

Appendix C. Information of 102 EST-SSR markers obtained by validity screening

Gene ID	Primer name		Primer sequence (5'-3')	Annealing temperature (°C)	Expected size (bp)	Repeat motif
PB.50081.1	PS1	F	CACTTGGACTTGTAGCCTTGG	51.6	172	(T)12
		R	TCGATTGACAAGGATGGACA			
PB.55834.2	PS2	F	GCTCGTAGCTCTCACTGTCTGA	60.4	194	(GA)6
		R	CTTCTCTTGGCGAAGGTCAC			
PB.49089.1	PS5	F	AGTTGCTTAGCGCCTCCTCT	53	234	(T)16
		R	AATCTCCGAGCATGAATTGC			
PB.12206.1	PS7	F	CGTCAAGACTTATTCTTACCGTGTT	58.3	297	(A)10
		R	AACCAACCATGGCGACAC			
PB.44222.1	PS8	F	AACCTCGACGAATCAACG	57.5	256	(T)10
		R	CGATGCCGACGGTCTAGTAT			
PB.43415.1	PS9	F	TCTGCTGCTGTTGTGCGTAT	52.9	249	(T)15
		R	ATCCGCTTCCGATCTTCTTC			
PB.32979.2	PS10	F	GTCTCTGCTCATCGTGTCCA	59.9	292	(T)13
		R	ACGCTGCCTCTCCTTCATT			
PB.59960.1	PS12	F	CACTCTCTCCTCCTGCCAAG	59.6	200	(CT)11
		R	TATCTTCCTCGGCTGTCCAT			
PB.48075.9	PS13	F	ATCATCACCACCACCTCCTC	57.4	175	(A)11
		R	AAGCTTGTGTAACGCCTCGT			
PB.53756.4	PS17	F	AATACGGCACTGCAGCTTCT	58.3	198	(T)11
		R	AAGAACCTAACCTAGACAATCTTCC			
PB.50898.1	PS19	F	CCTCAGTCTTCACCTTCTCTC	56.7	173	(A)13
		R	CTGGTACCACTTCCAACACG			

PB.16895.1	PS21	F	TGGACCGGAAGATATGAAGC	57.8	282	(TC)10
		R	GGCGGCACATCTGATTAAGT			
PB.56852.1	PS22	F	AATCATCTCTCTCAGGCGTAAT	57.3	224	(T)12
		R	TGTACTTGGCAGGACCTGAA			
PB.56852.1	PS23	F	TCGCTGGACTCTTATCTCACA	52.5	170	(AT)9
		R	TGTACTTGGCAGGACCTGAA			
PB.48645.2	PS24	F	TTGAGCAATCAGGTTTCATTAGG	56.4	155	(CAA)5
		R	TAGCCTCCGGTTCTGAATTG			
PB.39602.1	PS25	F	GGCGTTGAATCATGTGTTCC	55.6	279	(T)14
		R	CGTGAATGAGCGACTGCATA			
PB.35869.3	PS26	F	CCACAACCACTCTCCAACG	59.3	193	(CT)6
		R	TTACTCGGCGATGGTTCAGT			
PB.60194.1	PS27	F	CGCAGACTAGAATGCACCTG	52	136	(A)12
		R	GGTTGGCTACTATCAATACAAGGA			
PB.33711.4	PS29	F	CCTGCGCTTACCTGTGAATA	57.2	261	(T)10
		R	GCCTTGCATTAATGGCTTGT			
PB.38966.1	PS30	F	TGAGATAGAAGCGGCAAGGT	56.3	217	(T)11
		R	TAGCAGCGGCGAATATCTCT			
PB.46556.4	PS31	F	TCCGGTGGACGATATTGATT	56	248	(T)16
		R	GACAACAACAACATCGAAGTGA			
PB.12882.2	PS33	F	CAGGACGACTACCTGCGTTA	56.7	207	(GT)6(AT)10
		R	TCTTCCTGGCAATCTGAGGT			
PB.36620.1	PS34	F	GTGGTGACCAAGACCAGTCC	59	188	(A)11
		R	CCAACCGAAGATCATCAAGG			
PB.53994.4	PS36	F	TCCAAGCTACTCCATGCCTTA	58.8	277	(TCT)5
		R	GAATACTCACTCGCGGCTTC			

PB.41344.7	PS40	F	TGCATCGGATGAAGATGGTA	57.4	287	(ACA)5
		R	GAAGAGACTCATCACCCTTGC			
PB.41344.7	PS42	F	TCACGCGTGCGTTAGACTTA	52	102	(T)13
		R	tcaACACATAAGAGGTAAGTCAGG			
PB.45322.6	PS43	F	TTCCTGCACTTAATCCAGTAGG	56.7	239	(AG)10AAAGGAATTGGGAGCGAGAGAGGA
		R	GGCCGCATGCTATTAATGTT			ATTGGG(GA)8
PB.48873.1	PS44	F	CAGGTATCCTGTCATTAACATTCC	57.9	220	(GA)7
		R	CTGTGGTGGGAAGGATCTGGT			
PB.48506.7	PS45	F	TTGTTATCCAGGTATCTCCTGTCA	57.8	219	(GA)7
		R	GAAGGATCTGGTAGAAGAGTTGC			
PB.51785.1	PS46	F	TCCAGGTATCTCCTGTCATTAACAT	57.8	210	(GA)7
		R	GGATCTGGTAGAAGAGTTGCTG			
PB.36910.10	PS47	F	TCTCAGCTTCTAATCTTCTCCTCA	57.5	246	(AG)6
		R	ATGTCATGCCTCCAATCTCC			
PB.31359.3	PS49	F	CATGCAATCTGCTTCTCAGG	56.5	267	(T)20
		R	CTGATGCAGGATGCAATGTT			
PB.61740.1	PS50	F	TTACAGCAGGCCACGACTG	55.9	262	(AGC)6
		R	CATGACATCATGTGGTCCAA			
PB.30344.6	PS52	F	TCTCCACCACACAATCAAGG	59.3	265	(TCA)5
		R	GTGGTTGGAACCTGACTGCT			
PB.50380.4	PS53	F	CCGCCTTCTAAGGAGGATTC	53.2	275	(A)13
		R	CCAGAAGCACCTGTGTATGGA			
PB.19925.5	PS55	F	GGCAATGGCAACTGTATGAG	56	265	(A)12
		R	CAGCAATTACAACCTGTTTCATGG			
PB.45037.5	PS56	F	TTCGACCATCCATAAGTTGG	56.5	276	(T)11
		R	AAGACAGGTTGCCTCGATTG			

PB.42060.4	PS57	F	GCGACAGTACATTCCATCAA	57.7	128	(TC)7
		R	GTCAACCACACGTCTGCAAG			
PB.47737.1	PS59	F	CTTGATACCTGTCCGCCATT	56.6	205	(GAA)5
		R	CATAACCATGAGCCATTCAAGA			
PB.36595.1	PS60	F	TCCTTCGACGCTCGTAAGTAT	58.2	193	(AT)7
		R	AACAGGTTTCATGACTGTTTACG			
PB.47891.2	PS62	F	GAACAAGGCAAGGTTGGTGT	55.9	225	(T)10CTTCTCTTGTTTIGATTGTCTTTGTTGT
		R	TTACCAGGCAGTACTGAAGTTG			TATCT(GA)7
PB.52165.4	PS64	F	GATTCTGTCTGGCATTGACG	58.1	293	(GA)6
		R	CCATCTGTCTGGATCGACCT			
PB.52165.4	PS65	F	CGCCTTATCCGTTCTCTCTG	57.9	219	(T)10
		R	GCATATAAGCAAGAGTGGAAGTGA			
PB.48536.1	PS66	F	GGAATTCTTGACCGCTCTTC	57.9	221	(A)10GGTTTAGTTGAATTCACCATCCATCT
		R	CGTCAACCAACTGGTACGTC			TTAGCTAC(T)12
PB.29004.2	PS67	F	TCTGGACCGAGAAGACCATC	59.3	207	(AGA)5
		R	TCTCCTCAGGCTTCCTCATC			
PB.26141.3	PS68	F	GGCTCCTGAGGCTGAGTATG	54.2	264	(T)21
		R	AGCAGTGGTATCAACGCAGA			
PB.33995.1	PS70	F	CTTGCTGAGGCTGAGGAGTT	59.5	182	(GAT)6
		R	CCTCGATCTTAGGACCTGGA			
PB.24581.10	PS71	F	ACGCTCCATGTGTCGAGAA	57.6	165	(A)13
		R	TAACGCATTTCGCAATGAGAG			
PB.55174.1	PS72	F	GTTACTGGCCGAATCGCTAA	53.4	285	(A)14
		R	GTCGAGCAGTGTTGGAGGTT			
PB.55233.1	PS73	F	TGTCTGTACTTCATGACAGAACCTC	59.3	251	(T)11
		R	ACAGCCAAGAACATCCAGGT			

PB.30998.3	PS75	F	TTGAACAGGCAATTCAGTGG	56.7	271	(C)16
		R	CGCTTCCACCACTACCAATA			
PB.30233.1	PS77	F	TTGTCCATGACCAGACCATAA	56	212	(T)11
		R	CAACCTTGCCATATGTATATCAGAC			
PB.34613.1	PS81	F	TGTTACACCAGCCGCAATTA	58.2	129	(CAA)5
		R	TCGAACTGTGAGGCTCGAAT			
PB.53716.1	PS85	F	GGTGAAGATGATTATGGCTTCC	56.3	275	(A)10
		R	CATTCATTAGCACCACTAACC			
PB.37366.1	PS90	F	CACGTCATGGCAATGTGAA	57.2	251	(T)15
		R	TCCATAGAGTGGCAACATGC			
PB.28598.3	PS91	F	GTGGATCCAGAGGTTCTGA	59.5	283	(T)15
		R	AGTGCCATAGAGTGGCAACA			
PB.40592.8	PS92	F	TGCATAGGTCAAGTCAAGTTGG	57.6	215	(GCTAAG)5
		R	AAGTCATGGAGCGCAAGAAT			
PB.57254.2	PS93	F	TGCTGCAAGATGAACTCCAG	57.3	122	(T)11
		R	TCTCTCAACAAGCAAGAACTCA		122	
PB.57368.1	PS94	F	TCGATCTATATCCATGGCTCAC	57.4	255	(TC)8
		R	AGTCTCTCTCCTTGCTTGGAA			
PB.49311.9	PS96	F	AAGAGTAACATGCGCCAACA	58.8	242	(CT)18
		R	AACACTACAAGACCTCCACTGC			
PB.35930.1	PS97	F	ATTGCCGTATTCCTCGTGAC	52.9	181	(T)11
		R	CCACGTGCTACTACACTATGCTT			
PB.54752.2	PS98	F	CAGCAACAACCGATAATGGA	51.7	289	(CAA)5
		R	CATCCACTTCCTCGTCGTCT			
PB.42155.1	PS101	F	CAGCACCACAAGATGTTGGA	59.7	273	(GTG)5
		R	GGAGTGGATGGTGAGTAGGC			

PB.49578.3	PS102	F	TGAGTGAACCTCCTCCTTG	59	282	(T)11
		R	CCACTAGATGAAGCCATGGTG			
PB.48852.3	PS103	F	AAGATGCAGAGGATCGAGGA	58.1	214	(T)15
		R	CATGTCTGAAGCACTGTAACCA			
PB.44308.2	PS104	F	TTGAGTCATGCAAGCAACTT	56.4	218	(T)10
		R	TTGGATTCCACCACCTTGAG			
PB.40196.1	PS105	F	TTCATATCGGACACGCAGAG	59	279	(GTA)5
		R	AGTTCTGCACTCGAGCTTCC			
PB.35331.4	PS106	F	CACTTGAGGAATTCTTGGTGAA	57.8	293	(TAA)5
		R	CTGTTGTGGCTGCAAGGAAG			
PB.42554.1	PS108	F	TGGTCATTGGTGGTTGTATCTT	53.2	195	(T)18GG(T)10
		R	AGTGAAGGTGCCACGAGACT			
PB.58209.1	PS109	F	TCCTCCAGCTATGTTGGTAGC	53.7	276	(CA)7
		R	GGCAGGTTGGTAGATGTGC			
PB.47997.1	PS110	F	CTGCTGCACCTGTGAAGACT	59.6	267	(TGC)6TGTTGA(TGC)7
		R	CAACAAGCACAACCTCCGAGA			
PB.47997.1	PS111	F	CAACAAGCACAACCTCCGAGA	57.3	267	(CAG)7CATCAA(CAG)6
		R	CTGCTGCACCTGTGAAGACT			
PB.36647.2	PS112	F	TAAGAAGTCGGCCAATACGG	56.2	184	(T)17
		R	AACAATGAGAGGAAGGATTGG			
PB.46529.2	PS113	F	CATTAGCTCAGCTGCCTCAG	53.7	259	(T)16
		R	GCGACTGACATTCTGACTCGT			
PB.51687.1	PS114	F	TCCATCATCATCGTCATCAGA	48.7	287	(T)14
		R	GCCAATAATGGCAACAACA			
PB.51383.1	PS115	F	TGGATGTCTTCCAAGATGAGG	54.5	259	(AAC)5
		R	GCCGAATTCCACAAGCATT			

PB.51634.2	PS116	F	GACTTGCACTCGAACCATCA	57.6	190	(A)10
		R	CATAATCTCCGCCGGTTCTA			
PB.48336.1	PS117	F	CATAATCTCCGCCGGTTCTA	57.6	190	(T)11
		R	GACTTGCACTCGAACCATCA			
PB.45875.1	PS118	F	GGATTACATGTGAAGCGGATG	58.2	290	(TC)6
		R	GCGCCACAGACTTCAATACC			
PB.19800.1	PS120	F	TCGATGGTATGAGATTCACCTG	55.8	292	(T)11GGCTAATTAATTGAGTTTAGTCAATC TTAATCTCATTGAGA(T)10AAGTTAATGTT GTAA(T)10CTATCAGTCGGAAGCA(T)10
		R	ATGGTGCAACTGGTCGTACA			
PB.28010.1	PS122	F	TTGCTCCTAGGTATCGCAATC	57	295	(T)12
		R	AAGGACGTATTGACGCAGAA			
PB.32099.6	PS123	F	TTCAGCAGCAACAACAACAA	55.9	245	(ACA)5
		R	CTGAGCGAGAACCACCAGTT			
PB.32099.6	PS124	F	ATGGCTTGAATTGCTCCTGT	57.8	268	(T)14
		R	GGAACACGCATAGACCAACA			
PB.53405.1	PS125	F	GCCATCTCCAGCTTCAACA	58.8	280	(AGC)5
		R	GGCCGTACTIONCCTCCATCTA			
PB.49343.1	PS129	F	GATTCTCCATGCCATTGTCC	57.3	168	(T)13
		R	CAGCCACCTTCATGCTGATA			
PB.28626.1	PS130	F	GCCATCTCCAACAACAGGA	58.9	260	(T)11
		R	TGTTCTCTCAGAGGCTGTTCC			
PB.52783.1	PS131	F	CAACCTTGGTCTTGCTCTCC	57.7	210	(GAA)6
		R	GCTCTAATCCTCGAATATTACCTGA			
PB.58798.1	PS135	F	TATGGAGTTGAAGCGCAATG	57.1	245	(AGA)5
		R	TCCAGTGATCACCTGTCTGAA			
PB.45858.2	PS139	F	ATTGAGGTGTCCGAACATGG	58.9	245	(AGA)5
		R	CATCTATCACCGCCTGTCT			

PB.35178.2	PS140	F	GGTTCAGGAGGAGTGCTGAG	60.3	282	(AAG)7
		R	TTGCTACTTGCGTGGAAGAGT			
PB.44073.2	PS142	F	TCCAAGATGAGAAGTGCATCC	58.6	218	(A)10
		R	AGCAACTGCGGAAGATGAGT			
PB.18100.1	PS145	F	CAGTGGATCATCGCACAAATC	57.1	258	(T)10
		R	AAGACCAGCCAATGAACCAA			
PB.50274.1	PS147	F	GGCCTCTCTGCAGTCGTTA	56.2	145	(T)12
		R	GACGACTAGCAACTATTCCACAA			
PB.46379.1	PS149	F	GAGGTTACACCACACCTGTT	52	212	(G)11
		R	CTGTCATGACGCGATAATCAA			
PB.45714.1	PS150	F	TGCAGTGGTCCTCTTCACAG	54.6	270	(T)13
		R	TTGGCAGAGAATGATTGACA			
PB.46107.3	PS151	F	GCCACACCTCACTTGGTCTT	59.1	210	(T)13
		R	AGGCGCAATTCTCATGTCTT			
PB.33081.1	PS157	F	GCTCCATCTGCTTCATCTCC	52.7	268	(AT)7
		R	GAGTTCGGCATCTGTGGTAG			
PB.35830.3	PS159	F	TTATGGAGCAGTGATGCTTCT	57.7	245	(T)13
		R	ATCCACCTGCCTGTCTGATT			
PB.35071.1	PS160	F	ATGCACCTGTGGAGGTGTG	60	265	(T)13
		R	CAAGGTACTACGCGAACCTG			
PB.30575.1	PS161	F	TGCGTTCACATCAATCTCTGA	54.9	274	(A)10CCCGAGA(T)11
		R	GGTGAATTCAGTCCTCTTAGGC			
PB.45295.1	PS163	F	CTCGAGCAAGAGTTGGTGGT	61	276	(TC)6CT(CA)7
		R	ACAGGAGTCTCGCCTAGCAA			
PB.36887.1	PS164	F	AAGCACAGGCAGAAGAGGAA	58.6	130	(GAA)5
		R	CAATTCCTCTCGCACAGCTA			

Appendix D. Information of 58 EST-SSR markers obtained by polymorphic screening

Gene ID	Primer name		Primer sequence (5'-3')	Repeat motif	Function annotation
PB.55834.2	PS2	F	GCTCGTAGCTCTCACTGTCTGA	(GA)6	MADS-box protein 5
		R	CTTCTCTTGGCGAAGGTCAC		[<i>Paeonia suffruticosa</i>]
PB.12206.1	PS7	F	CGTCAAGACTTATTCTTACCGTGTT	(A)10	putative E3 ubiquitin-protein ligase RING1a
		R	AACCAACCATGGCGACAC		[<i>Durio zibethinus</i>]
PB.44222.1	PS8	F	AACCTCGACGAATCAACG	(T)10	ethylene-responsive transcription factor CRF4-like
		R	CGATGCCGACGGTCTAGTAT		[<i>Durio zibethinus</i>]
PB.32979.2	PS10	F	GTCTCTGCTCATCGTGTCCA	(T)13	Myb_DNA-bind_6 domain-containing protein
		R	ACGCTGCCTCTCCTTCATT		[<i>Cephalotus follicularis</i>]
PB.59960.1	PS12	F	CACTCTCTCCTCTGCCAAG	(CT)11	PREDICTED: transcription factor MYB114
		R	TATCTTCCTCGGCTGTCCAT		[<i>Ricinus communis</i>]
PB.53756.4	PS17	F	AATACGGCACTGCAGCTTCT	(T)11	transcription factor MYB41
		R	AAGAACCTAACCTAGACAATCTTCC		[<i>Herrania umbratica</i>]
PB.50898.1	PS19	F	CCTCAGTCTTCACCTTTCTCTC	(A)13	PREDICTED: AP2/ERF and B3 domain-containing transcription factor RAV1-like
		R	CTGGTACCACTTCCAACACG		[<i>Vitis vinifera</i>]
PB.16895.1	PS21	F	TGGACCGGAAGATATGAAGC	(TC)10	AP2-like ethylene-responsive transcription factor AIL6
		R	GGCGGCACATCTGATTAAGT		[<i>Theobroma cacao</i>]
PB.48645.2	PS24	F	TTGAGCAATCAGGTTCATTAGG	(CAA)5	PREDICTED: ethylene-responsive transcription factor RAP2-4-like isoform X1
		R	TAGCCTCCGGTTCTGAATTG		[<i>Vitis vinifera</i>]
PB.39602.1	PS25	F	GGCGTTGAATCATGTGTTCC	(T)14	PREDICTED: ethylene-responsive transcription factor RAP2-7 isoform X2
		R	CGTGAATGAGCGACTGCATA		[<i>Cucumis sativus</i>]
PB.60194.1	PS27	F	CGCAGACTAGAATGCACCTG	(A)12	PREDICTED: ethylene-responsive transcription factor 3-like
		R	GGTTGGCTACTATCAATACAAGGA		[<i>Vitis vinifera</i>]
PB.38966.1	PS30	F	TGAGATAGAAGCGGCAAGGT	(T)11	PREDICTED: ethylene-responsive transcription factor RAP2-7 isoform X2
		R	TAGCAGCGGCGAATATCTCT		[<i>Theobroma cacao</i>]

PB.46556.4	PS31	F	TCCGGTGGACGATATTGATT	(T)16	ethylene-responsive transcription factor 3-like
		R	GACAACAACAACATCGAAGTGA		[Jatropha curcas]
PB.12882.2	PS33	F	CAGGACGACTACCTGCGTTA	(GT)6(AT)10	bHLH transcription factor
		R	TCTTCCTGGCAATCTGAGGT		[Paeonia suffruticosa]
PB.53994.4	PS36	F	TCCAAGCTACTCCATGCCTTA	(TCT)5	PREDICTED: transcription factor bHLH147 isoform X1
		R	GAATACTCACTCGCGGCTTC		[Vitis vinifera]
PB.45322.6	PS43	F	TTCCTGCACTTAATCCAGTAGG	(AG)10AAAGGAATTGGG	transcription factor bHLH68 isoform X1
		R	GGCCGCATGCTATTAATGTT	AGCGAGAGAGGAATTG GG(GA)8	[Quercus suber]
PB.51785.1	PS46	F	TCCAGGTATCTCCTGTCATTAACAT	(GA)7	PREDICTED: transcription factor bHLH93
		R	GGATCTGGTAGAAGAGTTGCTG		[Vitis vinifera]
PB.36910.10	PS47	F	TCTCAGCTTCTAATCTTCTCCTCA	(AG)6	PREDICTED: transcription factor bHLH96-like
		R	ATGTCATGCCTCCAATCTCC		[Nelumbo nucifera]
PB.31359.3	PS49	F	CATGCAATCTGCTTCTCAGG	(T)20	PREDICTED: transcription factor PIF4
		R	CTGATGCAGGATGCAATGTT		[Vitis vinifera]
PB.61740.1	PS50	F	TTACAGCAGGCCACGACTG	(AGC)6	PREDICTED: transcription factor TCP11
		R	CATGACATCATGTGGTCCAA		[Vitis vinifera]
PB.50380.4	PS53	F	CCGCCTTCTAAGGAGGATTC	(A)13	PREDICTED: transcription factor TCP20
		R	CCAGAAGCACCTGTGTATGGA		[Vitis vinifera]
PB.19925.5	PS55	F	GGCAATGGCAACTGTATGAG	(A)12	PREDICTED: transcription factor TCP4
		R	CAGCAATTACAACGTTCATGG		[Vitis vinifera]
PB.45037.5	PS56	F	TTCGACCATCCATAAGTTGG	(T)11	PREDICTED: transcription factor TCP7
		R	AAGACAGGTTGCCTCGATTG		[Nelumbo nucifera]
PB.42060.4	PS57	F	GCGACAGTACATTCCATCAA	(TC)7	PREDICTED: transcription factor CYCLOIDEA
		R	GTCAACCACACGTCTGCAAG		[Vitis vinifera]
PB.47737.1	PS59	F	CTTGATACCTGTCCGCCATT	(GAA)5	PREDICTED: scarecrow-like protein 4
		R	CATAACCATGAGCCATTCAAGA		[Vitis vinifera]

PB.47891.2	PS62	F	GAACAAGGCAAGGTTGGTGT	(T)10CTTCTCTTGTGTTGA	PREDICTED: heat stress transcription factor B-4-like
		R	TTACCAGGCAGTACTGAAGTTG	TTGTCTTTGTTGTTATCT (GA)7	[Juglans regia]
PB.52165.4	PS64	F	GATTCTGTCTGGCATTGACG	(GA)6	heat stress transcription factor C-1
		R	CCATCTGTCTGGATCGACCT		[Ziziphus jujuba]
PB.48536.1	PS66	F	GGAATTCTTGACCGCTCTTC	(A)10GGTTTAGTTGAAT	PREDICTED: heat shock factor protein HSF24
		R	CGTCAACCAACTGGTACGTC	TCACCATCCATCTTTAG CTAC(T)12	[Vitis vinifera]
PB.55233.1	PS73	F	TGTCTGTACTTCATGACAGAACCTC	(T)11	PREDICTED: 17.1 kDa class II heat shock protein-like
		R	ACAGCCAAGAACATCCAGGT		[Fragaria vesca subsp. vesca]
PB.30998.3	PS75	F	TTGAACAGGCAATTCAGTGG	(C)16	Heat shock cognate 70 kDa protein
		R	CGCTTCCACCACTACCAATA		[Cajanus cajan]
PB.53716.1	PS85	F	GGTGAAGATGATTATGGCTTCC	(A)10	PREDICTED: NAC domain-containing protein 21/22
		R	CATTCATTAGCACCACTAACC		[Vitis vinifera]
PB.37366.1	PS90	F	CACGTCATGGCAATGTGAA	(T)15	PREDICTED: NAC domain-containing protein 82
		R	TCCATAGAGTGGCAACATGC		[Vitis vinifera]
PB.28598.3	PS91	F	GTGGATCCAGAGGTTCTCTGA	(T)15	PREDICTED: NAC domain-containing protein 82
		R	AGTGCCATAGAGTGGCAACA		[Vitis vinifera]
PB.57254.2	PS93	F	TGCTGCAAGATGAACTCCAG	(T)11	PREDICTED: axial regulator YABBY 1
		R	TCTCTCAACAAGCAAGAACTCA		[Theobroma cacao]
PB.57368.1	PS94	F	TCGATCTATATCCATGGCTCAC	(TC)8	PREDICTED: axial regulator YABBY 5 isoform X1
		R	AGTCTCTCTCCTTGCTTGAA		[Vitis vinifera]
PB.49311.9	PS96	F	AAGAGTAACATGCGCCAACA	(CT)18	PREDICTED: protein YABBY 4
		R	AACACTACAAGACCTCCACTGC		[Vitis vinifera]
PB.35930.1	PS97	F	ATTGCCGTATTCCTCGTGAC	(T)11	PREDICTED: expansin-B3-like
		R	CCACGTGCTACTACACTATGCTT		[Nelumbo nucifera]
PB.54752.2	PS98	F	CAGCAACAACCGATAATGGA	(CAA)5	PREDICTED: B3 domain-containing protein At2g36080-like
		R	CATCCACTTCTCGTCGTCT		[Vitis vinifera]

PB.49578.3	PS102	F	TGAGTGAACTCCTCCTCCTTG	(T)11	PREDICTED: bZIP transcription factor 53
		R	CCACTAGATGAAGCCATGGTG		[Ricinus communis]
PB.48852.3	PS103	F	AAGATGCAGAGGATCGAGGA	(T)15	bZIP transcription factor 60
		R	CATGTCTGAAGCACTGTAACCA		[Jatropha curcas]
PB.40196.1	PS105	F	TTCATATCGGACACGCAGAG	(GTA)5	putative basic leucine-zipper transcription factor fragment, partial
		R	AGTTCTGCACTCGAGCTTCC		[Diospyros kaki]
PB.46529.2	PS113	F	CATTAGCTCAGCTGCCTCAG	(T)16	PREDICTED: transcription factor E2FC isoform X1
		R	GCGACTGACATTCTGACTCGT		[Vitis vinifera]
PB.51687.1	PS114	F	TCCATCATCATCGTCATCAGA	(T)14	PREDICTED: GATA transcription factor 12
		R	GCCAATAATGGCAACAACA		[Nelumbo nucifera]
PB.51634.2	PS116	F	GACTTGCACTCGAACCATCA	(A)10	PREDICTED: GATA transcription factor 5
		R	CATAATCTCCGCCGGTTCTA		[Vitis vinifera]
PB.48336.1	PS117	F	CATAATCTCCGCCGGTTCTA	(T)11	PREDICTED: GATA transcription factor 5
		R	GACTTGCACTCGAACCATCA		[Vitis vinifera]
PB.45875.1	PS118	F	GGATTACATGTGAAGCGGATG	(TC)6	PREDICTED: GATA transcription factor 8-like
		R	GCGCCACAGACTTCAATACC		[Vitis vinifera]
PB.28010.1	PS122	F	TTGCTCCTAGGTATCGCAATC	(T)12	PREDICTED: probable WRKY transcription factor 20 isoform X1
		R	AAGGACGTATTGACGCAGAA		[Vitis vinifera]
PB.32099.6	PS123	F	TTCAGCAGCAACAACAACAA	(ACA)5	PREDICTED: probable WRKY transcription factor 21
		R	CTGAGCGAGAACCACCAGTT		[Prunus mume]
PB.49343.1	PS129	F	GATTCTCCATGCCATTGTCC	(T)13	probable WRKY transcription factor 7 isoform X1
		R	CAGCCACCTTCATGCTGATA		[Populus trichocarpa]
PB.52783.1	PS131	F	CAACCTTGGTCTTGCTCTCC	(GAA)6	WRKY transcription factor 22
		R	GCTCTAATCCTCGAATATTACCTGA		[Manihot esculenta]
PB.44073.2	PS142	F	TCCAAGATGAGAAGTGCATCC	(A)10	C2H2-like zinc finger protein
		R	AGCAACTGCGGAAGATGAGT		[Theobroma cacao]

PB.18100.1	PS145	F	CAGTGGATCATCGCACAATC	(T)10	WD repeat-containing protein 75
		R	AAGACCAGCCAATGAACCAA		[Manihot esculenta]
PB.50274.1	PS147	F	GGCCTCTCTGCAGTCGTTA	(T)12	PREDICTED: ribosome biogenesis protein WDR12 homolog
		R	GACGACTAGCAACTATTCCACAA		[Nicotiana tomentosiformis]
PB.45714.1	PS150	F	TGCAGTGGTCTCTTCACAG	(T)13	WD40 protein
		R	TTGGCAGAGAATGATTGACA		[Paeonia suffruticosa]
PB.46107.3	PS151	F	GCCACACCTCACTTGGTCTT	(T)13	PREDICTED: WD repeat domain-containing protein 83
		R	AGGCGCAATTCTCATGTCTT		[Nelumbo nucifera]
PB.35830.3	PS159	F	TTATGGAGCAGTGATGCTTCT	(T)13	WD repeat-containing protein 76 isoform X1
		R	ATCCACCTGCCTGTCTGATT		[Quercus suber]
PB.35071.1	PS160	F	ATGCACCTGTGGAGGTGTG	(T)13	PREDICTED: WD repeat-containing protein 11 isoform X1
		R	CAAGGTACTACGCGAACCTG		[Gossypium raimondii]
PB.45295.1	PS163	F	CTCGAGCAAGAGTTGGTGGT	(TC)6CT(CA)7	PREDICTED: transcription initiation factor TFIID subunit 15b
		R	ACAGGAGTCTCGCCTAGCAA		[Vitis vinifera]
