

Appendix A. Composition of Murashige and Skoog (MS) medium

Essential element	Concentration in stock solution (mg/L)	Concentration in medium (mg/L)
<i>Macro elements(a)</i>		
NH ₄ NO ₃	16500	1650
KNO ₃	19000	1900
CaCl ₂ .2H ₂ O	4400	440
MgSO ₄ .7H ₂ O	3700	370
H ₂ PO ₄	1700	170
<i>Microelements(b)</i>		
KI	83	0.83
H ₃ BO ₃	620	6.2
MnSO ₄ .4H ₂ O	2230	22.3
ZnSO ₄ .7H ₂ O	860	8.6
CuSO ₄ .5H ₂ O	25	0.25
CoCl ₂ .6H ₂ O	2.5	0.025
Na ₂ MoO ₇ .2H ₂ O	2.5	0.025
<i>Iron source(b)</i>		
FeSO ₄ .7H ₂ O	2780	27.8
Na ₂ EDTA.2H ₂ O	3730	37.3
<i>Organic supplement(b)</i>		
Myoinositol	10000	100
Nicotinic acid	50	0.5
Pyridoxine-HCl	50	0.5
Thiamine-HCl	50	0.5
Glycine	200	2
<i>Carbon source(c)</i>		
Sucrose	Added as solid	30 000

a: 100 ml of stock solution used per liter of medium.

b: 5ml of stock solution used per liter of medium.

c: 30g used per liter of medium.

Appendix B. Autoclaving

Volume(ml)	Pressure (psi)	Duration (min)
1-200	15	15
200-1000	15	30
1000-2000	15	40

Appendix C. LB agar medium preparation

To make 1 liter LB agar medium, 35g of LB agar (LENNOX) (PRONADISA) were added onto 900 ml distilled water followed by heat and agitating until boiling and dissolve completely. Solution was adjusted to final volume (1000 ml) and autoclaved at 121°C for 15 min. Agar was left to cool to approximately 55°C. Ampicillin (50µg/ml) plus 50µg/ml X-gal were added and subsequently a thin layer of LB agar (approximately 20 ml) was poured in to each plate (9 cm diameter Petri dish). After solidification, Plates were stored at 4°C.

Appendix D. LB broth medium preparation

To prepare 1 liter LB broth medium, 20 g of LB broth (LENNOX) (PRONADISA) were suspended in 900 ml distilled and dissolved by heating and frequent agitation until complete dissolution. Solution was adjusted to final volume (1000 ml) and autoclaved at 121°C for 15 min. After cooling down, medium was stored at 4°C.

Appendix E. Reagents and chemicals for CTAB method

Extraction buffer: mM Tris-HCl (pH 8.0); 25 mM EDTA; 2 M NaCl; 2% CTAB (w/v); 2 % PVP (w/v); 2% B-mercaptoethanol (v/v)

Chloroform/Isomylalcohol 24/1 (v/v)

70 % alcohol and isopropanol

Appendix F. Reagents and chemicals for CTAB modified method

Extraction buffer: mM Tris-HCl (pH 8.0); 25 mM EDTA; 2 M NaCl; 2% CTAB (w/v); 4 % PVP (w/v); 2% B-mercaptoethanol (v/v)

Proteinase K (20 mg/ml)

Saturated phenol

Chloroform/Isomylalcohol 24/1 (v/v)

70 % alcohol and isopropanol

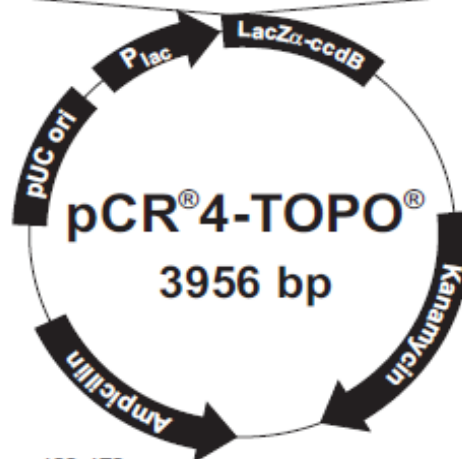
Appendix G. pCR4-TOPO map

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                LacZα initiation codon
                |
M13 Reverse priming site | T3 priming site
201 CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCA GAATTAACCC TCACTAAAGG
    GTGTGTCCTT TGTCGATACT GGTACTAATG CGGTTCGAGT CTTAATTGGG AGTGATTCC

                Spe I       Pst I       Pme I       EcoR I
261 GACTAGTCCT GCAGGTTTAA ACGAATTGCG CCTT PCR Product AAGGGC GAATTCGCGG
    CTGATCAGGA CGTCCAAATT TGCTTAAGCG GGA TTCCCG CTTAAGCGCC

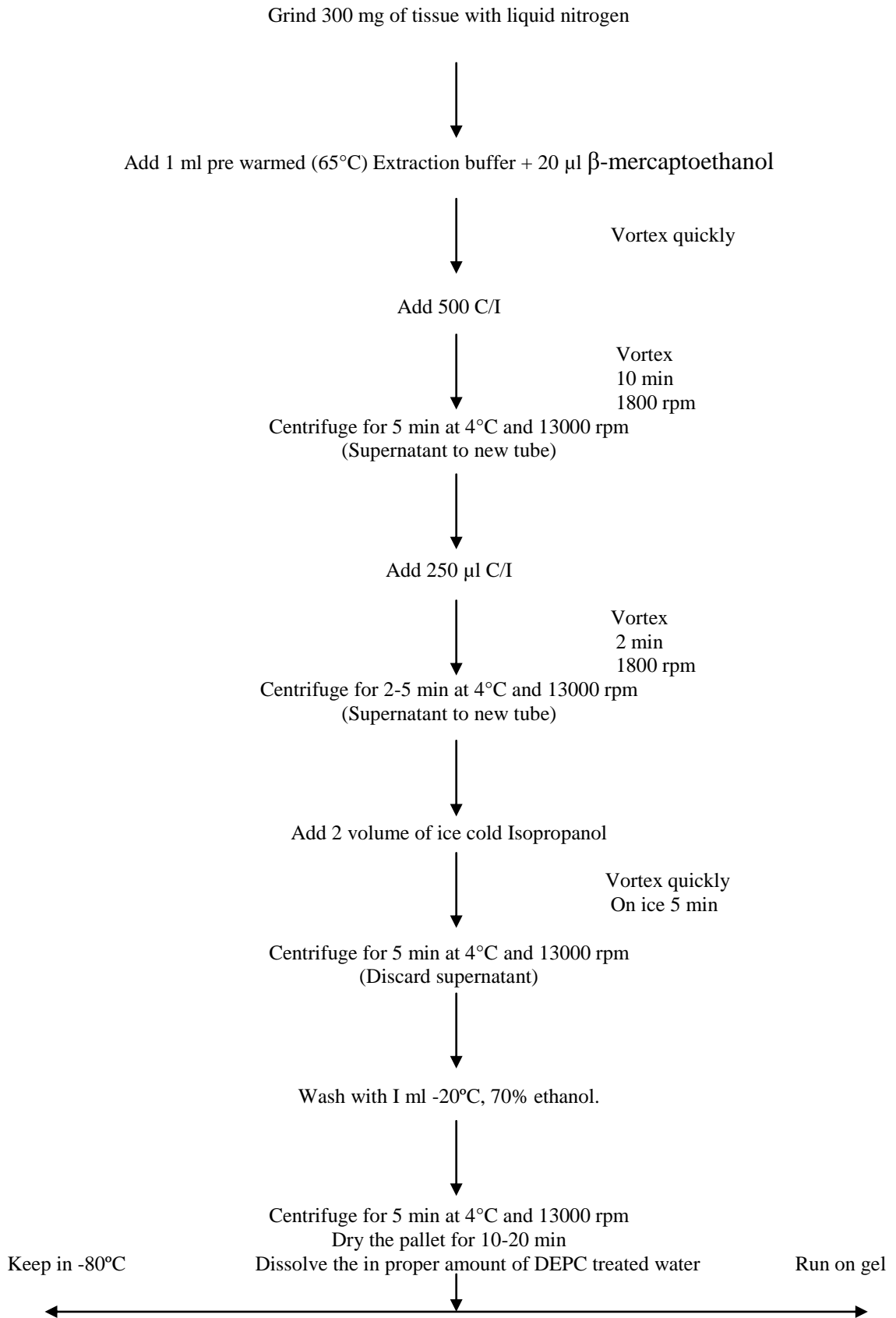
                T7 priming site
311 CCGCTAAATT CAATTGCGCC TATAGTGAGT CGTATTACAA TTCACTGGCC GTCGTTTAC
    GCGGATTTAA GTTAAGCGGG ATATCACTCA GCATAATGTT AAGTGACCGG CAGCAAATG
    M13 Forward (-20) priming site
  
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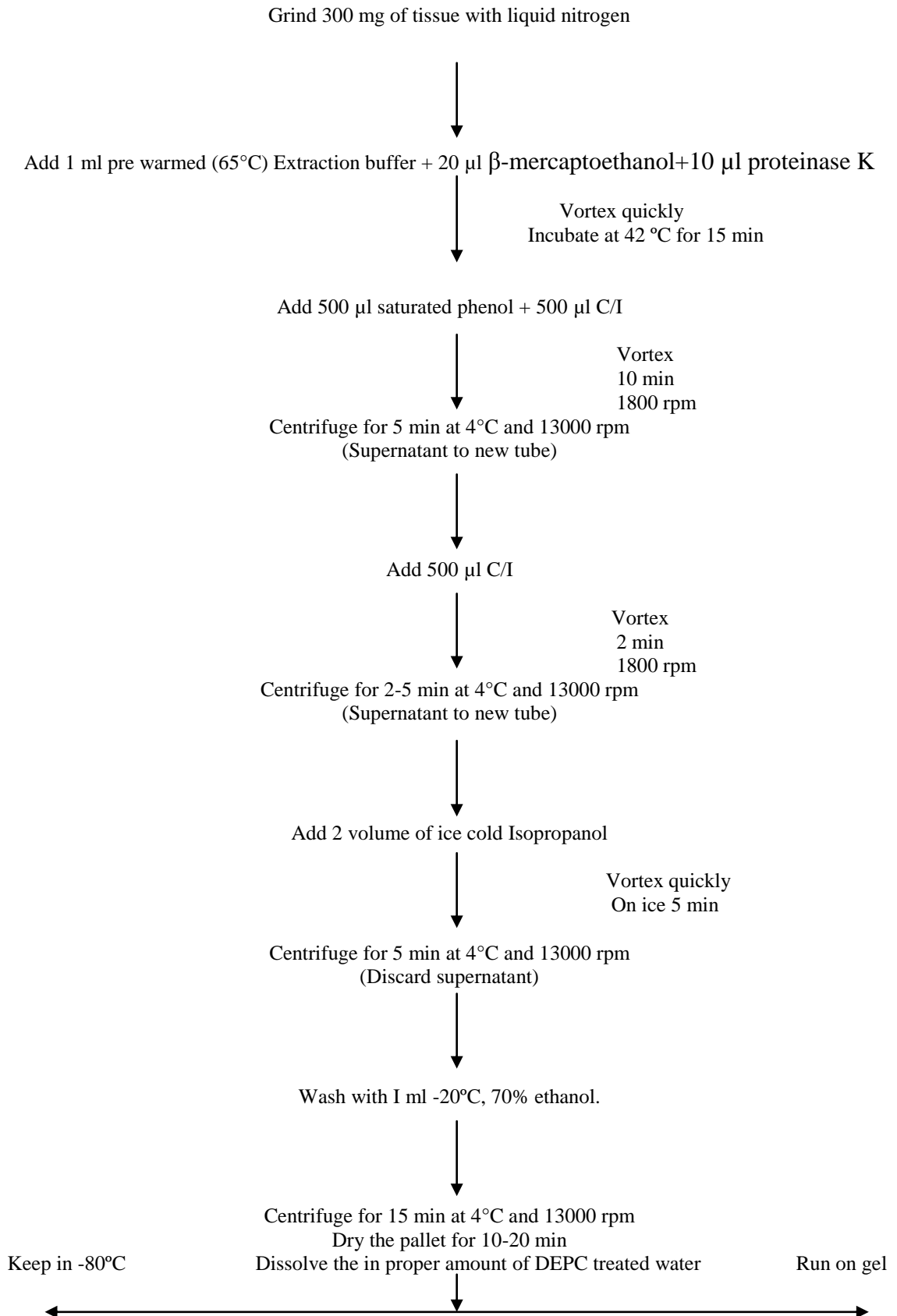
Comments for pCR[®]4-TOPO[®] 3956 nucleotides

lac promoter region: bases 2-216
 CAP binding site: bases 95-132
 RNA polymerase binding site: bases 133-178
 Lac repressor binding site: bases 179-199
 Start of transcription: base 179
 M13 Reverse priming site: bases 205-221
 LacZ α -*ccdB* gene fusion: bases 217-810
 LacZ α portion of fusion: bases 217-497
 ccdB portion of fusion: bases 508-810
 T3 priming site: bases 243-262
 TOPO[®] Cloning site: bases 294-295
 T7 priming site: bases 328-347
 M13 Forward (-20) priming site: bases 355-370
 Kanamycin promoter: bases 1021-1070
 Kanamycin resistance gene: bases 1159-1953
 Ampicillin (*b/a*) resistance gene: bases 2203-3063 (c)
 Ampicillin (*b/a*) promoter: bases 3064-3160 (c)
 pUC origin: bases 3161-3834
 (c) = complementary strand

Appendix H. CTAB RNA extraction procedures



Appendix I. CTAB modified RNA extraction procedures



Appendix J. The number of new shoots in 3, 5 and 7mg/L BAP of after four weeks.

Sample	BAP concentration mg/L	Shoot No	Time
1	3 mg/L	0	4 weeks
2	3 mg/L	0	4 weeks
3	3 mg/L	0	4 weeks
4	3 mg/L	0	4 weeks
5	3 mg/L	0	4 weeks
6	3 mg/L	0	4 weeks
7	3 mg/L	0	4 weeks
8	3 mg/L	0	4 weeks
9	3 mg/L	0	4 weeks
10	3 mg/L	0	4 weeks
1	5 mg/L	1	4 weeks
2	5 mg/L	1	4 weeks
3	5 mg/L	1	4 weeks
4	5 mg/L	0	4 weeks
5	5 mg/L	1	4 weeks
6	5 mg/L	1	4 weeks
7	5 mg/L	1	4 weeks
8	5 mg/L	0	4 weeks
9	5 mg/L	1	4 weeks
10	5 mg/L	1	4 weeks
1	7 mg/L	1	4 weeks
2	7 mg/L	1	4 weeks
3	7 mg/L	1	4 weeks
4	7 mg/L	1	4 weeks
5	7 mg/L	0	4 weeks
6	7 mg/L	1	4 weeks
7	7 mg/L	1	4 weeks
8	7 mg/L	1	4 weeks
9	7 mg/L	1	4 weeks
10	7 mg/L	1	4 weeks

Appendix K. The numbers of new leaf production at three different concentrations of BAP.

Replicate	NaCl concentration mM	No of new leaf
1	0	8
2	0	8
3	0	7
4	0	7
5	0	8
1	60	6
2	60	7
3	60	6
4	60	6
5	60	6
1	80	5
2	80	5
3	80	4
4	80	5
5	80	4
1	100	5
2	100	4
3	100	4
4	100	4
5	100	4

Note: Five replicates were used for each concentration.

Appendix L. Analysis of variance (ANOVA) of number of new leaf production at different NaCl concentrations

Source	DF	SS	MS	F	F _{Criteria(3,16)}
Concentration (NaCl)	3	36.55	12.183	48.73	3.24
Error	16	4.00	0.25	---	---
Total	19	40.55	---	---	---

$F \geq F_{\text{Criteria (3, 16)}}$, therefore NaCl Concentrations (60, 80, 100 mM) have a significant (at $p < 0.05$) effect on the number of new leaves production.

Appendix M. Proline Data analysis

Roots:

Source	DF	SS	MS	F	F _{Criteria(3,4)}
NaCl Concentrations	3	0.4118	0.1373	13.08	6.59
Error	4	0.0420	0.0105	---	---
Total	7	0.4538	---	---	---

$F \geq F_{\text{Criteria (3, 4)}}$, therefore there is a significant difference (at $p < 0.05$) in proline concentrations with increasing NaCl.

Leaves :

Source	DF	SS	MS	F	F _{Criteria(3,4)}
NaCl Concentrations	3	0.92009	0.30670	142.33	6.59
Error	4	0.00862	0.00215	---	---
Total	7		---	---	---

$F \geq F_{\text{Criteria (3, 4)}}$, there fore there is a significant difference (at $p < 0.05$) in proline concentrations with increasing NaCl.

Appendix N. Nucleotide collection (nr/nt) Blast results for clone-12

Clone	Name and Description	E value	Identity score
12	HM139753.1 - <i>Oryza sativa Japonica</i> Group cultivar Padi Kasalle precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139751.1 - <i>Oryza sativa Japonica</i> Group cultivar Chahora 144 precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139750.1 - <i>Oryza sativa Japonica</i> Group cultivar Kaw Luyoeng precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139749.1 - <i>Oryza sativa Japonica</i> Group cultivar Chodongji precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139748.1 - <i>Oryza sativa Japonica</i> Group cultivar NPE 253 precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139747.1 - <i>Oryza sativa Indica</i> Group cultivar Binulawan precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139746.1 - <i>Oryza sativa Indica</i> Group cultivar GIE57 precursor microRNA 393 gene	2e-34	108/119
	HM139745.1 - <i>Oryza sativa Indica</i> Group cultivar Kalukantha precursor microRNA 393 gene, complete sequence	2e-34	108/119
	HM139744.1 - <i>Oryza sativa Indica</i> Group cultivar DA7 precursor microRNA 393 gene, complete sequence	2e-34	108/119
	GQ419317.2 - <i>Oryza barthii</i> strain IRGC 104287 putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419316.2 - <i>Oryza sativa Japonica</i> Group cultivar N22 putative precursor microRNA	2e-34	108/119
	GQ419315.2 - <i>Oryza sativa Japonica</i> Group cultivar Khao Hawm putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419314.2 - <i>Oryza sativa Japonica</i> Group cultivar Cich Beton putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419313.2 - <i>Oryza sativa Japonica</i> Group cultivar Darmali putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419312.2 - <i>Oryza sativa Japonica</i> Group cultivar Nep Hoa Vang putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419311.2 - <i>Oryza sativa Indica</i> Group cultivar IR36 putative precursor microRNA R393 gene, complete sequence	2e-34	108/119

Appendix N, continued'

Clone	Name and Description	E value	Identity score
12	GQ419310.2 - <i>Oryza sativa</i> Indica Group cultivar Guang Lu Ai 4 putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419309.2 - <i>Oryza sativa</i> Indica Group cultivar Aizhizhan putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419308.2 - <i>Oryza sativa</i> Indica Group cultivar Khao Dawk Mali 105 putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419307.2 - <i>Oryza sativa</i> Indica Group cultivar Zhenxian97 putative precursor microRNA R393 gene, complete sequence	2e-34	108/119
	GQ419306.2 - <i>Oryza sativa</i> Indica Group cultivar CO25 putative precursor microRNA	2e-34	108/119
	GQ419305.2 - <i>Oryza sativa</i> Indica Group cultivar Kasalath putative precursor microRNA R393 gene, complete sequence	2e-34	108/119

Appendix O: Plant EST results

Clone	Name and Description	E value	Identity score
1	AJ853689.1 - <i>Oryza sativa</i> (<i>indica</i> cultivar-group) salt stress associated EST <i>Oryza sativa Indica</i> Group cDNA clone OsSsp130, mRNA sequence	4e-54	180/212
2	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5-, mRNA sequence	9e-76	160/163
3	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	9e-76	160/163
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza</i>	7e-57	124/126
4	CI308521.1 -CI308521 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M013F-B05 5', mRNA sequence	2e-116	243/250
5	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	2e-72	158-163
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	3e-55	123/126
6	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	1e-73	158/163
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	1e-54	122-126
7	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	3e-70	156/163
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	1e-54	122/126

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
8	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequenc	6e-38	98/105
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	6e-38	95/108
9	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	3e-45	126/138
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	2e-42	119/130
12	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	4e-74	162/167
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	9e-56	122/124
14	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	3e-61	156/169
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	2e-48	118/124
16	CB967048.1 -NL47_A01 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL47_A01 3', mRNA sequence	9e-81	164/165
	CB966675.1 -NL41_C04 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL41_C04 3', mRNA sequence	9e-81	164/165
	CB965007.1 -NL15_A04 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL15_A04 3', mRNA sequence	9e-81	164/165
	BI305563.1 -NL_0_K11 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL_0_K11 3', mRNA sequence	9e-81	164/165
	BI305450.1 -NLP_1_I21 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NLP_1_I21 3', mRNA sequence	9e-81	164/165

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
16	CB967359.1 -NL51_D08 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL51_D08 3', mRNA sequence	1e-79	163/165
	CB967237.1 -NL49_H11 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL49_H11 3', mRNA sequence	1e-79	163/165
	CB965928.1 -NL28_H09 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL28_H09 3', mRNA sequence	1e-79	163/165
	CB964596.1 -NL8_G06 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL8_G06 3', mRNA sequence	1e-79	163/165
	CB964605.1 -NL9_A04 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL9_A04 3', mRNA sequence	4e-79	163/165
	BI306658.1 -NL_5_J22 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL_5_J22 3', mRNA sequence	4e-79	161/162
	CB964850.1 -NL12-D10 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL12-D10 3', mRNA sequence	9e-76	161/165
	EX452105.1 -SSH002525 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	1e-54	119/121
	EX451719.1 -SSH001964 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	1e-54	119/121
	EX451695.1 -SSH001940 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	1e-54	119/121
	EX451687.1 -SSH001932 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	1e-54	119/121
	EX451718.1 -SSH001963 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	5e-53	118/121
	EX451698.1 -SSH001943 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	5e-53	118/121
	EX451678.1 -SSH001923 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	5e-53	118/121
EX451675.1 -SSH001920 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA sequence	5e-53	118/121	

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
16	EX451663.1-SSH001908 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA	5e-53	118/121
	EX451650.1-SSH001895 Salt stress SSH library <i>Oryza sativa Indica</i> Group cDNA, mRNA	5e-53	118/121
17	CI308356.1-CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	1e-39	123/138
	CI308607.1-CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	3e-36	115/129
18	CI308356.1-CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	7e-42	114/124
	CI308607.1-CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	3e-40	111/121
21	CI308356.1-CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	7e-22	114/140
	CI308607.1-CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	2e-18	106/131
23	CI308356.1-CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	1e-44	124/136
	CI308607.1-CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	7e-42	117/128
24	CI308356.1-CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	2e-28	113/134
	CI308607.1-CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	9e-26	108/129

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
25	GT284596.1- NL6_6_93 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL6_6_93(3'), mRNA sequence	3e-40	89/89
	AJ853684.1- AJ853684 <i>Oryza sativa (indica</i> cultivar-group) salt stress associated EST	4e-39	88/89
	BU099176.1-S234-TP4 Rice cold stress germination cDNA library <i>Oryza sativa Japonica</i> Group cDNA clone S234-TP4 5' similar to putative arginine transport ATP-binding protein, mRNA sequence	9e-26	66/67
28	CA765497.2- AF53-Rpf_07_L19_T7_078.ab1 IRR1 Drought Stress Panicle Library <i>Oryza sativa Indica</i> Group cDNA clone C0002587 5' similar to unknown, mRNA sequence	7e-37	108/119
29	CI308356.1-CI308356 <i>Oryza sativa (Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	3e-25	106/125
	CI308607.1-CI308607 <i>Oryza sativa (Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	6e-23	102/121
30	CI308356.1-CI308356 <i>Oryza sativa (Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	3e-36	117/132
	CI308607.1-CI308607 <i>Oryza sativa (Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	4e-34	113/128
31	CI308356.1-CI308356 <i>Oryza sativa (Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	9e-61	152/164
	CI308607.1-CI308607 <i>Oryza sativa (Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	7e-42	116/127
32	CB964596.1-NL8_G06 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL8_G06 3', mRNA sequence	2e-37	92/96
	BI305563.1-NL_0_K11 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL_0_K11 3', mRNA sequence	4e-34	80/81

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
32	CB967359.1 -NL51_D08 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL51_D08 3', mRNA sequence	2e-34	79/80
	CB967237.1 -NL49_H11 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL49_H11 3', mRNA sequence	6e-33	78/79
	CB966675.1 -NL41_C04 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL41_C04 3', mRNA sequence	6e-33	78/79
	CB965928.1 -NL28_H09 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL28_H09 3', mRNA sequence	6e-33	78/79
	CB964850.1 -NL12-D10 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL12- D10 3', mRNA sequence	6e-33	78/79
	CB964605.1 -NL9_A04 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL9_A04 3', mRNA sequence	6e-33	78/79
	BI306658.1 -NL_5_J22 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL_5_J22 3', mRNA sequence	6e-33	78/79
	BI305450.1 -NLP_1_I21 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NLP_1_I21 3', mRNA sequence	6e-33	78/79
	BU673093.1 -NL_10_75 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL	7e-32	83/87
	CB966770.1 -NL42_A12 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL42_A12 3', mRNA sequence	3e-31	73/79
	CB965007.1 -NL15_A04 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL15_A04 3', mRNA sequence	3e-31	78/80
	CF330848.1 -NACL-06-L19.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa</i> <i>Japonica</i> Group cDNA clone NACL--06-L19, mRNA sequence	4e-39	90/91
	CF330239.1 -NACL--05-O01.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa</i> <i>Japonica</i> Group cDNA clone NACL--05-O01, mRNA sequence	4e-39	90/91
	CF332208.1 -NACL-08-K01.b1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa</i> <i>Japonica</i> Group cDNA clone NACL--08-K01, mRNA sequence	2e-37	90/92

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
32	CF332014.1-NACL-08-F17.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-08-F17, mRNA sequence	2e-37	90/92
	CF331927.1-NACL-08-D19.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-08-D19, mRNA sequence	2e-37	90/92
	CF331207.1-NACL-07-D20.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-07-D20, mRNA sequence	2e-37	90/92
	CF331108.1-NACL-07-B14.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-07-B14, mRNA sequence	2e-37	90/92
	CF330429.1-NACL-06-C06.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-06-C06, mRNA sequence	2e-37	90/92
	CF330199.1-NACL-05-N05.b1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-05-N05, mRNA sequence	2e-37	90/92
	CF330169.1-NACL-05-M12.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-05-M12, mRNA sequence	2e-37	90/92
	CF329645.1-NACL-05-A18.b1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-05-A18, mRNA sequence	2e-37	90/92
	CF328946.1-NACL-04-B09.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-04-B09, mRNA sequence	2e-37	90/92
	CF328814.1-NACL-03-O10.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-03-O10, mRNA sequence	2e-37	90/92
	CF328813.1-NACL-03-O10.b1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-03-O10, mRNA sequence	2e-37	90/92
	CF328430.1-NACL-03-F08.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-03-F08, mRNA sequence	2e-37	90/92
	CF328176.1-NACL-02-P08.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-02-P08, mRNA sequence	2e-37	90/92
	CF327316.1-NACL-01-M02.g1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-01-M02, mRNA sequence	2e-37	90/92
	CF326953.1-NACL-01-D21.b1 Rice callus plasmid cDNA library (NACL) <i>Oryza sativa Japonica</i> Group cDNA clone NACL-01-D21, mRNA sequence	2e-37	90/92

Appendix O, continued⁷

Clone	Name and Description	E value	Identity score
33	AJ853684.1 -AJ853684 <i>Oryza sativa</i> (<i>indica</i> cultivar-group) salt stress associated EST <i>Oryza sativa Indica</i> Group cDNA clone OsSsp125, mRNA sequence	2e-28	80/88
34	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	4e-64	149/157
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	9e-46	116/124
38	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	4e-74	159/163
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	3e-55	123/126
39	AJ853684.1 -AJ853684 <i>Oryza sativa</i> (<i>indica</i> cultivar-group) salt stress associated EST <i>Oryza sativa Indica</i> Group cDNA clone OsSsp125, mRNA sequence	9e-51	109/110
	GT284596.1 -NL6_6_93 Drought stress (leaf) <i>Oryza sativa Indica</i> Group cDNA clone NL6	3e-50	107/107
	AJ853637.1 -AJ853637 <i>Oryza sativa</i> (<i>indica</i> cultivar-group) salt stress associated EST <i>Oryza sativa Indica</i> Group cDNA clone OsSsp78, mRNA sequence	4e-34	103/115
42	CI308356.1 -CI308356 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M005F-B06 5', mRNA sequence	2e-67	151/157
	CI308607.1 -CI308607 <i>Oryza sativa</i> (<i>Japonica</i> cultivar-group) BAP treated callus <i>Oryza sativa Japonica</i> Group cDNA clone 015-M018F-A09 5', mRNA sequence	4e-49	118/124

Appendix P. Sequences of clone-1, Clone-16, Clone-25, Clone-32, Clone-33 and

Clone-39.

Clone-1 sequence of sequence of miRNA library clones

AAGCTATCTACTTCTGGTACAACCCACTCCCATGGTGTGACGGGCGGTGTGT
ACAAGGCCCGGGAACGTATTCACCGCAACATTCTGATTTGCGATTACTAGC
GATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTTAGATGCA
CTTTCTGAGATTCGCTCCCCCTCGCAGGCTCGCTTCCCTCTGTATGCACCATT
GT

Clone-16 sequence of sequence of miRNA library clones

ATTGATTGCGGAAGACACCTTCTTGGTCAGGCCGGCATTGTGAAGAAGGA
ACACATCAAGATTCATGGTTTCTGAGCAACTGCCAAAACCATTGCAAAGAC
TATAGTTTGGGGTGGAGTATACTTGGTTGTGTACATGCCTGCGTGTTCATT
GTACACACAAAACCTAGCCACCTCTTGACTC

Clone-25 sequence of sequence of miRNA library clones

AATCGCCTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAG
GCCCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCCTATACGTACGGCAGT
TTAAGGTTTACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGT
ACAGAGTGATATTATTGACACGCCGGGGCGACGGATGGTGATCCCCCTGGC
CAGTGCACGTCTGCTGTCAGATAAAGTCTC

Clone-32 sequence of sequence of miRNA library clones

AACGAATGGNGCTCTCCCGTATGGTCGACCTGCAGGCCGGCCGCAATTCAC
TAGTGATTGCGAGCACAGAATTAATACGACTCACTATAGGTTTTTTTTTTTT
GCGCTCTCAAAGTAGCATATATTATTCAATCTTGATGAAAGAGGGACACTA
GCCATCATCTATAGTGATGGTGCCTCTT

Clone-33 sequence of sequence of miRNA library clones

AATCACCTTGACCCACATCCCCCTTCCCAACTGGCGTGGTACCGAAGAGG
CCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCGATACGTGCGGCATTT
GAAGGTTTACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGTA
CAGAGTGATATTATTGACACGCCGGGGCGACGGATGGTGATCCCCCTGGCC
AGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTT

Clone-39 sequence of sequence of miRNA library clones

AACCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGCCA
GCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGC
GCAGCCTATACGTACGGCAGTTTAAGGTTTACACCTATAAAAGAGAGAGCC
GTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCCGGGGCG
ACGGATGGTGATCCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCC
CGTGAACTT