

Table 1. Real-time qRT-PCR verification of eight DEGs.

Gene ID	Gene description	Gene expression comparisons	RNA-seq log ₂ (FC)	Up/down	Primer sequence (5' → 3')
BMK.10019	Uncharacterized protein LOC100777071	JL2 vs YZ9253	1.63	Up	F: TCTGGTGCTTATCGTCCT
		JL2 vs JL7	2.26	Up	R: ATGTCCTTTGTCGCTTGT
BMK.11023	UPF0481 protein At3g47200-like	YZ9253 vs JL7	1.83	Up	F: CAAGAACGCAGAAAGGAA
		JL2 vs JL7	3.35	Up	R: GTGAATGGAAGGGAAAAGA
BMK.14924	Tyramine N-feruloyltransferase 4/11-like	JL2 vs YZ9253	-3.52	Down	F: CTTCCACTCCTTCACCAT
		JL2 vs JL7	-3.61	Down	R: GAGCCTCAGATTCACGAC
BMK.1585	Patatin group A-3-like	JL2 vs YZ9253	2.81	Up	F: GACCCGTTCCAGCCTTTT
		YZ9253 vs JL7	-4.03	Down	R: CTGCCACAATCTTCCT
BMK.10824	Uncharacterized protein LOC100305850	JL2 vs YZ9253	1.73	Up	F: TTCTACTTGATGGGTTTGAG
		YZ9253 vs JL7	-3.51	Down	R: GAGGAAGAGGTTTCGTTTG
BMK.1780	Drought responsive element-binding protein	JL2 vs YZ9253	4.55	Up	F: TTTCTTATCAACCACAACC
		JL2 vs JL7	3.68	Up	R: CCCAGCCAAATCCTACTC
BMK.20465	Serine-threonine kinase	JL2 vs YZ9253	-3.81	Down	F: ACAATCTGGCACAATCTTTC
		JL2 vs JL7	-3.13	Down	R: CGTAGCATACAGGGAGCA
BMK.13095	Heat-shock protein	JL2 vs YZ9253	2.58	Up	F: CAGCACCACCCTGATACA
		YZ9253 vs JL7	-4.09	Down	R: AAGGCAGAGGATGAAGAG

Table 2. SSR loci selected for validating the amplification and polymorphism.

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T_M (F)	T_M (R)	Product	Polymorphism
HAAS_VR_1	BMK.7	(T) ₁₀	ACAGCTCTGTGGTGTTCAC	CGGATATGTGCTTGCCCTACC	59.95	60.45	249	M
HAAS_VR_2	BMK.10	(TG) ₇	TCTTCCGATCTGGGACATCT	TCCTTCACTTCAITTTCAATCCA	59.61	59.55	229	M
HAAS_VR_6	BMK.55	(A) ₁₂	GAACCAAAATCAAGCTCGTCA	CCCTTTGGAATCACGCTGT	60.24	59.97	246	M
HAAS_VR_24	BMK.255	(GAG) ₅	TGAAGCGGTAGTTGTGAAGC	CCACGTTTCCATCACACTT	59.08	59.44	186	M
HAAS_VR_25	BMK.286	(A) ₁₀	TGGCTGTTGCCCTAGGTATT	TGGCATCACCGTTTAGCATA	59.59	60.10	162	M
HAAS_VR_26	BMK.288	(A) ₁₁	CGAACTGTGGAACAAGCAAA	TTTGGTTGCAAAATCAATGTC	59.88	59.96	229	M
HAAS_VR_35	BMK.346	(ACT) ₅	ACCAGGAGCTGGGAATAAC	CAC TTGCAGACCAACAAAGG	60.33	59.33	242	P
HAAS_VR_36	BMK.360	(GCT) ₆	AAGCACTGGCTTACCAGAT	TGCAGCATTTGAAAAATCA	59.87	60.33	182	P
HAAS_VR_37	BMK.374	(A) ₁₁ gftaatcaaacataggtgtggt	TTCCGCCCTGAACTCTTCCTA	CTCCACTTTCTTGCGTGACA	59.95	60.02	246	P
HAAS_VR_49	BMK.485	aattaatttaagtttaattttacgttac(A) ₁₁	TGGGTTGGGAACAAAGAAAC	CCAGGCTTCCCACAATTA	59.94	59.93	242	None
HAAS_VR_51	BMK.501	(CT) ₇	CGTCTGGAATCCTCTCACAA	GAAGACGAAAGCGGTGGAGA	58.80	60.39	223	P
HAAS_VR_65	BMK.631	(GTC) ₆	CCATCAGTGGAAACCTTGCT	TGACAAACCGGTCTACGACA	60.11	60.15	240	None
HAAS_VR_80	BMK.801	(TGC) ₅	TAGGCCCTGGTTGTTCCATC	GATGCCCTGGCAGAAAGAG	59.93	60.10	226	P
HAAS_VR_83	BMK.807	(CCA) ₅	ATTTCGCCCTTTCCTCACCT	AGACGGAACGTTTTGTGGAG	59.94	60.15	208	P
HAAS_VR_84	BMK.810	(TTCA) ₆	GGTGGAGTCTGTAGGGTTT	AGCTAGTTCTGGTGCAGATGA	60.23	57.71	202	P
HAAS_VR_94	BMK.1018	(AT) ₇	CCGGTGCATAAGAAACACAC	CTTCTGCAGCAGGAATCAC	60.37	60.94	205	M
HAAS_VR_95	BMK.1020	(GAA) ₅	CACCGCTAAATCCACACT	TGCATCGAGCAITTTGTTCT	59.99	59.96	190	M
HAAS_VR_96	BMK.1021	(T) ₁₂	AGAGAGAGATGAAAGTACAGC	GCAGGGTAAAGTCCGTAGA	58.44	59.48	238	M
HAAS_VR_105	BMK.1137	(GGT) ₆	GCCACCGAGTACCACACTAT	CTCCCAGTGAACACCCACA	60.00	59.70	238	None
HAAS_VR_116	BMK.1245	(TGG) ₅	CATGGAGGAGAGGAGTCTGG	TTAATCCCAGGTGCAAAAGG	59.79	59.93	212	M
HAAS_VR_118	BMK.1251	(T) ₁₀	CAAAACGGCAAAAGAAATCCAT	ACGATCAAGGGCTTATGTGC	59.94	60.10	248	P
HAAS_VR_130	BMK.1353	(T) ₁₅	TGCTGGAAAACACAAAGCAA	GAAAAGAAAATCTCCCCAAA	60.41	59.41	217	None
HAAS_VR_146	BMK.1584	(AGG) ₅	CTGGTGGGGATACAAATCAC	CATGTTGAAACACACGCTCG	60.05	60.00	239	M
HAAS_VR_152	BMK.1689	(ATG) ₆	CCGGATAGCATCTCCTGAAG	TGGCCAAAGTTTGACCCGATA	59.79	61.39	243	M
HAAS_VR_162	BMK.1843	(GAT) ₆	TCAAATGATTTGGGTCCAT	CATCGAGAGGAGGTTTGT	60.17	60.11	246	None
HAAS_VR_164	BMK.1863	(CTT) ₅	GGGTAGCAACGTTGGTGT	AACAATGGGGAGGTATCTG	59.90	59.96	179	M
HAAS_VR_178	BMK.2109	(A) ₁₀	GCGACTGCAGAGATCAITCAA	GCAGAACAGGGCGTATTTTT	60.10	59.23	234	M
HAAS_VR_179	BMK.2111	(A) ₁₄	TGGGATTTACCTCCACCTT	GCGGACTGTACTGCCATTT	59.69	60.14	205	M
HAAS_VR_199	BMK.2293	(AGA) ₅	AAITGGAGCTCGTGTGTGCT	CACCAAGAAAGTTCGCCAAA	59.88	59.94	204	M
HAAS_VR_201	BMK.2313	(T) ₁₁	CAAACCTCCGTTTCCATTT	TCAGGCTGAACTCGATCCTT	59.83	59.95	220	M
HAAS_VR_219	BMK.2572	(A) ₁₄	TCCAAATGCAAGTCTGTCTC	GCAGTCAACATGGTCACTCACT	59.00	60.23	188	None
HAAS_VR_220	BMK.2578	(AG) ₆	ATCCATGAGAGCCGAAAATG	TTCCACCCCTTTGGTGAAAG	60.04	59.94	242	P
HAAS_VR_221	BMK.2585	(AG) ₆	TGCACACAAACAGCAATAGCA	GTCCGCTCCCTTCTCTCCT	60.06	59.81	232	P
HAAS_VR_232	BMK.2773	(A) ₁₂	CAAAACCAACCCCTTCCCTT	CCACTTCATGGCCAACTTCT	60.19	60.11	218	P
HAAS_VR_233	BMK.2780	(T) ₁₄	GCGATCTACTCCGCTGTCAT	AGCAAGCAAGGACATTTCTCTG	60.39	59.63	176	P
HAAS_VR_235	BMK.2810	(TTC) ₅	TGCTGCATTATAICAGACCTTGA	CAGCAGATTTATTTCCAGCA	59.76	58.87	194	M
HAAS_VR_249	BMK.3015	(T) ₁₅	TACCCCTCCCGTACTAATG	TTGCCAATACCTAGGTCCA	60.07	60.32	189	M
HAAS_VR_250	BMK.3019	(TCT) ₅	TTCCCTCCACCTGTTCTTC	TGTCCGAATCCGGTCAATGAA	59.11	59.92	151	M
HAAS_VR_263	BMK.3139	(ATA) ₅	TACGATGCCGTGGATGATAA	TTGGCGCCTAACATCTCTTT	59.91	59.85	203	P
HAAS_VR_265	BMK.3153	(A) ₁₄	TTTAGTGCATCCGCATAACC	GACAAAAGGGGTGGAGAAA	58.65	59.94	186	P
HAAS_VR_266	BMK.3155	(TA) ₆	GCGTGACTTGGTTGTCTAA	TTTCAATGTGCTTGTGACC	60.06	59.85	210	M
HAAS_VR_283	BMK.3462	(A) ₁₀	CCCTCGTGTGGAAAGAAA	TTGAAGCCCATATTCGGAAC	60.08	59.90	182	None
HAAS_VR_285	BMK.3490	(T) ₁₁	TTCCATCTAGGAGCAAAACAAA	TGAACACTTGACCCCAAAA	60.11	59.00	198	M
HAAS_VR_289	BMK.3545	(T) ₁₀	ACAAAAGGGGAAACTGGGACT	TGGCTCGCAGAAAATTAGACA	59.83	59.57	162	M

Table 2 (cont'd)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T_M (F)	T_M (R)	Product	Polymorphism
HAAS_VR_299	BMK.3633	(T) ₁₂	GTGGCTGAGGGCGAAATG	AATGCTCGAAGGGTGTGTTG	62.77	60.11	156	None
HAAS_VR_301	BMK.3650	(AAO) ₅	CGATGTCGAAAAACAACCTCA	TTGGCGAGAGGTTGAAAGAGT	59.69	59.99	234	P
HAAS_VR_315	BMK.3880	(AAC) ₅	CTTAATGTGCACGCCAATGT	GTTTCCCAATCGTAGTCCA	59.61	59.79	207	M
HAAS_VR_318	BMK.3885	(TCG) ₆	CAGACGAAAGACAGCAAG	TGGAATGGGTTCAAGAAGGAG	59.92	60.04	250	P
HAAS_VR_335	BMK.4123	(CTT) ₅	GAGAAATTCAGGCTTGCTG	GTAACCTGGTGGGCTTTT	60.01	60.22	171	P
HAAS_VR_336	BMK.4133	(GAA) ₅	GGCCAGAACAAITGAGGAGAA	GCATGATTTGGCTGGAAITT	60.20	59.91	157	P
HAAS_VR_338	BMK.4160	(C) ₁₀	TAGCCCAACCACTTCACTTT	TGAACCAACCCCAACAAACA	59.59	59.83	178	M
HAAS_VR_360	BMK.4456	(T) ₁₄	CCACATGCAAAACCTTCCCT	TGCACGAGTTCAATGGGTA	59.97	60.11	239	P
HAAS_VR_361	BMK.4456	(GA) ₆	GGTGAGCCAGAGAGAGCA	TTTCTTCTTCACTCCCTCTTT	60.85	59.76	188	P
HAAS_VR_376	BMK.4704	(TCC) ₅	GCCCCAACCAACCCATAAT	GGGATCGTAGGAGGTGGAAT	59.91	60.15	239	M
HAAS_VR_377	BMK.4715	(GA) ₈	CAGTGTTAATTTTCGGGTGTG	CCCATGTTGGAGAGGGAATA	59.42	59.74	212	P
HAAS_VR_378	BMK.4715	(CTT) ₅	GGGGCTGACACAAITGTTAC	CGGTATTACAAATGACGAAAAGG	60.24	59.79	231	P
HAAS_VR_395	BMK.4956	(TCT) ₅	TGTTGAGGTTCTTCAACCTTC	GGTAATATGCCCGGAGGAAT	58.43	60.01	172	M
HAAS_VR_397	BMK.4968	(T) ₁₀	AGCGGTTGCCATATAAACAC	TTCCAAGGAGGCCAATCTA	59.85	59.64	209	M
HAAS_VR_414	BMK.5319	(TCA) ₈	GGGTCCGAGTGCCTTAAITT	TGTGGGATGTGTGTGTGTG	60.32	59.88	182	None
HAAS_VR_415	BMK.5319	(T) ₁₃	GATTCACGTGTGCCATCATC	TGGACAATTCATTCAAAAGAAAA	59.93	59.87	372	M
HAAS_VR_417	BMK.5329	(AG) ₆	ATCCCGGGTGA AAAATAAAA	AGAAATGGTGCATGGGTTT	60.36	59.80	157	M
HAAS_VR_431	BMK.5583	(GAC) ₅ ;gaggaaaggaaaggaggacc gaaagggaaaggatttcgcgigaagacaagsg aaaaagggaaaatgtaacaagaagacag(GAT) ₅	CAAAAACGACGTTGAGGATGA	CCTGGACGGCAGAATGTTAT	59.69	59.96	249	M
HAAS_VR_433	BMK.5615	(TTG) ₅	CCAGAAAGCAACTGGGAGAAC	CAGCTTTTGTGTCTGCTC	59.84	58.65	239	M
HAAS_VR_434	BMK.5628	(TGT) ₅	CATATTCGCCACCCCTTCT	TGATGAAGCCACATGGAAGA	60.01	60.20	208	M
HAAS_VR_446	BMK.5786	(ATA) ₅	CGCACTCCAATCAAAATCAAA	TCGACGGAGAGAAGACCACT	59.66	59.99	184	P
HAAS_VR_451	BMK.5815	(T) ₁₃	CCAAAATGGCTCACTGGAT	AATCTTCTCCCGTGGATTT	60.11	59.77	194	P
HAAS_VR_468	BMK.6146	(A) ₁₃	TGATTTCCGATGCAACAGAGC	CTCAACTCGTCTCACACA	59.96	59.86	273	M
HAAS_VR_469	BMK.6150	(A) ₁₀	CAGGTTGGTTCGATACA	TGGCTGAGAAAACAACACAGC	58.11	60.03	112	P
HAAS_VR_470	BMK.6152	(GAA) ₅	CGCCTTTGCAAAATCATGTA	AGCAGGTGTGACCTTTGCTC	59.70	60.45	278	P
HAAS_VR_487	BMK.6439	(AAT) ₅	GATCTTTGCATGGAGGTGT	AAGGTGGCTTCATCTCACC	59.93	59.14	257	M
HAAS_VR_489	BMK.6475	(TCA) ₇	AGTTCATGGTGACGGAGGAA	TGCTCCCTTGTACTTGGTCC	60.51	60.11	179	M
HAAS_VR_509	BMK.7039	(TGA) ₅	TCCAAAATGAAAATCCGTGTT	GCAGTGTTCCTCATTCAGA	60.17	59.99	140	P
HAAS_VR_510	BMK.7057	(GTT) ₅	AGCTCCTTTGGCATCACACT	TAAGCATGGCTCTGAAGGCT	59.87	60.12	100	P
HAAS_VR_534	BMK.7514	(CTT) ₅	TGGTTAGTGGGTGTGACAA	GCTAAAACAACATCCATGTTCCG	59.85	59.47	203	P
HAAS_VR_535	BMK.7529	(AG) ₈	AGAAAGAAATGCTGGGAAGC	TCAAACCTGCAATTCCTTC	59.85	60.05	220	M
HAAS_VR_541	BMK.7729	(CT) ₆	TCCACCAAAATGAGCCCTC	TGTGTTCTCTGCCTTCTCC	60.05	59.52	266	P
HAAS_VR_558	BMK.8042	(T) ₁₀	TCGTTCTGTTGGTGTGTTT	AGGTGATAAATCTGCGGGTTG	60.05	59.99	241	M
HAAS_VR_559	BMK.8058	(CT) ₈	TCAAGATCATGACCAACAGC	TGATGCCTGGGAGATGTA	59.95	60.07	157	M
HAAS_VR_560	BMK.8059	(GTT) ₅	CCGGGAGATCAAAITCAAAA	CGATTTTGTGACAACGGAAAA	61.07	59.56	278	M
HAAS_VR_582	BMK.8450	(T) ₁₀	TTGAAAGGGGCGACTTAAATG	ACGAAAATCCCAACAACAAT	60.07	60.42	203	M
HAAS_VR_583	BMK.8493	(AG) ₆	TCATTTCCAGACGACATGTA	CCGTTCTGGGATTACCAATG	58.78	60.18	191	M
HAAS_VR_584	BMK.8493	(ATC) ₅	GACAAGCTTCCAGTCCGAC	CCCAATCTCCAAAATACCC	59.85	60.37	234	M
HAAS_VR_601	BMK.8712	(TG) ₉	TGGGTGAATGCTCTGTGCTA	AGGGGAATGAATGCTCTCA	60.11	59.63	231	M
HAAS_VR_602	BMK.8712	(A) ₁₄	TCCACAAAATGATGAAGCCA	CCCTCCTCTCAACTGCTTG	60.05	59.98	144	P
HAAS_VR_603	BMK.8722		TGCAGGTTCTGCAITTTCAAG	CTCGCTTGAATTAGCCCTCAC	59.99	59.98	153	M

Table 2 (contd)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T_M (F)	T_m (R)	Product	Polymorphism
HAAS_VR_621	BMK.9042	(TCA) ₆	CCGGTGAATAAATTCCTGAG	CGAGAGCGGAAAAGAGAGAGA	60.46	59.97	206	P
HAAS_VR_623	BMK.9053	(CTC) ₆	CCAAAACCCCTCACCTCCAAA	TTCACTCTCCATCCGAATC	59.94	60.01	166	M
HAAS_VR_625	BMK.9082	(TA) ₆	GGGATACTGCCACACCATCT	GAGGCTTAGTAATGCAGGCG	59.81	60.00	179	P
HAAS_VR_635	BMK.9150	(T) ₁₀	CTCTGCTGTAGCCACCACAA	AAATAAAAAGCCTGGGCAAC	60.05	60.31	127	P
HAAS_VR_636	BMK.9166	(T) ₁₀	CATCAGCAGCAAAAGACCAAA	GATGCATGAAGATGCAGGTG	59.99	60.23	130	M
HAAS_VR_637	BMK.9181	(A) ₁₀	TCCAAATGTTGGTTTCATGTTT	TCTGAGCTCTGAGGTGGGAT	59.23	59.95	249	P
HAAS_VR_659	BMK.9676	(GAT) ₅	GGAGGGAGATGGGATAAAA	CCAAATCCGACTTCTCCAAA	60.09	60.04	215	M
HAAS_VR_662	BMK.9708	(T) ₁₁	ACCATCAACCCCTTCTCTCC	TTTAAAGCCTTGTGGGAAA	60.17	59.83	104	M
HAAS_VR_664	BMK.9771	(T) ₁₀	AAGCAAAACGTCTTGCACACTCA	CCTATGCCTACTTCCAAACCG	59.64	59.59	275	P
		(GCA) ₅	gttccccagaagaagcaggat					
			aacccatacaaatcaggat(CAG) ₅					
HAAS_VR_694	BMK.10415	(CT) ₈	AGTACCAAAGCCAGCTTCAA	TTTGACCTTGGATAGCCTGC	59.88	60.21	267	M
HAAS_VR_695	BMK.10427	(ACA) ₅	AGTGAGATTGAAGCCAGCGT	AAATCCGGCAACCTCTTTT	60.02	59.95	279	P
HAAS_VR_696	BMK.10441	(CAT) ₅	CATGCCCTCAGCAACATTCAC	TGCTGTGAAAAGCATCCTCTG	60.27	60.14	225	M
HAAS_VR_714	BMK.10846	(T) ₁₀	TCCCGGAAATTAATACGAC	GCCATGTGGACCCCTAGAGAA	59.93	60.07	237	M
HAAS_VR_715	BMK.10918	(AGA) ₅	CCCACCTGTAATTTGCTTT	ACCCCAATCAAGCATCAAC	59.97	59.93	228	M
HAAS_VR_716	BMK.10918	(T) ₁₃	GTGGGTTAAGTGTGGAGGA	ACCACCTGGTTCTGATGGAG	60.11	59.96	263	M
HAAS_VR_741	BMK.11442	(A) ₁₀	AAACCGCATTTTGATTTCTGG	TGTCACGAGATCCAGACGAC	59.94	59.83	226	P
HAAS_VR_744	BMK.11450	(A) ₁₃	TTTCCCACCTTCTCCTTTG	ACTGGCGGAAAGCTTATCAGA	59.10	59.98	186	P
HAAS_VR_749	BMK.11539	(AGA) ₇	ACAAAACATTTGGACCCCC	TGGGAGCTCCAGTATCAGG	60.82	60.21	180	M
HAAS_VR_776	BMK.12396	(A) ₁₀	TTGCTTTTGGAGTGGCAGC	TTTCCCTTTCCCAATCAATGC	60.03	59.88	128	M
HAAS_VR_790	BMK.12922	(A) ₁₀	AAATCGGGATTAACAGATGC	TCCTTCTTTGCATGATCTTGA	59.80	59.99	257	P
HAAS_VR_791	BMK.12954	(AG) ₇	ATCAATGGCACAGCAATG	AAACATTTTCGGTACTGCC	59.68	59.98	241	M
HAAS_VR_813	BMK.13523	(CCG) ₅	TACAGAATCAGGACACCC	GCTGGCTAGAGTATGCAACC	60.07	59.87	254	M
HAAS_VR_817	BMK.13653	(GAA) ₅	AGACCATGTCTGCACCTTCC	GAACTTACCAATGACCGGT	60.12	60.00	280	M
HAAS_VR_836	BMK.14117	(T) ₁₁	TTGTGCGTTTCTTGAAGCTG	AAACAATGCACGCATCTCTG	60.17	59.91	221	P
HAAS_VR_838	BMK.14303	(GGC) ₅	CAAAACACACCTTGCAGTGG	GCTGCAACCCAGCAAATCTAA	60.19	59.07	188	M
HAAS_VR_840	BMK.14322	(TA) ₇	TTCCCATTCCAAAATCTTTCG	TGGCGTCAATCAATGACATT	60.04	59.93	269	M
HAAS_VR_855	BMK.14493	(AGC) ₅	TTCCCCTTCTGCTTCTCA	ACGCTGACGTTGACTCCTCT	59.93	60.06	271	P
HAAS_VR_860	BMK.14575	(CAG) ₅	TCAGACATCACGCTCTCGTC	CCTTGTGGTTGTCTCCAT	60.15	60.11	146	P
HAAS_VR_861	BMK.14575	(CAT) ₇	ATGGAGAACAACCAGCAAAGG	TTGAAATCGTTGACGTGCTC	60.11	60.03	182	M
HAAS_VR_880	BMK.14979	(AGC) ₅	TACCCGGTTTCTGTCTCTG	TGTGTAGAGCTTGGCATTCC	60.10	59.89	243	P
HAAS_VR_882	BMK.15001	(AGC) ₅	TTTATCTCCTGCAAGGC	CAGTCTCCCAACCTGTGTA	59.41	60.25	272	P
HAAS_VR_915	BMK.15732	(A) ₁₃	CTTTTGGCTTCTGCTGGAG	TGTGCTTCTATCCCTCCAC	60.13	60.07	264	M
HAAS_VR_916	BMK.15740	(GGT) ₅	GAGGTTCCGATTTGTGGAGGA	CCAACTGCAGCAACAACACT	60.05	59.95	254	M
HAAS_VR_947	BMK.16589	(T) ₁₂	AACTGCTGTGGTAGATGGGG	GGCAGCAGTAAAATGGAGC	59.99	59.85	249	P
HAAS_VR_969	BMK.17268	(AAT) ₆	AGATCAACGTCACCCGATTC	GACCTGGGAAAACAACATGGA	59.93	59.94	278	M
			cacacaaaacaactca(CT) ₇ tc(CT) ₇					
HAAS_VR_972	BMK.17308	(TA) ₈	TACAAAACAAGATCGTCGGCA	CCATTGCTGCAACAGAAAGAA	60.26	59.99	262	M
HAAS_VR_994	BMK.17824	(T) ₁₁	GAAATTGAATTGTGCCTGGAA	GAAAAGCAATATCTTGGGCA	59.93	60.04	250	P
HAAS_VR_996	BMK.17937	(AG) ₉	ATTTGCCGACTCAACCGACTT	CAAAAGCCGAAAATTCACAAA	59.74	60.05	268	M
HAAS_VR_1016	BMK.18328	(TGT) ₅	GAGGTAGGGGAGACGACGAT	CCGACAGGGGAAAAGTACA	60.48	59.96	277	M
HAAS_VR_1017	BMK.18348	(A) ₁₁	TGATGATGGAAAGGAAAGGG	AAGCCCTTGAAAACAACCCCT	60.00	59.98	254	P
HAAS_VR_1036	BMK.18816	(A) ₁₁	AAGAAAGAAATCGCGGAGGAT	TTGGAGAGTCCCGTTTGTCC	60.17	60.09	194	M

Table 2 (cont'd)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T _M (F)	T _m (R)	Product	Polymorphism
HAAS_VR_1037	BMK.18826	(GA) ₈	GTGAAATTGGGATTGTTAATTGT	ACATCCTCGATCACTCACCC	57.02	59.93	118	P
HAAS_VR_1056	BMK.19290	(GGC) ₆	CGTAGAAGCTCGGAACAACC	AAGGAGCTGGGTTAGCATCA	59.88	59.84	259	M
HAAS_VR_1057	BMK.19322	(AC) ₆	GCATCCACACACAAAACAAGG	TTCCAAITTTCTCGACACC	60.01	59.77	241	P
HAAS_VR_1080	BMK.19774	(AG) ₆	TGAAGGCAGAGAGAAAGGGAA	TCTCTGGAAAGAAAGGAGAAAA	60.07	58.77	274	P
HAAS_VR_1082	BMK.19806	(T) ₁₂	AAAAATTGACACCCCCGAC	GTGGTGGCGGAATAGTCAGT	59.64	60.00	156	M
HAAS_VR_1096	BMK.20071	(T) ₁₁	GTGAATCAGAGTGGGGCAAT	CTTCCCGGGTGTGTAITTG	59.93	60.22	212	P
HAAS_VR_1102	BMK.20195	(TGG) ₅	CTTCGAGGACACAGATGTGT	CTCTCTTCCACCATGCCCTC	60.11	59.95	193	M
HAAS_VR_1125	BMK.20653	(T) ₁₃	GC AAGTTTGAAGAAATAGGGGG	TTTTGACACGTGGTACAACAA	59.95	60.06	274	M
HAAS_VR_1132	BMK.20830	(T) ₁₃	AGGCTGATACGGTGGAGTTG	TCAGCATCAATGACAAACCA	60.13	58.62	207	P
HAAS_VR_1161	BMK.21468	(T) ₁₀	ACATCGGAGGTATGCTGGAC	GTGCAATTC AAGCACCCCTTT	59.96	60.12	161	M
HAAS_VR_1183	BMK.21908	(TGA) ₅	CAAGTGTCCGTTCTTGGGAT	CCACGTAGCTTTTGTCAACA	59.97	59.76	258	P
HAAS_VR_1187	BMK.21989	(TA) ₆	TCAATCCATTAGTAGCATGAAGATG	TAIGGT CAGGCCTCAITTC	59.55	59.89	213	M
HAAS_VR_1209	BMK.22656	(A) ₁₀	GTGCTGTGGAGCATTTAGA	TGTTGGAGGGATGGAAACAT	60.02	60.17	280	M
HAAS_VR_1210	BMK.22677	(GA) ₁₀	GGGGTCTCCTCCTCTCA	TTAGGGAGTGTGGATCTGG	60.73	60.07	248	M
HAAS_VR_1235	BMK.23694	(T) ₁₁	GAGCATGACAAAGTCCAGCAA	CAGTTACAGAGTGTGCTGA	59.99	59.25	150	P
HAAS_VR_1236	BMK.23705	(ACC) ₆	CTCTTCAACCTCAAACCCCA	GG AAGTAGTGG AAGGGGAGG	60.08	59.93	260	P
HAAS_VR_1262	BMK.24550	(T) ₁₁	TGCTATGTGTGTGGCTCTG	AGGGAAGGTTCCGAGATGAT	60.01	59.90	117	P
HAAS_VR_1263	BMK.24580	(T) ₁₂	AGTTGTGCTGCCATTAT	AAITCCATTGCAACCCACCAT	60.53	60.06	133	P
HAAS_VR_1274	BMK.24962	(GA) ₈	CCAGCTTTCTCCATACGAA	AGCAAGGCTGTGTAACCAT	60.21	59.90	247	P
HAAS_VR_1280	BMK.25106	(CAA) ₅	TTCATCCATTCTCAAAGGC	ACCCCTCACCCATATTC	60.01	60.02	225	M
HAAS_VR_1306	BMK.26012	(T) ₁₀	GGAATTTGGCAAAGTAAAGGC	TCAAACTGAAGACCATTTGGAAA	59.57	59.59	145	M
HAAS_VR_1307	BMK.26022	(CCG) ₆	TCTCTCCACCTGATCAACC	CTACCCGCTGAGTGTGGTAA	60.05	59.78	128	P
HAAS_VR_1319	BMK.26425	(T) ₁₁	GCCACATCAATTGGACAACA	GGATTTTCAAGAATGACCGAA	59.01	59.01	273	M
HAAS_VR_1321	BMK.26546	(T) ₁₀	ACGATTCCTGACAGACCACC	GCGATA CAGAATGGAAGGA	59.97	60.04	233	P
HAAS_VR_1341	BMK.26950	(TGA) ₅	ACCCCTTCAAACCTTCTGCT	GTACAGAGCACCTGTTC	60.11	60.71	254	M
HAAS_VR_1343	BMK.27030	(A) ₁₁	CACATGCATTACCATGACA	ACAACATACCAAGGCCAAGC	59.96	60.00	160	P
HAAS_VR_1360	BMK.27541	(CT) ₆	TGAGCAAAATTTGATTGAGATGTG	TCACCAGAGAAAGGAGAAA	60.12	58.90	121	P
HAAS_VR_1363	BMK.27666	(A) ₁₀	GAGGTTCCAAACATCTCAGCC	GGATGGACAATGTTGTGCTG	59.66	59.97	148	P
HAAS_VR_1378	BMK.28224	(A) ₁₂	GGCAAAGCACAAACAATTGA	AGAAACGGAGGCTCTGATGA	59.89	59.95	170	M
HAAS_VR_1381	BMK.28303	(T) ₁₀	TCAAATTC AAGCAAAGGGAAGA	GCTGTGATGGACAGAGGGTT	59.81	60.12	208	P
HAAS_VR_1402	BMK.28899	(T) ₁₁	AAAAATTTGATCCCTTTGCC	AACCCATCATAGTGC	60.13	59.92	270	P
HAAS_VR_1409	BMK.29131	(T) ₁₂	GCTTGATGCACCTCTCTCC	AACCTGGCAACCAACGACTC	59.96	60.16	226	M
HAAS_VR_1433	BMK.29686	(CAA) ₅	GCCACCAACTTTTCCAAAAC	AACCC TACTGGGTGAGTGA	59.45	59.43	261	P
HAAS_VR_1437	BMK.29721	(AG) ₆	CCCCAGAATCAAGAAATCCA	GCTCTGTTACTGGAGGCAC	59.86	60.02	142	P
HAAS_VR_1446	BMK.29976	(T) ₁₀	GGGCAGTAAAATCAACAATCT	TTGGTTGCCCTTCAAAACTC	57.33	60.09	145	P
HAAS_VR_1449	BMK.30117	(AGA) ₅	GCATGGAGAAAGGGTTTTTGA	GCGATGCAGAACAAAGCATA	60.05	59.98	227	P
HAAS_VR_1482	BMK.31091	(T) ₁₁	CCGAGCTTTTGTCTCTGCT	TTAAATCC AAGGCATTTGGC	59.76	59.91	218	M
HAAS_VR_1483	BMK.31111	(CCG) ₅	GCGAATATTCAAGCCGAAG	ACAAATGGGCAGAACTCTT	59.98	59.88	190	M
HAAS_VR_1505	BMK.31574	(T) ₁₂	GATCTGTGAGGGGTGAAGA	ACAAAAGCCAAACAAGTCCG	60.05	60.15	280	M
HAAS_VR_1507	BMK.31676	(A) ₁₁	GG AAGCGGCTTTTCTTTCT	GAATTCATGGGCAAAACACC	59.97	60.18	169	P
HAAS_VR_1528	BMK.32467	(A) ₁₅	CCATCCCAGAATGTGGTTC	ATTTGGTTCTGCCACTGAG	60.17	60.11	243	P
HAAS_VR_1529	BMK.32502	(GAA) ₇	AACTTCCATTGTGTGAGCAT	GAACACAAGCGTTTGTGAA	57.19	60.04	145	P
HAAS_VR_1548	BMK.33153	(ACC) ₆	AATACCGGCATCTTTTGGACG	TTTGGCAAGGGGTGATAGGAC	59.96	59.93	259	P
HAAS_VR_1549	BMK.33153	(GAA) ₅	AATGCAATGCTTGGTATGA	AAAGCCGAGGAATTGAGGAT	60.08	60.04	145	M
HAAS_VR_1571	BMK.33568	(TCA) ₇	GGAAGCAGAAAGCACCTAGCA	GGAGATGGATTGCAGGCTTA	60.68	60.18	101	P

Table 2 (contd)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T_m (F)	T_m (R)	Product	Polymorphism
HAAS_VR_1572	BMK.33597	(A) ₁₁	GTCCCTTTGTTGGTGCTA	ACTGGCGAACCCAAAATCAAG	59.97	60.11	255	P
HAAS_VR_1588	BMK.34141	(TC) ₇	GTCATGATGACGGACACGAG	TGTTGGCTTGCTACATGG	60.28	59.57	184	P
HAAS_VR_1589	BMK.34219	(A) ₁₁	AATGAAACCCAAAACCCAA	TGCAAAATCCCACTACTGAA	60.07	60.24	248	P
HAAS_VR_1601	BMK.34654	(AAG) ₅	AAAGGCTAAGTTTCATGGC	CCAAAATCAATCTTCTCCCC	60.10	59.65	129	P
HAAS_VR_1605	BMK.34738	(T) ₁₄	TGAACCTCAAGAAGGCAACA	CCGGGTAAAGAACAAGAACCA	59.42	59.96	242	P
HAAS_VR_1619	BMK.35227	(A) ₁₁	GATCAGGACCCGAAACCTAA	TCATTTCTCCCTCCCATCTG	60.07	60.00	218	M
HAAS_VR_1620	BMK.35245	(GA) ₆	AGCGGAAAGGAAGATGAGAT	GGCACAGCTCCCTCTAATTG	60.18	59.84	147	P
HAAS_VR_1646	BMK.36044	(T) ₁₀	TGAGGAAAAGCGTTGGTAG	ATCATCAATTTCTGTCCGCC	60.24	59.90	266	M
HAAS_VR_1647	BMK.36073	(A) ₁₀	TTCCGCTTATGCTATCTGTGCA	TTGAGATTTGCCAAAAGCAGTG	59.51	59.99	278	M
HAAS_VR_1670	BMK.36776	(TCA) ₅	CCTCCGTCCTTCACTGG	ATTTCTGTTCACTGATCGCC	59.98	60.04	160	M
HAAS_VR_1672	BMK.36827	(CTT) ₅	TCCCATTTTGTGGCCAGTAT	GGATTTACGAGCGCATGTG	60.19	60.10	165	M
HAAS_VR_1685	BMK.37253	(T) ₁₁	AATTGTGACCCCTTCTCGCAC	GCGGAGTGGAGAGATCTGAG	60.12	60.10	141	P
		(T) ₁₀ ctttcaataataactataaa						
		ctgaaaggcaacaacaataaaga						
		ttacaatttcaact(ATC) ₅						
HAAS_VR_1691	BMK.37360	(TTC) ₇	TTACCAACAAGGGGGAAGA	CTGTGCCACAATACTCTGC	59.40	59.62	278	P
HAAS_VR_1702	BMK.37436	(A) ₁₀	CACCAACCACCTCTCACTCT	AGACGGATGGACGAAAACATC	59.21	59.93	198	P
HAAS_VR_1707	BMK.37476	(TC) ₈	CACAAACGACATTTGAAAGCA	TGGAACCACTCCAAGAAGG	59.76	60.08	137	P
HAAS_VR_1719	BMK.37548	(GCC) ₅	TCCTTCTCAIATTTCCCTCTGC	GAGGCATGTGGTTGGAGAIT	59.69	59.93	235	P
HAAS_VR_1720	BMK.37548	(CT) ₆	TATTTCCCAAGTCTCCATCGG	AGTGCAACTGTCTCTCGGAT	59.89	60.02	218	P
HAAS_VR_1730	BMK.37626	(AG) ₉	GCCATCAAAGTGAAGGAAG	GGAGAATGGAGTTGCTCTG	59.67	59.80	253	P
HAAS_VR_1731	BMK.37634	(ATT) ₅	GGTCAAGCATAAACCCTAA	CTGCTTTGTCTCCCTCATCAC	59.93	59.60	280	P
HAAS_VR_1743	BMK.37703	(T) ₁₁	GTGAGAACCCGGGTGACAGTT	GCTTGTCCAAAATCCAAAACA	60.01	58.60	259	P
HAAS_VR_1744	BMK.37707	(ATT) ₅	CGTAATGGAAGTGGCAAT	TTGTAAACGAATTTGGGGA	60.10	60.16	266	M
HAAS_VR_1759	BMK.37797	(CT) ₈	GAAACGGTCTTCCCGTAIT	CCCACGATCAGAGGACTGTT	60.19	60.11	170	P
HAAS_VR_1760	BMK.37822	(GAGC) ₅	GGAGAAAGCCATGAAAATGA	AAATGAGGGAATTTGGCAA	60.01	60.31	196	P
HAAS_VR_1770	BMK.37875	(AGG) ₅	GGCGTGAGTTTGAAGAGACC	TCTTTTCATGCTGTTTCGCA	59.85	60.52	256	M
HAAS_VR_1774	BMK.37887	(ACO) ₅	GACCTTCAIACCCTCACCTGGA	GCCTCAICTTCCACACCAAT	60.05	59.93	134	M
HAAS_VR_1785	BMK.37950	(A) ₁₂	TGTGGCATGACTGACCTCAT	TGGACCTCTGATGTGTGAA	60.12	59.96	152	P
HAAS_VR_1787	BMK.37967	(T) ₁₁	TGAGTTCACCAACCACAGCA	CTCCTGGAAGGGAAGCTTTT	60.13	59.82	229	P
HAAS_VR_1801	BMK.38014	(T) ₁₁ (TTA) ₆ *	CTTCCACATGTAAGGCAITGG	CCTGGCTGATGTAIACCCT	59.00	59.95	228	P
HAAS_VR_1802	BMK.38014	(TA) ₉	AGAGAAAAGGTGCGAGACA	TTCTTCTTTTCCATAATAAGACTTTG	60.13	59.54	174	P
HAAS_VR_1816	BMK.38099	(TC) ₇	TCACATCAGAGAGCGGTGAC	GTGAAATAACAACGGCCCTG	59.99	60.37	202	M
HAAS_VR_1817	BMK.38116	(GAT) ₅	CAAAGGAAAAGGAAAAGGC	CCTGGTTACCAACCTCCTCA	60.05	59.96	132	M
HAAS_VR_1826	BMK.38145	(T) ₁₀	TGAAAAGATACACCAGGGCA	AAGGCAAAAGTAACTTCCG	60.64	60.73	234	M
HAAS_VR_1827	BMK.38148	(T) ₁₂	ATCTCGACTCAACGTGGCT	CGTTTGTATGGTCTTCCTG	59.83	60.13	262	M
HAAS_VR_1837	BMK.38225	(TA) ₇	TATGTCCGAGTTCGAGTTC	TGAACCAACCGTTGAACATTTT	59.87	58.54	238	P
HAAS_VR_1838	BMK.38228	(A) ₁₀	CATGATGGATGGGATTTTC	GAGAAGAAAAGTGGCCAGGA	59.95	59.41	201	P
HAAS_VR_1851	BMK.38356	(CT) ₈	CATCAATCACCCGTACCAC	CCTCCTTCCATTGGTTGTGT	59.99	59.82	184	P
HAAS_VR_1852	BMK.38362	(T) ₁₀	GGACTCAAGGTTCCCTCTCC	ATTAGCTCACGGGCCATAAA	60.05	59.57	233	P
HAAS_VR_1863	BMK.38432	(TG) ₇	ACGTCGTGATCCGAAAAGAC	TTCCAAAAGTCAACCCACCA	60.12	59.98	115	M
HAAS_VR_1864	BMK.38432	(A) ₁₅	TGTGGGTGTTGACTTTGGAA	AGCTGAGTGGCCAGAGAAA	59.98	60.13	215	P
HAAS_VR_1873	BMK.38486	(A) ₁₀	AGAAAGGAAACCACGATCTCA	GCAGAGGACGAAAATGGAAAG	59.66	59.81	159	P
HAAS_VR_1874	BMK.38488	(T) ₁₄	GGCAGCATAAGAGAAGCCAC	AACCCCTTTTTCATGCTCTT	59.99	59.94	164	P
HAAS_VR_1887	BMK.38550	(TCAC) ₅	CTTCGCTTCCCTTTTACC	CCAGAGAAAAGCCGTTCAAG	60.07	59.99	261	P

Table 2 (contd)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T _m (F)	T _m (R)	Product	Polymorphism
HAAS_VR_1888	BMK.38562	(GT) ₈	TCTGTCCATTTCCACATTCCC	AACCTCTCACTGGTTGGTGG	59.90	60.00	236	P
HAAS_VR_1898	BMK.38638	(CIT) ₅	TGGTGGCATAAGTAATCGTCG	GATGAAGGGTCGTTGGTGT	59.57	59.83	223	M
HAAS_VR_1910	BMK.38746	(A) ₁₁	TGATTTCAATTACAATCAAGGATGA	TAGAAGTGGGGTGAATTTGG	59.74	59.78	148	P
HAAS_VR_1912	BMK.38768	(A) ₁₀	AAAAAGAGGGGAAAAAGAGAAA	GACTGGCACTTTCTGCTCCTC	57.66	60.14	261	M
HAAS_VR_1922	BMK.38847	(A) ₁₀	TTCCTTTACAAAGTGTGTC	TGACCCCAATGGCTTTTAAACT	59.05	59.88	163	M
HAAS_VR_1923	BMK.38858	(GA) ₇	CGTGTGCTCTCCGATCTCT	AAATTCGATTTATGCGCAAC	60.56	59.94	142	M
HAAS_VR_1934	BMK.38910	(TTG) ₅	TAATGACCTCCATGCCTTCC	CACCGGAAAATACCATGGAC	59.89	60.05	155	P
HAAS_VR_1936	BMK.38919	(A) ₁₂	TCTCCCTTCATCAGATCGCT	GAAATCTCTTCTGGGCTGT	59.91	59.58	204	M
HAAS_VR_1947	BMK.39000	(GAG) ₅	AAGCGTGGAAAGGAAGAGAT	TCCAAGCTGGTTGAACTGAA	60.21	60.13	231	M
HAAS_VR_1948	BMK.39002	(GAA) ₆	AGGGATGGTGACTGGTGAAG	CCGATCTTCTCACCTCGCT	59.96	59.70	176	P
HAAS_VR_1958	BMK.39042	(A) ₁₀	TTCCTGTAGGGTTGGTGAAC	GGAATAAGGAGCATCCACAAA	59.83	60.05	183	M
HAAS_VR_1972	BMK.39153	(T) ₁₃	CTTTGAGCCCGTTTCTTC	ACAGAAGAGCACACGATCCC	59.80	60.27	218	M
HAAS_VR_1982	BMK.39195	(ATG) ₅	ACAAACCAAGTGCACCATCA	TGTTGTGTGAACCCGGTAA	60.01	59.86	196	M
HAAS_VR_1983	BMK.39198	(T) ₁₄	CCAACACCACTTCTCCACCT	CTGAAGTTGGTTCACTGCCA	60.00	59.87	134	P
HAAS_VR_1994	BMK.39240	(GAT) ₆	GGACCGTGAAGAAAGTGGAA	GGACCCAGTCTGCGTAAAGT	60.09	59.21	114	M
HAAS_VR_2004	BMK.39310	(T) ₁₁	TCTCCATCTCACCCACACA	CGCTCTGTCAACCCTTATTA	60.09	59.75	268	P
HAAS_VR_2005	BMK.39314	(A) ₁₄	CGCTACTTCCAAAAGAGAGCA	GTCGTGTTAGCCATGGATT	59.78	59.96	118	P
HAAS_VR_2018	BMK.39399	(A) ₁₀	TTGATGAAAGGCCGAAATTA	TTTTTTTTCTGCTCAGCC	60.40	60.50	169	M
HAAS_VR_2019	BMK.39435	(T) ₁₀	CCCCAGCCTTAGAAAAGAC	AGGAGCCCTAAAGCAAAGC	60.20	59.99	237	M
HAAS_VR_2030	BMK.39490	(A) ₁₀	TCACTCACAAAACCCGAGC	GTTGCAAGGCACACACTGT	59.88	59.95	180	M
HAAS_VR_2031	BMK.39495	(TAT) ₇	TGTTGTTGTTGGAAACAGGA	CGATCCAGGTGATGCTTCTT	59.98	60.22	103	P
HAAS_VR_2042	BMK.39601	(T) ₁₀	AGATGGCTTTGACCGCAAT	GTTGCCCTTTCAGATGAAA	59.88	60.20	273	P
HAAS_VR_2046	BMK.39607	(A) ₁₀	GAAATCAGGGAGCAATGTT	GGTACAACAGGACAGTGACCG	60.08	60.71	260	P
HAAS_VR_2058	BMK.39692	(TCT) ₆	GCITCCAAGAAATCGTCTCG	GATTC AACGTGGTGTCAITGC	59.96	59.98	235	P
HAAS_VR_2059	BMK.39696	(A) ₁₁	GGCAAAGCTCAGTCTCCTTG	TTTCAAAGAGGTGAAAACCCG	60.13	60.23	151	P
HAAS_VR_2070	BMK.39760	(AG) ₇	CTGATAAGTTGCCCCCAAGT	AGCCCGACAATAATCGACTG	60.51	60.10	279	P
HAAS_VR_2072	BMK.39785	(TGT) ₅	ATACATCCCTTTCGTTCCC	GAGAGGAGGAAAATCCGAGG	60.02	60.15	254	P
HAAS_VR_2082	BMK.39884	(TAG) ₅	CACCAAAGCTTGAGGTCCAA	AGGAGCAGGAAAAGAAAAGCC	60.11	59.96	236	M
HAAS_VR_2083	BMK.39888	(CT) ₈	TGTCCTCCGTTATCGAGGGTT	AACAGCAAAGAAAAGCGAGGA	59.55	60.13	149	P
HAAS_VR_2097	BMK.40007	(CAG) ₆	AACTCCAACATGCCGTTAGG	TACCCATTTCCCAATTTGGTT	59.99	59.91	151	P
		(CAG) ₅ caatcaacaaccccccaaca catcaacaatcccccaacaacccaacag cagttacaactcaacagcaatt(GCA) ₆						
HAAS_VR_2098	BMK.40007	(TG) ₈	GTCTGTCCGGTCTTTTCAATA	ATTGATGGAGATCCCACTG	60.07	59.74	259	P
HAAS_VR_2107	BMK.40093	(A) ₁₃	AGTTGGGTGCTAGAGCCAAA	AGAAAGCAAGAGGGAGGTGGT	59.88	60.25	207	M
HAAS_VR_2109	BMK.40105	(TTC) ₆	CAAAAACCTCCCATCTACATA	GGCTCTGAAATGTCCAGCTT	57.67	59.43	188	M
HAAS_VR_2123	BMK.40209	(T) ₁₂	TCACTGTGAAAACCTTCTTCG	GC ACTTGCAGGGTTAGAAGC	60.28	60.02	217	M
HAAS_VR_2124	BMK.40217	(ACC) ₇	GCTTCAGTGCCACCGTAITTT	CAAAGCTCAGACATAGCCA	60.14	60.16	129	M
HAAS_VR_2138	BMK.40295	(T) ₁₀	TTCAACTCCCAAACCCAAAC	GGGTTGAGGCTGTTCTTGAG	59.81	59.84	266	P
HAAS_VR_2139	BMK.40299	(TAC) ₇	TGTGACAAAAGACATGGGGA	ATTGCAATGCTTGGGAAAAC	59.94	59.95	275	M
HAAS_VR_2153	BMK.40401	(TGA) ₇	CACATCCCCACTTTGGAGGA	CTTTCTCAGCCCTCAGATG	59.96	59.94	274	M
HAAS_VR_2154	BMK.40403	(CIT) ₅	ACAAAGCTTAAACACAAGG	TACCAATGCCCTAAAGTGCC	60.03	59.96	270	P
HAAS_VR_2167	BMK.40456	(ATC) ₅	ACTCCCTCTGTGACACCCAC	TGTTCAATGACCGAGAAAGG	60.01	59.68	280	M
HAAS_VR_2169	BMK.40477	(A) ₁₀	TCATCCCCACCCCTGTAAAC	TGGCAATGGTTCAAGAACAG	59.65	59.69	243	M
HAAS_VR_2179	BMK.40573	(A) ₁₀	GCAAAGCGGAAATCTTCTGAC	CCTGTTTTCCCTCATCTCA	59.96	60.04	235	M

Table 2 (cont'd)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T_M (F)	T_m (R)	Product	Polymorphism
HAAS_VR_2180	BMK.40574	(TA) ₆	CGGGAAATCCTGACCTACAT	ATTTCTGTGGCTATGGGGT	58.86	60.58	265	P
HAAS_VR_2192	BMK.40662	(CAT) ₅	TTTTCCAAGGGAAACCATCTTG	TTTCTGCATTTGATCCCATGA	59.90	60.01	229	P
HAAS_VR_2193	BMK.40668	(AC) ₆	TGAGCGAGGAAGAAATCGT	TTTAGCTGAAATCCGTCGCT	59.99	59.98	249	M
HAAS_VR_2203	BMK.40750	(A) ₁₃	GGAGTTGACCCGAAGGAATCA	TTCCATTTCCATCTTCAGCC	60.05	60.01	153	P
HAAS_VR_2204	BMK.40757	(ATC) ₅	TTAAACAAATCCGTA GCCCG	AGAAAAACGGCGTGAAGAAGA	60.10	59.99	108	P
HAAS_VR_2215	BMK.40817	(GAA) ₅	GAGGACGAGAGATACGCTG	CGAICGAAAAGCATCAGACAA	59.97	59.95	111	M
HAAS_VR_2216	BMK.40819	(T) ₁₀	GTTTCTATGCTAGTCGCCGC	GCTTTTGTTCACCTCAAGCC	60.00	59.86	236	P
HAAS_VR_2228	BMK.40924	(TC) ₆	ATCTCCAATGTCAAGAGCC	TGCTAGTGCACAGTCCGTGC	60.22	60.06	260	M
HAAS_VR_2230	BMK.40934	(GCA) ₅	ATGGTGAATCAGACTCGG	ACTGCCCACTAACTGCTGCT	59.93	60.08	146	P
HAAS_VR_2244	BMK.41056	(CATC) ₅	ACTTGGGGTGAGAGCAGAGA	AAGAATGGGGTTGCAGAGTG	59.99	60.11	157	M
		(A) ₁₄ tcaatacagtaggatttat						
HAAS_VR_2245	BMK.41062	ggcgaacatgcatgct(A) ₁₀	TTCAAATTCACCGGAAAAGA	GGGAACATGGCCTAAAAGGAT	58.19	60.15	156	M
HAAS_VR_2255	BMK.41095	(ACC) ₅	TCGACTTTTCGACTGCATCAC	AGATAGGGTTGGCATAGGG	59.99	60.17	184	M
HAAS_VR_2256	BMK.41102	(GAA) ₇	AGCCACGGACTCAGAGAAGA	AATGGCATCAACCCCACTA	60.14	60.19	252	M
HAAS_VR_2265	BMK.41195	(CAC) ₆	AGAAAGCGAAGCATGAAAAA	CTCTCTGGTCCGCACTTC	59.96	59.99	162	M
HAAS_VR_2266	BMK.41205	(TTC) ₅	AGCTAGTCCCTTTCCCCAAA	GTCTTTGTGCTGTTGGGGTT	60.07	60.01	193	M
HAAS_VR_2279	BMK.41311	(T) ₁₀	CGTGAGAGAAAGCGAGAGAG	CACAAGAACACTGGCACCTG	60.42	60.35	138	P
HAAS_VR_2280	BMK.41322	(GT) ₆	CTCATGCCCTCCCTATGAAA	ATTATCCGCTCTCCGCTTT	60.03	60.06	147	P
HAAS_VR_2290	BMK.41413	(T) ₁₀	GAAGAAATGGGATTTGGGTT	TGCTGAGATCAAGAACAGCCA	60.00	60.98	105	P
HAAS_VR_2291	BMK.41439	(TA) ₆	TTTTCTGTGAGTGTGCTGCT	TGCAGATATGGCCTAATAAGG	59.78	60.22	132	P
HAAS_VR_2292	BMK.41444	(AG) ₆	CTACATGTGGAGCGCAGCT	CCTCTCTCTAATCCCAACCC	60.26	59.89	132	M
HAAS_VR_2302	BMK.41552	(T) ₁₀	AACGTTACAGGGGCTGTTG	CGCTCTCCGATCTAATTTGA	60.03	58.07	159	M
HAAS_VR_2307	BMK.41602	(A) ₁₁	CCCTGTGCATGCAACTAAGA	TTGGCGAGTTTGTCTTATGA	59.86	59.30	220	M
HAAS_VR_2309	BMK.41611	(TTC) ₅	TCCATGGAACACCCACAAC	CCAAGTTCAAGCACCGTCT	60.01	60.15	194	M
HAAS_VR_2318	BMK.41657	(GA) ₁₀	TCCTATAACAATCCCCACA	GGGATGTTGTGTGTGATGCTG	60.01	59.97	218	P
HAAS_VR_2319	BMK.41657	(GA) ₁₀	TGCTTCAGTGGGTTTGTGTTG	GGTGAATAAATGGTGGTGG	59.73	59.96	118	M
HAAS_VR_2320	BMK.41664	(CTC) ₆	CCGAACGGGTAGTGGTTTA	CCGGATATTACACGGATGG	59.86	60.03	106	P
HAAS_VR_2332	BMK.41728	(A) ₁₁	CTGAACCATAAACGGGCACT	TTTTCTGATGGTTCAACGGGC	59.96	60.11	133	P
HAAS_VR_2333	BMK.41734	(TGG) ₆	AGGGTTTCGAAGTTGAGGTT	GCAAAGTTTCCAGTTCCAC	59.97	59.57	249	M
HAAS_VR_2335	BMK.41776	(T) ₁₀	TCAACATTTTGCAGACGACC	GAGGGGATACCAATTCAGA	59.70	60.04	279	M
HAAS_VR_2346	BMK.41845	(A) ₁₁	ATCCCACCATTTGCAAACTTC	CAGAACCCTAAAATCCCAAAA	59.80	59.77	192	P
HAAS_VR_2349	BMK.41868	(ACA) ₅	CTGCAGTGTACTCCCAACA	GCGATGACTCCAGCTCTTT	60.05	59.58	209	P
HAAS_VR_2363	BMK.41944	(GA) ₆	CTGCGATTCAAAGGGAACAT	TTAAAACCCCAACCAATCAC	60.07	59.52	177	P
HAAS_VR_2364	BMK.41949	(CT) ₆	GCGTACCCCTAAATCCCAAT	ACCGTCAAACGTCAAATCCTC	60.04	59.97	133	P
HAAS_VR_2365	BMK.41952	(CAT) ₅	TGGGACTTACGTGGTGTGA	TGGAAGTTGGATTTGTGGAG	60.00	59.96	179	P
HAAS_VR_2375	BMK.42067	(T) ₁₀	ATTGGACGCAAGTTGTTGC	AAGCAATTCACCTGGCGAAGC	61.07	60.41	277	M
HAAS_VR_2376	BMK.42067	(T) ₁₀	GCAGCCCTGCTACTAAATC	AGTTCATTTGGCCACCGGTA	59.87	60.37	213	M
HAAS_VR_2377	BMK.42074	(CAG) ₅	AGGCTGATATCAACCCACC	TTTGGCTGGGACTATTCTGG	59.96	60.07	241	M
HAAS_VR_2385	BMK.42212	(GAG) ₅	CAAAGGCCATCTCAACTTC	TCCCGAAAAACAGTTCACTCC	59.67	60.09	166	P
HAAS_VR_2387	BMK.42218	(A) ₁₀	GTCTTAAAGAGCCTGTGGC	GAGGGAGCCAGACTCAGAAA	60.02	60.39	274	M
HAAS_VR_2388	BMK.42237	(AGA) ₆	TCACAAAGTCTCCACCACC	AGTGAGTTGGGTTGTCCGG	60.09	60.01	221	P
HAAS_VR_2398	BMK.42324	(TTC) ₆	GTTTTGCAAGCTTTCCCTTC	CCTCCATTTGGCATCTTGATT	60.23	59.89	280	M
HAAS_VR_2401	BMK.42357	(A) ₁₁	CCATCTCTCCTTCCTTTGTTG	GTCCCGTATGTTGGAGTG	60.10	60.01	203	M
HAAS_VR_2402	BMK.42362	(TC) ₆	TCTTCCACCTTCCCTCATTG	TGAGGGATCAAAGGCTATG	60.04	60.03	176	M
HAAS_VR_2412	BMK.42404	(GAG) ₅	GTGGCTTTGGAGATGGAAAA	TTTTCTCCGTCATACCTCCG	60.05	60.07	271	P

Table 2 (*contid*)

Primer ID	Unigene ID	Motif	Forward primer	Reverse primer	T_M (F)	T_m (R)	Product	Polymorphism
HAAS_VR_2415	BMK.42429	(AG) ₆	TTGAATGATCAACGGGACAA	TTCTTTCCACGGCTTAGTT	59.90	60.02	220	M
HAAS_VR_2416	BMK.42459	(A) ₁₀	ACAGGAAACCAACCAACCAAG	CCCATCTCATTTGGGTTTGT	59.86	59.65	181	M
HAAS_VR_2427	BMK.42587	(AG) ₈	GGCAGAGACTTGGACATGGT	AACGTCCTTTTCTCGCAG	60.12	60.38	181	M
HAAS_VR_2428	BMK.42607	(A) ₁₀	GCAAAGCTGCCCTTGATTAG	GGAGGTCATCTACCCCTTCC	59.98	59.76	207	M
HAAS_VR_2429	BMK.42612	(GA) ₆	CGTTTTAACGGAAAACGCAT	TGACAGAGCAACAGCAAACC	60.00	60.03	122	M
HAAS_VR_2441	BMK.42737	(A) ₁₀	TACCAGGTTCTCAAAAAGCC	GAGTTGGAGGCAGTGATGGT	60.11	60.12	245	M
HAAS_VR_2442	BMK.42742	(T) ₁₂	TGTGTGACAGAGCGTGCATA	CCAGAAACCAATGGCTGAGTT	60.05	60.11	181	P
HAAS_VR_2443	BMK.42745	(A) ₁₃	CACGCTGCAGTGGTACTGTT	GTCTTCAACCATGCAACCCTT	59.97	59.97	196	M
HAAS_VR_2454	BMK.42830	(T) ₁₁	TGTGCCACACACAAGATGA	ACTGAGGAAGAGTGCATGGC	59.71	60.42	273	P
HAAS_VR_2455	BMK.42833	(T) ₁₀	TCCTCTCAGCGCAATTAAACC	TCGCAACTTTTATTTGGGG	60.35	59.94	206	M
HAAS_VR_2456	BMK.42833	(AT) ₆	CCCCAAAATAAAAGTTGCCGA	TTTGGTCTTCGGTCACTTC	59.94	60.09	143	None
HAAS_VR_2469	BMK.43064	(CTT) ₆	AAACAACAACAATTCACCGTC	CGCTTGTGAGAGGAAGAACC	58.91	59.99	241	P
HAAS_VR_2470	BMK.43064	(T) ₁₀	TATCAGTGGCCTGTGACTGC	ACAAAAGCAAAAGAGGAACGA	59.86	59.99	233	M
HAAS_VR_2472	BMK.43077	(T) ₁₁	AACATCAGTACGGCAAAAGGG	GCGGGGATCCTCAAAGTTTTA	59.99	61.30	214	M
HAAS_VR_2481	BMK.43145	(CCT) ₅	ACTACCACCACCACCAAAAGC	AGCATAACAGAAAGGCGGCTA	59.89	60.00	241	M
HAAS_VR_2484	BMK.43154	(T) ₁₂	CACGTACCCTCAACACCCCTT	GGAAAAGCTCCAATTCATCCA	59.88	60.01	200	P
HAAS_VR_2485	BMK.43154	(TC) ₆	TGGATGAATTTGGAGCTTTCC	AGCACCCCTTAAAGAGCATGGA	60.01	59.84	262	M
HAAS_VR_2499	BMK.43260	(T) ₁₃	ACTCAGTGGGTTAGAGGCGA	ATTGCATTCATGATCGCTA	59.87	59.09	206	P
HAAS_VR_2501	BMK.43266	(CGT) ₅	GCCCCAAAATATGGGCTTTT	CACAGATCAAAAGCCCTGACA	60.15	59.83	228	P
HAAS_VR_2502	BMK.43272	(T) ₁₃	GTCCCCATATTTCCCTCACCC	GCAAAGTTGCAAAAAGGTGGAT	60.39	60.12	219	P

*M, morphism; P, polymorphism; none, no product.