCC 531
                              ***************** ********************************

gi|161970769|gb|EL692343.1|   TTCGGCAACCCTGCATTCCCAGTTCAGCCTACCGGCTCCATCCAATTTTC 600
gi|191194297|gb|EY408858.1|   TTCGGCAACCCTGCATTCCCAGTTCAGCCTACCGGCTCCATCCAATTTTC 581
                              **************************************************

gi|161970769|gb|EL692343.1|   GATTCAGGAGCTGAAATCCATGTGCTTGGACCAGTGTATGTATGCTCTAG 650
gi|191194297|gb|EY408858.1|   GATTCAGGAGCTGAAATCCATGTGCTTGGACCAGTGTATGTATGCTC--- 628
                              ***********************************************

gi|161970769|gb|EL692343.1|   ACCACCGACATC 662
gi|191194297|gb|EY408858.1|   ------------
```

Appendix 6. Blast of EST EL692343.1 Sequence in NCBI

Description: (A) Nucleotide blast of same candidate in NCBI. (B) Protein blast of candidate AP2-like sequence from oil palm EST through NCBI. Nucleotide identity is 69% while protein identity shows 58%.

(A)

```
>   gb|AF134116.3|AF134116  Hyacinthus orientalis APETALA2 protein homolog HAP2 (HAP2) mRNA,
complete cds
Length=1597

 Score =  215 bits (238),  Expect = 2e-52
 Identities = 333/480 (69%), Gaps = 33/480 (6%)
 Strand=Plus/Plus

Query  62    AAGGGCTTATGACAAGGCAGCTATAAAATGTAATGGAAGGGATGCTGTTACCAATTTTGA  121
             ||  ||||||||||||| ||  ||||| ||  | | |||||||| |||||  ||||||||||
Sbjct  919   AAAGGCTTATGACAAAGCGGCTATCAAGAGCAGTGGAAGGGAAGCTGTAACCAATTTTGA  978

Query  122   GCCCAGCACCTATGAAGGAGAACTGCTTACTGAGGCTAATAGTGAAGCAACTGGCCATGA  181
             ||| ||  | ||||||| | ||| |||| |||||||||  |||||| || | ||||||||||
Sbjct  979   GCCAAGTTCTTATGAACGGGAAGTGCTCACTGAGGCAGATAGTGATGCCATTGGCCATGA  1038

Query  182   TGTTGATCTGAACTTGAGGATTTCTCAACC---TGTTGCCCATAGTCCAAAGAAGGATCA  238
             | |||||||||||||||||| |||||||||    ||||  |    |||||||||  |  | |
Sbjct  1039  CATCGATCTGAACTTGAGGATATCTCAACCGAATGTTAGC---AGTCCAAAGAGGCGTGA  1095

Query  239   CAATTCAATAGGCATCCAATTCCACTATGGCTTGCTTGAATCTTCGGATGCCAAGAAAGT  298
             ||| || | ||| ||| |||||| |  ||||  | ||||| || || ||||||||||||||
Sbjct  1096  TAATCCAGTTGGCGTCCAGTTCCATTTGGGCTCCTTCGAATCGTCTGACGCCAAGAAAGC  1155

Query  299   AACGATTGACAGCACGTCTTCCCAATTGGCTGGTCAGCCGCAT-------------CAT-  344
             | ||||||||| |  || ||  ||||  |||| ||||||||| |||           ||||
Sbjct  1156  TATGATTGACACCCATTCATCAATTTTGGTTGGTCAGCCCCATACGGCGGCAATGACATC  1215

Query  345   -------------GTATGGACTGCTCAACGCCCAGCTCTCTTTCCTACCATTGAGGAAGG  391
                          |||||| |||| |   || | ||| ||| | |||||| | |
Sbjct  1216  CGAGGCTTCTCGAGTATGGTCTGCCCTTTATCCTGGATTCTATCCCCCTATTGAGCTACG  1275

Query  392   AGCAAGAGAGAAGAGGCTTGAGGTTGGTTCTCAAGCTCTACCCGCCTGNGCGTGGCAGAT  451
             ||| | ||| ||||  |  | ||| |||||   ||| |||||   || | ||||| |
Sbjct  1276  AGCCAAAGACAAGATGTCTATGGTCGGTTCAGCAGCCCTACCAAATTGGACATGGCAATT  1335

Query  452   GCATGGCCCTACTCCATTGCCGCTGTTCTCTTCTGCAGCATCATCAGGATTCTCAACTAC  511
             ||| ||  || |  |||| |||| ||||| |||||||||||||||||||||||| | || ||
Sbjct  1336  GCACGGGCCAATGCCATCGCCGATGTTCACTTCTGCAGCATCATCAGGATTCGCCACCAC  1395
```

(B)

```
 Score =  174 bits (441),   Expect = 6e-42
 Identities = 87/148 (58%), Positives = 105/148 (70%), Gaps = 9/148 (6%)
 Frame = +3

Query   63    RAYDKAAIKCNGRDAVTNFEPSTYEGELLTEANSEATGHDVDLNLRISQPVAHSPKKDHN   242
              +AYDKAAIK +GR+AVTNFEPS+YE E+LTEA+S+A GHD+DLNLRISQP   SPK+  N
Sbjct  181    KAYDKAAIKSSGREAVTNFEPSSYEREVLTEADSDAIGHDIDLNLRISQPNVSSPKRRDN   240

Query  243    SIGIQFHYGLLESSDAKKVTIDSTSSQLAGQPH---------HVWTAQRPALFPTIEEGA   395
               +G+QFH G  ESSDAKK  ID+ SS L GQPH             VW+A  P  +P IE  A
Sbjct  241    PVGVQFHLGSFESSDAKKAMIDTHSSILVGQPHTAAMTSEASRVWSALYPGFYPPIELRA   300

Query  396    REKRLEVGSQALPAXAWQMHGPTPLPLF   479
              ++K    VGS ALP   WQ+HGP P P+F
Sbjct  301    KDKMSMVGSAALPNWTWQLHGPMPSPMF   328


 Score = 44.7 bits (104),   Expect = 0.008
 Identities = 23/43 (53%), Positives = 28/43 (65%), Gaps = 0/43 (0%)
 Frame = +3

Query   18    RYIYLGLFDSEIEAARAYDKAAIKCNGRDAVTNFEPSTYEGEL   146
              + +YLG FD+    AARAYD+AAIK  G DA  NF  S Y  +L
Sbjct   88    KQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYNEDL   130
```

144

Appendix 7. Blastx Analysis of Oil Palm EST EL692343.1 Sequence

Description: (A) The nucleotide sequence deduced amino acid sequence was analyzed and the sequence comparison was conducted through blastx database search in NCBI, which showed a specific result in AP2-like supper family. The first red line indicates the most similarity which is APETALA2 protein homolog HAP2 (*Hyacinthus orientalis*) (B) and also showed a closely relation to other AP2-like genes.
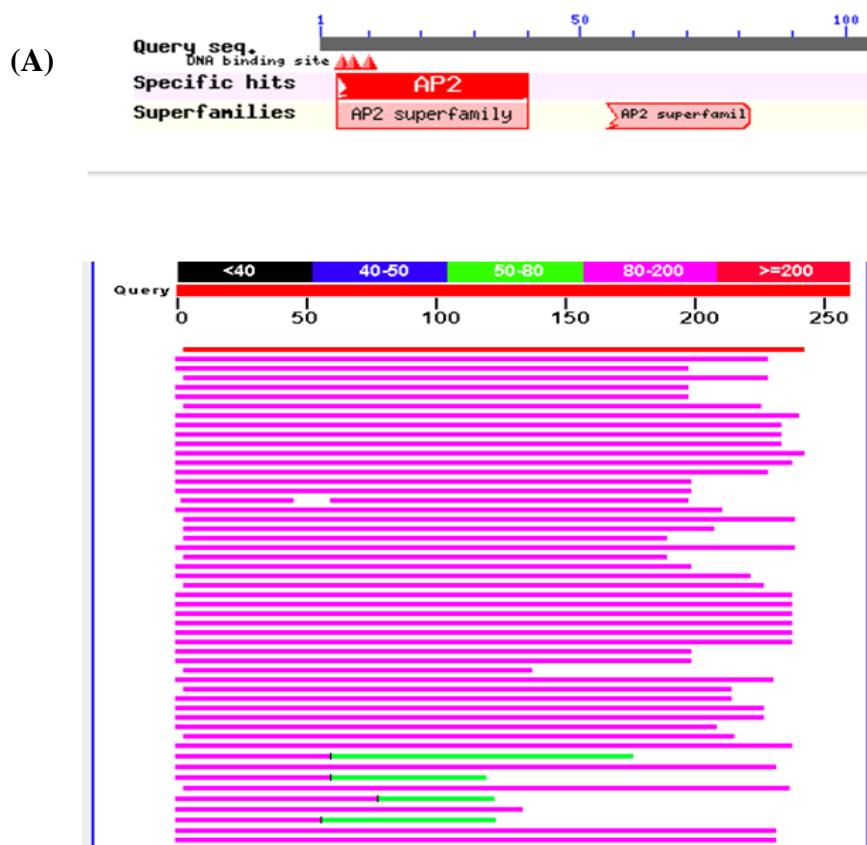
(B)

AP2-like families Producing Significant Alignments with EL692343.1:	Score (Bits)	E Value
gb|AAD22495.3| APETALA2 protein homolog HAP2 [Hyacinthus orientalis]	174	2e-39
gb|AAW78371.1| transcription factor AP2D23-like [Oryza sativa Japonica]	166	6e-42
gb|ABF99568.1| Floral homeotic protein APETALA2, putative, ex...	124	6e-27
gb|AAO65862.1| APETALA2-like protein [Oryza sativa Japonica Group]	124	6e-27
ref|XP_002326164.1| AP2 domain-containing transcription factor	124	7e-27
ref|XP_002322849.1| AP2 domain-containing transcription factor	123	1e-26
ref|XP_002525190.1| Floral homeotic protein APETALA2, putative…	120	1e-25
ref|NP_001104904.1| indeterminate spikelet1 [Zea mays]	116	2e-24
gb|AAD39440.1|AF132002_1 PHAP2B protein [Petunia x hybrida]	115	5e-24
gb|ABC71547.1| spikelet1-like AP2 transcription factor [Coix ...	114	1e-23
ref|XP_002312046.1| AP2 domain-containing transcription factor	112	2e-23
gb|ABR19871.1| AP2 domain transcription factor [Zea mays]	112	3e-23
gb|ABR19870.1| AP2 domain transcription factor [Zea mays]	111	5e-23
gb|ABY53104.1| APETALA2-like protein [Aegilops tauschii]	110	1e-22
gb|ACY30435.1| apetala 2-like protein [Nicotiana tabacum]	107	9e-22
gb|AAL50205.1| APETALA2-like protein [Hordeum vulgare subsp.]	106	2e-21
emb|CAE53890.1| putative AP2-like protein [Triticum aestivum]	103	1e-20
gb|ABC71546.1| spikelet1-like AP2 transcription factor [Setar...	100	2e-19
gb|AAO60032.1| putative transcription factor AP2 family protein	98.6	4e-19
dbj|BAE48514.1| APETALA2-like protein [Ginkgo biloba]	97.4	1e-18
ref|NP_001139539.1| sister of indeterminate spikelet 1 [Zea mayz]	94.0	1e-17
gb|ABM26976.1| APETALA2 L2 [Larix x marschlinsii]	95.1	5e-18
gb|ACN58224.1| sister of indeterminate spikelet 1 [Zea mays]	92.8	2e-17
dbj|BAE48516.1| APETALA2-like protein [Gnetum parvifolium]	92.8	2e-17
gb|ACD62792.1| APETALA2-like protein [Solanum lycopersicum]	92.0	4e-17
dbj|BAE48512.1| APETALA2-like protein 1 [Cycas revoluta]	92.0	4e-17
gb|AAY79346.1| AP2-related transcription factor AP2L3 [Picea ...	91.3	7e-17
gb|AAZ95247.1| APETALA2-like protein [Dendrobium crumenatum]	91.3	7e-17
gb|AAG32659.1| APETALA2-related transcription factor	90.9	9e-17
gb|AAX47049.1| AP2-like transcriptional factor [Brassica rapa]	90.5	1e-16
gb|AAD39439.1| PHAP2A protein [Petunia x hybrida]	90.5	4e-11
gb|ACG63707.1| transcription factor APETALA2 [Citrus trifoliata]	89.7	4e-11
gb|ABN10954.2| APETALA2-like protein [Ipomoea nil]	89.0	2e-11

gb|AAK14326.1| APETAL2-like protein [Pisum sativum]	87.8	9e-12
ref|XP_002310715.1| AP2 domain-containing transcription factor	87.4	1e-12
gb|ACO52508.1| transcription factor APETALA2 [Vitis vinifera]	87.4	1e-14
gb|AAG32658.1|AF253970_1 APETALA2-related transcription factor	87.4	1e-14
gb|AAM91531.1| APETALA2 protein [Arabidopsis thaliana]	86.7	1e-14
ref|NP_195410.1| AP2; transcription factor [Arabidopsis taliana]	86.7	9e-15
dbj|BAD16604.1| APETALA2-like protein 2 [Pinus thunbergii]	86.3	7e-15
ref|XP_002306481.1| AP2 domain-containing transcription factor	85.5	4e-15
ref|NP_201519.1| AP2 domain-containing transcription factor, ...	85.5	4e-15
dbj|BAD36744.1| APETALA2B [Ipomoea nil]	84.7	2e-15
gb|AAL57045.2| transcription factor AHAP2 [Malus x ...]	84.3	2e-15
gb|ABM26974.1| APETALA2 L1 [Larix x marschlinsii]	84.0	2e-15
dbj|BAD16603.1| APETALA2-like protein 1 [Pinus thunbergii]	84.0	1e-15
ref|XP_002315269.1| AP2 domain-containing transcription factor	83.6	1e-15
gb|ABR25960.1| transcription factor ap2d23-like protein [Oryza sativa]	77.0	1e-15
emb|CAR92295.1| relative to APETALA2 1 [Solanum tuberosum sub…]	74.3	8e-16
emb|CAE53889.1| putative APETALA2 protein [Triticum aestivum]	73.6	3e-16
gb|AAV83488.1| GLOSSY15 [Zea mays]	72.0	2e-16
ref|NP_001105890.1| glossy15 [Zea mays]	72.0	1e-16

Appendix 8. Raw Data Values for Figure 4.10

Description: (A) Raw data for relative expression of mature miR172 in 10, 11 and 12-month-old leaf (L), root (R) and shoot (Sh) (B) Raw data for relative expression of mature miR172 in flower (C) Raw data for relative expression of potential miR172 target (EST EL692343.1) in 10, 11 and 12-month-old leaf (L), root (R) and shoot (Sh) (D) Raw data for relative expression of potential miR172 target (EST EL692343.1) in flower.

(A)

Name	RQ	RQ2	RQ1(Min)	RQ3 (Max)	STDEV	Standard error
L10	1	0.997	0.945	1.058	0.05656	0.032655
L11	1.174	1.161	1.053	1.308	0.127996	0.073899
L12	2.294	2.289	2.18	2.413	0.11658	0.067308
R10	1.234	1.22	1.113	1.369	0.128573	0.074232
R11	1.531	1.514	1.382	1.697	0.158187	0.091329
R12	2.605	2.565	2.3	2.95	0.326841	0.188702
Sh10	0.629	0.614	0.544	0.729	0.093408	0.053929
Sh11	1.283	1.261	1.126	1.462	0.169077	0.097617
sh12	1.33	1.304	1.159	1.527	0.185373	0.107025

(B)

Name	RQ	RQ2	RQ1(Min)	RQ3 (Max)	STDEV	Standard error
Inflo (- fronds)	1	0.988	0.895	1.117	0.111485	0.064366
Inflo (+ fronds)	3.152	3.104	2.784	3.568	0.394198	0.22759
Emerged Flower	4.101	4.033	3.61	4.66	0.528293	0.30501
Mature Flower	45.56	45.486	43.759	47.435	1.839117	1.061815

(C)

Name	RQ	RQ2	RQ1(Min)	RQ3(Max)	STDEV	Standard error
L10	1	0.801	0.642	1.557	0.488883	0.282257
L11	0.442	0.181	0.208	0.937	0.428895	0.247623
L12	0.192	0.155	0.125	0.296	0.091307	0.052716
R10	0.395	0.26	0.222	0.703	0.267412	0.15439
R11	0.798	0.305	0.371	1.718	0.797426	0.460394
R12	2.749	2.447	1.975	3.825	0.961264	0.554986
Sh10	6.716	6.219	5.121	8.808	1.893079	1.09297
Sh11	0.389	0.32	0.257	0.59	0.176898	0.102132
Sh12	1.696	1.357	1.087	2.644	0.832017	0.480365

(D)

Name	RQ	RQ2	RQ1(Min)	RQ3(Max)	STDEV	Standard error
Inflo (- fronds)	1	0.995	0.929	1.076	0.073627	0
Inflo (+ fronds)	0.244	0.244	0.227	0.261	0.017	0.009815
Emerged Flower	1.993	1.782	1.442	2.755	0.681457	0.393439
Mature Flower	0.046	0.044	0.039	0.055	0.008185	0.004726